HUMAN RETROVIRUSES and AIDS 1994

A COMPILATION AND ANALYSIS OF

NUCLEIC ACID AND AMINO ACID SEQUENCES

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CONTENTS

More detailed tables of contents are to be found within the various parts of the compendium. The following provides merely an overview.

ACKNOWLEDGMENTS ii

INTRODUCTION iii

GLOSSARY and LANDMARKS v

PART I. NUCLEIC ACID ALIGNMENTS AND SEQUENCES

Introduction I-1

Contents I-3

A. HIV-1 Sequences

Nucleotide Alignments and Consensus Sequences I-A-2

Entries I-A-147

B. HIV-2/SIV Sequences

Nucleotide Alignments and Consensus Sequences I-B-1

Entries I-B-56

C. SIVAGM, SIVMND, and SIVSYK Sequences

Nucleotide Alignments and Consensus Sequences I-C-1

Entries I-C-20

PART II. AMINO ACID ALIGNMENTS

Introduction II-1

Contents II-2

A. HIV-1 Sequences

Amino Acid Alignments and Consensus Sequences II-A-2

B. HIV-2/SIV Sequences

Amino Acid Alignments and Consensus Sequences II-B-1

C. SIVAGM, SIVMND, and SIVSYK Sequences

Amino Acid Alignments and Consensus Sequences II-C-1

PART III Analysis

Contents III-1

A. Gag Proteins III-2

B. HIV-1 Tat: Structure and Function 11

C. HIV-1 and HIV-2 Sequence Subtypes 23

D. HIV Synonymous and Nonsynonymous Substitution Frequencies 34

E. Global Variation in the HIV-1 V3 Region 37

F. Mutations in HIV-1 RT and Protease 93

PART IV. RELATED SEQUENCES

Introduction IV-1

Contents IV-2

HIV and Cellular Factors 3

Sequence Entries 13

PART V. DATABASE COMMUNICATIONS

Introduction V-1

Roadmap to FTP Server V-2

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We thank the many researchers who have made their sequences available prior to publication. Of particular note, the Institute of Tropical Medicine in Antwerp allowed us to use their unpublished O group sequences for the figure shown on the cover of this compendium.

The summarization of RT and protease mutations by John Mellors, Raymond Schinazi, and Brendan Larder is updated from their publication in *International Antiviral News*. We thank them and the publishers for providing us with this section. Furthermore, we are pleased to report that John Mellors has agreed to come aboard as a database editor in 1995, for the purpose of continuing this effort.

We are grateful to Kim Millman, Andrew Farmer, Miranda McEvilly, and Anne Yesley, research assistants who have other roles in our group, for assisting the HIV Database staff with this publication.

INTRODUCTION

This compendium and the accompanying floppy diskettes are the result of an effort to compile and rapidly publish all relevant molecular data concerning the human immunodeficiency viruses (HIV) and related retroviruses. The scope of the compendium and database is best summarized by the five parts that it comprises: (I) Nucleic Acid Alignments and Sequences; (II) Amino Acid Alignments; (III) Analysis; (IV) Related Sequences; and (V) Database Communications. Information within all the parts is updated at least twice in each year, which accounts for the modes of binding and pagination in the compendium.

While this publication could take the form of a review or sequence monograph, it is not so conceived. Instead, the literature from which the database is derived has simply been summarized and some elementary computational analyses have been performed upon the data. Interpretation and commentary have been avoided insofar as possible so that the reader can form his or her own judgments concerning the complex information. In addition to the general descriptions below of the parts of the compendium, the user should read the individual introductions for each part.

Part I. Nucleic Acid Alignments and Sequences. Annotated nucleic acid sequences of HIV and SIV are presented in a form close to that of the GenBank Sequence Library. Our few modifications of standard GenBank format were instituted to better serve the particular community for which this database is intended.

The LOCUS name or identifier of an entry may differ slightly from that found in the GenBank or EMBL libraries, but the ACCESSION numbers are identical for entries in all three databases. Thus each entry is universally and uniquely traceable. Large sets of PCR-derived sequences are represented using a single sequence entry followed by an alignment of all the sequences in the set. When available, the entire range of ACCESSION numbers for the PCR set is usually indicated within the representative entry. The SOURCE line provides information, when available, about the infectivity or biological activity of the molecular clone from which a sequence has been derived. REFERENCES are limited to literature or personal communications having authority for the original sequence data; references that review sequence information, or that shed light upon the function or variation of coding and regulatory sequences, are listed in Part V.

Entries in Part I are annotated within the sequence, while their GenBank or EMBL-formatted versions on the floppy diskettes make use of FEATURES tables. The hard-copy annotation includes coding regions, regulatory structures, splice sites, and other features of functional significance. The authority for this annotation is largely invariance, the recurrence of patterns such as TATAA and AATAAA. Although our practice has been to conservatively annotate, we caution the user against docility: sequence information regarding transcripts, for example, is far from certain or complete at this time. Part I is divided into three subsections, A, B, and C, concerned with HIV-1s, HIV-2/SIVs, and SIVAGMs, SIVMND and SIVSYK.

Part II. Amino Acid Alignments. This section contains in alignment the amino acid sequences of all known coding regions and open reading frames of HIV-1, HIV-2, and SIVs. Beginning in 1993, Part II is broken down into subsections A, B and C, for HIV-1s, HIV-2/SIVs and SIVAGMs respectively. Consensus sequences and AACC consensus-like patterns are given with their respective alignments. Protein processing sites are annotated when known. The reader should consult the introduction to Part II for further explanation of the presentation and annotation of the amino acid sequences.

Part III. Analysis. This section is open-ended with the constraint that the sequence analyses and compilations be basic and of interest to the diversity of users. Currently the analyses include phylogenetic trees, HIV V3 Loop amino acid sequences, summaries of protein variability and molecular evolutionary patterns of the various regions of the HIV and SIV genomes, and envelope glycosylation patterns.

Part IV. Related Sequences. Heretofore, this section of the compendium has featured HIV related viral sequences—of nonprimate lentiviruses and the human T-cell lymphotropic viruses. Beginning in 1993, Part IV entries include, with greater emphasis, coding sequences for cellular proteins involved with HIV pathogenesis. Entries are presented in the same format as Part I entries.

Part V. Database Communications. In previous years this part contained a printed supplemental reference list which has been omitted this year to save space. As usual, diskettes of sequences are provided. The floppy diskettes contain the nucleic acid sequences from Part I and Part IV and the translated amino acid sequences of coding regions. A number of sequences not printed in this compendium may be found on the diskettes. Those sequences are listed in the table of contents of Part I. Beginning in 1993, sequence alignments are also included to meet user requests. For the most current information regarding database files, see the READ.ME file on each diskette. Nucleotide entries are presented in GenBank format for North American users and in EMBL format for European users (unless otherwise requested). Similarly, amino acid sequences are in either PIR or Swiss-Prot format. The diskettes themselves are either 5.25" IBM-DOS format or 3.5" Macintosh format, depending upon what has been requested. If there is any trouble using these files with software designed to work with the format we have sent, please let us know the name of the program you are using and the file that it could not handle.

A comprehensive compilation of the nucleic acid and protein sequences published in the Human Retroviruses and AIDS Database since 1987 is available in the NCBI Data Repository through Internet FTP (File Transfer Protocol). To transfer data over the Internet via anonymous FTP type: `ftp ncbi.nlm.nih.gov` or `ftp 130.14.20.1`. Enter `anonymous` for the login name and your electronic mail address for the password. Change directory to `'repository/aids-db'` to download the entries from the AIDS database.

The NCBI also offers several CD-ROMs containing HIV and SIV sequence information. The ENTREZ:Sequences CD contains the GenBank, NCBI backbone, PIR, SWISS-PROT, and MEDLINE databases with retrieval software for users with Macintosh and PC-compatible computers running Microsoft Windows. The second CD, NCBI-GenBank, will contain the complete GenBank database in the currently distributed flatfile format. Each release of this CD will contain a full GenBank release with new data incorporated from direct submissions, the NCBI Backbone (journal scanning), and the EMBL and DDBJ databases. The third CD, NCBI-Sequences, will include the integrated dataset provided on the Entrez:Sequences CD in the ASN.1 standard data description format. Questions about services or software provided by the NCBI may be directed to the NCBI via phone: (301) 496-2475, fax: (301) 480-9241, or email: `info@ncbi.nlm.nih.gov`.

We are prepared to quickly enter both protein and nucleotide sequences into the Human Retroviruses and AIDS database, and in the case of nucleotide sequences, oversee their entry into the GenBank and EMBL libraries. Submission of unpublished sequences is invited and encouraged. Sequence data or inquiries regarding the database should be addressed to

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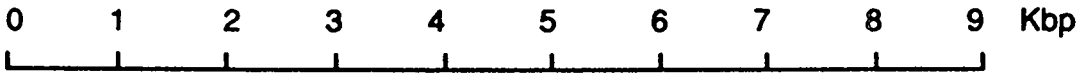
e-mail: glm%temin@lanl.gov

A short glossary follows.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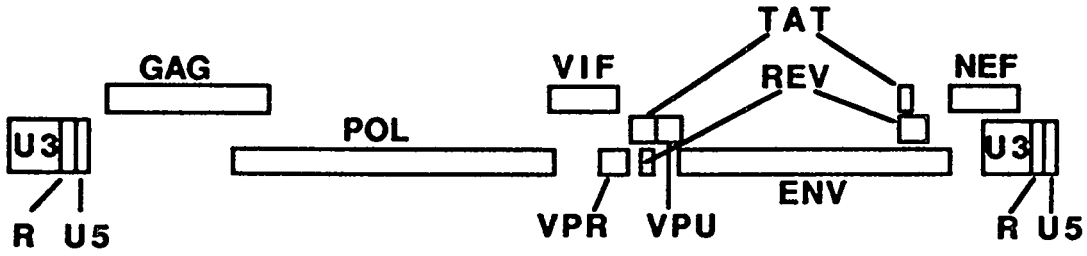
HIV-1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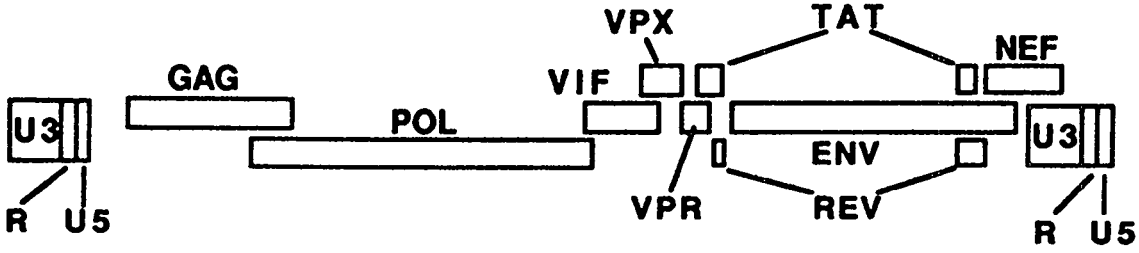
GAG
VIF
REV
NEF
U3
POL
U3
ENV
R U5
VPR VPU
R U5

HIV-2


VPX
TAT
NEF
GAG
VIF
U3
POL
U3
ENV
R U5
VPR
REV
R U5

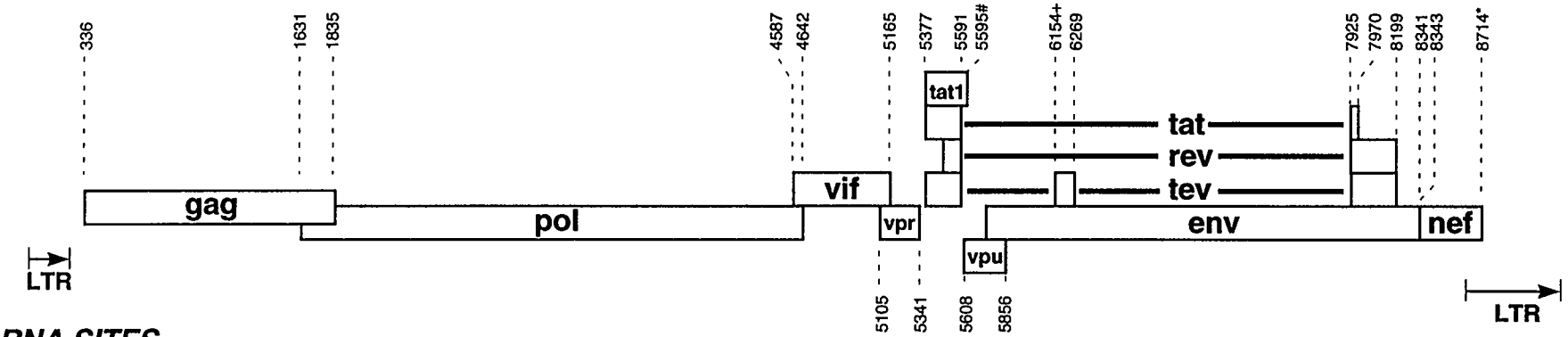
GLOSSARY

HIV/SIV PROTEINS

Name	Typical Size	Function	Localization
GAG	p55/p17/p24/p7 p6/p2/p1	structural capsid proteins	virion
POL	p66/p51/p32	viral enzymes	virion
ENV	gp120/gp41	viral surface (SU) and transmembrane (TM) glycoproteins	plasma membrane, virion envelope
TAT	p16/p14	viral transactivator	primarily in nucleolus/nucleus
REV	p19	RNA transport, stability and utilization factor (phosphoprotein)	primarily in nucleolus/nucleus
VIF	p23	promotes virion infectivity	Golgi?
VPR	p10–15	unknown, also called 'rap' (rapid)	virion
VPU	p16	promotes extra-cellular release of viral particles (phosphoprotein)	integral membrane protein
NEF	p27–p25	unknown (myristoylated protein)	cytoplasm, plasma membrane
VPX	p12-16	unknown, appears to be a duplication of VPR in HIV-2 and SIVs only	virion
TEV	p28	tripartite tat-env-rev protein (found only in HXB2; also named tnv)	primarily in nucleolus/nucleus

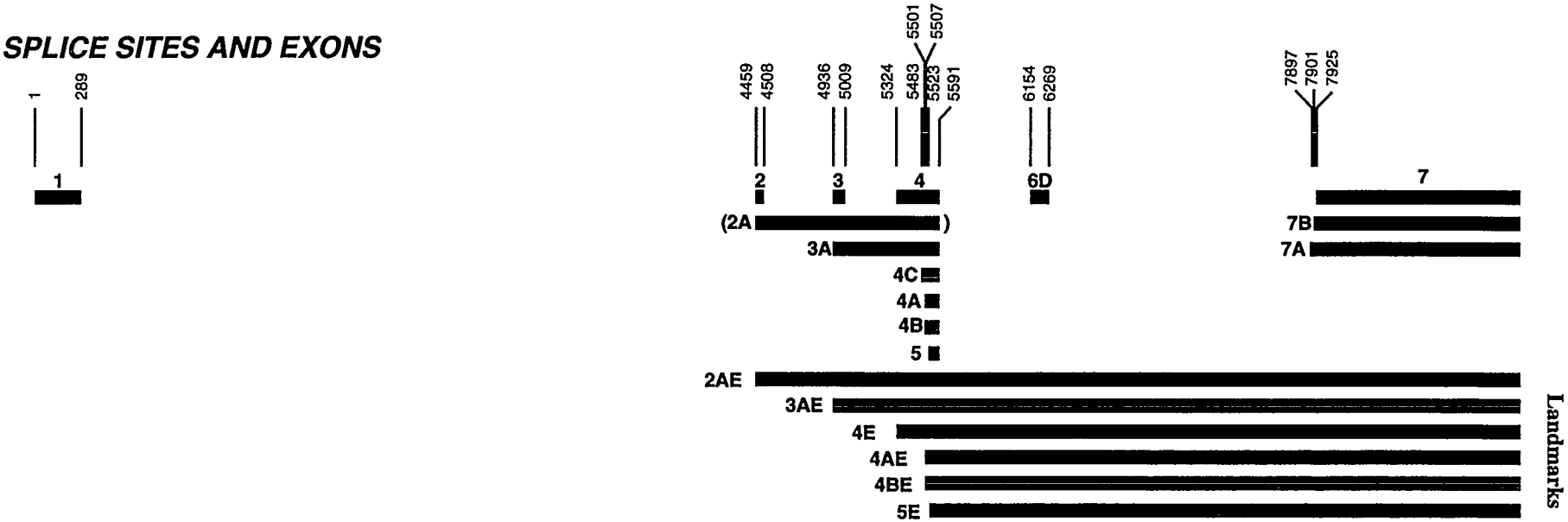
LANDMARKS ON THE HIV-1 GENOMIC RNA

PROTEINS



RNA SITES

SPLICE SITES AND EXONS



LANDMARKS:

HIV GENOMIC STRUCTURAL ELEMENTS

LTR Long terminal repeat, the DNA sequence flanking the genome of integrated proviruses. It contains important regulatory regions, especially those for transcription initiation (upstream and downstream promoters) and polyadenylation.

TAR Target sequence for viral transactivation, the binding site for Tat protein and for cellular proteins; consists of approximately the first 45 nucleotides of the viral mRNAs in HIV-1 (or the first 100 nucleotides in HIV-2 and SIV.) TAR forms a hairpin stem-loop structure with a side bulge; the bulge is necessary for Tat binding and function. May also be a DNA regulatory site.

RRE Rev responsive element (also named CAR), an RNA element encoded within the env region of HIV-1. It consists of approximately 200 nucleotides (positions 7327 to 7530 from the start of transcription in HIV-1HXB2R.) RRE is necessary for Rev function; it contains a high affinity site for Rev; in all, approximately seven binding sites for Rev exist within the RRE RNA. Other lentiviruses (HIV-2, SIV, visna, CAEV) have similar RRE elements in similar locations within env, while HTLVs have an analogous RNA element (RXRE) serving the same purpose within their LTR; RRE is the binding element for Rev protein, while RXRE is the binding element for Rex protein. RRE (and RXRE) form complex secondary structures important for specific protein binding.

CRS cis-acting repressive sequences postulated to inhibit structural protein expression in the absence of Rev. One such site was mapped within the pol region of HIV-1. The exact function has not been defined; splice sites have been postulated to act as CRS sequences.

INS Instability RNA sequences found within the structural genes of HIV-1 and of other complex retroviruses. Multiple INS elements exist within the genome and can act independently; one of the best characterized elements spans nucleotides 414 to 631 in the gag region of HIV-1HXB2R.

GENES AND GENE PRODUCTS

GAG group specific antigens or capsid proteins. The precursor is the p55 myristoylated protein, which is processed to p17 (MAtrix) p24 (CApsid) and p7 (NucleoCapsid) proteins by the viral protease. Other small proteins are generated from the gag polyprotein by protease cleavage.

POL generates the viral enzymes protease, reverse transcriptase and integrase after processing of a gag-pol precursor polyprotein by the viral protease; the Gag-Pol precursor is produced by ribosome frameshifting.

ENV viral glycoproteins produced as a precursor (gp160) and processed to the external glycoprotein gp120 and the transmembrane glycoprotein gp41. The mature proteins are held together by noncovalent interactions; as a result, a substantial amount of gp120 is released (shed) into the medium. gp120 contains the binding site for the CD4 receptor.

TAT Transactivator of HIV gene expression. One of the two necessary viral regulatory factors (Tat and Rev) for HIV gene expression. Two forms are known, Tat-1exon (minor form) of 72 amino acids and Tat-2exon (major form) of 86 amino acids. The electrophoretic mobility of these two forms in SDS gels is anomalous, with apparent sizes of approximately 16 kD and 14 kD for Tat-2exon and Tat-1exon, respectively. Low levels of both proteins are found in persistently infected cells. Tat has been localized primarily in the nucleolus/nucleus by immunofluorescence. It acts by binding to the TAR RNA element and activating transcription initiation and/or elongation from the

LTR promoter. It is the first eukaryotic transcription factor known to interact with RNA rather than DNA and may have similarities with prokaryotic anti termination factors.

REV The second necessary regulatory factor for HIV expression. A 19 kD phosphoprotein, localized primarily in the nucleolus/nucleus, Rev acts by binding to RRE and promoting the nuclear export, stabilization and utilization of the viral mRNAs containing RRE. Rev is considered the most functionally conserved regulatory protein of lentiviruses (although it is mutationally quite unstable).

VIF Viral infectivity factor, typically 23 kD. Required for the efficient transmission of cell-free virus in tissue culture. In the absence of Vif the produced viral particles are defective, while the cell-to-cell transmission of virus is not affected significantly. Accumulates in the Golgi system and is not found in the virion.

VPR Virion associated protein of unknown function found in HIV-1, HIV-2, SIVmac and SIVmnd; typically 15 kD. Probably homologous to VPX of HIV-2/SIVs.

VPU "oUt" protein, promotes extracellular release of viral particles. Found only in HIV-1. Integral membrane phosphoprotein of 16 kD; similar to M2 protein of influenza virus; may be involved in env maturation; not found in the virion.

NEF Approximately 27 kD non-virion protein found in the cytoplasm of infected cells. It is myristoylated and associated with the inner plasma membrane. One of the first HIV proteins to be produced in infected cells, it is the most immunogenic of the accessory proteins. During tissue culture propagation, Nef is dispensable and probably counter-selected. On the contrary, SIV Nef is required for viral propagation in animals. Nef affects the levels of CD4 and may modulate intracellular signaling pathways.

VPX Virion protein of 12 kD found only in HIV-2/SIVs. Function unknown. Vpu/Vpx may be used to distinguish between HIV-1 and HIV-2 infection.

TEV (also named tnv) Tripartite 28 kD viral phosphoprotein produced by some HIV-1 strains. Found primarily in the nucleolus/nucleus. Tev contains the first exon of Tat, a small part of Env and the second exon of Rev. It exhibits both Tat and Rev functions and can functionally replace both essential regulatory proteins of HIV-1. It is produced very early in infection.

STRUCTURAL PROTEINS/VIRAL ENZYMES The products of gag, pol and env genes, which are essential components of the retroviral particle.

REGULATORY PROTEINS Tat and Rev proteins of HIV/SIV and Tax and Rex proteins of HTLVs. Modulators of transcriptional and posttranscriptional steps of virus gene expression; essential for virus propagation.

ACCESSORY OR AUXILIARY PROTEINS additional virion and non-virion-associated proteins produced by HIV/SIV retroviruses: Vif, Vpr, Vpu, Vpx, Nef. Their exact function is mostly unknown. Although the accessory proteins are in general not necessary for viral propagation in tissue culture, they have been conserved in the different isolates; this conservation and experimental observations suggest that their role in vivo is very important.

COMPLEX RETROVIRUSES Retroviruses regulating their expression via viral factors and expressing additional proteins (regulatory and accessory) essential for their life cycle. By one interpretation, all retroviruses are "complex" and HIV is said to be merely one of the "more complex."

I

Nucleic Acid Alignments and Sequences

Nucleotide sequence alignments were generated using the PIMA program developed by Randy Smith and Temple Smith (*Protein Engineering* 5:35, 1992). By this approach, a protein pattern is created which then serves as a template for the nucleotide sequence alignment. Hand-editing, when required, was done with the MASE program (D. V. Faulkner and J. Jurka, *TIBS* 13:321, 1988). For information concerning either of these programs, contact Dr. Randall Smith, Institute of Molecular Genetics, Baylor College of Medicine, Houston, Texas, 713-798-4735.

With few exceptions, only full-length coding sequences were included in these alignments. Mixed case consensus sequences are used as the reference sequences for each alignment. Upper case letters indicate 100% conservation of nucleotide bases in a given position of the alignment, and lower case letters represent bases conserved in at least 50% of the sequences. To reduce the alignment uncertainty with the large HIV-1 set, sequence subtypes (see below and Part III) were constituted and consensus sequences were generated for each. Divergent sequences that could not be easily assigned to any given subtype are shown at the bottom of each block. Large deletions, if present in only one sequence (*e.g.*, the HIV2nihz *nef* coding region sequence), were also excluded from the consensus sequences.

In the 1994 compendium, HIV-1 alignments are presented for the *gag*, *tat*, and *env* coding sequences only, as little new information was obtained over the other coding regions. HIV-2 and related SIV sequence alignments are over *gag*, *pol*, and *env* coding sequences only. SIV-AGM sequence alignments are shown for the LTR and *env* region. All amino acid sequence alignments are given in Part II and all nucleotide sequence alignments are available on the FTP server. The 1993 compendium presented alignments for all coding sequences.

Prior to the 1992 database compendium, HIV-1 sequences had been roughly classified as 'U.S.' and 'African.' In light of many new HIV-1 *gag* and *env* sequences, it became more useful, starting with the 1992 compendium, to categorize HIV-1 sequences into five sequence subtypes, depending upon the coding sequence. HIV-1 subtypes now number eight (A through H). Collectively, these are called group M sequences, as they are significantly distinct from group O sequences. The bases for this classification, discussed at greater length in Part III, are:

i) subtypes are approximately equidistant from one another in *env* (a "star phylogeny");

ii) the *env* phylogenetic tree is for the most part congruent with *gag* phylogenetic trees;

iii) two or more samples are required to define a sequence subtype.

Subtype naming problems have arisen for several reasons. For example, viral samples such as MAL and TN243 appear to be hybrid, clustering with one sequence subtype in *gag* and another sequence subtype in envelope. We ask database users to be patient with these problems, most of which are unavoidable (recombination) or transitory (same name for different variants). In the case of hybrid viruses, gene sequences are aligned in this compendium according to the best fit with one of the existing subtypes.

The majority of HIV-1 variants being characterized in the centers of the pandemic fall into one of the five sequence subtypes, A through E, based upon *env* coding sequences. The discovery of the MVP5180 virus in Cameroon, its close relationship to ANT70 and the likelihood that 5% to 10% of infected Cameroonians carry this virus, is an interesting exception. These viral sequences are classified as group O.

There are at least five sequence subtypes for the HIV-2s, A through E.

The authority for some of the annotation is limited largely to invariance—the recurrence of patterns such as AATAAA, for example. The reader should be cautious in drawing upon this information.

Due to space limitations, only certain sequences are reported as entries in this section. The Table of Contents lists other sequences, in addition to these, that are available on diskettes and the FTP server. Short sequences, typically generated through PCR, of necessity must usually be presented as aligned sets rather than as GenBank-formatted entries, however accession numbers can usually be provided for the sequences that appear in alignment. Sequence entries from previous years are presented in the 1990–1993 compendiums. The Tables of Contents for those follow directly below.

PART I HIV and SIV Nucleic Acid Sequences

Introduction I-1
Contents(1994) I-3
Contents(1993) I-7
Contents(1992) I-10
Contents(1991) I-12
Contents(1990) I-14

A. HIV-1 Sequences

Nucleotide alignments of HIV-1 *gag* I-A-2
Nucleotide alignments of HIV-1 *tat* I-A-50
Nucleotide alignments of HIV-1 *env* I-A-56
HIVAMK101 (U08192) 147
HIVAMK82 (U08193) 148
HIVCA1 (X80438) 149
HIVCAR286A (pending) 155
HIVCAR4017 (pending) 156
HIVCAR4020 (pending) 157
HIVCAR4023 (pending) 158
HIVCAR4039 (pending) 159
HIVCAR4054 (pending) 160
HIVCAR4067 (pending) 161
HIVCAR4071 (pending) 162
HIVCAR4081 (pending) 163
HIVCAR423A (pending) 164
HIVCARELO (pending) 165
HIVCARGAN (pending) 166
HIVCARMBA (pending) 167
HIVCARSAS (pending) 168
HIVCI47 (X72049) 169
HIVD808 (U07012) 184
HIVDJ2581 (L11763) 189
HIVDJ2582 (L22939) 190
HIVDJ2591 (L11764) 192
HIVDJ2592 (L22940) 193
HIVDJ263A (L22941) 195
HIVDJ264A (L23064) 197
HIVDJ373A (L23065) 199
HIVGER (U11549) 201
HIVHYDA (L29091) 202
HIVK1241 (L11769) 203
HIVK124A2 (L22942) 204
HIVK986 (U12984) 206
HIVKENYA (L22943) 210
HIVN759 (U15576) 212
HIVRJ484 (U00409) 215
HIVRJSP3 (U08975) 219
HIVSE364A (L22944) 224
HIVSE3651 (L11797) 226
HIVSE365A2 (L22945) 227

HIVSM1451 (L11803) 229
HIVSM145A2 (L22946) 230
HIVUG2661 (L11798) 232
HIVUG266A2 (L22947) 233
HIVUG2681 (L11799) 235
HIVUG268A2 (L22948) 236
HIVUG269A (L22949) 238
HIVUG273A(L22957) 240
HIVUG2741 (L11801) 242
HIVUG274A2 (L22950) 243
HIVUG275A (L22951) 245
HIVVAU (X80020) 247
HIVVI1911 (L11783) 249
HIVVI191A2 (L22952) 250
HIVVI5251 (L11792) 252
HIVVI525A2 (L22953) 253
HIVZAM181 (L03705) 255
HIVZAM18A (L22954) 256
HIVZAM184 (L22955) 258
HIVZAM201 (L03707) 260
HIVZAM20A (L22956) 261

HIV-1 sequences stored on diskettes and FTP server only

HIVBR0141 (U08796)
HIVBR0204 (U08797)
HIVBR0259 (U15121)
HIVRW0914 (U08793)
HIVTH0065 (U08810)
HIVTH0224 (U15120)
HIVTH0266 (U08802)
HIVTH1412 (U08801)
HIVUG0205 (U08794)
HIVUG0219 (U08804)
HIVUG0314 (U08795)
HIVUG0317 (L34667)
HIVUG0378 (U15119)

B. HIV-2 and Related SIV Sequences

Nucleotide alignments of HIV-2 and SIV *gag* I-B-1
Nucleotide alignments of HIV-2 and SIV *pol* I-B-11
Nucleotide alignments of HIV-2 and SIV *env* I-B-32
HIV2EHOA (L14545) 56
HIV222381 (L33077) 60
HIV222382 (M87138) 61
HIV260415K1 (L33076) 62
HIV260667K1 (L33078) 63
HIV27312A1 (L33079) 64
HIV27312A2 (L33092) 65
HIV27312A3 (L33088) 66
HIV27312A4 (L33094) 67

HIV27810A1 (L33080) 68
HIV27924A1 (L33081) 69
HIV2ALI (L25445) 70
HIV2CI171 (X78505) 72
HIV2D1024 (U07104) 74
HIV2D1071 (U07105) 75
HIV2D766 (U07106) 76
HIV2D808 (U07107) 77
HIV2D868 (U07108) 78
HIV2FA1 (L33082) 79
HIV2FA2 (L33089) 80
HIV2FA3 (L33095) 81
HIV2FO784 (L33083) 82
HIV2JA1 (L33085) 83
HIV2JA2 (L33090) 84
HIV2JA3 (L33096) 85
HIV2ONFT1 (L33086) 86
HIV2ONFT2 (L33091) 87
HIV2ONFT3 (L33097) 88
HIV2ONFT4 (L33084) 89
HIV2PA1 (L33087) 90
HIV2PA2 (L33093) 91
SIVCPZGAB2 (U11495) 92
SIVHUB670 (S67406) 93
SIVSMCI2 (X78508) 94

HIV-2/SIV sequences stored on diskettes and FTP server only

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HIV2CAM3E (U05355)
HIV2CAM4E (U05356)
HIV2CAM5E (U05357)
HIV2CAM6E (U05358)
HIV2CBL21E (U05350)
HIV2CBL22E (U05351)
HIV2CBL23E (U05352)
HIV2CBL24E (U05353)

C. SIVAGM and SIVMND Sequences

Nucleotide alignments of AGM *ltr* I-C-1
Nucleotide alignments of AGM *env* I-C-8
SIVSAB1C (U04005) 20
SIV2010E (U10897) 24
SIV2010G (U10899) 25
SIVGRI2E (U03995) 26
SIVGRI2L (U04007) 27
SIVGRI3E (U03994) 28
SIVGRI3L (U04006) 29
SIVSAB2E (U03996) 30
SIVSAB3E (U03997) 32

SIVSAB3L18 (U04012) 34
SIVSAB4E (U03998) 36
SIVSAB4L10 (U04014) 38
SIVSABD37P (U04018) 40
SIVTAN17E (U04000) 41
SIVTAN1E (U03999) 42
SIVTAN40E (U04001) 43
SIVTAN49E (U04002) 44
SIVVER1E (U04003) 45
SIVVER266E (U10896) 46
SIVVER2E (U04004) 47
SIVVER2L (U04017) 48
SIVVER385E (U10898) 49

SIVAGM sequences stored on diskettes and FTP server only

SIVSAB1L15 (U04008)
SIVSAB2L16 (U04010)

PART I HIV and SIV Nucleic Acid Sequences

A. HIV-1 Sequences

Nucleotide alignments of HIV-1 sequences I-A-9
HIVANT70C (L20587, M31171) 173
HIVMVP5180 (L20571) 177
HIVBCSG3C (L02317) 181
HIVBZ162 (L11751) 185
HIVBZ167 (L11752) 186
HIVBZ190 (L11753) 187
HIVBZ200 (L11754) 188
HIVCI20 (L11755) 189
HIVCI32 (L11756) 190
HIVCI4 (L11757) 191
HIVCI51 (L11758) 192
HIVCI59 (L11759) 193
HIVDJ258 (L11763) 194
HIVDJ259 (L11764) 195
HIVG109 (L11765) 196
HIVG141 (L11766) 197
HIVIC144 (L11767) 198
HIVK112 (L1168) 199
HIVK124 (L11769) 200
HIVK29 (L11770) 201
HIVK31 (L11771) 202
HIVK7 (L11772) 203
HIVK88 (L11773) 204
HIVK89 (L11774) 205
HIVK98 (L11775) 206
HIVLBV105 (L11776) 207
HIVLBV23 (L11777) 208
HIVLBV217 (L11778) 209
HIVLBV2310 (L11779) 210
HIVPH136 (L11780) 211
HIVPH153 (L11781) 212
HIVSE365 (L11797) 213
HIVSM145 (L11803) 214
HIVTN238 (L11760) 215
HIVTN240 (L11761) 216
HIVTN245 (L11762) 217
HIVUG266 (L11798) 218
HIVUG268 (L11799) 219
HIVUG270 (L11800) 220
HIVUG274 (L11801) 221
HIVUG280 (L11802) 222
HIVVI174 (L11782) 223
HIVVI191 (L11783) 224
HIVVI203 (L11784) 225
HIVVI205 (L11785) 226
HIVVI310 (L11786) 227
HIVVI313 (L11787) 228

HIVVI32 (L11788) 229
HIVVI325 (L11789) 230
HIVVI354 (L11790) 231
HIVVI415 (L11791) 232
HIVVI525 (L11792) 233
HIVVI557 (L11793) 234
HIVVI57 (L11794) 235
HIVVI59 (L11795) 236
HIVVI69 (L11796) 237
HIV17M1234 (L04602) 238
HIVA101MA (M96458, M96493-M96496) 239
HIVA151RW (M96459) 240
HIVA161RW (M96460) 241
HIVA171RAW (M96461) 242
HIVA81SE (M96456) 243
HIVB54CH (M96497, M96457, M96499, M96498) 244
HIVLAIB2M2 (M96466) 245
HIVLAIB8M2 (M96464, M96463, M96465, M96467-M96470) 246
HIVLAIC319 (M96481, M96471-M96480, M96482-M96492) 247
HIVDLC23 (M96462) 250
HIV109A11X (L16594, L16591-L16593, L16595-L16620) 251
HIVNET12 (L01282, L01283-L01297) 253
HIVAMTAN (L01298, L01299-L01339) 254
HIVZ6555 (L19623, L19624-L19636) 259
HIVFLPI01 (L22590, L22591-L22605) 261
HIVFLPID (L22606) 264
HIV1789V (M93383, M93364-M93382) 265
HIVP896 (M96155) 269
HIVB10561 (L19226, L19225-L19237, L19240-L19246, L20963) 271
HIVC11893X (L11457, L11458-L11525) 277
HIVM12199 (L15721, L15722-L15735) 281
HIVRA14018 (L19571, L19572-L19579) 283
HIVMA236X (L15143, L15138-L15142, L15144-L15187) 285
HIVMB293X (L15098, L15085-L15097, L15099-L15137) 292

B. HIV-2 and Related SIV Sequences

Nucleotide alignments of HIV-2 and SIV sequences 1-B-1
HIV2UC1 (L07625) 82
HIV21971P6 (L16971) 86
HIV25132P1 (L16970) 87
HIV25132E2 (L16963, L16970-L16971) 88
HIV2GB1221 (L10638) 90
HIV2GB1222 (L10637) 91
HIV2GH2P22 (D10458) 92
HIV2S52907 (S52907) 93
HIV21888A (L08462) 94
SIVSMP209 (L20008, L20009, L20098-L20099) 96

C. SIVAGM and SIVMND Sequences

Nucleotide alignments of AGM sequence 1-C-1
SIVAGMT17 (L19250) 44
SIVAGMT27 (L19251) 45

SIVAGMT40 (L19252) 46
SIVAGMT49 (L19253) 47
SIVAGMT9 (L19254) 48
SIVAGMTBO5 (M81070) 49
SIVAGMTB14 (M80208) 50
SIVAGMTB30 (M81071) 51
SIVAGMTB53 (M81072) 52
SIVAGMSD29 (M81073) 53
SIVAGMSD30 (M81074) 54
SIVAGMSD37 (M81075) 55
SIVAGMSD45 (M81076) 56
SIVSYK (L06042) 57

PART I HIV and SIV Nucleic Acid Sequences

A. HIV-1 Sequences

Nucleotide alignments of HIV-1 sequences I-A-9
HIVCAM1 (D10112) 118
HIVYU10 (M93259 M89974) 122
HIVYU2 (M93258 M89974) 126
HIVGUN (M59192 M59193) 130
HIVD31 (X61240 X16109) 132
HIVSF2B13 (L07422) 136
HIVNH5 (L07423) 138
HIVGLNEF1 and related sequences (X63040-X63045) 141
HIVGD110 and related sequences (M92995) 144
HIVH5986 and related sequences (L07145) 147
HIVZAM18 (L03705) 170
HIVZAM19 (L03706) 171
HIVZAM20 (L03707) 172
HIVTB1321 (L03696) 173
HIVTB1322 (L03697) 174
HIVTN2431 (L03702) 175
HIVTN2432 and related sequences (L03698-L03704) 176
HIVT7787 and related sequences (L07442) 183
HIVNOF (L07426) 187
HIVD687 (L07652) 188
HIVD747 (L07653) 189
HIVD757 (L07654) 190
HIVD760 (L07655) 191
HIVD1044 (L07651) 192
HIVM6506 and related sequences (L15731) 193
HIVZ6555 and related sequences (L07465) 196
HIVU3079 and related sequences (M98912) 199
HIVU44342 (M98408-M98416) 212
HIVSIMI (L07421) 218
HIVKIGA93 and related sequences (L07082) 220

B. HIV-2 and Related SIV Sequences

Nucleotide alignments of HIV-2 and SIV sequences 1-B-1
HIV2FO784 (M87115-M87117; M87111-M87114;
M87106-M87110; M87069-M87105) 61
HIV22238 (M87135-M87139; M87118-M87134) 78
HIV27312A (M87144-M87145; M87140-M87143) 85
HIV2STV (M86924 M31113) 89
HIV2ISYR (J04498) 91
HIV2GB12 and related sequences (L10638) 95
HIV2GHLTR (M69108) 98
SIVSMMLIB1 (M62651) 99
SIVSMM9 (M80194) 100

C. SIVAGM and SIVMND Sequences

Nucleotide alignments of AGM sequences 1-C-1

PART I. HIV and SIV Nucleic Acid Sequences

A. HIV-1 Sequences

Nucleotide alignments of HIV-1 sequences I-A-3
HIVLAI (K02013; M64186-190; M64194-198; M64203-223) 70
HIVNL43 (M19921) 76
HIVJB01 (X57447) 80
HIVJB02 (X57450) 83
HIVJB03 (X57465) 89
HIVBAL (M68893) 92
HIVADA (M60472) 95
HIVSWB40 (M27951; M27946) 96
HIVSWB88 (M27952; M31462; M27947; M58206) 97
HIVM77, HIVV77, HIVT77 (see M61277-M61407, M36997) 100
HIVM82, HIVV82, HIVT82 (M61365, M36997, M61402, M77602, see M61277-M61407) 103
HIVNJA (M61028-M61045 117
HIVU455 (M62320) 122
HIVCBL4 (M63474; M63475) 126
HIVSF170 (four segments) (M66533-M66535; M81729) 127
HIVABA2 (M75686) 132
HIVACP1 (M80660) 135
HIVACH9 (M80661) 136
HIVJM (M80662) 137
HIVWM (M80663) 138
HIVHP200 (M81692) 139
HIVHP1089 (M81693) 140
HIVHP1098 (M81694) 141
HIVJRFL (pending, and M74978-M75007) 142
HIVSPBL14 (M74960; M74955-M74977) 148
HIVSPBR1 (M74964) 149
HIVTIBL7 (M75016; M75008-M75028) 152
HIVTIBR1 (M75022) 153
HIVRJS (M37491; M37573-M37577) 156
HIVSB (three segments) (M77228-M77230) 158
HIVFLD (Florida Dental Case V3V4V5 Sequences)
(M90847-M90966; M91084-M91115; M91121-M91149)
(M91153-M91156; M92100-M92150) 161
HIVHEI (X61351-X61359; X64746-X64745) 306
HIVYU10 (M89974) 324
HIVAM113 (M74591-M74640) 327
HIVAM49501 (M74641-M74684) 328
HIVMA208 (M79342-M79354; M90025-M90046) 333
HIVMOM1 (two segments) (M76789-M76799; M76900-M76912) 346
HIVTOT1 (two segments) (M76842-M76862; M76942-M76947) 346
HIVMOM2 (two segments) (M76800-M76818; M76913-M76925) 351
HIVTOT2 (two segments) (M76863-M76875; M76948-M76963) 351
HIVMOM3 (two segments) (M76819-M76841; M76926-M76941) 356
HIVTOT3 (two segments) (M76876-M76899; M76964-M76973) 356

B. HIV-2 and Related SIV Sequences

Nucleotide alignments of HIV-2 and SIV sequences I-B-1
HIV2D194 (J04542; X52223) 58
HIV2D205 (X16109; X61240) 62
SIVMM251 (M19499; X06393; M15897; M16125; Y00283; X06879; Y00294; Y00295; X06391) 66
SIVMM239 (M33262) 71
SIVMM1A1 (M76764) 76
SIVMM32H (D01065) 80
Nucleotide alignments of SIVMM 84
SIVSTAK (three segments) (X57323; X60667; X60668) 109
HIVCAM2 (D00835) 112

C. SIVAGM and SIVMND Sequences

Nucleotide alignments of AGM sequences I-C-1
SIVAGM677 (M66437) 22
SIVMND121 (M62883; M62884) 26
SIVAGM381 (M73537; M73538) 27
SIVAGM384 (M73539) 27
SIVAGM385 (M81730-M81733 28
SIVAGM386 (M81734) 29

PART I. HIV AND SIV NUCLEIC ACID SEQUENCES

A. HIV-1 Sequences

Nucleotide alignments of HIV-1 sequences I-A-3
HIVBRU (K02013) 60
HIVNL43 (M19921) 64
HIVHXB2R (K03455 M38432) 68
HIVPCV12 (M11840) 72
HIVMN (M17449) 74
HIVSC (M17450) 78
HIVJH3 (two segments)(M21137 M21138) 80
HIVBRVA (M21098) 83
HIVSF2 (K02007) 85
HIVHAN (EMBL assignment) 89
HIVOYI (M26727) 93
HIVCDC451(two segments)(M13136 M13137) 97
HIVNY5(K03346) 101
HIVJFL (M31451) 102
HIVTRA (two segments)(M27956 M27948) 104
HIVBAN (two segments)(M27953 M27944) 105
HIVBOS1 (M27910) 106
HIVPHIL1 (M27911) 107
HIVMAB (M27955) 108
HIVSWB88 (three segments)(M27952 M31462 M27947) 109
HIVSWB40 (two segments)(M27951) 111
HIVWMJ2 (two segments)(K03457 M12507) 112
HIVRF (M17451 M12508) 115
HIVMAL (K03456) 119
HIVELI (K03454) 123
HIVZ2Z6 (M22639) 127
HIVZ6 (K03458) 131
HIVZ321 (M15896 J00001) 134
HIVJY1(J03653) 136
HIVZ3 (K03347) 138
HIVNDK (M27323) 140
HIVANT70 (M31171) 144
HIVJRCSF (M38429) 145
HIVJRFL (pending and M74978-M75007) 149
HIVMFA (M33943) 153
HIVN1TE (M36998) 155
HIVSF33 (M38427) 156
HIVSF162 (M38428) 158
HIVALA1 (M38430) 160
HIVNY5CG (M38431) 162
SIVCPZCG (X52154) 166

B. HIV-2 and related SIV sequences

Nucleotide alignments of HIV-2 and SIV sequences I-B-1
HIV2ROD (M15390) 46
HIV2NIHZ (J03654) 50
HIV2ISY (J04498) 54
HIV2ST (M31113) 58
HIV2GH1 (M30895) 62
HIV2BEN (M30502) 66
HIV2D205 (X16109) 70
HIV2D194 (J04542) 73
SIVMM142 (M16403 Y00277) 77
SIVMM251 (M19499X06393) 81
SIVMM239 (M33262) 86
SIVMMP11 (M23164) 90
SIVMNE (M32741) 91
SIVSMMH4 (X14307) 95
SIVSMMM7 (M27256) 99
SIVSMMPBJ (M31325) 100

C. SIVAGM and SIVMND Sequences

Nucleotide alignments of AGM sequences I-C-1
SIVAGMTYO (X07805) 19
SIVAGM385 (M21311) 23
SIVAGM266 (M22974) 24
SIVAGM155 (M29975) 25
SIVAGM677 (M29973) 29
SIVAGM90 (M33718) 30
SIVAGM692 (two segments)(M33719 M29974) 31
SIVAGM3 (M30931) 33
SIVMNDGB1 (M27470 X15781) 37

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HIV1 GAG

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CONSENSUS.A ATgGGTGCGAGAGcGTCagTatTaAgtGggggaaaATTaGATgcaTgGgAgAaaATTcgGtTAaGGCCaGg  71
HIVU455     -------------------------C---AA----------T-------------------------------  71
HIVMAL      -------------------------C-------------------------------------------------  71
HIVVI59     --A---------------------C-A-----------------A-------------------------------  71
HIVVI310    -------------------------C---------------AAG-------------------------------  71
HIVVI57     -------------------------C--A----------------------------------------------  71
HIVK112     -------------------------------------------------------------------------  71
HIVK88      ----------------------------------------------------G--------------------  71
HIVK29      -------------------------------------------------------------------------  71
HIVK124     -------------------------C-------------------------------------------------  71
HIVK7       --A---------------------C------C--------AG--A-------------------------------  71
HIVK98      ------------A-----------------------------------------------------------  71
HIVK89      -------------------------C---------------A-G---------------------------  71
HIVVI32     ------------------------------------------------------------A------------  71
HIVVI415    -------------------------------------------------------------------------  71
HIVCI4      ---------------------------------------------G---------------C----------  71
HIVG141     -------------------------C-----------G----AT-----A-------A----C-------  71
HIVLBV23    -------------------------C---------------------A-G----A-------------  71
HIVTN243    ----------------------------------------------A------------C-------  71
HIVTN245    ----------------------------------------------A------------C-------  71
HIVTN240    ----------------------------------------------A------------C-------  71
HIVCI20     ----------------------G-------------------------------------------------  71
HIVCI59     ----------------G-------------------------------------------------------  71
HIVLBV2310  ---------------------------------------T-----------------------------  71
HIVCI51     ----------------A-----------------------T-----------------------------  71
HIVLBV105   --------------------G-----C--------------A----------------C----------  71
HIVCI32     ----------------G---------------CG-------------------------------------  71
HIVIC144    -------------------------C--A--------G-----------------------------------  71
HIVDJ258    ---------------------------------------T----------G--------------------  71
HIVCM238    -------------------------C---------------------A------------C-------  71
HIVUG266    ------------T------------C-A---G-------------A----------------------A  71
HIVVI354    ------------------A--C----C---------------------A-A-G---------------G--  71

CONSENSUS.B ATGGGTGCGAGAGCGTCaGTAtTaAGcGggGGagAATTaGAtagaTGGgAaAaaATTCGGtTAaGGCCAgG  71
HIVSF2      ----------------G-------------------------A-----------------------------  71
HIVBZ167    ----------------G-------------------------G-----------------------------  71
HIVPH153    ---------------------------------GA-------------------------C----------  71
HIVPH136    ---------------------------------------C----------G--------------------  71
HIVBZ200    --------------------C---------------------A-----------------------------  71
HIVTB132    ---------------------------------C--------------A-G------------C-------  71
HIVBZ190    ---------------------------------A---------A-----------------------------  71
HIVLAI      ---------------------------------------C-----------------------------  71
HIVHXB2R    ---------------------------------------C-----------------------------  71
HIVMN       ----------------G-------------------------C----------C------------------  71
HIVJH3      ---------------------------------------C-------G--------------------  71
HIVJRCSF    ---------------------------------G-----G-----------------------------  71
HIVOYI      ---------------------------------------A-----------------------------  71
HIVNY5CG    ----------------G-------------------------A-----------------------------  71
HIVNL43     ----------------G-------------------------A-----------------------------  71
HIVCDC4     -------------------------------------------------------------------------  71
HIVHAN      ---------------------------------------C-A-----------------------------  71
HIVCAM1     ---------------------------------------A-----------------------------  71
HIVRF       ---------------------------C---A-------C-A-------------------------A-  71
HIVD31      -------------------------------------------------------------------------  71
HIVBH102    ---------------------------------------C-----------------------------  71
HIVPV22     ---------------------------------------C-----------------------------  71
HIVJRFL     --------------------------------A----G----A-----------------------------  71
HIVUG280    -------------------------------------------------------------C-------  71
HIVYU2      -------------------------T-C---G----------AG-------------------------  71
HIVBCSG3C   ----------------------G---------A----G----AG-----G--------------------  71
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CONSENSUS.C ATGGGTGCGAGAGCGTCAaTATTAAgAGGcGgAAAATTAGATacaTGGGAaAaAATTAgGtTAAgGCCAGG  71
HIVUG268    ------------------G-------------------------C-------------A------------  71
HIVSM145    ----------------------------------------G---------G------------------  71
HIVZAM18    -------------------------A---G-----------------------------------------  71
HIVZAM19    -------------------------N---G------------G--------------------------  71
HIVZAM20    ----------------------------G-------------A------G---------------------  71
HIVDJ259    --------------------------------A----------G-C-------------A-C----------  71
HIVVI313    ---------------------------------------------C-------G-----A-----A------  71

CONSENSUS.D ATGGGTGCGAGAGCGTCaGTATTAAgCGGGGGAaAAtTaGATgaaTGGGAAAaAATTCgGTTACGGCCAGG  71
HIVELI      ------------------------------------------A-----------------------------  71
HIVZ2Z6     ----------------------------------------G----C-------------------------  71
HIVNDK      ------------------------------------------AC--------G------------------  71
HIVVI205    ------------------------------------------C-----------------------------  71
HIVG109     ----------------------------------C---------C--------G------------------  71
HIVK31      ------------------------------------------------------------A------------  71
HIVUG274    ------------------------------------------------------------------------  71
HIVUG270    ------------------G-----------------C-----------------------------------  71
HIVSE365    ----------------------------------C--------CG-----------------------------  71
HIVVI203    -------------------------C----------------TCG-----------------------------  71

CONSENSUS.F ATGGGTGCGAGAGCGTCAGTATTAAGCGGgGGAAAAtTaGATgCATGGGAAAAAATTCggTTAAGgCC?GG  70
HIVVI174    ------------------------------------------------------------A---------G--  71
HIVVI69     ------------------------------------------------------------A-----A--G--  71
HIVBZ162    ----------------------------A-------C-------------------------------A--  71
HIVVI325    ---------------------------------------G---A-------------------------A--  71

CONSENSUS.G ATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAAAA?TAGATG?ATGGGAAAAAAATT?GG?TGAGGCCAGG  67
HIVLBV217   ------------------------------------T------A-------------A--C----------  71
HIVVI191    ------------------------------------C------C-------------C--T----------  71

CONSENSUS.H ATGGGTGCGAGAGCGTCAGTATT?AGCGGGGGAA?ATTAGATGC?TGGGAGAAAATTCGGTT?AGGCCAGG  67
HIVVI525    ----------------------G----------G---------T-----------------A--------  71
HIVVI557    ------------------------A----------A---------A-----------------G--------  71

CONSENSUS.O ATGGGTGCGAG?GCGTCTGTGTTGACAGG?AG?AAATTGGATGCATGGGAAC?AATTAGGTTAA?GCCAGG  66
HIVANT70    -----------T-----------------A--C-------------------A-----------A------  71
HIVMVP51    -----------A-----------------G--T-------------------G-----------G------  71

SIVCPZGAB   ATGGGTGCGAGAGCGTCAGTTCTAACAGGGGGAAAATTAGATCGCTGGGAAAAAGTTCGGCTTAGGCCCGG  71
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HIV1 GAG

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CONSENSUS.A gGGAAagAAAaaaTATagacTgAAaCAT?TAgTaTgGGCaaGCagggAGcTgGAaagATTcgCACTTaAcC    141
HIVU455     ------C--------------------T-------------------------A----A---------    142
HIVMAL      ----------------------------T-------------------------------------------    142
HIVVI59     A---------C-----------------T----G-A--------A------A------------------    142
HIVVI310    ----------C----------A--G---C----G-------------------------------------    142
HIVVI57     ----------------------------C-------------------------------------------    142
HIVK112     -------------------A-C------C---------------------------A---T----------    142
HIVK88      -------------------A--------T-------------------------C-----T----------    142
HIVK29      -------------------A--------T-------------------------------T----------    142
HIVK124     ------------G--------------T-------------------------------T----------    142
HIVK7       ----------------------------C-------------------------------------------    142
HIVK98      ------T----G-----A---A------A-------------------------------------------    142
HIVK89      ------------------A----------T-------------------------------------------    142
HIVVI32     --------------------A--------T-------------------------C----------------    142
HIVVI415    -----G-------------A--------C-------------------------C----------------    142
HIVCI4      --------------------A--------C--A--------G----A------------------------    142
HIVG141     -----CC----GG----AG--A------A-------------------------C----T------G-T-    142
HIVLBV23    --------------------A--------C-------------------------------T----------    142
HIVTN243    -----GA-----G-----GA--------T----------------A---T-A--------------------    142
HIVTN245    -----GA-----G----AGA--------T----------------A---T-A--------------------    142
HIVTN240    -----GA-----------G---------T----------------A---T-A--------------------    142
HIVCI20     ---------------------A------C-------------------------------------------    142
HIVCI59     ---------------------A------C-------------------------------------------    142
HIVLBV2310  ---------------------A------C-------------------------------------------    142
HIVCI51     -----G----C----------A------C-------------------------------------------    142
HIVLBV105   -------------------A--------C-------------------------------T----------    142
HIVCI32     -----------------A---A------T-------------------------------------------    142
HIVIC144    ---------------------A------C--------------------T-----------------------    142
HIVDJ258    ---------------------A------C----------G-------------------------------    142
HIVCM238    -----G-----------AGA-A------T-------------C-A---T-A--------------------    142
HIVUG266    -----------------A----------C----G-A---------------A----A--------------    142
HIVVI354    ------------G---CAGA-A------A----G------------A-------G-A---T----------    142

                /<- INS-1
CONSENSUS.B gGGAAAGAAAaaaTATaaatTAAAaCATaTAGTATGGGCAAGCAGggAgCTAGAACGaTTcGCagTtaAtC    142
HIVSF2      ------------------G-------------------------------------------------C----    142
HIVBZ167    -----------------GG---------G-------------------A----------------------    142
HIVPH153    ----------------C--------------------------------------------------------    142
HIVPH136    ---------------------------------------------------------------------------    142
HIVBZ200    ----------GC-------------------------------------------------------------C-    142
HIVTB132    ----------------G--------------------------------------------------------    142
HIVBZ190    -----------GG---C--C-------------------------A-------------------------    142
HIVLAI      ---------------------------------------------------------------------------    142
HIVHXB2R    ---------------------------------------------------------------------------    142
HIVMN       --------------------------G-----------------------------------C----    142
HIVJH3      ---------------------------------------------------------T----------    142
HIVJRCSF    A----------------G-----------------------------------------T--------C----    142
HIVOYI      ----------------C--C-----------------------------------------A------    142
HIVNY5CG    ----------C------G-C-----------------------------A----------------------    142
HIVNL43     ----------C--------C-------------------------------------------------    142
HIVCDC4     ----------C-----CG------G--------------------A-------------------C----    142
HIVHAN      ----------------C--------------------------------------------------------    142
HIVCAM1     ---------------------------------------------------------------------------    142
HIVRF       -----------G------G-----------------------------------------T--T--C----    142
HIVD31      ----------------G-----------------------------A----------------------    142
HIVBH102    ---------------------------------------------------------------------------    142
HIVPV22     ---------------------------------------------------------------------------    142
HIVJRFL     ----------------G-----------------------------------T-------------    142
HIVUG280    ---------------------------------------------------------------------------    142
HIVYU2      ----------C------G-----------------------------------------------G---    142
HIVBCSG3C   ---------------------------C-------------------------------------------    142
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CONSENSUS.C gGGAAaGAAAcacTATATGaTaAAACAccTAGTaTGGGCAAGCAGGGAGCTgGaAAgATTTGCACTTaACc 142
HIVUG268    ----------TG---------G-----------C------------------G----------------T 142
HIVSM145    ------------------------------------------------------------------------ 142
HIVZAM18    ------------------------------------------------------------------------ 142
HIVZAM19    ------------T-----------------------------------------A------------------ 142
HIVZAM20    ------------T--------------TT------------------------------------------- 142
HIVDJ259    A----G-----G-------C-------------C----------------------A-------------- 142
HIVVI313    ---------------------G-------------------------------------------------G--- 142

CONSENSUS.D aggAaagAAAAAATATaaaCTaAAACATaTagTATGGGCAAGCAGgGAgCTagAACGATtTgCAcTTAATC 142
HIVELI      -----------------G-------------------------------------------A---------- 142
HIVZ2Z6     -----------------G----------C------------------------------------------- 142
HIVNDK      ----------------GC----------T-GA-----------------------------A---------- 142
HIVVI205    -AA--GC----------G-----------------------------------A------------------ 142
HIVG109     G----------------C---------------------------------A---------------------- 142
HIVK31      G---C-C-------------------------------------------------------------A------ 142
HIVUG274    G-----C-------------------------------------------G------------A------ 142
HIVUG270    G-----C--------------------C------------------------------------------- 142
HIVSE365    ------------------G-----------------------------A---------------------- 142
HIVVI203    -----------------G---G----------------------A--------------------------- 142

CONSENSUS.F gGGaA?gAAAAAATAtAgaaTgAAgCATCTAgTATGGGCAAGCAGGGAgcTAGAAcGATTTGCA?TT?AtC 138
HIVVI174    ---G-A-------------------------------------------------------------A--G--- 142
HIVVI69     -----G---------C-A-----------A---------------AT-----A--------C--G--- 142
HIVBZ162    -----A----------T-------------------------------------------A--A--- 142
HIVVI325    A----GC----------GC-A--A-----------------------------------C--A-C- 142

CONSENSUS.G GGGAAAGAAA?AATATAGAAT?AA?CAT?TAGTATGGGCAAGCAGGGAGCTGGA?A?ATTTGCACTTAACC 132
HIVLBV217   ----------A----------G--A---T-----------------------G-G-------------- 142
HIVVI191    ----------C----------A--G---C-------------------------A-A-------------- 142

CONSENSUS.H GGGAAAGAAA?AATATAG?CT?AAACAT?TAGTATGGGCAAGCAG?GAGCTGGAAAGATTTGCACT?AACC 132
HIVVI525    ----------C-------G--A------C----------------A--------------------T---- 142
HIVVI557    ----------A-------A--G------T----------------G--------------------C----- 142

CONSENSUS.O ATCTAAAAAG??ATATAG?CTAAAACA?TTAGTATGGGCAAGCAG?GAGCTGGAAAGAT?CGCATGTAATC 131
HIVANT70    ----------AA------A--------C-----------------A-------------T----------- 142
HIVMVP51    ----------GC------G--------T-----------------G-------------A----------- 142

SIVCPZGAB   GGGAAGAAAAAGATATATGATGAAACATTTAGTATGGGCAAGCAGGGAGCTGGAAAGATTCGCATGTGACC 142
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HIV1 GAG

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CONSENSUS.A CtaGccTTtTagAaACAgcaGaagGatGTcAacaaaTAaTggaACAgtTacAatCAgcTcTcaagACAGga   212
HIVU455     --G-------------------------------G------C---G---A------C--------C--------   213
HIVMAL      --G---------------G-------------------------C--------A---------------------   213
HIVVI59     -----------------A----------------------A-----A------C-----------------------   213
HIVVI310    -----------------A-G--------------------A------------C-----------------------   213
HIVVI57     -----------------A--------------------C-------------C--------A---------------   213
HIVK112     -------------G---A-----------------------------------------------------------   213
HIVK88      -C----------------------------------------------------------------------------   213
HIVK29      -----------------A----------------------A------------C----------A------------   213
HIVK124     -----------------A-------------------------------------T-----------------------   213
HIVK7       -----------------A-----A-G-----------------------------------------------------   213
HIVK98      --G--------------A-------G-----G---------A--------------------C--------------   213
HIVK89      -----------------A-------G--------------------A------C---------------G-------   213
HIVVI32     --------C-G------AA----------------G---------------G-----------------------   213
HIVVI415    --G-------------------------------C-------------GC-----------------------   213
HIVCI4      -----------------A----------------G--------C-----------------------------   213
HIVG141     -C------C----G---T----G--C---A--------C-A-G----C-----C-------T---------   213
HIVLBV23    --G-----------------------------------------G----------A--------C-------G   213
HIVTN243    --G-------------------------------------A-----------G---A--------------   213
HIVTN245    --G----------------------C-------------AAG---------G---A--------------   213
HIVTN240    -----T-----------------------------------A-----------G---A--------------   213
HIVCI20     -C-------------------G---------G---C-----------------G--CA-----G--------   213
HIVCI59     --G--------------------T-----------C-----------------------G--------------   213
HIVLBV2310  --G-------------------------------T-------------------------G--------------   213
HIVCI51     ---------------------------------------A----------------------A------------   213
HIVLBV105   --G-----------------------------------C-A-----------C--T--G-T--A------------   213
HIVCI32     -----------------T-----------------C----A--------C------A-----GG-------------   213
HIVIC144    --G--T-------------------------C-------------------A--------------------------   213
HIVDJ258    --G-------------------------------GT-------------------------GG-----A-------   213
HIVCM238    --G----------------T-----------------------A-----------G---A--------------   213
HIVUG266    -----------------A--------------AG----C-A-----A------C--------C-------------   213
HIVVI354    -CG-T------A----------------------G-----------A-----------------A------------   213

                                        - - - INS-1 - - -
CONSENSUS.B CtgGCCTgtTaGAaaCatCagaaGGcTGtaGAcAaATAcTgggACAgcTACaaCCatcCCTTcAGACaGGA   213
HIVSF2      ----------------------------C---------T-------------G------------------   213
HIVBZ167    -------AC-------GG---C-------------------------------G--------------T---   213
HIVPH153    ------------------------------------------------T---G--------------------   213
HIVPH136    ---------------------G----------------T---A-------------G--------------   213
HIVBZ200    -C-----TC--------------------C--A-----A-A-------------------------------   213
HIVTB132    -------A--G-----G-------------------------------------AG--------------   213
HIVBZ190    -------------G---G-------------------------------------------------------   213
HIVLAI      -------------------------------------------------------------------------   213
HIVHXB2R    -------------------------------------------------------------------------   213
HIVMN       -------------------------------------------------------------------------   213
HIVJH3      --A----------------G-------------------------------------------------------   213
HIVJRCSF    --------------T-------------------------------A---------------A---------   213
HIVOYI      -------------------------T-----------------------------------A---------   213
HIVNY5CG    -------T-----G---------------------------A---------------------------   213
HIVNL43     -------T-----G-------------------------------------------------------   213
HIVCDC4     -------T------------A-------------------------T-----------------------   213
HIVHAN      ---------------------------------G---A----------------G---------------   213
HIVCAM1     -------T-----G---------------------------------------G---------------   213
HIVRF       --A----T-----G---G----G-----------------------------G--------------   213
HIVD31      ------------------------------------T-------------------------------   213
HIVBH102    -------------------------------------------------------------------------   213
HIVPV22     -------------------------------------------------------------------------   213
HIVJRFL     --------------T-----------------------------A----T----G-----A---------   213
HIVUG280    -------A-----------------------------------------------G--------------   213
HIVYU2      ---------------------------------------------------G---------------   213
HIVBCSG3C   -C---------------G-----------------------------------G---------------   213
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CONSENSUS.C CTgGcCTTTTAGAgACAtCAgAaGGCTGTAaAcAAATAATaAaAcAGCTaCAaCCAgCTcTTCAGACAGGa 213
HIVUG268    ------------A-------------------------G---------------------------G 213
HIVSM145    ----------------------------------------G--------G------------------- 213
HIVZAM18    ------------------------------------------------------T--A----------- 213
HIVZAM19    ----T-------------------------------------------------------------- 213
HIVZAM20    ------------------G----C-------------------G---------T------------- 213
HIVDJ259    --A-------------------------------------G---------------------------- 213
HIVVI313    --------------------C---------G-G-----------A---------------------- 213

CONSENSUS.D CTGGCCTTTTAGAgACatCAGAaGGcTGTAaACAAATAATaGgaCAGCTACAaCCAgcTaTtcagaCAGGA 213
HIVELI      ------------A------------------------------G---------------------- 213
HIVZ2Z6     ----------------------T-------------------------------------C-G------- 213
HIVNDK      ------------------------------------------------------T-------A------ 213
HIVVI205    ------------------------------G-----------A---------------------- 213
HIVG109     ------------------G------------------------A---------C---AA-C-----T----- 213
HIVK31      --------------A---C----------------------G-----------C------------- 213
HIVUG274    -------------A-------------------------G-----------------C--A------- 213
HIVUG270    -------------A--C-------------------------G---------------T--------- 213
HIVSE365    ------------------------T----G---------------------------------------- 213
HIVVI203    ------------------------------------------A-------------T---------- 213

CONSENSUS.F CtgGcCTTcTAGAaACAtCAGAAGGCTGT?g?aAAATAATAgGACAgtTACAAcCATCCCTTCAGACAGGA 207
HIVVI174    ----T------------C-----------A-G---------------C-----A------------- 213
HIVVI69     ----------------------------A-A---------------------------------------- 213
HIVBZ162    ----------------------------CAA.---------------------------------------- 212
HIVVI325    -CA-----T----G---A----------C-GC--------A----A------------------------ 213

CONSENSUS.G CTGGCCT?TTAGAAACAACAGAAGG?TGTCAACAAATA?TG??ACAGTTGCAACCA?CTCTCCAGACAGGA 197
HIVLBV217   -------C----------------T-----------C--CA-----------T--------------- 213
HIVVI191    -------T----------------C-----------A--AG-----------G--------------- 213

CONSENSUS.H C?G?CCTTTTAGA?ACA?CAGAAGGCTGTCTACA??TAATAGAACAGCTACA?CCAGCTCTTAAGACAGGA 196
HIVVI525    -T-G---------A---T----------------GA----------------G---------------- 213
HIVVI557    -C-A---------C---G----------------AT----------------A---------------- 213

CONSENSUS.O CTG??CTA?TAGAAACTGCAGA?GGTA?TGAG?A?CTGCTACAGCAGTTAGAGCCAGCTCTCAAGACAGGG 195
HIVANT70    ---AG---C-------------G----A----A-G------------------------------------ 213
HIVMVP51    ---GT---T-------------A----C----C-A------------------------------------ 213

SIVCPZGAB   CCGGGCTAATGGAAAGTAAGGAAGGATGTACTAAATTGTTACAACAATTAGAGCCAGCTCTCAAAACAGGC 213
```

HIV1 GAG

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CONSENSUS.A ?CAgAAGAAcTtAaaTCaTTAtttAAtaCagTAGcAacCCTcTatTGcgTaCAtcaaaggATAgA?gTAAa  281
HIVU455     A----------G--------A----------GT---------T----------------T-----  284
HIVMAL      T--------A----------A----------------------T----------------T-----  284
HIVVI59     A----------G----------G--------GT----------------C-------TA----  284
HIVVI310    A----------A-G----------------A-----GT---------T---------C-------G-----  284
HIVVI57     A-------------------------------GT----------------C-------G-----  284
HIVK112     A----------G-----------------------------------------------T-----  284
HIVK88      A----------G---------C----------------------T----------A-----T-----  284
HIVK29      A----------G-----------------------------------------C-------G-----  284
HIVK124     A--------A---G----------G--------GT---------T---------C-------G-----  284
HIVK7       A----------GG-------A----------------------T-------G-CA------G-----  284
HIVK98      A----------G---G----A-------------------------------C-------T-----  284
HIVK89      A----------G-------------------------GG----------CAA---A-T-----  284
HIVVI32     A--------A----------A----------GT-----T---T---------C-------T-----  284
HIVVI415    A--------A----------A----------------------T--------G--------T-----  284
HIVCI4      A----------G--------A---C-------------------------C-------T-----  284
HIVG141     T----------C-----C----A----------------------T------GC---A-----AA----  284
HIVLBV23    A----------A---------CA----------GT----------G--------------T-----  284
HIVTN243    T-------------------------------------GG--------C----------G-----  284
HIVTN245    T---------------------------------T--------GG-----G--C----------G-----  284
HIVTN240    T-------------------------------------GG--------C----------G-----  284
HIVCI20     T----------------------------A----------T-GG-------------------CA----  284
HIVCI59     T-------------------------G--A-----GT---T-GG-------------------CA----  284
HIVLBV2310  T----------------------------A----------T-GG-------------------C-----  284
HIVCI51     T----------G----------------------T-GG-------------------CA----  284
HIVLBV105   T----------G--------------------T--------TG--T---------C-------G----G  284
HIVCI32     T----------G--------A-------A----------T-GG--T-------G---------GA----  284
HIVIC144    T--------G--------------------A----------T------A----------------CA---G  284
HIVDJ258    T--A-----------------A------CA-----GT---T-GG-------------------CA----  284
HIVCM238    T-------------------------------------GG--------C----------G-----  284
HIVUG266    G----------G---C----A----------GT--------------------------GA----  284
HIVVI354    T-----------------------------------------T----------A----A-T-----  284

                                        - - - INS-1 - - -
CONSENSUS.B tCAGAAGAactTAgATCATTataTAAtaCAgTAGCaaccCTcTATTGTGtgCATCAAaggATAGAggTAAa  284
HIVSF2      ----------------------------------------------A--------------T-----  284
HIVBZ167    ----------------------------------------------A-------A------T----G  284
HIVPH153    A---------------------------------------------------------AC----------  284
HIVPH136    -------------A-------C-----------------------------------A------T-----  284
HIVBZ200    ---------------------------------GT----------C--------A------T-----  284
HIVTB132    ------------------------------A-----GT----------A-------A----------  284
HIVBZ190    -------------A--------T----G--------GT-----------------CA----------  284
HIVLAI      ------------------------------------------------------------A-----  284
HIVHXB2R    ------------------------------------------------------------A-----  284
HIVMN       -------------A-----------------------------------------A-------A-----  284
HIVJH3      -------------A--------T-----------------------------------A----------  284
HIVJRCSF    -------------C-----------------------------A--------------A-----  284
HIVOYI      ---------A-----------------------T--T---------------A----------  284
HIVNY5CG    ----------G----------T-----------GT-------------------------T-----  284
HIVNL43     ------------------------------A-----GT-------------------------T-----  284
HIVCDC4     ------------------------------------------------------------------G  284
HIVHAN      ------------------------------------------------------A----------  284
HIVCAM1     ------------------------------------------------------A------T-----  284
HIVRF       -------------A-------------G----------------------A-------AT----------G  284
HIVD31      ----------------------T---C-----------------------------------------  284
HIVBH102    ------------------------------------------------------------A-----  284
HIVPV22     ------------------------------------------------------------A-----  284
HIVJRFL     ----------------------------------------------A--------------------  284
HIVUG280    --------------------G-T-----------------------------------T-----  284
HIVYU2      --------G-------------------------C---------------A-------A----------  284
HIVBCSG3C   -------------A----------------A-----GT--------------------T------T-----  284
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CONSENSUS.C ACAgAgGAACTTAgATCATTATatAAcaCAGTAGcAactCTcTatTGTGTACATgaa?agATAgaggTACg  283
HIVUG268    -----T-----------------------------------------------A--GG------A-----  284
HIVSM145    ----------------------TC-------------------------------A-------------  284
HIVZAM18    -------------A--------TC----------T------A-GG-----------G-T---ACA-----  284
HIVZAM19    -------------A-------C-C---G--------GTC---------------A--N-T---ACA-----  284
HIVZAM20    ---------------------------------------------------------C-GG----------  284
HIVDJ259    -----A--------------------T-----------------------------C-AG-------A---A  284
HIVVI313    ---A---------T-------C----T-----------------------------GA--------A----  284

CONSENSUS.D tCagAaGAacTtAaATCATTAT?TAATACAgTAGCAACcCTCTATTGtGTACATgaaaggATAgAgGTaaa  283
HIVELI      A------------G--------A-------------------------------A--G-A-----T-----  284
HIVZ2Z6     -------------G--------T---------------------------------------------  284
HIVNDK      ---------A---G--------A---------------------------------------------  284
HIVVI205    ---A-----A------------T-----------------------------A-------------G--  284
HIVG109     --G-----C-------------A-----------------------------A-C--------------  284
HIVK31      -----G---A------------A-----------------C-------C-G-----A------C  284
HIVUG274    -----G---A-C----------T-----------------------------------A------C  284
HIVUG270    -----G---G------------T---------------T-------------------A-----GC  284
HIVSE365    -------------G--------A-------A---------------------------A------------  284
HIVVI203    A--------------------T-------------------------------C----------------  284

CONSENSUS.F TCAGAAGAGCTTAgATCATTaT?tAATACAgTAG?AgtcCTCTATTttGTACATCAaAgGgTAGAG?TAAa  275
HIVVI174    --------------------G-T-------A---T----------A-------------------A----  284
HIVVI69     ----------------------A-----------C---T-------------------A-------G----  284
HIVBZ162    ----------------------A-----------C-------------------------------G----  283
HIVVI325    -------------A--------TC----------T-AC--------GC--------G---A-----A---G  284

CONSENSUS.G ACAGAGGAG?TTAAATCA?TAT?TAAT?CA?TAGCA??TCTCT??TGT?TACATCAAAGGATAGaggTAAA  258
HIVLBV217   ---------C--------T---T----G--G-----GT-----GG---A---------------G------  284
HIVVI191    ---------A--------C---A----A--A-----AC-----AT---G-----------------A----  284
HIVTAIG                                                                  -T-----    7

CONSENSUS.H ACAGAAGAACTTCAATCATTATTTAATCTATTAGCA??CCTCTATTG?GTACATCAAAGAATAGAT?TAAA  263
HIVVI525    ------------------------------------GT---------T------------------A----  284
HIVVI557    ------------------------------------AC---------C------------------G----  284

CONSENSUS.O TCAGA???CCTG?A?TC?CTCTGGAACGCAATAG?AGT?CTCTGGTG?GTTCACAACAGAT?T?A?AT??G  252
HIVANT70    -----CAG----C-G--A----------------T---G--------T-------------A-A-A--TG-  284
HIVMVP51    -----GGA----A-A--T----------------C---A--------C-------------T-G-C--CC-  284

SIVCPZGAB   TCAGAAGGACTGCGGTCCTTGTTTAACACTCTGGCAGTACTGTGGTGCATACATAGTGACATCACTGTAGA  284
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HIV1 GAG

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CONSENSUS.A aGACaCCAAgGAaGCttTagAtAaAaTAGAgGaAaTacAAAatAAgagcaagcaaaag????????????    339
HIVU455     ------------------A---------------G----------A--------G-.............    342
HIVMAL      ---------------GC---------------------------------G-------ACACAGCAGGCAG    355
HIVVI59     ---------A-----C--------------A-----G-----------T---------.............    342
HIVVI310    ------------------------------------------------------------.............    342
HIVVI57     ------------T-----------------------------G---------------.............    342
HIVK112     G---------------C-------------------------------------------.............    342
HIVK88      ------------G---C----C---------------------------------------.............    342
HIVK29      ----G-----------C-----------------T-G-----------------------.............    342
HIVK124     ----------------C----C--------------G--------------A-------.............    342
HIVK7       ---------A------C-------------------------------------------.............    342
HIVK98      ----------------C-------------------------------------------.............    342
HIVK89      ----------------C-G-----------------------------A---------A.............    342
HIVVI32     ---------------C--------------------A----------T---------.............    342
HIVVI415    ---------A---------------------------A---------A----------.............    342
HIVCI4      ------------------------------------------------------C--.............    342
HIVG141     ------------------------------------------C---------.....................    336
HIVLBV23    ----------------------G-----------------G-----------CC--.............    342
HIVTN243    ---------------------------------G--------------C--------.............    342
HIVTN245    ---------------------------------G--------------C--------.............    342
HIVTN240    ---------------------------------G--------------C--------.............    342
HIVCI20     ---------------C----------------T-------------------.....................    336
HIVCI59     ---------A-----C---------T--------G----------------A------.............    342
HIVLBV2310  ---------------C---------T-------------------------A------.............    342
HIVCI51     ---------------C-------------------------GC---CAA---A--.................    339
HIVLBV105   ----------------A----C-------------------------------------.............    342
HIVCI32     ---------------C-------------------------------------------ACACAGCAAGCAG    355
HIVIC144    ---------------C-------------------------------------------.............    342
HIVDJ258    ---------------C----------------C-G-----------------------.............    342
HIVCM238    ---------------------------------G--------------C--------.............    342
HIVUG266    ---------------------------------G----------------------.............    342
HIVVI354    ---------------------------------------------A-----------A.............    342

                INS-1 ->/
CONSENSUS.B AGACACCAAgGAAGCtTTAGA?AAgaTaGAGGAAGAgCAAaaCAaaAGTAagaAAAAa.............    341
HIVSF2      --------------------G-----------------------------------G.............    342
HIVBZ167    --------------------G---G-------------------------G----G.............    342
HIVPH153    --------------------A---------------------------C-----G.............    342
HIVPH136    --------------------G-------------------------------------.............    342
HIVBZ200    --------------------C-------------A---G----------------G.............    342
HIVTB132    --------------------G-------------A------------------G.............    342
HIVBZ190    --------------------T-----C---------------T-----------G.............    342
HIVLAI      --------------------C-------------------------------------.............    342
HIVHXB2R    --------------------C-------------------------------------.............    342
HIVMN       --------------------G--A----------------------------------.............    342
HIVJH3      --------------------G-------------------------------------.............    342
HIVJRCSF    --------------------A------------------C--------T------G.............    342
HIVOYI      --------------------T-------------------------------------.............    342
HIVNY5CG    ----------------C-----T-----------------------------------G.............    342
HIVNL43     ----------------C-----T-----------------------------------G.............    342
HIVCDC4     ---------A-----------C-------------A--------------------.............    342
HIVHAN      --------------------C---G-----------------C-----------G.............    342
HIVCAM1     ----------------C-----G--A-------------------------------G.............    342
HIVRF       --------------------C-------------------------------------.............    342
HIVD31      --------------------T-------------------------------------.............    342
HIVBH102    --------------------C-------------------------------------.............    342
HIVPV22     --------------------C-------------------------------------.............    342
HIVJRFL     --------------------A-----------------GC-----------------.............    342
HIVUG280    --------------------C-----------------------------------G.............    342
HIVYU2      --------------------G-------------------------------------.............    342
HIVBCSG3C   --------------------G----------------------C------------.............    342
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CONSENSUS.C AGACACCAAgGAAGCctTAGACaagaTAgAGGAAGAACAAAACAAaagTCAGCAAAAA??????.....  341
HIVUG268    ----------------------------------------------G-T----------.....  342
HIVSM145    ------------------------------------------------------------.....  342
HIVZAM18    ----------------------G-T--------------------------------ACAAAA.....  348
HIVZAM19    ---------------N-------G---------------------GT----------.....  342
HIVZAM20    ----------------------G----------------------T----------.....  342
HIVDJ259    ---------A-----AC-----------------------------T----------.....  342
HIVVI313    ------------------------A---A----------------------------.....  342

CONSENSUS.D agAcACcAAgGAAGCttTAGAaAAgaTgGAgGAAGAaCaAAaCAAAAGTAAGAAaAAg?????????....  341
HIVELI      ------------------------------------G---------------------.....  342
HIVZ2Z6     ------------------------------------------------------C--AAAG.....  345
HIVNDK      ---------A------G-------------------------------------------.....  342
HIVVI205    ----------------C-------AC-------------------------------AAGA.....  345
HIVG109     ------------------------------------------------------------GCACAGCAA....  351
HIVK31      -A------------------C-----A-------------C---------------A.....  342
HIVUG274    ---------------------C-----A-------------C---------------.....  342
HIVUG270    ------A--------C-----C-----A--A-----G----C---------------A.....  342
HIVSE365    ---------------G---------------------G-------------------.....  342
HIVVI203    G--T-----------------C--AT-----------------------------.....  342

CONSENSUS.F GGACACCAAGGAAGCtTTAGAcAAgCTAGAgGAaGAACAAAACAAAAGTcAGCAAAAG.....  333
HIVVI174    ---------------------A-------------------------------------.....  342
HIVVI69     ---------------------G-----------G-----------------------.....  342
HIVBZ162    ------------------------------------------------------------.....  341
HIVVI325    ---------------C--------A-----A------------------A--------.....  342

CONSENSUS.G AGACACCaAAGAAGCTcTAgAGGAAGTGGAaAAggcaCAAAaGAAcAGTCAGCAAAAA.....  316
HIVLBV217   ----------------------------------AGG---------------------.....  342
HIVVI191    -------C--------T--C----------G--------------A------------.....  342
HIVTAIG     --------------------------------A-------G----------------.....   65

CONSENSUS.H AGACACCAAGGAAGCTTTA???AAG?TA?AGGA?G?ACAAAACAA?AG?CAG?A?A??.....  308
HIVVI525    -------------------AGT---A--G----A-T---------C--A---C-A-AA.....  342
HIVVI557    -------------------GAG---T--A----G-C---------A--C---A-C-GG.....  342

CONSENSUS.O AGATAC?CAGCAGGCAATACAAAAGTTAAAG...GAAGTAATGG??AGCAGGAAGTCT.....GC?G  307
HIVANT70    ------G-----------------------...----------GG----------.....--G-  343
HIVMVP51    ------A-----------------------...----------CA----------.....--A-  343

SIVCPZGAB   AGACACACAGAAAGCTCTAGAACAGCTAAAGCGGCATCATGGAGAACAACAGAGCAAAACTGAAAGTAACT  355
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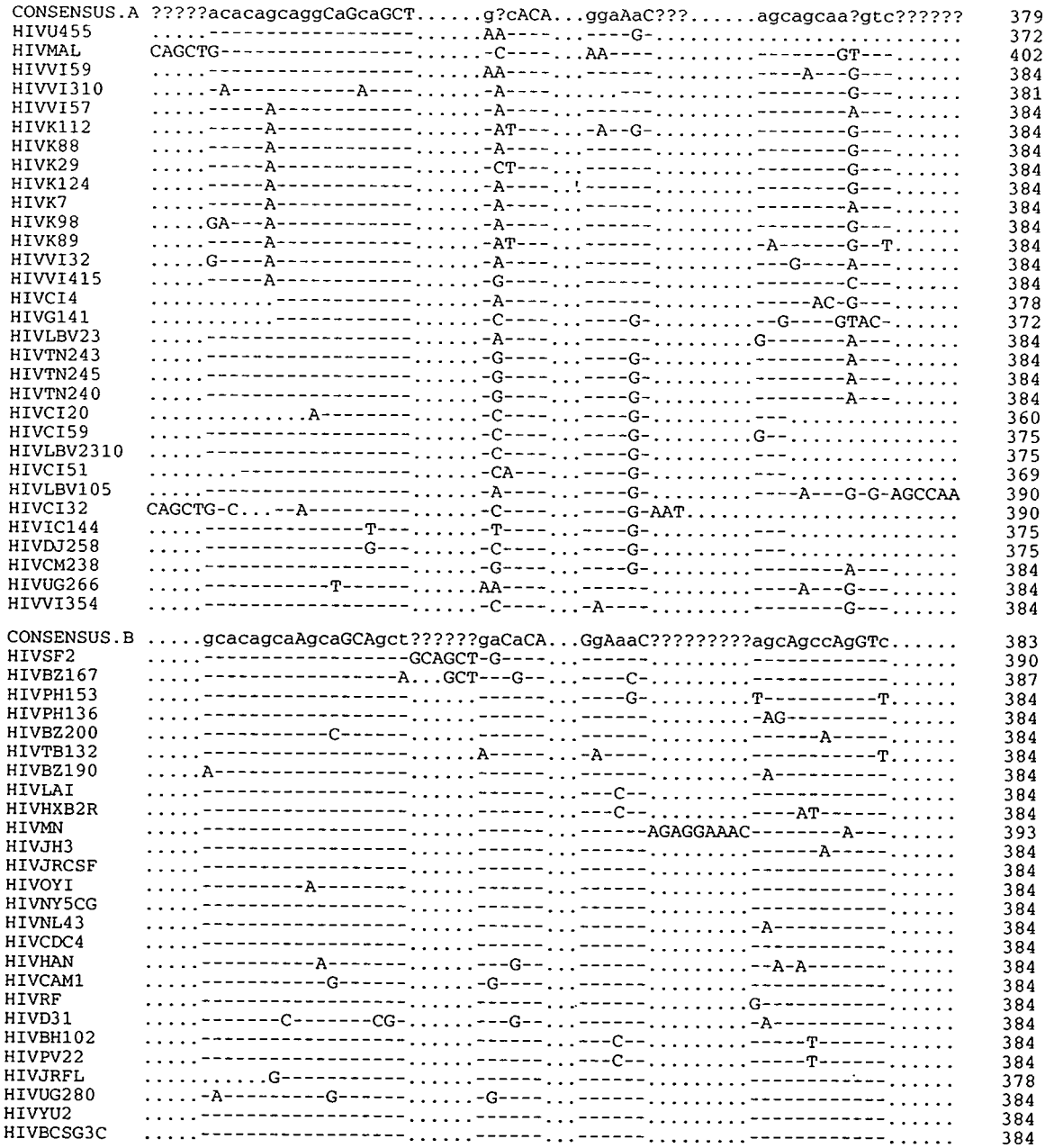
HIV1 GAG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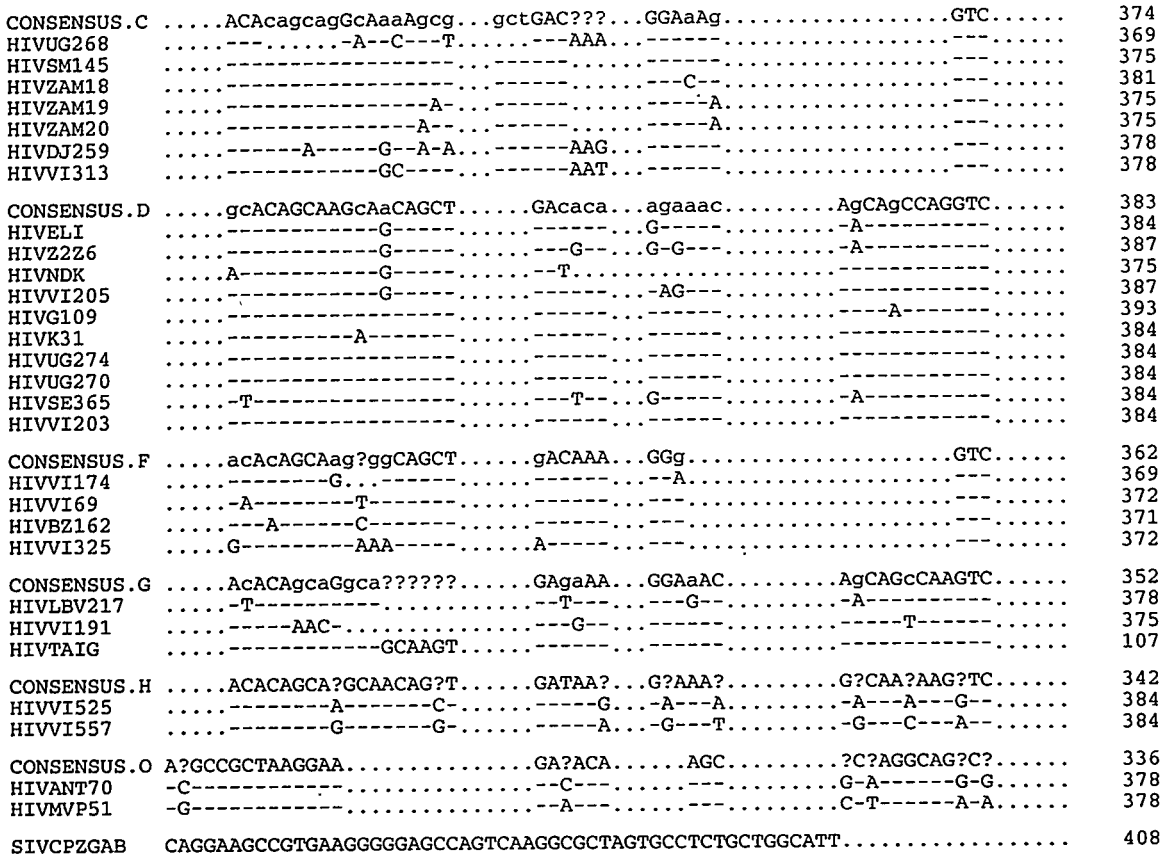
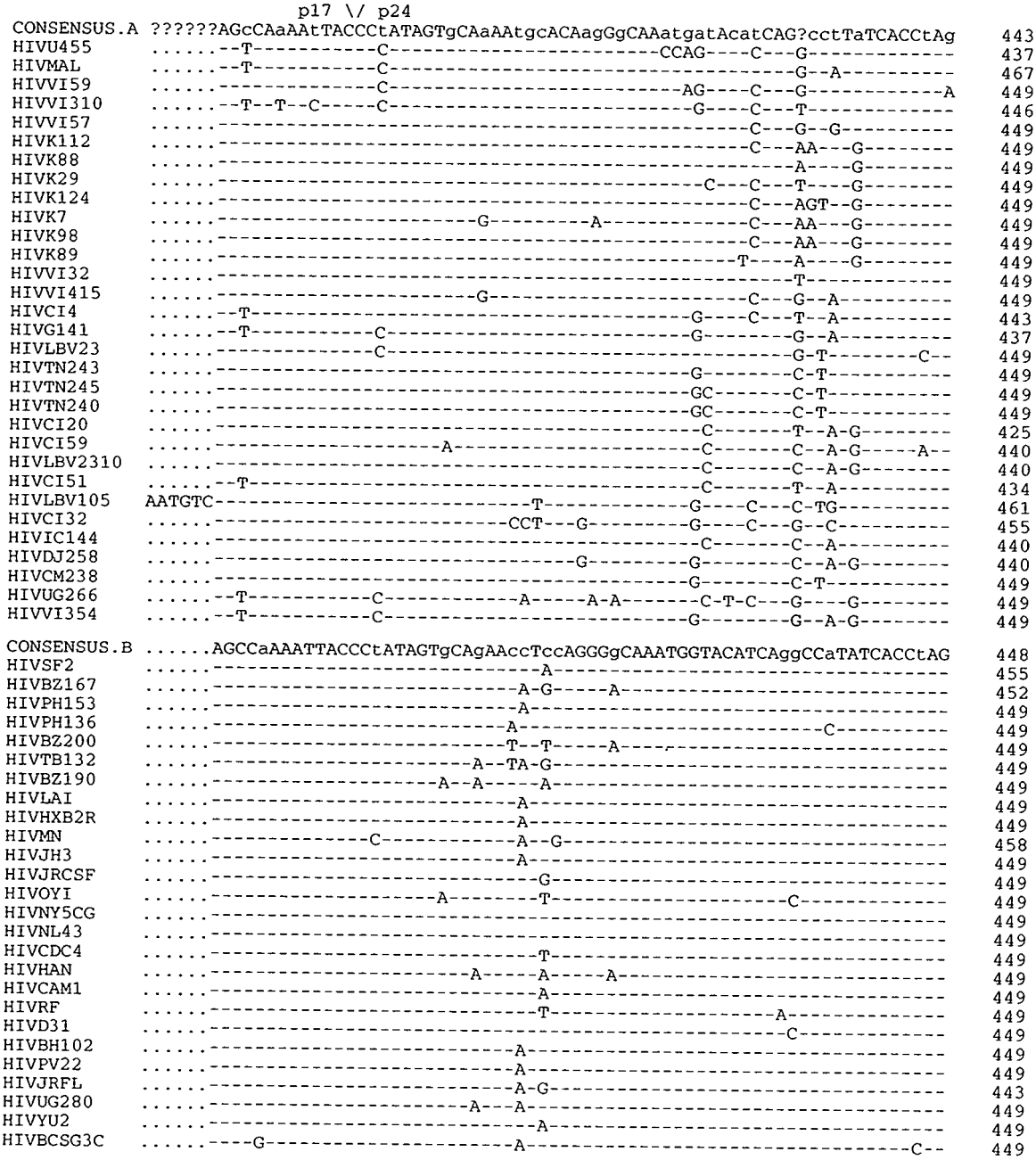
HIVU455 .....----------.....AA----...----G-..... 372
HIVMAL CAGCTG----------.....-C----...AA----.....-------GT---..... 402
HIVVI59 .....----------.....AA----...------.....----A---G---..... 384
HIVVI310 .....-A----------A----.....-A----...---.....-------G---..... 381
HIVVI57 .....-----A----------.....-A----...------.....-------A---..... 384
HIVK112 .....-----A----------.....-AT---...-A--G-.....-------G---..... 384
HIVK88 .....-----A----------.....-A----...------.....-------G---..... 384
HIVK29 .....-----A----------.....-CT---...------.....-------G---..... 384
HIVK124 .....-----A----------.....-A----..!------.....-------G---..... 384
HIVK7 .....-----A----------.....-A----...------.....-------A---..... 384
HIVK98 .....GA---A----------.....-A----...------.....-------G---..... 384
HIVK89 .....-----A----------.....-AT---...------.....-A------G--T..... 384
HIVVI32 .....G----A----------.....-A----...------.....---G----A---..... 384
HIVVI415 .....-----A----------.....-G----...------.....-------C---..... 384
HIVCI4 .....----------.....-A----...------.....-----AC-G---..... 378
HIVG141 .....----------.....-C----...----G-.....--G----GTAC-..... 372
HIVLBV23 .....----------.....-A----...------.....G-------A---..... 384
HIVTN243 .....----------.....-G----...----G-.....-------A---..... 384
HIVTN245 .....----------.....-G----...----G-.....-------A---..... 384
HIVTN240 .....----------.....-G----...----G-.....-------A---..... 384
HIVCI20 .....A--------.....-C----...----G-.....--- 360
HIVCI59 .....----------.....-C----...----G-.....G--..... 375
HIVLBV2310 .....----------.....-C----...----G-.....--- 375
HIVCI51 .....----------.....-CA---...----G-.....--- 369
HIVLBV105 .....----------.....-A----...----G-.....---A---G-G-AGCCAA 390
HIVCI32 CAGCTG-C...--A---------.....-C----...----G-AAT..... 390
HIVIC144 .....----------T---.....-T----...----G-.....--- 375
HIVDJ258 .....----------G---.....-C----...----G-.....--- 375
HIVCM238 .....----------.....-G----...----G-.....-------A---..... 384
HIVUG266 .....----------T------.....AA----...------.....----A---G---..... 384
HIVVI354 .....----------.....-C----...-A----.....-------G---..... 384
CONSENSUS.B .....gcacagcaAgcaGCAgct??????gaCaCA...GgAaaC?????????agcAgccAgGTc..... 383
HIVSF2 .....----------GCAGCT-G----...------.....----------..... 390
HIVBZ167 .....----------A...GCT---G--...----C-.....----------..... 387
HIVPH153 .....----------.....------...----G-.....T----------T..... 384
HIVPH136 .....----------.....------...------.....-AG---------..... 384
HIVBZ200 .....----------C------.....------...------.....------A-----..... 384
HIVTB132 .....----------.....A-----...-A----.....----------T..... 384
HIVBZ190 .....A----------.....------...------.....-A----------..... 384
HIVLAI .....----------.....------...---C--.....----------..... 384
HIVHXB2R .....----------.....------...---C--.....----AT------..... 384
HIVMN .....----------.....------...------AGAGGAAAC--------A---..... 393
HIVJH3 .....----------.....------...------.....------A-----..... 384
HIVJRCSF .....----------.....------...------.....----------..... 384
HIVOYI .....---------A--------.....------...------.....----------..... 384
HIVNY5CG .....----------.....------...------.....----------..... 384
HIVNL43 .....----------.....------...------.....-A----------..... 384
HIVCDC4 .....----------.....------...------.....----------..... 384
HIVHAN .....----------A-------.....---G--...------.....--A-A-------..... 384
HIVCAM1 .....----------G------.....-G----...------.....----------..... 384
HIVRF .....----------.....------...------.....G----------..... 384
HIVD31 .....-------C--------CG-.....---G--...------.....-A----------..... 384
HIVBH102 .....----------.....------...---C--.....-----T------..... 384
HIVPV22 .....----------.....------...---C--.....-----T------..... 384
HIVJRFL .....G----------.....------...------.....----------..... 378
HIVUG280 .....-A---------G------.....-G----...------.....----------..... 384
HIVYU2 .....----------.....------...------.....----------..... 384
HIVBCSG3C .....----------.....------...------.....----------..... 384


CONSENSUS.C .....ACAcagcagGcAaaAgcg...gctGAC???...GGAaAg.....GTC..... 374
HIVUG268 .....---.....-A--C---T.....---AAA...------.....---..... 369
HIVSM145 .....----------...------.....------.....---..... 375
HIVZAM18 .....----------...------.....---C--.....---..... 381
HIVZAM19 .....----------A-...------.....-----A.....---..... 375
HIVZAM20 .....----------A--...------.....-----A.....---..... 375
HIVDJ259 .....------A-----G--A-A...------AAG...------.....---..... 378
HIVVI313 .....----------GC----...------AAT...------.....---..... 378
CONSENSUS.D .....gcACAGCAAGcAaCAGCT......GAcaca...agaaac.....AgCAgCCAGGTC..... 383
HIVELI .....----------G-----.....------...G-----.....-A-----..... 384
HIVZ2Z6 .....----------G-----.....---G--...G-G---.....-A-----..... 387
HIVNDK .....A----------G-----.....--T.....----------..... 375
HIVVI205 .....----------G-----.....------...-AG---.....----------..... 387
HIVG109 .....----------.....------...------.....----A-------..... 393
HIVK31 .....----------A-------.....------...------.....----------..... 384
HIVUG274 .....----------.....------...------.....----------..... 384
HIVUG270 .....----------.....------...------.....----------..... 384
HIVSE365 .....-T----------.....---T--...G-----.....-A-----..... 384
HIVVI203 .....----------.....------...------.....----------..... 384
CONSENSUS.F .....acAcAGCAag?ggCAGCT......gACAAA...GGg.....GTC..... 362
HIVVI174 .....--------G...------.....------...--A.....---..... 369
HIVVI69 .....-A--------T-------.....------...---.....---..... 372
HIVBZ162 .....---A------C-------.....------...---.....---..... 371
HIVVI325 .....G---------AAA-----.....A-----...---.....---..... 372
CONSENSUS.G .....AcACAgcaGgca??????.....GAgaAA...GGAaAC.....AgCAGcCAAGTC..... 352
HIVLBV217 .....-T----------.....--T---.....---G--.....-A-----..... 378
HIVVI191 .....-----AAC-.....---G--...------.....-----T------..... 375
HIVTAIG .....----------GCAAGT.....------...------.....----------..... 107
CONSENSUS.H .....ACACAGCA?GCAACAG?T.....GATAA?...G?AAA?.....G?CAA?AAG?TC..... 342
HIVVI525 .....--------A-------C-.....-----G...-A---A.....-A---A---G--..... 384
HIVVI557 .....--------G-------G-.....-----A...-G---T.....-G---C---A--..... 384
CONSENSUS.O A?GCCGCTAAGGAA.....GA?ACA.....AGC.....?C?AGGCAG?C?..... 336
HIVANT70 -C----------.....--C---.....---.....G-A------G-G..... 378
HIVMVP51 -G----------.....--A---.....---.....C-T------A-A..... 378
SIVCPZGAB CAGGAAGCCGTGAAGGGGGAGCCAGTCAAGGCGCTAGTGCCTCTGCTGGCATT..... 408

HIV1 GAG


p17 \/ p24
CONSENSUS.A ??????AGcCAaAAtTACCCtATAGTgCAaAAtgcACAagGgCAAatgatAcatCAG?cctTaTCACCtAg 443
HIVU455 .....--T----------C----------CCAG----C---G---------- 437
HIVMAL .....--T----------C----------G--A---------- 467
HIVVI59 .....----------C----------AG----C---G----------A 449
HIVVI310 .....--T--T--C-----C----------G----C---T---------- 446
HIVVI57 .....----------C---G--G---------- 449
HIVK112 .....----------C---AA---G--------- 449
HIVK88 .....----------A----G--------- 449
HIVK29 .....----------C---C---T----G--------- 449
HIVK124 .....----------C---AGT--G--------- 449
HIVK7 .....----------G---------A----------C---AA---G--------- 449
HIVK98 .....----------C---AA---G--------- 449
HIVK89 .....----------T----A----G--------- 449
HIVVI32 .....----------T---------- 449
HIVVI415 .....----------G----------C---G--A---------- 449
HIVCI4 .....--T----------G----C---T--A---------- 443
HIVG141 .....--T----------C----------G--------G--A---------- 437
HIVLBV23 .....----------C----------G-T--------C-- 449
HIVTN243 .....----------G--------C-T---------- 449
HIVTN245 .....----------GC-------C-T---------- 449
HIVTN240 .....----------GC-------C-T---------- 449
HIVCI20 .....----------C-------T--A-G--------- 425
HIVCI59 .....----------A----------C-------C--A-G-----A-- 440
HIVLBV2310 .....----------C-------C--A-G--------- 440
HIVCI51 .....--T----------C-------T--A---------- 434
HIVLBV105 AATGTC----------T----------G----C---C-TG---------- 461
HIVCI32 .....----------CCT---G---------G----C---G--C---------- 455
HIVIC144 .....----------C-------C--A---------- 440
HIVDJ258 .....----------G---------G--------C--A-G--------- 440
HIVCM238 .....----------G--------C-T---------- 449
HIVUG266 .....--T----------C----------A-----A-A-------C-T-C---G----G--------- 449
HIVVI354 .....--T----------C----------G--------G--A-G--------- 449
CONSENSUS.B .....AGCCaAAATTACCCtATAGTgCAgAAccTccAGGGgCAAATGGTACATCAggCCaTATCACCtAG 448
HIVSF2 .....----------A---------- 455
HIVBZ167 .....----------A-G-----A---------- 452
HIVPH153 .....----------A---------- 449
HIVPH136 .....----------A----------C---------- 449
HIVBZ200 .....----------T--T-----A---------- 449
HIVTB132 .....----------A--TA-G---------- 449
HIVBZ190 .....----------A--A-----A---------- 449
HIVLAI .....----------A---------- 449
HIVHXB2R .....----------A---------- 449
HIVMN .....----------C----------A--G---------- 458
HIVJH3 .....----------A---------- 449
HIVJRCSF .....----------G---------- 449
HIVOYI .....----------A--------T----------C---------- 449
HIVNY5CG .....---------- 449
HIVNL43 .....---------- 449
HIVCDC4 .....----------T---------- 449
HIVHAN .....----------A-----A-----A---------- 449
HIVCAM1 .....----------A---------- 449
HIVRF .....----------T----------A---------- 449
HIVD31 .....----------C---------- 449
HIVBH102 .....----------A---------- 449
HIVPV22 .....----------A---------- 449
HIVJRFL .....----------A-G---------- 443
HIVUG280 .....----------A---A---------- 449
HIVYU2 .....----------A---------- 449
HIVBCSG3C .....----G----------A----------C-- 449

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                                p17 \/ p24
CONSENSUS.C .....AGTCAAAATTatCCTATAGTgCAgAATCTcCAAGGGCAAATGgTACAcCAGgCCaTaTCACCTAG  439
HIVUG268    .....----------------------------------------------------------C----------  434
HIVSM145    .....----------------------------------------------------------------------  440
HIVZAM18    .....----------C-----------------------------A----------------------------  446
HIVZAM19    .....----------C----------------------------------------------------------  440
HIVZAM20    .....----------T---------A--------T-----------------T----------------------  440
HIVDJ259    .....----------T---------A-----------------------------C--C----------------  443
HIVVI313    .....----------------------A-----------------------------C----G---------  443

CONSENSUS.D .....AGCCAAAATTAtCCTATAGTgCAaAACcTaCAgGGGCAaATGGTACAcCAgGcCaTaTCACCTAG  448
HIVELI      .....----------------------G----------------------T-----------------  449
HIVZ2Z6     .....----------------------G----------------------T-----------------  452
HIVNDK      .....----------C-----------G----------------------T-----------------  440
HIVVI205    .....----------------------G--------A-------------T-----------------  452
HIVG109     .....--------------------------G-------------------C-G---------------  458
HIVK31      .....-----------------------------------------------T---G---------  449
HIVUG274    .....----------------------------------------------------------------  449
HIVUG270    .....--------------------A------T------------------------------------  449
HIVSE365    .....----------C-----------------------------------A---C----------  449
HIVVI203    .....----------C--------------------------G---------------C----------  449

CONSENSUS.F .....AGTCAaAATTACCCTATAGTACA?AATcTtCAGGGaCAAATGGTACA?CAGgC?aTATCACCTAG  424
HIVVI174    .....-----G-----------------A----------------------T-----T----------  434
HIVVI69     .....----------------------A----------------------C-----C----------  437
HIVBZ162    .....----------------------G----------------------T---T-T----------  436
HIVVI325    .....----------------------G---A-G-----G----------C---C-CC----------  437

CONSENSUS.G .....AGtCAAAATTAtCCTATAGTGCAGAatgcaCAAGGGCAAatGgTACACCAGcCCaTAtCACCTAG  417
HIVLBV217   .....--C----------------------------------------------------------  443
HIVVI191    .....----------------------------------------------------T--A-------  440
HIVTAIG     .....----------C-------------NNATC---------CC-A--------G-------------  172

CONSENSUS.H .....AGTCAAAATTATCC?ATAGTACA?AATGCCCAAGG?CAG??GGTACACCAGGCCATATCACCTAG  402
HIVVI525    .....--------------C--------G----------G---AT-------------------------  449
HIVVI557    .....--------------T--------A----------A---CC-------------------------  449

CONSENSUS.O .....?GTCAAAATTACCCTATAGTA?CAAATGC?CAGGGACAAATGGTACATCA?GCCATCTCCCCCAG  397
HIVANT70    .....G----------------------T-------G--------------------G-------------  443
HIVMVP51    .....A----------------------A-------A--------------------A-------------  443

SIVCPZGAB   .....AGTGGAAATTACCCCCTCGTACAAAATGCTCAAGGGCAGATGGTGCATCAGGCCATCTCACCCAG  473
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HIV1 GAG

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CONSENSUS.A gACttTgaAtGCATgGGTgAAaGtaaTAGAagAaAagGcTTTcAgcCcAGAaGTaATACCCAtGTTctCaG  514
HIVU455     ---C--------------------G-------C------------------------------T----  508
HIVMAL      ------------------------------------------------------G---------------  538
HIVVI59     ---C--A--C----A----------G---------------------------------------------  520
HIVVI310    ------------------------------------G---------------G--------------T----  517
HIVVI57     --------------------G-----------------------------------------------------  520
HIVK112     ------------------A-----------------------------------------------------G-  520
HIVK88      ------------------A-----------------------------------------------------  520
HIVK29      ------------------A-----------------------------------------------------  520
HIVK124     ----C-------------A-----------------------------------------------------  520
HIVK7       ------A-------A---A-----------------------------T------------------T----  520
HIVK98      ------A-----------A-----------------A-------------------------------------  520
HIVK89      ---A--A-----------A-----------------------------------------------------  520
HIVVI32     ----------------------------------------T------------------C--------  520
HIVVI415    ------------------A-----------------------------------------------------  520
HIVCI4      ------------------A-----------------------------------------------T----  514
HIVG141     ------A-----------------------------------------------------------------  508
HIVLBV23    ---CC--------------------C-----------------T------------------------A---  520
HIVTN243    A------------------A------G------------G---T-A-------------------------  520
HIVTN245    A------------------------G------------G---T-A-------------------------  520
HIVTN240    A------------------------G------------G---T-A-------------------------  520
HIVCI20     ---------------------G--------G-------------------------------------TA---  496
HIVCI59     ---------------------G-----------------------------------------------TA---  511
HIVLBV2310  ---------------------G-----------------------------------------------T----  511
HIVCI51     ------A--------------G-C-----------G------T----------------------T----  505
HIVLBV105   A-----AG-----------A--G--G--------G----G-----A-------------------------  532
HIVCI32     ------------------A--------------G--------------------G-----------TA---  526
HIVIC144    ------A--------------G-----------------------------------------------T----  511
HIVDJ258    ---------------------G--------G-----------------------------------TA---  511
HIVCM238    A------------------A------G-----A------G---T-A-------------------------  520
HIVUG266    ---C--A-------A---A------G----G-----------------------------------T----  520
HIVVI354    ------A-----------A------------------A-G------T-------------------------  520

CONSENSUS.B AACTTTAAATGCATGGGTAAAAGTagTaGAAGAgAAGGCtTTcAGCCCaGAaGTaATACCCATGTTTtCAG  519
HIVSF2      ----------------------------------A-----------------------------------  526
HIVBZ167    ----------------------GA------------------------------------------------  523
HIVPH153    ------------------------------------------------------------------------  520
HIVPH136    ------------------------------------------------------------------------  520
HIVBZ200    ----------------------------------------------------G-------------------  520
HIVTB132    ----------------------------------A-----------------G-------------------  520
HIVBZ190    ----------------------------------A-------------------------------------  520
HIVLAI      ----------------------------------------------------G-------------------  520
HIVHXB2R    ----------------------------------------------------G-------------------  520
HIVMN       ------------------------------------------------------------------------  529
HIVJH3      ------------------------------------T-------------------------------------  520
HIVJRCSF    ----------------------A-----------------------C---------------------------  520
HIVOYI      ------------------------------------------------------------------------  520
HIVNY5CG    ------------------------------------------------------------------------  520
HIVNL43     ------------------------------------------------------------------------  520
HIVCDC4     ----------------------A-----------------------------T------------G---  520
HIVHAN      ----------------------G-------------------------------------------------  520
HIVCAM1     ------------------------------------------------------------------------  520
HIVRF       ----------------------------------------T---------------------------------  520
HIVD31      ------------------------------------------------------------------------  520
HIVBH102    ------------------------------------------------------------------------  520
HIVPV22     ----------------------------------------------------G-------------------  520
HIVJRFL     ------------------------------------------C---------------------------  514
HIVUG280    ------------------------------------T---------------------------------  520
HIVYU2      ----------------------G-----------G---------------------------------  520
HIVBCSG3C   ------------------------------------------------------------------------  520
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CONSENSUS.C AACtTTGAATGCaTGGGTaAAAGTAATAGAgGagAAgGCtTTcAGCCcagag?taatacccatgtttacag  509
HIVUG268    ------------------------------------A-------------------G-----------------  505
HIVSM145    ---C--------------------------A--------C--T-----G---A-------------------  511
HIVZAM18    --------------------------------GA--A--C--T---------A-------------------  517
HIVZAM19    ---A--------------G-------------NA---------------.....................  489
HIVZAM20    ------------------------------------------A----AGAG-A-----------------  511
HIVDJ259    ------------------------------------------------AG------------------  514
HIVVI313    ------------G-----------------------------------G---G-----------------  514

CONSENSUS.D aACtTTgAAcGCATGGGTaaAAGTAATAGAaGA?AAGGctTTcAgcCCaGAaGTaAtACCCATGTTTtCAG  518
HIVELI      ---------------------------------A-------------------------------------  520
HIVZ2Z6     ---------------------------------A-------------------------------------  523
HIVNDK      ---------------------------------A-----C--------G-----------------------  511
HIVVI205    ------A--T---------G-------------A--------------C-----G-C---------------  523
HIVG109     ---------------------------------G----------A------G---------------G---  529
HIVK31      G--C--------------------------G--G--------T-----------------------------  520
HIVUG274    ---------T--------------------G--G--------T-------------------------A---  520
HIVUG270    ------------------------------G--G--------T-----------------------------  520
HIVSE365    G-----------------C--------------G----A---------------G------------A---  520
HIVVI203    ------------------------------G--A----------AT--------------------------  520

CONSENSUS.F AACTTTAAATGCATGGGTaAAgGTgATAGAAGAgAAgGCTTTtAGcCCAGAAGTAATACCCATGTTtTCAG  495
HIVVI174    ---------------------------------------A-----------------------------C----  505
HIVVI69     ------------------------------------------------T-------------------------  508
HIVBZ162    ------------------------------------------------------------------------  507
HIVVI325    ------------------G--A--A--------A--------C-----------------------------  508

CONSENSUS.G aACTTTgAATGCATGGGTAAAAGTAgTAGAAGAAAAGgcCTTCAGTCCAGAAGTAATACCCATGTTTTCAG  488
HIVLBV217   G-----A-------------------------------------------------------------------  514
HIVVI191    ------------------------A-----------AA---------------------------------  511
HIVTAIG     ------------------------------------------------------------------------  243

CONSENSUS.H GACCTTAAATGCATGGGTAAAAGTAGTAGAAGA?AAGGCTTTTAGCCCAGAAGTAATACC?ATGTTTTCAG  471
HIVVI525    ---------------------------------A-------------------------T-----------  520
HIVVI557    ---------------------------------G-------------------------C-----------  520

CONSENSUS.O GACTTTAAATGCATGGGTAAAGGCAGTAGAAGA?AA?GCCTTTAACCCTGAAAT?ATTCCTATGTT?ATGG  464
HIVANT70    ---------------------------------A--A-----------------C-----------C-----  514
HIVMVP51    ---------------------------------G--G-----------------T-----------T-----  514

SIVCPZGAB   AACCTTGAATGCATGGGTAAAAGTGGTAGAGGAAAAGGCATTTAGCCCTGAGGTAATACCAATGTTTTCAG  544
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CONSENSUS.A caTTaTCAGAgGGaGCcACccCaCAagATtTaAAtatgATGcTgAAcatAGTggggGGaCAcCAgGCAGCt  585
HIVU455     ----------------------------------------------TG----------------------  579
HIVMAL      ------------G-------------------------------------T--A---------------  609
HIVVI59     A---------A-------------------------------A--TG----A--A---------------  591
HIVVI310    ------------------------------------------------T-----A----------------C  588
HIVVI57     ----------A--------------------G-------------------------G------------  591
HIVK112     ----------A---------------------------------A--------------------------  591
HIVK88      ----------A--------------------------------------------------------------  591
HIVK29      ----------A-----------------------------------------------------T--------  591
HIVK124     ----------A--------------------------------------------------------------  591
HIVK7       ----------A-----------------------G----------------A--------------------  591
HIVK98      -T--------A-----------------------G--------------------------------------  591
HIVK89      ----------A-----------------------------------T--------------------------  591
HIVVI32     ----G-----A---------------------------------A--T--------------------------  591
HIVVI415    ----------A--------T-------------------------------A--------------------  591
HIVCI4      ----------A-----------------------------------T-----------------A------  585
HIVG141     ----------A-------------------------------------T--A---------------------  579
HIVLBV23    ----------------------------------------------------------------------  591
HIVTN243    ------------------------------------------A--T-----------------------A  591
HIVTN245    ------------------------------------------A--T-----------------------A  591
HIVTN240    ------------------------------------------T-A--T-----------------------A  591
HIVCI20     ------------------------------------------A--------------------A-----A  567
HIVCI59     ------------------------------G-----------A-------------------------A  582
HIVLBV2310  ------------------------------G-----------A-------------------------A  582
HIVCI51     ----------------------G-------------------A-------------------------A  576
HIVLBV105   ----------------T----------------------------------------------------  603
HIVCI32     ----------A--------------G---------C-CC---T-A----C---A-----------A-----C  597
HIVIC144    ----------------------G--------------------A-------------------------A  582
HIVDJ258    ----------------------------C-------------A-------------------------A  582
HIVCM238    ------------------------------------------A--T----------------------A  591
HIVUG266    ----------A---------T-------------------------TG----A-AA---------------  591
HIVVI354    --------------------------A--C-------A-----A--------TAAA-----T---------  591

CONSENSUS.B CATTAtCAGAAGGaGCCACCCCaCAAGATtTAAAcACcATGcTAAACACAGTGGGGGGACAtCAAGCAGCc  590
HIVSF2      ----------------------------------------------------------------------  597
HIVBZ167    ------------------------------------------T-------------------C---------  594
HIVPH153    ----------------------------------------------------------------------  591
HIVPH136    ------------------------------------T---------------------------------  591
HIVBZ200    ----------------------------------------------------------------------  591
HIVTB132    ----------------------------------------------------------------------  591
HIVBZ190    -----G----------------------------------------------------------------  591
HIVLAI      ----------------------------------------------------------------------  591
HIVHXB2R    ----------------------------------------------------------------------  591
HIVMN       ----------------------------------------------------------------------  600
HIVJH3      ----------------------G---------------------------------------------------  591
HIVJRCSF    ----------------------------------------------------------------------T  591
HIVOYI      -----G-----------------------C---------------------------------------  591
HIVNY5CG    ---------------------------------T------------------------------------  591
HIVNL43     ------------------------------------T---------------------------------  591
HIVCDC4     -------------C--------------------------------------------------------  591
HIVHAN      ----------------------------------------------------------------------  591
HIVCAM1     ----------------------------------------------------------------------  591
HIVRF       ----------------------------------------------------------------------  591
HIVD31      ----------------------------------------------------------------------  591
HIVBH102    ----------------------------------------------------------------------  591
HIVPV22     ----------------------------------------------------------------------  591
HIVJRFL     ----------------------------------------------------------------------  585
HIVUG280    ----------------------------------------------------------------------  591
HIVYU2      ------------------------------------------------------------C---------  591
HIVBCSG3C   ----------------------------------------------------------------------T  591
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CONSENSUS.C cattatcagaaggagccaccccacaagatttaaacaccatgttaaatacagtgggggacatcaagcagcc  580
HIVUG268    ------------------------------------------C-----------------------------  576
HIVSM145    ----------------------G-------------------------------------------------  582
HIVZAM18    -------------------------------------------------------------------------  588
HIVZAM19    .........................................................................  489
HIVZAM20    ----------------------------C-------------------------------C---------  582
HIVDJ259    -------------------------------------------------------------------------  585
HIVVI313    --------------------------------G--------------------A------------------  585

CONSENSUS.D CAtTaTCAGAAGGAGCCACcCCACAaGATtTAAAcaCCATGcTAAAcACaGtGGGGGGaCATCAaGCAGCc  589
HIVELI      -------------------------------------------------------------------------  591
HIVZ2Z6     ----------------------------------T--------------------------------------  594
HIVNDK      -------------------------------------------------------------------------  582
HIVVI205    --------------------T-----G-----------------------------------------T-----T  594
HIVG109     ----G-----------------------C-----------T----T----C-------------------T  600
HIVK31      ---------------------------------------------------G--------G------------  591
HIVUG274    ------------------------G-----------------------------------------------  591
HIVUG270    ------------------------------------G-------------------------------------  591
HIVSE365    --C----------------------G---------------T-----------------------------  591
HIVVI203    -------------------------------------------------T-----------------------  591

CONSENSUS.F CATTAtCAGAaGG?GCCACtCCACAAGATTTAAACACCATGcTAAA?ACAGTGGGGGGACATCAaGCAGC?  563
HIVVI174    -------------G-----C--------------------------T----------------------T  576
HIVVI69     -------------A--------------------------------C-----------------G-----C  579
HIVBZ162    -------------G-----------------------T----T-------------------------C  578
HIVVI325    -----G----T--A--------------------------C-----------------------T  579

CONSENSUS.G CATTATCAGAAGGaGCCACcCCACAAGATtTAAAtAcCatGctAAAcACAGTGGGGGGgCATCAAGCAGCT  559
HIVLBV217   -------------------T---------C----------------T-----------A------------  585
HIVVI191    -------------------------------------------------------------------------  582
HIVTAIG     -------------G--------------------C-T-TA-TC-------------------------------  314

CONSENSUS.H CATTATCAGAAGGAGCCACCCCACAAGA?TTAAATGCCATG?TAAATA?AGTGGGGGG?CATCAAGCAGCC  538
HIVVI525    ----------------------------C------------C------C---------G------------  591
HIVVI557    ----------------------------T------------T------T---------A------------  591

CONSENSUS.O CATT?TCAGA?GG?GC??T??CCTATGATAT?AATAC?ATGCT?AATGCCATAGG?GGACA?CAAGG?GCT  522
HIVANT70    ----G-----G--A--AA-TT----------T-----T-----A-----------A-----T-----A---  585
HIVMVP51    ----A-----A--G--TG-CC----------C-----C-----G-----------G-----C-----G---  585

SIVCPZGAB   CTCTATCAGAGGGAGCCTTACCTCAGGATGTTAACACCATGTTAAATGCAGTAGGGGGACATCAAGGAGCC  615
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HIV1 GAG

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CONSENSUS.A ATGCAaATGtTaAAagAtaCcATcAATGagGAaGCTGCAGaaTgGGAcAGg?tACAtCCAGTaCatGCAgG  655
HIVU455     ----------------------------------------G---------T----------G--------  650
HIVMAL      ----------------------------------------C---------G-------------------  680
HIVVI59     ----------------------------A-------------A-------T----------G------A-  662
HIVVI310    ------------------------------------------------G-------------G------  659
HIVVI57     ------------------------------------------------T-------------------  662
HIVK112     ------------------------------------------------T-------------------  662
HIVK88      ------------------------------------------------T-------------------  662
HIVK29      ------------------------------------------------T-------------------  662
HIVK124     ---------------A------------------------------------T-----------------  662
HIVK7       ----------------C-----------A-------------A-------T-------------------  662
HIVK98      ----------------C-----------A----------------T---T-------------------  662
HIVK89      ------------------------------------------------T-------------------  662
HIVVI32     ------------------G--------------------G----------T-------------------  662
HIVVI415    --------------------A------------------------------T-------------------  662
HIVCI4      --------------------------G----------------------G-------------------  656
HIVG141     ------------------------------------------C---------AC----------------  650
HIVLBV23    ----------------------T--------G-----------------G-------------G------  662
HIVTN243    ------------------A------------------------------T---G----C-----------  662
HIVTN245    ------------------A------------------------------T---G----C-----------  662
HIVTN240    ------------------A------------------------------T---G----C-----------  662
HIVCI20     -----G----------------------A---------------------G-------------C------  638
HIVCI59     -----G-------------------------------------------G-------------G------  653
HIVLBV2310  ------------------------------------------------AG-------------------  653
HIVCI51     -----G--------G-----------------------------------AAC-----------------  647
HIVLBV105   ------------------------------------------------AC-----------G------  674
HIVCI32     ------------------------------------------------T--AG-----------------  668
HIVIC144    -----G-----G-------------------------------------G-------------------  653
HIVDJ258    -----G-------------------------------------------G-------------------  653
HIVCM238    ------------------A------------------------------T---G----C-----------  662
HIVUG266    ---------C----G--------------A-------------A-------T----------G--A---A-  662
HIVVI354    ------------------------------------------------A-------------G------  662

CONSENSUS.B ATGCAAATGtTAAAAGAgACcATCAATGAGGAAGCTGCAGAATgGGATAGAtTgCAtCCAGtgCAtGCAGG  661
HIVSF2      --------------------T------------------------------G-------------------  668
HIVBZ167    ------------------T-------------------------------------------------------  665
HIVPH153    -------------------------------------------------------------------------  662
HIVPH136    -------------------------------------------------------------------------  662
HIVBZ200    ------------------A-------------------------A-------------------------  662
HIVTB132    -------------------------------------------------------------------------  662
HIVBZ190    -------------------------------------------------------------------------  662
HIVLAI      ------------------------------------------------G-------------------  662
HIVHXB2R    ------------------------------------------------G-------------------  662
HIVMN       -------------------------------------------------------------------------  671
HIVJH3      ----------------A-----------------------------------------C---G------  662
HIVJRCSF    ---------C-------A-------------------------------------------------------  662
HIVOYI      ------------------------------------------------------------A--------  662
HIVNY5CG    -------------------------------------------------------------------------  662
HIVNL43     -------------------------------------------------------------------------  662
HIVCDC4     -------------------------------------------------------------------------  662
HIVHAN      ------------------A-----------------------------------C--------------  662
HIVCAM1     -------------------------------------------------------------------------  662
HIVRF       --------------------T------------------------------------------------------  662
HIVD31      -------------------------------------------------------------------------  662
HIVBH102    ------------------------------------------------G-A------------------  662
HIVPV22     ------------------------------------------------G-------------------  662
HIVJRFL     ---------C-------------------------------------------------------------  656
HIVUG280    -------------------------------------------------------------------------  662
HIVYU2      -------------------------------------------------------------------------  662
HIVBCSG3C   ------------------------------------------------------------A------  662
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CONSENSUS.C atgcaaatgttaaaagataccatcaatgaggaggctgcagaatgggatag?ttacatccagt?catgcagg   649
HIVUG268    ----------------C-------------------------------G-----------G--------   647
HIVSM145    ---------------------------------------------------A-----------A--G-----   653
HIVZAM18    -----G-----------------------------------------------A-----------A--------   659
HIVZAM19    ..........................................................................   489
HIVZAM20    ----------------C-------------------------------AA----------A--------   653
HIVDJ259    ---------------------------------------------------G-----------G--------   656
HIVVI313    --------------------A-------------------------------G-----------G--G-----   656

CONSENSUS.D ATGCAAATGtTAAAaGAgACCATCAaTGAgGAAGCTGCAGAATGGGAtAGgcTACATCCAGtgCATGCAGG   660
HIVELI      ---------C------------------A----------------------T-------------------   662
HIVZ2Z6     ---------C----G-------------------------------------T-------------------   665
HIVNDK      ---------C-------------------C-----------------C--AT-------------------   653
HIVVI205    ---------C---------------T-----------------------------------------------   665
HIVG109     ---------------------------------------------------------------------------   671
HIVK31      ---------------------------------------------------------C---------   662
HIVUG274    ----------------A-------------------------------G-------------------   662
HIVUG270    ---------------------------------------------------------A--------   662
HIVSE365    ----------------A---------------------------------AT-------------------   662
HIVVI203    ---------------------------------------------------------------------------   662

CONSENSUS.F ATGCAAATGTTAAAAGAcACcATCAATGAGGAaGCTGCAGAATGGGAcAGaTTACAtCCAGtGCA?GCAGG   633
HIVVI174    ---------------------------------------------------------------G-----   647
HIVVI69     ---------------------------------------------------T-----------T-----   650
HIVBZ162    ---------------------------------------------------------C---G-----   649
HIVVI325    ----------------T--T----------G----------------G-----C--------T-----   650

CONSENSUS.G ATGCAAATGctAAAGGATACtATCAATGAGGAaGCTGCAGAGTGGGAcAGGATACATCCACcACAgGCAGG   630
HIVLBV217   ---------------------------------------------T-------------A---------   656
HIVVI191    --------------------------------G-----------------------------------   653
HIVTAIG     ---------TC---------A-------------------------------------------A-----   385

CONSENSUS.H ATGCAAAT??TAAAAGATACAATCAATGAGGAAGCTGCAGAATGGGATAGG?TACATCCAGTGCATGCAGG   606
HIVVI525    --------AC-----------------------------------------C-------------------   662
HIVVI557    --------GT-----------------------------------------G-------------------   662

CONSENSUS.O TTACAAGTG?T?AAGGAAGTAATCAATGAGGAAGCAG?AGA?TGGGATAGAACTCA?CCACCA?C??T?GG   584
HIVANT70    ---------C-A-------------------------T---G--------------C------C-GG-A--   656
HIVMVP51    ---------T-G-------------------------C---A--------------T------G-AA-G--   656

SIVCPZGAB   ATGCAAGTGCTAAAGGAAGTCATTAATGAGGAAGCCGCCGAGTGGGATCGCTTACATCCCACTCATGCTGG   686
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HIV1 GAG

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CONSENSUS.A GCCTattcCaCcagGcCAgaTgAGaGAACCAAggGGaAGtGAcATAGCAGGaacTACTAGtAcCctTcaaG  726
HIVU455     ------------------------------------------------------------C---G------  721
HIVMAL      ---------C-----------------------A-----------------------------------  751
HIVVI59     ------------------------------AA-------------------------------------  733
HIVVI310    ----G-----------------------------------------------------------------  730
HIVVI57     ------------------A-----------------G----------------------C----C-----  733
HIVK112     ------------------------------------------------------------C-----C-----  733
HIVK88      ------------------------------------------------------------C-----C-----  733
HIVK29      ------------------------------------------------------------C-----C-----  733
HIVK124     ---------------------------------------C--------------------C-----C-----  733
HIVK7       ------C--------------------------A-----------------------------C-----C-----  733
HIVK98      ------------------------------------------------------------C-----C-----  733
HIVK89      ------------------A-----------------------------------------C-----C-----  733
HIVVI32     ------------------A-----------------------------------------C-----C-----  733
HIVVI415    ------------------A-------------------------------------------AC-----C-----  733
HIVCI4      -----------T-----------------------------------------------------------  727
HIVG141     ----GC------------A-----------------------------------------------------  721
HIVLBV23    ----TA--------------C----G-----------------------------------------GC--  733
HIVTN243    ------------------------G-----------------------------------------------  733
HIVTN245    ------------T-----------G-----------------------------------------------  733
HIVTN240    ------------------------G-----------------------------------------------  733
HIVCI20     -----------------------------------------------------------------------  709
HIVCI59     ------------------------G-------------------------G----------A--------  724
HIVLBV2310  ------------------------G-----------------------------------A--------  724
HIVCI51     ------------------------G-------------------------GT-----------------  718
HIVLBV105   -----------------------------------------------------------------------  745
HIVCI32     -------G-----------------------------------T-------------------------G-  739
HIVIC144    ------------------------G-----------------------------------A--------  724
HIVDJ258    ------------------A-----G-----------------------------------------------  724
HIVCM238    ------------------------G-----------------------------------------------  733
HIVUG266    ------------T--------------------A-----------------------------G------  733
HIVVI354    -------------A-T-----A--------------------T--------------------AC-----  733

CONSENSUS.B GCCTaTTgCaCCAGGcCAgATGAGAGAACCAAGGGGAAGTGACATAGCAGGaACtACTAGTACCCTTCAGG  732
HIVSF2      ------------------A-----------------------------------------------------  739
HIVBZ167    ------------------A-----------------------------------------------------  736
HIVPH153    -----------------------------------------------------------------------  733
HIVPH136    ----G----G------------------------------------------------------------  733
HIVBZ200    -----------------------------------------------------------------------  733
HIVTB132    -----------------------------------------------------------------------  733
HIVBZ190    -----------------------------------------------------------------------  733
HIVLAI      -----------------------------------------------------------------------  733
HIVHXB2R    -----------------------------------------------------------------------  733
HIVMN       -------A---------------------------------------------------------------  742
HIVJH3      -----------------------------------------------------------------------  733
HIVJRCSF    ----------------------------------------------------G------------------  733
HIVOYI      -----------------------------------------------------------------------  733
HIVNY5CG    -----------------------------------------------------------------------  733
HIVNL43     -----------------------------------------------------------------------  733
HIVCDC4     -----------------------------------------------------------------------  733
HIVHAN      -----------------------------------------------------------------------  733
HIVCAM1     -----------------------------------------------------------------------  733
HIVRF       ---------------T-------------------------------------C-----------------  733
HIVD31      -----------------------------------------------------------------------  733
HIVBH102    -----------------------------------------------------------------------  733
HIVPV22     -----------------------------------------------------------------------  733
HIVJRFL     ------------------A-----------------------------------------------------  727
HIVUG280    ----------------------------------------------------G------------------  733
HIVYU2      -----------------------------------------------------------------------  733
HIVBCSG3C   ----G-------------------------------------------------------------------  733
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CONSENSUS.C gcctgttgcaccaggccaaaTgAGAGAaCCAAGGGGAAGTGACATAGCAGGAACTACTAGTAcCCTTCAgG  720
HIVUG268    ------------------------------------------------------------------A-  718
HIVSM145    -------------------------C------------------------------------------  724
HIVZAM18    ----AA-------------T-------------------------------------------------  730
HIVZAM19    ..................-------------------------------------------------  541
HIVZAM20    -------------------------------------------------------------------  724
HIVDJ259    ----A-----------------------------------------------------A--------  727
HIVVI313    ------C--------------A-----G-------------------------------------  727

CONSENSUS.D gCCTaTTGCACCAGGcCAgATGAGAGAaCCAAGGGGAAGTGATATAGCaGGAACtACtAGTAcCCTTCAGG  731
HIVELI      -------------------------------------------------------------------  733
HIVZ2Z6     -------------------------------------------------------------------  736
HIVNDK      ----G-------------A-----------------------------------------------  724
HIVVI205    -------------------------------------------------------------------  736
HIVG109     -------------------------------------------------------------------  742
HIVK31      ------------------A-----------------------------------A------------  733
HIVUG274    A--------------A--A-----------------------------C-------------------  733
HIVUG270    ------------------A--------G-----------------------------C----T-----  733
HIVSE365    -------------------------------------------------------------------  733
HIVVI203    -------------------------------------------------------------------  733

CONSENSUS.F gCCTAtCCCACCAGGCCAGAT?AGgGAACCTAGGGGaAGTGAtATAGCtGGAACTACtAGtACCCTTCAGG  703
HIVVI174    ---------------------A--------------------C------------------------  718
HIVVI69     -----A---------------G-------------------------------------------  721
HIVBZ162    A-------------------A---------------------------------------------  720
HIVVI325    ---------------------G--A-----------G-----------A--------C--C-----  721

CONSENSUS.G gCCTATTcCACCAGGcCAGATAAGaGA?CCaAGGGGAAGTGATATAGCAGGaACTACTAGTACCCTaCAGG  700
HIVLBV217   --------------------------C----------------------G--------------G----  727
HIVVI191    A----------------------G--A--G-----------------------------------  724
HIVTAIG     -------G-------T-----------T-------------------------------------  456

CONSENSUS.H GCCTATTCCACCAGGCCA?ATGAGAGAACCAAGGGGAAG?GATATAGCAGGAACTACTAGTACCCTTCAGG  675
HIVVI525    ------------------A--------------------C--------------------------  733
HIVVI557    ------------------G--------------------T--------------------------  733

CONSENSUS.O GCCGTT?CCACCAGGGCAGATAAGGGAACCAACAGGAAGTGACATTGCTGG?ACAACTAGCAC?CAGCAAG  652
HIVANT70    ------G-----------------------------------------G-----------C-------  727
HIVMVP51    ------A-----------------------------------------A-----------A-------  727

SIVCPZGAB   TCCGATAGCCCCAGGACAGCTAAGGGAGCCAAGGGGTAGTGATATAGCAGGGACCACCAGCACACTGCAGG  757
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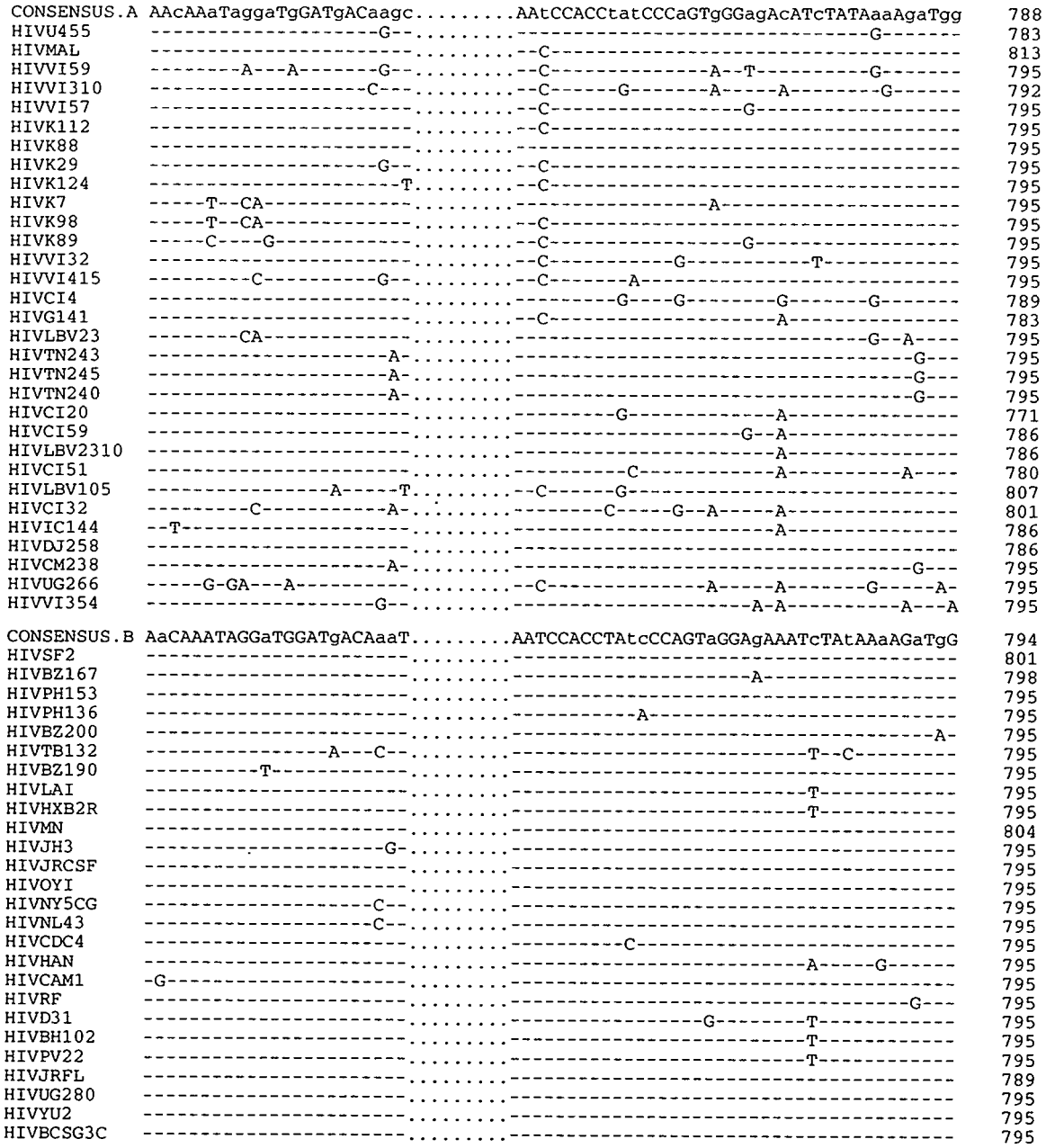
HIV1 GAG


CONSENSUS.A AAcAAaTaggaTgGATgACaagc.....AAtCCACCtatCCCaGTgGGagAcATcTATAaaAgaTgg 788
HIVU455 ----------G--.....----------G------- 783
HIVMAL ----------.....--C---------- 813
HIVVI59 --------A---A-------G--.....--C----------A--T----------G------- 795
HIVVI310 ----------C---.....--C------G-------A-----A--------G------ 792
HIVVI57 ----------.....--C----------G---------- 795
HIVK112 ----------.....--C---------- 795
HIVK88 ----------..... 795
HIVK29 ----------G--.....--C---------- 795
HIVK124 ----------T.....--C---------- 795
HIVK7 -----T--CA----------.....----------A---------- 795
HIVK98 -----T--CA----------.....--C---------- 795
HIVK89 -----C----G----------.....--C----------G---------- 795
HIVVI32 ----------.....--C----------G----------T---------- 795
HIVVI415 ---------C----------G--.....--C-------A---------- 795
HIVCI4 ----------.....---------G----G--------G-------G------- 789
HIVG141 ----------.....--C----------A---------- 783
HIVLBV23 --------CA----------.....----------G--A---- 795
HIVTN243 ----------A-.....----------G--- 795
HIVTN245 ----------A-.....----------G--- 795
HIVTN240 ----------A-.....----------G--- 795
HIVCI20 ----------.....---------G----------A---------- 771
HIVCI59 ----------.....----------G--A---------- 786
HIVLBV2310 ----------.....----------A---------- 786
HIVCI51 ----------.....----------C----------A----------A---- 780
HIVLBV105 ----------A-----T.....--C------G---------- 807
HIVCI32 ---------C----------A-.....--------C-----G--A-----A---------- 801
HIVIC144 --T----------.....----------A---------- 786
HIVDJ258 ----------..... 786
HIVCM238 ----------A-.....----------G--- 795
HIVUG266 -----G-GA---A----------.....--C----------A-----A-------G-----A- 795
HIVVI354 ----------G--.....----------A-A----------A---A 795
CONSENSUS.B AaCAAATAGGaTGGATgACAaaT.....AATCCACCTAtcCCAGTaGGAgAAATcTAtAAaAGaTgG 794
HIVSF2 ----------..... 801
HIVBZ167 ----------.....----------A---------- 798
HIVPH153 ----------..... 795
HIVPH136 ----------.....----------A---------- 795
HIVBZ200 ----------.....----------A- 795
HIVTB132 ----------A---C--.....----------T--C---------- 795
HIVBZ190 ----------T----------.....---------- 795
HIVLAI ----------.....----------T---------- 795
HIVHXB2R ----------.....----------T---------- 795
HIVMN ----------..... 804
HIVJH3 ----------G-.....---------- 795
HIVJRCSF ----------..... 795
HIVOYI ----------..... 795
HIVNY5CG ----------C--..... 795
HIVNL43 ----------C--..... 795
HIVCDC4 ----------.....----------C---------- 795
HIVHAN ----------.....----------A-----G------ 795
HIVCAM1 -G----------..... 795
HIVRF ----------.....----------G--- 795
HIVD31 ----------.....----------G--------T---------- 795
HIVBH102 ----------.....----------T---------- 795
HIVPV22 ----------.....----------T---------- 795
HIVJRFL ----------..... 789
HIVUG280 ----------..... 795
HIVYU2 ----------..... 795
HIVBCSG3C ----------..... 795

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CONSENSUS.C AACAaATAgcaTGGATGACAa?T.........AACCCaCCTaTTCCAGTgGGAGAcATCTATAAAAGATGG  781
HIVUG268    --------AAT----------G-.........----------------------A---------------  780
HIVSM145    --------------------G-.........-------------------------------------  786
HIVZAM18    ----G----------------A-.........---------G-----------------------------  792
HIVZAM19    ----G----------------A-.........---------G-----------------------------  603
HIVZAM20    --------------------GC-.........---------G-------------A---------------  786
HIVDJ259    --------------------G-.........-----C-----------------------------------  789
HIVVI313    --------------------A-.........----------------A---------------------  789

CONSENSUS.D AaCAAaTAG?aTGGATGACAagc.........AAtCCaCCtATCCCAGTAggAgAAATcTAtAAAAgATGG  792
HIVELI      ---------C------------T.........--C-------------------------------------  795
HIVZ2Z6     ---------C-------------.........--C-------------------------------------  798
HIVNDK      ---------C-------------.........--C-------------------------------------  786
HIVVI205    ---------C-------------.........--C---------------AA-A-----------------  798
HIVG109     ---------CC---------GC-.........--------------------------A-------A-----  804
HIVK31      -G-------G-----------A-.........-----------------------------C---------  795
HIVUG274    ---------G-------------.........-----G-----------------------------------  795
HIVUG270    -----G---G-------------.........-------------------------------------  795
HIVSE365    ---------G-----------AT.........--------C-----------------------------  795
HIVVI203    ---------G------------T.........-------------------------------------  795

CONSENSUS.F AACAAATAcaaTGGATGACAAgC.........AAcCCACCTgTCCCAGTGGGAGAaATCTATAAAAGATGG  765
HIVVI174    --------------------A-.........-------------------------------------  780
HIVVI69     ----------G------------.........--T------A------------C---------------  783
HIVBZ162    ----------------------.........-------------------------------------  782
HIVVI325    --------AC-------------.........-------------------------------------  783

CONSENSUS.G AACAAATaAGATGGATGACCAGc.........AATCCACCTATCCCAGTgGGAGAaATTTATAAAAGATGG  762
HIVLBV217   ----------------------.........-------------------------------------  789
HIVVI191    -------C--------------T.........----------------------C---------------  786
HIVTAIG     ----------------------.........-----------------A---------------------  518

CONSENSUS.H AACAAATAGCATGGATGACA?GC.........AATCC??CTATCCCAGTGGGAGACATCTATAAAAGATGG  734
HIVVI525    --------------------G--.........-----AG---------------------------------  795
HIVVI557    --------------------A--.........-----CC---------------------------------  795

CONSENSUS.O AGCAAATT???TGGACTAC?AG?...????C?AAC????CTATCCCAGTAGGAGACATCTATAGAAAATGG  706
HIVANT70    --------CAC--------C--G......C-C---CAAC---------------------------------  792
HIVMVP51    --------ATA--------T--A...GGGG-T---...T---------------------------------  792

SIVCPZGAB   AACAAATTGGGTGGACAACAGCA.........AATCCTCCCATCCCAGTAGGGGATGTTTATAGAAGATGG  819
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HIV1 GAG

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CONSENSUS.A ATAaTccTgGGatTAAATAAaATAGTaAGaATGTATAGcCCTgttAGCATttTgGAcaTAAgaCAAgggCC  859
HIVU455     ------------------------------------------------------------------------  854
HIVMAL      ----------------------------------------C-------------------------------  884
HIVVI59     --------A-------------------------------------A------------G--------A----  866
HIVVI310    ------------------------------------------------C----------------A--  863
HIVVI57     ------------------------------------------------------------A---------  866
HIVK112     ------------------------------------------------------T----A---------  866
HIVK88      ------------------------------------------------------TG---A------A--  866
HIVK29      ------------------------------------------------------T----A---------  866
HIVK124     ------------------------------------------------------------A---------  866
HIVK7       --------A-------------------------------------------A--T---------A----  866
HIVK98      ------------------------------------------------------T----A---------  866
HIVK89      ------------------------------------------------------T----A---------  866
HIVVI32     ------------------------------------------------------------A---------  866
HIVVI415    ------T-------------------G---------------AC-------C----TG---A---------  866
HIVCI4      --------------------G-------------------------------------------------  860
HIVG141     ------------------------------------------C-------------------------  854
HIVLBV23    --------A--------------------G-------------------A--------------------  866
HIVTN243    ----------------------------------------A-------------------------------  866
HIVTN245    ------------------------------------------------------------------------  866
HIVTN240    ------------------------------------------------------------------------  866
HIVCI20     ---G-------------------------------T-----C----------------------A--  842
HIVCI59     ---G-T--------------------C-----------------C-------------------------  857
HIVLBV2310  ---G-T-----------------------------------C-------------------------  857
HIVCI51     ----------G-------------------------------C-------------------------  851
HIVLBV105   ----------G-------------------------------C----------------AG--------  878
HIVCI32     ----------------------------------------C-----C-----T---------------  872
HIVIC144    ---G--------------------------------------C-------------------------  857
HIVDJ258    ----------------------------------------C-------------------------  857
HIVCM238    ----------------------------------------A-------------------------  866
HIVUG266    --------A---C-----------------------------------------A-------------A---  866
HIVVI354    ----------------------------------------C-------------------------  866

CONSENSUS.B ATAATccTgGGaTTAAATAAAATAGTAAGaATGTATAGcCCtaccAGcATTcTgGAcATAAgaCAAGGaCC  865
HIVSF2      ------------------------------------------------------------------------  872
HIVBZ167    ----------------------------G-------------T-------T--------------------  869
HIVPH153    --------A-------------------G-----------------T--------T---------------  866
HIVPH136    -----TA----------------------G---------T-----T----------------A---------  866
HIVBZ200    ----------------------------G-----------------------------------------G--  866
HIVTB132    -----A-----------------------G---------------------T--------------------  866
HIVBZ190    ------A-------------------------------------------------------A---------  866
HIVLAI      ------------------------------------------------------------------------  866
HIVHXB2R    ------------------------------------------------------------------------  866
HIVMN       ----------------------------G------------T-----------------------------  875
HIVJH3      ----------------------------G------------T-----------------------------  866
HIVJRCSF    ----------G-----------------G------------GT-----------------------------  866
HIVOYI      ------------------------------------------------------------------------  866
HIVNY5CG    ------------------------------------------------------------------------  866
HIVNL43     ------------------------------------------------------------------------  866
HIVCDC4     ----------------------------------------C-T---------A-----------------  866
HIVHAN      ------------------------------------------------------T----A---------  866
HIVCAM1     -----T-----------------------------------------------------------G-------  866
HIVRF       -----T-----------------------------------C-T-------------------------  866
HIVD31      ------------------------------------------------------------------------  866
HIVBH102    ------------------------------------------------------------------------  866
HIVPV22     ------------------------------------------------------------------------  866
HIVJRFL     ----------G-----------------G-------------------------------------------  860
HIVUG280    -----T----------------------G---------T----------------------A---------  866
HIVYU2      ----------------------------------------T-------------------------------  866
HIVBCSG3C   ----------------------------G---------T---T-T----------------------------  866
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CONSENSUS.C ATAATTCTGGGGTTAAATAAaATAGTaAGAATGTATAGCCCTGTCAGCATTTTgGACATAAaACAAGGGCC 852
HIVUG268    ------------------------------------------------------------------------ 851
HIVSM145    ---------------------------------------------------------A-------------- 857
HIVZAM18    -------------------------C---------------------------------------------- 863
HIVZAM19    --------------------G-----C-----------------------------------G--------- 674
HIVZAM20    ------------------------------------------------------------G--------- 857
HIVDJ259    ------------------------------------------------------------G--------- 860
HIVVI313    ------------------------------------------------------------------------ 860

CONSENSUS.D ATAATccTgGGATTAAATAAaATAGTAAgAATGTATAGcCCTGTcAGcATtTTGGACATAAGACAaGGACC 863
HIVELI      -----TG-------------------------------------------------------------G----- 866
HIVZ2Z6     ------------------------------------------------------------------G----- 869
HIVNDK      ------------------------------------------------------------------G----- 857
HIVVI205    --------A-------------------A---------------T--------------------G----- 869
HIVG109     ------A------------------------------------------------------------------ 875
HIVK31      --------A------------------------------------------------------------------ 866
HIVUG274    --------A-----------------------------------T--A-------------------------- 866
HIVUG270    --------A------------------------------------------------------------------ 866
HIVSE365    --------------------G-----------------T------------------------------------ 866
HIVVI203    ---------------------------------------------T---------------------------- 866

CONSENSUS.F ATcATCCTaGGaTTAAATAAAATAGTAAGAATGTAtAGCCCTGTCAGCATTTTGGACATAAgACAAGGGCC 836
HIVVI174    ------------------------------------------------------------------------ 851
HIVVI69     ------------------------------------------------------------------------ 854
HIVBZ162    ------------------------------------------------------------------------ 853
HIVVI325    --A-----G--T-----------------------C-------------------------A--------- 854

CONSENSUS.G ATAATCCTGGGaTTAAAtAAAATAGTAAGAATGTATAGCCCTGTCAGCATTTTGGA?ATAAGACAAGGGCC 832
HIVLBV217   ----------G-------------------------------------------------C---------- 860
HIVVI191    ----------------C-------------------------------------T---------------- 857
HIVTAIG     ------------------------------------------ 560

CONSENSUS.H ATAATCCTGGGATTAAATAA?ATAGTAAGAATGTATAG?CCTGTCAGCATTTTGGACATAA?ACAAGG?CC 801
HIVVI525    --------------------G-----------------T----------------------A------A-- 866
HIVVI557    --------------------A-----------------C----------------------G------G-- 866

CONSENSUS.O ATAGTG?TAGGACTAAACAAAATGGTAAAAATGTACAG?CCAGTGAGCATCTTAGATATTA?GCAGGGACC 774
HIVANT70    ------T-------------------------------C----------------------A--------- 863
HIVMVP51    ------C-------------------------------T----------------------G--------- 863

SIVCPZGAB   GTAATTTTAGGGTTAAACAAAGTGGTTAGAATGTATTGCCCAGTAAGTATCCTTGACATCAGACAAGGGCC 890
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HIV1 GAG

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CONSENSUS.A aAAaGAaCCcTTcAgaGAcTATGTagAtAggTTCTtTAAaactcTcAGAGCtgAgcAaGCTaCaCAgGagG  930
HIVU455     --------------G--T----------A-----------------------------------------T-  925
HIVMAL      ---G-----T--T-------------------------------------------------------------  955
HIVVI59     --------------AG----------C--A----------T---------------------------------  937
HIVVI310    ---------T--------------------A-------------------------G----------CA-  934
HIVVI57     G--------T-----------------------------GGT-------------------T-------C-  937
HIVK112     -----------------T--------------------------------------------------------  937
HIVK88      -----------------T----------------------C---------------------------------  937
HIVK29      -----------------T--------------------------------------------------------  937
HIVK124     -----------------T--------------------------------------------------------  937
HIVK7       ----------------------------------------G-------------A------T-------T-  937
HIVK98      ------G-------------------------------------G---------------------------  937
HIVK89      ------------------T-------------------------------------------G--A--C-  937
HIVVI32     ---------------------------A----------------------A----------------------  937
HIVVI415    ------------------------T----------------T---------------------------------  937
HIVCI4      ---------T-------------------------------TG-------------------------A-  931
HIVG141     ---------T--T--G-----------------------------------------------------------  925
HIVLBV23    ---------------------------------------------------------------------T-  937
HIVTN243    ------------------------------------A---------------G--A----------------  937
HIVTN245    ------------------------------------A---------------G--A----------------  937
HIVTN240    ------------------------------------A---------------G--A----------------  937
HIVCI20     ------------T-----T-----------------------T-G--------A--------G--------  913
HIVCI59     ------------T-----T-----------------------T-G--------AT-------G--------  928
HIVLBV2310  ------------T-----T---------------------GT-T-G--------A--------G--------  928
HIVCI51     ---G--------T-----T-----------------------T-G--------A--------G--------  922
HIVLBV105   ------------T--------------C---------------T-A-----------------------C-  949
HIVCI32     ------------T-----T---------------A--------T-G--------A------T----------  943
HIVIC144    ------------T-----T-------------------------G--------A------T-G--------  928
HIVDJ258    ------------T-----T-----------------------T-G--------A--------G--------  928
HIVCM238    ---------------------------------A---------------G--A----------------  937
HIVUG266    ------------T-A---A----------A-----------------------------------------T-  937
HIVVI354    ---------------G--A------A----------------G---------A------------------  937

CONSENSUS.B aAAgGAAcCcTTTAGAGAcTATgTAGAccGgTTCTATAAaACtcTAAGAGCcGAgCAaGCttCACAgGAgG  936
HIVSF2      ------------------T-----------------------------------A--------------T-  943
HIVBZ167    ---------------------------------------------------------G-----------T-  940
HIVPH153    ---------------------------------------------------------------------T-  937
HIVPH136    ---------------------------------------------------------------------A-  937
HIVBZ200    ---------------------------T-----------G-------------------------------  937
HIVTB132    ----------------------------------------G--------------------C----------  937
HIVBZ190    ---------T-----------------------------------------------------------A-  937
HIVLAI      ---A-----------------------------------------------------------------  937
HIVHXB2R    ---------------------------------------------------------------------  937
HIVMN       ---------------------------------------------------------------------  946
HIVJH3      ---------------------------------------------------------------------  937
HIVJRCSF    ------------------------------------------C------------------A---------  937
HIVOYI      ---------------------------------------------------------------------T-  937
HIVNY5CG    ---------------------------------------------------------------------  937
HIVNL43     ----------------------------A-----------------------------------A----  937
HIVCDC4     ---A-------------------------------------G--------T-------------------  937
HIVHAN      ---A--------------T----------------------C------------------A-------A-  937
HIVCAM1     ---------------------------A---------------------T--A----------------  937
HIVRF       T---------------------------------------------------------------------T-  937
HIVD31      ---------------------------------------------------------------A---------  937
HIVBH102    ---A-----T-----------------------------------------------------------  937
HIVPV22     ---A------------------C-----------------------------------------------  937
HIVJRFL     ---------------------------------------------------------------------  931
HIVUG280    ---------------------------------------------------------------------  937
HIVYU2      ------------------T-------------------------------------------------  937
HIVBCSG3C   -------T----------T---------A--------------T---------------------------  937
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CONSENSUS.C AAAGGAACCcTTTAGAGACTATGTAGAtCGGTTCTTTAAAACtTTAAGAGCTGAACAAGCtaCaCAAGATG  923
HIVUG268    ----------------------------------------C----------------------------  922
HIVSM145    --------------------------C-------------------------------------------  928
HIVZAM18    ---------T----------------C-------------------------------------------  934
HIVZAM19    ------------------------------------------------------------------------  745
HIVZAM20    --------------------------C-------------------------------------------  928
HIVDJ259    ---------T--------------------------------C-----------------AT-T-------  931
HIVVI313    ------------------------------------------------------------------------  931

CONSENSUS.D AAAggAACCcTTTAGAGAcTATGTAGA?CGGTTCTATAAAACtcTAAGaGCcGAGCAAGCTtCACAgGAtG  933
HIVELI      ---------T----------------C-------------------------------------------  937
HIVZ2Z6     ---------T----------------C-------------------------------------------A-  940
HIVNDK      ---------T----------------C-------------------------------------------  928
HIVVI205    ---AA----T----------------C-------------------------------------------  940
HIVG109     ---A-----------------------C-------------------------------------------  946
HIVK31      --------------------------T---------------T-------T--------------A----  937
HIVUG274    --------------------------T--------------------G----------------------  937
HIVUG270    ---------A----------------T-------------A-----G----------------A----  937
HIVSE365    ---A--------------T--------T-----------------------------------A-------G-  937
HIVVI203    --------------------------T-----------------------------------A----A--G-  937

CONSENSUS.F AAAAGAacCCTTTAGAGACTATGTAGACAGgTTcTTtAAAAC?CTAAGAGCTGAgcAAGCtACACAGGAAG  906
HIVVI174    ------------------------------------------T-----------------------------  922
HIVVI69     ------------------------------A-----------C------------G----------------  925
HIVBZ162    ------G-------------------------------------C-----------------------------  924
HIVVI325    -------T--------------------------T--C-----T-----------A-----C----------  925

CONSENSUS.G AAAAGAACCCTTTAGAGATTATGTAGATAGGTTCTTTAAAAC??TGAGAGCTGAGCAAGCTACACAGGA?G  900
HIVLBV217   ------------------------------------------TT--------------------------T-  931
HIVVI191    ------------------------------------------AC----------------------------A-  928

CONSENSUS.H AAAAGAACCCTTTAGAGACTATGTAGA?AGGTTCTTTAAA?CTTTAAGAGCTGA?CAAGC?ACACAGGA?G  867
HIVVI525    --------------------------C------------A-------------G-----C--------T-  937
HIVVI557    --------------------------T------------G-------------A-----T--------G-  937

CONSENSUS.O AAA?GAACCATT?AGAGA?TATGTAGATCGGTT?TACAAAACATTAAGAGCTGAGCAAGCTACTCAAGAAG  841
HIVANT70    ---G---------T-----C--------------C-------------------------------------  934
HIVMVP51    ---A---------C-----T--------------T-------------------------------------  934

SIVCPZGAB   AAAGGAGCCCTTTAGAGATTATGTGGACAGATTCTACAAAACTTTAAGGGCTGAGCAAGCTTCACAGGAAG  961
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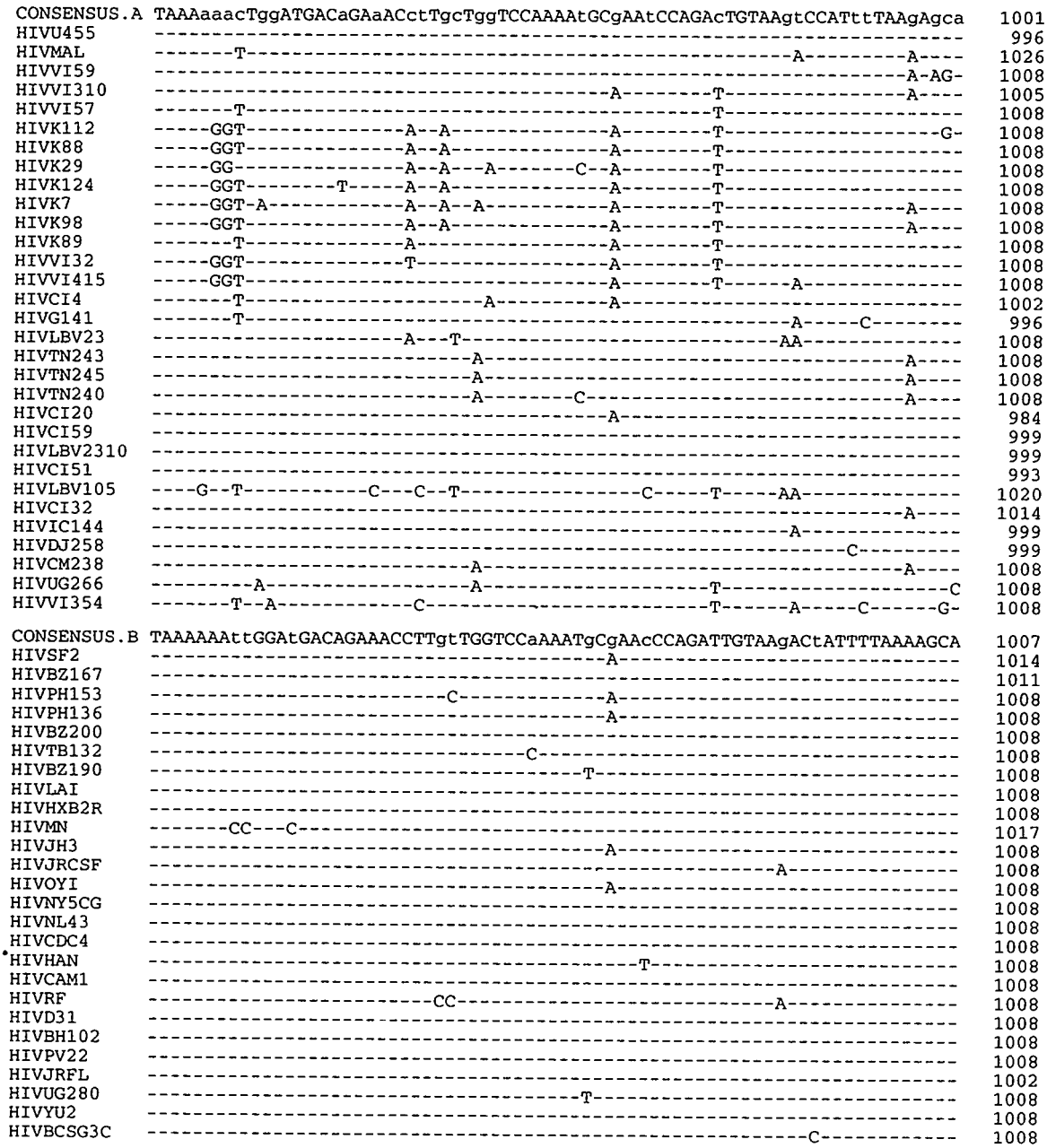
HIV1 GAG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HIVU455 996
HIVMAL 1026
HIVVI59 1008
HIVVI310 1005
HIVVI57 1008
HIVK112 1008
HIVK88 1008
HIVK29 1008
HIVK124 1008
HIVK7 1008
HIVK98 1008
HIVK89 1008
HIVVI32 1008
HIVVI415 1008
HIVCI4 1002
HIVG141 996
HIVLBV23 1008
HIVTN243 1008
HIVTN245 1008
HIVTN240 1008
HIVCI20 984
HIVCI59 999
HIVLBV2310 999
HIVCI51 993
HIVLBV105 1020
HIVCI32 1014
HIVIC144 999
HIVDJ258 999
HIVCM238 1008
HIVUG266 1008
HIVVI354 1008
CONSENSUS.B TAAAAAAttGGAtGACAGAAACCTTgtTGGTCCaAAATgCgAAcCCAGATTGTAAgACtATTTTAAAAGCA 1007
HIVSF2 1014
HIVBZ167 1011
HIVPH153 1008
HIVPH136 1008
HIVBZ200 1008
HIVTB132 1008
HIVBZ190 1008
HIVLAI 1008
HIVHXB2R 1008
HIVMN 1017
HIVJH3 1008
HIVJRCSF 1008
HIVOYI 1008
HIVNY5CG 1008
HIVNL43 1008
HIVCDC4 1008
HIVHAN 1008
HIVCAM1 1008
HIVRF 1008
HIVD31 1008
HIVBH102 1008
HIVPV22 1008
HIVJRFL 1002
HIVUG280 1008
HIVYU2 1008
HIVBCSG3C 1008

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CONSENSUS.C TAAAAAAtTGGATGACAGAcACCTTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACCATTtTAAGAGCA   994
HIVUG268    ------------------------------------------------------------------------   993
HIVSM145    ------------------------------------------------------------------------   999
HIVZAM18    ------------------A-----------------------------------------------------  1005
HIVZAM19    ------------------A-----------------------------------------------------   816
HIVZAM20    -------C-------------------------------------------------------C--------   999
HIVDJ259    ------------------------------------------------------------------------  1002
HIVVI313    ------------------------------------------------------------------------  1002

CONSENSUS.D TaAAAaatTGGATGAC?GAAACCTTGTTGGTcCAAAATGCgAACCCAGATTGTaaaActATCTTAAAAGCA  1003
HIVELI      ----------------A----------------------A-----------C--G----------------  1008
HIVZ2Z6     -----GG---------A----------------------A-------------G--C--------------  1011
HIVNDK      -------C--------A----------------------A-------------------------------   999
HIVVI205    -G-----C--------A----------------------A-------------------------------  1011
HIVG109     -------C--------C------------------------------------------------------  1017
HIVK31      ----------------C--------------T---------------------------------------  1008
HIVUG274    ----------------T-------------------------------------G----------------  1008
HIVUG270    ----------------T------------------------------------------------------  1008
HIVSE365    ----------------T---------------------------------------A--------------  1008
HIVVI203    ----------------C------------------------------------------------------  1008

CONSENSUS,F TAAAgggTTGGATGACAGACACctTGTTGgTCCAaAAtGCgAACCCaGATTGTAAgACCAT?TTAAAAGCa  976
HIVVI174    ----------------------T-----------------------------------------C-------  993
HIVVI69     ----------------------------A----G-----------G--------A-----C---------  996
HIVBZ162    ------------------------------------------------------------T---------  995
HIVVI325    ----AAA----------------C-------------C--A--------------------T--------G  996

CONSENSUS.G TAAAA??CTGGATGACAGACAC?TTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACCATCTTAA?AGCA  967
HIVLBV217   -----AA---------------T-----------------------------------------A-----  1002
HIVVI191    -----GG---------------C-------------------------------------------G-----  999

CONSENSUS.H T?AA???TTGGATGACAGACACCTTGTTGGTCCAAAATGCGAATCCAGATTG?AAGA?TATTTTAA?AGCA  931
HIVVI525    -A--GAA-------------------------------------------C----A--------A-----  1008
HIVVI557    -G--AGG-------------------------------------------T----C--------G-----  1008

CONSENSUS.O TAAA?AATTGGATGACAGAAAC??TGCTTGTTCA?AAT?C?AA?CCAGATTG?AAACA?ATT?TGAAA?CA  901
HIVANT70    ----A----------------TC----------A---G-C--T--------C-----G---T-----T--  1005
HIVMVP51    ----G----------------CT----------G---T-A--C--------T-----A---C-----G--  1005

SIVCPZGAB   TGAAAAATTGGATGACTGACACTCTCTTAGTGCAGAATGCAAACCCAGATTGTAAGCAAATTCTAAAAGCA  1032
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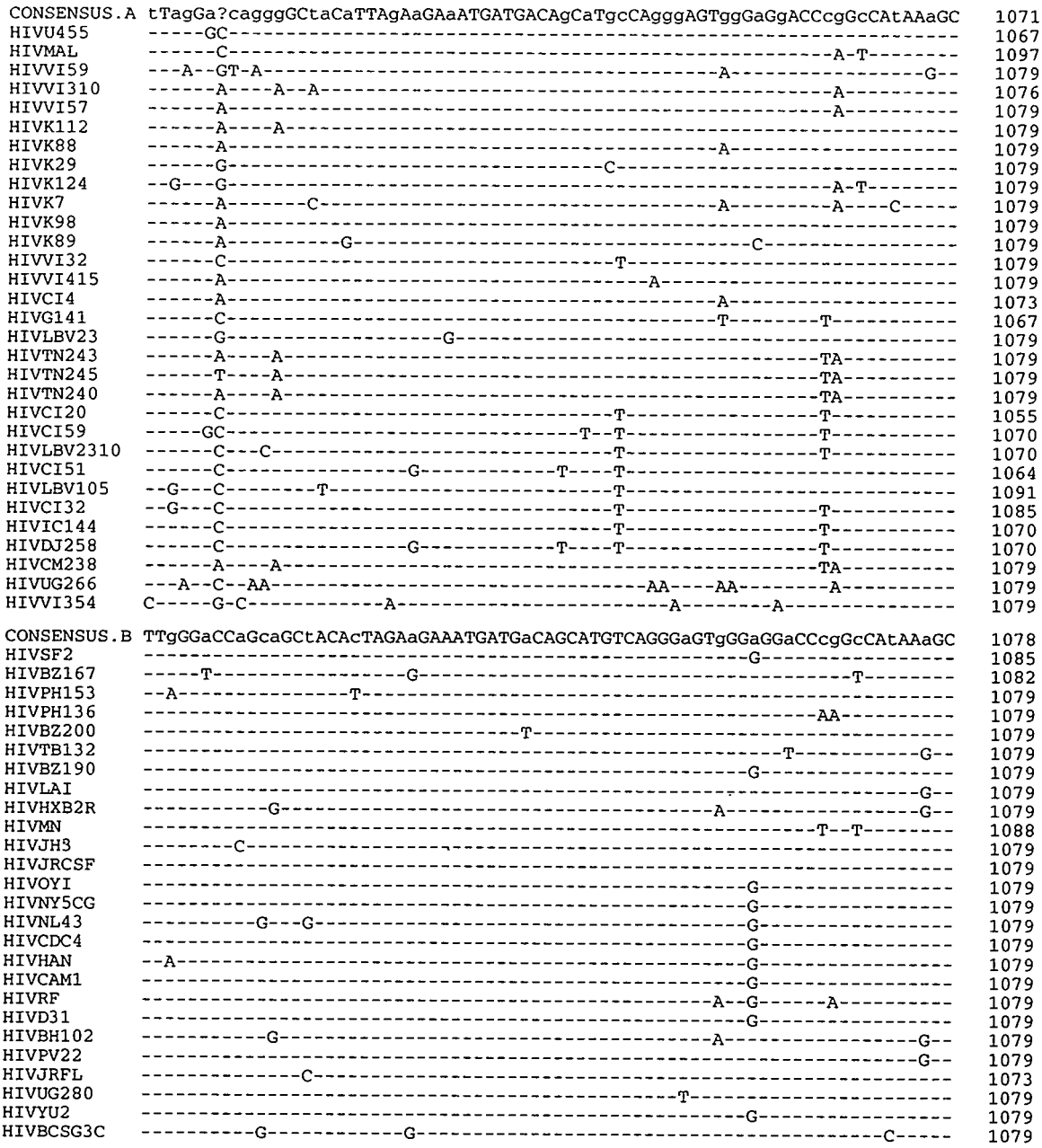
HIV1 GAG


CONSENSUS.A tTagGa?cagggGCtaCaTTAgAaGAaATGATGACAgCaTgcCAgggAGTggGaGgACCcgGcCAtAAaGC 1071
HIVU455 -----GC---------- 1067
HIVMAL ------C----------A-T-------- 1097
HIVVI59 ---A--GT-A----------A----------G-- 1079
HIVVI310 ------A----A--A----------A---------- 1076
HIVVI57 ------A----------A---------- 1079
HIVK112 ------A----A---------- 1079
HIVK88 ------A----------A---------- 1079
HIVK29 ------G----------C---------- 1079
HIVK124 --G---G----------A-T-------- 1079
HIVK7 ------A-------C----------A---------A----C----- 1079
HIVK98 ------A---------- 1079
HIVK89 ------A----------G----------C---------- 1079
HIVVI32 ------C----------T---------- 1079
HIVVI415 ------A----------A---------- 1079
HIVCI4 ------A----------A---------- 1073
HIVG141 ------C----------T--------T---------- 1067
HIVLBV23 ------G----------G---------- 1079
HIVTN243 ------A----A----------TA---------- 1079
HIVTN245 ------T----A----------TA---------- 1079
HIVTN240 ------A----A----------TA---------- 1079
HIVCI20 ------C----------T----------T---------- 1055
HIVCI59 -----GC----------T--T----------T---------- 1070
HIVLBV2310 ------C---C----------T----------T---------- 1070
HIVCI51 ------C----------G-----------T----T---------- 1064
HIVLBV105 --G---C--------T----------T---------- 1091
HIVCI32 --G---C----------T----------T---------- 1085
HIVIC144 ------C----------T----------T---------- 1070
HIVDJ258 ------C----------G-----------T----T----------T---------- 1070
HIVCM238 ------A----A----------TA---------- 1079
HIVUG266 ---A--C--AA----------AA----AA--------A---------- 1079
HIVVI354 C-----G-C----------A----------A--------A---------- 1079
CONSENSUS.B TTgGGaCCaGcaGCtACAcTAGAaGAAATGATGaCAGCATGTCAGGGaGTgGGaGGaCCcgGcCAtAAaGC 1078
HIVSF2 ----------G---------- 1085
HIVBZ167 -----T----------G----------T--------- 1082
HIVPH153 --A----------T---------- 1079
HIVPH136 ----------AA---------- 1079
HIVBZ200 ----------T---------- 1079
HIVTB132 ----------T----------G-- 1079
HIVBZ190 ----------G---------- 1079
HIVLAI ----------G-- 1079
HIVHXB2R ----------G----------A----------G-- 1079
HIVMN ----------T--T--------- 1088
HIVJH3 --------C---------- 1079
HIVJRCSF ---------- 1079
HIVOYI ----------G---------- 1079
HIVNY5CG ----------G---------- 1079
HIVNL43 ----------G---G----------G---------- 1079
HIVCDC4 ----------G---------- 1079
HIVHAN --A----------G---------- 1079
HIVCAM1 ----------G---------- 1079
HIVRF ----------A--G------A---------- 1079
HIVD31 ----------G---------- 1079
HIVBH102 ----------G----------A----------G-- 1079
HIVPV22 ----------G-- 1079
HIVJRFL --------------C---------- 1073
HIVUG280 ----------T---------- 1079
HIVYU2 ----------G---------- 1079
HIVBCSG3C ----------G----------G----------C----- 1079

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CONSENSUS.C TTAGGaCCAGggGCTtCAtTAGAAGAAATGATGACAGCATGTCAGGGAGTGGGAGGACCTagCCACAAAGC  1065
HIVUG268    -----G-----A-----------------------------------------------G----------  1064
HIVSM145    ------------------------------------------------------------GC---------  1070
HIVZAM18    ----------C----A-------------------------------------------------------  1076
HIVZAM19    ----------C----A-------------------------------------------------------   887
HIVZAM20    ----------------A-------------------------------------------------------  1070
HIVDJ259    -----G------------C-----------------------------------------------------  1073
HIVVI313    -----G-----------------------------------------------------G----------  1073

CONSENSUS.D TTgGGACCAg?gGCTACAtTAgAaGAAATGATGACaGCaTGtCAGGgaGTGGGgGgaCCCaGtCATAAAGC  1073
HIVELI      ---------CA-------C-------------------------------------G-----C--------  1079
HIVZ2Z6     ---------CA-------C-------------------------------------G-----C--------  1082
HIVNDK      ---------CA-------C----------------------C--------------G---G-C--------  1070
HIVVI205    ---------CA-------C--A-----------------------A---------G-----C--------  1082
HIVG109     ----------CA-----------------------------------------------------------  1088
HIVK31      ----------G-----------------------------------------A------G----------  1079
HIVUG274    ----------G-----------------------------------------A------------------  1079
HIVUG270    ----------C------------G-----------G-----------------------------------  1079
HIVSE365    --A-------G----------------------------C---------G-------A--------------  1079
HIVVI203    ----------G-----------------------------------------------------------  1079

CONSENSUS.F tTGGGACCAGGGGCTaCAcTAGAaGAAATGATGACAGCATGTCAgGGAGTGGGAGGACCTGGCCATAAgGC  1047
HIVVI174    -----------------------------------------------------------------------  1064
HIVVI69     A----------------------------------------------------------------------  1067
HIVBZ162    -----------------------------------------------------------------------  1066
HIVVI325    ---------------T--T----G-------------------A----------------------A--  1067

CONSENSUS.G TTAGGACCAGGAGCTACACTAGAAGAAATGATGACAGCATGCCAGGGAGTGGGAGGACCC?GCCATAAAGC  1037
HIVLBV217   -----------------------------------------------------------A----------  1073
HIVVI191    -----------------------------------------------------------G----------  1070

CONSENSUS.H TTAGGA??AGGGGCTTCAATAGAAGAAATGATGACAGC?TG?CAGGGAGTGGGAGG?CCT?GCCA?AAAGC   995
HIVVI525    ------AC-------------------------------A--T--------------A---A----C-----  1079
HIVVI557    ------CA-------------------------------C--C--------------G---G----T-----  1079

CONSENSUS.O TTAGG?CCAG?AGCTAC?TTAGAAGA?ATGATGGTAGCCTGTCA?GGAGTAGGAGG?CCAACTCA?AAGGC   965
HIVANT70    -----G----G------C--------G-----------------G-----------A--------T-----  1076
HIVMVP51    -----A----A------T--------A-----------------A-----------G--------C-----  1076

SIVCPZGAB   TTGGGACCTGGGGCCACCCTAGAGGAAATGATGACAGCTTGTCAAGGAGTAGGAGGACCATCTCATAAGGC  1103
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HIV1 GAG

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                 p24 \/
CONSENSUS.A AagggTtTTgGCTGAgGCAATgAGtCAaGtacaacAt?caAac.....????????aTAATGATgC  1123
HIVU455     ------------------------------------GA---G-.....----------          1120
HIVMAL      ---A--------------------C----C-AC-A--T---CT.....GCTGCC----------     1156
HIVVI59     --A-----------------A-------------GA---G-.....----------            1132
HIVVI310    ----A-C--------A----------G-C-------A-----.....--------T-            1129
HIVVI57     ------------------------------------GC-----.....----------          1132
HIVK112     ----A-------------------------------A-----.....----------          1132
HIVK88      ---------------------------G---------A-----.....----------          1132
HIVK29      -----------------------------G------A-----.....----------          1132
HIVK124     ---A--C-----------------C----C-AC-A--AAT-TA.....AATGCTGCTG---------  1141
HIVK7       --A------A-------------------C------GA----T.....----------          1132
HIVK98      ---------A--------------C----------GG-----.....----------           1132
HIVK89      ---------------------------G---------A-----.....----------          1132
HIVVI32     ----------------------------C--------GG-----.....----------          1132
HIVVI415    ------------------------------------A-----.....----------          1132
HIVCI4      ------------------------------------A-C---.....----------          1126
HIVG141     ---A-----A-----A-----------------A--G-C---.....----------          1120
HIVLBV23    ---------------A--------------------A-----.....G---------          1132
HIVTN243    ------------------------C--C-C-------G----T.....----------          1132
HIVTN245    ------------------------C--C-C-------G----T.....----------          1132
HIVTN240    ---------------A--------C--C-C-------G---CT.....----------          1132
HIVCI20     ------------------------------------GT-C---.....----------          1108
HIVCI59     ------------------------------------GT-C---.....----------          1123
HIVLBV231C  ------------------------------------GA-C---.....----------          1123
HIVCI51     ------------------------------------GT-C---.....----------          1117
HIVLBV105   ------C--------A--------------------C-----.....----------          1144
HIVCI32     ------------------------------------GT-C---.....----------          1138
HIVIC144    ------------------------------------GT-C---.....----------          1123
HIVDJ258    ---------------------------G--------AT-C---.....----------          1123
HIVCM238    ------------------------C--C-C------GG---GT.....----------          1132
HIVUG266    -CA------A-------------------------GA---G-.....----------          1132
HIVVI354    ---------------A-----------------CA--A---G-.....----------          1132

CONSENSUS.B AAGAgTTTTGGCtGAAGCaATGAGCcAAGtaacaaat.....???tCAgctaccataATGaTgC  1134
HIVSF2      ------------------C-----------------.....C------A----------          1141
HIVBZ167    ------------A-----------------C-----.....AGT-------------------     1141
HIVPH153    ----------------------------C------C.....----------G---C---        1135
HIVPH136    ------------G-----G-------------------.....---------GCC-------      1135
HIVBZ200    ------------A------------T-----------.....-----AG------------       1135
HIVTB132    ------------G-----------------G------.....-------------------      1135
HIVBZ190    ------------------------------------.....-------------------      1135
HIVLAI      ------------------------------------.....-------------------      1135
HIVHXB2R    ------------------------------------.....-------------------      1135
HIVMN       ------------G-----G-------------------.....-------------------      1144
HIVJH3      ------------------------------------.....---A---------------      1135
HIVJRCSF    ------------------------------------.....C-------------------      1135
HIVOYI      ------------------------------.....---.....----TC---G---------     1132
HIVNY5CG    ------------------------------------.....C----------------A-       1135
HIVNL43     ------------------------------------.....C----------------A-       1135
HIVCDC4     ------------------------------------.....-------------------      1135
HIVHAN      ----------------------------------GG-.....------G------------      1135
HIVCAM1     ------------------------------------.....-------------------      1135
HIVRF       ----A--------------------------------.....---------------C---      1135
HIVD31      ------------------------------------.....--------TG---------      1135
HIVBH102    ------------------------------------.....A-------------------      1135
HIVPV22     ------------------------------------.....A-------------------      1135
HIVJRFL     ------------------------------------.....C-------------------      1129
HIVUG280    ------------A-----------------------.....C---T--A----------        1135
HIVYU2      ------------------------------------.....-------------------      1135
HIVBCSG3C   ------------G-----------------------.....-----C----------          1135
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                p24 \/
CONSENSUS.C AAGAGTGTTgGCtGAGGCAATGAGCCAAgCAAaCAatacAAac.................aTAaTGATGC   1118
HIVUG268    ------------------------------------T----.................----------   1117
HIVSM145    ------------------------------------T----.................---C------   1123
HIVZAM18    ---------A--------------------------------.................---C------   1129
HIVZAM19    ---------A-------------------------G-----CN.................N---------    940
HIVZAM20    ----------------------------A------G-G----T.................G---------   1123
HIVDJ259    --------------------------------C---C------.................----------   1126
HIVVI313    ------------C-------------------------T----.................----------   1126

CONSENSUS.D AAGAGTttTGGCtGAgGCAATGAGCCAAGca......acaaaT......tcA?aT?ctgC?atAATgATGC   1129
HIVELI      -------C-----------------------.....------.....---GT-A--A-AGC--------   1138
HIVZ2Z6     -------C-----------------------.....------.....---GC-G-C--AG---------   1141
HIVNDK      ----------------------------T-.....---GG-.....---GC-A----AG---------   1129
HIVVI205    -------------------------------.....----G-.....---GC-A----AG----A----   1141
HIVG109     -------------------------------.....----G-.....---A--G----C----------   1147
HIVK31      -------------------------------.....---.....GG-A--A----T----------   1135
HIVUG274    ------C-----------------------C.....------.....G--A--A----T----------   1138
HIVUG270    ------------C-----------------C.....T-----.....G--A--G----T----------   1138
HIVSE365    ------C-----------------------.....----G-.....---GC-G----C----------   1138
HIVVI203    ------C--------A--------------.....------.....A--A--GT---C----------   1138

CONSENSUS.F aAGAgTTTTGGCTGAGgCAATGAGCCAaGcA......ACAAAT......??????gCA?CcATAaTGATGC   1099
HIVVI174    -------------------------------.....------.....ACAGCA---G------------   1123
HIVVI69     ----------------A--------------.....------.....---G------------------   1120
HIVBZ162    G------------------------------.....------.....---A-T---C------------   1119
HIVVI325    ----A----------------------G-T-.....------.....A--A------------------   1120

CONSENSUS.G AAGAGTTTTAGCTGAAGC?ATGAGCCA?GCA......TCAGGT......??AGCA?CAGCCAT?ATGATGC   1090
HIVLBV217   ------------------G--------G---.....------.....AC----A-------A-------   1132
HIVVI191    ------------------A--------A---.....------.....GT----G-------G-------   1129

CONSENSUS.H AA?AGTTTTGGCTGAGGCAATGAGCCAAGTA???...ACAAAT......??????GCAG??AT?ATGATGC   1044
HIVVI525    --G------------------------------.....------.....ACACAT----CC--A-------   1138
HIVVI557    --A----------------------------AAT...------.....----TT--G-------------   1135

CONSENSUS.O ?A?A?T?CTAGCAGAAGCAATGGCT?C?GCCCAGCAAGATTT?AAAGGAGGATACACAGCAGTATTCATGC   1029
HIVANT70    C-G-G-G------------------A-A--------------G----------------------------   1147
HIVMVP51    A-A-A-A------------------T-T--------------A----------------------------   1147

SIVCPZGAB   AAGGGTTCTAGCTGAAGCCATGTCAATGGTTCAG...AATCAA......GGGAGAGCAGATGTTTTCTTCC   1165
```

HIV1 GAG

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CONSENSUS.A AgAgaGGcaAttTt...aggGGccagaaaaga???aTtAAgTGtTTcAAcTGTGGcAaAGAaGGaCAccTA   1188
HIVU455     --------------...-------C--G----...-----------------------------------   1185
HIVMAL      -------T------...-A-------------...-----------------------------------   1221
HIVVI59     --------------...-A-------------...-------------------------------T---   1197
HIVVI310    ----G---------...-A------A------...-----A-----------------------T---   1194
HIVVI57     --------------...----------G-G--...-----------------------------------   1197
HIVK112     ----------C---...--------------G...-----------------------------------   1197
HIVK88      --------------...--------------G...-----------------------------------   1197
HIVK29      --------------...--------------G...-----------------------------------   1197
HIVK124     --------------...-A-----CA--G-A-ATC-----A----------------------G---A--   1209
HIVK7       --------------...-AA-----A----CG...----------T--T--------------------   1197
HIVK98      -A------------...--------A-----G...----------T--T--------------------   1197
HIVK89      ----G---------...--A----------G...-----------------------------------   1197
HIVVI32     -A---------A-C...------GGCT-G-A-AGA-----------------------------------   1200
HIVVI415    --------------...-AA-------G----...--------C-----T--------------------   1197
HIVCI4      ---A----------...-----T---------...-----------------------------------   1191
HIVG141     --A----------...-A-------------...-----------------------------------   1185
HIVLBV23    ----------C---...-----T---------...-----------------------------------   1197
HIVTN243    --------------...-A------A------...--------C--------------------------   1197
HIVTN245    --------------...-A------A------...--------C-------------G------------   1197
HIVTN240    -------------C...-A-------------...--------C----------T-G------------   1197
HIVCI20     --------------...--------A-G--C-...--A--A-------------------------------   1173
HIVCI59     ---------------...G---------G--C-...--A-------------------------------   1188
HIVLBV2310  --------------...----------G--C-...--A-------------------------------   1188
HIVCI51     --------------...----------G--C-...--A-------------------------------   1182
HIVLBV105   --------------...-A------------ATC-------------------------------T---   1212
HIVCI32     ----------C---...-A------A-G--AGTTCG----------------------G------A--   1206
HIVIC144    --------------...----------G--C-...--A-------------------------------   1188
HIVDJ258    --------G-----...----------G--C-...--A-------------------------------   1188
HIVCM238    --------------...-A----------G--...--------C-------------G------------   1197
HIVUG266    --------------...-AA------------...-----------------------------------   1197
HIVVI354    --------------...-A------A----A-...-----------------------------------   1197

CONSENSUS.B AgAgaGGcAAtTTT...AggaaccaaagAAAgActgTtAAgTGtTTCAAtTGTGGCAAAGaaGGgCAcatA   1202
HIVSF2      --------------...-----------------------------------------------------   1209
HIVBZ167    ---A----------...--A-------------T-----------------------------------   1209
HIVPH153    --------------...------AC-----------------------------------------A---   1203
HIVPH136    --------------...--------------A-T-----------------------------------   1203
HIVBZ200    --------------...-----------------------------------------------------   1203
HIVTB132    ---A------A---...----------------T-----------------------------------   1203
HIVBZ190    --------------...---------------------A-------------------------A---   1203
HIVLAI      -A------------...----------------T-----------------------------------   1203
HIVHXB2R    --------------...----------------T-----------------------------------C-   1203
HIVMN       --------------...-----T----------T-A-C-----C-------------------------   1212
HIVJH3      --------------...----------------T-A-------------------------------T--   1203
HIVJRCSF    ----------C---...----------------A-----------------------------------   1203
HIVOYI      ---A----------...-A-------------------------------------------------   1200
HIVNY5CG    --------------...--A-----G-A-----------------------------------------   1203
HIVNL43     ---A----------...-------------------------------------------------   1203
HIVCDC4     ----------C---...----GA---G-------------------------------------------   1203
HIVHAN      --------------...-----------------------------------------------------   1203
HIVCAM1     --------------...--------------------------------C----------TC---------   1203
HIVRF       ---A---T------...---G----------A-T--------------C----------T----------   1203
HIVD31      --------------...-----------------------------------------------------   1203
HIVBH102    --------------...----------------TG-----------------------------------C-   1203
HIVPV22     --------------...----------------TG-----------------------------------C-   1203
HIVJRFL     ----------C---...----------------T-----------------------------------   1197
HIVUG280    ---AC---------...----------------T--------------C----------T----------   1203
HIVYU2      --------------...--------------A-----------------------------------   1203
HIVBCSG3C   --------------...-----------------------------------------------T---   1203
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CONSENSUS.C AgAgAaGCAATTTT...AAaGGccCtAaaagAAtTgTTAAATGTTTCAAcTGTGGCAAgGAAGGGCACaTA 1186
HIVUG268    --------------...--G--------G------A-------------T------------------C-- 1185
HIVSM145    -A---G--------...------T-----------------------------------A------------ 1191
HIVZAM18    --------------...-----A----------G------------------------------------- 1197
HIVZAM19    --------------...-----A----G-N---------------------------------------- 1008
HIVZAM20    -----G--------...----------------C------------------------------------- 1191
HIVDJ259    ---A----------...--G-------G--A--C-A-----------------------------C-- 1194
HIVVI313    ---A----------...--------G---------A-----------------------------T-- 1194

CONSENSUS.D AgAgAGgcAAtTTt...AAgGGcCcAAgaAaAattaTTAAGTGTTTCAAcTGTGGCAaaGAAGGgCACatA 1197
HIVELI      --------------...-------------------------------T---------------------- 1206
HIVZ2Z6     --------------...----------------C------------------------------------- 1209
HIVNDK      --------------...----------------G-----------------------G----------C- 1197
HIVVI205    --------------...----------A------A------------------------------------ 1209
HIVG109     ---A---T------...--A------------G--G---------------------G------------- 1215
HIVK31      --------------...-------A---G-----C-----------------------------A---C-- 1203
HIVUG274    -------T------...----------G-----C------------------------------------- 1206
HIVUG270    -A----C---C---...-----T----AG-G--AC-----------------------------------C-- 1206
HIVSE365    --------------...-----T-A---G-----CG----------------------------------- 1206
HIVVI203    -------------C...----------A--G---------------------------G-----A---C-- 1206

CONSENSUS.F AGAaAaGtAAcTTT...AAGGGCCAAAGAAgAAtTgTTAAATGTTTtAATTGTGGCAaAgaaGGACAcaTA 1167
HIVVI174    --------------...------------------------------------------------------ 1191
HIVVI69     ----------T---...----------------C-----------------------------------G-- 1188
HIVBZ162    --------------...-------------------------------------------AC---------- 1187
HIVVI325    ---G-G-A------...-------------A----A----------C----------G---G-----T--- 1188

CONSENSUS.G A?AAA?GC???TTT...AAGGGCCCGA?AA?AA?TATTAAGTGTTTC?ACTGTGGCAAGGAAGGACATCTA 1149
HIVLBV217   -G---G--AAT---...----------G--A--A----------G----------------------- 1200
HIVVI191    -A---A--GGG---...----------A--G--C----------A----------------------- 1197

CONSENSUS.H AGAAAGG?AACTT?...AAGGG?CAAAGAAGAATT?TTAAATGTTTCAA?TGTGGCAAAGAAGGACAC?TA 1106
HIVVI525    -------C-----T...-----T------------G----------C------------------A-- 1206
HIVVI557    -------T-----C...-----C------------A----------T------------------C-- 1203

CONSENSUS.O AAAGAGGGCA?AAT...CCAA?TAG?AAAGG??C?ATAAAATG?TTCAA?TGTGGAAAAGAGGGACATATA 1089
HIVANT70    ----------A---...----T---G-----AA-T--------T-----C---------------------- 1215
HIVMVP51    ----------G---...----A---A-----GC-C--------C-----T---------------------- 1215

SIVCPZGAB   AGAAGGGACAAGGT...GCGGGCCCAAAAAGAAAAATAAAATGCTTTAATTGTGGGAAAGAAGGTCACCTA 1233
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HIV1 GAG

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CONSENSUS.A GCcAgAAATTGcAggGCcCCTAggAAAAagGGcTGTTgGAAaTGtgggAagGAaGGaCAcCAAaTgAAagA  1259
HIVU455     ----A------T-------------------------------C-----A--------------------  1256
HIVMAL      ------------------------------------------------------------------------  1292
HIVVI59     ----------------------------A-------A-------A----A--------------------  1268
HIVVI310    ----------------------A-------------------------T--G-----T-----------  1265
HIVVI57     ------------------------------------------------G---------------------  1268
HIVK112     --------------------------G-----------------------G-----T-----------  1268
HIVK88      ------------------------------------------------G---------------------  1268
HIVK29      -----------T--A-------------------------------A-----G-----------------  1268
HIVK124     --A-A-----------T----------G-----------------A-G---------------------  1280
HIVK7       ----------------------A-----A-------A-------A-----------------T-------  1268
HIVK98      ------------------------------------------------G---------------------  1268
HIVK89      -----------T-----------------------------------G---------------------  1268
HIVVI32     ------------------------------------------------G---------------------  1271
HIVVI415    ----------------------A-----------------G-----------------------------  1268
HIVCI4      ------------------------------------------------G---------------------  1262
HIVG141     ------------------------------------------------------------------------  1256
HIVLBV23    ------------------------------------------------------------------------  1268
HIVTN243    ----------------------A--------T----------------G---------T-----------  1268
HIVTN245    ----------------------A--------T-------------------------T-----------  1268
HIVTN240    ----------------------A--------T-----------C--------------T-----------  1268
HIVCI20     -------------A--------------G-----------------------------------------  1244
HIVCI59     -------------A--------------G-----------------------------------------  1259
HIVLBV2310  --A----------A--------------G---------------------------------------G--  1259
HIVCI51     -------------A-------------------------G-------G----------------------  1253
HIVLBV105   ------------------------------------------A-----------T-----------  1283
HIVCI32     --A-A-------------------A-------------------------------------------  1277
HIVIC144    -------------A---------------------------------------------------------  1259
HIVDJ258    -------------A---T-----A----------------------A-----G-----------------  1259
HIVCM238    ----------------------A--------T-------------------------T-----------  1268
HIVUG266    -------------A--------A--------------A-------AA---A--------------A-----  1268
HIVVI354    -------------A---------------------------------A--------C--T-----A---A-  1268

CONSENSUS.B GCcAaAAAtTGCAgGGCcCCTAGgAaaAaGGGCTGtTGGAaATGTGGAAagGAAGGACAcCAAATGAAaGA  1273
HIVSF2      ----------------------------------------G--------G-----------------  1280
HIVBZ167    --------------------------G-------------------------------------------  1280
HIVPH153    ----G--------A---------A-------------------------G-------------------  1274
HIVPH136    ------------------------------------------------G-------------------  1274
HIVBZ200    --A---------------------------------------------GA-------------------  1274
HIVTB132    ----------------------------------------G-------------------------------  1274
HIVBZ190    --------C---------------------------------------------------------------  1274
HIVLAI      ----G-------------------------------------------------------------------  1274
HIVHXB2R    ----G-------------------------------------------------------------------  1274
HIVMN       --------------------------G---------------------------------------------  1283
HIVJH3      ----G-------------------------------------------------------------------  1274
HIVJRCSF    ----G-------------------------------------------------------------------  1274
HIVOYI      -----------------T----------------------------G-------------------  1271
HIVNY5CG    ------------------------------------------------------------------------  1274
HIVNL43     ------------------------------------------------------------------------  1274
HIVCDC4     --T-G--------A----------------------------------G-------------------  1274
HIVHAN      ----G-------------------------------------------------------T--------G--  1274
HIVCAM1     --T---------------------------------------------------------T-----------  1274
HIVRF       ------------------------------------------------------------------------  1274
HIVD31      ------------------------G-------------------------------------------  1274
HIVBH102    ----G-------------------------------------------------------------------  1274
HIVPV22     ----G-------------------------------------------------------------------  1274
HIVJRFL     ----G-------------------------------------------------------------------  1268
HIVUG280    ------------------------------------------------------------------------  1274
HIVYU2      -----------------T-------------------------------------------------------  1274
HIVBCSG3C   ----G--------A--------------G------C----------------------------------  1274
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CONSENSUS.C GCcAgAAaTTGCAGGGCcCCTaGGAAAAAgGGCTGTTGGAAATGTGGAA?GGAAGGACACCAAATGAAAGA 1256
HIVUG268    ----------------------------A-------------------G-------------------- 1256
HIVSM145    --T--------------T-----------------------------A--------------------- 1262
HIVZAM18    ----A------------------------A-----------------A--------------------- 1268
HIVZAM19    ----A--T---------------------A-----------------N--------------------- 1079
HIVZAM20    ----------------T---C--------------------------G--------------------- 1262
HIVDJ259    ------------------------------------------------G--------------------- 1265
HIVVI313    ------------------------------------------------A--------------------- 1265

CONSENSUS.D GCaAaAAATTGcAggGCcCCTAg?AaaAaGGGCTGTTggAaATGtGGAaagGAAGGaCACCAAaTgAAaGA 1267
HIVELI      ----------------------G----------------G----------------------C-A----- 1277
HIVZ2Z6     ----------------------G-G--------------------------------------C----G-- 1280
HIVNDK      ----------------------A-------------------C----G--------------------- 1268
HIVVI205    ----------------------AA------------------------G---------------A----- 1280
HIVG109     --------------A--------G----G----------------------A-----G------------- 1286
HIVK31      ----------------T-----G--G----------------------G--------------------- 1274
HIVUG274    -----------T-----T-----G------------------------------------------------ 1277
HIVUG270    ----------------T-----A-------------AA----------G---------------A----- 1277
HIVSE365    ----G--------A---------A------------------------C-------------------G-- 1277
HIVVI203    --C--------------------A------------------------------------------------ 1277

CONSENSUS.F GCCAaAaAaTTGcAGGGCCCCTAGAAAAAAGGGCTGTTGGAAATGTGGaAgaGAaGGACACCAAATGAAAGA 1238
HIVVI174    ----G------------------------------------------------------------------ 1262
HIVVI69     ------------------------------------------------------G----------------- 1259
HIVBZ162    -----------T------------------------------------------------------------ 1258
HIVVI325    ------C-------------------------------------------G-AG-------------------- 1259

CONSENSUS.G GCCAGAAATTGCAGGGCCCCTAGGAAAA?GGGCTGTTGGAAATGTGGAA?GGA?GGACATCAAATGAAAGA 1217
HIVLBV217   ----------------------------G-------------------A---G----------------- 1271
HIVVI191    ----------------------------A-------------------G---A----------------- 1268

CONSENSUS.H GC?AGAAATTGCAGGGCCCCTAGGAAAAAGGG?TGTTGGAAATG?GGAA?GGAAGGACATCAG?TGAAAGA 1172
HIVVI525    --T-----------------------------C-----------T----G-------------A------- 1277
HIVVI557    --C-----------------------------A-----------C----A-------------C------- 1274

CONSENSUS.O GCAA?AAA?TGTCGAGCACCTAG?AAAA?GGGTTGCTGGAAATGTGGACAGGAAGGTCACCAAATGAAAGA 1156
HIVANT70    ----G---T--------------G----A------------------------------------------ 1286
HIVMVP51    ----A---C--------------A----G------------------------------------------ 1286

SIVCPZGAB   GCTAGAAATTGTAAAGCACCAAGAAGAAAAGGCTGTTGGCGGTGTGGGCAAGAGGGACACCAAATGAAAGA 1304
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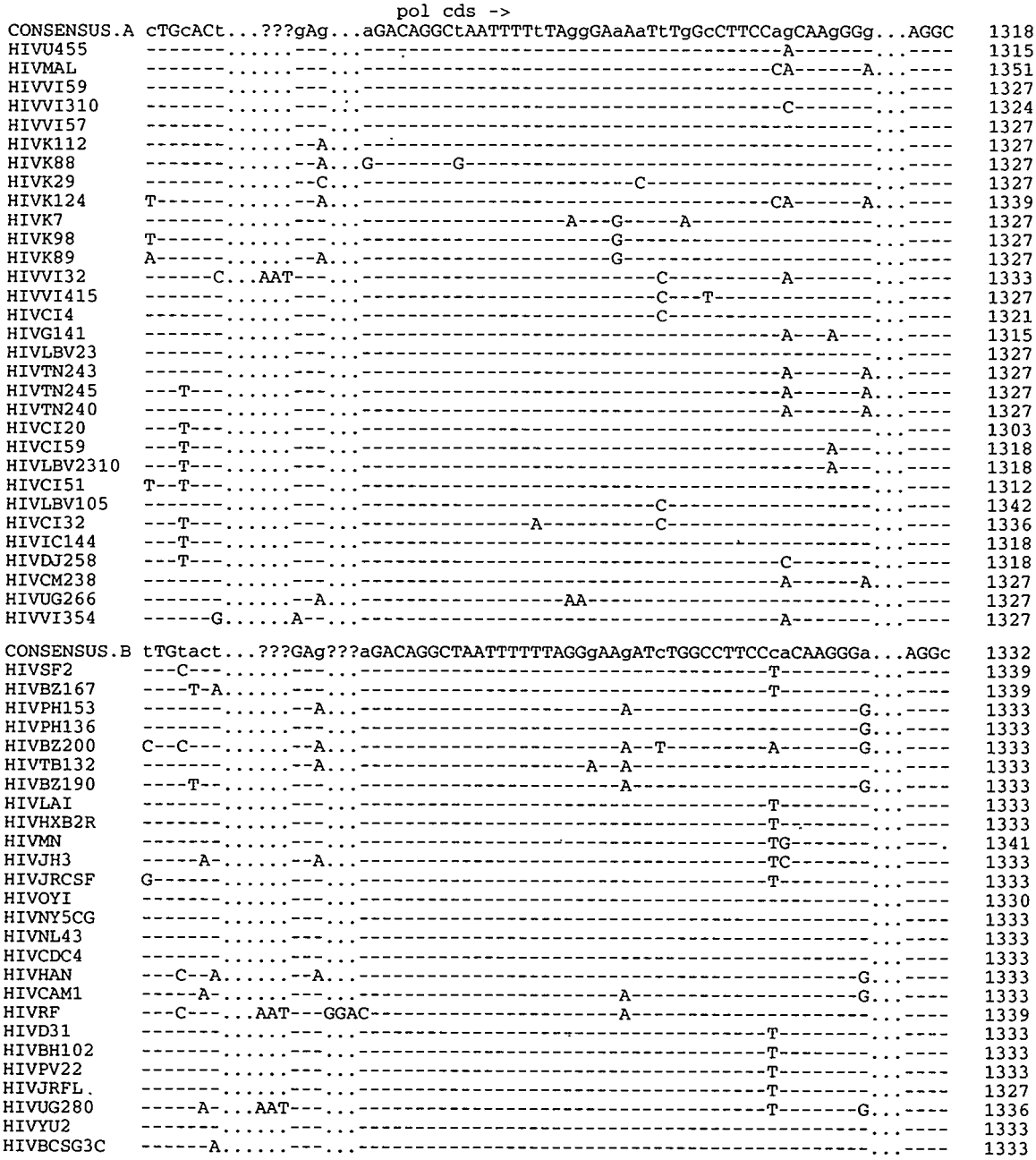
HIV1 GAG


pol cds ->
CONSENSUS.A cTGcACt...???gAg...aGACAGGCtAATTTTTtTAggGAaAaTtTgGcCTTCCagCAAgGGg...AGGC 1318
HIVU455 -------.....---...----------A------...---- 1315
HIVMAL -------.....---...----------CA------A...---- 1351
HIVVI59 -------.....---...---------- 1327
HIVVI310 -------.....---...----------C------...---- 1324
HIVVI57 -------.....---...---------- 1327
HIVK112 -------.....--A...---------- 1327
HIVK88 -------.....--A...G-------G---------- 1327
HIVK29 -------.....--C...----------C---------- 1327
HIVK124 T------.....--A...----------CA------A...---- 1339
HIVK7 -------.....---...----------A---G-----A---------- 1327
HIVK98 T------.....---...----------G---------- 1327
HIVK89 A------.....--A...----------G---------- 1327
HIVVI32 ------C...AAT---...----------C----------A------...---- 1333
HIVVI415 -------.....---...----------C---T---------- 1327
HIVCI4 -------.....---...----------C---------- 1321
HIVG141 -------.....---...----------A---A---...---- 1315
HIVLBV23 -------.....---...---------- 1327
HIVTN243 -------.....---...----------A------A...---- 1327
HIVTN245 ---T---.....---...----------A------A...---- 1327
HIVTN240 -------.....---...----------A------A...---- 1327
HIVCI20 ---T---.....---...---------- 1303
HIVCI59 ---T---.....---...----------A---...---- 1318
HIVLBV2310 ---T---.....---...----------A---...---- 1318
HIVCI51 T--T---.....---...---------- 1312
HIVLBV105 -------.....---...----------C---------- 1342
HIVCI32 ---T---.....---...----------A----------C---------- 1336
HIVIC144 ---T---.....---...---------- 1318
HIVDJ258 ---T---.....---...----------C------...---- 1318
HIVCM238 -------.....---...----------A------A...---- 1327
HIVUG266 -------.....--A...----------AA---------- 1327
HIVVI354 ------G.....A--...----------A------...---- 1327
CONSENSUS.B tTGtact...???GAg???aGACAGGCTAATTTTTTAGGgAAgATcTGGCCTTCCcaCAAGGGa...AGGc 1332
HIVSF2 ---C---.....---...----------T--------...---- 1339
HIVBZ167 ----T-A.....---...----------T--------...---- 1339
HIVPH153 -------.....--A...----------A----------G...---- 1333
HIVPH136 -------.....---...----------G...---- 1333
HIVBZ200 C--C---.....--A...----------A--T---------A-------G...---- 1333
HIVTB132 -------.....--A...----------A--A----------...---- 1333
HIVBZ190 ----T--.....---...----------A----------G...---- 1333
HIVLAI -------.....---...----------T--------...---- 1333
HIVHXB2R -------.....---...----------T--------...---- 1333
HIVMN -------.....---...----------TG-------...---. 1341
HIVJH3 -----A-.....--A...----------TC-------...---- 1333
HIVJRCSF G------.....---...----------T--------...---- 1333
HIVOYI -------.....---...---------- 1330
HIVNY5CG -------.....---...---------- 1333
HIVNL43 -------.....---...---------- 1333
HIVCDC4 -------.....---...---------- 1333
HIVHAN ---C--A.....--A...----------G...---- 1333
HIVCAM1 -----A-.....---...----------A----------G...---- 1333
HIVRF ---C---...AAT---GGAC----------A----------...---- 1339
HIVD31 -------.....---...----------T--------...---- 1333
HIVBH102 -------.....---...----------T--------...---- 1333
HIVPV22 -------.....---...----------T--------...---- 1333
HIVJRFL -------.....---...----------T--------...---- 1327
HIVUG280 -----A-...AAT---...----------T-------G...---- 1336
HIVYU2 -------.....---...---------- 1333
HIVBCSG3C ------A.....---...---------- 1333

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                                    pol cds ->
CONSENSUS.C cTGTACt......GAG...AGgCAGGCtAATTTTTTAGGGAAaATtTGGCCTtCCcAcAAGGGG...AGGC   1315
HIVUG268    -------.......---...--A-----C----------G---------C--A--------...----   1315
HIVSM145    -------.......---...-------------------------------------------...----   1321
HIVZAM18    ------C.......---...-------------------------C-----------------...----   1327
HIVZAM19    -------.......---...-------------------------C-----------------...----   1138
HIVZAM20    T------.......---...--A-----------------------------------A------...----   1321
HIVDJ259    -------.......---...--A---------------------------------A--------...----   1324
HIVVI313    -------.......---...---------------------------------------T--------...----   1324

CONSENSUS.D tTGCACt......Gaa...AGACAGGCTAATTTTTTAGGGAaaaTtTGGCCTTCCcaCAAGGGa...aGGC   1326
HIVELI      -------.......--G...----------------------G----------------------...----   1336
HIVZ2Z6     -------.......---...----------------------G----------------------...----   1339
HIVNDK      -------.......---...----------------------G----------------------...----   1327
HIVVI205    -------.......---...-------------------------------------T--------...----   1339
HIVG109     -------.......---...-----------------------------------A-------G...----   1345
HIVK31      -------.......---...----------------------G-C----------G--------...G---   1333
HIVUG274    G------.......---...-------------------------------------------G...----   1336
HIVUG270    ------A.......---...-------------------------C----------------G...----   1336
HIVSE365    -------.......-G-...-----------------------------------AG------G...----   1336
HIVVI203    -------.......---...----------------------G----------------------...----   1336

CONSENSUS.F CTGCACt......GAa...aGaCAGGCtAATTTTTTAGGGAAAATTTGGCCTTCCaACAAgGGG...AgGC   1297
HIVVI174    -------.......---...-------------------------------------------...----   1321
HIVVI69     -------.......--G...--------C-------------------------------------...----   1318
HIVBZ162    -------.......---...G-----------------------------C---------...----   1317
HIVVI325    ------C.......---...--G-----G---------------------------A---...-A--   1318

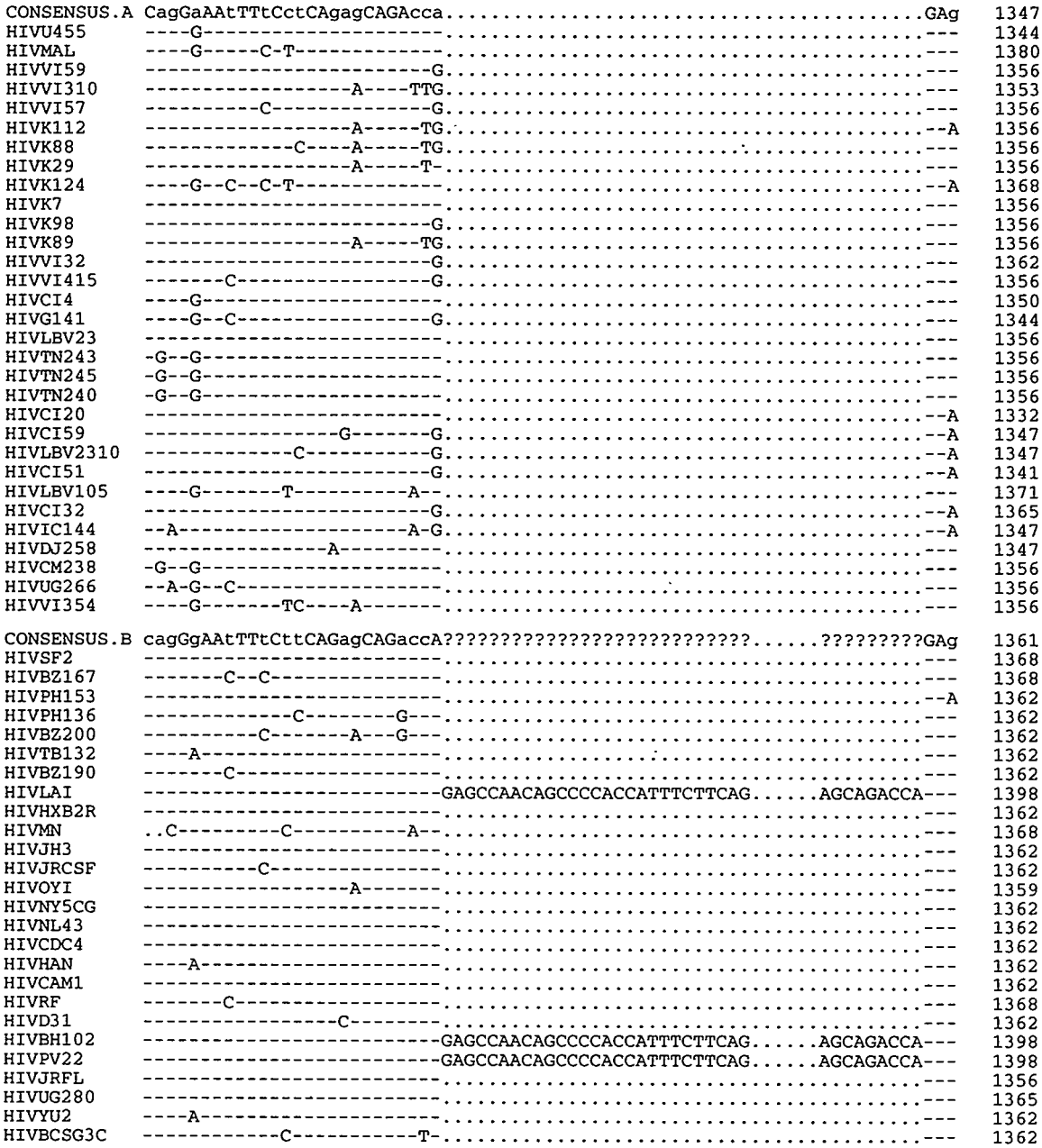
CONSENSUS.G CTGCACA......GAG...AGACAGGCTAATTTTTTAGGGA?AAT?TGGCCTTCCCACAAGGGG...AGGC   1274
HIVLBV217   -------.......---...----------------------A---C--------------...----   1330
HIVVI191    -------.......---...----------------------G---T--------------...----   1327

CONSENSUS.H ?TGCACA......GA?...AGACAGGCTAATTTTTTAGGGAAAAT?TGG?CT?CCA?CAAAGGG...AGGC   1225
HIVVI525    T------.......--G...-------------------------C---C--T---G--------...----   1336
HIVVI557    C------.......--A...-------------------------T---T--C---A--------...----   1333

CONSENSUS.O TTGCA?A......AATGGAA?ACAGGCAAATTTTTTAGG?AA?TACTGGCCTCCGGGGGGCACG...AGGC   1214
HIVANT70    -----G-......-------A----------------C--A----------------------...----   1348
HIVMVP51    -----A-......-------G----------------G--G----------------------...----   1348

SIVCPZGAB   CTGCACA......GGA...AGACAGGTGAATTTTTTAGGGAAAGGTTGGCCTTCCCGCAGCGGG...AGGC   1363
```

HIV1 GAG


CONSENSUS.A CagGaAAtTTtCctCAgagCAGAcca.....GAg 1347
HIVU455 ----G----------.....--- 1344
HIVMAL ----G-----C-T----------.....--- 1380
HIVVI59 ----------G.....--- 1356
HIVVI310 ----------A----TTG.....--- 1353
HIVVI57 ----------C----------G.....--- 1356
HIVK112 ----------A-----TG.....--A 1356
HIVK88 ----------C----A-----TG.....--- 1356
HIVK29 ----------A-----T-.....--- 1356
HIVK124 ----G--C--C-T----------.....--A 1368
HIVK7 ----------.....--- 1356
HIVK98 ----------G.....--- 1356
HIVK89 ----------A-----TG.....--- 1356
HIVVI32 ----------G.....--- 1362
HIVVI415 -------C----------G.....--- 1356
HIVCI4 ----G----------.....--- 1350
HIVG141 ----G--C----------G.....--- 1344
HIVLBV23 ----------.....--- 1356
HIVTN243 -G--G----------.....--- 1356
HIVTN245 -G--G----------.....--- 1356
HIVTN240 -G--G----------.....--- 1356
HIVCI20 ----------.....--A 1332
HIVCI59 ----------G-------G.....--A 1347
HIVLBV2310 ----------C----------G.....--A 1347
HIVCI51 ----------G.....--A 1341
HIVLBV105 ----G-------T----------A--.....--- 1371
HIVCI32 ----------G.....--A 1365
HIVIC144 --A----------A-G.....--A 1347
HIVDJ258 ----------A---------.....--- 1347
HIVCM238 -G--G----------.....--- 1356
HIVUG266 --A-G--C----------.....--- 1356
HIVVI354 ----G-------TC----A-------.....--- 1356
CONSENSUS.B cagGgAAtTTtCttCAGagCAGaccA??????????????????????????.....?????????GAg 1361
HIVSF2 ----------.....--- 1368
HIVBZ167 -------C--C----------.....--- 1368
HIVPH153 ----------.....--A 1362
HIVPH136 ----------C--------G---.....--- 1362
HIVBZ200 ----------C-------A---G---.....--- 1362
HIVTB132 ----A----------.....--- 1362
HIVBZ190 -------C----------.....--- 1362
HIVLAI ----------GAGCCAACAGCCCCACCATTTCTTCAG.....AGCAGACCA--- 1398
HIVHXB2R ----------.....--- 1362
HIVMN ..C---------C----------A--.....--- 1368
HIVJH3 ----------.....--- 1362
HIVJRCSF ----------C----------.....--- 1362
HIVOYI ----------A-------.....--- 1359
HIVNY5CG ----------.....--- 1362
HIVNL43 ----------.....--- 1362
HIVCDC4 ----------.....--- 1362
HIVHAN ----A----------.....--- 1362
HIVCAM1 ----------.....--- 1362
HIVRF -------C----------.....--- 1368
HIVD31 ----------C--------.....--- 1362
HIVBH102 ----------GAGCCAACAGCCCCACCATTTCTTCAG.....AGCAGACCA--- 1398
HIVPV22 ----------GAGCCAACAGCCCCACCATTTCTTCAG.....AGCAGACCA--- 1398
HIVJRFL ----------.....--- 1356
HIVUG280 ----------.....--- 1365
HIVYU2 ----A----------.....--- 1362
HIVBCSG3C ----------C----------T-.....--- 1362

```
CONSENSUS.C CAGGGAATTTCCTtCAGAgCAGgCCa??????????????????????????????????????????gag  1344
HIVUG268    ----------------------A---.....................................................--A  1344
HIVSM145    ------------------A-------GAGCCAACAGCCCCACCAGCAGAGAGCTTCAGGGTCAGGCCA---  1392
HIVZAM18    -------------------------GAGCCAACAGCCCCT.....................AGGCCA---  1377
HIVZAM19    ------------------------.....................................................--N  1167
HIVZAM20    -------------C----A-------GAGCCAACAGCCCCACCAGCAGAGAACTTCAGG.............  1380
HIVDJ259    ----------------------A--T.....,.....................................---  1353
HIVVI313    -------------C----A---A---.....................................---  1353

CONSENSUS.D CaGGgAAcTT?CttCAgAGCAGACca.....................................GAG  1354
HIVELI      -G--------T--C--A---------.....................................---  1365
HIVZ2Z6     -G--------T---------------.....................................---  1368
HIVNDK      -G-----T--T---------------.....................................---  1356
HIVVI205    -G-----T--T---------------.....................................---  1368
HIVG109     ----A-----C---------------.....................................---  1374
HIVK31      -T--A-----C--------------G.....................................---  1362
HIVUG274    ----------C-------------TG.....................................---  1365
HIVUG270    ----------C---------------.....................................---  1365
HIVSE365    ----------T-C-------------.....................................---  1365
HIVVI203    ----------C---------------.....................................---  1365

CONSENSUS.F C?GG?AATTTtCT?CAGAgCAGaCCA.....................................GAG  1323
HIVVI174    -C--A--------T------------.....................................---  1350
HIVVI69     -A--G--------T------------.....................................---  1347
HIVBZ162    -C--A-----C--C----A---G---.....................................---  1346
HIVVI325    -A--G--------C------------.....................................---  1347

CONSENSUS.G C?GGGAATTTTCTTCAGA?CAG??CA.....................................GAG  1299
HIVLBV217   -A----------------A---AC--.....................................---  1359
HIVVI191    -G----------------T---GA--.....................................---  1356

CONSENSUS.H CAGGGAATTTTCT?CAGAGCAGGCCA.....................................GAG  1253
HIVVI525    -------------T------------.....................................---  1365
HIVVI557    -------------C------------.....................................---  1362

CONSENSUS.O CAGGCAATTATGTGCAGA?AC?AG??.....................................??C  1237
HIVANT70    ------------------G--C--CA.....................................CA-  1377
HIVMVP51    ------------------A--A--TG.....................................TC-  1377

SIVCPZGAB   CAGGCAACTTTGTGCAGAACAGAACA.....................................GAA  1392
```

HIV1 GAG

```
CONSENSUS.A CCaaCAGCcCCACcaGCAGAg.....................a?cttt???gGgatgggggaagAgataac   1393
HIVU455     --------------------A.....................-T----...-----------A----G--   1391
HIVMAL      --------------------.....................-G---C...---T-T-----G-------A   1427
HIVVI59     --------------------.....................-T---G...A----AA--A----A--G--   1403
HIVVI310    --------T-----------.....................-G----...--------------C-----   1400
HIVVI57     --------------------.....................CT----...--A---------------G-   1403
HIVK112     --------------------.....................-T----...-----------------GG-   1403
HIVK88      --------------------.....................-T--G-...-----------------G-   1403
HIVK29      --------------------.....................-T----...--------------------   1403
HIVK124     --------------------.....................-G---C...---T-T-----G--------   1415
HIVK7       --------------------.....................-T----...A----A-A----------G-   1403
HIVK98      --------------------.....................-T----...--------------------   1403
HIVK89      --------------------.....................-T--G-...-----------------G-   1403
HIVVI32     ---T----------------.....................-T----...-----------------G-   1409
HIVVI415    --------------------.....................-T-G--...----------G------C..   1401
HIVCI4      --------------------.....................CT-C-G...--------A--G--------   1397
HIVG141     ---T----------------.....................-G---C...---T-T-----G--------   1391
HIVLBV23    --------------------.....................-TGA-CTTT-------------------   1406
HIVTN243    --------------------A.....................GA--GG...----G-----------C---   1403
HIVTN245    --------------------A.....................-A--GG...--------------------   1403
HIVTN240    --------------------A.....................-A--GG...--------------------   1403
HIVCI20     --------------------.....................-G----...------A-------------   1379
HIVCI59     --------------------.....................-A----...-------A----C-------   1394
HIVLBV2310  --------------------.....................-G----...--------------------   1394
HIVCI51     --------------------.....................-G----...---T----------------   1388
HIVLBV105   --CT----------C------.....................-G----...---T-C--A--G--AG----   1418
HIVCI32     --------------------.....................-G---C...-------A----------G-   1412
HIVIC144    --------------------.....................-G----...-------A----A---C---   1394
HIVDJ258    -------------T-------.....................-G----...--------------------   1394
HIVCM238    --------------------A.....................-A--GG...--------------------   1403
HIVUG266    --------------------.....................-T---G...A-----AAA--------G--   1403
HIVVI354    ----------------------.....................-G---C...---T-C--A--G------G-   1403

CONSENSUS.B CCaACAGCcCCacCAGaagAG.....................AgCtTC...aGGTttgggGaaGagAcaaC   1408
HIVSF2      --------------------.....................------...----------G----A---   1415
HIVBZ167    --------------------.....................-T----...--------------------   1415
HIVPH153    --------------------.....................------...-----CA-------------   1409
HIVPH136    --------------------.....................------...--------------------   1409
HIVBZ200    ----------------C----.....................------...G----C--A--G----TG--   1409
HIVTB132    --G-------------C----.....................------...--------------------   1409
HIVBZ190    ----------------G----.....................------...--------------------   1409
HIVLAI      --------------------.....................------...----C-----T---------   1445
HIVHXB2R    --------------------.....................------...----C-----T---------   1409
HIVMN       --------------------.....................------...--------------------   1415
HIVJH3      ----------T-----G----.....................------...--------------------   1409
HIVJRCSF    --------------------.....................------...------------------G-   1409
HIVOYI      ----------------C----.....................------...G-------------------   1406
HIVNY5CG    --------------------.....................------...--------------------   1409
HIVNL43     --------------------.....................------...--------------------   1409
HIVCDC4     ----------------G----.....................------...-----------C--------   1409
HIVHAN      --------------------.....................------...-------------CA---G-   1409
HIVCAM1     --------------------.....................------...----------------A---   1409
HIVRF       --------------------.....................------...--------------------   1415
HIVD31      --------------------.....................------...------------------G-   1409
HIVBH102    --------------------.....................------...----C-----T---------   1445
HIVPV22     --------------------.....................------...----C-----T---------   1445
HIVJRFL     ------------------A--.....................------...------------------G-   1403
HIVUG280    --------------------.....................------...-------T---------C--   1412
HIVYU2      ------------T--------.....................---G--...--------A-----------   1409
HIVBCSG3C   --------T------------.....................------...----------G--------   1409
```

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CONSENSUS.C CCAAcAGCCcCACcAGCAGAG??????????????????????AGCTTC...aGGTTC...GAGGaGaCaAC  1388
HIVUG268    --------------------CCAACAGCCCCACCGGCAGAG------...------...----G------  1409
HIVSM145    --------------------.....................------...------...----------  1436
HIVZAM18    --------------------.....................------...------...--------G--  1421
HIVZAM19    ----N----N---N-------.....................------...------...----------  1211
HIVZAM20    --------------------.....................------...------...----------  1424
HIVDJ259    --------------------.....................------...G-----...------C-G--  1397
HIVVI313    --------------------.....................------...------...----------  1397

CONSENSUS.D CCaACAGCCCCACCAGCAgAG.....................AGcTTC...GGGTTtGGgGAggAgAtaaC  1401
HIVELI      --------------------.....................------...----------A--------  1412
HIVZ2Z6     --------------------.....................------...----------A--------  1415
HIVNDK      --------------------.....................------...--------------------  1403
HIVVI205    ------------------A-.....................------...--------------------  1415
HIVG109     --------------------.....................------...--------------A--G--  1421
HIVK31      --G-----------------.....................--T---...--------------------  1409
HIVUG274    --------------------.....................------...----------A--------  1412
HIVUG270    --------------------.....................------...--------------------  1412
HIVSE365    --------------------.....................------...----------------CG--  1412
HIVVI203    --------------------.....................------...-----C--A-------A-G-  1412

CONSENSUS.F CCaaCAGCCCCaCCAGCAGAG.....................AgCTTc...GGGTTC?GaGAGGAGATAAc  1369
HIVVI174    --------------------.....................------...------G-------------  1397
HIVVI69     ---T-------G---------.....................-----T...------A-------------  1394
HIVBZ162    --------------------.....................------...------A------------A  1393
HIVVI325    --G-----------------.....................-A----...------G-G-----------  1394

CONSENSUS.G CCA?CAGCCCCACC?GCAGA?.....................agcctc...gggttcgggGAGGAGATA?C  1342
HIVLBV217   ---T----------C-----G.....................------...------------------G-  1406
HIVVI191    ---A----------T-----A.....................------------------------A-  1388

CONSENSUS.H CCAACAGCCCCACCAGCAGAG.....................AGCTT?...GGGTT?GGAGAGGA?ATGAC  1297
HIVVI525    --------------------.....................-----T...-----C--------G-----  1412
HIVVI557    --------------------.....................-----C...-----T--------A-----  1409

CONSENSUS.O CCATCAGCCCCACC?ATGGAG.....................................GAGG?AGTGAA  1267
HIVANT70    --------------G------.....................................----A------  1409
HIVMVP51    --------------A------.....................................----C------  1409

SIVCPZGAB   CCAACGGCCCCACCGATAGAG.....................AGTTAT...GGGTACCAGGAGGAAGAGAA  1439
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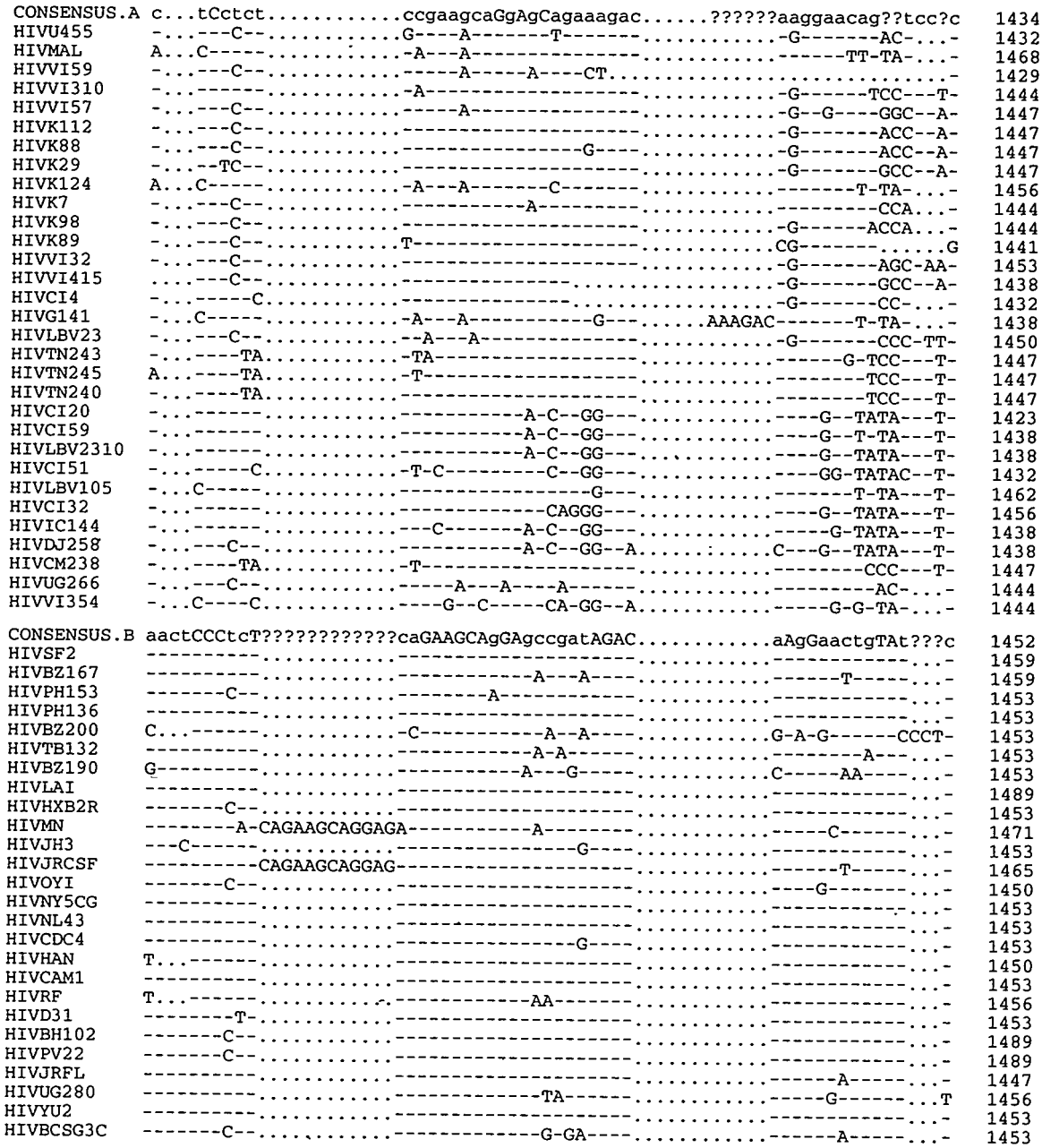
HIV1 GAG


CONSENSUS.A c...tCctct.....ccgaagcaGgAgCagaaagac.....??????aaggaacag??tcc?c 1434
HIVU455 -...---C--.....G----A-------T-------.....-G-------AC-...- 1432
HIVMAL A...C-----.....-A---A----------.....------TT-TA-...- 1468
HIVVI59 -...---C--.....-----A-----A----CT.....- 1429
HIVVI310 -...------.....-A----------.....-G------TCC---T- 1444
HIVVI57 -...---C--.....-----A----------.....-G--G----GGC--A- 1447
HIVK112 -...---C--.....----------.....-G-------ACC--A- 1447
HIVK88 -...---C--.....----------G----.....-G-------ACC--A- 1447
HIVK29 -...--TC--.....----------.....-G-------GCC--A- 1447
HIVK124 A...C-----.....-A---A-------C-------.....-------T-TA-...- 1456
HIVK7 -...---C--.....----------A---------.....---------CCA...- 1444
HIVK98 -...---C--.....----------.....-G------ACCA...- 1444
HIVK89 -...---C--.....T----------.....CG-------.....G 1441
HIVVI32 -...---C--.....----------.....-G-------AGC-AA- 1453
HIVVI415 ...---C--.....----------.....-G-------GCC--A- 1438
HIVCI4 -...-----C.....----------.....-G-------CC-...- 1432
HIVG141 -...C-----.....-A---A----------G---.....AAAGAC-------T-TA-...- 1438
HIVLBV23 -...---C--.....--A---A----------.....-G-------CCC-TT- 1450
HIVTN243 -...----TA.....-TA----------.....------G-TCC---T- 1447
HIVTN245 A...----TA.....-T----------.....--------TCC---T- 1447
HIVTN240 -...----TA.....----------.....--------TCC---T- 1447
HIVCI20 -...------.....----------A-C--GG---.....----G--TATA---T- 1423
HIVCI59 -...------.....----------A-C--GG---.....----G--T-TA---T- 1438
HIVLBV2310 -...------.....----------A-C--GG---.....----G--TATA---T- 1438
HIVCI51 -...-----C.....-T-C---------C--GG---.....----GG-TATAC--T- 1432
HIVLBV105 -...C-----.....----------G---.....-------T-TA---T- 1462
HIVCI32 -...------.....----------CAGGG---.....----G--TATA---T- 1456
HIVIC144 -...------.....---C-------A-C--GG---.....-----G-TATA---T- 1438
HIVDJ258 -...---C--.....----------A-C--GG--A.....C---G--TATA---T- 1438
HIVCM238 -...----TA.....-T----------.....--------CCC---T- 1447
HIVUG266 -...---C--.....-----A---A----A------.....---------AC-...- 1444
HIVVI354 -...C----C.....----G--C-----CA-GG--A.....-----G-G-TA-...- 1444
CONSENSUS.B aactCCCtcT???????????caGAAGCAgGAgccgatAGAC.....aAgGaactgTAt???c 1452
HIVSF2 ----------.....----------.....----------...- 1459
HIVBZ167 ----------.....----------A---A----.....------T-----...- 1459
HIVPH153 -------C--.....--------A----------.....----------...- 1453
HIVPH136 ----------.....----------.....----------...- 1453
HIVBZ200 C...------.....-C----------A--A----.....G-A-G------CCCT- 1453
HIVTB132 ----------.....----------A-A------.....--------A---...- 1453
HIVBZ190 G---------.....----------A---G-----.....C-----AA----...- 1453
HIVLAI ----------.....----------.....----------...- 1489
HIVHXB2R -------C--.....----------.....----------...- 1453
HIVMN --------A-CAGAAGCAGGAGA----------A--------.....-----C-------...- 1471
HIVJH3 ---C------.....----------G----.....----------...- 1453
HIVJRCSF ----------CAGAAGCAGGAG----------.....------T------...- 1465
HIVOYI -------C--.....----------.....----G-------...- 1450
HIVNY5CG ----------.....----------.....----------...- 1453
HIVNL43 ----------.....----------.....----------...- 1453
HIVCDC4 ----------.....----------G----.....----------...- 1453
HIVHAN T...------.....----------.....----------...- 1450
HIVCAM1 ----------.....----------.....----------...- 1453
HIVRF T...------.....----------AA-------.....----------...- 1456
HIVD31 --------T-.....----------.....----------...- 1453
HIVBH102 -------C--.....----------.....----------...- 1489
HIVPV22 -------C--.....----------.....----------...- 1489
HIVJRFL ----------.....----------.....------A-----...- 1447
HIVUG280 ----------.....----------TA------.....-----G------...T 1456
HIVYU2 ----------.....----------.....----------...- 1453
HIVBCSG3C -------C--.....----------G-GA----.....------A-----...- 1453

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CONSENSUS.C c...CCcgCT...........CcGAAgCAGGAGCcgAaAGAc???????????agggaa?????????C   1423
HIVUG268    T...---C--..........--------------------.....------.........-   1444
HIVSM145    -...------..........-------------T------A.....................-   1465
HIVZAM18    -...------..........-----T---------------.....------.........-   1456
HIVZAM19    -...--N---..........-----T---------------.....------.........-   1246
HIVZAM20    -...------..........----------------G----.....--TCCTACAGGGGAA-   1468
HIVDJ259    -...---C--..........-A-----------TA------AAGGAACCCTAC-A---G.....-   1444
HIVVI313    -...---T--..........----------------------.....-A----.........-   1432

CONSENSUS.D c...CCCtCt...........cagAAaCAgGAGCagAAaGAc???????????aagGAactgtaT...C   1442
HIVELI      -...------..........--A------------------.....------------...-   1453
HIVZ2Z6     -...------..........----------------------.....------------...-   1456
HIVNDK      -...------..........----------------------.....------------...-   1444
HIVVI205    -...------..........--------A------------.....--------AA--...-   1456
HIVG109     -...---C--..........--------A------------AAGGAAAAAGAC----------...-   1474
HIVK31      A...------..........----------------------.....-----GA-----...-   1450
HIVUG274    A...------..........----------------------.....-----G-CA-G-...-   1453
HIVUG270    A...------..........----------------------.....-----G------...-   1453
HIVSE365    -...------..........----------------------.....------------...-   1453
HIVVI203    -...-----C..........GC---G-------CA--G--G.....------G--A---...-   1450

CONSENSUS.F C...CCCTCT...........CCGAaGCAGGAGcaGAA?Gac...........gAGGgACtGtatcCTC   1412
HIVVI174    -...------..........----------------G-G-.....----------------   1441
HIVVI69     -...------..........----------------G---.....----------C-----   1438
HIVBZ162    -...------..........----------------A--A.....----------C----   1437
HIVVI325    -...------..........----G-------AC---A---.....A---A--A-GG-T---   1438

CONSENSUS.G C...?CCTC?...........CCGAAGCAGGA?CC?agggac...........AAGGA?CTATATcctC   1381
HIVLBV217   -...C----C..........----------G--A.....-----G------...-   1441
HIVVI191    -...T----T..........----------A--G------.....-----A----------   1432

CONSENSUS.H C...CCC?CT...........CC?AA?CAGGAG???A?GGA?...........???GAA......?CTC   1323
HIVVI525    -...---T--..........--G--G------CCC-G---C...........AAG---.....C---   1450
HIVVI557    -...---C--..........--A--A------AGG-A---T...........GCA---.....T---   1447

CONSENSUS.O G...G?ACA?...........GAGAATCAG???CAGAA?GGG......G??C?G?A?GAGCT?TA?...C   1301
HIVANT70    -...-G---G..........---------GAA-----A---.....-GC-C-A-C-----C--T...-   1456
HIVMVP51    -...-A---A..........---------AGT-----G---.....-AT-A-G-A-----G--C...-   1456

SIVCPZGAB   G...AGCCAG...........GAGAAGAAAGAGGGAGAGAGC.............AGTCTATATCCAC   1480
```

HIV1 GAG

```
CONSENSUS.A CtTtAgttTCCcTCAAATCACTCTTTGGCAACGACCccTTGTCACAG  1481
HIVU455     -------------------------------------------------  1479
HIVMAL      ------C-----------------------------AG---------  1515
HIVVI59     ---C-A--------------                               1449
HIVVI310    -C------------------                               1464
HIVVI57     --------------------                               1467
HIVK112     -C-C-A-C------------                               1467
HIVK88      --------------------                               1467
HIVK29      -C---AC-------------                               1467
HIVK124     ------C----G--------                               1476
HIVK7       ---C----------------                               1464
HIVK98      --------------------                               1464
HIVK89      ---C-A--------------                               1461
HIVVI32     --------------------                               1473
HIVVI415    --------------------                               1458
HIVCI4      ---C-A--------------                               1452
HIVG141     ------C-------------                               1458
HIVLBV23    ---C---C------------                               1470
HIVTN243    ------------------------------------              1485
HIVTN245    --------------------                               1467
HIVTN240    --------------------                               1467
HIVCI20     ------C-------------                               1443
HIVCI59     -----AC-------------                               1458
HIVLBV2310  -----AC-------------                               1458
HIVCI51     ------C-------------                               1452
HIVLBV105   -C---AC-------------                               1482
HIVCI32     ------C-------------                               1476
HIVIC144    -----AC-------------                               1458
HIVDJ258    -C---AC-------------                               1458
HIVCM238    --------------------                               1467
HIVUG266    -----A--------------                               1464
HIVVI354    -----ACC------------                               1464

CONSENSUS.B CtTtAgCttCCCTCAgaTcACTCTTTGGCAaCGACCCcTcGTCACaa  1499
HIVSF2      -----A---------------------------------------------  1506
HIVBZ167    ---------------A----                               1479
HIVPH153    ---C-----------A--T-                               1473
HIVPH136    ---------------A----                               1473
HIVBZ200    -C------------------                               1473
HIVTB132    -----A--G------A----------------------             1491
HIVBZ190    -C------G-----------                               1473
HIVLAI      -----A---------------------------------------------  1536
HIVHXB2R    -----A----------G-----------------------------------  1500
HIVMN       ---------------A--------------------A-T-------     1518
HIVJH3      ---------------------------------------------CC     1500
HIVJRCSF    -----A---------------------------------------------  1512
HIVOYI      -----A-C-----------------------------A---------     1497
HIVNY5CG    ------------------------------G----------------     1500
HIVNL43     ------------------------------G----------------     1500
HIVCDC4     -------------------------------------A---------     1500
HIVHAN      -C-----C-------A--------------G----------------     1497
HIVCAM1     ----------------------------------------------      1500
HIVRF       ---------------A--------------------A--------G     1503
HIVD31      -------------------------------------------------   1500
HIVBH102    -----A---------------------------------------------  1536
HIVPV22     -----A---------------------------------------------  1536
HIVJRFL     -----A---------------------------------------------  1494
HIVUG280    ---C-----------------                              1476
HIVYU2      ------------------------------G----------------     1500
HIVBCSG3C   -C-------------------------------------------------  1500
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CONSENSUS.C CCTTAAcTtCCCTCAaATCACTCTTTGGCAACGACCCCT                    1462
HIVUG268    ------T-------------                                       1464
HIVSM145    ---------------------                                      1485
HIVZAM18    --------------------                                       1476
HIVZAM19    ----------------------------------------                   1285
HIVZAM20    --------G-----------                                       1488
HIVDJ259    --------G------G----                                       1464
HIVVI313    --------------------                                       1452

CONSENSUS.D CtttAgCttCCCTCAaATCACTCTTTGGCAACGACCCCTtGTcaCAA            1489
HIVELI      -----A----------------------------------------G---        1500
HIVZ2Z6     ---C-A--G--------------------------------------T----      1503
HIVNDK      ------------------------------------------C-------        1491
HIVVI205    -----A-C-----------                                        1476
HIVG109     -C---A---------G----                                       1494
HIVK31      -C------------------                                       1470
HIVUG274    --------------------                                       1473
HIVUG270    ---C----G-----------                                       1473
HIVSE365    --------------------                                       1473
HIVVI203    --G-----------------                                       1470

CONSENSUS.F CcTTAgCtTCCCTCAAATCA                                       1432
HIVVI174    -------C-----------                                        1461
HIVVI69     --------------------                                       1458
HIVBZ162    --------------------                                       1457
HIVVI325    -T---A--------------                                       1458

CONSENSUS.G CTTTA??TTCCCTCAAATCA                                       1399
HIVLBV217   -----AC-----------                                         1461
HIVVI191    -----GT-----------                                         1452

CONSENSUS.H C?TTA?CTTCCCTCAAATCA                                       1341
HIVVI525    -C---G--------------                                       1470
HIVVI557    -T---A--------------                                       1467

CONSENSUS.O C?TTTGCCTCCCTCAAATCCCTCTTTGGGACAGACCAATAG                  1341
HIVANT70    -G-------------------------------------                   1494
HIVMVP51    -A-----------------------------------------               1497

SIVCPZGAB   CA...ACCTCCCTCAAATCACTCTTTGGCAGCGACCCCTCATCCCAG            1524
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HIV1 TAT

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                                <- vpR
CONSENSUS.A   ATGGA?CC?GTAGATCCTAaCCTAGAGCCCTGGAAcCA?CCGGGAAGTcAGCCTACAACTgCTTGTAgCAAg   69
HIVU455       -----G--A-------------------------A--C-------------------------------C   72
HIVSF170      -----T--A-----------------------------T---------------------C----------A   72
HIV1UG273A    -----T--G-------------------------T--T---------A----------C-----------   72
HIV1UG275A    -----T--G-----------------------------T---------------------C------A----   72
HIV1DJ263A    -----G--G----------G-----------------C-------------------------------   72
HIV1DJ264A    -----G--A----------G-----------------C-------------------------------T   72
HIV1DJ258A                                                                 ----------   16

CONSENSUS.B   ATGGAgCCAGTAGATCCTAgacTAGAGCCCTGGaAGCATCCAGGAAGtCAGCCTAagaCtgcttGtAccaat   72
HIVLAI        ---------------------------------------------------------A-------------C-   72
HIVTH475A     ---------------------------------------------------------A-------------C-   72
HIVHXB2R      ---------------------------------------------------------A---------------   72
HIVNL43       ---------------------------------------------------------A---------------   72
HIVMN         ------------------------------------------------------------------------C-   72
HIVSC         -----T-----------------------------------------------AG-----------TC-   72
HIVBAL1       -------------------A-------------------------------------------------C-   72
HIVJRCSF      -------------------C---------------------------------------------------   72
HIVJRFL       -------------------C-------------------------------------------------C-   72
HIVNH5        ------------------------------------------------------C---------C-   72
HIVOYI        ------------------------------------------------------------A---A----   72
HIVSF2        -------------------AT-----------------------------------G-----------A----   72
HIVNY5CG      ---------------------------------------------------------A---------------   72
HIVSF162      ---------------------T-----------------------------------------------A---   72
HIVCAM1       ---------------------------------------------C-------G---------------   72
HIVCDC4       ---------------------------------------------------------A---------------   72
HIVSF33       -------------------AC-----------------------------------G---------C-----C   72
HIVRJS        ---------------------------------------------------------A----AG---------   72
HIVHAN        ---------------------------------------------------------G---CC----------   72
HIVD31        ---------------------------------G-------------------------------------   72
HIVRF         ------------------------------------------------------------------A----   72
HIVYU2        -------------------AC-----------------------------------G----------A----   72
HIVBCSG3C     ---------------------------------------------C--------A--------------A   72

CONSENSUS.C   atgGa?ccagTAGAtCCTAaaCTAGAGCCCTGGAACCATCCaGGAaGTCAgCCTAAAACTgCTTGTActAAg   71
HIV1SM145A                                        ----------T----A----------A---T   37
HIV1ZAM184    -----T--------C-------------------------G-------------------------C---   72
HIV1DJ259A    TCC-TCTAGA---------G-------------------------------------------------A----   72
HIV1DJ373A    -----G--------------C-------------------------------------------------A   72
HIV1UG268A                                        ----------------------C----------   32

CONSENSUS.D   atgGatccagTAGATCCTAaccTAGAGcCCTGGAACCATCCAGGaAGTCAGCCTAggACtcCTTGTAAcAag   72
HIVELI        ------------------------------------------------------------------------   72
HIVZ2Z6       --------------------A---------------------------------A----G---------G-   72
HIVNDK        --------------------T------T-------------------------------G-------T---   72
HIVMAL        --------------------T---------------------G--------------G--------T---   72
HIV1SE365A    ---------------------------------------------------------A---------------C   72
HIV1UG274A    TCC-TCTAGA---------GA-----------------------------------C--------------A   72

CONSENSUS.O   ATGGATCCAGTAGATCCTGAG?TGCCCCCTTGGCA?CACCCTGG?AG??AGCCCCA?A?CCCTTGTAATAAT   65
HIVANT70      --------------------G-------------C---------A--TC-------G-T-------------   72
HIVMVP5180    --------------------A-------------T--------G--CA-------A-C-------------   72

CONSENSUS.CPZ ATGGA?CC??TAGA??CTGA???????CC?TGG??ACACCC??????T???CCA??AAC????TG?AATAA?   40
SIVCPZGAB     -----T--AA----TC----CCTGGAG--C---AA------AGGCAG-CAG---AG---AGTT--T-----T   72
```

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                                                                                \/3'sj\/3' sj   -> rev cds
CONSENSUS.A   TGTTAcTGTAAAatgTGtTGCTggCATTGccaA?ttTGCTTTCTgaacAAaGGCTTAGGCATcTCCTATGGC    140
HIVU455       -----T------G-------------------C-------------A--------------T---------    144
HIVSF170      ------------G---------AT-------C-GC---------ACG-------------------------    144
HIV1UG273A    ------------G---------AT-------C-G----------A--------------------------    144
HIV1UG275A    -------------A--------AT-----TAC-G-----------------------------------------    144
HIV1DJ263A    ---------------A--C-----------T---T-G--------------G---------------------    144
HIV1DJ264A    ---------------A--C--------------T-G--------------G---------------------    144
HIV1DJ258A    -------------AA--C--------------T-G--------------G---------------------     88

CONSENSUS.B   TGCTATTGTAAAaagTGtTGCtttCAtTGccAaGttTGtTTcacaAcAAAAGgCTTAgGCATcTCCTATGGC    144
HIVLAI        ------------------------------------------------------C-------------------    144
HIVTH475A     ------------------------------------------TG-------C-------------------    144
HIVHXB2R      ------------------------------------------T--------C-------------------    144
HIVNL43       ------------------------------------------TG-------C-------------------    144
HIVMN         ---------------------------------------------A-----C-------------------    144
HIVSC         ------------------------------------------------------------------------    144
HIVBAL1       ---------------------------------------C----T--------------------------    144
HIVJRCSF      --------------------C-------------------------------------------------    144
HIVJRFL       ----------------------C-------------C-------T--------------------------    144
HIVNH5        ---------------------A-------------------------------------------------    144
HIVOYI        -------------G-------C----C--T----------------A---------------T---------    144
HIVSF2        ----------------------------T-C-CG----------G--------------------------    144
HIVNY5CG      -------------G-----------------------------------------C-------------------    144
HIVSF162      ------------------------------------------T-------------------------    144
HIVCAM1       ------------C-----------------------------T-------------------------    144
HIVCDC4       ---------------------------------------G-A-----C-------------------    144
HIVSF33       ---------------------------------------C----T------------------A---------    144
HIVRJS        ------------------------------------------------------------------------    144
HIVHAN        --------------------C-----------------------G----------A--------------    144
HIVD31        --------------A--C-----------------------A--------------------------    144
HIVRF         ----------------------A---------------C---TT-------------------------    144
HIVYU2        ------------------------------------------T----A--------------------    144
HIVBCSG3C     ----------------------A--------------------TG-------------------------    144

CONSENSUS.C   TGTTaTtGTAAAaaaTGTaGcTAtCATTGtCtAGTtTGCTTTCagAcaAAAGGcTTAGGCATtTCCTATGGC    143
HIV1SM145A    -----------CTC--------C-----C-------------------------------------------    109
HIV1ZAM184    --------------G---T----------C-C---G-------TA-AC--------------C---------    144
HIV1DJ259A    ------------------------------------------------T-----------------------    144
HIV1DJ373A    ------------------------------------------------------------------------    144
HIV1UG268A    ----T-G-------------T----------A----------T--AC--------------C---------    104

CONSENSUS.D   TGt?ATTGTAAAAAGTGtTGcTATCATTGCCaAgttTGCTTCaTAAcgAAaGGCTTAGGCATcTCCTATGGC    143
HIV1UG269A                                                              ----------T---------     20
HIVELI        ---C-------------------------C----------T---AC--------------------------    144
HIVZ2Z6       ---C------------------------------------------------------------------    144
HIVNDK        ---C------------------------------------------------------------------    144
HIVMAL        ---T-------------C--------------A-G-------------------------------------    144
HIV1SE365A    ---T----------------T------------AA------------A--G---------------------    144
HIV1UG274A    --CT-------------C--------------T-G-------------------------------------    144

CONSENSUS.O   TGCTATTGCAAAAGATGCTGCTATCATTGCTATGTTTGTTTC??AA??AAGGGTTTGGGAATCTCC?ATGGC    132
HIVANT70      ------------------------------------------GT--GA------------------T-----    144
HIVMVP5180    ---------------------------------------AC--AG------------------C-----    144

CONSENSUS.CPZ TG?TA?TG?AAA???TGTTGTTA?CA?TG???????TGCTTCACAAAAAAAGGCTT?GG?AT?TCCTATGGC     94
SIVCPZGAB     --C--T--C---GCT--------T--C--TATATAT--------------------A--A--C---------    144
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HIV1 TAT

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                \/3' sj
CONSENSUS.A     AgGAAGAAGCGG......AgaC?cCGACGAgGAaCTCCTCAaaGcagTaAGGAtCaTCAAAaTCcTaTAcCA    205
HIVU455         -A----------......-A--C----------C--------G------------------C--T-------    210
HIVSF170        ------------......----AG----------------------A------------------------    210
HIV1UG273A      ------------......--T-AG----------------------A------------------------    210
HIV1UG275A      ------------......-AG-AG------A-----------T---A------------------------    210
HIV1DJ263A      ------------......----G------------------G--TC--C-----------------G-----    210
HIV1DJ264A      ------------......----G------------------G--TC--C------G----------G--T--    210
HIV1DJ258A      ------------......----G------------------G--TC--C----C------------G-----    154

CONSENSUS.B     AGGAAGAAGcGG......AGaCAGCGAcgaaGAgCTCcTcaagaCAGTcAGacTCATCAAgtttCTcTAtCA    210
HIVLAI          ------------......---------------C---------G--------------------------    210
HIVTH475A       ------------......--------------------A---GA------------------C----------    210
HIVHXB2R        ------------......--------------------A---GA------------------C----------    210
HIVNL43         ------------......--------------------A---GA------------------C----------    210
HIVMN           ------------......----------------------G------------------------------C--    210
HIVSC           ------------......---------A--------------------------------------------C--    210
HIVBAL1         ------------......-----------------------------G------------------------    210
HIVJRCSF        ------------......---------------C----------------------------------------C--    210
HIVJRFL         ------------......--------------------------------------------C----------    210
HIVNH5          ------------......------------------------------------------------------    210
HIVOYI          ------------......-------------------------------A------------------------    210
HIVSF2          ------------......------------------------G------------------C----------    210
HIVNY5CG        ------------......-------------------------------G------------------------    210
HIVSF162        ------------......----------------------C-------G--GT----------------C--    210
HIVCAM1         ------------......---------------A---------AG----A------------C----------    210
HIVCDC4         ------------......-------------------A--------------A--------CA---------    210
HIVSF33         ------------......--G-------AG---------G-CAG----i---A--------A----------    210
HIVRJS          ------------......-------------------A----A---------A-------A--C-----C--    210
HIVHAN          ------------......--------------------------------------------------C--    210
HIVD31          ------------......----------------------G-------------------------------    210
HIVRF           ---------A--......------------G--C---------G------------------C---T-----    210
HIVYU2          ------------......---------------C-------G------------------AG----------    210
HIVBCSG3C       ------------......-----------------------------------------C----------    210

CONSENSUS.C     AGGAAGAAGCGG......AGACagCGACGAAgcgCTCCTccaAgCAGtGAGGATCATCAaAaTCcTATAtCA    209
HIV1SM145A      ------------......----------------------AG-------------------------------    175
HIV1ZAM184      ------------......----CC--------AT------A--A---C----------------------C--    210
HIV1DJ259A      ------------......-----------------------------------------G-C----------    210
HIV1DJ373A      ------------......-------------------------T-----------------------T-------    210
HIV1UG268A      ------------......-------------A-------------------------------T--------    170

CONSENSUS.D     AGGAAGAAGCGG......AGACAGcGACGaagAcCTcCTcAagGCggTCAggCTCATCAAGtTcCTaTACCA    209
HIV1UG269A      ------------......--------------T-----A-------------------------------     86
HIVELI          ------------......------------G-----------------------------------------    210
HIVZ2Z6         ------------......------A----------T--------------A---------A----------    210
HIVNDK          ------------......------------A--------------A------------------------    210
HIVMAL          ------------......----------------------G---AA--------------A----C-----    210
HIV1SE365A      ------------......---------------A----------AA----A----------T--G-----    210
HIV1UG274A      ------------......-----------C------------A--A----A----------A----------    210

CONSENSUS.O     AGGAAGAAGCGA.........????GAC?A?CAGCTGCTGCAAGC?ATCCAGAT?ATAAAGATCCTGTACCA    187
HIVANT70        ------------.....G---G-C--------------C--------C-----------------          204
HIVMVP5180      ------------.....AGAA---C-G--------------T--------A-----------------          207

CONSENSUS.CPZ   AGGAAGA???GA?C????A??A???GACG?AC??CT?CTG?A?GCAGT?AAAATAATCAAGAT?CT?TA?CA    143
SIVCPZGAB       -------AGC--A-C...-CA-GAC----C--GG--C---C-G-----A--------------T--A--C--    213
```

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                    /- env -> (for more information, see the ENV CDS that follow)
                exon\/exon
CONSENSUS.A     AAGCAAcCCtTaCCCcaaaCccaagGGgtC???cCGaCAGgCCcGaAAGAATCGaAGAAGaAGGTGGagAGC   274
HIVU455         ----------G------T----GA-----...T--G------A-G-------------------------   279
HIVSF170        ------T--A--------------------...--------------------------------------   279
HIV1UG273A      ---------A----------------A--...T--------------------C-----------------   279
HIV1UG275A      ---------A--------------------...T----------G----------------------A---   279
HIV1DJ263A      ---------------ACC---AG-----A-...-------A-------------------G------C----   279
HIV1DJ264A      ---------------ACC---AG----AA-...-------------------------G-----------   279
HIV1DJ258A      ---------------ACC--TGG----AA-CAC-------A-------------------G------C----   226

CONSENSUS.B     AAGCaACCC?CctCCCAgccccgAGGGGAC...CCgacagGCCCGaaGgAAtcGAAGaAGaAGGTGGAGagA   278
HIVLAI          ---------A-------A----------...--------------------A-------------------   279
HIVTH475A       ---------A-------AT---------...--------------------A-------------------   279
HIVHXB2R        ---------A-------A----------...--------------------A-------------------   279
HIVNL43         ---------A-------AT---------...--------------------A-------------------   279
HIVMN           ---------G--C-----TT---------...--------------------------------------   279
HIVSC           ---------G-------AG--A-------...--------------------------------------   279
HIVBAL1         ---------A-------T--T--------...-----------G--------------------------   279
HIVJRCSF        ---------T---------AA--------...--------------------------------------   279
HIVJRFL         ---------T-------------------...--------------------------------------   279
HIVNH5          ---------T-------------------...--CGACA-------------------------------   279
HIVOYI          ---------G-------A---A-------...--------------------------------------   279
HIVSF2          ---------G--------T----------...-------------C------------------------   279
HIVNY5CG        ---------G----------A--------...--------------------------------------   279
HIVSF162        ---------G-T---------A-------...--------------------------------------   279
HIVCAM1         ---------G-T------TT--A-------...-------------------------------------G--   279
HIVCDC4         ---------T-------AA----------...-------------------C--------G----------   279
HIVSF33         ---------T-A---------A-------...----------------------------G----------   279
HIVRJS          ---------G-------A----------...--------------------------------------   279
HIVHAN          ---------T---------AA--------...--CGACA--------A-----------------------   279
HIVD31          ---------G-------------------...-------------------------------------C-   279
HIVRF           ---------A-------------------...-------------------------G-------------   279
HIVYU2          ---------A---------T-A-------...------------C-------------------------   279
HIVBCSG3C       ----G----A-------A----------...--------------------------------------   279

CONSENSUS.C     AAGCAAcCCtTAcCCCaaaCCCgagGGGaC...cCGACAGGCcCgGAggAATCGAAGAAGaAGGTGGAGAGC   278
HIV1SM145A      ----------------------------...---------T----A-----------------------   244
HIV1ZAM184      ------T--C-------C----AGA---T-...T------------A-----------G----------   279
HIV1DJ259A      ----------------------------...--------------------------------------   279
HIV1DJ373A      ----------T---G-----A-------...----------A-------------------------   279
HIV1UG268A      ----------------C----------...---------------A-----------------------   239

CONSENSUS.D     aAgCAACCCTCCTCCCAgccCCGAGGGgAC???CCGACAGGCCCGAAGgAAtAGAAGAAGAAGGTGGAGAGC   278
HIV1UG269A      ----------------------------...--------------------------------------   155
HIVELI          ----------------------------...------------------C-------------------   279
HIVZ2Z6         ----------------------------...--------------------------------------   279
HIVNDK          G----------------T----------...---------------A----------------------   279
HIVMAL          G---------------A-A----------CAC--------------------------------------   282
HIV1SE365A      --A----------------A---------...--------------------------------------   279
HIV1UG274A      ----------------------------A--...---------------A----------------------   279

CONSENSUS.O     ?AGCAATCCC???CC??CACC???AGGAAG...CAG?AACGCCAGGAAGAACAGGAG?AG?AGGTGGAGAAG   244
HIVANT70        A---------CAA--AT----AAG------...---G-------------------G--G-----------   273
HIVMVP5180      G---------TGT--CA----GGC------...---A-------------------A--A-----------   276

CONSENSUS.CPZ   AA?????CC?TA?CC?A??CCAG??GGA?C...?AG????GC??G?AGAAAT????GAAG?AGGTGG?????   181
SIVCPZGAB       --GCAAC--T--T--C-GT----AG---A-...A--GAAG--TC-G------CGAC----G------CGAGC   282
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HIV1 TAT

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CONSENSUS.A   AAGaCAgAGACAGATCgattCgcTTAG                                                                  301
HIVU455       ---G--A-----------------                                                                      303
HIVSF170      ---G------------------A-                                                                     303
HIV1UG273A    -------------------------                                                                    306
HIV1UG275A    --------------------A-----                                                                   306
HIV1DJ263A    ----------------AGGG--A----                                                                  306
HIV1DJ264A    ------A---------CG-G--A----                                                                  306
HIV1DJ258A    ------A---------A--A-------                                                                  253

CONSENSUS.B   GAGaCAGAGaCagATCCggtcgattAG                                                                  305
HIVLAI        -----------------AT--------                                                                  306
HIVTH475A     -----------------AT--------                                                                  306
HIVHXB2R      -----------------AT--------                                                                  306
HIVNL43       -----------------AT--------                                                                  306
HIVMN         ------------C-----------                                                                     303
HIVSC         -------------------------                                                                    303
HIVBAL1       --------------------C--                                                                      303
HIVJRCSF      ------------------A-A--                                                                      303
HIVJRFL       ------------------A----                                                                      303
HIVNH5        -----------G---------C--                                                                     303
HIVOYI        ------------------AA---                                                                      303
HIVSF2        ------------------T-----                                                                     303
HIVNY5CG      ------------------A-C--                                                                      303
HIVSF162      -----------------A---C--                                                                     303
HIVCAM1       ------------C------G----                                                                     303
HIVCDC4       ---G-------G-----AC-----                                                                     303
HIVSF33       ----------------AC-----                                                                      303
HIVRJS        ---------------------C--                                                                     303
HIVHAN        ---------G--------T-----                                                                     303
HIVD31        -----------------AA-----                                                                     303
HIVRF         ------------------CG-TGC--                                                                   306
HIVYU2        ---------------------C--                                                                     303
HIVBCSG3C     -------------------------                                                                    303

CONSENSUS.C   AAGaCAgAGaCAGATCcattcGATTAg                                                                  305
HIV1SM145A    ------A--------------------                                                                  271
HIV1ZAM184    ---G------------G----------                                                                  306
HIV1DJ259A    ---------G------G----------                                                                  306
HIV1DJ373A    ------A--G--------C--------                                                                  306
HIV1UG268A    -----------------G-GA-----A                                                                  266

CONSENSUS.D   aAGGCAGAGaCAGATCcaTtcGATTggTGA                                                               308
HIV1UG269A    ---------G---------------A-                                                                  182
HIVELI        G----------------G-GA-----C---                                                               309
HIVZ2Z6       G-----------------------------                                                               309
HIVNDK        G-----------------------------                                                               309
HIVMAL        ---------G------A-------------                                                               312
HIV1SE365A    ----------------A----------                                                                  306
HIV1UG274A    ---------G-----------------                                                                  306

CONSENSUS.O   ?AG?CAGGCCCA?GTGGA?A?CCT?GCC?C?AGG?TTCTTGC?AC?GTTGTACACGGA?CTCAG?ACAATAA                    303
HIVANT70      A--G--------G-----T-C---C---G-A---G-------C--T------------C-----A----                      342
HIVMVP5180    G--A--------A-----C-G---T---A-C---A-------A--A------------T-----G-------                    348

CONSENSUS.CPZ AAGACAG?A?CAG?T????G???TT??                                                                 196
SIVCPZGAB     -------A-G---A-CAGT-AGA--AG                                                                  309
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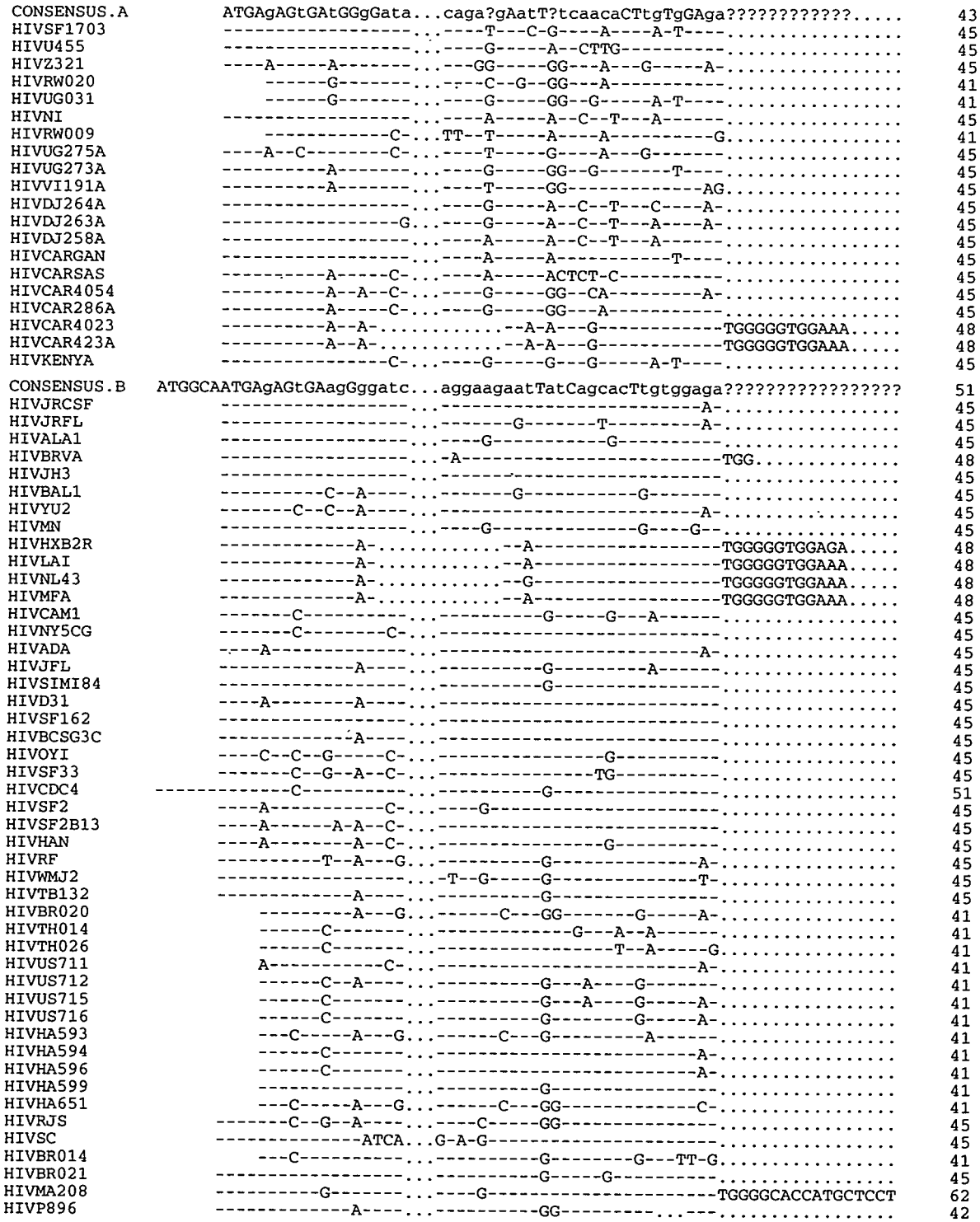
HIV1 ENV


CONSENSUS.A ATGAgAGtGAtGGgGata...caga?gAatT?tcaacaCTtgTgGAga????????????..... 43
HIVSF1703 ----------..----T---C-G----A----A-T---- 45
HIVU455 ----------..----G-----A--CTTG---------- 45
HIVZ321 ----A-----A-------..---GG-----GG---A---G-----A- 45
HIVRW020 ------G-------..---C--G--GG---A---------- 41
HIVUG031 ------G-------..----G-----GG--G-----A-T---- 41
HIVNI ----------..----A-----A--C--T---A------ 45
HIVRW009 ----------C-...TT--T-----A----A----------G 41
HIVUG275A ----A--C--------C-..----T-----G----A---G------- 45
HIVUG273A ----------A-------..----G-----GG--G-------T---- 45
HIVVI191A ----------A-------..----T-----GG----------AG 45
HIVDJ264A ----------..----G-----A--C--T---C----A- 45
HIVDJ263A ----------G..----G-----A--C--T---A----A- 45
HIVDJ258A ----------..----A-----A--C--T---A------ 45
HIVCARGAN ----------..----A-----A----------T---- 45
HIVCARSAS ----------A-----C-..----A-----ACTCT-C---------- 45
HIVCAR4054 ----------A--A--C-..----G-----GG--CA---------A- 45
HIVCAR286A ----------A-----C-..----G-----GG---A---------- 45
HIVCAR4023 ----------A--A-..........--A-A---G----------TGGGGGTGGAAA..... 48
HIVCAR423A ----------A--A-..........--A-A---G----------TGGGGGTGGAAA..... 48
HIVKENYA ----------C-..----G-----G---G-----A-T---- 45
CONSENSUS.B ATGGCAATGAgAGtGAagGggatc...aggaagaatTatCagcacTtgtggaga???????????????? 51
HIVJRCSF ----------..----------A- 45
HIVJRFL ----------..-------G-------T---------A- 45
HIVALA1 ----------..----G----------G---------- 45
HIVBRVA ----------...-A----------TGG 48
HIVJH3 ----------..---------- 45
HIVBAL1 ----------C--A----...-------G----------G------- 45
HIVYU2 -------C--C--A----...----------A- 45
HIVMN ----------..----G----------G----G-- 45
HIVHXB2R ----------A-..........--A----------TGGGGGTGGAGA..... 48
HIVLAI ----------A-..........--A----------TGGGGGTGGAAA..... 48
HIVNL43 ----------A-..........--G----------TGGGGGTGGAAA..... 48
HIVMFA ----------A-..........--A----------TGGGGGTGGAAA..... 48
HIVCAM1 -------C----------...----------G-----G---A------ 45
HIVNY5CG -------C--------C-...---------- 45
HIVADA ---A----------...----------A- 45
HIVJFL ----------A----...----------G---------A------ 45
HIVSIMI84 ----------...----------G---------- 45
HIVD31 ----A--------A----...---------- 45
HIVSF162 ----------...---------- 45
HIVBCSG3C ----------A----...---------- 45
HIVOYI ----C--C--G-----C-...----------G---------- 45
HIVSF33 -------C--G--A--C-...----------TG---------- 45
HIVCDC4 ----------C----------...----------G---------- 51
HIVSF2 ----A----------C-...----G---------- 45
HIVSF2B13 ----A------A-A--C-...---------- 45
HIVHAN ----A--------A--C-...----------G---------- 45
HIVRF ----------T--A---G...----------G----------A- 45
HIVWMJ2 ----------...-T--G-----G----------T- 45
HIVTB132 ----------A----...----------G---------- 45
HIVBR020 ---------A---G...------C---GG-------G-----A- 41
HIVTH014 ------C-------...----------G---A--A------ 41
HIVTH026 ------C-------...----------T--A-----G 41
HIVUS711 A----------C-...----------A- 41
HIVUS712 ------C--A----...----------G---A----G------- 41
HIVUS715 ------C-------...----------G---A----G-----A- 41
HIVUS716 ------C-------...----------G--------G-----A- 41
HIVHA593 ---C-----A---G...------C---G---------A------ 41
HIVHA594 ------C-------...----------A- 41
HIVHA596 ------C-------...----------A- 41
HIVHA599 ----------...----------G---------- 41
HIVHA651 ---C-----A---G...------C---GG----------C- 41
HIVRJS -------C--G--A----...----C-----GG---------- 45
HIVSC ----------ATCA...G-A-G---------- 45
HIVBR014 ---C----------...----------G--------G---TT-G 41
HIVBR021 ----------...----------G-----G---------- 45
HIVMA208 ----------G-------...----G----------TGGGGCACCATGCTCCT 62
HIVP896 ----------A----...----------GG---------...---... 42

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CONSENSUS.C     ATGAgAGTGAgGGgGAta...ctGagGAAtTg?CaACaaTGGtGGaTA.....  44
HIVMA959            --------------...-C-C-------G---------------.....  41
HIVMA960            --------------...TC---------G---------------.....  41
HIVZAM20A       ------------------...----------T---------------.....  45
HIVD1024        ------------------...----------AT---------G-----.....  45
HIVSM145A       ------------------...----------G---------------.....  45
HIVZAM18A       -------------A----...----------G---------------.....  45
HIVDJ259A       ----A-----T-----C-...-A------C--G-C--GG------G--.....  45
HIVDJ373A       ----------T--------...-A--T---C--T---------------.....  45
HIVSE364A       ----------C------G...T----------T----C----------.....  45
HIVUG268A       ----------T--------...-A---------T---------------.....  45

CONSENSUS.D     ATGAGAGtGAgGGaGAta...gagAggAATTaTCA?cacttgTgGaga?????????????????  44
HIVJY1          ----------T--G-----...AG--T---------A----------A-.....  45
HIVNDK          -------C--------A-...----------G---AA---------A-.....  45
HIVMAL          ------------------...C--------------AA---G-------.....  45
HIVELI          -------C-----G----...-----A----G---AA---G-----A-.....  45
HIVZ2Z6         -------------G----...----------G---AA---------A-.....  45
HIVUG024        ----------------G...C----------G--T--A----A-.....  45
HIVUG021            -------------G...AG--------G---G--T------G--.....  41
HIVUG038        ----------T--------...AT----------GAG---A------.....  45
HIVUG046        ----------T--G----...--------------G--TC-----GAGAGGAATCAGCACTCGTT  62
HIVUG266A       ----------A--G----...CC-------------AA----A-T----.....  45
HIVUG269A       ------------------...--------------G------------.....  45
HIVUG274A       ------------------...--------------G----------T-.....  45
HIVSE365A       -------C---------G...A-A-----------G------------.....  45
HIVCAR4020      -------------G----...--------------A-----A------.....  45

CONSENSUS.E     ATGAGAGTGAaGGaGaca...cagatgAatTggCcaaACTtgTGGAaA????????????.....  45
HIVTH966            --------------...----------------------------.....  41
HIVTH975            --------------...----------------------------.....  41
HIVTH022            --------------...----------------------------.....  41
HIVTN243        ------------------...----------------------------.....  45
HIVTH006            --------------...----------------------------.....  41
HIVTH011        ------------------...----------------------------.....  45
HIVCARELO       -------------G----...--------------C------------.....  45
HIVCAR4017      ----------------A-TAT---CACTTG---AG-TGGGG-------.....  48
HIVCAR4039      ----------G--G----...----A---------------A------.....  45
HIVCAR4071      -------------G----...----------------------------.....  45
HIVCARMBA       -------------G----...-------C----------G-------.....  45

CONSENSUS.F     ATGAGAGTGAGGGGGATG...CAGAGGAA?TGGCA?CACTTGGGGAAA.....  43
HIVBZ163A       ------------------...--------C-----G------------.....  45
HIVBZ126A       ------------------...--------T-----A------------.....  45

CONSENSUS.G     ATGAGAGtGAaGGGGATA...CaGAgGAATTGGCAacACTTgTGGAAa.....  45
HIVVI525A       ----------G--------...----C----------A----------T.....  45
HIVLBV217       -------C----------...-T-------------------------.....  45
HIVCAR4067      ------------------...--------------G-----A------.....  45

CONSENSUS.O     ATGAcAGtGAcTATGAAA...GcAATGgaGAAGAggAACAgGAAGTtAtGG.....  48
HIVANT70        ----T-------------...--------------------A----------.....  48
HIVMVP5180      ------------------...-T----A------AC----------C----.....  48
HIVVAU          -------C--T-------...-------G------------------G--.....  48

CONSENSUS.CPZ   ATGA?????A?G??GA??...????????????????????????T????.....   9
SIVCPZGAB       ----AAGTA-T-GA--AG...AAGAAGAGAGACTGGAACAGCT-ATCC.....  45

CONSENSUS.U     ATGAgAGTGAtGG?GAtA...CaGAgGAATTgtCaaCacTt?TgGagA.....  43
HIVZAM184       ----------G--G----...-C--A------G-----A-GG----T-.....  45
HIVCAR4081      ----A--------A--C-...--------------C--G--CA------.....  45
HIVK124A        -------------G----...--------------G-T---A-T-G--.....  45
HIVZ3           ----------A--A----...----------A---------G----A-.....  45
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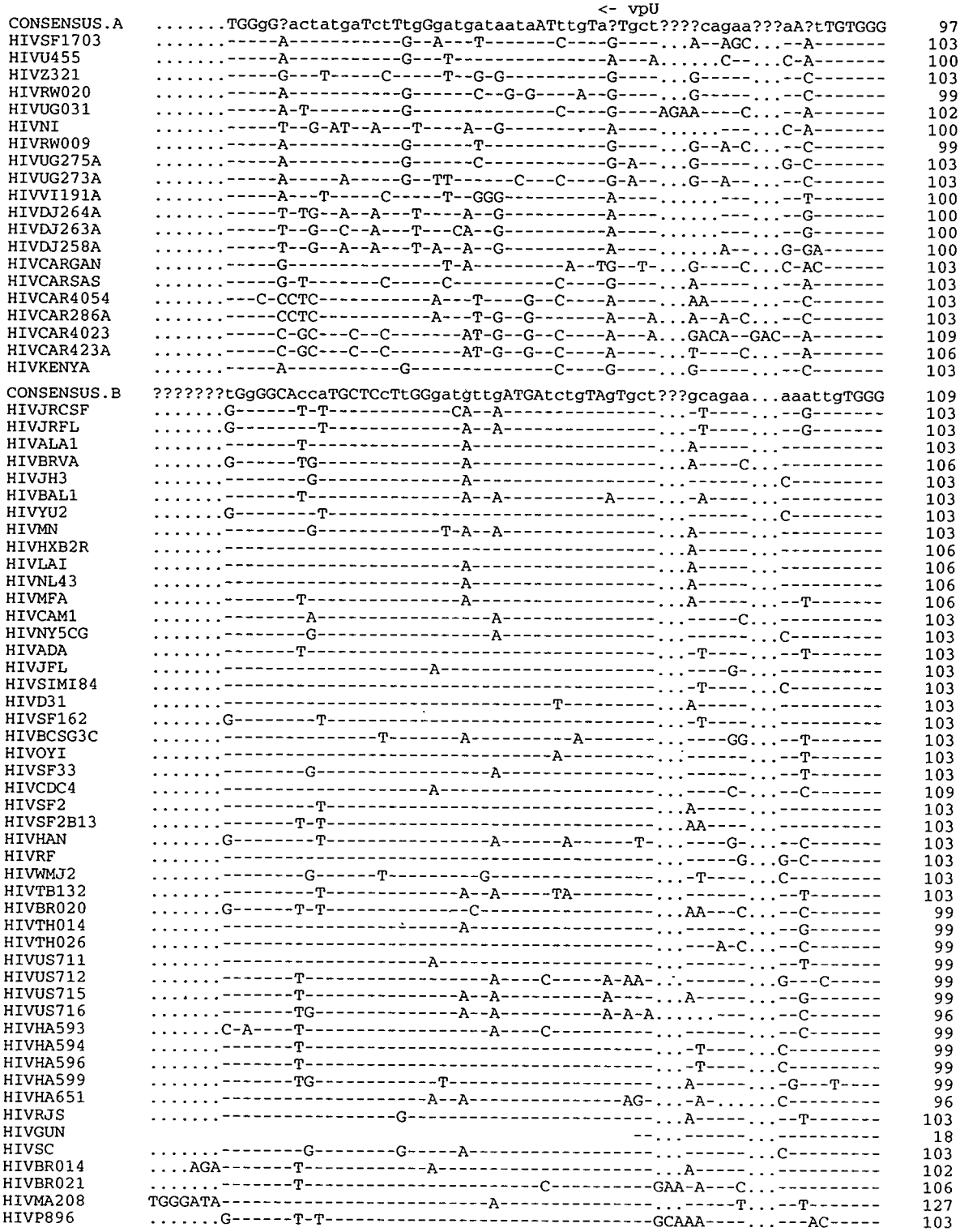
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CONSENSUS.A
HIVSF1703
HIVU455
HIVZ321
HIVRW020
HIVUG031
HIVNI
HIVRW009
HIVUG275A
HIVUG273A
HIVVI191A
HIVDJ264A
HIVDJ263A
HIVDJ258A
HIVCARGAN
HIVCARSAS
HIVCAR4054
HIVCAR286A
HIVCAR4023
HIVCAR423A
HIVKENYA
CONSENSUS.B
HIVJRCSF
HIVJRFL
HIVALA1
HIVBRVA
HIVJH3
HIVBAL1
HIVYU2
HIVMN
HIVHXB2R
HIVLAI
HIVNL43
HIVMFA
HIVCAM1
HIVNY5CG
HIVADA
HIVJFL
HIVSIMI84
HIVD31
HIVSF162
HIVBCSG3C
HIVOYI
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HIVCDC4
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HIVSF2B13
HIVHAN
HIVRF
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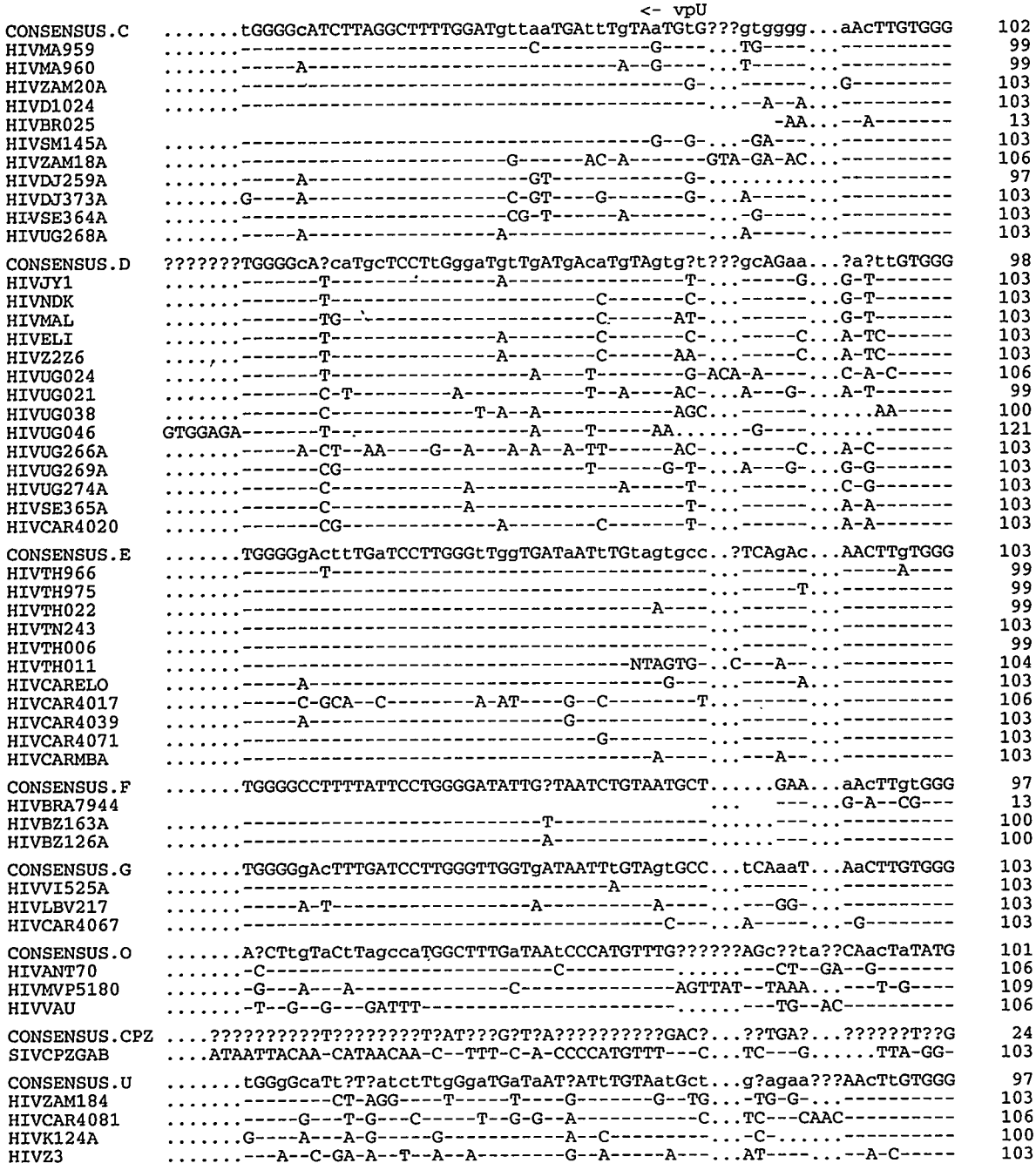
HIVUS716
HIVHA593
HIVHA594
HIVHA596
HIVHA599
HIVHA651
HIVRJS
HIVGUN
HIVSC
HIVBR014
HIVBR021
HIVMA208
HIVP896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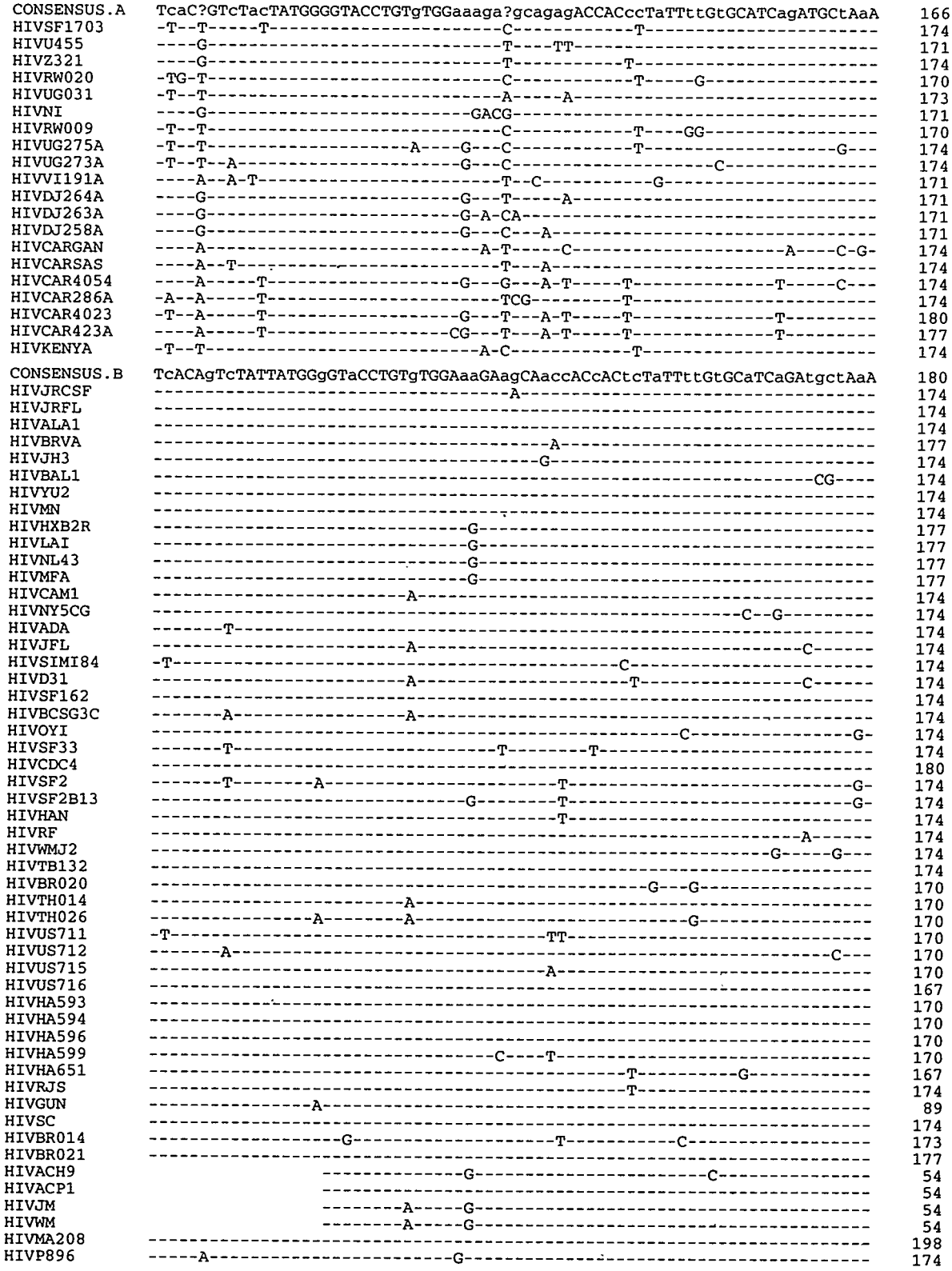
HIVMA959 .....----------C----------G----...TG----...---------- 99
HIVMA960 .....-----A----------A--G----...T------...---------- 99
HIVZAM20A .....----------G-...-------...G--------- 103
HIVD1024 .....---------...--A--A...---------- 103
HIVBR025 -AA...--A------- 13
HIVSM145A .....----------G--G-...-GA---...---------- 103
HIVZAM18A .....----------G------AC-A-------GTA-GA-AC...---------- 106
HIVDJ259A .....-----A----------GT----------G-...---------- 97
HIVDJ373A .....G----A----------C-GT----G-------G-...A-----...---------- 103
HIVSE364A .....----------CG-T------A-------...-G----...---------- 103
HIVUG268A .....-----A----------A----------...A-----...---------- 103
CONSENSUS.D ???????TGGGGcA?caTgcTCCTtGggaTgtTgATgAcaTgTAgtg?t???gcAGaa...?a?ttGTGGG 98
HIVJY1 .....-------T----------A----------T-...-----G...G-T------- 103
HIVNDK .....-------T----------C-------C-...--------...G-T------- 103
HIVMAL .....-------TG----------C------AT-...--------...G-T------- 103
HIVELI .....-------T----------A--------C-------C-...-----C...A-TC------ 103
HIVZ2Z6 ....,..-------T----------A--------C------AA-...-----C...A-TC------ 103
HIVUG024 .....-------T----------A----T--------G-ACA-A----...C-A-C----- 106
HIVUG021 .....-------C-T---------A----------T--A----AC-...A---G-...A-T------- 99
HIVUG038 .....-------C----------T-A--A----------AGC...------.....AA----- 100
HIVUG046 GTGGAGA-------T----------A----T-----AA.....-G----.....------- 121
HIVUG266A .....-----A-CT--AA----G--A---A-A--A-TT------AC-...-----C...A-C------- 103
HIVUG269A .....-------CG----------T------G-T-...A---G-...G-G------- 103
HIVUG274A .....-------C----------A----------A-----T-...--------...C-G------- 103
HIVSE365A .....-------C----------A----------T-...--------...A-A------- 103
HIVCAR4020 .....-------CG----------A--------C-------T-...--------...A-A------- 103
CONSENSUS.E .....TGGGGgActtTGaTCCTTGGGtTggTGATaATtTGtagtgcc..?TCAgAc...AACTTgTGGG 103
HIVTH966 .....-------T----------...-------...-----A---- 99
HIVTH975 .....----------...-----T...---------- 99
HIVTH022 .....----------A----...------...---------- 99
HIVTN243 .....----------...-------...---------- 103
HIVTH006 .....----------...------...---------- 99
HIVTH011 .....----------NTAGTG-..C---A--...---------- 104
HIVCARELO .....-----A----------G---...-----A...---------- 103
HIVCAR4017 .....-----C-GCA--C--------A-AT----G--C--------T...-------...---------- 106
HIVCAR4039 .....-----A----------G----------...-------...---------- 103
HIVCAR4071 .....----------G---------...------...---------- 103
HIVCARMBA .....----------A----...---A--...---------- 103
CONSENSUS.F .....TGGGGCCTTTTATTCCTGGGGATATTG?TAATCTGTAATGCT......GAA...aAcTTgtGGG 97
HIVBRA7944 ... ---...G-A--CG--- 13
HIVBZ163A .....----------T----------.....---...---------- 100
HIVBZ126A .....----------A----------.....---...---------- 100
CONSENSUS.G .....TGGGGgAcTTTGATCCTTGGGTTGGTgATAATTtGTAgtGCC...tCAaaT...AaCTTGTGGG 103
HIVVI525A .....----------A--------...------...---------- 103
HIVLBV217 .....-----A-T----------A----------A----...---GG-...---------- 103
HIVCAR4067 .....----------C---...A-----...-G-------- 103
CONSENSUS.O .....A?CTtgTaCtTagccaTGGCTTTGaTAAtCCCATGTTTG??????AGc??ta??CAacTaTATG 101
HIVANT70 .....-C----------C----------.....---CT--GA--G------- 106
HIVMVP5180 .....-G---A---A----------C----------AGTTAT--TAAA...---T-G---- 109
HIVVAU .....-T--G--G---GATTT----------.....---TG--AC---------- 106
CONSENSUS.CPZ ....??????????T?????????T?AT???G?T?A??????????GAC?...??TGA?...??????T??G 24
SIVCPZGAB ....ATAATTACAA-CATAACAA-C--TTT-C-A-CCCCATGTTT---C...TC---G.....TTA-GG- 103
CONSENSUS.U .....tGGgGcaTt?T?atctTtgGgaTGaTaAT?ATtTGTAatGct...g?agaa???AAcTtGTGGG 97
HIVZAM184 .....--------CT-AGG----T-----T----G-------G--TG...-TG-G-...---------- 103
HIVCAR4081 .....-----G---T-G---C-----T--G-G--A----------C...TC---CAAC---------- 106
HIVK124A .....G----A---A-G-----G----------A--C---------...-C-.....---------- 100
HIVZ3 .....---A--C-GA-A--T--A--A--------G--A-----A---...AT----...--A-C----- 103

HIV1 ENV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HIVSF1703 -T--T-----T----------C----------T---------- 174
HIVU455 ----G----------T----TT---------- 171
HIVZ321 ----G----------T----------T---------- 174
HIVRW020 -TG-T----------C----------T-----G---------- 170
HIVUG031 -T--T----------A-----A---------- 173
HIVNI ----G----------GACG---------- 171
HIVRW009 -T--T----------C----------T----GG---------- 170
HIVUG275A -T--T----------A----G---C----------T----------G--- 174
HIVUG273A -T--T--A----------G---C----------C---------- 174
HIVVI191A ----A--A-T----------T--C----------G---------- 171
HIVDJ264A ----G----------G---T-----A---------- 171
HIVDJ263A ----G----------G-A-CA---------- 171
HIVDJ258A ----G----------G---C---A---------- 171
HIVCARGAN ----A----------A-T-----C----------A----C-G- 174
HIVCARSAS ----A--T----------T---A---------- 174
HIVCAR4054 ----A-----T----------G---G---A-T-----T----------T-----C--- 174
HIVCAR286A -A--A-----T----------TCG---------T---------- 174
HIVCAR4023 -T--A-----T----------G---T---A-T-----T----------T---------- 180
HIVCAR423A ----A-----T----------CG---T---A-T-----T----------T---------- 177
HIVKENYA -T--T----------A-C----------T---------- 174
CONSENSUS.B TcACAgTcTATTATGGgGTaCCTGTgTGGAaaGAagCAaccACcACtcTaTTttGtGCaTCaGAtgctAaA 180
HIVJRCSF ----------A---------- 174
HIVJRFL ---------- 174
HIVALA1 ---------- 174
HIVBRVA ----------A---------- 177
HIVJH3 ----------G---------- 174
HIVBAL1 ----------CG---- 174
HIVYU2 ---------- 174
HIVMN ---------- 174
HIVHXB2R ----------G---------- 177
HIVLAI ----------G---------- 177
HIVNL43 ----------G---------- 177
HIVMFA ----------G---------- 177
HIVCAM1 ----------A---------- 174
HIVNY5CG ----------C--G---------- 174
HIVADA -------T---------- 174
HIVJFL ----------A----------C------ 174
HIVSIMI84 -T----------C---------- 174
HIVD31 ----------A----------T----------C------ 174
HIVSF162 ---------- 174
HIVBCSG3C -------A----------A---------- 174
HIVOYI ----------C----------G- 174
HIVSF33 -------T----------T--------T---------- 174
HIVCDC4 ---------- 180
HIVSF2 -------T--------A----------T----------G- 174
HIVSF2B13 ----------G--------T----------G- 174
HIVHAN ----------T---------- 174
HIVRF ----------A------ 174
HIVWMJ2 ----------G-----G--- 174
HIVTB132 ---------- 174
HIVBR020 ----------G---G---------- 170
HIVTH014 ----------A---------- 170
HIVTH026 ----------A--------A----------G---------- 170
HIVUS711 -T----------TT---------- 170
HIVUS712 -------A----------C--- 170
HIVUS715 ----------A---------- 170
HIVUS716 ---------- 167
HIVHA593 ---------- 170
HIVHA594 ---------- 170
HIVHA596 ---------- 170
HIVHA599 ----------C----T---------- 170
HIVHA651 ----------T----------G---------- 167
HIVRJS ----------T---------- 174
HIVGUN ----------A---------- 89
HIVSC ---------- 174
HIVBR014 ----------G----------T----------C---------- 173
HIVBR021 ---------- 177
HIVACH9 ----------G----------C---------- 54
HIVACP1 ---------- 54
HIVJM --------A-----G---------- 54
HIVWM --------A-----G---------- 54
HIVMA208 ---------- 198
HIVP896 -----A----------G---------- 174

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CONSENSUS.C  TCACAGTcTATTATGGGGTACCtGTGTGGaaaGAaGCAAaaaCTaCtcTaTTtTGTGCATCaGAtgCTAAA 173
HIVMA959     ------------------------------------C-----------------C------------------ 170
HIVMA960     ------------------------------------------------------C------------------ 170
HIVZAM20A    ---------------------------------G--------------------C------------------ 174
HIVD1024     ------------------------------------------------------C------------------ 174
HIVBR025     ------------------------------------------------------------------------C------ 84
HIVSM145A    ----------------------G-------G------------------G----------------T----- 174
HIVZAM18A    ------------------------------------------------T----C------------------ 177
HIVDJ259A    ---------------------------------T-----CC--C-C------------------------- 168
HIVDJ373A    ---------------------------------C----------CC------------------------- 174
HIVSE364A    -------A-------------------------------------------------------G--------- 174
HIVUG268A    ------------------------------------C------------------------------------ 174

CONSENSUS.D  TcACaGTtTAtTATGGGGTaCCtgTgTGgAAaGAaGCAaccACcACtcTATTttGtGCATCAGAtGCTAAA 169
HIVJY1       ------------------------------------------------G------------------------ 174
HIVNDK       ------------------G---A-A-----G--------T------------------------------- 174
HIVMAL       -T-------------------------------------------T---------------------------- 174
HIVELI       ------------------G-----A-----G------------------------------------------ 174
HIVZ2Z6      -------G-----------G-----A-----G------------------------------------------ 174
HIVUG024     ------------------------------------------T--------C------------------- 177
HIVUG021     ------------------------------------------T---------------------------- 170
HIVUG038     ----------C-------------------------------A---------------------------- 171
HIVUG046     ------------------------------------------T----------C---------------- 192
HIVUG266A    -T--T--C--C----------------------T---GAG-----CT-----G-G---------------- 174
HIVUG269A    ------------------------------------------T--------C------------------- 174
HIVUG274A    -------G-----------------------------------T--------------------C------ 174
HIVSE365A    ----------------------G-------------------------------------------------- 174
HIVCAR4020   ------------------------------------GAA---------------------------------- 174

CONSENSUS.E  TTACAGttTATTATGGGGTTCCTGtGTGGAgAGAtGCAgAtACCAcCCTATtttGTGCATCAGATGCCAAA 174
HIVTH966     ------------------------------------------------------------------------ 170
HIVTH975     ------------------------------------------------------------------------ 170
HIVTH022     -------------------------------A---------------------------------------- 170
HIVTN243     ------------------------------------------------------------------------ 174
HIVTH006     ------G----------------------------------------------G------------------ 170
HIVTH011     ------------------------------------C---------------------------------- 175
HIVCARELO    -------C----------------C----------C-----A---------------------------- 174
HIVCAR4017   ------------------------C------A---------------------------------------- 177
HIVCAR4039   ------------------------------------A-G----A-------------------------- 174
HIVCAR4071   ------------------------------------------------------------------------ 174
HIVCARMBA    -------------------------------A--------------------GC------------------ 174

CONSENSUS.F  TCACAGTCTATTATGGGGTACCTGTGTGGAAAGAaGCAACcACTACTCTATTCTGTGCATCAGATGCTAAA 168
HIVBRA7944   ------------------------------------T---------------------------------- 84
HIVBZ163A    ---------------------------------T------------------------------------ 171
HIVBZ126A    ------------------------------------------------------------------------ 171

CONSENSUS.G  TCACAGTCTAtTATGGGGTaCCTGtGTGGGAAGAtgcAGAtaCCcCtCTATTTTGTGCATCTGATGCTAaa 174
HIVVI525A    ----------C-------------------------------A---------------------------- 174
HIVLBV217    ------------------------C----------C---------A-G------------------------ 174
HIVCAR4067   -------------------G---------------CG----G----------------------------GG 174

CONSENSUS.O  CcACAGTcTATtCTGGGGTaCCTGTATGGGAAGAtGCAacACCAgtAcTaTTCTGTGCTTCAGATGCTAAC 172
HIVANT70     -A---------G-------G-------------------------------------------------- 177
HIVMVP5180   -------T-------------------------G---G---------------------------------- 180
HIVVAU       ------------------------------------A----AC-T-G---------------------- 177

CONSENSUS.CPZ TAACAGTAT??TATGGAGT?CCTGT?TGG????ATGC????CC????CT?TTTTGTGCC?CA?A?GC???? 71
SIVCPZGAB    ----------AT---------A-----T---CATG----TGAC--GGTA--C----------T--G-C--TAAG 174

CONSENSUS.U  TcACaGT?TAtTATGGGGTACCTGTGTGGA?AGAtGCAgA?ACcACtcTATTtTGTGCATCaGATGCTAAa 165
HIVZAM184    -------C----------------------G---A---A-A--T---------C------------------ 174
HIVCAR4081   -------T----------------------A---------G-----C--------------T---------- 177
HIVK124A     -T--T--T--C--------------------G---------G------T-------------G---------- 171
HIVZ3        -------C----------------------A---------A----------------------------G 174
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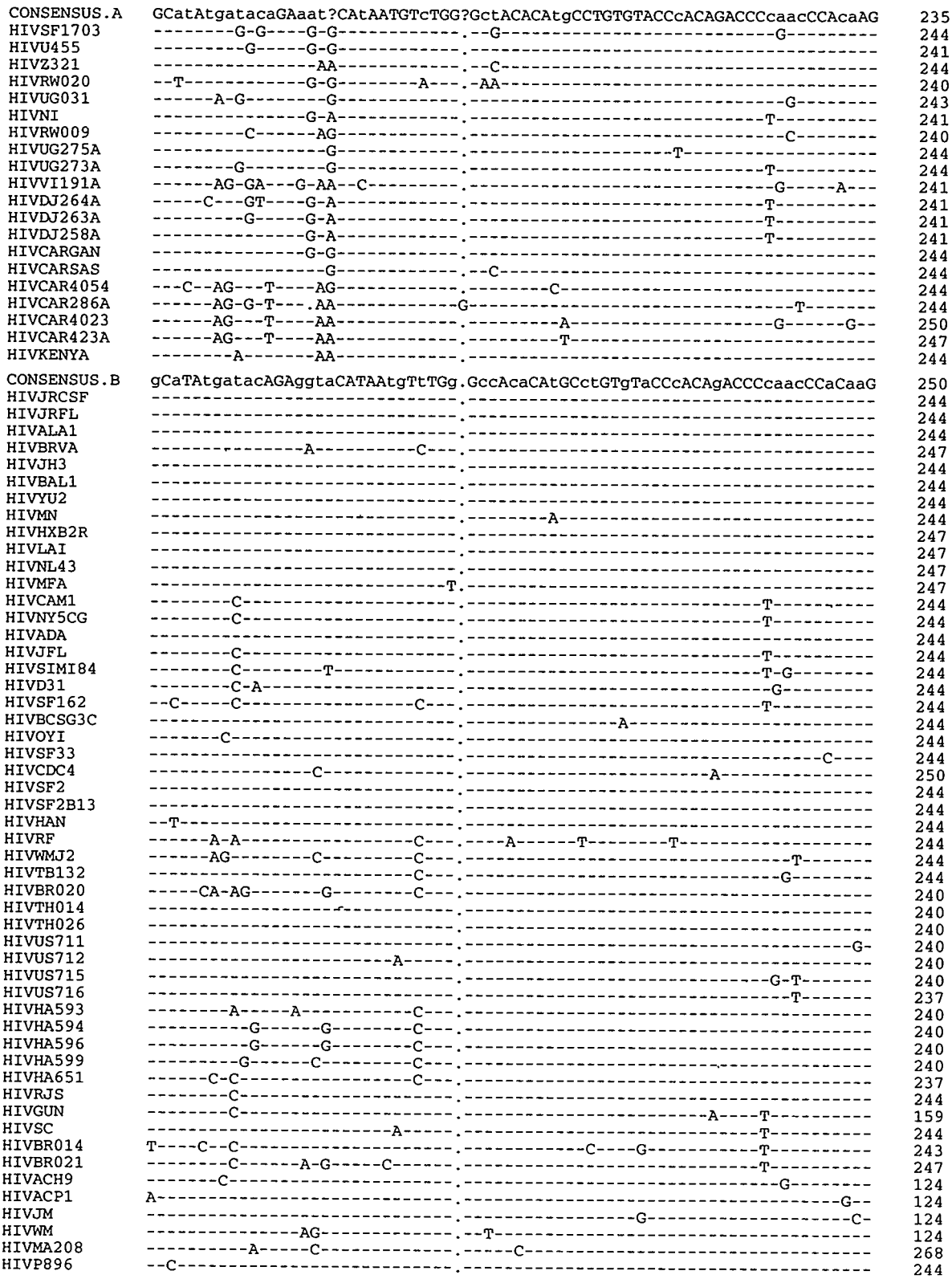
HIV1 ENV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HIVSF1703 244
HIVU455 241
HIVZ321 244
HIVRW020 240
HIVUG031 243
HIVNI 241
HIVRW009 240
HIVUG275A 244
HIVUG273A 244
HIVVI191A 241
HIVDJ264A 241
HIVDJ263A 241
HIVDJ258A 241
HIVCARGAN 244
HIVCARSAS 244
HIVCAR4054 244
HIVCAR286A 244
HIVCAR4023 250
HIVCAR423A 247
HIVKENYA 244
CONSENSUS.B gCaTAtgatacAGAggtaCATAAtgTtTGg.GccAcaCAtGCctGTgTaCCcACAgACCCcaacCCaCaaG 250
HIVJRCSF 244
HIVJRFL 244
HIVALA1 244
HIVBRVA 247
HIVJH3 244
HIVBAL1 244
HIVYU2 244
HIVMN 244
HIVHXB2R 247
HIVLAI 247
HIVNL43 247
HIVMFA 247
HIVCAM1 244
HIVNY5CG 244
HIVADA 244
HIVJFL 244
HIVSIMI84 244
HIVD31 244
HIVSF162 244
HIVBCSG3C 244
HIVOYI 244
HIVSF33 244
HIVCDC4 250
HIVSF2 244
HIVSF2B13 244
HIVHAN 244
HIVRF 244
HIVWMJ2 244
HIVTB132 244
HIVBR020 240
HIVTH014 240
HIVTH026 240
HIVUS711 240
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HIVUS715 240
HIVUS716 237
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HIVHA594 240
HIVHA596 240
HIVHA599 240
HIVHA651 237
HIVRJS 244
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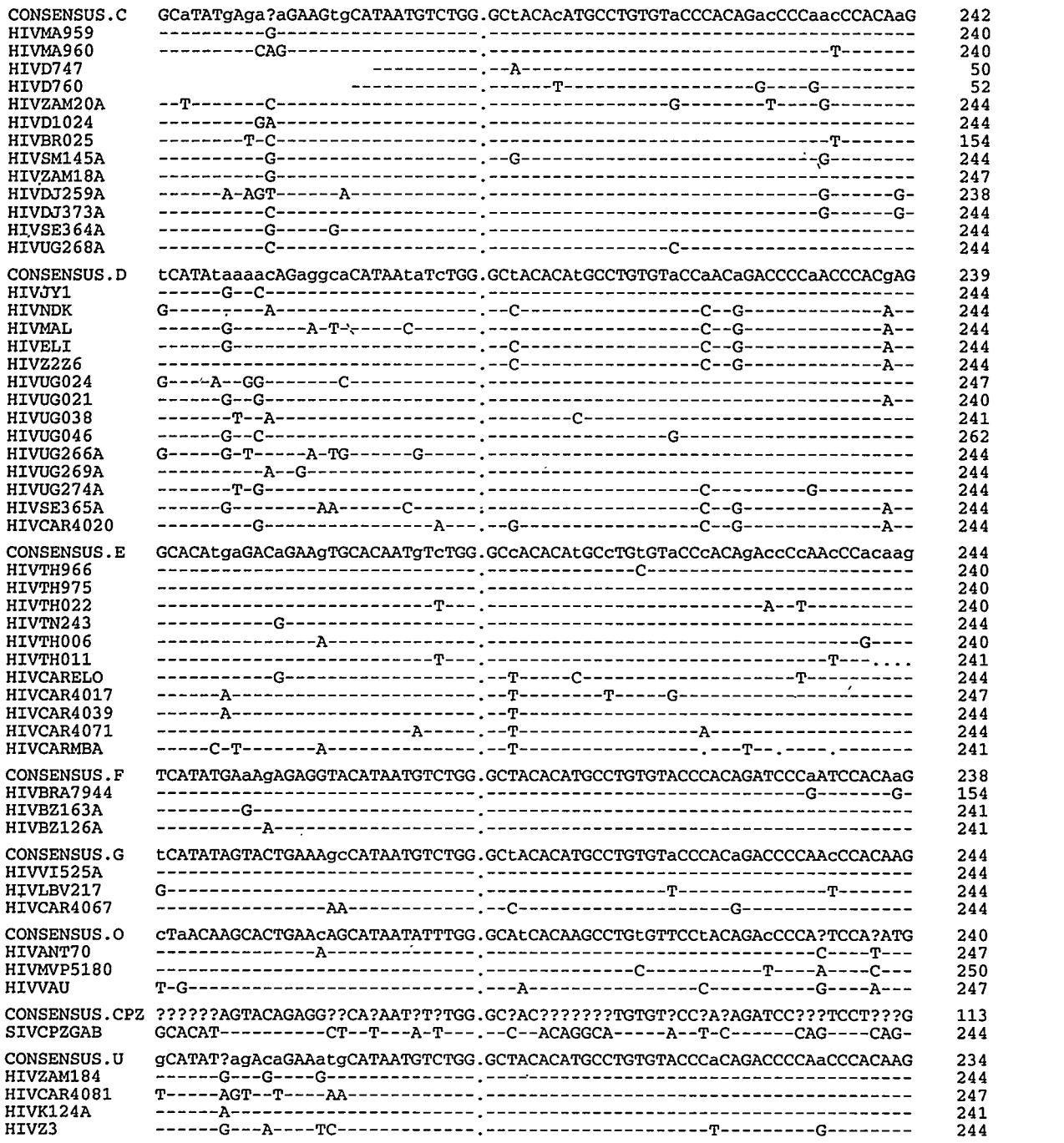
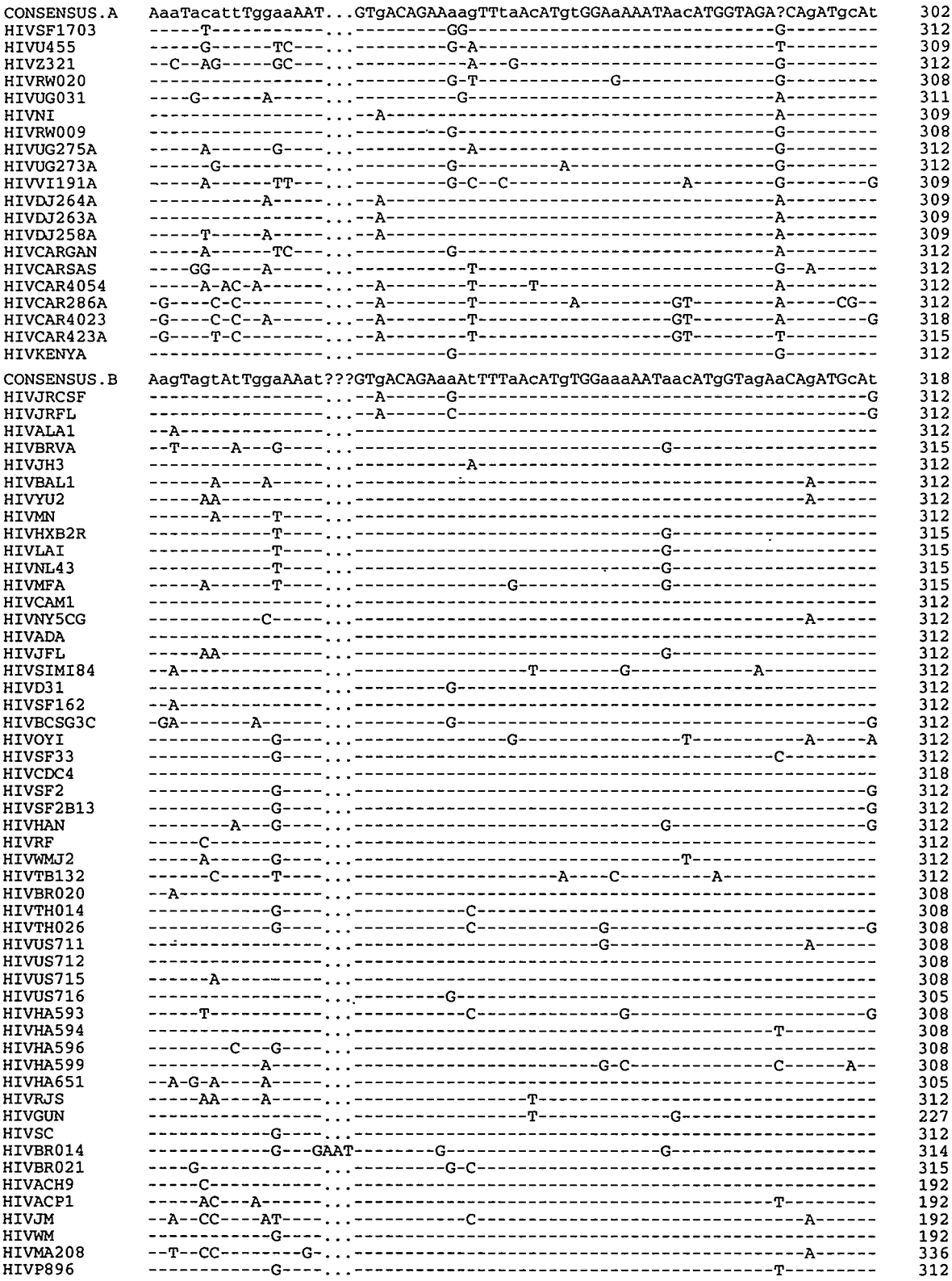
HIVACH9 124
HIVACP1 124
HIVJM 124
HIVWM 124
HIVMA208 268
HIVP896 244



HIV1 ENV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HIVSF1703 -----T----------...---------GG---------- 312
HIVU455 -----G------TC---...---------G-A---------- 309
HIVZ321 --C--AG-----GC---...----------A---G---------- 312
HIVRW020 ----------...---------G-T----------G---------- 308
HIVUG031 ----G-----A-----...---------G---------- 311
HIVNI ----------...--A---------- 309
HIVRW009 ----------...--------G---------- 308
HIVUG275A -----A------G----...----------A---------- 312
HIVUG273A ------G---------...---------G---------A---------- 312
HIVVI191A -----A------TT---...---------G-C--C----------A--------G--------G 309
HIVDJ264A ----------A-----...--A---------- 309
HIVDJ263A ----------...--A---------- 309
HIVDJ258A -----T-----A-----...--A---------- 309
HIVCARGAN -----A------TC---...---------G---------- 312
HIVCARSAS ----GG-----A-----...----------T----------G--A------ 312
HIVCAR4054 -----A-AC-A------...--A--------T-----T----------A--------- 312
HIVCAR286A -G----C-C--------...--A--------T---------A---------GT--------A-----CG-- 312
HIVCAR4023 -G----C-C--A------...--A--------T----------GT--------A--------G 318
HIVCAR423A -G----T-C--------...--A--------T----------GT--------T--------- 315
HIVKENYA ----------...---------G----------G--------- 312
CONSENSUS.B AagTagtAtTggaAAat???GTgACAGAaaAtTTTaAcATgTGGaaaAATaacATgGTagAaCAgATGcAt 318
HIVJRCSF ----------...--A------G----------G 312
HIVJRFL ----------...--A------C----------G 312
HIVALA1 --A----------...---------- 312
HIVBRVA --T-----A---G----...----------G---------- 315
HIVJH3 ----------...----------A---------- 312
HIVBAL1 ------A----A-----...----------A------ 312
HIVYU2 -----AA----------...----------A------ 312
HIVMN ------A-----T----...---------- 312
HIVHXB2R ----------T----...----------G---------- 315
HIVLAI ----------T----...----------G---------- 315
HIVNL43 ----------T----...----------G---------- 315
HIVMFA -----A------T----...----------G----------G---------- 315
HIVCAM1 ----------...---------- 312
HIVNY5CG ----------C-----...----------A------ 312
HIVADA ----------...---------- 312
HIVJFL -----AA----------...----------G---------- 312
HIVSIMI84 --A----------...----------T--------G----------A---------- 312
HIVD31 ----------...---------G---------- 312
HIVSF162 --A----------...---------- 312
HIVBCSG3C -GA-------A------...---------G----------G 312
HIVOYI ----------G----...----------G----------T----------A-----A 312
HIVSF33 ----------G----...----------C--------- 312
HIVCDC4 ----------...---------- 318
HIVSF2 ----------G----...----------G 312
HIVSF2B13 ----------G----...----------G 312
HIVHAN --------A---G----...----------G----------G 312
HIVRF -----C----------...---------- 312
HIVWMJ2 -----A------G----...----------T---------- 312
HIVTB132 ------C-----T----...----------A----C---------A---------- 312
HIVBR020 --A----------...---------- 308
HIVTH014 ----------G----...----------C---------- 308
HIVTH026 ----------G----...----------C----------G----------G 308
HIVUS711 ----------...----------G----------A------ 308
HIVUS712 ----------...---------- 308
HIVUS715 ------A----------...---------- 308
HIVUS716 ----------...---------G---------- 305
HIVHA593 -----T----------...----------C----------G----------G 308
HIVHA594 ----------...----------T--------- 308
HIVHA596 --------C---G----...---------- 308
HIVHA599 ----------A-----...----------G-C----------C------A-- 308
HIVHA651 --A-G-A----A-----...---------- 305
HIVRJS -----AA----A-----...----------T---------- 312
HIVGUN ----------...----------T----------G---------- 227
HIVSC ----------G----...---------- 312
HIVBR014 ----------G---GAAT--------G----------G---------- 314
HIVBR021 ----G----------...---------G-C---------- 315
HIVACH9 -----C----------...---------- 192
HIVACP1 -----AC---A------...----------T--------- 192
HIVJM --A--CC----AT----...----------C----------A------ 192
HIVWM ----------G----...---------- 192
HIVMA208 --T--CC--------G-...----------A------ 336
HIVP896 ----------G----...----------T--------- 312

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CONSENSUS.C   AaaT?gtTttGGaAAAT...GTAACAGaAaatTTTAACATGTGGaaAAATGacATgGTggAtCAgATGCAT   309
HIVMA959      ----A----G-------...-------------------------------------A--A------------   308
HIVMA960      --G-A-------G----...-------------------------------------A-----A------   308
HIVD747       -G--G-------G----...-------------------------G-------------A------------   118
HIVD760       ----A------------...-------G-----------------------------------A------   120
HIVZAM20A     ---G-------C-----...----------C-------------------------------------   312
HIVD1024      ----G------------...-----------------------------------------A------------   312
HIVBR025      ----G------------...-------------------------G----------------A----------   222
HIVSM145A     ----GC------G----...-------------------------------T------------------   312
HIVZAM18A     ----A-------G----...-------------------------------------------------   315
HIVDJ259A     --C-A-C----------...-----------------------------------G------------------   306
HIVDJ373A     --C-A---A--------...-----------------------------------G------------------   312
HIVSE364A     ----G----G-------...---------T---------------------------A------------   312
HIVUG268A     ----A--C--------...----------G-------------------------------------------   312

CONSENSUS.D   AAaTagaacTggaaAAT...GTcaCaGAaaacTTTaACATgTGGAaAAATaAcATGGTGGAgCagATGCAT   307
HIVJY1        --------A----G---...--T---------------------------------------------------   312
HIVNDK        --------T--------...--G-----------------------------------------A--A------   312
HIVMAL        -----------------...---------GGG-----------------------------------------   312
HIVELI        ------C----------...--G-------------------------------------A---------   312
HIVZ2Z6       -----------------...--G----------------------G--------------A---------   312
HIVUG024      -----C----A------...-------------------------------------------A--A------   315
HIVUG021      ------T---A------...--------G-----------C-------------------------------   308
HIVUG038      -------------G---...-------------------------------------------------   309
HIVUG046      -----A-----------...-----------------------------------G---------------   330
HIVUG266A     -----A----A------...-------------------------------------------G-------   312
HIVUG269A     --.--A--T-A------...-----C-------------------------T------------------   311
HIVUG274A     -----AG---A------...---------------G-----------------------------A------   312
HIVSE365A     ----------C------...-------------------------------------------------   312
HIVCAR4020    ----G--G---A-----...---T-----------------------------------------A---------   312

CONSENSUS.E   aaatatac?tggaaaat...gtaacagaaaattttaacatgtggaaaaataacatggtagagcagatgcag   311
HIVTH966      -----C--C--------...A-------------------------------------------------   308
HIVTH975      -----C--C--------...-------------------------------------------------   308
HIVTH022      --------C--------...-------------------------------------------------   308
HIVTN243      --------C--------...-------------------------C-----------------------   312
HIVTH006      -----C--C--------...-------------------------------------------------   308
HIVTH011      .....................................................................   241
HIVCARELO     --------A--------...---------C---------------------------------------   312
HIVCAR4017    --------A--------...-------------------------------------C-------------   315
HIVCAR4039    --------A--------...-------------------------------------------------   312
HIVCAR4071    ------T-T--------...-------------------------------------------------   312
HIVCARMBA     --G-----A--------...-----------------------------T--------A--------T   309

CONSENSUS.F   AAGTAGttCTGgAAAAT...GTAACAGAAAATTTTGATATGTGGAAAAATAaCATGGTAGAACAAATGCAt   306
HIVBRA7944    ------AG---A-----...-------------------------------------------------C   222
HIVBZ163A     -----------------...-----------------------------G-------------------   309
HIVBZ126A     -----------------...-------------------------------------------------   309

CONSENSUS.G   AgATAtcTCTGgAaAAT...GTAACAGAAAATTTTAAcATGTGGAAAAATAAcATGGTAGAACAGATGCAT   312
HIVVI525A     -----------------...-----------------------------A-------------------   312
HIVLBV217     -A---------A-C---...-------------------------------------------------   312
HIVCAR4067    -----GT----------...-----------------T-------------------------------   312

CONSENSUS.O   AATaTccacTa?acAAT...GTGACAGaTaAcTTtaATATATGGAAAAATTAcATgGTaGAcCAAATGCA?   306
HIVANT70      --------T-GC-----...---------G-------------------------------A--------G   315
HIVMVP5180    ---T--------GG---...-------------G-----------------------G-----------T   318
HIVVAU        -----GAG---A-A---...-------G---A--C----------------T--A--------------C   315

CONSENSUS.CPZ ?AGT????CT????AAT...?????AG??T??TTTAA????T??AAAAAT?ATATGGT?GA????ATG???   148
SIVCPZGAB     A---ATTT--TCCA---...GTAAT--AA-CA-----CATG-GG------A-------G--CCAA---CAT   312

CONSENSUS.U   AaaTA?tTTTgGaAAAT...GTaACAGAAAAtTTTAACATGTGGAAaAATaAcATGGTaGAaCAGATGCAT   301
HIVZAM184     -----G-----------...-------------------------------G-------G--T---------   312
HIVCAR4081    -----C----A------...-----------G-------------------------------------   315
HIVK124A      -----CA----------...--G-----------------------------------------------   309
HIVZ3         -GC--G------G----...-----------C--------------G-----A--------G---------   312
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                                                                                                <-tev or tnv in
LAI/IIIb
                                                                                                \/3'sj in LAI/IIIb
CONSENSUS.A   gaaGATaTaAtcAGtcTATGGGAccAaAGcCTAaAgCCATGTgTaaAgtTAaCCCCTCTCTGcGTtACtTT    373
HIVSF1703     AC----------------------G--T-------------------------------------------    383
HIVU455       ------------------------------------------------------------------G--    380
HIVZ321       --G---G--------T-------T-----T-------------------------------------C-----    383
HIVRW020      AC--------------------T--G--------A-----------A----------------------    379
HIVUG031      AC------------------------------------------------------------T-----G--    382
HIVD687                 T-------------------------------------------------------C-----     60
HIVNI         ----------T-------------------------------------------------------------    380
HIVRW009      AC-----------------------------------------------C--------------------    379
HIVUG275A     ----------------------T-----------------------C--------------------------    383
HIVUG273A     AC-------------------------------------------------------------------    383
HIVVI191A     -------------------------G-----------------G--------------------------    380
HIVDJ264A     ----------T-----------------------------------G------------------------    380
HIVDJ263A     ----------T-------------------------------------------------T--------    380
HIVDJ258A     ----------T-------------------------------------------------------------    380
HIVCARGAN     AC--------C----------------------C-----------------------------------C--    383
HIVCARSAS     AC------------C-------------------------------C---------------T--------    383
HIVCAR4054    --G------------T-------TG----T-----A-----------AC-------------T--------    383
HIVCAR286A    --G------------T-------TG-----------------A--G----------------T--------    383
HIVCAR4023    --G-----T-----CT-------TG----------A------------C-------------T--------    389
HIVCAR423A    --G------------T-------TG----------------------C-------------T--------    386
HIVKENYA      AC----------------------T--------------------T-----------------------C--    383

CONSENSUS.B   GAgGATaTAatcAgttTATGGGAtcAAAGccTAAAgCCaTGTGTaAaatTAaCcCCaCTcTGTGTtActtT    389
HIVJRCSF      ------G------A----------------T-------------------------------------------    383
HIVJRFL       -------------------------------------------------------------------------    383
HIVALA1       -------------------------------------------------------------------------    383
HIVBRVA       -------------------------------------------------------------------------    386
HIVJH3        -------------------------------------------------------------------------    383
HIVBAL1       -------------------------------------------------------------------------    383
HIVYU2        ---------------------------------------------------T---------------------    383
HIVMN         -------------------------------------------------------------------------    383
HIVHXB2R      ----------------------------------------------------------------------G---    386
HIVLAI        ----------------------------------------------------------------------G---    386
HIVNL43       ----------------------------------------------------------------------G---    386
HIVMFA        ----------------------------------------------------------------------A---    386
HIVCAM1       -------------------------------------------------------------------------    383
HIVNY5CG      ------------------------------------A------------------------------C--    383
HIVADA        -------------------------------------------------------------------------    383
HIVJFL        -------------------------------------------------------------------------    383
HIVSIMI84     -------------------------------------------------------------------------    383
HIVD31        -------------------------------------------------------------------------    383
HIVSF162      ----------------------------T-----------------G----------------------C-    383
HIVBCSG3C     -------------------------------------------------------------------------C-    383
HIVOYI        --A----------------------------------------------------------------------    383
HIVSF33       ---------G----------------------------------------------------------------    383
HIVCDC4       --------------C-----------------------------------C----------------------    389
HIVSF2        -------------------------------------------------------------------------    383
HIVSF2B13     -------------------------------------------------------------------------    383
HIVHAN        --A----------------------------------------------------------------------    383
HIVRF         -------------------------------------------------------------------------    383
HIVWMJ2       ------------------------------------A----------------------------------    383
HIVTB132      ------------------------------------A--------G--------T-----------------    383
HIVBR020      ---------------------------------------T--------G-----------------------    379
HIVTH014      --A----------------------------------------------------------------------    379
HIVTH026      --A----------------------------------------------------------------------    379
HIVUS711      ----------G-------------------------------------------T-----------------    379
HIVUS712      --A--------T-------------------------------------------T-----------------    379
HIVUS715      ----------T-------------------------------------------------------------C-    379
HIVUS716      --A--------T-------------------------------------------------------------    376
HIVHA593      -------------------------------------------------------------------------    379
HIVHA594      ------------------------------------A----------------------------------    379
HIVHA596      ------------------------------------A---------------G------------------    379
HIVHA599      ---------------------------------------------C-A----A-----------G------    379
HIVHA651      -------------------------------------------------------------------------    376
HIVRJS        -------------------------------------------------------------------------    383
HIVGUN        ----------------------G----TT-----------------------G--------------------    298
HIVSC         -------------------------------------------------------------------------    383
HIVBR014      -------------------------------------------------------------------------    385
HIVBR021      ---------------C-------------------------------------------------------    386
HIVACH9       -------------------------------------------------------------------------    263
HIVACP1       -------------------------------------------------------------------------C-    263
HIVJM         -------------------------------------------------------------------------    263
HIVWM         -------------A-----------------------------------------------------A-----    263
HIVMA208      ----------------------G----------A----------------------------------------    407
HIVP896       ----------------------G-------------------------------------------------    383
HIVBWB11A                                                                          --      2
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                                                                                                                  <-tev or tnv in
LAI/IIIb                                                                                                          \/3'sj in LAI/IIIb
CONSENSUS.C   gAGGATaTAATCaGttTATGGGaTcaAagccTaAAGCCATGTGTaAaagtTgACcCCACTcTGTgTcActTT    380
HIVMA959      --------------C-------------------------------------------------------------    379
HIVMA960      ------G-----------------------------------------------A---------------------    379
HIVD757                 ---------------------------------------------------------------------     60
HIVD747       ------G-------------------------------------------------------------------------    189
HIVD760       ------G-------------------------------------------------------------------------    191
HIVNOF                                                        A-GTT-------------------------     28
HIVZAM20A     ---------------------------------------------AA----A-----------A------          383
HIVD1044                                                                    ---------------T-----     21
HIVD1024      ------G--------C-----------------------------------------------------------C--    383
HIVD744                 C--G------------C-------------------------------------------------------     59
HIVD766                                                                          -----------          11
HIVD808                 ----------------C-------------------------------------------------------     62
HIVD868                 --------C------G-------------------------------------------------------     53
HIVBR025      C-------------C---\----G-----------------------------------------T--G--    293
HIVSM145A     ----------------------------T-------------------------------------------------    383
HIVZAM18A     --------------G--------------T-------------------------------------------------    386
HIVDJ259A     C--------------C-----------------------------------------T-----T-----          377
HIVDJ373A     C----------------------G--G-------------------------------------T-----          383
HIVSE364A     -------------------------------------------------------------------------------    383
HIVUG268A     C-----G--------C-----------------------------------------------------T-----    383

CONSENSUS.D   GAgGATaTAATCAGTtTAtGGGAtcAAAgcCTaAAaCCATGTGTAAAatTAaCcCCaCTCTGTGTCACtTT    378
HIVJY1        --A-----------------------AT-------------------------------------------------    383
HIVNDK        -------------------------------------------------T-----------------          383
HIVMAL        ------------------------------------------GC---------------------          383
HIVELI        -------------------------------------------------------------------------------    383
HIVZ2Z6       -------------------------------------------------------------------------------    383
HIVUG024      ------G-------------------------------------------------------------------------    386
HIVUG021      --T-----------------------------------------------C-------------------          379
HIVUG038      ----------------------------------G----------------------------------------          380
HIVUG046      ------G--------C---------------G-------------------------------------          401
HIVUG266A     ----------------------G-----------------------------------------C--          383
HIVUG269A     ----------------------G-------------------------------------------          382
HIVUG274A     -------------------------------------------------------------------------------    383
HIVSE365A     --A-------------------------------------------------------------------------    383
HIVCAR4020    ---------------------------------------------A--T---------------          383

CONSENSUS.E   gaggatgTAATCAgtTTATGGGATcAaAGtCTaAAgCCATGtGTAAagtTAACTCCTCTCTGcGTTActTT    382
HIVTH966      -------------C-------------------------------------------------------          379
HIVTH975      ------------------------G-------------------------------------------          379
HIVTH022      -------------------------------------------------------T---------          379
HIVTN243      -------------------------------------------------------------------          383
HIVTH006      -------------------------------------------------------------------          379
HIVTH011      .......------C--------------G----------------G----------------------          305
HIVCARELO     ---------------------------------------------A-----------------------          383
HIVCAR4017    ------A-----------------G----G--C-------------------------------------          386
HIVCAR4039    ----------------------------------------C-----------------------T---          383
HIVCAR4071    -------------------------------------------------------T---------          383
HIVCARMBA     -----CA----------------G----C-----A-----------C-------------T-----C--          380

CONSENSUS.F   ACAGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTGAAGTTAACCCCACTCTGTGTTACTTT    377
HIVBRA7944    -------------------------------------------------------------------------------    293
HIVBZ163A     -------------------------------------------------------------------------------    380
HIVBZ126A     -------------------------------------------------------------------------------    380

CONSENSUS.G   GAGGATATAATCaGttTATGGGATGAAAGCtTAaAGCCATGTGTAaAGcTAACCCCTCTCTGTGTTACtTT    383
HIVVI525A     ----------------------------------------------G--------------------          383
HIVLBV217     --------------C---------------C----------------T-------------------C--          383
HIVCAR4067    -----------T---------------------G-------------------------------------          383

CONSENSUS.O   GAAGACATtATtagTTTgTGGGAcCAGAGTtTaAAaCCTTGTGttcAAATGACTTTCtTgTGTGTACAAAT    377
HIVANT70      ----------------A----------C-T-----------------------C--------------          386
HIVMVP5180    --------C--------------A-----------G-------AGA-------------A-----------          389
HIVVAU        -----------AGA-------------------------------------------------------          386

CONSENSUS.CPZ GAAGA?AT??T?????T?T???A?CA?AG?C??AAGCC?TGTGTAAA??T?AC?CCT?T?TGT?TAA???T    191
SIVCPZGAB     -----C--TA-CAGTC-C-GGG-T--G--T-TC-----T--------GT-G--C---T-A---G---CCT-    383

CONSENSUS.U   gagGATATAATCAGTtTaTGGGAtcAAAGCCTaAAgCCATGTGTAAAgtTAACCccTCT?TG?GT?ACTTT    369
HIVZAM184     ----------------G----------------------------A----------C--C--C-----          383
HIVCAR4081    ----------------------G----------A----------C----------T--T--T-----          386
HIVK124A      ACA------------C-------C-------------------------------C--C--T-----          380
HIVZ3         --------------------------------T--------------------TT---T--T--C-----          383
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CONSENSUS.A   aaatTGta?t??????????????????????????????aa??tcac????????????????????????   388
HIVSF1703     --------GCCAT.....................................--CA----CACCCAT.............   411
HIVU455       -G----CCA-.......................................--CA----CATT.................   402
HIVZ321       --G---CCA-.......................................................................   393
HIVRW020      -G------A-.....................................GCCAC-G-CTCC.....................   401
HIVUG031      ---C----CC.....................................-CTG--GAC.......................   401
HIVD687       G-------G-.....................................G-CG----C.......................    79
HIVNI         -G-----CA-AATKTC.....................................--CAA--GCTACAGC.............   411
HIVRW009      -G-G----AC.......................................--CA----CAATGTC.............   404
HIVUG275A     --------G-GATGTCAAT...............................--TG----TGTCACC.............   417
HIVUG273A     --------CCAATGCC..................................--CC----CAATGCC.............   414
HIVVI191A     -G-A---CA-.......................................................................   390
HIVDJ264A     -G-----CA-.....................................--C.............................   393
HIVDJ263A     -G-----CA-AATGTC.....................................--CAG--GC.................   405
HIVDJ258A     -G-G---CA-.....................................--TG---GCAATAGC.............   405
HIVCARGAN     -G-A--CCA-.....................................--ACC-.........................   399
HIVCARSAS     -G-C----C-.....................................--TG-AG-T.....................   402
HIVCAR4054    --------C-GATGTAAAGAAG...........................--TAG---T.....................   414
HIVCAR286A    ---C----C-GATGCAAAGATAGACTGTACTAATGGAAGG--TAA--GTGCTGGAGGACAGACCTGTACTG        454
HIVCAR4023    ---C----C-GATGTAAAA..............................--TA----TGTG.................   420
HIVCAR423A    ---C----C-.....................................--TG-A--TGTAACC.............   411
HIVKENYA      --------GC.....................................--TG--..........................   399

CONSENSUS.B   AaatTGcactgaTttg??g???????????.....??????????????????????????????.           406
HIVJRCSF      --------AA---G--.................................................................   399
HIVJRFL       --------AG---G--.................................................................   399
HIVALA1       -C------T-----ATTT-..............................................................   402
HIVBRVA       -------CA------C.................................................................   402
HIVJH3        --------T-----G-GG-.....................AATGATACTAGCCCC.............   417
HIVBAL1       ----------------AG-.....................AATGCTACTAATGGG.............   417
HIVYU2        ---------------AAG-.............................................................   402
HIVMN         ----------------AG-.....................AATACTACTAATACCAAT..........   420
HIVHXB2R      ---G------------AA-.............................................................   405
HIVLAI        ---G------------GG-.....................AATGCTACTAATACC.............   420
HIVNL43       ---G------------AA-.............................................................   405
HIVMFA        ---G------------AA-.............................................................   405
HIVCAM1       --T-------A--G-A.................................................................   399
HIVNY5CG      ----------------AC-.............................................................   402
HIVADA        ----------------AG-.............................................................   402
HIVJFL        --------T-A-----AA-.............................................................   402
HIVSIMI84     ----------A---G-AA-AGTGCT.......................................................   408
HIVD31        -------------C--AA-.............................................................   402
HIVSF162      -C--------A-----AA-.............................................................   402
HIVBCSG3C     -------------GA-TT-AAG...........................................................   405
HIVOYI        -G-----------G-T.....................AATACCACTAGTAGTAGTTTGAGG.......   423
HIVSF33       --------------ATTT-GGG..........................................................   405
HIVCDC4       ----------------AATACTAAT.......................................................   414
HIVSF2        ----------------GG-.............................................................   402
HIVSF2B13     ----------------GG-.............................................................   402
HIVHAN        ---A----------ATAAT.............................................................   402
HIVRF         -------------GCTAACTTG..........................................................   405
HIVWMJ2       --------T----AA-................................................................   399
HIVTB132      ----------A-----AG-.............................................................   402
HIVBR020      --------T-------.....................AATAATAGTACTAAC.............   410
HIVTH014      ---C------------AG-.............................................................   398
HIVTH026      ----------------AG-.............................................................   398
HIVUS711      -------------AA-TT-.............................................................   398
HIVUS712      -------------C--AGT.............................................................   398
HIVUS715      ---------CA--C--AG-.............................................................   398
HIVUS716      ---G--T------C--GG-.............................................................   395
HIVHA593      -G-G--TCA----G--AATGTGAATGGCACT.....GCTAATAATGGCACTACTAATGTCACTGAG.             440
HIVHA594      ------------G--GA-..............................................................   398
HIVHA596      ------------G--AA-..............................................................   398
HIVHA599      -C----------GC-AG-..............................................................   398
HIVHA651      ----------C-GCAGA-..............................................................   395
HIVRJS        ----------A---G-AA-.............................................................   402
HIVGUN        ----------A-----GT-.............................................................   317
HIVSC         ----------A-----AG-.....................AATGATACTAGCACC.............   417
HIVBR014      -------------G--................................................................   401
HIVBR021      ----------A--G-T.....................AATACCAATAGTACT.............   417
HIVACH9       -------------AATTT-.............................................................   282
HIVACP1       -------------GATTT-AGG..........................................................   285
HIVJM         --------A----GCCTC-AGG.....................AATGTTACTAAGAGG.............   300
HIVWM         -------------GTGTAACTTCA........................................................   288
HIVMA208      -------------GCCACTATTAGA.....................................ACTAATACC.        441
HIVP896       ----------A-----.....................AATATCACTAAG.....................   411
HIVBWB11A     ----------A--GATTT-GGG.....................GATGCTACTAATACC.............    39
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CONSENSUS.C   AaA?TGtaga????????????.....aatg?ta????t?????????.....  396
HIVMA959      ---T-----C.....----C--AC.....  398
HIVMA960      ---T---GCT.....  389
HIVD757       ---T----C-.....----CA.....  76
HIVD747       -C-T----C-.....----C--CCTA-AGT.....  214
HIVD760       -G-G---G--AATGTT.....----C--CC.....  216
HIVNOF        ---T----C-GATGTAAAAGTT.....  50
HIVZAM20A     -G-A---G--.....----TG-CTGT-CCCAAGGAT.....  414
HIVD1044      -G-A------CAGGCT.....---TT--CC.....  46
HIVD1024      -G-A---G--AAGGTT.....----C--CC.....  408
HIVD744       ---A---GAT.....-C--CCAG-.....  78
HIVD766       -G-A------.....----T--CCAG-AATGGT.....  39
HIVD808       -G-A------.....----T--GCAG-AATGGT.....  90
HIVD868       -G-A------GAGGTT.....----A--CTAGAAATGGGGTT.....  90
HIVBR025      -C-C--C--T.....--CAGA-CTAT-GACTACAAT.....  324
HIVSM145A     ---T----C-GAA.....GC-AA--TT.....  405
HIVZAM18A     -G-A---G--.....----T-.....  402
HIVDJ259A     ---C-----T.....----T-CAGAG-.....  399
HIVDJ373A     ---C-----T.....---AAGGTTAC-GCTACCGGT.....  414
HIVSE364A     ---C-----G.....  393
HIVUG268A     ---T----C-.....----T--ATGT-.....  405

CONSENSUS.D   aaAcTGcActgatg?g??g?????????.....aa????act?????????????????....  399
HIVJY1        ---T------A---CTGG-GGG.....  405
HIVNDK        ----------AATT-AGG.....  405
HIVMAL        ----------A---T-.....--TGGG---GCTGTG.....  414
HIVELI        ------T-G-----AATT-AGGAAC.....  408
HIVZ2Z6       --------TA----AAGT-ATGGAG.....  408
HIVUG024      --------T---ATG-AA-AATGAA.....--TGAA---AAGGGG.....  426
HIVUG021      ----------ATG-AA-.....  398
HIVUG038      -C----------T-.....--TAGT---.....  405
HIVUG046      -C-T--------ATATAA-GCCCCT.....--TGCC---ATT.....  438
HIVUG266A     --------G---A-G-AG-GTT.....-CAGAT--A.....  414
HIVUG269A     ---T--------A-CCAAATTC.....--TGTC---AGAGCCACTAATGGAAAG....  431
HIVUG274A     ----------ATG-AA-.....  402
HIVSE365A     --------GG---ATTTCTAGT.....G-CGCC---AGTAACACCATTAGT.....  429
HIVCAR4020    GC--------CGATT-GA-AATATTGCA.....--CAGT-GCCTTACAAAC.....  429

CONSENSUS.E   AaatTGTAccaatgct???????????????.....??????????????????????...???.  398
HIVTH966      --------T-------.....AATTTGACCAATGTCAATAACATA...ATC.  422
HIVTH975      ---------T-CATTGACCAAAGTC.....AACATAACC.....  413
HIVTH022      ----------.....AATTTGATCAATGTCAAT.....  413
HIVTN243      --T----------AAGTTGACCAATGCT.....AATTTGACCAATGTCAAT.....  432
HIVTH006      ----------AAAGTGACCAAT.....GTCAGT.....  413
HIVTH011      ----------T----N.....NT.....AATTTGACCAATGTCAAG.....  341
HIVCARELO     --GG----------.....  399
HIVCAR4017    ----------G---.....  402
HIVCAR4039    -C---------GG---.....  399
HIVCAR4071    -G----------A---GATTTT.....  405
HIVCARMBA     ----------GG---AATCTT.....  402

CONSENSUS.F   AaATTGTACTaaTGCCact?cT.....AATGCCACT.....  407
HIVBRA7944    ----------G--------G--.....---------.....  324
HIVBZ163A     ----------...AT-.....---------.....  408
HIVBZ126A     -C---------G-------C--.....---------.....  411

CONSENSUS.G   AAACTGTACTaA?GtaA?C?ac.....AAT?g?ACta??g?C???.....  412
HIVVI525A     ----------G----C-T--.....---A-C---GCA-C-AAC.....  423
HIVLBV217     ----------T-C--T-GCT.....---GTA--C-ACAG-.....  420
HIVCAR4067    ----------G-A--G-A-A--.....---T-T----GG-A-.....  420

CONSENSUS.O   GaA?TGTacAgat?t??aaa????????.....AAtA?aaCa????????c?ta?????????.  404
HIVANT70      -G-G------.....--C-T-G-T.....  405
HIVMVP5180    ---C---GT----C-GC---CA.....----A----.....GG-C--.....TTA.  429
HIVVAU        ---T---------A-CA---ATAGTATT.....----CC---AACAGTCC-T--AACTCA....  441

CONSENSUS.CPZ G?A?TG?A?????????????????????????.....  196
SIVCPZGAB     -C-G--C-GTAAGGCTAACTTTAGCCAGGCAAAA.....  417

CONSENSUS.U   AAa?TGTAgTgatgtc???????????????.....AAtagcACtaa????.....  395
HIVZAM184     ---T----------C-ACTAGTACCAATAGC.....--C-C----.....  423
HIVCAR4081    --CC----C-.....----TA--C--A.....  408
HIVK124A      ---T------A-----.....---G----GGGTGGC.....  411
HIVZ3         ---C----T------AAAG.....-----T-----C.....  414
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CONSENSUS.A  ????????aaca?cac?a??????????????????aa?a??ac???????.....??????   401
HIVSF1703    .....----T---C-CCAACAACCCC.....--T-TC--C.....                    441
HIVU455      .....----A---C-AT.....--C-AC--C.....AATATC                       429
HIVZ321      .....----T---C-TCAAGGAC.....--T-AC--C.....AATGTA                 426
HIVRW020     .....--TGT---C-AT.....                                           413
HIVUG031     .....----C---G-AT.....GTC--C-TCT-G.....                          425
HIVD687      .....----A---CTTTAGC.....--CGTAT-T.....                          103
HIVNI        .....----GT-GC.....--CCTA--T.....                                429
HIVRW009     .....----A---TGTC.....--C-TT--G.....                             425
HIVUG275A    .....--TCAT-GT-TT.....                                           429
HIVUG273A    .....--T-AA-ATGCCAAGGTCAACAGCGCCACG--TGGC--C.....                453
HIVVI191A    .....----G---C-CCCCAGAT.....--C-AT--C.....ACC                    420
HIVDJ264A    .....---GT---CTCTAAC.....--T-GG--C.....ATA                       420
HIVDJ263A    .....--T-G--GC-CCTCTATC.....--C-GG--C.....ATA                    435
HIVDJ258A    .....--T-C-T-T-GCTACAGG.....--C-TAT-T.....                       432
HIVCARGAN    .....----C---AGATAGCACCAAA.....--C-AC-GCGCAGAA.....AACATG        441
HIVCARSAS    .....---GA--GT-CA.....                                           414
HIVCAR4054   .....                                                            414
HIVCAR286A   GAGTACAG--T-G---TGCT.....                                        474
HIVCAR4023   .....--T-GT--T-GT...ACTGGGAATAGTGCT--T-CA-TA.....               456
HIVCAR423A   .....----G--GT-AT.....--TGTA--C.....AAAACC                       438
HIVKENYA     .....--TGT---TGCCACG.....-GTGGC--A.....ACA                       426

CONSENSUS.B  .....aatg?tact??t??????????????????aata?ta?t??????????????????????gg   424
HIVJRCSF     .....----C----.....----CC-C-.....AGTAGTAGTGA-                    429
HIVJRFL      .....----C----.....----CC-C-.....AATGATAGCGA-                    429
HIVALA1      .....----C----.....----CC-C-.....AGTAGTAACG--                    432
HIVBRVA      .....----C----.....---GCC-C-.....AGTAATAGCG--                    432
HIVJH3       .....----C----.....----CC-C-.....AGTAGTGGCG--                    447
HIVBAL1      .....----AC---.....----CC-C-.....AGTAGTAGCA--                    447
HIVYU2       .....----C----.....----CC-C-.....AGTAGTAGCT--                    432
HIVMN        .....---AG----GC-AAT.....--C-A--G-.....AATAGCGA-                 453
HIVHXB2R     .....----A----AA-ACC.....----G--G-.....AGCG--                    435
HIVLAI       .....---AG--G-AA-ACC.....----G--G-.....AGCG--                    450
HIVNL43      .....----A----AA-ACC.....----G--G-.....AGCG--                    435
HIVMFA       .....----A----AA-ACC.....----G--G-.....AACG--                    435
HIVCAM1      .....---AA----AGGACC.....----G--G-.....GATTGGGACAGGA--           438
HIVNY5CG     .....----C----TA-GCC.....---GG--G-.....                          426
HIVADA       .....----T----AA-ATC.....----A--G-.....AGTGA-                    432
HIVJFL       .....----T----AA-ATC.....----A--G-.....T--                       429
HIVSIMI84    .....---AG---CAG-AATACC.....----G--G-.....                       435
HIVD31       .....----C----AA-ACCAAT.....----G--G-.....TGGACGAT-              438
HIVSF162     .....----C----.....----CC-AG.....AGTAGTAAT                       429
HIVBCSG3C    .....----C----.....----CC-C-AGTACTAATACCCCTAGTGGTA-C              447
HIVOYI       .....----C----.....----CC-CA.....AGTAGTAGTT--                    453
HIVSF33      .....----C----AA-ACC.....--C-A--G-.....AGTG--                    435
HIVCDC4      .....---AC----.....----C--C-GAACTATCAATAATAGTAGTTT--              456
HIVSF2       .....--G-C----AA-ACC.....----G--G-.....AATT--                    432
HIVSF2B13    .....--G-C---AACC.....----G--A-.....AATT--                       429
HIVHAN       .....----CC---.....--C-G--G-.....T--                             423
HIVRF        .....----G----.....---GTC-C-AGTAGTAGCGGG.....G-A                 438
HIVWMJ2      .....--CAT----GA-TGGAAG.....----CA-CAATA.....                    429
HIVTB132     .....----A----.....                                              411
HIVBR020     .....--CAA--A-.....-G--G-GGGGTAAA.....A                          434
HIVTH014     .....----C----AA-ACC.....-G--G--CA.....                          422
HIVTH026     .....----C----.....----CC-G-.....AGTACG.....                     422
HIVUS711     .....-T-AA-G--ACCTATAGCAAT.....-T--G-TTG.....                    428
HIVUS712     .....----C----AA-ACGAAT.....GC--C--CAACCACG...AATAGTAGCGCGG-A    446
HIVUS715     .....----A----AA-ACCACG.....-GG-A-GC-ACTAAT...ACCACGAGTAGTGA-    446
HIVUS716     .....----C----.....----CC-CG.....AGTAGC...G--                    422
HIVHA593     .....-G--G-GTCAA-AGTAGTGATGTCACTAGT----A-GTC.....ACTAATAGTAATT--  494
HIVHA594     .....---AG----AA-GCC.....-C--A--G-.....AGTG--                    428
HIVHA596     .....---AG----AA-GTC.....-C--A--G-.....AGTG--                    428
HIVHA599     .....---AG----AA-GTC.....-C--T-GAG.....GT-                       425
HIVHA651     .....-GGAA-GA-AC-GGG.....-GCTC--A-.....A-T                       422
HIVRJS       .....----A----GA-ACT.....----CC-C-.....AATAGTAGTAGTG--           441
HIVGUN       .....----C----TA-AGT.....----G--G-.....T--                       344
HIVSC        .....----C----.....----CC-C-.....AGTAGTAATC--                    447
HIVBR014     .....----T----AA-ACTAAT.....----C--C-AGTACAAATAGTAGTAGG...TT-    449
HIVBR021     .....---ACC---.....----G--C-.....AATGCCACTAGTAGTT--              453
HIVACH9      .....---AG----AA-TTGGGG.....----A--C-.....                      309
HIVACP1      .....----A-.....T--                                              294
HIVJM        .....----A----AA-GAGAATGCTACTGATAGT----A-GGGACTGCTACTAGTGGGAAT...AAA  360
HIVWM        .....---TGC---AA-TTGAGG.....---GT--CCAATACCAAAAGTAGTAGC...AA-    336
HIVMA208     .....---AC----AA-ACT.....----G--GC.....G--                       468
HIVP896      .....---AC----.....---CCC-C-.....AGTAGCAGC...T--                 441
HIVBWB11A    .....---AG--G-.....AGCGAG.....                                   54
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CONSENSUS.C  ........AAtg?taccaataat??????????????aat???ac?????????????????????????  415
HIVMA959     .........--CAC-G-T-CC---.....................---GTA--TGCTACCAATAATGTAACC......  440
HIVMA960     .........----T---T-TC-G-.....................---GAG--CTAT.....................  416
HIVD757      .........----T----T--G--AATGGT..........--CTAC--T.....................  106
HIVD747      .........---AG----T-C.....................---AGT--CTACAAT.....................  241
HIVD760      .........---AT----------GGGGAAAAT.....---CCT--CAATATTACCAATAATAGG......  267
HIVNOF       .........----C-----G---CAGTAAT.....--CATG--T.....................  80
HIVZAM20A    .........---AG----T-C---GGTGATATCAATAGT---ACT--CATGAAA.....................  459
HIVD1044     .........----C-------GC-AAC.....---GCT--G.....................  73
HIVD1024     .........---AT----------GGG.....  426
HIVD744      .........----C-----G--G-GGG.....  96
HIVD766      .........----G----T-C---GAGACCTAC.....---GAG-GCGTG.....  75
HIVD808      .........----G----T-C---GAGACCTAC.....---GAG-GCGTG.....  126
HIVD868      .........----T----------GGG.....  108
HIVBR025     .........--CAGA--TG--.....--CATGGGG.....  345
HIVSM145A    .........---AT-----G-GT-GGC.....---GTT--CAGTAATGACAATAAG.....  447
HIVZAM18A    .........----T----C--G-G.....---AGC--GAAG.....  429
HIVDJ259A    .........----C----T-CG-G.....---AGC--AAAA.....  426
HIVDJ373A    .........----G--GTGT--CCTAC.....---AGC--AGAA.....  444
HIVSE364A    .........----T-----CC-GCAAT.....---GCC--CAGT...AATGATAACCCTAAT...  438
HIVUG268A    .........---AT----------GCT.....---GCT--CAATAGCCCCTACGAAAATGGGAAA  456

CONSENSUS.D  ........AAt??cacta?ta????????.....aatg??act??????????????????????????  416
HIVJY1       .........---AAG----C--ATGGGAAT.....---ACT---AATCAGGAGGAACAGATGATGGAG  459
HIVNDK       .........--CAG--AGGGC.....----GG-AGGTAGAAGAGGAG.....  438
HIVMAL       .........---GGG----A-GCTGGGAGT.....---AGG---AATGCAGAATTGAAAATGGAAATT  468
HIVELI       .........---GG-----TGGGGAAC.....----TC---ACAGAGGAG.....  444
HIVZ2Z6      .........---GT---A-TG-AGAATAAT.....----TC--AGAGGAA.....  444
HIVUG024     .........---AAA---GTGGACCCT.....-AT-AGGAC.....  453
HIVUG021     .........---GC---C-C-.....----CC---.....  419
HIVUG038     .........---ATA----G--CTAATGTG.....---AAT---.....  435
HIVUG046     .........---GC----GA--GGGACATA.....  459
HIVUG266A    .........---GG-----T-GGA.....----GC---.....  438
HIVUG269A    .........--CACTGT--GA.....----CC---.....  452
HIVUG274A    .........---AC----GAACAGGAGAAG.....---ACCG--.....  432
HIVSE365A    .........--CGT----GGA-TACCG.....  447
HIVCAR4020   .........---GC--G-GCA-GAAGT.....----AT--AGACAATAACCATACA.....  471

CONSENSUS.E  ........aat?t?accaatg??????????????????aata??ac?????????????...?????????  415
HIVTH966     ........C--GGCC-T--C.....ATAATAGGA  443
HIVTH975     .....---TTCT-TAAA.....ATAGGA  431
HIVTH022     .........--CA-A-------TCTCTAACATAATAGGA----TA--A.....  452
HIVTN243     .........--CA-A-------TCTCTAACATAATAGGA----TA--A.....  471
HIVTH006     .........---ACA-T-----CCCCTGAC...ATAGGA----TA--A.....  449
HIVTH011     .........--CA-A-------TCCCTAACAAAATAGGA----TA--A.....  380
HIVCARELO    .........---T-T---.....---GCT--CGATGCT.....  423
HIVCAR4017   .........---T-T-----G-CT.....----GT--CGAGGCTGCTTTG.....  438
HIVCAR4039   .........---T-T------TCT.....---TAT--CAAGGGT.....  429
HIVCAR4071   .........--CACC--A--ATTT.....--C-CA--AGAAAAG.....  435
HIVCARMBA    .........---TCT-------CT.....---TCT--C.....AAT  429

CONSENSUS.F  ........??????.....?????????.....  407
HIVBRA7944   ........ACCACC.....AATGACACT.....  339
HIVBZ163A    .....  408
HIVBZ126A    .....  411

CONSENSUS.G  ........AAtAa?ac?act??????.....???a?ca?c?????????...??????????????  426
HIVVI525A    .....----GAT-AT-CACTGTC.....-C--C-CCT.....ACTAGTACTGTAACC  465
HIVLBV217    .....-----G--T-G-.....AAC-A--G-AGCCTTGGG.....  450
HIVCAR4067   .....--C--T-GC---GTG.....  435

CONSENSUS.O  ........aa?ga?ACAa?a.....  413
HIVANT70     .....-GA----C-.....  414
HIVMVP5180   .....--T--G----T-.....  441
HIVVAU       .....--CA-T---.....  450

CONSENSUS.CPZ ..........AA???AACA?????????????????????A?????ACA????C????...?????????  207
SIVCPZGAB    .....--CCT----.....-ACCAG---TCTT-T.....  441

CONSENSUS.U  ........aatagcactgaag?a???.....?????????????????.....  409
HIVZAM184    .....  423
HIVCAR4081   .....-----T-------T-.....AACAACAATAGCACTGTG.....  441
HIVK124A     .....--C------ACG-GTAAC.....AACATCACT.....  438
HIVZ3        .....----A--------A-.....  429
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CONSENSUS.A   ??????ga?atg??a.....??????????????????????????gg    409
HIVSF1703     ...AAAT-C---GA-.....                                  --    455
HIVU455       ACAGAT-GAG--AGG.....                                  -A    446
HIVZ321       GATACT--A---AA-.....                                  -A    443
HIVRW020      .....                                                      413
HIVUG031      ...AAG--C---AT-.....                                  --    439
HIVD687       ...TAT--C---AA-.....                                  --    117
HIVNI         ...AGT--C---AAT.....                                  --    443
HIVRW009      ...GAT--C---AA-.....                                  --    439
HIVUG275A     AGCAGT--C---AA-.....                                  --    446
HIVUG273A     ATCCAGAGC---GA-.....                                  A-    470
HIVVI191A     CAGTCCACT--CAT-.....                                  -A    437
HIVDJ264A     TCTAGG--C---CA-.....                                  --    437
HIVDJ263A     GATAGTA-A---CA-.....                                  -A    452
HIVDJ258A     ...AGT--A---CG-.....                                  -A    446
HIVCARGAN     ACCTTT--AGG-AT-.....                                  --    458
HIVCARSAS     .....                                                 AA    416
HIVCAR4054    .....                                                 CTGGAA--    422
HIVCAR286A    .....                                                 GAGGTT--    482
HIVCAR4023    AATAGAACT.....                                        GTGGATA-    473
HIVCAR423A    AACAGTAGC.....                                        --    473
HIVKENYA      CACGGG-GACG-.....                                     --    440

CONSENSUS.B   g?aa?g???atggagaaa???.....                            gg    439
HIVJRCSF      -G--T-...-------G-.....                               --    446
HIVJRFL       -G--C-...-------G-.....                               --    446
HIVALA1       AC--A-...-------G-.....                               --    449
HIVBRVA       AA--T-...------GG-.....                               --    449
HIVJH3        -A--A-...---------.....                               --    464
HIVBAL1       -G--T-...G---G-GG-.....                               --    464
HIVYU2        -A--C-...---------.....                               --    449
HIVMN         -G--CA...--AA--GG-.....                               --    470
HIVHXB2R      AG--T-ATA---------.....                               --    455
HIVLAI        -A--T-ATG---------.....                               --    470
HIVNL43       AG--T-ATA---------.....                               --    455
HIVMFA        AG--T-ATA---------.....                               --    455
HIVCAM1       -A-GGAGAA-A-AT----.....                               --    458
HIVNY5CG      ......AGTGA-----G-.....                               --    440
HIVADA        -G--T-AGA.....                                        --    443
HIVJFL        -G--A-...------G--.....                               --    446
HIVSIMI84     ......TTGGA-------.....                               --    449
HIVD31        AC-GGAGAA---...---.....                               --    455
HIVSF162      TGG-AAGAG-----C-G-.....                               --    449
HIVBCSG3C     TGG-AAAAG-----A-G-.....                               --    467
HIVOYI        -A--C-...---------.....                               --    470
HIVSF33       -G--C-...G--------.....                               -A    452
HIVCDC4       -A-CAA...CG--GT---.....                               --    473
HIVSF2        AA-GAA...GAAATA---.....                               --    449
HIVSF2B13     AA-GAA...GAAATA---.....                               --    446
HIVHAN        -G--G-...---------.....                               --    440
HIVRF         AC--T-...--------C.....                               --    455
HIVWMJ2       .....--A-GAGG-.....                                   --    440
HIVTB132      .....                                                 A-    413
HIVBR020      AC-GG-...--A--C--G.....                               --    451
HIVTH014      .....------GG-.....                                   --    433
HIVTH026      .....------GG-.....                                   --    433
HIVUS711      -A-GGA...GAAATA---.....                               --    433
HIVUS712      ATG-T-...-----C-GG.....                               --    445
HIVUS715      AC--T-...------G-G.....                               --    463
HIVUS716      AG--T-...-----AGGG.....                               --    463
HIVHA593      -G--CA...-----A--G.....                               --    439
HIVHA594      -G--TA...--A--C---.....                               --    511
HIVHA596      -GG-TA...--A---GG-.....                               --    445
HIVHA599      -A--A-...G-A------.....                               --    445
HIVHA651      AGTGGA...--A--T---.....                               --    442
HIVRJS        -A--AA...------G--.....                               --    439
HIVGUN        -A--A-...-----C-G-.....                               --    458
HIVSC         -G--A-...------GG-.....                               --    361
HIVBR014      -A-GA-...---------.....                               --    464
HIVBR021      -A-.....-ATAT---G.....                                --    466
HIVACH9       .....GATATC---.....                                   -A    467
HIVACP1       -A-CA-...---------.....                               --    320
HIVJM         ACT-T-...-----A--GTAT.....                            --    311
HIVWM         -A--TA...-----A---.....                               -C    380
HIVMA208      -A-GT-...-A-----G-.....                               --    353
HIVP896       -G--T-...---------.....                               -A    485
HIVBWB11A     -G--T-...-----A-T-.....                               --    458
                                                                    --     71
```

```
CONSENSUS.C ????????????.....ga  417
HIVMA959    .....AG  442
HIVMA960    .....A-  418
HIVD757     .....--  108
HIVD747     .....--  243
HIVD760     .....--  269
HIVNOF      .....-G   82
HIVZAM20A   .....--  461
HIVD1044    .....--   75
HIVD1024    .....--  428
HIVD744     .....--   98
HIVD766     .....A-   77
HIVD808     .....A-  128
HIVD868     .....--  110
HIVBR025    .....-G  347
HIVSM145A   .....--  449
HIVZAM18A   .....-G  431
HIVDJ259A   .....--  428
HIVDJ373A   .....A-  446
HIVSE364A   .....-G  440
HIVUG268A   CTCATGGAACAG.....-G  470

CONSENSUS.D a????????????????????????????????????.....g?  418
HIVJY1      -AA.....-G  464
HIVNDK      .....-A  440
HIVMAL      .....-G  470
HIVELI      .....AA  446
HIVZ2Z6     .....AT  446
HIVUG024    .....AT  455
HIVUG021    -ATGAGGGC.....AT  430
HIVUG038    -GCATAGAGAAA.....-G  449
HIVUG046    .....  459
HIVUG266A   -TT.....-G  443
HIVUG269A   -AGGGGGGC.....CT  463
HIVUG274A   GTACCGGGGAGTACAACATCTGAC.....AC  458
HIVSE365A   -TGATGGGGAAA.....-G  461
HIVCAR4020  -ACAGTACCAATACTAGATGGGTATATGACGGAATGGAA.....AA  512

CONSENSUS.E ??t???a????????????????????????????????????.....gA  419
HIVTH966    AA-ATA-CA.....--  454
HIVTH975    AA-ATA-CA.....--  442
HIVTH022    .....--  454
HIVTN243    .....--  473
HIVTH006    .....--  451
HIVTH011    .....--  382
HIVCARELO   AA-GTT-CCAATGCTACTGCTAAATTTAATGCTACAAAAGAAATGGAA.....A-  473
HIVCAR4017  AA-GGC-GTTACAGTAATGAAACAGCAGAAATGGAA.....A-  476
HIVCAR4039  AA-GAA-CTGTTGAAATGGAA.....A-  452
HIVCAR4071  CCAGAA-TAGAAATATCAGAAATGCAA.....A-  464
HIVCARMBA   GC-AAT-CCCTAAAAATGGAA.....A-  452

CONSENSUS.F .....gcca?tCAA?ACgG????acCcTGAAGGAAGaaCCA.....GG  439
HIVBRA7944  .....---C--A-C...---T---------G---.....--  368
HIVBZ163A   .....----T----G----G...GA----------G----.....--  443
HIVBZ126A   .....----C----A----AACA----------.....--  449

CONSENSUS.G AAtagta??g?????ag???????.....GA  438
HIVVI525A   --C-A--GCACTGTG--TGGCAAA.....--  491
HIVLBV217   -----C-CT-TGAGT--CATA.....--  473
HIVCAR4067  ---T--GAG-AA.....--  449

CONSENSUS.O .....AA  415
HIVANT70    .....--  416
HIVMVP5180  .....--  443
HIVVAU      .....--  452

CONSENSUS.CPZ ??????????????T???.....?T  209
SIVCPZGAB   .....CCGCC-.....C-  449

CONSENSUS.U ?????????.....ga  411
HIVZAM184   .....--  425
HIVCAR4081  GATAATAAA.....--  452
HIVK124A    AGGGAGGAC.....AT  449
HIVZ3       .....-C  431
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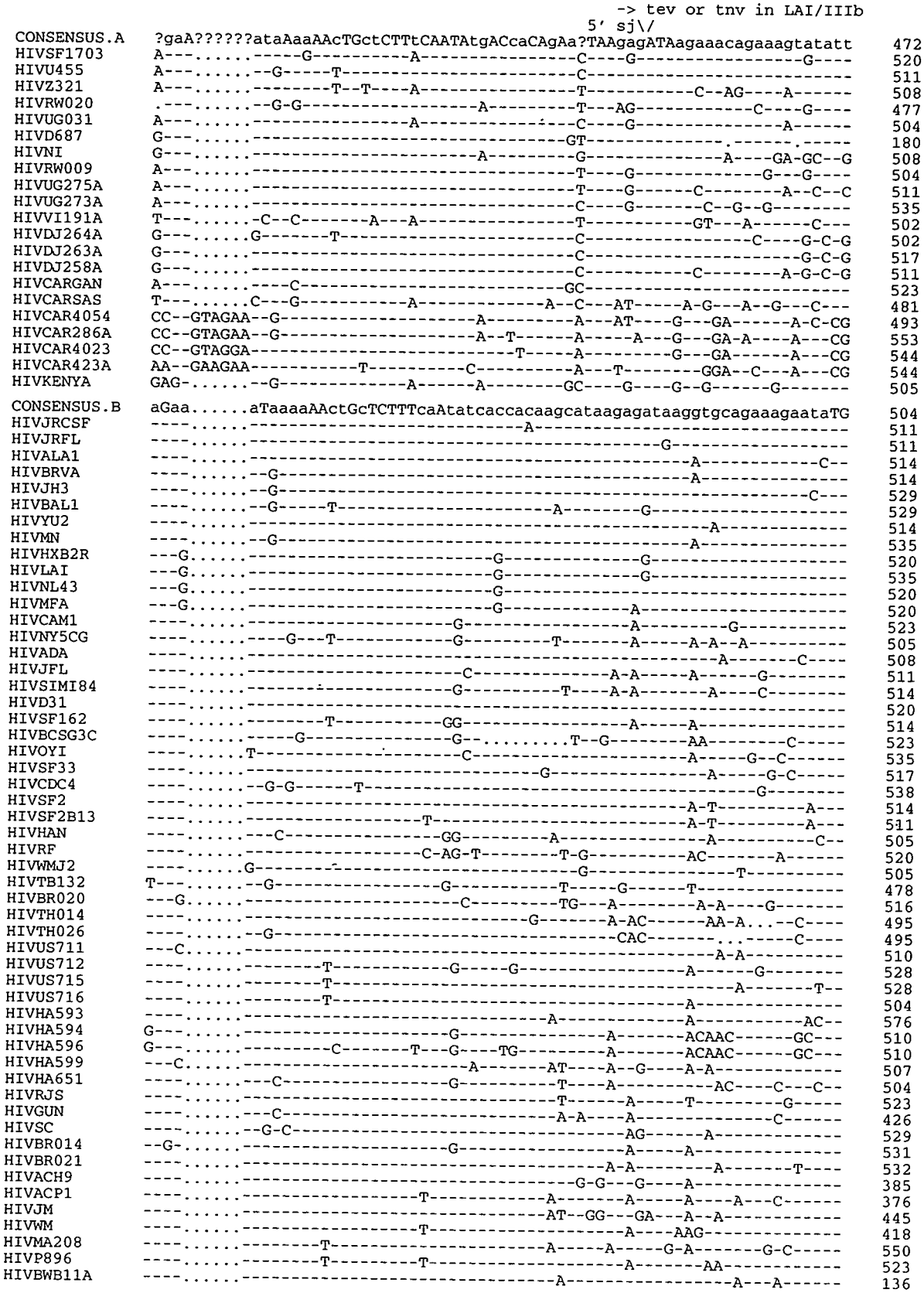
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5' sj\/
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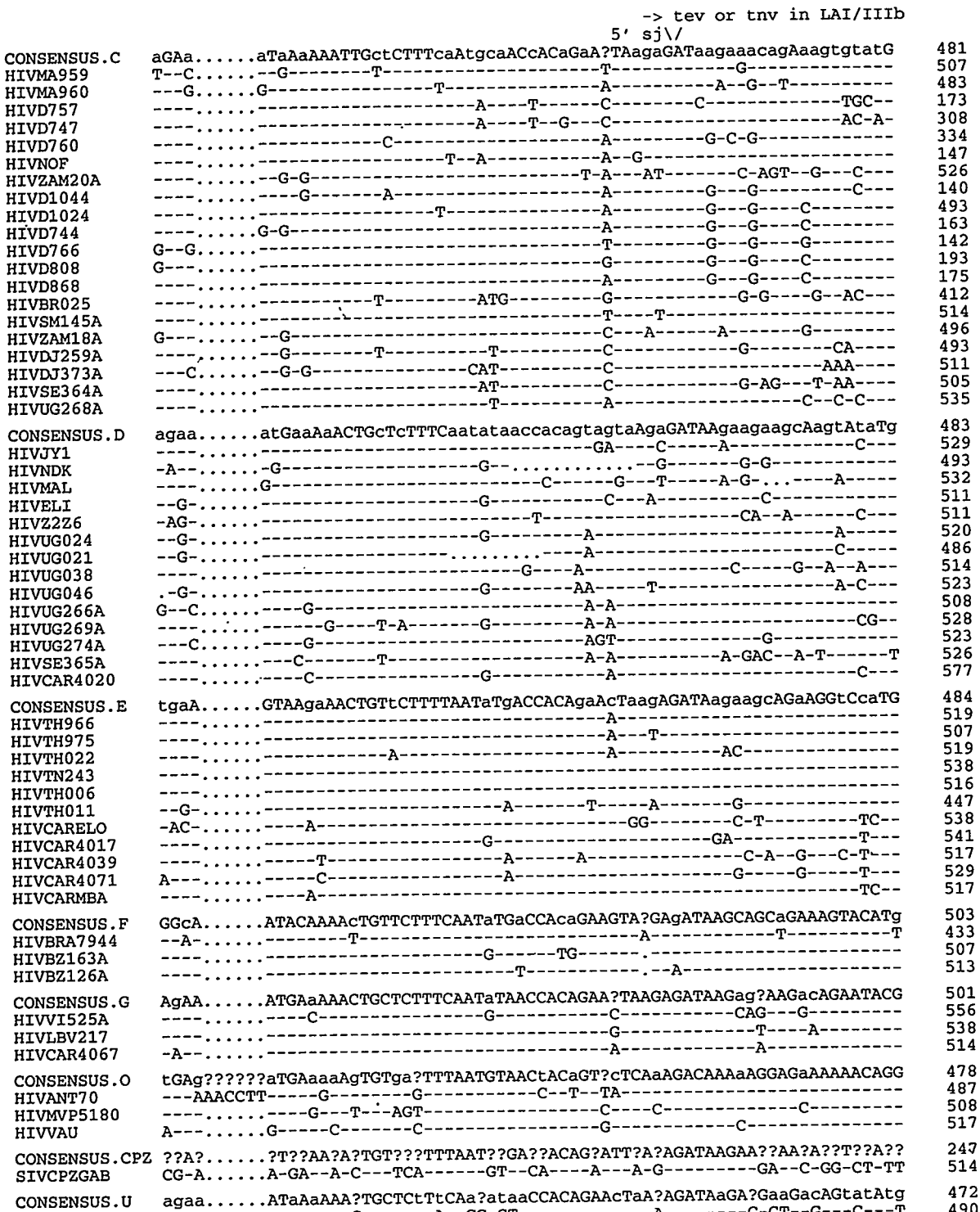
HIVSF1703 A---.....-----G----------A----------C----G----------G---- 520
HIVU455 A---.....--G-----T---------- 511
HIVZ321 A---.....--------T--T----A----------T----------C--AG----A------ 508
HIVRW020 .---.....--G-G----------A---------T---AG----------C----G---- 477
HIVUG031 A---.....----------A----------C----G----------A------ 504
HIVD687 G---.....----------GT----------.------.----- 180
HIVNI G---.....----------A---------G----------A----GA-GC--G 508
HIVRW009 A---.....----------T----G----------G---G---- 504
HIVUG275A A---.....----------T----G------C--------A--C--C 511
HIVUG273A A---.....----------C----G-------C--G--G-------- 535
HIVVI191A T---.....-C--C-------A---A----------T----------GT---A------C--- 502
HIVDJ264A G---.....G-------T----------C----------C----G-C-G 502
HIVDJ263A G---.....----------C----------G-C-G 517
HIVDJ258A G---.....----------C----------C--------A-G-C-G 511
HIVCARGAN A---.....----C----------GC---------- 523
HIVCARSAS T---.....C---G----------A----------A--C---AT-----A-G---A--G---C--- 481
HIVCAR4054 CC--GTAGAA--G----------A---------A---AT----G---GA------A-C-CG 493
HIVCAR286A CC--GTAGAA--G----------A--T------A-----A---G---GA-A----A---CG 553
HIVCAR4023 CC--GTAGGA----------T-----A---------G---GA------A---CG 544
HIVCAR423A AA--GAAGAA----------T----------C----------A---T--------GGA--C---A---CG 544
HIVKENYA GAG-.....--G----------A------A--------GC----G----G--G------G------- 505
CONSENSUS.B aGaa.....aTaaaaAActGcTCTTTcaAtatcaccacaagcataagagataaggtgcagaaagaataTG 504
HIVJRCSF ----.....----------A---------- 511
HIVJRFL ----.....----------G---------- 511
HIVALA1 ----.....----------A----------C-- 514
HIVBRVA ----.....--G----------A---------- 514
HIVJH3 ----.....--G----------C--- 529
HIVBAL1 ----.....--G-----T----------A--------G---------- 529
HIVYU2 ----.....----------A---------- 514
HIVMN ----.....--G----------A---------- 535
HIVHXB2R ---G.....----------G----------G---------- 520
HIVLAI ---G.....----------G----------G---------- 535
HIVNL43 ---G.....----------G---------- 520
HIVMFA ---G.....----------G----------A---------- 520
HIVCAM1 ----.....----------G----------A---------G---------- 523
HIVNY5CG ----.....----G---T----------G---------T-------A-----A-A--A---------- 505
HIVADA ----.....----------A-------C---- 508
HIVJFL ----.....----------C----------A-A-----A------G-------- 511
HIVSIMI84 ----.....----------G----------T----A-A-------A----C-------- 514
HIVD31 ----.....---------- 520
HIVSF162 ----.....--------T----------GG----------A-----A---------- 514
HIVBCSG3C ----.....-----G----------G--.....T--G--------AA--------C----- 523
HIVOYI ----.....T----------C----------A-----G--C------ 535
HIVSF33 ----.....----------G----------A-----G-C----- 517
HIVCDC4 ----.....--G-G------T----------G-------- 538
HIVSF2 ----.....----------A-T---------A--- 514
HIVSF2B13 ----.....----------T----------A-T---------A--- 511
HIVHAN ----.....---C----------GG---------A----------A----------C-- 505
HIVRF ----.....----------C-AG-T--------T-G----------AC-------A------ 520
HIVWMJ2 ----.....G----------G----------T----------T---------- 505
HIVTB132 T---.....--G----------G----------T-----G------T---------- 478
HIVBR020 ---G.....----------C---------TG---A--------A-A----G------- 516
HIVTH014 ----.....----------G-------A-AC------AA-A...--C---- 495
HIVTH026 ----.....--G----------CAC-------...-----C---- 495
HIVUS711 ---C.....----------A-A---------- 510
HIVUS712 ----.....--------T----------G-----G----------A------G-------- 528
HIVUS715 ----.....--------T----------A-------T-- 528
HIVUS716 ----.....--------T----------A---------- 504
HIVHA593 ----.....----------A----------A----------AC-- 576
HIVHA594 G---.....----------G----------A-------ACAAC------GC--- 510
HIVHA596 G---.....----------C-------T---G----TG---------A-------ACAAC------GC--- 510
HIVHA599 ---C.....----------A--------AT----A--G----A-A---------- 507
HIVHA651 ----.....---C----------G----------T----A----------AC-----C---C-- 504
HIVRJS ----.....----------T------A-----T---------G----- 523
HIVGUN ----.....---C----------A-A----A----------C------ 426
HIVSC ----.....--G-C----------AG------A---------- 529
HIVBR014 --G-.....----------G----------A-----A---------- 531
HIVBR021 ----.....----------A-A--------A-------T---- 532
HIVACH9 ----.....----------G-G---G----A---------- 385
HIVACP1 ----.....----------T----------A-------A-----A----A---C------ 376
HIVJM ----.....----------AT--GG---GA---A--A---------- 445
HIVWM ----.....----------T----------A----AAG---------- 418
HIVMA208 ----.....--------T----------A-----A-----G-A-------G-C----- 550
HIVP896 ----.....--------T---------T----------A-------AA---------- 523
HIVBWB11A ----.....----------A----------A---A------ 136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5' sj\/
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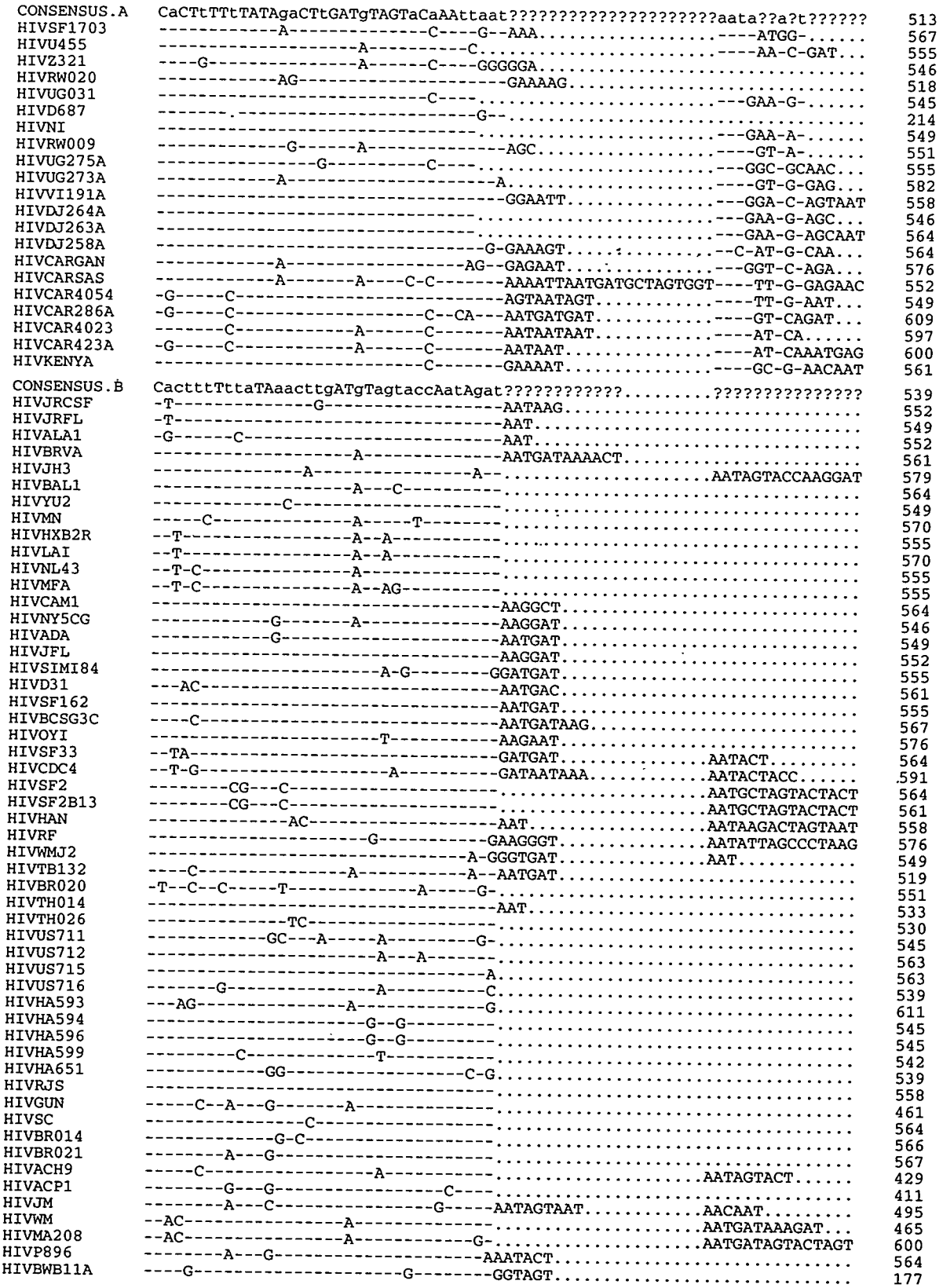
HIVMA959 T--C.....--G--------T---------T----------G---------- 507
HIVMA960 ---G.....G----------T----------A----------A--G--T---------- 483
HIVD757 ----.....----------A----T------C--------C----------TGC-- 173
HIVD747 ----.....----------A----T--G---C----------AC-A- 308
HIVD760 ----.....----------C----------A---------G-C-G---------- 334
HIVNOF ----.....----------T--A----------A--G---------- 147
HIVZAM20A ----.....--G-G----------T-A---AT-------C-AGT--G---C--- 526
HIVD1044 ----.....----G-------A----------A---------G---G---------C--- 140
HIVD1024 ----.....----------T----------A---------G---G----C--------- 493
HIVD744 ----.....G-G----------A---------G---G----C--------- 163
HIVD766 G--G.....----------T---------G---G----G--------- 142
HIVD808 G---.....----------G---------G---G----C--------- 193
HIVD868 ----.....----------A---------G---G----C--------- 175
HIVBR025 ----.....----------T---------ATG---------G----------G-G----G--AC--- 412
HIVSM145A ----.....----------T----T---------- 514
HIVZAM18A G---.....--G----------C---A------A-------G--------- 496
HIVDJ259A ----.....--G--------T----------T----------C----------G---------CA---- 493
HIVDJ373A ---C.....--G-G----------CAT----------C----------AAA---- 511
HIVSE364A ----.....----------AT----------C----------G-AG---T-AA---- 505
HIVUG268A ----.....----------T----------A----------C--C-C--- 535
CONSENSUS.D agaa.....atGaaAaACTGcTcTTTCaatataaccacagtagtaAgaGATAAgaagaagcAagtAtaTg 483
HIVJY1 ----.....----------GA----C-----A----------C--- 529
HIVNDK -A--.....-G----------G--.....--G-------G-G---------- 493
HIVMAL ----.....G----------C------G---T-----A-G-...----A----- 532
HIVELI --G-.....----------G----------C---A----------C---------- 511
HIVZ2Z6 -AG-.....----------T----------CA--A------C--- 511
HIVUG024 --G-.....----------G---------A----------A----- 520
HIVUG021 --G-.....----------.....----A----------C----- 486
HIVUG038 ----.....----------G----A----------C-----G--A--A--- 514
HIVUG046 .-G-.....----------G---------AA-----T----------A-C--- 523
HIVUG266A G--C.....----G----------A-A---------- 508
HIVUG269A ----.....------G----T-A-------G---------A-A----------CG-- 528
HIVUG274A ---C.....----G----------AGT----------G---------- 523
HIVSE365A ----.....---C-------T----------A-A----------A-GAC--A-T------T 526
HIVCAR4020 ----.....----C----------G----------A----------C--- 577
CONSENSUS.E tgaA.....GTAAgaAACTGTtCTTTTAATaTgACCACAgaAcTaagAGATAagaagcAGaAGGtCcaTG 484
HIVTH966 ----.....----------A---------- 519
HIVTH975 ----.....----------A---T---------- 507
HIVTH022 ----.....----------A----------A----------AC---------- 519
HIVTN243 ----.....---------- 538
HIVTH006 ----.....---------- 516
HIVTH011 --G-.....----------A-------T-----A-------G---------- 447
HIVCARELO -AC-.....----A----------GG--------C-T---------TC-- 538
HIVCAR4017 ----.....----------G----------GA----------T--- 541
HIVCAR4039 ----.....-----T----------A------A----------C-A--G---C-T--- 517
HIVCAR4071 A---.....-----C----------A----------G-----G-----T--- 529
HIVCARMBA ----.....----A----------TC-- 517
CONSENSUS.F GGcA.....ATACAAAAcTGTTCTTTCAATaTGaCCAcaGAAGTA?GAgATAAGCAGCaGAAAGTACATg 503
HIVBRA7944 --A-.....--------T----------A----------T----------T 433
HIVBZ163A ----.....----------G------TG------.---------- 507
HIVBZ126A ----.....----------T----------.--A---------- 513
CONSENSUS.G AgAA.....ATGAaAAACTGCTCTTTCAATaTAACCACAGAA?TAAGAGATAAGag?AAGacAGAATACG 501
HIVVI525A ----.....----C----------G----------C----------CAG---G--------- 556
HIVLBV217 ----.....----------G----------T----A--------- 538
HIVCAR4067 -A--.....----------A----------A---------- 514
CONSENSUS.O tGAg??????aTGAaaaAgTGTga?TTTAATGTAACtACaGT?cTCAaAGACAAAaAGGAGaAAAAACAGG 478
HIVANT70 ---AAACCTT-----G--------G----------C--T--TA---------- 487
HIVMVP5180 ----.....----G---T---AGT----------C----C----------C--------- 508
HIVVAU A---.....G-----C-------C----------G----------C---------- 517
CONSENSUS.CPZ ??A?.....?T??AA?A?TGT???TTTAAT??GA??ACAG?ATT?A?AGATAAGAA??AA?A??T??A?? 247
SIVCPZGAB CG-A.....A-GA--A-C---TCA------GT--CA----A---A-G---------GA--C-GG-CT-TT 514
CONSENSUS.U agaa.....ATaAaAAA?TGCTCtTtCAa?ataaCCACAGAAcTaA?AGATAaGA?GaaGacAGtatAtg 472
HIVZAM184 ----.....--------C-------A--GG-CT----------A---------C-CT--G---C---T 490
HIVCAR4081 ----.....--------T----------T----------A---G--------A--------C---C- 517
HIVK124A --G-.....--G-----C----------T----------G---G-----G--A----CA--------- 514
HIVZ3 TACC.....--C-C---T-----C-----GG--C----------G-A---------C-G---------C--A 496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HIVU455 ----------A----------C.....----AA-C-GAT... 555
HIVZ321 ----G----------A------C----GGGGGA..... 546
HIVRW020 ----------AG----------GAAAAG..... 518
HIVUG031 ----------C----.....---GAA-G-..... 545
HIVD687 -------.----------G--..... 214
HIVNI ----------.....---GAA-A-..... 549
HIVRW009 ----------G------A----------AGC.....----GT-A-..... 551
HIVUG275A ----------G----------C----.....---GGC-GCAAC... 555
HIVUG273A ----------A----------A.....----GT-G-GAG... 582
HIVVI191A ----------GGAATT.....---GGA-C-AGTAAT 558
HIVDJ264A ----------.....---GAA-G-AGC... 546
HIVDJ263A ----------.....---GAA-G-AGCAAT 564
HIVDJ258A ----------G-GAAAGT.....--C-AT-G-CAA... 564
HIVCARGAN ----------A----------AG--GAGAAT.....---GGT-C-AGA... 576
HIVCARSAS ----------A-------A----C-C-------AAAATTAATGATGCTAGTGGT----TT-G-GAGAAC 552
HIVCAR4054 -G-----C----------AGTAATAGT.....----TT-G-AAT... 549
HIVCAR286A -G-----C----------C--CA---AATGATGAT.....----GT-CAGAT... 609
HIVCAR4023 -------C----------A------C-------AATAATAAT.....----AT-CA..... 597
HIVCAR423A -G-----C----------A------C-------AATAAT.....----AT-CAAATGAG 600
HIVKENYA ----------C-------GAAAAT.....----GC-G-AACAAT 561
CONSENSUS.B CactttTttaTAaacttgATgTagtaccAatAgat????????????.....???????????????? 539
HIVJRCSF -T----------G----------AATAAG..... 552
HIVJRFL -T----------AAT..... 549
HIVALA1 -G------C----------AAT..... 552
HIVBRVA ----------A----------AATGATAAAACT..... 561
HIVJH3 ----------A----------A--.....AATAGTACCAAGGAT 579
HIVBAL1 ----------A---C----------..... 564
HIVYU2 ----------C----------..... 549
HIVMN -----C----------A-----T--------..... 570
HIVHXB2R --T----------A--A----------..... 555
HIVLAI --T----------A--A----------..... 570
HIVNL43 --T-C----------A----------..... 555
HIVMFA --T-C----------A--AG----------..... 555
HIVCAM1 ----------AAGGCT..... 564
HIVNY5CG ----------G-------A----------AAGGAT..... 546
HIVADA ----------G----------AATGAT..... 549
HIVJFL ----------AAGGAT..... 552
HIVSIMI84 ----------A-G--------GGATGAT..... 555
HIVD31 ---AC----------AATGAC..... 561
HIVSF162 ----------AATGAT..... 555
HIVBCSG3C ----C----------AATGATAAG..... 567
HIVOYI ----------T----------AAGAAT..... 576
HIVSF33 --TA----------GATGAT.....AATACT..... 564
HIVCDC4 --T-G----------A----------GATAATAAA.....AATACTACC..... 591
HIVSF2 --------CG---C----------.....AATGCTAGTACTACT 564
HIVSF2B13 --------CG---C----------.....AATGCTAGTACTACT 561
HIVHAN ----------AC----------AAT.....AATAAGACTAGTAAT 558
HIVRF ----------G----------GAAGGGT.....AATATTAGCCCTAAG 576
HIVWMJ2 ----------A-GGGTGAT.....AAT..... 549
HIVTB132 ----C----------A----------A--AATGAT..... 519
HIVBR020 -T--C--C-----T----------A-----G-..... 551
HIVTH014 ----------AAT..... 533
HIVTH026 ----------TC----------..... 530
HIVUS711 ----------GC---A-----A---------G-..... 545
HIVUS712 ----------A---A--------..... 563
HIVUS715 ----------A..... 563
HIVUS716 -------G----------A----------C..... 539
HIVHA593 ---AG----------A----------G..... 611
HIVHA594 ----------G--G----------..... 545
HIVHA596 ----------G--G----------..... 545
HIVHA599 ---------C----------T----------..... 542
HIVHA651 ----------GG----------C-G..... 539
HIVRJS ----------..... 558
HIVGUN -----C--A---G-------A----------..... 461
HIVSC ----------C----------..... 564
HIVBR014 ----------G-C----------..... 566
HIVBR021 --------A---G----------..... 567
HIVACH9 -----C----------A----------.....AATAGTACT..... 429
HIVACP1 --------G---G----------C----..... 411
HIVJM --------A---C----------G-----AATAGTAAT.....AACAAT..... 495
HIVWM --AC----------A----------.....AATGATAAAGAT... 465
HIVMA208 --AC----------A----------G-.....AATGATAGTACTAGT 600
HIVP896 --------A---G----------AAATACT..... 564
HIVBWB11A ----G----------G--------GGTAGT..... 177

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CONSENSUS.C  CACttTTtTATAgacttGATaTAGTAccacTtaat????????????.....???aataa?a?t??????  523
HIVMA959     ----------A----------.....G-G--GGA-.....  551
HIVMA960     ----------.....G-G--TGAGAAT...  530
HIVD757      ----------A-------G----------G--GGT.....---G-T.....  217
HIVD747      ----------A-------G----------.....----CT-C-GAT...  352
HIVD760      ----------G--.....-----T-A-.....  378
HIVNOF       ----------A--C----G----------.....---G-G-GG.....  188
HIVZAM20A    ----------GG----------GATGAGAATAGT.....--C--G-C-AATGCC  588
HIVD1044     ----------A----------G--.....---G-G-G-AAG...  187
HIVD1024     ----------G--AG--.....-G---C.....  534
HIVD744      ---N----------G--.....G---GG-A-GAGAGA  213
HIVD766      ----C-------CC----------T-------.....--G--G-ACTCT...  189
HIVD808      ----------T-----.....--G--G.....  234
HIVD868      ----------G--.....-----G-AGAAG...  222
HIVBR025     ----------G.....---G-G-G-AGT...  459
HIVSM145A    ----------GAGGGTGAA.....--C--CTC-AGGAAG  573
HIVZAM18A    ----------A----------GAGAAT.....AAC--CTCT-G-GAG...  552
HIVDJ259A    -------C----------GAG.....-----T-G-GAA...  543
HIVDJ373A    ----------A----------GGG.....---GGG-A-GAGGAA  561
HIVSE364A    ----------G-GGGAGTAAA.....--C-GTTCC.....  558
HIVUG268A    ----------A-------G-----T-----G-AGGGAATAGT.....--C-CT.....  585

CONSENSUS.D  CActtTTTTATAaaCTtGATgTaGTaCaaATagat?at????????????????aata?tagt??????  528
HIVJY1       ----------G----------C-------G--GATAATAGT.....GCT----CC---AATACC  594
HIVNDK       ----------A----G-C------CA--AAT.....----GG-CC.....  543
HIVMAL       --AC---------C-------C----------G--AGTGAT.....  576
HIVELI       ----------G-------A------C------C.....---GA----AGTACC  561
HIVZ2Z6      ----------G-------A------CC-----CA--GAT.....----G--CC.....  561
HIVUG024     ----------G--GA--G--.....----A--C-.....  567
HIVUG021     ----------G--------G--------GA--G--GAT.....----G--C-.....  536
HIVUG038     --A---------GG--------G--------GACA.....----A----AATGAT  564
HIVUG046     ----------G--------G---.....G---A----ACT...  570
HIVUG266A    ----------G----C-------G--.....AAT----G--C-.....  558
HIVUG269A    ----------GA--A--AGTGAGAGT.....ATT--C-CC--C.....  587
HIVUG274A    ----------G----------G--.....AAT----G--C-.....  573
HIVSE365A    ----------G-------T------C-----GCA--AGTAATAAG.....----GC-CC.....  582
HIVCAR4020   ----C----------A---A------C------GG--GAGGATAATATTAAAGGT----C----GATAAT  648

CONSENSUS.E  CActtTTTTATaagctTGAT?TAGTAccAaTtga?g??????????????...???AAtagTAGtgag???  530
HIVTH966     ----------C------A------A-ATAAA.....----------...  572
HIVTH975     ----------C------A---G--A-GG.....----C-------...  557
HIVTH022     ----------G-------A------A---GC-TAATGAA.....----------...  572
HIVTN243     ----------A------A-----GA-ATAAG.....----------...  591
HIVTH006     ----------A------A-G--.....----------...  560
HIVTH011     ----C----------A----------GA-AT.....AAT--CG-----AGTGAG  503
HIVCARELO    ----------T----------T-GCAATATTGATGGC.....----A-------...  600
HIVCAR4017   ----------AC----A-----T-------T.....--C------AGTGAT  591
HIVCAR4039   ---C----------A----C----------AA-G-AA.....---------AGTGAG  570
HIVCAR4071   ----C-------G-TC----C----------GAGAAATAGTGGGGAA...AAT---G-----AGT...  594
HIVCARMBA    --A--------GTATC----C-----T----GA-T-CA.....----A---C.....  564

CONSENSUS.F  CACTtTTTtATAgACTTGATATAGTACCAATtAGcaat?g?ag?.....AATaaCAGT???gga  556
HIVBRA7944   ----------C--T.....---------...---  480
HIVBZ163A    ----G---.----------G-A--A.....---GG----GGA-AC  565
HIVBZ126A    ----------A----------A-C--T.....----------...A--  569

CONSENSUS.G  CgCTTTTCTATAgACTTGATGTaGTACCAATTaATgataAT?aa.....AATagTAGT.....  553
HIVVI525A    ----------A----------G--A-----AG-.....---GA----.....  609
HIVLBV217    -T----------G----------G----G--.....---------.....  591
HIVCAR4067   ----------GG--C-G.....---------.....  567

CONSENSUS.O  CTCTATTCTATGTatCAGATtTGattaAg?TtAAtGacaCAa???????a.....AATgaaACA??????  529
HIVANT70     ----------GG-AC-G-----G----GCAGCAC-.....---A-G---AACAGC  552
HIVMVP5180   ----------C---G----G--------T---ATGCAGT-.....----G----.....  567
HIVVAU       ----------GA--------G-----A----C-C----TCA.....---------.....  570

CONSENSUS.CPZ C??TATTTTAT???G??GAT?T??T?AA??????G???.....AA????.....  267
SIVCPZGAB    -AC---------GTG-AG---G-GG-A--CCTAGG-.....--TGAG.....  555

CONSENSUS.U  CaCTtTTtTATAaACTtGATgTAGTaC?AaTtaATgaaaat??????.....???AATAatacTag????  523
HIVZAM184    ----G----------A----G--CC-.....AGT----------TG...  543
HIVCAR4081   -G-----C----G---A----------C---------T---AAT.....-------A-.....  570
HIVK124A     ----------A------A---G---------CAGGAT.....----GC-G---CGGT  576
HIVZ3        ----------G--------G-C-C------TG-CA.....------T----TATA  552
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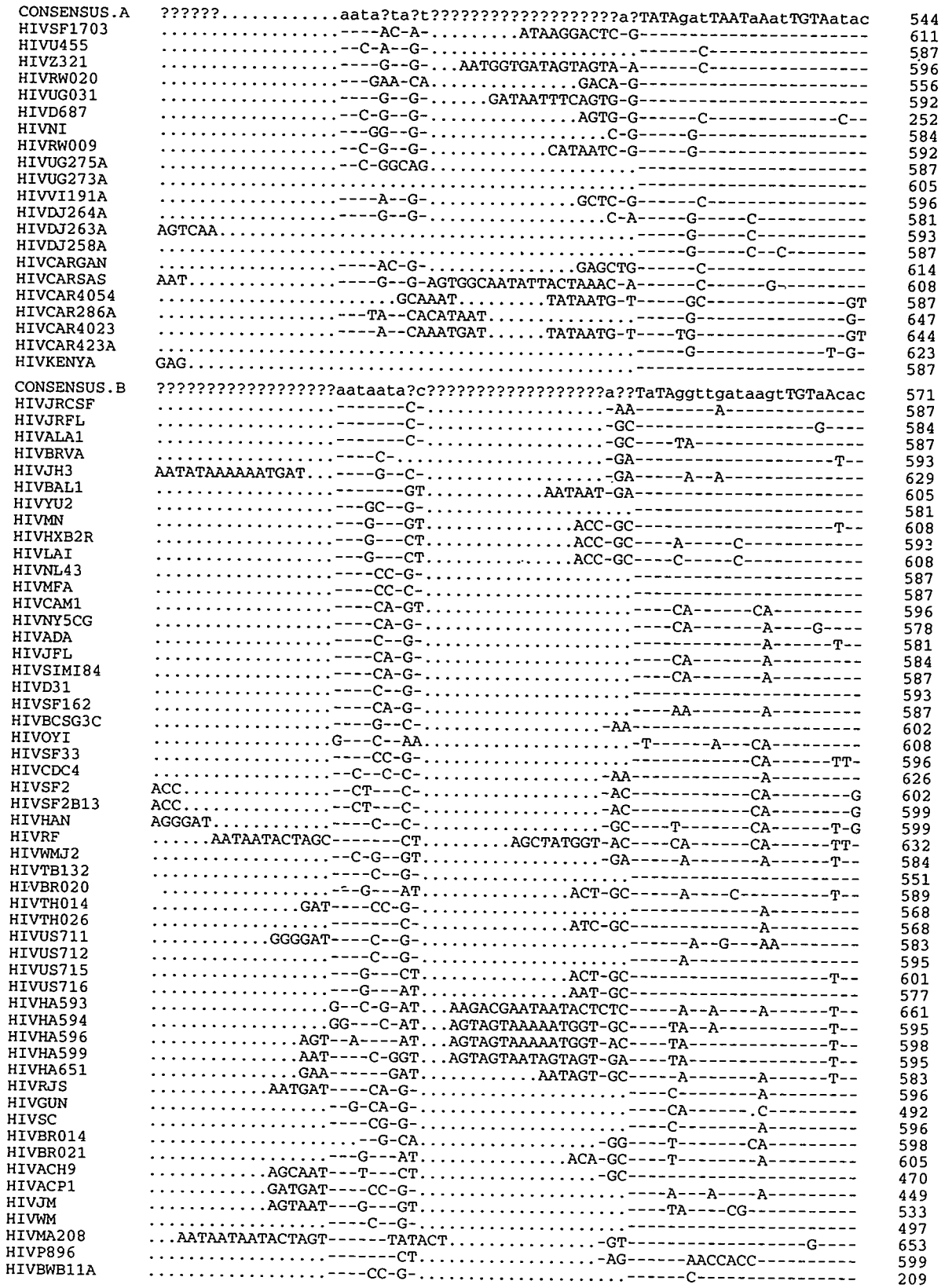
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HIVU455
HIVZ321
HIVRW020
HIVUG031
HIVD687
HIVNI
HIVRW009
HIVUG275A
HIVUG273A
HIVVI191A
HIVDJ264A
HIVDJ263A
HIVDJ258A
HIVCARGAN
HIVCARSAS
HIVCAR4054
HIVCAR286A
HIVCAR4023
HIVCAR423A
HIVKENYA
CONSENSUS.B
HIVJRCSF
HIVJRFL
HIVALA1
HIVBRVA
HIVJH3
HIVBAL1
HIVYU2
HIVMN
HIVHXB2R
HIVLAI
HIVNL43
HIVMFA
HIVCAM1
HIVNY5CG
HIVADA
HIVJFL
HIVSIMI84
HIVD31
HIVSF162
HIVBCSG3C
HIVOYI
HIVSF33
HIVCDC4
HIVSF2
HIVSF2B13
HIVHAN
HIVRF
HIVWMJ2
HIVTB132
HIVBR020
HIVTH014
HIVTH026
HIVUS711
HIVUS712
HIVUS715
HIVUS716
HIVHA593
HIVHA594
HIVHA596
HIVHA599
HIVHA651
HIVRJS
HIVGUN
HIVSC
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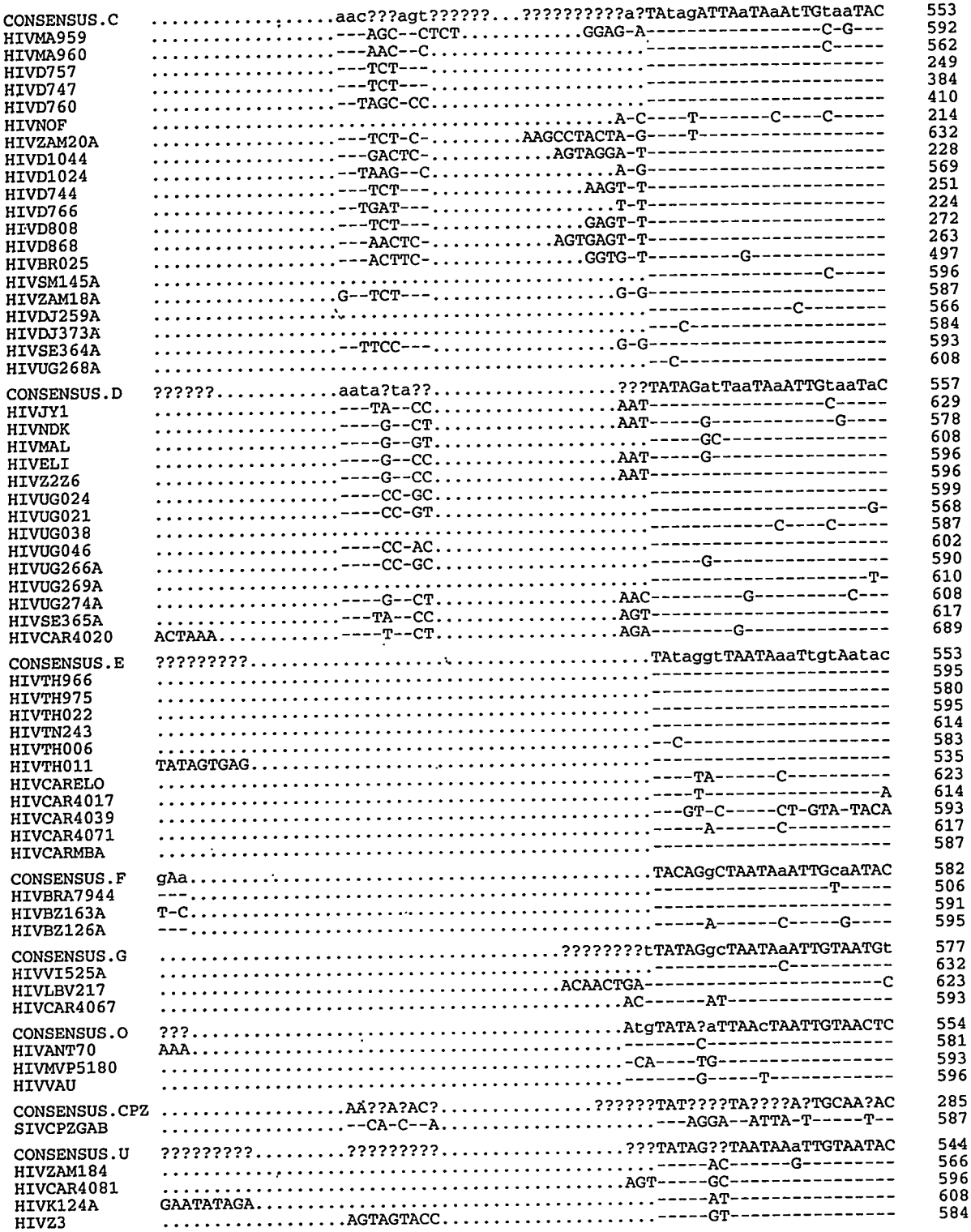
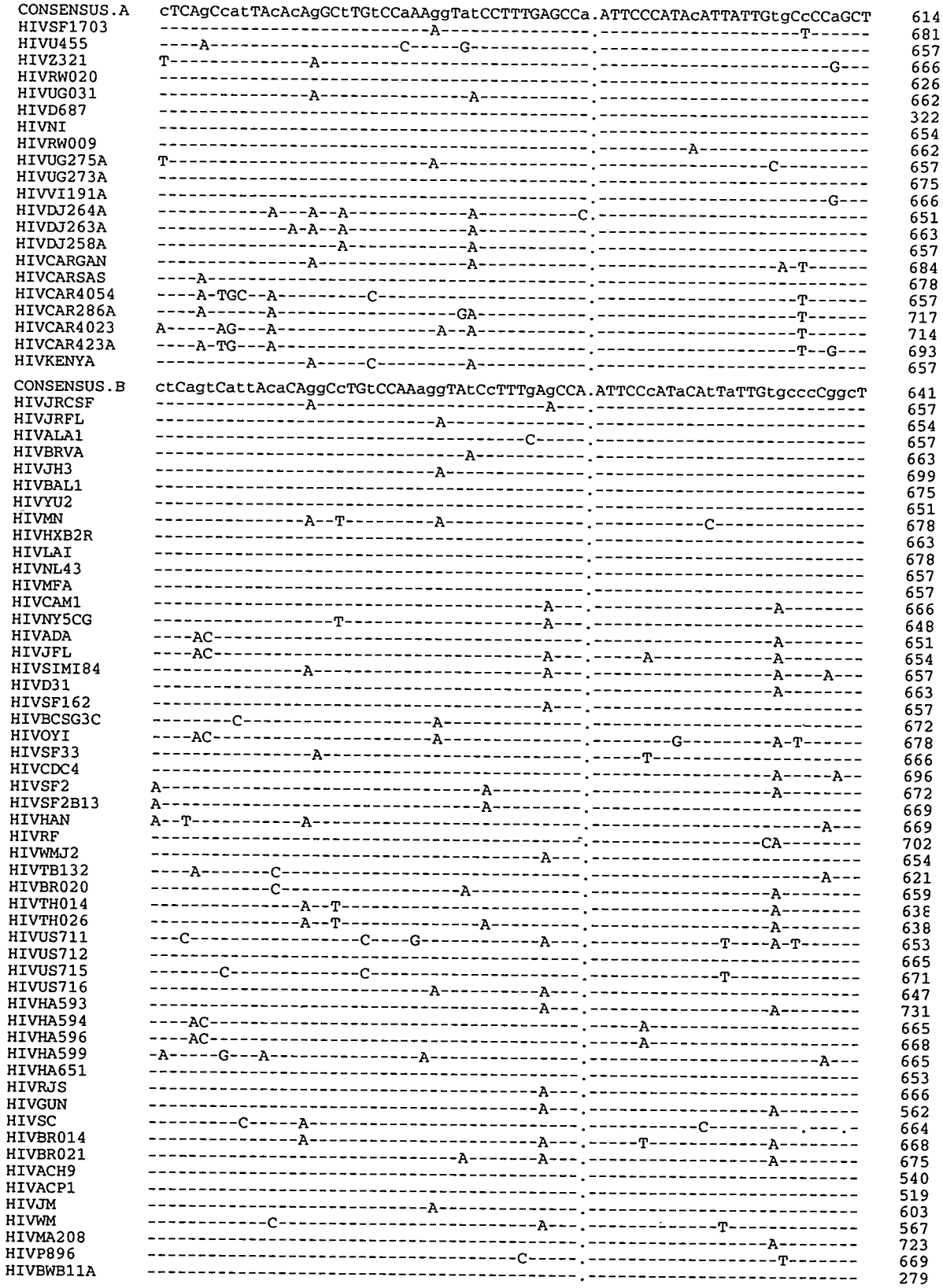
HIVBR021
HIVACH9
HIVACP1
HIVJM
HIVWM
HIVMA208
HIVP896
HIVBWB11A

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HIVU455 ----A----------C-----G----------.---------- 657
HIVZ321 T----------A----------.----------G--- 666
HIVRW020 ----------.---------- 626
HIVUG031 ----------A----------A----------.---------- 662
HIVD687 ----------.---------- 322
HIVNI ----------.---------- 654
HIVRW009 ----------.---------A---------- 662
HIVUG275A T----------A----------.----------C--------- 657
HIVUG273A ----------.---------- 675
HIVVI191A ----------.----------G--- 666
HIVDJ264A ----------A---A--A----------A---------C.---------- 651
HIVDJ263A ----------A-A--A----------A----------.---------- 663
HIVDJ258A ----------A----------A----------.---------- 657
HIVCARGAN ----------A----------A----------.----------A-T------ 684
HIVCARSAS ----A----------.---------- 678
HIVCAR4054 ----A-TGC--A---------C----------.----------T------ 657
HIVCAR286A ----A------A----------GA----------.----------T------ 717
HIVCAR4023 A-----AG---A----------A--A----------.----------T------ 714
HIVCAR423A ----A-TG---A----------.----------T--G--- 693
HIVKENYA ----------A-----C---------A----------.---------- 657
CONSENSUS.B ctCagtCattAcaCAggCcTGtCCAAaggTAtCcTTTgAgCCA.ATTCCcATaCAtTaTTGtgcccCggcT 641
HIVJRCSF ----------A----------A---.---------- 657
HIVJRFL ----------A----------.---------- 654
HIVALA1 ----------C-----.---------- 657
HIVBRVA ----------A----------.---------- 663
HIVJH3 ----------A----------.---------- 699
HIVBAL1 ----------.---------- 675
HIVYU2 ----------.---------- 651
HIVMN ----------A--T---------A----------.----------C---------- 678
HIVHXB2R ----------.---------- 663
HIVLAI ----------.---------- 678
HIVNL43 ----------.---------- 657
HIVMFA ----------.---------- 657
HIVCAM1 ----------A---.----------A--------- 666
HIVNY5CG ----------T----------A---.---------- 648
HIVADA ----AC----------.----------A--------- 651
HIVJFL ----AC----------A---.-----A----------A--------- 654
HIVSIMI84 ----------A----------A---.----------A----A--- 657
HIVD31 ----------.----------A--------- 663
HIVSF162 ----------A---.---------- 657
HIVBCSG3C --------C----------A----------.---------- 672
HIVOYI ----AC----------A----------.--------G---------A-T------ 678
HIVSF33 ----------A----------.-----T---------- 666
HIVCDC4 ----------.----------A-----A-- 696
HIVSF2 A----------A---------.----------A--------- 672
HIVSF2B13 A----------A---------.---------- 669
HIVHAN A--T----------A----------.----------A--- 669
HIVRF ----------.----------CA--------- 702
HIVWMJ2 ----------A---.---------- 654
HIVTB132 ----A-------C----------.----------A--- 621
HIVBR020 ----------C----------A----------.----------A--------- 659
HIVTH014 ----------A--T----------.----------A--------- 638
HIVTH026 ----------A--T----------A---------.----------A--------- 638
HIVUS711 ---C----------C----G----------A---.----------T----A-T------ 653
HIVUS712 ----------.---------- 665
HIVUS715 -------C----------C----------.----------T---------- 671
HIVUS716 ----------A---------A---.---------- 647
HIVHA593 ----------A---.----------A--------- 731
HIVHA594 ----AC----------.-----A---------- 665
HIVHA596 ----AC----------.-----A---------- 668
HIVHA599 -A-----G---A----------A----------.----------A--- 665
HIVHA651 ----------.---------- 653
HIVRJS ----------A---.---------- 666
HIVGUN ----------A---.----------A--------- 562
HIVSC ---------C-----A----------.----------C---------.---.- 664
HIVBR014 ----------A----------A---.-----T----------A--------- 668
HIVBR021 ----------A-------A---.----------A--------- 675
HIVACH9 ----------.---------- 540
HIVACP1 ----------.---------- 519
HIVJM ----------A----------.---------- 603
HIVWM ----------C----------A---.----------T---------- 567
HIVMA208 ----------.----------A--------- 723
HIVP896 ----------C-----.----------T-------- 669
HIVBWB11A ----------.---------- 279

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CONSENSUS.C  GTCAgCcaTAACaCAaGCCTGtCCAAAGGtCtctTTtGacCCa.ATtCCTATACAtTAtTGtgCtccaGCt  623
HIVMA959     ----A-TG-------------------------------------.------------------A--------  662
HIVMA960     ----A-------------------------AG----------.--------------------G------  632
HIVD757      ----------------------------------------.--C-----------------------  319
HIVD747      ------------------------------A---------.----------------------GG----  454
HIVD760      ----------------------------A-------T---.----------C---------------  480
HIVNOF       ----A----------------C-------------------.-------------------------  284
HIVZAM20A    ----A-------------------------AG---G-G----.-------------------------  702
HIVD1044     ----------------------------A----C------.----------C--C--CA--------  298
HIVD1024     ----------------------------A-------T---.----------C---------------  639
HIVD744      ----------------------------A-------T---.----------C------A--------  321
HIVD766      ----------------------------A-------T---.----------C------A----G---  294
HIVD808      ----------------------------A-------T---.----------C-----CA--------  342
HIVD868      --------------------------C-A-------T---.----------C---------------  333
HIVBR025     ----------------------------------------.-------------------------G  567
HIVSM145A    ----------------------------------------.-------------------------  666
HIVZAM18A    ----------------------------A----G--T---.-------------------------  657
HIVDJ259A    ------------------------------------G---.-------------------------  636
HIVDJ373A    ----T-------------------------------A---.-------------------------  654
HIVSE364A    ----------------------------------G-----C.-------------------------  663
HIVUG268A    ----------G-----------------A----G------.-------------------------  678

CONSENSUS.D  CTCAgccATTAcACAggctTGTCCaAAGgTaacCTTTGAgCCA.ATTCCCATaCATTaTTGTGCcCCAGCT  627
HIVJY1       ----------------------------------------.-------------------------  699
HIVNDK       ----A------------------------A--T-------A---.-------------T-------  648
HIVMAL       -----TA----------------------------------T---.-------------------------  678
HIVELI       ----------------------------T-----------.-------------------------  666
HIVZ2Z6      --------------------------GT-----------.-------------------------  666
HIVUG024     ----------------AG----------------------.-------------------------  669
HIVUG021     ----A-----------G---------A--T----------.-------------------------  638
HIVUG038     ----A-----------------------A----------.-------------------------  657
HIVUG046     -----T-----------G----------------------.-------------------T-------  672
HIVUG266A    ----------------A-G----------------------.--------T----------------  660
HIVUG269A    ----------------G-----T---A-------------.-------------------------  680
HIVUG274A    ----------A--G----------------------.-------------------------  678
HIVSE365A    -----T-----A--------------------A----------.-------------------------  687
HIVCAR4020   ----------------T----------A----------.-------------------------  759

CONSENSUS.E  TTCAGTCATTAAgCaGGCTTGTCcAAAggTatCCTTTGAtCCa?ATTCCtATACATTATTGtgCtCCaGCT  623
HIVTH966     ----------------------------A----------.----------------A--------  665
HIVTH975     ----------------------------A----------.----------------A--------  650
HIVTH022     ----------------------------A----------.----------------A--------  665
HIVTN243     ----------------------------A----------.----------------A--------  684
HIVTH006     ----------------------------A----------.-------------------------  653
HIVTH011     ----------G----------------------------.----------------A--------  605
HIVCARELO    ----------------------------G----------.A-----C--------------C--G---  693
HIVCAR4017   ----------------------------------------.-------------------------  684
HIVCAR4039   ----------A----------------A-------G---.-----C--------------C------  663
HIVCAR4071   ----------------------A---A----------.-----C----------C---------  687
HIVCARMBA    ----------------------------G----------.-----C--------------------  657

CONSENSUS.F  CTCAACCATTACACAGGCTTGTCCAAAgGTATCTTGGGaTCCA.ATTCCCATACATTAtTGTGCTCCAGCT  652
HIVBRA7944   ----------------------------------------.----------C-------------  576
HIVBZ163A    ----------------------------A----------G----.-------------------------  661
HIVBZ126A    ----------------------------n----------.-------------------------  665

CONSENSUS.G  CTCAACCATTAAACAgGCTTGTCCaAAGGTgaCTTTTGA?CCA.ATTCCCATACATTATTGtGCTCCAGCT  646
HIVVI525A    ----------------------C-----AT-------A---.-------------------------  702
HIVLBV217    ----------A----------------------C---.----------------C---------  693
HIVCAR4067   ----------------------------------G---.-------------------------  663

CONSENSUS.O  CACAAccATCA?GCAgGCCTGTCCaAAGGTAtcTTTTGAgCCc.ATTCCcATACACTATTGTGCTCCAgCa  623
HIVANT70     ----------C---A----------------------A--A.-----A----------------------  651
HIVMVP5180   -----TT----A----------G------AG----------.----------------------A--  663
HIVVAU       ----------G----------------------------.-------------------------G  666

CONSENSUS.CPZ ?ACA?C?AT?ACACAA?C?TGT??AAA??C??C?TTTGA?CC?.ATTCC?ATACA?TATTGTGC?CCAGCA  337
SIVCPZGAB    T---G-C--A------G-A---CC---AA-GT-C-----G--T.-----A-----C--------A------  657

CONSENSUS.U  CTCAgCCATtacACAgGCtTGtCCAAAGGTATCCTTTGAGCCA.ATTCC?ATACATTATTGTgC?CCaGCT  612
HIVZAM184    ---------CG----A----------------------.-----T----------A-C------  636
HIVCAR4081   ----------A----------------------------.-----C----------T------  666
HIVK124A     ----------------G--C-------------------.-----C----------T------  678
HIVZ3        ----A-------------------------------------.-----T----------C--T---  654
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CONSENSUS.A   GGtTTtGCgATtCTAAagTGTAa?GataaggagTTcaatGGAAcAGGGccatgcAagAATGTcAGcaCaGT   684
HIVSF1703     ----------------------T---GCA-----------------------------------------   752
HIVU455       ----------------------G---CCT------------A----------G---------------   728
HIVZ321       --A-------------------GG---G-------TG-A----A----------G---------------   737
HIVRW020      --C-------------------G----CA------------------------------------------   697
HIVUG031      ----------------GA-----T--GG-T--T---------------T---------------------   733
HIVD687       ----------------------G-GC---A-A---------------T-...--GC-----A--------   390
HIVNI         ----------------------G-----A-G-----------------------A--------------   725
HIVRW009      -----C----------------A-----AA------------------------------------------   733
HIVUG275A     ----------------------T---C--------------------AT---T--T--------------   728
HIVUG273A     -----------C-----A-----T-------------------------T----------------T----   746
HIVVI191A     ----------------A----GA-----------------------------G----------T----   737
HIVDJ264A     ----------------------T------A-----------------------------T--------   722
HIVDJ263A     --G-----A--------A-----T------A------------------T------------T--------   734
HIVDJ258A     ----------------------T------A-----------------------------T--------   728
HIVCARGAN     ----------------------T--G--AA----T-------------------G----------T----   755
HIVCARSAS     ----------------------G----C---------A----------------T--T-----   749
HIVCAR4054    ----------------------T----CAA-A-------------------------------------   728
HIVCAR286A    --.-------------------GG-------------------------------------.--------   786
HIVCAR4023    ----------------------T----C-A------G-------------------------------   785
HIVCAR423A    ----------------------GG---G--A----------------------T-----------C--   764
HIVKENYA      -----------C-----------A------A----------------------C---------------   728

CONSENSUS.B   GGtTtTGcgaTtcTAaAgTGTAatgataagaagTTcAatGGaacaGGaccaTGtAcaAAtGTcAGcACaGT   712
HIVJRCSF      ----------------------A------CA----------A-----A-----A---------------   728
HIVJRFL       ----------------------------C-----------A----------A---------------   725
HIVALA1       ----------------------A-----------------A----A------A---C-----------   728
HIVBRVA       ----------------------A-------------------------------------------   734
HIVJH3        ----------A-------------------------------------------------------   770
HIVBAL1       ----------------------A-----------------A-------------------------   746
HIVYU2        ----------------A-----------A-------------------------------------   722
HIVMN         ----------------A-----C-----A-------G-----A----T------A---------------   749
HIVHXB2R      ----------------A------A------C-------------------------------------   734
HIVLAI        ----------------A------A------C-------------------------------------   749
HIVNL43       ----------------A------A------C-------------------------------------   728
HIVMFA        ----------------A-----------C---------------------------------------   728
HIVCAM1       ---------------------------------------A-------------------------   737
HIVNY5CG      ----------------------C--------A-----------------------s---T--T-----   719
HIVADA        ----------------------A--C-------------------G-------A---------------   722
HIVJFL        ---------------------------------------A----------A---------------   725
HIVSIMI84     ---------------------------------------------------A---------------   728
HIVD31        ----------G----------A-------G----------A-----A-----A---C-----------   734
HIVSF162      ------------------------------------T-------------------------------   728
HIVBCSG3C     ----------------------A-----------------T------A---------------   743
HIVOYI        -------------------------------------------------------------------   749
HIVSF33       ----------------------A-----------G-----A---T-A-------------------   737
HIVCDC4       --------AC-------------C----------------G-------------------------   767
HIVSF2        ------------------------A----A-C----------A-------------------------   743
HIVSF2B13     ----------------------A----A-C----------A-------------------------   740
HIVHAN        ------------T----------------A-------------A----------A---------------   740
HIVRF         ---------------------------------------------------A---------------   773
HIVWMJ2       ----------------A-----------------------------------T---------------   725
HIVTB132      ----------------------GA------------G-----AC----------A---------------   692
HIVBR020      ----A--------------------G-----------------------C-------------------   730
HIVTH014      ---------------C-------CA----A-----------------------------------T-----   709
HIVTH026      ------------A----------C-----A-----------------------------------T-----   709
HIVUS711      ----------------------CA------C----------A-------------------------   724
HIVUS712      ----------------------C-----------------------------A---------------   736
HIVUS715      --------A-------------A-------------------------------------------   742
HIVUS716      ----------------------C---------------------T---------------------   718
HIVHA593      --------------------------G---T-------------------A---------------   802
HIVHA594      ----------A------------A------CA-----------------------------------   736
HIVHA596      ----------A------------A------C-----------------------------------   739
HIVHA599      --------A-----------------------------T-----------A---------------   736
HIVHA651      ----------------------GG---CCA--A-----G-------------------------------   724
HIVRJS        -------T---------------G--------T-----------------------------------   737
HIVGUN        ---------C-------------------------------------------A---------T-----   633
HIVSC         --.---------------T------A-------------------------------------------   734
HIVBR014      -------T----------------A------T-----------------------------------G--   739
HIVBR021      --G-----------------------T----C-----A----A------A---------------   746
HIVACH9       ----------------------A-------------------------A---------------   611
HIVACP1       ----------------------A-------------------------A------T---------   590
HIVJM         ----------------------GA---G--C-----------A----A-----------------   674
HIVWM         ----------------------CA------C-----G-----A-----------------------   638
HIVMA208      ---------C-------------C----C---------------------A---------------   794
HIVP896       --G--------G-----------CA------CA---------T----------C-----------   740
HIVBWB11A     ---------------------------------T-------------------G---------------   350
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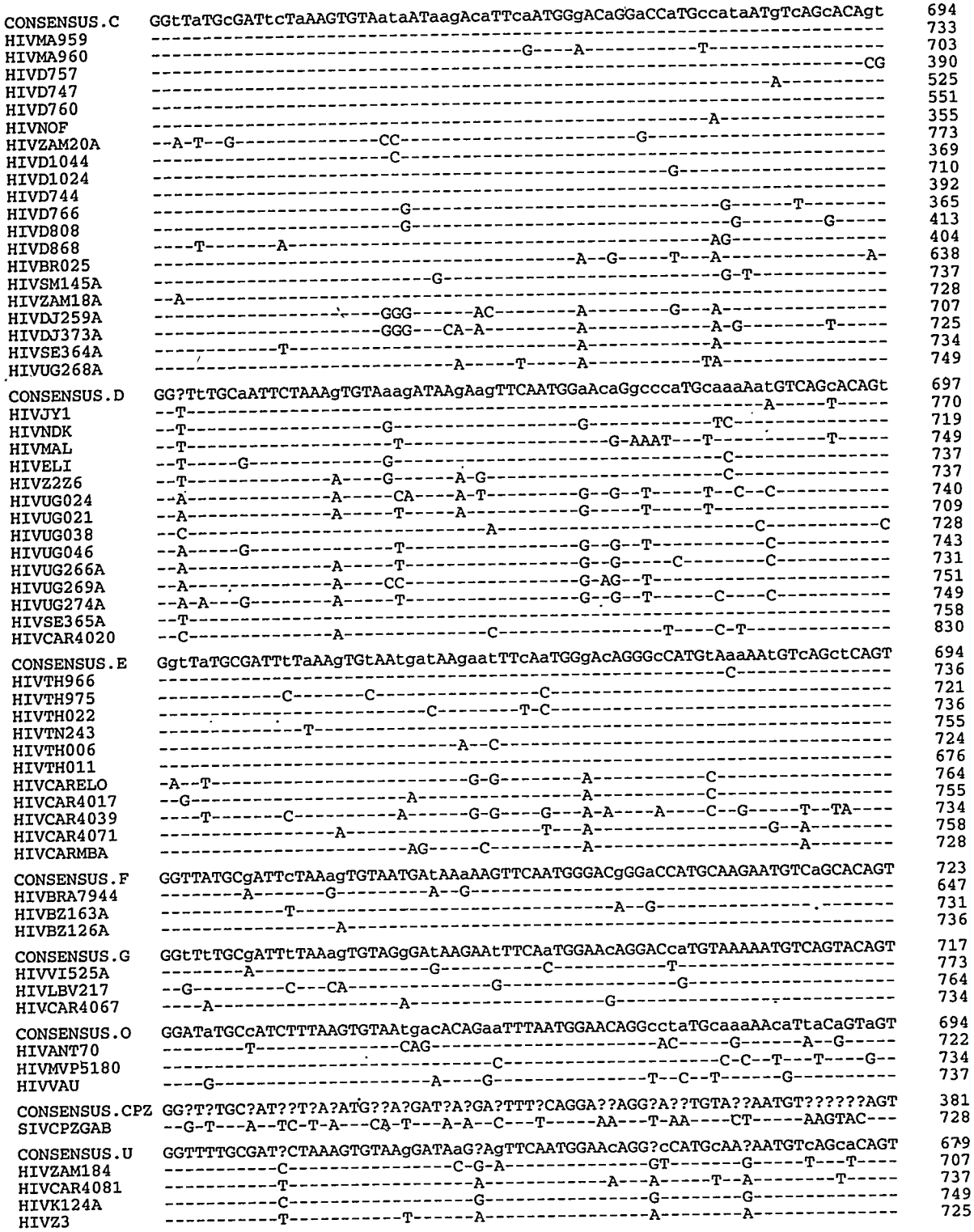

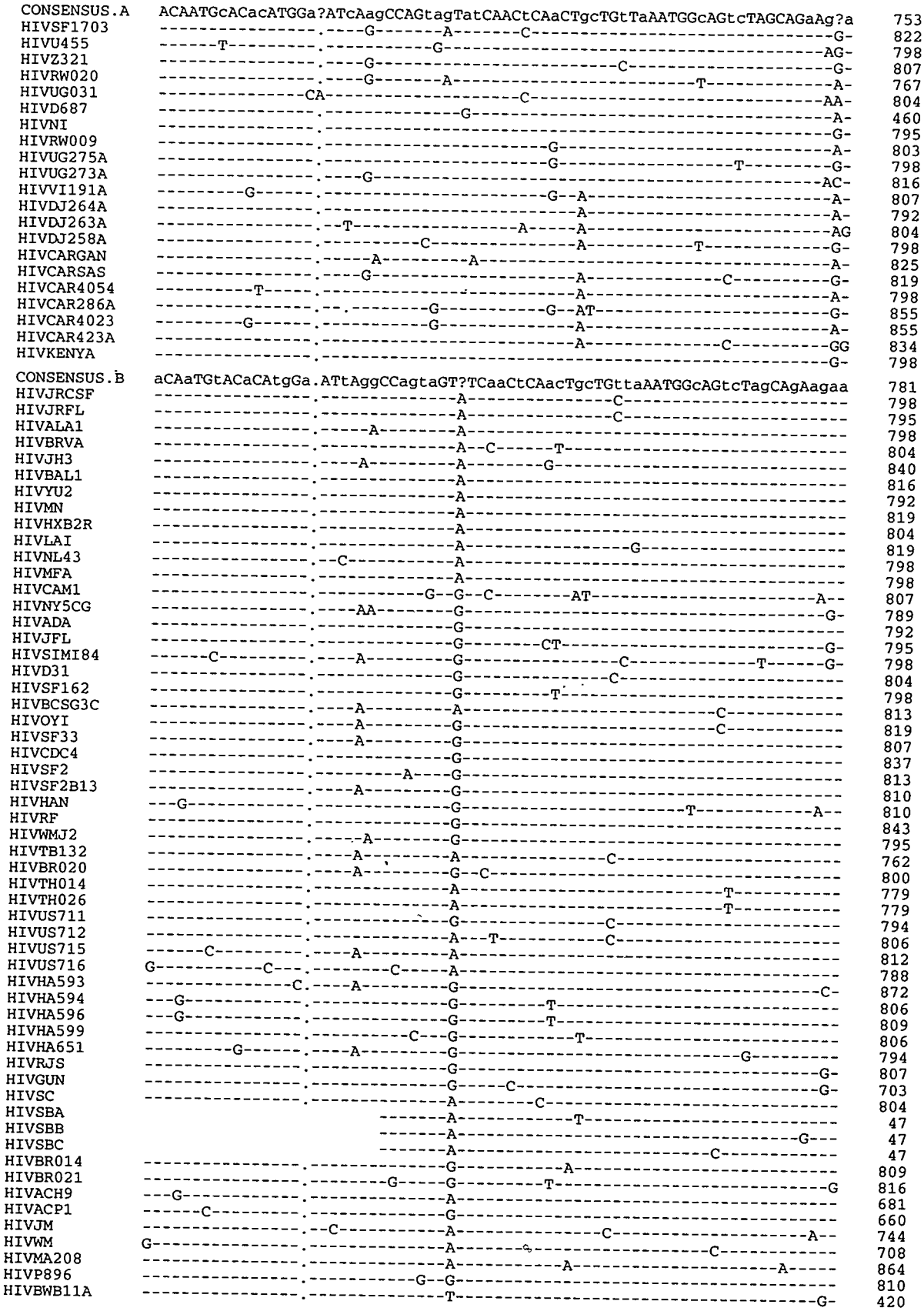
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HIVCARGAN 825
HIVCARSAS 819
HIVCAR4054 798
HIVCAR286A 855
HIVCAR4023 855
HIVCAR423A 834
HIVKENYA 798
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HIVJRCSF 798
HIVJRFL 795
HIVALA1 798
HIVBRVA 804
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HIVBR021 816
HIVACH9 681
HIVACP1 660
HIVJM 744
HIVWM 708
HIVMA208 864
HIVP896 810
HIVBWB11A 420

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CONSENSUS.C   acaaTgTACACAtGGa.ATtAagCCAGTggTaTCAaCtCAacTacTGTTAaATGGTAGcctagCAGAagga  764
HIVMA959      ---G----------.--------------------------------------------------------  803
HIVMA960      T-------------.--------------------------------------------------------  773
HIVD757       TAC-----------.----------A---------------------------------------------  460
HIVD747       ----------------.----------A---------------------------------------------  595
HIVD760       ----------------.----GC------------------------------------------------  621
HIVNOF        ----------------.----------------------T-----------------------------G  425
HIVZAM20A     ----------------.-----------------------------------------------T------A-  843
HIVD1044      ----------------.-------------------------GT---------------------------  439
HIVD1024      ----------------.--------------------------------------------------------  780
HIVD744       ----------------.--------------------G---------------------T-------G---  462
HIVD766       ----------------.-----------A----------------------------------------A--  435
HIVD808       ---G-T---------C.--------------------------------------------------A--  483
HIVD868       ----------------.-----------------------------------G------------------A-  474
HIVBR025      ---G----------.-----------AA-G--------C----------------T----------A-  708
HIVSM145A     ------------C--G.--------------------------------------------------------  807
HIVZAM18A     ------------C---.--C-----------------------------------------------------A-  798
HIVDJ259A     ----------------.-----A----------------------T-------------T----------AT  777
HIVDJ373A     ----------------.-----A----------------------T-------------TAC------G-AG  795
HIVSE364A     ----------------.-----------------------------------------T------------  804
HIVUG268A     ----------------.-----A------A-------------T-------------TA---------A-  819

CONSENSUS.D   aCAaTGtACACATGGa.ATtAggCCAGTaGTgTCAACtCAACTgctgttgAATGGCAGTcTAGCAGAAGAA  767
HIVJY1        ----------------.--C--------G-------------A--A-------------------------  840
HIVNDK        ----------------.-----A-----G--------------------------------------------  789
HIVMAL        ----------------.----A------G--------------------A-----------------------  819
HIVELI        ----------------.----------G--------------------------------------------  807
HIVZ2Z6       ----------------.----------G--------------------------------------------  807
HIVUG024      ---G--C--------G.-------------------------T-------------------------------  810
HIVUG021      ---G----------G.----A-----------------------T-------------------------------  779
HIVUG038      ----------------.-----------------------------------------T------------  798
HIVUG046      G--G----------G.-----C--------------C------T-------------------------------  813
HIVUG266A     G--G----------.-------------A------------T-------------------------------  801
HIVUG269A     ---G----------G.----A-----------------------T-------------------------------  821
HIVUG274A     ---G----------G.--C-------------------------T-------------------------------  819
HIVSE365A     ----------------C.----A------G--------------------A-----------------------  828
HIVCAR4020    ---G----------.----A------G-----------------C-----------------------------  900

CONSENSUS.E   ACAATGCACACATGGA.ATtAAGCCAGTgGTaTCAACTCAAtTGCTGTTAAATGGcAGTcTaGCAGAAgAA  764
HIVTH966      ----------------.--------------------------------------------------------  806
HIVTH975      ----------------.--------------------------------------------------------  791
HIVTH022      ----------------.--------------------------------------------------------  806
HIVTN243      ----------------.--------------------------------------------------------  825
HIVTH006      ----------------.--------------------------------------------------------  794
HIVTH011      ----------------.--------------------------------------------------------  746
HIVCARELO     ----------------.-----------------------------------------T------------  834
HIVCAR4017    ----------------.-------------------------C------------------------------  825
HIVCAR4039    ----------------.--C--------A--G---------C-------------------G------A--  804
HIVCAR4071    ----------------.-----------------------------------------T--------------  828
HIVCARMBA     ----------------.--------------------------------------------------------  798

CONSENSUS.F   ACAaTGTACACATGGA.ATTAAACCAGTgGTATCAACTCAATTGTTGTTAAATGGCAGCCTAGCAGAAGaA  793
HIVBRA7944    ----------------.----------A---------------------------------------------  717
HIVBZ163A     ---G------------.--------------------------------------------------------  801
HIVBZ126A     ----------------.--------------------------------------------------------  806

CONSENSUS.G   aCAATGTACACATGGA.ATTAAgCCAGTGGTATCAACTCAAcTACTgCTgAATGGcAGTtTAGCAGAAgaA  787
HIVVI525A     ----------------.-----------------------------------------------------A--  843
HIVLBV217     G---------------.-----------------------T--------------------------------  834
HIVCAR4067    ----------------.-----------------------T-------------------------------G-  804

CONSENSUS.H                                                                    ?A?    1
HIVCA13                                                                        G-A    3
HIVVI557                                                                       A-C    3

CONSENSUS.O   TACTTGTACACATGGC.ATcAagCCAACAGTAAGTACtCAaCTAATAcTaAATGGGACACTCTCTAaAGgA  764
HIVANT70      ----------------.--T-G----------------G------T---------------------------  792
HIVMVP5180    ----------------.-------------------------------G----------------G--A-  804
HIVVAU        ----------------.-----A-------------C-------------------------------------  807

CONSENSUS.CPZ ?CATTG?AC?CATGGA.AT?A??CCA?TGGT??C?AC???GTTACT??T?AATGGAA?TT???????A???  424
SIVCPZGAB     G-----T--A------.--T-AA---G----TA-C--TCA------TA-T-------G--TAGCTGA-GGA  798

CONSENSUS.U   aCAATGcACACATGGA.AT?A?GCCAGTaGTaTCAACTCAAcTgCTgTT?AATGGCAGtcTagCAGAAG?A  745
HIVZAM184     ------T---------.--T-G-------------------------G-------------------G-  777
HIVCAR4081    G---------------.--C-A-----------------------G---------C--G-------A-  807
HIVK124A      C---------------.--C-A-------------------------A-------------------G-  819
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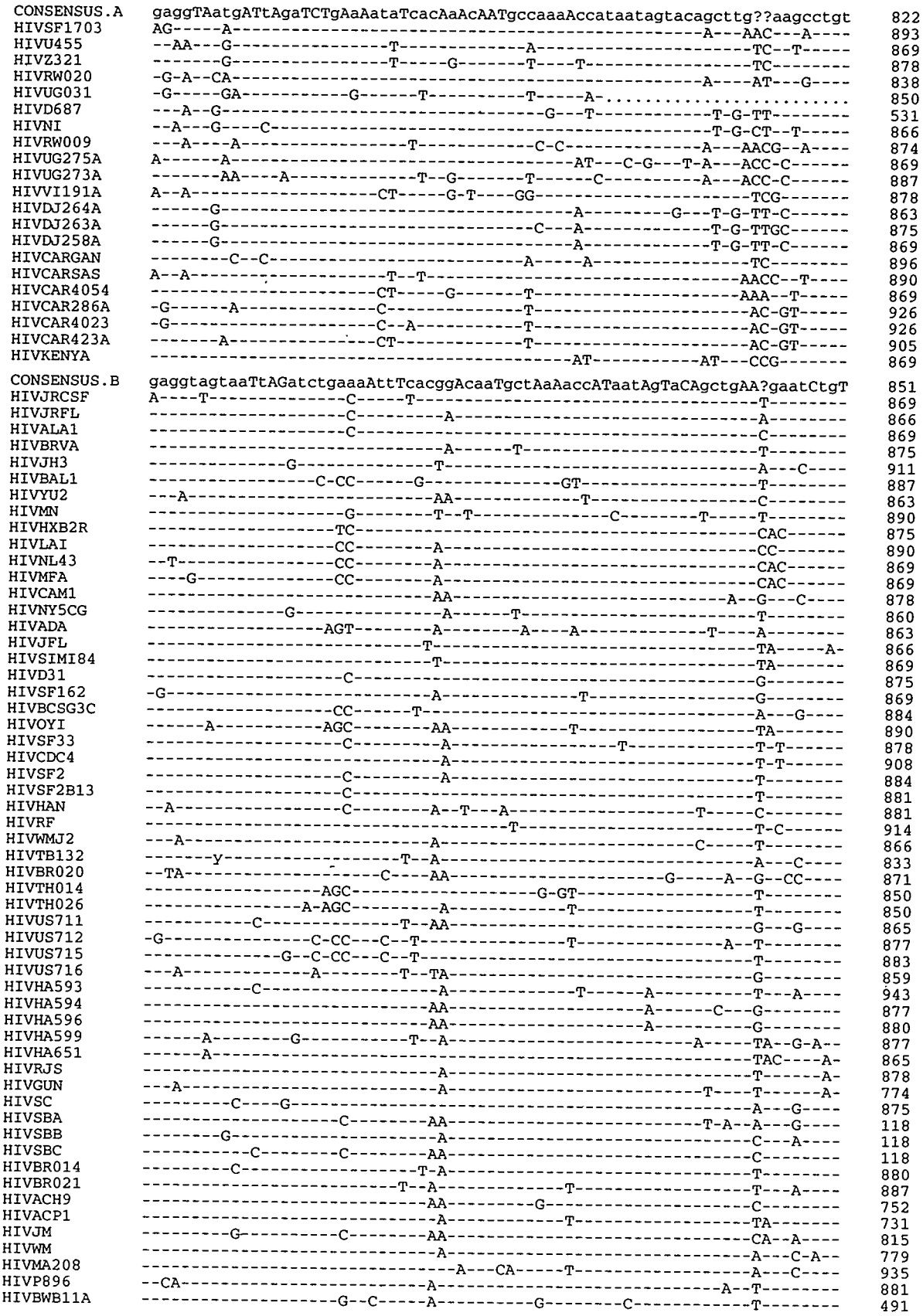
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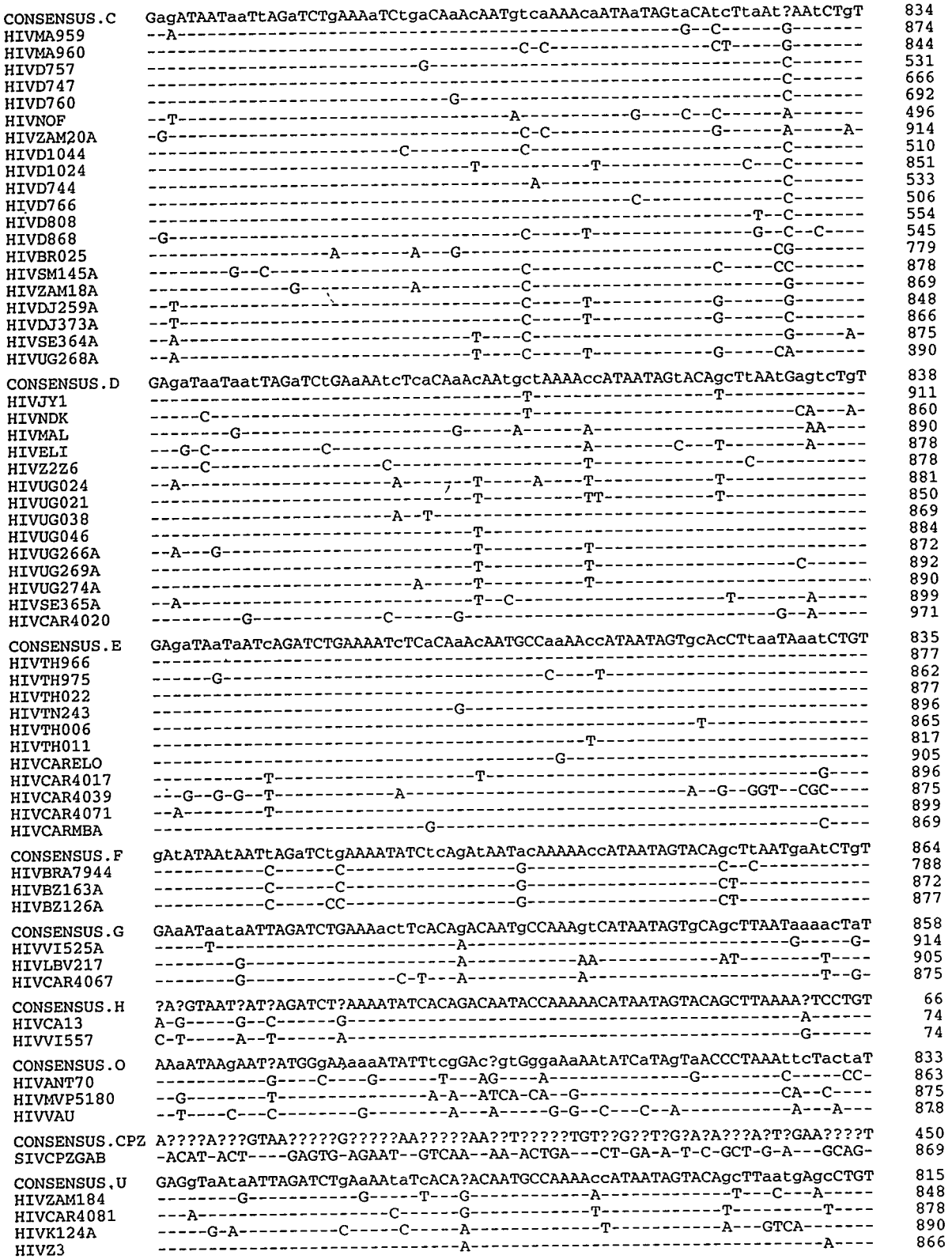
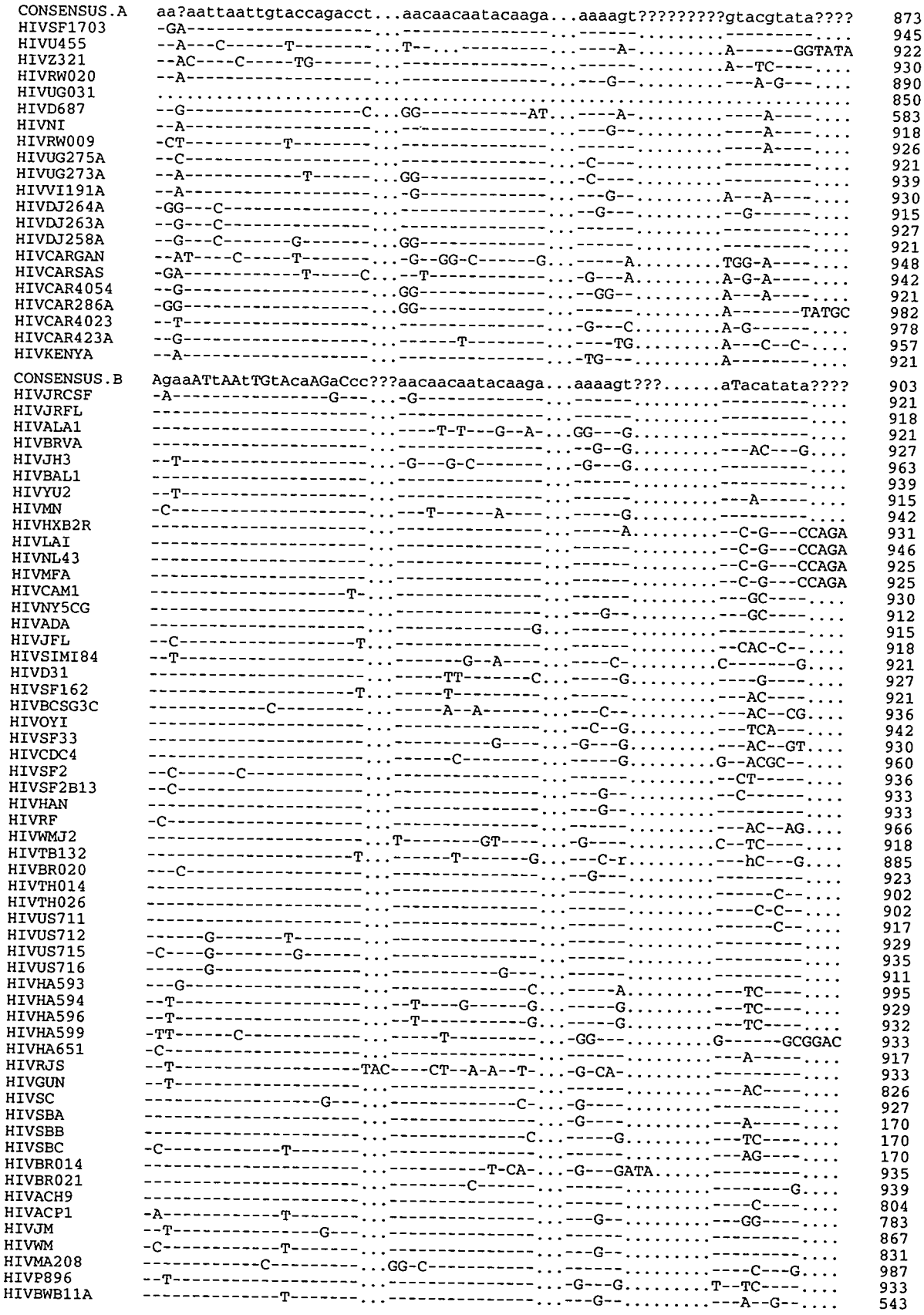
HIVU455 --AA---G---------- T---------- A---------- TC--T----- 869
HIVZ321 -------G---------- T-----G------- T----T---------- TC-------- 878
HIVRW020 -G-A--CA---------- A----AT---G---- 838
HIVUG031 -G-----GA---------- G------T---------- T-----A-..... 850
HIVD687 ---A--G---------- G---T---------- T-G-TT-------- 531
HIVNI --A---G----C---------- T-G-CT--T----- 866
HIVRW009 ---A----A---------- T---------- C-C---------- A---AACG--A---- 874
HIVUG275A A------A---------- AT---C-G---T-A---ACC-C------ 869
HIVUG273A -------AA----A---------- T--G------- T------C---------- A---ACC-C------ 887
HIVVI191A A--A---------- CT-----G-T----GG---------- TCG------- 878
HIVDJ264A ------G---------- A--------- G---T-G-TT-C------ 863
HIVDJ263A ------G---------- C---A---------- T-G-TTGC------ 875
HIVDJ258A ------G---------- A---------- T-G-TT-C------ 869
HIVCARGAN --------C--C---------- A-----A---------- TC-------- 896
HIVCARSAS A--A-------.---------- T--T---------- AACC--T---- 890
HIVCAR4054 ---------- CT-----G------- T---------- AAA--T----- 869
HIVCAR286A -G------A---------- C---------- T---------- AC-GT----- 926
HIVCAR4023 -G---------- C--A---------- T---------- AC-GT----- 926
HIVCAR423A -------A---------- CT---------- T---------- AC-GT----- 905
HIVKENYA ---------- AT---------- AT---CCG------- 869
CONSENSUS.B gaggtagtaaTtAGatctgaaaAttTcacggAcaaTgctAaAaccATaatAgTaCAgctgAA?gaatCtgT 851
HIVJRCSF A----T---------- C-----T---------- T-------- 869
HIVJRFL ---------- C--------- A---------- A-------- 866
HIVALA1 ---------- C---------- C-------- 869
HIVBRVA ---------- A------T---------- T-------- 875
HIVJH3 ---------- G---------- T---------- A---C---- 911
HIVBAL1 ---------- C-CC------G---------- GT---------- T-------- 887
HIVYU2 ---A---------- AA---------- T---------- C-------- 863
HIVMN ---------- G--------T--T---------- C--------T-----T-------- 890
HIVHXB2R ---------- TC---------- CAC------ 875
HIVLAI ---------- CC--------A---------- CC------- 890
HIVNL43 --T---------- CC--------A---------- CAC------ 869
HIVMFA ----G---------- CC--------A---------- CAC------ 869
HIVCAM1 ---------- AA---------- A--G---C---- 878
HIVNY5CG ---------- G---------- A------T---------- T-------- 860
HIVADA ---------- AGT--------A--------A----A---------- T----A-------- 863
HIVJFL ---------- T---------- TA-----A- 866
HIVSIMI84 ---------- T---------- TA------- 869
HIVD31 ---------- C---------- G-------- 875
HIVSF162 -G---------- A---------- T---------- G-------- 869
HIVBCSG3C ---------- CC------T---------- A---G---- 884
HIVOYI ------A---------- AGC--------AA---------- T---------- TA------- 890
HIVSF33 ---------- C---------A---------- T---------- T-T------ 878
HIVCDC4 ---------- A---------- T-T------ 908
HIVSF2 ---------- C---------A---------- T-------- 884
HIVSF2B13 ---------- C---------- T-------- 881
HIVHAN --A---------- C--------A--T---A---------- T-----C-------- 881
HIVRF ---------- T---------- T-C------ 914
HIVWMJ2 ---A---------- A---------- C-----T-------- 866
HIVTB132 -------y---------- T--A---------- A---C---- 833
HIVBR020 --TA---------- C----AA---------- G-----A--G--CC---- 871
HIVTH014 ---------- AGC---------- G-GT---------- T-------- 850
HIVTH026 ---------- A-AGC---------A---------- T---------- T-------- 850
HIVUS711 ----------C---------- T--AA---------- G---G---- 865
HIVUS712 -G---------- C-CC---C--T---------- T---------- A--T-------- 877
HIVUS715 ---------- G--C-CC---C--T---------- T-------- 883
HIVUS716 ---A---------- A--------T--TA---------- G-------- 859
HIVHA593 ----------C---------- A---------- T------A---------- T---A---- 943
HIVHA594 ---------- AA---------- A------C---G-------- 877
HIVHA596 ---------- AA---------- A----------G-------- 880
HIVHA599 ------A--------G---------- T--A---------- A-----TA--G-A-- 877
HIVHA651 ------A---------- TAC----A- 865
HIVRJS ---------- A---------- T------A- 878
HIVGUN ---A---------- A---------- T----T------A- 774
HIVSC ---------C----G---------- A---G---- 875
HIVSBA ---------- C---------AA---------- T-A--A---G---- 118
HIVSBB --------G---------- A---------- C---A---- 118
HIVSBC ----------C---------C---------AA---------- C-------- 118
HIVBR014 ---------C---------- T-A---------- T-------- 880
HIVBR021 ---------- T--A---------- T---------- T---A---- 887
HIVACH9 ---------- AA---------G---------- C-------- 752
HIVACP1 ---------- A---------- T---------- TA-------- 731
HIVJM ---------G---------- C---------AA---------- CA--A---- 815
HIVWM ---------- A---------- A---C-A-- 779
HIVMA208 ---------- A---CA-----T---------- A---C---- 935
HIVP896 --CA---------- A---------- A--T-------- 881
HIVBWB11A ---------- G--C-----A----------G---------C---------- T-------- 491

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HIVSF1703 -GA...AT...A...A...GGTATA 945
HIVU455 --A---C------T--------...T--...---------...----A-.....A------GGTATA 922
HIVZ321 --AC----C-----TG------...---------...------.....A--TC----.... 930
HIVRW020 --A---------...---------...---G--.....---A-G---.... 890
HIVUG031 850
HIVD687 --G---------C...GG----------AT...----A-.....----A----.... 583
HIVNI --A---------...---------...---G--.....----A----.... 918
HIVRW009 -CT----------T--------...---------...------.....----A----.... 926
HIVUG275A --C---------...---------...-C----.....---------.... 921
HIVUG273A --A----------T-------...GG---------...-C----.....---------.... 939
HIVVI191A --A---------...-G---------...---G--.....A---A----.... 930
HIVDJ264A -GG---C---------...---------...--G---.....--G------.... 915
HIVDJ263A --G---C---------...---------...------.....---------.... 927
HIVDJ258A --G---C-------G--------...GG---------...------.....---------.... 921
HIVCARGAN --AT----C-----T--------...-G--GG-C------G...------A.....TGG-A----.... 948
HIVCARSAS -GA----------T-----C...--T---------...-G---A.....A-G-A----.... 942
HIVCAR4054 --G---------...GG---------...--GG--.....A---A----.... 921
HIVCAR286A -GG---------...GG---------...------.....A-------TATGC 982
HIVCAR4023 --T---------...---------...-G---C.....A-G------.... 978
HIVCAR423A --G---------...------T--------...----TG.....A---C--C-.... 957
HIVKENYA --A---------...---------...-TG---.....A--------.... 921
CONSENSUS.B AgaaATtAAtTGtAcaAGaCcc???aacaacaatacaaga...aaaagt???.....aTacatata???? 903
HIVJRCSF -A----------G---...-G---------...------.....---------.... 921
HIVJRFL ---------...---------...------.....---------.... 918
HIVALA1 ---------...----T-T---G--A-...GG---G.....---------.... 921
HIVBRVA ---------...---------...--G--G.....---AC---G.... 927
HIVJH3 --T---------...-G---G-C--------...-G---G.....---------.... 963
HIVBAL1 ---------...---------...------.....---------.... 939
HIVYU2 --T---------...---------...------.....---A------.... 915
HIVMN -C---------...---T------A----...-----G.....---------.... 942
HIVHXB2R ---------...---------...------A.....--C-G---CCAGA 931
HIVLAI ---------...---------...------.....--C-G---CCAGA 946
HIVNL43 ---------...---------...------.....--C-G---CCAGA 925
HIVMFA ---------...---------...------.....--C-G---CCAGA 925
HIVCAM1 ----------T-...---------...------.....---GC----.... 930
HIVNY5CG ---------...---------...---G--.....---GC----.... 912
HIVADA ---------...----------G...------.....---------.... 915
HIVJFL --C---------T...---------...------.....--CAC-C--.... 918
HIVSIMI84 --T---------...-------G--A----...-----C-.....C-------G.... 921
HIVD31 ---------...-----TT-------C...-----G.....----G----.... 927
HIVSF162 ----------T...-----T---------...------.....---AC----.... 921
HIVBCSG3C ----------C---------...-----A--A------...---C--.....---AC--CG.... 936
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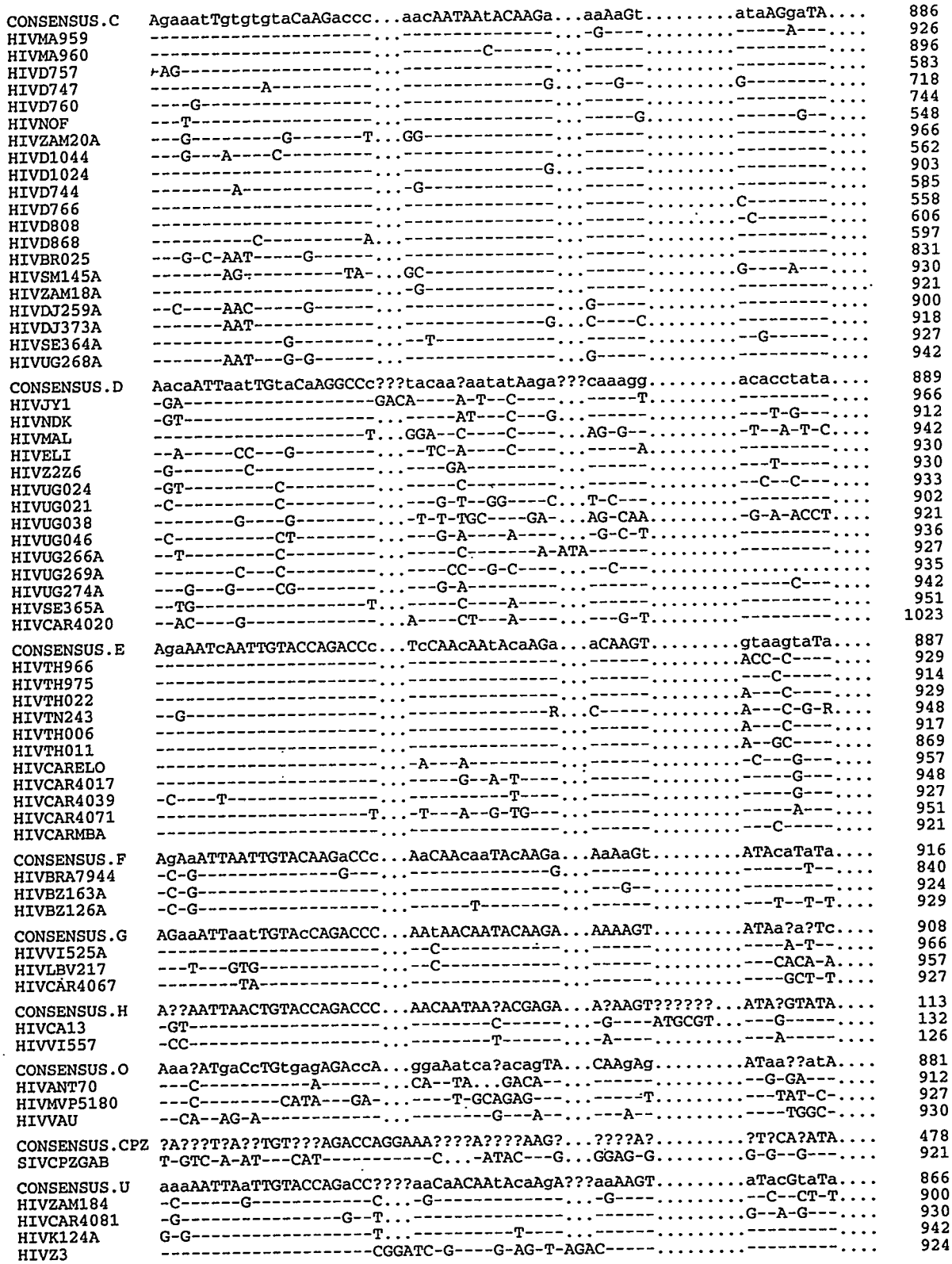
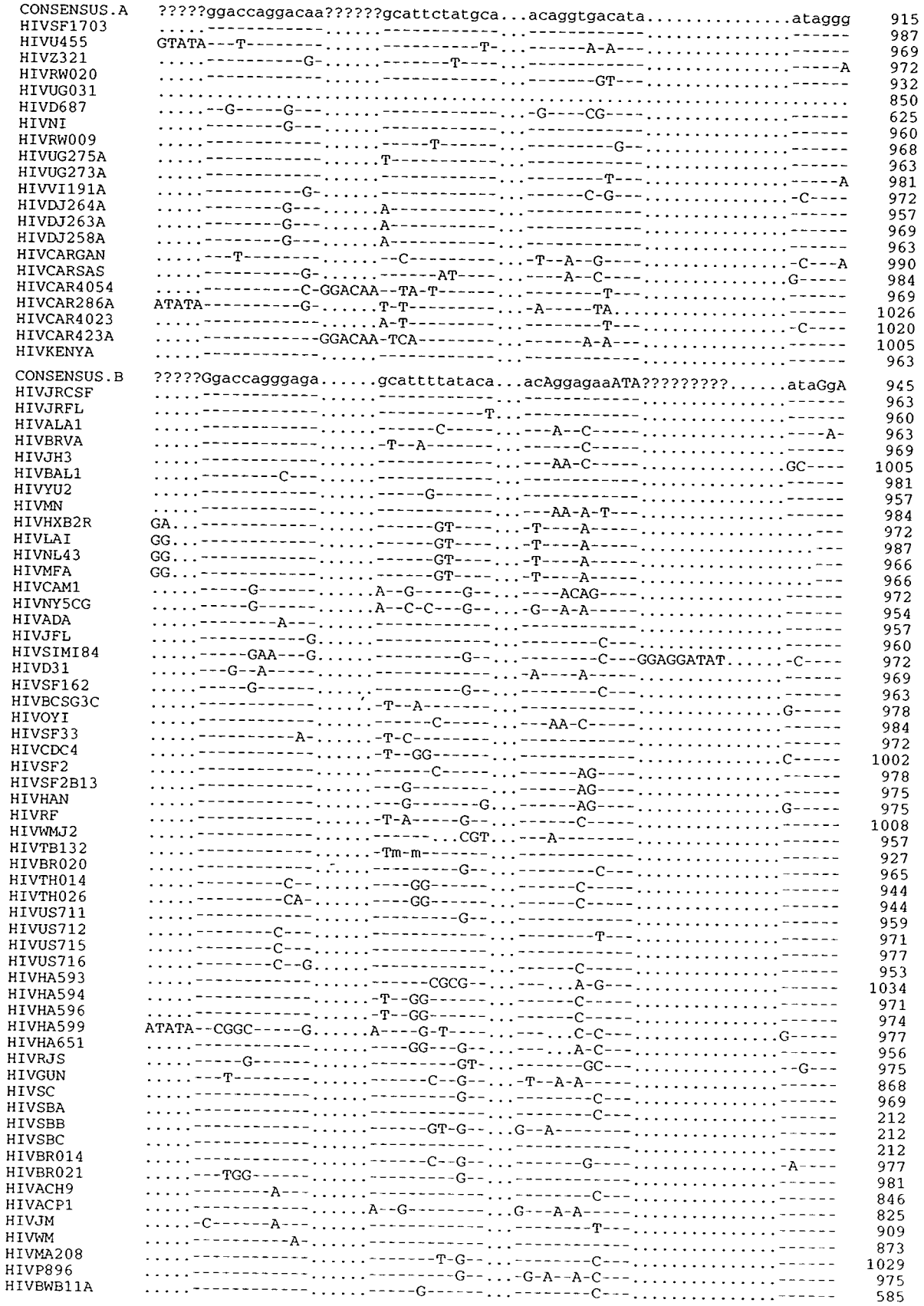
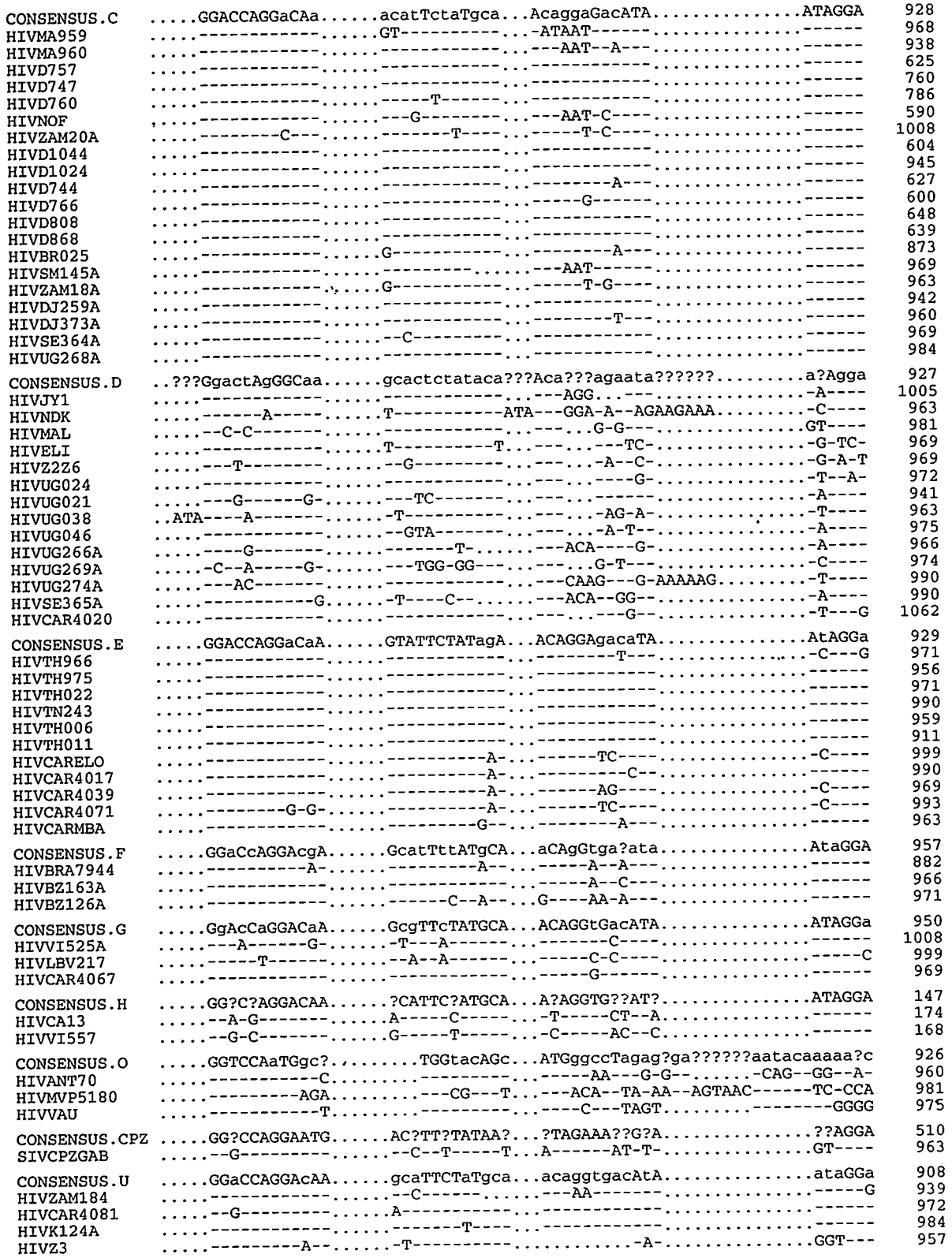
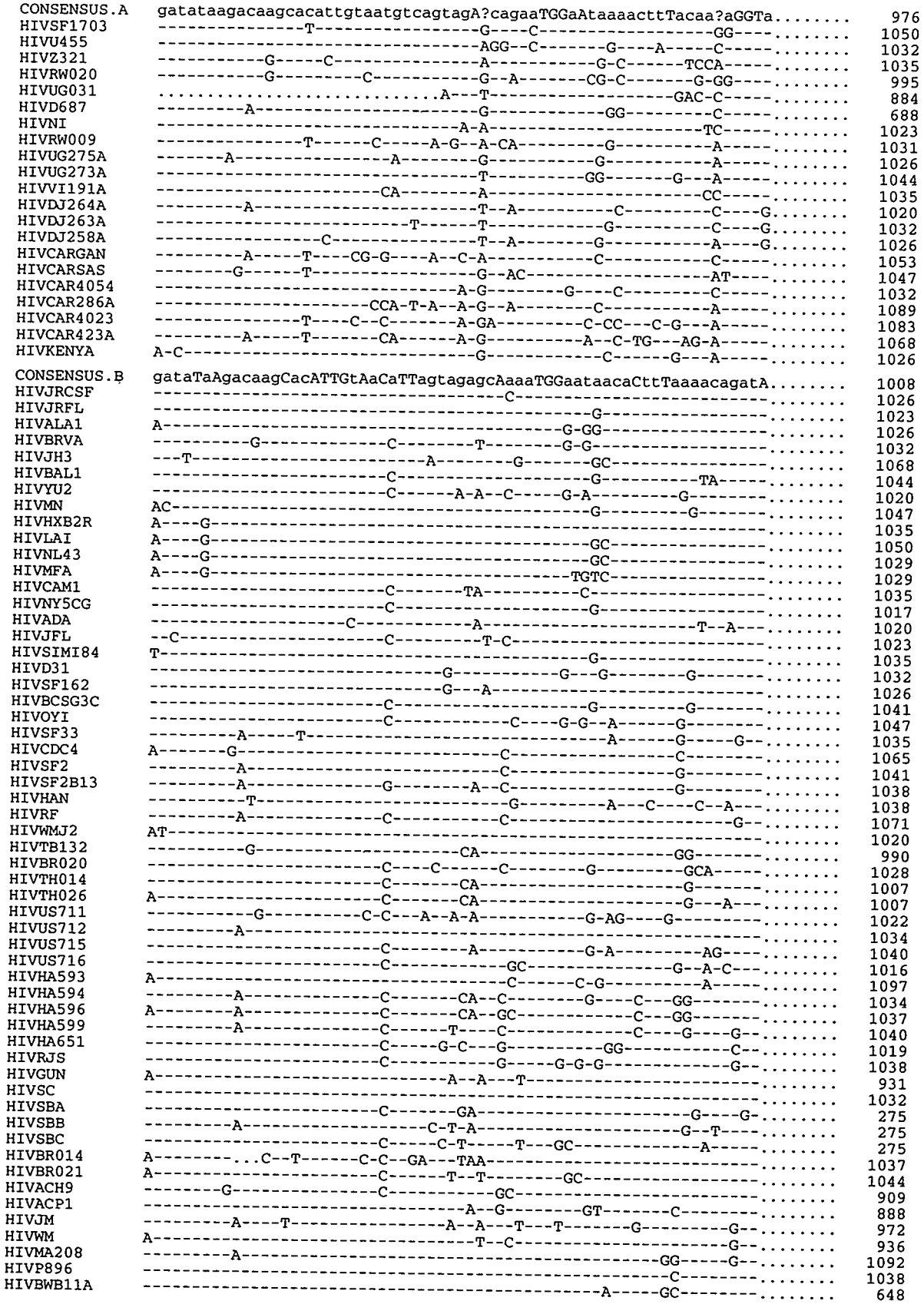
HIVCDC4 ---------...------C---------...-----G.....G--ACGC--.... 960
HIVSF2 --C------C----------...---------...------.....--CT-----.... 936
HIVSF2B13 --C---------...---------...---G--.....--C------.... 933
HIVHAN ---------...---------...---G--.....---------.... 933
HIVRF -C---------...---------...------.....---AC--AG.... 966
HIVWMJ2 ---------...T--------GT----...-G----.....C--TC----.... 918
HIVTB132 ----------T...------T-------G...---C-r.....---hC---G.... 885
HIVBR020 ---C---------...---------...--G---.....---------.... 923
HIVTH014 ---------...---------...------.....------C--.... 902
HIVTH026 ---------...---------...------.....----C-C--.... 902
HIVUS711 ---------...---------...------.....------C--.... 917
HIVUS712 ------G--------T-------...---------...------.....---------.... 929
HIVUS715 -C----G--------G------...---------...------.....---------.... 935
HIVUS716 ------G---------...----------G---...------.....---------.... 911
HIVHA593 ---G---------...----------C...-----A.....---TC----.... 995
HIVHA594 --T---------...--T----G------G...-----G.....---TC----.... 929
HIVHA596 --T---------...--T----------G...-----G.....---TC----.... 932
HIVHA599 -TT------C----------...-----T---------...-GG---.....G------GCGGAC 933
HIVHA651 -C---------...---------...------.....---A-----.... 917
HIVRJS --T----------TAC----CT--A-A--T-...-G-CA-.....---------.... 933
HIVGUN --T---------...---------...------.....---AC----.... 826
HIVSC ----------G---...----------C-...-G----.....---------.... 927
HIVSBA ---------...---------...-G----.....---A-----.... 170
HIVSBB ---------...----------C...-----G.....---TC----.... 170
HIVSBC -C----------T-------...---------...------.....---AG----.... 170
HIVBR014 ---------...----------T-CA-...-G---GATA.....---------.... 935
HIVBR021 ---------...---------C------...------.....--------G.... 939
HIVACH9 ---------...---------...------.....----C----.... 804
HIVACP1 -A----------T-------...---------...---G--.....---GG----.... 783
HIVJM --T----------G---...---------...------.....---------.... 867
HIVWM -C----------T-------...---------...---G--.....---------.... 831
HIVMA208 ----------C---------...GG-C----------...------.....----C---G.... 987
HIVP896 --T---------...---------...-G---G.....T--TC----.... 933
HIVBWB11A ----------T-------...---------...---G--.....---A--G--.... 543







HIV1 ENV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HIVUG273A 1044
HIVVI191A 1035
HIVDJ264A 1020
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HIVDJ258A 1026
HIVCARGAN 1053
HIVCARSAS 1047
HIVCAR4054 1032
HIVCAR286A 1089
HIVCAR4023 1083
HIVCAR423A 1068
HIVKENYA 1026
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HIVJRCSF 1026
HIVJRFL 1023
HIVALA1 1026
HIVBRVA 1032
HIVJH3 1068
HIVBAL1 1044
HIVYU2 1020
HIVMN 1047
HIVHXB2R 1035
HIVLAI 1050
HIVNL43 1029
HIVMFA 1029
HIVCAM1 1035
HIVNY5CG 1017
HIVADA 1020
HIVJFL 1023
HIVSIMI84 1035
HIVD31 1032
HIVSF162 1026
HIVBCSG3C 1041
HIVOYI 1047
HIVSF33 1035
HIVCDC4 1065
HIVSF2 1041
HIVSF2B13 1038
HIVHAN 1038
HIVRF 1071
HIVWMJ2 1020
HIVTB132 990
HIVBR020 1028
HIVTH014 1007
HIVTH026 1007
HIVUS711 1022
HIVUS712 1034
HIVUS715 1040
HIVUS716 1016
HIVHA593 1097
HIVHA594 1034
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HIVHA651 1019
HIVRJS 1038
HIVGUN 931
HIVSC 1032
HIVSBA 275
HIVSBB 275
HIVSBC 275
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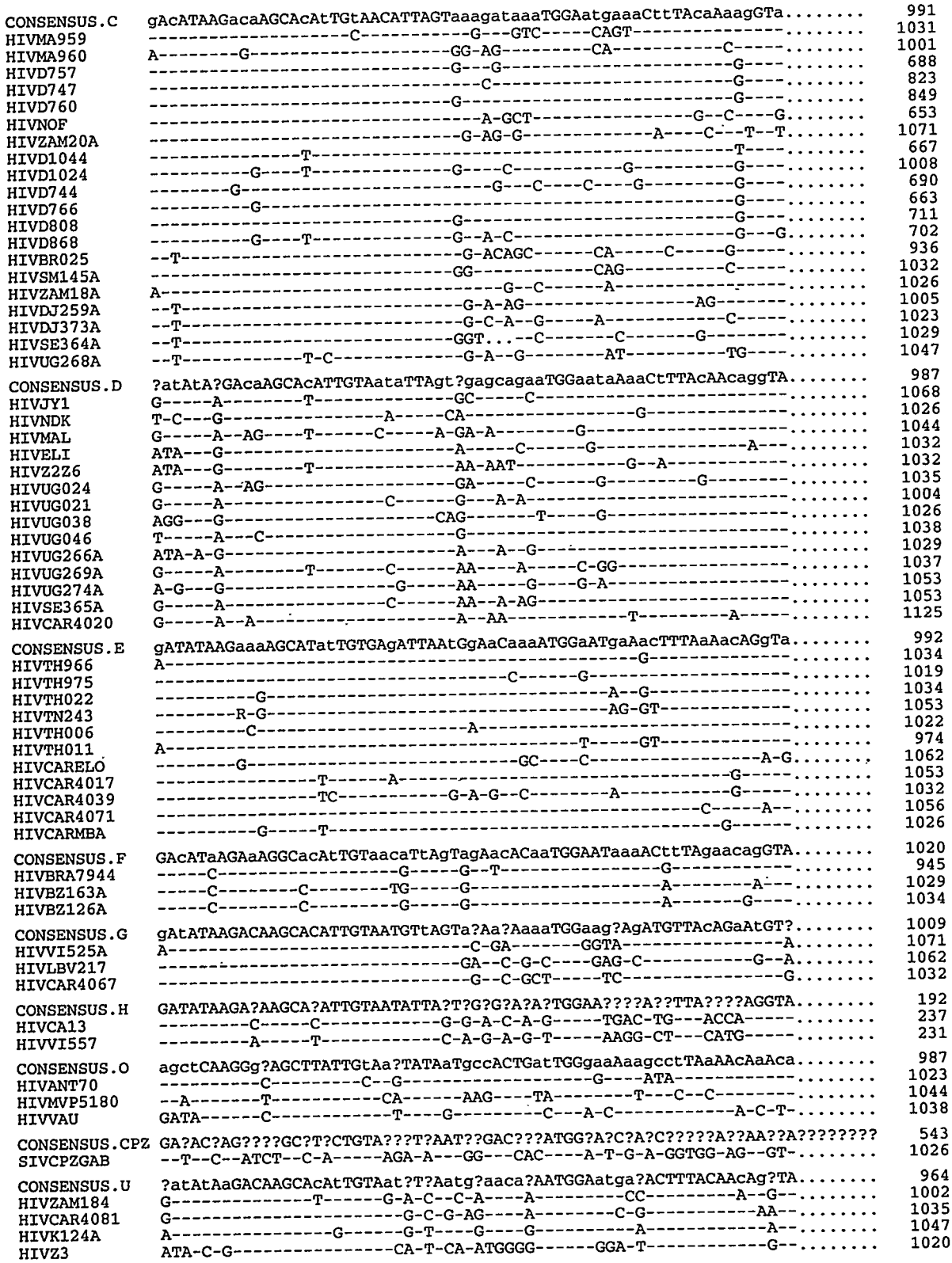

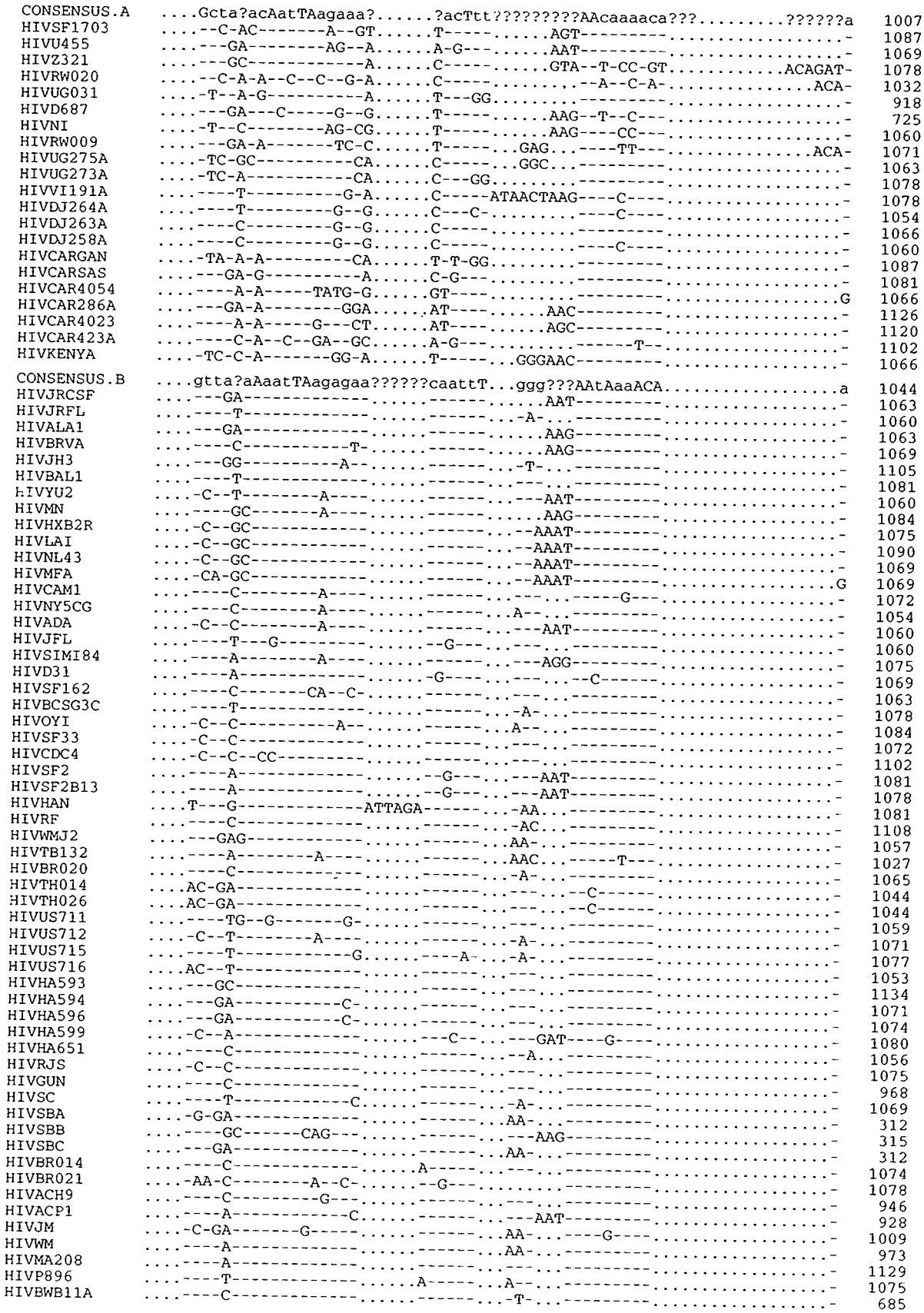

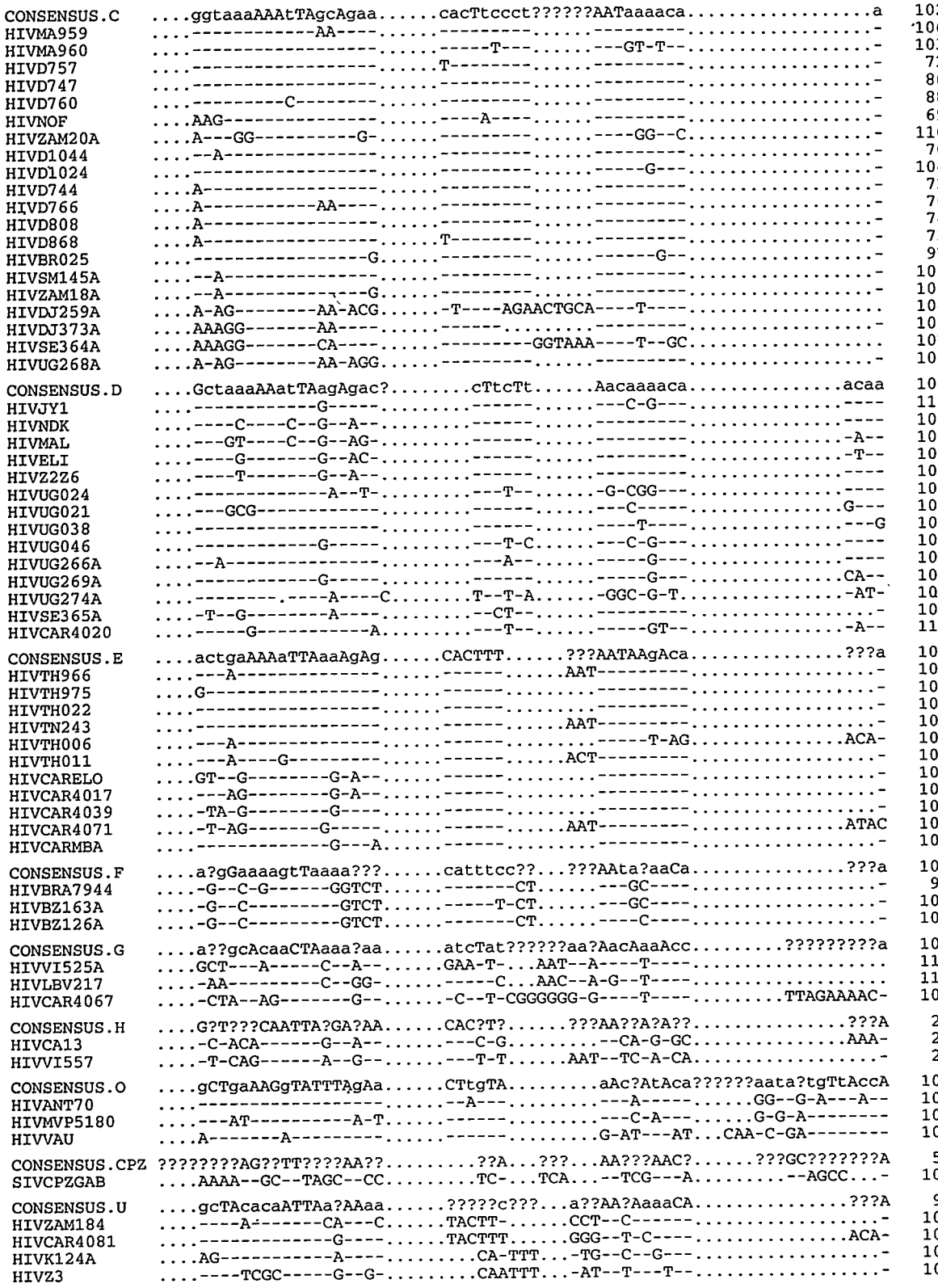

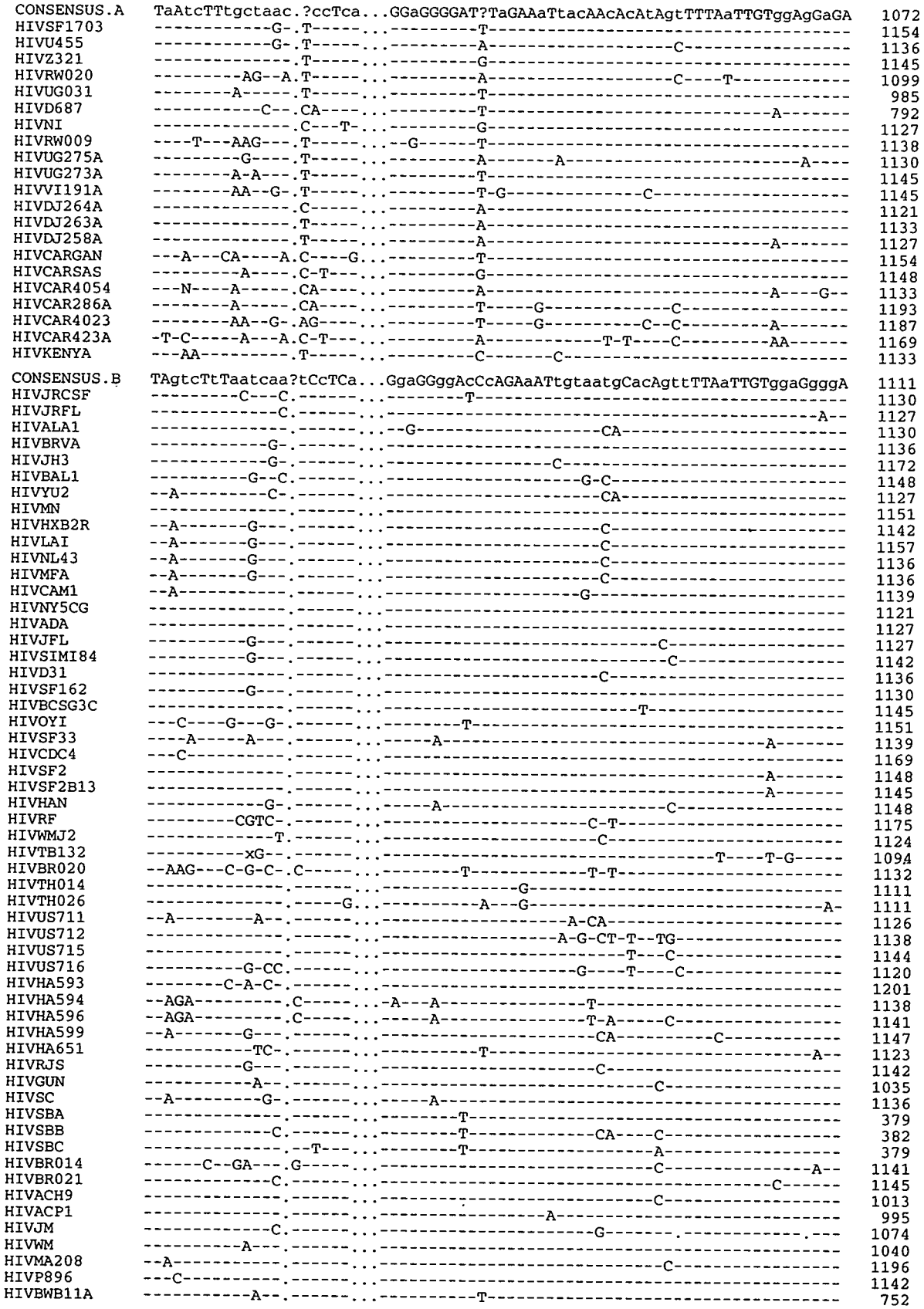
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HIVU455 ----------G-.T-----...---------A----------C---------- 1136
HIVZ321 ----------.T-----...---------G---------- 1145
HIVRW020 ---------AG--A.T-----...---------A----------C----T---------- 1099
HIVUG031 --------A-----.T-----...---------T---------- 985
HIVD687 ----------C--.CA----...---------T----------A-------- 792
HIVNI ----------.C---T-...---------G---------- 1127
HIVRW009 ----T---AAG---.T-----...--G------T---------- 1138
HIVUG275A ---------G----.T-----...---------A-------A----------A---- 1130
HIVUG273A --------A-A---.T-----...---------T---------- 1145
HIVVI191A --------AA--G-.T-----...---------T-G----------C---------- 1145
HIVDJ264A ----------.C-----...---------A---------- 1121
HIVDJ263A ----------.T-----...---------A---------- 1133
HIVDJ258A ----------.T-----...---------A----------A-------- 1127
HIVCARGAN ---A---CA----A.C----G...---------T---------- 1154
HIVCARSAS ---------A-----.C-T---...---------G---------- 1148
HIVCAR4054 ---N----A-----.CA----...---------A----------A----G-- 1133
HIVCAR286A --------A-----.CA----...---------T-----G----------C---------- 1193
HIVCAR4023 --------AA--G-.AG----...---------T-----G----------C--C---------A-------- 1187
HIVCAR423A -T-C-----A---A.C-T---...---------A----------T-T----C---------AA------ 1169
HIVKENYA ---AA----------.T-----...---------C-------C---------- 1133
CONSENSUS.B TAgtcTtTaatcaa?tCcTCa...GgaGGggAcCcAGAaATtgtaatgCacAgttTTAaTTGTggaGgggA 1111
HIVJRCSF ---------C---C.------...--------T---------- 1130
HIVJRFL ----------C.------...----------A-- 1127
HIVALA1 ----------.------...--G----------CA---------- 1130
HIVBRVA ----------G-.------...---------- 1136
HIVJH3 ----------G-.------...----------C---------- 1172
HIVBAL1 ----------G--C.------...----------G-C---------- 1148
HIVYU2 --A---------C-.------...----------CA---------- 1127
HIVMN ----------.------...---------- 1151
HIVHXB2R --A-------G---.------...----------C---------- 1142
HIVLAI --A-------G---.------...----------C---------- 1157
HIVNL43 --A-------G---.------...----------C---------- 1136
HIVMFA --A-------G---.------...----------C---------- 1136
HIVCAM1 --A----------.------...----------G---------- 1139
HIVNY5CG ----------.------...---------- 1121
HIVADA ----------.------...---------- 1127
HIVJFL ----------G---.------...----------C---------- 1127
HIVSIMI84 ----------G---.------...----------C---------- 1142
HIVD31 ----------.------...----------C---------- 1136
HIVSF162 ----------G---.------...---------- 1130
HIVBCSG3C ----------.------...----------T---------- 1145
HIVOYI ---C----G---G-.------...--------T---------- 1151
HIVSF33 ----A-----A---.------...-----A----------A------- 1139
HIVCDC4 ---C----------.------...---------- 1169
HIVSF2 ----------.------...----------A------- 1148
HIVSF2B13 ----------.------...----------A------- 1145
HIVHAN ----------G-.------...-----A----------C---------- 1148
HIVRF ---------CGTC-.------...----------C-T---------- 1175
HIVWMJ2 ----------T.------...----------C---------- 1124
HIVTB132 ----------xG--.------...----------T----T-G----- 1094
HIVBR020 --AAG---C-G-C-.C-----...--------T----------T-T---------- 1132
HIVTH014 ----------.------...----------G---------- 1111
HIVTH026 ----------.-----G...----------A---G----------A- 1111
HIVUS711 --A--------A--.------...----------A-CA---------- 1126
HIVUS712 ----------.------...----------A-G-CT-T--TG---------- 1138
HIVUS715 ----------.------...----------T---C---------- 1144
HIVUS716 ----------G-CC.------...----------G----T----C---------- 1120
HIVHA593 --------C-A-C-.------...---------- 1201
HIVHA594 --AGA---------.C-----...-A---A----------T---------- 1138
HIVHA596 --AGA---------.C-----...-----A----------T-A-----C---------- 1141
HIVHA599 --A-------G---.------...----------CA----------C---------- 1147
HIVHA651 ----------TC-.------...----------T----------A-- 1123
HIVRJS ----------G---.------...----------C---------- 1142
HIVGUN ----------A--.------...----------C---------- 1035
HIVSC --A---------G-.------...-----A---------- 1136
HIVSBA ----------.------...--------T---------- 379
HIVSBB ----------C.------...--------T----------CA----C---------- 382
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HIVBR014 ------C--GA---.G-----...----------C----------A-- 1141
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HIVJM ----------C.------...----------G-------.----------.--- 1074
HIVWM ----------A---.------...---------- 1040
HIVMA208 --A----------.------...----------C---------- 1196
HIVP896 ---C----------.------...---------- 1142
HIVBWB11A ----------A--.------...----------T---------- 752

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HIVMA959      ---C-----A-----.CA----...------A--T--------------------T----------------  1135
HIVMA960      ----------.------...--------T--------------------T----------------------  1105
HIVD757       -----------T--.------...-------G-------------------------------------------  792
HIVD747       ---G-------T--.------...-------------------------------------------------  927
HIVD760       -----------G--.------...-------------------------T----T-----------------  953
HIVNOF        --GC----AACT--.------...--------TT-----G-------------------------------  757
HIVZAM20A     ---T-----A----.------...-------------------------------------------------  1175
HIVD1044      ---G--C-------.------...-------------------------------------------------  771
HIVD1024      ----C------T--.------...-------------------------------------------------  1112
HIVD744       -----------T--.------...--G--------------------------------------------  794
HIVD766       ----------GT--.------...--G--------------------------------------------  767
HIVD808       -----------T--.------...-------------------------------------------------  815
HIVD868       --C--------T--.------...-------------------------------------------------  806
HIVBR025      -----------AAG.CA----...-------------------------------------------------  1040
HIVSM145A     ----G----A----.------...--------T----------------------------------------  1136
HIVZAM18A     ---------AC-A-.CA----...-------------------------------------------------  1130
HIVDJ259A     .....---CA----.------...-------------------------------------------G-------  1109
HIVDJ373A     ----------.------...-----A---A-----------------------------G-------------  1124
HIVSE364A     .....----A----.------...-----------------------C----------------------  1133
HIVUG268A     ----C---A-T-A-.C-----...---------T-------------------------------------  1151

CONSENSUS.D   TAattTTTaAacCa.tcctCa...GGAGGgGACCcAGAAaTtacAacACACAgctTTAATTGTggAGGgGa  1091
HIVJY1        ----------.C--G--...-----A---------------------------------------------  1172
HIVNDK        ---C------G---.------...----------------------T------TGC---------------  1130
HIVMAL        ----------TT--.------...-----------------------------T---------A-------  1148
HIVELI        ---AG---------.------...-----------------------------T-----------------  1136
HIVZ2Z6       ----------.------...-----------------------------T-----------------  1136
HIVUG024      --GA----------.-----G...-------------------------------------------------  1139
HIVUG021      ----------.-----G...-------------------------------------------------  1108
HIVUG038      ---A----------.------...----------C-------------------------------------  1130
HIVUG046      --------C-----.CA---G...-----------------------------C-----------------  1142
HIVUG266A     ----------.-----G...-------------------------------------------------  1133
HIVUG269A     --------G-----.-----G...----------G------A-------------------------  1141
HIVUG274A     ---C----------.------...-------------------------------------------------  1156
HIVSE365A     --------G-----.------...----------G----------T---------A-------  1154
HIVCAR4020    ---A----C----C.CAT---...-----A----T----G----------T---------CA------  1229

CONSENSUS.E   tAatctttCaaCcA.ccCTCA...GGAGGaGATCtagAAAtTAcAAtgCatcatTTTAATTGTaGAGGGGA  1093
HIVTH966      ----------.------...-------------------------------------------------  1138
HIVTH975      ----------.------...----------A-------------------------------------  1120
HIVTH022      ----------.------...-------------------------------------------------  1135
HIVTN243      ----------.------...----------G-------------------------------------  1157
HIVTH006      ----------C---.------...-----------------T--C-------------------------  1126
HIVTH011      ----------.------...-----------------------C-------------------------  1078
HIVCARELO     ----------.T-----...----------C----------A-----------------  1163
HIVCAR4017    --CA-----G----.T-----...-----G----C-----C-----AT---AT----------------  1154
HIVCAR4039    ----------G-.T-----...----------C----------T-ACC---------G-------  1133
HIVCAR4071    A-T-TAAA-C-----.TA----...-----------------------C-------------------  1163
HIVCARMBA     --G-T---------.------...-----------------------AG------------------  1127

CONSENSUS.F   TAA?aTTTaa??cA.tCctCA...GGAGGGGACCtAGAAaTTACAAtgCATAgtTTTAATTGtAGAGGAgA  1114
HIVBRA7944    ---A------CT--.------...-------------------------------------------------  1049
HIVBZ163A     ---A------TT--.------...-------------------------------------------------  1133
HIVBZ126A     ---A------CT--.------...-------------------------------------------------  1138

CONSENSUS.G   taa?cTTTAaCTCA.tCtgCA...GGAGGGGACCTAGAAaTTACaacACATAGTTTtAATTGTaGAGGAGA  1108
HIVVI525A     .....----------.--CT--...-------------------------------------------------  1172
HIVLBV217     .....----------.--CT--...----------------------G-------------------  1163
HIVCAR4067    ---C----------.C-----...----------------G------A----------------G-------  1151

CONSENSUS.H   TA???TT??AACCA.TCCTCA...GGAGG?GACAT?GAAATTA?AA??CA?A??TTTAA?TGT??AGGAGA  264
HIVCA13       --CAA--TA-----.------...-----A-----A-------T--CA--C-TG-----C---GC------  341
HIVVI557      --ATT--CG-----.------...-----G-----G-------C--TG--T-CT-----T---AG------  335

CONSENSUS.O   TgA?ATTCaatca?.agcAgt???GgtGgAGATgcaGAggtAAcccATtT?catTTTAACTGtCAtGGaGA  1095
HIVANT70      ---C---------C.-----C...---------CT---------------A--C-----------------  1136
HIVMVP5180    -A-T-----GCAGA.-CT---...--------------A----G------A-------------------  1157
HIVVAU        ---A----GG-A-T.CA----...-----A---------A-----AA----CTT-----------------  1154

CONSENSUS.CPZ ?????ACA?TC?A????.?????????GGAGATCC?GA?GT?A?A???CAT??GTTTAATTG???AGGAGA  596
SIVCPZGAB     ACATA---C--A-CAGA.GCCTCTGGA--------A--G--C-C-CAT---AT---------TGG------  1136

CONSENSUS.U   TAAtcTTTaata?a.TCcTCa...GGAGGgGAcctAGAaATTACAACACA?A?tTTTAAtTGTgGAGGaGA  1056
HIVZAM184     ---G----GC--AC.--T---...-------------------------T-G-----------------  1106
HIVCAR4081    ---A-----G--A-.------...-----A--TT----------------C-C-----------------  1142
HIVK124A      ----T-----ACC-.-----G...----------C----------------C-GC---------A----G--  1151
HIVZ3         ----A-----CTC-.------...---------A----G----------T-C------C-----------  1124
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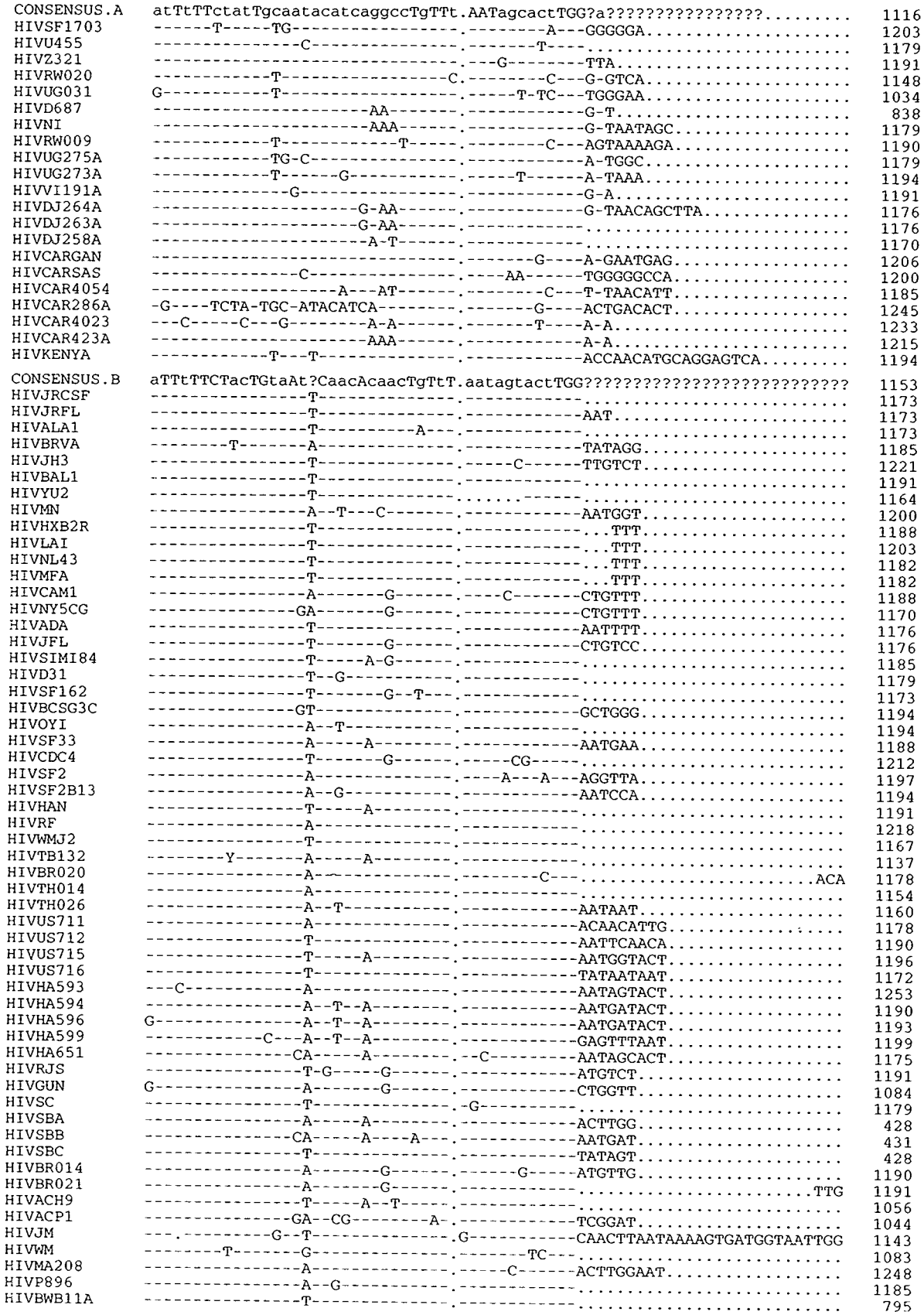

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CONSENSUS.C  ATTTTTCTAtTGcaAtACatCAaaccTGTTt.aaTagtacatac????????????a??cct???.....  1142
HIVMA959     ----------------------GGG------.-------AC-TT.....------------------.....  1178
HIVMA960     ------------T----------GA------.-----C------.....-AT---.....------.....  1154
HIVD757      ------------------------------.------------.....-TG---.....------.....  841
HIVD747      ----------------------G--------.---G--------.....-TG---.....------.....  976
HIVD760      ----------------------GG------C.---G--------.....-TG---.....------.....  1002
HIVNOF       --------------------A--G--------.TC-GCA.....------------------.....  794
HIVZAM20A    ------------------C----T-------.-----AT--C--TTAGGC.....TTGTT-.....  1230
HIVD1044     ------------T------------------.------------AATAGTACATAC-TG-T-.....  832
HIVD1024     ---------------C--------------.------------.....-TG---.....------.....  1161
HIVD744      ------------------------------.------G-----.....-TG---.....------.....  843
HIVD766      ------------T---------GG-------.---G--------.....-TG-A-.....------.....  816
HIVD808      ------------T---------GG-------.---G--------.....-TG---.....------.....  864
HIVD868      ------------------------------.---G--------.....-TG.....------.....  852
HIVBR025     ----------------------G-------.------------.....-CA---.....------.....  1089
HIVSM145A    ----------------------GG-------.------------.....-AT---.....------.....  1185
HIVZAM18A    ------------------------------.-----------T.....-AG---.....------.....  1179
HIVDJ259A    ---------C------------G--------.---.....------------------.....  1143
HIVDJ373A    ------------T---------GC-T-----.---GA-T--ATTACAAAT.....GCA--CATT.....  1182
HIVSE364A    ------------G----------G-------.---G-----ACACATACT.....------------  1182
HIVUG268A    ----------------------G-------.-------GTG-TAATAAT.....------------  1200

CONSENSUS.D  atTtTTCTaCTGcaATaCATCAagAcTgTTT.AAtagtAcatgg????????????.....------  1134
HIVJY1       ------------------------------.------------.....------------------  1215
HIVNDK       C--C--------T------------------.------------.....------------------  1173
HIVMAL       ------------T----------A-------.------------CAG.....------------  1194
HIVELI       ---C--------T---------G--------.------------.....------------------  1179
HIVZ2Z6      ---C--------T---------G--------.------------.....------------------  1179
HIVUG024     ----------------------A-T-----.---CA--GTGTAGGGGAG.....------------  1188
HIVUG021     ----------------------G--------.--C-A--GTGTATGGACATCA.....------  1160
HIVUG038     ----------------------CA-------.------------...GGGAGT.....------  1179
HIVUG046     ------------G--G--------------.-----G--T-AT.....------------------  1185
HIVUG266A    ----------------------G--------.----A--GTGTATGGAGG.....------  1182
HIVUG269A    ------------G-----------------.---GA--GT-AT.....------------------  1184
HIVUG274A    ------------------------A---.----A--GTG-ATGGGAAAATTAT.....------  1211
HIVSE365A    ----------------------G--------.------------AAAACA.....------------  1203
HIVCAR4020   ----------------------CA-------.---CA--A----.....------------------  1272

CONSENSUS.E  ATTTTTCTATTGCAATACAaCAaaacTGTTt.AaTagtActtgga?a??a???.....------  1139
HIVTH966     ----------------------G------C.----A------C-TTGG-.....------------  1187
HIVTH975     ------------------------------.------------T-GG-.....------------  1169
HIVTH022     ----------------------CG-------.-G--A------C-T-AA-.....------------  1184
HIVTN243     ----------------------CG-------.----A------C-T-GG-.....------------  1206
HIVTH006     --------------------C-----T-----.---G-A--CAT-GAGGGGCCT.....------  1178
HIVTH011     ----------------------C--------.----A------C-T-GG-.....------------  1127
HIVCARELO    ------------------------C------.------------GA-AT-.....------------  1212
HIVCAR4017   ----------------------C--------.------------G-AT-.....------------  1203
HIVCAR4039   ----------------------G-------.------------GG-AC-.....------------  1182
HIVCAR4071   ----------------------G-------.----T--GCACA.....------------------  1206
HIVCARMBA    ------------------------------.------------GA-ATG.....------------  1176

CONSENSUS.F  aTTTTTcTACTgCAAtACa?cagaaCTGTTT.AatgAcac?g?at????????.....------  1155
HIVBRA7944   ------------------GT--A--------.--------                            1088
HIVBZ163A    ------------------T---G-------.-C-----A-G--CC.....------------  1179
HIVBZ126A    ------------------T---G-------.--------A-G--CC.....------------  1184

CONSENSUS.G  aTTTTTcTATTGtAAtACATCAGgacTGTTt.AATaata?t?t??????????.....------  1148
HIVVI525A    ------T--------G-------AG------.----G--C-TGGTTGTTT.....------------  1221
HIVLBV217    ------------------------------.----G--G-A-ATTATCT.....------------  1212
HIVCAR4067   ------------------------------C.----G-.....------------------  1188

CONSENSUS.H  ATTTTTCTATTG?AATACA?CAAAA?TGTTT.AA?AGTAC?TGG????????????.....------  302
HIVCA13      ------------T------A-----C-----.--T-----C---ACGACTAACACC.....------  396
HIVVI557     ------------C------T-----T-----.--C-----T---GTT.....------------  381

CONSENSUS.O  aTTCTTTTATTGtAACACatcT?ggaTGTTT.AAttATAccTTTtcatgt?????????????????????  1143
HIVANT70     ------------------G--AA-------.------------------.....------------  1185
HIVMVP5180   ----------------------G--------.--C-----T---ATC.....------------  1203
HIVVAU       --------------------AA-C--C-----.---C----------C--CAAGAAGAATATGACCAATAAC  1224

CONSENSUS.CPZ ATT?TT?TATTGT?ATA??A??C?????TT?.A?TG?C??????????????.....------  618
SIVCPZGAB    ---T--C------A---CT-GC-AAATA--T.-C--A-.....------------------  1173

CONSENSUS.U  aTTTTTCTAtTGCAAtACATCAaaccTGTTT.AaTaGtat?Tggaaa???.....------  1101
HIVZAM184    ------------------------------.-------CA-AC--TCCT.....------------  1155
HIVCAR4081   ----------------------CG-T-----.-----C-GT------GGA.....------  1191
HIVK124A     ---------C--------------A------.------G-A---GG-.....------------  1197
HIVZ3        G--------------C------G-G------.-C-G----T---.....------------------  1167
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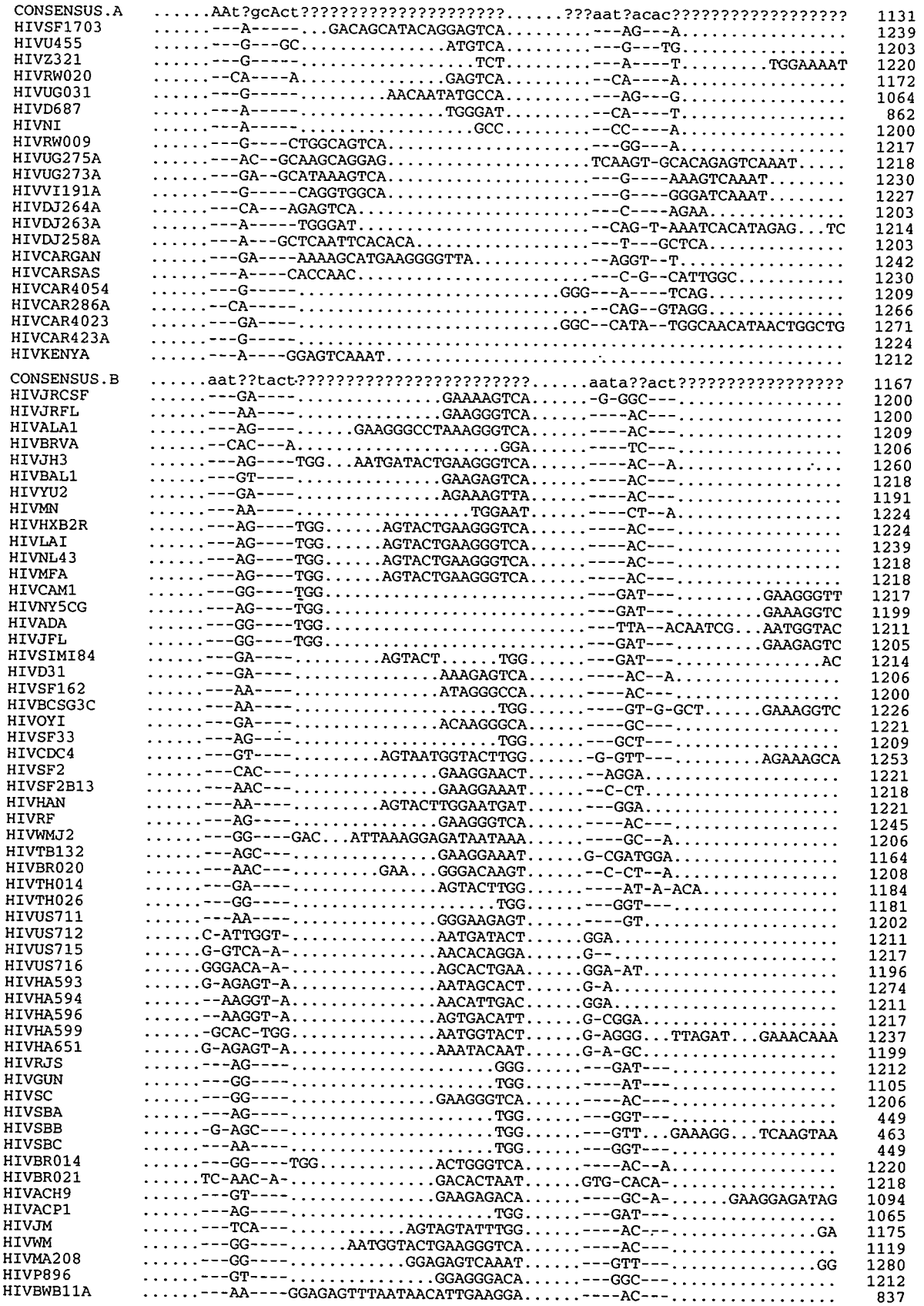

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CONSENSUS.C  ......aatggtaca??aa?t??????????????????????...aat???a?????......????????  1158
HIVMA959     ......----A----GA-GG-.....................---TCA-CT.....................  1202
HIVMA960     ......---------GT--G-.....................---GAT-CAGAA.....................  1181
HIVD757      ......---------AA-GG-.....................---TCA.........................  862
HIVD747      ......---------AA--G-.....................---TCA-GC.....................  1000
HIVD760      ......---------AA--G-.....................---TTA-AC.....................  1026
HIVNOF       .......--C-CA---AA-TT-.....................---GAA-GT.....................  818
HIVZAM20A    ......---------GA-.........................---AATTCA.....................  1251
HIVD1044     ......---------AC--G-.....................---TCA-CC.....................  856
HIVD1024     ......---------AA--G-.....................---TCA-AC.....................  1185
HIVD744      ......---------TAT-TGTTTAATGGTACATACATGTTT...---AGT-CA.....................  888
HIVD766      ......---------AA--G-.....................---TCA-GC.....................  840
HIVD808      ......---------AA--G-.....................---TCA-GC.....................  888
HIVD868      ......---------AA--G-.....................---TCA-GC.....................  876
HIVBR025     .......---A-----GT                                                        1100
HIVSM145A    .......---AAC---GG--G-GAGTCAAAC...........................................  1209
HIVZAM18A    .......----A----...........................---AGT-CA.....................  1197
HIVDJ259A    .......---CAG-GTATC-CA.....................................................  1158
HIVDJ373A    .......---AA-T-GAGT-CA.....................................................  1197
HIVSE364A    .......GCAAA-T--...........................................................  1191
HIVUG268A    .......---A----C...........................................................  1209

CONSENSUS.D  ......aAta?taca?ca?????????????????.....aatagtaca???......????????  1153
HIVJY1       .......----G--GTA--TGGAAT.....................---GA----.....................  1242
HIVNDK       .......---CAG--T.....................................---------.....................  1191
HIVMAL       .......----A-GGTG--AGACTAAGT.....................-----C---.....................  1224
HIVELI       .......----T--GTG--......TGGAAT.....................----T----.....GAGTCAAA  1214
HIVZ2Z6      ......G---T--GTAA-TCAGAATGGGCT.....................---------.....GAGTCAGA  1220
HIVUG024     .......----A---TCT-TCA.....................-T---C-AC.....................  1212
HIVUG021     .......----G---G.....................................................AT  1171
HIVUG038     .......---GA----T--.....................................---------TAT.....  1203
HIVUG046     .......----CAT--GGT.....................................------.....  1203
HIVUG266A    .......---GA-TATC--TCA.....................------------.....  1206
HIVUG269A    .......----CAT--G--TTAAATAGTACACAGGGA.....---GAG-GT.....  1223
HIVUG274A    .......----TAT--.....................------------.....  1229
HIVSE365A    .......--ATCAGGT.....  1212
HIVCAR4020   .......---GA----A--GGAGAAATGTCAGAACAG.....--C-A--ATACA......GAGTCA..  1320

CONSENSUS.E  ......AATgaaACcatg.....g?gg?gt?t......AAtggcAct.....  1166
HIVTH966     .....----------A.....-G--G--G-.....----A----.....  1217
HIVTH975     .....----G-------.....-A--G-CG-.....---A---GC.....  1199
HIVTH022     .....----------.....-C--G--G-.....--C------.....  1214
HIVTN243     .....----------.....AAT-G--G-.....---------.....  1236
HIVTH006     .....---A-C--GGA-.....-G-CCTAA-.....--CACT---.....  1208
HIVTH011     .....----------.....AA--G--G-.....----A----.....  1157
HIVCARELO    .....---A--------.....AA--C-.....----A---A.....  1239
HIVCAR4017   .....----------.....-AAAA-GT-.....--------A.....  1233
HIVCAR4039   .....----------A.....-A--C-.....----T---A.....  1209
HIVCAR4071   .....----G----.....ACA.....---------.....  1227
HIVCARMBA    .....---A-------A.....-A--A-CT-.....---------.....  1206

CONSENSUS.F  ......AAtaacact??????????????????.....  1164
HIVBZ163A    .......---GG----.....  1188
HIVBZ126A    .......---GG----.....  1193

CONSENSUS.G  ...???AAtaatAct?????????????????????.....aat???ac???????.....  1162
HIVVI525A    .....----G----GGGCTGGTTAATAGTACTTGG.....---GAT--ACGA.....  1263
HIVLBV217    .....--C----A-GCACCATCT.....---AGC-GT.....  1239
HIVCAR4067   .....----GC---AAGACTACAAATGATACTAAGACA.....---GAT--T.....  1230

CONSENSUS.H  ......AA??G?A??T????????...AAT?A?A????A.....AATGG?AC?.....  320
HIVCA13      .....--TG-C-GC-ATGTGAGC...---A-C-CAGA-.....-----T--T.....  435
HIVVI557     .....--CA-T-CA-CA.....---G-T-TCTC-.....-----C--A.....  414

CONSENSUS.O  ??????AAt?gtAcc?????????tg???????????aag?ta?cAATgt?ActaAt??t.....  1171
HIVANT70     .....--CG-A---.....ACC--T.....AGT-T--GT-----T-G-C-AGG-.....  1224
HIVMVP5180   .....--CT----AAAGTCCGGA--CCAGGAGATCA---GG-G-----AG--C---.....  1254
HIVVAU       AAGATC---T----T.....---A-T-GC---AA-.....  1254

CONSENSUS.CPZ .....??CAT?ACA.....  624
SIVCPZGAB    .....AA---T---.....  1182

CONSENSUS.U  ......AAttgtA?t?????????t?a????????????.....aatg?cact??????...????????  1119
HIVZAM184    .....---A---CA.....GA-AGTAATTCA.....  1176
HIVCAR4081   .....--G-AC-G-GGGCATGAG-C-.....----A----.....  1221
HIVK124A     .....----CA-G-.....----TG--AAAGGTA.....AATGG  1226
HIVZ3        .....---G---C-.....-GGGAT.....AAG.....---TG----AGCACT...GAGAGTAA  1208
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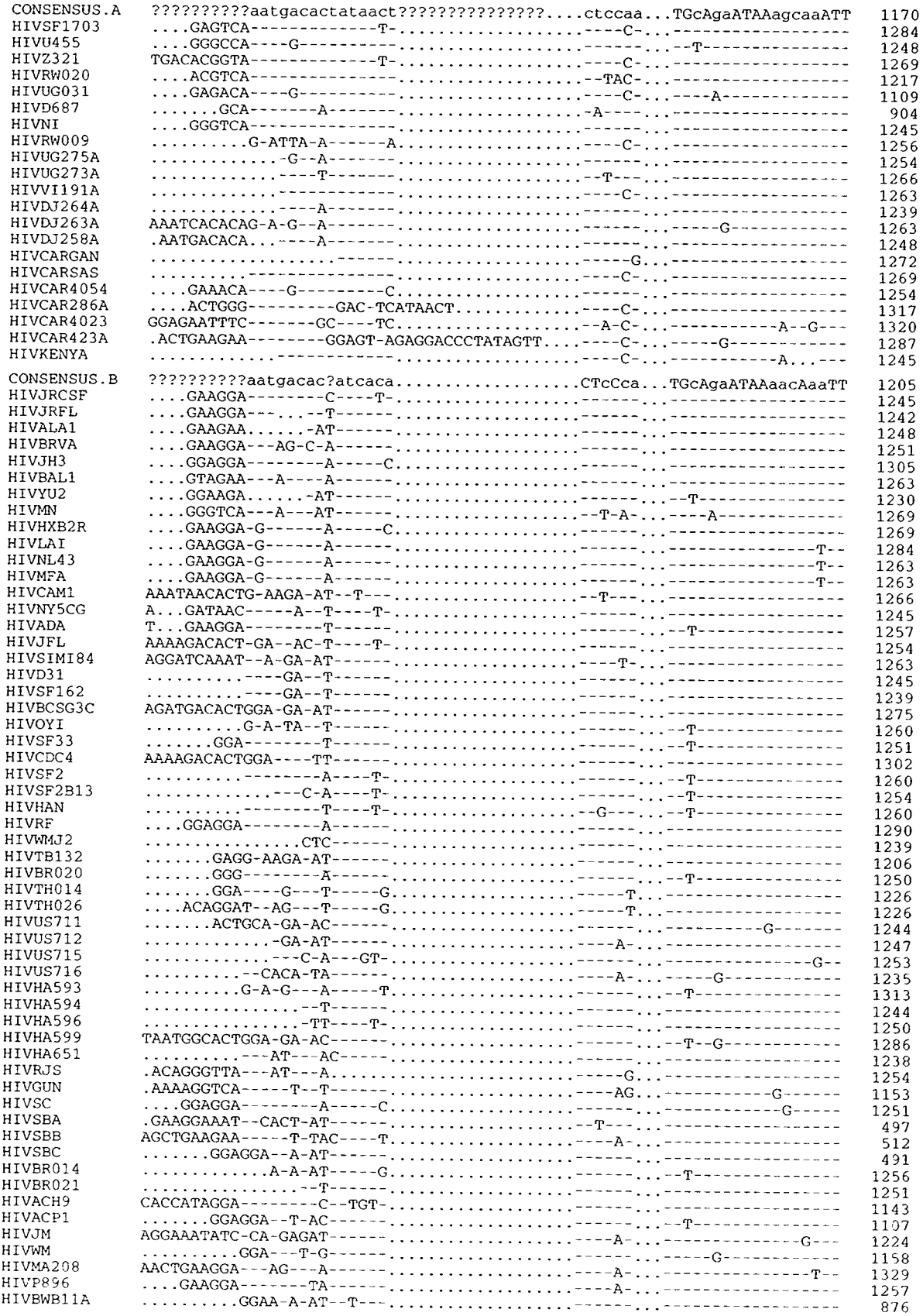

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CONSENSUS.C  ??????????????caa?cATcACa.....................cTcCcA...TgcAGaATAAAaCAaaTT  1192
HIVMA959     .............TT--G---A--C.....................------...------------------  1238
HIVMA960     .......AGTAATT---C-------.....................------...------------------  1223
HIVD757      ..........AACT---C-------.....................A---A-...------------------  901
HIVD747      .............T---C-------.....................A-T---...------------------  1036
HIVD760      .............T---C-------.....................A------...------------------  1062
HIVNOF       ....GATCCAAACG---C-------.....................------...-----G------------  863
HIVZAM20A    .......CCCCAA...-A------T.....................A------...----------C------  1290
HIVD1044     .............TT--A-------.....................A------...------------------  892
HIVD1024     .............T-C-C-------.....................A---T-...--T--T------------  1221
HIVD744      .......AGTAATG---C-------.....................A------...------------------  930
HIVD766      .............T---T-------.....................A------...----------G------  876
HIVD808      .............T---T-------.....................A------...----------G------  924
HIVD868      .............T---C-------.....................A---T-...----------------G--  912
HIVSM145A    ............AAC-A-------.....................----A-...------------------  1245
HIVZAM18A    .TATAATCCTAATGAT-CA------.....................------...------------------  1245
HIVDJ259A    ..........AATGA--A-------.....................--T-A-...------------------  1197
HIVDJ373A    ..........GATG---A-------.....................--T-A-...------------------  1236
HIVSE364A    ................-A-------.....................A---A-...----------G---  1224
HIVUG268A    ................-T-------.....................------...------------------  1242

CONSENSUS.D  ??????????aata??acaaTcAcA.....................cTcCcA...TGCAgAATAAaACAaATT  1190
HIVJY1       .TTAAATAGTG-AGGA-------A-.....................------...------------------  1290
HIVNDK       .GGGTTCAAT---GGC---G-----.....................------...------------------  1239
HIVMAL       ....GAGTCA-C-GGT-GT------.....................------...------------------  1269
HIVELI       TAATAGCACA--C-CA-AC------.....................----A-...------------------  1263
HIVZ2Z6      TGATAAA.........C---------.....................----A-...------------------  1260
HIVUG024     .GGGGTA...----CT-AC------.....................------...----A-------------  1257
HIVUG021     AGGGGCA...---GGG---------.....................------...------------------  1217
HIVUG038     ..........----AC-------A-.....................A------...----------G-------  1242
HIVUG046     .GGGGTAAAT--C-GT-------A-.....................------...------------------  1251
HIVUG266A    .GGAGTAAATG-G-GCGT-------.....................------...----A-------------  1254
HIVUG269A    ............GAA-AC------.....................------...------------------  1259
HIVUG274A    .GGGGGA...---GAG-------G-.....................----A-...------------------  1274
HIVSE365A    ............GAT-AT--T---.....................------...--------------G---  1248
HIVCAR4020   ............GAA-AT------.....................------...----------G-------  1356

CONSENSUS.E  .......????????????ATCacA.....................CTTCCA...TGCAagATAAaGCAAatT  1196
HIVTH966     ..................----T-.....................------...------------------  1247
HIVTH975     ..........GATACACCT---GT-.....................------...------------------  1238
HIVTH022     ..................----T-.....................------...------------------  1244
HIVTN243     ..................------.....................------...------------------  1266
HIVTH006     ..................----T-.....................------...------------------  1238
HIVTH011     ..................----T-.....................------...------------------  1187
HIVCARELO    .......AACTTAAGCAAT------.....................------...----GA----------  1281
HIVCAR4017   .......AACTCAAACATG------.....................------...----G-----G-------  1275
HIVCAR4039   .......AACCCAAGAAAT------.....................------...----------G-----A-  1251
HIVCAR4071   ..................------.....................------...----G----------G--  1257
HIVCARMBA    ..................------.....................------...----G----------  1236

CONSENSUS.F  .......??????????????????????.....CTcc?a???TGTagaATAAgACAa?Tt  1186
HIVBZ163A    ..................ATCACT.....................----T-...---C------A----A-G  1218
HIVBZ126A    ..................ATCACT.....................----T-...---C-C---------A--  1223

CONSENSUS.G  .......??????aa????atta??ac???????.....CTcCcA...TGtAgaATAAAACAAATT  1194
HIVVI525A    ............--AGAT----CA.....................--G-A-...--C-A----------  1299
HIVLBV217    ............--GAAT--C-CA.....................------...------------------  1275
HIVCAR4067   ..................--C-CA.....................----A-...------------------  1260

CONSENSUS.H  ..................A??A?A??????.....CTGC?A...TGCAGAATAAAACAAATT  346
HIVCA13      ..................-TT-C-.....................----A-...------------------  465
HIVVI557     ..................-CA-T-ATTGAA.....................----C-...------------------  450

CONSENSUS.O  .......a??AATGgcACT?a????.....aTACCT...TGCAggtTaAgACAagTg  1206
HIVANT70     .......-AC---------.....C-------...----AAC-G-----G---  1260
HIVMVP5180   .......-AA-----T---.....------...----A---------GC-A  1290
HIVVAU       .......-GC---------C-GGCA.....-------...---------G--------A  1296

CONSENSUS.CPZ  ..........AA?GG?????T?ATA.....???C??...TGCAGAATTA??CAGATA  649
SIVCPZGAB    ..........--T--CATTA-A---.....CTG-CA...----------GA------  1221

CONSENSUS.U  ??????????????ga?a??Ataaca.....CTCCCa...TGcA?aATAAaACAAaTt  1151
HIVZAM184    .......GACTTAA-C-TC-C-.....-------...----G----------  1215
HIVCAR4081   ..................-----T.....-----G...----A-----G-------  1251
HIVK124A     GACAAAGGTAAAA--G-CA--C---.....-------...--T-A----------  1275
HIVZ3        TTGCACT......-GA-AT--T---.....-------...----GG---------G-G  1251
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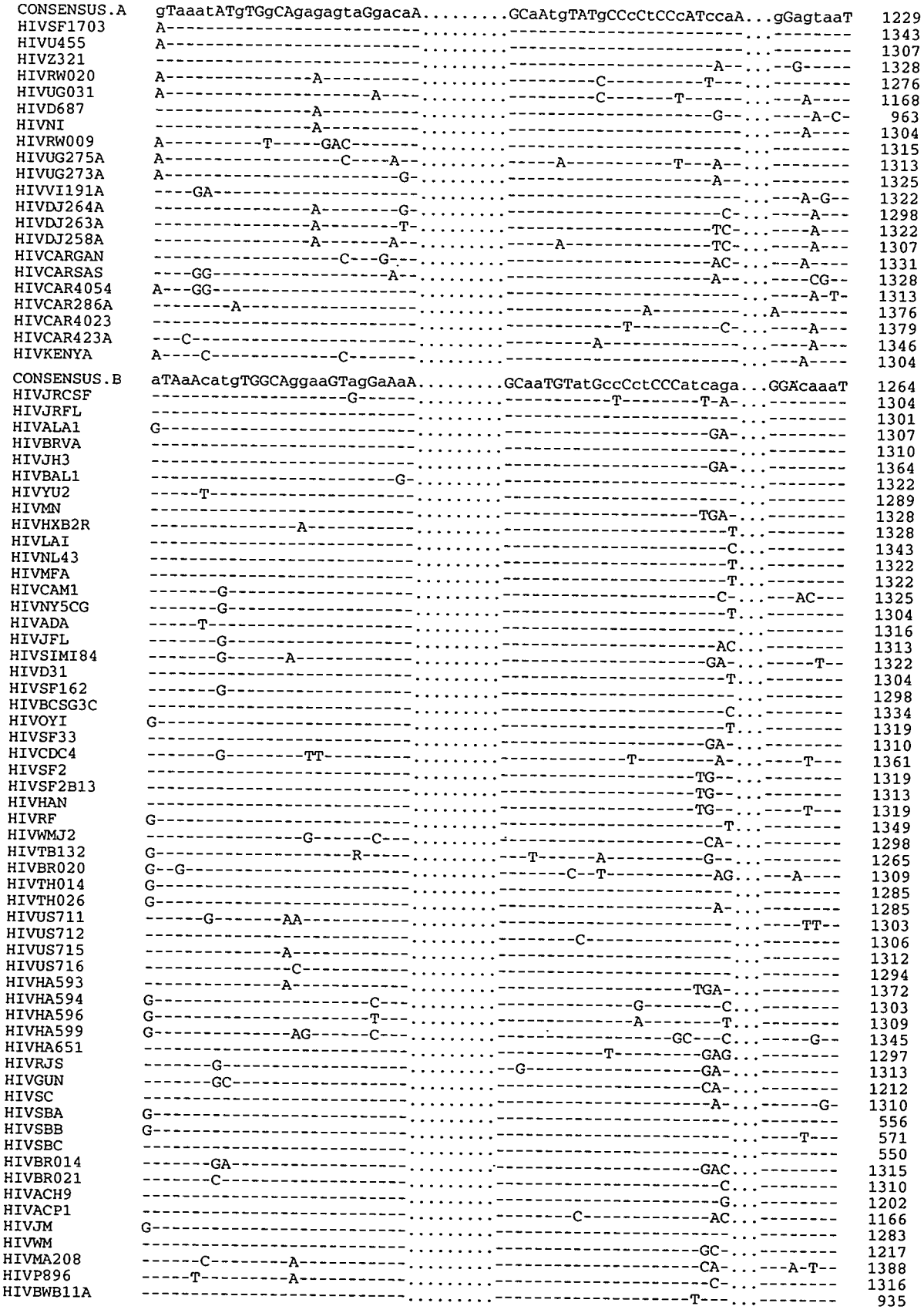
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HIVSF1703 A---------- 1343
HIVU455 A---------- 1307
HIVZ321 ---------- 1328
HIVRW020 A---------- 1276
HIVUG031 A---------- 1168
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HIVNI ---------- 1304
HIVRW009 A---------- 1315
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HIVVI191A ---------- 1322
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HIVDJ258A ---------- 1307
HIVCARGAN ---------- 1331
HIVCARSAS ---------- 1328
HIVCAR4054 A---------- 1313
HIVCAR286A ---------- 1376
HIVCAR4023 ---------- 1379
HIVCAR423A ---------- 1346
HIVKENYA A---------- 1304
CONSENSUS.B aTAaAcatgTGGCAggaaGTagGaAaA.....GCaaTGTatGccCctCCCatcaga...GGAcaaaT 1264
HIVJRCSF ---------- 1304
HIVJRFL ---------- 1301
HIVALA1 G---------- 1307
HIVBRVA ---------- 1310
HIVJH3 ---------- 1364
HIVBAL1 ---------- 1322
HIVYU2 ---------- 1289
HIVMN ---------- 1328
HIVHXB2R ---------- 1328
HIVLAI ---------- 1343
HIVNL43 ---------- 1322
HIVMFA ---------- 1322
HIVCAM1 ---------- 1325
HIVNY5CG ---------- 1304
HIVADA ---------- 1316
HIVJFL ---------- 1313
HIVSIMI84 ---------- 1322
HIVD31 ---------- 1304
HIVSF162 ---------- 1298
HIVBCSG3C ---------- 1334
HIVOYI G---------- 1319
HIVSF33 ---------- 1310
HIVCDC4 ---------- 1361
HIVSF2 ---------- 1319
HIVSF2B13 ---------- 1313
HIVHAN ---------- 1319
HIVRF G---------- 1349
HIVWMJ2 ---------- 1298
HIVTB132 G---------- 1265
HIVBR020 G---------- 1309
HIVTH014 G---------- 1285
HIVTH026 G---------- 1285
HIVUS711 ---------- 1303
HIVUS712 ---------- 1306
HIVUS715 ---------- 1312
HIVUS716 ---------- 1294
HIVHA593 ---------- 1372
HIVHA594 G---------- 1303
HIVHA596 G---------- 1309
HIVHA599 G---------- 1345
HIVHA651 ---------- 1297
HIVRJS ---------- 1313
HIVGUN ---------- 1212
HIVSC ---------- 1310
HIVSBA G---------- 556
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HIVSBC ---------- 550
HIVBR014 ---------- 1315
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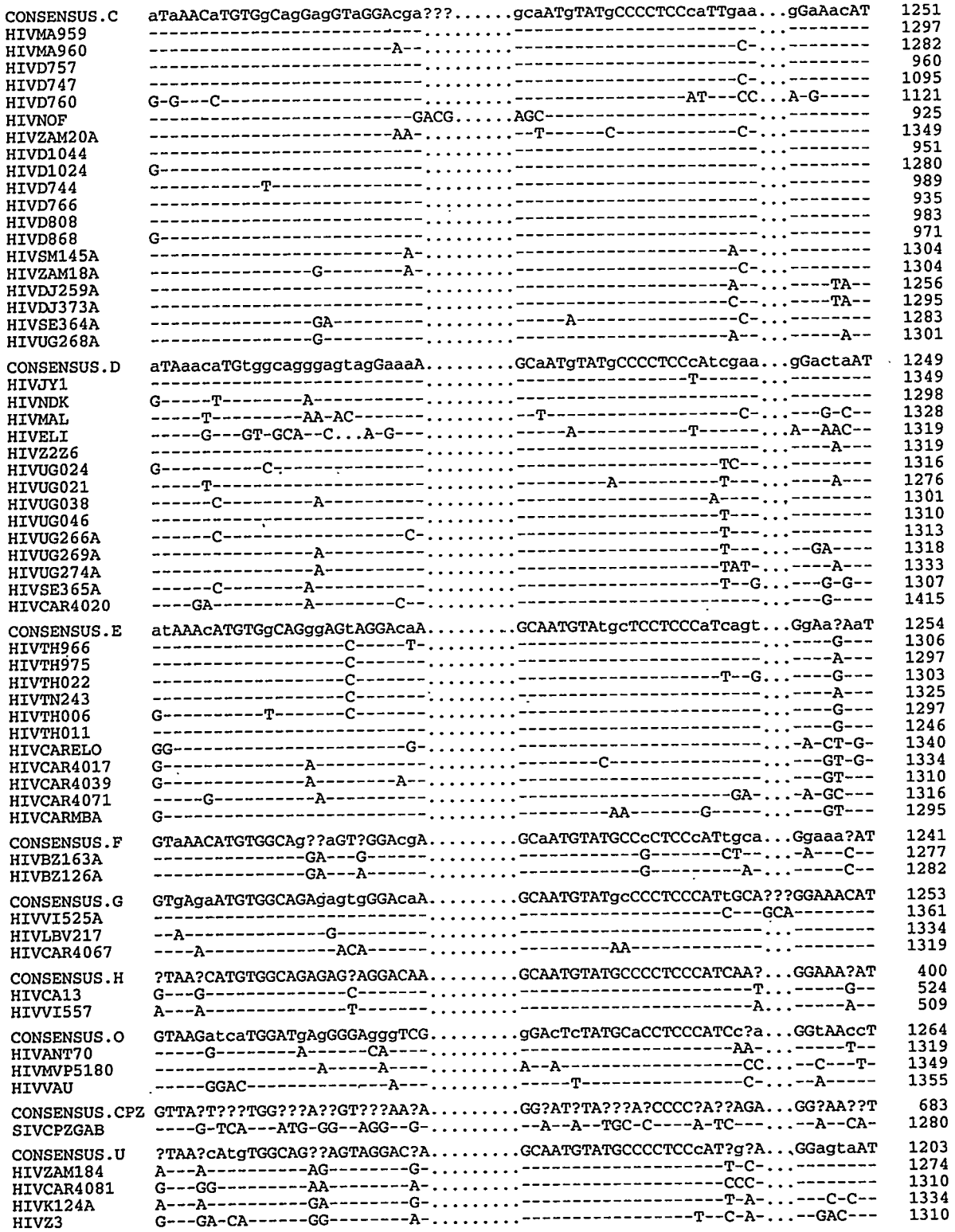
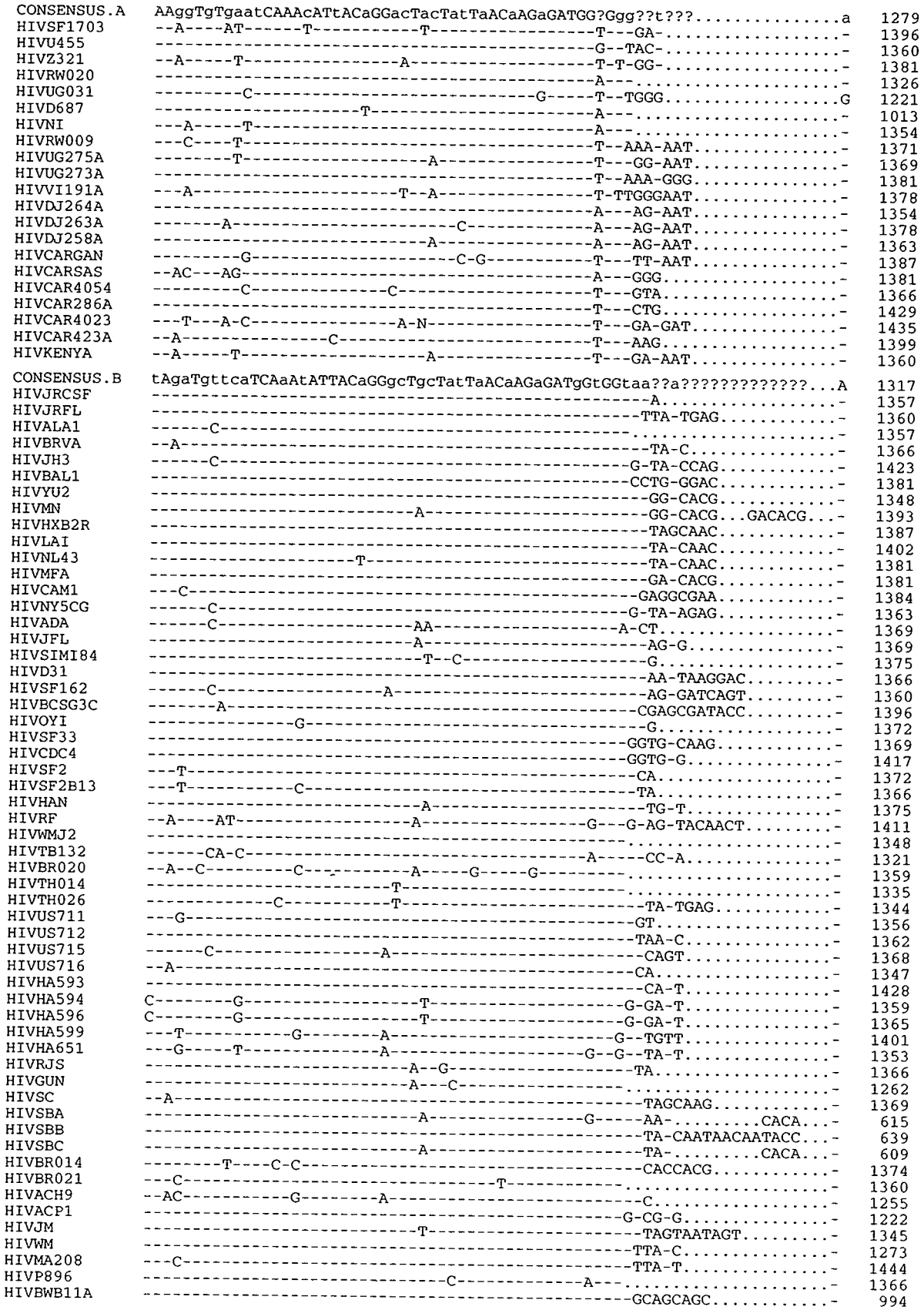


HIV1 ENV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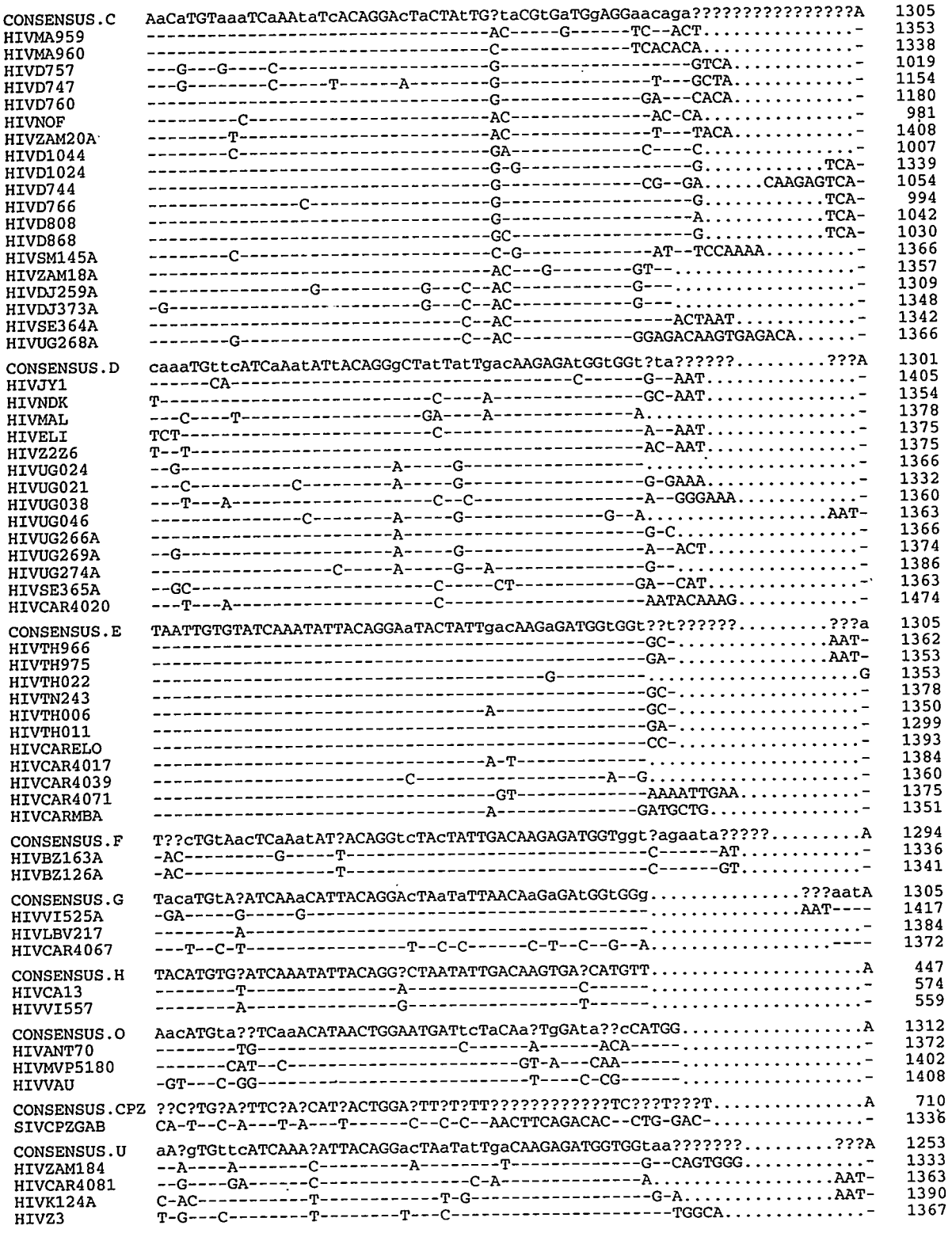
HIVSF1703 --A----AT------T----------T----------T---GA-.....- 1396
HIVU455 ----------G--TAC-.....- 1360
HIVZ321 --A-----T----------A----------T-T-GG-.....- 1381
HIVRW020 ----------A---.....- 1326
HIVUG031 ---------C----------G-----T--TGGG.....G 1221
HIVD687 ----------T----------A---.....- 1013
HIVNI ---A-----T----------A---.....- 1354
HIVRW009 ---C----T----------T--AAA-AAT.....- 1371
HIVUG275A --------T----------A----------T---GG-AAT.....- 1369
HIVUG273A ----------T--AAA-GGG.....- 1381
HIVVI191A ---A----------T--A----------T-TTGGGAAT.....- 1378
HIVDJ264A ----------A---AG-AAT.....- 1354
HIVDJ263A -------A----------C----------A---AG-AAT.....- 1378
HIVDJ258A ----------A----------A---AG-AAT.....- 1363
HIVCARGAN ---------G----------C-G----------T---TT-AAT.....- 1387
HIVCARSAS --AC---AG----------A---GGG.....- 1381
HIVCAR4054 ---------C----------C----------T---GTA.....- 1366
HIVCAR286A ----------T---CTG.....- 1429
HIVCAR4023 ---T---A-C----------A-N----------T---GA-GAT.....- 1435
HIVCAR423A --A----------C----------T---AAG.....- 1399
HIVKENYA --A-----T----------A----------T---GA-AAT.....- 1360
CONSENSUS.B tAgaTgttcaTCAaAtATTACaGGgcTgcTatTaACaAGaGATgGtGGtaa??a???????????...A 1317
HIVJRCSF ----------A.....- 1357
HIVJRFL ----------TTA-TGAG.....- 1360
HIVALA1 ------C----------..... 1357
HIVBRVA --A----------TA-C.....- 1366
HIVJH3 ------C----------G-TA-CCAG.....- 1423
HIVBAL1 ----------CCTG-GGAC.....- 1381
HIVYU2 ----------GG-CACG.....- 1348
HIVMN ----------A----------GG-CACG...GACACG...- 1393
HIVHXB2R ----------TAGCAAC.....- 1387
HIVLAI ----------TA-CAAC.....- 1402
HIVNL43 ----------T----------TA-CAAC.....- 1381
HIVMFA ----------GA-CACG.....- 1381
HIVCAM1 ---C----------GAGGCGAA.....- 1384
HIVNY5CG ------C----------G-TA-AGAG.....- 1363
HIVADA ------C----------AA----------A-CT.....- 1369
HIVJFL ----------A----------AG-G.....- 1369
HIVSIMI84 ----------T--C----------G.....- 1375
HIVD31 ----------AA-TAAGGAC.....- 1366
HIVSF162 ------C----------A----------AG-GATCAGT.....- 1360
HIVBCSG3C -------A----------CGAGCGATACC.....- 1396
HIVOYI ----------G----------G.....- 1372
HIVSF33 ----------GGTG-CAAG.....- 1369
HIVCDC4 ----------GGTG-G.....- 1417
HIVSF2 ---T----------CA.....- 1372
HIVSF2B13 ---T----------C----------TA.....- 1366
HIVHAN ----------A----------TG-T.....- 1375
HIVRF --A----AT----------A----------G---G-AG-TACAACT.....- 1411
HIVWMJ2 ----------..... 1348
HIVTB132 ------CA-C----------A-----CC-A.....- 1321
HIVBR020 --A--C---------C---------A-----G-----G---------..... 1359
HIVTH014 ----------T----------..... 1335
HIVTH026 ----------C----------T----------TA-TGAG.....- 1344
HIVUS711 ---G----------GT.....- 1356
HIVUS712 ----------TAA-C.....- 1362
HIVUS715 ------C----------A----------CAGT.....- 1368
HIVUS716 --A----------CA.....- 1347
HIVHA593 ----------CA-T.....- 1428
HIVHA594 C--------G----------T----------G-GA-T.....- 1359
HIVHA596 C--------G----------T----------G-GA-T.....- 1365
HIVHA599 ---T----------G--------A----------G--TGTT.....- 1401
HIVHA651 ---G-----T----------A----------G--G--TA-T.....- 1353
HIVRJS ----------A--G----------TA.....- 1366
HIVGUN ----------A---C----------..... 1262
HIVSC --A----------TAGCAAG.....- 1369
HIVSBA ----------A----------G-----AA-.....CACA...- 615
HIVSBB ----------TA-CAATAACAATACC...- 639
HIVSBC ----------A----------TA-.....CACA...- 609
HIVBR014 --------T----C-C----------CACCACG.....- 1374
HIVBR021 ---C----------T----------..... 1360
HIVACH9 --AC----------G--------A----------C.....- 1255
HIVACP1 ----------G-CG-G.....- 1222
HIVJM ----------T----------TAGTAATAGT.....- 1345
HIVWM ----------TTA-C.....- 1273
HIVMA208 ---C----------TTA-T.....- 1444
HIVP896 ----------C----------A---..... 1366
HIVBWB11A ----------GCAGCAGC.....- 994



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CONSENSUS.C  AaCaTGTaaaTCaAAtaTcACAGGAcTaCTAtTG?taCGtGaTGgAGGaacaga??????????????????A  1305
HIVMA959     ------------------------------------AC-----G------TC--ACT.................-  1353
HIVMA960     ------------------------------------C------------TCACACA................-  1338
HIVD757      ---G---G----C----------------------G---------------------GTCA............-  1019
HIVD747      ---G---------C-----T------A--------G---------------T---GCTA............-  1154
HIVD760      ------------------------------------G--------------GA---CACA............-  1180
HIVNOF       ---------C-------------------------AC--------------AC-CA.................-   981
HIVZAM20A    --------T-------------------------AC--------------T---TACA.............-  1408
HIVD1044     --------C-------------------------GA-------------C----C.................-  1007
HIVD1024     ------------------------------------G-G-----------------G...........TCA-  1339
HIVD744      ------------------------------------G--------------CG--GA......CAAGAGTCA-  1054
HIVD766      ---------------C--------------------G-------------------G............TCA-   994
HIVD808      ------------------------------------G-------------------A............TCA-  1042
HIVD868      ------------------------------------GC------------------G............TCA-  1030
HIVSM145A    --------C--------------------------C-G-------------AT--TCCAAAA.........-  1366
HIVZAM18A    ------------------------------------AC---G--------GT--.................-  1357
HIVDJ259A    ----------------G----------G---C--AC------------G---.................-  1309
HIVDJ373A    -G---------------------------G---C--AC------------G---.................-  1348
HIVSE364A    ------------------------------C--AC---------------ACTAAT.............-  1342
HIVUG268A    --------G----------------------C--AC------------GGAGACAAGTGAGACA......-  1366

CONSENSUS.D  caaaTGttcATCaAatATtACAGGgCTatTatTgacAAGAGAtGGtGGt?ta??????.........???A  1301
HIVJY1       ------CA-----------------------------------------C------G--AAT.............-  1405
HIVNDK       T-------------------------C----A--------------GC-AAT.................-  1354
HIVMAL       ---C----T-----------------GA----A-------------A.....................-  1378
HIVELI       TCT-------------------------C--------------------A--AAT.............-  1375
HIVZ2Z6      T--T-------------------------------------------------AC-AAT.........-  1375
HIVUG024     --G---------------------A-----G-----------------.....................-  1366
HIVUG021     ---C----------C---------A-----G-----------------G-GAAA.............-  1332
HIVUG038     ---T---A-------------------C--C-----------------A--GGGAAA..........-  1360
HIVUG046     ---------------C--------A-----G-------------G--A.................AAT-  1363
HIVUG266A    ----------------------A-----------------------G-C.................-  1366
HIVUG269A    --G---------------------A-----G-----------------A--ACT.............-  1374
HIVUG274A    ------------------C-----A-----G--A---------------G--.................-  1386
HIVSE365A    --GC-----------------------C-----CT------------GA--CAT.............-  1363
HIVCAR4020   ---T---A--------------------C--------------------AATACAAAG.........-  1474

CONSENSUS.E  TAATTGTGTATCAAATATTACAGGAaTACTATTgacAAGaGATGGtGGt??t??????.........???a  1305
HIVTH966     ------------------------------------------------------GC-.............AAT-  1362
HIVTH975     ------------------------------------------------------GA-.............AAT-  1353
HIVTH022     ---------------------------------------G--------.....................G  1353
HIVTN243     ------------------------------------------------------GC-.............-  1378
HIVTH006     ----------------------------------A---------------GC-.................-  1350
HIVTH011     ------------------------------------------------------GA-.............-  1299
HIVCARELO    ------------------------------------------------------CC-.............-  1393
HIVCAR4017   ----------------------------------A-T-------------.....................-  1384
HIVCAR4039   ------------------------C-------------------A--G.....................-  1360
HIVCAR4071   ----------------------------------GT-------------AAAATTGAA...........-  1375
HIVCARMBA    ----------------------------------A--------------GATGCTG.............-  1351

CONSENSUS.F  T??cTGtAacTCaAatAT?ACAGGtcTAcTATTGACAAGAGATGGTggt?agaata?????.........A  1294
HIVBZ163A    -AC---------G-----T-------------------------------C------AT..........-  1336
HIVBZ126A    -AC---------------T-------------------------------C------GT..........-  1341

CONSENSUS.G  TacaTGtA?ATCAAaCATTACAGGAcTAaTaTTAACAaGaGAtGGtGGg..............???aatA  1305
HIVVI525A    -GA-----G-----G-----------------------------------.............AAT----  1417
HIVLBV217    --------A-----------------------------------------.....................-  1384
HIVCAR4067   ---T--C-T---------------T--C-C------C-T--C--G--A.....................----  1372

CONSENSUS.H  TACATGTG?ATCAAATATTACAGG?CTAATATTGACAAGTGA?CATGTT.....................A   447
HIVCA13      --------T---------------A-----------------C------.....................-   574
HIVVI557     --------A---------------G-----------------T------.....................-   559

CONSENSUS.O  AacATGta??TCaaACATAACTGGAATGATtcTaCAa?TgGAta??cCATGG..................A  1312
HIVANT70     ---------TG--------------------C------A------ACA-----.................-  1372
HIVMVP5180   --------CAT--C----------------------GT-A---CAA------.................-  1402
HIVVAU       -GT---C-GG-------------------------T----C-CG------.....................-  1408

CONSENSUS.CPZ ??C?TG?A?TTC?A?CAT?ACTGGA?TT?T?TT?????????????TC???T???T.............A   710
SIVCPZGAB    CA-T--C-A---T-A---T------C--C-C--AACTTCAGACAC--CTG-GAC-.............-  1336

CONSENSUS.U  aA?gTGttcATCAAA?ATTACAGGacTAaTatTgaCAAGAGATGGTGGtaa???????.........???A  1253
HIVZAM184    --A----A-------C---------A--------T-------------G--CAGTGGG..........-  1333
HIVCAR4081   --G----GA------C---------------C-A-------------A.................AAT-  1363
HIVK124A     C-AC----------T-----------T-G----------------G-A.................AAT-  1390
HIVZ3        T-G---C--------T--------T---C--------------------TGGCA.............-  1367
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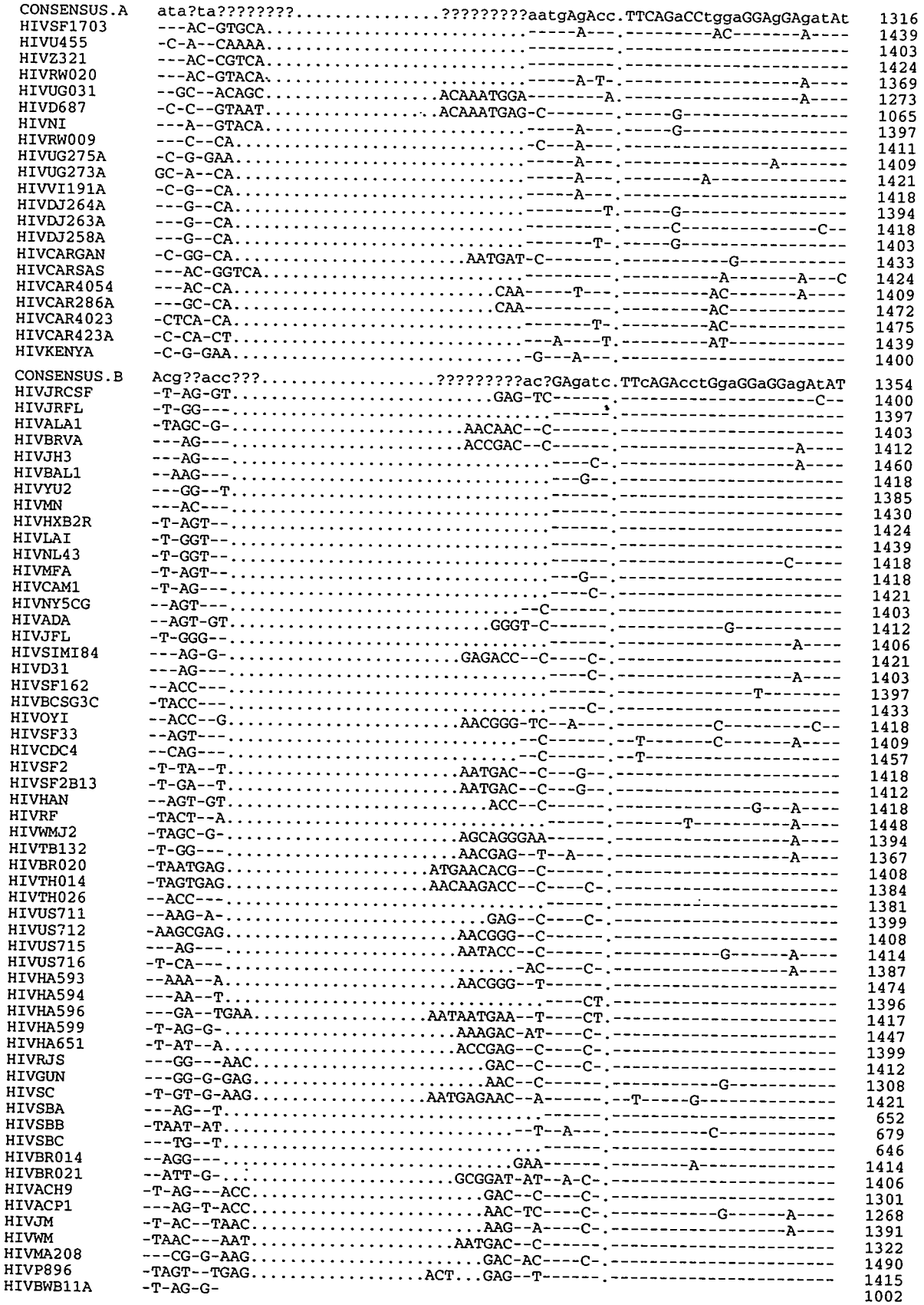
HIV1 ENV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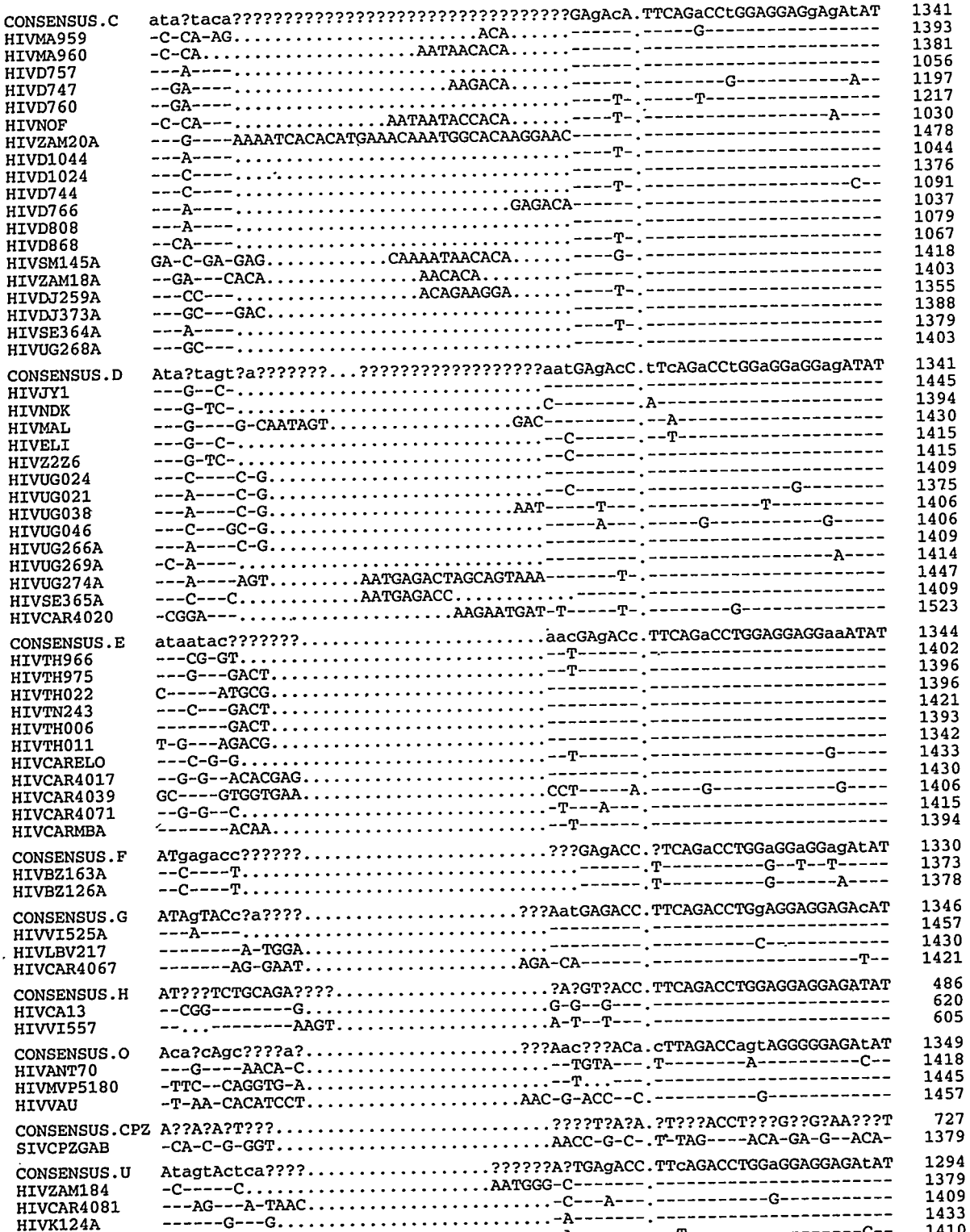
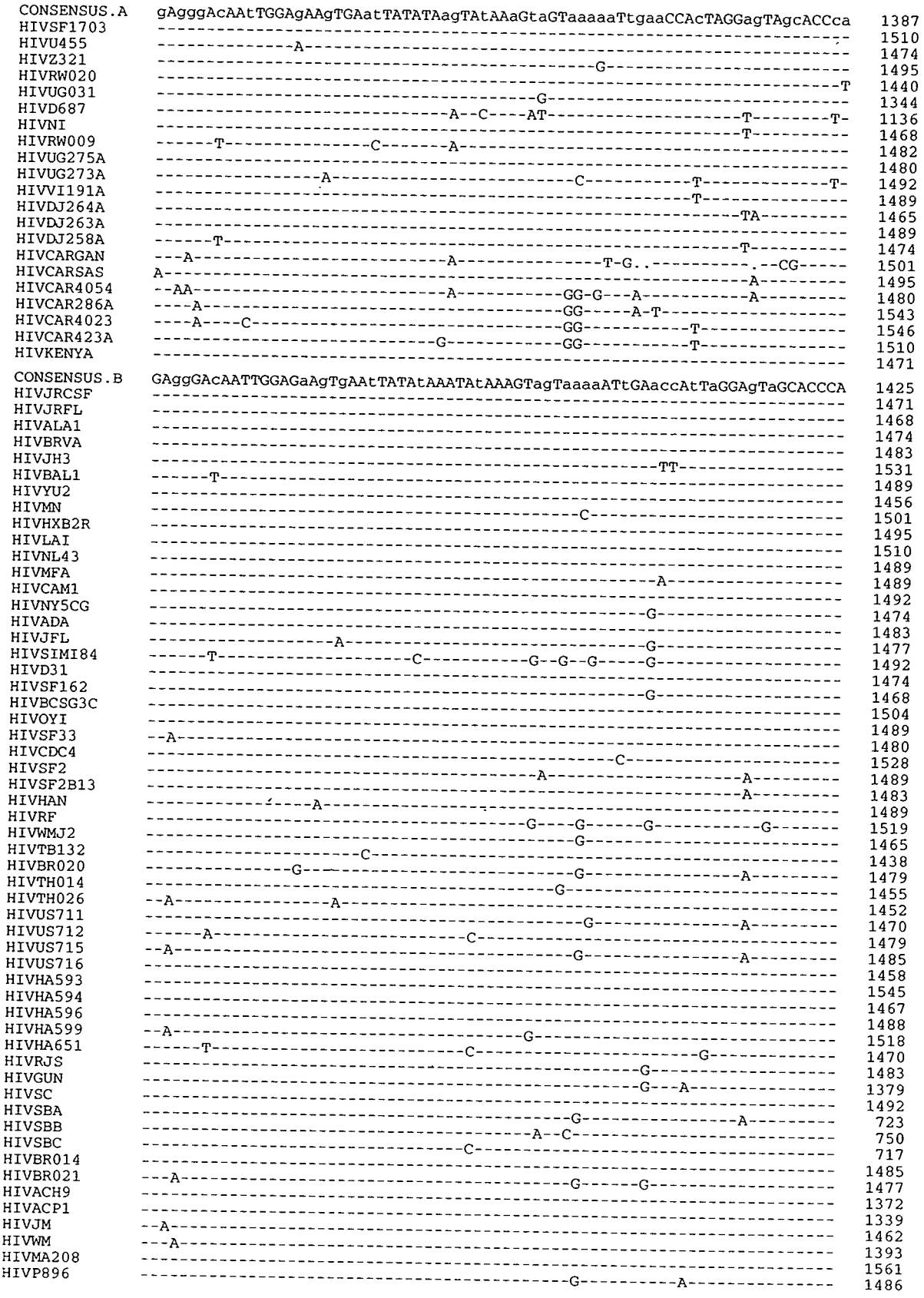
HIVSF1703 ---AC-GTGCA.....-----A---.---------AC-------A---- 1439
HIVU455 -C-A--CAAAA.....---------.---------- 1403
HIVZ321 ---AC-CGTCA.....---------.---------- 1424
HIVRW020 ---AC-GTACA.....-----A-T-.----------A---- 1369
HIVUG031 --GC--ACAGC.....ACAAATGGA--------A.----------A---- 1273
HIVD687 -C-C--GTAAT.....ACAAATGAG-C--------.-----G---------- 1065
HIVNI ---A--GTACA.....-----A---.-----G---------- 1397
HIVRW009 ---C--CA.....-C---A---.---------- 1411
HIVUG275A -C-G-GAA.....-----A---.----------A------- 1409
HIVUG273A GC-A--CA.....-----A---.--------A--------- 1421
HIVVI191A -C-G--CA.....-----A---.---------- 1418
HIVDJ264A ---G--CA.....---------T.-----G---------- 1394
HIVDJ263A ---G--CA.....---------.-----C----------C-- 1418
HIVDJ258A ---G--CA.....-------T-.-----G---------- 1403
HIVCARGAN -C-GG-CA.....AATGAT-C--------.----------G---------- 1433
HIVCARSAS ---AC-GGTCA.....---------.----------A-------A---C 1424
HIVCAR4054 ---AC-CA.....CAA-----T---.---------AC-------A---- 1409
HIVCAR286A ---GC-CA.....CAA---------.---------AC---------- 1472
HIVCAR4023 -CTCA-CA.....-------T-.---------AC---------- 1475
HIVCAR423A -C-CA-CT.....---A----T.---------AT---------- 1439
HIVKENYA -C-G-GAA.....-G---A---.---------- 1400
CONSENSUS.B Acg??acc???.....????????ac?GAgatc.TTcAGAcctGgaGGaGGagAtAT 1354
HIVJRCSF -T-AG-GT.....GAG-TC------.----------C-- 1400
HIVJRFL -T-GG---.....------.---------- 1397
HIVALA1 -TAGC-G-.....AACAAC--C------.---------- 1403
HIVBRVA ---AG---.....ACCGAC--C------.----------A---- 1412
HIVJH3 ---AG---.....----C-.----------A---- 1460
HIVBAL1 --AAG---.....---G--.---------- 1418
HIVYU2 ---GG--T.....------.---------- 1385
HIVMN ---AC---.....------.---------- 1430
HIVHXB2R -T-AGT--.....------.---------- 1424
HIVLAI -T-GGT--.....------.---------- 1439
HIVNL43 -T-GGT--.....------.----------C----- 1418
HIVMFA -T-AGT--.....---G--.---------- 1418
HIVCAM1 -T-AG---.....----C-.---------- 1421
HIVNY5CG --AGT---.....--C------.---------- 1403
HIVADA --AGT-GT.....GGGT-C------.----------G---------- 1412
HIVJFL -T-GGG--.....------.----------A---- 1406
HIVSIMI84 ---AG-G-.....GAGACC--C----C-.---------- 1421
HIVD31 ---AG---.....----C-.----------A---- 1403
HIVSF162 --ACC---.....------.----------T-------- 1397
HIVBCSG3C -TACC---.....----C-.---------- 1433
HIVOYI --ACC--G.....AACGGG-TC--A---.----------C---------C-- 1418
HIVSF33 --AGT---.....--C------.--T-------C-------A---- 1409
HIVCDC4 --CAG---.....--C------.--T---------- 1457
HIVSF2 -T-TA--T.....AATGAC--C---G--.---------- 1418
HIVSF2B13 -T-GA--T.....AATGAC--C---G--.---------- 1412
HIVHAN --AGT-GT.....ACC--C------.----------G---A---- 1418
HIVRF -TACT--A.....------.-------T----------A---- 1448
HIVWMJ2 -TAGC-G-.....AGCAGGGAA------.----------A---- 1394
HIVTB132 -T-GG---.....AACGAG--T--A---.----------A---- 1367
HIVBR020 -TAATGAG.....ATGAACACG--C------.---------- 1408
HIVTH014 -TAGTGAG.....AACAAGACC--C----C-.---------- 1384
HIVTH026 --ACC---.....------.---------- 1381
HIVUS711 --AAG-A-.....GAG--C----C-.---------- 1399
HIVUS712 -AAGCGAG.....AACGGG--C------.---------- 1408
HIVUS715 ---AG---.....AATACC--C------.----------G------A---- 1414
HIVUS716 -T-CA---.....-AC----C-.----------A---- 1387
HIVHA593 --AAA--A.....AACGGG--T------.---------- 1474
HIVHA594 ---AA--T.....----CT.---------- 1396
HIVHA596 ---GA--TGAA.....AATAATGAA--T----CT.---------- 1417
HIVHA599 -T-AG-G-.....AAAGAC-AT----C-.---------- 1447
HIVHA651 -T-AT--A.....ACCGAG--C----C-.---------- 1399
HIVRJS ---GG---AAC.....GAC--C----C-.---------- 1412
HIVGUN ---GG-G-GAG.....AAC--C------.----------G---------- 1308
HIVSC -T-GT-G-AAG.....AATGAGAAC--A------.--T-----G---------- 1421
HIVSBA ---AG--T.....------.---------- 652
HIVSBB -TAAT-AT.....--T--A---.----------C---------- 679
HIVSBC ---TG--T.....------.---------- 646
HIVBR014 --AGG---.....GAA------.--------A---------- 1414
HIVBR021 --ATT-G-.....GCGGAT-AT--A-C-.---------- 1406
HIVACH9 -T-AG---ACC.....GAC--C----C-.---------- 1301
HIVACP1 ---AG-T-ACC.....AAC-TC----C-.----------G------A---- 1268
HIVJM -T-AC--TAAC.....AAG--A----C-.----------A---- 1391
HIVWM -TAAC---AAT.....AATGAC--C------.---------- 1322
HIVMA208 ---CG-G-AAG.....GAC-AC----C-.---------- 1490
HIVP896 -TAGT--TGAG.....ACT...GAG--T------.---------- 1415
HIVBWB11A -T-AG-G- 1002

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HIVSF1703 1510
HIVU455 1474
HIVZ321 1495
HIVRW020 1440
HIVUG031 1344
HIVD687 1136
HIVNI 1468
HIVRW009 1482
HIVUG275A 1480
HIVUG273A 1492
HIVVI191A 1489
HIVDJ264A 1465
HIVDJ263A 1489
HIVDJ258A 1474
HIVCARGAN 1501
HIVCARSAS 1495
HIVCAR4054 1480
HIVCAR286A 1543
HIVCAR4023 1546
HIVCAR423A 1510
HIVKENYA 1471
CONSENSUS.B GAggGAcAATTGGAGaAgTgAAtTATAtAAATAtAAAGTagTaaaaATtGAaccAtTaGGAgTaGCACCCA 1425
HIVJRCSF 1471
HIVJRFL 1468
HIVALA1 1474
HIVBRVA 1483
HIVJH3 1531
HIVBAL1 1489
HIVYU2 1456
HIVMN 1501
HIVHXB2R 1495
HIVLAI 1510
HIVNL43 1489
HIVMFA 1489
HIVCAM1 1492
HIVNY5CG 1474
HIVADA 1483
HIVJFL 1477
HIVSIMI84 1492
HIVD31 1474
HIVSF162 1468
HIVBCSG3C 1504
HIVOYI 1489
HIVSF33 1480
HIVCDC4 1528
HIVSF2 1489
HIVSF2B13 1483
HIVHAN 1489
HIVRF 1519
HIVWMJ2 1465
HIVTB132 1438
HIVBR020 1479
HIVTH014 1455
HIVTH026 1452
HIVUS711 1470
HIVUS712 1479
HIVUS715 1485
HIVUS716 1458
HIVHA593 1545
HIVHA594 1467
HIVHA596 1488
HIVHA599 1518
HIVHA651 1470
HIVRJS 1483
HIVGUN 1379
HIVSC 1492
HIVSBA 723
HIVSBB 750
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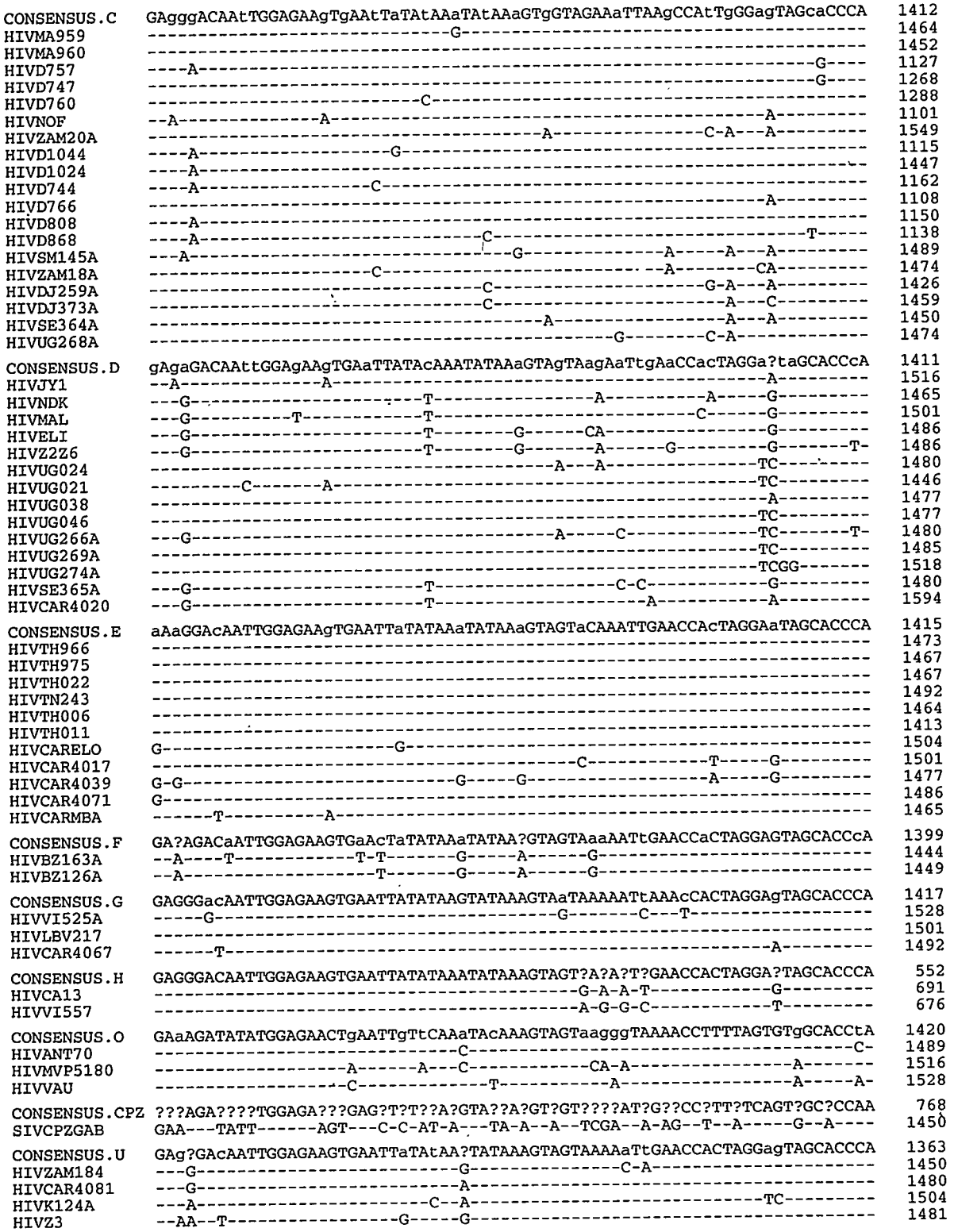
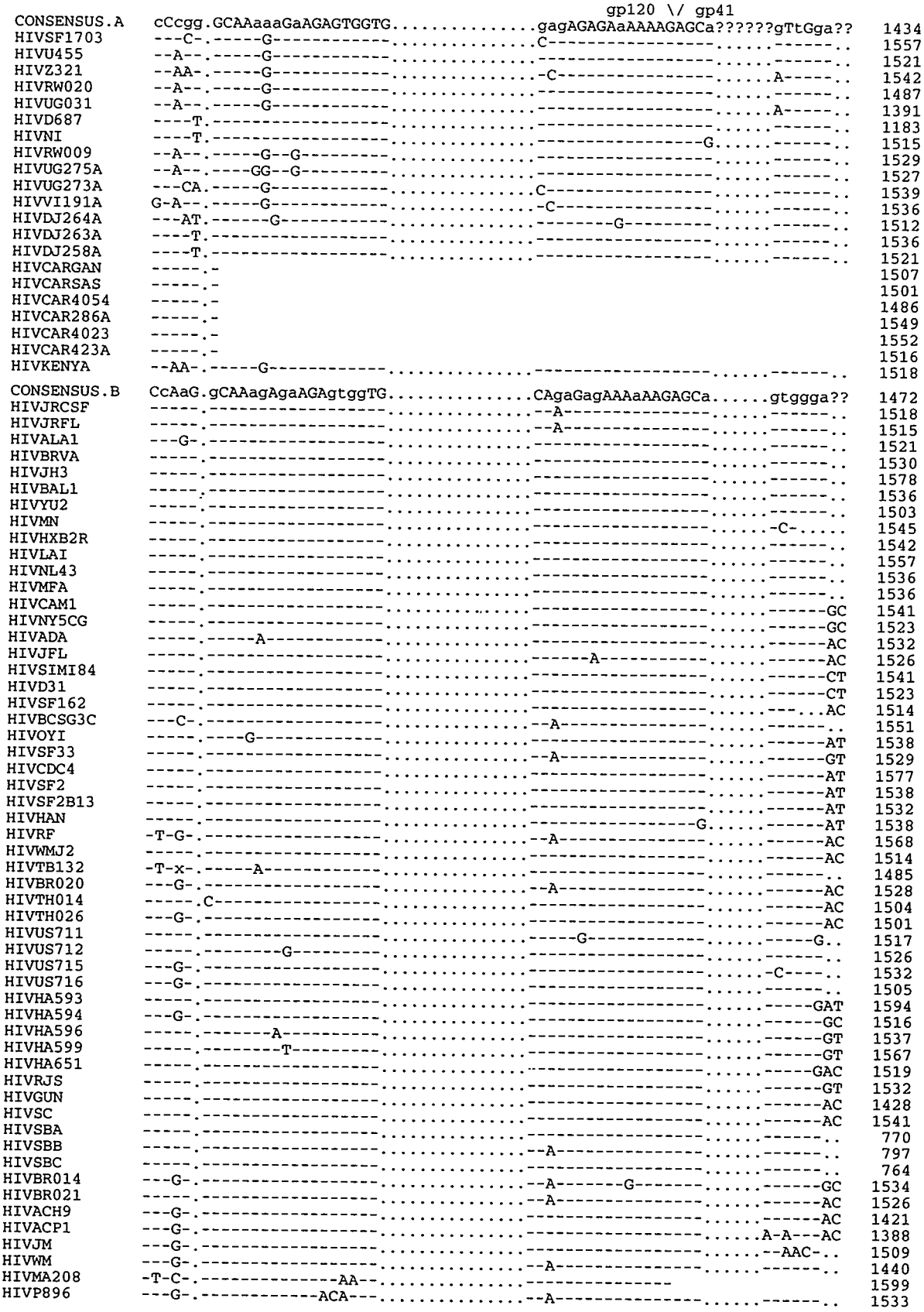
HIVMA208 1561
HIVP896 1486




gp120 \/ gp41
CONSENSUS.A cCcgg.GCAAaaaGaAGAGTGGTG.....gagAGAGAaAAAAGAGCa??????gTtGga?? 1434
HIVSF1703 ---C-.-----G----------.....C----------.....------.. 1557
HIVU455 --A--.-----G----------.....----------.....------.. 1521
HIVZ321 --AA-.-----G----------.....-C----------.....A-----.. 1542
HIVRW020 --A--.-----G----------.....----------.....------.. 1487
HIVUG031 --A--.-----G----------.....----------.....A-----.. 1391
HIVD687 ----T.----------.....----------.....------.. 1183
HIVNI ----T.----------.....----------G.....------.. 1515
HIVRW009 --A--.-----G--G---------.....----------.....------.. 1529
HIVUG275A --A--.----GG--G---------.....----------.....------.. 1527
HIVUG273A ---CA.-----G----------.....C----------.....------.. 1539
HIVVI191A G-A--.-----G----------.....-C----------.....------.. 1536
HIVDJ264A ---AT.------G---------.....--------G---------.....------.. 1512
HIVDJ263A ----T.----------.....----------.....------.. 1536
HIVDJ258A ----T.----------.....----------.....------.. 1521
HIVCARGAN -----.- 1507
HIVCARSAS -----.- 1501
HIVCAR4054 -----.- 1486
HIVCAR286A -----.- 1549
HIVCAR4023 -----.- 1552
HIVCAR423A -----.- 1516
HIVKENYA --AA-.-----G----------.....----------.....------.. 1518
CONSENSUS.B CcAaG.gCAAagAgaAGAgtggTG.....CAgaGagAAAaAAGAGCa.....gtggga?? 1472
HIVJRCSF -----.----------.....--A----------.....------.. 1518
HIVJRFL -----.----------.....--A----------.....------.. 1515
HIVALA1 ---G-.----------.....----------.....------.. 1521
HIVBRVA -----.----------.....----------.....------.. 1530
HIVJH3 -----.----------.....----------.....------.. 1578
HIVBAL1 -----.----------.....----------.....------.. 1536
HIVYU2 -----.----------.....----------.....------.. 1503
HIVMN -----.----------.....----------.....-C-..... 1545
HIVHXB2R -----.----------.....----------.....------.. 1542
HIVLAI -----.----------.....----------.....------.. 1557
HIVNL43 -----.----------.....----------.....------.. 1536
HIVMFA -----.----------.....----------.....------.. 1536
HIVCAM1 -----.----------.....----------.....------GC 1541
HIVNY5CG -----.----------.....----------.....------GC 1523
HIVADA -----.-----A----------.....----------.....------AC 1532
HIVJFL -----.----------.....------A----------.....------AC 1526
HIVSIMI84 -----.----------.....----------.....------CT 1541
HIVD31 -----.----------.....----------.....------CT 1523
HIVSF162 -----.----------.....----------.....---...AC 1514
HIVBCSG3C ---C-.----------.....--A----------.....------.. 1551
HIVOYI -----.----G----------.....----------.....------AT 1538
HIVSF33 -----.----------.....--A----------.....------GT 1529
HIVCDC4 -----.----------.....----------.....------AT 1577
HIVSF2 -----.----------.....----------.....------AT 1538
HIVSF2B13 -----.----------.....----------.....------AT 1532
HIVHAN -----.----------.....----------G.....------AT 1538
HIVRF -T-G-.----------.....--A----------.....------AC 1568
HIVWMJ2 -----.----------.....----------.....------AC 1514
HIVTB132 -T-x-.-----A----------.....----------.....------.. 1485
HIVBR020 ---G-.----------.....--A----------.....------AC 1528
HIVTH014 -----.C----------.....----------.....------AC 1504
HIVTH026 ---G-.----------.....----------.....------AC 1501
HIVUS711 -----.----------.....-----G----------.....-----G.. 1517
HIVUS712 -----.--------G---------.....----------.....------.. 1526
HIVUS715 ---G-.----------.....----------.....-C----.. 1532
HIVUS716 ---G-.----------.....----------.....------.. 1505
HIVHA593 -----.----------.....----------.....-----GAT 1594
HIVHA594 ---G-.----------.....----------.....------GC 1516
HIVHA596 -----.-------A---------.....----------.....------GT 1537
HIVHA599 -----.--------T---------.....----------.....------GT 1567
HIVHA651 -----.----------.....----------.....-----GAC 1519
HIVRJS -----.----------.....----------.....------GT 1532
HIVGUN -----.----------.....----------.....------AC 1428
HIVSC -----.----------.....----------.....------AC 1541
HIVSBA -----.----------.....----------.....------.. 770
HIVSBB -----.----------.....--A----------.....------.. 797
HIVSBC -----.----------.....----------.....------.. 764
HIVBR014 ---G-.----------.....--A-------G-------.....------GC 1534
HIVBR021 -----.----------.....--A----------.....------AC 1526
HIVACH9 ---G-.----------.....----------.....------AC 1421
HIVACP1 ---G-.----------.....----------.....A-A---AC 1388
HIVJM ---G-.----------.....----------.....--AAC-.. 1509
HIVWM ---G-.----------.....--A----------.....------.. 1440
HIVMA208 -T-C-.----------AA--.....---------- 1599
HIVP896 ---G-.----------ACA---.....--A----------.....------.. 1533

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                                                                gp120 \/ gp41
CONSENSUS.C   CTa?g.gCaAAAAGgAGAGTGGTG??????.........gagagaGaaAAaAGAGCA......Gtggga??   1458
HIVMA959      ---A-.------------------.............------------------.....------..   1511
HIVMA960      --GA-.------------------.............------------------.....------..   1499
HIVD757       ---CT.------------------.............------------------.....------..   1174
HIVD747       ---CT.------------------.............------------------.....------..   1315
HIVD760       ---CA.------------------.............------------------.....------..   1335
HIVNOF        --GGA.T----------------.............------------------.....------..   1148
HIVZAM20A     --GG-.C-C--------------GAGAAG.......C---T---G--G------.....------..   1602
HIVD1044      ---CA.C----------------.............------------------.....------..   1162
HIVD1024      --GCA.-----------------.............------------------.....------..   1494
HIVD744       --GCA.-----------------.............-------G----------.....------..   1209
HIVD766       --GCA.-----------------.............------------------.....------..   1155
HIVD808       ---CA.-----------------.............------------------.....------..   1197
HIVD868       ---CA.-----------------.............------------------.....------..   1185
HIVSM145A     --GG-.-----------------.............------------------.....------..   1536
HIVZAM18A     --GC-.----------------GAG...........AC----------------.....------..   1524
HIVDJ259A     ---A-.-----------------.............-G----------------.....-CA.....   1470
HIVDJ373A     ---A-.-----------------.............------------------.....-CA.....   1503
HIVSE364A     ---A-.-----------------.............------------------.....------..   1497
HIVUG268A     ---A-.-----------------.............------------------.....------..   1521

CONSENSUS.D   Cca?g.gCAAagAGaAGAGTGGTG.............gaaAGAGAAaAAAGAGCA......ATAGGA..   1457
HIVJY1        ---G-.-----------------.............------------------.....------..   1563
HIVNDK        ---A-.----G------------.............------------------.....------..   1512
HIVMAL        ---A-.-----------------.............------------------.....------..   1548
HIVELI        ---G-.-----------------.............------------------.....------..   1533
HIVZ2Z6       ---G-.-----------------.............------------------.....------..   1533
HIVUG024      ---G-.-----------------.............-C----------------.....------..   1527
HIVUG021      ---A-.----G------------.............------------------.....------..   1493
HIVUG038      ---T-.T----------------.............--G---------------.....------..   1524
HIVUG046      -TGA-.-----------------.............------------------.....------..   1524
HIVUG266A     ---G-.-----------------.............------------------.....------..   1527
HIVUG269A     ---C-.-----------------.............------------------.....------..   1532
HIVUG274A     ---G-.-----A--G--------.............------------------.....------..   1565
HIVSE365A     ---CA.-----------------.............A-----------------.....------..   1527
HIVCAR4020    --CG-.-                                                               1600

CONSENSUS.E   CCaGG.GCAAAGAGAAGAGTGGTG.............GAGAGAGAAAAAAGAGCA......GTGGGA..   1462
HIVTH966      -----.-----------------.............------------------.....------..   1520
HIVTH975      -----.-----------------.............------------------.....------..   1514
HIVTH022      -----.-----------------.............------------------.....------..   1514
HIVTN243      -----.-----------------.............------------------.....------..   1539
HIVTH006      -----.-----------------.............------------------.....------..   1511
HIVTH011      -----.-----------------.............------------------.....------..   1460
HIVCARELO     --C--.-                                                               1510
HIVCAR4017    --C--.-                                                               1507
HIVCAR4039    --C--.-                                                               1483
HIVCAR4071    --C--.-                                                               1492
HIVCARMBA     --C--.-                                                               1471

CONSENSUS.F   CCAgg.GCAAaaAGAcaAGTGGTg.............aaGAGAGaAAaAAGAGCA?????GTgGGA..   1446
HIVBZ163A     -----.-----------------.............-G----------------.....------..   1491
HIVBZ126A     -----.----------------A.............------------------GTA...------..   1499

CONSENSUS.G   CCagG.GCAAGGAGAAGAGTGGTG.............G?GAGAGAAAAAAGAGCA......ATT???..   1460
HIVVI525A     -----.-----------------.............-A----------------.....---GGA..   1575
HIVLBV217     ---A-.-----------------.............-G----------------.....---.....   1545
HIVCAR4067    --C--.-                                                               1498

CONSENSUS.H   C?A?G.GCAA?GAGAAGAGTGGTG.............G??AGAGAAAAAAGAGC?......GT?GGA..    592
HIVCA13       -T-A-.----A------------.............-GG--------------A.......--T---..    738
HIVVI557      -C-G-.----G------------.............-AA--------------T.......--G---..    723

CONSENSUS.O   CAaaa.ATtgCAAGgCCAatcATAggcAcT?g?aCt???CAtAGaGAaAAAAGAGCA......GtAGGa..   1477
HIVANT70      --CGT.------------G-----A-----A-A---...-----------------.....------..   1548
HIVMVP5180    -----.--GT----A-----A---AA--T-CAC--CCCT--C--G------------.....------..   1578
HIVVAU        -----.-------------CT-----A---A-AT--...--------G---------.....-C---T..   1587

CONSENSUS.CPZ CAA?A.G??A?AAGGC?????G????AA?ACA??A?...??CAGACA?AAAAGAG??...????T?GG?..    802
SIVCPZGAB     ---A-.-CA-G-----ATACA-TGGC--G---GA-A...GA------G-------CA...GCCT-C--T..   1512

CONSENSUS.U   CCagg.gCAAagAGAAGAGTGGTG.............GAgAGAGAAAAAAGAGCA......gT?GGa..   1409
HIVZAM184     ---A-.C---G------------.............------------------.....--T---..   1497
HIVCAR4081    --C--.-                                                               1486
HIVK124A      ----C.-----------------.............--A----------------.....A-A---..   1551
HIVZ3         -----.-----A-----------.............------------------.....--G--G..   1528
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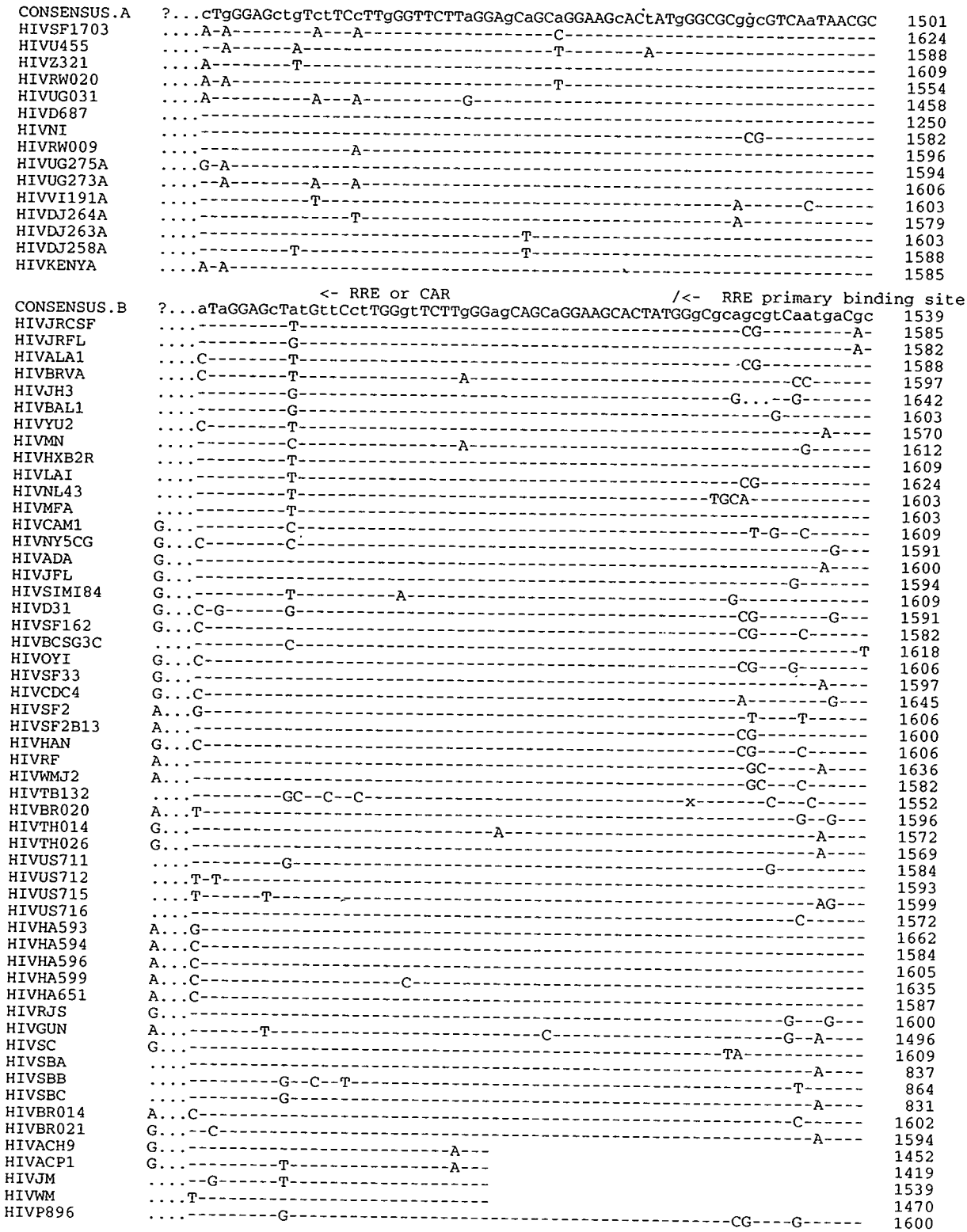
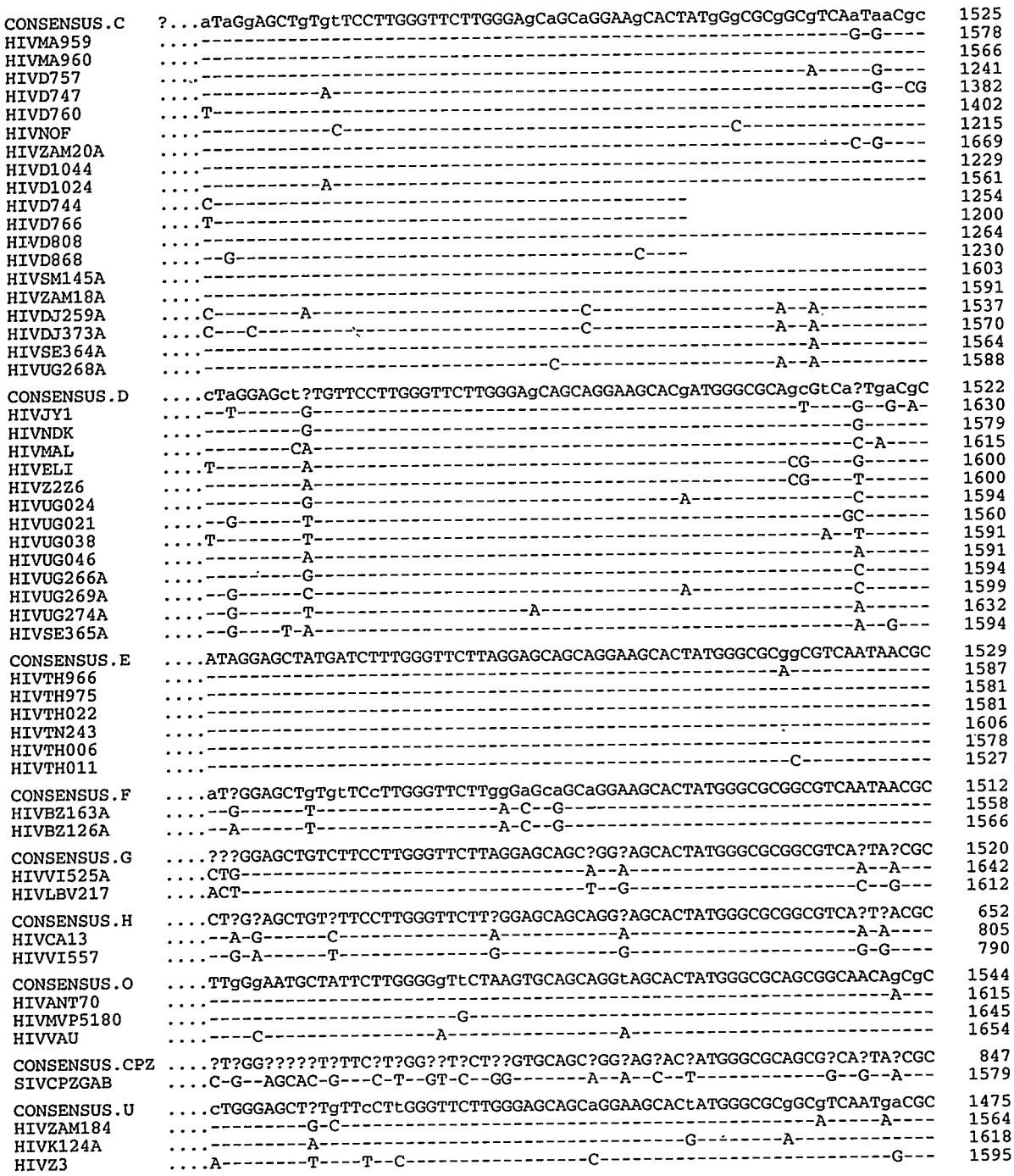
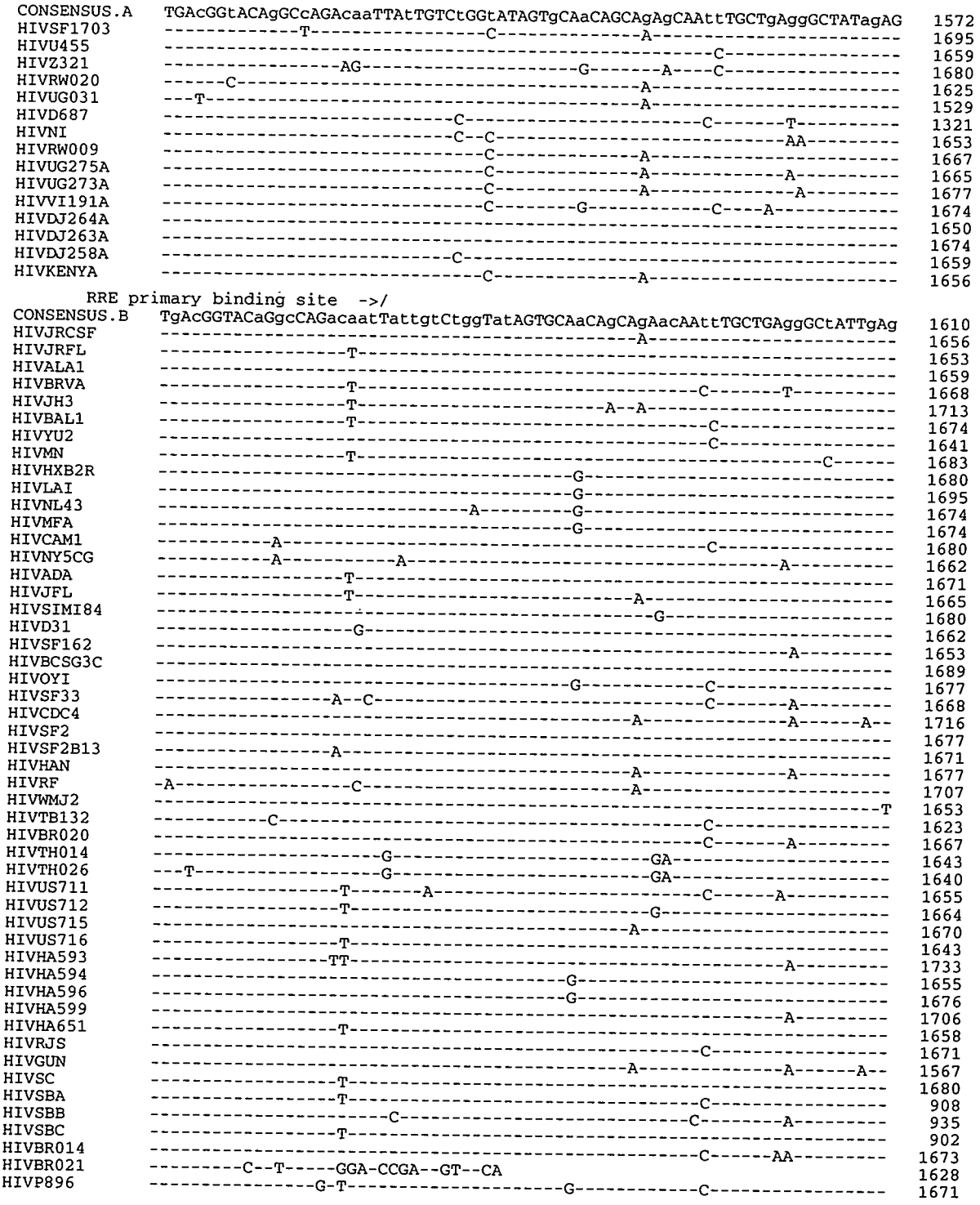
HIV1 ENV


CONSENSUS.A ?...cTgGGAGctgTctTCcTTgGGTTCTTaGGAgCaGCaGGAAGcACtATgGGCGCggcGTCAaTAACGC 1501
HIVSF1703 ....A-A--------A---A----------C---------- 1624
HIVU455 ....--A------A----------T--------A---------- 1588
HIVZ321 ....A--------T---------- 1609
HIVRW020 ....A-A----------T---------- 1554
HIVUG031 ....A----------A---A----------G---------- 1458
HIVD687 ....---------- 1250
HIVNI ....----------CG---------- 1582
HIVRW009 ....----------A---------- 1596
HIVUG275A ....G-A---------- 1594
HIVUG273A ....--A--------A---A---------- 1606
HIVVI191A ....----------T----------A------C------ 1603
HIVDJ264A ....----------T----------A---------- 1579
HIVDJ263A ....----------T---------- 1603
HIVDJ258A ....---------T----------T---------- 1588
HIVKENYA ....A-A---------- 1585
<- RRE or CAR /<- RRE primary binding site
CONSENSUS.B ?...aTaGGAGcTatGttCctTGGgtTCTTgGGagCAGCaGGAAGCACTATGGgCgcagcgtCaatgaCgc 1539
HIVJRCSF ....---------T----------CG---------A- 1585
HIVJRFL ....---------G----------A- 1582
HIVALA1 ....C--------T----------CG---------- 1588
HIVBRVA ....C--------T----------A----------CC------ 1597
HIVJH3 ....---------G----------G...--G------- 1642
HIVBAL1 ....---------G----------G---------- 1603
HIVYU2 ....C--------T----------A---- 1570
HIVMN ....---------C----------A----------G------ 1612
HIVHXB2R ....---------T---------- 1609
HIVLAI ....---------T----------CG---------- 1624
HIVNL43 ....---------T----------TGCA---------- 1603
HIVMFA ....---------T---------- 1603
HIVCAM1 G...---------C----------T-G--C------ 1609
HIVNY5CG G...C--------C----------G--- 1591
HIVADA G...----------A---- 1600
HIVJFL G...----------G------- 1594
HIVSIMI84 G...---------T----------A----------G---------- 1609
HIVD31 G...C-G------G----------CG-------G--- 1591
HIVSF162 G...C----------CG----C------ 1582
HIVBCSG3C ....---------C----------T 1618
HIVOYI G...C----------CG---G------- 1606
HIVSF33 G...----------A---- 1597
HIVCDC4 G...C----------A--------G--- 1645
HIVSF2 A...G----------T----T------ 1606
HIVSF2B13 A...----------CG---------- 1600
HIVHAN G...C----------CG----C------ 1606
HIVRF A...----------GC-----A---- 1636
HIVWMJ2 A...----------GC---C------ 1582
HIVTB132 ....---------GC--C--C----------x-------C---C----- 1552
HIVBR020 A...T----------G--G--- 1596
HIVTH014 G...----------A----------A---- 1572
HIVTH026 G...----------A---- 1569
HIVUS711 ....---------G----------G---------- 1584
HIVUS712 ....T-T---------- 1593
HIVUS715 ....T------T---------- 1599
HIVUS716 ....----------C------ 1572
HIVHA593 A...G---------- 1662
HIVHA594 A...C---------- 1584
HIVHA596 A...C---------- 1605
HIVHA599 A...C----------C---------- 1635
HIVHA651 A...C---------- 1587
HIVRJS G...----------G---G--- 1600
HIVGUN A...-------T----------C----------G--A---- 1496
HIVSC G...----------TA---------- 1609
HIVSBA ....----------A---- 837
HIVSBB ....---------G--C--T----------T------ 864
HIVSBC ....---------G----------A---- 831
HIVBR014 A...C----------C------ 1602
HIVBR021 G...--C----------A---- 1594
HIVACH9 G...----------A--- 1452
HIVACP1 G...---------T----------A--- 1419
HIVJM ....--G------T---------- 1539
HIVWM ....T---------- 1470
HIVP896 ....---------G----------CG----G------ 1600


CONSENSUS.C ?...aTaGgAGCTgTgtTCCTTGGGTTCTTGGGAgCaGCaGGAAgCACTATgGgCGCgGCgTCAaTaaCgc 1525
HIVMA959 ....-----G-G---- 1578
HIVMA960 ....---------- 1566
HIVD757 ....----------A-----G---- 1241
HIVD747 ....----------A----------G--CG 1382
HIVD760 ....T---------- 1402
HIVNOF ....----------C----------C---------- 1215
HIVZAM20A ....----------C-G---- 1669
HIVD1044 ....---------- 1229
HIVD1024 ....----------A---------- 1561
HIVD744 ....C---------- 1254
HIVD766 ....T---------- 1200
HIVD808 ....---------- 1264
HIVD868 ....--G----------C---- 1230
HIVSM145A ....---------- 1603
HIVZAM18A ....---------- 1591
HIVDJ259A ....C--------A----------C----------A--A---------- 1537
HIVDJ373A ....C---C---------?----------C----------A--A---------- 1570
HIVSE364A ....----------A---------- 1564
HIVUG268A ....----------C----------A--A---------- 1588
CONSENSUS.D ....cTaGGAGct?TGTTCCTTGGGTTCTTGGGAgCAGCAGGAAGCACgATGGGCGCAgcGtCa?TgaCgC 1522
HIVJY1 ....--T------G----------T----G--G-A- 1630
HIVNDK ....---------G----------G------ 1579
HIVMAL ....--------CA----------C-A---- 1615
HIVELI ....T--------A----------CG----G------ 1600
HIVZ2Z6 ....---------A----------CG----T------ 1600
HIVUG024 ....---------G----------A----------C------ 1594
HIVUG021 ....--G------T----------GC------ 1560
HIVUG038 ....T--------T----------A--T------ 1591
HIVUG046 ....---------A----------A------ 1591
HIVUG266A ....----------G----------C------ 1594
HIVUG269A ....--G------C----------A----------C------ 1599
HIVUG274A ....--G------T----------A----------A------ 1632
HIVSE365A ....--G----T-A----------A--G--- 1594
CONSENSUS.E ....ATAGGAGCTATGATCTTTGGGTTCTTAGGAGCAGCAGGAAGCACTATGGGCGCggCGTCAATAACGC 1529
HIVTH966 ....----------A---------- 1587
HIVTH975 ....---------- 1581
HIVTH022 ....---------- 1581
HIVTN243 ....---------- 1606
HIVTH006 ....---------- 1578
HIVTH011 ....----------C---------- 1527
CONSENSUS.F ....aT?GGAGCTgTgtTCcTTGGGTTCTTggGaGcaGCaGGAAGCACTATGGGCGCGGCGTCAATAACGC 1512
HIVBZ163A ....--G------T----------A-C--G---------- 1558
HIVBZ126A ....--A------T----------A-C--G---------- 1566
CONSENSUS.G ....???GGAGCTGTCTTCCTTGGGTTCTTAGGAGCAGC?GG?AGCACTATGGGCGCGGCGTCA?TA?CGC 1520
HIVVI525A ....CTG----------A--A----------A--A--- 1642
HIVLBV217 ....ACT----------T--G----------C--G--- 1612
CONSENSUS.H ....CT?G?AGCTGT?TTCCTTGGGTTCTT?GGAGCAGCAGG?AGCACTATGGGCGCGGCGTCA?T?ACGC 652
HIVCA13 ....--A-G------C----------A----------A----------A-A---- 805
HIVVI557 ....--G-A------T----------G----------G----------G-G---- 790
CONSENSUS.O ....TTgGgAATGCTATTCTTGGGGgTtCTAAGTGCAGCAGGtAGCACTATGGGCGCAGCGGCAACAgCgC 1544
HIVANT70 ....----------A--- 1615
HIVMVP5180 ....----------G---------- 1645
HIVVAU ....----C----------A----------A---------- 1654
CONSENSUS.CPZ ....?T?GG?????T?TTC?T?GG??T?CT??GTGCAGC?GG?AG?AC?ATGGGCGCAGCG?CA?TA?CGC 847
SIVCPZGAB ....C-G--AGCAC-G---C-T--GT-C--GG-------A--A--C--T----------G--G--A--- 1579
CONSENSUS.U ....cTGGGAGCT?TgTTcCTtGGGTTCTTGGGAGCAGCaGGAAGCACtATGGGCGCgGCgTCAATgaCGC 1475
HIVZAM184 ....---------G-C----------A-----A---- 1564
HIVK124A ....---------A----------G----------A---------- 1618
HIVZ3 ....A--------T----T--C----------C----------G--- 1595


CONSENSUS.A TGAcGGtACAgGCcAGAcaaTTAtTGTCtGGtATAGTgCAaCAGCAgAgCAAttTGCTgAggGCTATagAG 1572
HIVSF1703 ----------T----------C----------A---------- 1695
HIVU455 ----------C---------- 1659
HIVZ321 ----------AG----------G-------A----C---------- 1680
HIVRW020 ------C----------A---------- 1625
HIVUG031 ---T----------A---------- 1529
HIVD687 ----------C----------C-------T---------- 1321
HIVNI ----------C--C----------AA---------- 1653
HIVRW009 ----------C----------A---------- 1667
HIVUG275A ----------C----------A----------A---------- 1665
HIVUG273A ----------C----------A----------A---------- 1677
HIVVI191A ----------C--------G----------C----A---------- 1674
HIVDJ264A ---------- 1650
HIVDJ263A ---------- 1674
HIVDJ258A ----------C---------- 1659
HIVKENYA ----------C----------A---------- 1656
RRE primary binding site ->/
CONSENSUS.B TgAcGGTACaGgcCAGacaatTattgtCtggTatAGTGCAaCAgCAgAacAAttTGCTGAggGCtATTgAg 1610
HIVJRCSF ----------A---------- 1656
HIVJRFL ----------T---------- 1653
HIVALA1 ---------- 1659
HIVBRVA ----------T----------C-------T---------- 1668
HIVJH3 ----------T----------A--A---------- 1713
HIVBAL1 ----------T----------C---------- 1674
HIVYU2 ----------C---------- 1641
HIVMN ----------T----------C------ 1683
HIVHXB2R ----------G---------- 1680
HIVLAI ----------G---------- 1695
HIVNL43 ----------A---------G---------- 1674
HIVMFA ----------G---------- 1674
HIVCAM1 ----------A----------C---------- 1680
HIVNY5CG ----------A----------A----------A---------- 1662
HIVADA ----------T---------- 1671
HIVJFL ----------T----------A---------- 1665
HIVSIMI84 ----------G---------- 1680
HIVD31 ----------G---------- 1662
HIVSF162 ----------A---------- 1653
HIVBCSG3C ---------- 1689
HIVOYI ----------G----------C---------- 1677
HIVSF33 ----------A--C----------C-------A---------- 1668
HIVCDC4 ----------A----------A------A-- 1716
HIVSF2 ---------- 1677
HIVSF2B13 ----------A---------- 1671
HIVHAN ----------A----------A---------- 1677
HIVRF -A----------C----------A---------- 1707
HIVWMJ2 ----------T 1653
HIVTB132 ----------C----------C---------- 1623
HIVBR020 ----------C-------A---------- 1667
HIVTH014 ----------G----------GA---------- 1643
HIVTH026 ---T----------G----------GA---------- 1640
HIVUS711 ----------T-------A----------C------A---------- 1655
HIVUS712 ----------T----------G---------- 1664
HIVUS715 ----------A---------- 1670
HIVUS716 ---------- 1643
HIVHA593 ----------TT----------A---------- 1733
HIVHA594 ----------G---------- 1655
HIVHA596 ----------G---------- 1676
HIVHA599 ----------A---------- 1706
HIVHA651 ----------T---------- 1658
HIVRJS ----------C---------- 1671
HIVGUN ----------A----------A------A-- 1567
HIVSC ----------T---------- 1680
HIVSBA ----------T----------C---------- 908
HIVSBB ----------C----------C--------A---------- 935
HIVSBC ----------T---------- 902
HIVBR014 ----------C------AA---------- 1673
HIVBR021 ---------C--T-----GGA-CCGA--GT--CA 1628
HIVP896 ----------G-T----------G----------C---------- 1671

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CONSENSUS.C   TGACGGtACaggcCAGACAA?TgtTGTcTGGtATAGTGCAaCAgcAAAgcAATTTGCTGAggGCtATAGAG  1595
HIVMA959      ----------A---------C------T---C-------------------------------------  1649
HIVMA960      --------------------C------------------G-------------------------------  1637
HIVD757       --------------------T---------------------------------------------------  1312
HIVD747       --------------------T---------------------------------------------------  1453
HIVD760       --------------------T-AC------------------------------------------------  1473
HIVNOF        --------------------C-----------------------------------------A---------  1286
HIVZAM20A     --------------------G-----------------------------------------A---------  1740
HIVD1044      ---------C-CT---                                                          1245
HIVD1024      --------                                                                  1569
HIVD808       --------                                                                  1272
HIVSM145A     --------------------C---------------------------T-----------A---------  1674
HIVZAM18A     ------C-------------G-----------------------------------------A--C------  1662
HIVDJ259A     --------------------T-A-------------------------------------------------  1608
HIVDJ373A     --------------------T-A-----------------------------------------A-------  1641
HIVSE364A     --------------------T-------------------------------------------A-------  1635
HIVUG268A     --------------------T-A-------------------------A---------------------  1659

CONSENSUS.D   TGACGGtACAGGCCAGACagtTAtTGTCtGGtATAGTgCAaCAGCAAAACAATTTGCTGAggGCTATAgAG  1593
HIVJY1        ------G------------A-------------------------------------------------  1701
HIVNDK        ----------------------A----------------C-------------------------------  1650
HIVMAL        ----------------------C-------------------------------------------------  1686
HIVELI        --------------------A---A---------------------------------------------  1671
HIVZ2Z6       -------------------------------------------------------------------------  1671
HIVUG024      ----------------------A-------------------------------------------------  1665
HIVUG021      ----------------------C-------------------------------------------------  1631
HIVUG038      ----------                                                                1600
HIVUG046      ----------                                                                1600
HIVUG266A     ------------------T-----------------------------------------T----------  1665
HIVUG269A     --------------------AG-------C--C-------------------------------------  1670
HIVUG274A     --------------------G-----------------------------------------------A--  1703
HIVSE365A     --------------------C-----------------------------------------A---------  1665

CONSENSUS.E   TGACGGTACAGGCCAGaCAATTAtTGTCTGGTATAGTGCAaCAGCAaAGCAATTTGCTGAGGGCTATaGAG  1600
HIVTH966      ----------------------G----------------G-------------------------------  1658
HIVTH975      ----------------G-------------------------------------------------------  1652
HIVTH022      -------------------------------------------------------------------------  1652
HIVTN243      ---------------------------------------------R---------------------W---  1677
HIVTH006      -------------------------------------------------------------------------  1649
HIVTH011      ----------                                                                1536

CONSENSUS.F   TGACGGTACAGGCCAgACAATTAtTGTCTGgtATAGTGCAACAGCA?A?cAATtTGCTGAaGGCtATaGAA  1581
HIVBZ163A     ------------------------------A--------------G-GT---C------G------T---  1629
HIVBZ126A     ----------------------------AA--------------G-A----C------G------T---  1637

CONSENSUS.G   TGACGGTACAGGTCAGACAATTATTGTCTGGCATAGTGCAACAGCAAA?CAATTTGCTGAGGGCTATAGAG  1590
HIVVI525A     -------------------------------------------------G-----------------------  1713
HIVLBV217     -------------------------------------------------A-----------------------  1683

CONSENSUS.H   TGACGGTACAGGC?AGACAATTATTGTCTGG?ATAGTGCAACAGCAAAG?AATTTGCTG???GCTATA?AG   716
HIVCA13       -------------T----------------C----------------T---------AGG------G--   876
HIVVI557      -------------C----------------T----------------C---------CAA------C--   861

CONSENSUS.O   TGaCGGTACaGaCCCAcacTtTgaTgAAGGGTATAGTGCAACAGCAGGAcAACCTGCTaAGAGCaATACAG  1615
HIVANT70      --G-------------------C-------------------------------------------------  1686
HIVMVP5180    ---------G--------G-G-AC-----------------------------------G-----G------  1716
HIVVAU        ---------G------GCA-C----A----------------------T----------------------  1725

CONSENSUS.CPZ TGACGG?ACAG?CC?G??A?TTG?T????GGTAT?GT?CA?CA?CAG???AATCTG?TG?AAGC?ATAGAG   897
SIVCPZGAB     ------T----G--C-AC-G---C-GTCG-----A--G--G--A---AAT------T--A----A------  1650

CONSENSUS.U   TGACGGtACAGGCCAGACAatTatTGTCTGGTATAGTGCAaCAGCAAAaCAATTTGCTGAgGGCTATAGAg  1546
HIVZAM184     --------------------C-G----------------------G----------A---------------  1635
HIVK124A      ------------------G---A-------------------------------------------------  1689
HIVZ3         ------C---------------------------------G-----------------------------  1666
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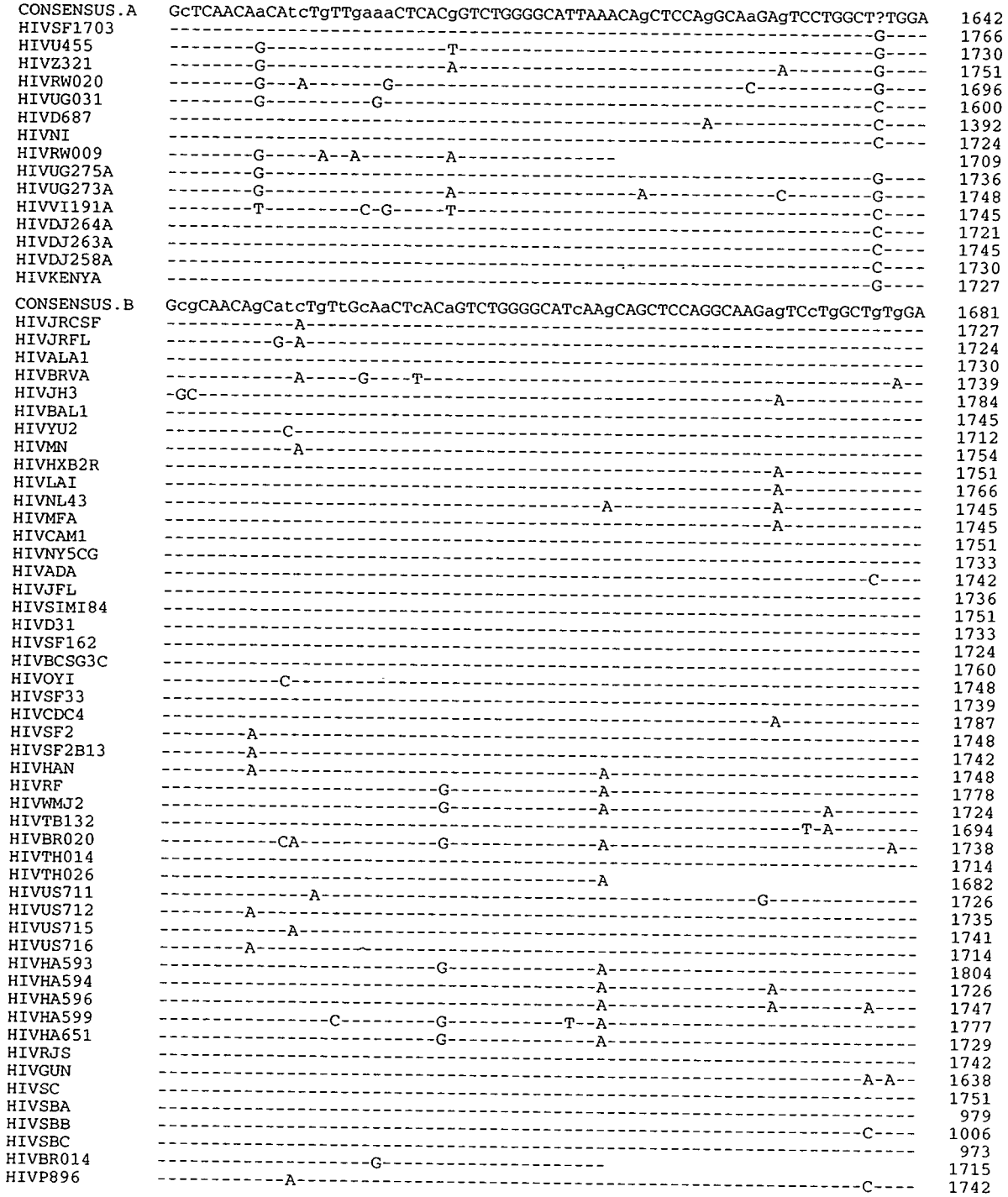
CONSENSUS.A GcTCAACAaCAtcTgTTgaaaCTCACgGTCTGGGGCATTAAACAgCTCCAgGCAaGAgTCCTGGCT?TGGA 1642
HIVSF1703 ----------G---- 1766
HIVU455 --------G----------T----------G---- 1730
HIVZ321 --------G----------A----------A--------G---- 1751
HIVRW020 --------G---A-------G----------C----------G---- 1696
HIVUG031 --------G----------G----------C---- 1600
HIVD687 ----------A----------C---- 1392
HIVNI ----------C---- 1724
HIVRW009 --------G-----A--A--------A---------- 1709
HIVUG275A --------G----------G---- 1736
HIVUG273A --------G----------A----------A----------C--------G---- 1748
HIVVI191A --------T---------C-G-----T----------C---- 1745
HIVDJ264A ----------C---- 1721
HIVDJ263A ----------C---- 1745
HIVDJ258A ----------C---- 1730
HIVKENYA ----------G---- 1727
CONSENSUS.B GcgCAACAgCatcTgTtGcAaCTcACaGTCTGGGGCATcAAgCAGCTCCAGGCAAGagTCcTgGCTgTgGA 1681
HIVJRCSF ----------A---------- 1727
HIVJRFL ----------G-A---------- 1724
HIVALA1 ---------- 1730
HIVBRVA ----------A-----G----T----------A-- 1739
HIVJH3 -GC----------A---------- 1784
HIVBAL1 ---------- 1745
HIVYU2 ----------C---------- 1712
HIVMN ----------A---------- 1754
HIVHXB2R ----------A---------- 1751
HIVLAI ----------A---------- 1766
HIVNL43 ----------A----------A---------- 1745
HIVMFA ----------A---------- 1745
HIVCAM1 ---------- 1751
HIVNY5CG ---------- 1733
HIVADA ----------C---- 1742
HIVJFL ---------- 1736
HIVSIMI84 ---------- 1751
HIVD31 ---------- 1733
HIVSF162 ---------- 1724
HIVBCSG3C ---------- 1760
HIVOYI ----------C---------- 1748
HIVSF33 ---------- 1739
HIVCDC4 ----------A---------- 1787
HIVSF2 --------A---------- 1748
HIVSF2B13 --------A---------- 1742
HIVHAN --------A----------A---------- 1748
HIVRF ----------G----------A---------- 1778
HIVWMJ2 ----------G----------A----------A-------- 1724
HIVTB132 ----------T-A--------- 1694
HIVBR020 ----------CA----------G----------A----------A-- 1738
HIVTH014 ---------- 1714
HIVTH026 ----------A 1682
HIVUS711 ----------A----------G---------- 1726
HIVUS712 --------A---------- 1735
HIVUS715 ----------A---------- 1741
HIVUS716 --------A---------- 1714
HIVHA593 ----------G----------A---------- 1804
HIVHA594 ----------A----------A---------- 1726
HIVHA596 ----------A----------A--------A---- 1747
HIVHA599 ----------C---------G----------T--A---------- 1777
HIVHA651 ----------G----------A---------- 1729
HIVRJS ---------- 1742
HIVGUN ----------A-A-- 1638
HIVSC ---------- 1751
HIVSBA ---------- 979
HIVSBB ----------C---- 1006
HIVSBC ---------- 973
HIVBR014 ----------G---------- 1715
HIVP896 ----------A----------C---- 1742

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CONSENSUS.C  GcGCaaCAgCATaTgtTGCAACTCACggTCTGGGGcATTAAGCAGCTCCaGaCAAGAGTCcTGGCtATaGA 1666
HIVMA959     --------T---C--C------------------------------------------------------- 1720
HIVMA960     ----G-------------------------------------------------G------------------ 1708
HIVD757      ----------C------------------------------------------------------------- 1383
HIVD747      ----------C-------------A-------G--------------G------------------------ 1524
HIVD760      ----------C------------------------------------------------------------- 1544
HIVNOF       ------------------------------------------------------------T---------- 1357
HIVZAM20A    ----------A-------------------------------------G-------------C------- 1811
HIVSM145A    ------------------------------------------G-G--------T---------------- 1745
HIVZAM18A    ----------C------------------------------------------T-------G--------- 1733
HIVDJ259A    -----G------------------------------------------------------------------ 1679
HIVDJ373A    -T---T--------------------A------------------------------------------- 1712
HIVSE364A    ------------------------A------------------------------------------- 1706
HIVUG268A    ------------------------------------------------------------------------ 1730

CONSENSUS.D  GCGCAACAgCATcTgTTGCAACTCAC?gTcTGGGGCATTAAACAGCTCCAGGCAAGAgTCCTGGCTGTgGA 1663
HIVJY1       ----------A-------------A------------------------------------------- 1772
HIVNDK       --------A---------------G------------------------------------------- 1721
HIVMAL       ------------------------G------------------------------------------- 1757
HIVELI       ------------------------G-----------------------------A------------- 1742
HIVZ2Z6      ------------------------G-----------------------------A----------A-- 1742
HIVUG024     ------------------------A------------------------------------------- 1736
HIVUG021     ----------T-------------A--T------------                               1673
HIVUG266A    --------------A----------A------------------------------------------- 1736
HIVUG269A    --------A----------------A------------------------------------------- 1741
HIVUG274A    ------------------------A-----------------------------A------------- 1774
HIVSE365A    ------------------------G-----------------------------A------------- 1736

CONSENSUS.E  GCGCAgCAGCATcTGTTGCAACTCACAGTCTGGGGCATtAAaCAGCTCCAGGCAAGAGTCcTgGCTGTGGA 1671
HIVTH966     ------------------------------------------------------------------------ 1729
HIVTH975     ------------------------------------------------------------------------ 1723
HIVTH022     ----------A------------------------------------------------------------- 1723
HIVTN243     -----A-----------------------------Y--R------------------Y-R--------- 1748
HIVTH006     ------------------------------------------------------------------------ 1720

CONSENSUS.F  GCGCAACAGCATCTGTTGCAgCTCACAGTCTGGGGCATTAAACAGCTCCAGGCAAGAGTCCTGGC?GTGGA 1651
HIVBZ163A    ------------------------------------------------------------C------ 1700
HIVBZ126A    ------------------------------------------------------------T------ 1708

CONSENSUS.G  GCGCA?CA?CATCTGTTGCAACTCACAGTCTGGGGCATTAAACAGCTCCAGGCAAGAGTCCTGGCTGTAGA 1659
HIVVI525A    -----G--G--------------------------------------------------------- 1784
HIVLBV217    -----A--A--------------------------------------------------------- 1754

CONSENSUS.H  GC?CAACAGCAT?TGTTGAA?CTCAC?                                          739
HIVCA13      --T---------C--------A-----A                                         903
HIVVI557     --A---------A-------G-----G                                          888

CONSENSUS.O  GCCCAGCAacAaTTGCTGAGGctATCTgTATGGGGTATtAGACAACTCCGAGCTCGCCTGCtAGCCTTAGA 1686
HIVANT70     --------G----------------R----------C--------------------------------- 1757
HIVMVP5180   ----------C---------T-------------------------------------A---------- 1787
HIVVAU       ----------C---------C------------------------------------------------- 1796

CONSENSUS.CPZ ?C?CA?CA?CA?CT??T?CA?CT?TC??TCTGGGGAGTAAAACAACT?CA?GC?AGA?TGCTTGC?GT?GA 950
SIVCPZGAB    G-T--A--G--C--AT-G--A--A--AA-----------------A--A--C---T-------T--A-- 1721

CONSENSUS.U  GCgCAACAGCATCTGTTGcAACTCACaGTCTGGGGCATTAAACAGCTCCAGGCAAGAGtCCTGGCTgTGGA 1617
HIVZAM184    --T--------------A-------G-----------------------------C-------A---- 1706
HIVK124A     ------------------------------------------------------------------------ 1760
HIVZ3        ------------------------------------------------------------------------ 1737
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CONSENSUS.A   AAGaTACCTaagGGATCAACAGCTCCTAGGAATTTGGGGcTGCTCTGGaAAacTCATCTGCaCCACTAaTG  1713
HIVSF1703     ----------A---------------------------------------------------------  1837
HIVU455       ----------CA--------------------------------------G----------------C--  1801
HIVZ321       ----------A---------------------------A------------A--------C---------  1822
HIVRW020      ----------A---------------------------------------------------------  1767
HIVUG031      ------------------------------------T---------------------------------  1671
HIVD687       ----------A---------------------------------------------------------C--  1463
HIVNI         ----------                                                              1735
HIVUG275A     ---------------------------------------------------------------------  1807
HIVUG273A     ---------------------------------------------------------------------C--  1819
HIVVI191A     ---------T---------------------------A--------C------------C---------  1816
HIVDJ264A     ---------------------------------------------------------------------C--  1792
HIVDJ263A     ---T-----------------------------------------------------------------  1816
HIVDJ258A     ---T-----------------------------------------------------------------C--  1801
HIVKENYA      ------------------------------------------------A--------------------  1798

          RRE or CAR ->/
CONSENSUS.B   AAGATaCcTaaagGAtCaACAGCTCcTagggaTtTGGGGtTGCTCTGGAAAaCtcaTtTGCaCCACTgctG  1752
HIVJRCSF      ------------------------A-G-----------------------------------------  1798
HIVJRFL       ----------GG--------------G-----------------------------------------  1795
HIVALA1       ----------G---------------G-A---------------------------------------A---  1801
HIVBRVA       ----------C----------G-----------------------------------------------  1810
HIVJH3        ------------------------G---------------------------------------------  1855
HIVBAL1       ----------G--------------G----------------------------C-------------  1816
HIVYU2        ----------G---------------------------------------------------------A---  1783
HIVMN         ------------------------G---T-----------------------------------------A---  1825
HIVHXB2R      ------------------------G---------------------------------------------  1822
HIVLAI        ------------------------G---------------------------------------------  1837
HIVNL43       ------------------------G---------------------------------------------  1816
HIVMFA        ------------------------G---------------------------------------------  1816
HIVCAM1       ---------------------------------------------------------C-------------  1822
HIVNY5CG      ----------------------------A-------------------------C---------A---  1804
HIVADA        ----------G---------------------------------------------C-------------  1813
HIVJFL        ----------C----------------G-----------------------------------------A---  1807
HIVSIMI84     ----------------C-------------------------------------G----------A---  1822
HIVD31        ----------G-----------------------------------------T----------------  1804
HIVSF162      ---------------------------------------------------------------------  1795
HIVBCSG3C     ------------------------G---------------------------------------------  1831
HIVOYI        ---------------------------------------------------G--------------A---  1819
HIVSF33       ----------GA----------------------------------------------------------A---  1810
HIVCDC4       ---------------------------T-----------------------------------------  1858
HIVSF2        ----------G---------------------------------------------------------  1819
HIVSF2B13     ----------G---------------------------------------------C-------------  1813
HIVHAN        ----------G---------------------------------------------C---------A---  1819
HIVRF         ----------G-----------------A--------A-------------------------A---  1849
HIVWMJ2       ----------G---------------------------------------------------------A---  1795
HIVTB132      ------------------------G--A-------------------------C---------A---  1765
HIVBR020      ----------GG--------------G-----C-------------------------------A---  1809
HIVTH014      ---------------------------------------------------------------------  1785
HIVUS711      ---------------------------------------------------------------------A---  1797
HIVUS712      ------------------------G--------------------------------------------AA--  1806
HIVUS715      ----------GA-------------G----------C-------------------------A---  1812
HIVUS716      ------------------------G-----------------------------------------A---  1785
HIVHA593      ---------------------------------------------------------------------A---  1875
HIVHA594      ------------------------------------A------------------------------  1797
HIVHA596      ------------------------------------A------------------------------  1818
HIVHA599      ---------------------------------------------------C---C-------G-  1848
HIVHA651      ----------------G-----------------------------------C-------------T---  1800
HIVRJS        -------T-------------------------------------------------------------  1813
HIVGUN        -----T-----G---------------------------------------C---------A---  1709
HIVSC         ----------G--------------G-----------------------------------A---  1822
HIVSBA        ---------G-G--------------G-----A-----------------------------------  1050
HIVSBB        ------------------------G-------------------------------------------  1077
HIVSBC        ---------G-G--------------G-----A---------------------C-------------  1044
HIVP896       ----------G-------------A-G--A-----------------------------------T---  1813
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CONSENSUS.C  AAGATACCTaaAGGAtCAACAGCTcCTAGGGaTtTGGGGCtGCTCTGGAAAACTCATCTGCACCACtgctG  1737
HIVMA959     ------------------------------------------------------------------------  1791
HIVMA960     ----------C----------------T-G-------------------------------CA---------  1779
HIVD757      ---------------------------------------C--------------------------AA--  1454
HIVD747      ---------------A--------------------------------------------------A---  1595
HIVD760      ---------------------------------G--------------------------------------  1615
HIVNOF       --------------------                                                      1377
HIVZAM20A    ------------------------------------------------------------------------  1882
HIVSM145A    ----------G-------------------------------------------------------------  1816
HIVZAM18A    ------------------------------------------------------------------------  1804
HIVDJ259A    ---------T--------------T-----------------------------------------------C-  1750
HIVDJ373A    ---------G-------------------------------------------------------AA----  1783
HIVSE364A    ------------------------------------------------------------------------  1777
HIVUG268A    ----------C-------------------------------------------------------------  1801

CONSENSUS.D  aAGaTACCTAaaGGATCAaCaGCTCCTaGGaATtTGGGGTTGCTCTGGAAaaCaCATTTGCaCCACtaatG  1734
HIVJY1       ---C--------------------------------------------------------------C--  1843
HIVNDK       ----------G-----------------------------------------GG-------------  1792
HIVMAL       ----------C---------G------------G-------------------------------ATT--  1828
HIVELI       ------------------------------------------------------------------------  1813
HIVZ2Z6      G-----------------------------------------------T--------------C--  1813
HIVUG024     ---C-------------------------G-------------------G----------C-----C-G-  1807
HIVUG266A    ---C--------------------------------------------------------------G--  1807
HIVUG269A    ---C------GG------G--------G----------------------G-------------------  1812
HIVUG274A    ---C------GG------G--------G----------------------G-------------------  1845
HIVSE365A    ----------------------------------A-------------------------------C--  1807

CONSENSUS.E  aAGATACCTAAAGGATCAAAAGtTCCTaGGACTTTGGGGcTGCTCTGGAAAAATCATCTGCACCACTGCTG  1742
HIVTH966     ------------------------------------------------------------------------  1800
HIVTH975     ------------------------------------------------------------------------  1794
HIVTH022     ------------------------------------------------------------------------  1794
HIVTN243     ----------------------C----R----------Y-------------------------------  1819
HIVTH006     G-----------------------------------------------------------------------  1791

CONSENSUS.F  AAGATACCTACAGGATCAACAGCTCCTAGGACTTTGGGGCTGCTCTGGAAAACTCATCTGCACCACTAATG  1722
HIVBZ163A    ------------------------------------------------------------------------  1771
HIVBZ126A    ------------------------------------------------------------------------  1779

CONSENSUS.G  AAGAT?CCTA?AGGATCAACAGC?CCTAGGGATTTGGGGCTGCTCTGGAAAACTCATCTGCACCACTAATG  1727
HIVVI525A    -----T----A----------C-------------------------------------------------  1855
HIVLBV217    -----A----C----------T-------------------------------------------------  1825

CONSENSUS.O  AACCtTtaTACAGAATCAGCAACtCCTaAaCCTaTGGGGCTGtAAaggaAaaCTAaTCTGcTACACATCAG  1757
HIVANT70     ------AC-------------------G---------G---G----------T----------------  1828
HIVMVP5180   ----C----------------G-------------------------------------T----------  1858
HIVVAU       ------------------------T-----G--------C--GAAT-G-------------------  1867

CONSENSUS.CPZ ?A?GTACCT????GATCA?CA??T??TG?GCCT?TGGGG?TG??CTG??AAGG????CTGT?A?AC?ACGG  996
SIVCPZGAB    A-G------GCAG-----G--GA-TC--G----G-----C--CT---GA----CTGT----T-T--C----  1792

CONSENSUS.U  AAGaTACCTA?AGgaTCAACAGCTCCTaGGaaTTTGGGGcTGCTCTGGAAAACtCATcTGCACCACTAcTG  1687
HIVZAM184    ----------C----------------G-------------------------------------------  1777
HIVK124A     ---C------A-----------------------------T------------A---T----------A--  1831
HIVZ3        ----------G--AG---------------GC----------------------------------------  1808
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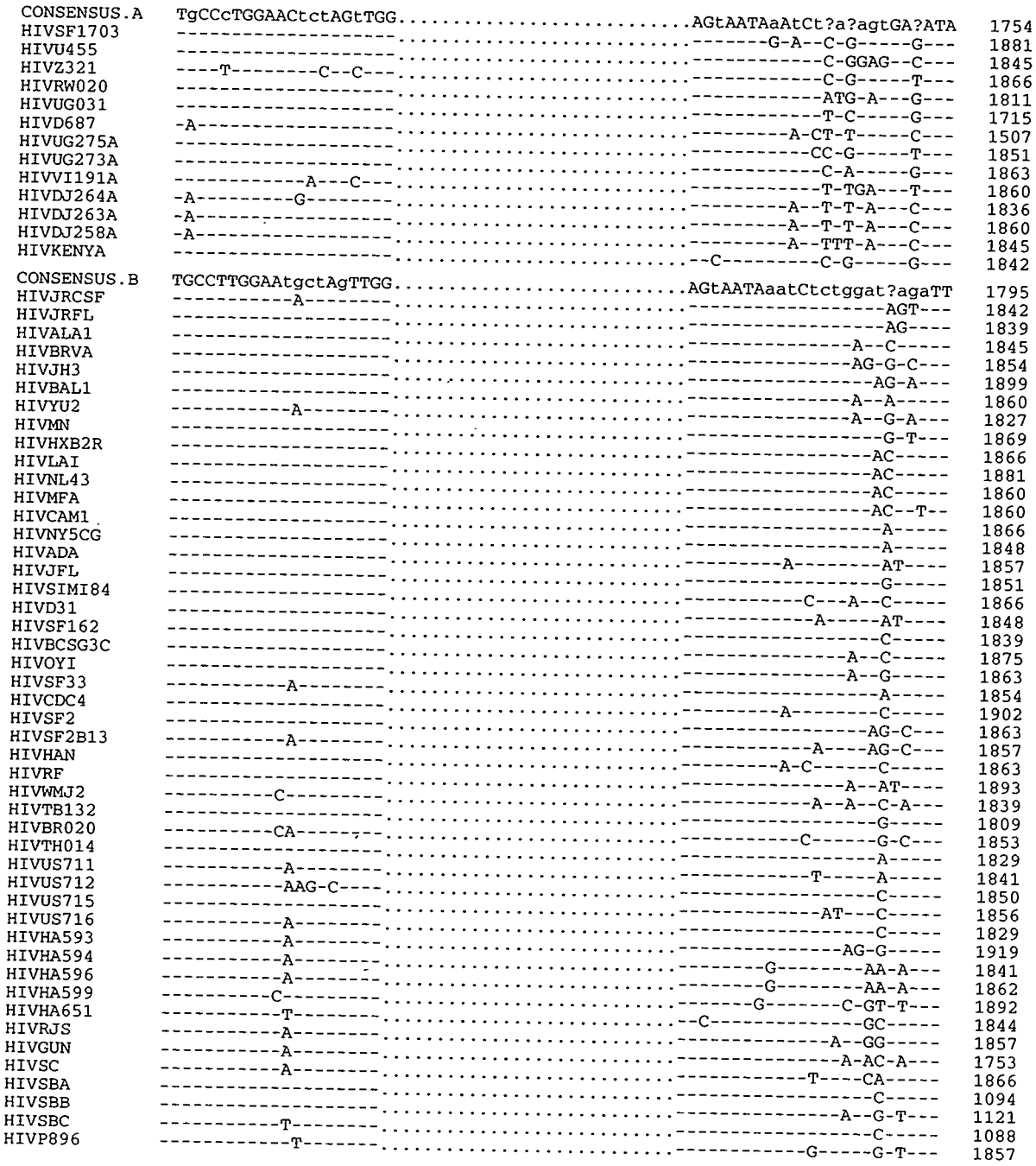
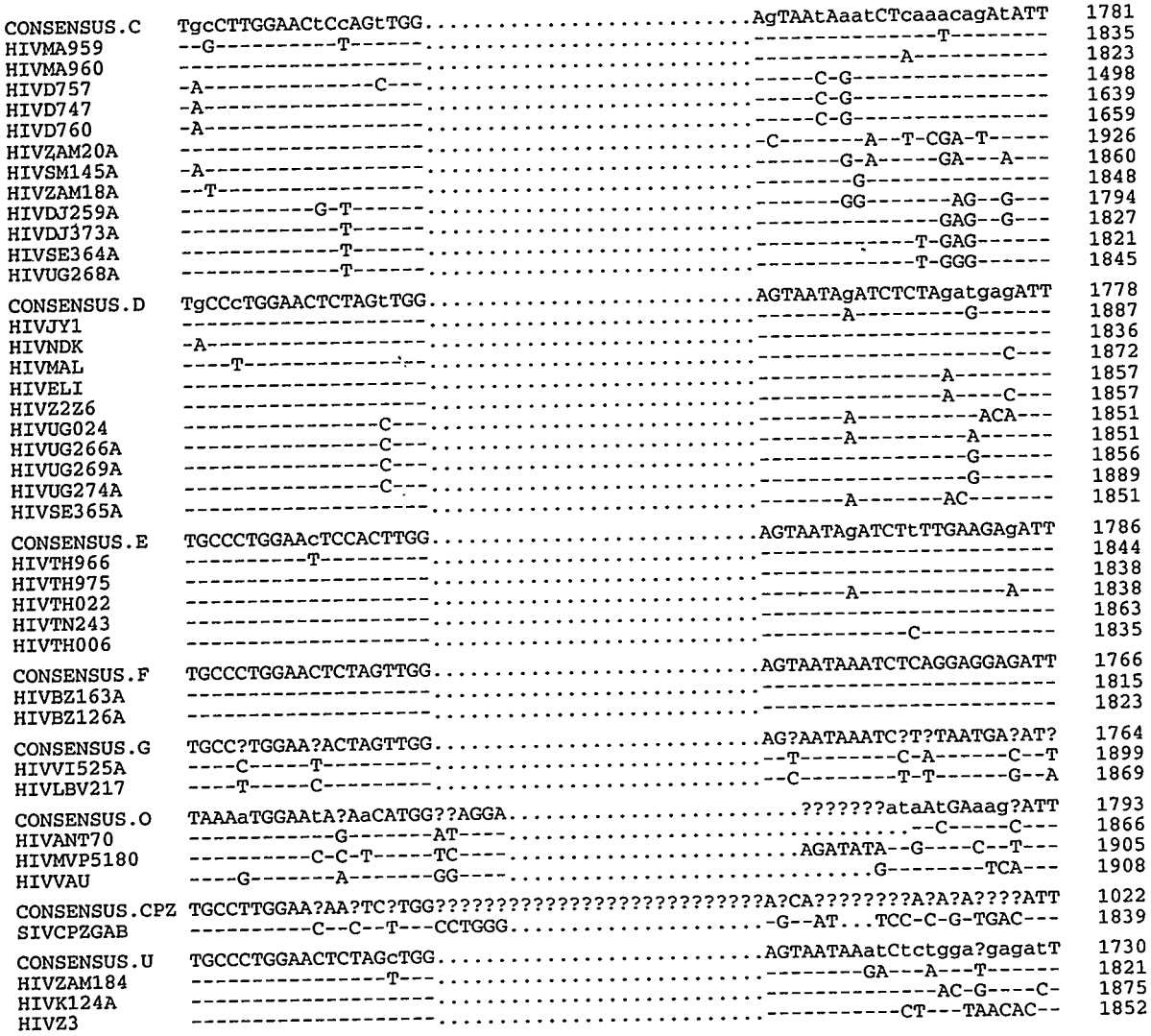
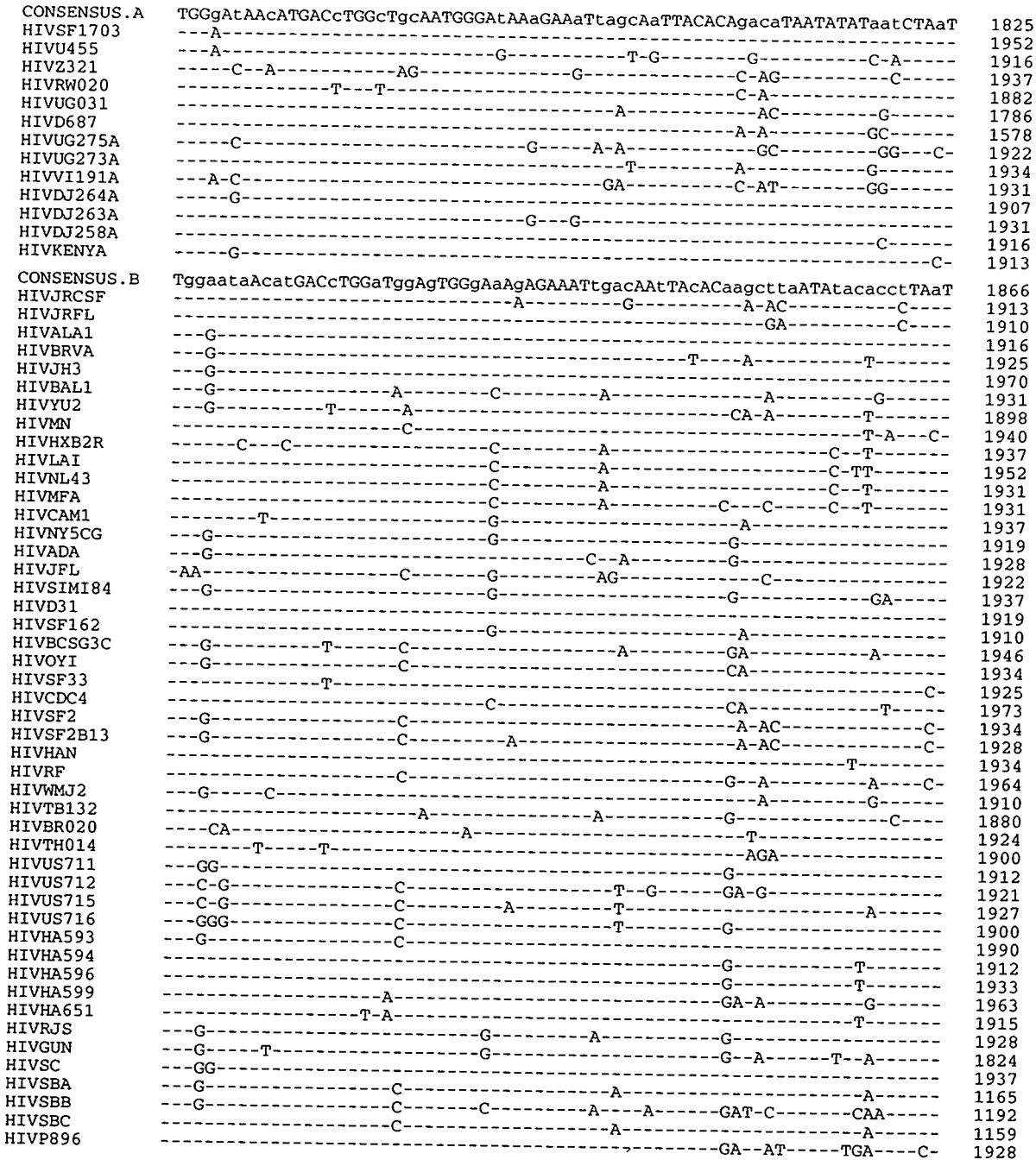
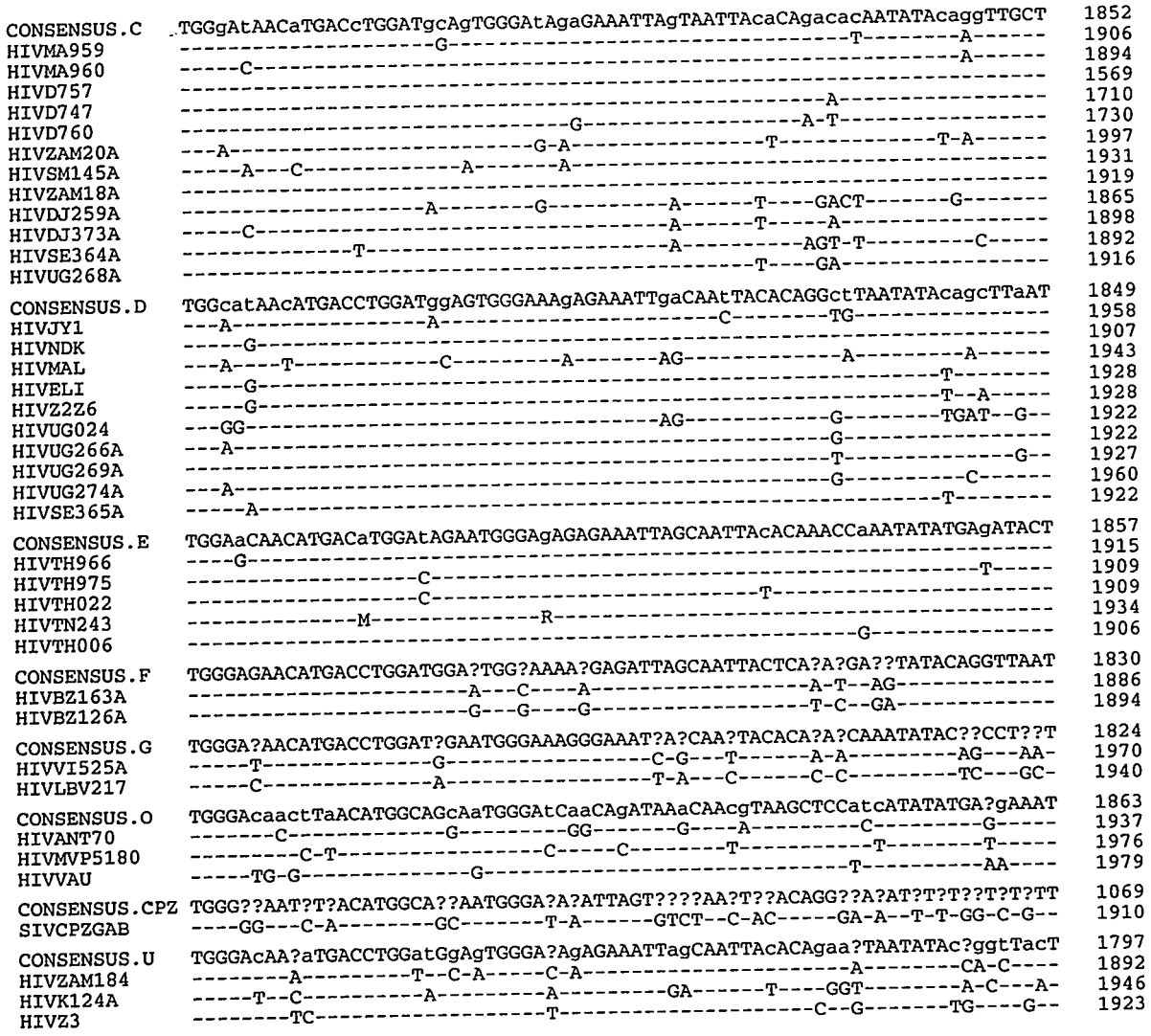

CONSENSUS.A TgCCcTGGAACtctAGtTGG AGtAATAaAtCt?a?agtGA?ATA 1754
HIVSF1703 ------- -------G-A--C-G-----G--- 1881
HIVU455 ------- ----------C-GGAG--C--- 1845
HIVZ321 ----T--------C--C--- ----------C-G-----T--- 1866
HIVRW020 ------- ----------ATG-A---G--- 1811
HIVUG031 ------- ----------T-C-----G--- 1715
HIVD687 -A------- ---------A-CT-T-----C--- 1507
HIVUG275A ------- ----------CC-G-----T--- 1851
HIVUG273A ------- ----------C-A-----G--- 1863
HIVVI191A ----------A---C--- ----------T-TGA---T--- 1860
HIVDJ264A -A---------G-------- ---------A--T-T-A---C--- 1836
HIVDJ263A -A------------------ ---------A--T-T-A---C--- 1860
HIVDJ258A -A------------------ ---------A--TTT-A---C--- 1845
HIVKENYA ------- --C---------C-G-----G--- 1842
CONSENSUS.B TGCCTTGGAAtgctAgTTGG AGtAATAaatCtctggat?agaTT 1795
HIVJRCSF ----------A-------- ----------AGT--- 1842
HIVJRFL ------- ----------AG---- 1839
HIVALA1 ------- ----------A--C----- 1845
HIVBRVA ------- ----------AG-G-C--- 1854
HIVJH3 ------- ----------AG-A--- 1899
HIVBAL1 ------- ----------A--A----- 1860
HIVYU2 ----------A-------- ----------A--G-A--- 1827
HIVMN ------- ----------G-T--- 1869
HIVHXB2R ------- ----------AC----- 1866
HIVLAI ------- ----------AC----- 1881
HIVNL43 ------- ----------AC----- 1860
HIVMFA ------- ----------AC--T-- 1860
HIVCAM1 ------- ----------A----- 1866
HIVNY5CG ------- ----------A----- 1848
HIVADA ------- ---------A--------AT---- 1857
HIVJFL ------- ----------G----- 1851
HIVSIMI84 ------- ----------C---A--C----- 1866
HIVD31 ------- ----------A-----AT---- 1848
HIVSF162 ------- ----------C----- 1839
HIVBCSG3C ------- ----------A--C----- 1875
HIVOYI ------- ----------A--G----- 1863
HIVSF33 ----------A-------- ----------A----- 1854
HIVCDC4 ------- ---------A--------C----- 1902
HIVSF2 ------- ----------AG-C--- 1863
HIVSF2B13 ----------A-------- ----------A----AG-C--- 1857
HIVHAN ------- ---------A-C------C----- 1863
HIVRF ------- ----------A--AT---- 1893
HIVWMJ2 ----------C--------- ----------A--A--C-A--- 1839
HIVTB132 ------- ----------G----- 1809
HIVBR020 ----------CA------- ----------C------G-C--- 1853
HIVTH014 ------- ----------A----- 1829
HIVUS711 ----------A-------- ----------T-----A----- 1841
HIVUS712 ----------AAG-C---- ----------C----- 1850
HIVUS715 ------- ----------AT---C----- 1856
HIVUS716 ----------A-------- ----------C----- 1829
HIVHA593 ----------A-------- ----------AG-G----- 1919
HIVHA594 ----------A-------- --------G--------AA-A--- 1841
HIVHA596 ----------A-------- --------G--------AA-A--- 1862
HIVHA599 ----------C--------- -------G-------C-GT-T--- 1892
HIVHA651 ----------T-------- --C--------GC----- 1844
HIVRJS ----------A-------- ----------A--GG----- 1857
HIVGUN ----------A-------- ----------A-AC-A--- 1753
HIVSC ----------A-------- ----------T----CA----- 1866
HIVSBA ------- ----------C----- 1094
HIVSBB ------- ----------A--G-T--- 1121
HIVSBC ----------T-------- ----------C----- 1088
HIVP896 ----------T------- ----------G-----G-T--- 1857




CONSENSUS.A TGGgAtAAcATGACcTGGcTgcAATGGGAtAAaGAAaTtagcAaTTACACAgacaTAATATATaatCTAaT 1825
HIVSF1703 ---A 1952
HIVU455 ---A 1916
HIVZ321 1937
HIVRW020 1882
HIVUG031 1786
HIVD687 1578
HIVUG275A 1922
HIVUG273A 1934
HIVVI191A 1931
HIVDJ264A 1907
HIVDJ263A 1931
HIVDJ258A 1916
HIVKENYA 1913
CONSENSUS.B TggaataAcatGACcTGGaTggAgTGGgAaAgAGAAATtgacAAtTAcACaagcttaATAtacacctTAaT 1866
HIVJRCSF 1913
HIVJRFL 1910
HIVALA1 1916
HIVBRVA 1925
HIVJH3 1970
HIVBAL1 1931
HIVYU2 1898
HIVMN 1940
HIVHXB2R 1937
HIVLAI 1952
HIVNL43 1931
HIVMFA 1931
HIVCAM1 1937
HIVNY5CG 1919
HIVADA 1928
HIVJFL 1922
HIVSIMI84 1937
HIVD31 1919
HIVSF162 1910
HIVBCSG3C 1946
HIVOYI 1934
HIVSF33 1925
HIVCDC4 1973
HIVSF2 1934
HIVSF2B13 1928
HIVHAN 1934
HIVRF 1964
HIVWMJ2 1910
HIVTB132 1880
HIVBR020 1924
HIVTH014 1900
HIVUS711 1912
HIVUS712 1921
HIVUS715 1927
HIVUS716 1900
HIVHA593 1990
HIVHA594 1912
HIVHA596 1933
HIVHA599 1963
HIVHA651 1915
HIVRJS 1928
HIVGUN 1824
HIVSC 1937
HIVSBA 1165
HIVSBB 1192
HIVSBC 1159
HIVP896 1928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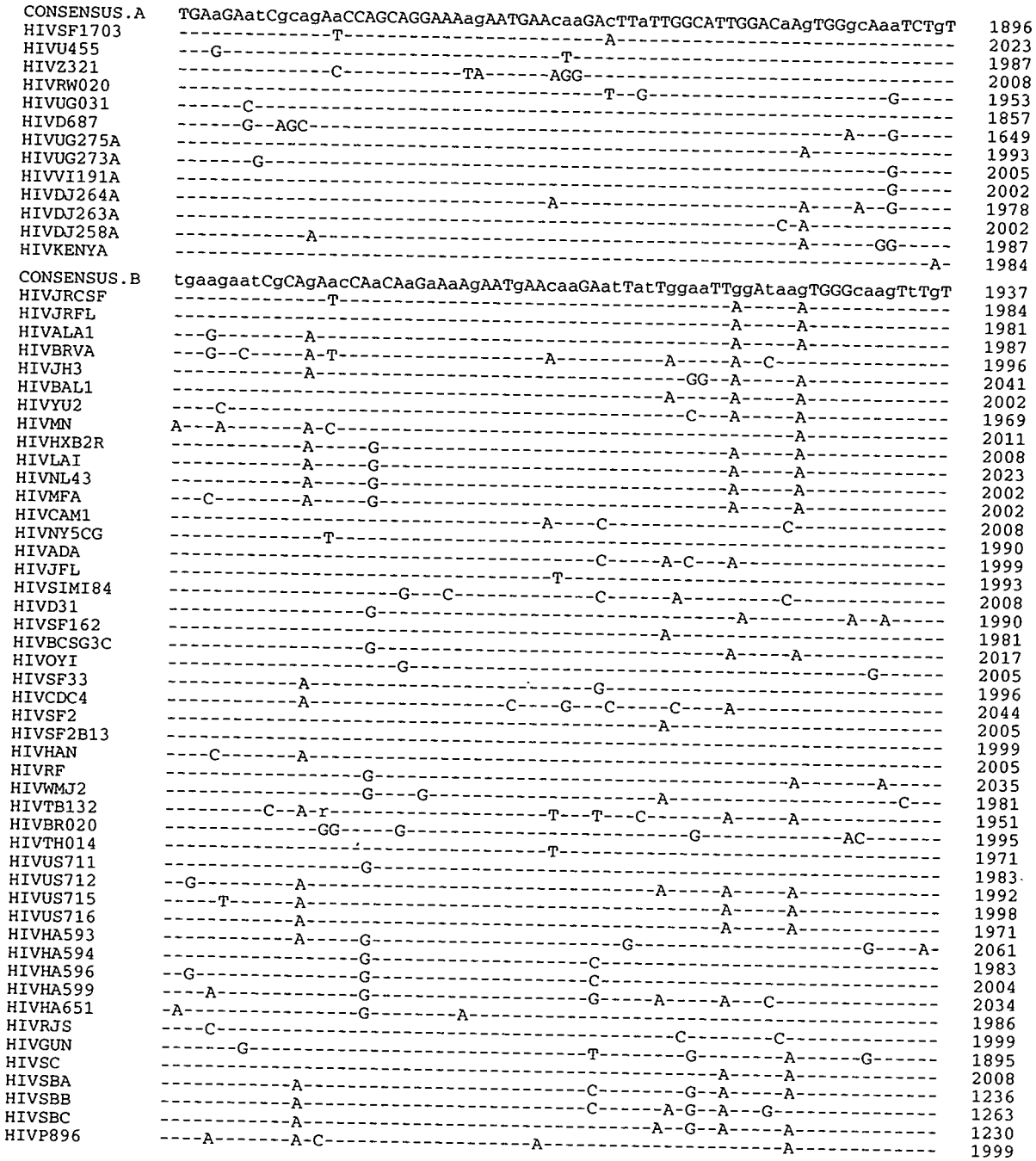
HIVMA959 1906
HIVMA960 1894
HIVD757 1569
HIVD747 1710
HIVD760 1730
HIVZAM20A 1997
HIVSM145A 1931
HIVZAM18A 1919
HIVDJ259A 1865
HIVDJ373A 1898
HIVSE364A 1892
HIVUG268A 1916
CONSENSUS.D TGGcatAAcATGACCTGGATggAGTGGGAAAgAGAAATTgaCAAtTACACAGGctTAATATAcagcTTaAT 1849
HIVJY1 1958
HIVNDK 1907
HIVMAL 1943
HIVELI 1928
HIVZ2Z6 1928
HIVUG024 1922
HIVUG266A 1922
HIVUG269A 1927
HIVUG274A 1960
HIVSE365A 1922
CONSENSUS.E TGGAaCAACATGACaTGGAtAGAATGGGAgAGAGAAATTAGCAATTAcACAAACCaAATATATGAgATACT 1857
HIVTH966 1915
HIVTH975 1909
HIVTH022 1909
HIVTN243 1934
HIVTH006 1906
CONSENSUS.F TGGGAGAACATGACCTGGATGGA?TGG?AAAA?GAGATTAGCAATTACTCA?A?GA??TATACAGGTTAAT 1830
HIVBZ163A 1886
HIVBZ126A 1894
CONSENSUS.G TGGGA?AACATGACCTGGAT?GAATGGGAAAGGGAAAT?A?CAA?TACACA?A?CAAATATAC??CCT??T 1824
HIVVI525A 1970
HIVLBV217 1940
CONSENSUS.O TGGGAcaactTaACATGGCAGcAaTGGGAtCaaCAgATAAaCAAcgTAAGCTCCatcATATATGA?gAAAT 1863
HIVANT70 1937
HIVMVP5180 1976
HIVVAU 1979
CONSENSUS.CPZ TGGG??AAT?T?ACATGGCA??AATGGGA?A?ATTAGT????AA?T??ACAGG??A?AT?T?T??T?T?TT 1069
SIVCPZGAB 1910
CONSENSUS.U TGGGAcAA?aTGACCTGGatGgAgTGGGA?AgAGAAATTagCAATTAcACAgaa?TAATATAc?ggtTacT 1797
HIVZAM184 1892
HIVK124A 1946
HIVZ3 1923


CONSENSUS.A TGAaGAatCgcagAaCCAGCAGGAAAagAATGAAcaaGAcTTaTTGGCATTGGACaAgTGGgcAaaTCTgT 1896
HIVSF1703 ----------T----------A---------- 2023
HIVU455 ---G----------T---------- 1987
HIVZ321 ----------C----------TA------AGG---------- 2008
HIVRW020 ----------T--G----------G----- 1953
HIVUG031 ------C---------- 1857
HIVD687 ------G--AGC----------A---G----- 1649
HIVUG275A ----------A---------- 1993
HIVUG273A -------G----------G----- 2005
HIVVI191A ----------G----- 2002
HIVDJ264A ----------A----------A----A--G----- 1978
HIVDJ263A ----------C-A---------- 2002
HIVDJ258A ----------A----------A------GG----- 1987
HIVKENYA ----------A- 1984
CONSENSUS.B tgaagaatCgCAgAacCAaCAaGaAaAgAATgAAcaaGAatTatTggaaTTggAtaagTGGGcaagTtTgT 1937
HIVJRCSF ----------T----------A-----A---------- 1984
HIVJRFL ----------A-----A---------- 1981
HIVALA1 ---G--------A----------A-----A---------- 1987
HIVBRVA ---G--C-----A-T----------A----------A-----A--C---------- 1996
HIVJH3 ----------A----------GG--A-----A---------- 2041
HIVBAL1 ----------A-----A-----A---------- 2002
HIVYU2 ----C----------C---A-----A---------- 1969
HIVMN A---A-------A-C----------A---------- 2011
HIVHXB2R ----------A-----G----------A-----A---------- 2008
HIVLAI ----------A-----G----------A-----A---------- 2023
HIVNL43 ----------A-----G----------A-----A---------- 2002
HIVMFA ---C--------A-----G----------A-----A---------- 2002
HIVCAM1 ----------A----C----------C---------- 2008
HIVNY5CG ----------T---------- 1990
HIVADA ----------C-----A-C---A---------- 1999
HIVJFL ----------T---------- 1993
HIVSIMI84 ----------G---C----------C------A---------C---------- 2008
HIVD31 ----------G----------A---------A--A----- 1990
HIVSF162 ----------A---------- 1981
HIVBCSG3C ----------G----------A-----A---------- 2017
HIVOYI ----------G----------G------ 2005
HIVSF33 ----------A----------G---------- 1996
HIVCDC4 ----------A----------C----G---C-----C----A---------- 2044
HIVSF2 ----------A---------- 2005
HIVSF2B13 ---------- 1999
HIVHAN ----C-------A---------- 2005
HIVRF ----------G----------A-------A----- 2035
HIVWMJ2 ----------G----G----------A----------C--- 1981
HIVTB132 ---------C--A-r----------T---T---C-------A-----A---------- 1951
HIVBR020 ----------GG-----G----------G----------AC------- 1995
HIVTH014 ----------T---------- 1971
HIVUS711 ----------G---------- 1983
HIVUS712 --G---------A----------A-----A-----A---------- 1992
HIVUS715 -----T------A----------A-----A---------- 1998
HIVUS716 ----------A----------A-----A---------- 1971
HIVHA593 ----------A-----G----------G----------G----A- 2061
HIVHA594 ----------G----------C---------- 1983
HIVHA596 --G----------G----------C---------- 2004
HIVHA599 ----A----------G----------G-----A-----A---C---------- 2034
HIVHA651 -A----------G---------A---------- 1986
HIVRJS ----C----------C---------C---------- 1999
HIVGUN -------G----------T--------G---------A------G------ 1895
HIVSC ----------A---------- 2008
HIVSBA ----------A----------C--------G--A-----A---------- 1236
HIVSBB ----------A----------C-------A-G--A---G---------- 1263
HIVSBC ----------A----------A--G--A-----A---------- 1230
HIVP896 ----A-------A-C----------A----------A---------- 1999

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CONSENSUS.C   TGAAGacTCgCAAAacCAGCAGGAaaaAAATGAAaAaGAttTAtTAGCATTGGACAgtTGGaaaAaTCTgT  1923
HIVMA959      ------------------------G---------------C-------------------------------  1977
HIVMA960      ------------------------------------------------------------------T-------  1965
HIVD757       -------------------------G-----------------------------------------------  1640
HIVD747       -------------------------G-----------------------------------------------  1781
HIVD760       -------------------------G-----------------------------------------------  1801
HIVZAM20A     -------------C----------C-------------G----------------AG-----T-T-------  2068
HIVSM145A     -----T-------------------------------C--------------------GG--G-------  2002
HIVZAM18A     ------A--------TT----------G-----------C---------------------------A-  1990
HIVDJ259A     ------------------------G---------C--------C------------AA---C-G-------  1936
HIVDJ373A     -----T--------C---------GC----------------C------------AA---C---------  1969
HIVSE364A     ------A----------------G-----------C------C------------A------C-------  1963
HIVUG268A     ---------A--------------G-----------------C------------AA---C---------  1987

CONSENSUS.D   TGAagAaTCgCAaatCCAGCAAGAAAAgAATGAacAaGAatTaTTGgaATTGGAcAAaTGGGCAAGTtTGT  1920
HIVJY1        ----A-T--A--------------A-----------CC-----C-------------------------  2029
HIVNDK        -----------G---------------------A-------------------------------------  1978
HIVMAL        ------------------------------A-G--------------------G---------------  2014
HIVELI        ---G--------G-C-------------------A-------G--------------G-------------  1999
HIVZ2Z6       --------------C-----------------------------------------G-------------  1999
HIVUG024      ---------------------------------A----TC--------------------------------  1993
HIVUG266A     -------------G-------------------------------C-------------------------  1993
HIVUG269A     --------------C------------A------------C-----C-------------------------  1998
HIVUG274A     --------------A-------------------------C-----C--------T------------G---  2031
HIVSE365A     ---G----------C-----------------G-------------C---------G-------------  1993

CONSENSUS.E   tACagAATCGCAgaACCAGCAGGACAGgAATGAAAAgGAtTTGTTAGaatTGGATAAATGGGCAAGtCTGT  1928
HIVTH966      ---G--------A-------------------------------------------------------------  1986
HIVTH975      ------------------------------------A----------G-------------------------  1980
HIVTH022      ---------------------------------------------------C---------------------  1980
HIVTN243      ------------------------------------------------------------------C----  2005
HIVTH006      G--GA--------G-------------A-----------C--------G-------------------------  1977

CONSENSUS.F   TGAA?AATCACAGAACCAGCAGGAAAAGAATGAACAAG?ATTATTGGCATTGGACAAATGGGCAAGTCTGT  1899
HIVBZ163A     ----A-------------------------------G-------------------------------------  1957
HIVBZ126A     ----C-------------------------------A-------------------------------------  1965

CONSENSUS.G   ?GAAGAATCGCAGATCCAGCAGGAAAAGAATGAACAAGACTTATTGGCATTGGACAAATGGG?AAG?TTGT  1892
HIVVI525A     T-------------------------------------------------------------C---T----  2041
HIVLBV217     C-------------------------------------------------------------A---C----  2011

CONSENSUS.O   ACAAgagGCACAAGaaCAaCAGGAaaAaAATGagAAAgaaTTGcTGGAGtTAGATGAATGGGCCTCTaTTT  1934
HIVANT70      ----A---------T---G------C-----------A-G-----------------------------  2008
HIVMVP5180    -----CA--------C-----------G----TA----C----T-----C-----------------C---  2047
HIVVAU        ------------------------G-------------------------------------------  2050

CONSENSUS.CPZ A?A???AGCACA????CAACAAGAGA?AAAT?AAA?GGA??TAT??GAA?T?GA??AATGG??C???TT?T  1115
SIVCPZGAB     -G-GGA------ATCA----------A----G---G---CC---TG---T-G--TC-----GC-AGC--G-  1981

CONSENSUS.U   TGAagAcTCgCAaAacCAGCAgGAAAAGAaTGAacAAGA?tTAtTggaATTgGAcAAaTGGGCAAgTtTGT  1867
HIVZAM184     ---G--------G-------------------G-----C-------C---A-------------A-----  1963
HIVK124A      ----A-A-------C------A----------------GC----AC----------------------  2017
HIVZ3         ---------A-----A-------------G----A----T---C----------T--G---------C---  1994
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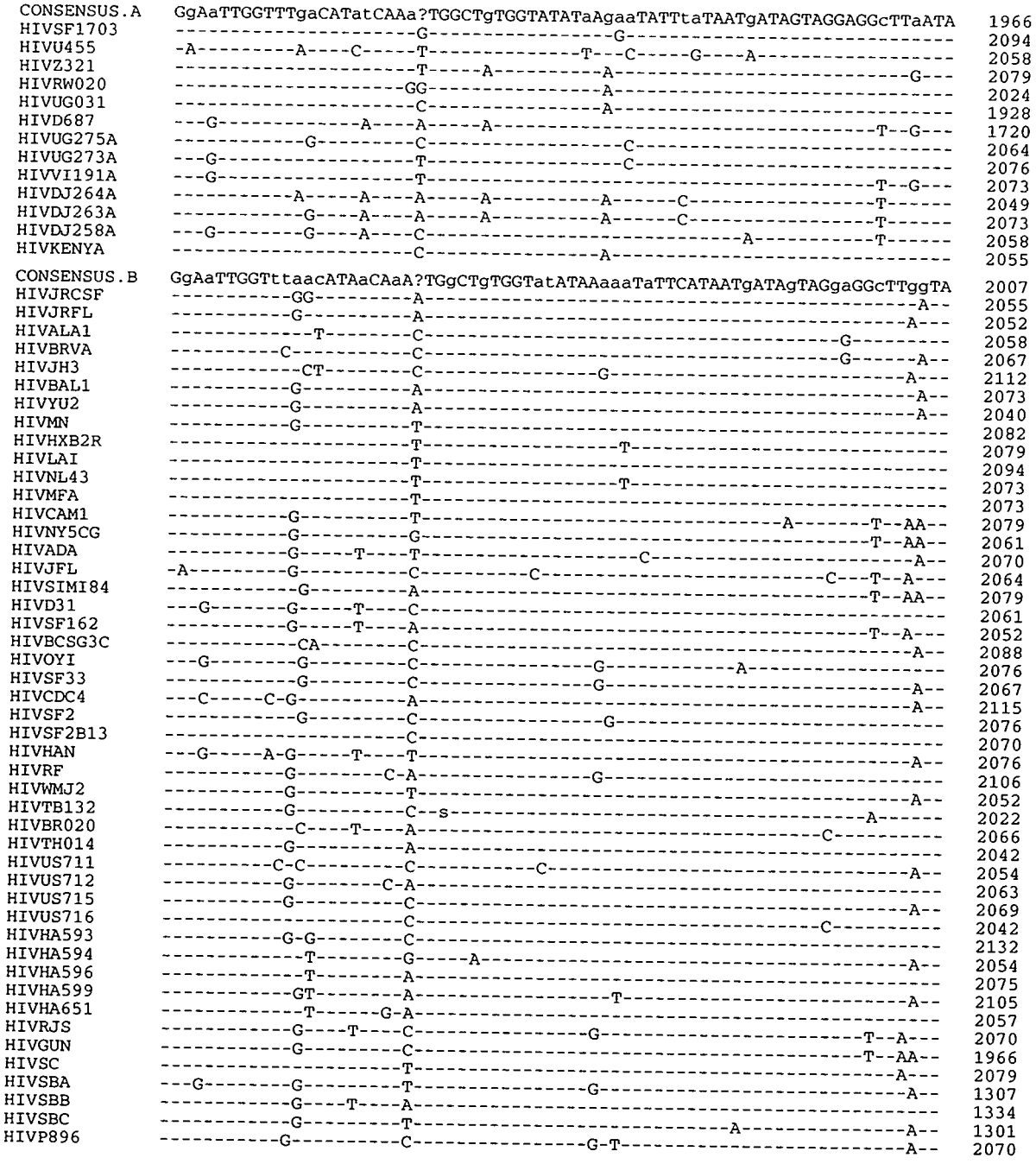
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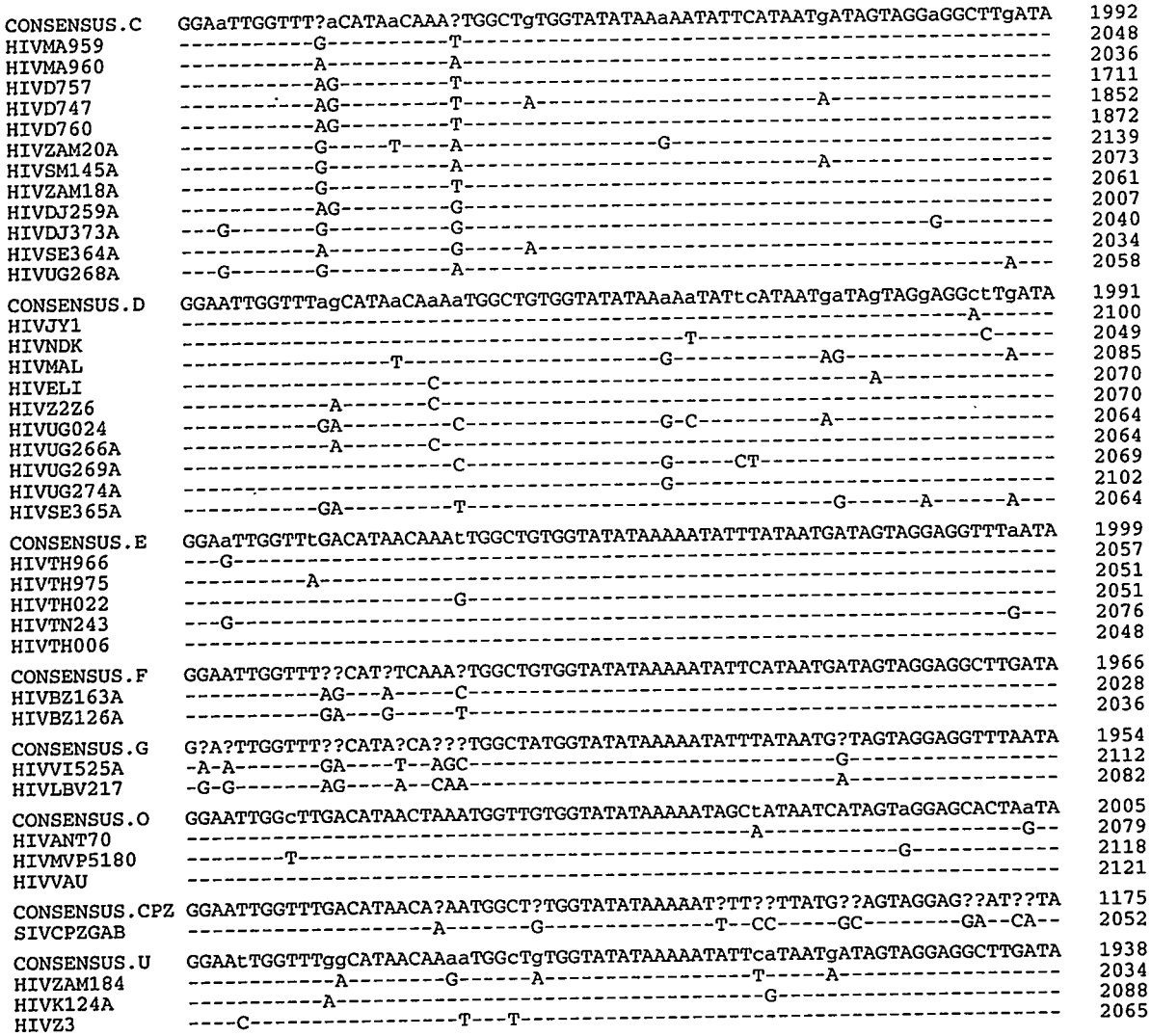
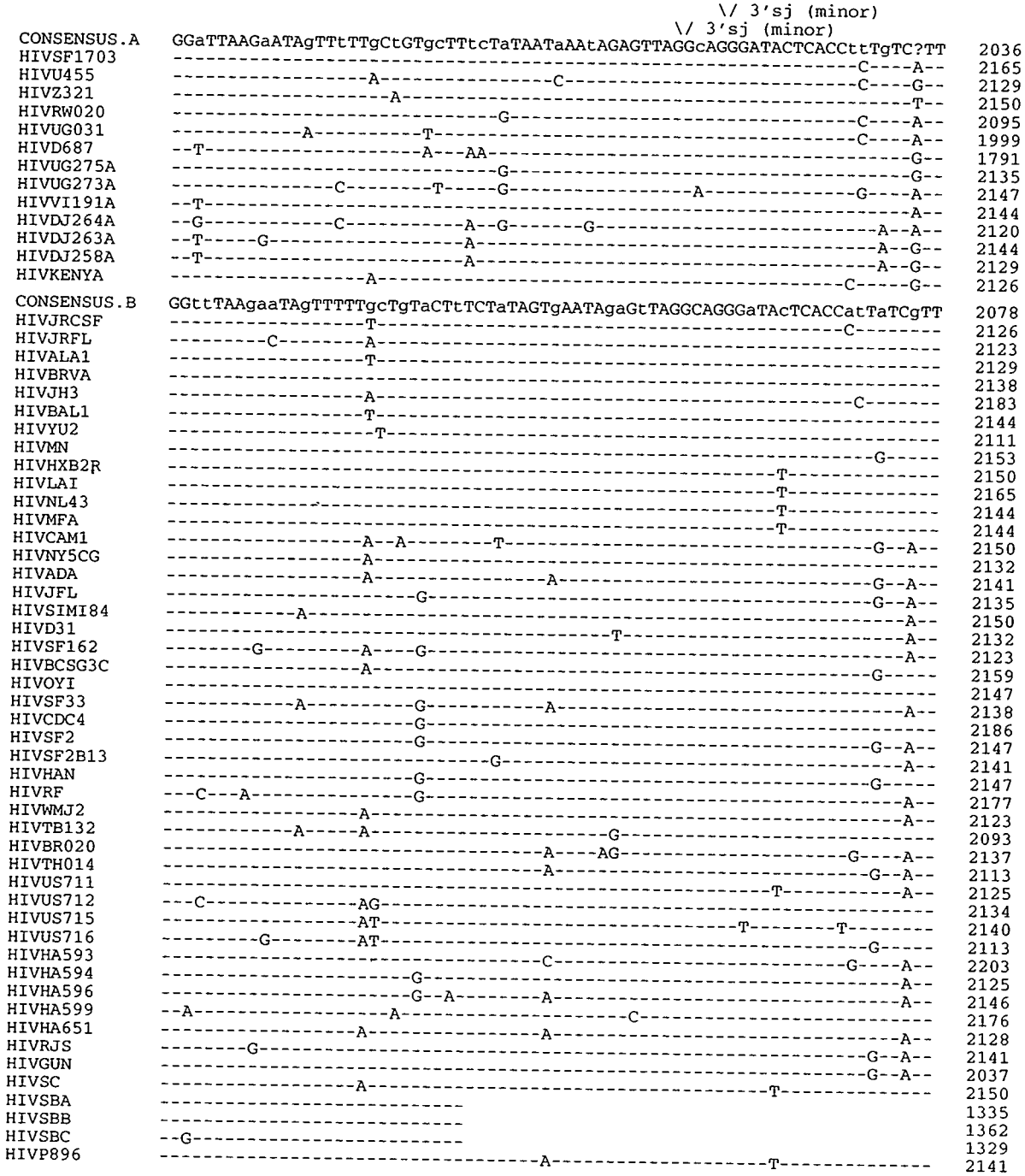
HIVSF1703 ----------G---------G---------- 2094
HIVU455 -A---------A----C-----T----------T---C-----G----A---------- 2058
HIVZ321 ----------T-----A----------A----------G--- 2079
HIVRW020 ----------GG----------A---------- 2024
HIVUG031 ----------C----------A---------- 1928
HIVD687 ---G----------A----A-----A----------T--G--- 1720
HIVUG275A ----------G---------C----------C---------- 2064
HIVUG273A ---G----------T----------C---------- 2076
HIVVI191A ---G----------T----------T--G--- 2073
HIVDJ264A ----------A-----A----A-----A----------A------C----------T------ 2049
HIVDJ263A ----------G----A----A-----A----------A------C----------T------ 2073
HIVDJ258A ---G--------G----A----C----------A----------T------ 2058
HIVKENYA ----------C----------A---------- 2055
CONSENSUS.B GgAaTTGGTttaacATAaCAaA?TGgCTgTGGTatATAAaaaTaTTCATAATgATAgTAGgaGGcTTggTA 2007
HIVJRCSF ----------GG---------A----------A--- 2055
HIVJRFL ----------G----------A----------A--- 2052
HIVALA1 ----------T--------C----------G---------- 2058
HIVBRVA ----------C----------C----------G------A-- 2067
HIVJH3 ----------CT--------C----------G----------A--- 2112
HIVBAL1 ----------G----------A----------A-- 2073
HIVYU2 ----------G----------A----------A-- 2040
HIVMN ----------G----------T---------- 2082
HIVHXB2R ----------T----------T---------- 2079
HIVLAI ----------T---------- 2094
HIVNL43 ----------T----------T---------- 2073
HIVMFA ----------T---------- 2073
HIVCAM1 ----------G----------T----------A-------T--AA-- 2079
HIVNY5CG ----------G----------G----------T--AA-- 2061
HIVADA ----------G-----T----T----------C----------A-- 2070
HIVJFL -A---------G----------C----------C----------C---T--A--- 2064
HIVSIMI84 ----------G---------A----------T--AA-- 2079
HIVD31 ---G-------G-----T----C---------- 2061
HIVSF162 ----------G-----T----A----------T--A--- 2052
HIVBCSG3C ----------CA--------C----------A-- 2088
HIVOYI ---G--------G---------C----------G----------A---------- 2076
HIVSF33 ----------G---------C----------G----------A-- 2067
HIVCDC4 ---C-----C-G----------A----------A-- 2115
HIVSF2 ----------G---------C----------G---------- 2076
HIVSF2B13 ----------C---------- 2070
HIVHAN ---G-----A-G-----T----T----------A-- 2076
HIVRF ----------G--------C-A----------G---------- 2106
HIVWMJ2 ----------G----------T----------A-- 2052
HIVTB132 ----------G----------C--s----------A------ 2022
HIVBR020 ----------C----T----A----------C---------- 2066
HIVTH014 ----------G----------A---------- 2042
HIVUS711 ----------C-C---------C----------C----------A-- 2054
HIVUS712 ----------G---------C-A---------- 2063
HIVUS715 ----------G----------C----------A-- 2069
HIVUS716 ----------C----------C---------- 2042
HIVHA593 ----------G-G--------C---------- 2132
HIVHA594 ----------T--------G-----A----------A-- 2054
HIVHA596 ----------T--------A---------- 2075
HIVHA599 ----------GT--------A----------T----------A-- 2105
HIVHA651 ----------T------G-A---------- 2057
HIVRJS ----------G----T----C----------G----------T--A--- 2070
HIVGUN ----------G---------C----------T--AA-- 1966
HIVSC ----------T----------A--- 2079
HIVSBA ---G--------G---------T----------G----------A-- 1307
HIVSBB ----------G----T----A---------- 1334
HIVSBC ----------G---------T----------A----------A-- 1301
HIVP896 ----------G----------C----------G-T----------A-- 2070


CONSENSUS.C GGAaTTGGTTT?aCATAaCAAA?TGGCTgTGGTATATAAaAATATTCATAATgATAGTAGGaGGCTTgATA 1992
HIVMA959 ----------G----------T---------- 2048
HIVMA960 ----------A----------A---------- 2036
HIVD757 ----------AG---------T---------- 1711
HIVD747 ----------AG---------T-----A----------A---------- 1852
HIVD760 ----------AG---------T---------- 1872
HIVZAM20A ----------G-----T----A----------G---------- 2139
HIVSM145A ----------G----------A----------A---------- 2073
HIVZAM18A ----------G----------T---------- 2061
HIVDJ259A ----------AG---------G---------- 2007
HIVDJ373A ---G-------G----------G----------G--------- 2040
HIVSE364A ----------A----------G-----A---------- 2034
HIVUG268A ---G-------G----------A----------A--- 2058
CONSENSUS.D GGAATTGGTTTagCATAaCAaAaTGGCTGTGGTATATAAaAaTATtcATAATgaTAgTAGgAGGctTgATA 1991
HIVJY1 ----------A------ 2100
HIVNDK ----------T----------C----- 2049
HIVMAL ----------T----------G----------AG----------A--- 2085
HIVELI ----------C----------A---------- 2070
HIVZ2Z6 ----------A-------C---------- 2070
HIVUG024 ----------GA---------C----------G-C----------A---------- 2064
HIVUG266A ----------A-------C---------- 2064
HIVUG269A ----------C----------G-----CT---------- 2069
HIVUG274A ----------G---------- 2102
HIVSE365A ----------GA---------T----------G------A------A--- 2064
CONSENSUS.E GGAaTTGGTTtGACATAACAAAtTGGCTGTGGTATATAAAAATATTTATAATGATAGTAGGAGGTTTaATA 1999
HIVTH966 ---G---------- 2057
HIVTH975 ----------A---------- 2051
HIVTH022 ----------G---------- 2051
HIVTN243 ---G----------G--- 2076
HIVTH006 ---------- 2048
CONSENSUS.F GGAATTGGTTT??CAT?TCAAA?TGGCTGTGGTATATAAAAATATTCATAATGATAGTAGGAGGCTTGATA 1966
HIVBZ163A ----------AG---A-----C---------- 2028
HIVBZ126A ----------GA---G-----T---------- 2036
CONSENSUS.G G?A?TTGGTTT??CATA?CA???TGGCTATGGTATATAAAAATATTTATAATG?TAGTAGGAGGTTTAATA 1954
HIVVI525A -A-A-------GA----T--AGC----------G---------- 2112
HIVLBV217 -G-G-------AG----A--CAA----------A---------- 2082
CONSENSUS.O GGAATTGGcTTGACATAACTAAATGGTTGTGGTATATAAAAATAGCtATAATCATAGTaGGAGCACTAaTA 2005
HIVANT70 ----------A----------G-- 2079
HIVMVP5180 --------T----------G---------- 2118
HIVVAU ---------- 2121
CONSENSUS.CPZ GGAATTGGTTTGACATAACA?AATGGCT?TGGTATATAAAAAT?TT??TTATG??AGTAGGAG??AT??TA 1175
SIVCPZGAB ----------A-------G----------T--CC-----GC--------GA--CA-- 2052
CONSENSUS.U GGAAtTGGTTTggCATAACAAaaTGGcTgTGGTATATAAAAATATTcaTAATgATAGTAGGAGGCTTGATA 1938
HIVZAM184 ----------A--------G------A----------T-----A---------- 2034
HIVK124A ----------A----------G---------- 2088
HIVZ3 ----C----------T---T---------- 2065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CONSENSUS.A GGaTTAAGaATAgTTtTTgCtGTgcTTtcTaTAATaAAtAGAGTTAGGcAGGGATACTCACCttTgTC?TT 2036
HIVSF1703 2036
HIVU455 2165
HIVZ321 2129
HIVRW020 2150
HIVUG031 2095
HIVD687 1999
HIVUG275A 1791
HIVUG273A 2135
HIVVI191A 2147
HIVDJ264A 2144
HIVDJ263A 2120
HIVDJ258A 2144
HIVKENYA 2129
CONSENSUS.B GGttTAAgaaTAgTTTTTgcTgTaCTtTCTaTAGTgAATAgaGtTAGGCAGGGaTAcTCACCatTaTCgTT 2078
HIVJRCSF 2126
HIVJRFL 2123
HIVALA1 2129
HIVBRVA 2138
HIVJH3 2183
HIVBAL1 2144
HIVYU2 2111
HIVMN 2153
HIVHXB2R 2150
HIVLAI 2165
HIVNL43 2144
HIVMFA 2144
HIVCAM1 2150
HIVNY5CG 2132
HIVADA 2141
HIVJFL 2135
HIVSIMI84 2150
HIVD31 2132
HIVSF162 2123
HIVBCSG3C 2159
HIVOYI 2147
HIVSF33 2138
HIVCDC4 2186
HIVSF2 2147
HIVSF2B13 2141
HIVHAN 2147
HIVRF 2177
HIVWMJ2 2123
HIVTB132 2093
HIVBR020 2137
HIVTH014 2113
HIVUS711 2125
HIVUS712 2134
HIVUS715 2140
HIVUS716 2113
HIVHA593 2203
HIVHA594 2125
HIVHA596 2146
HIVHA599 2176
HIVHA651 2128
HIVRJS 2141
HIVGUN 2037
HIVSC 2150
HIVSBA 1335
HIVSBB 1362
HIVSBC 1329
HIVP896 2141

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CONSENSUS.C   GGtTTaAgAATAAtTTTTGcTGTGCTcTcTATAGTgAATAGAGTtAgGcagGGaTACTCACCttTgTCgTT  2063
HIVMA959      ------------------------T--------A-----------------------------------  2119
HIVMA960      -----G-----------------------------A-----------------------------------  2107
HIVD757       -----G-A-------------------------------------------------------------A-----  1782
HIVD747       --C--G--------------------T-G------A----------A-GCA--------------------  1923
HIVD760       -----G-----------------------------------------------------------------  1943
HIVZAM20A     -------------------------A---------------------------------------------  2210
HIVSM145A     -------------------T---------------------------------------------------  2144
HIVZAM18A     --C----------G-----------T---------------------------------------------  2132
HIVDJ259A     -----------------------------------------------------G--------GC-A-----  2078
HIVDJ373A     -------------------------T-----------------------------------A--A--A--  2111
HIVSE364A     ---------------------------------------------C-------------------------  2105
HIVUG268A     ---------------------------------------------A-------------A--A-----  2129

CONSENSUS.D   GGtTTAAGaATAgTtTTTgCTGTGcTTTCTtTAGTAAATAGAGTTAGGCAGGGATAtTCACCTCTgTC?tT  2061
HIVJY1        -----------------A-----------------------------------------------A--  2171
HIVNDK        ----------------------------G-----------------------C-----------A--  2120
HIVMAL        ------------A---------------------------------------C-----------G--  2156
HIVELI        -----------------------------------------------------C-----------G--  2141
HIVZ2Z6       -----------------------------------------------------------------A--  2141
HIVUG024      -----------------------------------------------------------------A--  2135
HIVUG266A     --------G-----C-------------------------------------------------GC-  2135
HIVUG269A     --------G---------------T-----------------------------------C--G--  2140
HIVUG274A     -----------------------------------------------------------------A--  2173
HIVSE365A     --G---------A-----------------------------------------C-----------G--  2135

CONSENSUS.E   GGTTTAAGAATAATTTTTGCTGTgCTTTCTATAGTgAATAGAGTTAGGCAGGGATACTCACCTTTGTCTtT  2070
HIVTH966      -----------------------------------------------------------------------  2128
HIVTH975      ---------------------------------A-------------------------------------  2122
HIVTH022      -----------------------------------------------------------------------  2122
HIVTN243      ----------------------K------------------------------------------------C-  2147
HIVTH006      ------------------------------------A-------------------------------------  2119

CONSENSUS.F   GGCTTAAGAATAGTTTTTGCTGTGCTTTCTATAGTAAATAGAGTTAGGAAGG?ATACTCACCTTTGTCATT  2036
HIVBZ163A     ---------------------------------------------------C-------------------  2099
HIVBZ126A     ---------------------------------------------------G-------------------  2107

CONSENSUS.G   GGTTTAA?AATAGTTTTTGCTGTGCTTTCTATAGT?AATAGAGT?AGGCAGGGATACTCACCTCT?TCATT  2021
HIVVI525A     -------G---------------------------A--------C--------------------G-----  2183
HIVLBV217     -------A---------------------------G--------T--------------------A-----  2153

CONSENSUS.O   GGtgTaAGAGTtaTtATGATAgTACTTAATcTAGTgAAgAACATTAGGCAGGGATATCAACCCCTCTCGTT  2076
HIVANT70      --G--G--------C---------------A-------A---------------------------------  2150
HIVMVP5180    ---A-----------------A-----------------------------------------------  2189
HIVVAU        ----------AG----------------------A-----------------------------------  2192

CONSENSUS.CPZ GG??TAAGAATT?T??T???A?T??T?????????T?AG?A??GTTAGGCAGGG?TA????CCTCT?TC?TT  1216
SIVCPZGAB     --GT--------A-TA-GAC-G-TT-CTCAGTAG-C--G-GA----------C--CTCA-----C--G--  2123

CONSENSUS.U   GG?TTAAGaATAGTTtTTgCTaTg?TTTCT?TAgTAAATAGAGTTAGGCAGGGATAcTCACCTtTGTC?TT  2005
HIVZAM184     --A----------A-------AA-----G-----------------------------------------A--  2105
HIVK124A      --T-----G---------------C-----T-------------------------T------C----G--  2159
HIVZ3         --C---------------A--G--T-----A--A---------------------------------T--  2136
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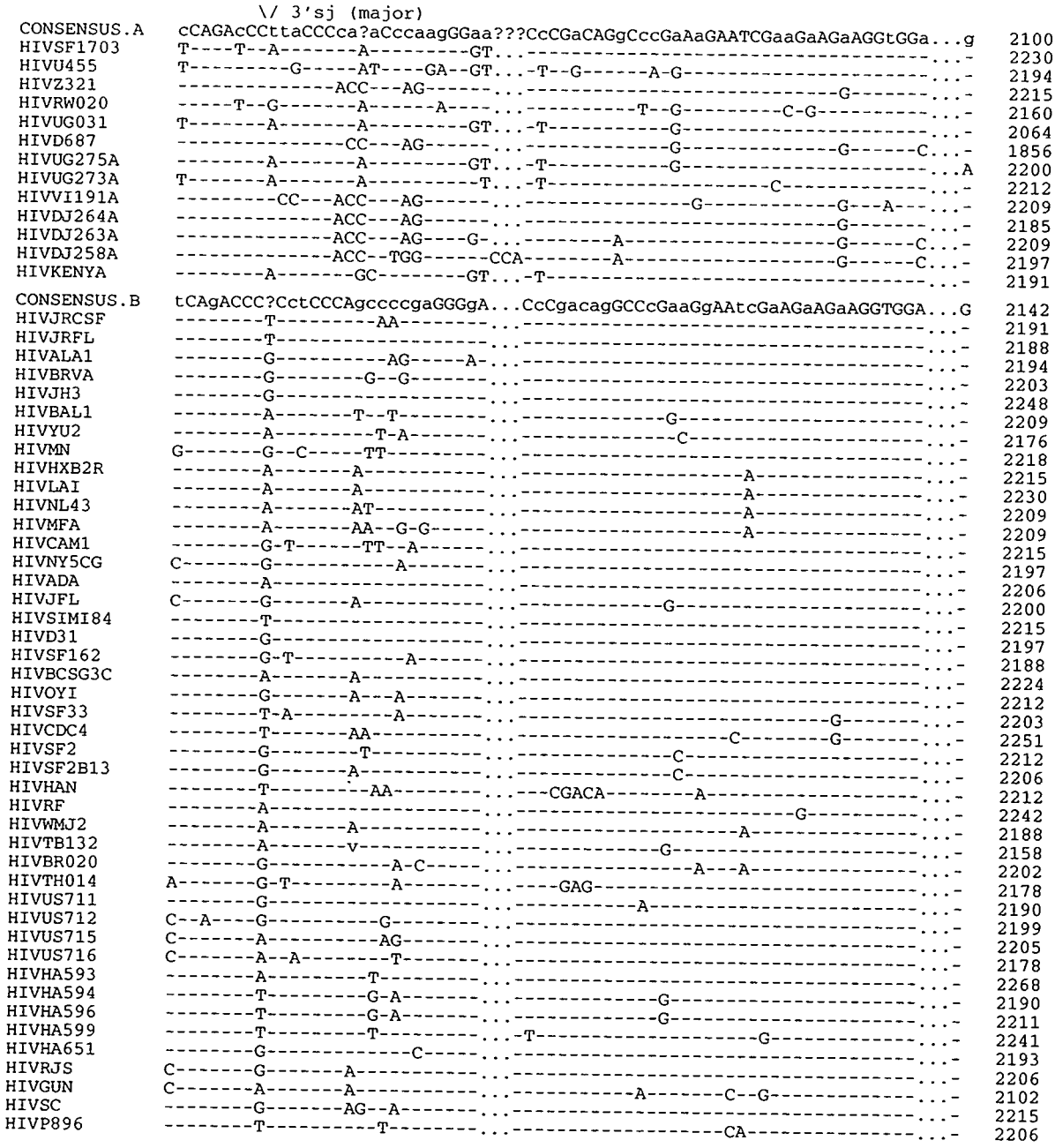
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CONSENSUS.A cCAGAcCCttaCCCca?aCccaagGGaa???CcCGaCAGgCccGaAaGAATCGaaGaAGaAGGtGGa...g 2100
HIVSF1703 T----T--A-------A---------GT... 2230
HIVU455 T---------G-----AT----GA--GT...-T--G------A-G---------- 2194
HIVZ321 -------------ACC---AG------... 2215
HIVRW020 -----T--G-------A------A----...----------T--G---------C-G---------- 2160
HIVUG031 T-------A-------A---------GT...-T----------G---------- 2064
HIVD687 ---------------CC---AG------...----------G----------G------C... 1856
HIVUG275A --------A-------A---------GT...-T----------G----------A 2200
HIVUG273A T-------A-------A---------T...-T----------C---------- 2212
HIVVI191A ---------CC---ACC---AG------...----------G----------G---A---... 2209
HIVDJ264A -------------ACC---AG------...----------G--------... 2185
HIVDJ263A -------------ACC---AG----G-...--------A----------G------C... 2209
HIVDJ258A -------------ACC--TGG------CCA--------A----------G------C... 2197
HIVKENYA --------A-------GC--------GT...-T---------- 2191
CONSENSUS.B tCAgACCC?CctCCCAgccccgaGGGgA...CcCgacagGCCcGaaGgAAtcGaAGaAGaAGGTGGA...G 2142
HIVJRCSF --------T---------AA--------... 2191
HIVJRFL --------T----------... 2188
HIVALA1 --------G----------AG-----A-... 2194
HIVBRVA --------G--------G--G-------... 2203
HIVJH3 --------G----------... 2248
HIVBAL1 --------A-------T--T--------...----------G---------- 2209
HIVYU2 --------A---------T-A-------...----------C---------- 2176
HIVMN G-------G--C------TT---------... 2218
HIVHXB2R --------A-------A----------...----------A---------- 2215
HIVLAI --------A-------A----------...----------A---------- 2230
HIVNL43 --------A-------AT---------...----------A---------- 2209
HIVMFA --------A-------AA--G-G-----...----------A---------- 2209
HIVCAM1 --------G-T------TT--A------... 2215
HIVNY5CG C-------G----------A-------... 2197
HIVADA --------A----------... 2206
HIVJFL C-------G-------A----------...----------G---------- 2200
HIVSIMI84 --------T----------... 2215
HIVD31 --------G----------... 2197
HIVSF162 --------G-T---------A------... 2188
HIVBCSG3C --------A-------A---------... 2224
HIVOYI --------G-------A---A-------... 2212
HIVSF33 --------T-A---------A-------...----------G-------- 2203
HIVCDC4 --------T-------AA---------...----------C--------G-------... 2251
HIVSF2 --------G--------T---------...----------C---------- 2212
HIVSF2B13 --------G-------A----------...----------C---------- 2206
HIVHAN --------T---------AA---------...---CGACA--------A---------- 2212
HIVRF --------A----------...----------G---------- 2242
HIVWMJ2 --------A-------A----------...----------A---------- 2188
HIVTB132 --------A-------v----------...----------G---------- 2158
HIVBR020 --------G----------A-C-----...----------A---A---------- 2202
HIVTH014 A-------G-T---------A-------...----GAG---------- 2178
HIVUS711 --------G----------...----------A---------- 2190
HIVUS712 C--A----G---------G--------... 2199
HIVUS715 C-------A----------AG-------... 2205
HIVUS716 C-------A--A--------T-------... 2178
HIVHA593 --------A---------T---------... 2268
HIVHA594 --------T---------G-A-------...----------G---------- 2190
HIVHA596 --------T---------G-A-------...----------G---------- 2211
HIVHA599 --------T---------T---------...-T----------G---------- 2241
HIVHA651 --------G----------C-----... 2193
HIVRJS C-------G-------A----------... 2206
HIVGUN C-------A-------A----------...----------A-------C--G---------- 2102
HIVSC --------G-------AG--A-------... 2215
HIVP896 --------T----------T--------...----------CA---------- 2206

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CONSENSUS.C     tCAGACCCTTAcCCCaAaCccgaGGGGa???CcCGACAGGCtCggAagAATCGAAGaAGaAGGTGGA...G  2128
HIVMA959        ----------------------------...----------------------------------...-  2184
HIVMA960        ----------------------------...-T--------------------------------...-  2172
HIVD757         ---------------G-----AG-----...-------------A-----------G--G-------...-  1847
HIVD747         ---------------G--                                                       1941
HIVD760         -------                                                                  1950
HIVZAM20A       ---------------G---ATC-----GGAA----------------------------------...-  2278
HIVSM145A       ----------------------------...----------------------------------...-  2209
HIVZAM18A       ---------------G-----A------...----------------------------------...-  2197
HIVDJ259A       ----------------------------...----------C----G--------------------...-  2143
HIVDJ373A       -----------T---G-----A------...----------C-A--G--------------------...-  2176
HIVSE364A       C----------T----------------...----------------------------------...-  2170
HIVUG268A       ----------------C----------...----------C----GA--------------------...-  2194

CONSENSUS.D     tCAGACCCTCCTCCCAgccCCGAGGGgA???CCCGACAGGCCCGaAGgAAtAGAAGAAGAAGGTGGA...G  2126
HIVJY1          ----------------------------...----------------------------------...-  2236
HIVNDK          ----------T----------...----------------A-------------------...-  2185
HIVMAL          G---------------A-A---------CCA----------------------------------...-  2224
HIVELI          ----------------------------...-------------------C----------------...-  2206
HIVZ2Z6         ----------------------------...----------------------------------...-  2206
HIVUG024        ----------A----------...-------------G--A--C----------------...-  2200
HIVUG266A       ----------------------------...-------------------C----------------...-  2200
HIVUG269A       ----------------------------...----------------------------------...-  2205
HIVUG274A       -------------------------A-...----------------A-------------------...-  2238
HIVSE365A       ----------------A----------...----------------------------------...-  2200

CONSENSUS.E     CCAGAcCCcTacCCATCAtCAGaGGGAA...CcCGACAGACCCGAAAGAATCGAAGAAGgAGGTGGC...G  2135
HIVTH966        ----------T------G---------...----------------------------------...-  2193
HIVTH975        ----------TA----------------...----------------------------A-------...-  2187
HIVTH022        -----T----C----------------...----------------------------------...-  2187
HIVTN243        ----------------------------...-T--------------------------------...-  2212
HIVTH006        --------T-------------G-----...----------------------------------...-  2184

CONSENSUS.F     ?CAGACCCATATCCCAAGCCCGAGGGAA...CCCGACAGGCCCGAAG?AATCGAAGAAGGAGGTGGA...G  2099
HIVBZ163A       T---------------------------...----------------A-------------------...-  2164
HIVBZ126A       A---------------------------...----------------G-------------------...-  2172

CONSENSUS.G     CCAGACCCTT?CCCA?CA?CA??GGGAA...CCCGACAGGC??GAAAGAATCGAAGAAGGAGGTGGC...G  2079
HIVVI525A       ----------A----T--C--AG-----...----------TC-----------------------...-  2248
HIVLBV217       ----------G----C--T--GA-----...----------CT-----------------------...-  2218

CONSENSUS.O     aCAGATCCCcatCCaaCAcCaagaGGAA...GcAGgAACGCCAGGAaGAACAGGAGaAGgAGGTGGA...G  2141
HIVANT70        -----------A---T------------...-------------------------G----------...-  2215
HIVMVP5180      G--------TG---C-----GGC-----...----A----------------------A-------...-  2254
HIVVAU          ------------------A----C----...-T-------------G--------------------...-  2257

CONSENSUS.CPZ   ?CAGA?CC?TA?CC?A??CCAG??GGA?...C?AG????GC??G?AGAAAT????GAAG?AGGTGG?...?  1256
SIVCPZGAB       G----C--T--T--C-GT----AG---A...-A--GAAG--TC-G------CGAC----G------C...G  2188

CONSENSUS.U     tCAGAcCCtcctCCCA?cCCCgagGGGa...CccGACAGGCCcGgAaGAAtcGAAGAAGaAGGTGGA...G  2069
HIVZAM184       -----T--CTAC----CA---AGA---T...-T----------------------------G-------...-  2170
HIVK124A        ----------------G-----------...--A----------A-G----A----------------...-  2224
HIVZ3           C---------------A-----------...-----------A-------C----------------...-  2201
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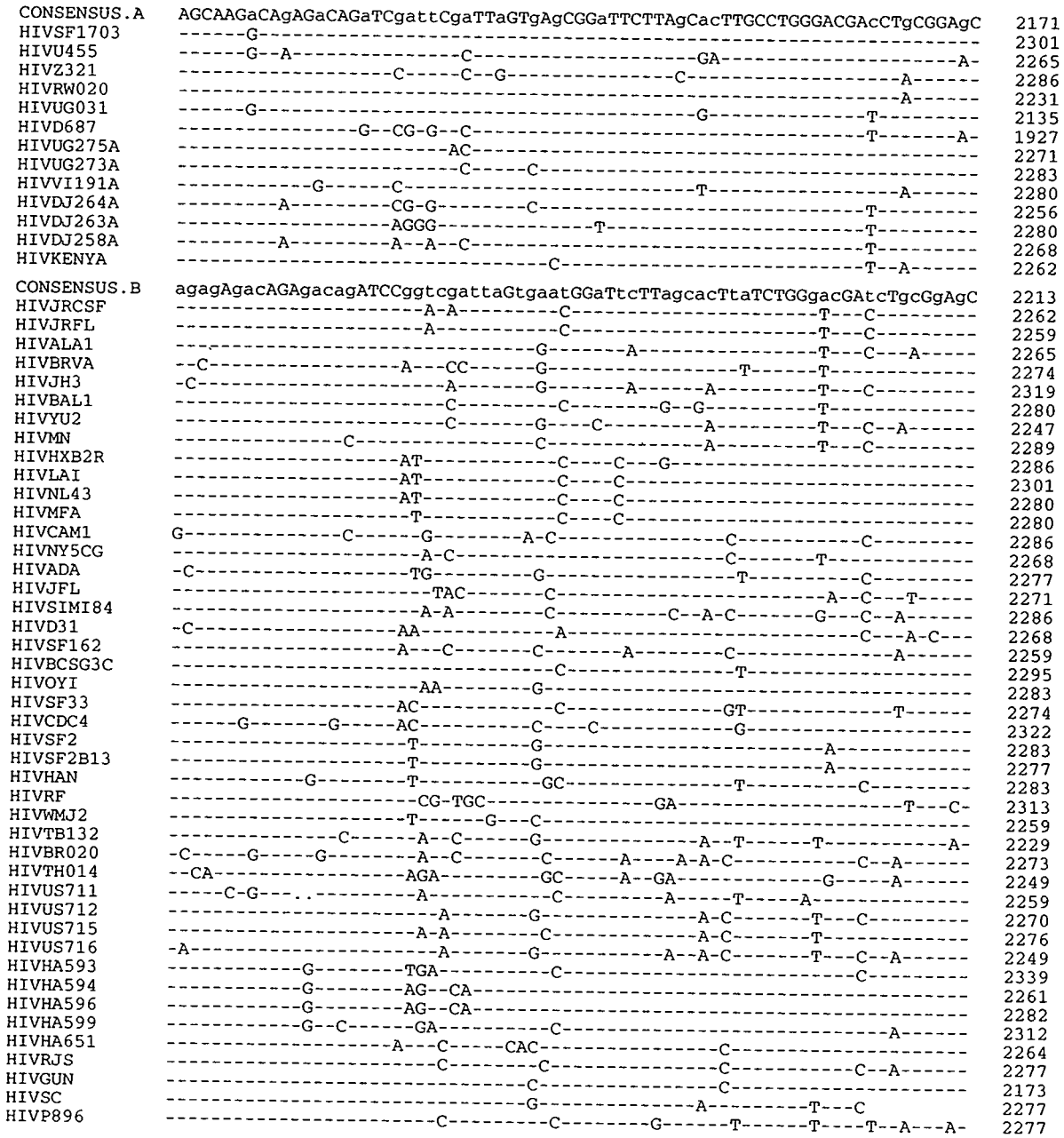
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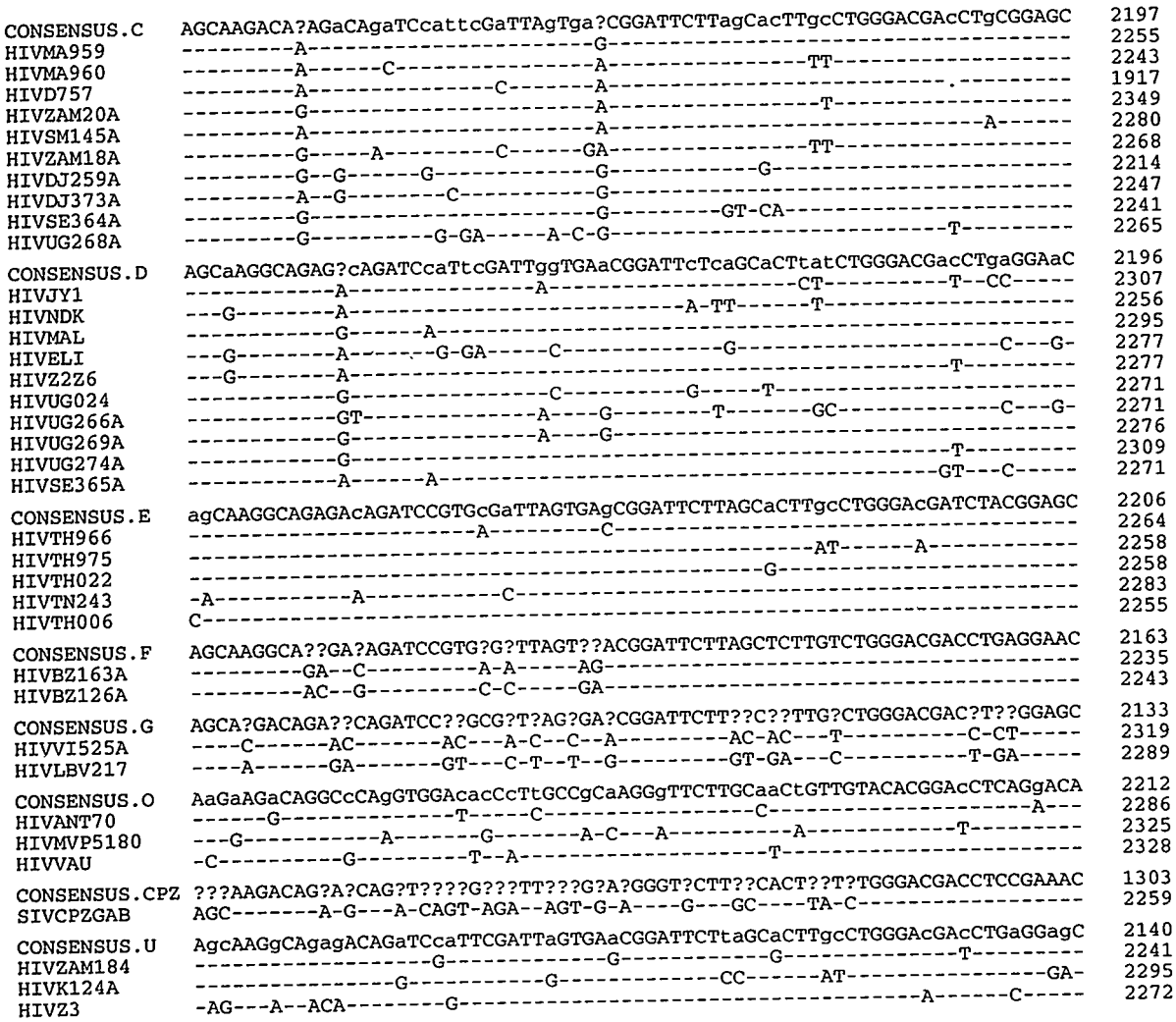
HIVSF1703 ------G---------- 2301
HIVU455 ------G--A----------C----------GA----------A- 2265
HIVZ321 ----------C-----C--G----------C----------A------ 2286
HIVRW020 ----------A------ 2231
HIVUG031 ------G----------G----------T--------- 2135
HIVD687 ----------G--CG-G--C----------T-------A- 1927
HIVUG275A ----------AC---------- 2271
HIVUG273A ----------C-----C---------- 2283
HIVVI191A ----------G------C----------T----------A------ 2280
HIVDJ264A ---------A---------CG-G--------C----------T--------- 2256
HIVDJ263A ----------AGGG----------T----------T--------- 2280
HIVDJ258A ---------A---------A--A--C----------T--------- 2268
HIVKENYA ----------C----------T--A------ 2262
CONSENSUS.B agagAgacAGAgacagATCCggtcgattaGtgaatGGaTtcTTagcacTtaTCTGGgacGAtcTgcGgAgC 2213
HIVJRCSF ----------A-A---------C----------T---C--------- 2262
HIVJRFL ----------A----------C----------T---C--------- 2259
HIVALA1 ----------G-------A----------T---C---A----- 2265
HIVBRVA --C----------A---CC------G----------T------T---------- 2274
HIVJH3 -C----------A-------G-------A------A---------T---C--------- 2319
HIVBAL1 ----------C---------C--------G--G----------T---------- 2280
HIVYU2 ----------C-------G----C---------A---------T---C--A------ 2247
HIVMN ----------C----------C----------A---------T---C--------- 2289
HIVHXB2R ----------AT----------C----C---G---------- 2286
HIVLAI ----------AT----------C----C---------- 2301
HIVNL43 ----------AT----------C----C---------- 2280
HIVMFA ----------T----------C----C---------- 2280
HIVCAM1 G----------C------G--------A-C----------C----------C--------- 2286
HIVNY5CG ----------A-C----------C-------T---------- 2268
HIVADA -C----------TG---------G----------T---------C--------- 2277
HIVJFL ----------TAC-------C----------A--C---T----- 2271
HIVSIMI84 ----------A-A--------C----------C--A-C-------G---C--A------ 2286
HIVD31 -C----------AA----------A----------C---A-C--- 2268
HIVSF162 ----------A---C-------C-------A--------C----------A------ 2259
HIVBCSG3C ----------C----------T---------- 2295
HIVOYI ----------AA--------G---------- 2283
HIVSF33 ----------AC----------C----------GT----------T------ 2274
HIVCDC4 ------G-------G-----AC----------C----C----------G---------- 2322
HIVSF2 ----------T----------G----------A---------- 2283
HIVSF2B13 ----------T----------G----------A---------- 2277
HIVHAN ----------G--------T----------GC----------T----------C--------- 2283
HIVRF ----------CG-TGC----------GA----------T---C- 2313
HIVWMJ2 ----------T------G---C---------- 2259
HIVTB132 ----------C------A--C------G----------A--T------T----------A- 2229
HIVBR020 -C-----G-----G--------A--C-------C------A----A-A-C----------C--A------ 2273
HIVTH014 --CA----------AGA---------GC-----A--GA----------G-----A------ 2249
HIVUS711 -----C-G---..---------A----------C---------A-----T-----A---------- 2259
HIVUS712 ----------A-------G----------A-C-------T---C--------- 2270
HIVUS715 ----------A-A--------C----------A-C-------T---------- 2276
HIVUS716 -A----------A-------G----------A--A-C-------T---C--A------ 2249
HIVHA593 ----------G--------TGA---------C----------C--------- 2339
HIVHA594 ----------G--------AG--CA---------- 2261
HIVHA596 ----------G--------AG--CA---------- 2282
HIVHA599 ----------G--C------GA----------C----------A------ 2312
HIVHA651 ----------A---C-----CAC----------C---------- 2264
HIVRJS ----------C---------C----------C----------C--A------ 2277
HIVGUN ----------C----------C----------T---C 2173
HIVSC ----------G----------A---------T---C 2277
HIVP896 ----------C---------C--------G------T------T----T--A---A- 2277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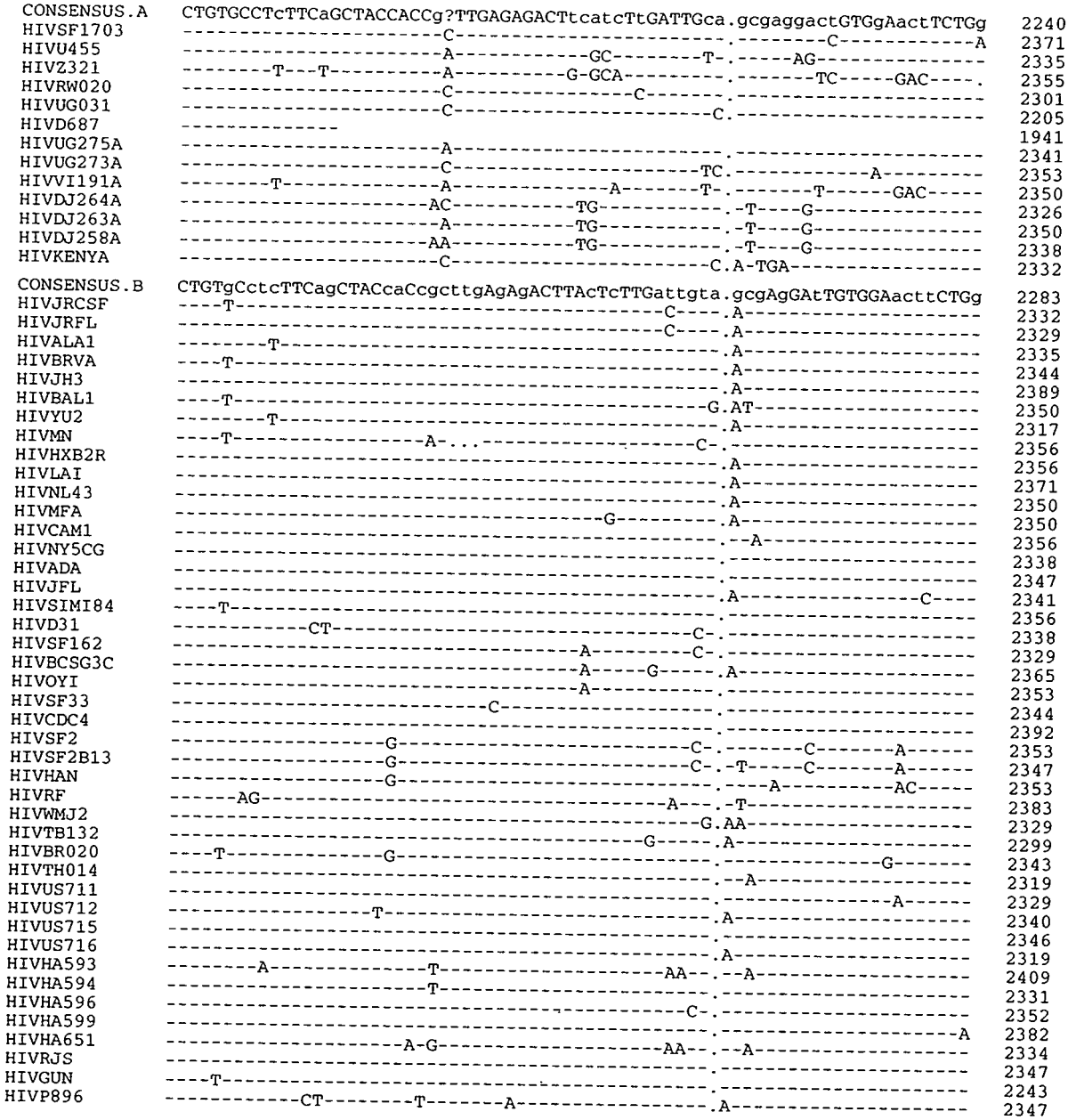
HIVMA959 ---------A----------G---------- 2255
HIVMA960 ---------A------C----------A----------TT---------- 2243
HIVD757 ---------A----------C-------A----------.--------- 1917
HIVZAM20A ---------G----------A----------T---------- 2349
HIVSM145A ---------A----------A----------A------ 2280
HIVZAM18A ---------G-----A---------C------GA----------TT---------- 2268
HIVDJ259A ---------G--G------G----------G----------G---------- 2214
HIVDJ373A ---------A--G--------C----------G---------- 2247
HIVSE364A ---------G----------G---------GT-CA---------- 2241
HIVUG268A ---------G----------G-GA-----A-C-G----------T--------- 2265
CONSENSUS.D AGCaAGGCAGAG?cAGATCcaTtcGATTggTGAaCGGATTcTcaGCaCTtatCTGGGACGacCTgaGGAaC 2196
HIVJY1 ----------A----------A----------CT----------T--CC----- 2307
HIVNDK ---G--------A----------A-TT------T---------- 2256
HIVMAL ----------G------A---------- 2295
HIVELI ---G--------A------G-GA-----C----------G----------C---G- 2277
HIVZ2Z6 ---G--------A----------T--------- 2277
HIVUG024 ----------G----------C----------G-----T---------- 2271
HIVUG266A ----------GT----------A----G--------T-------GC----------C---G- 2271
HIVUG269A ----------G----------A----G---------- 2276
HIVUG274A ----------G----------T--------- 2309
HIVSE365A ----------A------A----------GT---C----- 2271
CONSENSUS.E agCAAGGCAGAGAcAGATCCGTGcGaTTAGTGAgCGGATTCTTAGCaCTTgcCTGGGAcGATCTACGGAGC 2206
HIVTH966 ----------A---------C---------- 2264
HIVTH975 ----------AT------A---------- 2258
HIVTH022 ----------G---------- 2258
HIVTN243 -A----------A----------C---------- 2283
HIVTH006 C---------- 2255
CONSENSUS.F AGCAAGGCA??GA?AGATCCGTG?G?TTAGT??ACGGATTCTTAGCTCTTGTCTGGGACGACCTGAGGAAC 2163
HIVBZ163A ---------GA--C---------A-A-----AG---------- 2235
HIVBZ126A ---------AC--G---------C-C-----GA---------- 2243
CONSENSUS.G AGCA?GACAGA??CAGATCC??GCG?T?AG?GA?CGGATTCTT??C??TTG?CTGGGACGAC?T??GGAGC 2133
HIVVI525A ----C------AC-------AC---A-C--C--A---------AC-AC---T----------C-CT----- 2319
HIVLBV217 ----A------GA-------GT---C-T--T--G---------GT-GA---C----------T-GA----- 2289
CONSENSUS.O AaGaAGaCAGGCcCAgGTGGAcacCcTtGCCgCaAGGgTTCTTGCaaCtGTTGTACACGGAcCTCAGgACA 2212
HIVANT70 ------G----------T-----C----------C----------A--- 2286
HIVMVP5180 ---G----------A-------G-------A-C---A----------A----------T--------- 2325
HIVVAU -C----------G---------T--A----------T---------- 2328
CONSENSUS.CPZ ???AAGACAG?A?CAG?T????G???TT???G?A?GGGT?CTT??CACT??T?TGGGACGACCTCCGAAAC 1303
SIVCPZGAB AGC-------A-G---A-CAGT-AGA--AGT-G-A----G---GC----TA-C---------- 2259
CONSENSUS.U AgcAAGgCAgagACAGaTCcaTTCGATTaGTGAaCGGATTCTtaGCaCTTgcCTGGGAcGAcCTGaGGagC 2140
HIVZAM184 ----------G----------G----------G----------T--------- 2241
HIVK124A ----------G----------G----------CC------AT----------GA- 2295
HIVZ3 -AG---A--ACA--------G----------A------C----- 2272

HIV1 ENV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HIVSF1703 2371
HIVU455 2335
HIVZ321 2355
HIVRW020 2301
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HIVD687 1941
HIVUG275A 2341
HIVUG273A 2353
HIVVI191A 2350
HIVDJ264A 2326
HIVDJ263A 2350
HIVDJ258A 2338
HIVKENYA 2332
CONSENSUS.B CTGTgCctcTTCagCTACcaCcgcttgAgAgACTTAcTcTTGattgta.gcgAgGAtTGTGGAacttCTGg 2283
HIVJRCSF 2332
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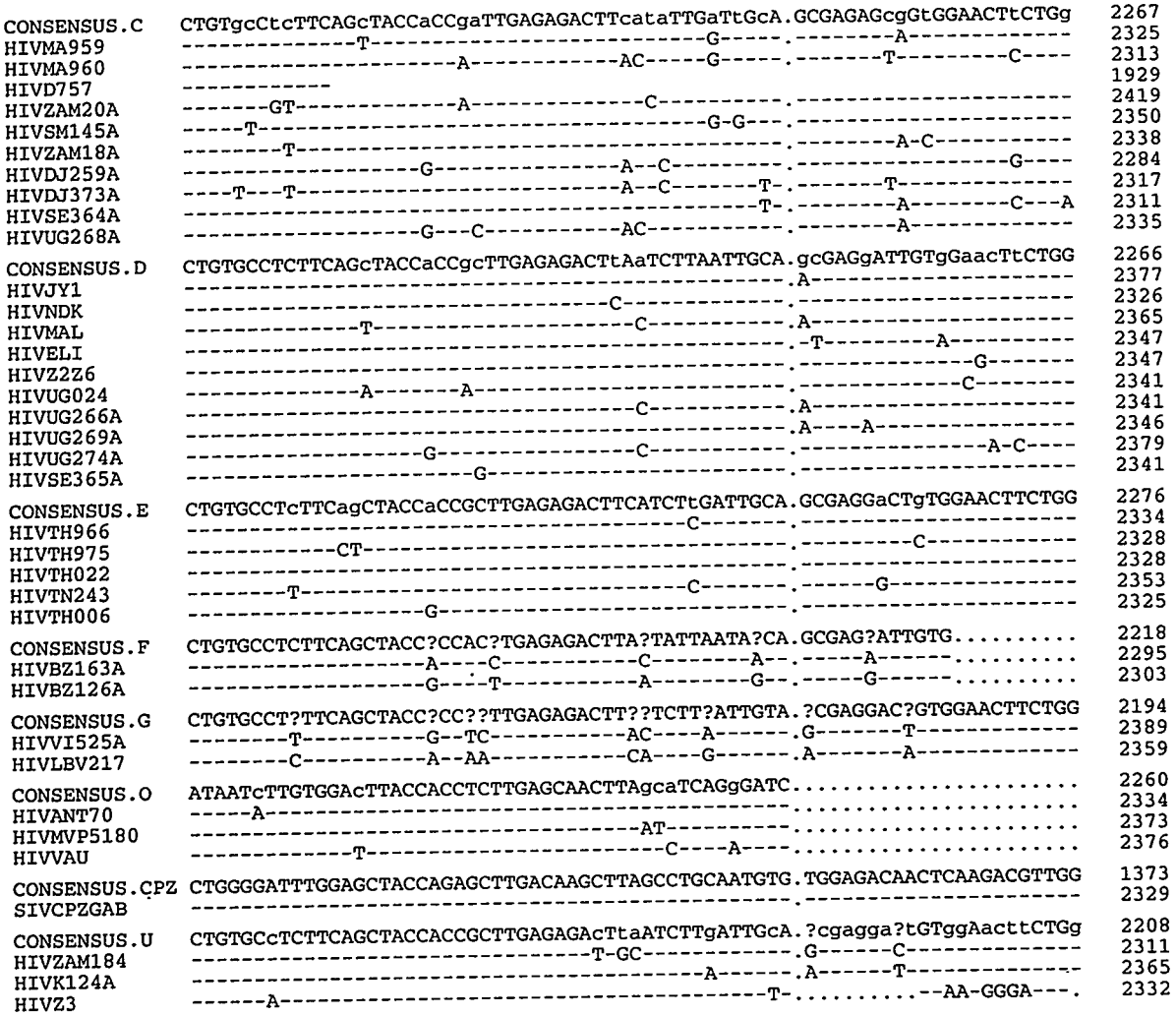
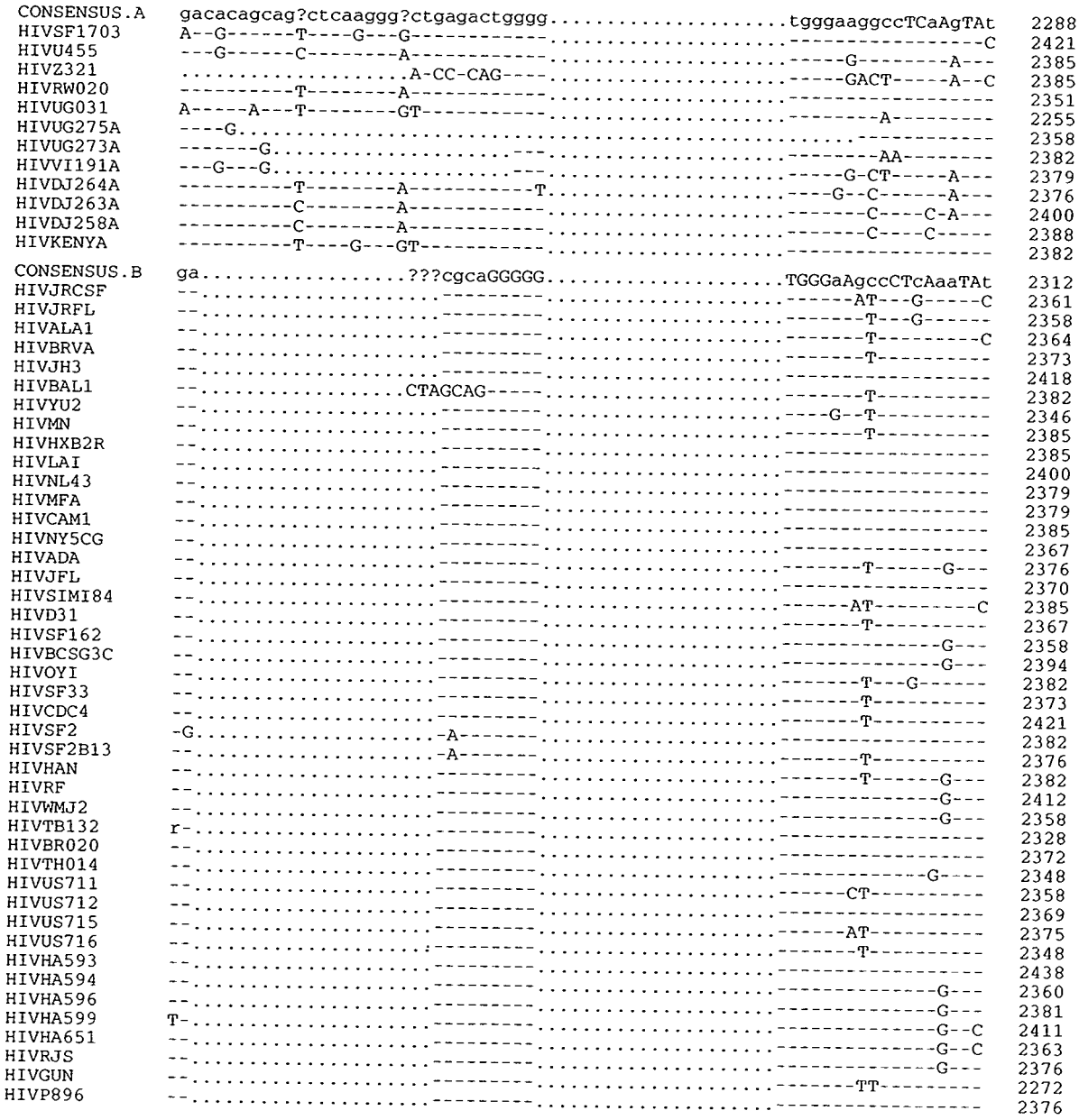
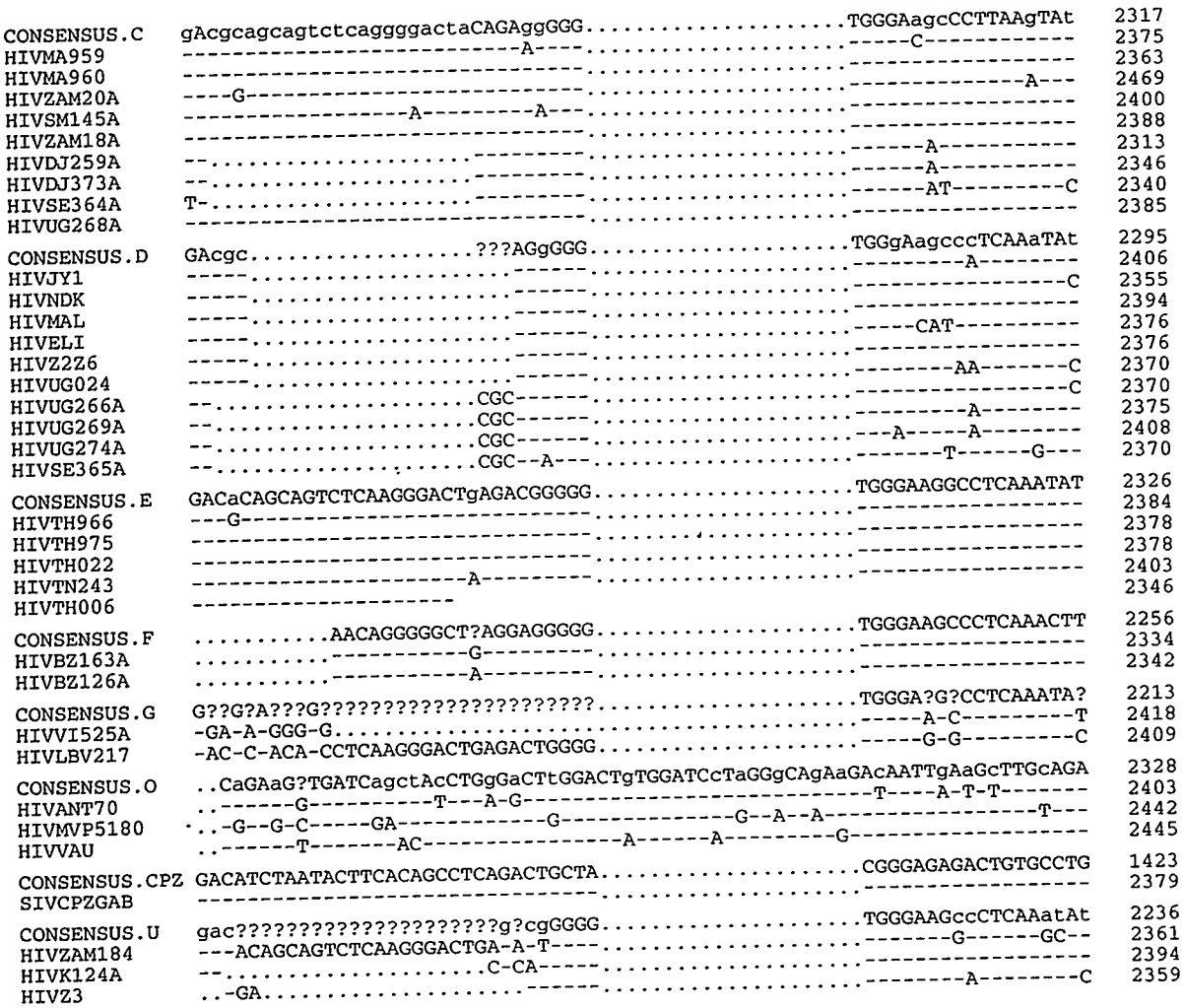
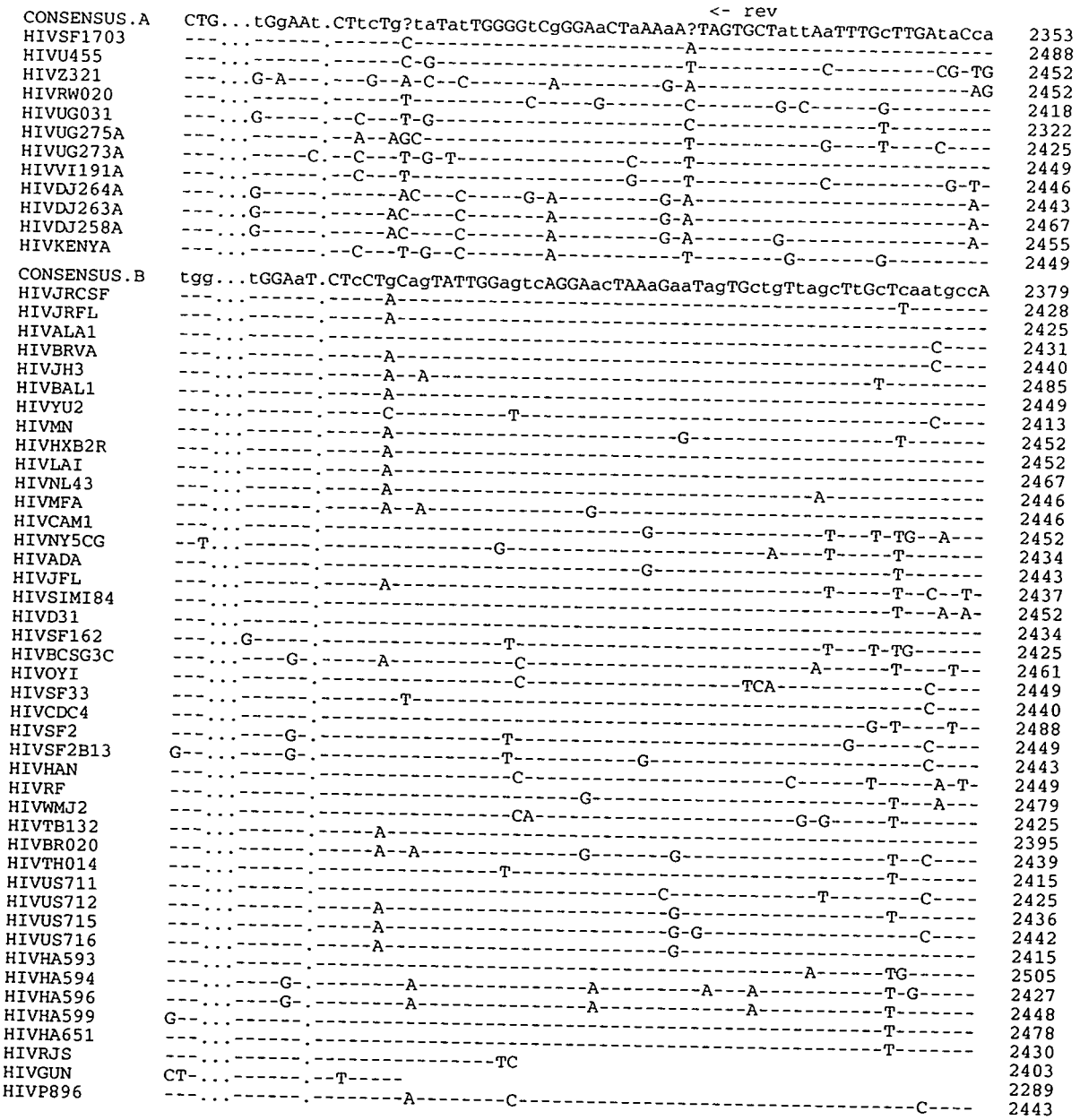
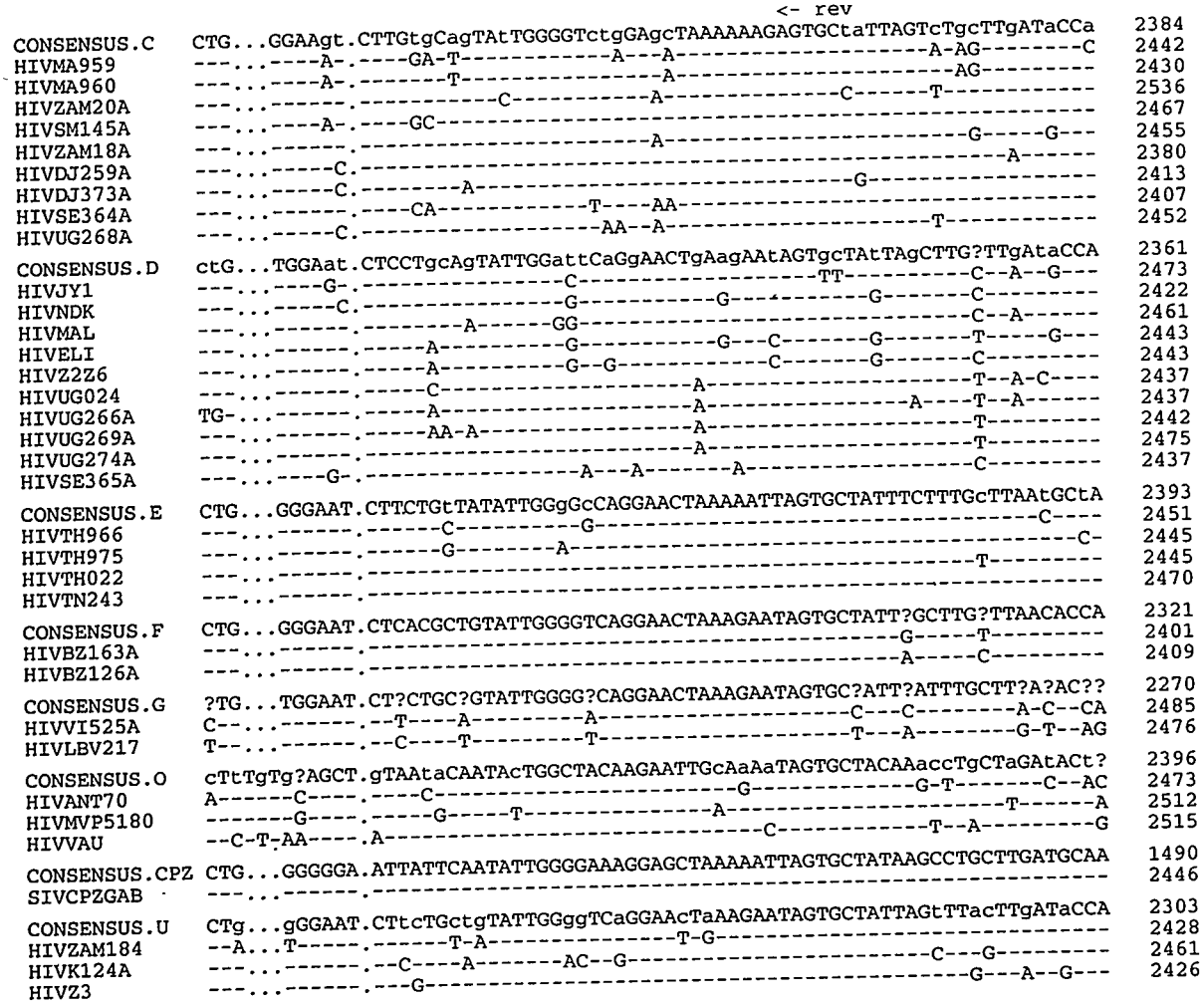
HIVGUN 2243
HIVP896 2347

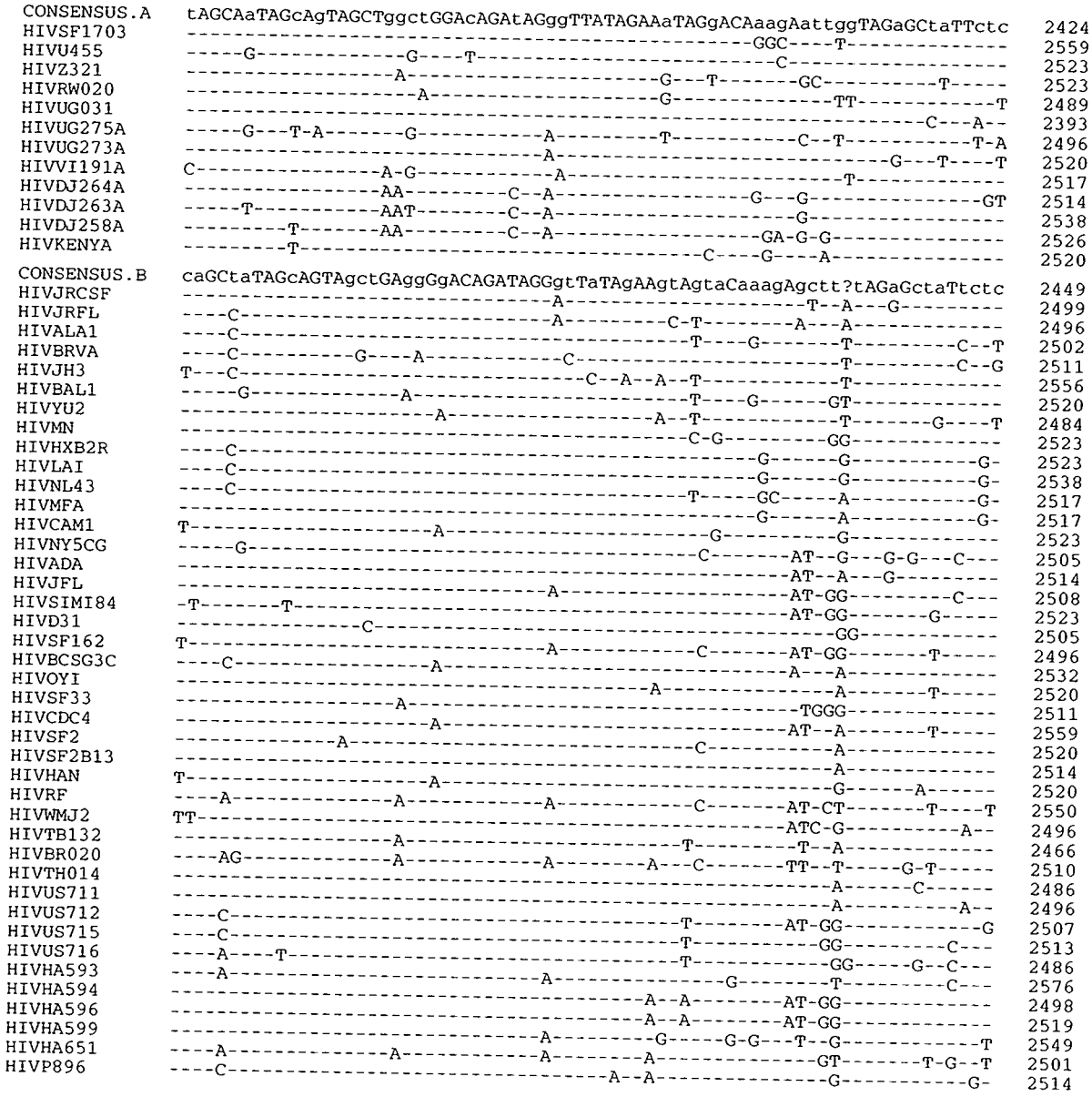



CONSENSUS.A gacacagcag?ctcaaggg?ctgagactgggg.....tgggaaggccTCaAgTAt 2288
HIVSF1703 A--G------T----G---G----------.....----------C 2421
HIVU455 ---G------C--------A----------.....-----G--------A--- 2385
HIVZ321 .....A-CC-CAG----.....-----GACT-----A--C 2385
HIVRW020 ----------T--------A----------.....---------- 2351
HIVUG031 A-----A---T--------GT----------.....--------A--------- 2255
HIVUG275A ----G.....---.....---------- 2358
HIVUG273A -------G.....---.....--------AA-------- 2382
HIVVI191A ---G---G.....---.....-----G-CT-----A--- 2379
HIVDJ264A ----------T--------A----------T.....----G--C------A--- 2376
HIVDJ263A ----------C--------A----------.....-------C----C-A--- 2400
HIVDJ258A ----------C--------A----------.....-------C----C----- 2388
HIVKENYA ----------T----G---GT----------.....---------- 2382
CONSENSUS.B ga.....???cgcaGGGGG.....TGGGaAgccCTcAaaTAt 2312
HIVJRCSF --.....---------.....------AT---G-----C 2361
HIVJRFL --.....---------.....-------T---G------ 2358
HIVALA1 --.....---------.....-------T---------C 2364
HIVBRVA --.....---------.....-------T---------- 2373
HIVJH3 --.....---------.....---------- 2418
HIVBAL1 --.....CTAGCAG-----.....-------T---------- 2382
HIVYU2 --.....---------.....----G--T---------- 2346
HIVMN --.....---------.....-------T---------- 2385
HIVHXB2R --.....---------.....---------- 2385
HIVLAI --.....---------.....---------- 2400
HIVNL43 --.....---------.....---------- 2379
HIVMFA --.....---------.....---------- 2379
HIVCAM1 --.....---------.....---------- 2385
HIVNY5CG --.....---------.....---------- 2367
HIVADA --.....---------.....-------T------G--- 2376
HIVJFL --.....---------.....---------- 2370
HIVSIMI84 --.....---------.....------AT---------C 2385
HIVD31 --.....---------.....-------T---------- 2367
HIVSF162 --.....---------.....----------G--- 2358
HIVBCSG3C --.....---------.....----------G--- 2394
HIVOYI --.....---------.....-------T---G------ 2382
HIVSF33 --.....---------.....-------T---------- 2373
HIVCDC4 --.....---------.....-------T---------- 2421
HIVSF2 -G.....-A-------.....---------- 2382
HIVSF2B13 --.....-A-------.....-------T---------- 2376
HIVHAN --.....---------.....-------T------G--- 2382
HIVRF --.....---------.....----------G--- 2412
HIVWMJ2 --.....---------.....----------G--- 2358
HIVTB132 r-.....---------.....---------- 2328
HIVBR020 --.....---------.....---------- 2372
HIVTH014 --.....---------.....----------G---- 2348
HIVUS711 --.....---------.....------CT---------- 2358
HIVUS712 --.....---------.....---------- 2369
HIVUS715 --.....---------.....------AT---------- 2375
HIVUS716 --.....---------.....-------T---------- 2348
HIVHA593 --.....---------.....---------- 2438
HIVHA594 --.....---------.....----------G--- 2360
HIVHA596 --.....---------.....----------G--- 2381
HIVHA599 T-.....---------.....----------G--C 2411
HIVHA651 --.....---------.....----------G--C 2363
HIVRJS --.....---------.....----------G--- 2376
HIVGUN --.....---------.....-------TT--------- 2272
HIVP896 --.....---------.....---------- 2376




CONSENSUS.A
HIVSF1703
HIVU455
HIVZ321
HIVRW020
HIVUG031
HIVUG275A
HIVUG273A
HIVVI191A
HIVDJ264A
HIVDJ263A
HIVDJ258A
HIVKENYA
CONSENSUS.B
HIVJRCSF
HIVJRFL
HIVALA1
HIVBRVA
HIVJH3
HIVBAL1
HIVYU2
HIVMN
HIVHXB2R
HIVLAI
HIVNL43
HIVMFA
HIVCAM1
HIVNY5CG
HIVADA
HIVJFL
HIVSIMI84
HIVD31
HIVSF162
HIVBCSG3C
HIVOYI
HIVSF33
HIVCDC4
HIVSF2
HIVSF2B13
HIVHAN
HIVRF
HIVWMJ2
HIVTB132
HIVBR020
HIVTH014
HIVUS711
HIVUS712
HIVUS715
HIVUS716
HIVHA593
HIVHA594
HIVHA596
HIVHA599
HIVHA651
HIVRJS
HIVGUN
HIVP896


<- rev
CONSENSUS.C CTG...GGAAgt.CTTGtgCagTAtTGGGGTctgGAgcTAAAAAAGAGTGCtaTTAGTcTgcTTgATaCCa 2384
HIVMA959 ---...----A-.----GA-T----------A---A----------A-AG--------C 2442
HIVMA960 ---...----A-.-------T----------A----------AG--------- 2430
HIVZAM20A ---...------.----------C----------A----------C------T---------- 2536
HIVSM145A ---...----A-.----GC---------- 2467
HIVZAM18A ---...------.----------A----------G-----G--- 2455
HIVDJ259A ---...-----C.----------A 2380
HIVDJ373A ---...-----C.--------A----------G---------- 2413
HIVSE364A ---...------.----CA----------T----AA---------- 2407
HIVUG268A ---...-----C.----------AA--A----------T---------- 2452
CONSENSUS.D ctG...TGGAat.CTCCTgcAgTATTGGattCaGgAACTgAagAAtAGTgcTAtTAgCTTG?TTgAtaCCA 2361
HIVJY1 ---...----G-.----------C----------TT----------C--A--G--- 2473
HIVNDK ---...-----C.----------G----------G----------G--------C---------- 2422
HIVMAL ---...------.--------A------GG---------- 2461
HIVELI ---...------.-----A----------G----------G---C-------G-------T-----G--- 2443
HIVZ2Z6 ---...------.-----A----------G--G----------C-------G-------C---------- 2443
HIVUG024 ---...------.-----C----------A----------T--A-C---- 2437
HIVUG266A TG-...------.-----A----------A----------A----T--A------ 2437
HIVUG269A ---...------.-----AA-A----------A----------T-------- 2442
HIVUG274A ---...------.----------A----------T--------- 2475
HIVSE365A ---...----G-.----------A---A-------A----------C--------- 2437
CONSENSUS.E CTG...GGGAAT.CTTCTGtTATATTGGgGcCAGGAACTAAAAATTAGTGCTATTTCTTTGcTTAAtGCtA 2393
HIVTH966 ---...------.------C----------G----------C---- 2451
HIVTH975 ---...------.------G--------A----------C- 2445
HIVTH022 ---...------.----------T--------- 2445
HIVTN243 ---...------.---------- 2470
CONSENSUS.F CTG...GGGAAT.CTCACGCTGTATTGGGGTCAGGAACTAAAGAATAGTGCTATT?GCTTG?TTAACACCA 2321
HIVBZ163A ---...------.----------G-----T--------- 2401
HIVBZ126A ---...------.----------A-----C--------- 2409
CONSENSUS.G ?TG...TGGAAT.CT?CTGC?GTATTGGGG?CAGGAACTAAAGAATAGTGC?ATT?ATTTGCTT?A?AC?? 2270
HIVVI525A C--...------.--T----A---------A----------C---C--------A-C--CA 2485
HIVLBV217 T--...------.--C----T---------T----------T---A--------G-T--AG 2476
CONSENSUS.O cTtTgTg?AGCT.gTAAtaCAATAcTGGCTACAAGAATTGcAaAaTAGTGCTACAAaccTgCTaGAtACt? 2396
HIVANT70 A------C----.----C----------G----------G-T-------C--AC 2473
HIVMVP5180 -------G----.-----G-----T----------A----------T------A 2512
HIVVAU --C-T-AA----.A----------C----------T--A---------G 2515
CONSENSUS.CPZ CTG...GGGGGA.ATTATTCAATATTGGGGAAAGGAGCTAAAAATTAGTGCTATAAGCCTGCTTGATGCAA 1490
SIVCPZGAB ---...------.---------- 2446
CONSENSUS.U CTg...gGGAAT.CTtcTGctgTATTGGggTCaGGAAcTaAAGAATAGTGCTATTAGtTTacTTgATaCCA 2303
HIVZAM184 --A...T-----.------T-A----------T-G---------- 2428
HIVK124A ---...------.--C----A-------AC--G----------C---G--------- 2461
HIVZ3 ---...------.---G----------G---A--G--- 2426


CONSENSUS.A tAGCAaTAGcAgTAGCTggctGGAcAGAtAGggTTATAGAAaTAGgACAaagAattggTAGaGCtaTTctc 2424
HIVSF1703 2424
HIVU455 2559
HIVZ321 2523
HIVRW020 2523
HIVUG031 2489
HIVUG275A 2393
HIVUG273A 2496
HIVVI191A 2520
HIVDJ264A 2517
HIVDJ263A 2514
HIVDJ258A 2538
HIVKENYA 2526
CONSENSUS.B caGCtaTAGcAGTAgctGAggGgACAGATAGGgtTaTAgAAgtAgtaCaaagAgctt?tAGaGctaTtctc 2520
HIVJRCSF 2449
HIVJRFL 2499
HIVALA1 2496
HIVBRVA 2502
HIVJH3 2511
HIVBAL1 2556
HIVYU2 2520
HIVMN 2484
HIVHXB2R 2523
HIVLAI 2523
HIVNL43 2538
HIVMFA 2517
HIVCAM1 2517
HIVNY5CG 2523
HIVADA 2505
HIVJFL 2514
HIVSIMI84 2508
HIVD31 2523
HIVSF162 2505
HIVBCSG3C 2496
HIVOYI 2532
HIVSF33 2520
HIVCDC4 2511
HIVSF2 2559
HIVSF2B13 2520
HIVHAN 2514
HIVRF 2520
HIVWMJ2 2550
HIVTB132 2496
HIVBR020 2466
HIVTH014 2510
HIVUS711 2486
HIVUS712 2496
HIVUS715 2507
HIVUS716 2513
HIVHA593 2486
HIVHA594 2576
HIVHA596 2498
HIVHA599 2519
HIVHA651 2549
HIVP896 2501

```
CONSENSUS.C   tAGCaATAgCAGTAgCTGAAGGAACAGATAGgATTaTAgAAtta?tACAAaGaaTttGtAGaGcTaTCcgc  2454
HIVMA959      ----C-------------------------------T------C-C----------G-------------  2513
HIVMA960      ----C-----------------------------------------A--------C--G-----------TA-  2501
HIVZAM20A     ---------------------------------------G-------------------------------T  2607
HIVSM145A     --------A---------------------------------GC-----------------G-G-----  2538
HIVZAM18A     --------A-----------------------------------CA-------------------------  2526
HIVDJ259A     C-------A-------------------------------A----CA-----G-GC----G---------T--  2451
HIVDJ373A     C---------------------------------------A--A----------G------T--T--  2484
HIVSE364A     --------A---------------------A-----------G----------C-----G------A--  2478
HIVUG268A     --------------T---------------A---------G-GGG----G-----G-G----------T-  2523

CONSENSUS.D   ?AGCAATAGcAGTAGCTGAggGgACAGATAGggtTATAGAaaTAgtACaAAGAgcT?gtAGAGCT?TTCTt  2429
HIVJY1        C-------------------------------A--------C--A---G-------TT-------G-----  2544
HIVNDK        T-----------------A-------------------G-------------T-C------A-----  2493
HIVMAL        C-----------------AT-C----------------------G-------TT-G--------A----C  2532
HIVELI        T-------------------------------A-----------A----------T-C------G-----  2514
HIVZ2Z6       T---------------------------------------------G-------T-C------G-----  2514
HIVUG024      C--------T---------------------A--------C----------AT-G--------A-----  2508
HIVUG266A     C-------------------------------C----------------------GT-------A-----  2508
HIVUG269A     T--------T-----------------------------G--A----------GT-------G-----  2513
HIVUG274A     C-----------------A-----------A-------G--------------GT-------G-----  2546
HIVSE365A     T-------------------------------A-------CG-------------T--------A-----  2508

CONSENSUS.E   CAGCAATAGCAGTAGCGGGGTGGACAGATAgggTTATAGAaGTAGCACAAgGAgcTTGGAGAGCCATTCTC  2464
HIVTH966      ---------------------------------------G-----------AT---------------  2522
HIVTH975      -------------------------------A---------------------------------------  2516
HIVTH022      -------------------------------A----------------A--------------------  2516
HIVTN243      -------------------------------A---------------------------------------  2541

CONSENSUS.F   CAGCAATAGTAGTA?CTGAGGGAACAGATAGAATTATAGCAGCTTTGCAAAGAATTGGTAGAGCTATT?T?  2389
HIVBZ163A     --------------G-------------------------------------------------------T-G  2472
HIVBZ126A     --------------A-------------------------------------------------------C-T  2480

CONSENSUS.G   ?AGCAATAGCA??AGCT?A??G?ACAGATAGGGT?ATAGAA?TAG?GCAAA?AGCTTGCAGAGCT?TTCT?  2328
HIVVI525A     C----------GT----G-GG-A----------T------A---T-----T-------------G----T  2556
HIVLBV217     T----------AC----A-CT-G----------C------G---C-----G-------------A----C  2547

CONSENSUS.O   TTGCAGTGgCAGTtGCcAATTGGACTGACgGCAtaATCttAGG?aTACAAAGaATAGGaa?AGGaaTtCtT  2465
HIVANT70      -------------A-----------------------GC---G---------------C--------G-  2544
HIVMVP5180    --------T-------------------------C--------TC--------------CA-----T-C---  2583
HIVVAU        ----------------T------------A---C---------C--------C-----G-G---G------  2586

CONSENSUS.CPZ CAGCTATTGCAGTAGCAGAAGGTACAGATAGAATAATAGAAGCTTTTCAAGTTACACTTAGAATTATTAGA  1561
SIVCPZGAB     ---------------------------------------------------------------------  2517

CONSENSUS.U   tAGCAaTAGtAGTAGCTGagtGgACAGAtAG?ATTATAgAAaTaGGACAAAGA?tTtGtAGaGCTaTTCtC  2372
HIVZAM184     ---------C-------------------G---------------------GC---C----------G-  2499
HIVK124A      -----G------------GC--------C--T------A--------------C--G--------T-----  2532
HIVZ3         C-------------------G-A--------A---------G-G---------A-------G---------  2497
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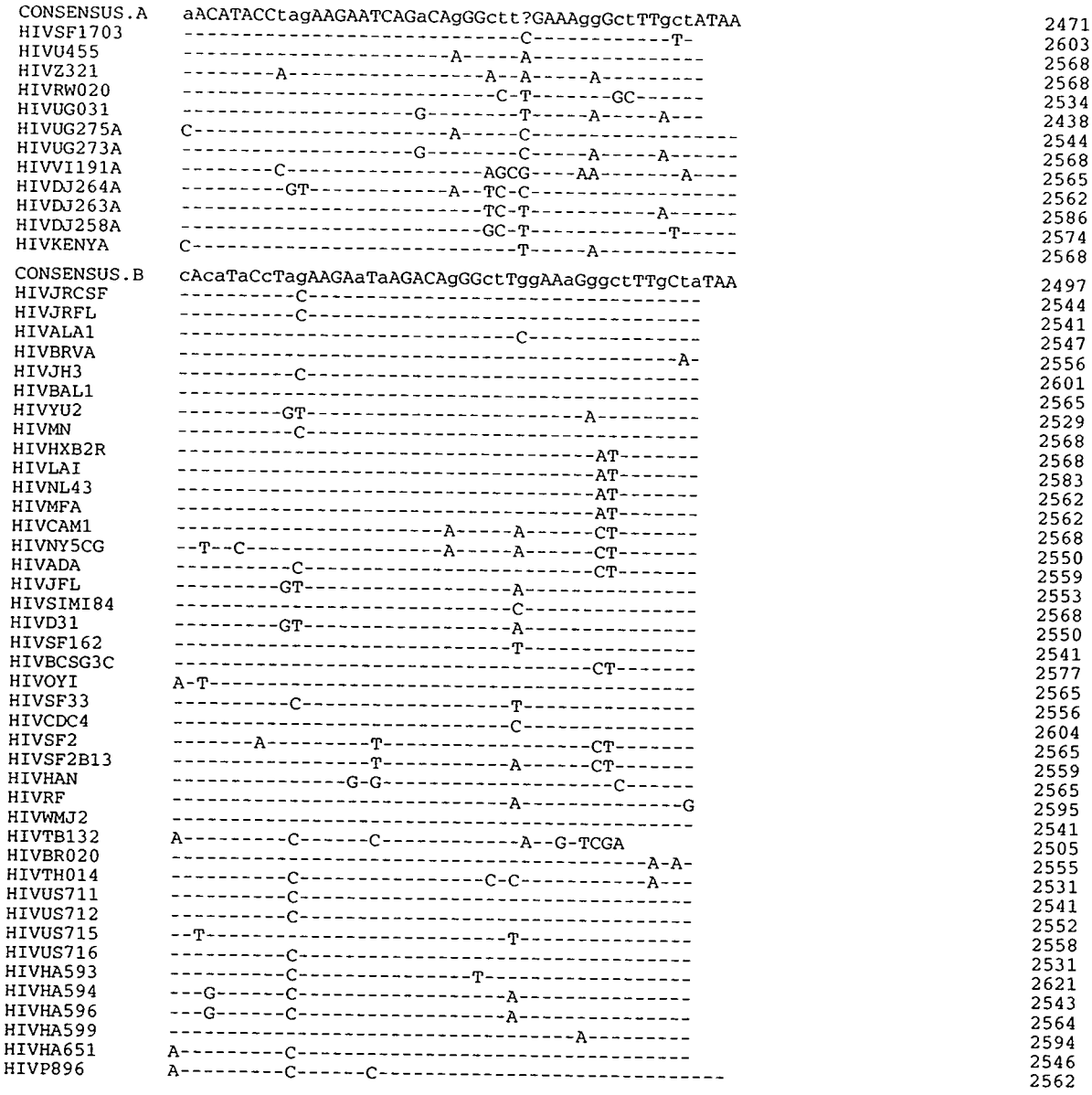
HIV1 ENV


CONSENSUS.A aACATACCtagAAGAATCAGaCAgGGctt?GAAAggGctTTgctATAA 2471
HIVSF1703 ----------C----------T- 2603
HIVU455 ----------A-----A---------- 2568
HIVZ321 --------A----------A--A-----A--------- 2568
HIVRW020 ----------C-T-------GC------ 2534
HIVUG031 ----------G--------T-----A-----A--- 2438
HIVUG275A C----------A-----C---------- 2544
HIVUG273A ----------G--------C-----A-----A------ 2568
HIVVI191A --------C----------AGCG----AA-------A---- 2565
HIVDJ264A ---------GT----------A--TC-C---------- 2562
HIVDJ263A ----------TC-T----------A------ 2586
HIVDJ258A ----------GC-T----------T----- 2574
HIVKENYA C----------T-----A---------- 2568
CONSENSUS.B cAcaTaCcTagAAGAaTaAGACAgGGctTggAAaGggctTTgCtaTAA 2497
HIVJRCSF ----------C---------- 2544
HIVJRFL ----------C---------- 2541
HIVALA1 ----------C---------- 2547
HIVBRVA ----------A- 2556
HIVJH3 ----------C---------- 2601
HIVBAL1 ---------- 2565
HIVYU2 ---------GT----------A--------- 2529
HIVMN ----------C---------- 2568
HIVHXB2R ----------AT------- 2568
HIVLAI ----------AT------- 2583
HIVNL43 ----------AT------- 2562
HIVMFA ----------AT------- 2562
HIVCAM1 ----------A-----A------CT------- 2568
HIVNY5CG --T--C----------A-----A------CT------- 2550
HIVADA ----------C----------CT------- 2559
HIVJFL ---------GT----------A---------- 2553
HIVSIMI84 ----------C---------- 2568
HIVD31 ---------GT----------A---------- 2550
HIVSF162 ----------T---------- 2541
HIVBCSG3C ----------CT------- 2577
HIVOYI A-T---------- 2565
HIVSF33 ----------C----------T---------- 2556
HIVCDC4 ----------C---------- 2604
HIVSF2 -------A---------T----------CT------- 2565
HIVSF2B13 ----------T----------A------CT------- 2559
HIVHAN ----------G-G----------C------ 2565
HIVRF ----------A----------G 2595
HIVWMJ2 ---------- 2541
HIVTB132 A---------C------C----------A--G-TCGA 2505
HIVBR020 ----------A-A- 2555
HIVTH014 ----------C----------C-C----------A--- 2531
HIVUS711 ----------C---------- 2541
HIVUS712 ----------C---------- 2552
HIVUS715 --T----------T---------- 2558
HIVUS716 ----------C---------- 2531
HIVHA593 ----------C----------T---------- 2621
HIVHA594 ---G------C----------A---------- 2543
HIVHA596 ---G------C----------A---------- 2564
HIVHA599 ----------A--------- 2594
HIVHA651 A---------C---------- 2546
HIVP896 A---------C------C---------- 2562

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CONSENSUS.C   aAcATACCTagAAGAATaagacagggctttgaagcagctttgc?ataa   2501
HIVMA959      ---------GC------------------------------T-      2558
HIVMA960      ----------------------------------------T-      2546
HIVZAM20A     --T----------------                              2625
HIVSM145A     ----------C------------------------------T----   2586
HIVZAM18A     ------------------                                2544
HIVDJ259A     ----------------T------------------------A----   2499
HIVDJ373A     ---------------------------------------A----     2532
HIVSE364A     --------------------------A-----------G----A---- 2526
HIVUG268A     C----------------------A-------------------A----  2571

CONSENSUS.D   ?ACaTACCcA?A?GAaTaAGACAGGGcTTgGAAAGGgcTTT?CTataa  2473
HIVJY1        C---------G-C--G------------------------A---     2589
HIVNDK        A--G------G-A-----------------------CT---G---    2538
HIVMAL        C-------T-G-A----T-----------C-----------G---    2577
HIVELI        A---------G-A----------------A------T----A--T    2559
HIVZ2Z6       C---------C-A----------------A------CT---G--T    2559
HIVUG024      A---------C-C-----------------------CT---G---    2553
HIVUG266A     A---------C-A----------------C-----------A------ 2556
HIVUG269A     C---------G-C----------------T-----------A------ 2561
HIVUG274A     A---------C-C----------------------------G------ 2594
HIVSE365A     C---------C-C-------------G--------------A------ 2556

CONSENSUS.E   CACATACCTAGaAGAATCAGACAGGGCTTAGAAAGGGCTTTGCTA      2509
HIVTH966      ----------------------------------------------   2567
HIVTH975      ----------------------------------------------   2561
HIVTH022      -----------G----------------------------------   2561

CONSENSUS.F   AACATACCTACAAGAATAAGACAGGGCTTCGAAAGGGCTTTGCT?TAA  2436
HIVBZ163A     ----------------------------------------------A---  2520
HIVBZ126A     ----------------------------------------------G---  2528

CONSENSUS.G   ?A?ATACCTAGAAG?ATAAGACA?GGCTT?GAAAG?GCTTTGCTATAA  2370
HIVVI525A     C-C-----------A--------G-----T-----G------------  2604
HIVLBV217     A-T-----------G--------A-----G-----A------------  2595

CONSENSUS.O   aACATcCCAAGaAGaATTAGACAgGGc?taGAAaGAatctTatTg     2509
HIVANT70      -----------G--------------T---------GT------     2589
HIVMVP5180    C----------------------A--TGC-------------G--     2628
HIVVAU        -----A--------G------------C-T---C--C--C-G--A    2631

CONSENSUS.CPZ AACATCCCTAGGCGCATAAGACAAGGGCTGGAAAGAGCTTTACTT     1606
SIVCPZGAB     ----------------------------------------------   2562

CONSENSUS.U   aAtATACCTAgAAGAATaAGACAGGGcTTcGAaAGGGCTTTaCTgTAA  2420
HIVZAM184     ----------C------------------T-------------------  2547
HIVK124A      C-C--------------C--------------G--------G--A---  2580
HIVZ3         --------------------------T---------------------  2545
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LOCUS HIVAMK101 947 bp ss-RNA VRL 09-MAY-1994
DEFINITION Human immunodeficiency virus type 1 (HIV-1) gag sequence, sample AMK10, partial cds.
ACCESSION U08192
SOURCE Human immunodeficiency virus type 1 uncultured PCR-amplified PBMC DNA derived from a 40 year old male student originally from Zaire who had moved to Alabama, U.S.A. and was suffering with AIDS.
REFERENCE 1 (bases 1 to 947)
AUTHORS Gao,F., Yue,L., Hill,S.C., Robertson,D.L., Graves,A.H., Saag,M.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE HIV-1 Sequence Subtype D in the United States
JOURNAL AIDS Res. Hum. Retroviruses 10, 625-627 (1994)
COMMENT The viral strain derived from patient AMK produced the first identified case of a non-subtype B infection in the United States [1]. This sequence was derived from a 40 year old male student who was originally from Zaire and had subsequently moved to Alabama, U.S.A. In 1992 he was identified as HIV positive when he sought medical care for Staphylococcus aureus endocarditis, tuberculosis, and acute renal failure. Gao et al. report that the patient's clinical history suggests that he was infected before his move to the United States. Although a wife and three children who still lived in Zaire were healthy, two brothers who both lived in Zaire had died of AIDS. This gag sequence clusters with HIV-1 subtype D gag sequences. Also see accession number U08193 <HIVAMK82>, another sample from this individual.
NCBI gi: 483777
BASE COUNT 362 a 183 c 213 g 189 t
ORIGIN 83 bp downstream from beginning of gag cds.

```
        1 aatatagact aaaacatata gtatgggcaa gcagagagct agaacgattt gcaattaatc
 gag cds ->
       61 ctggcctttt agaaacatca gaaggctgta gacaaataat aggacagcta caaccatccc
      121 tccagacagg gtcagaagaa cttagatcat tgtttaatac agtagcaacc ctctattgtg
      181 tacatgaaag aatagaggta aaggacacca aggaagcctt agacaaagtg gaggaagaac
      241 aaaacaaaag taagaaaaag gtacagcaag aaacagctga cacaagaaac agcagccagg
      301 tcagccagaa ttatcctata gtgcaaaatc tgcaggggca aatggtacac cagcccctat
      361 cacctagaac tttgaatgca tgggtaaaag taatagaaga caaggctttc agtccagaag
      421 taatacccat gttcacagta ttatcagaag gagccacccc acaagattta accaccgtgt
      481 taaacacagt gggggggacat caagcagcca tgcaaatgtt aaaagagacc atcaatgagg
      541 aagcggcaga atgggacagg atgcatccag tgcatgcagg acctgttgca ccaggtcagc
      601 tgagagaacc aaggggaagt gatatagcag gaactactag caaccttcag gaacaaatag
      661 gatggatgac aagcaatcca cctatcccag taggagaaat ctataaaaga tggataatcc
      721 tgggattaaa taaaatagta agaatgtata gccctgtcag cattttggac ataagacaag
      781 gaccaaagga acctttttaga gactatgtag atcggttcta taaaactcta agagccgagc
      841 aagcttcaca ggatgtaaaa aattggatga ctgaaacctt gttggtccaa aatgcgaacc
      901 cagattgtaa aactatctta aaagcattgg gaccaggggc ttcatta
                                                        gag ->
```

HIVAMK82

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LOCUS       HIVAMK82      612 bp ss-RNA             VRL       09-MAY-1994
DEFINITION  Human immunodeficiency virus type 1 (HIV-1) env sequence,
            sample AMK8, partial cds.
ACCESSION   U08193
SOURCE      Human immunodeficiency virus type 1 uncultured PCR-amplified PBMC
            DNA derived from a 40 year old male student originally from Zaire
            who had moved to Alabama, U.S.A. and was suffering with AIDS.
REFERENCE   1  (bases 1 to 612)
  AUTHORS   Gao,F., Yue,L., Hill,S.C., Robertson,D.L., Graves,A.H., Saag,M.S.,
            Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     HIV-1 Sequence Subtype D in the United States
  JOURNAL   AIDS Res. Hum. Retroviruses 10, 625-627 (1994)
COMMENT     The viral strain derived from patient AMK produced the first
            identified case of a non-subtype B infection in the United States
            [1].  This sequence was derived from a 40 year old male student
            who was originally from Zaire and had subsequently moved to Alabama,
            U.S.A.  In 1992 he was identified as HIV positive when he sought
            medical care for Staphylococcus aureus endocarditis, tuberculosis,
            and acute renal failure.  Gao et al. report that the patient's
            clinical history suggests that he was infected before his move to
            the United States.  Although a wife and three children who still
            lived in Zaire were healthy, two brothers who both lived in Zaire
            had died of AIDS. Interestingly, this envelope amino acid
            sequence contains an extremely rare GQGQ V3 loop crown.  The env and
            gag sequences cluster with HIV-1 subtype D sequences (U08192,
            <HIVAMK101>).
            NCBI gi: 483779
BASE COUNT      252 a    101 c    121 g    138 t
ORIGIN      805 bp downstream from beginning of env cds.
        1 gaagagataa taattagatc tgaaaatatc acaaataatg ctaaaaccat aatagtacag
 env cds ->
       61 cttaatgagt ctgtatcaat taattgtaca aggccctaca gcaaggaaag actaaagaca
                            V3 loop ->
      121 tctataggac aagggcaagc actctacaca acaagggtaa aggtaacagg agatataaga
      181 caagcacatt gtaatgttag tgaaataaaa tggaataaaa cattacaaca ggtagctgca
                    <- V3 loop
      241 aaattaaaag gccttcttaa tattagtagt acaatacatt ttaaaccatc ctcaggaggg
      301 gacccagaaa ttacaacaca cagttttaat tgtggagggg aattcttcta ctgcaataca
      361 tcaaaactgt ttaatatatc aataggtaat agtagtgcaa cgagtagtac aacaaatagt
      421 acagggggta ctataacaat cccatgcagg ataaaacaaa ttataaacat gtggcaggga
      481 gtaggaaaag caatgtatgc ccctcccatc gaaggaacaa ttagatgtac atcaaacatt
      541 acaggactat tactgacaag agatgggggt gcaaacagta ctaacgagac cttcagacct
      601 ggaggaggaa at
                  env ->
```

LOCUS HIVCA1 897 bp ss-RNA VRL 16-SEP-1994
DEFINITION Human immunodeficiency virus type 1 (HIV-1) env sequence, isolate CA1, partial cds.
ACCESSION X80438
SOURCE Human immunodeficiency virus type 1 cocultured PCR-amplified PBMC DNA derived from an asymptomatic patient from Yaounde, Cameroon.
REFERENCE 1 (bases 1 to 897)
AUTHORS Nkengasong,J.N., Janssens,W., Heyndrickx,L., Fransen,K., Ndumbe,P.M., Motte,J., Leonaers,A., Ngolle,M., Ayuk,J., Piot,P. and van der Groen,G.
TITLE Genotypic subtypes of HIV-1 in Cameroon
JOURNAL AIDS 8, 1405-1412 (1994)
COMMENT Nkengasong et al. conducted a survey designed to determine the prevalence of different HIV-1 subtypes in Cameroon. As a part of this study, viruses were isolated from nine symptomatic (CA5, CA7, CA11, CA15, CA16, CA17, CA18, CA20, and CA21) and nine asymptomatic (CA1, CA2, CA4, CA6, CA9, CA10, CA13, CA19 AND CA22) HIV-1 infected individuals. Isolates CA21 and CA22 were derived from patients in Douala, while all other samples were from patients in Yaounde. All of the strains except for isolate CA9 were sequenced over the envelope region (V3, V4, V5 and a segment of gp41). Isolate CA9 was sequenced over a 280 bp region of pol. From phylogenetic analysis, the following subtype designations were assigned [1]:

A	CA7, CA6, CA1, CA17, CA22, CA21, CA11, CA2, CA15, CA19, CA18
B	CA5
E	CA10
F	CA4, CA20, CA16
H	CA13
O	CA9 (based on analysis of pol)

Sequence analysis also revealed significant diversity at the tip of the V3 loop. An alignment of envelope sequences in this set is shown below (accession numbers X80438-X80454).

BASE COUNT 334 a 154 c 209 g 200 t
ORIGIN 796 bp downstream from the beginning of env cds

```
        1 gaaaaggtag taattcgatc tgaaaatatc acaaacaatg caaaaagcat actagtacag
 env cds ->
       61 ttggctaagc ctgtaaaaat taattgtacc agacctaaca acaatacaag aacaagtgtg
                          V3 loop ->
      121 cgtatagggc cagggcaagc attctatgca acaggtgaca taatagggga tacaagacaa
      181 gcacattgta atgtcagtag aacagaatgg aatacaactt tacaacaggt agttacacaa
                <- V3 loop
      241 ttaaggacgt actttgggaa tgacacaaca ataatctttg ctaaaccctc aggaggggat
      301 ttagaaatta caacacatag ttttaattgt ggaggagaat ttttctattg caatacatca
      361 aaactattta atagcacttg gaatagcaat accactgtca gcccaaatga cacagagtca
      421 aatgacacta taactctcca atgcagaata aagcaaattg taaatatgtg gcagagagta
      481 ggacaagcaa tgtatgcccc tcccatccaa ggagtaataa ggtgtgaatc aaacattaca
      541 ggactaatat taacaagaga tggaggggct aataatagta caaatgagac attcaggcct
      601 ggaggaggag atatgaggga caattggaga agtgagttat ataagtataa agtagtagaa
      661 attgaaccgc taggtgtagc acccacccct gcaaaaagaa gagtggtgga gagagaaaaa
      721 agagcagttg gactgggagc tgtcttcctt gggttcttag gagcagcagg aagcactatg
      781 ggcgcggcgt caataacgct gacggtacag gccagacaat tattgtccgg tatagtgcga
      841 cagcaggata atttgctgaa ggctatagag gctcaacaac atctgttgaa actcacg
                                                              env cds ->
```

HIVCA1

```
CONSENSUS GAAGAGATAATGATTAGATCTGAAAATATCACAAACAATGCCAAAACCATAATAGTACAGTTTAATAAGC    70
CA1       --GA----------------------CT-----G-----A-T----A-----------------C-GTT    70
CA10      --------C--A--A-----------C----C----------------------G--CC-C-----AT    70
CA11      -G-A--G--G-------------------------------T---------------------GGC-G---    70
CA13      ---A--G-------C-----------------G-----A------A-------------C----A--T-    70
CA15      ------G--G-----------------G----G---------------------------AGT-G---    70
CA16      -----T-----A---------------------G-----A-A----A-------------C------GAT    70
CA17      -G-A-------------G-------------------------------------------GG---C--    70
CA18      A-----GA-G-------------------------------------------------GGT-----    70
CA19      ------G--G-----------------------------------T----------A--AGT---T-    70
CA2       ----G-------G-----------------------------T---------G-----GGC-GC--    70
CA20      -----T-----A-----------------T--G-T---A-A-------------------------GAT    70
CA21      ---A--G--G-A---C-------------------------A----G----C----------GGC-----    70
CA22      ---A--G--GCA---------------C-----------------------------------C-T-----    70
CA4       ---A-T----CA-------------------G---A---ATA----TT------------C------GAT    70
CA5       ----G----G-AC--------------T---GTG-------T-----------------C-GG----AT    70
CA6       -G--GA----GA--------------CT-----G-------T---------C-------AC----C-GTA    70
CA7       -G--GAG---G-G-------------CT-----G-------T---------C--------C----C-GTA    70

CONSENSUS CTGTAAAAATTAATTGTACCAGACCTAACAACAATACAAGAA?AAGTATACGTATAGGACCAGGA.....    134
CA1       ------G-----------------------------------A-G------A------------.....    135
CA10      ----GG----C--------------CTC--CA-C--T-----C----TC-A-G------------.....    135
CA11      -----C-----------------------------------C-G------A------------.....    135
CA13      -----GT------C-----------C-----T--C--G----G------G--------TAT----CGAGG    140
CA15      ------------------------------------------G----G----------------.....    135
CA16      --A--G-------------A-----C-G---A-C--T-----G---G-----------C-T----.....    135
CA17      -------T----C-----T---------------C-------A----G---------------G.....    135
CA18      --------------------------GG--------------G----G----------------.....    135
CA19      ------G-----------------T--G--------------A----G---------------G.....    135
CA2       ------G---------------G-------------------A----G----------------.....    135
CA20      -----G-------------A-----C----------------A---C----A------------.....    135
CA21      ------------------------------------------C----G-G--------G-----G.....    135
CA22      ------T-------------------GG--------------G----G-G--------------G.....    135
CA4       -----G-------------A-----C--------------G-A----------------------.....    135
CA5       -----G------C------A-----C----------------A-G------A------------G.....    135
CA6       ------G----------T----------------------G-G------C-A-T-C---------.....    135
CA7       ------G-----------------------------------G-G------C---------T-----.....    135

CONSENSUS .CAAGCATTCTATGCAACAGGTGACATAATAGGGGATATAAGACAAGCACATTGTAATGTCAGTAGAACA    203
CA1       .AGT--TA----------------T-------------------------------------------C-G--    204
CA10      .--------T---AA--T--AA-G----TC---AA--------GC----T-----G-GA-T-A-G-----    204
CA11      .---A-------------------A---------A-----------------------------G-----    204
CA13      A---A-----C------T-----CT--------A----------------------A-T---G--G--    210
CA15      .---A-------------------C-------------------------------------------A----    204
CA16      .-G--T-----------------TA...-AT--A---------A-G---T-----GTCA-T-A-------    201
CA17      .---A-----------G-------------------------------------------A--------CA-    204
CA18      .----------------------A-----------C------A-------------C------------    204
CA19      .---A----T--------------A-------------------G-------------------GA----    204
CA2       .---A----------------G-------------------------------G--------------    204
CA20      .AG-----------------------------A---------A-G---T-C---GTCA-T-A-------    204
CA21      .-----------------------------------C-----------------------------    204
CA22      .------A-----------------------------------A-------------------C------    204
CA4       .----T-----------------T--------A---------A-G---T------GCA-T-A--T----    204
CA5       .AGG-----T---A------ACATA...-----A-------------------C-CCC-T-A-G-----    201
CA6       .---A-TC--------------A-T---------------C---------------------------A-    204
CA7       .---A-T-C------------G--T---------A-----C--G----------C--------------    204
```

```
CONSENSUS GAATGGAATGA?ACTTTACAACAGGTAGCTACACAATTAAGAAAGTACTTT...AATAA?ACAACAATA.   267
CA1       --T------A-C---------Aa--------AG---------G--AT--AC.....--C-A-------.   267
CA10      A----------A-----TA--------A---A-A--------G---------...-----T-AG------.   270
CA11      ----------GAG---------------T----G-------G---------GGG-----C-A-------.   273
CA13      A-G--------C-TG---ACCA----------------G----AC--C-G...--C--G-GC-A----.   276
CA15      -G----G-AA-A-----------------------------G-----TC--AAG---G-T-AC----C-A   274
CA16      CTG--------C---C--GG-A------T-GA-A--G-CGA--GACT-C--.....--T-T-T--CC-A   265
CA17      A------CAA-A-AA----------G----A---------GG--C-----.....--C---------.   267
CA18      ----------GA---------AG--------T------T-A----------AAG---GTT---------.   273
CA19      --------GACA----------------------------G---------.....--C---------.   267
CA2       ---------A-C---------A--------G---------G---------GGG...--T-A-------.   270
CA20      CTG--------T------A-CA------T-GAGGCG--CCA-CGCA-AAGC.....--CCTT--TG--.   267
CA21      ---------ACA---------------T-----------G-C-------GGG---G-C---------.   273
CA22      --T------A-C-----G-GC-----G----A---------TGG-------GAG-----A----T---C.   273
CA4       CTG--------A------AC--------T-GA-G-G--C-A---ACTTGACCAC----TA--C-AT---.   273
CA5       C----------C------A--AT-A---TGGG-A-----G--G-AC-A---GGG-----T-A-------.   270
CA6       ------G-AA-C-TG-----------A-------C----A-G-AA-G---...--C--A----A----.   270
CA7       ------G-A--C-TG-----------------C---G--GGAA-G---...--C-CA----G----.   270

CONSENSUS ..ATCTTTACTAACTCCTCAGGAGGGGATTTAGAAATTACAACACATAGTTTTAATTGTGGAGGAGAATT   335
CA1       ..----------ACA----------G-------------------C-------------------   335
CA10      ..-AA---CAACCA---C-------A---CC-----------TG---------------A----G-----   338
CA11      ..------G-------------------------------------------T---------------   341
CA13      ..CAA----AACCA----------A--CA---------T------C-TG-----C----C---------   344
CA15      TACA----G-------------------------------------------------------------   344
CA16      TA------CAACCA--A----------CC-----G-------------C--------CA-------G--   335
CA17      ..------G---G---------------------------------------------------------   335
CA18      ..G-----G---------------A---G-----------------------------------------   341
CA19      ..--------------------------G-----------------------------------------   335
CA2       ..-------------------------------------------------------A----------   338
CA20      ..-C-----A--GA--AG----------CC----------------------------A----------   335
CA21      ..------G----AC-------------------------------------------------------   341
CA22      .....----------CAT--------A-------------------------------------------   338
CA4       ..-C-----GCCCA--------------CCC------------G---------------A-----A----   341
CA5       ..G-A--C-A-C-A--------------CC----------GTG----C---------------G-----   338
CA6       ..-C-----AG-G---------------------------------C---------A----G-----   338
CA7       ..-------AA-G-C-------------------------------C--C---------A----------   338

CONSENSUS TTTCTATTGCAATACATCAAAACTGTTTAATAGCACTTGG.................A..??.AATA??   380
CA1       --------------------G-T-----C-AG----A---.............GAC-AGAAA---GAC   390
CA10      ----------------A----------------T------.......................-GA-TA   384
CA11      --------------------TC---A--------------.........................-AT   384
CA13      ---------T------A----------------T--C---.............ACG-CTAAC-CC-AT   399
CA15      -------------------G----A--------T------.............ACA-ATAAC----CC   399
CA16      ---T--C-----C---AGT--G------.................................AC-CA-GT   371
CA17      ---T------------------------G-----------...AATACATCAACACTGTCTAAT-GC-CT   402
CA18      ----------------A--G----A--------------.................-ACGTA-C-GCC   393
CA19      ------------------GG-T-A--------------.............GCT-TATTT---GGC   390
CA2       ---------T--C-----------A---G----------.......................T---AC   384
CA20      ------C-----C---GATG-G----------A--GC-T-.........................     375
CA21      ------------------------A--------------.................-ATAGC----CC   393
CA22      --------------------CC-----------------.............TATAAT-GCACTTGGGGT   396
CA4       ------C-A---C---A--G-T----------A--TGGAA.........................     381
CA5       ------C--T---T--A--C--T-----G----T------...TATTTTAGTAATAGT-CTTGGT--TTT   405
CA6       ---------------------G----------------TT.......................-AT   381
CA7       --------------------GGG-----------------.........GATGTGGTA-ATAAC-C-GCC   399
```

```
CONSENSUS AATAA?AA?GAAA?TAACACAGAGGCAAAT.....GACACTATAACTCTCCCATGCAGAATAA  435
CA1       -C-TGG--TT-CCCAGGGT--A-T-AC---.....----------------------------  448
CA10      -----A-CT----CC-TGGAG----TT--A.....--------C-TG--T-------AG----  442
CA11      --C--T-CCA-T-GC-CTTGG----T----.....----A------C----A-----------  442
CA13      GGC-GCT-T-TG-GC--T-ACACA-A----.....-GT-----T--A--G-A-----------  457
CA15      ---GTC-GACC--A-G------G-T-----AAT.....-----C----------A-----------  460
CA16      T--CTG-TGTTG-A------T-CCA.....CTA--ATC-CTCT--TGG--T-A-----  424
CA17      TGGG-G-GCA-T-GC-GTGTCAGCT--T--.....--A-A----------A-----A-----  460
CA18      -GCTCA--CT-C-CAG-GT--A-CT-----.....----G----------------------  451
CA19      -----T--CACC-TC-G-T--A-T------.....----A----------A-------C---  448
CA2       -----C-CT-GC-TAGTGG---G-------GACACTATAAAT----------T----------  454
CA20      .....TTG---AACACAAAAAAA--A-A---C-----T-----T-------  421
CA21      -C-GTC-GCCC--A-G--------T-----.....----------A-----------  451
CA22      G-C--T-GCTC--CATC-----G-TT----AAT.....--A----------A-----------  457
CA4       .....-A-ACTAAC---.....A-------C-T---------T-A-----  421
CA5       ----GT-CT-TG-A-GGT--TC-A-G----.....-----A--C--A----------------  463
CA6       GGC-CT-TG----A-----TT-CA-A----.....--A---C--TA----A------A-----  439
CA7       -GC-TCC-TA---C--TA-ATA-TA-T-CCAGCAGCAATAAT--A--------A---A------A-----  469

CONSENSUS AGCAAATTGTAAATATGTGGCAGAGAGTAGGACAAGCAATGTATGCCCCTCCCATCCAAGGAGAAATAAG  505
CA1       ----------C----------A-----GA  518
CA10      ----------C---------G----------T---------AGT--G-T---T-A  512
CA11      ----------C----------G----------A------T------  512
CA13      -A----------GC----------C----------A-T---A-G--T-C  527
CA15      --------A----------A-------T---A------T------  530
CA16      GA---T----T--C---------GAG------A----------TG----GAC---TCA  494
CA17      --------A----------G-----T-----A  530
CA18      -A--------G---T-A-------A----------  521
CA19      ----------GG----------AG----------T----------  518
CA2       ----------GA----------T-C-----C------  524
CA20      -A---T-------C--------A--G----------T--AGCC---C----TCA  491
CA21      ----------T------  521
CA22      --------A----------A--------G----------C----------  527
CA4       GA---T-------C--------A-----G----G---C----------TGCC---C----TCA  491
CA5       -A------A----C---------GAG------A----C----------A----CA--T----  533
CA6       ----G-------GGC----------T----  509
CA7       ----G---A-----C----------  539

CONSENSUS GTGTGAATCAAACATTACAGGACTACTATTAACAAGAGATGGTGGG......AATAATAATACAAATAAT  569
CA1       ----A----------T----------.....-----A-CACA----...  579
CA10      T----T------T----------T.....GG-----G---TG-C-CA  576
CA11      ----------G-----A---.....-G---CGGC------...  573
CA13      A----T------T----------A----G-----T--CCA--TT.....---CGGTC-G--G-GG-G  591
CA15      ----------A---.....--A-------GTG-G---  594
CA16      A---A-C----GT--C-----T---A----G----------T.....-T--CC-CC-A----G-A  558
CA17      ----------A---.....T--------GGTGCA---  594
CA18      ----------T----------A---.....-------G-------...  582
CA19      ----------T-G---C----------A--AGATGGAGGG--A----G--G-GCA  588
CA2       ------C----------G-----A---.....G---C-----GT-CA-C-  588
CA20      ---CA-C----GT--C-----T--------G----------AAC.....--A---GGGT-C.....  549
CA21      ----------A----------A---.....GC--------GT-CA---  585
CA22      -----T----------G----------A---.....G------G--ATGCA---  591
CA4       ----A-T-----G--C-----T--------G----------A.....G-G----CA-ATGGGTCC  555
CA5       A--C-T------T--------G--G----------T.....G---GG--C-GC-CC-C-  597
CA6       ------C----------G----------.....T-------C---G-GG-G  573
CA7       ------C-----T--------G----------.....--G-----C------...  600
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```
CONSENSUS ......GAGACCTTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAGTATA  633
CA1       ......--A----------AC---------C-----------------------------------  643
CA10      ......-------------------------A------A---------------------------A----  640
CA11      ......-----A-------------------------------C-----------------------  637
CA13      ......-T-----------------------------------------------------------A----  655
CA15      AATAAT-----A-----G-------------------------------------------------  664
CA16      ACC...--C---C-------------G---A------AA-----------------C-G-----A----  625
CA17      ......-----T-----G-------------------------------------------------  658
CA18      ......-----A-----G-------------------------------------------------  646
CA19      AAT...-----A-----G-------------------------------------------------  655
CA2       ......-----A-----G-------------------------------------------------  652
CA20      ......------C-----------A-G----------A-----------------C-------A----  613
CA21      ......-----A-----G-------------------------------------G-------------  649
CA22      ......----------G-----------------------------------------------A----  655
CA4       ......------C----G-------------------A-----------------C-------A----  619
CA5       ......----T-------------------A------A-----------------------G---A----  661
CA6       AGC...----------------C-------------------------------------------  640
CA7       ......---------------AT-------------------------------------------  664

CONSENSUS AAGTAGTAAAAATTGAACCACTAGGAGTAGCACCCACCAAGGCAAAAAGAAGAGTGGTGGAGAGA...GA  700
CA1       -------GG-----AG-----------------------------------------C-----...--  710
CA10      -----A--C----------------A----------------GG-----------------...--  707
CA11      -G------C----------------T--G---------CGT--------------------A---...-G  704
CA13      -------G-----------------------------T--------G-------------G----...--  722
CA15      -G------C----------------T--G---------CGT----G--------------------...--  731
CA16      -G-------------------------------------C----C----C--------A-----...--  692
CA17      -------------------------T------------CGT------------------A-----...--  725
CA18      -G------C---------T------T--G---------C-------------------------...--  713
CA19      -G------C----------------T--G---------CGT--------G---------------...--  722
CA2       -G------C----------------T--G---------C-T-----------------------...--  719
CA20      -G-----------------C--------------------G----------CA-------A-----...--  680
CA21      --------G----------G-----T------------CCT-------------------------...--  716
CA22      ----------------------G--T------------CGT-------------------------...--  722
CA4       -G-------G---A--------------------T---------------CA-------C-----...-G  686
CA5       -------G------------T-------------------------G------------C-----GAGAG  731
CA6       ----G--GG-G---A-------------------------------------TG------A-----...--  707
CA7       ----G--GG-G---A----------------------G------------G------------...--  731

CONSENSUS AAAAAGAGCAGTG...GGACTAGGAGCTGTCTTC?TTGGGTTCTTAGGAGCAGCAGGAAGCACTATGGGC  766
CA1       ------------...-A-A----------GC--T----------G-----------------------  777
CA10      ------------...---A--------C-GA--T-----------------------------------  774
CA11      ------------AGTT-----G------------C-----------------------------------  774
CA13      ------------T...-----------------C-----------------------------------  789
CA15      ------------T...-----G------------C-----------------------------------  798
CA16      ------------...-----G--------G---A----------G-----------------------  759
CA17      ------------T...-----G------------C-----------------------------------  792
CA18      ------------T...---A-------------C-----------------------------------  780
CA19      ------------C...---A-G--------TC--T-----------------------------------  789
CA2       ------------ACTT---A-------------T-----------------------------------  789
CA20      --G----------...---A----------G---C----------G-----------------------  747
CA21      ------------T...-----G------------C-----------------------------------  783
CA22      ------------T...-----G------------T-----------------------------------  789
CA4       ------------...---A----------AC--T-----------------------------------  753
CA5       -G-----AG--CAGTG---A-G------A-G---C----------G-C---------------------  801
CA6       ------------...-------------GC--T----------G-----------------------  774
CA7       ------------...-------------GC--T----------G-----------------------  798
```

HIVCA1

```
CONSENSUS GCGGCGTCAATAACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAGCAAAGCAATT  836
CA1       --------------A----------A-------------------C---------------G------  847
CA10      --A------T-----------------------------A-------------------------------  844
CA11      ------------------------------------------C-----------------G------C  844
CA13      ----------------------------T-----------------C-----------------T----  859
CA15      ------------------------------------------C-----------------G-------  868
CA16      ------------------------------A-------A------------------------A-----  829
CA17      ------------------------------------------C-----------------G-A-----  862
CA18      ---------C-------------------------------------------------------G------C  850
CA19      --A-------------------------------------------------------G-------------  859
CA2       ------------------------------------------------------------------------  859
CA20      ------------------------------------------------------------------------  817
CA21      ------------------------------------------C----------G------GGAT----  853
CA22      ------------------------------------------C-------------------------  859
CA4       ------------------------------------------------------------------G-AT----  823
CA5       --A------C-G-----------------------------------------------------------A-----  871
CA6       --A-------------------------------------------C----------------------  844
CA7       --A-------------------------T-----------------C-----------------A-----  868

CONSENSUS TGCTGAAGGCTATAGAGGCTCAACAGCATCTGTTGAAACTCACG  880
CA1       -------------C-----G--------A--------------T  891
CA10      ------G------------G--G---------C--C-------A  888
CA11      ------G-------------------A-----------------  888
CA13      ------G-------------------------------------A  903
CA15      ------GA--C--------------A-----------------  912
CA16      ----------C-----A--G---------------C-G-----A  873
CA17      ------G-----------------A---A--------------  906
CA18      ------G-----------------A-----------------  894
CA19      ------GA----------------A-----------------  903
CA2       -------------------------A-----------------  903
CA20      ----------------A--G---------------C-------A  861
CA21      -------------------------A-----------------  897
CA22      --------------A----------A--GA------G-------  903
CA4       ----------------A--G---------------C-G-----A  867
CA5       ------G------T-----G---------------C-------A  915
CA6       -------------C--T--A-G-------A-------------T  888
CA7       -------------C-----A---------A-------------T  912
```

```
LOCUS       HIVCAR286A   1549 bp ss-DNA              VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 1286CL1,  env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), isolate 1286CL1.
REFERENCE   1  (bases 1 to 1546)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env A subtype sequences.
            It represents one of 14 CAR isolates that have been integrated
            into a "hybrid" gp160 sequence for expression from a vaccinia
            virus expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      579 a    258 c    336 g    376 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggggacaca gaggaattgg caaaacttgt ggagatgggg cctcatgatc
env start ->
       61 tttggaatgt tgatgatttg taatgcaaca aacaacttgt gggtaacagt ctattatggg
      121 gtacctgtgt ggaaagatcg agagaccact ctattttgtg catcagatgc taaagcatat
      181 agtgctgaaa acataatgtc tggggctaca catgcctgtg tacccacaga ccccaatcca
      241 caagagatac ctctggaaaa tgtaacagaa aattttaaca tgaggaaaaa tagtatggta
      301 gaacagatcg atgaggatat aatcagttta tgggatgaaa gcctaaagcc atgtatagag
      361 ttaacccctc tctgtgttac tttaaactgt actgatgcaa agatagactg tactaatgga
      421 aggaataaca gtgctggagg acagacctgt actggagtac agaatagcac tgctgaggtt
      481 ggccaagtag aaatgaaaaa ctgctctttc aatataacta cagaaataag aaataggaag
      541 aaaaaagaat acgcgctttt ctatagactt gatgtagtac caacaaataa tgatgataat
      601 agtacagata attatacaca taattatagg ttaataaatt gtaatgcctc aaccattaaa
      661 caggcttgtc caaaggtgac ctttgagcca attcccatac attattgtgc tccagctggt
      721 ttgcgattct aaagtgtagg gataaggagt tcaatggaac agggccatgc aagaatgtag
      781 cacagtacaa tgcacacatg gaataagcca gtggtatcaa ctcagctatt gttaaatggc
      841 agtctagcag aaggaggggt aataattaga tctgaaaaca tcacaaacaa tgctaaaacc
      901 ataatagtac agcttgacag tcctgtagga attaattgta ccagacctgg caacaataca
                                      v3 loop ->
      961 agaaaaagta tacgtattat gcatatagga ccaggacgat ctttctatgc aaaaggtgta
     1021 ataggggata taagacaagc acattgtacc attaataaag caaaatggaa tcaaacttta
                                   <- v3 loop
     1081 caaaaggtag ctgaaaaatt aagaggaatc tttaacaaca aaacaataat ctttactaac
     1141 cactcaggag gggatttaga agttacaaca catagcttta attgtggagg agaagttttt
     1201 ctattgcaat acatcagcct gtttaatagc agttggactg acactaacag cactaacagc
     1261 agtaggactg ggaatgacac tgacatcata actctcccat gcagaataaa gcaaattgta
     1321 aatatatggc agagagtagg acaagcaatg tatgccccac ccatccaaag agtaataagg
     1381 tgtgaatcaa acattacagg actactatta acaagagatg gtgggctgaa tagcacacaa
     1441 aatgagacct tcagacctac aggaggagat atgaggaaca attggagaag tgaattatat
     1501 aagtataaag tagtggaaat taatccacta ggagtagcac ccacccggg
                                                        env cds ->
```

HIVCAR4017

```
LOCUS       HIVCAR4017       1507 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4017-1, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), isolate 4017-1.
REFERENCE   1  (bases 1 to 1507)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P..
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env E subtype sequences.
            It is one of 14 CAR isolates that have been integrated into a
            "hybrid" gp160 sequence for expression from a vaccnia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      565 a    240 c    322 g    380 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggagaaata tcagcacttg tggagatggg ggtggaaatg gggcagcatg
env start ->
       61 ctccttggga tattgatgat ctgtagtgct tcagacaact tgtgggttac agtttattat
      121 ggggttcctg cgtggaaaga tgcagatacc accctatttt gtgcatcaga tgccaaagca
      181 cataagacag aagtgcacaa tgtctgggct acacatgctt gtgtgcccac agaccccaac
      241 ccacaagaaa tatacatgga aaatgtaaca gaaaatttta acatgtggaa aaataacatg
      301 gcagagcaga tgcaggagga tataatcagt ttatgggatg aaaggctcaa gccatgtgta
      361 aagttaactc ctctctgcgt tactttaaat tgtaccaagg ctaattttac caaggctaat
      421 agtaccgagg ctgctttgaa tggcagttac agtaatgaaa cagcagaaat ggaaaatgaa
      481 gtaagaaact gttcttttaa tgtgaccaca gaactaagag atagaaagca gaaggtctat
      541 gcacttttt ataagactga tatagtatca attgataaca gtagtagtga ttatatgtta
      601 ataaattgta ataattcagt cattaagcag gcttgtccaa aggtatcctt tgatccaatt
      661 cctatacatt attgtgctcc agctgggtat gcgattttaa agtgtaataa taagaatttc
      721 aatggaacag ggccatgcaa aaatgtcagc tcagtacaat gcacacatgg aattaagcca
      781 gtggtatcaa ctcaactgct gttaaatggc agtctagcag aagaagagat aataattaga
      841 tctgaaaatc tcacaaataa tgccaaaacc ataatagtgc accttaataa agctgtagaa
      901 atcaattgta ccagaccctc caagaaaata agaacaagtg taaggatagg accaggacaa
        v3 loop ->
      961 gtattctata aaacaggaga cctaatagga gatataagaa aagcattttg tgaaattaat
                                                              <- v3 loop
     1021 ggaacaaaat ggaatgaaac tttaaaagag gtaactagaa aattaagaaa gcactttaat
     1081 aagacaatac actttcgacc atcctcagga ggggatccag aaactacaaa tcatattttt
     1141 aattgtagag gggaattttt ctattgcaat acaacacaac tgtttaatag tacttggaga
     1201 ataaatgaaa ccatggaaaa ggttaatggc acaaactcaa acatgatcac acttccatgc
     1261 aggataaggc aaattgtaaa catgtggcag agagtaggac aagcaatgta cgctcctccc
     1321 atcagtggag tagttaattg tgtatcaaat attacaggaa tactattaat aagagatggt
     1381 ggtaatgaga cacacgagaa cgagaccttc agacctggag gaggaaatat aaaggacaat
     1441 tggagaagtg aattatataa atataaagta gtccaaattg aaccattagg agtagcaccc
     1501 acccggg
         env cds ->
```

```
LOCUS       HIVCAR4020     1600 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4020-19, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 4020-19.
REFERENCE   1  (bases 1 to 1600)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P..
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic virus, clusters with env D subtype sequences.
            It is one of 14 CAR isolates that have been integrated into a
            "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      629 a    266 c    327 g    378 t
ORIGIN      Beginning of env cds
        1 ATGagagtga gggggataga gaggaattat caacacttat ggagatgggg cacgatgctc
env start ->
       61 cttgggatat tgatgacctg tagtgttgca gaaaaattgt gggtcacagt ttattatggg
      121 gtacctgtgt ggaaagaagc agaaaccact ctattttgtg catcagatgc taaatcatat
      181 aaagcagagg cacataatat atgggcgaca catgcctgtg tacccacgga ccccaaccca
      241 caagaaatgg agctgaaaaa tgtctcagaa aactttaaca tgtggaaaaa taacatggtg
      301 gaacagatgc atgaggatat aatcagttta tgggatcaaa gcctaaaacc atgtgtaaaa
      361 ttaacacctc tctgtgtcac tttgcactgc actcgattgg agaatattgc aaacagtagc
      421 cttacaaaca atgccagtgc aagaagtaat gatacagaca ataaccatac aaacagtacc
      481 aatactagat gggtatatga cggaatggaa aaagaaatga caaactgctc tttcaatgta
      541 accacagtaa taagagataa gaagaagcaa gtacatgcac tcttttataa actagatata
      601 gtaccaatag aggatgagga taatattaaa ggtaatacta gtgataatac taaaaatatt
      661 actagatata gattgataaa ttgtaatacc tcagccatta cacagtcttg tccaaaggta
      721 aactttgagc caattcccat acattattgt gccccagctg gctttgcaat tctaaaatgt
      781 aaagataaga acttcaatgg aacaggccta tgccataatg tcagcacagt acagtgtaca
      841 catggaatta agccagtggt gtcaactcaa ctgctgctga atggcagtct agcagaagaa
      901 gagataatag ttagatctga aaacctcaca gacaatgcta aaaccataat agtacagctt
      961 aaggaatctg taaacattag ttgtacaagg cccaacaact ataaaagaca aggtacacct
                        v3 loop ->
     1021 ataggactag ggcaagcact ctatacaaca agagtaatag gggatataag aaaagcacat
     1081 tgtaatatta gtagaaaaga atggaataat actttacaaa aggtagctaa gaaattaaga
           <- v3 loop
     1141 gaacttttta acaagtcaaa aataaatttt caaccccatt caggaggaga cctagaagtt
     1201 acaacacaca gttttaattg tcaaggggaa tttttctact gcaatacatc acaactgttt
     1261 aatcataaat ggaatgatac aacaggagaa atgtcagaac agaacaataa tacagagtca
     1321 gaaaatatca cactcccatg cagaataaga caaattataa gaatgtggca gagagtagga
     1381 caagcaatgt atgcccctcc catcgaagga gtaatcaatt gtacatcaaa tattacaggg
     1441 ctactattga caagagatgg tggtaataca aagaacggaa gtaagaatga tattgagatc
     1501 ttcagaccgg gaggaggaga tatgagggac aattggagaa gtgaattata taaatataaa
     1561 gtagtaagaa ttaaaccact aggaatagca cccacccggg
                                              env cds ->
```

HIVCAR4023

```
LOCUS       HIVCAR4023       1552 bp ss-DNA              VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4023-2, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 4023-2.
REFERENCE   1  (bases 1 to 1552)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P..
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic virus, clusters with env A subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT     590 a    255 c    324 g    382 t      1 others
ORIGIN      Beginning of env cds
        1 ATGagagtga aggagaaata tcagcacttg tggagatggg ggtggaaatg gggcagcatg
env start ->
       61 ctccttggga tattgatgat ctgtaatgca gacaaagaca aattgtgggt tacagtctat
      121 tatggggtac ctgtgtggag agatgcaaat accactctat tttgtgcatc tgatgctaaa
      181 gcatatagta ctgaaaaaca taatgtctgg gctacacata cctgtgtacc cacagacccc
      241 gacccacgag agatacctct gaaaaatgta acagaaaatt ttaacatgtg gaaaaatagt
      301 atggtagaac agatgcagga ggatattatc agcttatggg atgaaagcct aaaaccatgt
      361 gtaaagctaa ccctctctg tgttacttta aactgtactg atgtaaaaaa tatcactgtg
      421 aatagtacta gtactgggaa tagtgctaat acaataaata gaactgtgga tagccaagta
      481 ggaataaaaa actgctcttt caatatgacc tcagaaataa gagataggaa gaagaaagaa
      541 tacgcacttt tctatagact tgatatagta ccaattaata ataataataa taatacaaat
      601 aatacaaatg attataatga ttatatgtta ataaattgta atgtatcagc agttaaacag
      661 gcttgtccaa agataacctt tgagccaatt cccatacatt attgtgctcc agctggtttt
      721 gcgattctaa agtgtaatga tacgaagttc agtggaacag ggccatgcaa gaatgtcagc
      781 acagtacaat gcacgcatgg aatcaagcca gtggtatcaa ctcaactact gttaaatggc
      841 agtctagcag aagaaggggt aatgattaga tctgaaaaca taacaaacaa tgctaaaacc
      901 ataatagtac agcttgacag tcctgtaata attaattgta ccagacctaa caacaataca
                                        v3 loop ->
      961 agaagaagca tgcgtatagg accaggacaa actttctatg caacaggtga tataacaggg
     1021 gatataagac aagcatattg caacgtcagt aaagaagaat ggaacaccac tctgcaaaag
                               <- v3 loop
     1081 gtagctaaaa aattaggaac tatctttagc aacaaaacaa taatctttaa tagcagctca
     1141 ggaggggatt tagaagttac aacacacagc tttaattgta gaggagaatt cttctactgc
     1201 gatacatcaa gactgtttaa tagcatttgg aaaaatgaca ctggcaacat aactggcaac
     1261 ataactggct gggagaattt caatgacagc ataatcctac catgcagaat aaaacagatt
     1321 gtaaatatgt ggcagagagt aggacaagca atgtatgcct ctcccatccc aggagaaata
     1381 agttgtaact caaacattac aggaatncta ttaacaagag atggtgggga tgataactca
     1441 acaaatgaga tcttcagacc tacaggagga gatatgagga acaactggag aagtgaatta
     1501 tataagtata aagtagtgga aattgaacca ttaggagtag cacccacccg gg
                                                            env cds ->
```

```
LOCUS       HIVCAR4039   1483 bp ss-DNA              VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4039-TG2, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 4039-TG2.
REFERENCE   1  (bases 1 to 1483)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env E subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      548 a    240 c    328 g    367 t
ORIGIN      Beginning of env cds
        1 ATGagagtga gggggacaca gaagaattgg ccaaacttat ggaaatgggg aactttgatc
env start ->
       61 cttgggttgg tgatgatttg tagtgcctca gacaacttgt gggttacagt ttattatggg
      121 gttcctgtgt ggagagatgc aaagaccaac ctattttgtg catcagatgc caaagcacat
      181 aagacagaag tgcacaatgt ctgggctaca catgcctgtg tacccacaga ccccaaccca
      241 caagaaatat acatggaaaa tgtaacagaa aattttaaca tgtggaaaaa taacatggta
      301 gagcagatgc aggaggatgt aatcagttta tgggatcaaa gtctaaagcc atgcgtaaag
      361 ttaactcctc tctgcgttat tttacattgt accagggcta attttaccaa ttctaattat
      421 accaagggta atgaaactgt tgaaatggaa aatgaagtaa gtaactgttc ttttaatata
      481 accacaaaac taagagataa gacgaaggag gcctatgcac ctttttataa gcatgatcta
      541 gtaccaataa aggaaaatag tagtagtgag tatgtgctaa tacttgtaat acattcagtc
      601 attaaacagg cttgtccaaa ggtaaccttt gagccaattc ccatacatta ttgtgcccca
      661 gctggttttg cgattctaaa gtgtaaagat aaggagttca gtggaaaagg gacatgcaag
      721 aatgttagta cagtacaatg cacacatgga atcaagccag tagtgtcaac tcaactgctg
      781 ttaaatggca gtctggcaga aaaagaggta gtgattagat ctgaaaatat cacaaacaat
      841 gccaaaacca taatagtaca gctggttacg cctgtacaaa ttaattgtac cagaccctcc
                                                  v3 loop ->
      901 aacaatataa gaacaagtgt aaggatagga ccaggacaag tattctataa aacaggaagc
      961 ataacaggag atataagaaa agcattctgt gagattaagg aagcacaatg gaataaaact
                                        <- v3 loop
     1021 ttaaaagagg taataggaaa attaagagag cactttaata agacaataat ctttcaacga
     1081 tcctcaggag gagatccaga aattacaatg cttaccttta attgtggagg ggaatttttc
     1141 tattgcaata caacaagact gtttaatagt acttggggaa caaatgaaac catagagtct
     1201 aatgtcacaa acccaagaaa tatcacactt ccatgcaaga taaggcaaaa tgtaaacatg
     1261 tggcagagag taggaaaagc aatgtatgct cctcccatca gtggagtaat taattgtgta
     1321 tcaaatatta caggactact attgacaaga gatggaggga gcaatagtgg tgaacctgag
     1381 acattcaggc ctggaggagg agatatgagg gacaattgga gaagtgaatt atataagtat
     1441 aaggtagtac aaattgaacc aataggagta gcacccaccc ggg
                                                  env cds ->
```

HIVCAR4054

```
LOCUS       HIVCAR4054   1486 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4054-TG2, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 4054-TG2.
REFERENCE   1  (bases 1 to 1486)
  AUTHORS   Kieny,M.P., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Schmitt, D.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env A subtype sequences.
            It represnts one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      573 a    249 c    299 g    364 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggagacaca gaggaattgg cacaacttgt ggaaatggcg cctcatgatc
env start ->
       61 tttggaatgt taatgatctg taatgctaaa gaaaacttgt gggtcacagt ctattatggg
      121 gtacctgtgt ggagagaggc aaataccact ctattttgtg catctgatgc caaagcacat
      181 agtactgaaa agcataatgt ctgggctaca cacgcctgtg tacccacaga ccccaaccca
      241 caagaaataa aactagaaaa tgtaacagaa aattttaata tgtggaaaaa taacatggta
      301 gaacagatgc atgaggatat aatcagttta tgggatgaaa gtctaaaacc atgtgtaaaa
      361 ctaacccctc tctgtgttac tttaaattgt actgatgtaa agaagaatag cactctggaa
      421 ggccaagtag aaatgaaaaa ctgctctttc aatataacca cagaaataaa tgataggaag
      481 aagaaagaac acgcgctttt ctatagactt gatgtagtac aaattaatag taatagtaat
      541 attagtaatg caaattataa tgattatagg ctaataaatt gtaatgtctc aactgctaaa
      601 caggcttgcc caaaggtatc ctttgagcca attcccatac attattgtgc tccagctggt
      661 tttgcgattc taaagtgtaa tgatacaaaa ttcaatggaa cagggccatg caagaatgtc
      721 agcacagtac aatgcacata tggaatcaag ccagtagtat caactcaact actgttaaat
      781 ggcagtctag cagaagaaga ggtaatgatt agatctgaaa acttcacaga caatgctaaa
      841 accataatag tacagcttaa aaatcctgta agaattaatt gtaccagacc tggcaacaat
                                          v3 loop ->
      901 acaagaaagg gtatacatat aggaccagga ccaggacaag ctatttatgc aacaggtgat
      961 ataatagggg atataagaca agcacattgt aatgtcagta aagcagaatg ggataacact
                                       <- v3 loop
     1021 ttacaacagg tagctaaaaa attatatgag gtctttaaca aaacagtaan ctttactaac
     1081 cactcaggag gggatataga aattacaaca catagtttta attgtagagg ggaatttttc
     1141 tattgcaata caacagatct gtttaatagc acctggtata acattaatgg cactgggaat
     1201 aacactcagg aaacaaatgg cactataacc ctccaatgca gaataaagca aattataagg
     1261 atgtggcaga gagtaggaca agcaatgtat gcccctccca tccaaggaga attaaggtgt
     1321 gactcaaaca ttacaggcct actattaaca agagatggtg gggtaaataa cacacaaaat
     1381 gataccttca gacctacagg aggaaatatg aaagacaatt ggagaagtga attatataaa
     1441 tataaagtag tggagattaa accactagga atagcaccca cccggg
                                                    env cds ->
```

```
LOCUS       HIVCAR4067     1498 bp ss-DNA              VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4067-68, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 4067-68.
REFERENCE   1  (bases 1 to 1498)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env G subtype sequences.
            It represents one of 14 CAR isolates that have been integrated
            into a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      563 a    239 c    320 g    376 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggggataca gaggaattgg cagcacttat ggaaatgggg gactttgatc
env start ->
       61 cttgggttgg tgataatttg tagcgccaca aatagcttgt gggtcacagt ctattatggg
      121 gtgcctgtgt gggaagatcg agatgcccct ctattttgtg catctgatgc taggtcatat
      181 agtactgaaa aacataatgt ctgggccaca catgcctgtg tacccacgga ccccaaccca
      241 caagagatag ttctggaaaa tgtaacagaa aattttaata tgtggaaaaa taacatggta
      301 gaacagatgc atgaggatat aattagttta tgggatgaaa gcttagagcc atgtgtaaag
      361 ctaacccctc tctgtgttac tttaaactgt actgaagtga acaacaattg tactagggac
      421 aacaatagca ctgtgaattg tgaggaagaa aaaatgaaaa actgctcttt caatataacc
      481 acagaaataa gagataagag aaagacagaa tacgcgcttt tctatagact tgatgtagta
      541 ccaattaatg aggatcagaa tagtagtact tatagattaa taaattgtaa tgtctcaacc
      601 attaaacagg cttgtccaaa ggtgactttt gagccaattc ccatacatta ttgtgctcca
      661 gctggttatg cgattttaaa gtgtagagat aagaatttca atggaagagg accatgtaaa
      721 aatgtcagta cagtacaatg tacacatgga attaagccag tggtatcaac tcaattactg
      781 ctgaatggca gtttagcaga aggagaaata atgattagat ctgaaaacct tacaaacaat
      841 gccaaaatca taatagtgca gcttaataaa tctgtagaaa ttatatgtac cagacccaat
                                                    v3 loop ->
      901 aacaatacaa gaaaaagtat aagctttgga ccaggacaag cgttctatgc aacaggggac
      961 ataataggag atataagaca agcacattgt aatgttagta gaacagcttg gaatcagatg
                                      <- v3 loop
     1021 ttacagaatg tgactacaag actaaaagaa acctttcggg gggagaacat aaccttagaa
     1081 aacataacct ttaactcacc tgcaggaggg gacctagaag ttacaaaaca tagttttaat
     1141 tgtggaggag aatttttcta ttgtaataca tcaggactgt tcaatagtaa tagcactaag
     1201 actacaaatg atactaagac aaatgatact atcacactcc aatgtagaat aaaacaaatt
     1261 gtgaaaatgt ggcagagaac aggacaagca atgtataacc ctcccattgc aggaaacatt
     1321 acttgcatat caaacattac aggattactc ttaacacgtg acgggggaaa taatagtaca
     1381 gagaatagaa cagagacctt cagacctgga ggaggagata tgagggataa ttggagaagt
     1441 gaattatata agtataaagt aataaaaatt aaaccactag gaatagcacc cacccggg
                                                                  env cds ->
```

```
LOCUS       HIVCAR4071   1492 bp ss-DNA              VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4071-TG2, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 4071-TG2.
REFERENCE   1  (bases 1 to 1492)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env E subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      572 a    235 c    306 g    379 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggggacaca gatgaattgg ccaaacttgt ggaaatgggg gactttgatc
env start ->
       61 cttgggttgg tgataatgtg tagtgcctca gacaacttgt gggttacagt ttattatggg
      121 gttcctgtgt ggagagatgc agataccacc ctattttgtg catcagatgc caaagcacat
      181 gagacagaag tgcacaatat ctgggctaca catgcctgtg taccaacaga ccccaaccca
      241 caagaaatat tcttggaaaa tgtaacagaa aattttaaca tgtggaaaaa taacatggta
      301 gagcagatgc aggaggatgt aatcagttta tgggatcaaa gtctaaagcc atgtgtaaag
      361 ttaactcctc tctgtgttac tttagattgt accaaagctg attttaacac cacaaaattt
      421 aacacaacag aaaagccaga aatagaaata tcagaaatgc aaaaagaagt aagcaactgt
      481 tcttttaata taaccacaga actaagagat aaggagcagg aggtctatgc actcttttat
      541 aggtctgatc tagtaccaat tgagagaaat agtggggaaa ataatggtag tagttataga
      601 ttaatacatt gtaatacttc agtcattaag caggcttgtc aaaaagtatc ctttgatcca
      661 attcccatac attattgcgc tccagctggt tatgcgattt taaaatgtaa tgataagaat
      721 ttcattggaa cagggccatg taaaaaggta agctcagtac aatgcacaca tggaattaag
      781 ccagtggtat caactcaatt gctgttaaat ggtagtctag cagaagaaga aataataatt
      841 agatctgaaa atctcacaaa caatgccaaa accataatag tgcaccttaa taaatctgta
      901 gaaatcaatt gtaccagacc tttcaaaaag atgagaacaa gtgtaagaat aggaccaggg
           v3 loop ->
      961 cgagtattct ataaaacagg atccataaca ggagatataa gaaaagcata ttgtgagatt
                                              <- v3 loop
     1021 aatggaacaa aatggaatga aactttacaa cagataatta gaaaattaga agagcacttt
     1081 aataataaga caatacaatt taaaccacca tactcaggag gagatctaga aattacaatg
     1141 caccatttta attgtagagg ggaatttttc tattgcaata caacaagact gtttaatatt
     1201 agcacaaatg gaaccacaaa tggcactatc acacttccat gcaggataaa gcaagttata
     1261 aagatgtggc aggaagtagg acaagcaatg tatgctcctc ccatcgatga agcaattaat
     1321 tgtgtatcaa atattacagg aatactattg gtaagagatg gtggtaaaat tgaaaatgag
     1381 accatcgaaa ccttcagacc tggaggagga aatatgaagg acaattggag aagtgaatta
     1441 tataaatata aagtagtaca aattgaacca ctaggaatag cacccacccg gg
                                                          env cds ->
```

```
LOCUS       HIVCAR4081   1486 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 4081, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 4081.
REFERENCE   1  (bases 1 to 1486)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env G subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression sysytem for study by Transgene and Pasteur Merieux.
BASE COUNT      577 a    245 c    298 g    366 t
ORIGIN      Beginning of env cds
        1 ATGaaagtga tggagacaca gaggaattgt ccacgctcat ggagatgggg gattttgatc
env start ->
       61 cttgggttgg tgataatttg taatgcctca gacaacaact tgtgggtcac agtttattat
      121 ggggtacctg tgtggaaaga tgcagagacc accctatttt gtgcatctga tgctaaatca
      181 tatagtactg aaaaacataa tgtctgggct acacatgcct gtgtacccac agaccccaac
      241 ccacaagaaa tacttttaga aaatgtaaca gaaaagttta acatgtggaa aaataacatg
      301 gtagaacaga tgcatgagga tataatcagt ttatgggatg aaagcctaaa accatgtgta
      361 aagctaaccc ctctttgtgt tactttaacc tgtactaata taaccaaaaa tagtactgaa
      421 gtaaacaaca atagcactgt ggataataaa gaagaaataa aaaattgctc tttcaatata
      481 accacagaaa taagagataa gaagaagaca gcatacgcgc ttttctatag actagatgta
      541 gtaccaatta atgataataa taataataat agttataggc taataaattg taatacctca
      601 gccattaaac aggcttgtcc aaaggtatcc tttgagccaa ttcccataca ttattgtgct
      661 ccagctggtt ttgcgattct aaagtgtaag gataagaagt tcaatggaaa aggaccatgt
      721 aaaaatgtca gtacagtgca atgcacacat ggaatcaagc cagtagtatc aactcaactg
      781 ctgttgaatg gcagcctggc agaagaagag ataataatta gatctgaaaa catcacagac
      841 aatgccaaaa tcataatagt acatcttaat gagtctgtag aaattaattg taccaggcct
             v3 loop ->
      901 aacaacaata caagaaaaag tgtaaggata gggccaggac aaacattcta tgcaacaggt
      961 gacataatag gagatataag acaagcacat tgtaatgtca gtagaacaaa atggaatcag
                                          <- v3 loop
     1021 actttacaac aaatagctac acaattaaga aaatactttg ggaatacaac aacaataaac
     1081 tttagtaaat cctcaggagg agatttagaa attacaacac acacttttaa ttgtggagga
     1141 gaatttttct attgcaatac atcacgcttg tttaatagca gttggaaagg aaagtacagt
     1201 gggcatgagt caaatgacac tataactctc ccgtgcaaaa taagacaaat tgtaaggatg
     1261 tggcagaaag taggacaagc aatgtatgcc cctcccatcc caggagtaat aaggtgtgaa
     1321 tcaaacatta caggactaat actaacaaga gatggtggaa ataataagac taataacact
     1381 gaaaccttca gacctggggg aggagatatg agggacaatt ggagaagtga attatataaa
     1441 tataaagtag taaaaattga accactagga gtagcaccca cccggg
                                                    env cds ->
```

HIVCAR423A

```
LOCUS       HIVCAR423A   1516 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate 11423-21,
            env glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate 11423-21.
REFERENCE   1  (bases 1 to 1516)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny, M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env A subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into a
            "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      577 a    255 c    313 g    371 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggagaaata tcagcacttg tggagatggg ggtggaaatg gggcagcatg
env start ->
       61 ctccttggga tattgatgat ctgtaatgct tcagacaaat tgtgggtcac agtctattat
      121 ggggtacctg tgtggcgaga tgcaaatacc actctatttt gtgcatctga tgctaaagca
      181 tatagtactg aaaaacataa tgtctgggct acacattcct gtgtacccac agaccccaac
      241 ccacaagaga tacttctgga aaatgtaaca gaaaatttta acatgtggaa aaatagtatg
      301 gtagatcaga tgcatgagga tataatcagt ttatgggatg aaagcctaaa gccatgtgta
      361 aagctaaccc ctctctgtgt tactttaaac tgtactaatg taactgtaac caacagcagt
      421 aataatgtaa ccaaaaccaa cagtagccaa tcctctaagt ataacattga tggaaaagaa
      481 gaaataaaaa actgttcttt caatacgacc acagaaataa tagataagag gaagcaagaa
      541 tacgcgcttt tctatagact tgatatagta ccaattaata ataataataa tacaaatgag
      601 tataggttaa taaattgtat tgcctcaact gttaaacagg cttgtccaaa ggtatccttt
      661 gagccaattc ccatacatta ttgtgctccg gctggttttg cgattctaaa gtgtagggat
      721 gagaagttca atggaacagg gccatgcaat aatgtcagca ccgtacaatg cacacatgga
      781 atcaagccag tagtatcaac tcaactactg ttaaatggca gcctagcaga aggggaggta
      841 aagattagat ctgaaaactt cacaaacaat gctaaaacca taatagtaca gcttgacagt
      901 cctgtaagaa ttaattgtac cagacctaac aactatacaa gaaaaatgat acctacagga
                V3 loop ->
      961 ccaggacaag gacaagtcat ctatgcaaca ggtaaaataa taggggatat aagaaaagca
     1021 tattgtaaca tcagtaaagc agaatggaaa aacatgttaa gaaaggtagc tacaaaacta
            <- V3 loop
     1081 gaaagcaagt ttaacaaatc aattaccttt gataaacctt caggagggga tatagaaatt
     1141 acaatatata gctttaattg taaaggagaa tttttctatt gcaatacatc aaaactgttt
     1201 aatagcactt ggaaaaatgg cactactgaa gaaaatgaca cggagtcaga ggaccctata
     1261 gttctcccat gcaggataaa gcaaattgta catatgtggc agagagtagg acaagcaatg
     1321 tatacccctc ccatccaagg agaaataaag tgtgaatcaa acatcacagg actactatta
     1381 acaagagatg gtgggaagaa cacaactaat aagactttca gacctatagg aggagatatg
     1441 agggacaatt ggagaagtga attatatagg tataaagtag tggaaattga accattagga
     1501 gtagcaccca cccggg
                  env cds ->
```

```
LOCUS       HIVCARELO    1510 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate ELO, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate ELO.
REFERENCE   1  (bases 1 to 1510)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env E subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgaene and Pasteur Merieux.
BASE COUNT      550 a    257 c    314 g    389 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggggacaca gatgaattgg ccacacttgt ggaaatgggg aactttgatc
env start ->
       61 cttgggttgg tgataatttg tagggcctca gaaaacttgt gggttacagt ctattatggg
      121 gttcctgcgt ggagagacgc agaaaccacc ctattttgtg catcagatgc caaagcacat
      181 gagacggaag tgcacaatgt ctgggctaca cacgcctgtg tacccacaga ccctaaccca
      241 caagaaatat acatggaaaa tgtaacagaa cattttaaca tgtggaaaaa taacatggta
      301 gagcagatgc aggaggatgt aatcagttta tgggatcaaa gtctaaagcc atgtgtaaaa
      361 ttaactcctc tctgcgttac tttaaggtgt accaatgcta attttaccaa tgctaccgat
      421 gctaatgtta ccaatgctac tgctaaattt aatgctacaa aagaaatgga aaatacagta
      481 aaaaactgtt cttttaatat gaccacagaa ctgggagata agcatcagaa ggtctctgca
      541 ctttttttata agcttgattt agtaccaatt gatggcaata ttgatggcaa taatagtgag
      601 tatatattaa tacattgtaa tacttcagtc attaagcagg cttgtccaaa ggtgtccttt
      661 gatccaattc ccatacatta ttgtgccccg gctgattttg cgattttaaa gtgtaatgat
      721 aaggagttca atggaacagg gccatgcaaa aatgtcagct cagtacaatg cacacatgga
      781 attaagccag tggtatcaac tcaattgctg ttaaatggca gtttagcaga agaagagata
      841 ataatcagat ctgaaaatct cacaaacaat gccagaacca taatagtgca ccttaataaa
      901 tctgtagaaa tcaattgtac cagaccctac aaaaatacaa gaacaagtgc aaggatagga
                  v3 loop ->
      961 ccaggacaag tattctataa aacaggatcc ataacaggag atataaggaa agcatattgt
                   <- v3 loop
     1021 gagattaatg gaacagcatg gcatgaaact ttaaaacaga tggttggaaa attaagaaag
     1081 cactttaata agacaataat ctttcaacca tcctcaggag gagatccaga aattacaatg
     1141 cataatttta attgtagagg ggaatttttc tattgcaata caacaaacct gtttaatagt
     1201 acttgggaaa taaataaaac catgaagtct aatgacacaa acttaagcaa tatcacactt
     1261 ccatgcagaa taaagcaaat tggaaacatg tggcagggag taggacgagc aatgtatgct
     1321 cctcccatca gtgaactagt taattgtgta tcaaatatta caggaatact attgacaaga
     1381 gatggtggtc ctaatactgc gaatgagacc ttcagacctg gaggagggaa tatgaaggac
     1441 aattggagaa gtgaattgta taaatataaa gtagtacaaa ttgaaccact aggaatagca
     1501 cccacccggg
            env cds ->
```

HIVCARGAN

```
LOCUS       HIVCARGAN    1507 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate GAN, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate GAN.
REFERENCE   1  (bases 1 to 1507)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env D subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      574 a    264 c    316 g    353 t
ORIGIN      Beginning of env cds
        1 ATGagagtga tggggataca gaagaattat caacacttgt tgagatgggg gactatgatc
env start ->
       61 tttgggttaa taataattag ttgtgttgca gaccaactgt gggtcacagt ctactatggg
      121 gtacctgtgt ggaaaaatgc agacaccacc ctattttgtg catcaaatgc cagagcatat
      181 gatacagaag tgcataatgt ctgggctaca catgcctgtg tacccacaga ccccaaccca
      241 caagaaataa atttggtcaa tgtgacagaa gagtttaaca tgtggaaaaa taacatggta
      301 gaacagatgc atacagatat aaccagtcta tgggaccaaa gcctacagcc atgtgtaaag
      361 ttaacccctc tctgcgttac cttagaatgc cataaaccca acaccacaga tagcaccaaa
      421 aacaacagcg cagaaaacat gacctttgaa gggataggag aaataacaaa ctgctctttc
      481 aatatgacca cagagctaag agataagaaa cagaaagtat attcactttt ttataaactt
      541 gatgtagtac aaatagatga gaataatggt actagaaata acagtgagct gtatagacta
      601 ataaattgta atacctcagc cattacacaa gcttgtccaa aggtaacctt tgagccaatt
      661 cccatacatt attgtactcc agctggtttt gcgattctaa agtgtaatga gaaaaagttt
      721 aatggaacag ggccatgcag gaatgtcagc tcagtacaat gcacacatgg aatcaaacca
      781 gtagtaacaa ctcaactgct gttaaatggc agtctagcag aagaagaggt aatcatcaga
      841 tctgaaaata tcacaaacaa tgcaaaaaca ataatagtac agcttgtcaa gcctgtaaat
      901 attacttgta tcagacctag caggactaca aggaaaagat ggcatatagg atcaggacaa
        v3 loop ->
      961 gccttctatg caatagatgg cataacagga gatataagaa aagcatattg cgaggtcaat
                                                              <- v3 loop
     1021 acaacagaat ggaatcaaac tttacaacag gtagtaaaaa aattaagaac atattggaac
     1081 aaaacaataa acttcactaa accctcggga ggggatttag aaattacaac acatagtttt
     1141 aattgtggag gagaattttt ctattgcaat acatcaggcc tgtttaatag cagttggaag
     1201 aatgagaatg acactaaaag catgaagggg ttaaaaggta ctataactct ccagtgcaga
     1261 ataaagcaaa ttgtaaatat gtggcagaga gcagggcaag caatgtatgc ccctcccatc
     1321 acaggaataa taaggtgtga gtcaaacatt acaggactac tactgacaag agatggtggg
     1381 tttaataaca ggacaaatga tactgagacc ttcagacctg ggggaggaga tatgagagac
     1441 aattggagaa gtgaattata taaatataaa gtagtaaaat tgaccactag gatacgaccc
     1501 acccggg
         env cds ->
```

```
LOCUS       HIVCARMBA    1471 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate MBA, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate MBA.
REFERENCE   1  (bases 1 to 1471)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env E subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      552 a    239 c    298 g    382 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggggacaca gatgacttgg ccaaactggt ggaaatgggg gactttgatc
env start ->
       61 cttgggttgg tgataatttg taatgcctca aacaacttgt gggttacagt ttattatggg
      121 gttcctgtgt ggaaagatgc agataccacc ctatgctgtg catcagatgc caaagcacac
      181 gtgacagaaa tgcacaatgt ctgggctaca catgcctgtg taccacatac ccaaccacaa
      241 gaagtataca tggaaaatgt aacagaaaat tttaacatgt ggaaaaataa tatggtagaa
      301 cagatgcatg aggacataat cagtttatgg gatgaaagcc taaaaccatg tgtaaagcta
      361 actcctctct gtgttacctt aaattgtacc agggctaatc ttaattctac caatgctaat
      421 tctaccaatg ctaataccct aaaaatggaa aatgaagtaa aaaactgttc ttttaatatg
      481 accacagaac taagagataa gaagcagaag gtctctgcaa ttttttatgt atctgatcta
      541 gtatcaatga atgcaaataa tagctatagg ttaataaatt gtaatacttc agtcattaag
      601 caggcttgtc caaaggtgtc ctttgatcca attcccatac attattgtgc tccagctggt
      661 tatgcgattt taaagtgtaa tagtaagact ttcaatggaa cagggccatg taaaaatgta
      721 agctcagtac aatgcacaca tggaattaag ccagtggtat caactcaatt gctgttaaat
      781 ggcagtctag cagaagaaga gataataatc agatctgaaa atctcgcaaa caatgccaaa
      841 accataatag tgcaccttaa taaacctgta gaaatcaatt gtaccagacc ctccaacaat
                                                  v3 loop ->
      901 acaagaacaa gtgtacgtat aggaccagga caagtattct atggaacagg agaaataata
      961 ggagatataa gaagagcatt ttgtgagatt aatggaacaa aatggaatga aactttaaag
                                  <- v3 loop
     1021 caggtaactg aaaaattaag agaacacttt aataagacaa tagtttttca accaccctca
     1081 ggaggagatc tagaaattac aatgcatagt tttaattgta gaggggaatt tttctattgc
     1141 aatacaacaa aactgtttaa tagtacttgg gaaatgaata aaaccataga ggagcttaat
     1201 ggcactatca cacttccatg caggataaag caaattgtaa acatgtggca gggagtagga
     1261 caagcaatgt ataatcctcc cgtcagtgga gtaattaatt gtgtatcaaa tattacagga
     1321 atactattaa caagagatgg tgggatgctg aataatacac aaaatgagac cttcagacct
     1381 ggaggaggaa atataaagga taattggaga aatgaattat ataaatataa agtagtacaa
     1441 attgaaccac taggaatagc acccacccgg g
                                     env cds ->
```

HIVCARSAS

```
LOCUS       HIVCARSAS    1501 bp ss-DNA             VRL       01-OCT-1994
DEFINITION  Human immunodeficiency virus type 1, CAR isolate SAS, env
            glycoprotein gp120, partial cds.
ACCESSION
SOURCE      Human immunodeficiency virus type 1 (HIV-1), CAR isolate SAS.
REFERENCE   1  (bases 1 to 1501)
  AUTHORS   Schmitt,D., Mathiot,C., Levy,J.-P., Girard,M., You,B.,
            Barre-Sinoussi,F., Deslandres,A., and Kieny,M.P.
  TITLE     ;
  JOURNAL   Unpublished
COMMENT     Kindly provided prior to publication by Dr. Marie Paule Kieny
            of Transgene in Strasbourg, France. This sequence, from a Central
            African Republic isolate, clusters with env A subtype sequences.
            It represents one of 14 CAR isolates that have been integrated into
            a "hybrid" gp160 sequence for expression from a vaccinia virus
            expression system for study by Transgene and Pasteur Merieux.
BASE COUNT      569 a    263 c    307 g    362 t
ORIGIN      Beginning of env cds
        1 ATGagagtga aggggacaca gaagaattac tctcccttgt ggagatgggg gattatgatc
env start ->
       61 cttgggctga taataatctg tagtgctaca gaaaaattgt gggtcacagt ttactatggg
      121 gtacctgtgt ggaaagatgc aaagaccacc ctattttgtg catcagatgc taaagcatat
      181 gatacagaaa tgcataatgt ctgggccaca catgcctgtg tacccacaga ccccaaccca
      241 caagaaatgg atttgaaaaa tgtgacagaa aattttaaca tgtggaaaaa taacatggta
      301 gagcaaatgc atacagatat aatcagccta tgggaccaaa gcctaaagcc atgtgtacag
      361 ttaacccctc tctgtgttac tttagactgt actaatgtag ctaacgacag tacaaatgaa
      421 ctaagaaact gctcttacaa tatgaccaca aaactaaatg ataaaagaca aaaggtacat
      481 tcacttttt ataaacttga tatagtccca attaataaaa ttaatgatgc tagtggtaat
      541 attagtgaga acaataatag tagtagtggc aatattacta aacaatatag actaataagt
      601 tgtaatacct caaccattac acaggcttgt ccaaaggtat cctttgagcc aattcccata
      661 cattattgtg ccccagctgg ttttgcgatt ctaaagtgta aggatacgga gttcaaagga
      721 acagggccat gcaagaatgt tagtacagta caatgcacac atggaatcag gccagtagta
      781 tcaactcaac tactgttaaa tggcagccta gcagaaggaa agataatgat tagatctgaa
      841 aatttctcaa acaatgccaa aaccataata gtacagctta accagtctgt agaaattaat
      901 tgtactagac ccaataacaa tacaagaaga agaatgcata taggaccagg acgagcattc
 v3 loop ->
      961 attgcaacag atgccatagt aggggatata aggcaagcat attgtaatgt cagtagagca
                                                        <- v3 loop
     1021 acatggaata aaactttaca aatggtagct gaagaattaa gaaaacagtt taacaaaaca
     1081 ataatctttg ataaccttc aggaggggat gtagaaatta caacacatag ttttaattgt
     1141 ggaggagaat ttttctattg caacacatca ggcctgttta ataaaacttg gtgggggcca
     1201 aatagcacca ccaacaatca gaccattggc aatgacacta taactctccc atgcagaata
     1261 aagcaaattg taaggatgtg gcagagagta ggaaaagcaa tgtatgcccc tcccatcaaa
     1321 ggagcgataa actgtagatc aaacattaca ggactactat taacaagaga tggaggggg
     1381 aataacaggt caaatgagac cttcagacct gaaggaggaa atacaaggga caattggaga
     1441 agtgaattat ataagtataa agtagtaaaa attgaaccac taggaatagc acccacccgg
     1501 g
```

```
LOCUS       HIVCI47      900 bp ss-RNA              VRL       31-MAR-1994
DEFINITION  Human immunodeficiency virus type 1 (HIV-1) V3-V5 region envelope
            sequence, Ivory Coast sample CI-47, clone 1.
ACCESSION   X72049
SOURCE      Human immunodeficiency virus type 1 cocultivated PCR-amplified
            PBMC DNA derived from a patient from Cote d'Ivoire
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Janssens,W., Heyndrickx,L., Van de Peer,Y., Bouckaert,A.,
            Fransen,K., Motte,J., Gershy-Damet,G.M., Peeters,M., Piot,P. and
            Van der Groen,G.
  TITLE     Molecular phylogeny of part of the env gene of human
            immunodeficiency virus type 1 isolated in Cote d'Ivoire
  JOURNAL   AIDS 8, 21-26 (1994)
COMMENT     Janssens et al. conducted a survey designed to determine the
            genetic HIV-1 variation present in Cote d'Ivoire.  As a part
            of this study, viruses were isolated from eleven symptomatic (CI-3,
            CI-13, CI-21, CI-22, CI-42, CI-45, CI-47, CI-326, CI-327, CI-329,
            and CI-330) and two asymptomatic (CI-14 and CI-20) HIV-1 infected
            individuals.  Isolates CI-13, CI-14, CI-45 and CI-47 were derived
            from patients whose sera were dually reactive to both HIV-1 and
            HIV-2 antibodies.  These thirteen isolates were sequenced over
            the envelope region including V3, V4, V5 and the beginning of
            gp41.  In phylogenetic analysis, isolates CI-22 and CI-13
            cluster with subtype B and subtype D respectively.  The
            remaining eleven of the thirteen HIV-1 isolates cluster with
            HIV-1 subtype A, with significant variation among these sequences.
            Janssens et al. propose this variation suggests either a local
            burst of particular variants, or a recent spread of the epidemic
            in Abidjan.  The envelope sequences in this set are shown
            in the alignment below (accession numbers X72024-X72065).
            NCBI gi: 468672
BASE COUNT      350 a    142 c    202 g    206 t
ORIGIN      790 bp downstream from the beginning of env cds
        1 gaaggaatag tgattagatc tgaaaatatc acaaacaatg ccaaaaccat aatagtacag
 env cds ->
       61 ttaagtaagc ctgtaaaaat taattgtacc agacctggca actatacaag aaaaagtgta
                          V3 loop ->
      121 cgtacaggta taggaccagg gcaaacattc tatgcaacag gtaaaataat aggggatata
      181 agacaagcac attgtaatgt cagtagaaga gactggaata acactttaca acaggtagct
                     <- V3 loop
      241 acaaaattaa gggagtactt taataaaaca ataatctttg ataaatcctc aggaggggat
      301 gtagaaatta caacacatag ttttaattgt ggaggagaat ttttctattg ctatacatca
      361 aaactgttta atagcacttg gaataacaat gacactgcca gctcaaataa catagagtca
      421 aatgataata taactctcca atgcagaata aagcaaattg taaatatgtg gcagaaagtg
      481 ggacaagcaa tgtatgcccc tcccatccaa ggagaaataa agtgtgtatc aaacatcaca
      541 ggactactat taacaagaga tggagggaat aataataata gtatgaatga gactttcagg
      601 cctggaggag gagatatgag ggacaattgg agaagtgaat tatataagta taaagtagta
      661 aaaattgaac cactaggtgt agcacccacc catgcaaaaa gaagagtggt ggagagagaa
      721 aaaagagcag ttggactggg agcgttcttc cttgggttct taggagcagc aggaagcact
      781 atgggcgcgg cgtcaataac gctgacggta caggccagac aattattgtc cggtatagtg
      841 caacagcaaa gcaatttgct gagggctata gaggctcaac aacatctgtt gaaactcacg
                                                                    env ->
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HIVCI47

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CONSENSUS GGAGA?...GTAGTGATTAGATCTGAAAATATCACAAACAATGCCAAAACCATAATAGTACAGTT?G?TA   64
CI-3-1    ---A-T...----CA----------G-------------------G----------------TAC-G   67
CI-3-2    ---A-T...---ACA----------G-------------------G----------------TAC-G   67
CI-3-3    ---A-T...---ACA----------G-------------------G----------------TAC-G   67
CI-45-3   -A-A-G...----C---A------A-----C-------------------------------C-T-C--   67
CI-13-3   -A---A...A--A-A----------G---C-T-----T-----A----T------------C-TAA-G   67
CI-13-4   -A---A...A--A-A----------G---C-T-----T-----A----T------------C-TAA-G   67
CI-14-5   -A---G...A-------------------------------------------------------G-T--   67
CI-14-13  -A---G...----------------------T-------------------------------G-T--   67
CI-14-21  -A---G...A-------------------------------------------------------G-T--   67
CI-20-1   -AGA-G...A---C---------------------G----------A--------------G-T--   67
CI-20-2   -AGA-G...A---C---------------------G----------A--------------G-T--   67
CI-20-3   -AGA-G...A---C---------------------G----------A--------------G-T--   67
CI-20-5   -AGA-G...A---C---------------------G----------A--------------G-T--   67
CI-21-1   -----G...---AGA-------------------G-T---------A-----------AC-T-CC-   67
CI-21-2   -----G...---AGA-------------------G-T---------A-----------AC-T-CC-   67
CI-21-4   -----G...---AGA-------------------G-T---------A-----------AC-T-CC-   67
CI-22-3   -A---A...-----A---------C-----T----GG-------T----------------C-GAACG   67
CI-22-6   -A---A...-----A---------C-----T----GG-------T----------------C-GAACG   67
CI-22-10  -A---A...-----A---------C-----T----GG-------T----------------C-GAACG   67
CI-42-1   -----TGAT---A--------------G-C--G--G-----A------------------C-T-T-G   70
CI-42-2   -----TGAT---A--------------G-C--G--G-----A------------------C-T-T-G   70
CI-42-3   -----TGAT---A--------------G-C--G--G-----A------------------C-T-T-G   70
CI-42-4   -----TGAT---A--------------G-C--G--G-----A------------------C-T-T-G   70
CI-45-1   -A-A-G...----C---A------A-----C-------------------------------C-T-C--   67
CI-45-2   -A-A-G...----C---A------A-----C-------------------------------C-T-C--   67
CI-47-1   -A--GA...A-------------------------------------------------------AAG--   67
CI-47-3   -A--GA...A-------------------------------------------------------AAG--   67
CI-47-8   -A--GA...A-------------------------------------------------------AAG--   67
CI-326-2  -----A...----C---------------------------------------------------GTC--   67
CI-326-3  -----A...-------------------------------------------------------GTC--   67
CI-326-4  -----A...-------------------------------------------------------GTC--   67
CI-327-1  -----G...A-----------------------------------------------G-----AAA-G   67
CI-327-2  -----G...A-----------------------------------------------G-----AAA-G   67
CI-327-3  -----G...A---C-------------------------------------------G-----AAA-G   67
CI-327-4  -----G...A-----------------------------------------------G-----AAA-G   67
CI-329-1  ---A-T...---ACA----------------T-A-------------------------------AAA--   67
CI-329-3  ---A-T...---ACA----------------G---------------------------------AAA--   67
CI-329-5  ---A-T...---ACA----------------T-A-------------------------------AAA--   67
CI-330-1  -----T...---A-------G---------C-----------------------------C-T-A-G   67
CI-330-2  -----T...---A-------G---------C-----------------------------C-T-A-G   67
CI-330-3  -----T...---A-------G---------C-----------------------------C-T-A-G   67
CI-330-4  -----T...---A-------G---------C-----------------------------C-T-A-G   67
```

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CONSENSUS AGCCTGTAA?AATTAATTGTACCAGACCTAGCAACAATACAAGAAAAAGTGTA.....C?TATAGG  123
CI-3-1    ---------G--------------------A----------------------.....-G------  128
CI-3-2    ---------G--------------------A-------------C-------.....-G------  128
CI-3-3    ---------G--------------------AT---------------------.....-G------  128
CI-45-3   ---------A------------------C-A---------------------.....-G------  128
CI-13-3   -AT------C------C--------G--C-A-------------C--G--AC-.....-A------  128
CI-13-4   -AT------C------C--------G--C-A-------------C--G--AC-.....-A------  128
CI-14-5   ---------G-------------------------------------------.....-CA-----  128
CI-14-13  ---------G-------------------------------------------.....-CA-----  128
CI-14-21  ---------G-------------------------------------------.....-CA-----  128
CI-20-1   ---------G----------------------------------C------A--.....-G------  128
CI-20-2   ---------G----------------------------------C------A--.....-G------  128
CI-20-3   ---------G----------------------------------C------A--.....-G------  128
CI-20-5   ---------G----------------------------------C------A--.....-G------  128
CI-21-1   -AAA-----C----G------T-----------------------------------.....AA-----  128
CI-21-2   -AAA-----C----G------T-----------------------------------.....AA-----  128
CI-21-4   -AAA-----C----G------T-----------------------------------.....AA-----  128
CI-22-3   --T-----GT-----------A-----C-A---T---------------A--.....-A---G--  128
CI-22-6   --T-----GT-----------A-----C-A---T---------------A--.....-A---G--  128
CI-22-10  --T-----GT-----------A-----C-A---T---------------A--.....-A---G--  128
CI-42-1   ---------A----------T------C-AT----------G---------.....-A------  131
CI-42-2   ---------A----------T------C-AT----------G---------.....-A------  131
CI-42-3   ---------A----------T------C-AT----------G---------.....-A------  131
CI-42-4   ---------A----------T------C-AT----------G---------.....-A------  131
CI-45-1   ---------A------------------C-A---------------------.....-G------  128
CI-45-2   ---------A------------------C-A---------------------.....-G------  128
CI-47-1   ---------A-------------------G-----T----------------CGTACA...GG------  134
CI-47-3   ---------A-------------------G-----T----------------CGTACA...GG------  134
CI-47-8   ---------A-------------------G-----T----------------CGTACA...GG------  134
CI-326-2  ---------G-------------------G-T----------G------TGGAGAAGTTGG-A------  137
CI-326-3  ---------G-------------------G-T----------G------TGGAGAAATTGG-A------  137
CI-326-4  ---------G-------------------G-T----------G------TGGAGAAGTTGG-A------  137
CI-327-1  --A------A----------T-------G----------------G-----.....-A------  128
CI-327-2  --A------A----------T-------G----------------G----G.....-A------  128
CI-327-3  --A------A----------T-------G----------------G-----.....-A------  128
CI-327-4  --A------A----------T-------G----------------G-----.....-A------  128
CI-329-1  ---------A-------------------G--------------------T--.....-G------  128
CI-329-3  ---------A-------------------G--------------------T--.....-G------  128
CI-329-5  ---------A-------------------G--------------------T--.....-G------  128
CI-330-1  ---------C------------------C-A------C---------------.....-G------  128
CI-330-2  ---------C------------------C-A------C---------------.....-G------  128
CI-330-3  ---------C------------------C-A------C---------------.....-G------  128
CI-330-4  ---------C------------------C-A------C---------------.....-G------  128
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HIVCI47

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CONSENSUS ACCAGGGCAAGCATTCTATGCAACAGGTGACATAATAGGGGATATAAGACAAGCACATTGTAATGTCAGT  193
CI-3-1    ------------------------------------------------------------------------  198
CI-3-2    ------A-----------------------------------------------------------------  198
CI-3-3    ------------------------------------------------------------------------  198
CI-45-3   ----------A-------------------------------------------G-G---------------  198
CI-13-3   ---------G---C-----A-----...-GGG-------A---------A--------------A-T---  195
CI-13-4   ---------G---C-----A-----...-GGG-------A---------A--------------A-T---  195
CI-14-5   -------------------------A------------------------------------------  198
CI-14-13  --------G-----------------A------------------------------------------  198
CI-14-21  -------------------------A------------------------------------------  198
CI-20-1   ----------A----T-----------CCG-------------------------------------  198
CI-20-2   ----------A----T-----------CCG-------------------------------------  198
CI-20-3   ----------A----T-----------CCG-------------------------------------  198
CI-20-5   ----------A----T-----------CCG-------------------------------------  198
CI-21-1   ------A-------------------------------------------------------T---  198
CI-21-2   ------A-------------------------------------------------------T---  198
CI-21-4   ------A-------------------------------------------------------T---  198
CI-22-3   -------AGC---A-T-----------A--A--------A---------A-----T----C--CA-T---  198
CI-22-6   -------AGC---A-T-----------A--A--------A---------A-----T----C--CA-T---  198
CI-22-10  -------AGC---A-T-----------A--A--------A---------A-----T----C--CA-T---  198
CI-42-1   ------A--------T-----------------------------------------T------------A-  201
CI-42-2   ------A--------T-----------------------------------------T------------A-  201
CI-42-3   ------A--------T-----------------------------------------T------------A-  201
CI-42-4   ------A--------T-----------------------------------------T------------A-  201
CI-45-1   ----------A-------------------------------------------G---------------  198
CI-45-2   ----------A-----------------A------------------A------G---------------  198
CI-47-1   ----------A-----------------A-A-----------------------------------------  204
CI-47-3   ----------A-----------------A-A-----------------------------------------  204
CI-47-8   ----------A-----------------A-A-----------------------------------------  204
CI-326-2  --------G----------A------A--G---------T---------A-----T--------------  207
CI-326-3  --------G----------A------A--G---------T---------A-----T--------------  207
CI-326-4  --------G----------A------A--G---------T---------A-----T--------------  207
CI-327-1  ----------------------G-------------------------------------------------  198
CI-327-2  ----------------------G-------------------------------------------------  198
CI-327-3  ----------------------G-------------------------------------------------  198
CI-327-4  ----------------------G-------------------------------------------------  198
CI-329-1  ----------A-------------------------------------------------------------C  198
CI-329-3  ----------A-------------------------------------------------------------C  198
CI-329-5  ----------A-------------------------------------------------------------C  198
CI-330-1  ------A-------------------------------------------------------------A-  198
CI-330-2  ------A-------------------------------------------------------------A-  198
CI-330-3  ------A-------------------------------------------------------------A-  198
CI-330-4  ------A-------------------------------------------------------------A-  198
```

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CONSENSUS AGAACAGAATGGAATAAAACTTTACAACAGGTAGCTA?ACAATTAAGG?AGCACTTT...AA?AA?ACAA  256
CI-3-1    -A-GAG----------T-A----GG-A---------T-A--------G-AT-----AAG--T--C----  268
CI-3-2    -A--A----------A----GG-A---------T-A--------G--T-----AAG--T--C----  268
CI-3-3    -A--A----------A----GG-A---------T-A--------G--T-----AAG--T--C----  268
CI-45-3   G-------G------G-------G--GA----G---GCG---------A--------.....--T-A--  262
CI-13-3   G-G-A--C----------A------T-A-------AA-C-TTC--...--C--G----  262
CI-13-4   G-G-A--C----------A------T-A-------AA-C-TTC--...--C--G----  262
CI-14-5   -A----------G---------G----------C--------A-A--------...--G--TG---  265
CI-14-13  -A----------G----------C--------A-A--------...--G--TG---  265
CI-14-21  -A----------G---------G----------C--------A-A--------...--G--TG---  265
CI-20-1   ----------G----C---------AGG-T-----...--A--TG---  265
CI-20-2   ----------G----C---------AGG-T-----...--A--TG---  265
CI-20-3   ----------G----C---------AGG-T-----...--A--TG---  265
CI-20-5   ----------G----C---------AGG-T-----...--A--TG---  265
CI-21-1   ---G---C---------C-----G---G-------C-AC-------AAATA------...G-G--C-A--  265
CI-21-2   ---G---C---------C-----G---G-------C-AC-------AAATA------...G-G--C-A--  265
CI-21-4   ---G---C---------C-----G---G-------C-AC-------AAATA------...G-G--C-A--  265
CI-22-3   G--G--A----------C------A-----A---T-GG-A-------AG-A--A---GGA--T--T-A--  268
CI-22-6   G--G--A----------C------A-----A---T-GG-A-------AG-A--A---GGA--T--T-A--  268
CI-22-10  G--G--A----------C------A-----A---T-GG-A-------AG-A--A---GGA--T--T-A--  268
CI-42-1   GA----------G--G------G-A--------GG--------TAC-A------...--C--A----  268
CI-42-2   GA----------G--G------G-A--------GG--------TAC-A------...--C--A----  268
CI-42-3   GA----------G--G------G-A--------GG--------TAC-A------...--C--A----  268
CI-42-4   GA----------G--G------G-A--------GG--------TAC-A------...--C--A----  268
CI-45-1   G-------G------G-------G--GA----G---GCG---------A--------.....--T-A--  262
CI-45-2   GA----A-G--A----------GA----GA--GCG---------A--------.....--T-A--  262
CI-47-1   ----G---C---------C----------C-A--------G--T-----.....--T-A--  268
CI-47-3   ----G---C---------C----------C-A--------G--T-----.....--T-A--  268
CI-47-8   ----G---C---------C----------C-A--------G--T-----...--T-GT-A--  271
CI-326-2  -A-----TG-----GG-C------A-------G----G----------A--T-G---...--T--T-AC-  274
CI-326-3  -A-----TG-----GG-C------A-------G----G----------A--T-T---...--T--T-AC-  274
CI-326-4  -A-----TG-----GG-C------A-------G----G----------A--T-T---...--T--T-AC-  274
CI-327-1  -A-G--A---------GC----------G----C----------A--T-----AGG--TG-C----  268
CI-327-2  -A-G--A---------GC----------G----C----------A--T-----AGG--TG-C----  268
CI-327-3  ---G--A---------GC----------G----C-A--------A--T-----AGG--TG-C----  268
CI-327-4  -A-G--A---------GC----------G----C-A--------G--T-----AGG--TG-C----  268
CI-329-1  ----A----------G----------G----G----C----------GG-T-----AGG--TG-C----  268
CI-329-3  ----A----------G----------G----G----C----------A--------AGG--TG-C----  268
CI-329-5  ----A----------G----------G----G----C----------A--------AGG--TG-C----  268
CI-330-1  --------C-------G----------A--------GA-------G-AC-A------.....--C-A--  262
CI-330-2  --------C-------G----------A--------GA-------G-AC-A------.....--C-A--  262
CI-330-3  --------C-------G----------A--------GA-------G-AC-A------.....--C-A--  262
CI-330-4  --------C-------G----------A--------GA-------G-AC-A------.....--C-A--  262
```

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CONSENSUS CAATAATCTTTGCTAAC?CCTCAGGAGGGGAT?TAGAAATTACAACACATAGTTTTAATTGTGGAGGAGA  324
CI-3-1    ----------A-----CA----------G-------------------------------------  338
CI-3-2    ----------A-----CA----------G-------------------------------------  338
CI-3-3    ----------A-----CA----------G-------------------------------------  338
CI-45-3   ---------------G-C----------G-------------------------------------  332
CI-13-3   -------T---AACTCAT----G-------GCCC--------T------C----------------G--  332
CI-13-4   -------T---AACTCAT----G-------GCCC--------T------C----------------G--  332
CI-14-5   -----------------C----------T-----G--GT-------------------------  335
CI-14-13  -----------------C----------T-----G--GT-------------------------  335
CI-14-21  -----------------C----------T-----G--GT-------------------------  335
CI-20-1   GT----C--------G-G----------T----------------------C------------  335
CI-20-2   GT----C--------G-G----------T----------------------C------------  335
CI-20-3   GT----C--------G-G----------T----------------------C------------  335
CI-20-5   GT----C--------G-G----------T----------------------C------------  335
CI-21-1   ----------A-----T-A----------C-------------------------------------  335
CI-21-2   ----------A-----T-A----------C-------------------------------------  335
CI-21-4   ----------A-----T-A----------C-------------------------------------  335
CI-22-3   -----G-----AACC-TT----------CCC-------GT--TG--C-C---------------G--  338
CI-22-6   -----G-----AACC-TT----------CCC-------GT--TG--C-C---------------G--  338
CI-22-10  -----G-----AACC-TT----------CCC-------GT--TG--C-C---------------G--  338
CI-42-1   T-----A-----A---AT----------T----------------C-----------------  338
CI-42-2   T-----A-----A---AT----------T----------------C-----------------  338
CI-42-3   T-----A----AA---AT----------T----------------C-------------A---  338
CI-42-4   T-----A-----A---AT----------T----------------C-----------------  338
CI-45-1   ---------------G-C----------G-------------------------------------  332
CI-45-2   ---------------G-C----------G-------------------------------------  332
CI-47-1   ----------A---AT----------G-------------------------------------  338
CI-47-3   ----------A---AT----------G-------------------------------------  338
CI-47-8   ----------A---AT----------G-------------------------------------  341
CI-326-2  ----------------CA----------G-------------------------------------  344
CI-326-3  ----------------CA----------G-------------------------------------  344
CI-326-4  ----------------CA----------G-------------------------------------  344
CI-327-1  ----------------TG----------T----------------------C------------  338
CI-327-2  ----------------TG----------T----------------------C------------  338
CI-327-3  ----------------G----------T----------------------C------------  338
CI-327-4  ----------------TG----------T----------------------C------------  338
CI-329-1  A---------------AC----------T-------------------------------------  338
CI-329-3  A----------A---AC----------T-------------------------------------  338
CI-329-5  A---------------AC----------T-------------------------------------  338
CI-330-1  ------C----A-----T----------A----------------AC----------------  332
CI-330-2  ------C----A-----T----------A----------------AC----------------  332
CI-330-3  ------C----A-----T----------A----------------AC----------------  332
CI-330-4  ------C----A-----T----------A----------------AC----------------  332
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CONSENSUS ATTTTTCTATTGCAATACATCAGAACTGTTTAATAGCACTTGGAAT...AACAATA?CA?TGCC..... 383
CI-3-1    ------------G-----A--A----------------C-------...-G----GA--C----..... 399
CI-3-2    ------------G-----A--A----------------C-------...-G----GA--C----..... 399
CI-3-3    ------------G-----A--A----------------C-------...-G----GA--C----..... 399
CI-45-3   ----------------------A-----------------------...-------C--T----..... 393
CI-13-3   ---------C------------A----A--------T--A----G-ATAG-G-G--AT-T-A-A..... 396
CI-13-4   ---------C------------A----A--------T--A----G-ATAG-G-G--AT-T-A-A..... 396
CI-14-5   ----------------------------------------G--...--T----C--T-A--..... 396
CI-14-13  ----------------------------------------G--...--T----C--T-A--..... 396
CI-14-21  ----------------------------------------G--...--T----C--T-A--..... 396
CI-20-1   ----------------------AC-----------------...GG----GA--C----..... 396
CI-20-2   ----------------------AC-----------------...GG----GA--C----..... 396
CI-20-3   ----------------------AC-----------------...GG----GA--C----..... 396
CI-20-5   ----------------------AC-----------------...GG----GA--C----..... 396
CI-21-1   ------------T--C-------GC--A----------------GGC-CTGTCGG--A--T-..... 399
CI-21-2   ------------T--C-------GC--A----------------GGC-CTGTCGG--A--T-..... 399
CI-21-4   ------------T--C-------GC--A----------------GGC-CTGTCGG--A--T-..... 399
CI-22-3   G-----------T---T-----C-------------T------T--ACG--TGG--CT-A-AA-..... 402
CI-22-6   G-----------T---T-----C-------------T------T--ACG--TGG--CT-A-AA-..... 402
CI-22-10  G-----------T---T-----C-------------T------T--ACG--TGG--CT-A-AA-..... 402
CI-42-1   ----------------------------------------------...----T--C--T----..... 399
CI-42-2   ----------------------------------------------...----T--C--T----..... 399
CI-42-3   ----------------------------------------------...----T--C--T----..... 399
CI-42-4   ----------------------------------------------...----T--C--T----..... 399
CI-45-1   ----------------------A-----------------------...-------C--A----..... 393
CI-45-2   ----------------------A------------A-----AA---...-------C--A----..... 393
CI-47-1   -------------T--------A-----------------------...------GA--C----..... 399
CI-47-3   -------------T--------A-----------------------...------GA--C----..... 399
CI-47-8   -------------T--------A-----------------------...------GA--C----..... 402
CI-326-2  ----------------------A---------------T-------GAT-G--C-TTG-A-A--..... 408
CI-326-3  ----------------------A---------------T-------GAT-G--C-TTG-A-A--..... 408
CI-326-4  ----------------------A---------------T-------GAT-G--C-TTG-A-A--..... 408
CI-327-1  -----------------------T-------------------G-G...-G-----G--C----..... 399
CI-327-2  -----------------------T-------------------G-G...-G-----G--C----..... 399
CI-327-3  -----------------------T-------------------G-G...-G-----G--C----..... 399
CI-327-4  -----------------------T-------------------G-G...-G-----G--C----..... 399
CI-329-1  ----------------------------------------GC-...-------G--A-AG-..... 399
CI-329-3  ----------------------------------------C-...-------G--A-AG-..... 399
CI-329-5  --------------------C----------------------GC-...----G--G--A-AG-..... 399
CI-330-1  ----------------------GC-----------T---------...TGG---GG--C----ATCACG 399
CI-330-2  ----------------------GC-----------T---------...TGG---GG--C----ATCACG 399
CI-330-3  ----------------------GC-----------T---------...TGG---GG--C----ATCACG 399
CI-330-4  ----------------------GC-----------T---------...TGG---GG--C----ATCACG 399
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HIVCI47

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CONSENSUS ...AGCTCAAAT?ACACAGAGTCAAAT...GA?ACTATAACTCTCCAATGCAGAATAAAGCAAATTGTAA  445
CI-3-1    ...--A------A-T---A--------...--C-------------------------------------  463
CI-3-2    ...--A------A------G-------GACACT-T---------------------------------  466
CI-3-3    ...--A------A-T---A--------...--C-------------------------------------  463
CI-45-3   ............AG-T-----------...-GC------------------A-----------------  448
CI-13-3   ..................---------GATAGT--A--C-TA--T-C------------A--G-------  448
CI-13-4   ..................---------GATAGT--A--C-TA--T-C------------A--G-------  448
CI-14-5   ...---G----CC--------------...AGC-------------------------------------  460
CI-14-13  ...---G----CC--------------...AGC-------------------------------------  460
CI-14-21  ...---G----CC--------------...AGC-------------------------------------  460
CI-20-1   ...----------T------GA------...--T-------------------------------------  460
CI-20-2   ...----------T------GA------...--T-------------------------------------  460
CI-20-3   ...----------T------GA------...--T-------------------------------------  460
CI-20-5   ...----------T------GA------...--T-------------------------------------  460
CI-21-1   ...---AGGC-GG-GT--............--A-A-----------------------------------  454
CI-21-2   ...---AGGC-GG-GT--............--A-A-----------------------------------  454
CI-21-4   ...---AGGC-GG-GT--............--A-A-----------------------------------  454
CI-22-3   ATTGAAAG----G-----..................C-C-TA----C------------A------A---  454
CI-22-6   ATTGAAAG----G-----..................C-C-TA----C------------A------A---  454
CI-22-10  ATTGAAAG----G-----..................C-C-TA----C------------A------A---  454
CI-42-1   ...----------G----G-G-------...-GT-A----------C----------G-----------  463
CI-42-2   ...----------G----G-G-------...-GT-A----------C----------G-----------  463
CI-42-3   ...----------G----G-G-------...-GT-A----------C----------G-----------  463
CI-42-4   ...----------G----G-G-------...-GT-A----------C----------G-----------  463
CI-45-1   ...------G-G.........------...-GC------------------A-----------------  448
CI-45-2   ...--------G.........------...-GC------------------A-----------------  448
CI-47-1   ...----------A---T----------...--T-A-------------------------------------  463
CI-47-3   ...----------A--GT----------...--T-A-------------------------------------  463
CI-47-8   ...----------A---T----------...--T-A-------------------------------------  466
CI-326-2  AGT---AGTGTCAG-T-----------...--CC------T-T----------------A----------  475
CI-326-3  AGT---AGTGTCAG-T-----------...--CC------T-T----------------A----------  475
CI-326-4  AGT---AGTGTCAG-T-----------...--CC------T-T----------------A----------  475
CI-327-1  ...---------CC-------A------...--C-----------------------------------A---  463
CI-327-2  ...---------CC-------A------...--C-----------------------------------A---  463
CI-327-3  ...--T-----CC-------A------...--C-----------------------------------A---  463
CI-327-4  ...---------CC-------A------...--C-----------------------------------A---  463
CI-329-1  ......------G-----A--------...--C-------T-----------------------------  463
CI-329-3  ......------A---TGACA-T----...--C-------T-----------------------------  460
CI-329-5  ......------G-----A--------...--C-------T-----------------------------  460
CI-330-1  CAG-A--T-GC-G----G----T----...AGT-------------C------------A--------GC  460
CI-330-2  CAG-A--T-GC-G----G----T----...AGT-------------C------------A--------GC  466
CI-330-3  CAG-A--T-GC-G----G----T----...AGT-------------C------------A--------GC  466
CI-330-4  CAG-A--T-GC-G----G----T----...AGT-------------C------------A--------GC  466
```

```
CONSENSUS ATATGTGGCAGAGAGTAGGACAAGCAATGTATGCCCCTCCCATCCAAGGAGTAATAAGGTGTGAATCAAA  515
CI-3-1    -A----------A-------A----------------------C------------------T-----  533
CI-3-2    ------------A-------A----------------------C------------------T-----  536
CI-3-3    -A----------A-------A----------------------C------------------T-----  533
CI-45-3   ------------A-------------------------------------A------------------  518
CI-13-3   -C------------------A----------------------TG-----A----C--A---TC------  518
CI-13-4   -C------------------A----------------------TG-----A----C--A---TC------  518
CI-14-5   GA---------G-----------------------------------A-----------------A-T-----  530
CI-14-13  -----------G-----------------------------------A-----------------A-T-----  530
CI-14-21  GA---------G-----------------------------------A-----------------A-T-----  530
CI-20-1   -C----------------------C------------------A-----AA-----A-----G------  530
CI-20-2   -C----------------------C------------------A-----AA-----A------------  530
CI-20-3   -C----------------------C------------------A-----AA-----A-----G------  530
CI-20-5   -C----------------------C------------------A-----AA-----A-----G------  530
CI-21-1   ---------------C------------A--------------A-----------------A-------  524
CI-21-2   ---------------C------------A--------------A-----------------A-------  524
CI-21-4   ---------------C------------A--------------A-----------------A-------  524
CI-22-3   -C---------GA-------A----------------------AG----CA---T--A--CTC------  524
CI-22-6   -C---------GA-------A----------------------AG----CA---T--A--CTC------  524
CI-22-10  -C---------GA-------A----------------------AG----CA---T--A--CTC------  524
CI-42-1   -G-------------------------------------------------------------------  533
CI-42-2   -G-------------------------------------------------------------------  533
CI-42-3   -G-------------------------------------------------------------------  533
CI-42-4   -G-------------------------------------------------------------------  533
CI-45-1   ------------A-------------------------------------A------------------  518
CI-45-2   ------------A----A-----------------------------A-A----------A-------  518
CI-47-1   ------------A---G-----------------------------------A-----A-----T-----  533
CI-47-3   ------------A---G-----------------------------------A-----A-----T-----  533
CI-47-8   ------------A---G-----------------------------------A-----A-----T-----  536
CI-326-2  ---------------------------------------------T-C------------------C-----  545
CI-326-3  ---------------------------------------------T-C------------------C-----  545
CI-326-4  ---------------------------------------------T-C------------------C-----  545
CI-327-1  ----------A-A-------------------------------C----------A------------  533
CI-327-2  ----------A-A-------------------------------C----------A------------  533
CI-327-3  ----------A-A-------------------------------C----------A------------  533
CI-327-4  ----------A-A-------------------------------C----------A------------  533
CI-329-1  GA--------A-C-------------------------------------A-------------C----  530
CI-329-3  GA----------C-------------------------------------A---------C--------  530
CI-329-5  GA--------A-C-------------------------------------A------------------  530
CI-330-1  ---------------------------------------------T------A------AC----TG-----  536
CI-330-2  ---------------------------------------------T------A------AC----TG-----  536
CI-330-3  ---------------------------------------------T------A------AC----TG-----  536
CI-330-4  ---------------------------------------------T------A------AC----TG-----  536
```

```
CONSENSUS CATTACAGGACTACTATTAACAAGAGATGGAGGGAATAATAATAGT......ACAAATGAGACCTTCAGG   579
CI-3-1    --------------------G------------G-----------.......-AT---------------   597
CI-3-2    --------------------G------------G-----------.......-AT---------------   600
CI-3-3    --------------------G------------G-----------.......-AT---------------   597
CI-45-3   T-----------------------------------G-----------.....----------T------   582
CI-13-3   T--------G--------GCT-G-------T---GTA------CA-.......-GT-------------A   582
CI-13-4   T--------G--------GCT-G-------T---GTA------CA-.......-GT-------------A   582
CI-14-5   ----------A----------------------A------------AGT...-------------------   597
CI-14-13  ----------A----------------------A------------AGT...-------------------   597
CI-14-21  ----------A----------------------A------------AGT...-------------------   597
CI-20-1   ---------------------------------A--G----G----AAT...----G------------A   597
CI-20-2   ---------------------------------A--G----G----AAT...----G------------A   597
CI-20-3   ---------------------------------A--G----G----AAT...----G------------A   597
CI-20-5   ---------------------------------A--G----G----AAT...----G------------A   597
CI-21-1   T------------A----------------T---GG----------.....--------A--------A   588
CI-21-2   T------------A----------------T---GG----------.....--------A--------A   588
CI-21-4   T------------A----------------T---GG----------.....--------A--------A   588
CI-22-3   T--------G--G----------------T--TG----C-CG-ACAGC...--C-C------------A   591
CI-22-6   T--------G--G----------------T--TG----C-CG-ACAGC...--C-C------------A   591
CI-22-10  T--------G--G----------------T--TG----C-CG-ACAGC...--C-C------------A   591
CI-42-1   T---------T----C--------G----------GG------A-.....T--CC-----T-------   597
CI-42-2   T---------T----C--------G----------GG------A-.....T--CC-----T-------   597
CI-42-3   T---------T----C--------G----------GG------A-.....T--CC-----T-------   597
CI-42-4   T---------T----C--------G----------GG------A-.....T--CC-----T-------   597
CI-45-1   T-----------------------------------G-----------.....-----------T------   582
CI-45-2   T-------A-------------------------G-----------.....-----------T------   582
CI-47-1   ---C-------------------------------------------A-AGT...-TG--------T------   600
CI-47-3   ---C-------------------------------------------A-AGT...-T---------T------   600
CI-47-8   ---C-------------------------------------------A-AGT...-TG--------T------   603
CI-326-2  ------------------------------------------G----.....-----------T------   609
CI-326-3  ------------------------------------------G----.....-----------T------   609
CI-326-4  ------------------------------------------G----.....-----------T------   609
CI-327-1  T-----T---------------------------------G-A---.....-T--C-------------   597
CI-327-2  T-----T---------------------------------G-A---.....-T--C-------------   597
CI-327-3  T-----T---------------------------------G-A---.....-T--C-------------   597
CI-327-4  T-----T-----------------------------C----G-A---.....-T--C-------------   597
CI-329-1  ------------------------------G-------------A-AATAGTG----------T------   600
CI-329-3  ------------------------------G-------------A-AATAGTG----------T------   600
CI-329-5  ------------------------------G-------------A-AATAGTG----------T------   600
CI-330-1  ---------G-----GC-------------T---GT-G-G----T-.....---GC------G-----A   600
CI-330-2  ---------G-----GC-------------T---GT-G-G----T-.....---GC------G-----A   600
CI-330-3  ---------G-----GC-------------T---GT-G-G----T-.....---GC------G-----A   600
CI-330-4  ---------G-----GC-------------T---GT-G-G----T-.....---GC------G-----A   600
```

```
CONSENSUS CCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAGTATAAAGTAGTAAAAATTGAAC 649
CI-3-1    ------------------------------------------------------------G------- 667
CI-3-2    ------------------------------------------------------------G------- 670
CI-3-3    ------------------------------------------------------------G------- 667
CI-45-3   --------------------A----------------G------------------------------ 652
CI-13-3   ----------------A-----------------------------A-------------G-C------ 652
CI-13-4   ----------------A-----------------------------A-------------G-C------ 652
CI-14-5   ---------------------------------------C------------------------------ 667
CI-14-13  ---------------------------------------C------------------------------ 667
CI-14-21  ---------------------------------------C------------------------------ 667
CI-20-1   ------------------------------------------------------------C---------- 667
CI-20-2   ------------------------------------------------------------C---------- 667
CI-20-3   ------------------------------------------------------------C---------- 667
CI-20-5   ------------------------------------------------------------C---------- 667
CI-21-1   ---------------------------------------------------G-----G---------- 658
CI-21-2   ---------------------------------------------------G-----G---------- 658
CI-21-4   ---------------------------------------------------G-----G---------- 658
CI-22-3   ----------------------A----------------------A---------------------- 661
CI-22-6   ----------------------A----------------------A---------------------- 661
CI-22-10  ----------------------A----------------------A---------------------- 661
CI-42-1   -------------------A------------------------------------------------- 667
CI-42-2   -------------------A------------------------------------------------- 667
CI-42-3   -------------------A------------------------------------------------- 667
CI-42-4   -------------------A------------------------------------------------- 667
CI-45-1   --------------------A----------------G------------------------------ 652
CI-45-2   --------------------A----------------G------------------------------ 652
CI-47-1   ------------------------------------------------------------------- 670
CI-47-3   ------------------------------------------------------------------- 670
CI-47-8   ------------------------------------------------------------------- 673
CI-326-2  ---------------------------------------------C----------G--------- 679
CI-326-3  -------------G-------------------------------C----------G--------- 679
CI-326-4  ---------------------------------------------C--G-------G--------- 679
CI-327-1  ------------------------------------------------------------------- 667
CI-327-2  ------------------------------------------------------------------- 667
CI-327-3  ------------------------------------------------------------------- 667
CI-327-4  ------------------------------------------------------------------- 667
CI-329-1  --------------C---------------------------------------------------- 670
CI-329-3  ------------------------------------------------T------G--------- 670
CI-329-5  ------A------------------------------------------T------G--------- 670
CI-330-1  ------------A------A----------------------------A---------------------- 670
CI-330-2  ------------A------A----------------------------A---------------------- 670
CI-330-3  ------------A------A----------------------------A---------------------- 670
CI-330-4  ------------A------A----------------------------A---------------------- 670
```

HIVCI47

```
CONSENSUS CACTAGGTGTAGCACCCACCCATGCAAAAAGAAGAGTGGTGGAGAGAGAAAAAAGAGCAGTTGGACTGGG  719
CI-3-1    --A--------------A--G-------------------------------------------------  737
CI-3-2    --A--------------A--G-------------------------------------------------  740
CI-3-3    --A--------------A--G-------------------------------------------------  737
CI-45-3   ----------------------------------------A-------------------------  722
CI-13-3   -------A------------AGG-----G-------------A---------------A-A---T-A--  722
CI-13-4   -------A------------AGG-----G-------------A---------------A-A---T-A--  722
CI-14-5   --------------------T-------------------------------------------------  737
CI-14-13  ----------T-------------------------------------------------------------  737
CI-14-21  --------------------T-------------------------------------------------  737
CI-20-1   ----------------T-A--G-----------------------------------------G-T--  737
CI-20-2   ----------------T-A--G-----------------------------------------G-T--  737
CI-20-3   ----------------T-A--G-----------------------------------------G-T--  737
CI-20-5   ----------------T-A--G-----------------------------------------G-T--  737
CI-21-1   --T----A------------ATG-----G-----------------------------------A-A--  728
CI-21-2   --T----A------------ATG-----G-----------------------------------A-A--  728
CI-21-4   --T----A------------ATG-----G-----------------------------------A-A--  728
CI-22-3   --T----A------------A-G-----G-----------C-------------------G---T-A--  731
CI-22-6   --T----A------------A-G-----G-----------C-------------------G---T-A--  731
CI-22-10  --T----A------------A-G-----G-----------C-------------------G---T-A--  731
CI-42-1   ---------------------C-------------------------------------------------  737
CI-42-2   ---------------------C-------------------------------------------------  737
CI-42-3   ---------------------C-------------------------------------------------  737
CI-42-4   ---------------------C-------------------------------------------------  737
CI-45-1   ----------------------------------------A-------------------------  722
CI-45-2   ----------------------------------------A-------------------------  722
CI-47-1   -------------------------------------------------------------------  740
CI-47-3   -------------------------------------------------------------------  740
CI-47-8   -------------------------------------------------------------------  743
CI-326-2  ----------------------------------------C-------------------------  749
CI-326-3  ----------------------------------------C-------------------------  749
CI-326-4  ----------------------------------------C-------------------------  749
CI-327-1  ----------------------C----------------C-------------------G---A-A--  737
CI-327-2  -------------------------------------------------------G---A-A--  737
CI-327-3  -------------------------------------------------------G---A-A--  737
CI-327-4  ----------------------C-------------------------------G---A-A--  737
CI-329-1  -------------------------------------------------------------A--  740
CI-329-3  ----------------------------------------A-------------------------  740
CI-329-5  ----------------------------------------A-------------------------  740
CI-330-1  -------A------------A-G-----G-----------------------------------  740
CI-330-2  -------A------------A-G-----G-----------------------------------  740
CI-330-3  -------A------------A-G-----G-------------G---------------------  740
CI-330-4  -------A------------A-G-----G-----------------------------------  740
```

```
CONSENSUS A......GCTGTCTTCCTTGGGTTCTTAGGAGCAGCAGGAAGCACTATGGGCGCGGCGTCAATAACGCTG  783
CI-3-1    -......---T-------------------------------------------------------------  801
CI-3-2    -......---T-------------------------------------------------------------  804
CI-3-3    -......---T-------------------------------------------------------------  801
CI-45-3   -.......--C-------------------------------------------------------------  786
CI-13-3   -.......---A-G-------------G-----------------G--------A--------G------  786
CI-13-4   -.......---A-G-------------G-----------------G--------A--------G------  786
CI-14-5   -.......-----------------------------------------------A---------------  801
CI-14-13  -.......-------------------------------A---------------A----------T----  801
CI-14-21  -.......-----------------------------------------------A---------------  801
CI-20-1   -CTGGGA--A-------------------------------------------------------C-------  807
CI-20-2   -CTGGGA--A-------------------------------------------------------C-------  807
CI-20-3   -CTGGGA--A-------------------------------------------------------C-------  807
CI-20-5   -CTGGGA--A-------------------------------------------------------C-------  807
CI-21-1   -.......------C-----------------A-----------------------------------------  792
CI-21-2   -.......------C-----------------A-----------------------------------------  792
CI-21-4   -.......------C-----------------A-----------------------------------------  792
CI-22-3   -.......---T-G---A-----------------------------------------A-T----G-G------  795
CI-22-6   -.......---T-G---A-----------------------------------------A-T----G-G------  795
CI-22-10  -.......---T-G---A-----------------------------------------A-T----G-G------  795
CI-42-1   -.......-------------------------------------------------------------------  801
CI-42-2   -.......-------------------------------------------------------------------  801
CI-42-3   -.......-------------------------------------------------------------------  801
CI-42-4   -.......-------------------------------------------------------------------  801
CI-45-1   -.......--C----------------------------------------------------------------  786
CI-45-2   -.......--C----------------------------------------------------------------  786
CI-47-1   -.......--GT---------------------------------------------------------------  804
CI-47-3   -.......-TGT---------------------------------------------------------------  804
CI-47-8   -.......--GT---------------------------------------------------------------  807
CI-326-2  -.......-G-C---------------------------------------------------------------  813
CI-326-3  -.......-T-C---------------------------------------------------------------  813
CI-326-4  -.......-T-C---------------------------------------------------------------  813
CI-327-1  -.......---------A---------------------------------------------------------  801
CI-327-2  -.......---------A---------------------------------------------------------  801
CI-327-3  -.......-------------------------------------------------------------------  801
CI-327-4  -.......---------A---------------------------------------------------------  801
CI-329-1  -.......------------A---------------------------A-----A--------------------  804
CI-329-3  -.......-----------------------------------------------A--------------------  804
CI-329-5  -.......-----------------------------------------------A--------------------  804
CI-330-1  -.......-------------------------------------T----------------------------  804
CI-330-2  -.......-------------------------------------T----------------------------  804
CI-330-3  -.......-------------------------------------T----------------------------  804
CI-330-4  -.......-------------------------------------T----------------------------  804
```

HIVCI47

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CONSENSUS ACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAGCAGAGCAATTTGCTGAGGGCTATAGAGG  853
CI-3-1    ------------------------C------------------------------A----------  871
CI-3-2    ------------------------C------------------------------A----------  874
CI-3-3    ------------------------C------------------------------A----------  871
CI-45-3   ------------------------C----------------------------------------  856
CI-13-3   ----------------TG---C--------------------A-A----------------------  856
CI-13-4   ----------------TG---C--------------------A-A----------------------  856
CI-14-5   --------A-----------C----C------------------------------A----------  871
CI-14-13  --------A-----------C----C------------------------------A----------  871
CI-14-21  --------A-----------C----C------------------------------A----------  871
CI-20-1   ------------------------C----------------------------------------  877
CI-20-2   ------------------------C----------------------------------------  877
CI-20-3   ------------------------C----------------------------------------  877
CI-20-5   ------------------------C----------------------------------------  877
CI-21-1   ----------------------------C-------------A--------------------T----  862
CI-21-2   ----------------------------C-------------A--------------------T----  862
CI-21-4   ----------------------------C-------------A--------------------T----  862
CI-22-3   ----------------T--------------------------A-A-----------A-----T----  865
CI-22-6   ----------------T--------------------------A-A-----------A-----T----  865
CI-22-10  ----------------T--------------------------A-A-----------A-----T----  865
CI-42-1   ------------------------------------------------------------------A---  871
CI-42-2   ------------------------------------------------------------------A---  871
CI-42-3   ------------------------------------------------------------------A---  871
CI-42-4   ------------------------------------------------------------------A---  871
CI-45-1   ------------------------C----------------------------------------  856
CI-45-2   ------------------------C----------------------------------------  856
CI-47-1   ------------------------C----------------A-----------------------  874
CI-47-3   ------------------------C----------------A-----------------------  874
CI-47-8   ------------------------C----------------A-----------------------  877
CI-326-2  ----------------G---A----------------------------C----------------  883
CI-326-3  ----------------G---A----------------------------C----------------  883
CI-326-4  ----------------G---A----------------------------C----------------  883
CI-327-1  ------------------------------------------------C----------------  871
CI-327-2  ------------------------------------------------C----------------  871
CI-327-3  ------------------------------------------------C----------------  871
CI-327-4  ------------------------------------------------C----------------  871
CI-329-1  ------------------------C----------------A-----------------------  874
CI-329-3  ------------------------C----------------G-----------------------  874
CI-329-5  ------------------------C----------------G-----------------------  874
CI-330-1  ----C----------------------C-----A---------------C----------------  874
CI-330-2  ----C----------------------C-----A---------------C----------------  874
CI-330-3  ----C----------------------C-----A---------------C----------------  874
CI-330-4  ----C----------------------C-----A---------------C----------------  874
```

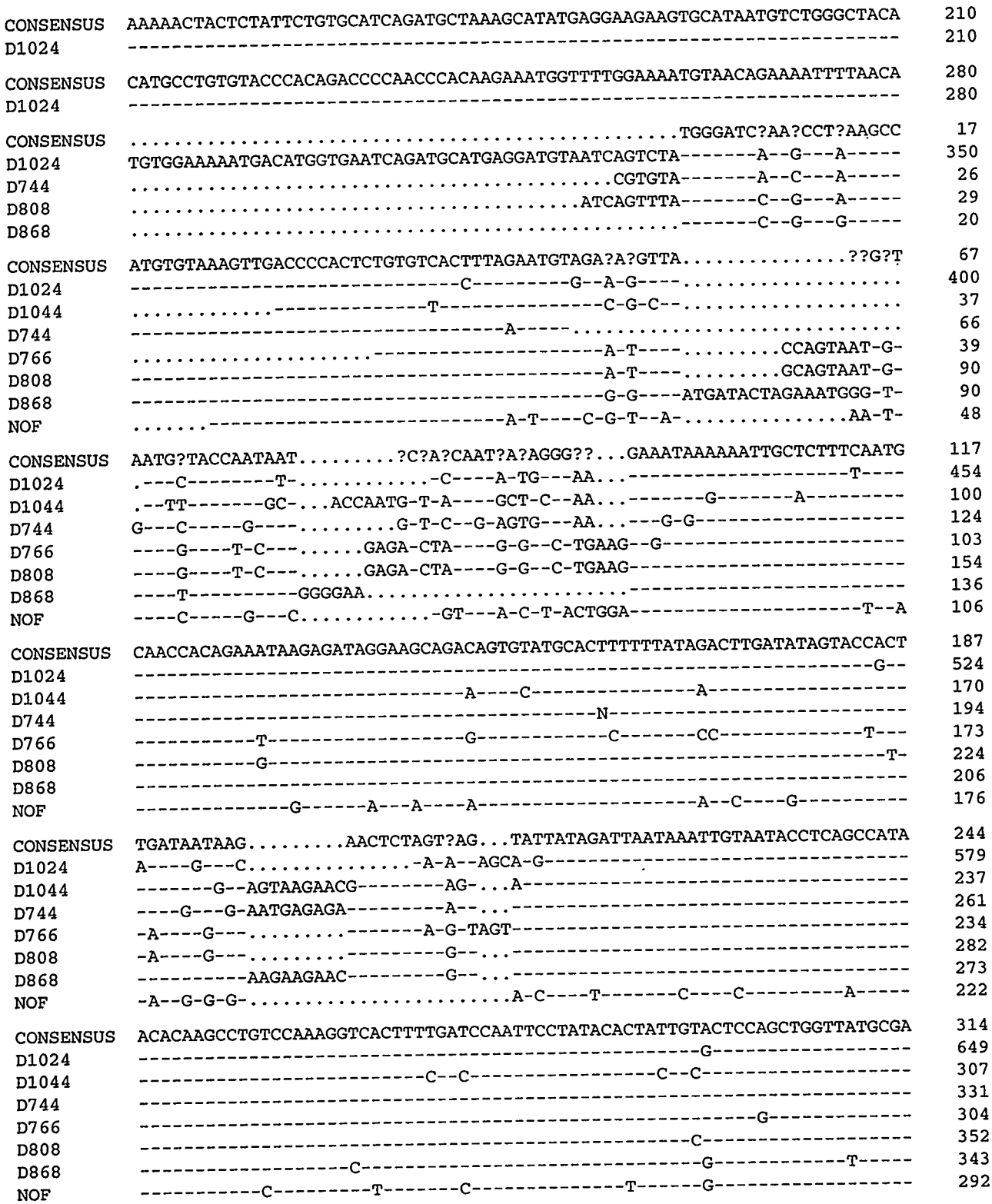
```
CONSENSUS CTCAACAACATCTGTTGAAACTCACG    879
CI-3-1    -------------------------     897
CI-3-2    -------------------------     900
CI-3-3    -------------------------     897
CI-45-3   -------------------------     882
CI-13-3   -G-----G---------C--------    882
CI-13-4   -G-----G---------C--------    882
CI-14-5   -------------------------     897
CI-14-13  -------------------------     897
CI-14-21  -------------------------     897
CI-20-1   -------------------------     903
CI-20-2   -------------------------     903
CI-20-3   -------------------------     903
CI-20-5   -------------------------     903
CI-21-1   -------G------------------    888
CI-21-2   -------G------------------    888
CI-21-4   -------G------------------    888
CI-22-3   -G-----G---------C-------A    891
CI-22-6   -G-----G---------C-------A    891
CI-22-10  -G-----G---------C-------A    891
CI-42-1   ----------A---------------    897
CI-42-2   ----------A---------------    897
CI-42-3   ----------A---------------    897
CI-42-4   ----------A---------------    897
CI-45-1   -------------------------     882
CI-45-2   -------------------------     882
CI-47-1   -------------------------     900
CI-47-3   -------------------------     900
CI-47-8   -------------------------     903
CI-326-2  -----------A------G-------    909
CI-326-3  A----------A------G-------    909
CI-326-4  -----------A------G-------    909
CI-327-1  ------------------------A     897
CI-327-2  ------------------------A     897
CI-327-3  ------------------------A     897
CI-327-4  ------------------------A     897
CI-329-1  ----------AT------G-------    900
CI-329-3  -------------------------     900
CI-329-5  -------------------------     900
CI-330-1  -------G--A-------G-------    900
CI-330-2  -------G--A-------G-------    900
CI-330-3  -------G--A-------G-------    900
CI-330-4  -------G--A-------G-------    900
```

HIVD808

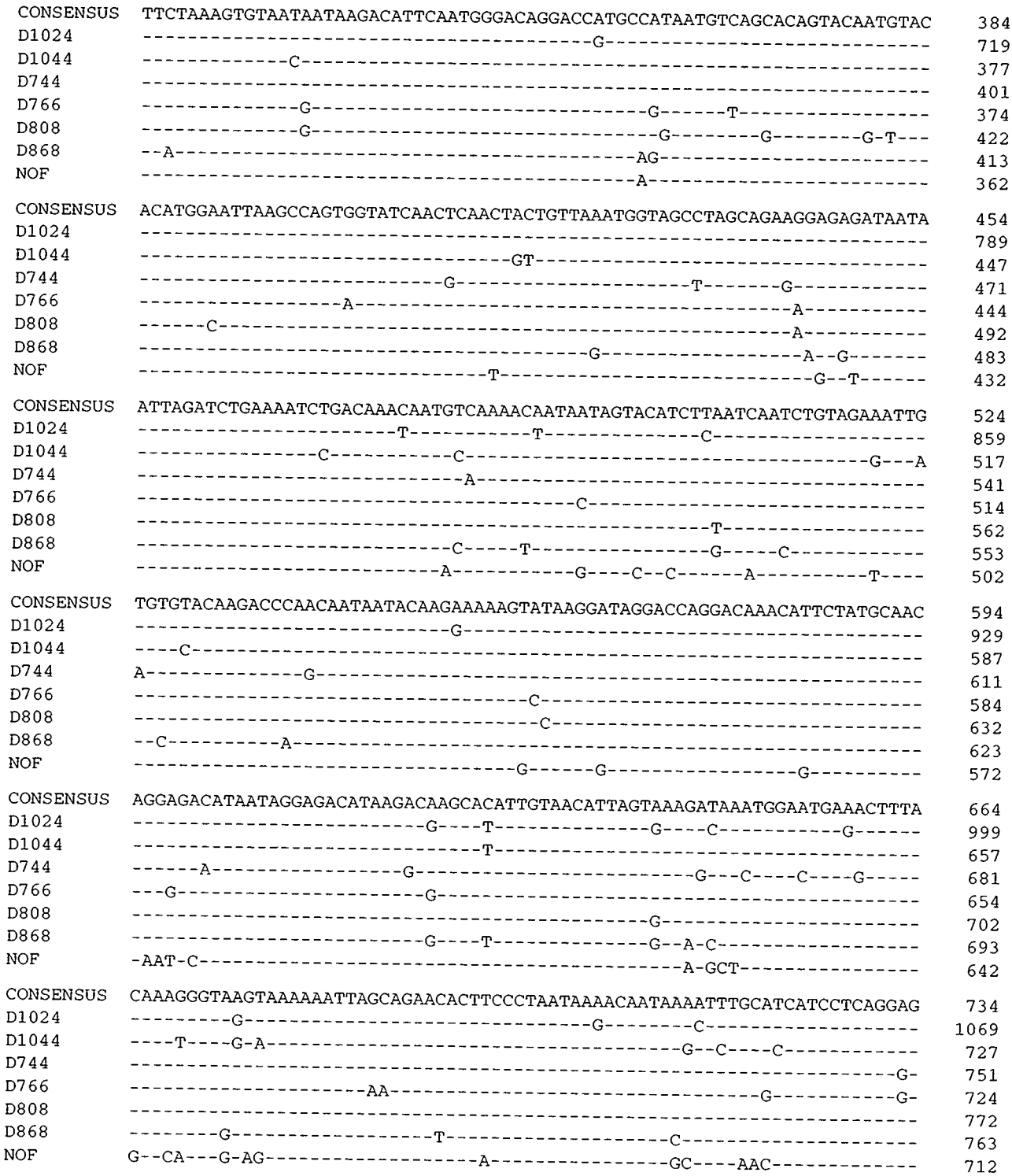
```
LOCUS       HIVD808         1236 bp    DNA             VRL       15-APR-1994
DEFINITION  Human immunodeficiency virus type 1 sample D808, env gene,
            partial cds (gp120).
ACCESSION   U07102
SOURCE      Human immunodeficiency virus type 1, sample D808, PCR amplification
            of uncultured PBMC proviral DNA.
REFERENCE   1  (bases 1 to 1236)
  AUTHORS   Grez,M., Dietrich,U., Balfe,P., Von Briesen,H., Maniar,J.K.,
            Mahambre,G., Delwart,E.L., Mullins,J.I. and Ruebsamen-Waigmann,H.
  TITLE     Genetic analysis of human immunodeficiency virus type 1 and 2
            (HIV-1 and HIV-2) mixed infections in India reveals a recent spread
            of HIV-1 and HIV-2 from a single ancestor for each of these viruses
  JOURNAL   J. Virol. 68, 2161-2168 (1994)
COMMENT     The variants in this study were isolated from HIV-1/HIV-2
            dually infected individuals.  Phylogenetic analysis
            of the HIV-1 and HIV-2 sequences indicates a significant
            degree of conservation within the two HIV types.  The HIV-1
            variants cluster with HIV-1 subtype C strains and are highly
            similar to sequences isolated in East and South Africa. Grez.
            et al. propose that the low degree of diversity between isolates
            (of a given type) indicates a relatively brief period of HIV-1
            infection in India.  Other sequences in this set are included in
            the alignment below (accession numbers U06716, U07098-U07101,
            and U07103).
            NCBI gi: 47174
BASE COUNT      489 a    211 c    267 g    305 t
ORIGIN      310 bp downstream from the beginning of env cds
        1 atcagtttat gggatccaag cctaaagcca tgtgtaaagt tgaccccact ctgtgtcact
     env ->
       61 ttagaatgta gaaatgttag cagtaatggt aatggtacct acaatgagac ctacaatgag
      121 agcgtgaagg aaataaaaaa ttgctctttc aatgcaacca cagaagtaag agataggaag
      181 cagacagtgt atgcactttt ttatagactt gatatagtac catttaataa gaagaactct
      241 agtgagtatt atagattaat aaattgtaat acctcagcca taacacaagc ctgtccaaag
      301 gtcacttttg atccaattcc tatacactat tgcactccag ctggttatgc gattctaaag
      361 tgtaatgata agacattcaa tgggacagga ccatgccaga atgtcaggac agtacagttt
      421 acacatggca ttaagccagt ggtatcaact caactactgt taaatggtag cctagcagaa
      481 agagagataa taattagatc tgaaaatctg acaaacaatg tcaaaacaat aatagtacat
      541 ctttatcaat ctgtagaaat tgtgtgtaca agacccaaca ataatacaag aaaaagtaca
                          V3 loop ->
      601 aggataggac caggacaaac attctatgca acaggagaca taataggaga cataagacaa
      661 gcacattgta acattagtga agataaatgg aatgaaactt tacaaagggt aagtaaaaaa
                <- V3 loop
      721 ttagcagaac acttccctaa taaaacaata aaatttgcat catcctcagg aggggaccta
      781 gaaattacaa cacatagctt taattgtaga ggagaatttt tctattgtaa tacatcaggc
      841 ctgtttaatg gtacatacat gcctaatggt acaaaaagta attcaagctc aatcatcaca
      901 atcccatgca gaataaagca aattataaac atgtggcagg aggtaggacg agcaatgtat
      961 gcccctccca ttgaaggaaa cataacatgt aaatcaaata tcacaggact actattggta
     1021 cgtgatggag gaacagaatc aaataataca gagacattca gacctggagg aggagatatg
     1081 aggaacaatt ggagaagtga attatataaa tataaagtgg tagaaattaa gccattggga
     1141 gtagcaccca ctacagcaaa aaggagagtg gtggagagag aaaaaagagc agtgggaata
     1201 ggagctgtgt tccttgggtt cttgggagca gcaggaagca ctatgggcgc ggcgtcaata
     1261 acgctgacgg ta
                env ->

CONSENSUS  ATGAGAGTGAGGGGGATACTGAGGAATTATCAACAATGGGGGATATGGGGCATCTTAGGCTTTTGGATGT    70
D1024      ------------------------------------------------------------------    70

CONSENSUS  TAATGATTTGTAATGTGGTAGGAAACTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGAAGC   140
D1024      ------------------------------------------------------------------   140
```


CONSENSUS AAAAACTACTCTATTCTGTGCATCAGATGCTAAAGCATATGAGGAAGAAGTGCATAATGTCTGGGCTACA 210
D1024 ---------- 210
CONSENSUS CATGCCTGTGTACCCACAGACCCCAACCCACAAGAAATGGTTTTGGAAAATGTAACAGAAAATTTTAACA 280
D1024 ---------- 280
CONSENSUS .....TGGGATC?AA?CCT?AAGCC 17
D1024 TGTGGAAAAATGACATGGTGAATCAGATGCATGAGGATGTAATCAGTCTA-------A--G---A----- 350
D744 .....CGTGTA-------A--C---A----- 26
D808 .....ATCAGTTTA-------C--G---A----- 29
D868 .....-------C--G---G----- 20
CONSENSUS ATGTGTAAAGTTGACCCCACTCTGTGTCACTTTAGAATGTAGA?A?GTTA.....??G?T 67
D1024 ----------C---------G--A-G----..... 400
D1044 .....----------T----------C-G-C--..... 37
D744 ----------A-----..... 66
D766 .....----------A-T----.....CCAGTAAT-G- 39
D808 ----------A-T----.....GCAGTAAT-G- 90
D868 ----------G-G----ATGATACTAGAAATGGG-T- 90
NOF .....----------A-T----C-G-T--A-.....AA-T- 48
CONSENSUS AATG?TACCAATAAT.....?C?A?CAAT?A?AGGG??...GAAATAAAAAATTGCTCTTTCAATG 117
D1024 .---C--------T-.....-C----A-TG---AA...----------T---- 454
D1044 .--TT-------GC-...ACCAATG-T-A----GCT-C--AA...-------G-------A--------- 100
D744 G---C-----G----.....G-T-C--G-AGTG---AA...---G-G---------- 124
D766 ----G----T-C---.....GAGA-CTA----G-G--C-TGAAG--G---------- 103
D808 ----G----T-C---.....GAGA-CTA----G-G--C-TGAAG---------- 154
D868 ----T----------GGGGAA.....---------- 136
NOF ----C-----G---C.....-GT---A-C-T-ACTGGA----------T--A 106
CONSENSUS CAACCACAGAAATAAGAGATAGGAAGCAGACAGTGTATGCACTTTTTTATAGACTTGATATAGTACCACT 187
D1024 ----------G-- 524
D1044 ----------A----C----------A---------- 170
D744 ----------N---------- 194
D766 ----------T----------G----------C-------CC----------T--- 173
D808 ----------G----------T- 224
D868 ---------- 206
NOF ----------G------A---A----A----------A--C----G---------- 176
CONSENSUS TGATAATAAG.....AACTCTAGT?AG...TATTATAGATTAATAAATTGTAATACCTCAGCCATA 244
D1024 A----G---C.....-A-A--AGCA-G---------- 579
D1044 -------G--AGTAAGAACG--------AG-...A---------- 237
D744 ----G---G-AATGAGAGA---------A--...---------- 261
D766 -A----G---.....-------A-G-TAGT---------- 234
D808 -A----G---.....---------G--...---------- 282
D868 ----------AAGAAGAAC---------G--...---------- 273
NOF -A--G-G-G-.....A-C----T-------C----C---------A----- 222
CONSENSUS ACACAAGCCTGTCCAAAGGTCACTTTTGATCCAATTCCTATACACTATTGTACTCCAGCTGGTTATGCGA 314
D1024 ----------G---------- 649
D1044 ----------C--C----------C--C---------- 307
D744 ---------- 331
D766 ----------G---------- 304
D808 ----------C---------- 352
D868 ----------C----------G----------T----- 343
NOF ----------C---------T-------C----------T------G---------- 292

HIVD808


CONSENSUS TTCTAAAGTGTAATAATAAGACATTCAATGGGACAGGACCATGCCATAATGTCAGCACAGTACAATGTAC 384
D1024 719
D1044 377
D744 401
D766 374
D808 422
D868 413
NOF 362
CONSENSUS ACATGGAATTAAGCCAGTGGTATCAACTCAACTACTGTTAAATGGTAGCCTAGCAGAAGGAGAGATAATA 454
D1024 789
D1044 447
D744 471
D766 444
D808 492
D868 483
NOF 432
CONSENSUS ATTAGATCTGAAAATCTGACAAACAATGTCAAAACAATAATAGTACATCTTAATCAATCTGTAGAAATTG 524
D1024 859
D1044 517
D744 541
D766 514
D808 562
D868 553
NOF 502
CONSENSUS TGTGTACAAGACCCAACAATAATACAAGAAAAAGTATAAGGATAGGACCAGGACAAACATTCTATGCAAC 594
D1024 929
D1044 587
D744 611
D766 584
D808 632
D868 623
NOF 572
CONSENSUS AGGAGACATAATAGGAGACATAAGACAAGCACATTGTAACATTAGTAAAGATAAATGGAATGAAACTTTA 664
D1024 999
D1044 657
D744 681
D766 654
D808 702
D868 693
NOF 642
CONSENSUS CAAAGGGTAAGTAAAAAATTAGCAGAACACTTCCCTAATAAAACAATAAAATTTGCATCATCCTCAGGAG 734
D1024 1069
D1044 727
D744 751
D766 724
D808 772
D868 763
NOF 712

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CONSENSUS  GGGACCTAGAAATTACAACACATAGCTTTAATTGTAGAGGAGAATTTTTCTATTGCAATACATCAAACCT  804
D1024      ----------------------------------------------------------C----------  1139
D1044      ----------------------------------------------------------T----------  797
D744       ---------------------------------------------------------------------  821
D766       ----------------------------------------------------------T---------GG---  794
D808       ----------------------------------------------------------T---------GG---  842
D868       ---------------------------------------------------------------------  833
NOF        ----TT-----G-------------------------------------------------------A--G----  782

CONSENSUS  GTTTAAT?GTACATAC...........ATGC?TAATGGTACA.........................  833
D1024      -------A--------...........----C----------.........................  1170
D1044      -------A--------AATAGTACATAC----T----------.........................  840
D744       -------A--G-----...........----C----------TATATGTTTAATGGTACATACATGTTT  879
D766       -------G--------...........----A----------.........................  825
D808       -------G--------...........----C----------.........................  873
D868       -------G--------...........---...---------.........................  861
NOF        ----.............................TCT-C-A-..........CGCAACAAAATTTAAT  810

CONSENSUS  AAAAGTAATTCAA?CTCAACCATCACAATCCCATGCAGAATAAAACAAATTATAAACATGTGGCAGGAGG  902
D1024      ------------A---C------------T---T--T-----------G----------------  1240
D1044      -C----------C--T--A-------------------------------------------------  910
D744       --T----CAAGT-ATG-------------------------------------------------T-------  949
D766       ------------G-----T----------------------G-------------------------  895
D808       ------------G-----T----------------------G-------------------------  943
D868       ------------G----------------T----------------G--G----------------  931
NOF        G-----G--C---A-G----------C----------G-------------------------------  880

CONSENSUS  TAGGACGAGCA...ATGTATGCCCCTCCCATTGAAGGAAACATAACATGTAAATCAAATATCACAGGACT  969
D1024      ----------...-------------------------------------------------------  1307
D1044      ----------...-----------------------------------C------------------  977
D744       ----------...-------------------------------------------------------  1016
D766       ----------...-----------------------------------------------C-------  962
D808       ----------...-------------------------------------------------------  1010
D868       ----------...-------------------------------------------------------  998
NOF        -------GA-GAGC-----------------------------------------C------------  950

CONSENSUS  ACTATTGGTACGTGATGGAGGAACAGA?......TCAAATAATACA...GAGATA......TTCAGACCT  1023
D1024      ---------G----------------G......-------C----...----C-.....---------  1362
D1044      --------A-------------C----C.........---------...------.....---------  1029
D744       ----------------------CG--GACAAGAG-------C----...------.....---------  1077
D766       --------------------------G.....------------...----C-GAGACA---------  1023
D808       --------------------------A.....------------...----C-.....---------  1065
D868       --------C----------------G.....------C-----...------.....---------  1053
NOF        -------AC--------------AC-CAAACACAA----------CACA------.....---------  1014

CONSENSUS  GGAGGAGGAGATATGAGGAACAATTGGAGAAGTGAATTATATAAATATAAAGTGGTAGAAATTAAGCCAT  1093
D1024      -------------------------------------------------------------------  1432
D1044      ----------------------------------G--------------------------------  1099
D744       ----------C----------------------C--------------------------------  1147
D766       ----------------G-------------------------------------------------  1093
D808       -------------------------------------------------------------------  1135
D868       ------------------------------------------C------------------------  1123
NOF        ---------A------A-G----------A-------------------------------------  1084
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HIVD808

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CONSENSUS  TGGGAGTAGCACCCACTGCAGCAAAAAGGAGAGTGGTGGAGAGAGAAAAAAGAGCAGTGGGAATAGGAGC  1163
D1024      ------------------------------------------------------------------------  1502
D1044      ----------------A--C--------------------------------------------------  1169
D744       ----------------------------------------G---------------C-------------  1217
D766       -----A------------------------------------------------------T-------  1163
D808       ----------------A-----------------------------------------------------  1205
D868       ---------T-------A-----------------------------------------G-----  1193
NOF        -----A-----------G-T-------------------------------------------------  1154

CONSENSUS  TGTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCGGCGTCAATAACGCTGACGGTACAG  1233
D1024      ---A-------------------------------------------------------------      1569
D1044      ------------------------------------------------------------------     1236
D744       ----------------------------------                1254
D766       ----------------------------------      1200
D808       ------------------------------------------------------------------     1272
D868       --------------------------------C----                                  1230
NOF        ----C-----------------------------------C--------------------------    1224

CONSENSUS  GCCAGACAACTGTTGTCTGGTATAGTGCAACAGCAAAGCAATTTGCTGAGAGCTATAGAGGCGCAACAGC  1303
NOF        ------------------------------------------------------------------     1294

CONSENSUS  ATATGTTGCAACTCACGGTCTGGGGCATTAAGCAGCTCCAGACAAGAGTCTTGGCTATAGAAAGATACCT  1373
NOF        ------------------------------------------------------------------     1364

CONSENSUS  AAAGGATCAACAGCT    1388
NOF        ---------------    1379
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LOCUS HIVDJ2581 1459 bp ss-DNA VRL 27-MAY-1993
DEFINITION Human immunodeficiency virus type 1 (HIV-1) partial gag sequence, isolate DJ258.
ACCESSION L11763
SOURCE Human immunodeficiency virus type 1 cocultivated PCR-amplified PBMC DNA derived from a patient from Djibouti.
REFERENCE 1 (bases 1 to 1459)
AUTHORS Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T., Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K., Gershy-Damet,M., DeLeys,R. and Burke,D.
TITLE Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
JOURNAL AIDS 7, 769-780 (1993)
COMMENT 55 viral sequences were obtained from patients in fifteen countries (Belgium, Burundi, Gabon, The Ivory Coast, Kenya, Rwanda, Zambia Thailand, Somalia, the Philippines, Djibouti, Brazil, Uganda, Senegal, and Zaire) on four continents. These sequences were compared to another 15 previously sequenced isolates through phylogenetic analysis. With the inclusion of new gag sequences, Louwagie et al. report the emergence of three new HIV-1 genotypes, E-G, and the existence of an unclassified Belgian isolate, VI325. The env region of DJ258 has also been sequenced (L22939). This gag sequence (previously published on page I-A-194 AUG 93) groups with HIV1 A subtype gag sequences.
BASE COUNT 525 a 281 c 373 g 280 t
ORIGIN gag cds start

```
       1 ATGggtgcga gagcgtcagt attaagtggg ggaaaattag attcatggga gaagattcgg
gag start ->
      61 ttaaggccag ggggaaagaa aaaatataga ctaaaacatc tagtatgggc gagcagggag
     121 ctggaaagat tcgcacttaa ccctggcctt ttagaaacag cagaaggatg tcaacagtta
     181 atggaacagt tacaatcagc tctcgggaca gaatcaaaag aacttaaatc attatataat
     241 accatagcag tcctttggtg cgtacatcaa aggatagaca taaaagacac caaggaagcc
     301 ttagataaaa tagaggcagt acaaaataag agcaagcaaa agacacagca ggcagcggct
     361 gccacaggaa gcagcagcca aaattaccct atagtgcaaa atgcacaggg gcaaatggta
     421 catcagccca tgtcacctag gactttgaat gcatgggtga aggtaataga ggaaaaggct
     481 ttcagcccag aagtaatacc catgtttaca gcattatcag agggagccac cccacaagat
     541 ctaaatatga tgctaaacat agtgggggga caccaggcag caatgcagat gttaaaagat
     601 accatcaatg aggaagctgc agaatgggac agggtacatc cagtacatgc agggcctatt
     661 ccaccaggcc aaatgaggga accaagggga agtgacatag caggaactac tagtaccctt
     721 caagaacaaa taggatggat gacaagcaat ccacctatcc cagtgggaga catctataaa
     781 agatggataa tcctgggatt aaataaaata gtaagaatgt atagccctgt cagcattttg
     841 gacataagac aagggccaaa agaacccttt agagattatg tagataggtt ctttaaaact
     901 ttgagagctg aacaagctac gcaggaggta aaaaactgga tgacagaaac cttgctggtc
     961 caaaatgcga atccagactg taagtccatc ttaagagcat taggaccagg ggctacatta
    1021 gaggaaatga tgacatcatg tcagggagtg ggaggacctg gccataaagc aagggttttg
    1081 gctgaggcaa tgagtcaggt acaacaatcc aacataatga tgcagagagg cgattttagg
    1141 ggccagagaa caataaagtg tttcaactgt ggcaaagaag gacacctagc cagaaattgc
    1201 aaggctccta gaaaaaaggg ctgttggaaa tgtggaaagg agggacacca aatgaaagac
    1261 tgtactgaga gacaggctaa ttttttaggg aaaatttggc cttccaccaa ggggaggcca
    1321 ggaaattttc ctcaaagcag accagagcca acagccccac tagcagagag ctttgggatg
    1381 ggggaagaga taacctcccc tccgaagcag gaaccgaggg aacagggact atatcctccc
    1441 ttaacttccc tcaaatcac
                        gag ->
```

```
LOCUS       HIVDJ2582    3215 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1 (HIV-1) env, vpU, and
            nef sequences, isolate DJ258
ACCESSION   L22939
SOURCE      Human immunodeficiency virus type 1, sample DJ258, PCR-amplified
            PBMC
REFERENCE   1  (bases 1 to 3215)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.
            A., van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1994)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research
            Laboratory Rockville, Maryland. Twenty-one full length gp160 cds
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268,
            UG274, VI191, and VI525 have corresponding gag sequences that were
            published by Louwagie et. al. in AIDS 7, 769-780 (1993) and are
            represented in this compendium.  This sequence and a corresponding
            gag sequence (L11763) cluster with A subtype sequences.
            See also accession numbers L22940-L22957 and L23064-L23065.
            NCBI gi: 437342
BASE COUNT     1129 a    561 c    757 g    768 t
ORIGIN      85 bp upstream from the beginning of rev cds start
        1 aactgcttgt agcaagtgtt actgtaaaaa atgctgctgg cattgccaat tgtgctttct
       61 gaacaagggc ttaggcatct cctATGgcag gaagaagcgg agacgccgac gaggaactcc
                    rev cds start ->
      121 tcagagtcgt caggaccatc aaaatcctgt accaaagcaG Tgagtagtaa taattaatat
                                              5' sj /\
      181 atgtgATGaa ctctttagaa atagctgcaa tagtaggact agtagtagca ttcacagcag
 vpU cds start ->
      241 ccatagttgt gtggaccata gtattaattg aatataggaa aataaggaaa cagaagaaaa
      301 tagacaagtt gcttgataga ataagagaaa gagcagaaga tagtggcaAT Gagagtgatg
                                                  env cds start ->
      361 gggatacaga agaattatcc actcttatgg agatggggta cgataatatt ttgaaTAAtg
                                                                    <- vpU
      421 ataatttgta atgctaaaga gatgtgggtc acggtctact atggggtacc tgtgtggaga
      481 gacgcaaaga ccaccctatt ttgtgcatca gatgctaaag catatgatac agaagtacat
      541 aatgtctggg ctacacatgc ctgtgtaccc acagacccta acccacaaga aatatatttg
      601 aaaaatgtaa cagaaaagtt taacatgtgg aaaaataaca tggtagaaca gatgcatgaa
      661 gatataatta gtctatggga ccaaagccta aagccatgtg taaagttaac ccctctctgc
      721 gttactttag agtgtcataa tgtcagcaat agcaatacct ctagctacag gaacatatct
      781 agtgaaatgc gagaggaaat aaaaaactgc tctttcaata tgaccacaga actaagagat
      841 aagcaacaga aaatgtctgc actttttat agacttgatg tagtacaaat tagtgaaagt
      901 aacaatagtc aatataggtt aatcaactgt aatacctcag ccattacaca ggcatgtcca
      961 aaggtaacct ttgagccaat tcccatacat tattgtgccc cagctggttt tgcgattcta
     1021 aagtgtaatg ataagaagtt caatggaaca gggccatgca agaatgttag cacagtacaa
     1081 tgcacacatg gaatcaagcc agcagtatca actcaactac tgttaaatgg tagtctagca
     1141 gaaggagagg tagtgattag atctgaaaat atcacaaaca atgccaaaaa cataatagta
     1201 cagttggtta cgcctgtaag aatcaattgt agcagacctg gcaacaatac aagaaaaagt
                              v3 loop ->
     1261 gtacgtatag gaccagggca aacattctat gcaacaggtg acataatagg ggatataaga
     1321 caagcacact gtaatgtcag tagatcaaaa tggaatgaaa ctttacaaaa ggtggctaca
                         <- v3 loop
     1381 caattaagga agcactttaa cacaacaata atctttgcta actcctcagg aggggatata
     1441 gaaattacaa cacatagttt taattgtaga ggagaatttt tctattgcaa tacatcaagt
     1501 ctgtttaata gcacttggaa tagcagctca attcacacaa attacagctc aaatgacaca
```

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1561 gacaatataa ctctccaatg cagaataaag caaattgtaa atatgtggca gaaagtagga
1621 aaagcaatat atgcccctcc catctcagga gaaataaggt gtgaatcaaa cattacagga
1681 ctaatattaa caagagatgg agggagtaat aatagtacaa atgagatctt caggcctgga
1741 ggaggagata tgagggataa ttggagaagt gaattatata agtataaagt agtaaaaatt
1801 gaaccactag gtgtagcacc cacccgtgca aaaagaagag tggtggagag agaaaaaaga
1861 gcagttggac tgggagcttt cttccttggg ttcttaggag ctgcaggaag cactatgggc
1921 gcggcgtcaa taacgctgac ggtacaggcc agacaattat tgtccggtat agtgcaacag
1981 cagagcaatt tgctgagggc tatagaggct caacaacatc tgttgaaact cacggtctgg
2041 ggcattaaac agctccaggc aagagtcctg gctctggaaa gttacctaag ggatcaacag
2101 ctcctaggaa tttggggctg ctctggaaaa ctcatctgca ccactactgt accctggaac
2161 tctagttgga gtaataaaac ttttaatgac atatgggata acatgacctg gctgcaatgg
2221 gataaagaaa ttagcaatta cacagacata atatatactc taattgaaga atcgcaaaac
2281 cagcaggaaa agaatgaaca agacttattg gcattggaca aatgggcagg tctgtggagt
2341 tggtttggca taacaaactg gctgtggtat ataagaatat ttataataat agtaggaggt
2401 ttaataggtt taagaatagt ttttgctgtg cttactataa taaatagagt taggcaggga
2461 tactcacctt tatcgttccA Gacccttacc caccactgga gggaaccacc cgacagaccc
          3' sj (tat, rev) /\
2521 gaaagaatcg aagaaggagg tggcgagcaa gacaaagaca gatcaatacg cttgatgagc
2581 ggattcttag cacttgcctg ggacgatctg cggagcctgt gcctcttcag ctaccaccaa
2641 ttgagagact ttgtcttgat tgcagtgagg gctgtggaac ttctgggaca cagcagcctc
2701 aagggactga gactggggtg ggaagccctc cagtatctgg ggaatcttct actatactgg
2761 ggtcaggaac taaagaaTAG tgctgttaat ttgcttgata caatagcaat agtagtagct
                       <- rev cds end
2821 aactggacag acagagttat agaaatagga caagaagtgg gtagagctat tctcaacata
2881 cctagaagaa tcagacaggg gcttgaaagg gctttgttaT AAcATGggtg gcaagtggtc
                                                  <- env cds end
                                    nef cds start ->
2941 aaaaagcagc atagtgggat ggcctaaggt tagggaaaga ataagacaaa cccctccagc
3001 agcaacagga gtaggagcag catctcaaga tttagataga catggagcaa ttacaagtag
3061 taatacagca gctactaatg ctgattgtgc ctggctagaa gcacaagaag aagaggaggt
3121 aggctttcca gtcaggccgc aggtaccttt gagaccaatg acttataagg cagctttcga
3181 tctcggcttc tttttaaaag aaaaggggg actgg
                                  3' LTR ->
```

```
LOCUS       HIVDJ2591      1465 bp ss-DNA             VRL       27-MAY-1993
DEFINITION  Human immunodeficiency virus type 1, isolate DJ259 from Djibouti,
            gag region.
ACCESSION   L11764
SOURCE      Human immunodeficiency virus type 1 (HIV-1) blood DNA, Djibouti
            isolate DJ259 (cocultivation on PBMCs).
REFERENCE   1  (bases 1 to 1465)
  AUTHORS   Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T.,
            Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K.,
            Gershy-Damet,M., DeLeys,R. and Burke,D.
  TITLE     Phylogenetic analysis of gag genes from seventy international HIV-1
            isolates provides evidence for multiple genotypes
  JOURNAL   AIDS 7, 769-780 (1993)
  COMMENT   Viral isolates were obtained from 15 different countries
            (Belgium, Burundi, Gabon, The Ivory Coast, Kenya, Rwanda, Zaire,
            Thailand, Somalia, the Philippines, Djibouti, Brazil, Uganda,
            Senegal, and Zaire) on four continents.  From this study the
            authors identified 7 distinct genotypes with an average gag
            intra-genotypic variance of 7% and an average inter-genotypic
            variance of 14%.  The env region of this isolate has also been
            sequenced (L22940). This gag sequence (previously published on page
            I-A-195 AUG 93) groups with HIV1 C subtype gag sequences.
BASE COUNT      542 a    293 c    352 g    278 t
ORIGIN      gag cds start
        1 ATGggtgcga gagcgtcaat attaagaggc gaaaaattag atgcctggga aaaaattaag
gag start ->
       61 ctaaggccag gaggaaggaa acgctatatg ctaaaacacc tagtctgggc aagcagggag
      121 ctggaaaaat ttgcacttaa ccctagcctt ttagagacat cagaaggctg taaacaaata
      181 ataagacagc tacaaccagc tcttcagaca ggaacagaag aacttagatc attatataat
      241 acagtagcaa ctctctattg tgtacatgca aggatagaga tacaagacac caaagaagca
      301 ctagacaaga tagaggaaga acaaaacaaa tgtcagcaaa aaacacagaa ggcagaaaca
      361 gctgacaagg gaaaggtcag tcaaaatttt cctatagtac agaatctcca agggcaaatg
      421 gtacaccagc ccctatcacc tagaactttg aatgcatggg taaaagtaat agaggagaag
      481 gctttcagcc cagaagtaat acccatgttt acagcattat cagaaggagc caccccacaa
      541 gatttaaaca ccatgttaaa tacagtgggg ggacatcaag cagccatgca aatgttaaaa
      601 gataccatca atgaggaggc tgcagaatgg gataggttac atccagtgca tgcagggcct
      661 attgcaccag gccaaatgag agaaccaagg ggaagtgaca tagcaggaac tactagtaac
      721 cttcaggaac aaatagcatg gatgacaagt aacccccta ttccagtggg agacatctat
      781 aaaagatgga taattctggg gttaaataaa atagtaagaa tgtatagccc tgtcagcatt
      841 ttggacataa gacaagggcc aaaggaacct tttagagact atgtagatcg gttctttaaa
      901 accttaagag ctgaacaagc atctcaagat gtaaaaaatt ggatgacaga caccttgttg
      961 gtccaaaatg cgaacccaga ttgtaagacc attttaagag cattagggcc aggggcttca
     1021 ctagaagaaa tgatgacagc atgtcaggga gtgggaggac ctagccacaa agcaagagtg
     1081 ttggctgagg caatgagcca agcaaccaac acaaacataa tgatgcagaa aagcaatttt
     1141 aagggcccta gaaaaactat taaatgtttc aactgtggca aggaagggca cctagccaga
     1201 aattgcaggg cccctaggaa aaagggctgt tggaaatgtg gaagggaagg acaccaaatg
     1261 aaagactgta ctgagagaca ggctaatttt ttagggaaaa tttggccttc caacaagggg
     1321 aggccaggga atttccttca gagcagacct gagccaacag ccccaccagc agagagcttc
     1381 gggttcgagg agccgacccc ccctcagaag caggagctaa aagacaagga accctacaag
     1441 gagcccttaa ctgccctcag atcac
                               gag ->
```

```
LOCUS       HIVDJ2592    3234 bp ds-DNA              VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, DJ259 from Djibouti, proviral
            DNA encoding env, tat, vpU, rev, and nef
ACCESSION   L22940
SOURCE      Human immunodeficiency virus type 1 (HIV-1), DJ259 from Djibouti,
            PCR amplification of proviral DNA from cocultivated PBMC's
REFERENCE   1  (bases 1 to 3234)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1994)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences that were published
            by Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993 Human
            Retroviruses and AIDS compendium. This sequence and the corresponding
            gag sequence cluster with C subtype sequences. See also accession
            numbers L22939, L22941-L22957 and L23064-L23065.
            NCBI gi: 437343
BASE COUNT      1134 a    558 c    786 g    756 t
ORIGIN      144 bp upstream from the beginning of rev cds start
          1 ggcttccgtc tagatagatc ctagactaga gccctggaac catccaggaa gtcagcctaa
         61 aactgcttgt aataagtgtt attgtaaaaa atgtagctat cattgtctag tttgctttca
        121 gacaaaaggt ttaggcattt cctATGgcag gaagaagcgg agacagcgac gaagcgctcc
                    rev cds start ->
        181 tccaagcagt gaggatcatc agactcctat atcaaagcaG Taagtacaat agtagatgta
                                                 5' sj /\
        241 ATGatagatt taccagcaaa agtagactat agattagcag taggagcatt aatagtagca
   vpU start ->
        301 ctaatcatag caatagttgt gtggaccata gtatatatag aatataggaa attgttaaga
        361 caaagacaaa tagactggtt aattgaaaga attagggaaa gagcagaaga cagtggcaAT
                                                              env cds start ->
        421 Gaaagtgatg gggacacaga ggaactggcc acggtggtgg gtatggggaa tcttaggctt
        481 ttggatgttg ttgatttgTA Atgggaactt gtgggtcaca gtctattatg gggtacctgt
                                  <- vpU end
        541 gtggaaagat gcaaaccctc ccctattttg tgcatcagat gctaaagcat ataaagtaga
        601 agtacataat gtctgggcta cacatgcctg tgtacccaca gaccccagcc cacaggaact
        661 agctttggaa aatgtaacag aaaattttaa catgtggaaa aatggcatgg tggatcagat
        721 gcatcaggat ataatcagtc tatgggatca aagcctaaag ccatgtgtaa agttgacccc
        781 actttgtgtt actttaaact gtagtaatgt tcagagtaat gctacctacg agaatagcac
        841 aaaagaagaa atgaaaaatt gttctttcaa tgtaaccaca gaactaagag ataagagaca
        901 gaaagcatat gcacttttct atagacttga tatagtacca cttaatgaga ataatagtga
        961 atatagatta ataaactgta atacctcagc cataacacaa gcctgtccaa aggtctcttt
       1021 ggacccaatt cctatacatt attgtgctcc agctggttat gcgattctaa agtgtaggga
       1081 taagaacttc aatggaacag gaccgtgcaa taatgtcagc acagtacaat gtacacatgg
       1141 aattaaacca gtggtatcaa ctcaactatt gttaaatggt agtctagcag aagatgatat
       1201 aataattaga tctgaaaatc tgacaaacaa tgccaaaata ataatagtac agcttaatga
       1261 atctgtagca attaactgta cgagacccaa caataataca agagaaagta taaggatagg
                    v3 loop ->
       1321 accaggacaa acattctatg caacaggaga cataatagga gatataagac aagcacattg
       1381 taacattagt agaaaagaat ggaatgaaac tttaagaaag gtaagagaaa aattaaaaac
          <- v3 loop
       1441 gctcttcaga actgcaaata taacatttca accatcctca ggaggggacc tagaaattac
       1501 aacacatagc tttaattgtg gaggagaatt tttctactgc aatacatcag acctgtttaa
```

```
1561 taatcagagt atcacaaatg aaaacatcac acttcaatgc agaataaaac aaattataaa
1621 catgtggcag gaggtaggac gagcaatgta tgcccctccc attaaaggaa taataacatg
1681 taaatcaaat gtcacaggac tgctactgac acgtgatgga gggacaaata ccacaacaga
1741 aggagagata ttcagacctg gaggaggaga tatgagggac aattggagaa gtgaattata
1801 taaatacaaa gtggtagaaa ttaagccagt aggaatagca cccactaagg caaaaaggag
1861 agtggtgggg agagaaaaaa gagcagcact aggagctatg ttccttgggt tcttgggagc
1921 agccggaagc actatgggcg cagcatcaat aacgctgacg gtacaggcca gacaattatt
1981 gtctggtata gtgcaacagc aaagcaattt gctgagggct atagaggcgc agcagcatat
2041 gttgcaactc acggtctggg gcattaagca gctccagaca agagtcctgg ctatagaaag
2101 ataccttaag gatcaacagc ttctagggat ttggggctgc tctggaaaac tcatctgcac
2161 cactaatgtg ccttggaacg ctagttggag taataggtct caaaaggaga tttgggataa
2221 catgacctgg atacagtggg agagagaaat taataattat acaggactaa tatacgggtt
2281 gcttgaagac tcgcaaaacc agcaggagaa aaatgaacaa gatttactag cattggacaa
2341 atggcagaat ctgtggaatt ggtttagcat aacaaagtgg ctgtggtata taaaaatatt
2401 cataatgata gtaggaggct tgataggttt aagaataatt tttgctgtgc tctctatagt
2461 gaatagagtt aggcaggggt actcaccgct atcgtttcAG acccttaccc caaacccgag
                              3' sj (tat, rev) /\
2521 gggacccgac aggcccggag gaatcgaaga agaaggtgga gagcaagaca gaggcagatc
2581 gattcgatta gtgagcggat tcttagcgct tgcctgggac gacctgcgga gcctgtgcct
2641 cttcagctac cgccgattga gagacttaat cttgattgca gcgagagcgg tggaactgct
2701 gggacagagg gggtgggaaa cccttaagta tctgggaagc cttgtgcagt attggggtct
2761 ggagctaaaa aagagtgcta ttagtctgct taataccaca gcaataacag tagctgaagg
2821 aacagatagg attataaaat tcatacaagg gctttggaga gctatctgca acatacctag
2881 aagaattaga cagggctttg aagcagcttt gcaaTAAaAT Ggggagcacg tggtcaaaaa
                                          <- env
                                  nef cds start ->
2941 gtagtccagt gggatggcct gctgtaagag aaagaataag gcaaactgat ccagcagcaa
3001 ggcaaactga ttcagcacca aagggagtag gagcagcgtc tcaagactta gacaaatatg
3061 gggcacttac aagcagcaac acaccagcca ataatgctga ttgtgcttgg ctggcagcgc
3121 aagaggagga aggagaagta ggctttccag taagacctca ggtaccttta agaccaatga
3181 cttataaggg agcattcgat ctcggcttct ttttaaaaga aaaggggga ctgg
                                                    3' LTR ->
```

```
LOCUS       HIVDJ263A   3292 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, DJ263 from Djibouti, proviral
            DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L22941
SOURCE      Human immunodeficiency virus type 1 (HIV-1), DJ263 from Djibouti,
            PCR amplification of proviral DNA from cocultivated PBMC's
REFERENCE   1  (bases 1 to 3292)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences that were
            published by Louwagie et. al. in AIDS 7, 769-780 (1993) and in the
            1993 compendium. This sequence clusters with A subtype env sequences.
            See also accession numbers L22939-L22940, L22942-L22957 and L23064-
            L23065.
            NCBI gi: 437344
BASE COUNT      1149 a    581 c    787 g    775 t
ORIGIN      149 bp upstream from the beginning of rev cds start
          1 aggcaggaAT Ggagccggta gatcctagcc tagagccctg gaaccacccg ggaagtcagc
       tat cds start ->
         61 ctacaactgc ttgtagcaag tgttactgta aaatatgctg ctggcattgt caattgtgct
        121 ttctgaacaa gggcttaggc atctcctATG gcaggaagaa gcggagacgc cgacgaggaa
                          rev cds start ->
        181 ctcctcagag tcgtcaggat catcaaaatc ctgtaccaaa gcaGTgagta gtaataatta
                                                    5' sj /\
        241 gtaagtgtgA TGcaatcttt agaaataact gcaatagtag gactagtagt agcattcata
        vpU cds start ->
        301 gcagccatag ttgtgtgggc catagtattc attgaatata ggaaaataag gaaacagaag
        361 aaaatagaca agttacttga tagaataaga gaaagagcag aagatagtgg caATGagagt
                                                      env cds start ->
        421 gatggggatg cagaggaatt atccactctt atggaaatgg ggtacgatca tattttggac
        481 aatgataatt tgTAAtgctg aaaagttgtg ggtcacggtc tactatgggg tacctgtgtg
                         <- vpU cds end
        541 gagaaacaca gagaccaccc tattttgtgc atcagatgct aaagcatatg atgcagaagt
        601 acataatgtc tgggctacac atgcctgtgt acccacagac cctaacccac aagaaataca
        661 tttggaaaat gtaacagaaa agtttaacat gtggaaaaat aacatggtag aacagatgca
        721 tgaagatata attagtctat gggaccaaag cctaaagcca tgtgtaaagt taacccctct
        781 ctgtgttact ttagattgtc ataatgtcaa cagcagcaat agcagcacct ctatcaacag
        841 gaccatagat agtaaaatgc aagaggaaat aaaaaactgc tctttcaata tgaccacaga
        901 actaagagat aagaaacaga aagtgtctgc actttttat agacttgatg tagtacaaat
        961 taatgaaagt agcaatagtc aatataggtt aatcaattgt aatacctcag ccattacaaa
       1021 agcatgtcca aaggtaacct ttgagccaat tcccatacat tattgtgccc cagctgggtt
       1081 tgcaattcta aaatgtaatg ataagaagtt caatggaaca gggctatgca agaatgttag
       1141 cacagtacaa tgcacacatg gaattaagcc agtagtatca acacaactac tgttaaatgg
       1201 cagtctagca gaagaggagg tagtgattag atctgaaaat atcacaaaca atgcccaaaa
       1261 cataatagta cagttggttg cgcctgtaag aatcaattgt accagaccta acaacaatac
                                          v3 loop ->
       1321 aagaaaaagt gtacgtatag gaccagggca aacattctat gcaacaggtg acataatagg
       1381 ggatataaga caagcacatt gtaatgttag tagatcagaa tggaatagaa ctttacaaca
                                       <- v3 loop
       1441 ggtggctaca caattaagga agcactttaa caaaacaata atctttgcta actcctcagg
```

```
1501 aggggatata gaaattacaa cacatagttt taattgtgga ggagaatttt tctattgcaa
1561 tacatcggaa ctgtttaata gcacttggaa tagcacttgg gataacagct caaatcacat
1621 agagtcaaat cacacagaag gcaatataac tctccaatgc aggataaagc aaattgtaaa
1681 tatgtggcag aaagtaggac tagcaatgta tgcccctccc atctcaggag aaataaggtg
1741 taaatcaaac attacaggac tactactaac aagagatgga gggagtaata atagtacaaa
1801 tgagaccttc agccctggag gaggagacat gagggacaat tggagaagtg aattatataa
1861 gtataaagta gtaaaaattg aaccactagg agtagcaccc acccgtgcaa aaagaagagt
1921 ggtggagaga gaaaaaagag cagttggact gggagctgtc ttccttgggt tcttaggagc
1981 tgcaggaagc actatgggcg cggcgtcaat aacgctgacg gtacaggcca gacaattatt
2041 gtctggtata gtgcaacagc agagcaattt gctgagggct atagaggctc aacaacatct
2101 gttgaaactc acggtctggg gcattaaaca gctccaggca agagtcctgg ctctggaaag
2161 ttacctaagg gatcaacagc tcctaggaat ttggggctgc tctggaaaac tcatctgcac
2221 cactaatgta ccctggaact ctagttggag taataaaact tataatgaca tatgggataa
2281 catgacctgg ctgcaatggg ataaggaagt tagcaattac acagacataa tatataatct
2341 aattgaagaa tcgcagaacc agcaggaaaa gaatgaacaa gacttattgg cattggacca
2401 atgggcaaat ctgtggaatt ggtttggcat aacaaaatgg ctatggtata taaaaatatt
2461 cataatgata gtaggaggtt taataggttt aaggatagtt tttgctgtgc ttactataat
2521 aaatagagtt aggcagggat actcaccttt atcgttccAG acccttaccc accaccagag
                              3' sj (tat,rev) /\
2581 gggacccgac agacccgaaa gaatcgaaga aggaggtggc gagcaagaca gagacagatc
2641 agggcgatta gtgagcggtt tcttagcact tgcctgggac gatctgcgga gcctgtgcct
2701 cttcagctac caccgattga gagactttgt cttgattgca gtgagggctg tggaacttct
2761 gggacacagc agcctcaagg gactgagact ggggtgggaa gccctccaat atctggggaa
2821 tcttctacta tactggggtc aggaactaaa gaaTAGtgct attaatttgc ttgatacaat
                                          <- rev cds end
2881 agcattagca gtagctaatt ggacagacag agttatagaa ataggacaaa gagttggtag
2941 agctattctc aacataccta gaagaatcag acagggtctt gaaagggctt tactaTAAcA
                                                                  <- env
                                                     nef cds start ->
3001 TGggtggcaa gtggtcaaaa agcagcatag tgggatggtc taaggttagg gaaagaataa
3061 gacagacccc tccagcagca acaggagtag gagcagcatc tcaagattta gatagacatg
3121 gagcaatcac aagtagtaat acagcagata ctaatgctga ttgtgcctgg ctagaagcac
3181 aagaggaaga ggaggtaggc tttccagtca ggccacaggt acctttgaga ccaatgactt
3241 ataaggcagc attcgatctc ggcttctttt taaaagaaaa ggggggactg ga
                                                  3' LTR ->
```

```
LOCUS       HIVDJ264A   3328 bp ds-DNA              VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, DJ264 from Djibouti,
            proviral DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L23064
SOURCE      Human immunodeficiency virus type 1 (HIV-1), DJ264 from Djibouti,
            PCR amplification of proviral DNA from cocultivated PBMC's
REFERENCE   1  (bases 1 to 3328)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 proteins from
            eight African countries (Djibouti, Gabon, Kenya, Senegal, Somalia,
            Uganda, Zaire, and Zambia) were sequenced and analyzed with thirty-
            two previously published full-length gp160 env sequences. Sequences
            DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274, VI191, and
            VI525 have corresponding gag sequences published by Louwagie et. al.
            in AIDS 7, 769-780 (1993) and in the 1993 compendium. This sequence
            clusters with A subtype env sequences. See also accession numbers
            L22939-L22957 and L23065.
            NCBI gi: 437345
BASE COUNT      1160 a    583 c    797 g    788 t
ORIGIN      209 bp upstream from the beginning of rev cds start
          1 tgtttattca tttcagaatt gggtgtcaac atagcagaat aggcattatt cgagggagaa
         61 gaggcaggaA TGgagccagt agatcctagc ctagagccct ggaaccaccc gggaagtcag
       tat cds start ->
        121 cctacaactg cttgtagcaa ttgttactgt aaaatatgct gctggcattg ccaattgtgc
        181 tttctgaaca agggcttagg catctcctAT Ggcaggaaga agcggagacg ccgacgagga
                          rev cds start ->
        241 actcctcaga gtcgtcagga tcgtcaaaat cctgtatcaa agcaGTgagt agtaataatt
                                                    5' sj /\
        301 agtatatgtg ATGaaatctt tagaaatagc tgcaatagta ggactagtag tagcattcat
             vpU start ->
        361 agcagccata gttgtgtgga ccataatagt cattgaatat aggaaaataa ggaaacagaa
        421 gaaaatagac aaattacttg atagaataag agaaagagca gaagatagtg gcaATGagag
                                                    env cds start ->
        481 tgatggggat acagaggaat tatccactct tctggaaatg gggtatgata atattttgga
        541 taatgataat ttgTAAtgct gaaaagttgt gggtcacggt ctactatggg gtacctgtgt
                          <- vpU cds end
        601 ggagagatgc agaaaccacc ctattttgtg catcagatgc taaagcatac gatgtagaag
        661 tacataatgt ctgggctaca catgcctgtg tacccacaga ccctaaccca caagaaatac
        721 atttgaaaaa tgtaacagaa aagtttaaca tgtggaaaaa taacatggta gaacagatgc
        781 atgaagatat aattagtcta tgggaccaaa gcctaaagcc atgtgtagag ttaacccctc
        841 tctgcgttac tttagattgt cataacaacg tcacctctaa caataggacc atatctaggg
        901 acatgcaagg ggaagtaaaa aattgctctt tcaatatgac cacagaacta agagataaga
        961 aacagcaagt gtctgcactt ttttatagac ttgatgtagt acaaattaat gaaagtagca
       1021 atagtagtca atataggtta atcaattgta atacctcagc cattaaacaa gcatgtccaa
       1081 aggtaacctt tgagcccatt cccatacatt attgtgcccc agctggtttt gcgattctaa
       1141 agtgtaatga taagaagttc aatggaacag ggccatgcaa gaatgttagc acagtacaat
       1201 gcacacatgg aatcaagcca gtagtatcaa ctcaactact gttaaatggc agtctagcag
       1261 aagaagaggt agtgattaga tctgaaaata tcacaaacaa tgccaaaaac ataatagtgc
       1321 agttggttac gcctgtagga atcaattgta ccagacctaa caacaataca agaaagagtg
                                 v3 loop ->
       1381 tgcgtatagg accagggcaa acattctatg caacaggtga cataataggg gatataagaa
       1441 aagcacattg taatgtcagt agatcaaaat ggaataacac tttacaacag gtggctatac
                     <- v3 loop
       1501 aattaaggaa gcactctaac acaacaataa tctttgctaa cccctcagga ggggatatag
```

```
1561 aaattacaac acatagtttt aattgtggag gagaattttt ctattgcaat acatcggaac
1621 tgtttaatag cacttgggat aacagcttaa atcacacaga gtcaaatcac acagaagaca
1681 atataactct ccaatgcaga ataaagcaaa ttgtaaatat gtggcagaaa gtaggacgag
1741 caatgtatgc ccctcccatc ccaggagaaa taaggtgtga atcaaacatt acaggactac
1801 tattaacaag agatggaggg agtaataata gtacaaatga gactttcagg cctggaggag
1861 gagatatgag ggacaattgg agaagtgaat tatataagta taaagtagta aaaattgaac
1921 cactaggtat agcacccacc catgcaaaag gaagagtggt ggagagagag aaaagagcag
1981 ttggactggg agctgtcttc tttgggttct taggagcagc aggaagcact atgggcgcag
2041 cgtcaataac gctgacggta caggccagac aattattgtc tggtatagtg caacagcaga
2101 gcaatttgct gagggctata gaggctcaac aacatctgtt gaaactcacg gtctggggca
2161 ttaaacagct ccaggcaaga gtcctggctc tggaaagata cctaagggat caacagctcc
2221 taggaatttg gggctgctct ggaaaactca tctgcaccac tactgtaccc tggaacgcta
2281 gttggagtaa taaaacttat aatgacatat gggagaacat gacctggctg caatgggata
2341 aagaaattag caattacaca gacataatat ataatctaat tgaagaatcg cagaaccagc
2401 aggaaaagaa tgaaaaagac ttattggcat tggacaaatg ggaaagtctg tggaattggt
2461 ttaacataac aaaatggcta tggtatataa aaatattcat aatgatagta ggaggtttaa
2521 tagggttaag aatagttctt gctgtgctta ctgtaataaa gagagttagg cagggatact
2581 cacctttatc attccAGacc cttacccacc accagaggga acccgacagg cccgaaagaa
      3' sj (tat,rev) /\
2641 tcgaagaagg aggtggagag caagacaaag acagatccgt gcgattagtc agcggattct
2701 tagcacttgc ctgggacgat ctgcggagcc tgtgcctctt cagctaccac cacttgagag
2761 actttgtctt gattgcagtg agggctgtgg aacttctggg acacagcagt ctcaagggac
2821 tgagactggg ttggggagcc ctcaaatatc tggggaatct tctgacatac tgggggcagg
2881 aactaaagaa TAGtgctatt aatttgcttg atacaatagc aatagcagta gctaactgga
                <- rev cds end
2941 cagacagagt tatagaaata ggacagagag ttggtagagc tattcgtaac atacctgtaa
3001 gaatcagaca aggtctcgaa agggctttgc taTAAcATGg gtggcaagtg gtcaaaaagc
                                          <- env cds end
                              nef cds start ->
3061 agcttagtgg gatggcctaa ggttagggaa agaataatac agacccctcc agcagcaact
3121 ggagtaggag cagcatctca agatttagat agacatggag caatcacaag tagtaataca
3181 gcagaaacta atgctgattg tgcctggcta gaagcacaag aggacgagga ggtaggcttt
3241 ccagtcaagc cacaggtacc tttgagacca atgacttata agggagcttt cgatctcggc
3301 ttctttttaa aagaaaaggg gggactgg
                         3' LTR ->
```

```
LOCUS       HIVDJ373A   3340 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, DJ373 from Djibouti,
            proviral DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L23065
SOURCE      Human immunodeficiency virus type 1 (HIV-1), DJ273 from Djibouti,
            PCR amplification of proviral DNA from cocultivated PBMC's
REFERENCE   1  (bases 1 to 3340)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993 compen-
            dium. This sequence clusters with C subtype env sequences. See also
            accession numbers L22939-L22957 and L23064.
            NCBI gi: 437346
BASE COUNT      1191 a    568 c    791 g    790 t
ORIGIN      226 bp upstream from the beginning of rev cds start
          1 ggcttccgtc tagatgctgt ctattcattt cagaattggg tgcctgcata gcagaatagg
         61 catcatgcga cagagaagag caagaaATGg agccagtaga tcctaaccta gagccctgga
                       tat cds start ->
        121 accatccagg aagtcagcct aaaactgctt gtactaaatg ttattgtaaa aaatgtagct
        181 atcattgtct agtttgcttt cagacaaaag gcttaggcat ttcctATGgc aggaagaagc
                                            rev cds start ->
        241 ggagacagcg acgaagcgct ccttcaagca gtgaggatca tcaaaatctt atatcaaagc
        301 aGTgagtacc aaatagtaga tgtaATGata gacttactag caaaagtaga ttatagatta
      5' sj /\          vpU cds start ->
        361 gcagtagcag catttataat agcatttatc atagcaatag ttgtgtggac catagcatat
        421 atagaatata ggaaattgtt aagacaaaga aaaatagaca ggttaattga aagaattagg
        481 gaaagagcag aagacagtgg caATGagagt gatggggata cagatgaact gtcaacaatg
                    env cds start ->
        541 gtggataggg ggaatcttag gcttttggat gctgttgatg tgTAAtggga tggggaactt
                                                        <- vpU cds end
        601 gtgggtcaca gtctattatg gggtacctgt gtggcaagaa gcaaacccta ctctattttg
        661 tgcatcagat gctaaagcat atgagacaga agtgcataat gtctgggcta cacatgcctg
        721 tgtacccaca gaccccagcc cacaggaact agttatggaa aatgtaacag aaaatttaa
        781 catgtggaaa aatggcatgg tggatcagat gcatcaggat ataatcagtt tatgggatga
        841 aggcctaaag ccatgtgtaa agttgacccc actctgtgtt actttaaact gtagtaataa
        901 ggttactgct accggtaatg gtagtgttac ctacaatagc acagaaaaag acatgagaaa
        961 ttgctctttc aacataacca cagaactaag agataagaaa cagaaaaaat atgcactttt
       1021 ttataaactt gatatagtac cacttgggaa tgggaatgag gaatatcgat taataaattg
       1081 taatacctca tccataacac aagcctgtcc aaaggtctct tttgaaccaa ttcctataca
       1141 ttattgtgct ccagctggtt atgcgattct aaagtgtagg gatacaaaat tcaatggaac
       1201 aggaccatgc aagaatgtca gtacagtaca atgtacacat ggaattaaac cagtggtatc
       1261 aactcaacta ttgttaaatg gtagtacagc agaggaggat ataataatta gatctgaaaa
       1321 tctgacaaac aatgccaaaa taataatagt acagcttaat caatctgtag aaattaattg
                                                              v3 loop ->
       1381 tacaagaccc aacaataata caaggcaaag cataaggata ggaccaggac aaacattcta
       1441 tgcaacagga gatataatag gagatataag acaagcacat tgtaacatta gtagacaaaa
                                                    <- v3 loop
       1501 gtggaaagaa actttacaac aggtaaaagg aaaattaaaa gaacacttca ataaaacaat
       1561 aaaatttgca ccatcctcag gaggagacat agaaattaca acacatagct ttaattgtgg
```

```
1621 aggagaattt ttctattgta atacatcagc cttgtttaat gattcaatta caaatgcacc
1681 cattaataat tcgagtacag atgcaaacat cacacttcaa tgcagaataa aacaaattat
1741 aaacatgtgg caggaggtag gacgagcaat gtatgcccct cccattcaag gaataatagc
1801 atgtaaatca aatatcacag gactgctact gacacgtgat ggagggacaa atagcacaga
1861 cgagacattc agacctggag gaggagatat gagggacaat tggagaagtg aattatataa
1921 atacaaagtg gtagaaatta agccattagg actagcaccc actaaggcaa aaaggagagt
1981 ggtggagaga gaaaaaagag cagcactagc agctgtgttc cttgggttct tgggagcagc
2041 cggaagcact atgggcgcag catcaataac gctgacggta caggccagac aattattgtc
2101 tggtatagtg caacagcaaa gcaatttgct gaaggctata gaggtgcatc agcatatgtt
2161 gcaactcaca gtctggggca ttaagcagct ccagacaaga gtcctggcta tagaaagata
2221 cctgaaggat caacagctcc tagggatttg gggctgctct ggaaaactca tctgcaccac
2281 tgctgtgcct tggaactcta gttggagtaa taaatctcaa gaggagattt gggacaacat
2341 gacctggatg cagtgggata gagaaattaa taattataca gaaacaatat acaggttgct
2401 tgaagtctcg caaacccagc aggagcaaaa tgaaaaagat ttactagcat tggacaaatg
2461 gcaaaatctg tggagttggt ttgacataac aaagtggctg tggtatataa aaatattcat
2521 aatgatagta gggggcttga taggtttaag aataattttt gctgtgcttt ctatagtgaa
2581 tagagttagg cagggatact caccattatc atttcAGacc cttatcccga acccaagggg
                          3' sj (tat,rev) /\
2641 acccgacagg cccagaggaa tcgaagaaga aggtggagag caagacaaag gcagatccac
2701 tcgattagtg agcggattct tagcacttgc ctgggacgac ctgcggagcc tgttcctttt
2761 cagctaccac cgattgagag acttaatctt gattgtagcg agagtggtgg aacttctggg
2821 acagaggggg tgggaaaccc ttaagtatct gggaagcctt gtgcaatatt ggggtctgga
2881 gctaaaaaag agtgctgtTA Gtctgcttga taccacagca atagcagtag ctgaaggaac
                       <- rev cds end
2941 agataggatt atagaaataa tacaaagaat ttggagagct ttctgcaaca tacctagaag
3001 aataagacag ggctttgaag cagctttgca aTAAaATGgg gaacaagtgg tcaaagggat
                                      <- env cds end
                           nef cds start ->
3061 ggcctgctgt aagagaaaga ataagaaaaa ctaagccagc agcagaaaga gtagcagcag
3121 cagcagaagg agtaggggca gcgtctcaag acttagataa atatggggca cttacaacca
3181 gcaacacacc cgccaataat gctgattgtg cctggctgga aacacaagag gaggaagaag
3241 aagtaggctt tccagtaaga cctcaggtac cattaagacc aatgacttat aagggagcat
3301 ttgatctcag cttcttttta aaagaaaagg ggggactgga
                                    3' LTR ->
```

```
LOCUS       HIVGER         384 bp ss-DNA              VRL       27-JUN-1994
DEFINITION  Human immunodeficiency virus type 1 (HIV-1) gag sequence, isolate
            GER, partial cds.
ACCESSION   U11549
SOURCE      Human immunodeficiency virus type 1 PCR-amplified DNA from coculti-
            vated PBMCs.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Emiliani,S., Blanc,M., and Devaux,C.
  TITLE     p17gag sequence of HIV1GER, a new, highly replicative and
            highly cytopathic HIV Type 1 strain of D genotype
  JOURNAL   AIDS Res. Hum. Retroviruses 10, in press.
COMMENT     Isolate HIVGER has an SI phenotype with elevated replication in
            both PBMCs and human hematopoietic cells, i.e. rapid/high HIV-1
            strain.  The virus was isolated from a 37 year old French patient
            who contracted the virus through heterosexual contact.  HIVGER
            has the greatest nucleotide similarity to HIVNDK, a subtype D
            virus.  This subtype designation obtained through phylogenetic
            analysis is consistent with the presence of an isoleucine in the
            amino acid sequence at position 68 in p17gag, a characteristic
            of subtype D sequences.  Another characteristic common to both
            HIVNDK and HIVGER is the absence of three amino acids in the
            C-terminal region of p17gag.  Emiliani et al. suggest that this
            sequence similarity may result in a high fusogenic potential.
BASE COUNT      160 a     59 c     92 g     73 t
ORIGIN      Beginning of gag cds
        1 ATGggtgcga gagcgtcagt attaagcggg ggaaaattag atacatggga aagaattcgg
  gag cds ->
       61 ttacggccag gaggaaagaa aaaatatgca ctaaaacatt tgatatgggc aagcagggag
      121 ctagaacgat ttaaacttaa tcctggcctt ttagagacat cagaaggctg taaacaaata
      181 ataggacagc tacaaccatc tattcaaaca ggatcagaag aaattagatc attgtataat
      241 acagtagcaa ccctctattg tgtacatgaa aggatagagg taaaagacac caaagaagct
      301 gtagaaaaga tggaggaaga acaaaacaaa agtaagaaaa aggcacagca agcagctgat
      361 agcagccagg tcagccaaaa ttat
                               gag ->
```

HIVHYDA

```
LOCUS       HIVHYDA       267 bp ss-DNA              VRL       09-MAR-1994
DEFINITION  Human immunodeficiency virus type 1, sample HYDA (isolate 30008)
            from Hyderabad, India, C2-V3 of env region.
ACCESSION   L29091
SOURCE      Human immunodeficiency virus type 1 (HIV-1), sample HYDA from
            isolate 30008 from Hyderabad, India, PCR amplification of proviral
            DNA extracted from peripheral blood leukocytes (PBL's).
REFERENCE   1  (bases 1 to 267)
  AUTHORS   Baskar,P.V., Ray, S.C., Rao,R., Quinn,T.C., Hildreth,J.E.K. and
            Bollinger,R.C.
  TITLE     Presence in India of HIV type 1 similar to North American strains
  JOURNAL   AIDS Res. Hum. Retroviruses 10, 1039-1041 (1994)
COMMENT     These sequences, taken from four seropositive individuals, represent
            the first known subtype B infections in India.  Phylogenetic analysis
            of the C2-V3 regions of the four Hyderabad sequences indicates a closer
            similarity to North American and European HIV-1 subtype B sequences
            than to subtype B sequences in Thailand and subtype C sequences from
            India and South Africa.  Other sequences in this set are included in
            the alignment below (accession numbers L29091-L29094).
            NCBI gi: 459768
BASE COUNT      120 a     38 c     52 g     57 t
ORIGIN      790 bp downstream from the beginning of env cds
        1 tagcagaaga agaggtagta attagatctg acaacttcac agacaatgct aaaaccataa
 env cds ->
       61 tagtacagct gaaagaatct gtagaaatta attgtacaag acccggcaac aatacaagaa
                                    V3 loop ->
      121 gaagtataca tataggacca gggagagcat tttttgcaac aggagacata acaggagata
      181 taagacaagc acattgtaac cttagtagaa caaaatggaa tgaaacttta aaacagatag
                          <- V3 loop
      241 ttataaagtt aagagaacaa tttcaga
                               env cds ->
```

```
------
CONSENSUS .............???CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTCACAGACAATGCTAAAAC     52
HIVHYDA   .............TAG-----------------------------C--------------------     55
HIVHYDB   ..............-------------------------------------------------------     52
HIVHYDC   ...................-------------------------------------------------     49
HIVHYDD   TGTTAAATGGCAGTCTAG--------------------------G-----------------------     70

CONSENSUS CATAATAGTACAGCTGAACAAATCTGTAGAAATTAATTGTACAAGACCC?ACAAC?A?ATAA?AAGAAG?    117
HIVHYDA   ------------------AG----------------------------GG----A-T-C--G------T    125
HIVHYDB   -------------------------------------------------G-----G-G----G------T    122
HIVHYDC   ----------------------------------------------G---A-----AGT----A------A    119
HIVHYDD   -------------------------------------------------A-A---G-G----A------A    140

CONSENSUS AGAATACA?ATAGGACCAGGGAGAGCATTT?TTGCAACA...G?CACAG?AGGAGATACAAGACAAGCAC    180
HIVHYDA   -T-...--T---------------------T--------GGA-A--T-AC--------T-----------    192
HIVHYDB   ---C-T--GG--------------------G-----G--...-G-----C--------------------    189
HIVHYDC   --------T----------------------T---------...AA-----T--------------------    186
HIVHYDD   ------A-G----------------------G---------...-G-----T--------------------    207

CONSENSUS AGTGTAACCTTAGTAGAGCAAAATGGAATGAAACTTTAAAACAGATAGTTATAAAGTTAAGAGAACAATT    250
HIVHYDA   -T---------------A-----------------------------------------------------    262
HIVHYDB   --------------------------T--------------T------------------------      256
HIVHYDC   ---------------------------------------------------T-----------          250
HIVHYDD   ------------------------------------------------------------------      277

CONSENSUS T?AGA     254
HIVHYDA   -C---     267
HIVHYDD   -A        279
```

LOCUS HIVK1241 1477 bp ss-RNA VRL 20-APR-1993
DEFINITION Human immunodeficiency virus type 1, isolate K124 from Nairobi, Kenya, gag region.
ACCESSION L11769
SOURCE Human immunodeficiency virus type 1 (HIV-1), Nairobi, Kenya isolate K124.
REFERENCE 1 (bases 1 to 1477)
AUTHORS Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T., Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K., Gershy-Damet,M., DeLeys,R. and Burke,D.
TITLE Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
JOURNAL AIDS 7, 769-780 (1993)
COMMENT Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. Samples were obtained from 15 different countries (Belgium, Burundi, Gabon, Ivory Coast, Kenya, Rwanda, Zaire, Thailand, Somalia, Brazil, Philippines, Djibouti, Uganda, Senegal, and Zaire) on four continents. The authors identified 7 distinct genotypes with an average gag inter-genotypic variance of 7% and an average intra-genotypic variance of 14%. The env region of this isolate (L22942) has also been sequenced; it groups with subtype D sequences. This gag sequence, previously published on page I-A-200 of AUG 93, tends to cluster with HIV1 A subtype gag sequences.
BASE COUNT 553 a 275 c 363 g 286 t
ORIGIN gag cds start

```
       1 ATGggtgcga gagcgtcagt attaagcggg ggaaaattag atgcatggga gaaaattcgg
gag start ->
      61 ttaaggccag ggggaaagaa aaagtataga ctgaaacatt tagtatgggc aagcagggag
     121 ctggaaagat ttgcacttaa ccctagcctt ttagaaacaa cagaaggatg tcaacaaata
     181 atggaacagt tacaatcatc tctcaagaca ggaacagaag aaattagatc attatttaat
     241 gcagtagcag tcctctattg tgtacatcaa cggatagagg taaaagacac caaggaagct
     301 ctagacaaaa tagaggaaat gcaaaataag agcaaacaaa agacacaaca ggcagcagct
     361 gacacaggaa acagcagcaa ggtcagccaa aattacccta tagtgcaaaa tgcacaaggg
     421 caaatgatac accagagttt gtcacctagg actctgaatg catgggtaaa agtaatagaa
     481 gaaaaggctt tcagcccaga agtaataccc atgttctcag cattatcaga aggagccacc
     541 ccacaagatt taaatatgat gctgaacata gtgggggggac accaggcagc tatgcaaatg
     601 ttaaaaaata ccatcaatga ggaagctgca gaatgggaca ggttacatcc agtacatgca
     661 gggcctattc caccaggcca gatgagagaa ccaaggggaa gcgacatagc aggaactact
     721 agtacccctc aagaacaaat aggatggatg acaagtaacc cacctatccc agtgggagac
     781 atctataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctgtt
     841 agcattttgg acataaaaca agggccaaaa gaacccttca gagattatgt agataggttc
     901 tttaaaactc tcagagctga gcaagctaca caggaggtaa aaggttggat gactgaaaca
     961 ttactggtcc aaaatgcaaa tccagattgt aagtccattt taagagcatt gggagcaggg
    1021 gctacattag aagaaatgat gacagcatgc cagggagtgg gaggacccag tcataaagca
    1081 agagtcttgg ctgaggcaat gagccaagca acaaataata taaatgctgc tgtaatgatg
    1141 cagagaggca attttaaggg cccaaagaaa atcattaaat gtttcaactg tggcaaagaa
    1201 gggcacatag caaaaaattg cagggctcct aggaaaaggg gctgttggaa atgtggaagg
    1261 gaaggacacc aaatgaaaga ttgcactgaa agacaggcta atttttagg gaaaatttgg
    1321 ccttcccaca agggaaggcc agggaacttc cttcagagca gaccagaacc aacagcccca
    1381 ccagcagaga gcttcgggtt tggggaggag ataacaccct ctcagaaaca ggagccgaaa
    1441 gacaaggaac tgtatccttt agcttccgtc aaatcac
                                          gag ->
```

HIVK124A2

```
LOCUS       HIVK124A2    2581 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, K124 from Kenya,
            proviral envelope glycoprotein (env) gene.
ACCESSION   L22942
SOURCE      Human immunodeficiency virus type 1 (HIV-1), K124 from Kenya,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 2581)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 proteins from eight
            African countries (Djibouti, Gabon, Kenya, Senegal, Somalia, Uganda,
            Zaire, and Zambia) were sequenced and analyzed with thirty-two
            previously published full-length gp160 env sequences.  Sequences
            DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274, VI191, and
            VI525 have corresponding gag sequences published by Louwagie et. al.
            in AIDS 7, 769-780 (1993) and in the 1993 compendium. This sequence
            tends to cluster with D subtype env sequences, although the corres-
            ponding gag sequence (L11769) clusters with A subtype gag sequences.
            See also accession numbers L22939-L22941, L22943-L22957 and L23064-
            L23065.
            NCBI gi: 437347
BASE COUNT      905 a    451 c    611 g    614 t
ORIGIN      env cds start
          1 ATGagagtga tggggataca gaggaattgt cagctcttat tgggaggggg aattatgatc
    env cds ->
         61 ttggggatga taataatctg taatgctgca aacttgtggg ttactgttta ctatggggta
        121 cctgtgtgga gagatgcaga gaccacttta ttttgtgcat cggatgctaa agcatataag
        181 acagaaatgc ataatgtctg ggctacacat gcctgtgtac ccacagaccc caacccacaa
        241 gaaatacatt tggaaaatgt gacagaaaat tttaacatgt ggaaaaataa catggtagaa
        301 cagatgcata cagatataat cagtctatgg gaccaaagcc taaagccatg tgtaaagtta
        361 acccctctct gcgttacttt aaattgtagt aatgtcaatg gcacgggtgg caacagcact
        421 acgggtaaca acatcactag ggaggacata ggaatgaaaa actgctcttt caatataacc
        481 acagaagtaa gagataggaa gaagcaagta tatgcacttt tttataaact tgatatagta
        541 caaatgaatg aaaatcagga taatagcagt agcggtgaat atagatatag attaataaat
        601 tgtaatacct cagccattac acaggcgtgc ccaaaggtat cctttgagcc aattcccata
        661 cattattgtg ctccagctgg ttttgcgatc ctaaagtgta aggataagga gttcaatgga
        721 acagggccat gcaagaatgt cagcacagtc caatgcacac atggaatcaa gccagtagta
        781 tcaactcaac tgctgttaaa tggcagtcta gcagaaggag aggtgaaaat tagatctcaa
        841 aatctcacaa acaatgccaa aactataata gtacaacttg tcaagcctgt gagaattaat
        901 tgtaccagac ctaacaacaa tataagaaaa agtatacgta taggaccagg acaagcattc
    v3 loop ->
        961 tttgcaacag gtgacataat aggaaatata agacaagcac agtgtaatgt taatggaaca
                                                        <- v3 loop
       1021 gaatggaatg aaactttaca acagataagt acacaattaa aaaaacactt tatgaacaag
       1081 acaataattt ttaaaccatc ctcgggaggg gacccagaaa ttacaacaca cagctttaat
       1141 tgtagagggg aatttttcta ctgcaataca tcaaaactgt ttaatagtgt atggggaaat
       1201 tcaagtaatg tgacaaaggt aaatgggaca aaggtaaaag agacaatcac actcccatgt
       1261 aaaataaaac aaattataaa catgtggcag gaagtaggac gagcaatgta tgcccctccc
       1321 attgaaggac tcatcaactg ttcatcaaat attacaggac tattgttgac aagagatggt
       1381 ggtgaaaata atagtagtca gaatgagacc ttcagacctg gaggaggaga tatgagagac
       1441 aattggagaa gtgaattata caaatataaa gtagtaaaaa ttgaaccact aggtctagca
       1501 cccaccagcg caaagagaag agtggtggaa agagaaaaaa gagcaatagg actgggagct
       1561 atgttccttg ggttcttggg agcagcagga agcacgatgg gcgcagcgtc aatgacgctg
       1621 acggtacagg ccagacagtt aatgtctggt atagtgcaac agcaaaacaa tttgctgagg
       1681 gctatagatg cgcaacagca tctgttgcaa ctcacagtct ggggcattaa acagctccag
```

```
1741 gcaagagtcc tggctgtgga aagctaccta aaggatcaac agctcctagg aatttggggt
1801 tgctctggaa aacacatttg caccactaat gtgccctgga actctagctg gagtaataaa
1861 tctctacagg agacttggga taacatgacc tggaaggagt gggaaagaga aattgacaat
1921 tatacagggt taatatacag cttaattgaa aaatcgcaaa cccagcaaga aaagaatgaa
1981 caagagctat tacaattgga caaatgggca agtttgtgga attggtttag cataacaaaa
2041 tggctgtggt atataaaaat attcgtaatg atagtaggag gcttgatagg tttaaggata
2101 gtttttgcta tgctttcttt agtaaataga gttaggcagg gatattcacc tctgtcgttt
2161 cagaccctcc tcccagcccc gaggggacca gacAGgcccg aaggaataga agaagaaggt
                         3' sj (tat,rev) /\
2221 ggagagcaag gcagagacag gtccattcga ttggtgaacg gattctccgc acttatctgg
2281 gacgacctga gggacctgtg cctcttcagc taccaccgct tgagagactt aatcttaatt
2341 gcaacgagga ttgtggaact tctgggacgc agggggtggg aagccctcaa atatctgggg
2401 aatctcctgc agtattggac tcgggaacta aagaaTAGtg ctattagctt agttgatacc
                                              <- rev cds end
2461 atagcagtag tagtagctgg ctggacagac agtattataa aaataggaca aagacttggt
2521 agagcttttc tccacatacc tagaagaatc agacagggct tcgagagggc tttgctaTAA
                                                                    <- env
2581 c
```

HIVK986

```
LOCUS       HIVK986       252 bp ss-RNA             VRL       04-AUG-1994
DEFINITION  Human immunodeficiency virus type 1 (HIV-1) partial envelope sequence,
            V3 region, isolate K986.
ACCESSION   U12984
SOURCE      Human immunodeficiency virus type 1, PBMC DNA from a Kenyan patient,
            K986.
REFERENCE   1  (bases 1 to 252)
  AUTHORS   Janssens,W., Heyndrickx,L., Fransen,K., Temmerman,M., Leonaers,A.,
            Ivens,T., Motte,J., Piot,P. and van der Groen,G.
  TITLE     Genetic variability of HIV type 1 in Kenya
  JOURNAL   AIDS Res. Hum. Retroviruses 10, (1994) In press, Nov issue.
COMMENT     This sequence set was derived from a 1990-1992 cohort study designed
            to determine risk factors for mother to child HIV transmission.  In
            this study, samples were collected from twenty-two seropositive
            pregnant women and one infected infant(K88).  Of the set,
            nineteen cluster with subtype A sequences and are shown in alignment
            following their consensus sequence.  Classification of sequence K976
            is problematic, although it seems to cluster most often with subtype
            A sequences. The three remaining sequences cluster with subtype D
            sequences; they are also shown in alignment below their consensus
            sequence. Five members of the set (K29, K31, K88, K98, and K112)
            were previously sequenced over the gag coding region (Louwagie et al.
            AIDS 7: 769-780). Four of these (K29, K88, K98 and K112) strains
            cluster with sequences of the same subtype for both the env and gag
            coding regions. However, K31 clusters with subtype D in gag and
            subtype A in env.  Accession numbers for the sequence set are U12984-
            U13006.
BASE COUNT      111 a     43 c     41 g     57 t
ORIGIN      972 bp downstream from beginning of env cds
        1 gaagagataa taattagatc tgaaaatctc acaaataatg ctaaaatcat aatagtacag
 env cds ->
       61 cttaatgagt ctgtaccaat tacttgcaca aggccctaca acaatacaag acaaggtaca
                            V3 loop ->
      121 catataggac cagggcaaac actctttaca acaaaaataa taggagatat aagacaagca
      181 cattgtaata ttagtgaagc agaatggaac aaaactttac aactagtagc aagaaaatta
             <- V3 loop
      241 ggaggccttc tt
              env cds ->
```

```
CONSENSUS.A GAAGAGGTAA?AATTAGATCTGAAAATATCACAAACAATGCCAAAACTATAATAGTACAA  59
HIVK  29    ----------T----------------------------------------------------  60
HIVK  31    A-----A---T----------------------------------------------------  60
HIVK  88    ----------C-----------------------------AT--------------------  60
HIVK  98    -G--------A-------------------------------T----AC--T---------  60
HIVK  112   A--C-T----A---C-----------------------------------------------  60
HIVK  965   A--A------A---------------T------------T----------C---------  60
HIVK  967   ----------G-------------------T--G-------T-----C---C---------  60
HIVK  968   A-G---A---A-----------------------------T--------------------  60
HIVK  970   -G----A---G-------------------------------T----AC------------  60
HIVK  973   ------T---T----------------C-G-----------T-----A-----------G  60
HIVK  976   -GG--AA---TG-----------------T---G------------AC-----------G  60
HIVK  977   A----A----G-----------------T--G-------T-----C---------------  60
HIVK  978   --G-T-----GT--------------C-------------------AC--------G---  60
HIVK  979   A---------A---------------------T-------T-----T---------------  60
HIVK  980   A-G-------A-----------------------------------------------------  60
HIVK  981   A----A-A--T-------------------------------T--------------------  60
HIVK  982   ------A---TG-----G-----------------------T-----AC------------  60
HIVK  983   ----------A-----------------------------------A----C---------  60
HIVK  984   ---A------T-----------------------------------A---------------  60
HIVK  985   ---------GTC-----------------------------T--------------------  60

CONSENSUS.D GAAGAGATAATAATTAGATCTGAAAATCTCACAAATAATGCTAAAATCATAATAGTACAG  60
HIVK  966   -------------------------------------------------------------  60
HIVK  971   ----------------------------------------------C--------------  60
HIVK  986   -------------------------------------------------------------  60

CONSENSUS.A CTTG?CAAGCCTGTAAAAATTAATTGTACCAGACCTAACAACAATACAAGAAAAAGTATA 118
HIVK  29    ----TAG--------C-----------------------------------C-G-----  120
HIVK  31    ----A-G---------T------------------N-T---------------------  120
HIVK  88    ----C--C------G-C------------T----------------------C-------  120
HIVK  98    T--AA---C-------------------------------------------------G--  120
HIVK  112   T---T---T-----G-C----------------------T---------------------  120
HIVK  965   ----TT-------------------------------GG--------------C-------  120
HIVK  967   ---AC--C-------GC-----------------------------------G-------  120
HIVK  968   ----TT--T-----G-C----------G----------T-------------G-------  120
HIVK  970   T---A---C----------------------G-----------------------G--  120
HIVK  973   --CAAG-CC---------------------G-----------------------C---  120
HIVK  976   T--ACTG-----A--C-------------T-----C-----------------------  120
HIVK  977   T--AAA-C--------C-----------T----------------------C-------  120
HIVK  978   T--ACAG-------------------------------------------------G--  120
HIVK  979   ----C---------G-----------------------------------C-------  120
HIVK  980   ----T---------G-----------------------------------S-------  120
HIVK  981   ----T-G-------G----------------------G--------------C-------  120
HIVK  982   ---AATG--T------C-------------------------------------GC-  120
HIVK  983   T--AA-G--A----G-------------T---------T---------TT----G-----  120
HIVK  984   ----T--C------G-C----G------T---G---T----------------------  120
HIVK  985   ----T-G-------G-T-------------------------------------------  120

CONSENSUS.D CTTAATGAGTCTGTACCAATTAATTGCACAAGGCCCTACAACAATACAAGACAAGGTACG 120
HIVK  966   ---------------A-----------------------------------A-----  120
HIVK  971   -------------------------------------------------------  120
HIVK  986   ----------------------C-----------------------------------A  120
```

HIVK986

```
CONSENSUS.A CATATAGGACCAGGACAAGCATTCTATGCAACAGGTGACATAATAGGGGATATAAGACAA   178
HIVK  29    ------------------------------G---G-C-----C------------A--   180
HIVK  31    -------------------------------------T-----------------A--   180
HIVK  88    -G----------------A-------------------------------A-------   180
HIVK  98    --------G-------------------------------T---------A-------   180
HIVK  112   -------------------------------------------------A-------   180
HIVK  965   -G--------------------------G--G----A-------------------A--   180
HIVK  967   -G-------------------------------------T----C---------C-----   180
HIVK  968   ---------------------------...G--A-------------------------   177
HIVK  970   ------------------------------------------------------------   180
HIVK  973   -G------------------------A-------------------------------   180
HIVK  976   -GCT-T--------------C-------...---A-------------------------   177
HIVK  977   -G---------------G--------------------T--------A------------   180
HIVK  978   -C------------------------------G-A-A----------------------   180
HIVK  979   TG----------------A---------...G------GA--------A------------   177
HIVK  980   ------------------------------------------------------------   180
HIVK  981   -G------------------------------------------------------------   180
HIVK  982   A-------------T-----------------------A----------------------   180
HIVK  983   ------------------T-----------------AG----G-----A-----------   180
HIVK  984   ----------------------T---...G--A--CG------T---A-----------   177
HIVK  985   -G----------------A---------...G-------A---------A-----------   177

CONSENSUS.D CATATAGGACCAGGGCAAACACTCTTT...ACAACAAAAATAATAGGAGATATAAGACAA   177
HIVK  966   -G-------------------------...-------------------------------   177
HIVK  971   ----------------G-G--TA--A-...--------C----------------------   177
HIVK  986   ---------------------------...-------------------------------   177

CONSENSUS.A GCACATTGTAATGTCAGTAGATCAGAATGGAATAAAACTTTACAAAAGGTAGCTA?ACAA   237
HIVK  29    ---T--------------------C----------------GG-----------TG---   240
HIVK  31    -----------------------------------T------------------C----   240
HIVK  88    -------------------------C-------GC-------------------A----   240
HIVK  98    --------------T------A---C---------C-----G----------TC-GC---   240
HIVK  112   ---------------------A---C---------G---------G---------C----   240
HIVK  965   ------------------T----------------C---------G--------GA----   240
HIVK  967   ------------------------C--------G---------G-G------T--T----   240
HIVK  968   -----------------------------------GT----A--C-A-------C---C   237
HIVK  970   --------------T------A---C-------G-----C-G-----------C-A----   240
HIVK  973   ------------A-------------C-------C-------------------CA---G   240
HIVK  976   ---T--------A----C-A-A--A--------GCC-------------------A----   237
HIVK  977   ---------------------------------G-----------C------T--A----   240
HIVK  978   ---------------------GT-----------C-----G----G------C-A----   240
HIVK  979   ------------------GA-A----G------G-T-A----A--C-----A---C----   237
HIVK  980   ------------------------------------------------C------G--C----   240
HIVK  981   ------------------------------------------------------------GAC---   240
HIVK  982   ---------------------G--------------G----G-G-G-------C-G----   240
HIVK  983   ------------------G----------------T-A------------T--C----   240
HIVK  984   ----------------C-------A-C--------CG-----GG-C--------GAT---   237
HIVK  985   ------------------------A----------T-------------------C----   237

CONSENSUS.D GCACATTGTAACATTAGTGGAGCAGAATGGAACAAAACTTTACAAC?GGTAGCTAAAAAA   236
HIVK  966   -------------------------G------T-----------AG-------------   237
HIVK  971   ------------------A--------------------------A-----------G-   237
HIVK  986   -----------T-------A-------------------------TA-----A-G----   237
```

CONSENSUS.A		TTAAGAAAATACTTT	252
HIVK	29	---------------	255
HIVK	31	---------------	255
HIVK	88	---G--C----T---	255
HIVK	98	-------C-------	255
HIVK	112	-----G---C-----	255
HIVK	965	----A-G--C-----	255
HIVK	967	-----G---C---GG	255
HIVK	968	---------C-----	252
HIVK	970	----A--C-------	255
HIVK	973	---------Y-----	255
HIVK	976	---GAG---C----C	252
HIVK	977	---------C---GG	255
HIVK	978	-------C-------	255
HIVK	979	----AG---C-----	252
HIVK	980	-------C-------	255
HIVK	981	-------C-------	255
HIVK	982	-------C-GT----	255
HIVK	983	--------C------	255
HIVK	984	------C--------	252
HIVK	985	------G--C-----	252
CONSENSUS.D		TTAGGAGACCTTCTT	251
HIVK	966	---------------	252
HIVK	971	---------------	252
HIVK	986	-------G-------	252

HIVKENYA

```
LOCUS       HIVKENYA    2569 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, KENY proviral envelope
            glycoprotein (env) gene.
ACCESSION   L22943
SOURCE      Human immunodeficiency virus type 1 (HIV-1), isolate KENY from
            Kenya, PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 2569)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L.,
            Hegerich,P.A., van der Groen,G., McCutchan,F.F.E., Eddy,G. and
            Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland.  Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence clusters with A subtype env sequences. See
            also accession numbers L22939-L22942, L22944-L22957 and L23064-L23065.
            NCBI gi: 437348
BASE COUNT      896 a    462 c    607 g    604 t
ORIGIN      env cds start
          1 ATGagagtga tggggacaca gaggaattgt cagcacttat tgagatgggg aactatgatc
    env cds ->
         61 ttggggatga taataatctg tagtgctgca gaaaacttgt gggttactgt ctactatggg
        121 gtacctgtgt ggaaaaacgc agagaccacc ttattttgtg catcagatgc taaagcatat
        181 gaaacagaaa aacataatgt ctgggctaca catgcctgtg tacccacaga ccccaaccca
        241 caagaaatac atttggaaaa tgtgacagaa gagtttaaca tgtggaaaaa taacatggta
        301 gagcagatgc atacagatat aatcagtcta tgggatcaaa gcctaaagcc atgtgttaag
        361 ttaacccctc tctgcgttac cttaaattgt agcaatgtca atgtcactgc cacgagtggc
        421 acaacacacg ggggacgggg gagaatgaaa aactgctctt acaatataac cacagagcta
        481 agggatagga gacagaaggt atattcactt ttttatagac ttgatgtagt accaattaat
        541 gaaaataata gcagtaacaa tgagtataga ttaataaatt gtaatacctc agccattaca
        601 caagcttgcc caaaggtaac ctttgagcca attcccatac attattgtgc cccagctggt
        661 tttgcgatcc taaagtgtaa agataagaag ttcaatggaa cagggccatg cacgaatgtc
        721 agcacagtac aatgcacaca tggaatcaag ccagtagtat caactcaact gctgttaaat
        781 ggcagtctag cagaaggaga ggtaatgatt agatctgaaa atatcacaaa caatgccaaa
        841 aatataatag tacaatttgc cgagcctgta aaaattaatt gtaccagacc taacaacaat
                                                 v3 loop ->
        901 acaagaatga gtatacgtat aggaccagga caagcattct atgcaacagg tgacataata
        961 gggaacataa gacaagcaca ttgtaatgtc agtagagcag aatggaatac aactttgcaa
                                   <- v3 loop
       1021 aaggtagtca caaaattaag ggaatacttt gggaacaaca aaacaataaa atttgctaac
       1081 tcctcaggag gggatctaga aatcacaaca catagtttta attgtggagg agaatttttc
       1141 tattgtaatt catcaggcct gtttaatagc acttggacca acatgcagga gtcaaatagc
       1201 acggagtcaa atgacactat aactctccca tgcagaataa aaattataaa catgtggcag
       1261 agagcaggac aagcaatgta tgcccctccc atccaaggaa taataaagtg tgtatcaaac
       1321 attacaggac taatattaac aagagatggt ggggataata acagtgaaag tgaaaccttc
       1381 agacctggag gaggagatat gagggacaat tggagaagtg aattatataa gtataaagta
       1441 gtaaaaattg aaccactagg agtagcaccc accaaggcaa agagaagagt ggtggagaga
       1501 gaaaaaagag cagttggaat aggagctgtc ttccttgggt tcttaggagc agcaggaagc
       1561 actatgggcg cggcgtcaat aacgctgacg gtacaggcca gacaattatt gtctggcata
       1621 gtgcaacagc aaagcaattt gctgagggct atagaggctc aacaacatct gttgaaactc
       1681 acggtctggg gcattaaaca gctccaggca agagtcctgg ctgtggaaag atacctaagg
       1741 gatcaacagc tcctaggaat ttggggctgc tctggaaaaa tcatctgcac cactaatgtg
```

```
1801 ccctggaact ctagttggag caataaatct cagagtgaga tatgggagaa catgacctgg
1861 ctgcaatggg ataaagaaat tagcaattac acagacataa tatataatct acttgaagaa
1921 tcgcagaacc agcaggaaaa gaatgaacaa gacttattgg cattggacaa gtgggcaaat
1981 ctatggaatt ggtttgacat atcaaactgg ctgtggtata taaaaatatt tataatgata
2041 gtaggaggct taataggatt aagaatagtt tttactgtgc tttctataat aaatagagtt
2101 aggcagggat actcaccctt gtcgttccAG acccataccc cagccccaag gggtctcgac
                    3' sj (tat,rev) /\
2161 aggcccgaaa gaatcgaaga agaaggtgga gagcaagaca gagacagatc gattcgatta
2221 gtgaccggat tcttagcact tgcctgggac gatctacgga gcctgtgcct cttcagctac
2281 caccgcttga gagacttcat cttgattgcc actgagactg tggaacttct gggacacagc
2341 agtctcaggg ggttgagact ggggtgggaa ggcctcaagt atctgtggaa tctcctgttg
2401 tactggggtc aggaactaaa aattagtgct agtaatttgg ttgataccat agcaatagta
2461 gtagctggct ggacagatag ggttatagaa atagcacaag gaataggtag agctattctc
2521 cacataccta gaagaatcag acagggcttt gaaagagctt tgctaTAAc
                                                    <- env cds end
```

HIVN759

```
LOCUS       HIVN759       342 bp
DEFINITION  Human immunodeficiency virus type 1 (HIV-1) C2-V3 envelope sequence,
            sample N759 (patient THP01).
ACCESSION   U15576
SOURCE      Human immunodeficiency virus type 1 PCR-amplified PBMC DNA derived
            from Thai patient THP01
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Kalish,M.L., Luo,C., Weniger,B.G., Limpakarnjanarat,K., Young,K.,
            Ou,C. and Schochetman,G.
  TITLE     Early HIV type 1 strains in Thailand were not responsible for the
            current epidemic
  JOURNAL   AIDS Res. Hum. Retroviruses 10, (1994). In press, Nov issue
COMMENT     In this study, samples THP01-THP13 were collected from thirteen
            consenting Thai inmates, each classified as an IDU. Of these,
            ten (THP01-THP10) were diagnosed with infectious HIV in 1986 or
            1987. The ten viral sequences were found to be similar to B subtype
            viruses found in Europe and the Americas.  These samples were also
            found to be phylogenetically similar to the variants collected from
            IDUs infected in 1988 and 1989, however, they are distinguishable
            from the latter, which the authors designate B'. THP11 and THP12,
            from patients who were diagnosed with HIV in 1988 and 1992, were
            found to be subtype B' viruses, not subtype B.  The remaining
            patient, THP13, was infected in 1989 with an E subtype
            virus. This subtype is predominantly found in Thai cases of sexual
            transmission.  Kalish et al. suggest that the recent prevalence of
            subtypes B' and E over subtype B in Thailand may be explained by B'
            and E subtype infections of dynamic high-risk populations.
            They also propose  that conditions in the Thai population may be
            more conducive to the transmission of subtypes B' and E than subtype
            B. Hence, phylogenetic comparison of Thai HIV-1 strains isolated in
            the mid-1980s and Thai HIV-1 strains isolated in the late 1980s
            indicates that the earlier virus was not responsible for the Thai
            epidemic beginning in 1988.  Other sequences in this set are included
            in the alignment below (accession numbers U15577-U15588).
            Sequences kindly provided prior to publication by Dr. Marcia Kalish
            of the CDC Atlanta, Georgia.
BASE COUNT      145 a     49 c     66 g     82 t
ORIGIN
        1 acggacaata ctaaaaccat aatagtacag ctgaacaaat ctatagaaat taattgtaca
       61 agacccaaca acaatacaag aaagggtata catataggac cagggagagc attttataca
      121 acaggagaaa tagtaggaga tataaggcaa gcacattgta accttagtag aacagaatgg
      181 gataatactt taaaacagat agttggaaaa ttaagagaac aattagggaa caataaaaca
      241 atagtcttta atcaatcctc aggaggggac ccagaaattg taatgcacag ttttaattgt
      301 ggaggggaat ttttctactg taattcaaca cagctgttta at
```

```
CONSENSUS ACGGACAATACTAAAACCATAATAGTACAGCTGAATGAATCTATAGAAATTAATTGTACAAGACCCAACA  70
HIVTHP01  ----------------------------------CA--------------------------------  70
HIVTHP02  --A------G------T-----------A--------T------C-----------------------  70
HIVTHP03  ------------------------------------------------------------------  70
HIVTHP04  --A-------------------------------CC--------------------------------  70
HIVTHP05  --A-----------------------------------------T-----------------------  70
HIVTHP06  ----------------------------------C-C-------------------------------  70
HIVTHP07  --A-----------------------------------------------------------------  70
HIVTHP08  ----------------------------------C-C-------------------------------  70
HIVTHP09  ----------------------------------A--NC--G---------------------------  70
HIVTHP10  ---A-----GT-----A---------------A---------G---------------------------  70
HIVTHP11  ---------G---G-GT-------------------------G---------------------------  70
HIVTHP12  ---------G---G-GT---------------------C---G---------------------------  70
HIVTHP13  --AA-----G-C--------------G--C--T---A-----G-------C--G-----C------TC--  70

CONSENSUS ACAATACAAGAAAAGGTATACATATAGGACCAGGGAGAGCATTTTATACAACAGGAGAAATAATAGGAGA 140
HIVTHP01  ----------G-------------------------------------------------G-------  140
HIVTHP02  ----------T----------CC----------------------G--------NG------------  140
HIVTHP03  ----------------------C-----------------------------------C-----------  140
HIVTHP04  --------------A------C---------------G-----------------C-------------  140
HIVTHP05  ------------------------------------------------------------------  140
HIVTHP06  ------------------------------------------------------------------  140
HIVTHP07  ------------------------------------------------------------------  140
HIVTHP08  ------------------------------------------------------------------  140
HIVTHP09  ----------------------------------------------------G-G-------------  140
HIVTHP10  --------------A----------G----AG---------------G---------GC----------  140
HIVTHP11  ----------------------C-----------CA-----GG------------C-------------  140
HIVTHP12  ----------------------C-C---------CA-----GG------------C-------------  140
HIVTHP13  -----------C-A-----AC------------ACA--T---C----G---------C---------A-  140

CONSENSUS TATAAGACAAGCACATTGTAACCTTAGTAGAACAAAATGG?ATAATGCTTTAAAACAGATAGCT?AAAAA 208
HIVTHP01  ------G-----------------------------G-----G-----A---------------T-GG----  210
HIVTHP02  ----------------------A-----------G-C---A-G--G----------------T-G-----  210
HIVTHP03  ------G-----------------------------C-----G---------------------A-----  210
HIVTHP04  ------------------------------G-C------G-GG--------------------AC----  210
HIVTHP05  ----------------------A-----------------G---------------------T-G--C--  210
HIVTHP06  ---------------C-----------------------G---------------------T-A-----  210
HIVTHP07  ----------------------A-----------------G---------------------G--C--  210
HIVTHP08  ---------------C-----------------------G---------------------A-----  210
HIVTHP09  ------------------------------G--C-----A-----A-----G-C-------T-A-----  210
HIVTHP10  C------------T------C-A-----G--GA-------A----CA--C--C---------T-AC----  210
HIVTHP11  ------------------------------C---------A----CA----------------G-----  210
HIVTHP12  ---------------G-------------C---------AC---CA------G-------A--G-----  210
HIVTHP13  -------A-----T-----G-GA---A-G----------A--G-AA----------G-----A-----  210

CONSENSUS TTAAGAGAACAATTAGGGAATAAAACA...ATAGTCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTG 275
HIVTHP01  --------------------C--T-A-ACA-------------------------------------  280
HIVTHP02  ---G---------ATA-------T---...----C-------------------------T----G---  277
HIVTHP03  ---G------------------CC---ACA-------------------------------------  280
HIVTHP04  ----------------------C-----...-------------------------------------  277
HIVTHP05  --------G------------------...-----------------------------T--------  277
HIVTHP06  C-----------------------...-------------------------------------  277
HIVTHP07  ----------------------...-----------------------------T--------  277
HIVTHP08  C----------------------T---...-------------------------------------  277
HIVTHP09  -----------C--T-----------...-----------------------------TC---G---  277
HIVTHP10  -----------G--TAA-----G----...----C-------------A-----------------  277
HIVTHP11  --------------T-----C--C---...-----------------------------G----  277
HIVTHP12  --------------T-----C------...-----------------------C-----------G----  277
HIVTHP13  ----AC--G--C--TAA---G-C--T-......A-----C-C-C-C----------A--T-T--T-G--A  274
```

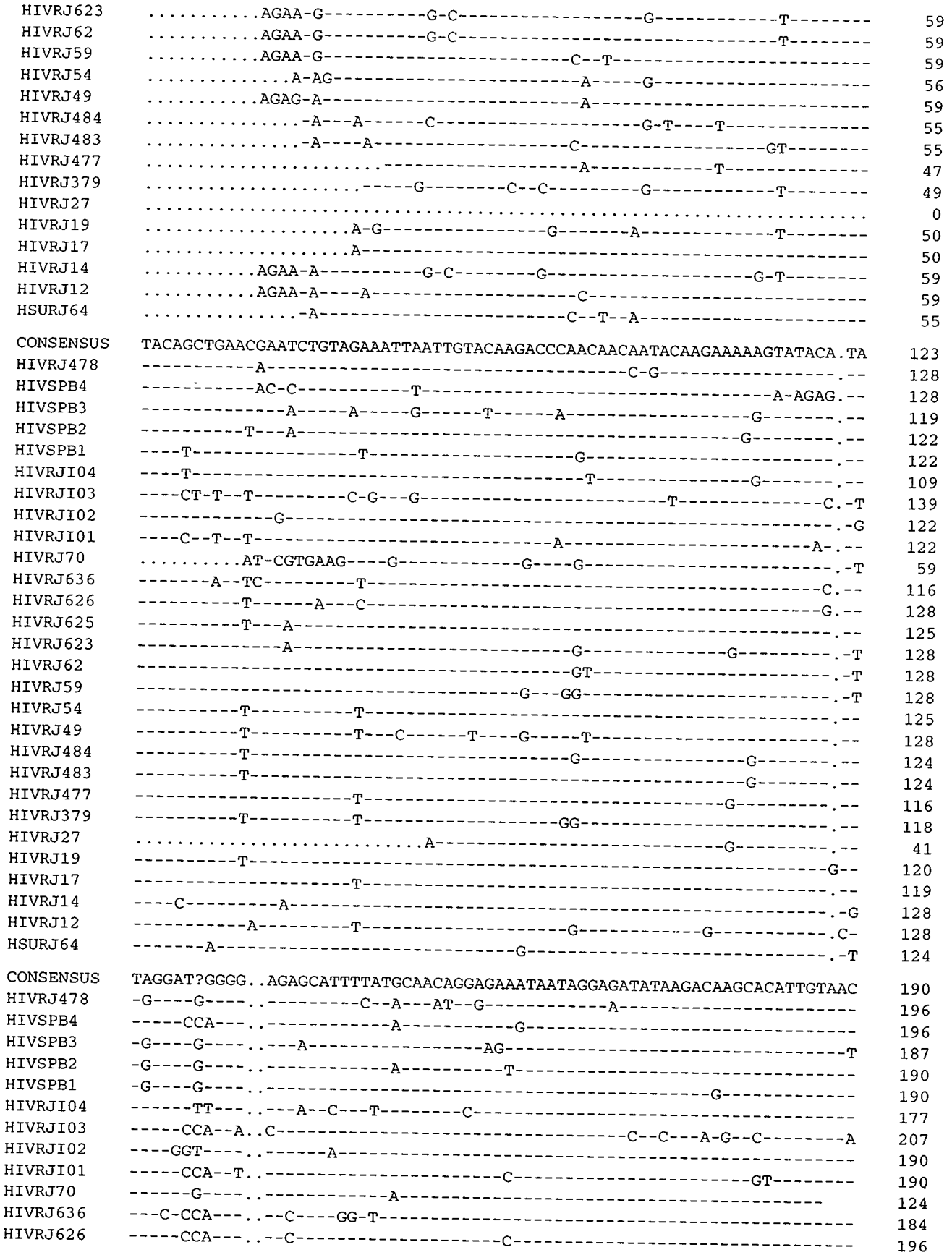
HIVN759

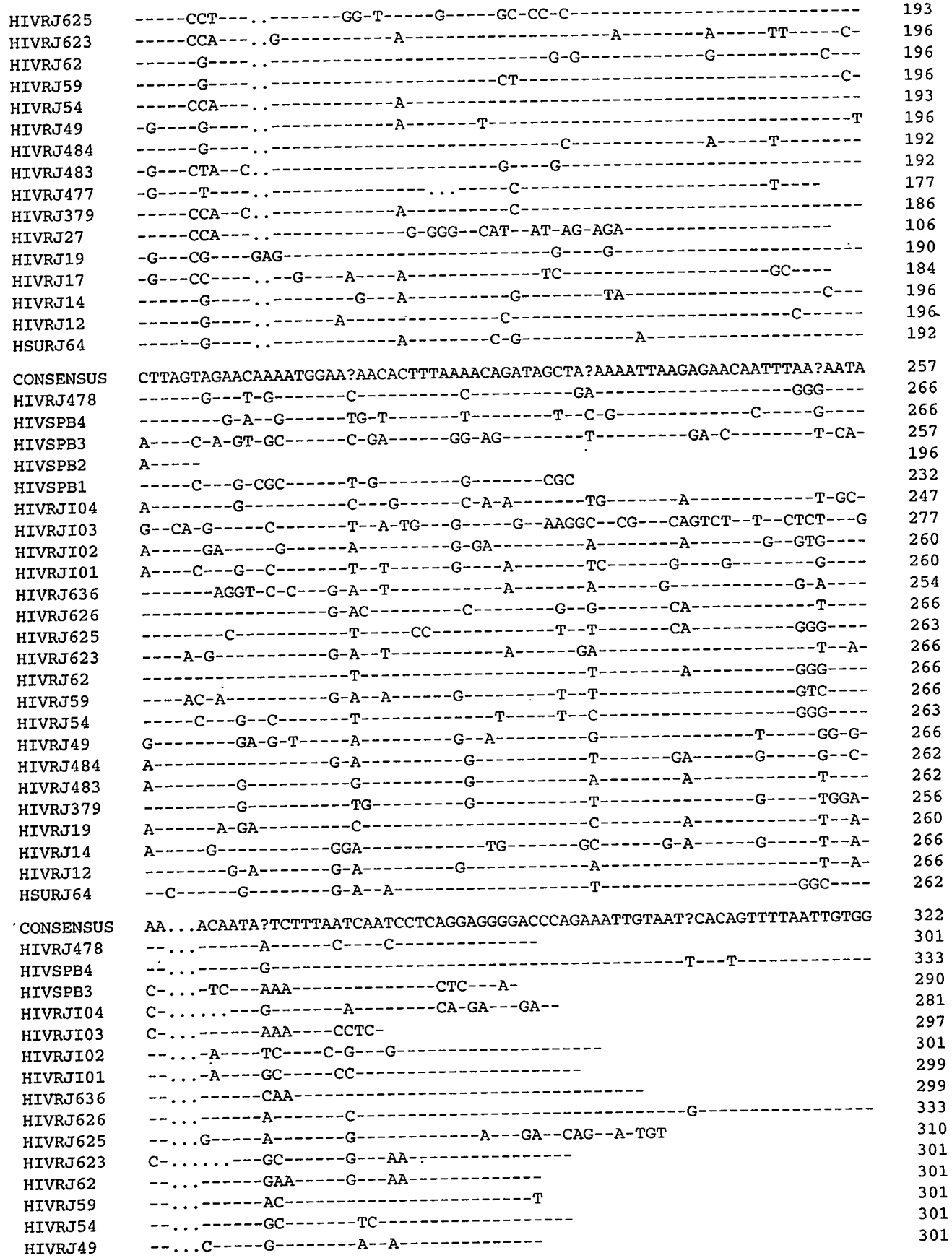
```
CONSENSUS TAATGCACAGTTTTAATTGTGGAGGGGAATTTTTCTACTGTAATACAACACAACTGTTTAAT   337
HIVTHP01  ----------------------------------------T-------G---------   342
HIVTHP02  ------------------------------------------------------------   339
HIVTHP03  --GC--------------------------------------T--G--------------   342
HIVTHP04  --C---------------------------------------C-----------------   339
HIVTHP05  ---C--------------------------------------------------------   339
HIVTHP06  ---C---------------------------------------T-----------------   339
HIVTHP07  ---C---------------------------------------G--------------   339
HIVTHP08  ---C---------------------------------------T-----------------   339
HIVTHP09  ---C-----------------------------------------------------C-----   339
HIVTHP10  -------T-----------------------------------------T----G------GG-   339
HIVTHP11  ------------------------------------------------T------------C-   339
HIVTHP12  ------------------------------------------------T--------------   339
HIVTHP13  C------TCA----------A----------------T------------AC-T--------   336
```

```
LOCUS       HIVRJ484     417 bp    RNA             VRL       25-MAY-1994
DEFINITION  Human immunodeficiency virus type 1, sample RJ484 from Brazil,
            partial env cds, C2-V3 region.
ACCESSION   U00409
SOURCE      Human immunodeficiency virus type 1 (HIV-1), sample HIVRJ484
            from Brazil, PCR amplified proviral DNA extracted from PBMCs.
REFERENCE   1  (bases 1 to 417)
  AUTHORS   Morgado,M.G., Sabino,E., Shpaer,E., Bongertz,V., Brigido,L.,
            Guimaraes,M., Castilho,E., Galvao-Castro,B., Mullins, J.I.,
            Hendry,R. and Mayer,A.
  TITLE     V3 region polymorphisms in HIV-1 from Brazil: Prevalence of
            subtype B strains divergent from North American/European
            prototype and detection of subtype F
  JOURNAL   AIDS Res. and Hum. Retroviruses 10, 569-576 (1994)
COMMENT     Submitted (04-AUG-1993) by Mariza G. Morgado, Instituto Oswaldo Cruz,
            Immunology, Av Brasil 4365, Rio de Janeiro, RJ 20000, Brazil.
            In an effort to assess the degree of HIV-1 genomic variation in
            Brazil, Morgado et al. collected HIV-1 samples from 28 infected
            individuals in Rio de Janeiro and four infected patients in Sao
            Paulo. The env V3 regions of these samples were PCR amplified and
            sequenced. The amino acid alignment of the sequences indicates
            that 26 of the 28 samples cluster with HIV-1 subtype B. RJ103 clusters
            with HIV-1 subtype F. Morgado et al. suggest that the remaining
            sequence, RJ101, may be a recombinant of HIV-1 subtypes B and F. RJ101
            clusters with HIV-1 subtype B sequences except for the N-terminal
            region which is more similar to HIV-1 subtype F sequences (see
            <HIVRJSP3>). Phylogenetic analysis of the tetrapeptide tip of the
            V3 loop reveals a high degree of variation between North American/
            European and Brazilian sequences. Other sequences in this set are
            included in the alignment below (accession numbers U00400-U00427).
            NCBI gi: 392389
BASE COUNT      176 a     54 c     81 g    106 t
ORIGIN      798 bp downstream from the beginning of env cds
        1 gaagaagtag tacttagatc tgaaaatttc acggataatg ttaaaaccat aatagtacag
 env cds ->
       61 ctgaatgaat ctgtagaaat taattgtaca agacccagca acaatacaag aaaaggtata
                           V3 loop ->
      121 catataggat gggggagagc attttatgca acaggagaaa taacaggaga tataagaaaa
      181 gcatattgta acattagtag aacaaaatgg gaaaacactt taagacagat agctataaaa
                <- V3 loop
      241 ttagaagaac agtttaagaa caaaacaata atctttaatc aatcctcagg aggagaccca
      301 gaaattgtaa cacacagttt taattgtgga ggggaatttt tctactgtga tacaacaaag
      361 ctgtttaata gtacttggaa tacaacacag ctgtctaata gttttaatag tactggg
                                                                  env ->
```

```
CONSENSUS   ...............G?AGAGGTAGTAATTAGATCTGAAAATTTCACGAACAATGCTAAAACCATAATAG     54
HIVRJ478    ...........AGAA-A-------------------------------------------------     59
HIVSPB4     ...........AGCA-A-A------G--------------------AG----------------G----     59
HIVSPB3     ....................AA---------A-------------T--G-------------A-------     50
HIVSPB2     .................----A--------------A-----------G-----A------T--------     53
HIVSPB1     .................----A-------------------------------------------------     53
HIVRJI04    ............................A-----------------A------CTA---T-A.------     40
HIVRJI03    AGCAGTCTAGCAGAA-A---TA--A----C--C-T-C-----A--T-AG-T-----A-------------     70
HIVRJI02    .................----A-----G-C--------------------------------T--------     53
HIVRJI01    .................----A--A----C------C-----A--T--G-T-----A----T--------     53
HIVRJ70     ...................................................................... .     0
HIVRJ636    ....................--G-----------------------------------T--------     47
HIVRJ626    ...........AGAA-G-------------------------------------------------     59
HIVRJ625    ............A-A--------------------------T---G------T--------------     56
```

HIVRJ484


HIVRJ623 ....AGAA-G----------G-C----------G----------T-------- 59
HIVRJ62 ....AGAA-G----------G-C----------T-------- 59
HIVRJ59 ....AGAA-G----------C--T---------- 59
HIVRJ54 ....A-AG----------A-----G---------- 56
HIVRJ49 ....AGAG-A----------A---------- 59
HIVRJ484 ....-A---A------C----------G-T----T---------- 55
HIVRJ483 ....-A----A----------C----------GT-------- 55
HIVRJ477 ....----------A----------T---------- 47
HIVRJ379 .....-----G--------C--C---------G----------T-------- 49
HIVRJ27 0
HIVRJ19 .....A-G----------G-------A----------T-------- 50
HIVRJ17 .....A---------- 50
HIVRJ14 ....AGAA-A----------G-C--------G----------G-T-------- 59
HIVRJ12 ....AGAA-A----A----------C---------- 59
HSURJ64 ....-A----------C--T--A---------- 55
CONSENSUS TACAGCTGAACGAATCTGTAGAAATTAATTGTACAAGACCCAACAACAATACAAGAAAAAGTATACA.TA 123
HIVRJ478 ----------A----------C-G----------.-- 128
HIVSPB4 ----------AC-C----------T----------A-AGAG.-- 128
HIVSPB3 ----------A-----A-----G------T------A----------G-------.-- 119
HIVSPB2 ----------T---A----------G--------.-- 122
HIVSPB1 ----T----------T----------G----------.-- 122
HIVRJI04 ----T----------T----------G-------.-- 109
HIVRJI03 ----CT-T--T---------C-G---G----------T----------C.-T 139
HIVRJI02 ----------G----------.-G 122
HIVRJI01 ----C--T--T----------A----------A-.-- 122
HIVRJ70 .....AT-CGTGAAG----G----------G----G----------.-T 59
HIVRJ636 -------A--TC---------T----------C.-- 116
HIVRJ626 ----------T------A---C----------G.-- 128
HIVRJ625 ----------T---A----------.-- 125
HIVRJ623 ----------A----------G----------G---------.-T 128
HIVRJ62 ----------GT----------.-T 128
HIVRJ59 ----------G---GG----------.-T 128
HIVRJ54 ----------T----------T----------.-- 125
HIVRJ49 ----------T----------T---C------T----G-----T----------.-- 128
HIVRJ484 ----------T----------G----------G-------.-- 124
HIVRJ483 ----------T----------G-------.-- 124
HIVRJ477 ----------T----------G---------.-- 116
HIVRJ379 ----------T----------T----------GG----------.-- 118
HIVRJ27 .....A----------G---------.-- 41
HIVRJ19 ----------T----------G-- 120
HIVRJ17 ----------T----------.-- 119
HIVRJ14 ----C---------A----------.-G 128
HIVRJ12 ----------A---------T----------G----------G----------.C- 128
HSURJ64 -------A----------G----------.-T 124
CONSENSUS TAGGAT?GGGG..AGAGCATTTTATGCAACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAAC 190
HIVRJ478 -G----G----..---------C--A---AT--G----------A---------- 196
HIVSPB4 -----CCA---..----------A----------G---------- 196
HIVSPB3 -G----G----..---A----------AG----------T 187
HIVSPB2 -G----G----..----------A----------T---------- 190
HIVSPB1 -G----G----..----------G---------- 190
HIVRJI04 ------TT---..---A--C---T--------C---------- 177
HIVRJI03 -----CCA--A..C----------C--C---A-G--C--------A 207
HIVRJI02 ----GGT----..------A---------- 190
HIVRJI01 -----CCA--T..----------C----------GT-------- 190
HIVRJ70 ------G----..----------A---------- 124
HIVRJ636 ---C-CCA---..--C----GG-T---------- 184
HIVRJ626 -----CCA---..--C----------C---------- 196


HIVRJ625 193
HIVRJ623 196
HIVRJ62 196
HIVRJ59 196
HIVRJ54 193
HIVRJ49 196
HIVRJ484 192
HIVRJ483 192
HIVRJ477 177
HIVRJ379 186
HIVRJ27 106
HIVRJ19 190
HIVRJ17 184
HIVRJ14 196
HIVRJ12 196
HSURJ64 192
CONSENSUS CTTAGTAGAACAAAATGGAA?AACACTTTAAAACAGATAGCTA?AAAATTAAGAGAACAATTTAA?AATA 257
HIVRJ478 266
HIVSPB4 266
HIVSPB3 257
HIVSPB2 196
HIVSPB1 232
HIVRJI04 247
HIVRJI03 277
HIVRJI02 260
HIVRJI01 260
HIVRJ636 254
HIVRJ626 266
HIVRJ625 263
HIVRJ623 266
HIVRJ62 266
HIVRJ59 266
HIVRJ54 263
HIVRJ49 266
HIVRJ484 262
HIVRJ483 262
HIVRJ379 256
HIVRJ19 260
HIVRJ14 266
HIVRJ12 266
HSURJ64 262
CONSENSUS AA...ACAATA?TCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAAT?CACAGTTTTAATTGTGG 322
HIVRJ478 301
HIVSPB4 333
HIVSPB3 290
HIVRJI04 281
HIVRJI03 297
HIVRJI02 301
HIVRJI01 299
HIVRJ636 299
HIVRJ626 333
HIVRJ625 310
HIVRJ623 301
HIVRJ62 301
HIVRJ59 301
HIVRJ54 301
HIVRJ49 301

HIVRJ484

```
HIVRJ484    --...------A----------------------A----------------CA-----------------  329
HIVRJ483    --...------G----------------------A--------G--------G-----------------  329
HIVRJ379    C-GAA------A--------------------------A--CAG                            299
HIVRJ19     C-.....---G-------------------------                                     290
HIVRJ14     C-.....---AAA---C-G.CCG----------A------                                 300
HIVRJ12     C-.....---G--------------------------------------                        311
HSURJ64     --...---G--A-----------------------GA--CAG--A-TGT-AT                     312

CONSENSUS   AGGGGAATTTTTCTACTGTAATACATCAA??CTGTTTAATAGTACTTGGAATACAACACAGCTGTCTAAT  390
HIVSPB4     -C-A--                                                                   339
HIVRJ626    ----------------------------                                             361
HIVRJ484    -------------------G-----A---AG-----------------------------------------  399
HIVRJ483    ----------------------------CA------------------                        378

CONSENSUS   AGTTTTAATAGTACTGGG    408
HIVRJ484    ------------------    417
```

```
LOCUS       HIVRJSP3        1270 bp    DNA              VRL       26-MAY-1994
DEFINITION  Human immunodeficiency virus type 1, sample RJI01, clone SP3
            from Brazil, envelope glycoprotein, partial cds (V1-V5).
ACCESSION   U08975
SOURCE      Human immunodeficiency virus type 1 (HIV-1), sample RJI01,
            clone SP3, from Brazil, PCR amplified from proviral DNA.
REFERENCE   1  (bases 1 to 1270)
  AUTHORS   Sabino,E.C., Shpaer,E.G., Morgado,M.M., Korber, B.T.M., Diaz,R.S.,
            Bongertz,V., Cavalcante,S., Galvao-Castro,B., Hendry,M., Mullins,J.I.
            and Mayer,A.
  TITLE     Identification of HIV-1 proviral genomes recombinant between
            subtypes B and F in two epidemiologically-linked individuals from
            Brazil
  JOURNAL   J. Virol. 68, 6340-6346 (1994)
  COMMENT   Submitted (15-APR-1994) Allen Mayer, Irwin Memorial Blood Centers,
            Scientific Service, 270 Masonic Ave., San Francisco, CA 94118, USA.
            Sequence analysis of the gp120 and C2-V3 regions of sample RJI01
            indicates a double recombinational event.  A region of the C2-V3
            gene of sample RJI01 clusters with HIV-1 subtype F while a
            large percentage of the gp120 region clusters with the HIV-1 B
            subtype.  PBMC DNA extracted from the subject's sexual partner also
            coded the recombinant env genes.  According to the authors, sample
            RJI01 reveals the plausibility of dual infection and recombination
            of distinct subtypes. Other sequences in this set are included in
            the alignment below (accession numbers U10019-U10026, U08953-U08960
            and U08962-U08975). RJI03 is a Brazilian F subtype sample.
            NCBI gi: 487388
BASE COUNT      484 a    203 c    269 g    314 t
ORIGIN      345 bp downstream from the beginning of env cds
        1 aaagccatgt gtgcaattaa ccccactctg tgttacttta cattgtactg attgtaatgc
 env cds ->
       61 taccaatatc aataatagca ccagtagtag tagttgcaat accaataata ccagcaccaa
      121 taatagtagt ttggggaaca tggagggaga aataaaaacc tgctctttta atatcacctc
      181 agatataaaa gataaggtgc gaaaagaaca tgcacttttt aatagacttg atatagtacc
      241 aatagataag aataatagta aaagctatat gttgataaat tgtaacacct cagtcattac
      301 tcaggcctgt ccaaaggtat cctttgaacc aatcccaata cattattgta ccccggctgg
      361 ttttgcgatt ctaaagtgta atgataagaa gttcaatgga acaggattct gtaaaaatgt
      421 cagtacagtg caatgtacac atggaattag gccagtggtg tcaactcaac tgctgttgaa
      481 tggcagtcta gcagaagaag atatagtaat taaatccgaa aatttctcgg acaatgctaa
      541 aacaataata gtacagctga acgaaactgt aaaaattgat tgtataagac caaacaacaa
                                          V3 loop ->
      601 tacaagaaaa ggtatacata tgggatgggg gagaacattt tatgcaacag gaagaataat
      661 aggagatata agacaagcac attgtaatct tagcaaagta gcatggaaca gaactttaga
                                  <- V3 loop
      721 aaggatagct ataaaattaa ggaaccaatt taattacaac aatgataaaa attttaatca
      781 atcctcagga ggggacccag aaattgtaat gcacagtttt aattgtggag gggaattttt
      841 ctactgtgat acaactcatc tgtttaatag tgcttggact aatgagagta ggactggcag
      901 agtcaaatgc actgaaaata ccacactctc atgcagaata aaacaaatta taaacaagtg
      961 gcaggaagta ggaaaagcaa tgtatgcccc tcccatcagt ggacaaatta gctgttcatc
     1021 aaatattaca gggctgctat tgacaagaga tggtggtaag aataacgggc ccaacgagtc
     1081 cgaaatcttc agacctggag gaggagatat gaagggcaat tggagaagtg aattatataa
     1141 atataaagta gtaaaaattg aaccattagg aatagcaccc accaaggcaa ggagaagagt
     1201 ggtgcaaaga caaaaaagag cagtgggaac gctaggagcc atgttccttg ggttcttggg
     1261 agcagcagga
            env ->
CONSENSUS    CGATCAAAGCCTAAAGCCATGTGT?GAATTAACCCC?CTCTGTGTTACTTTACATTG?ACTGATGCTAAC     67
HIVSP3       ............----------GC----------A--------------------T------TG---T     58
HIVRJIO3     ..........----------GA-G--------A----------------A----TT-------C-C-     60
HIVRJIO1-10  .-----------------------A----------G--------------------C----------     69
```

HIVRJSP3

```
HIVRJIO1-05  ------------------------A-----------G--------------------C-----------   70

CONSENSUS    ?CCACTAGAAG?.........GGTACTAATAACACCACTAGTAATAGT.............ACTGTTAACA  114
HIVSP3       G-T--C-AT-TC.............-A-----G-----G-----G----TGCAATACCAAT-A-ACC-G--  116
HIVRJIO3     GT----CC---C.........A-A--CCTG.....................................  81
HIVRJIO1-10  A----------T.........-------------------------.............----------  118
HIVRJIO1-05  A----------T.........-------------------------.............----------  119

CONSENSUS    CCGCTGTTAGTAGTGGGGGAAAGATGGAGGGAGAAATAAAAAA?TGC?CTTTCAATATCACCACAAGCAT  182
HIVSP3       --AA-AA-------TT---G--C-------------------CC---T----T---------T--GAT--  186
HIVRJIO3     ...................G-AGA-CCA--G-C----C----C--TT-------G--GG-------A-G  131
HIVRJIO1-10  ---------------------------------G--------T---A----------------------  188
HIVRJIO1-05  ----------------------------------------T---A----------------------  189

CONSENSUS    AA?AGATAAGGTGCAG?AAGAA?ATGCACTTTTTTATA?ACTTGAT?TAGTACCAATAG?CAATAATAGT  246
HIVSP3       --A-----------GAA-----C-----------A---G-------A------------AT--G----A-  256
HIVRJIO3     T-A-------CA----A---T-C---------------GC------A----------TAG--G---C---  201
HIVRJIO1-10  --G-------------G-----T---------------A-------G------------A----------  258
HIVRJIO1-05  --G-------------G-----T---------------A-------G------------G----------  259

CONSENSUS    A?T...AGTTATAGGTTGATAAATTGTAACACCTCAGTCATTA?ACAGGCCTGTCCAAAGGTATCCTTTG  311
HIVSP3       -G-AAA--C----T-----------------------------CT-------------------------  326
HIVRJIO3     GGA...GAA--C---C-A---C-------T------AC-----C------T--------------T-GG-  268
HIVRJIO1-10  -C-...-------------------------------------A-------------------------  325
HIVRJIO1-05  -C-...-------------------------------------A-------------------------  326

CONSENSUS    AGCCAATTCCCATACATTATTGTT?CCCGGCTGGTTTTGCGATTCTAAAGTGTAATGATAAGAAGTTCAA  380
HIVSP3       -A-----C--A------------AC-----------------------------------------------  396
HIVRJIO3     -T---------------------GCT--A-------A----------------------A--------  338
HIVRJIO1-10  ------------------------G-----------------------------------------------  395
HIVRJIO1-05  ------------------------G-------A-----------------------------------  396

CONSENSUS    TGGAACAGGACCATGTAAAAATGTCAGCACAGTACAATGTACACATGGAATTAAGCCAGTGGTATCAACT  450
HIVSP3       ----------TTC--------------T-----G-------------------G---------G------  466
HIVRJIO3     ---G-----G-----C-CG-----------------------------------A---------------  408
HIVRJIO1-10  ------------------------------------------------------------------  465
HIVRJIO1-05  ------------------------------------------------------------------  466

CONSENSUS    TGGAACAGGACCATGTAAAAATGTCAGCACAGTACAATGTACACATGGAATTAAGCCAGTGGTATCAACT  519
HIVRJ548-54  ..........................CTAC-TG-----------------------------------  42
HIVRJ548-35  ..........................CTAC-TGTG-------------------C-----A-------  42
HIVRJ548-82  ................GCAGTCTAGCAGAAGAAGA-------------------------A-------  54
HIVRJ548-2   ..........................CTAC-TG-------------------------A-------  42
HIVRJ548-169 ..........................CTAC-TG-------------------------A-------  42
HIVRJ548-160 ..........................CTAC-TG-------------------------A-------  42
HIVRJ548-155 ..........................CTAC-TGA----G-------------------------  42
HIVSP3       CAACTGCTGTTGAATGGCAGTCTAGCAGAAGAAGAT---G----T-A---CG-----T-------C----  536
HIVRJIO3     CAATTGTTGTTAAATGGCAGCCTAGCAGAAGA-GAT----------C-T----------A-------  478
HIVRJIO1-10  CAATTGTTGTTAAATGGCAGCCTAGCAGAAGAAGA-----------------------------------  535
HIVRJIO1-05  CAATTGTTGTTAAATGGCAGCCTAGCAGAAGAAGA-----------------------------------  536
HIVRJ549-113 ..............................-----------------------------------  35
HIVRJ549-111 ..........................CTAC-TG-------------------------A-------  42
HIVRJ549-94  ..........................CTAC-TG-----------------------------------  42
HIVRJ549-83  ..........................CTAC-TG-------------------------A-------  42
HIVRJ549-78  ..........................CTAC-TG-------------------------A-------  42
HIVRJ549-38  ..........................CTAC-TG-----------------------------------  42
HIVRJ549-2   ..............................-----------------------------------  35
HIVRJ548-153 ..........................CTAC-TGT----------------------------------  42
HIVRJ548-147 ..........................CTAC-TGA----------A----------------------  42
HIVRJ548-130 ................................A-------------------------A-------  35
HIVRJ548-123 ................................A----A-----A----------------------  35
HIVRJ548-116 ..............................-----------------------------------  35
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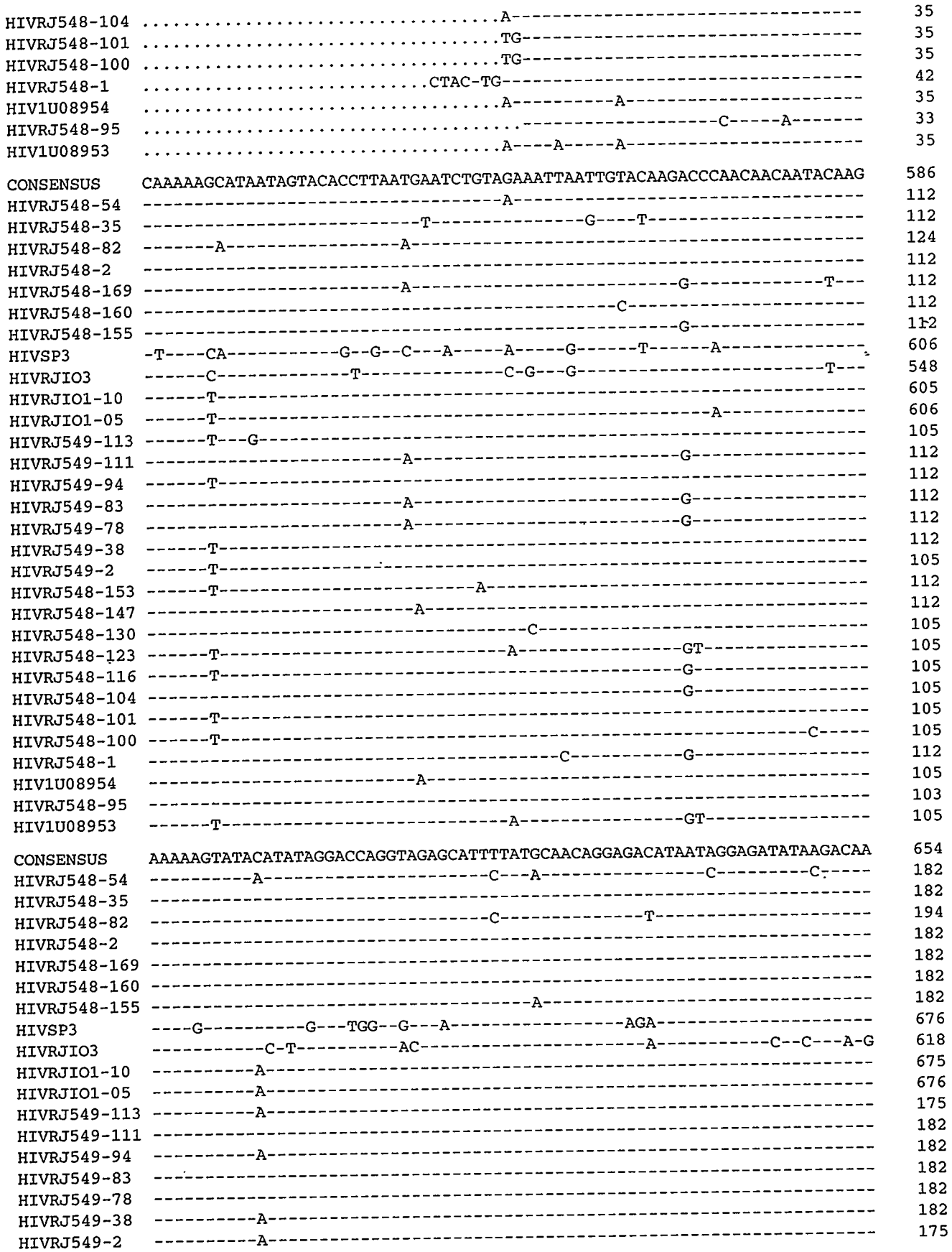
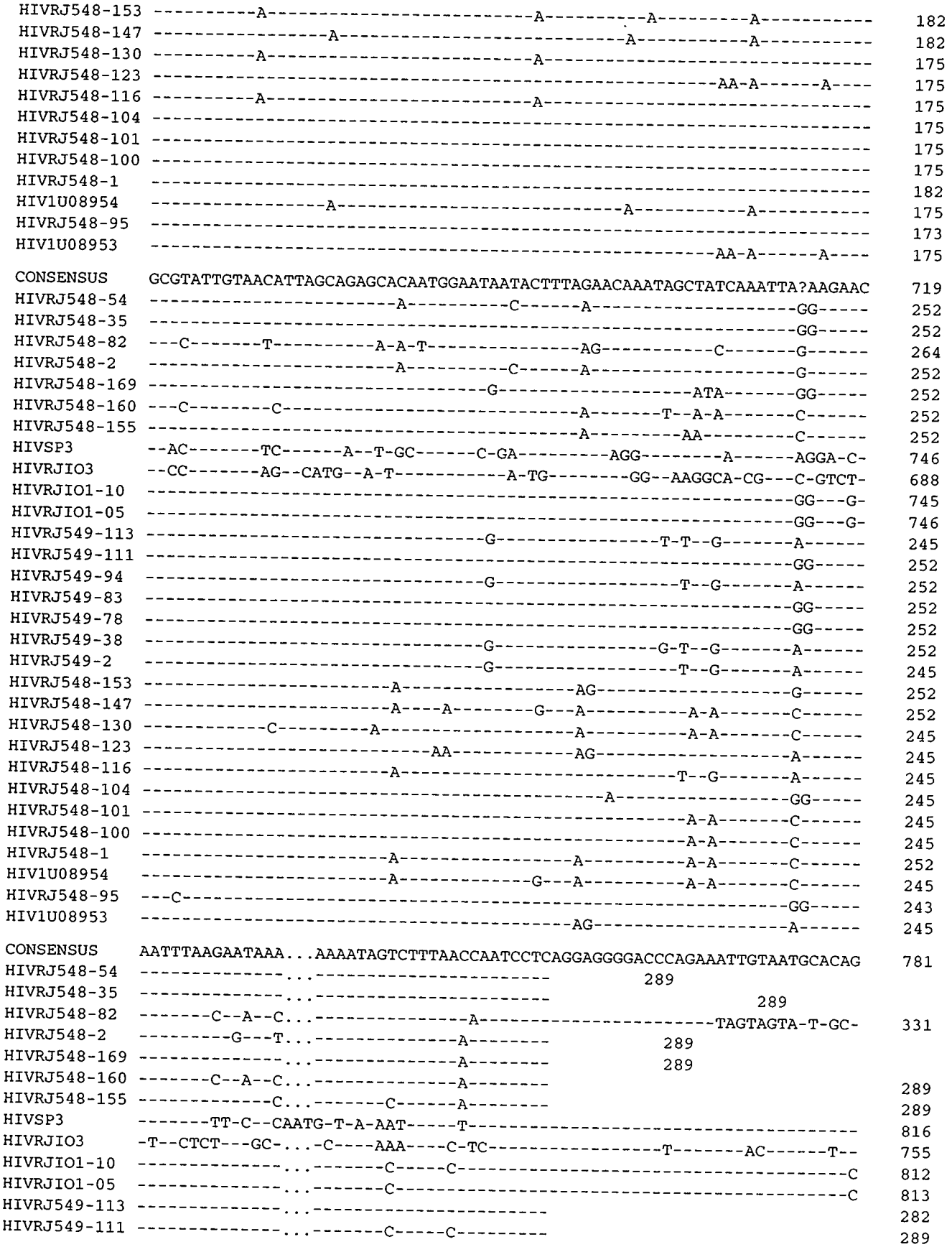
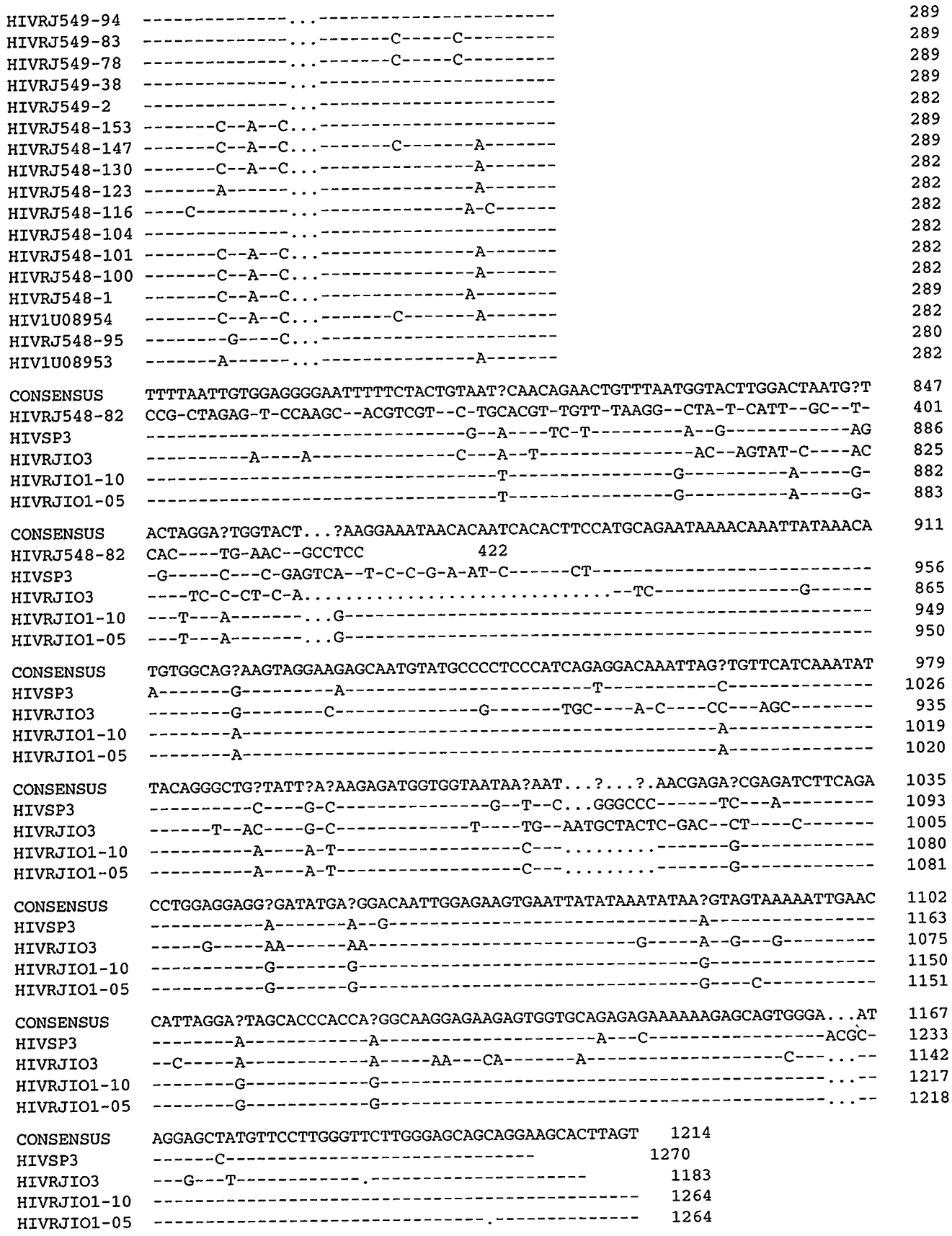

HIVRJ548-104 ..... A 35
HIVRJ548-101 ..... TG 35
HIVRJ548-100 ..... TG 35
HIVRJ548-1 ..... CTAC-TG 42
HIV1U08954 ..... A ..... A 35
HIVRJ548-95 ..... C ..... A 33
HIV1U08953 ..... A ..... A ..... A 35
CONSENSUS CAAAAAGCATAATAGTACACCTTAATGAATCTGTAGAAATTAATTGTACAAGACCCAACAACAATACAAG 586
HIVRJ548-54 ..... A 112
HIVRJ548-35 ..... T ..... G ..... T 112
HIVRJ548-82 ..... A ..... A 124
HIVRJ548-2 112
HIVRJ548-169 ..... A ..... G ..... T 112
HIVRJ548-160 ..... C 112
HIVRJ548-155 ..... G 112
HIVSP3 606
HIVRJIO3 548
HIVRJIO1-10 605
HIVRJIO1-05 606
HIVRJ549-113 105
HIVRJ549-111 112
HIVRJ549-94 112
HIVRJ549-83 112
HIVRJ549-78 112
HIVRJ549-38 112
HIVRJ549-2 105
HIVRJ548-153 112
HIVRJ548-147 112
HIVRJ548-130 105
HIVRJ548-123 105
HIVRJ548-116 105
HIVRJ548-104 105
HIVRJ548-101 105
HIVRJ548-100 105
HIVRJ548-1 112
HIV1U08954 105
HIVRJ548-95 103
HIV1U08953 105
CONSENSUS AAAAAGTATACATATAGGACCAGGTAGAGCATTTTATGCAACAGGAGACATAATAGGAGATATAAGACAA 654
HIVRJ548-54 182
HIVRJ548-35 182
HIVRJ548-82 194
HIVRJ548-2 182
HIVRJ548-169 182
HIVRJ548-160 182
HIVRJ548-155 182
HIVSP3 676
HIVRJIO3 618
HIVRJIO1-10 675
HIVRJIO1-05 676
HIVRJ549-113 175
HIVRJ549-111 182
HIVRJ549-94 182
HIVRJ549-83 182
HIVRJ549-78 182
HIVRJ549-38 182
HIVRJ549-2 175

HIVRJSP3


HIVRJ548-153 182
HIVRJ548-147 182
HIVRJ548-130 175
HIVRJ548-123 175
HIVRJ548-116 175
HIVRJ548-104 175
HIVRJ548-101 175
HIVRJ548-100 175
HIVRJ548-1 182
HIV1U08954 175
HIVRJ548-95 173
HIV1U08953 175
CONSENSUS GCGTATTGTAACATTAGCAGAGCACAATGGAATAATACTTTAGAACAAATAGCTATCAAATTA?AAGAAC 719
HIVRJ548-54 252
HIVRJ548-35 252
HIVRJ548-82 264
HIVRJ548-2 252
HIVRJ548-169 252
HIVRJ548-160 252
HIVRJ548-155 252
HIVSP3 746
HIVRJIO3 688
HIVRJIO1-10 745
HIVRJIO1-05 746
HIVRJ549-113 245
HIVRJ549-111 252
HIVRJ549-94 252
HIVRJ549-83 252
HIVRJ549-78 252
HIVRJ549-38 252
HIVRJ549-2 245
HIVRJ548-153 252
HIVRJ548-147 252
HIVRJ548-130 245
HIVRJ548-123 245
HIVRJ548-116 245
HIVRJ548-104 245
HIVRJ548-101 245
HIVRJ548-100 252
HIVRJ548-1 245
HIV1U08954 243
HIVRJ548-95 245
HIV1U08953
CONSENSUS AATTTAAGAATAAA...AAAATAGTCTTTAACCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAG 781
HIVRJ548-54 289
HIVRJ548-35 289
HIVRJ548-82 331
HIVRJ548-2 289
HIVRJ548-169 289
HIVRJ548-160 289
HIVRJ548-155 289
HIVSP3 816
HIVRJIO3 755
HIVRJIO1-10 812
HIVRJIO1-05 813
HIVRJ549-113 282
HIVRJ549-111 289


HIVRJ549-94 289
HIVRJ549-83 289
HIVRJ549-78 289
HIVRJ549-38 289
HIVRJ549-2 282
HIVRJ548-153 289
HIVRJ548-147 289
HIVRJ548-130 282
HIVRJ548-123 282
HIVRJ548-116 282
HIVRJ548-104 282
HIVRJ548-101 282
HIVRJ548-100 282
HIVRJ548-1 289
HIV1U08954 282
HIVRJ548-95 280
HIV1U08953 282
CONSENSUS TTTTAATTGTGGAGGGGAATTTTTCTACTGTAAT?CAACAGAACTGTTTAATGGTACTTGGACTAATG?T 847
HIVRJ548-82 CCG-CTAGAG-T-CCAAGC--ACGTCGT--C-TGCACGT-TGTT-TAAGG--CTA-T-CATT--GC--T- 401
HIVSP3 G--A----TC-T---------A--G----------AG 886
HIVRJIO3 C---A--T----------AC--AGTAT-C----AC 825
HIVRJIO1-10 T----------G----------A-----G- 882
HIVRJIO1-05 T----------G----------A-----G- 883
CONSENSUS ACTAGGA?TGGTACT...?AAGGAAATAACACAATCACACTTCCATGCAGAATAAAACAAATTATAAACA 911
HIVRJ548-82 CAC----TG-AAC--GCCTCC 422
HIVSP3 -G-----C---C-GAGTCA--T-C-C-G-A-AT-C------CT---------- 956
HIVRJIO3 ----TC-C-CT-C-A.....--TC----------G------ 865
HIVRJIO1-10 ---T---A-------...G---------- 949
HIVRJIO1-05 ---T---A-------...G---------- 950
CONSENSUS TGTGGCAG?AAGTAGGAAGAGCAATGTATGCCCCTCCCATCAGAGGACAAATTAG?TGTTCATCAAATAT 979
HIVSP3 A-------G---------A----------T----------C---------- 1026
HIVRJIO3 --------G--------C----------G-------TGC----A-C----CC---AGC-------- 935
HIVRJIO1-10 --------A----------A---------- 1019
HIVRJIO1-05 --------A----------A---------- 1020
CONSENSUS TACAGGGCTG?TATT?A?AAGAGATGGTGGTAATAA?AAT...?...?.AACGAGA?CGAGATCTTCAGA 1035
HIVSP3 ----------C----G-C----------G--T--C...GGGCCC------TC---A--------- 1093
HIVRJIO3 ------T--AC----G-C----------T----TG--AATGCTACTC-GAC--CT----C------- 1005
HIVRJIO1-10 ----------A----A-T----------C---.....-------G---------- 1080
HIVRJIO1-05 ----------A----A-T----------C---.....-------G---------- 1081
CONSENSUS CCTGGAGGAGG?GATATGA?GGACAATTGGAGAAGTGAATTATATAAATATAA?GTAGTAAAAATTGAAC 1102
HIVSP3 ----------A-------A--G----------A---------- 1163
HIVRJIO3 -----G-----AA------AA----------G-----A--G---G--------- 1075
HIVRJIO1-10 ----------G-------G----------G---------- 1150
HIVRJIO1-05 ----------G-------G----------G----C---------- 1151
CONSENSUS CATTAGGA?TAGCACCCACCA?GGCAAGGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGA...AT 1167
HIVSP3 --------A----------A----------A---C----------ACGC- 1233
HIVRJIO3 --C-----A----------A-----AA---CA-------A----------C---...-- 1142
HIVRJIO1-10 --------G----------G----------...-- 1217
HIVRJIO1-05 --------G----------G----------...-- 1218
CONSENSUS AGGAGCTATGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTTAGT 1214
HIVSP3 ------C---------- 1270
HIVRJIO3 ---G---T----------.---------- 1183
HIVRJIO1-10 ---------- 1264
HIVRJIO1-05 ----------.---------- 1264

```
LOCUS       HIVSE364A   3154 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, SE364 from Senegal,
            proviral DNA encoding env, vpU, rev, and nef genes.
ACCESSION   L22944
SOURCE      Human immunodeficiency virus type 1 (HIV-1), SE364 from Senegal,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3154)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence clusters with C subtype env sequences. See
            also accession numbers L22939-L22943, L22945-L22957 and L23064-L23065.
            Nucleotides 35 through 104 of this sequence have a perfect match to
            nucleotides 1 through 70 of a sequence, <BLVNADAA>, (Mansky and Temin,
            J. Virol. 68:494-499, 1994) that appears to be derived from a cloning
            vector related to pSG930 (U14118). This makes the first exons of tat
            and rev for this sequence problematic.
            NCBI gi: 437349
BASE COUNT      1124 a    527 c    747 g    756 t
ORIGIN      38 bp upstream from the beginning of rev cds start
          1 ccaagctatt taggtgacac tatagaatac tcaagctATG catcaagctt ggtaccgagc
                                     rev cds start ->
                                      insertion ->
         61 tcggatccac tagtaacggc cgccagtgtg ctggaattcg gcttaggatc atcaaaatcc
                                                        <- insertion
        121 tatatcaaag caGTaagtac tacatagtag ATGtaatggt agatttacta gccaaaagta
                  5' sj /\     vpU cds start ->
        181 gattatagat taggagtagg agcattgata gtagcactaa tcatagcaat aatttgtgtg
        241 gatcatagca tatatagaat ataggaaatt gttaagacaa aagaaattag attggttagt
        301 taagagaatt agggaaagag cagaagacag tggcaATGag agtgacgggg atgttgagga
                                   env cds start ->
        361 attgtcaacc atggtggata tggggcatct taggcttttg gatgcgattg atttaTAAtg
                                                                  <- vpU
        421 tgggggggaa cttgtgggtc acagtatatt atggggtacc tgtgtggaaa gaagcaaaaa
        481 ctactctatt ttgtgcatcg gatgctaaag catatgagag agaagggcat aatgtctggg
        541 ctacacatgc ctgtgtaccc acagacccca acccacaaga aatggtttgg gaaaatgtaa
        601 cagaatattt taacatgtgg aaaaatgaca tggtagatca gatgcatgag gatataatca
        661 gtttatggga tcaaagccta aagccatgtg taaagttgac cccactctgt gtcactttaa
        721 actgtaggaa tgttaccacc agcaataatg ccaccagtaa tgataaccct aatggagaaa
        781 taaaaaattg ctctttcaat ataaccacag aactaagaga taagagaagg aatgaatatg
        841 cacttttta tagacttgat atagtaccac ttagtgggag taaaaacagt tccaattcca
        901 gtgagtatag attaataaat tgtaatacct cagccataac acaagcctgt ccaaaggtct
        961 ctttggaccc cattcctata cattattgtg ctccagctgg ttatgcgatt ttaaagtgta
       1021 ataataagac attcaatgga acaggaccat gcaataatgt cagcacagta caatgtacac
       1081 atggaattaa gccagtggta tcaactcaac tactgttaaa tggtagtcta gcagaaggag
       1141 aaataataat tagatctgaa aatctgacaa ataatgccaa aacaataata gtacatctta
       1201 atgaatctat agaaattgtg tgtgcaagac ccaataataa tacaagaaaa agtatgagga
                         v3 loop ->
       1261 taggaccagg acaaaccttc tatgcaacag gagacataat aggagatata agacaagcac
```

```
1321 attgtaacat tagtggtaac tggaatgcaa ctttagaaaa ggtaaaagga aaattacaag
       <- v3 loop
1381 aacacttccc tggtaaaaat ataagctttg aaccatcctc aggaggggac ctagaaatta
1441 caacacacag ctttaattgt agaggagaat ttttctattg cgatacatca aagctgttta
1501 atggtacaac acatactgca aattcaaaca tcacaatcca atgcagaata aaacagatta
1561 taaacatgtg gcagggagta ggacgagcaa tatatgcccc tcccattgca ggaaacataa
1621 catgtaaatc aaatatcaca ggactactac tgacacgtga tggaggaaca actaataata
1681 atacagagat attcagacct ggaggaggag atatgaggga caattggaga agtgaattat
1741 ataaatataa agtagtagaa attaagccat taggaatagc acccactaag gcaaaaagga
1801 gagtggtgga gagagaaaaa agagcagtgg gaataggagc tgtgttcctt gggttcttgg
1861 gagcagcagg aagcactatg ggcgcggcat caataacgct gacggtacag gccagacaat
1921 tgttgtctgg tatagtgcaa cagcaaagca atttgctgag agctatagag gcgcaacagc
1981 atatgttgca actcacagtc tggggcatta agcagctcca gacaagagtc ctggctatag
2041 aaagatacct aaaggatcaa cagctcctag ggatttgggg ctgctctgga aaactcatct
2101 gcaccactgc tgtgccttgg aactctagtt ggagtaataa atctctagag gatatttggg
2161 ataacatgac ttggatgcag tgggatagag aaattaataa ttacacaagt ataatataca
2221 gcttgcttga agaatcgcaa aaccagcagg agaaaaatga aaacgattta ctagcattgg
2281 acaattggaa caatctgtgg aattggttta acataacaaa gtggctatgg tatataaaaa
2341 tattcataat gatagtagga ggcttgatag gtttaagaat aatttttgct gtgctctcta
2401 tagtgaatag agtcaggcag ggatactcac ctttgtcgtt ccAGaccctt atcccaaacc
                                    3' sj (tat, rev) /\
2461 cgaggggacc cgacaggctc ggaagaatcg aagaagaagg tggagagcaa gacagagaca
2521 gatccattcg attagtgagc ggattcttgt ccattgcctg ggacgacctg cggagcctgt
2581 gcctcttcag ctaccaccga ttgagagact tcatattgat tgtagcgaga gcagtggaac
2641 tcctgataca gaggggtgg gaaatcctta agtacctggg aagtcttgca cagtattggg
2701 gtttggaaat aaaaaagagt gctatTAGtc tgcttgatac catagcaata acagtagctg
                                  <- rev cds end
2761 aaggaacaga tagaattata gaattagtac aaagaatctg tagggctatc agcaacatac
2821 ctagaagaat aagacaggga tttgaagcag cgttgcaaTA AaATGggggg caagtggtca
                                                  <- env cds end
                                       nef cds start ->
2881 aaatgcagta tagtgggatg gccagaggta agagaaagaa taagaagaac taatccagca
2941 gcaacgggag taggagcagc gtctcaagac ttagataaat atggggcact tacaagcagc
3001 aacacagccg ccactaatga ggcttgtgcc cagctggaag cgcaagagca ggaagaagag
3061 gtaggctttc cagtcagacc tcaggtacct ttaagaccaa tgacttataa gggagcattt
3121 gatctcagcc atttttttaaa agaaaagggg ggac
```

```
LOCUS       HIVSE3651     1474 bp ss-DNA             VRL       27-MAY-1993
DEFINITION  Human immunodeficiency virus type 1, Senegalese isolate SE365,
            gag region.
ACCESSION   L11797
SOURCE      Human immunodeficiency virus type 1 (HIV-1) blood DNA, Senegalese
            isolate SE365 (cocultivation on PBMCs).
REFERENCE   1  (bases 1 to 1474)
  AUTHORS   Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T.,
            Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K.,
            Gershy-Damet,M., DeLeys,R. and Burke,D.
  TITLE     Phylogenetic analysis of gag genes from seventy international HIV-1
            isolates provides evidence for multiple genotypes
  JOURNAL   AIDS 7, 769-780 (1993)
COMMENT     Kindly provided prior to publication by Henry M. Jackson Foundation
            Research Laboratory, 1500 East Gude Drive, Rockville, MD  20850.
            Samples were obtained from 15 different countries (Belgium, Burundi,
            Gabon, Ivory Coast, Kenya, Rwanda, Zaire, Thailand, Somalia,
            Philippines, Djibouti, Brazil, Uganda, Senegal, and Zaire) on four
            continents.  From this study the authors identified 7 distinct
            genotypes with an average gag intra-genotypic variance of 7% and an
            average inter-genotypic variance of 14%. The env region of this
            isolate has also been sequenced (L22945).
            This gag sequence, previously published on page I-A-213 of the 1993
            compendium, groups with HIV1 D subtype gag sequences.
BASE COUNT      549 a    280 c    365 g    280 t
ORIGIN      gag cds start
        1 ATGggtgcga gagcgtcagt attaagcggg ggacaattag atcgatggga aaaaattcgg
gag start ->
       61 ttacggccag gaggaaagaa aaaatataag ctaaaacata tagtatgggc aagcagggaa
      121 ctagaacgat ttgcacttaa tcctggcctt ttagagacat cagaaggttg tagacaaata
      181 ataggacagc tacaaccagc tattcagaca ggatcagaag aacttagatc attatataat
      241 acaatagcaa ccctctattg tgtacatgaa aagatagagg taaaagacac caaggaagct
      301 gtagaaaaga tggaggaaga acgaaacaaa agtaagaaaa aggtacagca agcaacagct
      361 gactcaggaa acaacagcca ggtcagccaa aattacccta tagtgcaaaa cctacagggg
      421 caaatggtac accaagccct atcacctagg actttgaacg catgggtcaa agtaatagaa
      481 gagaaggatt tcagcccaga agtgataccc atgtttacag cactatcaga aggagccacc
      541 ccacaggatt taaacaccat gttaaacaca gtgggggggac atcaagcagc catgcaaatg
      601 ttaaaagaaa ccatcaatga ggaagctgca gaatgggata gattacatcc agtgcatgca
      661 gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgatatagc aggaactact
      721 agtacccttc aggaacaaat aggatggatg acaaataatc cacccatccc agtaggagaa
      781 atctataaaa gatggataat cctgggatta aataagatag taagaatgta tagtcctgtc
      841 agcattttgg acataagaca aggaccaaaa gaacccttta gagattatgt agatcggttc
      901 tataaaactc taagagccga gcaagctaca caggaggtaa aaaattggat gactgaaacc
      961 ttgttggtcc aaaatgcgaa cccagattgt aaaaatatct taaaagcatt aggaccaggg
     1021 gctacattag aagaaatgat gacagcctgt caggggtgg gggaacccag tcataaagca
     1081 agagtcttgg ctgaggcaat gagccaagca acaagttcag ctgctgccat aatgatgcag
     1141 agaggcaatt ttaagggtca aaggaaaatc gttaagtgtt tcaactgtgg caaagaaggg
     1201 cacatagcaa gaaattgcaa ggcccctaga aaaaagggct gttggaaatg tggacaggaa
     1261 ggacaccaaa tgaaggattg cactggaaga caggctaatt ttttagggaa aatttggcct
     1321 tccagcaagg ggaggccagg gaactttcct cagagcagac cagagccaac agccccacca
     1381 gcagagagct tcgggtttgg ggaggagacg acccccctctc agaaacagga gcagaaagac
     1441 aaggaactgt atcctttagc ttccctcaaa tcac
                                          gag ->
```

```
LOCUS       HIVSE365A2   3315 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, SE365  from Senegal,
            proviral DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L22945
SOURCE      Human immunodeficiency virus type 1 (HIV-1), SE365 from Senegal,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3315)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence and the corresponding gag sequence (L11797)
            cluster with  D subtype sequences. See also accession numbers L22939-
            L22944, L22946-L22957 and L23064-L23065.
            NCBI gi: 437350
BASE COUNT      1175 a    575 c    783 g    782 t
ORIGIN      209 bp upstream from the beginning of rev cds start
          1 tgtttattca tttcagaatt gggtgtcaac atagcagaat aggcattact ccacagagaa
         61 gaataagaaA TGgatccagt agatcctaac ctagagccct ggaaccatcc aggaagtcag
       tat cds start ->
        121 cctaagactc cttgtaacaa ctgttattgt aaaaagtgtt gttatcattg ccaaaattgc
        181 ttcataacaa agggcttagg catctcctAT Ggcaggaaga agcggagaca gcgacgaaga
                          rev cds start ->
        241 actcctcaag gcaatcagac tcatcaagtt tctgtaccaa aacaGTaagt aatatatgta
                                                    5' sj /\
        301 ATGcagtctt tagagatatt agcaatagca gcaattgtag tagcgctaat actagccata
  vpU start ->
        361 gttgtgtgga ccatagtatt catagaagtt aggaagataa gaaggcaaag gaaaatagac
        421 tggttaattg acagaataaa agaaagagca gaagatagtg gcaATGagag cgagggagat
                                          env cds start ->
        481 gaaaaggaat tatcagcact tgtggagatg gggcaccatg ctccttggaa tgttgatgac
        541 atgTAGtgtt gcagaaaaat tgtgggtcac agtttattat ggggtaccgg tgtggaaaga
              <- vpU end
        601 agcaaccacc actctatttt gtgcatcaga tgctaaatca tatgaaacag agaaacataa
        661 catctgggct acacatgcct gtgtacccac ggaccccaac ccacaagaaa tagaactggc
        721 aaatgtcaca gaaaacttta acatgtggaa aaataacatg gtggagcaga tgcatgaaga
        781 tataatcagt ttatgggatc aaagcctaaa accatgtgta aaattaaccc cactctgtgt
        841 cactttaaac tgcagggata tttctagtga cgccactagt aacaccatta gtaacgtcac
        901 tggaataccg atgatgggga aaggagaaat gcaaaactgt tctttcaata taaccacaga
        961 aataagagat aaaagacaga atgtatattc actttttat agacttgatt tagtaccaat
       1021 aggcaatagt aataagaata gcaccaatta taccagttat agattaataa attgtaatac
       1081 ctcagtcatt aaacaggctt gtccaaaggt aaactttgag ccaattccca tacattattg
       1141 tgccccagct ggttttgcaa ttctaaagtg taaagataag aagttcaatg gaacaggccc
       1201 atgcaaaaat gtcagcacag tacaatgtac acatggcatt aagccagtgg tgtcaactca
       1261 actgctgtta aatggcagtc tagcagaaga agaaataata attagatctg aaaatctcac
       1321 aaataacgct aaaaccataa tagtacagtt taatgaatct gtaatgatta attgtacaag
                                                          v3 loop ->
       1381 gccttacaac aataaaagac aaaggacacc tataggacta gggcaggtac tccatacaac
       1441 aagggtaaaa ggagatataa gacaagcaca ttgtaacatt agtaaagaaa gatggaataa
                                          <- v3 loop
```

```
1501 aactttacaa caggtagtta gaaaattaaa agacctcttt aacaaaacaa taatttttga
1561 accatcctca ggaggggacc cagaaattgc aacacacagt tttaattgta gaggggaatt
1621 tttctactgc aatacatcag gactgtttaa tagtacatgg aaaacaaaat caggtgataa
1681 tattacactc ccatgcagaa taaaacagat tataaacctg tggcagagag taggaaaagc
1741 aatgtatgcc cctcccattg agggagtgat cagctgttca tcaaatatta cagggctact
1801 attgctaaga gatggtggga tacataatac tagcaatgag accgagacct tcagacctgg
1861 aggaggagat atgagggaca attggagaag tgaattatat aaatataaag tagtaagact
1921 cgaaccacta ggagtagcac ccaccacagc aaagagaaga gtggtgaaaa gagaaaaaag
1981 agcaatagga ctgggagtta tgttccttgg gttcttggga gcagcaggaa gcacgatggg
2041 cgcagcgtca atggcgctga cggtacaggc cagacagcta ttgtctggta tagtgcaaca
2101 gcaaaacaat ttgctgagag ctatagaggc gcaacagcat ctgttgcaac tcacggtctg
2161 gggcattaaa cagctccagg caagaatcct ggctgtggaa agatacctaa gggatcaaca
2221 gctcctagga atttggggtt gctctggaag acacatttgc accactaatg tgccctggaa
2281 ctctagttgg agtaataaat ctctaactga gatttggcaa aacatgacct ggatggagtg
2341 ggaaagagaa attgacaatt acacaggctt aatatatagc ttaattgagg aatcgcaaac
2401 ccagcaagaa aagaatgagc aagaattatt ggcattggac aagtgggcaa gtttgtggaa
2461 ttggtttgac ataacaaatt ggctgtggta tataaaaata ttcataatgg tagtagaagg
2521 cttaataggg ttaagaataa tttttgctgt gctttcttta gtaaatagag ttaggcaggg
2581 atactcacct ctgtcgtttc AGaccctcct cccagcaccg aggggacccg acaggcccga
           3' sj (tat,rev) /\
2641 aggaatagaa gaagaaggtg gagagcaagg cagagacaga tcaattcgat tggtgaacgg
2701 attctcagca cttatctggg acggtctgcg gaacctgtgc ctcttcagct accaccggtt
2761 gagagactta atcttaattg cagcgaggat tgtggaactt ctgggacgca gagggtggga
2821 agtcctcaag tatctgtgga gtctcctgca gtattggata cagaaactga aaaaTAGtgc
                                                                  <- rev
2881 tattagcttg cttgatacca tagcaatagc agtagctgag gggacagata ggattataga
2941 cgtagtacaa agagcttgta gagctattct tcacataccc acacgaataa gacaggggtt
3001 ggaaagggct ttactaTAAa ATGggtggca aatggtcaaa aagtagtata gtaggatggc
                     <- env cds end
            nef cds start ->
3061 ctgctataag ggaaagaata agaagaactg agccagcagc agatggggtg ggagcagtat
3121 cgcgagacct ggaaaaacat ggggcagtca caagtagcaa tacaaaagat actaatgcgg
3181 actgtgcctg gctagaagca caagaagaga atgaaaaagt gggttttcca gtcaggcctc
3241 aggtaccttt aagaccaatg acttacaagg cagctgttga tcttagccac tttttaaaag
3301 aaaaggggag actgg
          3' LTR ->
```

LOCUS HIVSM1451 1486 bp ss-RNA VRL 20-APR-1993
DEFINITION Human immunodeficiency virus type 1, Somalian isolate SM145, gag region.
ACCESSION L11803
SOURCE Human immunodeficiency virus type 1 (HIV-1), Somalian isolate SM145. (cocultivation on PBMCs)
REFERENCE 1 (bases 1 to 1486)
AUTHORS Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T., Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K., Gershy-Damet,M., DeLeys,R. and Burke,D.
TITLE Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
JOURNAL AIDS 7, 769-780 (1993)
COMMENT Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. Samples were obtained from 15 different countries (Belgium, Burundi, Gabon, The Ivory Coast, Kenya, Rwanda, Zaire, Thailand, Somalia, the Philippines, Djibouti, Brazil, Uganda, Senegal, and Zaire) on four continents. From this study the authors identified 7 distinct genotypes with an average gag intra-genotypic variance of 7% and an average inter-genotypic variance of 14%. The env cds of this isolate (L22946) has also been sequenced. This gag sequence, previously published on page I-A-214 of AUG 93, groups with HIV1 C subtype gag sequences.
BASE COUNT 544 a 295 c 365 g 282 t
ORIGIN gag cds start

```
        1 ATGggtgcga gagcgtcaat attaagaggc ggaaaattag atgcatggga aagaattagg
gag start ->
       61 ttaaggccag ggggaaagaa acactatatg ataaaacacc tagtatgggc aagcagggag
      121 ctggaaagat ttgcacttaa ccctggcctt ttagagacat cagaaggctg taaacaaata
      181 atgaaacagc tgcaaccagc tcttcagaca ggaacagagg aacttagatc attattcaac
      241 acagtagcaa ctctctattg tgtacatgaa aagatagagg tacgagacac caaggaagcc
      301 ttagacaaga tagaggaaga acaaaacaaa agtcagcaaa aaacacagca ggcaaaagcg
      361 gctgacggaa aggtcagtca aaattatcct atagtgcaga atctccaagg gcaaatggta
      421 caccaggcca tatcacctag aaccttgaat gcatgggtaa aagtaataga agagaaggcc
      481 tttagcccgg agataatacc catgtttaca gcattatcag aaggagccac cccgcaagat
      541 ttaaacacca tgttaaatac agtgggggga catcaagcag ccatgcaaat gttaaaagat
      601 accatcaatg aggaggctgc agaatgggat agattacatc cagtacaggc agggcctgtt
      661 gcaccaggcc aaatgagaga cccaagggga agtgacatag caggaactac tagtaccctt
      721 caggaacaaa tagcatggat gacaagtaac ccacctattc cagtgggaga catctataaa
      781 agatggataa ttctggggtt aaataaaata gtaagaatgt atagccctgt cagcatttta
      841 gacataaaac aagggccaaa ggaacccttt agagactatg tagaccggtt ctttaaaact
      901 ttaagagctg aacaagctac acaagatgta aaaaattgga tgacagacac cttgttggtc
      961 caaaatgcga acccagattg taagaccatt ttaagagcat taggaccagg ggcttcatta
     1021 gaagaaatga tgacagcatg tcagggagtg ggaggacctg cccacaaagc aagagtgttg
     1081 gctgaggcaa tgagccaagc aaacaatata aacatactga tgcaaagagg caattttaaa
     1141 ggctctaaaa gaattgttaa atgtttcaac tgtggcaaag aagggcacat agctagaaat
     1201 tgcagggctc ctaggaaaaa gggctgttgg aaatgtggaa aggaaggaca ccaaatgaaa
     1261 gactgtactg agaggcaggc taatttttta gggaaaattt ggccttccca caaggggagg
     1321 ccagggaatt tccttcagaa caggccagag ccaacagccc caccagcaga gagcttcagg
     1381 gtcaggccag agccaacagc cccaccagca gagagcttca ggttcgagga gacaaccccc
     1441 gctccgaagc aggagctgaa agaacccctta acttccctca aatcac
                                                      gag ->
```

HIVSM145A2

```
LOCUS       HIVSM145A2   3228 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, SM145 from Somalia, proviral
            DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L22946
SOURCE      Human immunodeficiency virus type 1 (HIV-1), SM145 from Somalia,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3228)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland.  Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence and the corresponding gag sequence (L11803)
            cluster with C subtype env sequences. See also accession numbers
            L22939-L22945, L22947-L22957 and L23064-L23065.
            NCBI gi: 437351
BASE COUNT      1147 a    545 c    773 g    763 t
ORIGIN      105 bp upstream from the beginning of rev cds start
          1 ccatccagga tgtcaaccta aaactgcttg taataattgt tattgtaaac tctgtagcta
         61 ccattgccta gtttgctttc agacaaaagg cttaggcatt tcctATGgca ggaagaagcg
                                              rev cds start ->
        121 gagacagcga cgaagcgctc ctcagagcag tgaggatcat caaaatccta tatcaaagca
        181 GTgagtatct gtaATGttaa atttattagc aggagtagat tatagaatag caataggagc
  5' sj /\   vpU start ->
        241 atttagtgta gcactaatca tagcaatagt tgtgtggacc atagtatata tagaatatag
        301 gaaattgtta agacaaagaa aaatagactg gttagttaaa agaattaggg aaagagcaga
        361 agacagtggc aATGagagtg agggggatac tgaggaattg gcaacaatgg tggatatggg
          env cds start ->
        421 gcatcttagg cttttggatg ttaatgattt gTAGtggggg agggaacttg tgggtcacag
                                              <- vpU end
        481 tctattatgg ggtaccggtg tggagagaag caaaaactac tctgttttgt gcatcagatt
        541 ctaaagcata tgagagagaa gtgcataatg tctgggcgac acatgcctgt gtacccacag
        601 accccagccc acaagaaatg cttttgggaa atgtaacaga aaattttaac atgtggaaaa
        661 atgatatggt ggatcagatg catgaggata taatcagttt atgggatcaa agtctaaagc
        721 catgtgtaaa gttgacccca ctctgtgtca ctttaaattg tacagaagct aatattaata
        781 ttaccagtgt tggcaatgtt accagtaatg acaataagga agaaataaaa aattgctctt
        841 tcaatgcaac cacagaatta agtgataaga aacagaaagt gtatgcactt ttttatagac
        901 ttgatatagt accacttaat gagggtgaaa acaactctag gaagtataga ttaataaatt
        961 gcaatacctc agccataaca caagcctgtc caaaggtctc ttttgaccca attcctatac
       1021 attattgtgc tccagctggt tatgcgattc taaagtgtaa taatgagaca ttcaatggga
       1081 caggaccatg ccgttatgtc agcacagtac aatgtacaca cgggattaag ccagtggtat
       1141 caactcaact actgttaaat ggtagcctag cagaaggaga gataatgatc agatctgaaa
       1201 atctgacaaa caatgccaaa acaataatag tacaccttaa ccaatctgta gaaattaggt
                                                                v3 loop ->
       1261 gtacaagata cgccaataat acaagaaaaa gtgtaagaat aggaccagga caaacattct
       1321 atacaaatga cataatagga gacataagac aagcacattg taacattagt ggagataaat
                                                   <- v3 loop
       1381 ggaacagaac tttacaacag gtaggaaaaa aattagcaga acacttccct aataaaacaa
       1441 taaagtttga accatcctca ggaggggatc tagaaattac aacacatagc tttaattgta
       1501 gaggagaatt tttctattgc aatacatcag gcctgtttaa tagtacatac aatcctaata
       1561 acacaggaag tgagtcaaac aacaacatca cactccaatg cagaataaaa caaattataa
```

```
1621 acatgtggca ggaggtagga caagcaatgt atgcccctcc cattaaagga aacataacat
1681 gtacatcaaa tatcacagga ctactattgc tgcgtgatgg aggaaatgat ccaaaaagaa
1741 ctgaagagca aaataacaca gagagattca gacctggagg aggagatatg agagacaatt
1801 ggagaagtga attatataaa tataaggtgg tagaaattaa accattagga atagcaccca
1861 ctggggcaaa aaggagagtg gtggagagag aaaaaagagc agtgggaata ggagctgtgt
1921 tccttgggtt cttgggagca gcaggaagca ctatgggcgc ggcgtcaata acgctgacgg
1981 tacaggccag acaactgttg tctggtatag tgcaacagca aagtaatttg ctgagagcta
2041 tagaggcgca acagcatatg ttgcaactca cggtctgggg cattaagcag ctccgggcaa
2101 gagtcttggc tatagaaaga tacctagagg atcaacagct cctagggatt tggggctgct
2161 ctggaaaact catctgcacc actgctgtac cttggaactc cagttggagt aatagaactc
2221 aagaagaaat ttgggaaaac ctgacctgga tgcaatggga taaagaaatt agtaattaca
2281 cagacacaat atacaggttg cttgaagtct cgcaaaacca gcaggaaaaa aatgaaaaag
2341 atctattagc attggacagt tggggaagtc tgtggaattg gtttgacata acaaaatggc
2401 tgtggtatat aaaaatattc ataataatag taggaggctt gataggttta agaataattt
2461 ttgttgtgct ctctatagtg aatagagtta ggcagggata ctcacctttg tcgtttcAGa
                                                    3' sj (tat,rev) /\
2521 cccttacccc aaacccgagg ggacccgaca ggctcggaag aatcgaagaa gaaggtggag
2581 agcaagacaa agacagatcc attcgattag tgaacggatt cttagcactt gcctgggacg
2641 acctacggag cctgtgtctc ttcagctacc accgattgag agacttcata ttggtggcag
2701 cgagagcggt ggaacttctg ggacgcagca gtctcaggga actacagaga gggtgggaag
2761 cccttaagta tctgggaaat cttggccagt attggggtct ggagctaaaa aagagtgcta
2821 ttagtctgct tgataccata gcaataacag tagctgaagg aacagatagg attatagaat
2881 tagcacaaag aatttgtaga ggtgtccgca acatacctac aagaataaga cagggctttg
2941 aagcagcttt gctaTAAaAT Ggggggcaag tggtcaaaga gcagaatagt tggatgggct
                      <- env cds end
          nef cds start ->
3001 aatataagaa aaagaataag aagaactgag ccagcagcag agggagtagg agcagcatct
3061 aaagacttag ataaatatgg agcacttaca aacagcaaca cacccaccaa taatgctgat
3121 tgtgcttggc tgcaagcgca agaggaggaa gaggaagtag gctttccagt caaacctcag
3181 gtgcctttaa ggccaatgac tcataaggca gcatttgatc tcagcttc
```

```
LOCUS       HIVUG2661     1465 bp ss-DNA             VRL       27-MAY-1993
DEFINITION  Human immunodeficiency virus type 1, Ugandan isolate UG266,
            gag region.
ACCESSION   L11798
SOURCE      Human immunodeficiency virus type 1 (HIV-1) blood DNA, Ugandan
            isolate UG266.
REFERENCE   1  (bases 1 to 1465)
  AUTHORS   Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T.,
            Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K.,
            Gershy-Damet,M., DeLeys,R. and Burke,D.
  TITLE     Phylogenetic analysis of gag genes from seventy international HIV-1
            isolates provides evidence for multiple genotypes
  JOURNAL   AIDS 7, 769-780 (1993)
COMMENT     Kindly provided prior to publication by Henry M. Jackson Foundation
            Research Laboratory, 1500 East Gude Drive, Rockville, MD  20850.
             Samples were obtained from 15 different countries (Belgium, Burundi,
            Gabon, The Ivory Coast, Kenya, Rwanda, Zaire, Thailand, Somalia, the
            Philippines, Djibouti, Brazil, Uganda, Senegal, and Zaire) on four
            continents.  From this study the authors identified 7 distinct
            genotypes with an average gag intra-genotypic variance of 7% and an
            average inter-genotypic variance of 14%. The env region of this
            isolate has also been sequenced (L22947); it tends to cluster with
            D subtype sequences. This gag sequence, previously published on page
            I-A-218 of the 1993 compendium, groups with A subtype gag sequences.
BASE COUNT      591 a    281 c    318 g    275 t
ORIGIN      gag cds start
        1 ATGggtgcga gagtgtcagt attaagcgag gggaaattag atgcatagga gaaaattcgg
gag start ->
       61 ttaaggccag agggaaagaa aaaatataaa ctgaaacatc tagtgtaggc aagcagggag
      121 ctagaaaaat tcgcacttaa ccctagcctt ttagaaacaa cagaaggatg tcaaagaata
      181 ctagaacaat tacaaccagc tctccagaca ggagcagaag aacttagatc cttatataat
      241 acagtagcag tcctctattg cgtacatcaa aggatagaga taaaagacac caaggaagct
      301 ttagataaaa tagaggaaat gcaaaataag agcaagcaaa agacacagca ggctgcagct
      361 aacacaggaa acagcaacaa ggtcagtcaa aattacccca tagtgcaaaa tacacaaaga
      421 caaatgacat accaggcctt gtcacctagg accttaaatg cataggtaaa agtagtagag
      481 gaaaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc
      541 tcacaagatt taaatatgat gctgaatgta gtagaaggac accaggcagc tatgcaaatg
      601 ctaaaggata ccatcaatga agaagctgca gaataggaca ggttacatcc agtgcaagca
      661 aggcctattc cacctggcca gatgagagaa ccaagaggaa gtgacatagc aggaactact
      721 agtaccgttc aagaacaagt gagatagatg acaagcaacc cacctatccc agtaggagaa
      781 atctatagaa gatagataat cctaggacta aataaaatag taagaatgta tagccctgtt
      841 agcattttag acataagaca agagccaaaa gaacccttta aagaatatgt agataagttc
      901 tttaaaactc tcagagctga gcaagctaca caggatgtaa aaaactagat gacagaaacc
      961 ttgctagtcc aaaatgcgaa tccagattgt aagtccattt taagagcctt aagaccaaag
     1021 gctacattag aagaaatgat gacagcatgc caaagagtaa gaggacccag ccataaagca
     1081 caggttttag ctgaggcaat gagtcaagta caacagacaa gcataatgat gcagagaggc
     1141 aattttaaag gccagaaaag aattaagtgt ttcaactgtg gcaaagaagg acacctagcc
     1201 agaaattgca aggcccctaa gaaaaagggc tgttagaaat gtaagaaaga aggacaccaa
     1261 ataaaagact gcactgaaag acaggctaat tttttaaaga aaatttggcc ttccagcaag
     1321 gggaggccaa ggaactttcc tcagagcaga ccagagccaa cagccccacc agcagagatc
     1381 ttgaggatga aagaagagat gacctcccct ccgaaacaga agcaaaaaga caaggaacag
     1441 actcctttaa tttccctcaa atcac
                              gag ->
```

```
LOCUS       HIVUG266A2   3026 bp ds-DNA ·            VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, UG266 from Uganda, proviral
            DNA encoding env, vpU, and nef genes.
ACCESSION   L22947
SOURCE      Human immunodeficiency virus type 1 (HIV-1), UG266 from Uganda,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3026)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence clusters with D subtype sequences whereas
            the corresponding gag sequence (L11798) clusters with A subtype
            sequences.  See also accession numbers L22939-L22946, L22948-L22957
            and L23064-L23065.
            NCBI gi: 450599
BASE COUNT      1070 a    520 c    731 g    705 t
ORIGIN      169 bp upstream from the beginning of env cds start
          1 atgtaataaa tcctttagaa atctgggcaa tagtagcact gatagtggcg ctaatcttag
         61 caatagttgt gtgggctata gtatccatag agtgtagaaa attaaaaagg caaaggaaaa
        121 tagactggtt gattgataga ataagagaaa gagaagaaga cagtggcaAT Gagagtgaag
                                                  env cds start ->
        181 gggataccga ggaattatca aaacttattg agatggggaa ctataatcct gggaatgata
        241 ataatttgta gtactgcaga caacttgtgg gttactgtct actatggggt acctgtgtgg
        301 aaagatgcag agaccacctt atttggggca tcagatgcta aagcatatga tacagaagtg
        361 cataatgtct gggctacaca tgcctgtgta ccaacagacc ccaacccacg agaaataaaa
        421 ctagaaaatg tcacagaaaa ctttaacatg tggaaaaata acatggtgga gcggatgcat
        481 gaggatataa tcagtttatg ggagcaaagc ctaaaaccat gtgtaaaatt aaccccactc
        541 tgtgtcacct taaactgcag tgaagggagg gttacagata caaatggcac tattggaaat
        601 ggcactattg gggacatgag aaactgctct ttcaatataa ccacagaaat aagagataag
        661 aagaagcaag tatatgcact tttttataaa cttgatgtgg taccaataga tgataataat
        721 agtactaata ccagctatag gttaataaat tgtaatacct cagccattac acagacgtgt
        781 ccaaaggtaa cctttgagcc aattcccatt cattattgtg ccccagctgg atttgcaatt
        841 ctaaaatgta atgataagaa gttcaatggg acgggcccct gcaaaaacgt cagcacagtg
        901 cagtgtacac atggaattag gccagtagta tcaactcaac tgttgttgaa tggcagtcta
        961 gcagaagaag aaatagtaat tagatctgaa aatctcacaa ataatgctaa aatcataata
       1021 gtacagctta atgagtctgt aataattaat tgcacaaggc cctacaacaa tataaaaata
                                    v3 loop ->
       1081 caaaggacac ctataggacg agggcaagca ctctttacaa caagaagaaa aggaataaaa
       1141 ggacaagcac attgtaatat tagtagagaa ggatggaata aaactttaca acaggtagca
                          <- v3 loop
       1201 aaaaaattaa gagaccttat taacaagaca acaataattt ttaaaccatc ctcgggaggg
       1261 gacccagaaa ttacaacaca cagctttaat tgtggagggg aatttttcta ctgcaataca
       1321 tcaggactgt ttaataatag tgtatggagg aatgattatc catcaaatag tacaggagta
       1381 aatgagagcg taatcacact cccatgcaaa ataaaacaaa ttataaacct gtggcaggga
       1441 gtaggaacag caatgtatgc ccctcccatt gaaggactaa tcaaatgttc atcaaatatt
       1501 acaggactat tattgacaag agatggtggt gtcaataata gtcagaatga gaccttcaga
       1561 cctggaggag gagatatgag ggacaattgg agaagtgaat tatacaaata taaagtaata
       1621 agacttgaac cactaggtct agcacctacc agggcaaaga gaagagtggt ggaaagagaa
       1681 aaaagagcaa taggactagg agctgtgttc cttgggttct tgggagcagc aggaagcacg
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1741 atgggcgcag cgtcactgac gctgacggta caggccagac tgttattgtc tggtatagtg
1801 caacagcaaa acaatttgct gatggctata gaggcgcaac agcatctatt gcaactcaca
1861 gtctggggca ttaaacagct ccaggcaaga gtcctggctg tggaaagcta cctaaaggat
1921 caacagctcc taggaatttg gggttgctct ggaaaacaca tttgcaccac tagtgtgccc
1981 tggaactcta gctggagtaa taaatctcta gaagagattt ggaataacat gacctggatg
2041 gagtgggaaa gagaaattga caattacaca gggttaatat acagcttaat tgaagaatcg
2101 caagtccagc aagaaaagaa tgaacaagaa ttattgcaat tggacaaatg ggcaagtttg
2161 tggaattggt ttaacataac acaatggctg tggtatataa aaatattcat aatgatagta
2221 ggaggcttga taggtttaag gatagtcttt gctgtgcttt ctttagtaaa tagagttagg
2281 cagggatatt cacctctgtc gcttcAGacc ctcctcccag ccccgagggg acccgacagg
                3' sj (tat, rev) /\
2341 cccgaaggaa cagaagaaga aggtggagag caaggcagag gtagatccat tcgattagtg
2401 agcggattct tagcacttgc ctgggacgac ctgcggagcc tgtgcctctt cagctaccac
2461 cgcttgagag acttactctt aattgcaacg aggattgtgg aacttctggg acgcaggggg
2521 tgggaagccc tcaaatactg gtggaatctc ctacagtatt ggattcagga actaaagaat
2581 agtgctatta acttgtttaa taccacagca atagcagtag ctgaggggac agatagggct
2641 atagaaatag tacaaagagc tgttagagct attcttaaca tacccacaag aataagacag
2701 ggcttcgaaa gggctttact aTAAaATGgg tggcaaatgg tcaaaaagta gtatagttgg
                              <- env cds end
                    nef cds start ->
2761 atggactgct ataagggaaa gaataagaaa aactgatcca gcagcagaag gggtgggagc
2821 agtatctcgg gacctggaaa aacatggggc aatcacaagt agcaacacag cacagactaa
2881 ccctgactgt gcttgggtag aagcacaaga agaggacggg gaagtgggtt ttccagtcag
2941 acctcaggtt ccgttacgac caatgactta caagggagct ctagatctga gccacttttt
3001 aaaagaaaag gggggactgg aaagcc
               3' LTR ->
```

LOCUS HIVUG2681 1465 bp ss-DNA VRL 27-MAY-1993
DEFINITION Human immunodeficiency virus type 1, Ugandan isolate UG268, gag region.
ACCESSION L11799
SOURCE Human immunodeficiency virus type 1 (HIV-1) blood DNA, Ugandan isolate UG268.
REFERENCE 1 (bases 1 to 1465)
AUTHORS Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T., Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K., Gershy-Damet,M., DeLeys,R. and Burke,D.
TITLE Phylogenetic analysis of gag genes from seventy international HIV-1 isolates provides evidence for multiple genotypes
JOURNAL AIDS 7, 769-780 (1993)
COMMENT Kindly provided prior to publication by Henry M. Jackson Foundation Research Laboratory, 1500 East Gude Drive, Rockville, MD 20850. Samples were obtained from 15 different countries (Belgium, Burundi, Gabon, The Ivory Coast, Kenya, Rwanda, Zaire, Thailand, Somalia, the Philippines, Djibouti, Brazil, Uganda, Senegal, and Zaire) on four continents. From this study the authors identified 7 distinct genotypes with an average gag intra-genotypic variance of 7% and an average inter-genotypic variance of 14%. The env region of this isolate has also been sequenced (L22948). This gag sequence, previously published on page I-A-219 of the 1993 compendium, groups with HIV1 C subtype gag sequences.
BASE COUNT 539 a 288 c 357 g 281 t
ORIGIN gag cds start

```
       1 ATGggtgcga gagcgtcagt attaagaggc ggaaaattag atacctggga aaaaattaag
gag start ->
      61 ttaaggccag ggggaaagaa atgctatatg atgaaacacc tagtctgggc aagcagggag
     121 ctgggaagat ttgcacttaa ctctggcctt ttagaaacat cagaaggctg taaacaaata
     181 atgaaacagc tacaaccagc tcttcagaca gggacagatg aacttagatc attatataac
     241 acagtagcaa ctctctattg tgtacataaa gggatagaag tacgagacac caaggaagcc
     301 ttagacaaga tagaggaaga acaaaacaag attcagcaaa aaacagaaac agctgacaaa
     361 ggaaaggtca gtcaaaatta tcctatagtg cagaatctcc aagggcaaat ggtacaccag
     421 gccctatcac ctagaacttt gaatgcatgg gtaaaagtaa tagaggaaaa ggctttcagc
     481 ccagaggtaa tacccatgtt tacagcatta tcagaaggag ccaccccaca agatttaaac
     541 accatgctaa atacagtggg gggacatcaa gcagccatgc aaatgttaaa agacaccatc
     601 aatgaggagg ctgcagaatg ggataggtta catccagtgc atgcagggcc tgttgcacca
     661 ggccaaatga gagaaccaag gggaagtgac atagcaggaa ctactagtac ccttcaagaa
     721 caaataaatt ggatgacaag taacccacct attccagtgg gagaaatcta taaaagatgg
     781 ataattctgg ggttaaataa aatagtaaga atgtatagcc ctgtcagcat tttggacata
     841 aaacaagggc caaaggaacc ctttagagac tatgtagatc ggttctttaa aaccttaaga
     901 gctgaacaag ctacacaaga tgtaaaaaat tggatgacag acaccttgtt ggtccaaaat
     961 gcgaacccag attgtaagac cattttaaga gcattagggc caggagcttc attagaagaa
    1021 atgatgacag catgtcaggg agtgggagga cctggccaca aagcaagagt gttggctgag
    1081 gcaatgagcc aagcaaacaa tataaacata atgatgcaga gaagcaattt taagggccct
    1141 aagagaatta ttaaatgttt caattgtggc aaggaagggc acctagccag aaattgcagg
    1201 gcccctagga aaaaaggctg ttggaaatgt ggaagggaag gacaccaaat gaaagactgt
    1261 actgagagac aggccaattt tttagggaag atttggcctc ccaacaaggg gaggccaggg
    1321 aatttccttc agagcagacc agaaccaaca gccccaccag cagagccaac agccccaccg
    1381 gcagagagct tcaggttcga ggggacaact ccccctccga agcaggagcc gaaagacagg
    1441 gaacccttaa tttccctcaa atcac
                              gag ->
```

HIVUG268A2

```
LOCUS       HIVUG268A2   3228 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, UG268 from Uganda,
            proviral DNA encoding env, vpU, rev, and nef genes.
ACCESSION   L22948
SOURCE      Human immunodeficiency virus type 1 (HIV-1), UG268 from Uganda,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3228)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence and the corresponding gag sequence (L11799)
            cluster with C subtype sequences.  See also accession numbers L22939-
            L22947, L22949-L22957 and L23064-L23065.
            NCBI gi: 437352
BASE COUNT      1153 a    546 c    760 g    769 t
ORIGIN      100 bp upstream from the beginning of rev cds start
          1 caggaagtca gcctaaaact ccttgtacta agtgttttgg taaaaaatgt agttatcatt
         61 gtcaagtttg ctttctgaac aaaggcttag gcatctcctA TGgcaggaag aagcggagac
                                          rev cds start ->
        121 agcgacgaaa cgctcctcca agcagtgagg atcatcaaaa tcttatatca aagcaGTaag
                                                                  5' sj /\
        181 tattacatgg tagatgtaAT Gttaaattta ctagcaggag tagactatag aataggaata
                    vpU start ->
        241 ggagcattgc taatagcact aatcatagca atagttgtgt ggatcatagt atatatagaa
        301 tataggaaac tgttaaaaca aagaagaatg gacaggttaa ttaaaagaat tagggaaaga
        361 gcagaagata gtggcaATGa gagtgatggg gatacagagg aattgtcaac aatggtggat
               env cds start ->
        421 atggggaatc ttaggctttt ggatatTAAt gatttgtaat gtgatgggga acttgtgggt
                                          <- vpU cds end
        481 cacagtctat tatggggtac ctgtgtggaa agaagcaaca actactctat tttgtgcatc
        541 agatgctaaa gcatatgaga cagaagtgca taatgtctgg gctacacatg cctgtgtccc
        601 cacagacccc aacccacaag aaatagttct ggaaaatgta acagaaagtt ttaacatgtg
        661 gaaaaatgac atggtggatc agatgcatca ggatgtaatc agtctatggg atcaaagcct
        721 aaagccatgt gtaaagttga ccccactctg tgttacttta aattgtacaa atgttaatgt
        781 taatattacc aataatgcta atgctaccaa tagcccctac gaaaatggga aactcatgga
        841 acagggagaa ataaaaaatt gctctttcaa tgtaaccaca gaaataagag ataagaaaca
        901 gacagcgcat gcacttttt ataaacttga tgtagtatca cttgaaggga atagtaacac
        961 ttacagatta ataaattgta atacctcagc cataacgcaa gcctgtccaa aggtcacttt
       1021 ggacccaatt cctatacatt attgtgctcc agctggttat gcgattctaa agtgtaataa
       1081 taaaacattt aatggaacag gaccatgtaa taatgtcagc acagtacaat gtacacatgg
       1141 aattaaacca gtgatatcaa ctcaactatt gttaaatggt agtatagcag aagaagaaat
       1201 aataattaga tctgaaaatc tgacaaataa tgccaaaata ataatagtac agcttaacaa
       1261 atctgtagaa attaattgtg cgagacccaa caataataca agagaaagta taaggatagg
                      v3 loop ->
       1321 accaggacaa acattctatg caacaggaga cataatagga gatataagac aagcatactg
       1381 taacattagt agaaatgaat ggaatataac tttacaatgg gtaagagaaa aattaaaaag
          <- v3 loop
       1441 gcacttccct aataaaacaa taaactttac tcaaccctca ggaggggact tagaaattac
       1501 aacacatagc tttaattgta gaggagaatt tttctattgc aatacatcaa gcctgtttaa
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```
1561 tagtagtgat aataataata gtaccatcat cacactccca tgcagaataa aacaaattat
1621 aaacatgtgg caggggggtag gacgagcaat gtatgcccct cccattaaag gaaaaataac
1681 atgtagatca aatatcacag gactactact gacacgtgat ggaggggaga caagtgagac
1741 aaatagcaca gagacattca gacctggagg aggagatatg agggacaatt ggagaagtga
1801 attatataaa tataaagtgg tagaagttaa gccactagga gtagcaccca ctaaggcaaa
1861 aaggagagtg gtggagagag aaaaaagagc agtgggaata ggagctgtgt tccttgggtt
1921 cttgggagcc gcaggaagca ctatgggcgc agcatcaata acgctgacgg tacaggccag
1981 acaattattg tctggtatag tgcaacagca aaacaatttg ctgagggcta tagaggcgca
2041 acagcatatg ttgcaactca cggtctgggg cattaagcag ctccagacaa gagtcctggc
2101 tatagaaaga tacctacagg atcaacagct cctagggatt tggggctgct ctggaaaact
2161 catctgcacc actgctgtgc cttggaactc tagttggagt aataaatctc taggggatat
2221 ttgggataac atgacctgga tgcagtggga tagagaaatt agtaattata caggaacaat
2281 atacaggttg cttgaagact cacaaaacca gcaggagaaa aatgaaaaag atttactagc
2341 attggacaaa tggcaaaatc tgtggagttg gtttgacata acaaaatggc tgtggtatat
2401 aaaaatattc ataatgatag taggaggctt aataggttta agaataattt ttgctgtgct
2461 ctctatagtg aatagagtta ggaagggata ctcaccatta tcgtttcAGa cccttacccc
                                        3' sj (tat,rev) /\
2521 aaccccgagg ggacccgaca ggcccggaga aatcgaagaa gaaggtggag agcaagacag
2581 agacagatcc gtgagattaa tcagcggatt cttagcactt gcctgggacg atctgcggag
2641 cctgtgcctc ttcagctacc gccgcttgag agacttacta ttgattgcag cgagagcagt
2701 ggaacttctg ggacgcagca gtctcagggg actacagagg gggtgggaag ccctTAAgta
                                                                <- rev
2761 tctgggaagc cttgtgcagt attggggtca agaactaaaa aagagtgcta ttagtttgct
2821 tgataccata gcaatagcag tatctgaagg aacagataga attatagaag tgggacaagg
2881 aattgggaga gctatcctcc acatacctag aagaataaga caaggctttg aagcagcttt
2941 gcaaTAAaAT Ggggagcaag tggtcaacat gtagtccagt gggatggcct gatgtaagag
          <- env cds end
nef cds start ->
3001 aaagaataaa acgcactgct ccagcagcag agggagtagg agcagcgtct caggacttag
3061 acaaacatgg ggcactgaca accagcaaca cacccgccaa taatgctgat tgtgcctggc
3121 tggaggcgca agaggatgag gaggtaggct ttccagtcaa acctcaggta cctttaagac
3181 caataactta taaggcagca ttcgatctca gcttcttttt aaaagaaa
```

HIVUG269A

```
LOCUS       HIVUG269A   3132 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, UG269 from Uganda,
            proviral DNA encoding env, vpU, and nef genes.
ACCESSION   L22949
SOURCE      Human immunodeficiency virus type 1 (HIV-1), UG269  from Uganda,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3132)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993 compendium.
            This sequence clusters with D subtype env sequences. See also
            accession numbers L22939-L22948, L22950-L22957 and L23064-L23065.
COMMENT      NCBI gi: 437353
BASE COUNT      1090 a    547 c    764 g    731 t
ORIGIN      16 bp upstream from the beginning of rev cds start
          1 gcttaggcat ttcctATGgc aggaagaagc ggagacagcg acgaagatct cctaaaggcg
              rev cds start ->
         61 gtcaggctca tcaagttcct ataccaaagc aGTaagtagt acATGtatgc aacctttagt
                                      5' sj /\      vpU  ->
        121 gatattagca atagtagcat tagtagtagt gctaatacta gcaatagttg tgtggactat
        181 agtagtcata gagtgtataa gattaccaaa gcaaagaaaa atagactggt taattgatag
        241 aataagagaa agagcagaag atagtggccA TGagagtgag ggagatagag aggaattatc
                           env cds start ->
        301 agcacttgtg gagatggggc acgatgctcc ttgggatgtt gatgatatgt agggttacag
        361 gagagttgtg ggtcacagtt tattatgggg tacctgtgtg gaaagaagca accactactc
        421 tattctgtgc atcagatgct aaatcatata aaaaaggggc acataatatc tgggctacac
        481 atgcctgtgt accaacagac cccaacccac gagaaTAAaa ttagaaaatg tcaccgaaaa
                                                  <- env premature stop
        541 ctttaacatg tggaaaaatA atatggtgga gcagatgcat gaggatataa tcagtttatg
        601 ggatgaaagc ctaaaaccat gtgtaaaatt aaccccactc tgtgtcactt taaattgcac
        661 tgaagccaaa ttcaatgtca ctagagccac taatggaaag aacactgtta gaaatgccac
        721 taaggggggc ctagaaatga aagactgtta tttcaatgta accacagaaa taagagataa
        781 gaagaagcaa gtacgtgcac ttttttataa acttgatgta gtacaaatga ataatagtga
        841 gagtattaac accagctata gattaataaa ttgtaattcc tcagccatta cacaggcgtg
        901 tcctaagata acctttgagc caattcccat acattattgt gccccagctg gatttgcaat
        961 tctaaaatgt accgataaga agttcaatgg gaagggtcca tgcaaaaatg tcagcacagt
       1021 acagtgtaca catgggatta agccagtagt gtcaactcaa ctgttgttga atggcagtct
       1081 agcagaagaa gagataataa ttagatctga aaatctcaca aataatgcta aaatcataat
       1141 agtacagctt aatgcgtctg taacaattac ttgcacaagg ccctacacca agacaagaca
       1201 cagggcacaa gggcgagcat ggtggacaac aggtataaca ggagatataa gacaagcata
       1261 ttgtaacatt agtaaagcaa aatggcagga aactttacaa caggtagcta aaaaattagg
       1321 agaccttctt aacaagacac aaataatttt tgaaccatcc tcgggagggg acccagaagt
       1381 tacaaaacac agctttaatt gtggagggga atttttctac tgcgatacat caagactgtt
       1441 taatgatagt tataatacat cagcattaaa tagtacacag ggaaatgaga gtgaaaacat
       1501 cacactccca tgcagaataa aacaaattat aaacatgtgg caggaagtag gaaaagcaat
       1561 gtatgcccct cccattgaag ggataatcag atgttcatca aatattacag gactattgtt
       1621 gacaagagat ggtggtataa ctaacaatag taatgagacc ttcagacctg gaggaggaaa
       1681 tatgagagac aattggagaa gtgaattata caaatataaa gtagtaagaa ttgaaccact
       1741 aggtctagca cccaccacgg caaagagaag agtggtggaa agagaaaaaa gagcaatagg
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1801 actgggagct ctgttccttg ggttcttggg agcagcagga agcacaatgg gcgcagcgtc
1861 actgacgctg acggtacagg ccagacaagt attgtccggc atagtgcaac agcaaaacaa
1921 tttgctgagg gctatagagg cgcaacaaca tctgttgcaa ctcacagtct ggggcattaa
1981 acagctccag gcaagagtcc tggctgtgga aagctaccta ggggatcagc agctcctggg
2041 aatttggggt tgctctggaa gacacatttg caccactaat gtgccctgga actctagctg
2101 gagtaataga tctctagagg agatttggca taacatgacc tggatggagt gggaaagaga
2161 aattgacaat tacacaggtt taatatacag cttgattgaa gaatcgcaaa cccagcaaga
2221 aaaaaatgaa caagaactat tgcaattgga caaatgggca agtttgtgga attggtttag
2281 cataacaaac tggctgtggt atataagaat atctataatg atagtaggag gcttgatagg
2341 tttaaggata gtttttgctg tgttttcttt agtaaataga gttaggcagg gatattcacc
2401 tctctcgttt cAGaccctcc tcccagcccc gaggggaccc gacaggcccg aaggaataga
  3' sj (tat,rev) /\
2461 agaagaaggt ggagagcaag gcagaggcag atccattcga ttagtgagcg gattctcagc
2521 acttatctgg gacgacctga ggaacctgtg cctcttcagc taccaccgct tgagagactt
2581 aatcttaatt gcaacgagaa ttgtggaact tctgggacgc agggggtggg aagccatcaa
2641 atatctgtgg aatctcctaa aatattggat tcaggaacta aagaaTAGtg ctattagctt
                                                    <- rev cds end
2701 gtttgatacc atagcaatag tagtagctga ggggacagat agggttatag aagtaataca
2761 aagagctgtt agagctgttc ttcacatacc cagacgaata agacagggct ttgaaagggc
2821 tttactaTAA aATGggtggc aaatggtcca aaaagtagta tagttggatg gcctgctata
           <- env cds end
   nef cds start ->
2881 agagacagaa taagaagaac tgatccagca gcagaggggt gggagctgca tctagggact
2941 tggaaaaaca tggggcaatc acaagtagca atacaccaca cacaaattct gactgtgcct
3001 ggctagaagc acaagaagag gacggggacg tgggttttcc agtcagacct caggtaccgt
3061 taagaccaat gacttacaag gcggctgtag atctgagcca ctttttaaaa gaaaaggggg
3121 gactggaaag cc
3' LTR ->
```

HIVUG273A

```
LOCUS       HIVUG273A   3337 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, UG273 from Uganda, proviral
            DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L22957
SOURCE      Human immunodeficiency virus type 1 (HIV-1), UG273 from Uganda,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3337)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence clusters with A subtype env sequences. See
            also accession numbers L22939-L22956 and L23064-L23065.
            NCBI gi: 437354
BASE COUNT      1171 a    598 c    775 g    793 t
ORIGIN      209 bp upstream from the beginning of rev cds start
          1 tgtttattca tttcagaatt gggtgccaac acagcagaat aggcattatt cgagggagaa
         61 gagtcagggA TGgatccggt agatcctaac ctagagccct ggaatcatcc gggaagtaag
        tat cds start ->
        121 cctacaactc cttgtagcaa gtgttactgt aaagtgtgtt gctatcattg cccagtttgc
        181 tttctgaaaa aaggcttagg catctcctAT Ggcaggaaga agcggagtca gcgacgagga
                            rev cds start ->
        241 actcctcaaa gcaataagga tcatcaaaat cctataccaa agcaGTaagt attagtaatt
                                                    5' sj /\
        301 aatatatgta ATGcttcctt taaatatctg tgcaatagta ggactgatag tagcactaat
         vpU cds start ->
        361 cttagcaata gttgtgtgga ctatagtagg tatagactat aagaaattgt taaagcaaag
        421 aaaaatagac aggttaattg agagaataag agaaagagca gaagacagtg ccaATGagag
                                                    env cds start ->
        481 tgaaggggat acagaggaat tggcagcact tgttgagatg gggaactata atcttgggtt
        541 tgataacaat ctgTAGtact gcaaaaaact tgtgggttac tgtatactat ggggtacctg
                           <- vpU cds end
        601 tgtggagaga cgcagagacc accctatttt gcgcatcaga tgctaaagca tatgagacag
        661 aaatgcataa tgtctgggct acacatgcct gtgtacccac agaccctaac ccacaagaaa
        721 tacgtttgga aaatgtgaca gaagagttta acatatggaa aaataacatg gtagagcaga
        781 tgcatacaga tataatcagt ctatgggacc aaagcctaaa gccatgtgta aagttaaccc
        841 ctctctgcgt tactttaaat tgtaccaatg ccaacctcac caatgccaat aaaaatgcca
        901 aggtcaacag cgccacgaat ggcaccatcc agagcatgga aagagaaata aaaaactgct
        961 ctttcaatat gaccacagaa ctaagggata agacacggag agtatattca ctttttata
       1021 aacttgatgt agtacaaatt aaaaatagta gtgagtatag attaataaat tgtaatacct
       1081 cagccattac acaggcttgt ccaaaggtat cctttgagcc aattcccata cattattgtg
       1141 ccccagctgg ttttgcgatc ctaaaatgta atgataagga gttcaatgga acagggctat
       1201 gcaagaatgt cagctcagta caatgcacac atggaatcag gccagtagta tcaactcaac
       1261 tgctgttaaa tggcagtcta gcagaaacag aggtaaaaat taaatctgaa aatatctcag
       1321 acaatgctaa aaccctaata gtacaactta ccacgcctgt aaaaattaat tgtactagac
                                                      v3 loop ->
       1381 ctggcaacaa tacaagaaca agtgtacgta taggaccagg acaagcattc tatgcaacag
       1441 gtgatataat aggagatata agacaagcac attgtaatgt cagtagatca gaatggaagg
                                          <- v3 loop
       1501 aaactttgca aaaggtagtc aaacaattaa gaacacactg gaacaaaaca ataatcttta
```

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1561 caaactcctc aggaggggat ttagaaatta caacacatag ttttaattgt ggaggagaat
1621 ttttctattg taatacagca ggcctgttta atagtacttg gaataaaaat gacagcataa
1681 agtcaaatga cacaaagtca aatgacatta taactcttca atgcagaata aagcaaatta
1741 taaatatgtg gcagagagta ggacgagcaa tgtatgcccc tcccatcaaa ggagtaataa
1801 ggtgtgaatc aaacattaca ggactactat taacaagaga tggtggaaat gggagcaata
1861 caaatgaaac cttcagacca ggaggaggag atatgaggga caattggaga aatgaattat
1921 ataagtataa agtagtacaa attgaaccat taggagtagc acctacccca gcaaagagaa
1981 gagtggtgca gagagaaaaa agagcagttg gactaggagc tgtattcatt gggttcttag
2041 gagcagcagg aagcactatg ggcgcggcgt caataacgct gacggtacag gccagacaat
2101 tattgtctgg catagtgcaa cagcaaagca atttgctgag agctatagag gctcaacagc
2161 atctgttgaa actcacagtc tggggcatta aacaactcca ggcaagactc ctggctgtgg
2221 aaagatacct aagggatcaa cagctcctag gaatttgggg ctgctctgga aaactcatct
2281 gcaccactac tgtgccctgg aactctagtt ggagtaataa atctcaaagt gagatatggg
2341 ataacatgac ctggctgcaa tgggataaag aaattagtaa ttacacaaac ataatatatg
2401 atctaattga agaagcgcag aaccagcagg aaaagaatga acaagactta ttggcattgg
2461 acaagtgggc aagtctgtgg agttggtttg acatatcaaa ttggctgtgg tatataagac
2521 tatttataat gatagtagga ggcttaatag gattaagaat agttcttgct gtgttttctg
2581 taataaatag agttaggaag ggatactcac ctgtgtcatt tcAGacccat accccaaacc
                                    3' sj (tat,rev) /\
2641 caagggatct cgacaggccc gaaagaatcg cagaagaagg tggagagcaa gacagagaca
2701 gatcgattcg cttagtcagc ggattcttag cacttgcctg ggacgacctg cggagcctgt
2761 gcctcttcag ctaccaccgc ttgagagact tcatcttgat tgtcgcgagg actgtgaaac
2821 ttctgggaca caggggtgg gaaggaatca agtatctgtg gaacctcctg ttgttttggg
2881 gtcgggaact caaaatTAGt gctattaatt tgcttgatac catagcaata gcagtagctg
                      <- rev cds end
2941 gctggacaga tagagttata gaaataggac aaagaattgg tagggctttt cttaacatac
3001 ctagaagaat caggcagggc ttcgaaagag ctttactaTA AcATGggtag caagtggtca
                                                  <- env cds end
                                    nef cds start ->
3061 aaaagttggc ctcaggttag ggaaagaatg agacgagctc ctccagcagg acaagctcct
3121 ccagcagcaa aaggagtagg accagtatct caagatttag aaaaacatgg agcagtcaca
3181 agcagtaata taaatcaccc gagttgcacc tggctgcaag cgcaagaaga agatgatgag
3241 gtaggctttc cagtcaggcc acaagtacct ctaagaccaa tgactttcaa agcagctttt
3301 gatctcagcc acttttaaa agaaaagggg ggactgg
                                    3' LTR ->
```

```
LOCUS       HIVUG2741     1474 bp ss-DNA             VRL       27-MAY-1993
DEFINITION  Human immunodeficiency virus type 1, Ugandan isolate UG274,
            gag region.
ACCESSION   L11801
SOURCE      Human immunodeficiency virus type 1 (HIV-1) blood DNA, Ugandan
            isolate UG274.
REFERENCE   1  (bases 1 to 1474)
  AUTHORS   Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T.,
            Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K.,
            Gershy-Damet,M., DeLeys,R. and Burke,D.
  TITLE     Phylogenetic analysis of gag genes from seventy international HIV-1
            isolates provides evidence for multiple genotypes
  JOURNAL   AIDS 7, 769-780 (1993)
COMMENT     Kindly provided prior to publication by Henry M. Jackson Foundation
            Research Laboratory, 1500 East Gude Drive, Rockville, MD  20850.
             Samples were obtained from 15 different countries
            (Belgium, Burundi, Gabon, The Ivory Coast, Kenya, Rwanda, Zaire,
            Thailand, Somalia, the Philippines, Djibouti, Brazil, Uganda,
            Senegal, and Zaire) on four continents.  The authors identified 7
            distinct genotypes with an average gag intra-genotypic variance of
            7% and an average inter-genotypic variance of 14%. The env region
            of this isolate has also been sequenced (L22950). This gag sequence,
            previously published on page I-A-221 of the 1993 compendium, groups
            with HIV1 D subtype gag sequences.
BASE COUNT      555 a    276 c    361 g    282 t
ORIGIN      gag cds start
        1 ATGggtgcga gagcgtcagt attaagcggg ggaaaattag atgaatggga aaaaattcgg
gag start ->
       61 ttacggccag ggggaaacaa aaaatataaa ctaaaacata tagtatgggc aagcagggag
      121 ctggaacgat ttgcaattaa tcctggcctt ttagaaacat cagaaggctg taaacaaata
      181 atgggacagc tacaaccagc tcttaagaca ggatcagagg aaatcaaatc attatttaat
      241 acagtagcaa ccctctattg tgtacatgaa aggataaagg taacagacac caaggaagct
      301 ttagacaaga tagaggaaga acaaaccaaa agtaagaaaa aggcacagca agcaacagct
      361 gacacaagaa acagcagcca ggtcagccaa aattatccta tagtgcaaaa cctacagggg
      421 caaatggtac accaggccat atcacctaga actttgaatg catgggtaaa agtaatagag
      481 gagaaggctt ttagcccaga agtaataccc atgtttacag cattatcaga aggagccacc
      541 ccacaggatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg
      601 ttaaaagaaa ccatcaatga ggaagctgca gaatgggata gggtacatcc agtgcatgca
      661 ggacctattg caccaggaca aatgagagaa ccaaggggaa gtgatatagc cggaactact
      721 agtacccttc aggaacaaat aggatggatg acaagcaatc cgcctatccc agtaggagaa
      781 atctataaaa gatggataat cctaggatta aataaaatag taagaatgta tagccctgtc
      841 agtatattgg acataagaca aggaccaaag gaacccttta gagactatgt agatcggttc
      901 tataaaactc taagggccga gcaagcttca caggatgtaa aaaattggat gactgaaacc
      961 ttgttggtcc aaaatgcgaa cccagattgt agaactatct taaaagcatt gggaccaggg
     1021 gctacattag aagaaatgat gacagcatgt cagggagtgg gaggacccag tcataaagca
     1081 agagtcttgg ctgaggcaat gagccaagcc acaaatgcaa atactgctat aatgatgcag
     1141 agaggtaatt ttaagggccc aaggaaaatc attaagtgtt tcaactgtgg caaagaaggg
     1201 cacatagcaa aaaattgtag ggctcctagg aaaaagggct gttggaaatg tggaaaggaa
     1261 ggacaccaaa tgaaagagtg cactgaaaga caggctaatt ttttagggaa aatttggcct
     1321 tcccacaagg ggaggccagg gaacttcctt cagagcagac tggagccaac agccccacca
     1381 gcagagagct tcgggtttgg ggagaagata acaccctctc agaaacagga gcagaaagac
     1441 aaggagccat gtcctttagc ttccctcaaa tcac
                                          gag ->
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LOCUS       HIVUG274A2   3288 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, UG274 from Uganda, proviral
            DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L22950
SOURCE      Human immunodeficiency virus type 1 (HIV-1), UG274 from Uganda,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3288)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence and the corresponding gag sequence (L11801)
            cluster with  D subtype sequences.  See also accession numbers
            L22939-L22949, L22951-L22957 and L23064-L23065.
            NCBI gi: 437355
BASE COUNT      1164 a    566 c    794 g    764 t
ORIGIN      144 bp upstream from the beginning of rev cds start
          1 ggcttccgtc tagatagatc ctagactaga gccctggaac catccaggaa gtcagcctag
         61 cactccttgt aacaaatgct attgtaaaaa gtgctgctat cattgccaat tgtgcttcat
        121 aacgaaaggc ttaggcatct cctATGgcag gaagaagcgg agacagcgac gcagacctcc
                    rev cds start ->
        181 tcaaagcagt caagctcatc aagatcctat accaaagcaG Taagtagtac atgtaATGaa
                                              5' sj /\       vpU start ->
        241 acctttagtg atattagcaa tagtagcatt agtagtagcg ctaataatag caatagttgt
        301 gtggattata gtattcatag agtgtagaag attaaaaagg caaagaaaaa tagactggtt
        361 aattgataga ataagtgaaa gagcagaaga tagtggcaAT Gagagtgagg gagatagaga
                                        env cds start ->
        421 ggaattatca gcacttgtgg atatggggca ccatgctcct tggaatgttg atgacataTA
        481 Gtgttgcaga acagttgtgg gtcacagtgt attatggggt acctgtgtgg aaagaagcaa
          <- vpU end
        541 ccactactct attttgtgca tcagacgcta aatcatatat agcagaggca cataatatct
        601 gggctacaca tgcctgtgta cccacagacc ccgacccacg agaaataaga ctagaaaatg
        661 tcacagaaaa ctttgacatg tggaaaaata acatggtgga gcaaatgcat gaggatataa
        721 tcagtttatg ggatcaaagc ctaaaaccat gtgtaaaatt aaccccactc tgtgtcactt
        781 taaactgcac tgaatggaag aataccactg aacaggagaa gaataccgct gtaccgggga
        841 gtacaacatc tgacacagac atgagaaact gctctttcaa tataaccaca gagttaagag
        901 ataagaagga gcaagtatat gcacttttTt ataaacttga tgtggtacaa atagatgata
        961 ataatagtac taatagtact aactatagat tagtaaattg tactacctca gccattacac
       1021 aagcgtgtcc aaaggtaacc tttgagccaa ttcccataca ttattgtgcc ccagctggat
       1081 atgcgattct aaaatgtaat gataagaagt tcaatgggac gggtccatgc caaaacgtca
       1141 gcacagtaca gtgtacacat gggatcaggc cagtagtgtc aactcaactg ttgttgaatg
       1201 gcagtctagc agaagaagag ataataatta gatctgaaaa tctaacaaat aatgctaaaa
       1261 tcataatagt acagcttaat gagtctgtaa cgattgattg cgcaaggccc tacgaaaata
                                          v3 loop ->
       1321 taagacaaag gacacccata ggaacagggc aagcactcta tacaacacaa ggaagaaaaa
       1381 agataggaaa gataggacaa gcacattgta atgttagtaa agcaggatgg gaaaaaactt
                                      <- v3 loop
       1441 tacaacaggt agctaaaaat taaaagacct ttttaaggca gataatataa cttttaaacc
       1501 atcctcagga ggggacccag aaattacaac acacagcttt aattgtggag gggaattttt
       1561 ctactgcaat acatcaagac tatttaataa tagtggatgg gaaaattata atatatcaaa
```

```
1621 tagtacaggg ggaaatgaga caatcagact ccaatgcaga ataaaacaaa ttataaacat
1681 gtggcaggaa gtaggaaaag caatgtatgc ccctcccatt ataggacaaa tcaaatgttc
1741 atcaaatatc acaggactat tgttaacaag agatggtggt gtaaataata gtagtaatga
1801 gactagcagt aaaaatgaga tcttcagacc tggaggagga gatatgagag acaattggag
1861 aagtgaatta tacaaatata aagtagtaag aattgaacca ctaggtcggg cacccaccag
1921 ggcaaaaagg agagtggtgg aaagagaaaa aagagcaata ggactgggag ctttgttcct
1981 tgggttcttg ggaacagcag gaagcacgat gggcgcagcg tcaatgacgc tgacggtaca
2041 ggccagacag gtattgtctg gtatagtgca acagcaaaac aatttgctga gggctataaa
2101 ggcgcaacag catctgttgc aactcacagt ctggggcatt aaacagctcc aggcaagaat
2161 cctggctgtg gaaagatacc taaaggatca acagctccta ggaatatggg gttgctctgg
2221 aaaacacatt tgcaccacta ctgtgccctg gaactctagc tggagtaata gatctctaga
2281 ggagatttgg aataacatga cctggatgga gtgggaaaga gaaattgaca attacacagg
2341 gttaatatac accttaattg aagaatcgca aaaccagcaa gaaaagaatg aacaagaact
2401 attgcaattg gataaatggg caagtgtgtg gaattggttt agcataacaa aatggctgtg
2461 gtatataaga atattcataa tgatagtagg aggcttgata ggtttaagaa tagtttttgc
2521 tgtgctttct ttagtaaata gagttaggca gggatattca cctctgtcat ttcAGaccct
                                                  3' sj (tat,rev) /\
2581 cctcccagcc ccgagggaac ccgacaggcc cgaagaaata gaagaagaag gtggagagca
2641 aggcagaggc agatccattc gattggtgaa cggattctca gcacttatct gggacgatct
2701 gaggaacctg tgcctcttca gctaccgccg cttgagagac ttactcttaa ttgcagcgag
2761 gattgtggaa atcctgggac gcaggggtg gaaagccatc aaatatctgt ggaatctcct
2821 gcagtattgg attcaggaac TAAagaatag tgctattagc ttgtttgata ccacagcaat
                          <- rev cds end
2881 agcagtagct gaagggacag ataggattat agagatagta caaagagctg ttagagctgt
2941 tcttaacata cccacacgaa taagacaggg cttggaaagg gctttgctaT AAaATGggtg
                                                              <- env cds
                                                   nef cds start ->
3001 gcaaatggtc aaaaagtagt atagttggat ggcctgctat aagggaaaga atgagaagaa
3061 ctgctccagc agcagaaggg gtgggatcag tatctcggga tctggaaaaa catggggcaa
3121 tcacaagtag taatacagcc catactaatc ctgattgtgc ctgggtagaa gcacaagaag
3181 aggaagagga agtgggtttt tcagtcagac cccaggtacc gttaagacca atgacttaca
3241 agggggctgt agatctgagc cacttttaa aagaaaaggg gggactgg
                                              3' LTR ->
```

```
LOCUS       HIVUG275A   3311 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, UG275 from Uganda, proviral
            DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L22951
SOURCE      Human immunodeficiency virus type 1 (HIV-1), UG275  from Uganda,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3311)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence clusters with A subtype env sequences. See
            also accession numbers L22939-L22950, L22952-L22957 and L23064-L23065.
            NCBI gi: 437356
BASE COUNT      1152 a    579 c    789 g    791 t
ORIGIN      209 bp upstream from the beginning of rev cds start
          1 tgtttattca tttcagaatt gggtgcacac atagcagaat aggcattatt cgaaggagaa
         61 gagtcagggA TGgatccggt agatcctaac ctagagccct ggaaccatcc gggaagtcag
        tat cds start ->
        121 cctacaactc cttgtaacaa gtgttactgt aaaaagtgtt gctatcattg tacagtttgc
        181 tttctgaaca aaggcttagg catctcctAT Ggcaggaaga agcggaagca gcgacgaaga
                          rev cds start ->
        241 actcctcaat gcaataagga tcatcaaaat cctataccaa agcaGTaagt attagtaatt
                                                    5' sj /\
        301 agtatATGta atgtctcctt tgcctccttt gcatatctgt gcaatagtag gactggtagt
        vpU start ->
        361 ggcactaatc ctagcaaTAG ttgtgtggac tatagtaggt atagaatata agagattgct
                             <- vpU end
        421 aaagcaaagg aaaatagaca ggttaattaa gagaataagt gaaagagcag aagacagtgg
        481 caATGaaagc gatggggaca cagatgaatt gtcaaaactg gtggagatgg ggaactatga
  env cds start ->
        541 tcttggggat gctaataatt tgtagtactg cagaagactt gtgggttact gtctactatg
        601 gggtacctgt atggagagac gcagagacca ccttattttg tgcatcagat gcgaaagcat
        661 atgatacaga aatgcataat gtctgggcta cacatgcctg tgtacctaca gaccccaacc
        721 cacaagaaat aaatttggga aatgtgacag aaaaatttaa catgtggaaa aataacatgg
        781 tagagcagat gcatgaagat ataatcagtc tatgggatca aagcctaaag ccatgtgtaa
        841 agctaacccc tctctgcgtt actttaaatt gtagtgatgt caataatgtc actgtcacca
        901 atcatagtat tagcagtgac atgaaaggag aaataaaaaa ctgctctttc aatatgacca
        961 cagaattaag ggataagcaa cagaaaatac atccactttt ttatagactg gatgtagtac
       1021 caattaatgg cagcaacaac aggcagtata gattaataaa ttgtaatact tcagccatta
       1081 cacaggcttg tccaaaagta tcctttgagc caattcccat acattattgc gccccagctg
       1141 gttttgcgat tctaaagtgt aatgatcagg agttcaatgg aacagggata tgtaataatg
       1201 tcagcacagt acaatgcaca catggaatca agccagtagt atcaactcag ctgctgttaa
       1261 atggcagttt agcagaagga aaggtaaaga ttagatctga aaatatcaca aacaatgcca
       1321 aaaatatact ggtataactt accacgcctg taacaattaa ttgtaccaga cctaacaaca
                                                  v3 loop ->
       1381 atacaagaac aagtgtacgt ataggaccag gacaatcatt ctatgcaaca ggtgacataa
       1441 taggggatat aaaacaagca cattgtaata tcagtagagc agaatggaat gaaactttac
                                     <- v3 loop
       1501 aaaaggtagt cagccaatta agaacacact ttggcaacaa aacaataatc tttggtaact
```

```
1561 cctcaggagg ggatatagaa ataacaacac atagttttaa ttgtggaaga gaatttttct
1621 attgtgacac atcaggcctg tttaatagca cttggaatgg caataccagc aagcaggagt
1681 caagtagcac agagtcaaat ggcaatataa ctctccaatg cagaataaag caaattataa
1741 atatgtggca gagagcagga aaagcaatat atgcccctcc tatcaaagga gtaataaggt
1801 gtgtatcaaa cattacagga ctaatattaa caagagatgg tgggggtaat aacagtgaaa
1861 atgaaacctt cagacctgga ggaagagata tgagggacaa ttggagaagt gaattatata
1921 agtataaagt agtaaaaatt gaaccactag gagtagcacc caccagggca aggaggagag
1981 tggtggagag agaaaaaaga gcagttggag taggagctgt cttccttggg ttcttaggag
2041 cagcaggaag cactatgggc gcggcgtcaa taacgctgac ggtacaggcc agacaattat
2101 tgtctggcat agtgcaacag caaagcaatt tgctgaaggc tatagaggct caacagcatc
2161 tgttgaaact cacggtctgg ggcattaaac agctccaggc aagagtcctg gctgtggaaa
2221 gatacctaag ggatcaacag ctcctaggaa tttggggctg ctctggaaaa ctcatctgca
2281 ccactaatgt gccctggaac tctagttgga gtaataaatc ccagagtgat atatgggaca
2341 acatgacctg gctgcaatgg gataaggaaa taaacaatta cacagagcta atatataggc
2401 tacttgaaga atcgcagaac cagcaggaaa agaatgaaca agacttattg gcattggaca
2461 aatgggcaaa tctgtggaat tggtttggca tatcaaactg gctgtggtat ataagactat
2521 ttataatgat agtaggaggc ttaataggat taagaatagt ttttgctgtg ctttctgtaa
2581 taaatagagt taggcaggga tactcacctt tgtcgttccA Gacccatacc ccaaacccaa
                                3' sj (tat,rev) /\
2641 ggggtctcga caggcccgga agaatcgaag aagaaggtgg aaagcaagac agagacagat
2701 cgattcactt agtgagcgga ttcttagcac ttgcctggga cgacctgcgg agcctgtgcc
2761 tcttcagcta ccaccgattg agagacttca tcttgattgc agcgaggact gtggaacttc
2821 tgggacaggg cctcaagtat ctgtggaatc tactagcata ttggggtcgg gaactaaaaa
2881 tTAGtgctat tagtttgttt gacaccatag cagtagtaat agctgggtgg acagatagag
      <- rev cds end
2941 ttatagaatt aggacaaaga ctttgtagag ctattttaca catacctaga agaatcagac
3001 aaggcttcga aagggctttg ctaTAAcATG gggggcaagt ggtcaaaaaa aaaatagggg
                               <- env cds end
                     nef cds start ->
3061 atggtctgag gttagggaaa aaataagaca aactcctcca gcagcaaaag gagtaggagc
3121 agtatctcaa gatttagata aacatggagc agtcacaagc agcaatacaa atcatcctag
3181 ttgtgcctgg ctggaagcac aagaggaaga ggaggtaggc tttccagtca ggccacaggt
3241 acctctaagg ccaatgactt tcaagggagc ttttgatctc agccactttt taaaagaaaa
3301 ggggggactg g
     3' LTR ->
```

```
LOCUS       HIVVAU       2631 bp    RNA             VRL       06-JUL-1994
DEFINITION  Human immunodeficiency virus type 1, isolate VAU from France,
            env cds.
ACCESSION   X80020
SOURCE      Human immunodeficiency Virus type 1 (HIV-1), isolate VAU from
            France, proviral DNA extracted from PBMCs, PCR amplified.
REFERENCE   1  (bases 1 to 2631)
  AUTHORS   Charneau,P., Borman,A.M., Quillent,C., Guetard,D., Chamaret,S.,
            Cohen,J., Remy,G., Montagnier,L. and Clavel,F.
  TITLE     Isolation and envelope sequence of a highly divergent HIV-1
            isolate: definition of a new HIV-1 group
  JOURNAL   Virology 205:247-253 (1994).
COMMENT     Submitted (04-JUL-1994) to the EMBL/GenBank/DDBJ databases. F.
            Clavel, Institut Pasteur, Unite d'Oncologie Virale, Dept Sida et
            Retrovirus, 25 rue du Dr. Roux, 75015 Paris, FRANCE
            The VAU, ANT-70 and MVP-5180 samples define the recently identified
            O clade of outlier HIV-1 genomes. The VAU virus was isolated from a
            French woman who claimed to have never left Euorpe. Hence, the VAU
            sample indicates the spread of the group O HIV-1 virus outside of
            Africa. Genomic comparison of VAU with the prototypical
            HIV-1 isolate, HIVLAI, reveals a high degree of variability (50%)
            with the most extreme divergence occuring within the V3 region.
            Twenty-nine potential N-linked glycosylation sites were identified
            in the VAU env protein sequence; thirteen of these sites are
            conserved between VAU and M group HIV-1 variants.  In addition, the
            presence of 19 conserved cysteines suggests the basic structure
            is also conserved. Phylogenetic analysis of the three O group env
            sequences indicates that they are separated by distances comparable
            to the distances that exist between M group subtypes.
BASE COUNT      940 a    485 c    576 g    630 t
ORIGIN      env cds start
        1 ATGacagcga ttatgaaagc aatggggaag aggaacagga agttagggat ctggtgcttg
env start ->
       61 attttggctt tgataatccc atgtttgagc tgtaaccaac tatatgccac agtctattct
      121 ggggtacctg tatgggaaga tgcaaaacca acattgttct gtgcttcaga tgctaacttg
      181 acaagcactg aacagcataa tatttgggca acacaagcct gtgttcccac agaccccagt
      241 ccaaatgaat atgagctaaa aaatgtgaca ggtaaattca atatatggaa aaattatata
      301 gtagaccaaa tgcacgaaga cattatagat ttgtgggacc agagtttaaa accttgtgtt
      361 caaatgactt tcttgtgtgt acaaatgaat tgtacagata tcaaaaatag tattaatacc
      421 acaaacagtc ccttaaactc aaacaataca aaagaggtga aacagtgtga ctttaatgta
      481 actacagtgc tcaaagacaa acaggagaaa aaacaggctc tattctatgt gacagatttg
      541 gttaagatta acgccacatc aaatgaaaca atgtatagat taattaattg taactccaca
      601 accatcaggc aggcctgtcc aaaggtatct tttgagccca ttcccataca ctattgtgct
      661 ccagcgggat gtgccatctt taagtgtaat gaaacaggat ttaatggaac aggtctctgt
      721 aaaaacgtta cagtagttac ttgtacacat ggcatcaaac caacagtaag tacccaacta
      781 atactaaatg ggacactctc taaaggaaat ataacaatca tgggaaagaa tatttcagac
      841 agtggggaga acatcctaat aaccctaaat actaatataa caatagcatg tgagagacca
                                                        V3 loop ->
      901 ggaaatcaga caatacaaaa gataatggca ggtccaatgg cttggtacag catggccctt
      961 agtaatacaa agggggatac aagggcagct tattgtaatt atagtgccac tgactggaac
                                              <- V3 loop
     1021 aaagccttaa aaaacataac tgaaagatat ttagaacttg tagaatataa tcaaactgat
     1081 gttaccatga aattcggtaa tcacagtggt gaagatgcag aagtaacaaa tttctttttt
     1141 aactgtcatg gagaattctt ttattgtaac acaaatcggc tgtttaatca tacctttttcc
     1201 tgcaagaaga atatgaccaa taacaagatc aattgtacta atattagcaa taatagcaat
     1261 ggcactcagg caataccttg caggttgaga caagtagtaa gggactggat gaggggagga
     1321 tcgggacttt atgcacctcc catcccagga aacctagtat gcaggtcaaa cataactgga
     1381 atgattctac aattggacac gccatggaat aaaacacatc ctaacagcac cacccttaga
     1441 ccaggagggg gagatatgaa agatatatgg agaactcaat tgttcaaata taaagtagta
```

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1501 agagtaaaac cttttagtgt agcaccaaca aaaattgcaa ggccaactat aggaactaga
1561 tctcatagag agaaaagagc agcaggtttg gcaatgctat tcttggggat tctaagtgca
1621 gcaggaagca ctatgggcgc agcggcaaca gcgctgacgg tacggaccca gcatctgata
1681 aagggtatag tgcaacagca ggataacctg ctaagagcaa tacaggccca gcaacacttg
1741 ctgaggccat ctgtatgggg tattagacaa ctccgagctc gcctgctagc cttagaaacc
1801 tttatacaga atcagcaact ccttaacctg tggggctgca agaatagact aatctgctac
1861 acatcagtaa agtggaataa aacatgggga ggagataatg aatcaatttg ggatgagtta
1921 acatggcagc agtgggatca acagataaac aacgtaagct ccttcatata tgaaaaaata
1981 caagaggcac aagaacaaca ggagaaaaat gagaaagaat tgctggagtt agatgaatgg
2041 gcctctattt ggaattggct tgacataact aaatggttgt ggtatataaa aatagctata
2101 atcatagtag gagcactaat aggtgtaaga gtagttatga tagtacttaa tctagtaaag
2161 aacattaggc agggatatca acccctctcg ttacagatcc ccatccaaca acaagcggaa
2221 gtaggaacgc caggaggaac aggagaagga ggtggagacg aagacaggcg caggtggact
2281 ccattgccgc aagggttctt gcatctgttg tacacggacc tcaggacaat aatcttgtgg
2341 atttaccacc tcttgagcaa cttagcctca gagatccaga agttgatcag acacctggga
2401 cttggactat ggatcatagg gcagaggaca attgaagctt gcagactctt taaagctata
2461 atacaatact ggctacaaga attgcaaact agtgctacaa atctactaga tactgttgca
2521 gtggcagttg ctaattggac tgacagcaca atcttaggca tacaaagcat agggagaggg
2581 attcttaaca taccaagaag gattagacag ggccttgaac gactcctgtt a
                                                          env ->
```

```
LOCUS       HIVVI1911     1453 bp ss-RNA             VRL       20-APR-1993
DEFINITION  Human immunodeficiency virus type 1, Zairean isolate VI191, gag
            region.
ACCESSION   L11783
SOURCE      Human immunodeficiency virus type 1 (HIV-1), Zairean isolate VI191.
REFERENCE   1  (bases 1 to 1453)
  AUTHORS   Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T.,
            Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K.,
            Gershy-Damet,M., DeLeys,R. and Burke,D.
  TITLE     Phylogenetic analysis of gag genes from seventy international HIV-1
            isolates provides evidence for multiple genotypes
  JOURNAL   AIDS 7, 769-780 (1993)
COMMENT     Kindly provided prior to publication by Henry M. Jackson Foundation
            Research Laboratory, 1500 East Gude Drive, Rockville, MD  20850.
            Samples were obtained from 15 different countries
            (Belgium, Burundi, Gabon, The Ivory Coast, Kenya, Rwanda, Zaire,
            Thailand, Somalia, the Philippines, Djibouti, Brazil, Uganda,
            Senegal, and Zaire) on four continents.  From this study the
            authors identified 7 distinct genotypes with an average gag
            intra-genotypic variance of 7% and an average inter-genotypic
            variance of 14%. The env region of this isolate has also been
            sequenced (L22952). This gag sequence, previously published on page
            I-A-195 of the 1993 compendium, groups with LBV21-7 as subtype G,
            also found in Gabon and Taiwan.
BASE COUNT      535 a    282 c    363 g    273 t
ORIGIN      gag cds start
        1 ATGggtgcga gagcgtcagt attaagcggg ggaaaactag atgcatggga aaaaattcgg
gag start ->
       61 ttgaggccag ggggaaagaa acaatataga ataaagcatc tagtatgggc aagcagggag
      121 ctggaaaaat ttgcacttaa ccctggcctt ttagaaacaa cagaaggctg tcaacaaata
      181 atgagacagt tgcaaccagc tctccagaca ggaacagagg agattaaatc actatataat
      241 acaatagcaa ctctctattg tgtacatcaa aggatagaga taaaagacac ccaagaagct
      301 ttacaggaag tggagaaggc acaaaagaaa agtcagcaaa aaacacaaac ggaggaagga
      361 aacagcagtc aagtcagtca aaattatcct atagtgcaga atgcacaagg gcaaatggta
      421 caccagccct taacacctag aactttgaat gcatgggtaa aagtaataga agaaaagaac
      481 ttcagtccag aagtaatacc catgttttca gcattatcag aaggagccac cccacaagat
      541 ttaaatacca tgctaaacac agtgggggggg catcaagcag ctatgcaaat gctaaaggat
      601 actatcaatg aggaggctgc agagtgggac aggatacatc caccacaggc aggacctatt
      661 ccaccaggcc agataaggga accgagggga agtgatatag caggaactac tagtacccta
      721 caggaacaaa tcagatggat gaccagtaat ccacctatcc cagtgggaga catttataaa
      781 agatggataa tcctgggatt aaacaaaata gtaagaatgt atagccctgt cagcattttg
      841 gatataagac aagggccaaa agaacccttt agagattatg tagataggtt ctttaaaaca
      901 ctgagagctg agcaagctac acaggaagta aaaggctgga tgacagacac cttgttggtc
      961 caaaatgcga acccagattg taagaccatc ttaagagcat taggaccagg agctacacta
     1021 gaagaaatga tgacagcatg ccagggagtg ggaggacccg gccataaagc aagagtttta
     1081 gctgaagcaa tgagccaagc atcaggtgta gcagcagcca tgatgatgca aaaaagcggg
     1141 tttaagggcc cgaaaagaac tattaagtgt ttcaactgtg gcaaggaagg acatctagcc
     1201 agaaattgca gggcccctag gaaaaagggc tgttggaaat gtggaaggga aggacatcaa
     1261 atgaaagact gcacagagag acaggctaat tttttaggga gaatttggcc ttcccacaag
     1321 gggaggccgg ggaatttttct tcagatcagg acagagccaa cagccccacc tgcagaagag
     1381 gagataacct cctctccgaa gcaggaaccg agggacaagg aactatatcc tcctttagtt
     1441 tccctcaaat cac
                  gag ->
```

HIVVI191A2

```
LOCUS       HIVVI191A2   2566 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, VI191 from Zaire, proviral DNA,
            envelope glycoprotein (env) gene.
ACCESSION   L22952
SOURCE      Human immunodeficiency virus type 1 (HIV-1), VI191  from Zaire, PCR
            amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 2566)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland.  Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence clusters with A subtype sequences, whereas
            the corresponding gag sequence (L11783) clusters with G subtype
            sequences. See also accession numbers L22939-L22951, L22953-L22957
            and L23064-L23065.
            NCBI gi: 437357
BASE COUNT      878 a    458 c    610 g    620 t
ORIGIN      env cds start
          1 ATGagagtga aggggataca gatgaattgg caacacttgt ggaagtgggg aactttgatc
   env start ->
         61 cttgggttgg ggataatttg taatgctgaa aatttgtggg tcacagtatt ctatggggta
        121 cctgtgtgga aagatgccga gaccaccctg ttttgtgcat cagatgctaa agcatatagt
        181 gaagagaaac acaatgtctg ggctacacat gcctgtgtac ccacagaccc cgacccaaaa
        241 gaaataaatt tggttaatgt gacagaagac ttcaacatgt ggaaaaataa aatggtagag
        301 cagatgcagg aagatataat cagtctatgg gaccagagcc taaagccatg tgtgaagtta
        361 acccctctct gcgttacttt agaatgtcat aacagcacca ccccagataa caataccacc
        421 cagtccacta tcatagatga aacaacaaac tgcacttaca atatgaccac agaattaaga
        481 gataaggtac aaaaagtaca ttcacttttt tatagacttg atgtagtaca aattaatgga
        541 attaatggaa ctagtaataa taatagtgct cagtatagac taataaattg taatacctca
        601 gccattacac aggcttgtcc aaaggtatcc tttgagccaa ttcccataca ttattgtgcc
        661 ccggctggtt ttgcgattct aaaatgtaga gataaggagt tcaatggaac agggccatgc
        721 aggaatgtca gctcagtaca atgcacgcat ggaatcaagc cagtagtatc aactcagcta
        781 ctgttaaatg gcagtctagc agaagaaaag ataatgatta gatctgaaaa cttcacagat
        841 aatgggaaaa ccataatagt acagcttgtc gagcctgtaa aaattaattg taccagacct
                                                    v3 loop ->
        901 agcaacaata caagaaaagg tatacatata ggaccaggac gagcattcta tgcaacaggt
        961 cagataacag gggatataag acaagcacat tgtaacatca gtagaacaga atggaataaa
                                          <- v3 loop
       1021 actttacacc aggtagctat acaattaaga gaacacttta taactaagaa cacaacaata
       1081 atctttaata gctcctcagg aggggatttg gaaattacaa cacacagttt taattgtgga
       1141 ggagaatttt tctattgcag tacatcaggc ctgtttaata gcacttggga aaatggcact
       1201 caggtggcaa atgacacggg atcaaatgac actataactc tcccatgcag aataaagcaa
       1261 attgtaagaa tgtggcagag agtaggacaa gcaatgtatg cccctcccat ccaaggaatg
       1321 ataagatgtg aatcaaacat tacaggatta atattaacaa gagatggtgt tgggaataac
       1381 agtacaaatg aaaccttcag acctggagga ggagatatga gggacaattg gagaagtgaa
       1441 ttatataagt ataaagtagt aaaaattgaa ccattaggag tagcacccag cagggcaaag
       1501 agaagagtgg tggcgagaga aaaaagagca gttggactgg gagctgtttt ccttgggttc
       1561 ttaggagcag caggaagcac tatgggcgca gcgtcactaa cgctgacggt acaggccaga
       1621 caattattgt ctggcatagt gcagcagcag agcaatctgc taagggctat agaggctcaa
       1681 catcatctgt tgcagctcac tgtctggggc attaaacagc tccaggcaag agtcctggct
```

```
1741 ctggaaagat accttaggga tcaacagctc ctaggaattt ggggatgctc tggcaaactc
1801 atctgcccca ctaatgtgcc ctggaactat agctggagta ataaatctta tgatgatata
1861 tggaacaaca tgacctggct gcaatgggat aaagaaattg acaattacac acaattaata
1921 tatggtctaa ttgaagaatc gcagaaccag caggaaaaga atgaacaaga cttattggca
1981 ttggacaagt gggcaagtct gtggagttgg tttgacatat caaattggct gtggtatata
2041 agaatattta taatgatagt aggaggtttg ataggtttaa gaatagtttt tgctgtgctt
2101 tctataataa atagagttag gcagggatac tcacctttgt cattccAGac cctcccccac
                                      3' sj (tat,rev) /\
2161 caccagaggg aacccgacag gcccgaagga atcgaagaag gaggaggaga gcaagacaga
2221 ggcagatcca ttcgattagt gagcggattc ttagctcttg cctgggacga cctacggagc
2281 ctgtgccttt tcagctacca ccgattgaga gacttcatat tgattgtagc gaggattgtg
2341 gagactctgg gacgcagggg gtgggaggct ctcaaatatc tgtggaatct cctgttatat
2401 tggggtcggg aactgaaaat tagtgctatt actttgcttg atgctacagc aatagcagta
2461 gctaggtgga cagataggat tatagaaata ggacaaagaa ttgttagagc tattctcaac
2521 atacccagaa gaatcagaca gggagcggaa aaagctttgc aaTAAa
                                                  <- env cds end
```

HIVVI5251

```
LOCUS       HIVVI5251     1471 bp ss-RNA              VRL       20-APR-1993
DEFINITION  Human immunodeficiency virus type 1, Gabonese isolate VI525, gag
            region.
ACCESSION   L11792
SOURCE      Human immunodeficiency virus type 1 (HIV-1), Gabonese isolate VI525.
REFERENCE   1  (bases 1 to 1471)
  AUTHORS   Louwagie,J.J., McCutchan,F., Brennan,T., Peeters,M., Brennan,T.,
            Sanders-Buell,E., Eddy,G., van der Groen,G., Fransen,K.,
            Gershy-Damet,M., DeLeys,R. and Burke,D.
  TITLE     Phylogenetic analysis of gag genes from seventy international HIV-1
            isolates provides evidence for multiple genotypes
  JOURNAL   AIDS 7, 769-780 (1993)
COMMENT     Kindly provided prior to publication by Henry M. Jackson Foundation
            Research Laboratory, 1500 East Gude Drive, Rockville, MD  20850.
            Samples were obtained from 15 different countries
            (Belgium, Burundi, Gabon, The Ivory Coast, Kenya, Rwanda, Zaire,
            Thailand, Somalia, the Philippines, Djibouti, Brazil, Uganda,
            Senegal, and Zaire) on four continents.  From this study the
            authors identified 7 distinct genotypes with an average gag
            intra-genotypic variance of 7% and an average inter-genotypic
            variance of 14%. The env region of this isolate(L22953) has also
            been sequenced. This gag sequence, previously published on page
            I-A-195 of the 1993 compendium, groups as subtype H in gag but G
            in env.
BASE COUNT      543 a    279 c    361 g    288 t
ORIGIN      gag cds start
        1 ATGggtgcga gagcgtcagt attgagcggg ggaagattag atgcttggga gaaaattcgg
gag start ->
       61 ttaaggccag ggggaaagaa acaatatagg ctaaaacatc tagtatgggc aagcagagag
      121 ctggaaagat ttgcacttaa ccctggcctt ttagaaacat cagaaggctg tctacagata
      181 atagaacagc tacagccagc tcttaagaca ggaacagaag aacttcaatc attatttaat
      241 ctattagcag tcctctattg tgtacatcaa agaatagata taaaagacac caaggaagct
      301 ttaagtaaga tagaggaagt acaaaacaac agacagcaaa aaacacagca agcaacagct
      361 gataaggaaa aagacaaaaa ggtcagtcaa aattatccca tagtacagaa tgcccaaggg
      421 cagatggtac accaggccat atcacctagg accttaaatg catgggtaaa agtagtagaa
      481 gaaaaggctt ttagcccaga agtaatacct atgttttcag cattatcaga aggagccacc
      541 ccacaagact taaatgccat gctaaataca gtgggggggc atcaagcagc catgcaaata
      601 ctaaaagata caatcaatga ggaagctgca gaatgggata ggctacatcc agtgcatgca
      661 gggcctattc caccaggcca aatgagagaa ccaaggggaa gcgatatagc aggaactact
      721 agtacccttc aggaacaaat agcatggatg acaggcaatc cagctatccc agtgggagac
      781 atctataaaa gatggataat cctgggatta aataagatag taagaatgta tagtcctgtc
      841 agcattttgg acataaaaca aggaccaaaa gaacccttta gagactatgt agacaggttc
      901 tttaaaactt taagagctga gcaagccaca caggatgtaa agaattggat gacagacacc
      961 ttgttggtcc aaaatgcgaa tccagattgc aagaatattt taaaagcatt aggaacaggg
     1021 gcttcaatag aagaaatgat gacagcatgt cagggagtgg gaggacctag ccacaaagca
     1081 agagttttgg ctgaggcaat gagccaagta acaaatacac atgcagccat aatgatgcag
     1141 aaaggcaact ttaagggtca aagaagaatt gttaaatgtt tcaactgtgg caaagaagga
     1201 cacatagcta gaaattgcag ggcccctagg aaaaagggct gttggaaatg tggaagggaa
     1261 ggacatcaga tgaaagattg cacagagaga caggctaatt ttttagggaa aatctggcct
     1321 tccagcaaag ggaggccagg gaatttttctt cagagcaggc cagagccaac agccccacca
     1381 gcagagagct ttgggttcgg agaggagatg acccccctctc cgaagcagga gcccagggac
     1441 aaggaacctc ccttagcttc cctcaaatca c
                                        gag ->
```

```
LOCUS       HIVVI525A2   2604 bp ds-DNA              VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, VI525 from Gabon, proviral
            DNA, envelope glycoprotein (env) gene.
ACCESSION   L22953
SOURCE      Human immunodeficiency virus type 1 (HIV-1), VI525  from Gabon,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 2604)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland.  Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence clusters with G subtype sequences, however
            the corresponding gag sequence (L11792) clusters with H subtype
            sequences.  See also accession numbers L22939-L22952, L22954-L22957
            and L23064-L23065.
            NCBI gi: 437358
BASE COUNT      904 a    458 c    601 g    641 t
ORIGIN      env cds start
          1 ATGagagtga gggggataca gacgaattgg caaaacttgt ggaattgggg gactttgatc
   env start ->
         61 cttgggttgg tgataattag tagtgcctca aataacttgt gggtcacagt ctactatggg
        121 gtacctgtgt gggaagatgc agaaacccct ctattttgtg catctgatgc taaatcatat
        181 agtactgaaa gccataatgt ctgggctaca catgcctgtg tacccacaga ccccaaccca
        241 caagagatat ctctggaaaa tgtaacagaa aattttaaca tgtggaaaaa taaaatggta
        301 gaacagatgc atgaggatat aatcagttta tgggatgaaa gcttaaagcc atgtgtagag
        361 ctaacccctc tctgtgttac tttaaactgt actaaggtaa cctacaatag cactgcagcc
        421 aacaatagat catccactgt caccacccct actagtactg taaccaacaa tagcactgtg
        481 agtggcaaag aagaaatgac aaactgctct ttcaatgtaa ccacagaact aagagataag
        541 cagaaggcag aatacgcgct tttctataaa cttgatgtag taccaattga taataataga
        601 aatgatagtt ataggctaat acattgtaat gtctcaacca ttaaacaggc ttgtcccaag
        661 gtatcttttg aaccaattcc catacattat tgtgctccag ctggttttgc aattttaaag
        721 tgtagggaga agaatttcac tggaacagga ctatgtaaaa atgtcagtac agtacaatgt
        781 acacatggaa ttaagccagt ggtatcaact caactactgc tgaatggcag tttagcagaa
        841 aaagaaatta taattagatc tgaaaacttc acaaacaatg ccaaagtcat aatagtgcag
        901 cttaatgaaa ctgtagaaat taattgtacc agacccaaca acaatacaag aaaaagtata
                              v3 loop ->
        961 aaattcggaa caggacgagt gttatatgca acaggtgcca taataggaaa tataagacaa
       1021 gcacattgta atgttagtac agaaaaatgg ggtaagatgt tacagaatgt agctgcaaaa
                    <- v3 loop
       1081 ctacaaaaag aatttaataa aaacataacc tttaactcat cctcaggagg ggacctagaa
       1141 attacaacac atagttttaa ttgtagagga gaatttttt attgtaagac atcagagctg
       1201 tttaatagta cttggttgtt taatagtact gggctggtta atagtacttg gaatgataca
       1261 cgaaaagata ttacactgca atgcaaaata aaacaaattg tgagaatgtg gcagagagtg
       1321 ggacaagcaa tgtatgcccc tcccatcgca gcaggaaaca ttgaatgtag atcaagcatt
       1381 acaggactaa tattaacaag agatggtggg aataataata ataccaatga gaccttcaga
       1441 cctggaggag gagacatgag gggcaattgg agaagtgaat tatataagta taaagtagta
       1501 aaaatcaaat cactaggagt agcacccacc agggcaagga gaagagtggt ggagagagaa
       1561 aaaagagcaa ttggactggg agctgtcttc cttgggttct taggagcagc aggaagcact
       1621 atgggcgcgg cgtcaataac gctgacggta caggtcagac aattattgtc tggcatagtg
       1681 caacagcaaa gcaatttgct gagggctata gaggcgcagc agcatctgtt gcaactcaca
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1741 gtctggggca ttaaacagct ccaggcaaga gtcctggctg tagaaagatt cctaaaggat
1801 caacagcccc tagggatttg gggctgctct ggaaaactca tctgcaccac taatgtgccc
1861 tggaatacta gttggagtaa taaatcctat aatgacattt gggataacat gacctggatg
1921 gaatgggaaa gggaaatcag caattacaca aaacaaatat acagcctaat tgaagaatcg
1981 cagatccagc aggaaaagaa tgaacaagac ttattggcat tggacaaatg ggcaagtttg
2041 tgaaattggt ttgacatatc aagctggcta tggtatataa aaatatttat aatggtagta
2101 ggaggtttaa taggtttaag aatagttttt gctgtgcttt ctatagtaaa tagagtcagg
2161 cagggatact cacctctgtc attccAGacc cttacccatc accaagggga acccgacagg
                3' sj (tat,rev) /\
2221 ctcgaaagaa tcgaagaagg aggtggcgag cacgacagaa ccagatccac gcgatcagcg
2281 aacggattct taccacttgt ctgggacgac ctctggagcc tgtgcctttt cagctaccgc
2341 ctcttgagag acttactctt aattgtagcg aggactgtgg aacttctggg gagaaggggg
2401 tgggaagccc tcaaatatct gtggaatctt ctgcagtatt ggggacagga actaaagaat
2461 agtgccattc atttgcttaa caccacagca atagcagtag ctgagggaac agatagggtt
2521 atagaaatag tgcaaatagc ttgcagagct gttcttcaca tacctagaag aataagacag
2581 ggctttgaaa gggctttgct aTAA
                           <- env cds end
```

```
LOCUS       HIVZAM181    1477 bp ss-RNA             VRL       06-OCT-1992
DEFINITION  Human immunodeficiency virus type 1, ZAM18 core protein (gag)
            gene, 5' end.
ACCESSION   L03705
SOURCE      Human immunodeficiency virus type 1, individual_isolate ZAM18 from
            Zambia RNA.
REFERENCE   1  (bases 1 to 1477)
  AUTHORS   McCutchan,F., Ungar,B.L.P., Hegerich,P.A., Roberts,C.R.,
            Fowler,A.K., Hira,S.K., Perine,P.L. and Burke,D.S.
  TITLE     Genetic Analysis of HIV-1 Isolates from Zambia and an Expanded
            Phylogenetic Tree for HIV-1
  JOURNAL   J. Acquir. Immune Defic. Syndr. 5, 441-449 (1992)
COMMENT     See related env sequence (L22954). Both the ZAM18 gag and env
            sequences cluster with C subtype sequences. This sequence was
            previously presented on page I-A-170 of SEP92.
            NCBI gi: 325636
BASE COUNT      554 a    293 c    353 g    277 t
ORIGIN
        1 ATGggtgcga gagcgtcaat attaaaaggg ggaaaattag atacatggga aaaaattagg
gag start ->
       61 ttaaggccag ggggaaagaa acactatatg ataaaacacc tagtatgggc aagcagggag
      121 ctggaaagat ttgcacttaa ccctggcctt ttagagacat cagaaggctg taaacaaata
      181 ataaaacagc tacaaccatc tattcagaca ggaacagagg aacttaaatc attattcaac
      241 acagtagtaa ctctatggtg tgtacatgaa gatataacag tacgagacac caaggaagcc
      301 ttagacaggt tagaggaaga acaaaacaaa agtcagcaaa aaacaaaaac acagcaggca
      361 aaagcggctg acggacaggt cagtcaaaat taccctatag tgcagaatct ccaagggcaa
      421 atgatacacc aggccatatc acctagaact ttgaatgcat gggtaaaagt aatagaggga
      481 aaagccttta gcccagagat aatacccatg tttacagcat tatcagaagg agccacccca
      541 caagatttaa acaccatgtt aaatacagtg gggggacatc aagcagccat gcagatgtta
      601 aaagatacca tcaatgagga ggctgcagaa tgggatagat tacatccagt acatgcaggg
      661 cctaatgcac caggccaatt gagagaacca aggggaagtg acatagcagg aactactagt
      721 acccttcagg aacagatagc atggatgaca aataacccac ctgttccagt gggagacatc
      781 tataaaagat ggataattct ggggttaaat aaaatagtca gaatgtatag ccctgtcagc
      841 attttggaca taaaacaagg gccaaaggaa ccttttagag actatgtaga ccggttcttt
      901 aaaactttaa gagctgaaca agctacacaa gatgtaaaaa attggatgac agaaaccttg
      961 ttggtccaaa atgcgaaccc agattgtaag accattttaa gagcattagg accagcggct
     1021 acattagaag aaatgatgac agcatgtcag ggagtgggag gacctagcca caaagcaaga
     1081 gtgttagctg aggcaatgag ccaagcaaac aatacaaaca tactgatgca gagaagcaat
     1141 tttaaaggac ctaaaagaag tgttaaatgt ttcaactgtg gcaaggaagg gcacatagcc
     1201 aaaaattgca gggcccctag gaaaaaaggc tgttggaaat gtggaaagga aggacaccaa
     1261 atgaaagact gtaccgagag gcaggctaat tttttaggga aaatctggcc ttcccacaag
     1321 gggaggccag ggaatttcct tcagagcagg ccagagccaa cagcccctag gccagagcca
     1381 acagccccac cagcagagag cttcaggttc gaggagacga cccccgctcc gaatcaggag
     1441 ccgaaagaca gggaaccctt aacttccctc aaatcac
```

HIVZAM18A

```
LOCUS       HIVZAM18A   2544 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, ZAM18 from Zambia, proviral
            envelope glycoprotein (env) gene.
ACCESSION   L22954
SOURCE      Human immunodeficiency virus type 1 (HIV-1), ZAM18 from Zambia,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 2544)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L.,
            Hegerich,P.A., van der Groen,G., McCutchan,F.F.E., Eddy,G. and
            Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. This sequence and the corresponding gag sequence (L03705)
            cluster with C subtype sequences.  See also accession numbers
            L22939-L22953, L22955-L22957 and L23064-L23065.
            NCBI gi: 437359
BASE COUNT      904 a    439 c    598 g    603 t
ORIGIN      env cds start
          1 ATGagagtga gggagatact gaggaattgg caacaatggt ggatatgggg catcttaggc
  env start ->
         61 ttttggatgg taatgaacta taatgtggta ggagacaact tgtgggtcac agtctattat
        121 ggggtacctg tgtggaaaga agcaaaaact actttattct gtgcatcaga tgctaaagca
        181 tatgagagag aagtgcataa tgtctgggct acacatgcct gtgtacccac agaccccaac
        241 ccacaagaaa tagttttggg aaatgtaaca gaaaatttta acatgtggaa aaatgacatg
        301 gtggatcaga tgcatgagga tataatcagg ttatgggatc aaagcttaaa gccatgtgta
        361 aagttgaccc cactctgtgt cactttagaa tgtggaaatg ttaatgttac ccatgagaat
        421 agcacgaagg gggaaatgaa aaattgctct ttcaatgcaa ccacagaact aaaagataaa
        481 aaacagagag tgtatgcact tttttataaa cttgatatag taccacttaa tgagaataac
        541 aactctagtg aggactctag tgagtataga ttaataaatt gtaatacctc agccataaca
        601 caagcctgtc caaaggtcac tttggatcca attcctatac attattgtgc tccagctgga
        661 tatgcgattc taaagtgtaa taataagaca ttcaatggga caggaccatg ccataatgtc
        721 agcacagtac aatgtacaca cggaatcaag ccagtggtat caactcaact actgttaaat
        781 ggtagcctag cagaagaaga gataataatt aggtctgaaa atctaacaaa caatgccaaa
        841 acaataatag tacatcttaa tgaatctgta gaaattgtgt gtacaagacc cagcaataat
                                              v3 loop ->
        901 acaagaaaaa gtataaggat aggaccagga caagcattct atgcaacagg tggcataata
        961 ggaaacataa gacaagcaca ttgtaacatt agtaaagaga actggaataa aactttacaa
                                  <- v3 loop
       1021 aaggtaggaa aaaaattagc agagcacttc cctaataaaa caataaaatt tgaccaacac
       1081 tcaggagggg acctagaaat tacaacacat agctttaatt gtagaggaga atttttctat
       1141 tgcaatacat caaacctgtt taatagtaca tataagccta atgatacaaa tagtacatat
       1201 aatcctaatg atacaatcac actcccatgc agaataaaac aaattataaa catgtggcag
       1261 ggggtaggac aagcaatgta tgcccctccc attgcaggaa acataacatg taaatcaaat
       1321 atcacaggac tactattgac acgggatgga gggtcaaatg ataccacaaa cacagagaca
       1381 ttcagacctg gaggaggaga tatgagggac aattggagaa gtgaactata taaatataaa
       1441 gtggtagaaa ttaaaccatt gggcatagca cccactgcgg caaaaaggag agtggtggag
       1501 acgagagaaa aaagagcagt gggaatagga gctgtgttcc ttgggttctt gggagcagca
       1561 ggaagcacta tgggcgcggc gtcaataacg ctgacggcac aggccagaca agtgttgtct
       1621 ggtatagtgc aacagcaaag caatttgctg agagccatag aggcgcaaca gcatctgttg
       1681 caactcacgg tctggggcat taagcagctc cagacaagag tcttggctat ggaaagatac
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1741 ctaaaggatc aacagctcct agggatttgg ggctgctctg gaaaactcat ctgcaccact
1801 gccgtgtctt ggaactccag ttggagtaat aagtctcaaa cagatatttg ggataacatg
1861 acctggatgc agtgggatag agaaattagt aattacacag acacaatata caggttgctt
1921 gaagaatcgc aaattcagca ggaaagaaat gaaaaagact tattagcatt ggacagttgg
1981 aaaaatctat ggaattggtt tgacataaca aattggctgt ggtatataaa aatattcata
2041 atgatagtag gaggcttgat aggcttaaga ataagttttg ctgtgctttc tatagtgaat
2101 agagttaggc agggatactc acctttgtcg tttcAGaccc ttaccccgaa cccaagggga
                          3' sj (tat,rev) /\
2161 cccgacaggc tcggaagaat cgaagaagaa ggtggagagc aagacagaga caaatccatt
2221 cgcttagtgg acggattctt agcacttttc tgggacgacc tgcggagcct gtgccttttc
2281 agctaccacc gattgagaga cttcatattg attgcagcga gagcagcgga acttctggga
2341 cgcagcagtc tcaggggact acagaggggg tgggaagccc ttaagtatct gggaagtctt
2401 gtgcagtatt ggggtctgga actaaaaaag agtgctatta gtctggttga tgccatagca
2461 ataacagtag ctgaaggaac agataggatt atagaattca tacaaagaat ttgtagagct
2521 atccgcaaca tacctagaag aata
                           env ->
```

HIVZAM184

```
LOCUS       HIVZAM184   3307 bp ds-DNA             VRL       31-DEC-1993
DEFINITION  Human immunodeficiency virus type 1, ZAM184 from Zambia, proviral
            DNA encoding env, tat, vpU, rev, and nef genes.
ACCESSION   L22955
SOURCE      Human immunodeficiency virus type 1 (HIV-1), ZAM184  from Zambia,
            PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE   1  (bases 1 to 3307)
  AUTHORS   Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A.,
            van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
  TITLE     Genetic diversity of the HIV-1 envelope glycoprotein
  JOURNAL   Unpublished (1993)
COMMENT     These sequences were kindly provided prior to publication by Dr.
            Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory
            Rockville, Maryland. Twenty-one full length gp160 coding sequences
            from eight African countries (Djibouti, Gabon, Kenya, Senegal,
            Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with
            thirty-two previously published full-length gp160 env sequences.
            Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274,
            VI191, and VI525 have corresponding gag sequences published by
            Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993
            compendium. The subtype classification of ZAM184 is uncertain at
            this time. See also accession numbers L22939-L22954, L22956-L22957
            and L23064-L23065.
            NCBI gi: 437360
BASE COUNT      1133 a    594 c    794 g    786 t
ORIGIN      226 bp upstream from the beginning of rev cds start
          1 ggcttccgtc tagatgctgt ttattcattt cagaattggg tgccaacata gcagaatagg
         61 cattactcga agaagaagag taagggATGg atccagtaga ccctaaacta gagccctgga
                       tat cds start ->
        121 accatccggg aagtcagcct aaaactgctt gtaccaagtg ttattgtaaa aagtgttgct
        181 atcattgccc agtgtgcttt ctaaacaaag gcttaggcat ctcctATGgc aggaagaagc
                                            rev cds start ->
        241 ggagaccccg acgaagatct cctcaaaaca gcgaggatca tcaaaatcct ataccaaagc
        301 aGTaagtagt agtaattaat atatgtaATG ttacctttag caacattgtc aatagtagga
      5' sj /\             vpU cds start ->
        361 ctgatagtag cgttaatctt agcaatagtg gtatggacta tagtatttat agaatataaa
        421 aaaattaaga agcaaaagaa aatagactgg ctaatcgaga gaataagtga aagagcagaa
        481 gacagtgcca ATGagagtga gggggatacc gaagaattgg caacaatggt ggatatgggg
         env cds start ->
        541 catcttaggc ttttggatgt taatgatttg TAGtgtggtg ggaaacttgt gggtcacagt
                                            <- vpU cds end
        601 ctattatggg gtacctgtgt ggagagaagc aaaaactact ctattctgtg catcagatgc
        661 taaagcatat gagagagaag tgcataatgt ctgggctaca catgcctgtg tacccacaga
        721 ccccaaccca caagaaatag ttttggaaaa tgtaacagaa aattttaaca tgtggaaaaa
        781 tgacatggtg gatcagatgc atgaggatat aatcagtttg tgggatcaaa gcctaaagcc
        841 atgtgtaaaa ttaacccctc tctgcgtcac tttaaattgt agtgatgcca ctagtaccaa
        901 tagcaacacc actgaagaaa taaaaaactg ctcttacagg actaccacag aactaaaaga
        961 taagacgctg agagtctatt cactgtttta taaacttgat gtagtacaaa ttgatccaag
       1021 taataatact atgtatagac taataagttg taatacctca gccatcgcac aagcttgtcc
       1081 aaaggtatcc tttgagccaa ttcctataca ttattgtacc ccagctggtt ttgcgatcct
       1141 aaagtgtaag gatacggaat tcaatggaac agggtcatgc aagaatgtta gctcagtaca
       1201 atgtacacat ggaattaggc cagtagtatc aactcaactg ctgttgaatg gcagtctagc
       1261 agaaggagag gtaatgatta gatctgagaa tattacagac aatgccaaaa acataatagt
       1321 acagtttact gaacctgtac aaattagttg taccagaccc agcaacaata caagaagaag
                                 v3 loop ->
       1381 tatccgcttt ggaccaggac aagccttcta tacaaatgac ataatagggg atataagaca
       1441 agcatattgt agtatcaacg aaacaaaatg gaatgccact ttacaaaagg tagctaaaca
                    <- v3 loop
       1501 attacaaaac tacttcccta acaaaacaat aagctttgct aactcttcag gaggggacct
```

```
1561 agaaattaca acacatagtt ttaattgtgg aggagaattt ttctattgca atacatcaaa
1621 cctgtttaat agtacataca atcctaatag tacagaaagt aattcagact taaacatcac
1681 actcccatgc agaataaaac aaattataaa catgtggcag agagtaggac gagcaatgta
1741 tgcccctccc attgcaggag taataaagtg tacatcaaac attacaggaa taatattgtc
1801 aagagatggt gggaacagtg ggaacagtac caatgggact gagaccttca gacctggagg
1861 aggagatatg agggacaatt ggagaagtga attatataag tataaagtag taaaactaga
1921 accactagga gtagcaccca ccaagccaag gagaagagtg gtggagagag aaaaaagagc
1981 agttggactg ggagctgtct tccttgggtt cttgggagca gcaggaagca ctatgggcgc
2041 ggcatcaata acgctgacgg tacaggccag acaactgttg tctggtatag tgcaacagca
2101 aagcaatttg ctgaaggcta tagaggctca acagcatctg ttgaaactca cggtctgggg
2161 cattaaacag ctccaggcaa gagccctggc tatggaaaga tacctacagg atcaacagct
2221 cctgggaatt tggggctgct ctggaaaact catctgcacc actactgtgc cctggaactc
2281 tagttggagt aataagactc aggatgagat ttgggacaaa atgacctggt tgcaatggga
2341 caaagaaatt agcaattaca cagaaataat ataccagcta cttgaggact cgcagaacca
2401 gcaggaaaag aatgagcaag acttattggc attagacaaa tgggcaaatt tgtggaattg
2461 gtttgacata acaagatggc tatggtatat aaaaatattt ataataatag taggaggctt
2521 gataggatta agaatagtta ttgctataat ttctgtagta aatagagtta ggcagggata
2581 ctcacctttg tcatttcAGa tccctacccc acacccagag ggtctcgaca ggcccggaag
       3' sj (tat,rev) /\
2641 aatcgaagaa ggaggtggag agcaaggcag agacagatcg attcgattag tgagcggatt
2701 cttagcgctt gcctgggacg atctgaggag cctgtgcctc ttcagctacc accgcttgag
2761 agattgcatc ttgattgcag cgaggactgt ggaacttctg ggacacagca gtctcaaggg
2821 actgagactg gggtgggaag gcctcaagca tctatggaat cttctgttat attggggtca
2881 ggaattgaag aatagtgcta tTAGtttact tgataccata gcaatagcag tagctgagtg
                          <- rev cds end
2941 gacagatagg attatagaaa taggacaaag agcttgcaga gctattcgca atatacctac
3001 aagaataaga cagggctttg aaagggcttt actgTAAaAT Gggaggcaag tggtcaaaaa
                                          <- env cds end
                              nef cds start ->
3061 gtagcatagt gggatggcct gaagttaggg agagaatgaa aagaactcct ccagcagcag
3121 aaggagtagg agcagtgtct caagatttag ctgcacgtgg agcagtcaca agcagtaata
3181 cagcacatac taatcctgat tgtgcctggc tggaagcgca agaagagggg gagggagtag
3241 gcttcccagt caagccacag gtacctttaa gaccaatgac ctacaaggga gctgtggatc
3301 tcaccac
```

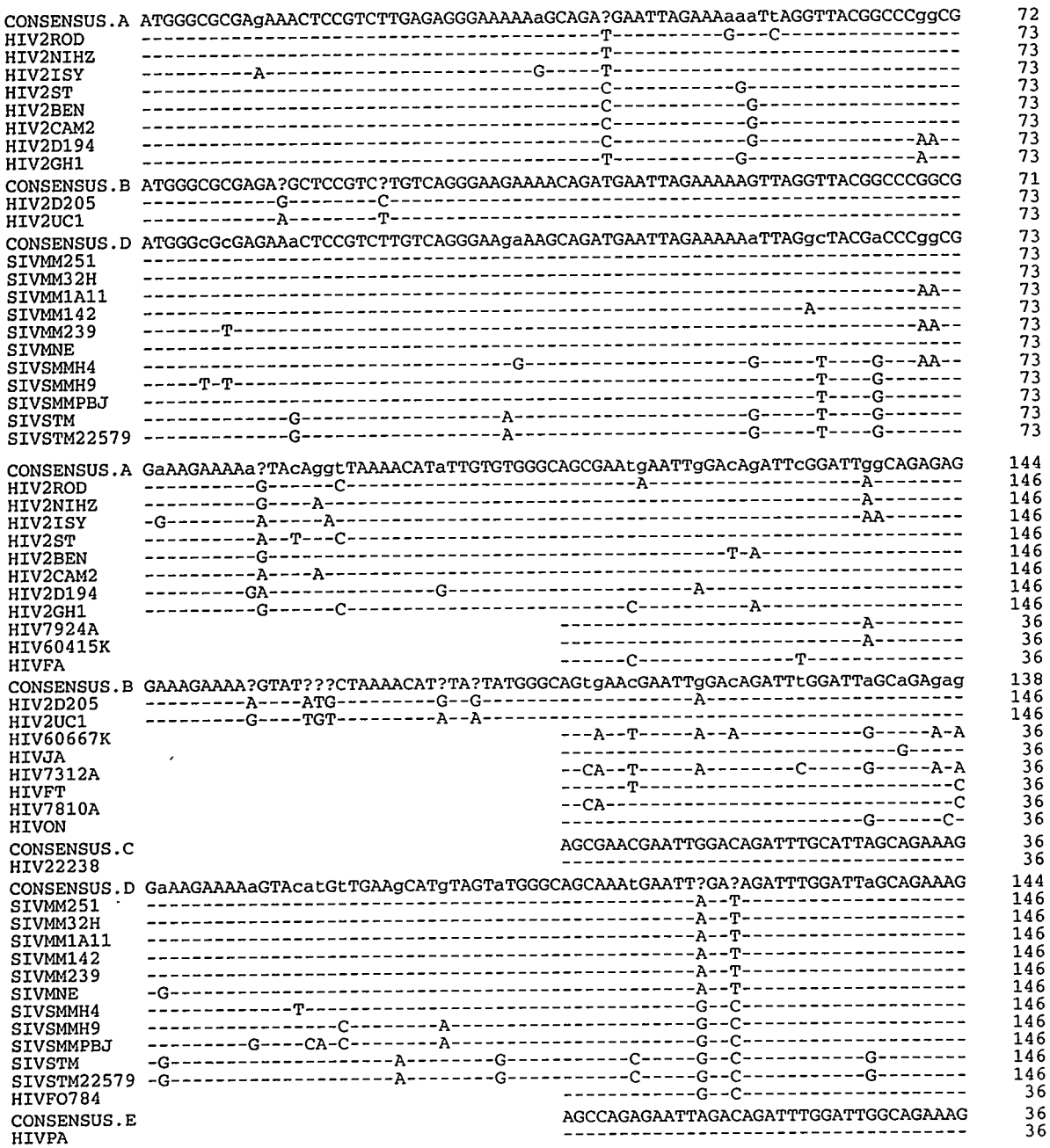
HIVZAM201

```
LOCUS       HIVZAM201    1488 bp ss-RNA             VRL       06-OCT-1992
DEFINITION  Human immunodeficiency virus type 1, ZAM20 core protein (gag)
            gene, complete cds.
ACCESSION   L03707
SOURCE      Human immunodeficiency virus type 1, individual_isolate ZAM20 from
            Zambia RNA.
REFERENCE   1  (bases 1 to 1488)
  AUTHORS   McCutchan,F., Ungar,B.L.P., Hegerich,P.A., Roberts,C.R.,
            Fowler,A.K., Hira,S.K., Perine,P.L. and Burke,D.S.
  TITLE     Genetic Analysis of HIV-1 Isolates from Zambia and an Expanded
            Phylogenetic Tree for HIV-1
  JOURNAL   J. Acquir. Immune Defic. Syndr. 5, 441-449 (1992)
COMMENT     See related env sequence (L22956). Both the ZAM20 gag and env
            sequences cluster with C subtype sequences. This sequence was
            previously published on page I-A-172 of SEP 92.
            NCBI gi: 325640
BASE COUNT      543 a    293 c    373 g    279 t
ORIGIN
        1 ATGggtgcga gagcgtcaat attaagaggg ggaaaattag ataaatggga gaaaattagg
gag start ->
       61 ttaaggccag ggggaaagaa acattatatg ataaaacatt tagtatgggc aagcagggag
      121 ctggaaagat ttgcacttaa ccctggcctt ttagagacag cagacggctg taaacaaata
      181 ataagacagc tacatccagc tcttcagaca ggaacagagg aacttagatc attatataac
      241 acagtagcaa ctctctattg tgtacatgca gggatagagg tacgagacac caaggaagcc
      301 ttagacgaga tagaggaaga acaaaacaaa tgtcagcaaa aaacacagca ggcaaaaacg
      361 gctgacggaa aagtcagtca aaatttcct atagtacaga atcttcaagg gcaaatggta
      421 catcaggcca tatcacctag aactttgaat gcatgggtaa aagtaataga gggagaaggc
      481 tttaagccag aggtaatacc catgtttaca gcattatcag aaggagccac cccacaagat
      541 ctaaacacca tgttaaatac agtgggggga caccaagcag ccatgcaaat gttaaaagac
      601 accatcaatg aggaggctgc agaatgggat agaatacatc cagtacatgc agggcctgtt
      661 gcaccaggcc aaatgagaga accaagggga agtgacatag caggaactac tagtaccctt
      721 caggaacaaa tagcatggat gacagctaac ccacctgttc cagtgggaga aatctataaa
      781 agatggataa ttctggggtt aaataaaata gtaagaatgt atagccctgt cagcattttg
      841 gacataagac aagggccaaa ggaacccttt agagactatg tagaccggtt ctttaaaact
      901 ttaagagctg aacaagctac acaagatgta aaaaactgga tgacagacac cttgttggtc
      961 caaaatgcga acccagattg taagaccatt ctaagagcat taggaccagg ggctacatta
     1021 gaagaaatga tgacagcatg tcagggagtg ggaggaccta gccacaaagc aagagtgttg
     1081 gctgaggcaa tgagccaaac aaacaggcaa atgtaatgat gcagagaggc aattttaaag
     1141 gccctaaaag aactgttaaa tgtttcaact gtggcaagga agggcacata gccagaaatt
     1201 gcagggctcc tcggaaaaag ggctgttgga aatgtggaag ggaaggacac caaatgaaag
     1261 attgtactga gagacaggct aatttttag ggaaaatttg gccttcccaa aaggggaggc
     1321 cagggaattt cctccagaac aggccagagc caacagcccc accagcagag aacttcaggc
     1381 caacagcccc accagcagag agcttcaggt tcgaggagac aacccccgct ccgaagcagg
     1441 agccgagaga cagtcctaca ggggaaccct taactgccct caaatcac
```

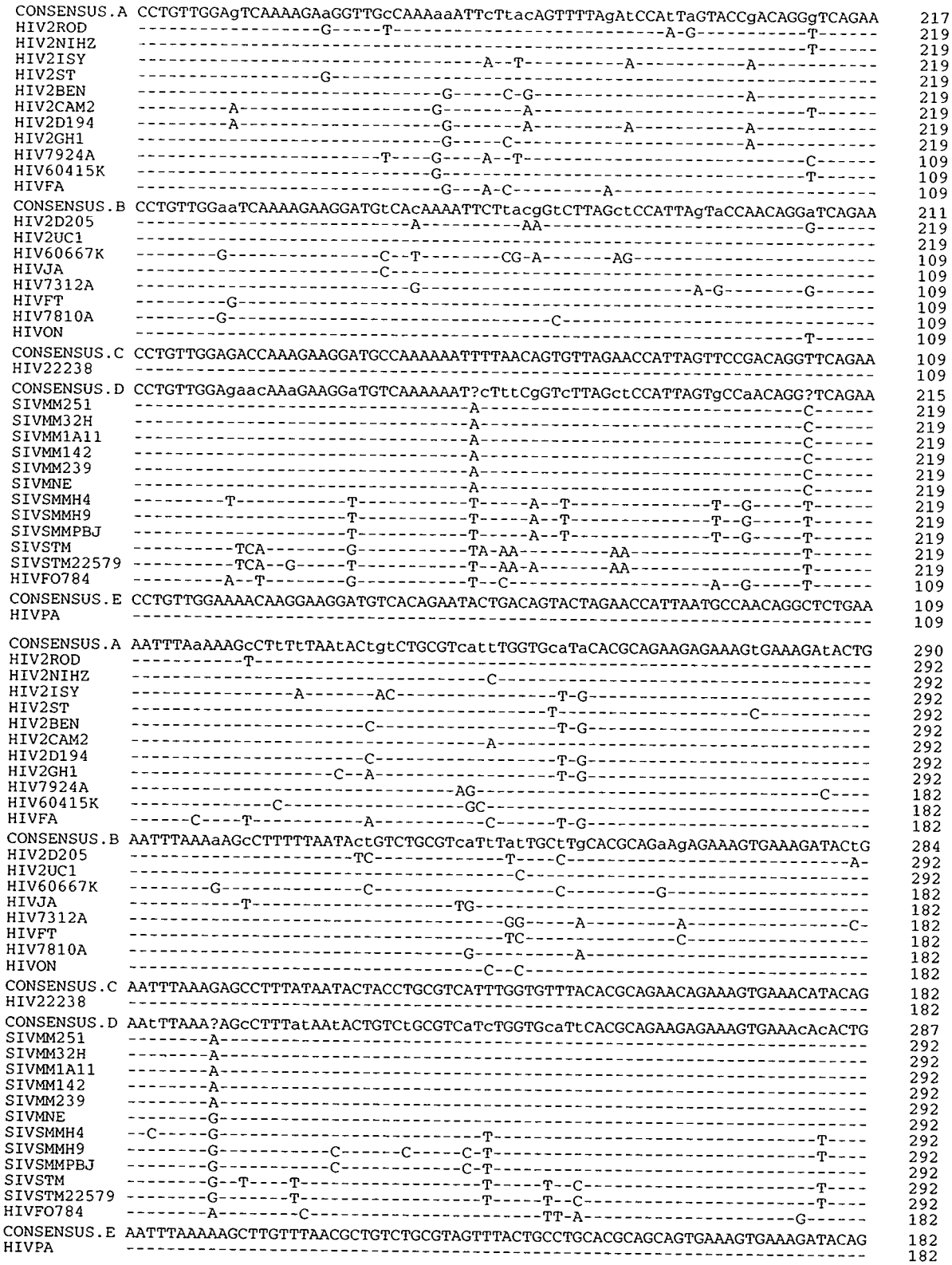
LOCUS HIVZAM20A 2625 bp ds-DNA VRL 31-DEC-1993
DEFINITION Human immunodeficiency virus type 1, ZAM20 from Zambia, proviral envelope glycoprotein (env) gene.
ACCESSION L22956
SOURCE Human immunodeficiency virus type 1 (HIV-1), ZAM20 A from Zambia, PCR amplification of proviral DNA from cocultivated PBMC's.
REFERENCE 1 (bases 1 to 2625)
AUTHORS Louwagie,J.J., Janssens,W., Mascola,J.J., Fischer,C.L., Hegerich,P.A., van der Groen,G., McCutchan,F.F.E., Eddy,G. and Burke,D.
TITLE Genetic diversity of the HIV-1 envelope glycoprotein
JOURNAL Unpublished (1993)
COMMENT These sequences were kindly provided prior to publication by Dr. Joost Louwagie of the Henry M. Jackson Foundation Research Laboratory Rockville, Maryland. Twenty-one full length gp160 coding sequences from eight African countries (Djibouti, Gabon, Kenya, Senegal, Somalia, Uganda, Zaire, and Zambia) were sequenced and analyzed with thirty-two previously published full-length gp160 env sequences. Sequences DJ258, DJ259, K124, SE365, SM145, UG266, UG268, UG274, VI191, and VI525 have corresponding gag sequences published by Louwagie et. al. in AIDS 7, 769-780 (1993) and in the 1993 compendium. This sequence, and the corresponding gag sequence (L03707) cluster with C subtype env sequences. See also accession numbers L22939-L22955, L22957, and L23064-L23065.
NCBI gi: 437361
BASE COUNT 910 a 455 c 620 g 640 t
ORIGIN env cds start

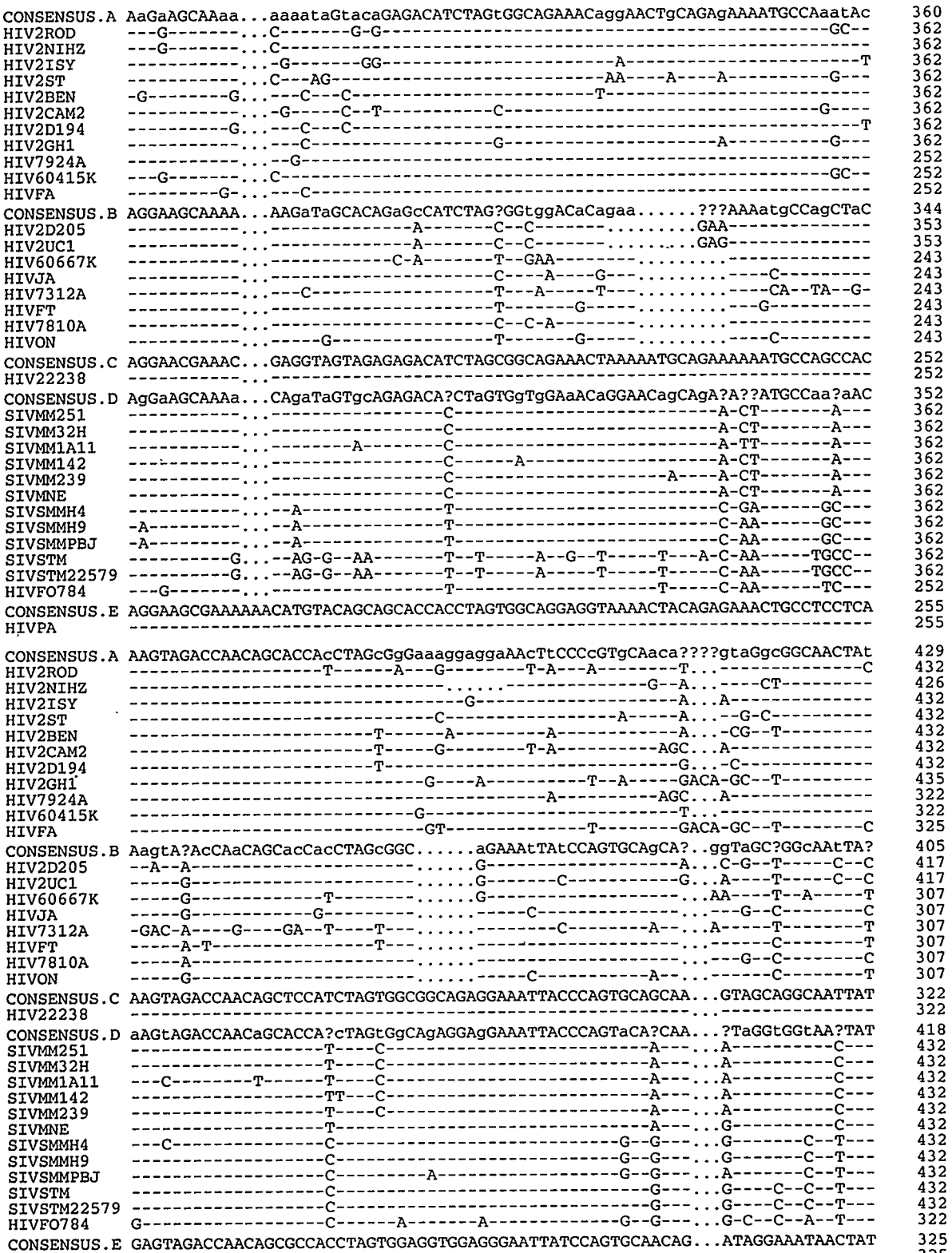
```
        1 ATGagagtga gggggatact gaggaattgt caacaatggt ggatatgggg catcttaggc
   env start ->
       61 ttttggatgt taatgatttg taatggggtg ggggacttgt gggtcacagt ctattatggg
      121 gtacctgtgt ggaaggaagc aaaaactact ctattctgtg catcagatgc taaagcttat
      181 gagacagaag tgcataatgt ctgggctaca catgcctgtg tgcccacaga tcccagccca
      241 caagaaatgg ttttggcaaa tgtaacagaa aactttaaca tgtggaaaaa tgacatggtg
      301 gatcagatgc atgaggatat aatcagttta tgggatcaaa gcctaaagcc atgtgtaaaa
      361 atgacaccac tctgtgtaac tttagaatgt ggaaatgtga ctgttcccaa ggataatagt
      421 acctacaatg gtgatatcaa tagtaatact accatgaaag aagaaatgag aaattgctct
      481 ttcaatgcaa ccacagtaat aaatgataag acaagtaagg tgcatgcact ttttatagg
      541 gttgatatag taccacttaa tgatgagaat agtaacaaga ctaatgccaa ctctactaag
      601 cctactaagt atatattaat aaattgtaat acctcaacca taacacaagc ctgtccaaag
      661 gtcagtttgg gcccaattcc tatacattat tgtgctccag ctggatttgg gattctaaag
      721 tgtaccaata agacattcaa tgggacaggg ccatgccata atgtcagcac agtacaatgt
      781 acacatggaa ttaagccagt ggtatcaact caactactgt taaatggtag cctatcagaa
      841 gaagggataa taattagatc tgaaaatctg acaaacaatg cccaaacaat aatagtacag
      901 cttaataaat ctatagagat tgtgtgtgca agacctggca ataatacaag aaaaagtata
                            v3 loop ->
      961 aggataggac caggccaaac attctttgca acaggtgcca taataggaga cataagacaa
     1021 gcacattgta acattagtag aagtgaatgg aatgaaacat taccaaatgt tagtaggaaa
                  <- v3 loop
     1081 ttagcaggac acttccctaa taggaccata atatttgaac catcctcagg aggggaccta
     1141 gaaattacaa cacatagctt taattgtaga ggagaatttt tctattgcaa tacctcaatc
     1201 ctgtttaata gatcacactt aggcttgttt aatggtacag aaaataattc accccaaaac
     1261 atcactatcc catgcagaat aaaccaaatt ataaacatgt ggcaggaggt aggaaaagct
     1321 atgtatcccc ctcccattgc aggaaacata acatgtatat caaatatcac aggactacta
     1381 ttgacacgtg atggaggaat agatacaaat agtacaaaaa tcacacatga aacaaatggc
     1441 acaaggaacg agacattcag acctggagga ggagatatga gggacaattg gagaagtgaa
     1501 ttatataaat ataaagtagt agaaattaag ccactaggaa tagcacccac tgggcccaaa
     1561 aggagagtgg tggagaagca gatagagaag agagcagtgg gaataggagc tgtgttcctt
     1621 gggttcttgg gagcagcagg aagcactatg ggcgcggcgt cactgacgct gacggtacag
     1681 gccagacaag tgttgtctgg tatagtgcaa cagcaaagca atttgctgag agctatagag
     1741 gcgcaacagc atatattgca actcacggtc tggggcatta agcagctcca ggcaagagtc
```

```
1801 ctggccatag aaagatacct aaaggatcaa cagctcctag ggatttgggg ctgctctgga
1861 aaactcatct gcaccactgc tgtgccttgg aactccagtt ggactaataa aacttacgaa
1921 tatatttgga ataacatgac ctggatgcag tgggagaaag aaattagtaa ttactcagac
1981 acaatatata agttgcttga agactcgcaa acccagcagg aacaaaatga aaaagagtta
2041 ttagcattgg acaagtggaa tattctgtgg aattggtttg acatatcaaa atggctgtgg
2101 tatataagaa tattcataat gatagtagga ggcttgatag gtttaagaat aatttttgct
2161 gtgctatcta tagtgaatag agttaggcag ggatactcac ctttgtcgtt tcAGaccctt
                                                  3' sj (tat,rev) /\
2221 accccgaaca tcaggggga acccgacagg ctcggaagaa tcgaagaaga aggtggagag
2281 caagacagag acagatccat tcgattagtg aacggattct tagcacttgt ctgggacgac
2341 ctgcggagcc tgtgccgttt cagctaccac caattgagag acttcacatt gattgcagcg
2401 agagcggtgg aacttctggg acggagcagt ctcaggggac tacagagggg gtgggaagcc
2461 cttaaatatc tgggaagtct tgtgcagtac tggggtctgg aactaaaaaa gagtgccatt
2521 agtttgcttg ataccatagc aatagcagta gctgaaggaa cagataggat tatagaatta
2581 gtacaaagaa tttgtagagc tatccgtaat atacctagaa gaata
                                                  env ->
```

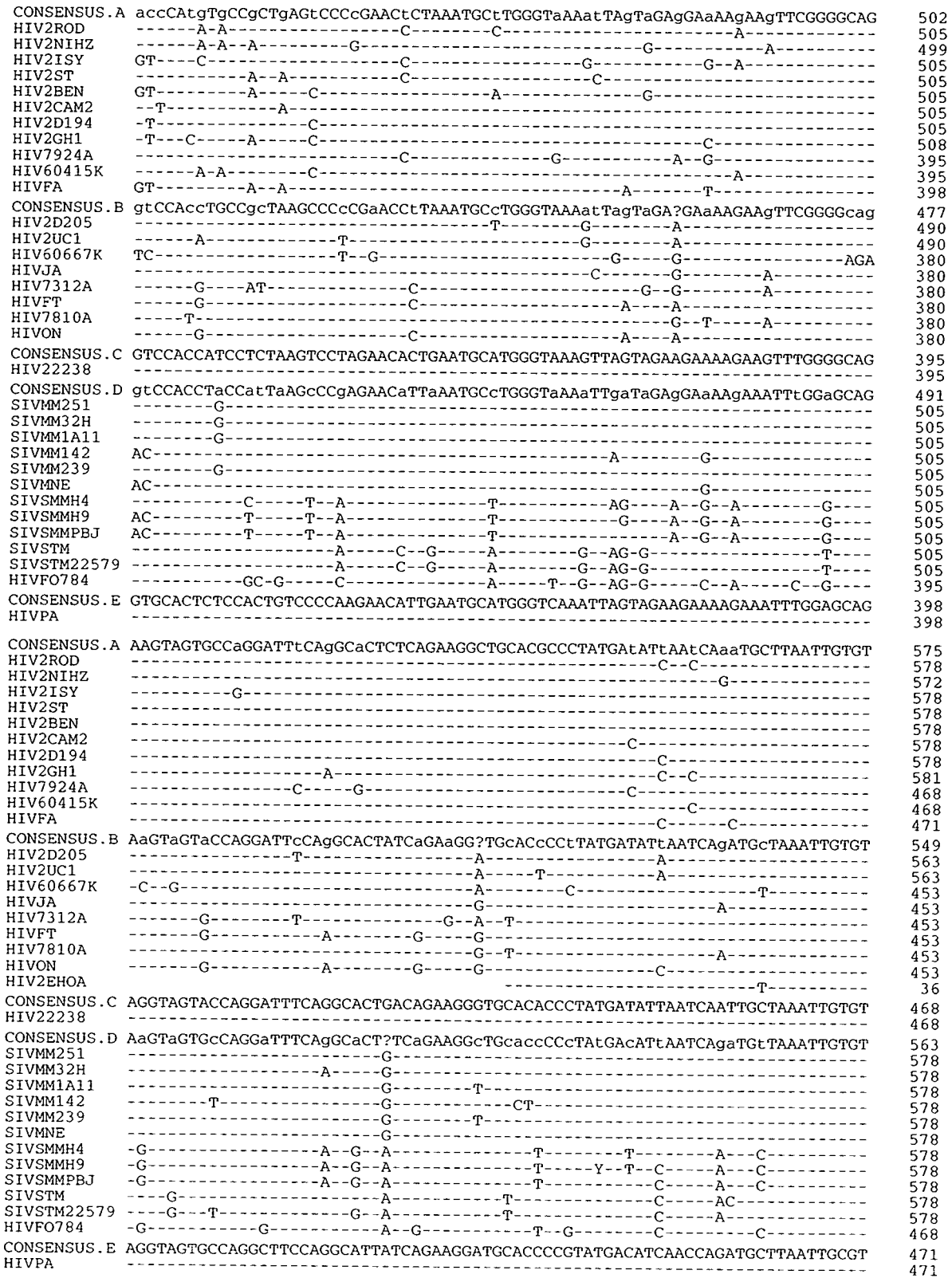


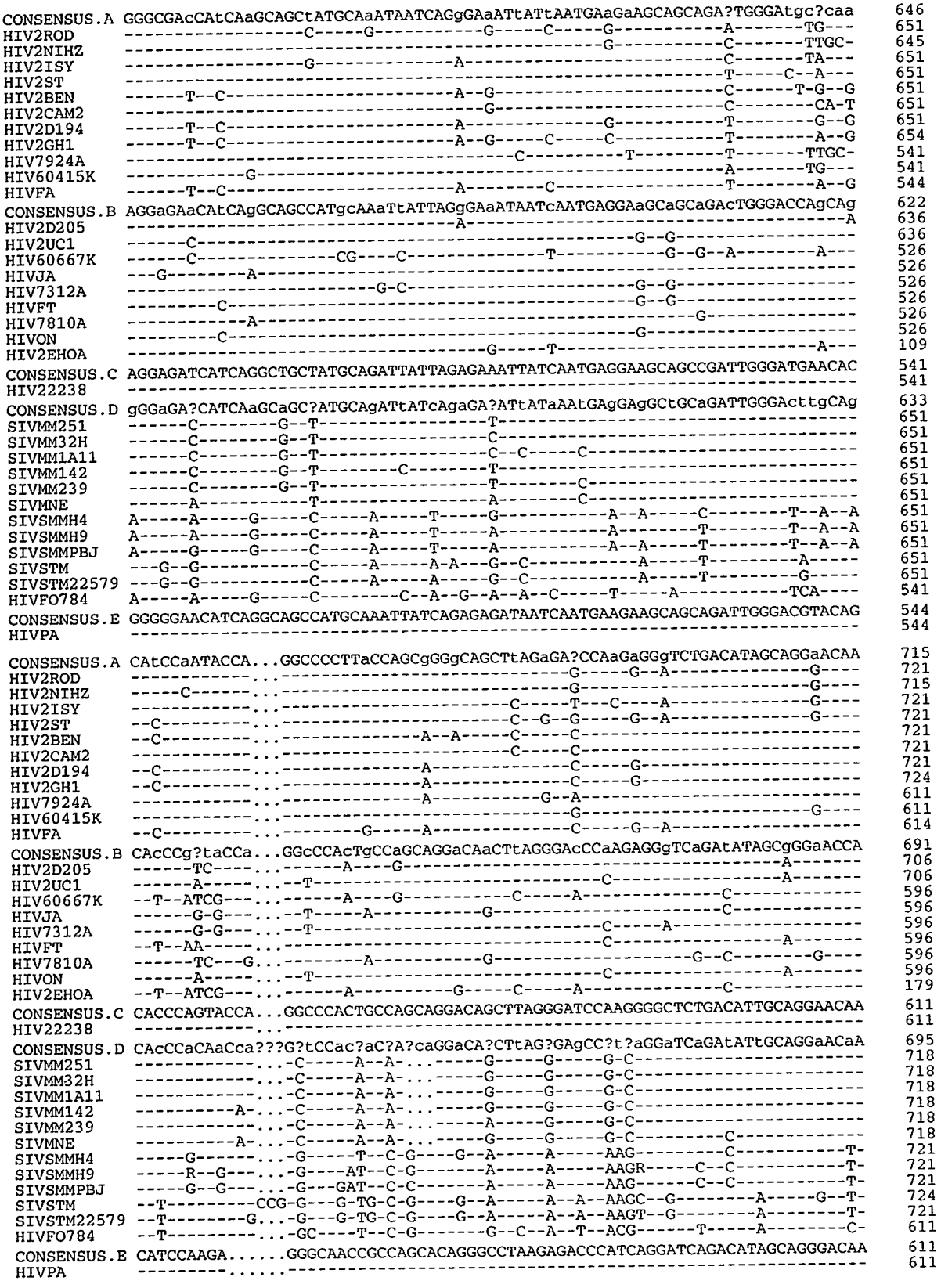
HIV2/SIV GAG


CONSENSUS.A CCTGTTGGAgTCAAAAGAaGGTTGcCAAAaaATTcTtacAGTTTTAgAtCCAtTaGTACCgACAGGgTCAGAA 217
HIV2ROD ----------G-----T----------A-G----------T------ 219
HIV2NIHZ ----------T------ 219
HIV2ISY ----------A--T----------A----------A---------- 219
HIV2ST ----------G---------- 219
HIV2BEN ----------G-----C-G----------A---------- 219
HIV2CAM2 ---------A----------G--------A----------T------ 219
HIV2D194 ---------A----------G-------A---------A----------A---------- 219
HIV2GH1 ----------G-----C----------A---------- 219
HIV7924A ----------T----G----A--T----------C------ 109
HIV60415K ----------G----------T------ 109
HIVFA ----------G---A-C---------A---------- 109
CONSENSUS.B CCTGTTGGaaTCAAAAGAAGGATGtCAcAAAATTCTtacgGtCTTAGctCCATTAgTaCCAACAGGaTCAGAA 211
HIV2D205 ----------A----------AA----------G------ 219
HIV2UC1 ---------- 219
HIV60667K --------G----------C--T--------CG-A-------AG---------- 109
HIVJA ----------C---------- 109
HIV7312A ----------G----------A-G--------G------ 109
HIVFT ---------G---------- 109
HIV7810A --------G----------C---------- 109
HIVON ----------T------ 109
CONSENSUS.C CCTGTTGGAGACCAAAGAAGGATGCCAAAAAATTTTAACAGTGTTAGAACCATTAGTTCCGACAGGTTCAGAA 109
HIV22238 ---------- 109
CONSENSUS.D CCTGTTGGAgaacAAaGAAGGaTGTCAAAAAAT?cTttCgGTcTTAGctCCATTAGTgCCaACAGG?TCAGAA 215
SIVMM251 ----------A----------C------ 219
SIVMM32H ----------A----------C------ 219
SIVMM1A11 ----------A----------C------ 219
SIVMM142 ----------A----------C------ 219
SIVMM239 ----------A----------C------ 219
SIVMNE ----------A----------C------ 219
SIVSMMH4 ---------T----------T----------T-----A--T----------T--G-----T------ 219
SIVSMMH9 ----------T----------T-----A--T----------T--G-----T------ 219
SIVSMMPBJ ----------T----------T-----A--T----------T--G-----T------ 219
SIVSTM ----------TCA--------G----------TA-AA---------AA----------T------ 219
SIVSTM22579 ----------TCA--G-----T----------T--AA-A-------AA----------T------ 219
HIVFO784 ---------A--T--------G----------T--C----------A--G-----T------ 109
CONSENSUS.E CCTGTTGGAAAACAAGGAAGGATGTCACAGAATACTGACAGTACTAGAACCATTAATGCCAACAGGCTCTGAA 109
HIVPA ---------- 109
CONSENSUS.A AATTTAaAAAGcCTtTtTAAtACtgtCTGCGTcattTGGTGcaTaCACGCAGAAGAGAAAGtGAAAGAtACTG 290
HIV2ROD ----------T---------- 292
HIV2NIHZ ----------C---------- 292
HIV2ISY ----------A-------AC----------T-G---------- 292
HIV2ST ----------T----------C---------- 292
HIV2BEN ----------C----------T-G---------- 292
HIV2CAM2 ----------A---------- 292
HIV2D194 ----------C----------T-G---------- 292
HIV2GH1 ----------C--A----------T-G---------- 292
HIV7924A ----------AG----------C---- 182
HIV60415K ----------C----------GC---------- 182
HIVFA ------C----T----------A----------C------T-G---------- 182
CONSENSUS.B AATTTAAAaAGcCTTTTTAATActGTCTGCGTcaTtTatTGCtTgCACGCAGaAgAGAAAGTGAAAGATACtG 284
HIV2D205 ----------TC----------T----C----------A- 292
HIV2UC1 ----------C---------- 292
HIV60667K --------G----------C----------C---------G---------- 182
HIVJA ----------T----------TG---------- 182
HIV7312A ----------GG-----A---------A----------C- 182
HIVFT ----------TC----------C---------- 182
HIV7810A ----------G----------A---------- 182
HIVON ----------C--C---------- 182
CONSENSUS.C AATTTAAAGAGCCTTTATAATACTACCTGCGTCATTTGGTGTTTACACGCAGAACAGAAAGTGAAACATACAG 182
HIV22238 ---------- 182
CONSENSUS.D AAtTTAAA?AGcCTTTatAAtACTGTCtGCGTCaTcTGGTGcaTtCACGCAGAAGAGAAAGTGAAAcAcACTG 287
SIVMM251 --------A---------- 292
SIVMM32H --------A---------- 292
SIVMM1A11 --------A---------- 292
SIVMM142 --------A---------- 292
SIVMM239 --------A---------- 292
SIVMNE --------G---------- 292
SIVSMMH4 --C-----G----------T----------T---- 292
SIVSMMH9 --------G----------C------C-----C-T----------T---- 292
SIVSMMPBJ --------G----------C----------C-T---------- 292
SIVSTM --------G--T----T----------T-----T--C----------T---- 292
SIVSTM22579 --------G-------T----------T-----T--C----------T---- 292
HIVFO784 --------A--------C----------TT-A----------G------ 182
CONSENSUS.E AATTTAAAAAGCTTGTTTAACGCTGTCTGCGTAGTTTACTGCCTGCACGCAGCAGTGAAAGTGAAAGATACAG 182
HIVPA ---------- 182

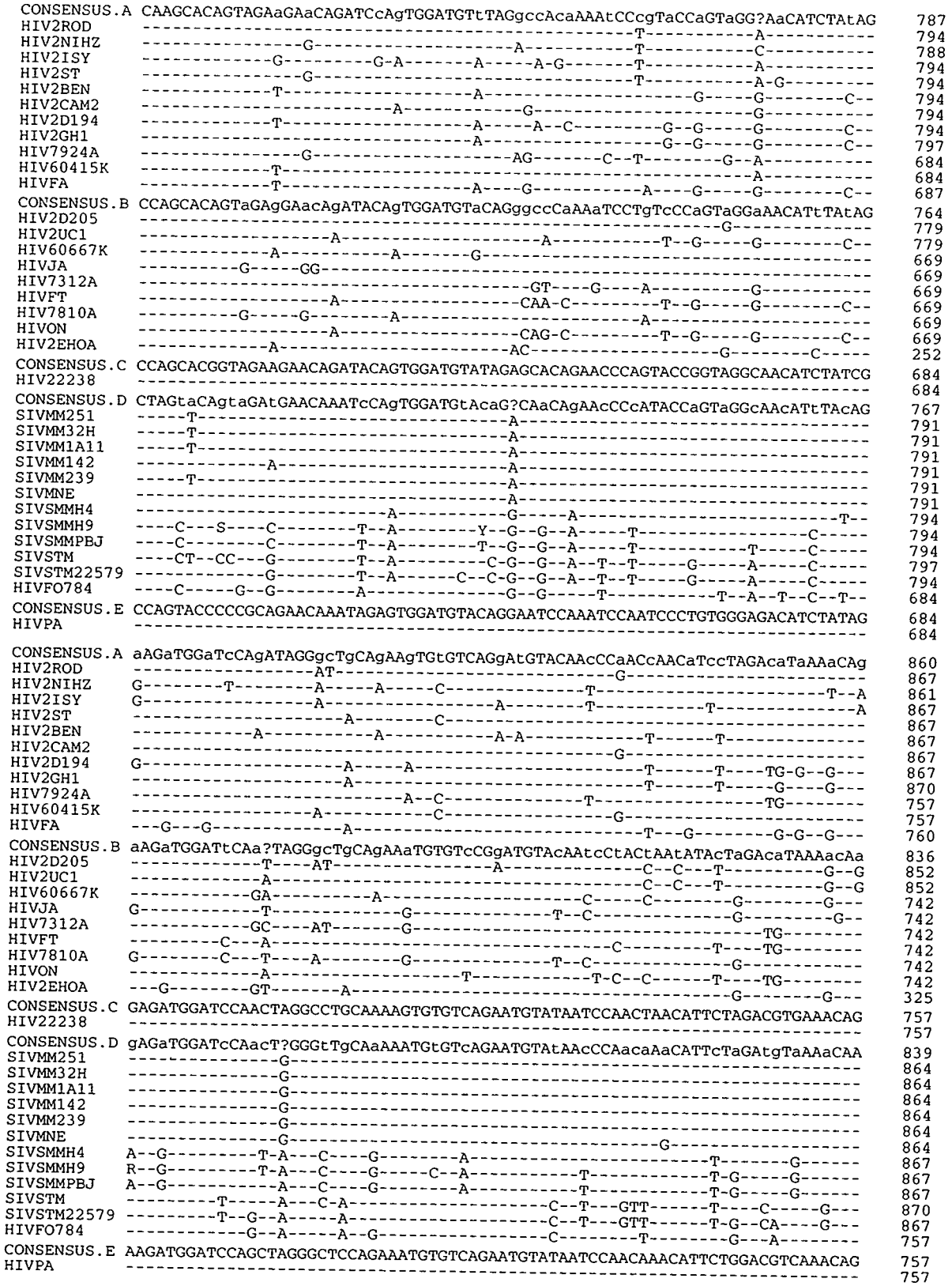


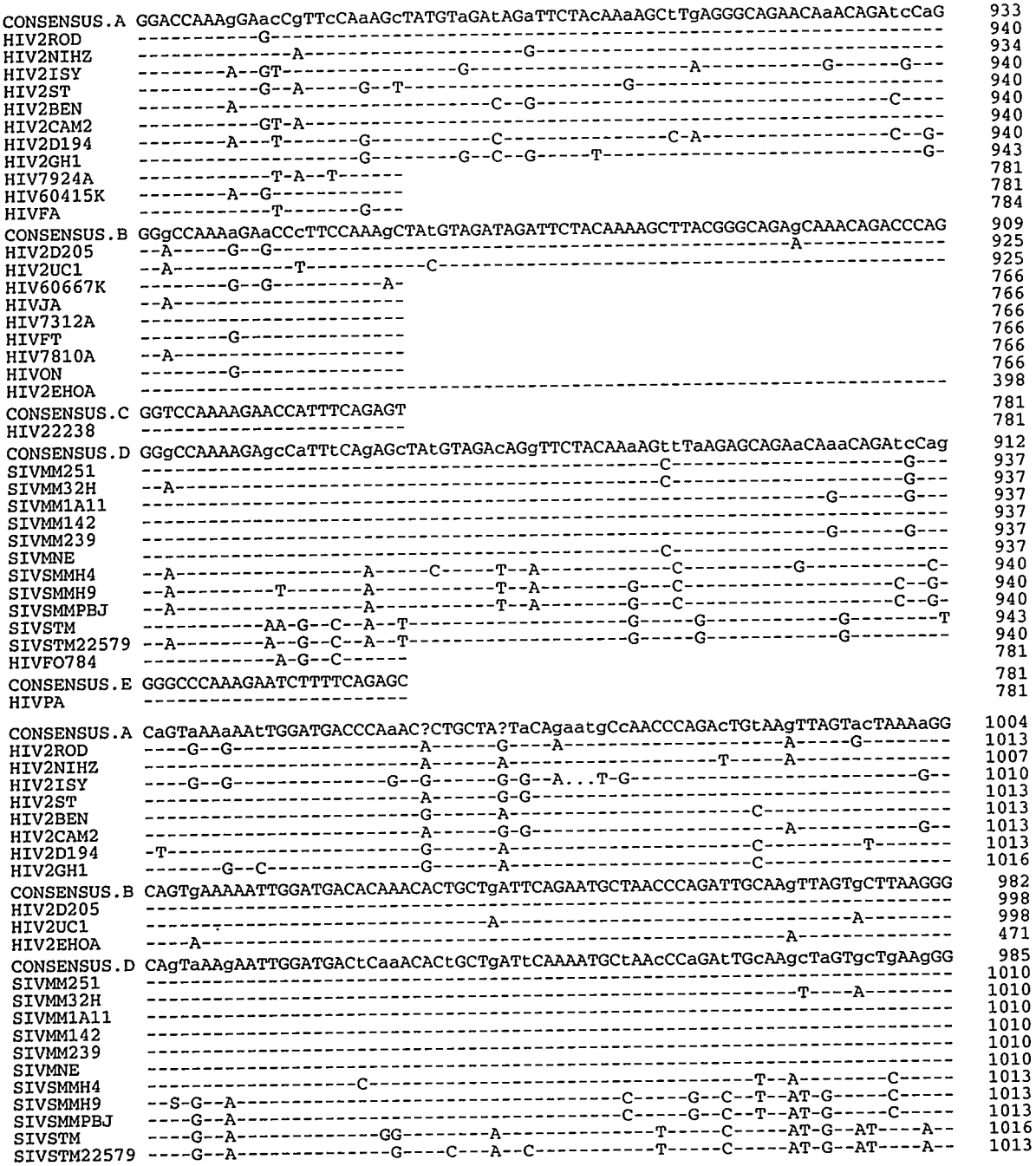
HIV2/SIV GAG



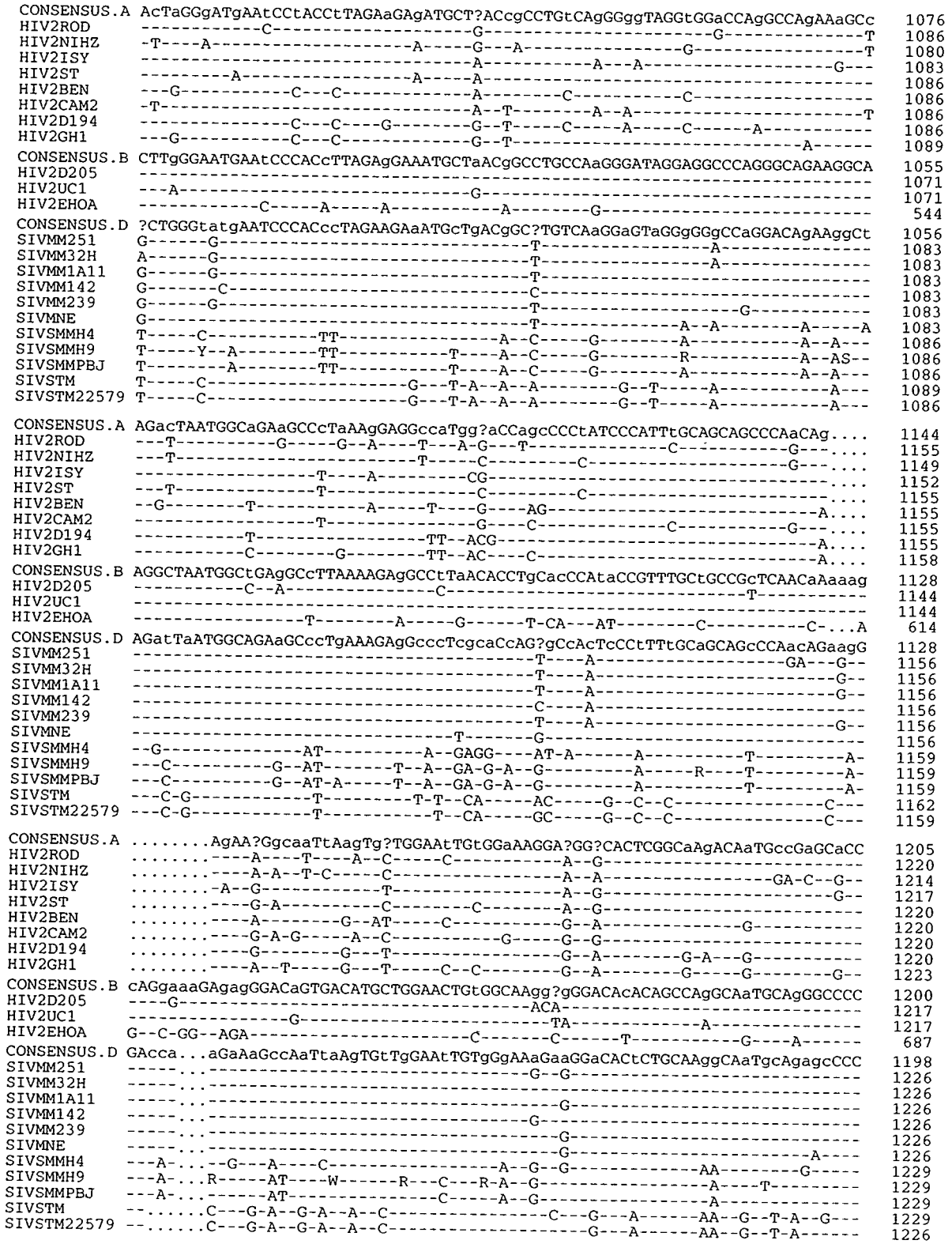


HIV2/SIV GAG


CONSENSUS.A CAAGCACAGTAGAaGAaCAGATCcAgTGGATGTtTAGgccAcaAAAtCCcgTaCCaGTaGG?AaCATCTAtAG 787
HIV2ROD 794
HIV2NIHZ 788
HIV2ISY 794
HIV2ST 794
HIV2BEN 794
HIV2CAM2 794
HIV2D194 794
HIV2GH1 797
HIV7924A 684
HIV60415K 684
HIVFA 687
CONSENSUS.B CCAGCACAGTaGAgGAacAgATACAgTGGATGTaCAGggccCaAAaTCCTgTcCCaGTaGGaAACATtTAtAG 764
HIV2D205 779
HIV2UC1 779
HIV60667K 669
HIVJA 669
HIV7312A 669
HIVFT 669
HIV7810A 669
HIVON 669
HIV2EHOA 669
CONSENSUS.C CCAGCACGGTAGAAGAACAGATACAGTGGATGTATAGAGCACAGAACCCAGTACCGGTAGGCAACATCTATCG 684
HIV22238 684
CONSENSUS.D CTAGtaCAgtaGAtGAACAAATcCAgTGGATGtAcaG?CAaCAgAAcCCcATACCaGTaGGcAAcATtTAcAG 767
SIVMM251 791
SIVMM32H 791
SIVMM1A11 791
SIVMM142 791
SIVMM239 791
SIVMNE 791
SIVSMMH4 794
SIVSMMH9 794
SIVSMMPBJ 794
SIVSTM 794
SIVSTM22579 797
HIVFO784 794
CONSENSUS.E CCAGTACCCCCGCAGAACAAATAGAGTGGATGTACAGGAATCCAAATCCAATCCCTGTGGGAGACATCTATAG 684
HIVPA 684
CONSENSUS.A aAGaTGGaTcCAgATAGGgcTgCAgAAgTGtGTCAGgAtGTACAAcCCaACcAACaTccTAGAcaTaAAaCAg 860
HIV2ROD 867
HIV2NIHZ 861
HIV2ISY 867
HIV2ST 867
HIV2BEN 867
HIV2CAM2 867
HIV2D194 867
HIV2GH1 870
HIV7924A 757
HIV60415K 757
HIVFA 760
CONSENSUS.B aAGaTGGATtCAa?TAGGgcTgCAgAAaTGTGTcCGgATGTAcAAtcCtACtAAtATAcTaGAcaTAAAacAa 836
HIV2D205 852
HIV2UC1 852
HIV60667K 742
HIVJA 742
HIV7312A 742
HIVFT 742
HIV7810A 742
HIVON 742
HIV2EHOA 325
CONSENSUS.C GAGATGGATCCAACTAGGCCTGCAAAAGTGTGTCAGAATGTATAATCCAACTAACATTCTAGACGTGAAACAG 757
HIV22238 757
CONSENSUS.D gAGaTGGATcCAacT?GGGtTgCAaAAATGtGTcAGAATGTAtAAcCCAacaAaCATTcTaGAtgTaAAaCAA 839
SIVMM251 864
SIVMM32H 864
SIVMM1A11 864
SIVMM142 864
SIVMM239 864
SIVMNE 864
SIVSMMH4 867
SIVSMMH9 867
SIVSMMPBJ 867
SIVSTM 867
SIVSTM22579 870
HIVFO784 867
CONSENSUS.E AAGATGGATCCAGCTAGGGCTCCAGAAATGTGTCAGAATGTATAATCCAACAAACATTCTGGACGTCAAACAG 757
HIVPA 757



HIV2/SIV GAG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HIV2ROD 1086
HIV2NIHZ 1080
HIV2ISY 1083
HIV2ST 1086
HIV2BEN 1086
HIV2CAM2 1086
HIV2D194 1086
HIV2GH1 1089
CONSENSUS.B CTTgGGAATGAAtCCCACcTTAGAgGAAATGCTaACgGCCTGCCAaGGGATAGGAGGCCCAGGGCAGAAGGCA 1055
HIV2D205 1071
HIV2UC1 1071
HIV2EHOA 544
CONSENSUS.D ?CTGGGtatgAATCCCACccTAGAAGAaATGcTgACgGC?TGTCAaGGaGTaGGgGGgCCaGGACAgAAggCt 1056
SIVMM251 1083
SIVMM32H 1083
SIVMM1A11 1083
SIVMM142 1083
SIVMM239 1083
SIVMNE 1083
SIVSMMH4 1083
SIVSMMH9 1086
SIVSMMPBJ 1086
SIVSTM 1086
SIVSTM22579 1089
CONSENSUS.A AGacTAATGGCaGAaGCCcTaAAgGAGGccaTgg?aCCagcCCCtATCCCATTtGCAGCAGCCCAaCAg.... 1144
HIV2ROD 1155
HIV2NIHZ 1149
HIV2ISY 1152
HIV2ST 1155
HIV2BEN 1155
HIV2CAM2 1155
HIV2D194 1155
HIV2GH1 1158
CONSENSUS.B AGGCTAATGGCtGAgGCcTTAAAAGAgGCCtTaACACCTgCacCCAtaCCGTTTGCtGCCGcTCAACaAaaag 1128
HIV2D205 1144
HIV2UC1 1144
HIV2EHOA 614
CONSENSUS.D AGatTaATGGCAGAaGCccTgAAAGAgGcccTcgcaCcAG?gCcAcTcCCtTTtGCaGCAGcCCAacAGaagG 1128
SIVMM251 1156
SIVMM32H 1156
SIVMM1A11 1156
SIVMM142 1156
SIVMM239 1156
SIVMNE 1156
SIVSMMH4 1159
SIVSMMH9 1159
SIVSMMPBJ 1159
SIVSTM 1162
SIVSTM22579 1159
CONSENSUS.A .....AgAA?GgcaaTtAagTg?TGGAAtTGtGGaAAGGA?GG?CACTCGGCaAgACAaTGccGaGCaCC 1205
HIV2ROD 1220
HIV2NIHZ 1214
HIV2ISY 1217
HIV2ST 1220
HIV2BEN 1220
HIV2CAM2 1220
HIV2D194 1220
HIV2GH1 1223
CONSENSUS.B cAGgaaaGAgagGGACaGTGACATGCTGGAACTGtGGCAAgg?gGGACAcACAGCCAgGCAaTGCAgGGCCCC 1200
HIV2D205 1217
HIV2UC1 1217
HIV2EHOA 687
CONSENSUS.D GAcca...aGaAaGccAaTtaAgTGtTgGAAtTGTgGgAAaGaaGGaCACtCTGCAAggCAaTgcAgagcCCC 1198
SIVMM251 1226
SIVMM32H 1226
SIVMM1A11 1226
SIVMM142 1226
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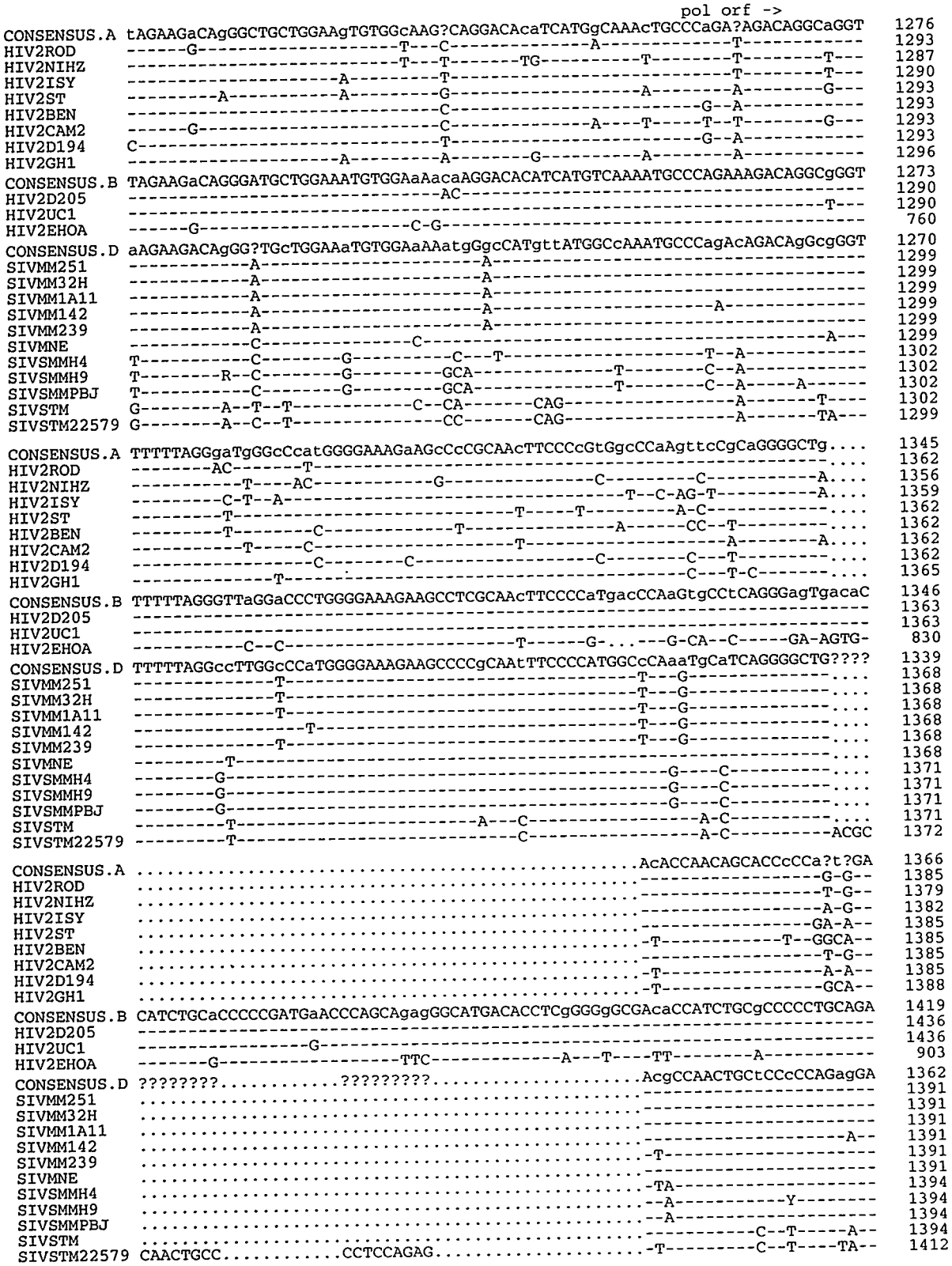
SIVSMMH9 1229
SIVSMMPBJ 1229
SIVSTM 1229
SIVSTM22579 1229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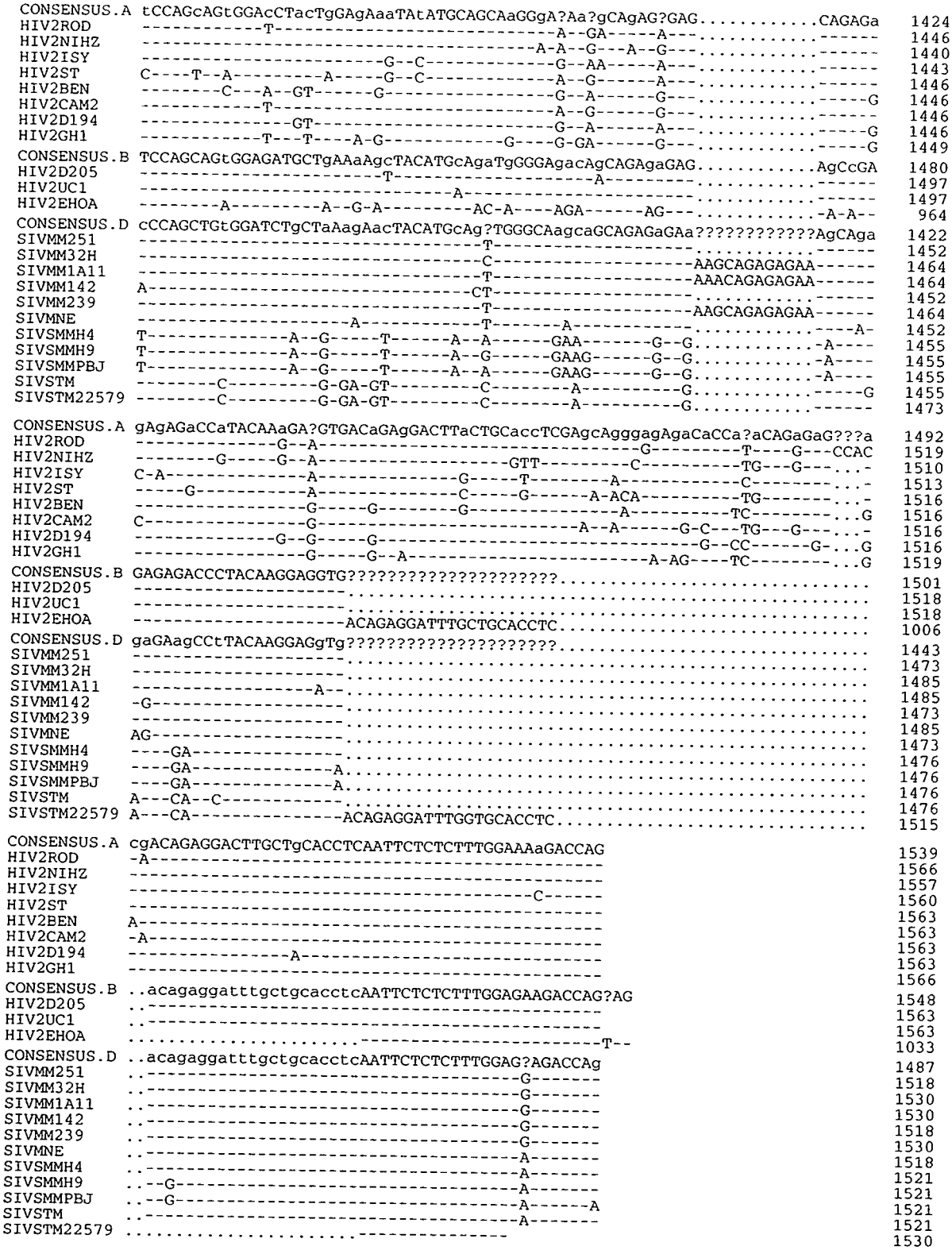
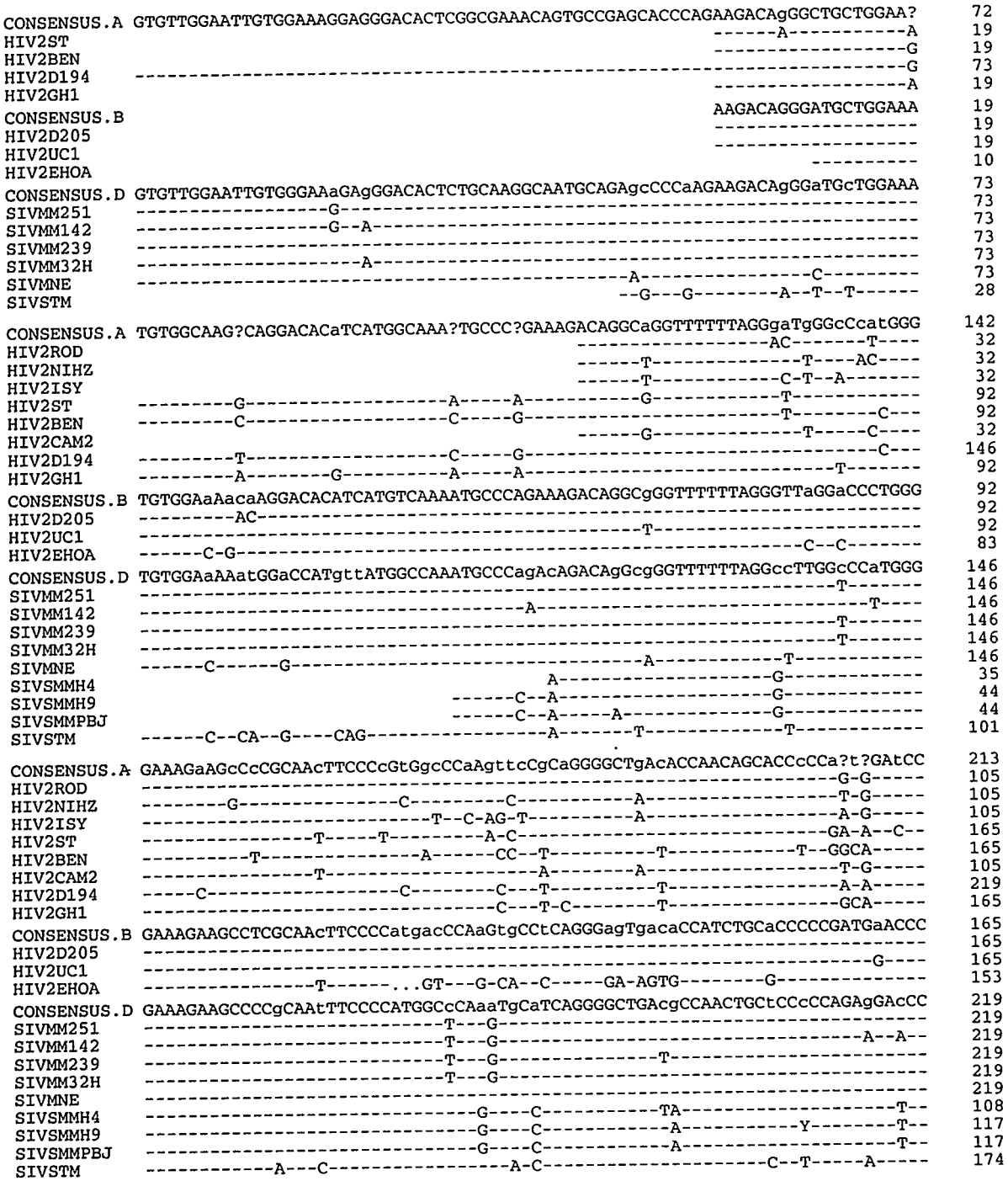
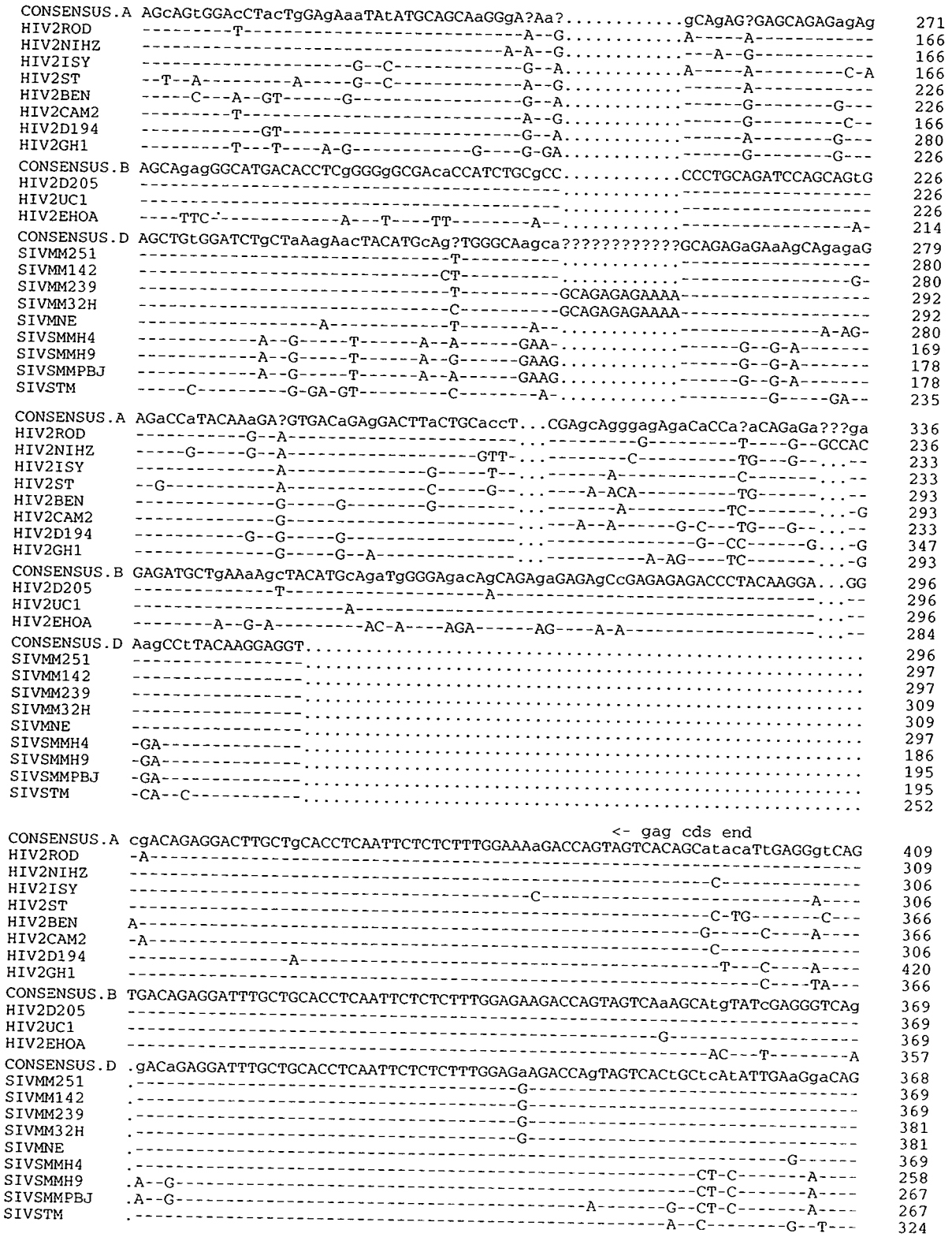
HIV2NIHZ 1287
HIV2ISY 1290
HIV2ST 1293
HIV2BEN 1293
HIV2CAM2 1293
HIV2D194 1293
HIV2GH1 1296
CONSENSUS.B TAGAAGaCAGGGATGCTGGAAATGTGGAaAacaAGGACACATCATGTCAAAATGCCCAGAAAGACAGGCgGGT 1273
HIV2D205 1290
HIV2UC1 1290
HIV2EHOA 760
CONSENSUS.D aAGAAGACAgGG?TGcTGGAAaTGTGGAaAAatgGgcCATgttATGGCcAAATGCCCagAcAGACAgGcgGGT 1270
SIVMM251 1299
SIVMM32H 1299
SIVMM1A11 1299
SIVMM142 1299
SIVMM239 1299
SIVMNE 1299
SIVSMMH4 1302
SIVSMMH9 1302
SIVSMMPBJ 1302
SIVSTM 1302
SIVSTM22579 1299
CONSENSUS.A TTTTTAGGgaTgGGcCcatGGGGAAAGaAGcCcCGCAAcTTCCCcGtGgcCCaAgttcCgCaGGGGCTg.... 1345
HIV2ROD ....
HIV2NIHZ 1362
HIV2ISY 1356
HIV2ST 1359
HIV2BEN 1362
HIV2CAM2 1362
HIV2D194 1362
HIV2GH1 1362
CONSENSUS.B TTTTTAGGGTTaGGaCCCTGGGGAAAGAAGCCTCGCAAcTTCCCCaTgacCCAaGtgCCtCAGGGagTgacaC 1365
HIV2D205 1346
HIV2UC1 1363
HIV2EHOA 1363
CONSENSUS.D TTTTTAGGccTTGGcCCaTGGGGAAAGAAGCCCCgCAAtTTCCCCATGGCcCAaaTgCaTCAGGGGCTG???? 830
SIVMM251 1339
SIVMM32H 1368
SIVMM1A11 1368
SIVMM142 1368
SIVMM239 1368
SIVMNE 1368
SIVSMMH4 1371
SIVSMMH9 1371
SIVSMMPBJ 1371
SIVSTM 1371
SIVSTM22579 1372
CONSENSUS.A 1366
HIV2ROD 1385
HIV2NIHZ 1379
HIV2ISY 1382
HIV2ST 1385
HIV2BEN 1385
HIV2CAM2 1385
HIV2D194 1385
HIV2GH1 1388
CONSENSUS.B CATCTGCaCCCCCGATGaACCCAGCAgagGGCATGACACCTCgGGGgGCGAcaCCATCTGCgCCCCCTGCAGA 1419
HIV2D205 1436
HIV2UC1 1436
HIV2EHOA 903
CONSENSUS.D ????????.....????????.....AcgCCAACTGCtCCcCCAGagGA 1362
SIVMM251 1391
SIVMM32H 1391
SIVMM1A11 1391
SIVMM142 1391
SIVMM239 1391
SIVMNE 1391
SIVSMMH4 1394
SIVSMMH9 1394
SIVSMMPBJ 1394
SIVSTM 1394
SIVSTM22579 CAACTGCC.....CCTCCAGAG..... 1412

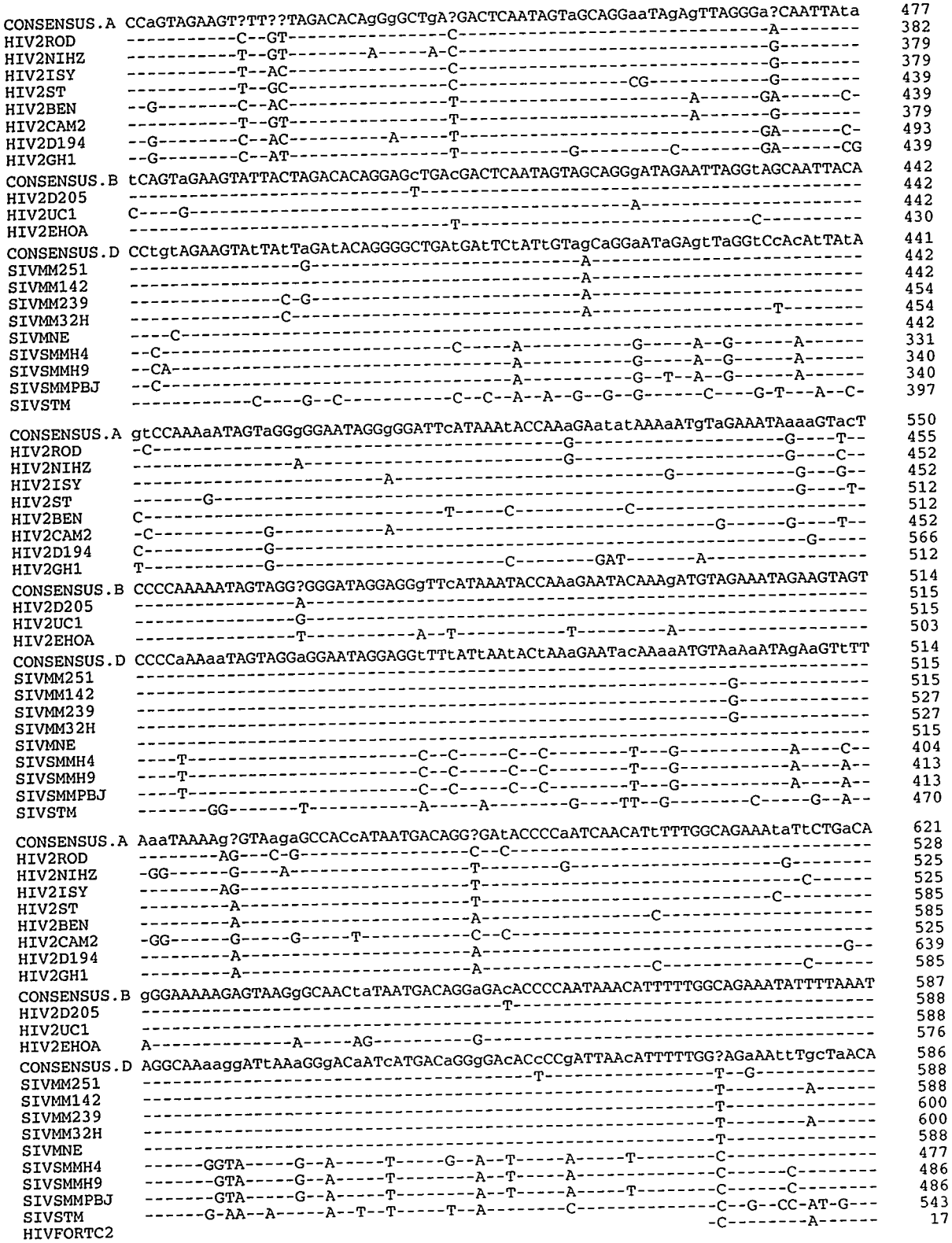
HIV2/SIV GAG



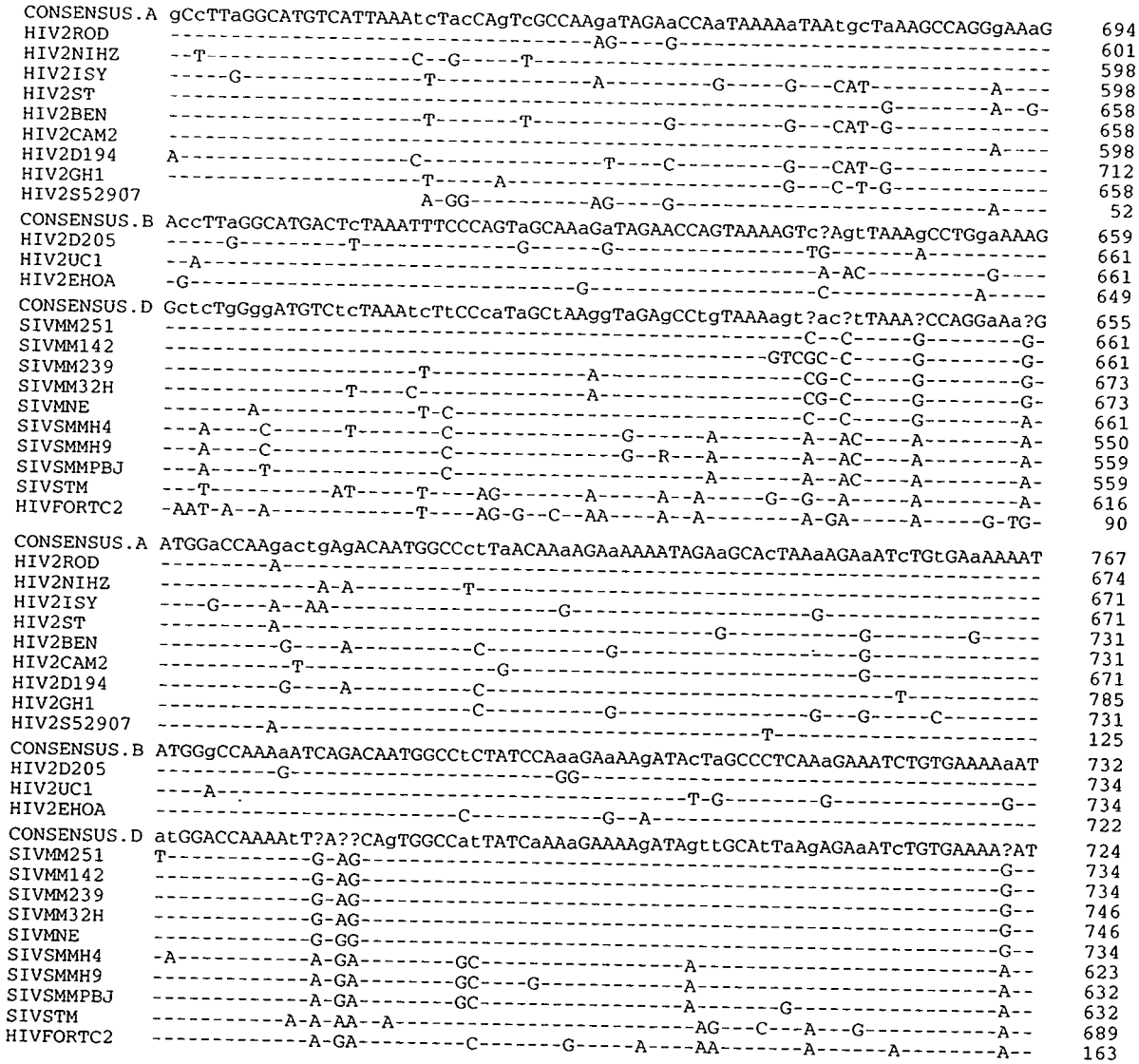


HIV2/SIV POL


CONSENSUS.A AGcAGtGGAcCTacTgGAgAaaTAtATGCAGCAaGGgA?Aa?.....gCAgAG?GAGCAGAGagAg 271
HIV2ROD ---------T----------A--G.....A-----A---------- 166
HIV2NIHZ ----------A-A--G.....---A--G---------- 166
HIV2ISY ----------G--C----------G--A.....A-----A---------C-A 166
HIV2ST --T--A---------A-----G--C----------A--G.....------A---------- 226
HIV2BEN -----C---A--GT------G----------G--A.....------G--------G--- 226
HIV2CAM2 ---------T----------A--G.....------G---------C-- 166
HIV2D194 ----------GT----------G--A.....------A--------G--- 280
HIV2GH1 ---------T---T----A-G----------G----G-GA.....------G--------G--- 226
CONSENSUS.B AGCAgagGGCATGACACCTCgGGGgGCGAcaCCATCTGCgCC.....CCCTGCAGATCCAGCAGtG 226
HIV2D205 ---------- 226
HIV2UC1 ---------- 226
HIV2EHOA ----TTC----------A---T----TT--------A--.....----------A- 214
CONSENSUS.D AGCTGtGGATCTgCTaAagAacTACATGcAg?TGGGCAagca????????????GCAGAGaGAaAgCAgagaG 279
SIVMM251 ----------T---------.....---------- 280
SIVMM142 ----------CT---------.....----------G- 280
SIVMM239 ----------T---------GCAGAGAGAAAA---------- 292
SIVMM32H ----------C---------GCAGAGAGAAAA---------- 292
SIVMNE ----------A----------T------A--.....----------A-AG- 280
SIVSMMH4 ----------A--G-----T------A--A------GAA-.....------G--G-A------- 169
SIVSMMH9 ----------A--G-----T------A--G------GAAG.....------G--G-A------- 178
SIVSMMPBJ ----------A--G-----T------A--A------GAAG.....------G--G-A------- 178
SIVSTM -----C---------G-GA-GT---------C--------A-.....---------G-----GA-- 235
CONSENSUS.A AGaCCaTACAAaGA?GTGACaGAgGACTTaCTGCaccT...CGAgcAgggagAgaCaCCa?aCAGaGa???ga 336
HIV2ROD ----------G--A----------...---------G---------T----G--GCCAC 236
HIV2NIHZ -----G-----G--A----------GTT-...---------C----------TG---G--...-- 233
HIV2ISY ----------A----------G-----T--...------A----------C---------...-- 233
HIV2ST --G----------A----------C-----G--...----A-ACA----------TG---------...-- 293
HIV2BEN ----------G-----G--------G---------...-------A----------TC-------...-G 293
HIV2CAM2 ----------G----------...---A--A------G-C---TG---G--...-- 233
HIV2D194 ----------G--G-----G----------...----------G--CC------G...-G 347
HIV2GH1 ----------G-----G--A----------...----------A-AG----TC--------...-G 293
CONSENSUS.B GAGATGCTgAAaAgcTACATGcAgaTgGGGAgacAgCAGAgaGAGAgCcGAGAGAGACCCTACAAGGA...GG 296
HIV2D205 ----------T----------A----------...--- 296
HIV2UC1 ----------A----------...-- 296
HIV2EHOA --------A--G-A---------AC-A----AGA------AG----A-A----------...-- 284
CONSENSUS.D AagCCtTACAAGGAGGT..... 296
SIVMM251 ----------..... 297
SIVMM142 ----------..... 297
SIVMM239 ----------..... 309
SIVMM32H ----------..... 309
SIVMNE ----------..... 297
SIVSMMH4 -GA----------..... 186
SIVSMMH9 -GA----------..... 195
SIVSMMPBJ -GA----------..... 195
SIVSTM -CA--C----------..... 252
<- gag cds end
CONSENSUS.A cgACAGAGGACTTGCTgCACCTCAATTCTCTCTTTGGAAAaGACCAGTAGTCACAGCatacaTtGAGGgtCAG 409
HIV2ROD -A---------- 309
HIV2NIHZ ---------- 306
HIV2ISY ----------C---------A---- 306
HIV2ST ----------C-TG-------C--- 366
HIV2BEN A----------G-----C----A---- 366
HIV2CAM2 -A----------C---------- 306
HIV2D194 ----------A----------T---C----A---- 420
HIV2GH1 ----------C----TA--- 366
CONSENSUS.B TGACAGAGGATTTGCTGCACCTCAATTCTCTCTTTGGAGAAGACCAGTAGTCAaAGCAtgTATcGAGGGTCAg 369
HIV2D205 ---------- 369
HIV2UC1 ----------G---------- 369
HIV2EHOA ----------AC---T--------A 357
CONSENSUS.D .gACaGAGGATTTGCTGCACCTCAATTCTCTCTTTGGAGaAGACCAgTAGTCACtGCtcAtATTGAaGgaCAG 368
SIVMM251 .----------G---------- 369
SIVMM142 .----------G---------- 369
SIVMM239 .----------G---------- 381
SIVMM32H .----------G---------- 381
SIVMNE .----------G------ 369
SIVSMMH4 .----------CT-C-------A---- 258
SIVSMMH9 .A--G----------CT-C-------A---- 267
SIVSMMPBJ .A--G----------A-------G--CT-C-------A---- 267
SIVSTM .----------A--C--------G--T--- 324



HIV2/SIV POL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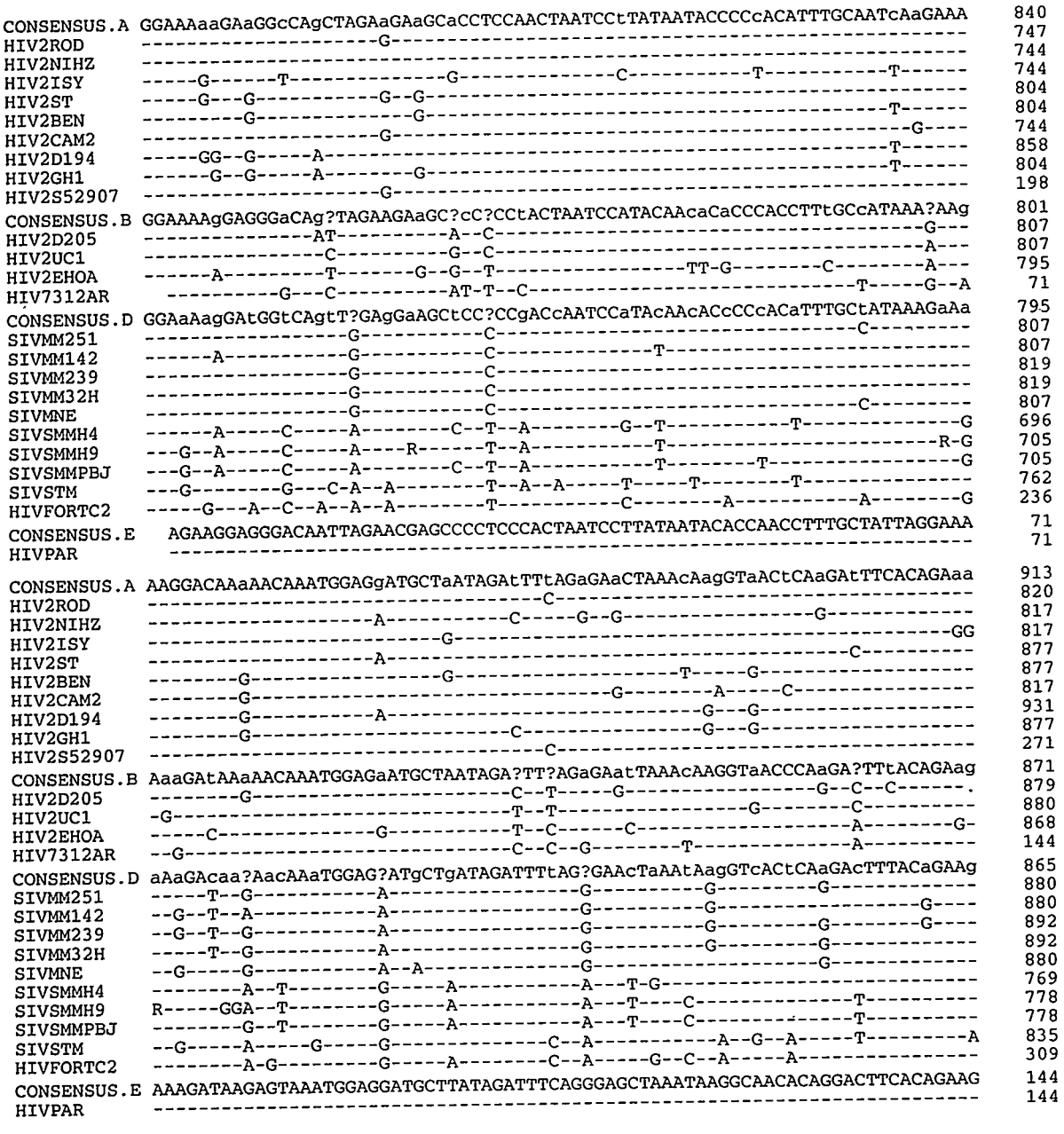
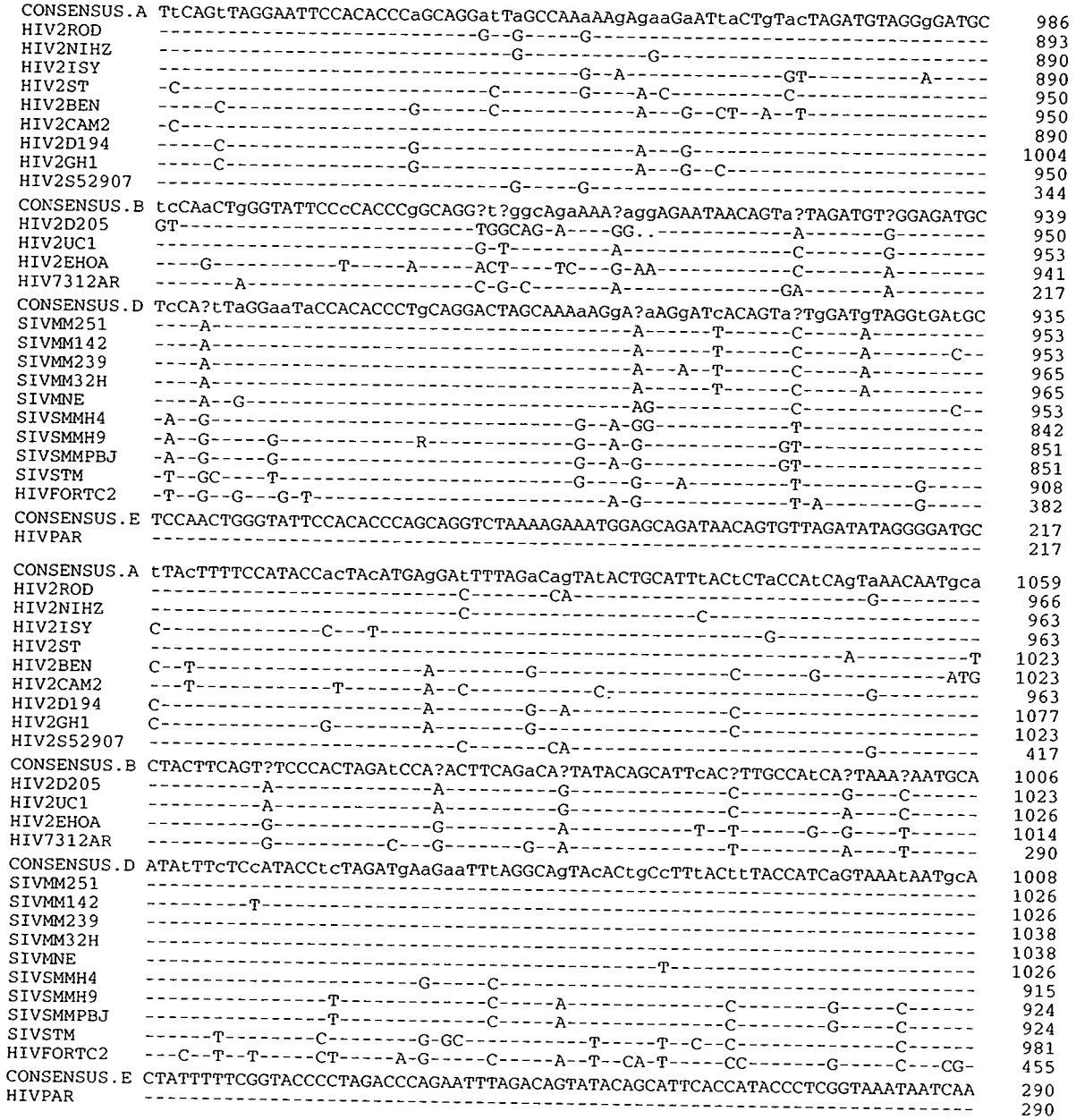
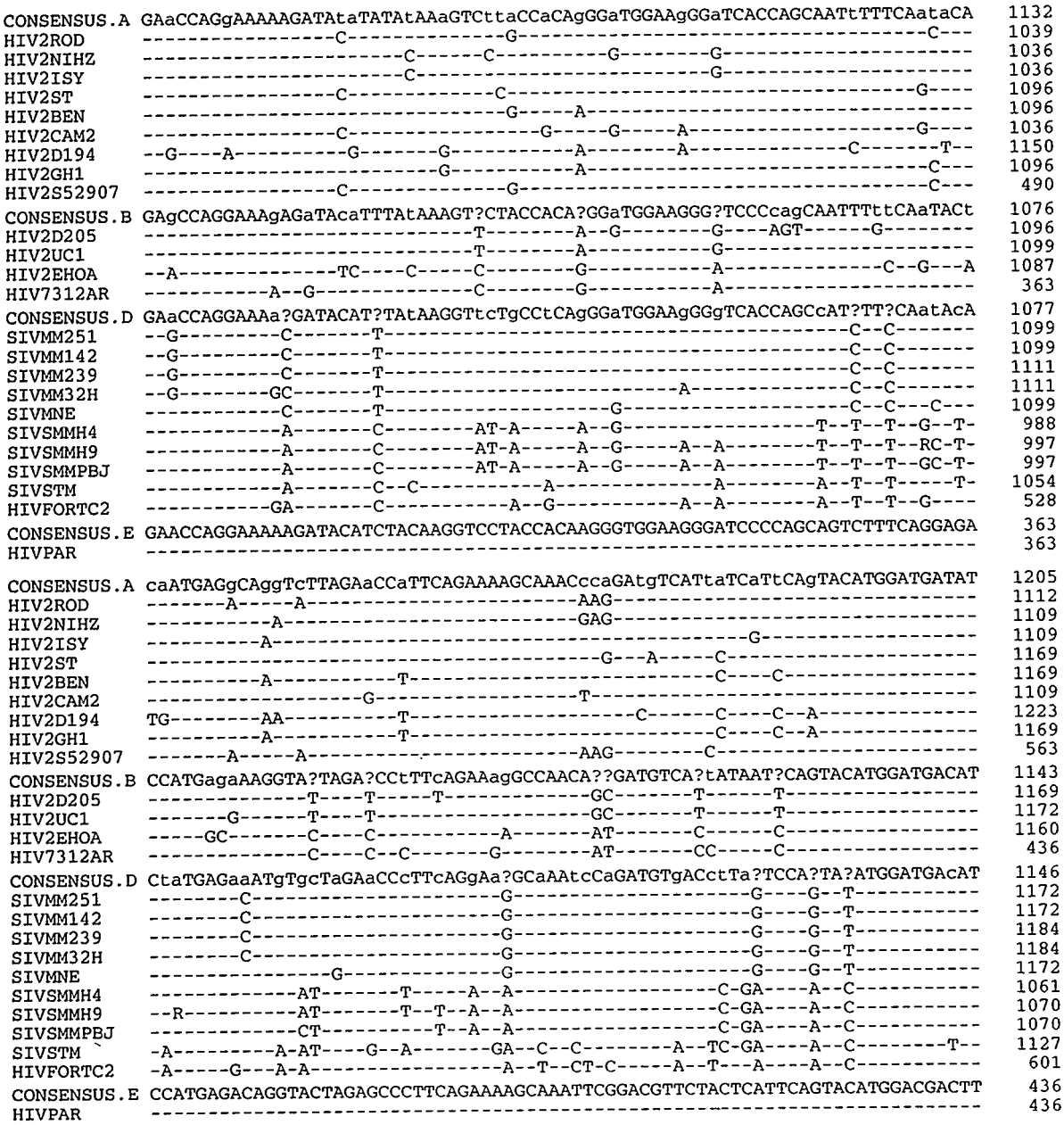
HIV2ROD
HIV2NIHZ
HIV2ISY
HIV2ST
HIV2BEN
HIV2CAM2
HIV2D194
HIV2GH1
HIV2S52907
CONSENSUS.B AccTTaGGCATGACTcTAAATTTCCCAGTaGCAAaGaTAGAACCAGTAAAAGTc?AgtTAAAgCCTGgaAAAG
HIV2D205
HIV2UC1
HIV2EHOA
CONSENSUS.D GctcTgGggATGTCtcTAAAtcTtCCcaTaGCtAAggTaGAgCCtgTAAAagt?ac?tTAAA?CCAGGaAa?G
SIVMM251
SIVMM142
SIVMM239
SIVMM32H
SIVMNE
SIVSMMH4
SIVSMMH9
SIVSMMPBJ
SIVSTM
HIVFORTC2
CONSENSUS.A ATGGaCCAAgactgAgACAATGGCCctTaACAAaAGAaAAAATAGAaGCAcTAAaAGAaATcTGtGAaAAAAT
HIV2ROD
HIV2NIHZ
HIV2ISY
HIV2ST
HIV2BEN
HIV2CAM2
HIV2D194
HIV2GH1
HIV2S52907
CONSENSUS.B ATGGgCCAAAaATCAGACAATGGCCtCTATCCAaaGAaAAgATAcTaGCCCTCAAaGAAATCTGTGAAAAaAT
HIV2D205
HIV2UC1
HIV2EHOA
CONSENSUS.D atGGACCAAAAtT?A??CAgTGGCCatTATCaAAaGAAAAgATAgttGCAtTaAgAGAaATcTGTGAAAA?AT
SIVMM251
SIVMM142
SIVMM239
SIVMM32H
SIVMNE
SIVSMMH4
SIVSMMH9
SIVSMMPBJ
SIVSTM
HIVFORTC2

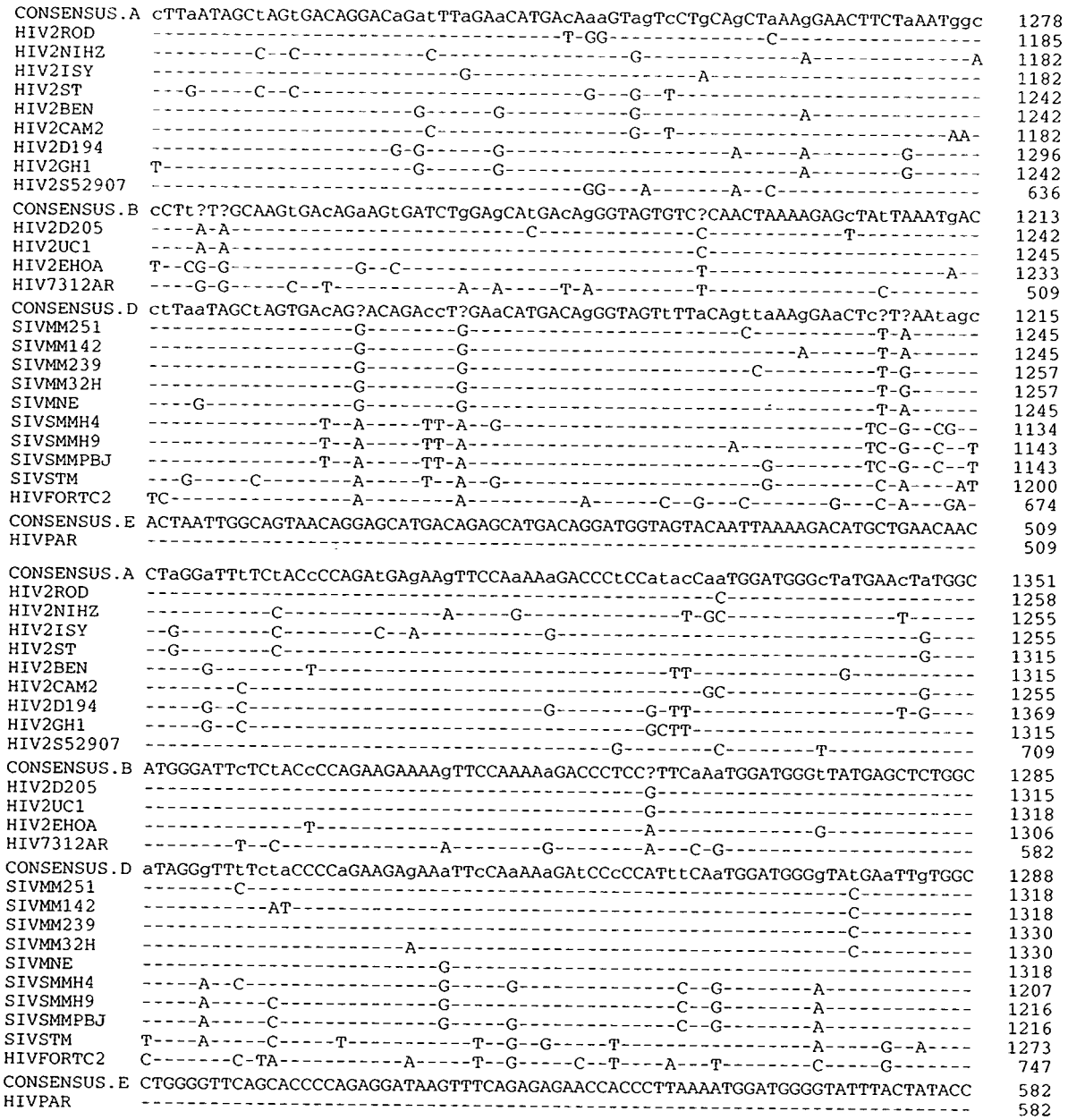


HIV2/SIV POL


CONSENSUS.A TtCAGtTAGGAATTCCACACCCaGCAGGatTaGCCAAaAAgAgaaGaATtaCTgTacTAGATGTAGGgGATGC 986
HIV2ROD ----------G--G-----G---------- 893
HIV2NIHZ ----------G----------G---------- 890
HIV2ISY ----------G--A----------GT----------A----- 890
HIV2ST -C----------C-------G----A-C----------C---------- 950
HIV2BEN -----C----------G------C----------A---G--CT--A--T---------- 950
HIV2CAM2 -C---------- 890
HIV2D194 -----C----------G----------A---G---------- 1004
HIV2GH1 -----C----------G----------A---G--C---------- 950
HIV2S52907 ----------G-----G---------- 344
CONSENSUS.B tcCAaCTgGGTATTCCcCACCCgGCAGG?t?ggcAgaAAA?aggAGAATAACAGTa?TAGATGT?GGAGATGC 939
HIV2D205 GT----------TGGCAG-A----GG..----------A-------G-------- 950
HIV2UC1 ----------G-T---------A----------C-------G-------- 953
HIV2EHOA ----G----------T-----A-----ACT----TC---G-AA----------C-------A-------- 953
HIV7312AR -------A----------C-G-C-------A----------GA-------A-------- 941
CONSENSUS.D TcCA?tTaGGaaTaCCACACCCTgCAGGACTAGCAAAaAGgA?aAGgATcACAGTa?TgGATgTAGGtGAtGC 935
SIVMM251 ----A----------A------T------C-----A---------- 217
SIVMM142 ----A----------A------T------C-----A-------C-- 953
SIVMM239 ----A----------A---A--T------C-----A---------- 953
SIVMM32H ----A----------A------T------C-----A---------- 965
SIVMNE ----A--G----------AG----------C----------C-- 965
SIVSMMH4 -A--G----------G--A-GG----------T---------- 953
SIVSMMH9 -A--G-----G----------R----------G--A-G----------GT---------- 842
SIVSMMPBJ -A--G-----G----------G--A-G----------GT---------- 851
SIVSTM -T--GC----T----------G----G---A---------T----------G----- 851
HIVFORTC2 -T--G--G---G-T----------A-G----------T-A--------G----- 908
CONSENSUS.E TCCAACTGGGTATTCCACACCCAGCAGGTCTAAAAGAAATGGAGCAGATAACAGTGTTAGATATAGGGGATGC 382
HIVPAR ---------- 217
CONSENSUS.A tTAcTTTTCCATACCacTAcATGAgGAtTTTAGaCagTAtACTGCATTtACtCTaCCAtCAgTaAACAATgca 1059
HIV2ROD ----------C-------CA----------G--------- 966
HIV2NIHZ ----------C----------C---------- 963
HIV2ISY C----------C---T----------G---------- 963
HIV2ST ----------A----------T 1023
HIV2BEN C--T----------A--------G----------C------G----------ATG 1023
HIV2CAM2 ---T----------T-------A--C----------C----------G--------- 963
HIV2D194 C----------A--------G--A----------C---------- 1077
HIV2GH1 C----------G--------A--------G----------C---------- 1023
HIV2S52907 ----------C-------CA----------G--------- 417
CONSENSUS.B CTACTTCAGT?TCCCACTAGAtCCA?ACTTCAGaCA?TATACAGCATTcAC?TTGCCAtCA?TAAA?AATGCA 1006
HIV2D205 ----------A----------A----------G----------C---------G----C------ 1023
HIV2UC1 ----------A----------A----------G----------C---------A----C------ 1026
HIV2EHOA ----------G----------G----------A----------T--T------G--G----T------ 1014
HIV7312AR ----------G----------C---G-------G--A----------T---------A----T------ 290
CONSENSUS.D ATAtTTcTCcATACCtcTAGATgAaGaaTTtAGGCAgTAcACtgCcTTtACttTACCATCaGTAAAtAATgcA 1008
SIVMM251 ---------- 1026
SIVMM142 ---------T---------- 1026
SIVMM239 ---------- 1038
SIVMM32H ---------- 1038
SIVMNE ----------T---------- 1026
SIVSMMH4 ----------G-----C---------- 915
SIVSMMH9 ----------T----------C-----A----------C--------G-----C------ 924
SIVSMMPBJ ----------T----------C-----A----------C--------G-----C------ 924
SIVSTM ------T--------C--------G-GC----------T-----T--C--C----------C------ 981
HIVFORTC2 ---C--T--T-----CT-----A-G-----C-----A--T--CA-T-----CC-------G-----C---CG- 455
CONSENSUS.E CTATTTTTCGGTACCCCTAGACCCAGAATTTAGACAGTATACAGCATTCACCATACCCTCGGTAAATAATCAA 290
HIVPAR ---------- 290



HIV2/SIV POL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HIV2ROD ----------T-GG----------C---------- 1185
HIV2NIHZ ---------C--C----------C----------G----------A----------A 1182
HIV2ISY ----------G----------A---------- 1182
HIV2ST ---G-----C--C----------G---G--T---------- 1242
HIV2BEN ----------G------G----------G----------A---------- 1242
HIV2CAM2 ----------C----------G--T----------AA- 1182
HIV2D194 ----------G-G------G----------A-----A--------G------ 1296
HIV2GH1 T----------G------G----------A--------G------ 1242
HIV2S52907 ----------GG---A-------A--C---------- 636
CONSENSUS.B cCTt?T?GCAAGtGAcAGaAGtGATCTgGAgCAtGAcAgGGTAGTGTC?CAACTAAAAGAGcTAtTAAATgAC 1213
HIV2D205 ----A-A----------C----------C----------T---------- 1242
HIV2UC1 ----A-A----------C---------- 1245
HIV2EHOA T--CG-G----------G--C----------T----------A-- 1233
HIV7312AR ----G-G-----C--T----------A--A-----T-A---------T----------C--------- 509
CONSENSUS.D ctTaaTAGCtAGTGAcAG?ACAGAccT?GAaCATGACAgGGTAGTtTTaCAgttaAAgGAaCTc?T?AAtagc 1215
SIVMM251 ----------G--------G----------C----------T-A------ 1245
SIVMM142 ----------G--------G----------A------T-A------ 1245
SIVMM239 ----------G--------G----------C----------T-G------ 1257
SIVMM32H ----------G--------G----------T-G------ 1257
SIVMNE ----G----------G--------G----------T-A------ 1245
SIVSMMH4 ----------T--A-----TT-A--G----------TC-G--CG-- 1134
SIVSMMH9 ----------T--A-----TT-A----------A----------TC-G--C--T 1143
SIVSMMPBJ ----------T--A-----TT-A----------G---------TC-G--C--T 1143
SIVSTM ---G-----C---------A-----T--A--G----------G---------C-A----AT 1200
HIVFORTC2 TC----------A--------A----------A------C--G---C-------G---C-A---GA- 674
CONSENSUS.E ACTAATTGGCAGTAACAGGAGCATGACAGAGCATGACAGGATGGTAGTACAATTAAAAGACATGCTGAACAAC 509
HIVPAR ---------- 509
CONSENSUS.A CTaGGaTTtTCtACcCCAGAtGAgAAgTTCCAaAAaGACCCtCCatacCaaTGGATGGGcTaTGAAcTaTGGC 1351
HIV2ROD ----------C---------- 1258
HIV2NIHZ ----------C----------A-----G----------T-GC----------T------ 1255
HIV2ISY --G---------C---------C--A----------G----------G---- 1255
HIV2ST --G---------C----------G---- 1315
HIV2BEN -----G---------T----------TT----------G---------- 1315
HIV2CAM2 --------C----------GC----------G---- 1255
HIV2D194 -----G--C----------G--------G-TT----------T-G---- 1369
HIV2GH1 -----G--C----------GCTT---------- 1315
HIV2S52907 ----------G--------C--------T---------- 709
CONSENSUS.B ATGGGATTcTCtACcCCAGAAGAAAAgTTCCAAAAaGACCCTCC?TTCaAaTGGATGGGtTATGAGCTCTGGC 1285
HIV2D205 ----------G---------- 1315
HIV2UC1 ----------G---------- 1318
HIV2EHOA ----------T----------A----------G---------- 1306
HIV7312AR --------T--C----------A--------G--------A---C-G---------- 582
CONSENSUS.D aTAGGgTTtTctaCCCCaGAAGAgAAaTTcCAaAAaGAtCCcCCATttCAaTGGATGGGgTAtGAaTTgTGGC 1288
SIVMM251 --------C----------C---------- 1318
SIVMM142 ----------AT----------C---------- 1318
SIVMM239 ----------C---------- 1330
SIVMM32H ----------A----------C---------- 1330
SIVMNE ----------G---------- 1318
SIVSMMH4 -----A--C----------G-----G----------C--G--------A---------- 1207
SIVSMMH9 -----A-----C----------G----------C--G--------A---------- 1216
SIVSMMPBJ -----A-----C----------G-----G----------C--G--------A---------- 1216
SIVSTM T----A-----C-----T----------T--G--G-----T----------A-----G--A---- 1273
HIVFORTC2 C--------C-TA----------A-----T--G-----C--T----A---T--------C-----G------- 747
CONSENSUS.E CTGGGGTTCAGCACCCCAGAGGATAAGTTTCAGAGAGAACCACCCTTAAAATGGATGGGGTATTTACTATACC 582
HIVPAR ---------- 582

```
CONSENSUS.A CAACtAAATGGAAgtTGCAgAaAaTACAatTgCCcCAaAAaGAaaTaTGGACAGTcAAtGACATCCAaAAgCT 1424
HIV2ROD     ----------------------------G-------------------------------------G----- 1331
HIV2NIHZ    -------------------A--------GC-------------G-------------------------- 1328
HIV2ISY     ----C---------A-----A--------------------G---G----------T-----------G--A-- 1328
HIV2ST      --------------C----A-G------------------G---G-------------------------A-- 1388
HIV2BEN     --------------C---------C-----C--------G-----C---------------------------- 1388
HIV2CAM2    ------------------------------------------G--GG-G---------------------------- 1328
HIV2D194    -------------AC----------------A--T--G-------------------------------A-- 1442
HIV2GH1     --------------C---------T-----C--------G--------------------C---------G----- 1388
HIV2S52907  ----------------------------G-------------------------------------G----- 782

CONSENSUS.B CAAA?AagTGGAAaCTGCAAAAAATACAacT?CCAGAAAa?GA?GTTTGGACAGT?AATGacATTCA?AAacT 1352
HIV2D205    ----A-------------------------G--------A--A----------G----CA-----A----- 1388
HIV2UC1     ----A-G-----------------------G--------G--A----------G----------A----- 1391
HIV2EHOA    ----G--A--------------------G--A--------A--G----------A----------G--GT- 1379
HIV7312AR   ----G--------G---------------A-A-------GG--G----------A----------G----- 655

CONSENSUS.D CaACaAAaTGGAA??TgCAaAA?ATAGAgtTgCCaCAaAgAGAgaccTGGACAGTgAATgAtATaCAgAA?tT 1357
SIVMM251    -G----------GT-------G-------------------------------------------------G-- 1391
SIVMM142    -G----------GT-------G-------------------------------------------------G-- 1391
SIVMM239    ----------GT-------G-------------------------------------------------G-- 1403
SIVMM32H    ----------GT-------G-------------------------------------------------G-- 1403
SIVMNE      ----------GT-------G----------------A-------------------------------G-- 1391
SIVSMMH4    ----C---------AC----G--A-------------------------------A-----C-----A--A-- 1280
SIVSMMH9    -C--C---------AC-------A----------G--------A----------A---A-------A--A-- 1289
SIVSMMPBJ   -C--C---------AC-------A--------------------A----------A----------A--A-- 1289
SIVSTM      -------G-----AC-------A-----A--A--T--G-----CGTT----------------C--A--AC- 1346
HIVFORTC2   -------G-----AC-A-----A------C-------G------GAT--------A-----C--T-----AC- 820

CONSENSUS.E CCAAGAAATGGAAACTACAAAAAATAGAGCTTCCTGAAAAAGAAAGATGGACAGTTAATGACATTCAGAAGTT 655
HIVPAR      ------------------------------------------------------------------------ 655

CONSENSUS.A aGTgGGtGTccTaAAtTGGGCaGCaCAaaTCTAccCAGGgATAAAgACCAaacActTaTGTAggtTaATtAgA 1497
HIV2ROD     ----------------------------C-----------------------------------------C--- 1404
HIV2NIHZ    ------------------------------------------------------C--------C-------- 1401
HIV2ISY     ----------------C-----G----------------A----------------------A-C-------- 1401
HIV2ST      G-------------------------------------------------------G-A---------------C--- 1461
HIV2BEN     ------A---T----------G-----------TT----A-----A----------------AC-------- 1461
HIV2CAM2    ---A------------------------------------------------------G-----A--------- 1401
HIV2D194    ---A--A--TT-G--C-----G--G--G-----T----------A-----G--T-------AA--G------ 1515
HIV2GH1     G-----A---T----------G-----------T-----A-----A--------T--G------C----C-A- 1461
HIV2S52907  ----------------------------C-----------------------------------------C--- 855

CONSENSUS.B aGTgGGAGTATTAAAcTGGGCAGCTCAACT?TT?CCtGGaATtAAgACaAGGCAcATATG?AaACTaATtAgG 1422
HIV2D205    G--A-------------------------C--T-------------------------C------------ 1461
HIV2UC1     ----------------------------C--T-------------------------T------------ 1464
HIV2EHOA    ---------------T-------------T--C--G--G--------C-----T-----T--------A--- 1452
HIV7312AR   -------------------------T--C--C-----C--A-------------C-G---G--C-A- 728

CONSENSUS.D aGTAGGaGTatTAAAtTGGGCAGC?CAAATTTATCCAGG?ATaAAaACcAAACATCTcTG?Ag?tTAATtAGA 1426
SIVMM251    ----------------------T--------------T--------------------T--G--------- 1464
SIVMM142    ----------------------T--------------T--------------------T--G--------- 1464
SIVMM239    ----------------------T--------------T--------------------T--G--------- 1476
SIVMM32H    ----------------------T--------------T--------------------T--G--------- 1476
SIVMNE      ----------------------T--------------T--------------------T--G--------- 1464
SIVSMMH4    ---------GC-------------A--------------A-----G--T--------T--C--AC----C--- 1353
SIVSMMH9    ---------GC-------------A--------------A-----G--T--------T--C--A-----C--- 1362
SIVSMMPBJ   ---------GC-------------A--------------A-----G--T--------T--C--A-----C--- 1362
SIVSTM      G-----G--C-----C--------A--------------A--T-----T--------G--C-AA-----C--- 1419
HIVFORTC2   G---------C-------------A--------------A----------------G--C--A--------- 893

CONSENSUS.E AGTAGGAATACTAAATTGGGCAGCACAAGTATATCCAGGAATCAAAACAAAAAATTTATGCAAGCTCATCAGA 728
HIVPAR      ------------------------------------------------------------------------ 728
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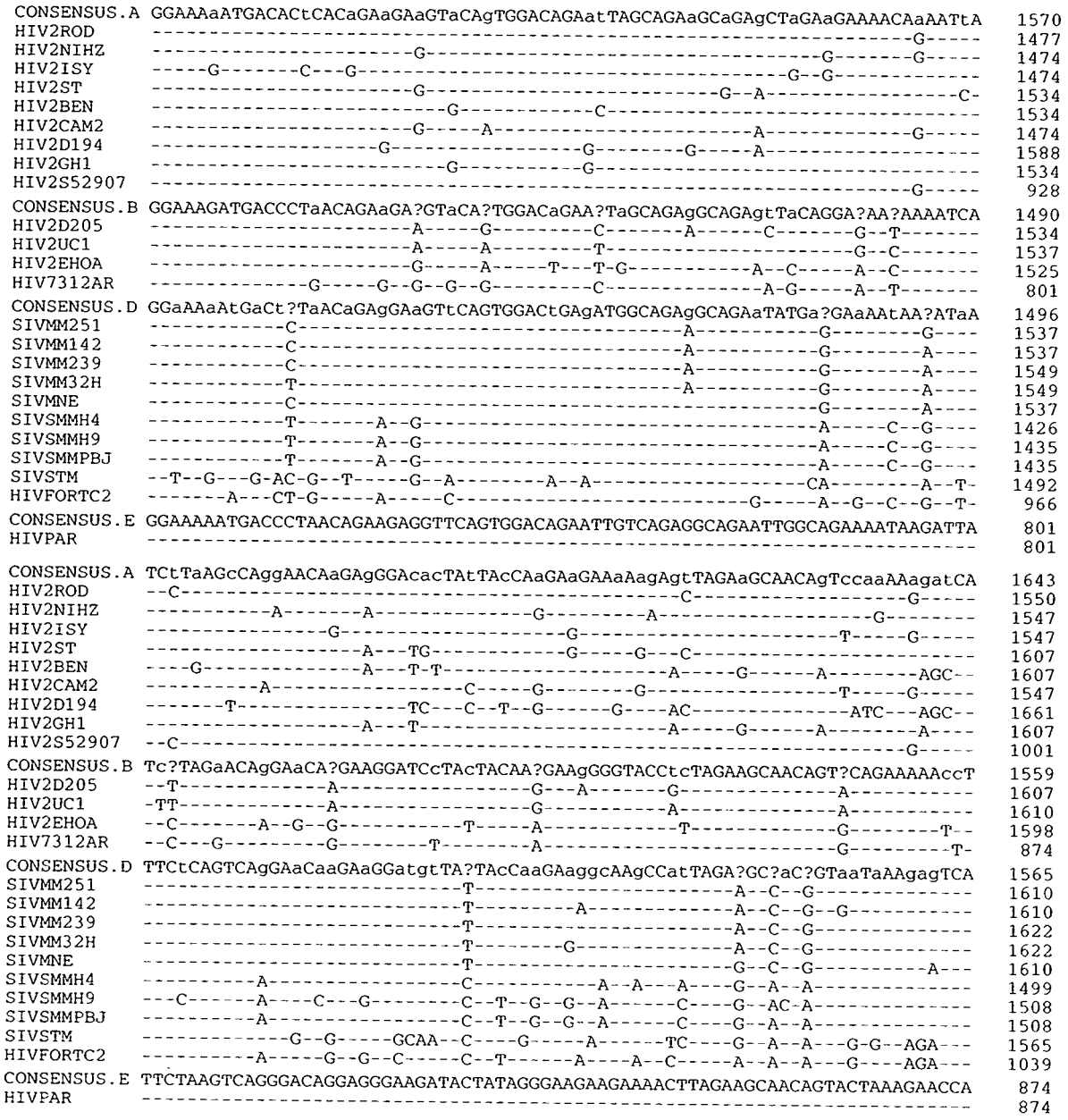
HIV2/SIV POL



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CONSENSUS.A AGacaATCAgTGGaCATAtAAaaTACACCAGGaaGa?AaaaTtCTaAAAGtaGGaAAatatgcaAAgataAAA 1715
HIV2ROD     ---G-------------------------------A-----------------------------G-G---  1623
HIV2NIHZ    ---------------------GG---------GG--G--------C----GT--G---ATATGC--AGAT---  1620
HIV2ISY     ----------------------G---------G---A-----------------------------------  1620
HIV2ST      ---------------------G----------G--GA-----------------------------G-----  1680
HIV2BEN     --GAC----A--------C-----------------G-----C--------------G---------------  1680
HIV2CAM2    ---------------------G--------------A-----------------------------A------  1620
HIV2D194    --------------G----C-------------G---G-GGG----------------G-----G---------  1734
HIV2GH1     -------------------C-----------------G-----C-----------G-----------------  1680
HIV2S52907  ------------------------------------C-------------------G---------G-----  1074

CONSENSUS.B AGCAAAtCAGTGGACATACAAaATTCATCAGGGAaATAaA?TccTAAAAGTAGGAAAATATGCAAAGGTTAAA 1631
HIV2D205    ------------------------------------------G-------------------------------  1680
HIV2UC1     ------------------------------------------G-A-TT---------------------------  1683
HIV2EHOA    ----------------------G------------G-----A-------------------------------  1671
HIV7312AR   ------C-------------------------------G-------------------------------  947

CONSENSUS.D GGAcAATCA?TGGTCtTAtAAaATtCAcCAaGAaGACAAAaTAcTgAAAGTaGGaAAaTtTGCAAAgaTaAAa 1637
SIVMM251    ---------G-------------------------------------------------------------G  1683
SIVMM142    ---------G-------------------------------------------------------------G  1683
SIVMM239    ---------G-------------------------------------------------------------G  1695
SIVMM32H    ---------G-----------------------------------------G--------------G  1695
SIVMNE      ---------G-----------G-----------------------A-------------------------  1683
SIVSMMH4    ---T-----A-----A-------------------G-------------T------------G-T---  1572
SIVSMMH9    ---T-----A-----A-----------------G-----------A--------C--------------T---  1581
SIVSMMPBJ   ---T-----A-----A-------------------------------C--------------T---  1581
SIVSTM      ---------A-----C-----G--A-------------------T----------C--G--------A------  1638
HIVFORTC2   ---T-----A-----C--C--------T--G------------T-A-----G--T--G-A------A--C---  1112

CONSENSUS.E AGATAATCAGTGGAGCTATAAGATTCATCAGGGAGACAGAATTCTTAAAGTAGGAAAATTTCCCCAAATAAAA  947
HIVPAR      ------------------------------------------------------------------------  947

CONSENSUS.A aAtaccCatacCaAtgGggTCAgatT?tTaGCACAgGTAGTtCAaAAAATAGGAAAaGAaGCACTaGTCATtT 1787
HIV2ROD     --C--------------AA-------G----------------G----------------------------  1696
HIV2NIHZ    --ATA--CATA-C-AC----------G------------------------------------------------  1693
HIV2ISY     --------------C--------G--G--G--------------G----------------------------  1693
HIV2ST      --------C-----C--A------C-CC-------A-------------------------------------  1753
HIV2BEN     -------------------------AC----------------G--------------G--------------  1753
HIV2CAM2    C----------------A----A---A------------------------------------------------  1693
HIV2D194    -----T-------------------C-AC-------A-----C--------------G--------G-------  1807
HIV2GH1     -------------------------AC----------------G-------------------------C-  1753
HIV2S52907  --C--------------AA-------G-----------------------------------G-------  1147

CONSENSUS.B AACACcCACACCAA?GG?GTAAGAcTAcTgGCaCATGTAGT?CA?AAAATAGGaAAaGAAGCccTaGTCATCT 1700
HIV2D205    -----G--------C--G----------------------T--G--------C----------------  1753
HIV2UC1     --------------C--G----------------------T--G--------------------------  1756
HIV2EHOA    -----T--------T--A---------T----T--------C--A----------G-----AT-G-------  1744
HIV7312AR   --------------T--A------A----A----------C--A---                          995

CONSENSUS.D AAtACACATAC?AATGGAGTtAGa?TAtTaGCACAtGTaaTaCAgAAaATAGGaAA?GAaGCAaTAgTgATcT 1707
SIVMM251    ----------C------------C-------------------------------G----------------  1756
SIVMM142    ----------C------------C-------------------------------G----------------  1756
SIVMM239    ----------C--------G---C-------------------------------G----------------  1768
SIVMM32H    ----------C------------C-------------------------------G----------------  1768
SIVMNE      ----------C------------C-------------------------------G----------------  1756
SIVSMMH4    ----------A--------C---T--C-------C---G-G--------------A------C----A--T-  1645
SIVSMMH9    ----------A--------C--CT--------------G-G--------------A----------A-A--T-  1654
SIVSMMPBJ   ----------A--------C---T--------------G-G--------------A----------A--T-  1654
SIVSTM      --C--------A------------T----G--------G--T-----G-----G--A----------------  1711
HIVFORTC2   ----------A------------T--------------G----A----------A--G--------A--T-  1185

CONSENSUS.E AATACCCATACAAATGGAGTAAGACTATTAGCTAGTGTAGTACAGAAA                          995
HIVPAR      -----------------------------------------------                           995
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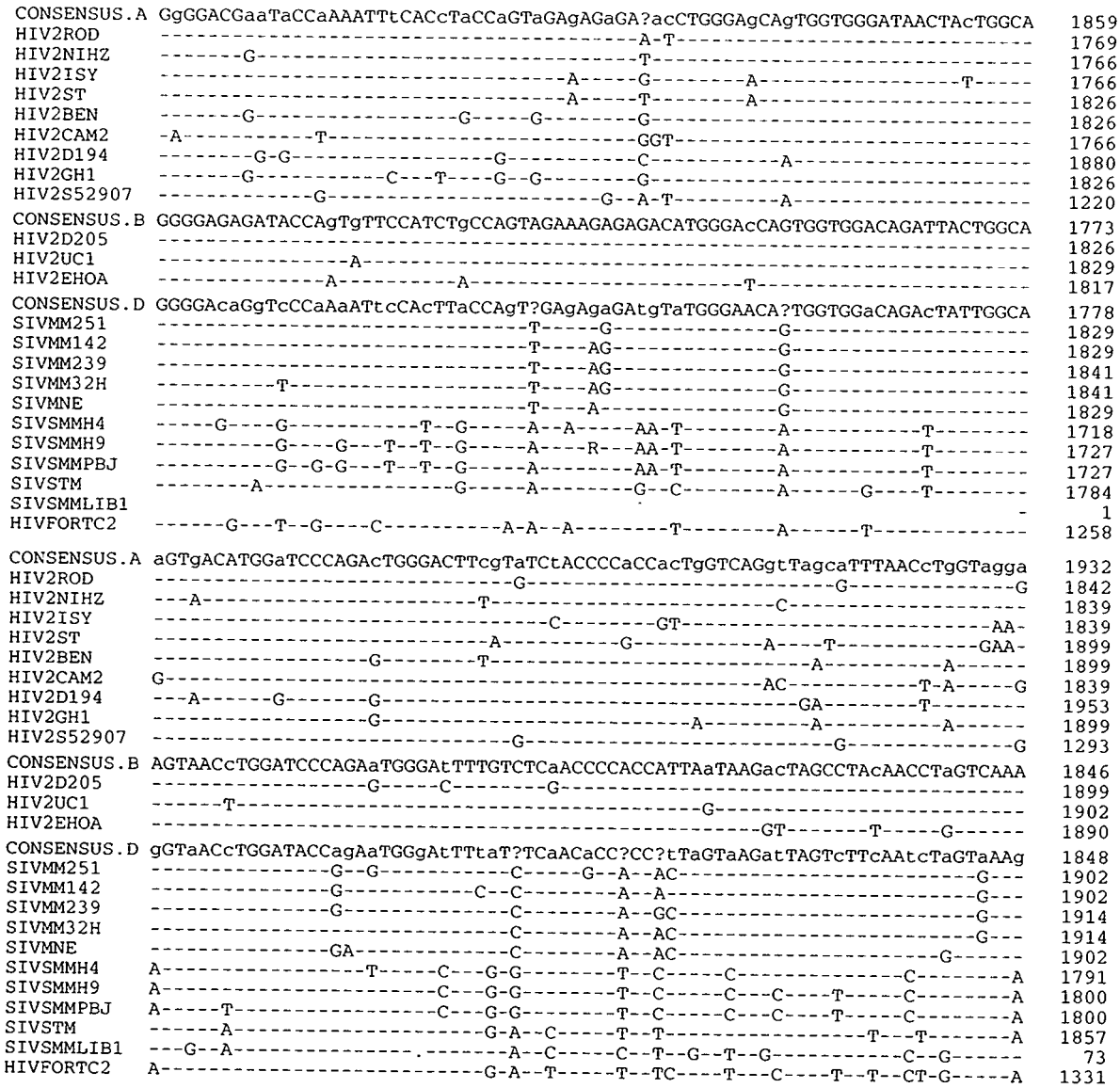
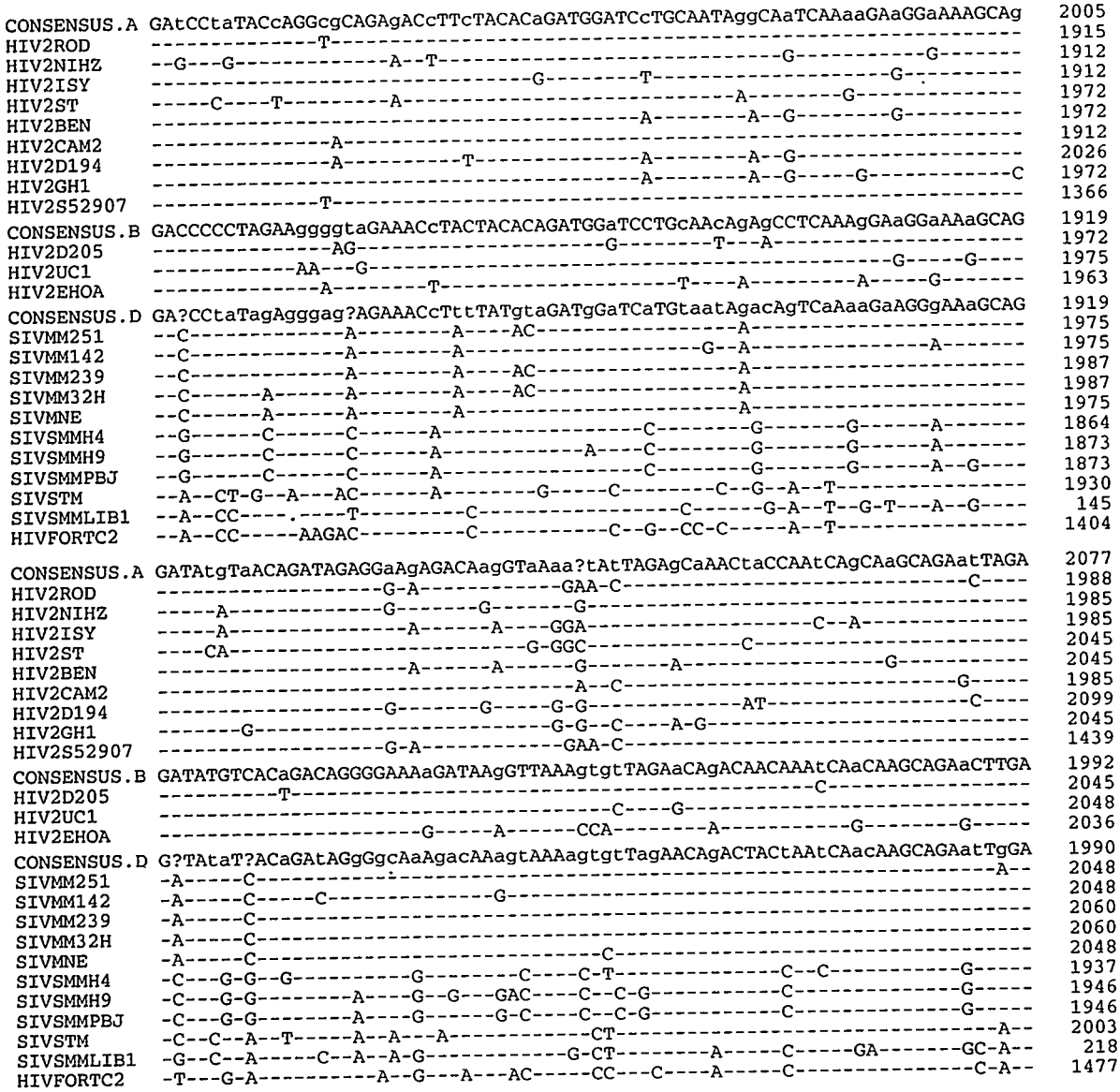
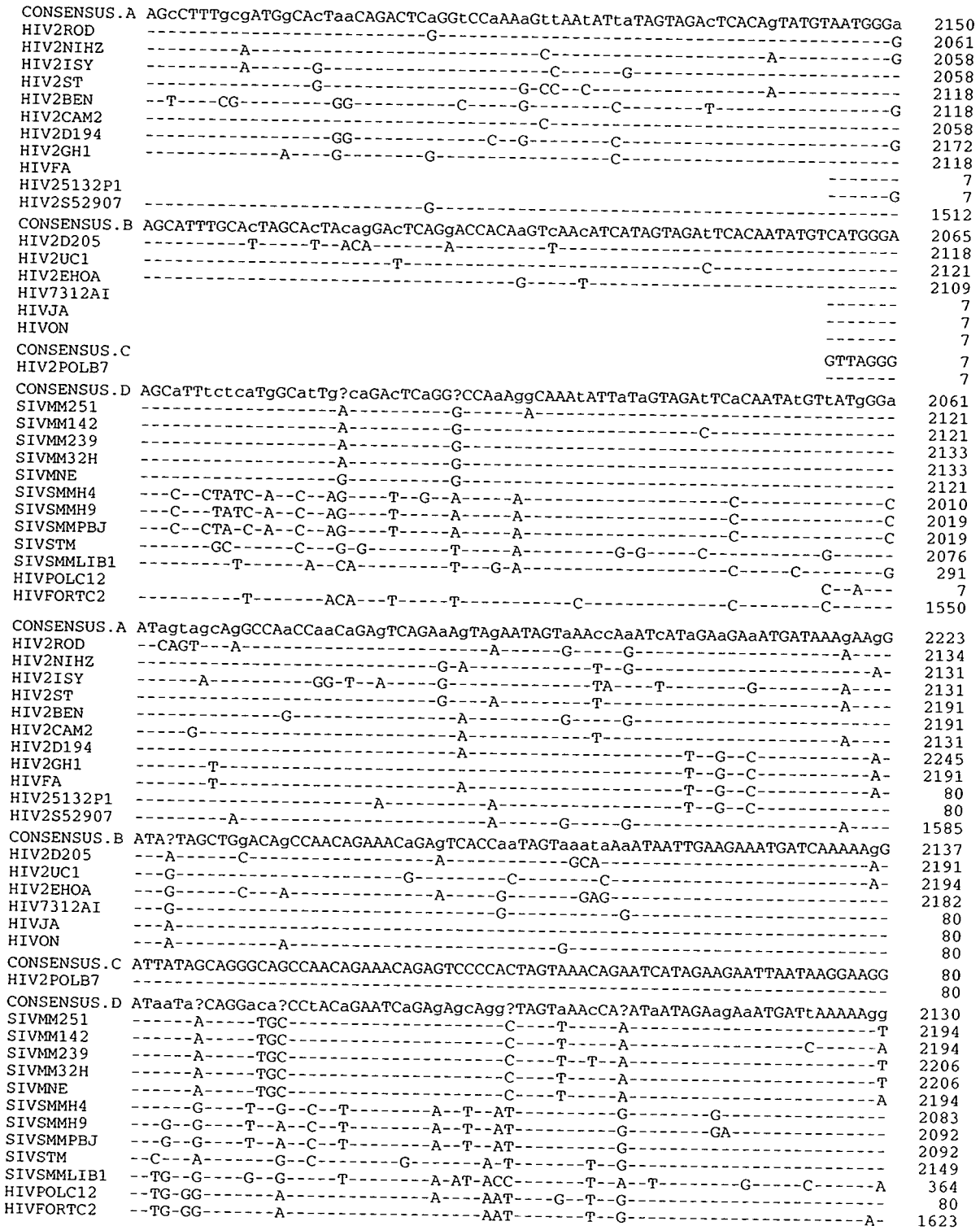
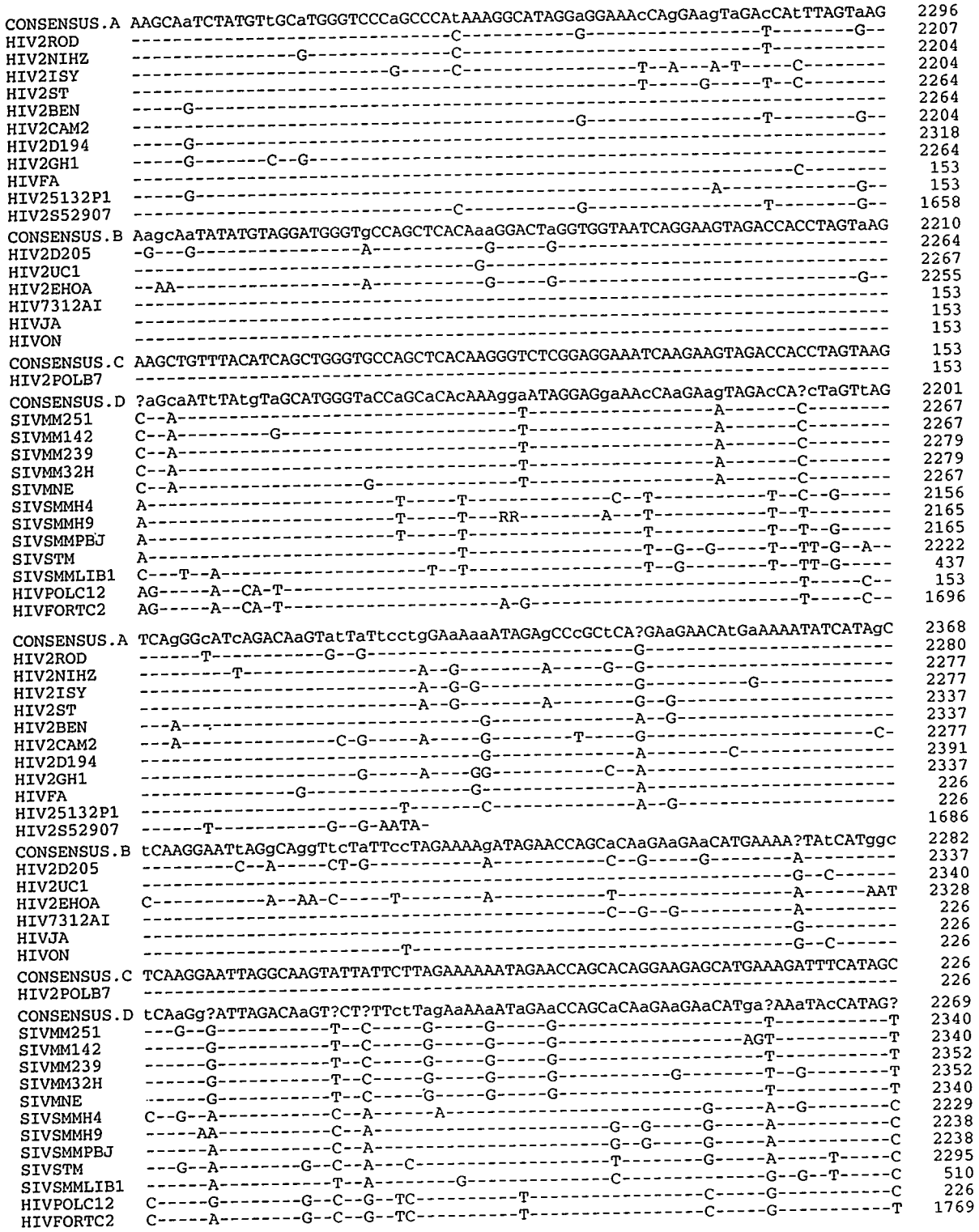
HIV2/SIV POL



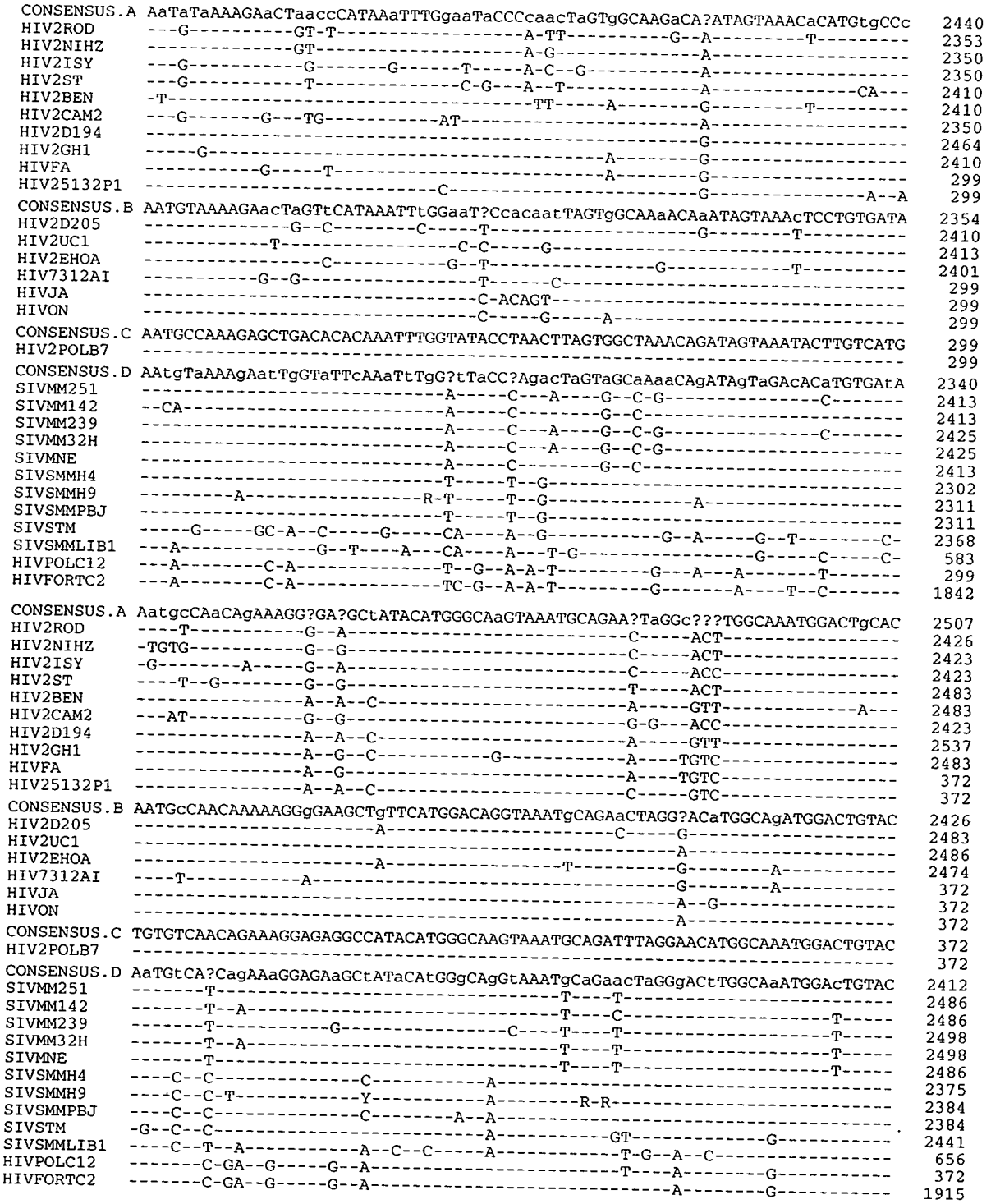


HIV2/SIV POL


CONSENSUS.A AGcCTTTgcgATGgCAcTaaCAGACTCaGGtCCaAAaGttAAtATtaTAGTAGAcTCACAgTATGTAATGGGa 2150
HIV2ROD ----------G---------- 2061
HIV2NIHZ ---------A----------C----------A----------G 2058
HIV2ISY ---------A------G----------C------G---------- 2058
HIV2ST ----------G----------G-CC--C----------A---------- 2118
HIV2BEN --T----CG---------GG----------C-----G--------C--------T----------G 2118
HIV2CAM2 ----------C---------- 2058
HIV2D194 ----------GG----------C--G--------C----------G 2172
HIV2GH1 ----------A----G--------G----------C---------- 2118
HIVFA ------- 7
HIV25132P1 ------G 7
HIV2S52907 ----------G---------- 1512
CONSENSUS.B AGCATTTGCAcTAGCAcTAcagGAcTCAGgACCACAaGTcAAcATCATAGTAGAtTCACAATATGTCATGGGA 2065
HIV2D205 ----------T-----T--ACA-------A---------T---------- 2118
HIV2UC1 ----------T----------C---------- 2121
HIV2EHOA ----------G-----T---------- 2109
HIV7312AI ------- 7
HIVJA ------- 7
HIVON ------- 7
CONSENSUS.C GTTAGGG 7
HIV2POLB7 ------- 7
CONSENSUS.D AGCaTTtctcaTgGCatTg?caGAcTCaGG?CCAaAggCAAAtATTaTaGTAGAtTCaCAATAtGTtATgGGa 2061
SIVMM251 ----------A----------G------A---------- 2121
SIVMM142 ----------A----------G----------C---------- 2121
SIVMM239 ----------A----------G---------- 2133
SIVMM32H ----------A----------G---------- 2133
SIVMNE ----------G----------G---------- 2121
SIVSMMH4 ---C--CTATC-A--C--AG----T--G--A-----A----------C----------C 2010
SIVSMMH9 ---C---TATC-A--C--AG----T-----A-----A----------C----------C 2019
SIVSMMPBJ ---C--CTA-C-A--C--AG----T-----A-----A----------C----------C 2019
SIVSTM -------GC------C---G-G--------T-----A---------G-G-----C----------G------ 2076
SIVSMMLIB1 ---------T------A--CA---------T---G-A----------C-----C--------G 291
HIVPOLC12 C--A--- 7
HIVFORTC2 ----------T-------ACA---T-----T----------C----------C--------C------ 1550
CONSENSUS.A ATagtagcAgGCCAaCCaaCaGAgTCAGAaAgTAgAATAGTaAAccAaATcATaGAaGAaATGATAAAgAAgG 2223
HIV2ROD --CAGT---A----------A------G-----G----------A---- 2134
HIV2NIHZ ----------G-A----------T--G----------A- 2131
HIV2ISY ------A----------GG-T--A-----G----------TA----T--------G--------A---- 2131
HIV2ST ----------G----A---------T----------A---- 2191
HIV2BEN --------------G----------A---------G-----G---------- 2191
HIV2CAM2 -----G----------A----------T----------A---- 2131
HIV2D194 ----------A----------T--G--C----------A- 2245
HIV2GH1 -------T----------T--G--C----------A- 2191
HIVFA -------T----------A----------T--G--C----------A- 80
HIV25132P1 ----------A----------A----------T--G--C---------- 80
HIV2S52907 ---------A----------A------G-----G----------A---- 80
CONSENSUS.B ATA?TAGCTGgACAgCCAACAGAAACaGAgTCACCaaTAGTaaataAaATAATTGAAGAAATGATCAAAAAgG 1585
HIV2D205 ---A------C----------A----------GCA----------A- 2137
HIV2UC1 ---G----------G---------C--------C----------A- 2191
HIV2EHOA ---G------C---A----------A-----G-------GAG---------- 2194
HIV7312AI ---G----------G----------G---------- 2182
HIVJA ---A---------- 80
HIVON ---A----------A----------G---------- 80
CONSENSUS.C ATTATAGCAGGGCAGCCAACAGAAACAGAGTCCCCACTAGTAAACAGAATCATAGAAGAATTAATAAGGAAGG 80
HIV2POLB7 ---------- 80
CONSENSUS.D ATaaTa?CAGGaca?CCtACaGAATCaGAgAgcAgg?TAGTaAAcCA?ATaATAGAagAaATGATtAAAAAgg 2130
SIVMM251 ------A-----TGC----------C----T-----A----------T 2194
SIVMM142 ------A-----TGC----------C----T-----A----------C------A 2194
SIVMM239 ------A-----TGC----------C----T--T--A----------T 2206
SIVMM32H ------A-----TGC----------C----T-----A----------T 2206
SIVMNE ------A-----TGC----------C----T----A----------A 2194
SIVSMMH4 ------G----T--G--C--T--------A--T--AT----------G--------G---------- 2083
SIVSMMH9 ---G--G----T--A--C--T--------A--T--AT----------G--------GA---------- 2092
SIVSMMPBJ ---G--G----T--A--C--T--------A--T--AT----------G---------- 2092
SIVSTM --C---A-------G--C--------G-------A-T-------T--G---------- 2149
SIVSMMLIB1 --TG--G----G--G-----T--------A-AT-ACC-------T--A--T--------G-----C------A 364
HIVPOLC12 --TG-GG-------A----------A----AAT----G--T--G---------- 80
HIVFORTC2 --TG-GG-------A----------AAT------T--G----------A- 1623



HIV2/SIV POL



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CONSENSUS.A ACActTAGaaGGAAAaaTCATtATAGTAGCAGTaCATGTTGCAAGTGGATT?ATAGAaGCAgAAGTcATCCCA 2579
HIV2ROD     ---T-----------G-----------------------------------T-------------------- 2499
HIV2NIHZ    ---T------------G----------------------------------T-----G--------T------ 2496
HIV2ISY     ------------------------------------------------------T-------------------- 2496
HIV2ST      ------------------------------------------------------T-------------------- 2556
HIV2BEN     ------------------------------------------------------C-------------------- 2556
HIV2CAM2    ---TC----G-----------C----------------------------------T-------------------- 2496
HIV2D194    ---------------------------------G--------------------C-------------------- 2610
HIV2GH1     ---------------G-------------------------------------C--------------T------ 2556
HIVFA       ------------------------------------------------------C---------A---------- 445
HIV25132P1  --------G--------------------------------------------C---------------------- 445
CONSENSUS.B ACA?TTAGAaGGaAAggTcATAATAGTgGCAGTcCATGTAGCCAGTGGaTTtATAGA?GCAGAgGTAATACCC 2497
HIV2D205    ---T-----------AA-T-------------------------------G--------A--------------- 2556
HIV2UC1     ---C-------------------------------------------------------G--------------- 2559
HIV2EHOA    ---T-----G--------T--------------T-----------------C-----A-----A--------- 2547
HIV7312AI   ---T--------G--A-----------A--------------------G--------A--------------- 445
HIVJA       ---C-------------------------------------------------------G-----A--------- 445
HIVON       ---C--------G---A-------------------------------------------G--------------- 445
CONSENSUS.C CCATTTAGAAGGAAAAGTTATCATAGTAGCAGTCCATGTGGCCAGTGGCTTTATAGAAGCAGAGGTAATCCCA 445
HIV2POLB7   ------------------------------------------------------------------------- 445
CONSENSUS.D aCAtcTAGAgGGaAAaaTAatcATAGTtGCaGTACATGTaGcTAGtGGaTTcATaGAaGCAGAaGTaATtCCa 2485
SIVMM251    C--------A---------G--------------------------------------------------- 2559
SIVMM142    C----------------G-------------------------------------------------------- 2559
SIVMM239    C-------------------------------------------------------------G--------- 2571
SIVMM32H    C------------------------------------------------------------------------ 2571
SIVMNE      C------------------------------------------------------------------------ 2559
SIVSMMH4    G--C-----A--C--------T----------------G-----------T-----G----------C--G 2448
SIVSMMH9    ---C--------C--------T----------------G-G---------G----------C--G 2457
SIVSMMPBJ   ---C--------C--------T----------------G---------G--------------G 2457
SIVSTM      ---------A--C--G-----T-----A--------------G--T-----G----------C--- 2514
SIVSMMLIB1  ----T--------C---------T-----G--T--------------C--T-----C----------G-----G 729
HIVPOLC12   ----------------G----------A--T--------G----------T--------------C------ 445
HIVFORTC2   ---C------------G---C------A--T--------G----------T-----                1972
CONSENSUS.A CAGgAATCAGgAAGgCA?ACaGCaCTcTTCcTAtTaAAAcTGGCcAGtAGGTGGCCAATAACaCActTgCAcA 2651
HIV2ROD     --------------A--A----------------G--------A-------------------------T- 2572
HIV2NIHZ    -----------------A--------G---T--C-G-------------------------------C------ 2569
HIV2ISY     -----------------A------------------------------------------------------- 2569
HIV2ST      -----------------A--G------------C-------------------------------T------- 2629
HIV2BEN     -----------------G-------------------------------------------G---------- 2629
HIV2CAM2    -----------------A--------------------T----T--C--------------------A---- 2569
HIV2D194    -----------------G------------------------------------------------------- 2683
HIV2GH1     -----------------G-----G-----------------------------------------A---- 2629
HIVFA       ---A------A---A--G-------------------------------C------------------------ 518
HIV25132P1  -----------------G-----C------------------------------------------------- 518
CONSENSUS.B CAAGAaACaGGAAGACA?ACAGCTCTCTTCCTgtTAAA?tTGGCcAGCAGATGGCCtATcACACACcTgCaCA 2568
HIV2D205    -----G----------G-------------AC----G-----------------------------A---- 2629
HIV2UC1     -----------------A-------------------A---------------------------------- 2632
HIV2EHOA    -----------------G-------------------GC---------------------------------- 2620
HIV7312AI   -----------------A-------------------GC----A----------C--T------T------- 518
HIVJA       --------G--------G-------------------A-----------------------------A----- 518
HIVON       -----------------A-------------A-----A-------------------------------G-- 518
CONSENSUS.C CAAGAAACTGGCAGACAAACAGCTCTTTTTCTGTTAAAATTGGCAGCAAGATGGCCTATTACCCACCTACACA 518
HIV2POLB7   ------------------------------------------------------------------------- 518
CONSENSUS.D CaaGAaACAGGaAGaCAgACAGCacTaTTtCTGtTaAAaTTgGcaaGCAGATGGCCtaTtACaCAtcTgCAcA 2558
SIVMM251    -----G-----------------------------------------G--------------------A---- 2632
SIVMM142    ------------------------------------------------------------------------- 2632
SIVMM239    -----G-----------------------------------------G--------------------A---- 2644
SIVMM32H    -----G-----------------------------------------G----------G----------A---- 2644
SIVMNE      -----G-------------------------------------------------------G-----A---- 2632
SIVSMMH4    --G--------------A--------G----------G--A--TG----------C--C----------T- 2521
SIVSMMH9    -RG--------------A--------G------C--------A--C----------C--C----------T- 2530
SIVSMMPBJ   --G--------------A--------G------C--------A--C----------C--C----------T- 2530
SIVSTM      -----------G------------T-G--------G--G--A---------------G-C-----C------- 2587
SIVSMMLIB1  -----G--------G---------T--G------C--------A-T-----------------C---T------ 802
HIVPOLC12   --G--------------A-----TT----C-------------------------G--C-----C------- 518
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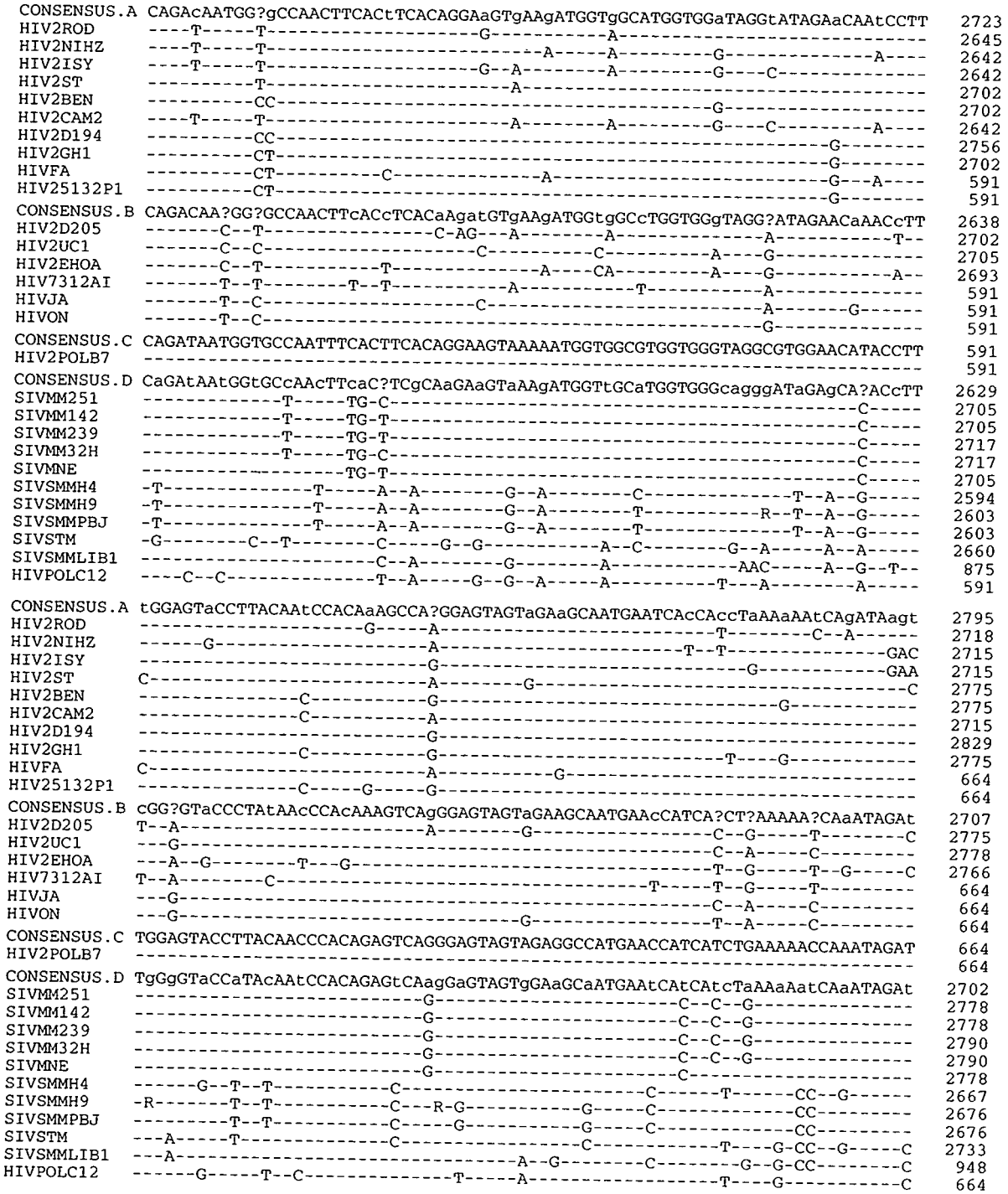
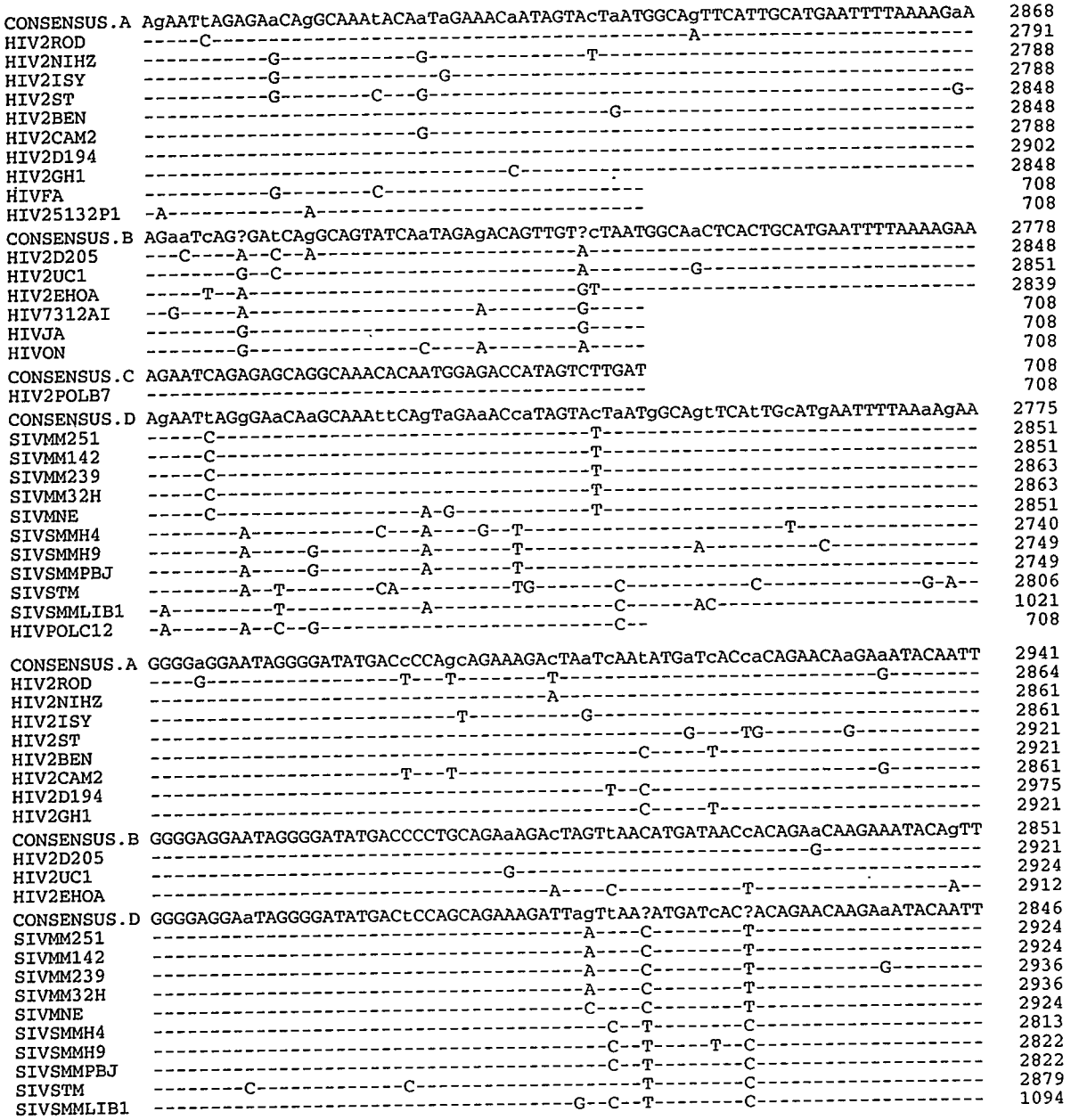
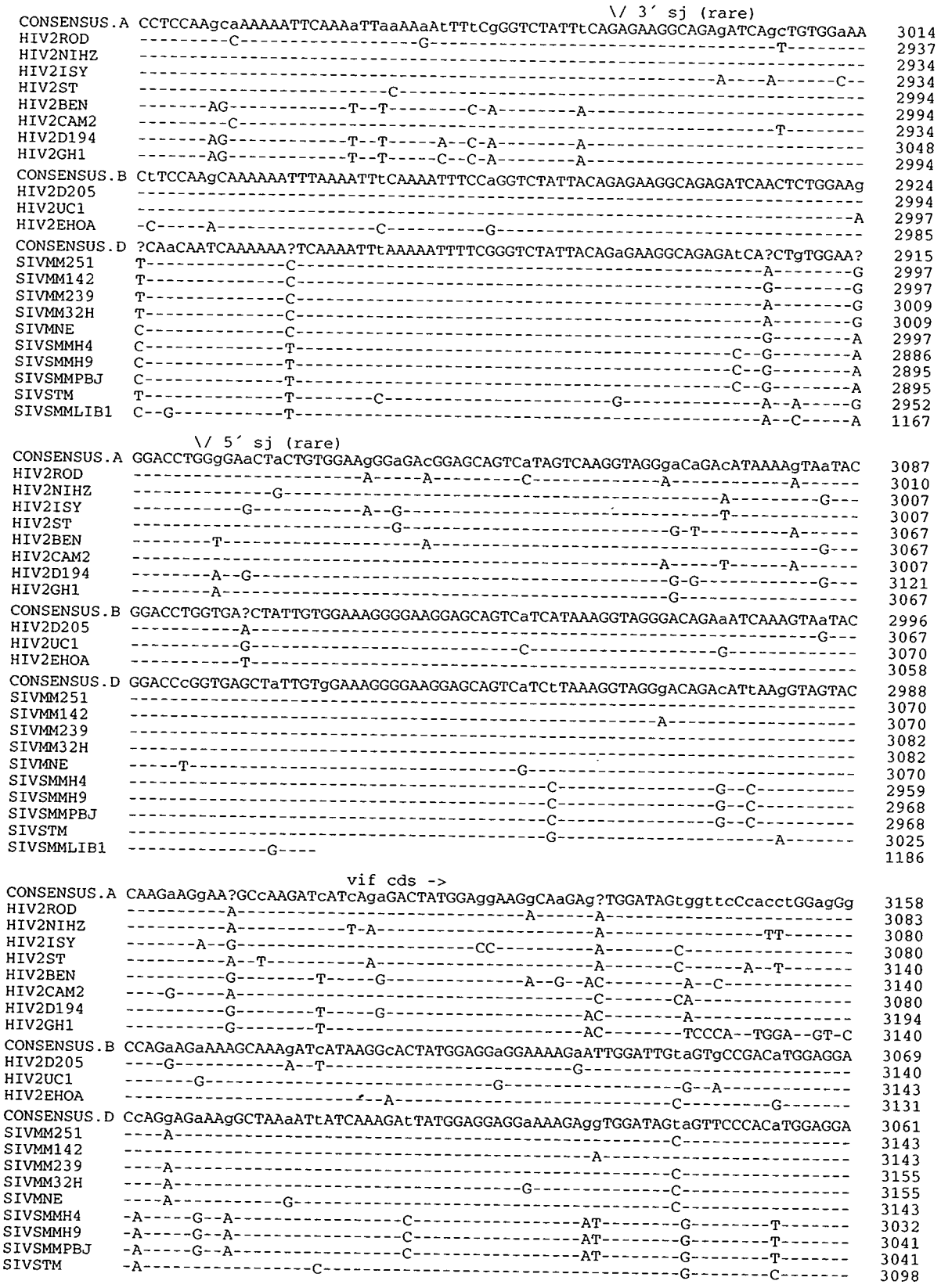
HIV2/SIV POL



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HIV2NIHZ 2934
HIV2ISY 2934
HIV2ST 2994
HIV2BEN 2994
HIV2CAM2 2934
HIV2D194 3048
HIV2GH1 2994
CONSENSUS.B CtTCCAAgCAAAAAATTTAAAATTtCAAAATTTCCaGGTCTATTACAGAGAAGGCAGAGATCAACTCTGGAAg 2924
HIV2D205 2994
HIV2UC1 2997
HIV2EHOA 2985
CONSENSUS.D ?CAaCAATCAAAAAA?TCAAAATTtAAAAATTTTCGGGTCTATTACAGaGAAGGCAGAGAtCA?CTgTGGAA? 2915
SIVMM251 2997
SIVMM142 2997
SIVMM239 3009
SIVMM32H 3009
SIVMNE 2997
SIVSMMH4 2886
SIVSMMH9 2895
SIVSMMPBJ 2895
SIVSTM 2952
SIVSMMLIB1 1167
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CONSENSUS.A GGACCTGGgGAaCTaCTGTGGAAgGGaGAcGGAGCAGTCaTAGTCAAGGTAGGgaCaGAcATAAAAgTAaTAC 3087
HIV2ROD 3010
HIV2NIHZ 3007
HIV2ISY 3007
HIV2ST 3067
HIV2BEN 3067
HIV2CAM2 3007
HIV2D194 3121
HIV2GH1 3067
CONSENSUS.B GGACCTGGTGA?CTATTGTGGAAAGGGGAAGGAGCAGTCaTCATAAAGGTAGGGACAGAaATCAAAGTAaTAC 2996
HIV2D205 3067
HIV2UC1 3070
HIV2EHOA 3058
CONSENSUS.D GGACCcGGTGAGCTaTTGTgGAAAGGGGAAGGAGCAGTCaTCtTAAAGGTAGGgACAGAcATtAAgGTAGTAC 2988
SIVMM251 3070
SIVMM142 3070
SIVMM239 3082
SIVMM32H 3082
SIVMNE 3070
SIVSMMH4 2959
SIVSMMH9 2968
SIVSMMPBJ 2968
SIVSTM 3025
SIVSMMLIB1 1186
vif cds ->
CONSENSUS.A CAAGaAGgAA?GCcAAGATcATcAgaGACTATGGAggAAGgCAaGAg?TGGATAGtggttcCcacctGGagGg 3158
HIV2ROD 3083
HIV2NIHZ 3080
HIV2ISY 3080
HIV2ST 3140
HIV2BEN 3140
HIV2CAM2 3080
HIV2D194 3194
HIV2GH1 3140
CONSENSUS.B CCAGaAGaAAAGCAAAgATcATAAGGcACTATGGAGGaGGAAAAGaATTGGATTGtaGTgCCGACaTGGAGGA 3069
HIV2D205 3140
HIV2UC1 3143
HIV2EHOA 3131
CONSENSUS.D CcAGgAGaAAgGCTAAaATtATCAAAGAtTATGGAGGAGGaAAAGAggTGGATAGtaGTTCCCACaTGGAGGA 3061
SIVMM251 3143
SIVMM142 3143
SIVMM239 3155
SIVMM32H 3155
SIVMNE 3143
SIVSMMH4 3032
SIVSMMH9 3041
SIVSMMPBJ 3041
SIVSTM 3098

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CONSENSUS.A tgccagGGAGgATGGAGA??TGGCA?GCCCTTGTCAAGTACCTGAAATACAGAACAAAAGACCTAGAGGAGGT 3228
HIV2ROD     ------------------AA------                                                 3108
HIV2NIHZ    ------------------GA------                                                 3105
HIV2ISY     ------------------AA------                                                 3105
HIV2ST      ------------------GG------                                                 3165
HIV2BEN     ------------------AA-----T---------------------------------------------- 3213
HIV2CAM2    ----------A-------AG------                                                 3105
HIV2D194    ------------------GG------                                                 3219
HIV2GH1     CAGGGA------------GG------                                                 3165

CONSENSUS.B TACCAgGCAGGCTAGAGAgaTGGCACAGTCTgaT?AAGTACCTGAAGCA                          3117
HIV2D205    ----------------------------------                                         3174
HIV2UC1     ------------------A-------------G-C--------------                          3192
HIV2EHOA    -----T-------------G-----------A--T--                                      3168

CONSENSUS.D TACCgGaGAGGCTaGAGAgGTGGCA                                                  3086
SIVMM251    -------------------------                                                  3168
SIVMM142    -------------------------                                                  3168
SIVMM239    -------------------------                                                  3180
SIVMM32H    -------------------------                                                  3180
SIVMNE      -------------------------                                                  3168
SIVSMMH4    -------------------------                                                  3057
SIVSMMH9    ------G------------A------                                                 3066
SIVSMMPBJ   ------G------------A------                                                 3066
SIVSTM      ----A-G------G-----------                                                  3123

CONSENSUS.A GCGCTATGTTCCCCACCACAAGGTGGGATGGGCATGGTGGACTTGCAGCAGGGTAATATTCCCACTACAAGGA 3301
HIV2BEN     ---------------------------------------------------------------------- 3286

CONSENSUS.A AAAAGTCATCTAGAAATACAGGCATATTGGAACCTAACACCAGAAAAAGGATGGCTCTCCTCTCATGCAGTAA 3374
HIV2BEN     ---------------------------------------------------------------------- 3359

CONSENSUS.A GATTAACCTGGTATACAGAAAAGTTCTGGACAGATGTTACCCCAGACTGTGCAGACATCCTAATACA      3441
HIV2BEN     ------------------------------------------------------------          3426
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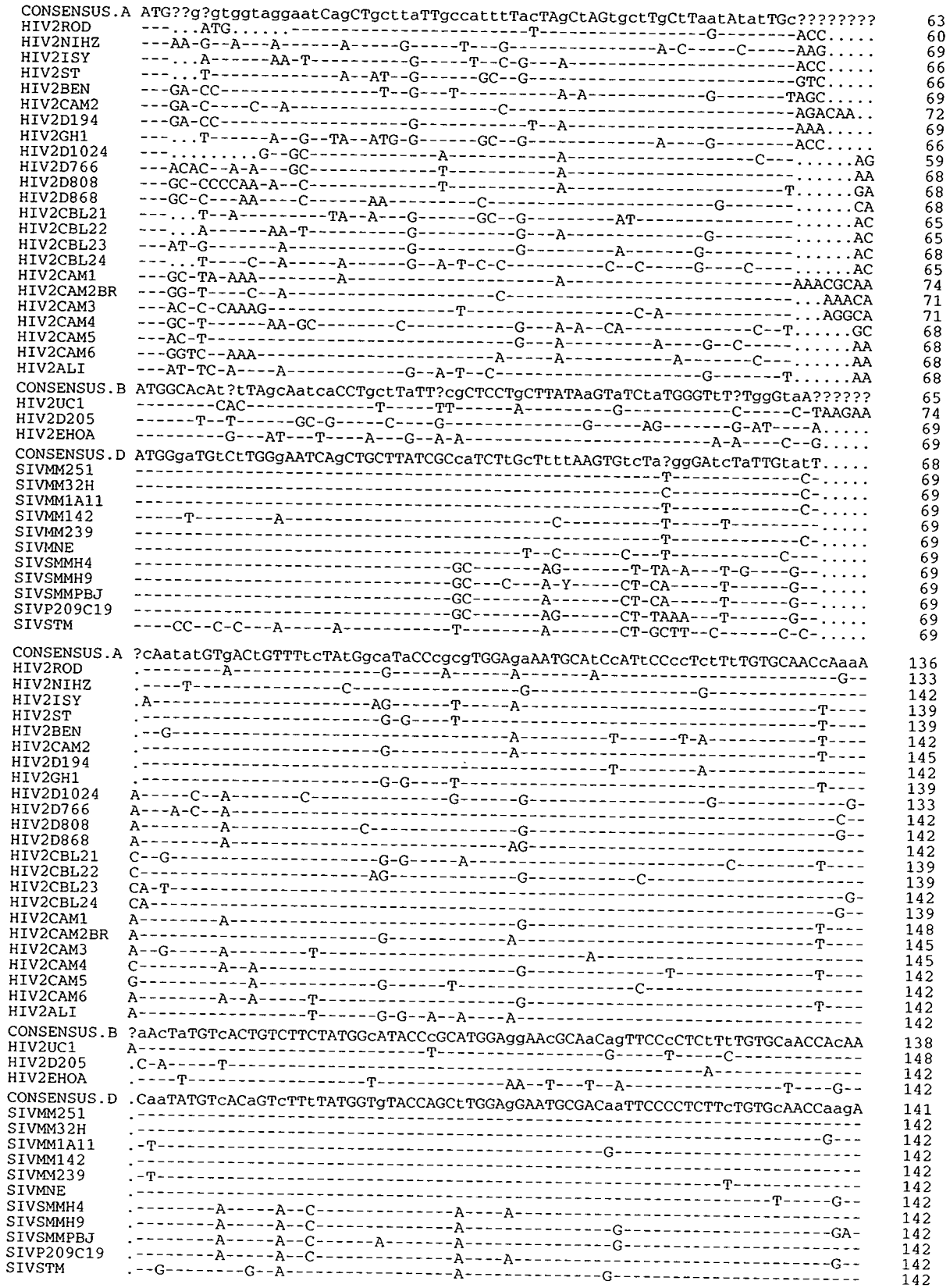
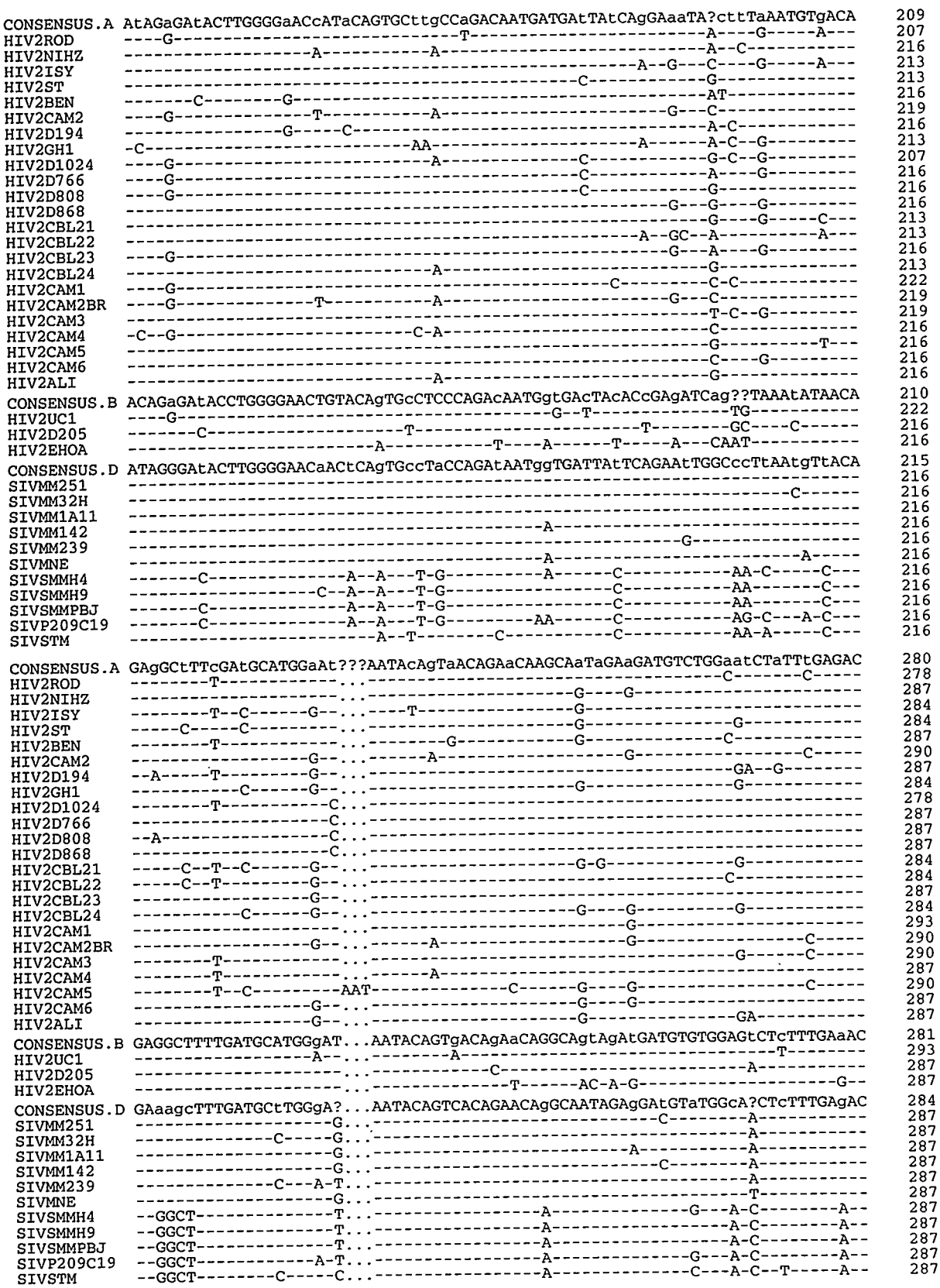
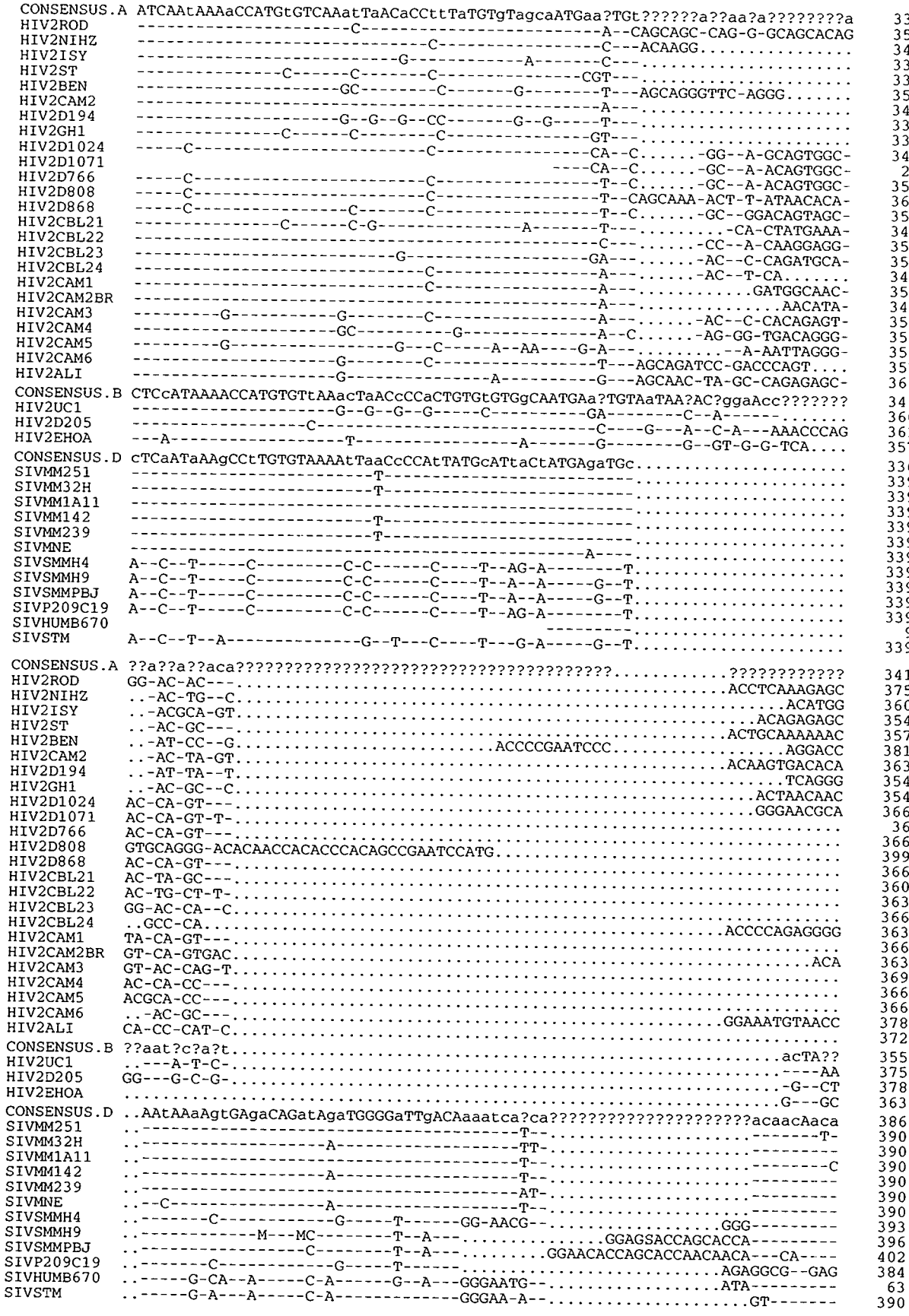
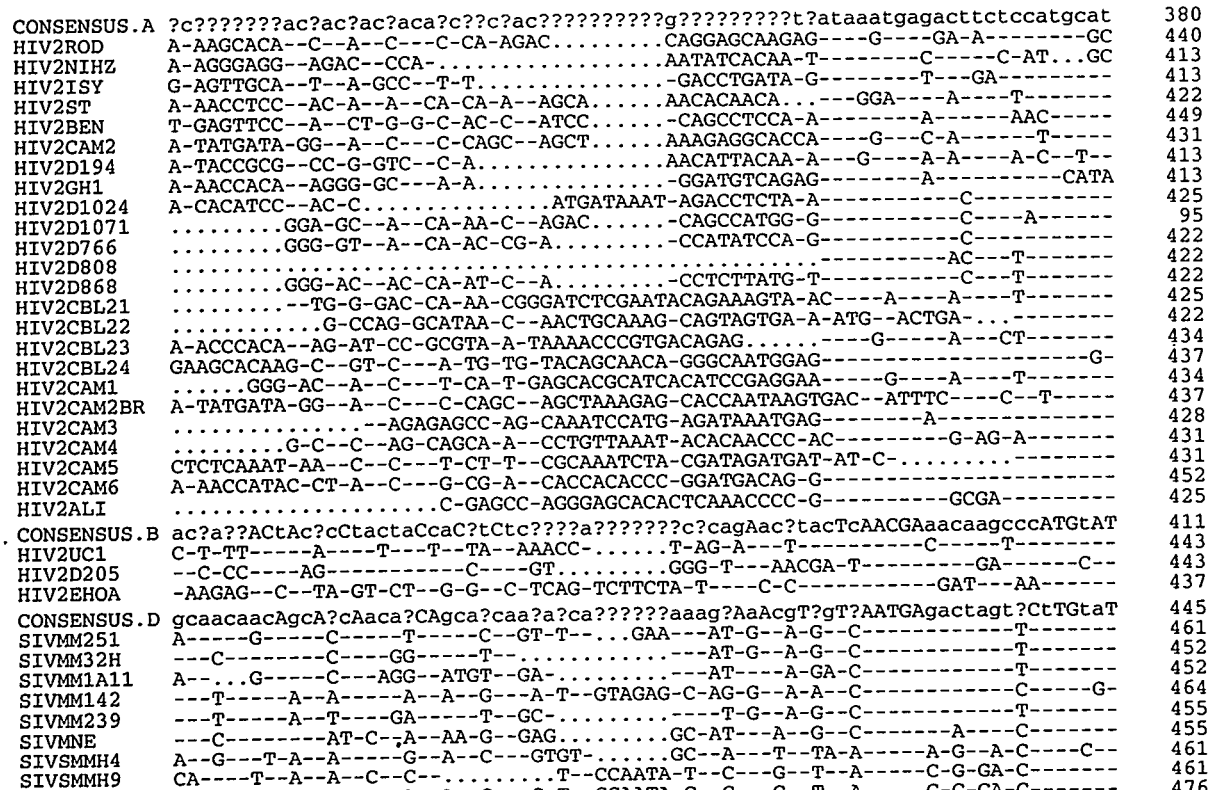
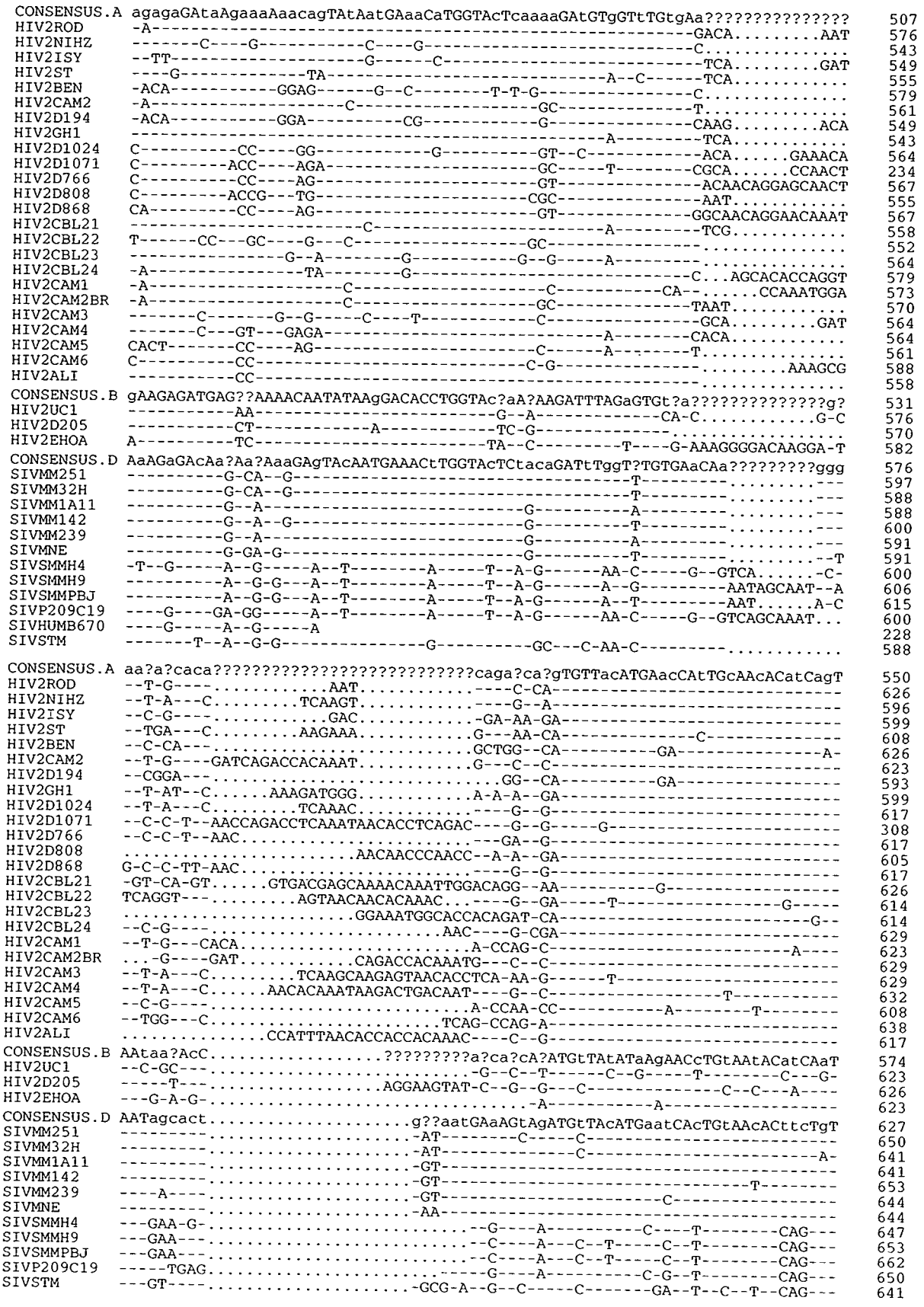


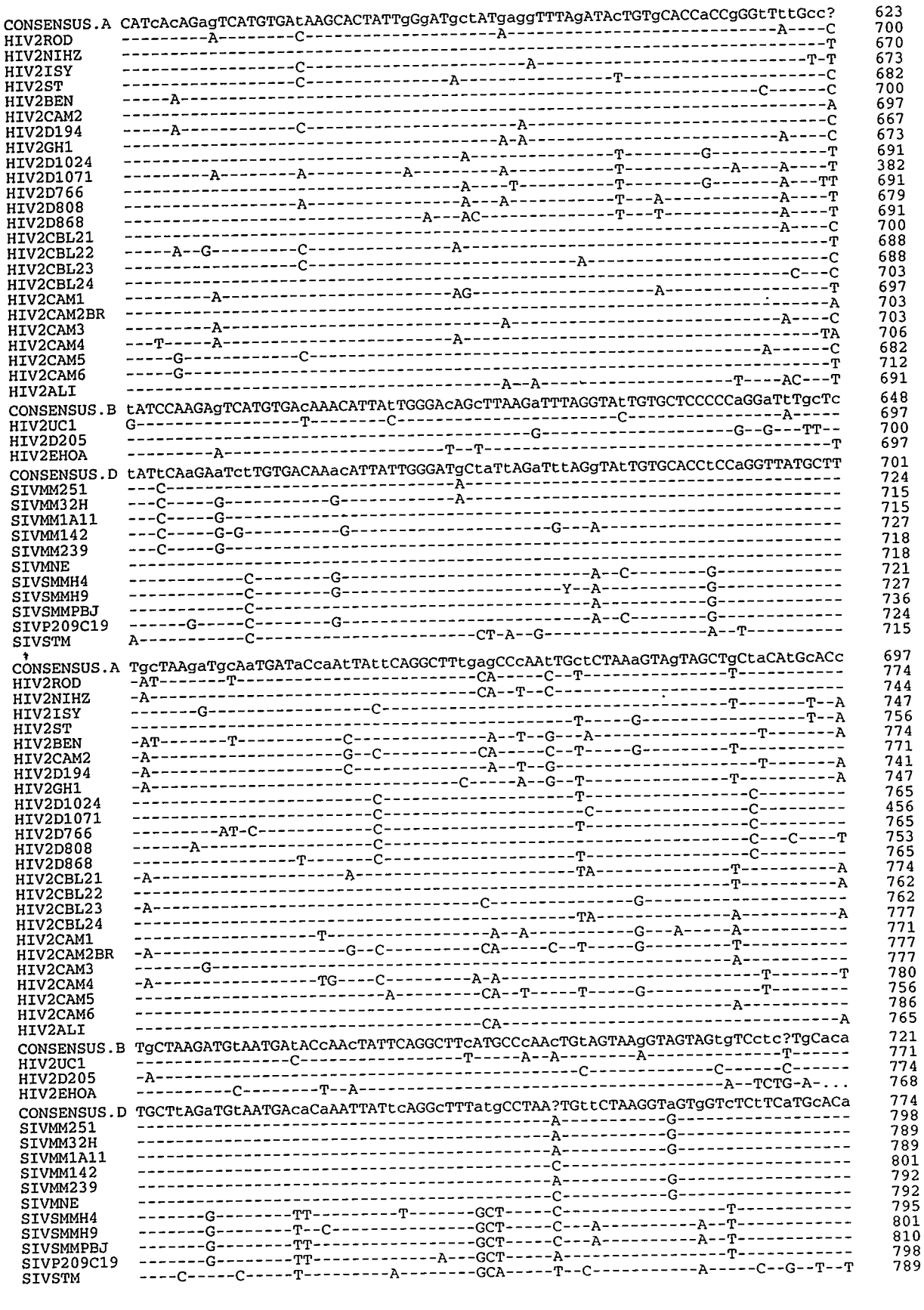


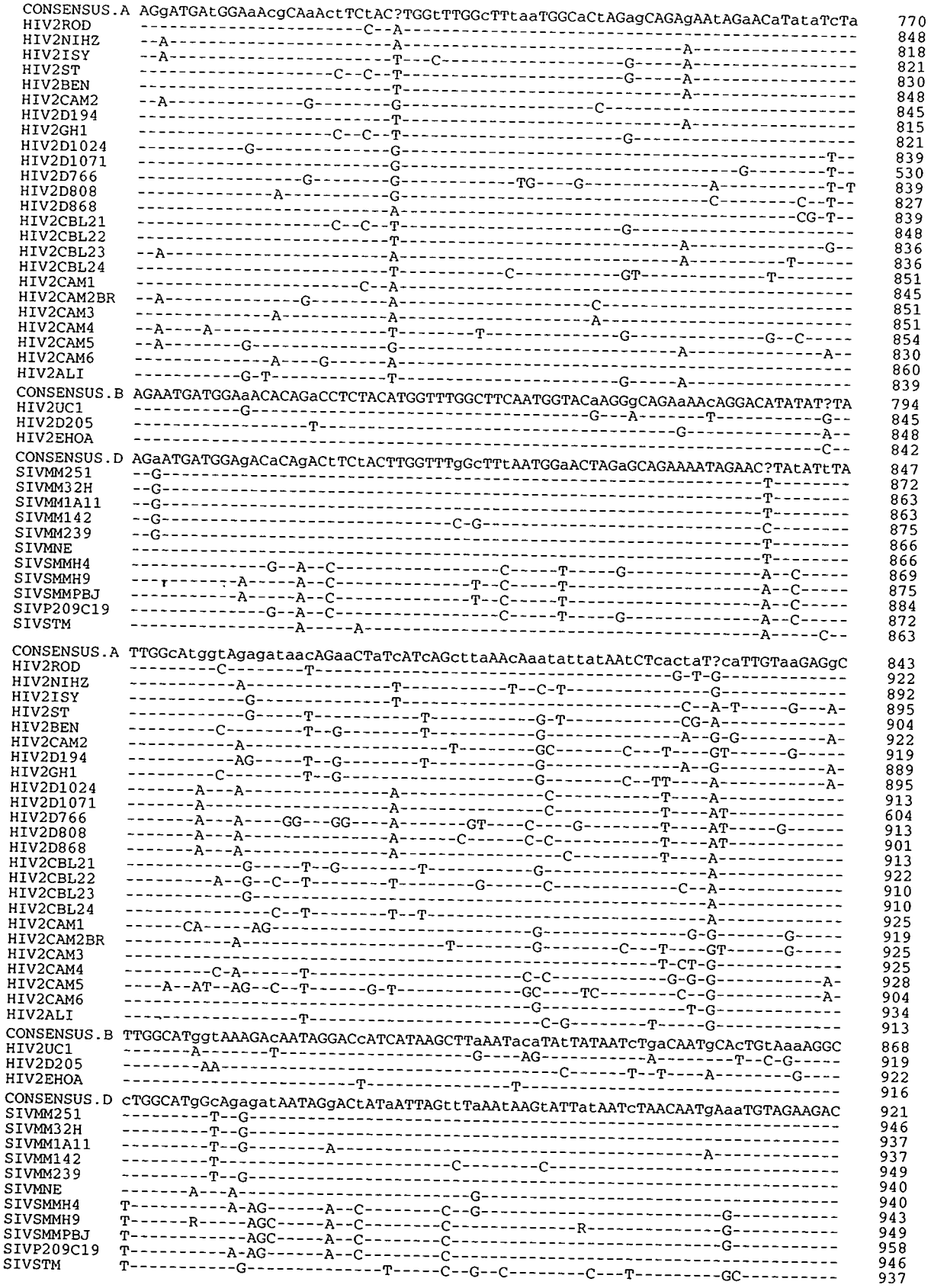
HIV2/SIV ENV

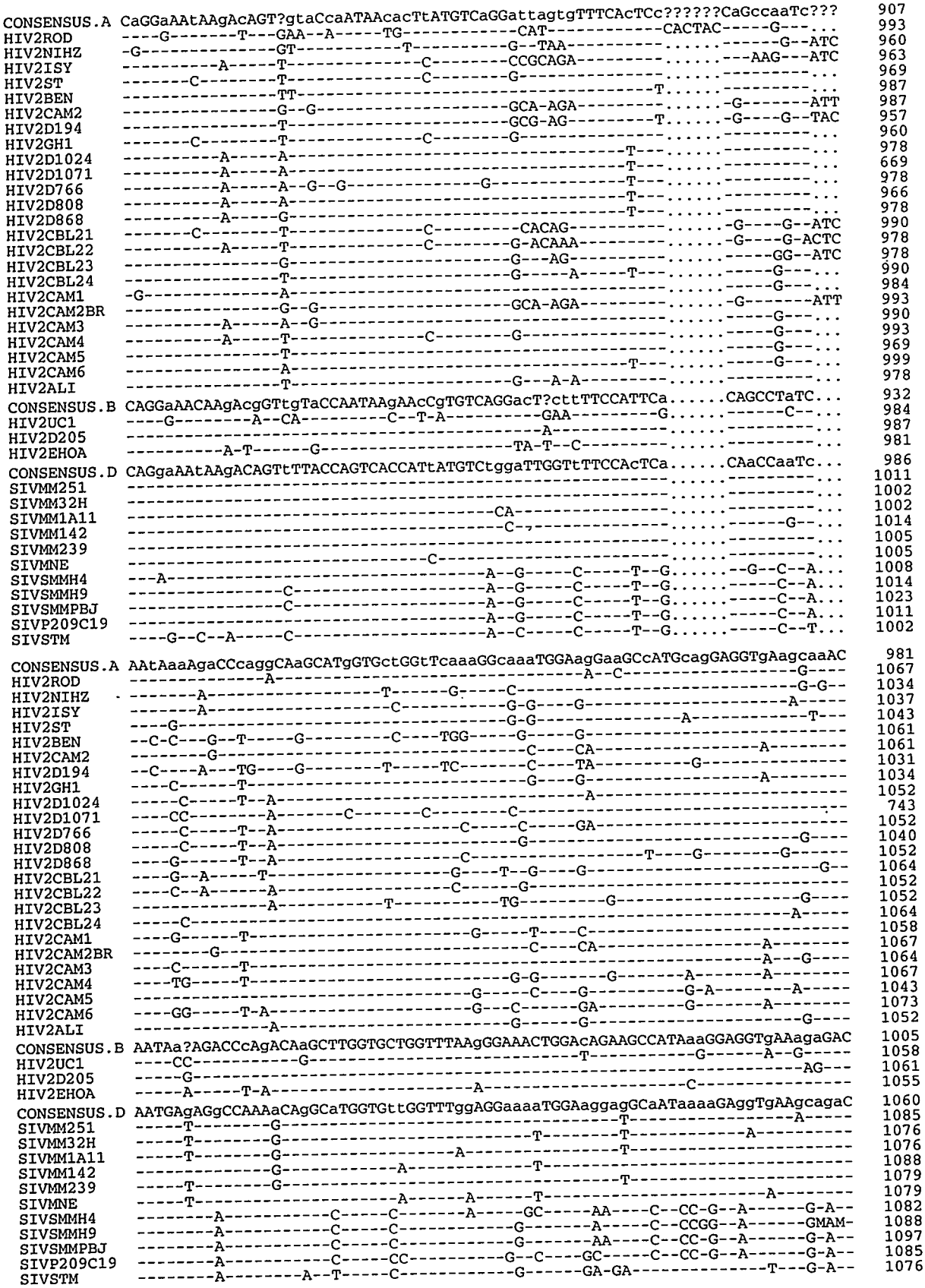


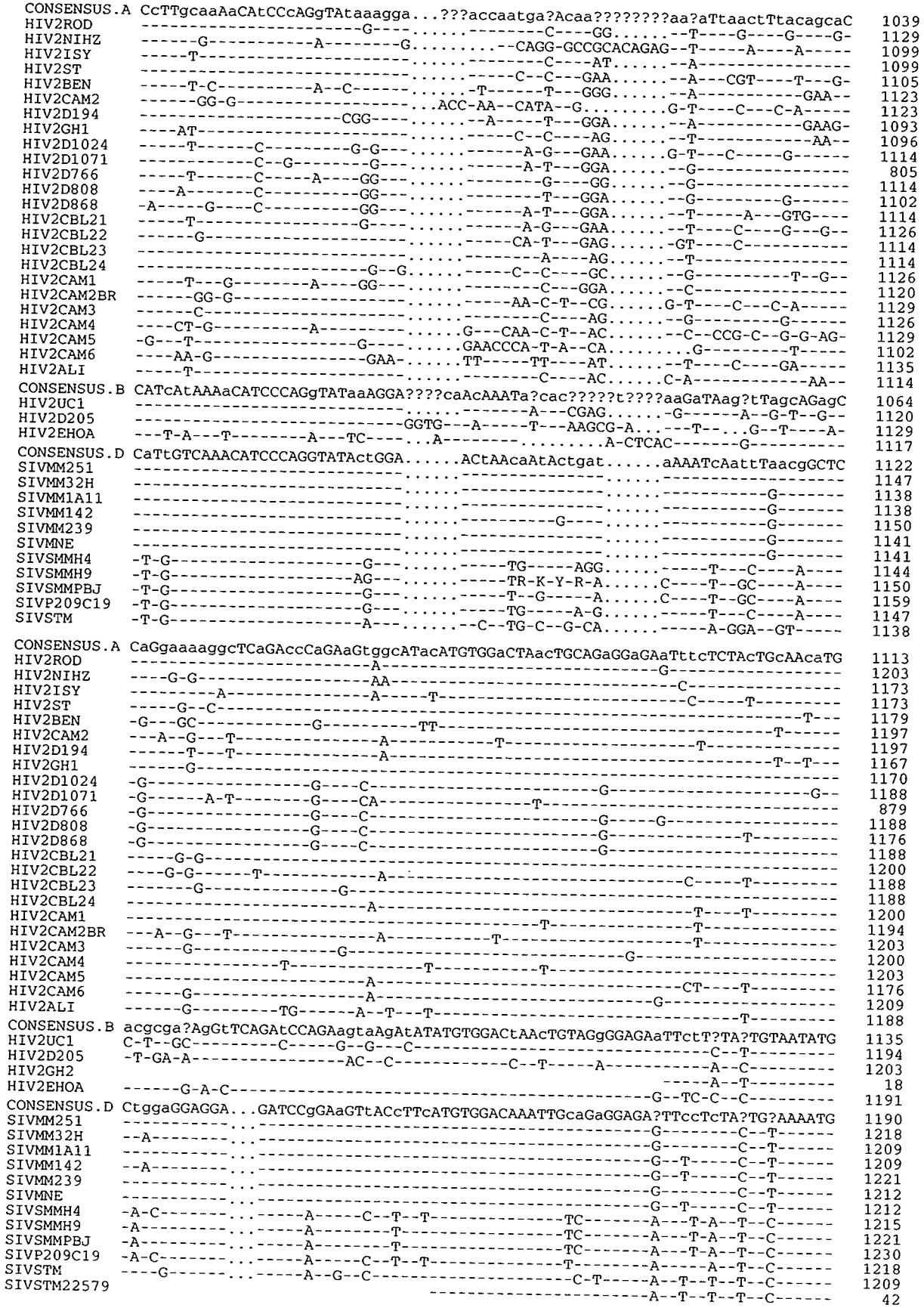


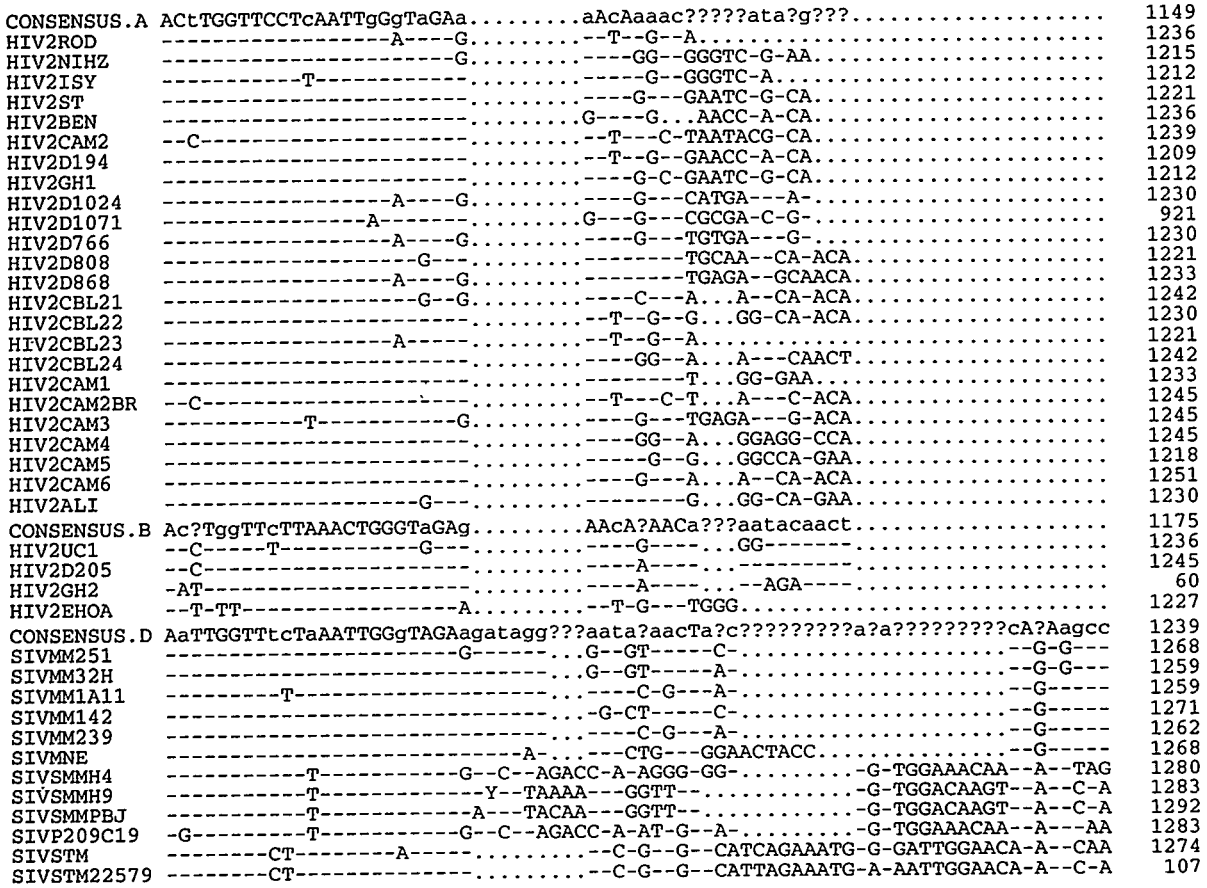




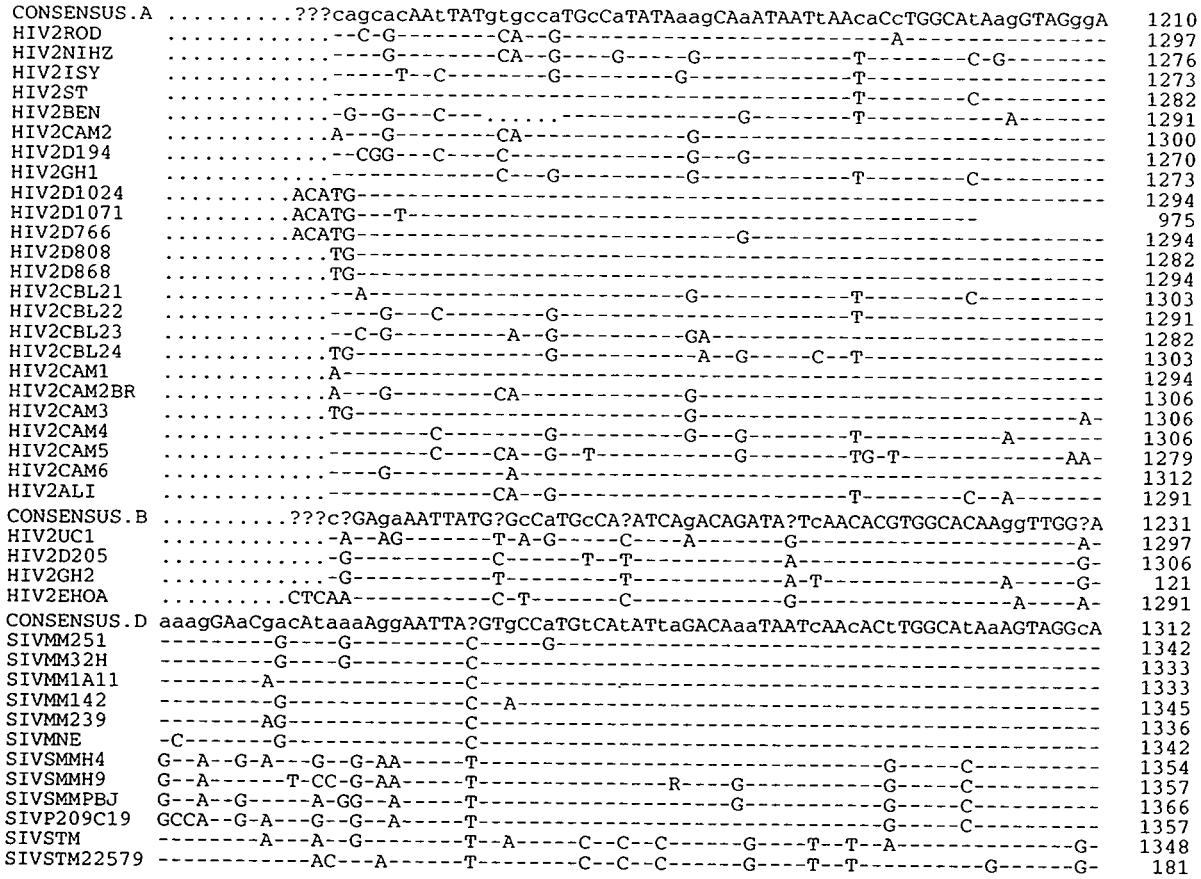








HIV2/SIV ENV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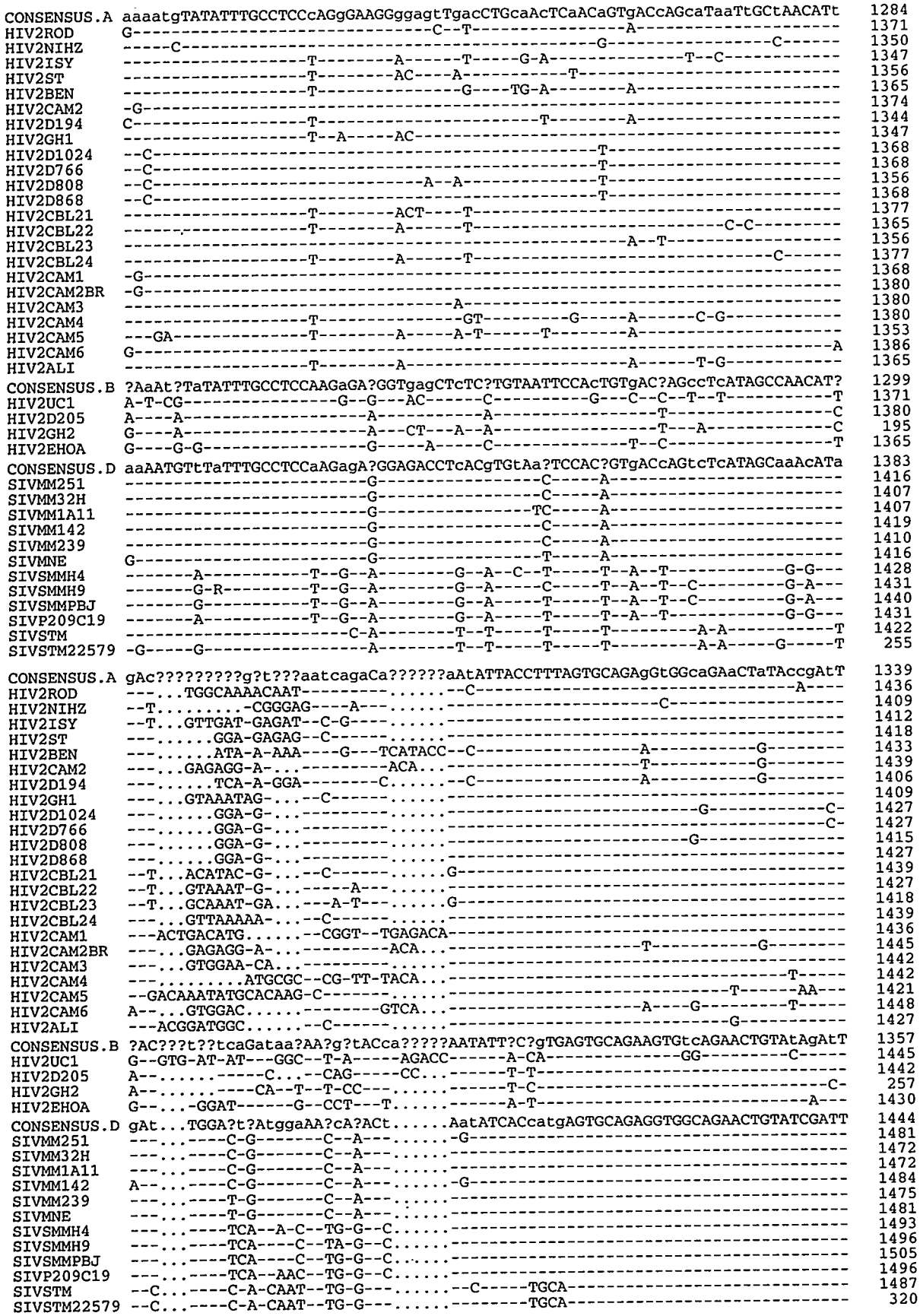
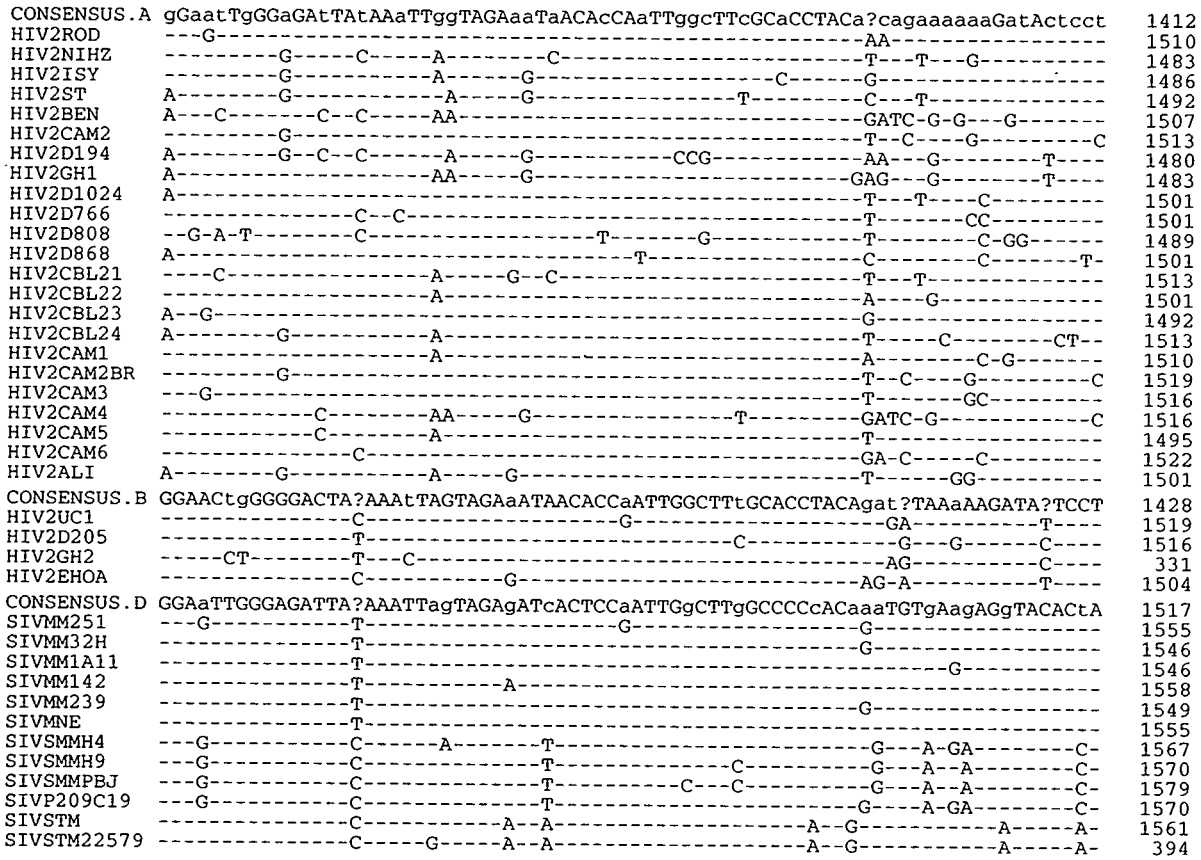
HIV2ROD .....--C-G--------CA--G----------A---------- 1297
HIV2NIHZ .....----G--------CA--G----G-----G----------T--------C-G-------- 1276
HIV2ISY .....-----T--C--------G---------G----------T---------- 1273
HIV2ST ----------T--------C---------- 1282
HIV2BEN .....-G--G---C---.....--------G--------T----------A------- 1291
HIV2CAM2 .....A---G--------CA----------G---------- 1300
HIV2D194 .....--CGG---C----C----------G---G---------- 1270
HIV2GH1 .....----------C---G---------G----------T--------C---------- 1273
HIV2D1024 .....ACATG---------- 1294
HIV2D1071 .....ACATG---T---------- 975
HIV2D766 .....ACATG----------G---------- 1294
HIV2D808 .....TG---------- 1282
HIV2D868 .....TG---------- 1294
HIV2CBL21 .....--A----------G----------T--------C---------- 1303
HIV2CBL22 .....----G---C--------G----------T---------- 1291
HIV2CBL23 .....--C-G---------A--G---------GA---------- 1282
HIV2CBL24 .....TG---------G----------A--G-----C--T---------- 1303
HIV2CAM1 .....A---------- 1294
HIV2CAM2BR .....A---G--------CA----------G---------- 1306
HIV2CAM3 .....TG----------G----------A- 1306
HIV2CAM4 .....--------C--------G---------G---G--------T----------A------- 1306
HIV2CAM5 .....--------C----CA--G--T----------G---------TG-T----------AA- 1279
HIV2CAM6 .....----G---------A---------- 1312
HIV2ALI .....----------CA--G----------T--------C--A------- 1291
CONSENSUS.B .....???c?GAgaAATTATG?GcCaTGcCA?ATCAgACAGATA?TcAACACGTGGCACAAggTTGG?A 1231
HIV2UC1 .....-A--AG-------T-A-G-----C----A-------G----------A- 1297
HIV2D205 .....-G----------C------T--T----------A----------G- 1306
HIV2GH2 .....-G----------T---------T----------A-T----------A-----G- 121
HIV2EHOA .....CTCAA----------C-T-------C----------G----------A----A- 1291
CONSENSUS.D aaagGAaCgacAtaaaAggAATTA?GTgCCaTGtCAtATtaGACAaaTAATcAAcACttGGCAtAaAGTAGGcA 1312
SIVMM251 ---------G----G---------C-----G---------- 1342
SIVMM32H ---------G----G---------C---------- 1333
SIVMM1A11 --------A----------C---------- 1333
SIVMM142 ---------G----------C--A---------- 1345
SIVMM239 --------AG----------C---------- 1336
SIVMNE -C-------G----------C---------- 1342
SIVSMMH4 G--A--G-A---G--G-AA-----T----------G-----C---------- 1354
SIVSMMH9 G--A------T-CC-G-AA-----T----------R----G----------G-----C---------- 1357
SIVSMMPBJ G--A--G-----A-GG--A-----T----------G----------G-----C---------- 1366
SIVP209C19 GCCA--G-A---G--G--A-----T----------G-----C---------- 1357
SIVSTM --------A---A--G--------T--A-----C--C--C------G----T--T--A----------G- 1348
SIVSTM22579 ----------AC---A------T--------C--C--C------G----T--T----------G------G- 181



HIV2/SIV ENV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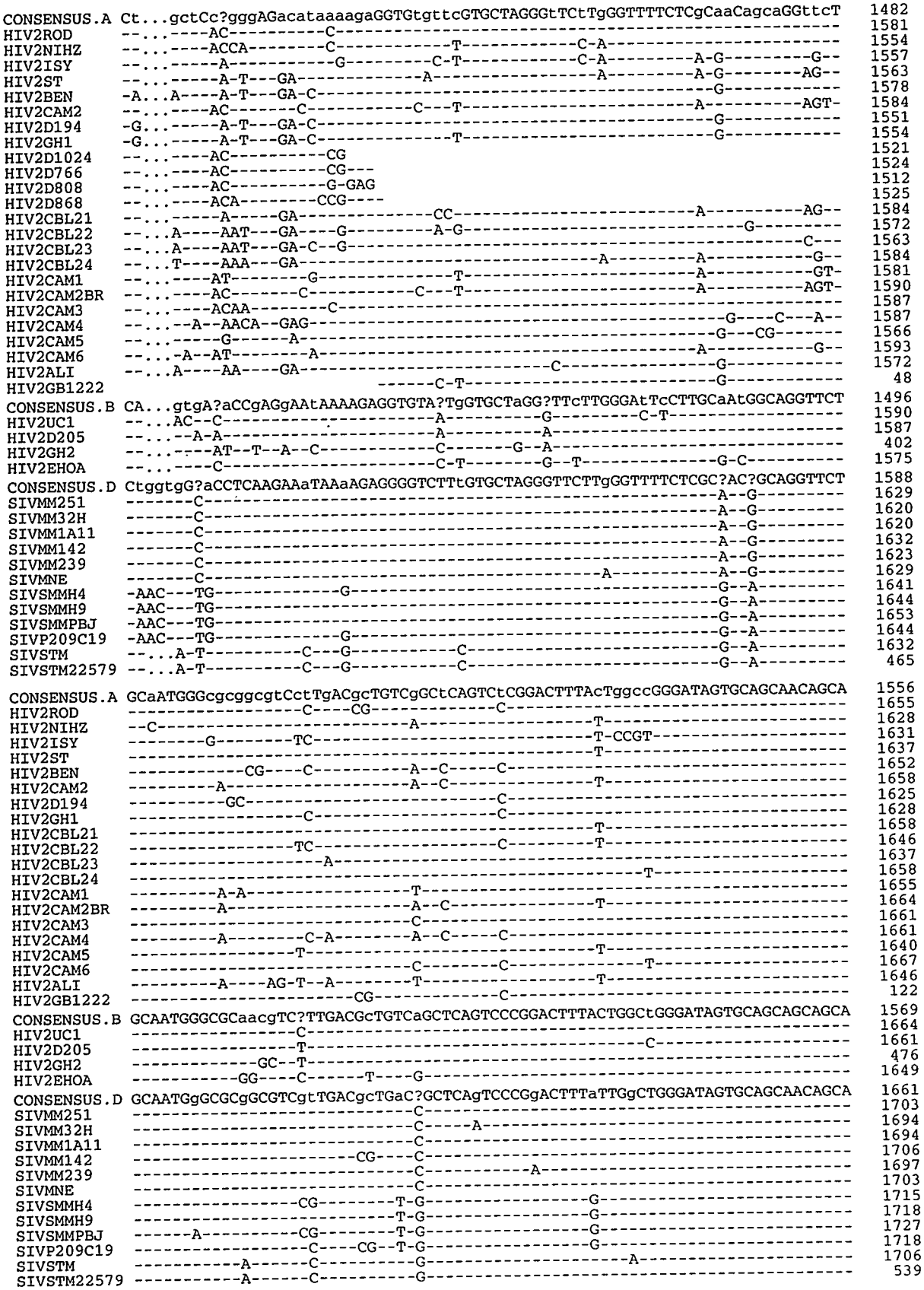
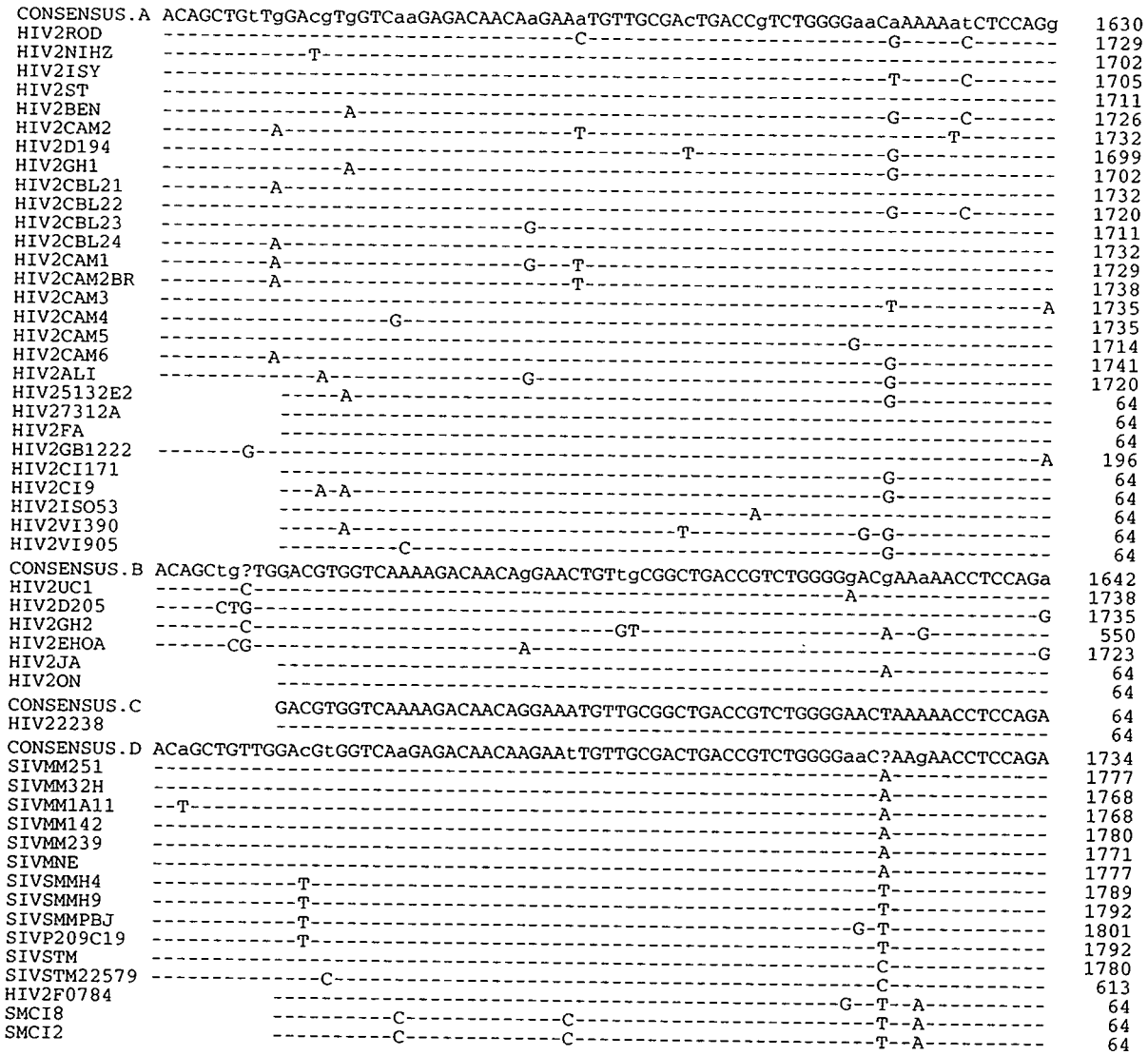
HIV2ROD ---G----------AA---------- 1510
HIV2NIHZ ---------G-----C-----A--------C----------T---T---G---------- 1483
HIV2ISY ---------G----------A------G----------C------G---------- 1486
HIV2ST A--------G----------A-----G----------T---------C---T---------- 1492
HIV2BEN A---C-------C--C-----AA----------GATC-G-G---G------- 1507
HIV2CAM2 ---------G----------T--C----G---------C 1513
HIV2D194 A--------G--C--C------A-----G----------CCG----------AA---G--------T---- 1480
HIV2GH1 A----------AA-----G----------GAG---G---------T---- 1483
HIV2D1024 A----------T---T----C--------- 1501
HIV2D766 ----------C--C----------T-------CC--------- 1501
HIV2D808 --G-A-T--------C----------T-------G----------T--------C-GG------ 1489
HIV2D868 A----------T----------C--------C-------T- 1501
HIV2CBL21 ----C----------A-----G--C----------T---T---------- 1513
HIV2CBL22 ----------A----------A----G---------- 1501
HIV2CBL23 A--G----------G---------- 1492
HIV2CBL24 A--------G----------A----------T-----C--------CT-- 1513
HIV2CAM1 ----------A----------A--------C-G------- 1510
HIV2CAM2BR ---------G----------T--C----G---------C 1519
HIV2CAM3 ---G----------T-------GC--------- 1516
HIV2CAM4 ----------C--------AA-----G----------T---------GATC-G----------C 1516
HIV2CAM5 ----------C--------A----------T---------- 1495
HIV2CAM6 ----------C----------GA-C-----C--------- 1522
HIV2ALI A--------G----------A-----G----------T------GG---------- 1501
CONSENSUS.B GGAACtgGGGGACTA?AAAtTAGTAGAaATAACACCaATTGGCTTtGCACCTACAgat?TAAaAAGATA?TCCT 1428
HIV2UC1 ----------C----------G----------GA----------T---- 1519
HIV2D205 ----------T----------C----------G---G------C---- 1516
HIV2GH2 -----CT--------T---C----------AG----------C---- 331
HIV2EHOA ----------C----------G----------AG-A----------T---- 1504
CONSENSUS.D GGAaTTGGGAGATTA?AAATTagTAGAgATcACTCCaATTGgCTTgGCCCCcACaaaTGTgAagAGgTACACtA 1517
SIVMM251 ---G----------T----------G----------G---------- 1555
SIVMM32H ----------T----------G----------G---------- 1546
SIVMM1A11 ----------T----------G---------- 1546
SIVMM142 ----------T----------A---------- 1558
SIVMM239 ----------T----------G---------- 1549
SIVMNE ----------T---------- 1555
SIVSMMH4 ---G----------C------A-------T----------G---A-GA--------C- 1567
SIVSMMH9 ---G----------C----------T----------C----------G---A--A--------C- 1570
SIVSMMPBJ ---G----------C----------T----------C---C----------G---A--A--------C- 1579
SIVP209C19 ---G----------C----------T----------G----A-GA--------C- 1570
SIVSTM ----------C----------A--A----------A--G----------A-----A- 1561
SIVSTM22579 ----------C-----G-----A--A----------A--G----------A-----A- 394



HIV2/SIV ENV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HIV2ROD 1729
HIV2NIHZ 1702
HIV2ISY 1705
HIV2ST 1711
HIV2BEN 1726
HIV2CAM2 1732
HIV2D194 1699
HIV2GH1 1702
HIV2CBL21 1732
HIV2CBL22 1720
HIV2CBL23 1711
HIV2CBL24 1732
HIV2CAM1 1729
HIV2CAM2BR 1738
HIV2CAM3 1735
HIV2CAM4 1735
HIV2CAM5 1714
HIV2CAM6 1741
HIV2ALI 1720
HIV25132E2 64
HIV27312A 64
HIV2FA 64
HIV2GB1222 196
HIV2CI171 64
HIV2CI9 64
HIV2ISO53 64
HIV2VI390 64
HIV2VI905 64
CONSENSUS.B ACAGCtg?TGGACGTGGTCAAAAGACAACAgGAACTGTtgCGGCTGACCGTCTGGGGgACgAAaAACCTCCAGa 1642
HIV2UC1 1738
HIV2D205 1735
HIV2GH2 550
HIV2EHOA 1723
HIV2JA 64
HIV2ON 64
CONSENSUS.C GACGTGGTCAAAAGACAACAGGAAATGTTGCGGCTGACCGTCTGGGGAACTAAAAACCTCCAGA 64
HIV22238 64
CONSENSUS.D ACaGCTGTTGGAcGtGGTCAaGAGACAACAAGAAtTGTTGCGACTGACCGTCTGGGGaaC?AAgAACCTCCAGA 1734
SIVMM251 1777
SIVMM32H 1768
SIVMM1A11 1768
SIVMM142 1780
SIVMM239 1771
SIVMNE 1777
SIVSMMH4 1789
SIVSMMH9 1792
SIVSMMPBJ 1801
SIVP209C19 1792
SIVSTM 1780
SIVSTM22579 613
HIV2F0784 64
SMCI8 64
SMCI2 64

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CONSENSUS.A CAAGAGTCACtGCTATcGAGAagTACtTAaaggAcCAGGCgCagcTAAATTCaTGGGGaTGtGcgTTtAGaCAa 1704
HIV2ROD     ----------------A---------C--C-----------G---------------------------------- 1803
HIV2NIHZ    ----------------A---------C---------------------------------------------------- 1776
HIV2ISY     ----------------T---------C--GCA----------GA---------------------------------- 1779
HIV2ST      ----------------------A--------------------A---------------------------------- 1785
HIV2BEN     ------------------------C-----C-T-----A----------------------------------G 1800
HIV2CAM2    ----------------A---------C-------T-----A---------------------------------- 1806
HIV2D194    ----------------------A-----------------A-----------------------------G--G 1773
HIV2GH1     ---------------------------------------A---T------------G-----------G--G 1776
HIV2CBL21   ----------------T-----A-------------------------------C----------------G--- 1806
HIV2CBL22   ---------------------------------------------------------G---------------- 1794
HIV2CBL23   ------------------------------------------A--------------------A--------- 1785
HIV2CBL24   ----------------------A-------------------G---------------------------------- 1806
HIV2CAM1    ----------------A---------C---------------TA--------------------A--C------- 1803
HIV2CAM2BR  ----------------A---------C-------T-----A---------------------------------- 1812
HIV2CAM3    ----------------A---------C-------------A--A-----------------------C------- 1809
HIV2CAM4    ----------G-----------A-----------------A--------------------C-T------G--- 1809
HIV2CAM5    ---------------------------------------A-G--------------------A--------G 1788
HIV2CAM6    ----------------A---------C-------------A---------------------------------- 1815
HIV2ALI     ----------------------A-------------------G---------------------A--------- 1794
HIV25132E2  ------------------------------------------A-----------------------------G--G 138
HIV27312A   ----------------T-----A--------------------A-------------------------G--- 138
HIV2FA      ----------------T-----A--------------------A-----------------C--------G--- 138
HIV2GB1222  ----------------A---------C-----------------CG------------------------------ 270
HIV2CI171   ----------------------A-------------------------------------------------G--G 138
HIV2CI9     ------------------------------------------A-----------------G-----------G--G 138
HIV2ISO53   ----------------------GA-------------------------------------C------------ 138
HIV2VI390   ----------------------A-----------------A-----------------------------G--G 138
HIV2VI905   ----------------A-----A---C-----------------A-----------------C-----------G 138
CONSENSUS.B CAAGAGTCACTGCcATCGAGAAATAcCTaAAgGAcCAGGCAC?ACTAAAtTCgTGGGGATGTGCTTT?AGaCAG 1714
HIV2UC1     ------------------------------------------T-------------------------T--G--- 1812
HIV2D205    ------------------------------------T-------A---------A---------------C------ 1809
HIV2GH2     ------------------------------------T-------A-----------------------C------- 624
HIV2EHOA    ------------------------T--C--A----------A---------A--------------C------- 1797
HIV2JA      ------------------------------------------T------C-----------------T------- 138
HIV2ON      ----------T-------------------------------T-----------------------T------- 138
CONSENSUS.C CTAGAGTCACTGCCATCGAGAAGTACCTAAAGGACCAAGCAAAACTAAATTCATGGGGATGTGCCTTTAGACAG 138
HIV22238    ------------------------------------------------------------------------------ 138
CONSENSUS.D CTAGaGTCaCTGCcATCGAGAAgTACcTaAAGGAtCAGGCgCagcTaAATTcCtTGGGGATGtGCgTTtAGaCAa 1808
SIVMM251    ----G----------------------T-------C---------------G------------------------ 1851
SIVMM32H    ----G----------------------T-------C-----------G---G------------------------ 1842
SIVMM1A11   ----G----------------A---T-------C-----------G---G------------------------ 1842
SIVMM142    ----G---T----------------T-------C---------------G------------------------ 1854
SIVMM239    ----G----------------------T-------C-----------G---G------------------------ 1845
SIVMNE      -------------------------T-------C---------------G-------------A---------- 1851
SIVSMMH4    -------------T--------------G-----------------------A-----------T-----G--- 1863
SIVSMMH9    -------------T-------------------------------CRN-------A-----------T-----G--G 1866
SIVSMMPBJ   -------------T-------------------------------------A-----------T-----G--G 1875
SIVP209C19  -------------T--------------G-----------------------A-----------T-----G--- 1866
SIVSTM      -------------T--------A-----------------A-------------------------------G 1854
SIVSTM22579 -------------T--------A-----------------A-------------------------------G 687
HIV2F0784   -------------T--------------------C-----------------A--------C-----C-----G 138
SMCI8       ----------------------A-----------------A-G----------------------A---------- 138
SMCI2       ----------------------A-----------------A-G-------G-------------A---------- 138
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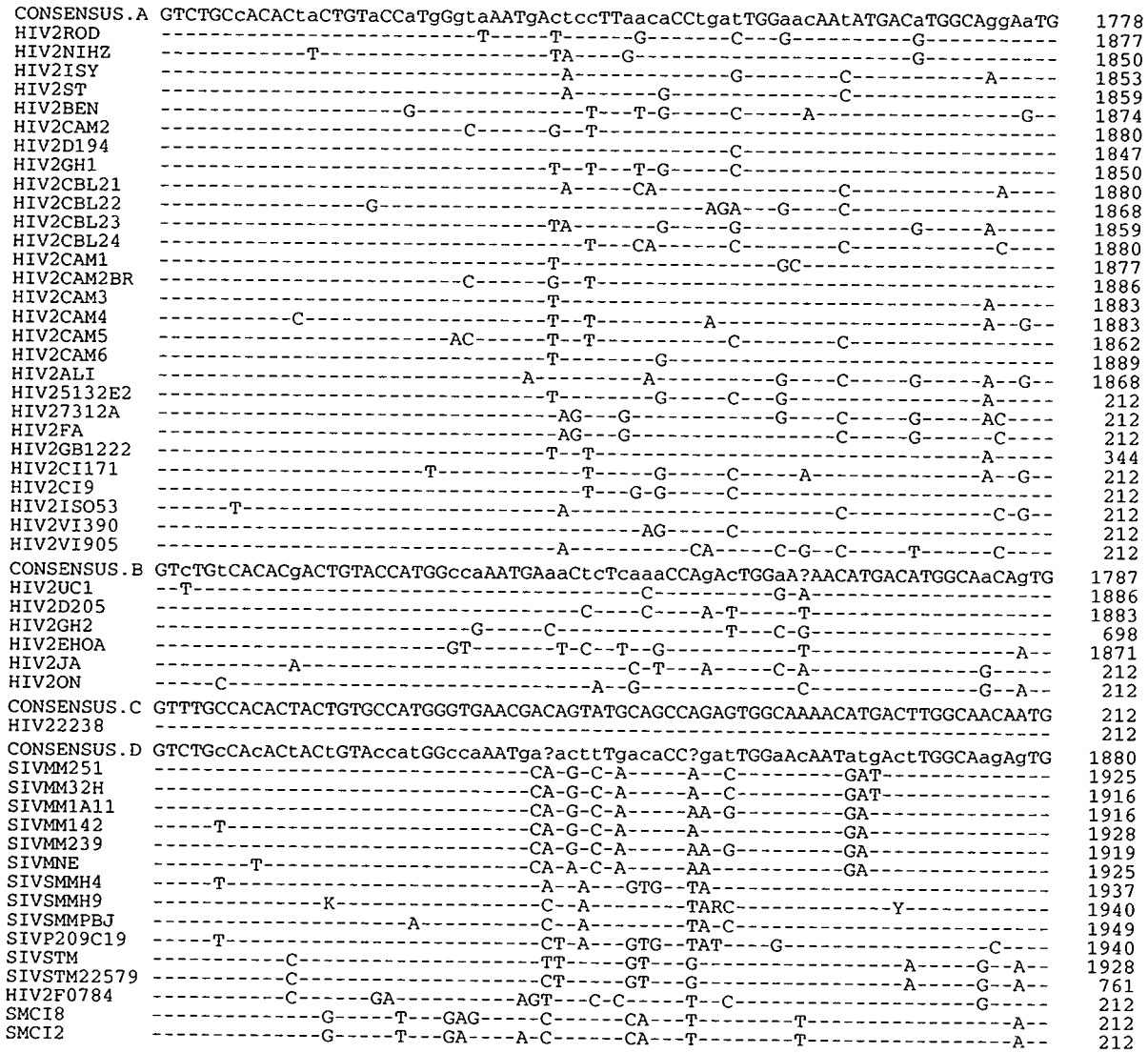
HIV2/SIV ENV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HIV2ROD 1877
HIV2NIHZ 1850
HIV2ISY 1853
HIV2ST 1859
HIV2BEN 1874
HIV2CAM2 1880
HIV2D194 1847
HIV2GH1 1850
HIV2CBL21 1880
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HIV2CAM1 1877
HIV2CAM2BR 1886
HIV2CAM3 1883
HIV2CAM4 1883
HIV2CAM5 1862
HIV2CAM6 1889
HIV2ALI 1868
HIV25132E2 212
HIV27312A 212
HIV2FA 212
HIV2GB1222 344
HIV2CI171 212
HIV2CI9 212
HIV2ISO53 212
HIV2VI390 212
HIV2VI905 212
CONSENSUS.B GTcTGtCACACgACTGTACCATGGccaAATGAaaCtcTcaaaCCAgAcTGGaA?AACATGACATGGCAaCAgTG 1787
HIV2UC1 1886
HIV2D205 1883
HIV2GH2 698
HIV2EHOA 1871
HIV2JA 212
HIV2ON 212
CONSENSUS.C GTTTGCCACACTACTGTGCCATGGGTGAACGACAGTATGCAGCCAGAGTGGCAAAACATGACTTGGCAACAATG 212
HIV22238 212
CONSENSUS.D GTCTGcCAcACtACtGTAccatGGccaAATga?acttTgacaCC?gatTGGaAcAATatgActTGGCAagAgTG 1880
SIVMM251 1925
SIVMM32H 1916
SIVMM1A11 1916
SIVMM142 1928
SIVMM239 1919
SIVMNE 1925
SIVSMMH4 1937
SIVSMMH9 1940
SIVSMMPBJ 1949
SIVP209C19 1940
SIVSTM 1928
SIVSTM22579 761
HIV2F0784 212
SMCI8 212
SMCI2 212

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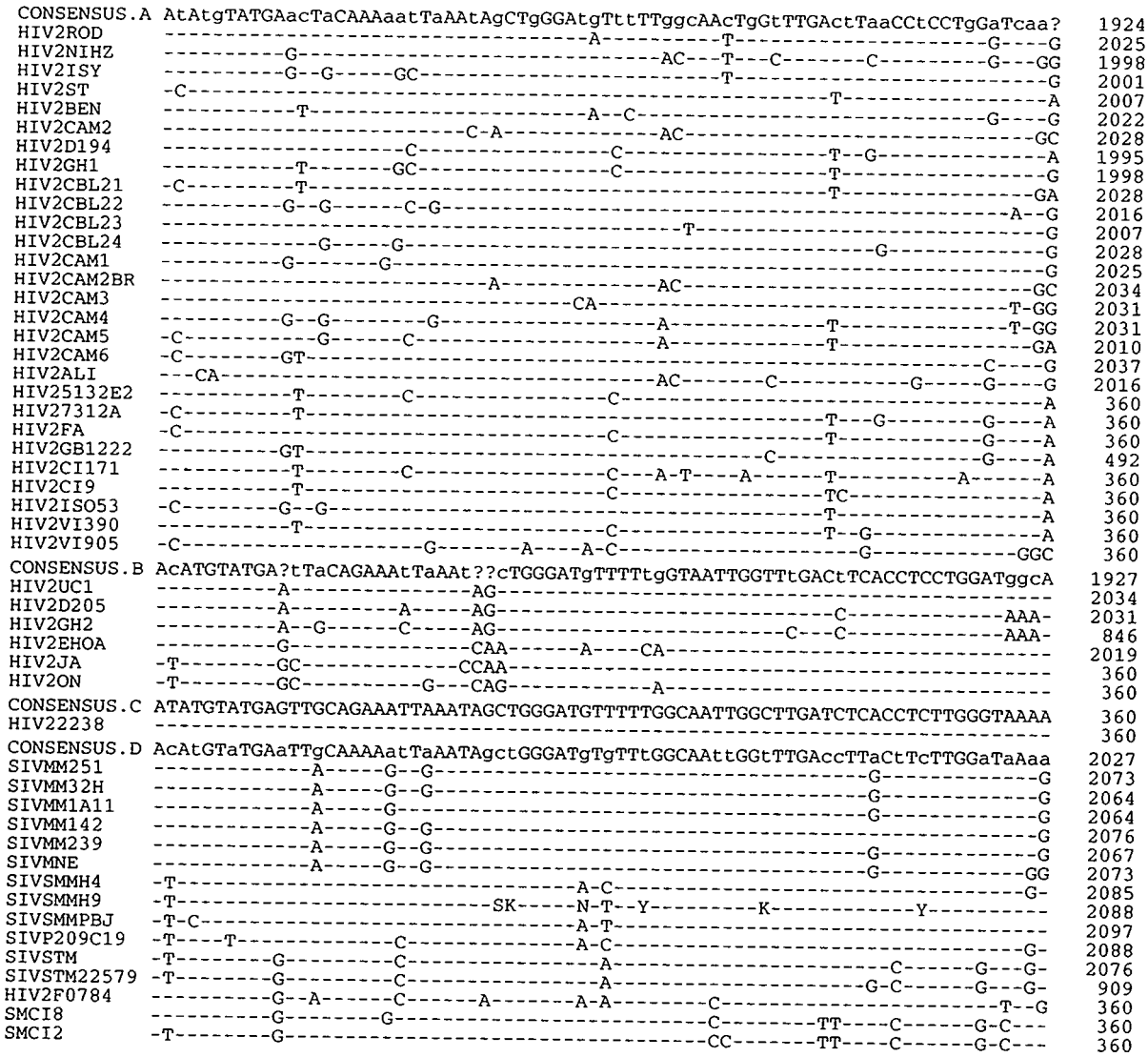
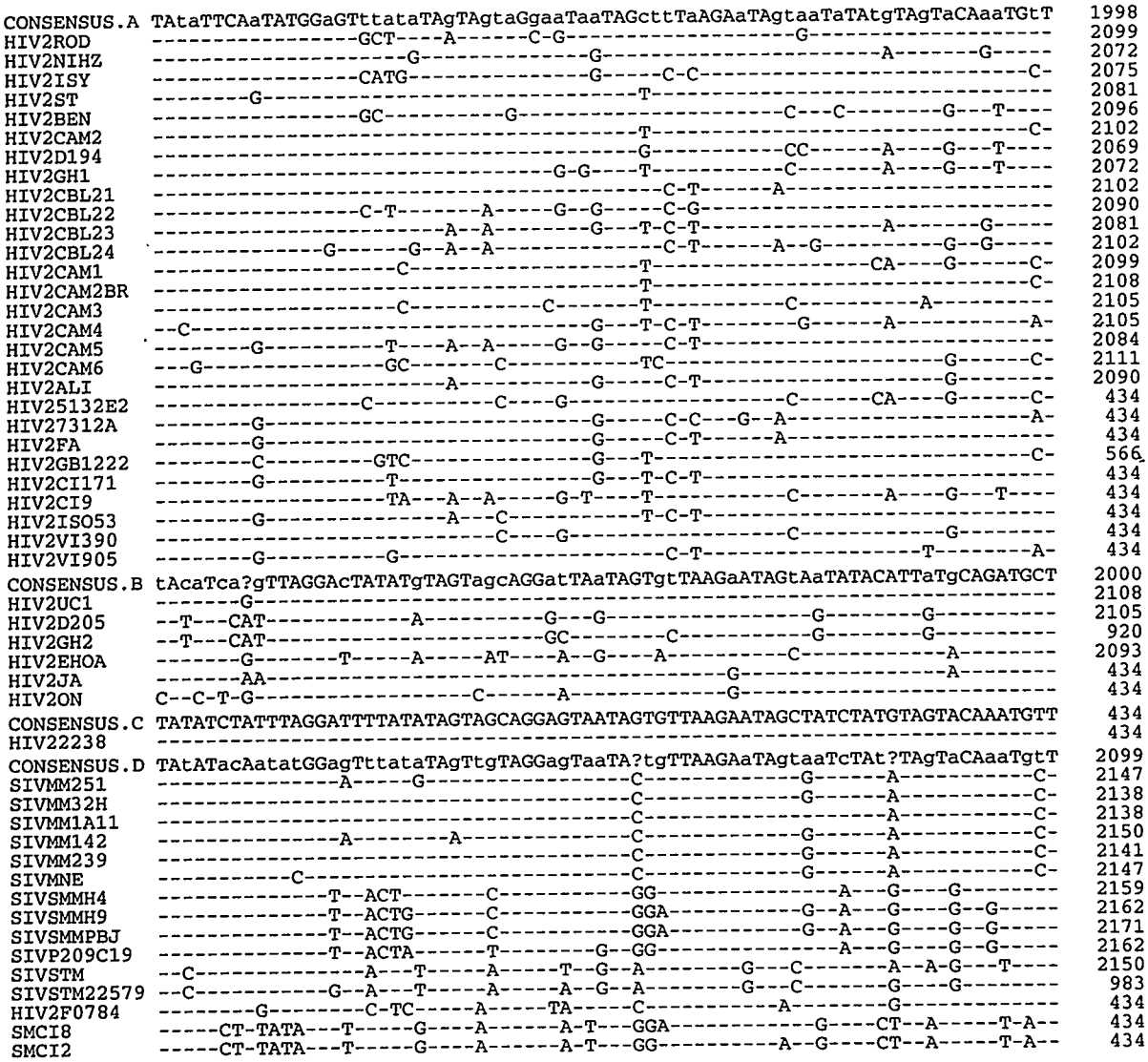
CONSENSUS.A GGaacaacaagtCCgctaCCTaGAgGCAAATATCAGT?aaagttTaGAacAgGCaCAAaTtCAgCAaGAaAAgA 1851
HIV2ROD     ----A----------------G--------------A-----------------------------G--A- 1951
HIV2NIHZ    -------A-------------G--------------C-----C-------A---------------------- 1924
HIV2ISY     ------CA--A------T-------------------G-G--------------------C------------- 1927
HIV2ST      ---G----G-A-----A--------------------G----------------------C------------- 1933
HIV2BEN     ---GA-------------------------------C-----------G-A--C--------A---------- 1948
HIV2CAM2    -------A-G----------G---------------C-----------G--------C--------------- 1954
HIV2D194    ----A---G-----A----------------------C-------------------------A---------- 1921
HIV2GH1     ----A-------------------------------C----------------------A------------- 1924
HIV2CBL21   ----------A--------------------------AC-----------A---------------------- 1954
HIV2CBL22   ---------GA--------------------------GGCCAG----------------C------------- 1942
HIV2CBL23   ----GGCA--A-----G----G--------------C--CAA--------A---------------------- 1933
HIV2CBL24   ---G--C-----------------------------G--CTG----------------C------------- 1954
HIV2CAM1    -------A-G----------G---------------C-------G--------------C--A--G------- 1951
HIV2CAM2BR  -------A-G----------G---------------C----------G--------C--------------- 1960
HIV2CAM3    -------A------A------G---------------G---TG-----------------C-----G------- 1957
HIV2CAM4    -----T--G-AC---T-----G--T-----------C--CT-----------------C--------G----- 1957
HIV2CAM5    ------CA--A----TG--------------------G-C---C-------A--------C------------- 1936
HIV2CAM6    ---G--GA-------------G---------------C----------------------C-----G------- 1963
HIV2ALI     ---------------T--------------------G--CAG------------------------------- 1942
HIV25132E2  ---GG---G-------------------------C-------------------------A-----G--A-  286
HIV27312A   ----A-----A-----G----G--------------G-----C----------------C------------- 286
HIV2FA      ----------A----------G---------------G-G--------------------C------------- 286
HIV2GB1222  ----------------------G--A----------G----AC-------A--------------G-----A- 418
HIV2CI171   ---GATG-----------------------------C--CAG---------------------A---------- 286
HIV2CI9     ---GG-------------------------------G---TC--------------------A-----G----- 286
HIV2ISO53   ------C---A-------------------------G--CAA----------G----------G------- 286
HIV2VI390   --CGA-G----------T------------------C--CAG--G--G-----------C--A-----G--A- 286
HIV2VI905   ----------A----T--------------------GC---------------------------------- 286
CONSENSUS.B GGAaaagcaaGTC?atTtCTTGGAtGCAAATATAACag?a?TatTAGAAGAgGC?CAGATACAaCA?GAAAaGA 1856
HIV2UC1     --------G----A-------------------------CCC-G----------T----------A----G-- 1960
HIV2D205    -------------C----------------------G-CTC-G----------T----------G------- 1957
HIV2GH2     ---G---------A----------A-------------CTC----------A--T----------A------- 772
HIV2EHOA    ---G-G-------CGC----------------------AA-T--C----------A----------A------- 1945
HIV2JA      ----C--A-G---A-C-A--------------------CA-T----------A--------G--G------- 286
HIV2ON      ----GCAA-G---C-A----------------------CA-T----------A--A--------G--G------- 286
CONSENSUS.C GGAAAAACAGATTGCCTTCTTGGAGGATAATATCACAGAGCTGTTAGAGCAAGCTCAAATACAGCAGGAGAAAA 286
HIV22238    ------------------------------------------------------------------------ 286
CONSENSUS.D GGAgagaaAGgTtgacttccTgGAgGcAAATATaaCagaactatTaGAagA?GCaCAAaTtCAaCAaGAaaAgA 1953
SIVMM251    ----C--------------T------A-----------CC--CC-------G----------------G----- 1999
SIVMM32H    ----C--------------T------A-----------CC--CC-------G----------------G----- 1990
SIVMM1A11   ----C--------------T------A-----------CC--CC----G--G----------------G----- 1990
SIVMM142    ----C-G------------T----------------G-CC--CC-------G----------------G----- 2002
SIVMM239    ----C--------------T----A-A-----------CC--CC----G--G----------------G----- 1993
SIVMNE      ----C--------------T------A---------G-CC--T--------G--------------------- 1999
SIVSMMH4    ---A---C------------A--------------TC--T----------A----------G---------- 2011
SIVSMMH9    ---A-A-C----GA-------A--------------TS--TY---G-----A----------G------M--- 2014
SIVSMMPBJ   ---A-A-C----GA-------A--------------TC--TC---G-----A----------G---------- 2023
SIVP209C19  ---A---C----------C---A--------------TC--T----------A----------G---------- 2014
SIVSTM      ------------------T--T---------------C----G--------A--T---G-------G------- 2002
SIVSTM22579 ------------------T--T---------------C-------------A--T---G-------G------- 835
HIV2F0784   ---A---C-------T-----A---------------C--T-------G--A----------G--G--G--A-  286
SMCI8       ---A-T----A-CAGAGAT--------------CT-----AA---G--GA-C--------A-------------  286
SMCI2       ---A-T----A-CAGAGAT--------------CT-----TC---G--G--G--------A-------------  286
```

HIV2/SIV ENV


CONSENSUS.A AtAtgTATGAacTaCAAAaatTaAAtAgCTgGGAtgTttTTggcAAcTgGtTTGActTaaCCtCCTgGaTcaa? 1924
HIV2ROD 2025
HIV2NIHZ 1998
HIV2ISY 2001
HIV2ST 2007
HIV2BEN 2022
HIV2CAM2 2028
HIV2D194 1995
HIV2GH1 1998
HIV2CBL21 2028
HIV2CBL22 2016
HIV2CBL23 2007
HIV2CBL24 2028
HIV2CAM1 2025
HIV2CAM2BR 2034
HIV2CAM3 2031
HIV2CAM4 2031
HIV2CAM5 2010
HIV2CAM6 2037
HIV2ALI 2016
HIV25132E2 360
HIV27312A 360
HIV2FA 360
HIV2GB1222 492
HIV2CI171 360
HIV2CI9 360
HIV2ISO53 360
HIV2VI390 360
HIV2VI905 360
CONSENSUS.B AcATGTATGA?tTaCAGAAAtTaAAt??cTGGGATgTTTTtgGTAATTGGTTtGACttCACCTCCTGGATggcA 1927
HIV2UC1 2034
HIV2D205 2031
HIV2GH2 846
HIV2EHOA 2019
HIV2JA 360
HIV2ON 360
CONSENSUS.C ATATGTATGAGTTGCAGAAATTAAATAGCTGGGATGTTTTTGGCAATTGGCTTGATCTCACCTCTTGGGTAAAA 360
HIV22238 360
CONSENSUS.D AcAtGTaTGAaTTgCAAAAatTaAATAgctGGGATgTgTTtGGCAAttGGtTTGAccTTaCtTcTTGGaTaAaa 2027
SIVMM251 2073
SIVMM32H 2064
SIVMM1A11 2064
SIVMM142 2076
SIVMM239 2067
SIVMNE 2073
SIVSMMH4 2085
SIVSMMH9 2088
SIVSMMPBJ 2097
SIVP209C19 2088
SIVSTM 2076
SIVSTM22579 909
HIV2F0784 360
SMCI8 360
SMCI2 360


CONSENSUS.A TAtaTTCAaTATGGaGTttataTAgTAgtaGgaaTaaTAGcttTaAGAaTAgtaaTaTAtgTAgTaCAaaTGtT 1998
HIV2ROD 2099
HIV2NIHZ 2072
HIV2ISY 2075
HIV2ST 2081
HIV2BEN 2096
HIV2CAM2 2102
HIV2D194 2069
HIV2GH1 2072
HIV2CBL21 2102
HIV2CBL22 2090
HIV2CBL23 2081
HIV2CBL24 2102
HIV2CAM1 2099
HIV2CAM2BR 2108
HIV2CAM3 2105
HIV2CAM4 2105
HIV2CAM5 2084
HIV2CAM6 2111
HIV2ALI 2090
HIV25132E2 434
HIV27312A 434
HIV2FA 434
HIV2GB1222 566
HIV2CI171 434
HIV2CI9 434
HIV2ISO53 434
HIV2VI390 434
HIV2VI905 434
CONSENSUS.B tAcaTca?gTTAGGAcTATATgTAGTagcAGGatTAaTAGTgtTAAGaATAGtAaTATACATTaTgCAGATGCT 2000
HIV2UC1 2108
HIV2D205 2105
HIV2GH2 920
HIV2EHOA 2093
HIV2JA 434
HIV2ON 434
CONSENSUS.C TATATCTATTTAGGATTTTATATAGTAGCAGGAGTAATAGTGTTAAGAATAGCTATCTATGTAGTACAAATGTT 434
HIV22238 434
CONSENSUS.D TAtATacAatatGGagTttataTAgTtgTAGGagTaaTA?tgTTAAGAaTAgtaaTcTAt?TAgTaCAaaTgtT 2099
SIVMM251 2147
SIVMM32H 2138
SIVMM1A11 2138
SIVMM142 2150
SIVMM239 2141
SIVMNE 2147
SIVSMMH4 2159
SIVSMMH9 2162
SIVSMMPBJ 2171
SIVP209C19 2162
SIVSTM 2150
SIVSTM22579 983
HIV2F0784 434
SMCI8 434
SMCI2 434

```
                                                                                                \/3´ sj
CONSENSUS.A AaGTAGacTtAGaAagGGCTATAGGCCTGTTTTCTCttCCcCcCCcGgTTAtaTcCAACAGaTCCAtATCCAca   2072
HIV2ROD     ------G-------------------------------------------------------------------   2173
HIV2NIHZ    ------------------------------------------------C---------------------------   2146
HIV2ISY     ------------------------------------------------------T--------------------   2149
HIV2ST      ------------------------------------------------C---CT---------------------   2155
HIV2BEN     -------T-----------------------------------------------C--------------------   2170
HIV2CAM2    ------G-----------------------------C---T---------------------------------   2176
HIV2D194    ------------------------------------C---------------C--------------------   2143
HIV2GH1     ----------------------------------------T---------C--------------------   2146
HIV2CBL21   -------T----G-----------------------C-------T-C----C--------G------------   2176
HIV2CBL22   ------G-------------------------------------------G--------------------   2164
HIV2CBL23   ------------------------------------------------CC---------------------   2155
HIV2CBL24   ------------------------------------------------CC-------------------TC   2176
HIV2CAM1    ------G-----------------------------------T--------------------------   2173
HIV2CAM2BR  ----------------------------------C--------------------------------------   2182
HIV2CAM3    ------GT-----------------------------------------------------------------   2179
HIV2CAM4    ------------------------------------------T---------C--------------C-----T-   2179
HIV2CAM5    ----------------------------------C---------------C----------------------   2158
HIV2CAM6    ------------------------------------------------C---------------------   2185
HIV2ALI     ------G--C--G-----------------------C-----T--------C---------------------   2164
HIV25132E2  ----------------                                                            450
HIV27312A   -G------------GA                                                            450
HIV2FA      --------------G-                                                            450
HIV2GB1222  ------------G-----------------------------------C----------------------   640
HIV2CI171   --------------G----                                                         453
HIV2CI9     --------------------                                                        453
HIV2ISO53   -G------------G----                                                         453
HIV2VI390   -------T-----------                                                         453
HIV2VI905   -G------------G----                                                         453
CONSENSUS.B AGCAAgaCTTAGGAAGGGCTATAGGCCAGTATTcTCCTCCCCTCCCTCTTATACTCAACAGATCCCTATCCGCA   2074
HIV2UC1     ------------------------------------------------------------------------   2182
HIV2D205    ------------------------------------------------------------------------   2179
HIV2GH2     ---------------------------------T----------------------------------------   994
HIV2EHOA    ------G-----------------------------------------------------------------   2167
HIV2JA      -----A----------                                                            450
HIV2ON      ------G---------                                                            450
CONSENSUS.C AATGAGACTTAGGAAGGGC                                                         453
HIV22238    --------------------                                                        453

                                                                        <- premature stop in
                                                                           some SIVs
                                                                         \/3´ sj
CONSENSUS.D aGcTAaGttaAGgcAgGG?TATaGGCCaGTGTTCTCTTCCCC?CCctCTTaTtt?cAGcAGA?cCaTAtCcaa?   2168
SIVMM251    ------------------G----------------------A----------C---T---CT----C----C   2221
SIVMM32H    ------------A-----G----------------------A----------C-------C----------C   2212
SIVMM1A11   ------------------G----------------------A----------C---T---C----------C   2212
SIVMM142    -----G------A-----G----------------------A----------C---T---C-----C----C   2224
SIVMM239    ------------------G----------------------A----------C-------C----------C   2215
SIVMNE      ---------------A--G----------------------A--T--------C---T---C--------G-C   2221
SIVSMMH4    -----G------A-----T----------------------T---G-----G-T-------T--C------CA   2233
SIVSMMH9    -----G------A-----T----------------------T---G---R-G-TY------T--C----Y-RA   2236
SIVSMMPBJ   -----G------A-----T----------------------T---G-----G-T-------T--C------GA   2245
SIVP209C19  -----G------A-----T----------------------T---G-----G-T-------T--C------CA   2236
SIVSTM      -----G-C-T---A-A--T---C----T--------------T-------G-CGT-------T--C------CA   2224
SIVSTM22579 -----G-C-T---A-A--T----------------------T--T------CAT-------T--T------CA   1057
HIV2F0784   ------------TA--                                                            450
SMCI8       G-G----CAT---A--                                                            450
SMCI2       --G----C-T---A--                                                            450
```

```
                \/3' sj
CONSENSUS.A aGgAccgGGaACAGCcagcCAgaGaAGaAACAGAAGaAGACGttgGa?aCaaCg?TGGagaCagaT?cTggCCt 2143
HIV2ROD     ---------G----------AC-----------------G----AG-----G----------A------C 2247
HIV2NIHZ    ------A-------------------------------------AG-----G----------CT------ 2220
HIV2ISY     -----T----------A-------------------------GA--G---T----AG-----C------- 2223
HIV2ST      ------------------------------------------A---G--T--------AT-GG-----C 2229
HIV2BEN     ---------G----------AC----G--------------C---GG-G--AG---TT--GAC-TG------ 2244
HIV2CAM2    ------C----------C-----------------------GG-----G----------C------- 2250
HIV2D194    C----A---G----------AC-----------------CC---G--G--AG---TTT-G-C-TG------ 2217
HIV2GH1     C---------G----------AC----G-----------ACA--G--G---A---TT--GAC-TG-A---- 2220
HIV2CBL21   --C------G-------C----C----------------G---G--T---------C-C------- 2250
HIV2CBL22   -----T----------A--------G-------------G------C----AG---C-C------- 2238
HIV2CBL23   -----T-------------------------------A------T---------C-TG--A--- 2229
HIV2CBL24   G-C--T----------A-----G----------------G------T---GAC---C-TG------ 2250
HIV2CAM1    ------T--------T-----------------------AG-----T----------T------C 2247
HIV2CAM2BR  ------C----------C-----------------------GG-----G----------C------- 2256
HIV2CAM3    ------A---------C-A---------------------CAT-----G----------C------- 2253
HIV2CAM4    C----AA----------G----------------------G------T---------C-TG------ 2253
HIV2CAM5    ----TT----------AC-G----------G-----G----A------C---------AC-C------C 2232
HIV2CAM6    ------T----------AC----G-----------------A------G----T------CT-----C 2259
HIV2ALI     ------A----------A------G----------------G------T---G-------TG-----C 2238
HIV2GB1222  ------A----------A-------------------AG-----T----------T------C 714

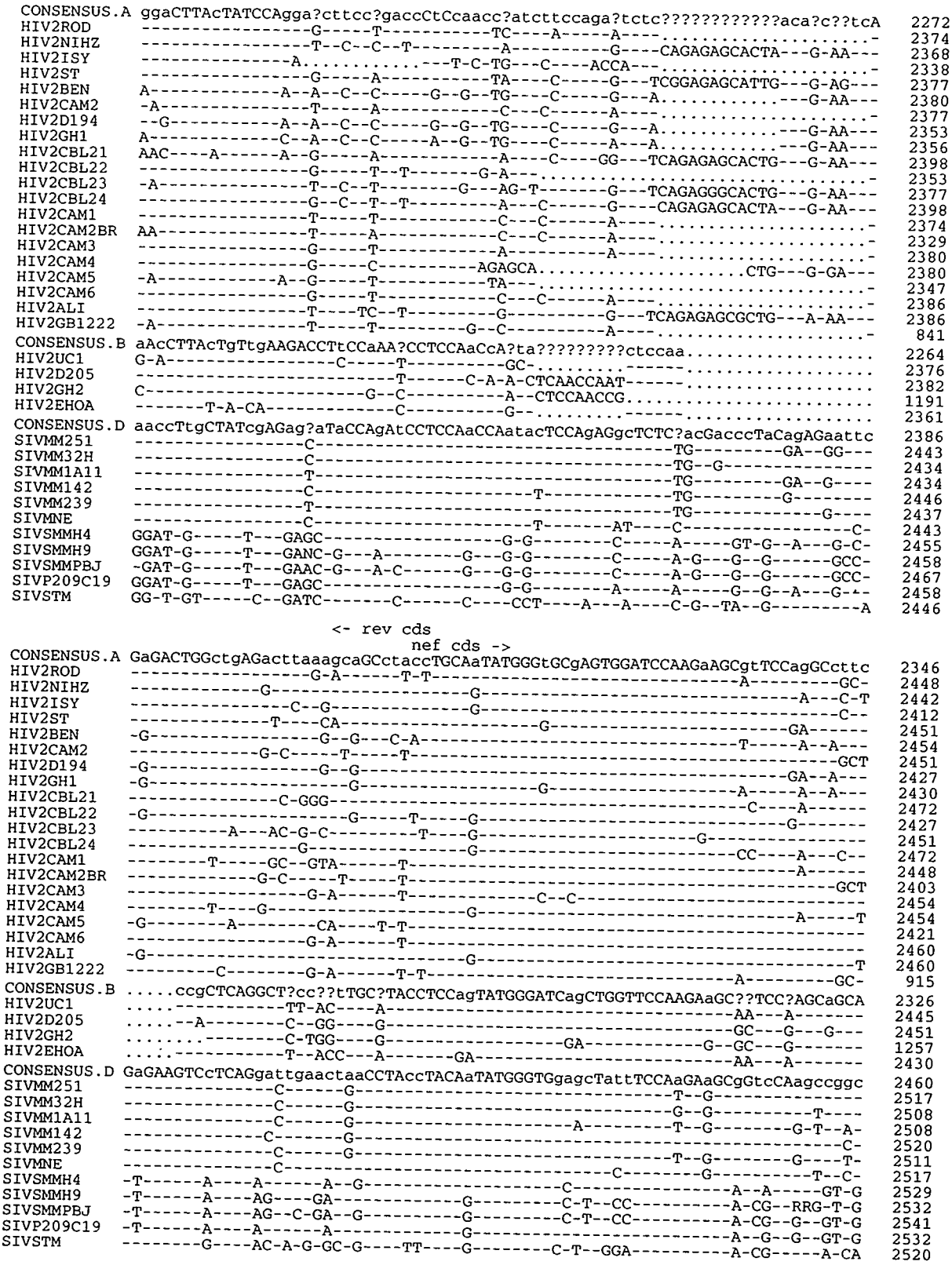
CONSENSUS.B AggaCCGGGGACAGCCAGCCAACGAAGAAACAGAAGAaGgAGGTGGAaAcgAcGgGGgcTACAGATCtTGGCCC 2148
HIV2UC1     -AC-------------------------------C-A----------A----CT-------------- 2256
HIV2D205    ------------------------------------------------A---------C------ 2253
HIV2GH2     ---G-------------------------------------G-A---------------------- 1068
HIV2EHOA    ------------------------------------------A---A------------------ 2241

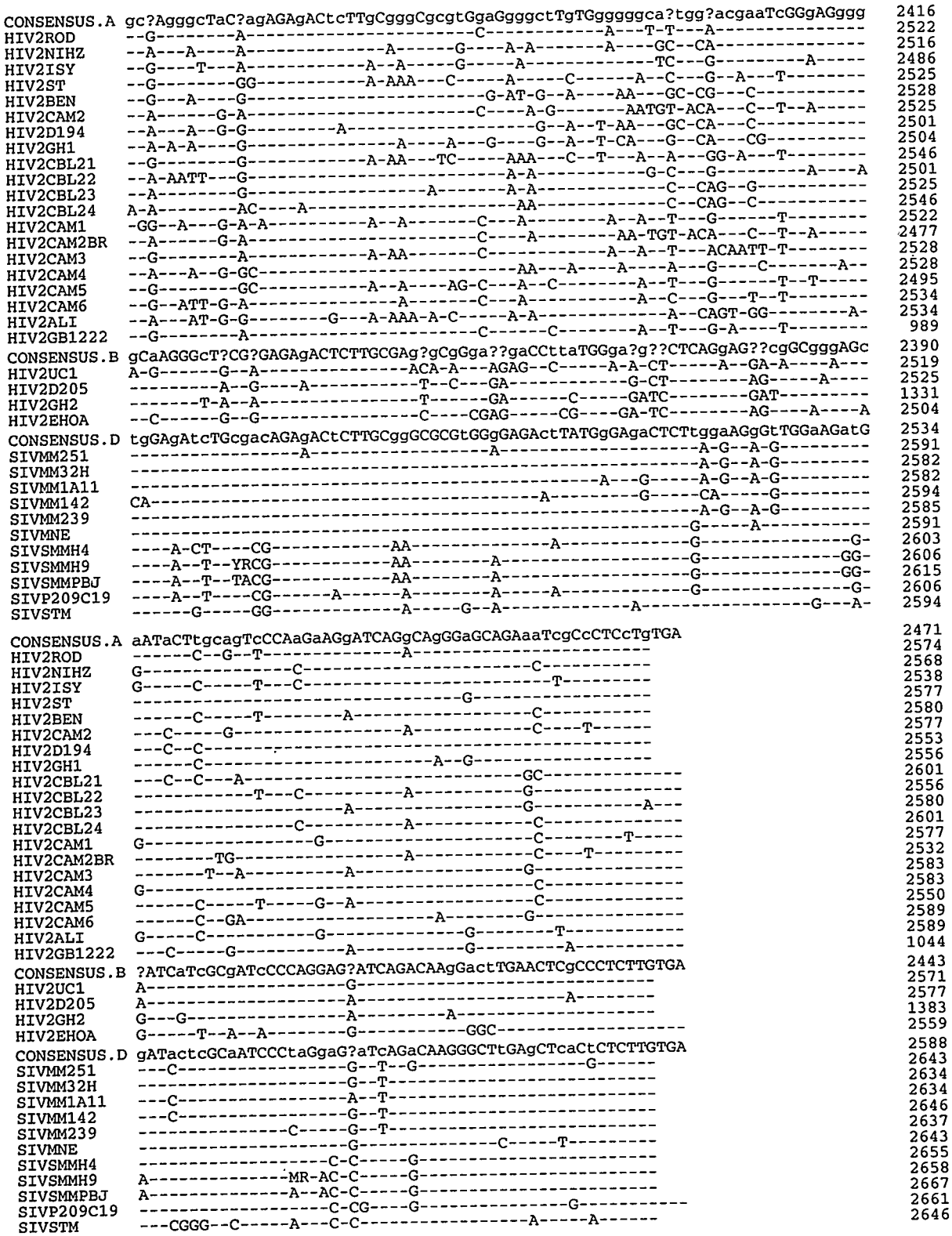
CONSENSUS.D aGG?cCaGG?aCtGCcAACCAaAGAAGGaaaAgAAggAGacGGTGGAGacaGcGGTGGcAaCAgcTCcTGGCCT 2240
SIVMM251    ---A--C--C----------G------C----------------AG---------------------- 2295
SIVMM32H    ---A--C--C----------G------C----------------AG---------------------- 2286
SIVMM1A11   ---A-----C----------G------C----------------AG---------------------- 2286
SIVMM142    ---AT-C--CT----------------C---A-------------G---------------------- 2298
SIVMM239    ---A--C--C----------G------C------A----------AG---------------------- 2289
SIVMNE      ---A-----C----------------C----------------G---------------------- 2295
SIVSMMH4    ---G-----A--C----------G----------------A-------G---A--T------ 2307
SIVSMMH9    C--G-----A----------G----------------R---A----------A--T------ 2310
SIVSMMPBJ   C--G-----A----------G----------------G---A----------A--T------ 2319
SIVP209C19  ---G-----A--C----------G----------A----------A-------G---A--T------ 2310
SIVSTM      ---G-----A--A----------C-----A--GA----------A-----A-T--A---------- 2298
SIVSTM22579 ---G-----A--A--T----------C-----A--GA 1098

                <- tat
CONSENSUS.A TggCcgaTagcatatatacatttcctgatccgcctgctgattcgcctcttgaccggactatacaacAtCTGCAG 2217
HIV2ROD     ----------------------------------A----------A---------G--------- 2321
HIV2NIHZ    ------------------------------------------------G---------------- 2294
HIV2ISY     ----------A----------C----------A----------G------ 2297
HIV2ST      ---------AG----------A----------A-A---------------- 2303
HIV2BEN     -----A---AAC---G-G--G----------A---A----C----------T---G---------------- 2318
HIV2CAM2    ----A-----A----------A------C---------------------------------- 2324
HIV2D194    -----AC--AAC--C-----A----------A---A----C----------G----------G------ 2291
HIV2GH1     ---------AAC----------A---A----C----------G--------G-------- 2294
HIV2CBL21   -A----------C----------TT---------- 2324
HIV2CBL22   --A------AG----------A---AG----------TT-G-------G--G------ 2312
HIV2CBL23   ---------AG----------A--A---------- 2303
HIV2CBL24   ----------A----------T---------- 2324
HIV2CAM1    ----------C----------A----------G------ 2321
HIV2CAM2BR  ----A-----A-.....-------- 2276
HIV2CAM3    ----------C----------C----------A----------G------ 2327
HIV2CAM4    ----------CC-G----------A----------A---------G--G------ 2327
HIV2CAM5    ----A----AG----------A----------G------ 2306
HIV2CAM6    ----------A---------G--G------ 2333
HIV2ALI     --------C------T----------A------AGC----------T---G--G----G---------- 2312
HIV2GB1222  ----------A----G----------T------G-------G------ 788

CONSENSUS.B TGGCAGATaGAATACattCAcTTtCtg?TtCGCCA?CtGAGGaACCTCTTgATTTGGCTaTACAaCgGCTGCAG 2220
HIV2UC1     ----------GC----------A-------A----------G---------- 2330
HIV2D205    ----------T-----AC-G-----G----------A---------- 2327
HIV2GH2     ----------C-A-----G-C----------A------ 1142
HIV2EHOA    --------C--------C-----C-C-A-------A------G----------G--------- 2315

CONSENSUS.D TgGCAgATAGAATATAtTCATTTCCTgATcCGCCAacTgaTACGCCTCTTGACTTGGcTaTtCAgCAacTgCAG 2314
SIVMM251    ---------- 2369
SIVMM32H    ---------- 2360
SIVMM1A11   ---------- 2360
SIVMM142    ---------- 2372
SIVMM239    ---------- 2363
SIVMNE      ----------A----------T---------- 2369
SIVSMMH4    ----------GT----------G------ 2381
SIVSMMH9    -R----------G----------GT----- 2384
SIVSMMPBJ   ----------GT----------GT----- 2393
SIVP209C19  ----------A--T----------G------ 2384
SIVSTM      -----A----------C----------G--AG----------G-A--A-----T--- 2372
```





HIV2EHOA

```
LOCUS       HIV2EHOA     8636 bp ds-DNA             VRL       11-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) complete genomic
            sequence, isolate HIV2EHOA.
ACCESSION   L14545
SOURCE      Human immunodeficiency virus type 2 DNA derived from the peripheral
            blood lymphocytes of a male patient from the Ivory Coast with full-
            blown AIDS.
REFERENCE   1  (bases 1 to 8636)
  AUTHORS   Rey-Cuille,M.A., Galabru,J., Laurent-Crawford,A., Krust,B.,
            Montagnier,L. and Hovanessian,A.G.
  TITLE     HIV-2 EHO isolate has a divergent envelope gene and induces single
            cell killing by apoptosis
  JOURNAL   Virology 202, 471-476 (1994)
COMMENT     The HIV-2 EHO sequence codes for a viral strain which is highly
            virulent, binds soluble CD4 receptors with high affinity,
            down-regulates CD4 receptors with accelerated kinetics and does
            not form syncytia.  The divergent genotype of HIV-2 EHO is most
            apparent in its cell surface glycoprotein, which is 25 kDa smaller
            than other currently identified HIV-2 strains.  However, this
            discrepency in protein size is not evident when comparing predicted
            molecular weights.  Rey-Cuille et al. report that the EHO envelope
            sequence contains fewer N-linked glycosylation sites than other
            HIV-2 sequences and further suggest that the presence of fewer
            oligosaccharide chains on the modified protein may in part explain
            the difference in protein size.  The fact that HIV2 EHO does not
            induce syncytia and is highly virulent is unusual since
            non-syncytium-inducing isolates are usually associated with
            decreased virulence.  HIV-2 EHO clusters with the B subtype HIV-2
            viruses.
BASE COUNT     2972 a   1759 c   2066 g   1839 t
ORIGIN      549 bp downstream from the start of gag
        1 caccccttat gatattaatc agatgttaaa ttgtgtagga gaacatcagg cagccatgca
        <- gag cds
       61 aattattagg gagataatta atgaggaagc agcagactgg gaccaacagc atccatcgcc
      121 aggcccaatg ccagcagggc aactcaggga accaagaggg tcagacatag cgggaaccac
      181 cagcacagta gaagaacaga tacagtggat gtacagaccc caaaatcctg tcccagtggg
      241 aaacatctat agaaggtgga ttcagttagg gctacagaaa tgtgtccgga tgtacaatcc
      301 tactaatata ctggacataa agcaagggcc aaaagaaccc ttccaaagct atgtagatag
      361 attctacaaa agcttacggg cagagcaaac agacccagca gtaaaaaatt ggatgacaca
      421 aacactgctg attcagaatg ctaacccaga ttgcaaatta gtgcttaagg gcttgggaat
      481 gaaccccaca ttagaagaaa tgctaacagc ctgccagggg ataggaggcc cagggcagaa
      541 ggcaaggcta atggctgagg ctttaaaaga agccttgaca ccttccacca atccgtttgc
      601 cgccgctcaa ccaagagcag ggaagaggac agtgacatgc tggaactgcg gcaaggcggg
      661 acatacagcc aggcagtgca aggcccctag aaggcagggA TGctggaaat gtggacagca
                                        pol cds start ->
      721 aggacacatc atgtcaaaat gcccagaaag acaggcgggt tttttagggt tcggcccctg
      781 gggaaagaag cctcgcaatt tccccgtcca ggcaccccag gggatagtgc catctgcgcc
      841 cccgatgaac ccagcattcg gcatgacacc tcagggtgcg attccatctg cacccctgc
      901 agatccagca gaggagatgc taaagaacta catgcaacta gggaagaagc agaaggagaa
      961 cagagagaga ccctacaagg aggtgacaga ggatttgctg cacctcaatt ctctctttgg
     1021 agaagaccag TAGtcaaagc aactattgag ggtcaatcag tagaagtatt actagacaca
                    <- gag cds end
     1081 ggagctgatg actcaatagt agcagggata gaattaggca gcaattacac cccaaaaata
     1141 gtaggtggga taggaggatt tataaatacc aatgaataca aaaatgtaga aatagaagta
     1201 gtaggaaaaa gagtaagagc aacagtaatg acaggggaca ccccaataaa cattttggc
     1261 agaaatattt taaatagctt aggcatgact ctaaatttcc cagtagcaag gatagaacca
     1321 gtaaaagtcc agttaaagcc tgaaaaagat gggccaaaaa tcagacaatg gcccctatcc
     1381 aaagagaaaa tactagccct caaagaaatc tgtgaaaaaa tggaaaaaga gggacagtta
     1441 gaagaggcgc ctcctactaa tccatacaat tcgcccacct tcgccataaa aaagaaagac
```

```
 1501 aaaaacaaat ggaggatgct aatagatttc agagaactaa acaaggtaac ccaagaattt
 1561 acagaggtcc agctgggtat tcctcaccca gcaggactgg catcaaagaa aagaataaca
 1621 gtactagatg taggagatgc ctacttcagt gtcccactag atccagactt cagacaatat
 1681 acagcattta ctttgccagc agtaaataat gcagaaccag gaaagagata tctttacaaa
 1741 gtcctaccac agggatggaa gggatcccca gcaattttcc agtacaccat ggcaaaggta
 1801 ctagaccctt tcagaaaagc caacaatgat gtcactataa tccagtacat ggatgacatt
 1861 ctcgtggcaa gtgacaggag cgatctggag catgacaggg tagtgtctca actaaaagag
 1921 ctattaaata acatgggatt ctctactcca gaagaaaagt tccaaaaaga ccctccattc
 1981 aaatggatgg ggtatgagct ctggccaaag aaatggaaac tgcaaaaaat acagctacca
 2041 gaaaaagagg tttggacagt aaatgacatt cagaagttag tgggagtatt aaattgggca
 2101 gctcaacttt tcccggggat taagaccagg catatatgta aactaataag gggaaagatg
 2161 accctaacag aagaggtaca atggactgaa ttggcagagg cagaattcca ggaaaacaaa
 2221 atcatcctag aacaagagca ggaaggatcc tattacaaag aaggggtacc tttagaagca
 2281 acagtgcaga aaaatctagc aaatcagtgg acatacaaga ttcatcaggg agataaaatc
 2341 ctaaaagtag gaaaatatgc aaaggttaaa aacactcaca ccaatggagt aagactattg
 2401 gctcatgtag tccaaaaaat aggaaaggaa gcattggtca tctggggaga gataccaatg
 2461 ttccatctac cagtagaaag agagacatgg gatcagtggt ggacagatta ctggcaagta
 2521 acctggatcc cagaatggga ttttgtctca accccaccat taataaggtt agcctataac
 2581 ctggtcaaag acccctaga aggagtagaa acttactaca cagatggatc ctgtaacaaa
 2641 gcctcaaaag aagggaaagc aggatatgtc acagacaggg gaaaggataa agttaaacca
 2701 ttagaacaaa caacaaatca gcaagcagag cttgaagcat ttgcactagc actacaggac
 2761 tcaggaccac aggtcaatat catagtagat tcacaatatg tcatgggaat agtagctgca
 2821 caaccaacag aaacagaatc accgatagta agagaaataa ttgaagaaat gatcaaaaag
 2881 gaaaaaatat atgtaggatg ggtaccagct cacaagggac tgggtggtaa tcaggaagta
 2941 gaccacctag tgagccaagg aattagacaa atcctatttc tagaaaaaat agaaccagct
 3001 caagaagaac atgaaaaata tcataataat gtaaaagaac tagtccataa atttgggatt
 3061 ccacaattag tggcaagaca aatagtaaat tcctgtgata aatgccaaca aaaaggggaa
 3121 gctattcatg gacaggtaaa ttcagaacta gggacatggc aaatggactg tacacattta
 3181 gagggaaagg ttataatagt ggcagttcat gtagccagtg gattcataga agcagaagta
 3241 ataccccaag aaacaggaag acagacagct ctcttcctgt taaagctggc cagcagatgg
 3301 cctatcacac acctgcacac agacaacggt gccaacttca cttcacaaga tgtgaaaatg
 3361 gcagcctggt ggatagggat agaacaaaca ttcggagtgc cctataatcc agaaagtcag
 3421 ggagtagtag aagcaatgaa ccatcatctg aaaaatcaga tagacagaat tagagatcag
 3481 gcagtatcaa tagagacagt tgtgttaatg gcaactcact gcatgaattt taaaagaagg
 3541 ggaggaatag gggatatgac ccctgcagaa agaatagtca acatgataac tacagaacaa
 3601 gaaatacaat tcctccaaac aaaaaattta aaattccaaa atttccgggt ctattacaga
 3661 gaaggcagag atcaactctg gaagggacct ggtgatctat tgtggaaagg ggaaggagca
 3721 gtcatcataa aggtagggac agaaatcaaa gtaataccca gaagaaaagc aaagatcata
 3781 aggaactATG gaggaggaaa agaattggat tgcagtgccg acgtggagga taccatgcag
vif cds start ->
 3841 gctagagagg tggcacagtc taatTAAata cctgaaatat aggacaaaag acttgcaaca
                                <- pol cds end
 3901 ggtctcttat gttcctcacc ataaggtagg atgggcttgg tggacttgca gtagagtaat
 3961 atttcccctg aaagaaggag cacatctaga agtccaagga tactggaacc tgaccccaga
 4021 aaggggattc ttgagttcct atgctgtaag actaacatgg tatgagagga gcttttatac
 4081 agatgtaact cctgatgtag cagaccgatt actgcatggg tcttatttct cttcgtttac
 4141 agctaatgaa gtaaggagag ccatcagggg agaaaagata ttgtcccact gcaactaccc
 4201 atcagctcat acaggccagg taccaagttt acagtttcta gccctaagag ttgtacaaga
 4261 aggaaaagAT Ggatcccagg gagagagtac caccaggaaa cagcggcgaa gaaacagtag
vpX cds start ->
 4321 gagaggcatt cgaatggcta gagacaacat tagaacatct caacagagta gcagtcaatc
 4381 acttgcccag ggaacttatt ttccaggtct ggcagaagtc ttgggcatat tggcgTGAgg
                                                                <- vif end
 4441 aacagggcat gtcaattagt tataccaaat ataggtattt gtgtctaatg caaaaagcaa
 4501 tgtttataca ctttgcaaag ggttgtggAT Gtctgcggga aggccatggg ccaggggGat
                        vpR cds start ->
 4561 ggagatcagg acctcctcct cctcctcccc caggtctagc cTAAtggcag aagcagtccc
                                                  <- vpX cds end
 4621 agagattcct ccagaggata aaaacccaca aagagaaccg tgggaacagt gggtagtgga
```

```
4681 cgtcctggag gaaataaaac aagaagcctt aaagcatttt gacccccgct tattaactgc
4741 acttggcaat tttatctaca ataggcATGg aaataccctt gaaggagcag gagagctcat
                  tat cds start ->
4801 taaactcctc cagcgggcac tcttcctcca cttcagaggg ggttgccaac actcaaggat
4861 tggacaaccg gggggaggaa atcctctctc agctataccg ccctctTAAg gcatgcagta
                                                        <- vpR cds end
4921 atacatgcta ctgtaaaaaa tgttcctacc attgccagct ttgctttctt aaaaagggcc
4981 tggggatatg ttATGaacgc tcgagaaaga gatcttcaaa aagggctaag actactacat
    rev cds start ->
5041 cttctgcacc aaacgagtga gtATGgcaca tgttaataat tacctacttg ttacactcct
              env cds start ->
5101 gcttataagt atctatgggt atatgggcaa gaactttgtc actgtcttct atggtatacc
5161 cgcatggaaa aatgcatcaa ttcccctctt ttgtgctacc agaaacagag atacctgggg
5221 aactgtacaa tgcctcccag ataatgatga ctataccgaa atccaattaa atataacaga
5281 ggcttttgat gcatgggata atacagtgac agatcaggca acaaaggatg tgtggagtct
5341 ctttgagacc tcaataaaac catgtgttaa attaacccca ctgtgtgtga caatgaagtg
5401 taataagacg tggagctcag ctagcaaaga gaccactacg tcctccgcgt ccctcagatc
5461 ttctactcag accctactca acgaagatag caaatgtatt caaaatgaca gctgtgcagg
5521 gataggacta gaagaaatga tagactgtca attcaaaatg acaggattaa aaagagatga
5581 gtcaaaacaa tataaggaca cctggtataa acaagattta gtgtgtgaaa aggggacaag
5641 gagtaatgaa agcaaatgtt atataaaaac ctgtaataca tcaattatcc aagaatcatg
5701 tgacaaacat tattgggata gtttaagatt taggtattgt gctcccccag gatttgcttt
5761 gctaagatgc aatgatacta aatattcagg cttcatgccc aactgtagta aggtagtagt
5821 atctctgtac agaatgatgg aaacacagac ctctacatgg tttggcttca atggtacaag
5881 ggcagaaaac aggacatata tctattggca tggtaaagac aataggacta tcataagctt
5941 aaattcatat tataatctga caatgcactg taaaaggcca ggaaacaaaa tggttgtgcc
         HIV-1 V3 loop equivalent ->
6001 aataagaacc gtgtcaggta ttctcttcca ttcacagcct atcaataaaa gacctaaaca
6061 agcttggtgc tggtttaaag gaaactggac agaagccata caggaggtga aagagaccat
           <-
6121 taaaaatcat cccagatatt caggaacaac aaatatctca cagataaggt tagcagagca
6181 cgcgagaagc tcagatccag aagtaagata tatgtggact aactgtaggg gagagtttct
6241 ctactgtaat atgacttttt tcttaaactg ggtagaaaat agaactgggc tcaagagaaa
6301 ttatgcgtca tgccacatca gacagatagt caacacgtgg cacaagattg gaagaaatgt
6361 gtatttgcct ccaagagagg gtgaactctc ctgtaattcc actgttacca gcctcatagc
6421 caacattgac tggatagata agaaccttac taatattact gtgagtgcag aagtgtcaga
6481 actgtataaa ttggaactgg gggactacaa attagtagag ataacaccaa ttggctttgc
6541 acctacaagt ataaaaagat attcctcagt gacaccgagg aataaaagag gtgtacttgt
6601 gctagggttt ttgggattcc ttgcgacggc aggttctgca atgggcgcgg cgtccttgac
6661 gttgtcggct cagtcccgga ctttactggc tgggatagtg cagcagcagc aacagctcgt
6721 ggacgtggtc aaaagacaac aagaactgtt gcggctgacc gtctggggga cgaaaaacct
6781 ccaggcaaga gtcactgcca tcgagaaata tctcaaagac caggcacaac taaattcatg
6841 gggatgtgct ttcagacagg tctgtcacac gactgtacca tgggtaaatg aatcccttaa
6901 gccagactgg aataacatga catggcaaca atgggagagg caagtccgct tcttggatgc
6961 aaatataaca aaattactag aagaggcaca gatacaacaa gaaaagaaca tgtatgagtt
7021 acagaaatta aatcaatggg atattttcag taattggttt gacttcacct cctggatggc
7081 atacatcagg ttaggattat atatagtaat aggaatagta gtattaagaa tagcaatata
7141 cattatacag atgctagcaa ggcttaggaa gggctatagg ccagtattct cctcccctcc
7201 ctcttatact caacagatcc ctatccgcaa ggaccgggga cagccagcca acgaagaaac
7261 agaagaagga ggtggaaaca acgagggcta cagatcttgg ccctggcaga tcgaatacat
7321 ccacttcccg attcgccaac TGAgggacct cttgatttgg ctatacagcg gctgcagaac
                          <- tat cds end
7381 cttattatca aagaccttcc aaaccctcca accagtactc caaccgctca ggcttccacc
7441 tgcatacctc cgatATGgga tcagctggtt ccaagaagca atccaagcag cagccagggc
     nef cds start ->
7501 tgcgggagag actcttgcga gcgcggcgag gacctcgtgg ggagtcctca ggagagcggc
7561 aggagagatc attgcaatac ccaggaggat cagacaaggg gcTGAactcg ccctcttgTG
                                                    <- rev cds end
```

```
7621 Atggacaaaa gactttggga gcagaagggg gaggaaaaca agattcagat gaggatgatg
    <- env cds end
7681 aggacaatga agtaggggtc cgtgtaagac ccggggtccc actgaggcca atgacattca
7741 aactagcagt agacatgtct catttttaa aagaaaaggg ggaactggaa gggattttct
                                                 LTR ->
7801 atagtgagag aaggcataaa atactagaca catacttaga aaatgaagaa ggcattgtgt
7861 ctggatggca gaactacaca catgggccag gagtaagata tcccaagttc tttggctggc
7921 tatggaagct agtgccaata aatatgatag cagaaccaga ggacgaggaa acccattgtc
7981 tggtgcatcc agcacagacc tccgcatggg atgaccccca cgaagagacc cttgtctggc
8041 agtttgactc cctcctagca tatgactatg tggccttcag caggttccca gaggagtttg
8101 ggtatcagtc aggaatgcca gagaaagagt ggaaggctaa actgagagca agaggaatac
8161 ctacagagTA Gacaggaaat aacagcacaa agaggaacta gctaacactg catagagaag
             <- nef cds end
8221 gaaactagct gatactGCAG GACTTTCCAG AAGGGGCTGT aacagtGGGA GGgacatggg
                     ->  enhancer    <-          Sp1 ->
                                enhancer ->    <-
8281 AGGAGCaGGG AGGaacgccc atcaagactc tgTATAAATg tacccgcttt gtgcattgta
 Sp1 -> Sp1 ->                   signal ->
8341 ttcagtcgct ctgcggagag gctggcagat cgagccctgg gaggttctct ccagcactag
    mRNA ->         |->          tar core I             <-|          |->
8401 caggtagagc ctgggtgttc cctgctagac tctcaccagc acttggccgg tgctgggcag
        tar core II                  <-|
8461 acggctccac gcttgcttgc ttaaaaccct cttAATAAAa ctgcctatta gaagcaagac
                                signal ->
8521 aagtgtgtgt tcccatctct cctagtcgcc gcctggtcat tcggtgctcc actagaaacc
8581 ctggtctgtt aggacccctt ctgctttggg aaaccaaggc aggaaaatcc ctagca
                                                                <- LTR
```

```
LOCUS       HIV222381     781 bp ss-DNA              VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
            sample 2238, clone 1, partial cds.
ACCESSION   L33077
SOURCE      Human immunodeficiency virus type 2 PCR-amplified PBMC DNA derived
            from a 47 year old asymptomatic male from rural Liberia.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient 2238 was a 47 year old asymptomatic male from rural Liberia
            who had no history of sexually transmitted disease, chronic illness,
            blood transfusion or homosexuality.  Primer pairs failed to amplify
            the pol (reverse transcriptase) region.  Sample 2238, a highly
            divergent strain, defines a new subtype which has been designated
            as subtype C [1].
            NCBI gi: 532129
BASE COUNT      280 a    155 c    190 g    156 t
ORIGIN      111 bp downstream from the start of gag
        1 agcgaacgaa ttggacagat ttgcattagc agaaagcctg ttggagacca aagaaggatg
 gag cds ->
       61 ccaaaaaatt ttaacagtgt tagaaccatt agttccgaca ggttcagaaa atttaaagag
      121 cctttataat actacctgcg tcatttggtg tttacacgca gaacagaaag tgaaacatac
      181 agaggaacga aacgaggtag tagagagaca tctagcggca gaaactaaaa atgcagaaaa
      241 aatgccagcc acaagtagac caacagctcc atctagtggc ggcagaggaa attacccagt
      301 gcagcaagta gcaggcaatt atgtccacca tcctctaagt cctagaacac tgaatgcatg
      361 ggtaaagtta gtagaagaaa agaagtttgg ggcagaggta gtaccaggat ttcaggcact
      421 gacagaaggg tgcacaccct atgatattaa tcaattgcta aattgtgtag gagatcatca
      481 ggctgctatg cagattatta gagaaattat caatgaggaa gcagccgatt gggatgaaca
      541 ccacccagta ccaggcccac tgccagcagg acagcttagg gatccaaggg gctctgacat
      601 tgcaggaaca accagcacgg tagaagaaca gatacagtgg atgtatagag cacagaaccc
      661 agtaccggta ggcaacatct atcggagatg gatccaacta ggcctgcaaa agtgtgtcag
      721 aatgtataat ccaactaaca ttctagacgt gaaacagggt ccaaaagaac catttcagag
      781 t
   gag cds ->
```

```
LOCUS       HIV222382     708 bp ss-RNA              VRL       24-SEP-1992
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) pol integrase sequence,
            sample 2238, partial cds.
ACCESSION   M87138
SOURCE      Human immunodeficiency virus type 2 PCR-amplified PBMC DNA derived
            from a 47 year old asymptomatic male from rural Liberia.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Gao,F., Yue,L., White,A.T., Pappas,P.G., Barchue,J., Hanson,A.P.,
            Greene,B.M., Sharp,P.M., Shaw,G.M. and Hahn,B.H.
  TITLE     Human infection by genetically-diverse SIVsm-related HIV-2 in West
            Africa
  JOURNAL   Nature 358, 495-499 (1992)
REFERENCE   2  (bases 1 to 781)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     Patient 2238 was a 47 year old asymptomatic male from rural Liberia
            who had no history of sexually transmitted disease, chronic illness,
            blood transfusion or homosexuality.  Virus isolation was attempted
            without success.  Sample 2238, a highly divergent strain, defines a
            new subtype which has been designated as subtype C [2].
            NCBI gi: 325740
BASE COUNT      260 a    131 c    168 g    149 t
ORIGIN      2184 bp downstream from the start of pol
        1 gttagggatt atagcagggc agccaacaga aacagagtcc ccactagtaa acagaatcat
 pol cds ->
       61 agaagaatta ataaggaagg aagctgttta catcagctgg gtgccagctc acaagggtct
      121 cggaggaaat caagaagtag accacctagt aagtcaagga attaggcaag tattattctt
      181 agaaaaaata gaaccagcac aggaagagca tgaaagattt catagcaatg ccaaagagct
      241 gacacacaaa tttggtatac ctaacttagt ggctaaacag atagtaaata cttgtcatgt
      301 gtgtcaacag aaaggagagg ccatacatgg gcaagtaaat gcagatttag gaacatggca
      361 aatggactgt acccatttag aaggaaaagt tatcatagta gcagtccatg tggccagtgg
      421 ctttatagaa gcagaggtaa tcccacaaga aactggcaga caaacagctc tttttctgtt
      481 aaaattggca gcaagatggc ctattaccca cctacacaca gataatggtg ccaatttcac
      541 ttcacaggaa gtaaaaatgg tggcgtggtg ggtaggcgtg gaacatacct ttggagtacc
      601 ttacaaccca cagagtcagg gagtagtaga ggccatgaac catcatctga aaaaccaaat
      661 agatagaatc agagagcagg caaacacaat ggagaccata gtcttgat
                                                    pol cds ->
```

HIV260415K1

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LOCUS       HIV260415K1   781 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
            sample 60415K, clone 8, partial cds.
ACCESSION   L33076
SOURCE      Human immunodeficiency virus type 2 PCR-amplified DNA recovered from
            a 34 year old heterosexual asymptomatic man from urban Senegal.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient 60415K was a heterosexual 34-year old asymptomatic man from
            urban Senegal, who was living in the Washington, D.C. area.  He
            traveled extensively before coming to the United States where he was
            identified as HIV-2 positive after seeking medical care for a STD.
            He was married to an American IV drug user.  Virus isolation was
            successfully performed at the University of Alabama at Birmingham.
            Virus 60415K clusters with the subtype A HIV-2 viruses.
            NCBI gi: 532131
BASE COUNT      277 a    165 c    194 g    145 t
ORIGIN      111 bp downstream from the start of gag
        1 agcgaatgaa ttggacagat tcggattagc agagagcctg ttggagtcaa aagaaggttg
 gag cds ->
       61 ccaaagaatt cttacagttt tagatccatt agtaccgaca ggttcagaaa atttaaaaag
      121 cctctttaat actgtctgcg tcgcttggtg catacacgca gaagagaaag tgaaagatac
      181 tgaaggagca aaacaaatag tacagagaca tctagtggca gaaacaggaa ctgcagagaa
      241 aatgccaagc acaagtagac caacagcacc acctagcggg gaaggaggaa acttccccgt
      301 gcaacatgta ggcggcaact atacccatat accgctgagc ccccgaactc taaatgcttg
      361 ggtaaaatta gtagaggaaa aaaagttcgg ggcagaagta gtgccaggat ttcaggcact
      421 ctcagaaggc tgcacgccct atgatattaa ccaaatgctt aattgtgtgg gcgaccatca
      481 ggcagctatg caaataatca gggaaattat taatgaagaa gcagcagaat gggatgtgca
      541 acatccaata ccaggccccc taccagcggg gcagcttaga gagccaagag ggtctgacat
      601 agcagggaca acaagcacag tagatgaaca gatccagtgg atgtttaggc cacaaaatcc
      661 cgtaccagta ggaaacatct atagaagatg gatccagata ggactgcaga agtgcgtcag
      721 gatgtacaac ccgaccaaca tcctagacat aaaacaggga ccaaaagagc cgttccaaag
      781 c
   gag cds ->
```

LOCUS HIV260667K1 766 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence, sample 60667K, clone 1, partial cds.
ACCESSION L33078
SOURCE Human immunodeficiency virus type 2 PCR-amplified DNA recovered from a 37 year old heterosexual female originally from Sierra Leone who showed HIV dual seroreactivity.
REFERENCE 1 (bases 1 to 766)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient 60667K was a heterosexual 37-year old female from Sierra Leone, who was living in the Washington, D.C. area. Originally she lived in an urban area in West Africa before traveling extensively and coming to the United States. After seeking medical care for a STD, patient 60667K was identified as HIV-2 positive. She had reduced CD4 counts but was otherwise asymptomatic. Her two teenage children were seronegative. Western blot analysis of patient 60667K's peripheral blood cells showed HIV dual reactivity. Virus isolation was successfully performed at the University of Alabama at Birmingham. Sample 60667K clusters with the subtype B viruses.
NCBI gi: 532133
BASE COUNT 275 a 160 c 187 g 144 t
ORIGIN 111 bp downstream from the start of gag

```
        1 agtaaatgaa ttagaaagat ttggattggc agaaaacctg ttgggatcaa aagaaggatg
 gag cds ->
       61 ccataaaatt ctcgcagtct tagagccatt agtaccaaca ggatcagaaa atttaaagag
      121 ccttttttaat accgtctgcg tcatttattg cctgcacgca ggagagaaag tgaaagatac
      181 tgaggaagca aaaaagatag cacagcgaca tctagtggga aacacagaaa aaatgccagc
      241 tacaagtaga ccaacagcac catctagcgg cggaaattat ccagtgcagc aaatagctgg
      301 aaattattcc cacctgccgc taagccctcg gaccttaaat gcctgggtaa aattggtaga
      361 ggaaaagaag ttcggggaga acgtggtacc aggattccag gcactatcag aaggatgcac
      421 cccctatgat attaatcaga tgttaaattg tgtaggagac catcaggcag ccatcgaaat
      481 cattagggaa ataattaatg aggaagcggc ggaatgggac caacagcatc catcgccagg
      541 cccaatgccg gcaggacaac tcagggaacc aagagggtca gacatagcgg gaaccaccag
      601 cacagtagaa gaacagatac aatggatgtg cagggcccaa aatcctgtcc cagtaggaaa
      661 catttataga agatggattc agatagggct gcaaaaatgt gtccggatgt acaaccctac
      721 caatatactg gacataaagc aagggccaaa ggagcccttc caaaac
                                                    gag cds ->
```

```
LOCUS       HIV27312A1    766 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency. virus type 2 (HIV-2) p16/p28 gag sequence,
            isolate 7312A, clone JK, partial cds.
ACCESSION   L33079
SOURCE      Human immunodeficiency virus type 2 DNA from cocultured PBMCs derived
            from a 32 year old male from urban Cote d'Ivoire with lymphadenopathy and
            who showed HIV dual seroreactivity.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient 7312A was a 32 year old male from urban Cote d'Ivoire who
            had reported frequent visits to urban prostitutes.  His sera was HIV
            dually reactive and he had lymphadenopathy.  Unlike other sequences
            in this study, gag, pol, and env sequences for patient 7312A were
            not PCR derived.  Instead, they were obtained from a full length
            proviral genome cloned from cultured PBMC DNA.  Virus isolation was
            successfully performed at the University of Alabama at Birmingham.
            Virus 7312A clusters with subtype B viruses for gag and pol(RT
            and int) and with the A viruses for env.  Gao et al. conclude that
            virus 7312A has arisen from the recombination of subtype A and B
            viruses.
            NCBI gi: 532137
BASE COUNT      269 a    157 c    188 g    152 t
ORIGIN      111 bp downstream from the start of gag
        1 agcaaatgaa ttagacagat tcggattggc agaaaacctg ttggaatcaa aagaaggatg
 gag cds ->
       61 tcagaaaatt cttacggtct tagctccatt aatgccaaca gggtcagaaa atttaaaaag
      121 ccttttttaat actgtctgcg tcatttggtg cttacacgca gaaaagaaag tgaaagatac
      181 cgaggaagca aaaaagctag cacagagcca tctagtggta gacactgaaa aaacacctac
      241 tgcagacaaa ccagcagcga catctagtgg cagaaattac ccagtgcaac aagtagctgg
      301 caattatgtc cacgtgccat taagcccccg aaccctaaat gcctgggtaa aattagtgga
      361 ggaaaagaaa ttcggggcag aagtagtgcc aggatttcag gcactatcag agggatgtac
      421 cccttatgat attaatcaga tgctaaattg tgtaggagaa catcaggcag ccatgcaagt
      481 cattagggaa ataatcaatg aggaggcggc agactgggac cagcagcacc cggtgccagg
      541 tccactgcca gcaggacaac ttagggaccc cagaggatca gatatagcgg gaaccaccag
      601 cacagtagag gaacagatac agtggatgta caggggtcaa agtcctatcc cagtagggaa
      661 catttataga agatggattc agctaggatt gcagaagtgt gtccggatgt acaatcctac
      721 taatatacta gatgtaaaac aagggccaaa agaacccttc caaagc
                                                    gag cds ->
```

LOCUS HIV27312A2 995 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human iummodeficiency virus 2 (HIV-2) pol reverse transcriptase sequence, isolate 7312A, clone JK, partial cds.
ACCESSION L33092
SOURCE Human immunodeficiency virus type 2 DNA from cocultured PBMCs derived from a 32 year old male from urban Cote d'Ivoire with lymphadenopathy and who showed HIV dual seroreactivity.
REFERENCE 1 (bases 1 to 995)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient 7312A was a 32 year old male from urban Cote d'Ivoire who had reported frequent visits to urban prostitutes. His sera was HIV dually reactive and he had lymphadenopathy. Unlike other sequences in this study, gag, pol, and env sequences for patient 7312A were not PCR derived. Instead, they were obtained from a full length proviral genome cloned from cultured PBMC DNA. Virus isolation was successfully performed at the University of Alabama at Birmingham. Virus 7312A clusters with subtype B viruses for gag and pol(RT and int) and with the A viruses for env. Gao et al. conclude that virus 7312A has arisen from the recombination of subtype A and B viruses.
NCBI gi: 532141
BASE COUNT 390 a 200 c 218 g 187 t
ORIGIN 806 bp downstream from the start of pol

```
        1 aaaaggaggg gcagctagaa gaagcatctc ccactaatcc atacaacaca cccacctttg
 pol cds ->
       61 ctataaagaa aaaggataaa aacaaatgga gaatgctaat agacttcagg gaattaaata
      121 aggtaaccca agaatttaca gaagtccaac taggtattcc ccacccggca ggctggccag
      181 aaaaaaggag aataacagtg atagatgtag gagatgccta cttcagtgtc ccactagacc
      241 cagacttcag gcaatataca gcattcactt tgccatcaat aaataatgca gagccaggaa
      301 aaaggtacat ttataaagtc ctaccacagg gatggaaggg atccccagca atttttcaat
      361 actccatgag aaaggtacta gacccttca gaagggccaa caatgatgtc accataatcc
      421 agtacatgga tgacatcctt gtggcaagcg atagaagtga tctagaacat gataaggtag
      481 tgtctcaact aaaagagcta ctaaatgaca tgggattttc caccccagaa gaaaaattcc
      541 aaaaggaccc tccattccag tggatgggtt atgagctctg gccaaagaag tggaagctgc
      601 aaaaaataca aataccagaa agggaggttt ggacagtaaa tgacattcag aaactagtgg
      661 gagtattaaa ctgggcagct caacttttcc ccggaatcaa aacaaggcac atatgcagac
      721 tgatcaaggg aaagatgacc ctgacagagg aggtgcagtg gacagaacta gcagaggcag
      781 agatgcagga aaataaaatc atcctaggac aggaacagga aggatcttac tacaaagaag
      841 gggtacctct agaagcaaca gtgcagaaaa acttagcaaa ccagtggaca tacaaaattc
      901 atcagggaaa taaagtccta aaagtaggaa aatatgcaaa ggttaaaaac acccacacca
      961 atggagtaag aatactagca catgtagtcc aaaaa
                                        pol cds ->
```

HIV27312A3

```
LOCUS       HIV27312A3    708 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus 2 (HIV-2) pol integrase sequence,
            isolate 7312A, clone JK, partial cds.
ACCESSION   L33088
SOURCE      Human immunodeficiency virus type 2 DNA from cocultured PBMCs derived
            from a 32 year old male from urban Cote d'Ivoire with lymphadenopathy and
            whose showed HIV dual seroreactivity.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient 7312A was a 32 year old male from urban Cote d'Ivoire who
            had reported frequent visits to urban prostitutes.  His sera was HIV
            dually reactive and he had lymphadenopathy.  Unlike other sequences
            in this study, gag, pol, and env sequences for patient 7312A were
            not PCR derived.  Instead, they were obtained from a full length
            proviral genome cloned from cultured PBMC DNA.  Virus isolation was
            successfully performed at the University of Alabama at Birmingham.
            Virus 7312A clusters with subtype B viruses for gag and pol(RT
            and int) and with the A viruses for env.  Gao et al. conclude that
            virus 7312A has arisen from the recombination of subtype A and B
            viruses.
            NCBI gi: 532139
BASE COUNT      275 a    121 c    167 g    145 t
ORIGIN      2184 bp downstream from the start of pol
        1 catgggaata gtagctggac agccaacaga aacagagtca ccgatagtaa ataagataat
 pol cds ->
       61 tgaagaaatg atcaaaaagg aagcaatata tgtaggatgg gtgccagctc acaaaggact
      121 aggtggtaat caggaagtag accacctagt aagtcaagga attaggcagg ttctattcct
      181 agaaaagata gaaccagccc aggaggaaca tgaaaaatat catggcaatg taaaagagct
      241 ggttcataaa tttggaattc cacaactagt ggcaaaacaa atagtaaact cctgtgataa
      301 atgtcaacaa aaaggagaag ctgttcatgg acaggtaaat gcagaactag ggacatggca
      361 aatggactgt acacatttag aagggaaagt cataatagta gcagtccatg tagccagtgg
      421 gtttatagaa gcagaggtaa taccccaaga aacaggaaga caaacagctc tcttcctgtt
      481 aaagctggca agcagatggc ccattacaca cttgcacaca gacaatggtg ccaactttac
      541 ttcacaagat gtaaagatgg tggcttggtg ggtaggaata gaacaaacct ttggagtacc
      601 ctacaaccca caaagtcagg gagtagtaga agcaatgaat catcatctga aaaatcaaat
      661 agataggatc agagatcagg cagtatcaat agaaacagtt gtgctaat
                                                      pol cds ->
```

LOCUS HIV27312A4 453 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immunodeficiency virus type 2 (HIV-2) gp41 env sequence, isolate 7312A, clone JK, partial cds.
ACCESSION L33094
SOURCE Human immunodeficiency virus type 2 DNA from cocultured PBMCs derived from a 32 year old male from urban Cote d'Ivoire with lymphadenopathy and who showed HIV dual seroreactivity.
REFERENCE 1 (bases 1 to 453)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient 7312A was a 32 year old male from urban Cote d'Ivoire who had reported frequent visits to urban prostitutes. His sera was HIV dually reactive and he had lymphadenopathy. Unlike other sequences in this study, gag, pol, and env sequences for patient 7312A were not PCR derived. Instead, they were obtained from a full length proviral genome cloned from cultured PBMC DNA. Virus isolation was successfully performed at the University of Alabama at Birmingham. Virus 7312A clusters with subtype B viruses for gag and pol(RT and int) and with the A viruses for env. Gao et al. conclude that virus 7312A has arisen from the recombination of subtype A and B viruses.
NCBI gi: 532135
BASE COUNT 162 a 76 c 110 g 105 t
ORIGIN 1861 bp downstream from the start of env

```
       1 gacgtggtca agagacaaca agaaatgttg cgactgaccg tctggggaac aaaaaatctc
 env cds ->
      61 caggcaagag tcactgctat tgagaaatac ttaaaggacc aggcgcaact aaattcatgg
     121 ggatgtgcgt ttaggcaagt ctgccacact actgtaccat gggtaaatga cagcttgaca
     181 cctgattggg acaacatgac gtggcaacaa tgggaaaaac aaatccgcga cctggaggca
     241 aatatcagtg aaagtctaga acaggcacaa atccagcaag aaaagaacat gtatgaatta
     301 caaaaattaa atagctggga tgtttttggc aactggtttg atttagcctc ctgggtcaaa
     361 tatattcagt atggagttta tatagtagta ggaatagtag ctctcagagt aataatatat
     421 gtagtacaaa tgataggtag acttagaaga ggc
                                        env cds ->
```

HIV27810A1

```
LOCUS       HIV27810A1    766 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
            sample 7810A, clone 2, partial cds.
ACCESSION   L33080
SOURCE      Human immunodeficiency virus type 2 PCR-amplified DNA recovered from
            an asymptomatic 31 year old heterosexual man originally from Cote
            d'Ivoire.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient 7810A was a heterosexual 31-year old student from
            Cote d'Ivoire, who was living in the Washington, D.C. area.
            Originally he lived in an urban area in West Africa before traveling
            extensively and coming to the United States.  After seeking medical
            care for a STD, patient 7810A was identified as HIV-2 positive.
            He had a heterosexual partner of 3 years who was HIV-2 seronegative.
            He was asymptomatic with normal CD4 counts.  Sample 7810A clusters
            with the subtype B viruses.
            NCBI gi: 532143
BASE COUNT      270 a    168 c    183 g    145 t
ORIGIN      111 bp downstream from the start of gag
        1 agcaaacgaa ttggacagat ttggattagc agagaccctg ttgggatcaa aagaaggatg
 gag cds ->
       61 tcacaaaatt cttacggcct tagctccatt agtaccaaca ggatcagaaa atttaaaaag
      121 ccttttaat actgtctgcg tcgtttattg cttacacgca gaagagaaag tgaaagatac
      181 tgaggaagca aaaaagatag cacagagcca tctagcggcg aacacagaaa aaatgccagc
      241 tacaagtaaa ccaacagcac cacctagcgg cagaaattat ccagtgcagc aggtggccgg
      301 caattacgtc catctgccgc taagcccccg aaccttaaat gcctgggtaa aattagtaga
      361 ggataagaaa ttcggggcag aagtagtacc aggattccag gcactatcag aagggtgtac
      421 cccttatgat attaatcaaa tgctaaattg tgtaggagaa catcaagcag ccatgcaaat
      481 tattagggaa ataatcaatg aggaagcagc ggactgggac cagcagcacc cgtcaccggg
      541 cccactacca gcaggacagc ttagggaccc aagagggtcg gacatagcgg ggaccaccag
      601 cacagtggag gagcagatac aatggatgta cagggcccaa aatcctatcc cagtaggaaa
      661 catttatagg agatggatcc aattaggact gcagaagtgt gtccggatgt ataaccctac
      721 taatatactg gacataaaac aaggaccaaa agaacccttc caaagc
                                                    gag cds ->
```

LOCUS HIV27924A1 781 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence, sample 7924A, clone 1, partial cds.
ACCESSION L33081
SOURCE Human immunodeficiency virus type 2 PCR-amplified DNA recovered from a 48 year old heterosexual male originally from urban Guinea Bissau who showed HIV dual seroreactivity.
REFERENCE 1 (bases 1 to 781)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient 7924 was a heterosexual 48-year old teacher from Guinea Bissau, who was living in the Washington, D.C. area. Originally he lived in an urban area in West Africa before traveling extensively and coming to the United States. After seeking medical care for a STD, patient 7924 was identified as HIV-2 positive. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Virus isolation was successfully performed at the University of Alabama at Birmingham. Sample 7924A clusters with the subtype A HIV-2 viruses.
NCBI gi: 532145
BASE COUNT 279 a 157 c 195 g 150 t
ORIGIN 111 bp downstream from the start of gag

```
        1 agcgaatgaa ttggacagat tcggattagc agagagcctg ttggagtcaa aagaaggttg
 gag cds ->
       61 tcaaagaatt atttcagttt tagatccatt agtaccgaca ggctcagaaa atttaaaaag
      121 ccttttttaat actgtctgcg tagtttggtg catacacgca gaagagaaag tgaaagacac
      181 tgaagaagca aaaaagatag tacagagaca tctagtggca gaaacaggaa ctgcagagaa
      241 aatgccaaat acaagtagac caacagcacc acctagcggg aaaggaggaa actaccccgt
      301 gcaaagcata ggcggcaact atacccatgt gccgctgagt ccccgaaccc taaatgcttg
      361 ggtgaaatta gtagaagaga agaagttcgg ggcagaagta gtgccaggat tccaggcgct
      421 ctcagaaggc tgcacgccct atgacattaa tcaaatgctt aattgtgtgg gcgaccatca
      481 agcagctatg caaataatca gggaaatcat taatgaagta gcagcagatt gggatgttgc
      541 acatccaata ccaggcccct taccagcagg gcagcttagg gaaccaagag ggtctgacat
      601 agcaggaaca acaagcacag tagaagagca gatccagtgg atgtttagag cacaaaaccc
      661 tgtaccagtg ggaaacatct atagaagatg gatccagata gggctgcaga aatgcgtcag
      721 gatgtacaat ccaaccaaca tcctagatgt aaaacaggga ccaaaggaat catttcaaag
      781 c
   gag cds ->
```

HIV2ALI

```
LOCUS       HIV2ALI      2589 bp ss-RNA             VRL       07-MAR-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) envelope glycoprotein
            sequence, non-syncytium-inducing isolate HIV-2ALI, complete cds.
ACCESSION   L25445
SOURCE      Human immunodeficiency virus type 2 from PCR-amplifed DNA extracted from
            cocultured PBMCs  derived from a male patient from Guinea-Bissau who had
            AIDS-related complex (ARC).
REFERENCE   1  (bases 1 to 2589)
  AUTHORS   Costa Taveira,N., Bex,F., Burny,A., Sharp,P., Santos Ferreira,M. and
            Moniz-Pereira,J.
  TITLE     Genetic analysis of the env gene from a non-syncytium-inducing HIV-2
            isolate (HIV-2 ALI)
  JOURNAL   Aids Res. Hum. Retroviruses 10, 223-224 (1994)
COMMENT     HIV2ALI is a non-syncytium-inducing isolate with a deduced V3 loop
            amino acid sequence that is similar to other HIV-2 V3 loop regions.
            Costa Taveira et al. note that the most significant difference between
            this isolate and others which induce synctium is the absence of
            positively charged amino acids within the flanks of the V3 loop.
            This difference suggests, as it does for HIV-1, that the synctium
            inducing phenotype may be due to the hydrophilic nature of the V3 loop.
            In addition, this isolate possesses a leucine at residue 7 with the
            TM protein fusion domain.  This characteristic is unique to all
            human retroviruses and may play a part in its inability to form
            synctium.  In phylogenetic analysis, HIV2ALI grouped with HIV-2
            subtype As from Guinea-Bissau, even though it is phenotypically
            different from others in the group with respect to ability to
            form synctium.
BASE COUNT      846 a    530 c    611 g    602 t
ORIGIN      env cds start
        1 ATGatgtcta gtagaaatca gctgcttgtt actatcttac tagctagtgc ttgcttagta
  env cds ->
       61 tattgtaaac aatatgtgac tgtttttttat ggcgtgccag catggaaaaa tgcatccatt
      121 ccctctcttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttaccagac
      181 aatgatgatt atcaggaaat agctttaaat gtgacagagg ctttcgatgc atgggataat
      241 acagtaacag aacaagcagt agaagatgtc tggagactat ttgagacatc aataaaacca
      301 tgtgtcaagt taacaccttt atgtatagca atgaagtgta gcaacataag cacagagagc
      361 acaaccacat ccccgagccc agggagcaca ctcaaacccc tgataaatga gagcgatcca
      421 tgcataaagg cagacaactg ccccagggga ctaggggatg aagagatggt caattgtcgg
      481 ttcaacatga caggattaca gagagataag ccaaaacagt ataatgaaac atggtactca
      541 aaagatgtgg tttgtgaacc atttaacacc accacaaacc agaccaggtg ttacatgaac
      601 cattgcaaca catcagtcat cacagagtca tgtgataagc actattggga tgctataaga
      661 tttagatact gtgcaccacc tggttacgcc ttgctaagat gcaatgatac caattattca
      721 ggctttgcac ccaattgctc taaagtagta gctgctacat gcacaaggat gatggagatg
                                 v3 loop equivalent ->
      781 caaacttcta cttggtttgg ctttaatggc actagggcag aaaatagaac atatatctat
      841 tggcatggta gagataatag aactatcatc agcttaaaca aacagtataa tcttactatg
      901 cattgTAAga ggccaggaaa taagacagtt gtaccaataa cacttatgtc agggttaata
              <- v3 loop equivalent
      961 tttcactccc agccaatcaa taaaagaccc agacaagcat ggtgctggtt caaaggcgaa
     1021 tggagggaag ccatgcagga ggtgaaggaa acccttgtaa aacatcccag gtataaagga
     1081 accaatgaca caaaccaaat taactttaca aaaccaggaa gaggctcaga tgcagaagag
     1141 gtatatatgt ggactaactg cagaggagaa tttctctatt gcaacatgac ttggttcctc
     1201 aattgggtgg aaaacaaaac gggtcaggaa cagcacaatt atgcaccgtg ccatataaag
     1261 caaataatta atacctggca caaagtaggg aaaaatgtat atttgcctcc tagggaagga
     1321 gagttgacct gcaactcaac agtaaccagc ttgattgcta acattgacac ggatggcaac
     1381 cagacaaata ttacctttag tgcagaggtg gcagagctat accgattaga attgggggat
     1441 tataaattag tagagataac accaattggc ttcgcaccta catcagaaag gagatactcc
     1501 tctactccaa ggaggaataa aagaggtgtg ttcgtgctag ggctcttggg ttttctcgcg
     1561 acagcaggtt ctgcaatggg cacggcagct ttaacgctgt ctgctcagtc tcggacttta
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1621 ttggccggga tagtgcagca acagcaacag ctgttggaca tggtcaagag acaacaggaa
1681 atgttgcgac tgaccgtctg gggaacgaaa aatctccagg caagagtcac tgctatcgag
1741 aaatacttaa aggaccaggc gcggctaaat tcatggggat gtgcatttag acaagtctgc
1801 cacactactg taccatgggt aaataactcc ttaaaacctg attgggacaa catgacgtgg
1861 caagagtggg aacaacaagt ccgttaccta gaggcaaata tcagtgaaca gttagaacag
1921 gcacaaattc agcaagaaaa gaatacatat gaactacaaa aattaaatag ctgggatgtt
1981 tttaccaact ggcttgactt aaccgcctgg gtcaagtata ttcaatatgg agtttatata
2041 atagtaggaa tagtagctct tagaatagta atatatgtag tgcaaatgtt aagtaggctc
2101 aggaagggct ataggcctgt tttctcctcc cctcccggtt acatccaaca gatccatatc
2161 cacaaggacc aggaacagcc aaccagagga gaaacagaag aagacgttgg agacaacgtt
2221 ggggacagat tgtggccctg gccgatcgca tatttacatt tcctgatcca cctgctagct
2281 cgcctcttga tcgggctgta cagcatctgc agggacttac tatccaggat cttctcgatc
2341 ctccaaccga tcttccagag tcttcAGaga gcgctgacaa caatcaggga ctggctgaga
                3´ sj (tat,rev) /\
2401 cttaaagcag cctacctgca gtatgggtgc gagtggatcc aagaagcgtt ccaggccttt
2461 gcaaggattg cgagagagac gcttacaaac acctggagag acttgtgggg ggcaatgcag
2521 tgggtcggga ggaggatact cgcagtccca aggaggatca ggcaggggGC agaaattgcc
2581 ctcctgTGA
          <- env cds end
```

HIV2CI171

```
LOCUS       HIV2CI171   453 bp ss-RNA              VRL       28-OCT-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) gp 36 envelope
            sequence, isolate HIV2CI171, partial cds.
ACCESSION   X78505
SOURCE      Human immunodeficiency virus type 2 from PCR-amplified DNA extracted
            from cocultured PBMCs derived from a patient from Cote d'Ivoire with
            AIDS.
REFERENCE   1 (bases 1 to 453)
  AUTHORS   Peeters,M., Janssens,W., Fransen,K., Brandfull,J., Hendrickx,L.,
            Koffi,K., Delaporte,E., Piot,P., Gershy-Damet,G., Van der Groen,G.
  TITLE     Isolation of simian immunodeficiency virus from two wild-captured
            sooty mangabeys in Cote d'Ivoire: virological and genetic
            characterization and relationship to either HIV-2 and SIVsm/mac
            strains.
  JOURNAL   AIDS Res. Hum. Retroviruses 10, 1289-1294 (1994)
COMMENT     This sequence, HIV2CI171, was obtained through a study designed to
            compare genetic isolates of HIV-2 and SIV from the same region of
            Africa, specifically Cote d'Ivoire.  During the study, blood samples
            were collected from five human patients (CI171, CI9, ISO53, VI390,
            and VI905) and two sooty mangabey monkeys (SMCI2 and SMCI8).  PBMCs
            from the animals and human patients were cocultured with those from
            a healthy human donor, and the viral sequences were PCR amplified,
            cloned, and sequenced.
            Both HIV-2 strains CI9 and CI171 were obtained from patients from
            Cote d'Ivoire with AIDS.  HIV-2 strain VI390 was isolated from an
            asymptomatic Ghanian patient living in Belgium.  HIV-2 strain
            VI905 was derived from an asymptomatic Senegalese patient also
            living in Belgium.  Finally, strain ISO53 was obtained from an
            asymptomatic Belgium homosexual who had never had contact with
            Africans.  Both strains SMCI8 and SMCI2 were derived from sooty
            mangabeys from Cote d'Ivoire.
            Through phylogenetic analysis, Peeters et al. determined that the
            SMCI2 and SMCI8 sooty mangabey sequences were equidistant from both
            the HIV-2 sequences and from other SIVsm and SIVmac sequences.
            Peeters et al. also determined that the HIV-2 isolates obtained in
            their laboratory cluster with the HIV-2 subtype A viruses.  Sequence
            CI171 and the other four HIV-2 viral sequences determined in this
            study are shown in alignment below: CI9 (X78506), ISO53 (X78507),
            VI390 (X78510), and VI905 (X78511).
BASE COUNT     161 a    73 c    105 g    114 t
ORIGIN      1861 bp downstream from the start of env
       1  gacgtggtca agagacaaca agaaatgttg cgactgaccg tctggggaac
 env cds ->
      51  gaaaaatctc caggcaagag tcactgctat cgagaaatac ttaaaggacc
     101  aggcgcagct aaattcatgg ggatgtgcgt ttaggcaggt ctgccacact
     151  actgtaccat tggtaaatga ctctttaacg cctgactgga aaaatatgac
     201  atggcaagag tgggagatgc aagtccgcta cctagaggca aatatcagtc
     251  aacagttaga acaggcacaa attcaacaag aaaagaatat gtatgaatta
     301  caaaaactaa atagctggga tgtctttagt aacTAGtttg atttaacctc
                premature termination of env  <-
     351  cTAGatcaaa tatattcagt atggagtttt tatagtagta ggaatagtag
            <- premature termination of env
     401  ttcttagaat agtaatatat gtagtacaaa tgttaagtag acttagaagg
     451  ggc
     env cds ->
```

```
CONSENSUS GACGTGGTCAAGAGACAACAAGAAATGTTGCGACTGACCGTCTGGGGAACGAAAAATCTC  60
HIV2CI171 ------------------------------------------------------------  60
HIV2CI9   ---A-A---------------------------------------------------------  60
HIV2ISO53 ----------------------------------------A---------A---------  60
HIV2VI390 -----A---------------------------T--------------G-----------  60
HIV2VI905 ----------C------------------------------------------------  60

CONSENSUS CAGGCAAGAGTCACTGCTATCGAGAAATACTTAAAGGACCAGGCGCAGCTAAATTCATGG 120
HIV2CI171 ------------------------------------------------------------ 120
HIV2CI9   -------------------------G-----------------A--------------- 120
HIV2ISO53 -------------------------G---------------------------------- 120
HIV2VI390 ---------------------------------------------A--------------- 120
HIV2VI905 --------------------A---------C----------------A------------ 120

CONSENSUS GGATGTGCGTTTAGGCAGGTCTGCCACACTACTGTACCATGGGTAAATGACTCCTTAACG 180
HIV2CI171 ----------------------------------------T------------T------ 180
HIV2CI9   --G-------------------------------------------------T---G-- 180
HIV2ISO53 -----C--------A--A------T--------------------------A-------A 180
HIV2VI390 ------------------------------------------------------------A- 180
HIV2VI905 -----C--------A---------------------------------A-------A 180

CONSENSUS CCTGACTGGAACAATATGACATGGCAGGAATGGGAG?A?CAAGTCCGCTACCTAGAGGCA 238
HIV2CI171 -----------A--------------A--G------ATG---------------------- 240
HIV2CI9   ------------------------------------G-A---------------------- 240
HIV2ISO53 -----T--------C------------C-G-----AC-C---A------------------ 240
HIV2VI390 ----------------------------------C-A-G----------T---------- 240
HIV2VI905 --CA-T---C-G--C-----T------C--------AC-A---A----T------------ 240

CONSENSUS AATATCAGTGAACA?TTAGAACAGGCACAAATTCAACAAGAAAAGAATATGTATGAATTA 297
HIV2CI171 ---------C----G------------------------------------------------ 300
HIV2CI9   ------------ATC-------------------------G------------------- 300
HIV2ISO53 --------------A-----------G--------G--G--------C--------GC-G 300
HIV2VI390 ---------C----G--G--G-----------C--------G--A---------------- 300
HIV2VI905 ----------C-AGT--------------------G-----------C---------C-- 300

CONSENSUS CAAAAATTAAATAGCTGGGATGTCTTTGGCAACTGGTTTGATTTAACCTCCTGGATCAAA 357
HIV2CI171 ------C-------------------A-T----A-----------------A------- 360
HIV2CI9   ------------------------------------------C------------------ 360
HIV2ISO53 ------------------------T---------------------------------- 360
HIV2VI390 ---------------------------------------------G--------------- 360
HIV2VI905 --------G-------A----A-------------------C--G------------GGC 360

CONSENSUS TATATTCAGTATGGAGTTT?TATAGTAGTAGGAATAATAGTTCTTAGAATAGTAATATAT 416
HIV2CI171 -------------------T----------------G----------------------- 420
HIV2CI9   --------A----------TA---A--A-----G-T------T-A-------C------- 420
HIV2ISO53 -------------------A----A---C------------------------------- 420
HIV2VI390 --------A----------A---------C----G------C-T-A-------C------- 420
HIV2VI905 -------------------G--------------------C------------------- 420

CONSENSUS GTAGTACAAATGTTAAGTAGACTTAGAAGGGGC    449
HIV2CI171 --------------------------------    453
HIV2CI9   A----G---T-----------------A----    453
HIV2ISO53 ---------------G-----------------    453
HIV2VI390 -----G---------------T------A----    453
HIV2VI905 ---T--------A--G-----------------    453
```

```
LOCUS       HIV2D1024    1521 bp    ss-RNA          VRL       15-APR-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) gp105 envelope
            glycoprotein sequence, sample D1024, partial cds.
ACCESSION   U07104
SOURCE      Human immunodeficiency virus type 2 from PCR-amplified DNA extracted
            from uncultured PBMCs derived from a patient from Bombay, India whose
            sera was dually reactive (HIV1/HIV2).
REFERENCE   1  (bases 1 to 1521)
  AUTHORS   Grez,M., Dietrich,U., Balfe,P., Von Briesen,H., Maniar,J.K.,
            Mahambre,G., Delwart,E.L., Mullins,J.I. and Ruebsamen-Waigmann,H.
  TITLE     Genetic analysis of human immunodeficiency virus type 1 and 2
            (HIV-1 and HIV-2) mixed infections in India reveals a recent spread
            of HIV-1 and HIV-2 from a single ancestor for each of these viruses
  JOURNAL   J. Virol. 68, 2161-2168 (1994)
COMMENT     This sequence was obtained as part of a study to determine the
            genetic breadth of HIV-2 variation in India.  In this study, blood
            samples were obtained from four patients from Bombay, India (D766,
            D808, D868, and D1024) and from one patient from Goa, India (D1071);
            each of the five patients was serologically dually reactive. The
            mean genetic divergence of the set of four sequences from Bombay was
            7.3%, while the sequence from Goa was from 7 to 10.5% different from
            each of the Bombay sequences.  The entire set of Indian sequences,
            including both the Bombay and Goa sequences, diverged from eleven
            non-Indian HIV-2 sequences by 23%.  Because of the similarity of the
            Indian sequences, Grez et al. suggest that similar HIV-2 strains
            might be found elsewhere in India.  All five of these sequences
            clustered with HIV-2 subtype A viruses.  HIV-1 env sequences from
            Indian patients D766, D808, D868, and D1024 clustered with HIV-1 C
            viruses, and as a set showed a similar degree of interpatient
            genetic similarity as did their HIV-2 counterparts.
BASE COUNT      526 a    305 c    336 g    354 t
ORIGIN      envelope cds start
        1 ATGggggctc agctgcttat taccatttta ctaactagtg cttgcttaat atactgcaga
  env cds ->
       61 caatacgtaa ctgtttccta tggcataccc gggtggagga atgcatccat tcccctcgtt
      121 tgtgcaacca agaataggga tacttgggga accatacagt gcttaccaga caatgatgac
      181 tatcaggaaa tagccttgaa tgtgacagag gcttttgatg catggaacaa tacagtaaca
      241 gaacaagcaa tagaagatgt ctggaatcta tttgagacat caacaaaacc atgtgtcaaa
      301 ttaacaccct tatgtgtagc aatgacatgc aggaaaagca gtggcaacac aagtacaggg
      361 aacgcaacca catccacacc catgataaat gagacctcta taataaatga gacctctcca
      421 tgcatacgca caaacaactg ctcaggattg agagaggaag agatggtcag ttgtcagttc
      481 aatatgacag gattagcgag agataagcca aaagggtata atgaaacgtg gtactcaagt
      541 gacgtggttt gtgaaacaga aacaaataac acctcaaacc agagcaggtg ttacatgaac
      601 cattgcaaca catcagtcat cacagagtca tgtgataagc actattggga tgatatgagg
      661 tttagatatt gtgcaccgcc gggttttgcc ttgctaagat gcaatgatac caattactca
      721 ggctttgagc ccaattgttc taaagtagta gctgccacat gcaccaggat gatggagacg
      781 caaacttcta cgtggtttgg ctttaatggc actagagcag agaatagaac atatatttat
      841 tggcatagta aagataacag aactataatc agcttaaaca aacattataa tctctctata
      901 cattgtaaga ggccaggaaa taaaacagta gtaccaataa cacttatgtc aggattagtg
      961 tttcattccc agccaatcaa taacagacct agacaagcat ggtgctggtt caaaggcaaa
     1021 tggaaagaag ccatgcagga ggtgaagcaa acccttgtaa aacaccccag gtatgaggga
     1081 accaataaga cagaagatat tcactttgca gcaccgggaa aaggctcaga cccggaagcg
     1141 gcatacatgt ggactaactg caggggagaa tttctctact gcaacgtgac ttggttcctc
     1201 aattggatag agaacagaac catgaataag acatggcaca attatgtgcc atgccatata
     1261 aagcaaataa ttaacacctg gcataaggta gggaaacatg tatatttgcc tcccagggaa
     1321 ggggagttga cctgcaactc aactgtgacc agcataattg ctaacattga cggaggtaat
     1381 cagacaaata ttacctttag tgcagaggtg gcggaactat accgactaga attgggagat
     1441 tataaattgg tagaaataac accaattggc ttcgcaccta catcagtaaa acgatactcc
     1501 tctgctcacg ggagacatac g
                    envelope cds ->
```

```
LOCUS       HIV2D1071     975 bp    ss-RNA          VRL       15-APR-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) gp105 envelope
            glycoprotein sequence, sample D1071, partial cds.
ACCESSION   U07105
SOURCE      Human immunodeficiency virus type 2 from PCR-amplified DNA extracted
            from uncultured PBMCs derived from a female prostitute from the state of
            Goa, India whose sera was dually reactive (HIV-1/HIV-2).
REFERENCE   1  (bases 1 to 975)
  AUTHORS   Grez,M., Dietrich,U., Balfe,P., Von Briesen,H., Maniar,J.K.,
            Mahambre,G., Delwart,E.L., Mullins,J.I. and Ruebsamen-Waigmann,H.
  TITLE     Genetic analysis of human immunodeficiency virus type 1 and 2
            (HIV-1 and HIV-2) mixed infections in India reveals a recent spread
            of HIV-1 and HIV-2 from a single ancestor for each of these viruses
  JOURNAL   J. Virol. 68, 2161-2168 (1994)
COMMENT     This sequence was obtained as part of a study to determine the
            genetic breadth of HIV-2 variation in India.  In this study, blood
            samples were obtained from four patients from Bombay, India (D766,
            D808, D868, and D1024) and from one patient from Goa, India (D1071);
            each of the five patients was serologically dually reactive. Patient
            D1071 was a female prostitute who was identified as HIV-2 positive
            in April, 1992 and dually seroreactive in July of 1992. The mean
            genetic divergence of the set of four sequences from Bombay was 7.3%.
            The sequence from Goa was from 7 to 10.5% different from each of the
            Bombay sequences.  The entire set of Indian sequences, including both
            the Bombay and Goa sequences, diverged from eleven non-Indian HIV-2
            sequences by 23%.  Because of the similarity of the Indian sequences,
            Grez et al. suggest that similar HIV-2 strains might be found elsewhere
            in India.  All five of these sequences clustered with HIV-2 subtype A
            viruses.  HIV-1 env sequences from Indian patients D766, D808, D868, and
            D1024 clustered with HIV-1 C viruses, and as a set showed a similar
            degree of interpatient genetic similarity as did their HIV-2
            counterparts.
BASE COUNT      355 a    208 c    203 g    209 t
ORIGIN      340 bp downstream from the start of envelope
        1 ATGacatgca gcaaaaacag tggcaacaca agtataggaa gcacaaccac aaccacagac
 env cds ->
       61 gcagccatgg tgataaatga gacctctcaa tgcatacgcg caaacaactg ctcaggattg
      121 agagaggaag agctagtcag ttgtcagttc gatatgacag gattaacgag agataaacca
      181 aaaagatata atgaaacatg gtactcaagc gatgttgttt gtgacgcacc aactaacacc
      241 tcaaaccaga cctcaaataa cacctcagac cagagcaggt gttgcatgaa ccattgcaac
      301 acatcagtca tcacagaatc atgtgaaaag cactatTAGg atgctataag gtttagatat
                  premature termination of env cds <-
      361 tgtgcaccac caggttatgc cttgctaaga tgcaatgata ccaattactc aggctttgag
      421 cccaattgcc ctaaagtagt agctgccaca tgcaccagga tgatggaaac gcaaacttct
      481 acgtggtttg gctttaatgg cactagagca gagaatagga catatattta ttggcatagt
      541 agagataaca gaactataat cagcttaaac aaacattata atctctctat atattgtaag
      601 aggccaggaa ataaaacagt agtaccaata acacttatgt caggattagt gtttcattcc
      661 cagccaatca ataccagacc cagacaagca tcgtgctggc tcaaaggcca atggaaggaa
      721 gccatgcagg aggtgaagca aacccttgca aaacacccga ggtataaggg aaccaataat
      781 acaggaaaga ttaactttac agcaccggga aaaagttcag acccggaagc agcatacatg
      841 tggactatct gcagaggaga atttctctac tgcaacatga cttggttcct caatTAGgta
                                      premature termination of env cds  <-
      901 gaagacagaa ccgcgaacag gacatggcat aattatgtgc catgccatat aaagcaaata
      961 attaacacct ggcat
             envelope cds ->
```

```
LOCUS       HIV2D766     1524 bp    ss-RNA          VRL       15-APR-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) gp105 envelope
            glycoprotein sequence, sample D766, partial cds.
ACCESSION   U07106
SOURCE      Human immunodeficiency virus type 2 from PCR-amplified DNA extracted
            from uncultured PBMCs derived from a patient from Bombay, India whose
            sera was dually reactive (HIV1/HIV2).
REFERENCE   1  (bases 1 to 1524)
  AUTHORS   Grez,M., Dietrich,U., Balfe,P., Von Briesen,H., Maniar,J.K.,
            Mahambre,G., Delwart,E.L., Mullins,J.I. and Ruebsamen-Waigmann,H.
  TITLE     Genetic analysis of human immunodeficiency virus type 1 and 2
            (HIV-1 and HIV-2) mixed infections in India reveals a recent spread
            of HIV-1 and HIV-2 from a single ancestor for each of these viruses
  JOURNAL   J. Virol. 68, 2161-2168 (1994)
COMMENT     This sequence was obtained as part of a study to determine the
            genetic breadth of HIV-2 variation in India.  In this study, blood
            samples were obtained from four patients from Bombay, India (D766,
            D808, D868, and D1024) and from one patient from Goa, India (D1071);
            each of the five patients was serologically dually reactive. The
            mean genetic divergence of the set of four sequences from Bombay was
            7.3%, while the sequence from Goa was from 7 to 10.5% different from
            each of the Bombay sequences.  The entire set of Indian sequences,
            including both the Bombay and Goa sequences, diverged from eleven
            non-Indian HIV-2 sequences by 23%.  Because of the similarity of the
            Indian sequences, Grez et al. suggest that similar HIV-2 strains
            might be found elsewhere in India.  All five of these sequences
            clustered with HIV-2 subtype A viruses.  HIV-1 env sequences from
            Indian patients D766, D808, D868, and D1024 clustered with HIV-1 C
            viruses, and as a set showed a similar degree of interpatient
            genetic similarity as did their HIV-2 counterparts.
BASE COUNT      512 a    307 c    346 g    359 t
ORIGIN      envelope cds start
        1 ATGacacgta gaagggctca gctgcttatt tccattttac taactagtgc ttgcttaata
  env cds ->
       61 tattgcaaac aaaacgtaac tgttttctat ggcatacccg cgtggagaaa tgcatccatt
      121 ccctctttt gtgcaaccac aaatagggat acttggggaa ccatacagtg cttgccagac
      181 aatgatgact atcaggaaat aactttgaat gtgacagagg ctttcgatgc atggaacaat
      241 acagtaacag aacaagcaat agaagatgtc tggaatctat ttgagacatc aacaaaacca
      301 tgtgtcaaat taacaccctt atgtgtagca atgaattgca gcaaaaacag tggcaacaca
      361 agtacaggga gtacaaccac acccgcagcc atatccatga taaatgagac ctctccatgc
      421 atacgcacag acaactgctc aggattaaga gaggaagaga tggtcagttg tcagttcagt
      481 atgacaggat taacgagaga taagccaaaa aggtataatg aaacatggta ctcaagtgat
      541 gtggtttgtg aaacaacagg agcaactaac acctcaaacc aggacaggtg ttacatgaac
      601 cattgcaaca catcagtcat cacagagtca tgtgataagc actattggga tgatatgtgg
      661 tttagatatt gtgcaccgcc gggttatgct ttgctaagat atactgatac caattactca
      721 ggctttgagc ccaattgttc taaagtagta gctgccacat gcaccaggat gatggaaacg
      781 cagacttcta cgtggtttgg cttttgtggc gctagagcag agaaaagaac atatattttt
      841 tggcatagta aagatggcag ggctataatc agctgtaaca catatgataa tctctctata
      901 tattgtgaga ggccaggaaa taaaacagta gtgccgataa cacttatgtc gggattagtg
      961 tttcattccc agccaatcaa taacagacct agacaagcat ggtgctggtt cacaggcaca
     1021 tggagagaag ccatgcagga ggtgaagcaa acccttgtaa aacaccccag atatagggga
     1081 accaatgaga caaggaagat taactttaca gcaccgggaa aaggctcaga cccggaagcg
     1141 gcatacatgt ggactaactg caggggagag tttctctact gcaacatgac ttggttcctc
     1201 aattggatag agaacagaac tgtgaatagg acatggcaca attatgtgcc atgccatata
     1261 aagcagataa ttaacacctg gcataaggta gggaaacatg tatatttgcc tcccagggaa
     1321 ggggagttga cctgcaactc aactgtgacc agcataattg ctaacattga cggaggtaat
     1381 cagacaaata ttacctttag tgcagaggtg gcagaactat accgactgga attgggagat
     1441 tacaacttgg tagaaataac accaattggc ttcgcaccta catcagaaaa ccgatactcc
     1501 tctgctcacg ggagacatac gaga
                      envelope cds ->
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```
LOCUS       HIV2D808     1512 bp    ss-RNA          VRL       15-APR-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) gp105 envelope
            glycoprotein sequence, sample D808, partial cds.
ACCESSION   U07107
SOURCE      Human immunodeficiency virus type 2 from PCR-amplified DNA extracted
            from uncultured PBMCs derived from a patient from Bombay, India whose
            sera was dually reactive (HIV1/HIV2).
REFERENCE   1  (bases 1 to 1512)
  AUTHORS   Grez,M., Dietrich,U., Balfe,P., Von Briesen,H., Maniar,J.K.,
            Mahambre,G., Delwart,E.L., Mullins,J.I. and Ruebsamen-Waigmann,H.
  TITLE     Genetic analysis of human immunodeficiency virus type 1 and 2
            (HIV-1 and HIV-2) mixed infections in India reveals a recent spread
            of HIV-1 and HIV-2 from a single ancestor for each of these viruses
  JOURNAL   J. Virol. 68, 2161-2168 (1994)
COMMENT     This sequence was obtained as part of a study to determine the
            genetic breadth of HIV-2 variation in India.  In this study, blood
            samples were obtained from four patients from Bombay, India (D766,
            D808, D868, and D1024) and from one patient from Goa, India (D1071);
            each of the five patients was serologically dually reactive. The
            mean genetic divergence of the set of four sequences from Bombay was
            7.3%, while the sequence from Goa was from 7 to 10.5% different from
            each of the Bombay sequences.  The entire set of Indian sequences,
            including both the Bombay and Goa sequences, diverged from eleven
            non-Indian HIV-2 sequences by 23%.  Because of the similarity of the
            Indian sequences, Grez et al. suggest that similar HIV-2 strains
            might be found elsewhere in India.  All five of these sequences
            clustered with HIV-2 subtype A viruses.  HIV-1 env sequences from
            Indian patients D766, D808, D868, and D1024 clustered with HIV-1 C
            viruses, and as a set showed a similar degree of interpatient
            genetic similarity as did their HIV-2 counterparts.
BASE COUNT      536 a    304 c    319 g    353 t
ORIGIN      envelope cds start
        1 ATGgcgcccc aaaagactca gctgcttatt tccattttac taactagtgc ttgcttaata
  env cds ->
       61 tattgtgaac aatatgtaac tgttttctat gccatacccg cgtggaggaa tgcatccatt
      121 ccctctttt gtgcaaccag aaatagggat acttggggaa ccatacagtg cttgccagac
      181 aatgatgact atcaggaaat agctttaaat gtgacagaag ctttcgatgc atggaacaat
      241 acagtaacag aacaagcaat agaagatgtc tggaatctat ttgagacatc aacaaaacca
      301 tgtgtcaaat taacaccctt atgtgtagca atgaattgca gcaaaaacta taataacaca
      361 agtgcaggga acacaaccac acccacagcc gaatccatga taaatgagaa ctcttcatgc
      421 atacgcgcaa acaactgctc aggattggaa gaggaagaga tagtcaattg tcagttcaat
      481 atggcaggat taccgagaga taaaccgaaa tggtataatg aaacatggta ctcacgcgat
      541 gtggtttgtg aaaataacaa cccaacccaa aacagatgtt acatgaacca ttgcaacaca
      601 tcagtcatca cagagtcatg tgaaaagcac tattgggatg atataaggtt tagatattgt
      661 acaccaccgg gttatgcctt gctaaaatgc aatgatacca attactcagg ctttgagccc
      721 aattgctcta aagtagtagc tgccacacgc actaggatga tggaaacaca aacttctacg
      781 tggtttggct ttaatggcac tagagcagag aacagaacat acatttattg gcatagtaaa
      841 gataacagaa ctataatcag cctaaacaca cattataatc tctctatata ttgtaagagg
      901 ccaggaaata aaacagtagt accaataaca cttatgtcag gattagtgtt tcattcccag
      961 ccaatcaata acagacctag acaagcatgg tgctggttca aaggcagatg gaaggaagcc
     1021 atgcaggagg tgaaggaaac ccttacaaaa caccccaggt ataggggaac caatgataca
     1081 ggaaagatta actttgcagc accgggaaaa ggctcagacc cggaagcggc atacatgtgg
     1141 actaactgca ggggagaatt tctctattgc aacatgactt ggttcctcaa ttgggtggaa
     1201 aacaaaactg caaatcagac atggcacaat tatgtgccat gccatataaa gcaaataatt
     1261 aacacctggc ataaggtagg gaaacatgta tatttgcctc ccagggaagg ggaattaacc
     1321 tgcaactcaa ctgtgaccag cataattgct aacattgacg gaggtaatca gacaaatatt
     1381 acctttagtg cagaggtggg agaactatac cgattgggaa ttggagatta caaattggta
     1441 gaaataacat caattgggtt cgcacctaca tcagaaaaac gggactcctc tgctcacggg
     1501 agacatagag ag
          envelope cds ->
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LOCUS       HIV2D868     1525 bp    ss-RNA          VRL       15-APR-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) gp105 envelope
            glycoprotein sequence, sample D868, partial cds.
ACCESSION   U07108
SOURCE      Human immunodeficiency virus type 2 from PCR-amplified DNA extracted
            from uncultured PBMCs derived from a patient from Bombay, India whose
            sera was dually reactive (HIV1/HIV2).
REFERENCE   1  (bases 1 to 1525)
  AUTHORS   Grez,M., Dietrich,U., Balfe,P., Von Briesen,H., Maniar,J.K.,
            Mahambre,G., Delwart,E.L., Mullins,J.I. and Ruebsamen-Waigmann,H.
  TITLE     Genetic analysis of human immunodeficiency virus type 1 and 2
            (HIV-1 and HIV-2) mixed infections in India reveals a recent spread
            of HIV-1 and HIV-2 from a single ancestor for each of these viruses
  JOURNAL   J. Virol. 68, 2161-2168 (1994)
COMMENT     This sequence was obtained as part of a study to determine the
            genetic breadth of HIV-2 variation in India.  In this study, blood
            samples were obtained from four patients from Bombay, India (D766,
            D808, D868, and D1024) and from one patient from Goa, India (D1071);
            each of the five patients was serologically dually reactive. The
            mean genetic divergence of the set of four sequences from Bombay was
            7.3%, while the sequence from Goa was from 7 to 10.5% different from
            each of the Bombay sequences.  The entire set of Indian sequences,
            including both the Bombay and Goa sequences, diverged from eleven
            non-Indian HIV-2 sequences by 23%.  Because of the similarity of the
            Indian sequences, Grez et al. suggest that similar HIV-2 strains
            might be found elsewhere in India.  All five of these sequences
            clustered with HIV-2 subtype A viruses.  HIV-1 env sequences from
            Indian patients D766, D808, D868, and D1024 clustered with HIV-1 C
            viruses, and as a set showed a similar degree of interpatient
            genetic similarity as did their HIV-2 counterparts.
BASE COUNT      526 a    301 c    335 g    363 t
ORIGIN      envelope cds start
        1 ATGgcgcgtg aaaggactca gctaattatt gccactttac tagctagtgc ttgcttaaga
  env cds ->
       61 tattgccaac aatatgtaac tgttttctat ggcatacccg cgtggaagaa tgcatccatt
      121 ccctctcttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac
      181 aatgatgatt atcaggagat agctttgaat gtgacagagg ctttcgatgc atggaacaat
      241 acagtaacag aacaagcaat agaagatgtc tggaatctat ttgagacatc aacaaaacca
      301 tgtgtcaaac taacaccctt atgtgtagca atgaattgca gcaaggacag tagcaacaca
      361 agtacaggga acacacccac atccacagcc tcttatgtta taaatgagac ctcttcatgc
      421 atacacacag acacctgctc aggattgaga gaggaagaga tagtcagttg tcagttcagt
      481 atgacaggat tagcaagaga taagccaaaa aggtataatg aaacatggta ctcaagtgat
      541 gtggtttgtg aggcaacagg aacaaatgac accttaaacc agagcaggtg ttacatgaac
      601 cattgcaaca catcagtcat cacagagtca tgtgataagc actattggaa tgacatgagg
      661 tttagatatt gttcaccacc gggttatgcc ttgctaagat gcaatgattc caattactca
      721 ggctttgagc ccaattgttc taaagtagta gctgccacat gcaccaggat gatggaaacg
      781 caaacttcta catggtttgg ctttaatggc actagagcag agaatagaac atacgtttat
      841 tggcatagta aagataacag aactataatc agcttaaaca aatactataa tctctctata
      901 cattgtaaga ggccaggaaa taaaacagtg gtaccaataa cacttatgtc aggattagtg
      961 tttcattccc agccaatcaa tagaagacct agacaagcat ggtgctggtt cacaggcaaa
     1021 tggaaggaag ctatgcggga ggtgaggcaa accattgcag aacaccccag gtataggga
     1081 accaataata caggaaatat taaatttgtg gcaccgggaa aaggctcaga cccggaagcg
     1141 gcatacatgt ggactaactg caggggagaa tttctctact gcaacatgac ttggttcctc
     1201 aattggatag agaacaaaac tgagaatgca acatggcaca attatgtgcc atgccatata
     1261 aagcaaataa ttaacacctg gcataaggta gggaaacatg tatatttgcc tcccagggaa
     1321 ggggagttga cctgcaactc aactgtgacc agcataattg ctaacattga cggaggtaat
     1381 cagacaaata ttacctttag tgcagaggtg gcagaactat accgattaga attgggagat
     1441 tataaattgg tagaaataac accatttggc ttcgcaccta caccagaaaa acgatactct
     1501 tctgctcaca ggagacatcc gagag
                       envelope cds ->
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LOCUS       HIV2FA1       784 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immnodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
            sample FA, clone 2, partial cds.
ACCESSION   L33082
SOURCE      Human immunodeficiency virus type 2 PCR-amplified DNA recovered from
            a 36 year old female living in urban Ghana.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient FA was a 36-year old female who was identified at the
            University of Ghana Medical Center in Accra as HIV-2 positive and
            who was admitted with pulmonary tuberculosis.  She had lived in both
            Ghana and Cote d'Ivoire where she suffered from AIDS dementia
            complex.  Virus isolation was successfully performed at the National
            Cancer Institute.  Virus FA clusters with one of the subsets of
            subtype A in gag and pol(int) and with the other subset in env and
            pol(RT).  Gao et al. conclude that it may be a recombinant virus
            derived from two subtype A viruses, one from each of the two subsets.
            NCBI gi: 532149
BASE COUNT      271 a    164 c    201 g    148 t
ORIGIN      111 bp downstream from the start of gag
        1 agcgaacgaa ttggacagat ttggattggc agagagcctg ttggagtcaa aagaaggttg
 gag cds ->
       61 ccaaaagatt atcacagttt taaatccatt agtaccgaca gggtcagaaa atttacaaag
      121 tctttttaat acagtctgcg tcatctggtg cttgcacgca gaagagaaag tgaaagatac
      181 tgaagaagca agaaaactag tacagagaca tctagtggca gaaacaggaa ctgcagagaa
      241 aatgccaaat acaagtagac caacagcacc acctagcggg agtggaggaa acttccctgt
      301 gcaacagaca ggcggtggca actacgtcca tgtgccacta agtccccgaa ctctaaatgc
      361 ttgggtaaaa ttaatagagg ataagaagtt cggggcagaa gtagtgccag gatttcaggc
      421 actctcagaa ggctgcacgc cctatgatat caatcaactg cttaattgtg tgggcgatca
      481 ccaagcagct atgcaaataa tcagagaaat tatcaatgaa gaagcagcag attgggatgc
      541 acagcaccca ataccaggcc ccttgccagc agggcagctt agagacccaa ggggatctga
      601 catagcagga acaacaagca cagtagatga acagatccag tggatgtata gggcacaaaa
      661 tcccataccg gtagggaaca tctacagaag gtgggtccag atagggctac agaagtgtgt
      721 caggatgtac aacccaacta acgtcctaga cgtgaagcag ggaccaaagg aatcgttcca
      781 gagc
      gag cds ->
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HIV2FA2

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LOCUS       HIV2FA2       708 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) pol integrase sequence,
            sample FA, clone 1, partial cds.
ACCESSION   L33089
SOURCE      Human immunodeficiency virus type 2 PCR-amplified PBMC DNA recovered
            from a 36 year old female living in urban Ghana.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient FA was a 36-year old female who was identified at the
            University of Ghana Medical Center in Accra as HIV-2 positive and
            who was admitted with pulmonary tuberculosis.  She had lived in both
            Ghana and Cote d'Ivoire where she suffered from AIDS dementia
            complex.  Virus isolation was successfully performed at the National
            Cancer Institute.  Virus FA clusters with one of the subsets of
            subtype A in gag and pol(int) and with the other subset in env and
            pol(RT).  Gao et al. conclude that it may be a recombinant virus
            derived from two subtype A viruses, one from each of the two subsets.
            NCBI gi: 532151
BASE COUNT      290 a    135 c    153 g    130 t
ORIGIN      2184 bp downstream from the start of pol
        1 aatgggaata gtagtaggcc aaccaacaga gtcagaaaat agaatagtaa accaaatcat
 pol cds ->
       61 tgaggacatg ataaagaaag aagcaatcta tgttgcatgg gtcccagccc ataaaggcat
      121 aggaggaaac caggaagtag accacttagt aagtcagggc atcagacagg tattattcct
      181 ggaaagaata gagcccgctc aagaagaaca tgaaaaatat catagcaata taaaagagct
      241 aactcataaa tttggaatac cccaactagt agcaagacag atagtaaaca catgtgccca
      301 atgccaacag aaaggagagg ctatacatgg gcaagtaaat gcagaaatag gtgtctggca
      361 aatggactgc acacacttag aaggaaaaat cattatagta gcagtacatg ttgcaagtgg
      421 attcatagaa gcaaaagtca tcccacagaa atcagaaaga cagacagcac tcttcctatt
      481 aaaactggcc agcaggtggc caataacaca cttgcacaca gacaatggct ccaacttcac
      541 ctcacaggaa gtgaaaatgg tggcatggtg gataggtata gagcaaacct tcggagtacc
      601 ttacaatcca caaagccaag gagtagtaga ggcaatgaat caccacctaa aaaatcagat
      661 aagtagaatt agagagcagg caaacacaat agaaacaata gtactaat
                                                      pol cds ->
```

LOCUS HIV2FA3 453 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immunodeficiency virus type 2 (HIV-2) gp41 env sequence, sample FA, clone 15, partial cds.
ACCESSION L33095
SOURCE Human immunodeficiency virus type 2 PCR-amplified DNA recovered from a 36 year old female living in urban Ghana.
REFERENCE 1 (bases 1 to 453)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient FA was a 36-year old female who was identified at the University of Ghana Medical Center in Accra as HIV-2 positive and who was admitted with pulmonary tuberculosis. She had lived in both Ghana and Cote d'Ivoire where she suffered from AIDS dementia complex. Virus isolation was successfully performed at the National Cancer Institute. Virus FA clusters with one of the subsets of subtype A in gag and pol(int) and with the other subset in env and pol(RT). Gao et al. conclude that it may be a recombinant virus derived from two subtype A viruses, one from each of the two subsets.
NCBI gi: 532147
BASE COUNT 161 a 78 c 108 g 106 t
ORIGIN 1861 bp downstream from the start of env

```
        1 gacgtggtca agagacaaca agaaatgttg cgactgaccg tctggggaac aaaaaatctc
 env cds ->
       61 caggcaagag tcactgctat tgagaaatac ttaaaggacc aggcgcaact aaattcatgg
      121 ggatgcgcgt ttaggcaagt ctgccacact actgtaccat gggtaaatga cagcttgaca
      181 cctgattgga acaacatgac gtggcagcaa tgggaacaac aaatccgcta cctggaggca
      241 aatatcagtg agagtttaga acaggcacaa atccagcaag aaaagaacat gtatgaacta
      301 caaaaattaa atagctggga tgtctttggc aactggtttg atttaacctc ctgggtcaaa
      361 tatattcagt atggagttta tatagtagta ggaatagtag ctcttagaat aataatatat
      421 gtagtacaaa tgttaagtag acttagaagg ggc
                                        env cds ->
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HIV2FO784

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LOCUS       HIV2FO784      781 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
            sample FO784, clone 103, partial cds.
ACCESSION   L33083
SOURCE      Human immunodeficiency virus type 2 PCR-amplified PBMC DNA recovered
            from a 46 year old asymptomatic man from rural Liberia who showed
            HIV dual seroreactivity.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient FO784 was a 46 year old asymptomatic male from rural
            Liberia who had no history of sexually transmitted disease, chronic
            illness, blood transfusion or homosexuality.  His serum was HIV
            dually reactive.  Virus isolation was attempted twice at the
            University of Alabama at Birmingham without success.  This sample
            defines a distinct subtype, which has been designated as subtype D
            by Gao et al.  Interestingly, virus FO784 clustered with SIVsm and
            SIVmac, rather than with other HIV-2 strains. This and other strong
            evidence suggest that human and macaque contact with infected sooty
            mangabeys may be the source of HIV-2 and SIVmac infection [1].
            NCBI gi: 532153
BASE COUNT      278 a    158 c    196 g    149 t
ORIGIN      111 bp downstream from the start of gag
        1 agcaaatgaa ttggacagat ttggattagc agaaagcctg ttggaaaata aagaagggtg
 gag cds ->
       61 tcaaaaaatt ctctcggtct tagctccatt agtaccgaca ggttcagaaa atttaaaaag
      121 cctttacaat actgtctgcg tcatctggtg tttacacgca gaagagaaag tgaaagacac
      181 tgagggagca aaacagatag tgcagagaca tctagtggtg gaaacaggaa ctgcagacaa
      241 aatgccatca acgagtagac caacagcacc acctagtgac agaggaagaa attacccagt
      301 gcagcaagtc ggcggaaatt atgtccacct accgctgagc cccagaacat taaatgcatg
      361 ggttaagtta gtggaggaca aaaaattcgg ggcagaggta gtgccagggt ttcaggcact
      421 atcggaaggc tgcactccgt atgacatcaa tcagatgcta aattgtgtag gagaacatca
      481 ggcagccatg cagatcataa gggaaataat caatgatgag gcagcagatt gggatcagca
      541 gcatccacaa ccaggcccac taccagcagg acagctcaga gatccacgag gatctgatat
      601 agcaggaacc actagcacag tggaggaaca aatacagtgg atgtacaggc agcagaatcc
      661 cataccagtt ggaaatatct ataggagatg gatccagcta gggttacaga aatgtgtcag
      721 aatgtacaac ccaactaaca ttctggatat aaaacaaggg ccaaaagaga cgttccagag
      781 c
   gag cds ->
```

LOCUS HIV2JA1 766 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence, sample JA, clone 1, partial cds.
ACCESSION L33085
SOURCE Human immunodeficiency virus type 2 PCR-amplified DNA recovered from a 27 year old female living in urban Ghana who showed HIV dual seroreactivity.
REFERENCE 1 (bases 1 to 766)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient JA was a 27-year old female, married to a Nigerian man. She had lived in Nigeria for five years before she became ill with chronic diarrhea, severe weight loss, anemia and alopecia and returned to Ghana. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Sample JA clusters with the subtype B viruses.
NCBI gi: 532159
BASE COUNT 265 a 163 c 193 g 145 t
ORIGIN 111 bp downstream from the start of gag

```
       1 agtgaacgaa ttggacagat ttggattagc ggagagcctg ttggaatcaa aagaaggatg
 gag cds ->
      61 ccacaaaatt cttacggtct tagctccatt agtaccaaca ggatcagaaa atttaaaaag
     121 tctttttaat actgtctgcg ttgtttattg cttgcacgca gaagagaaag tgaaagatac
     181 tgaggaagca aaaaagatag cacagagcca tctagcggtg aacacggaaa aaacgccagc
     241 tacaagtaga ccaacagcac cgcctagcgg cagaaactat ccagtgcagc aggtggccgg
     301 caattacgtc cacctgccgc taagcccccg aaccttaaat gcctgggtaa aactagtaga
     361 ggaaaagaaa ttcggggcag aagtagtacc aggattccag gcactatcag aagggtgcac
     421 cccttatgat attaatcaaa tgctaaattg tgtaggggaa catcaagcag ccatgcaaat
     481 tattagggaa ataatcaatg aggaagcagc agactgggac cagcagcacc cggtgccagg
     541 tccactacca gcaggacagc ttagggaccc aagagggtca gacatagcgg gaaccaccag
     601 cacagtggag gaggagatac agtggatgta cagggcccaa aatcctgtcc cagtaggaaa
     661 catttatagg agatggattc aattagggct gcagaagtgt gtccggatgt ataaccctac
     721 taatatactg gacataaaag aaggaccaaa agaacccttc caaagc
                                                    gag cds ->
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HIV2JA2

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LOCUS       HIV2JA2       708 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) pol integrase sequence,
            sample JA, clone 9, partial cds.
ACCESSION   L33090
SOURCE      Human immunodeficiency virus type 2 PCR-amplified PBMC DNA recovered
            from a 27 year old female living in urban Ghana who showed HIV dual
            seroreactivity.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient JA was a 27-year old female, married to a Nigerian man.
            She had lived in Nigeria for five years before she became ill with
            chronic diarrhea, severe weight loss, anemia and alopecia and
            returned to Ghana.  Subsequent Western blot analysis of peripheral
            blood cells showed HIV dual reactivity.  Sample JA clusters with
            the subtype B viruses.
            NCBI gi: 532161
BASE COUNT      275 a    130 c    167 g    136 t
ORIGIN      2184 bp downstream from the start of pol
        1 catgggaata atagctggac agccaacaga aacagagtca ccaatagtaa ataaaataat
 pol cds ->
       61 tgaagaaatg atcaaaaagg aagcaatata tgtaggatgg gtgccagctc acaaaggact
      121 aggtggtaat caggaagtag accacctagt aagtcaagga attaggcagg ttctattcct
      181 agaaaagata gaaccagcac aagaagaaca tgaaaagtat catggcaatg taaaagaact
      241 agttcataaa tttggaatcc acagtttagt ggcaaaacaa atagtaaact cctgtgataa
      301 atgccaacaa aaaggggaag ctgttcatgg acaggtaaat gcagaactag gaacgtggca
      361 gatggactgt acacacttag aaggaaaggt cataatagtg gcagtccatg tagccagtgg
      421 atttatagag gcagaagtaa taccccaaga aacgggaaga cagacagctc tcttcctgtt
      481 aaaattggcc agcagatggc ctatcacaca cctacacaca gacaatggcg ccaacttcac
      541 ctcacaagac gtgaagatgg tggcctggtg ggtaggaata gaacgaacct tcggggtacc
      601 ctataaccca caaagtcagg gagtagtaga agcaatgaac catcacctaa aaaaccaaat
      661 agatagaatc agggatcagg cagtatcaat agagacagtt gtgctaat
                                                        pol cds ->
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LOCUS HIV2JA3 453 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immunodeficiency virus type 2 (HIV-2) gp41 env sequence, sample JA, clone 12, partial cds.
ACCESSION L33096
SOURCE Human immunodeficiency virus type 2 PCR-amplified DNA recovered from a 27 year old female living in urban Ghana who showed HIV dual seroreactivity.
REFERENCE 1 (bases 1 to 453)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient JA was a 27-year old female, married to a Nigerian man. She had lived in Nigeria for five years before she became ill with chronic diarrhea, severe weight loss, anemia and alopecia, and returned to Ghana. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Sample JA clusters with the subtype B viruses.
NCBI gi: 532157
BASE COUNT 162 a 85 c 105 g 101 t
ORIGIN 1861 bp downstream from the start of env

```
        1 gacgtggtca aaagacaaca ggaactgttg cggctgaccg tctgggggac aaaaaacctc
 env cds ->
       61 cagacaagag tcactgccat cgagaaatac ctaaaggacc aggcactact aaactcgtgg
      121 ggatgtgctt ttagacaggt ctgtcacaca actgtaccat ggccaaatga aactctccat
      181 ccaaactggc aaaacatgac atggcagcag tgggaacaga aggtcaacta cttggatgca
      241 aatataacac aattattaga agaggcacag atacagcagg aaaagaatat gtatgagcta
      301 cagaaattaa accaatggga tgtttttggt aattggtttg acttcacctc ctggatggca
      361 tacatcaaat taggactata tgtagtagca ggattaatag tgttaaggat agtaatatac
      421 attatacaga tgctagcaaa acttaggaag ggc
                                          env cds ->
```

HIV2ONFT1

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LOCUS       HIV2ONFT1     766 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
            sample ON, clone 18, partial cds.
ACCESSION   L33086
SOURCE      Human immunodeficiency virus type 2 PCR-amplified DNA recovered from
            a 48 year old fisherman living in urban Ghana who showed HIV dual
            seroreactivity.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient ON was a 48 year old male fisherman who had sexual
            encounters with prostitutes in Ghana and in Cote d'Ivoire.  He was
            hospitalized at the University of Ghana Medical Center in Accra
            where he was identified to be HIV-2 positive and suffered from
            end-stage AIDS.  Subsequent Western blot analysis of peripheral
            blood cells showed HIV dual reactivity.
            Patient FT, patient ON's wife, was also identified at the University
            of Ghana Medical Center in Accra as HIV-2 positive.  She was
            clinically asymptomatic.  Samples ON and FT both cluster with the
            subtype B viruses.
            NCBI gi: 532165
BASE COUNT      267 a    166 c    188 g    145 t
ORIGIN      111 bp downstream from the start of gag
        1 agtgaacgaa ttggacagat ttggattggc agagcgcctg ttggaatcaa aagaaggatg
 gag cds ->
       61 tcacaaaatt cttacggtct tagctccatt agtaccaaca ggttcagaaa atttaaaaag
      121 ccttttaat actgtctgcg tcatctactg cttgcacgca gaagagaaag tgaaagatac
      181 tgaggaagca aaaaagatgg cacagagcca tctagtggtg gacgcagaaa aaacgccagc
      241 tacaagtaga ccaacagcac cacctagcgg cagaaactat ccagtgcaac aggtagccgg
      301 caattatgtc cacgtgccgc taagcccccg aaccctaaat gcctgggtaa aattaataga
      361 agaaaagaag ttcggggcag aagtagtgcc aggattccaa gcactatcgg aagggtgcac
      421 cccttatgat atcaatcaga tgctaaattg tgtaggagaa caccaggcag ccatgcaaat
      481 tattagggaa ataatcaatg aggaggcagc agactgggac cagcagcacc cgataccagg
      541 tccactgcca gcaggacaac ttagggaccc cagagggtca gatatagcag gaaccaccag
      601 cacagtagag gaacaaatac agtggatgta caggcagcca aatcctgttc cggtagggaa
      661 catttacaga agatggattc aaatagggct gcagaaatgt gttcggatgt acaattccac
      721 caatatatta gatgtaaaac aagggccaaa ggaacccttc caaagc
                                                      gag cds ->
```

LOCUS HIV2ONFT2 708 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immnodeficiency virus type 2 (HIV-2) pol integrase fragment, sample ON, clone 6, partial cds.
ACCESSION L33091
SOURCE Human immunodeficiency virus type 2 PCR-amplified PBMC DNA recovered from a 48 year old fisherman living in urban Ghana who showed HIV dual seroreactivity.
REFERENCE 1 (bases 1 to 708)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient ON was a 48 year old male fisherman who had sexual encounters with prostitutes in Ghana and in Cote d'Ivoire. He was hospitalized at the University of Ghana Medical Center in Accra where he was identified to be HIV-2 positive and suffered from end-stage AIDS. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity.
Patient FT, patient ON's wife, was also identified at the University of Ghana Medical Center in Accra as HIV-2 positive. She was clinically asymptomatic. Samples ON and FT both cluster with the subtype B viruses.
NCBI gi: 532167
BASE COUNT 277 a 130 c 164 g 137 t
ORIGIN 2184 bp downstream from the start of pol

```
        1 catgggaata atagctggac aaccaacaga aacagagtca ccaatagtga ataaaataat
 pol cds ->
       61 tgaagaaatg atcaaaaagg aagcaatata tgtaggatgg gtgccagctc acaaaggact
      121 aggtggtaat caggaagtag accacctagt aagtcaagga attaggcagg ttctattctt
      181 agaaaagata gaaccagcac aagaagaaca tgaaaagtac catggcaatg taaaagaact
      241 agttcataaa tttggaatcc cacagttagt agcaaaacaa atagtaaact cctgtgataa
      301 atgccaacaa aaaggggaag ctgttcatgg acaggtaaat gcagaactag gaacatggca
      361 gatggactgt acacacttag aagggaagat cataatagtg gcagtccatg tagccagtgg
      421 atttatagag gcagaggtaa taccccaaga aacaggaaga caaacagctc tcttcctatt
      481 aaaattggcc agcagatggc ctatcacaca cctgcgcaca gacaatggcg ccaacttcac
      541 ctcacaagat gtgaagatgg tggcctggtg ggtagggata gaacaaacct tcggggtacc
      601 ctataaccca caaagtcagg gagtagtgga agcaatgaac catcatctaa aaaaccaaat
      661 agatagaatc agggatcagg cagtatcact agaaacagtt gtactaat
                                                    pol cds ->
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HIV2ONFT3

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LOCUS       HIV2ONFT3     453 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) gp41 env sequence,
            sample ON, clone 12, partial cds.
ACCESSION   L33097
SOURCE      Human immunodeficiency virus type 2 PCR-amplified DNA recovered from
            a 48 year old fisherman living in urban Ghana who showed HIV dual
            seroreactivity.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient ON was a 48 year old male fisherman who had sexual
            encounters with prostitutes in Ghana and in Cote d'Ivoire.  He was
            hospitalized at the University of Ghana Medical Center in Accra
            where he was identified to be HIV-2 positive and suffered from
            end-stage AIDS.  Subsequent Western blot analysis of peripheral
            blood cells showed HIV dual reactivity.
            Patient FT, patient ON's wife, was also identified at the University
            of Ghana Medical Center in Accra as HIV-2 positive.  She was
            clinically asymptomatic.  Samples ON and FT both cluster with the
            subtype B viruses.
            NCBI gi: 532163
BASE COUNT      155 a     83 c    113 g    102 t
ORIGIN      1861 bp downstream from the start of env
        1 gacgtggtca aaagacaaca ggaactgttg cggctgaccg tctgggggac gaaaaacctc
 env cds ->
       61 cagacaagag tcactgctat cgagaaatac ctaaaggacc aggcactact aaattcgtgg
      121 ggatgtgctt ttagacaggt ctgccacacg actgtaccat ggccaaatga aactatcgaa
      181 ccagactgga acaacatgac atggcagcaa tgggaagcaa aggtccaatt cttggatgca
      241 aatataacac aattattaga agaagcacag atacagcagg aaaagaatat gtatgagcta
      301 cagaaattga atcagtggga tgtttttagt aattggtttg acttcacctc ctggatggca
      361 caccttaggt taggactata tgtagtcgca ggaataatag tgttaaggat agtaatatac
      421 attatgcaga tgctagcaag gcttaggaag ggc
                                        env cds ->
```

LOCUS HIV2ONFT4 766 bp ds-DNA VRL 23-AUG-1994
DEFINITION Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence, sample FT, clone 1, partial cds.
ACCESSION L33084
SOURCE Human immunodeficiency virus type 2 PCR-amplified DNA recovered from an asymptomatic female living in urban Ghana.
REFERENCE 1 (bases 1 to 766)
AUTHORS Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J., Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Genetic diversity of human immunodeficiency virus type 2: Evidence for five distinct sequence subtypes with differences in virus biology
JOURNAL J. Virol. 68, 7433-7447 (1994)
COMMENT This sequence was obtained as part of a study designed to determine the in vivo extent of HIV-2 genetic and biological variation. Up to now, HIV-2 sequences have been derived almost solely from cultured isolates. Since cultivation may select against viruses which can not grow in a particular cell type, Gao et al. argue that a greater variation may be elucidated by sequencing virus obtained from uncultured PBMCs. With this aim in mind, peripheral blood samples were collected from 12 HIV-2 seropositive patients (2238, 60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA) from six different West African countries, living in both urban and rural areas. Uncultured PBMC DNA was PCR amplified, and the recombinant clones were manually sequenced. Another portion of the cells was used for virus isolation.
Patient FT, patient ON's wife, was identified at the University of Ghana Medical Center in Accra as HIV-2 positive. She was clinically asymptomatic.
Patient ON, patient FT's husband, was a 48 year old male fisherman who had sexual encounters with prostitutes in Ghana and in Cote d'Ivoire. He was hospitalized at the University of Ghana Medical Center in Accra where he was identified to be HIV-2 positive and suffered from end-stage AIDS. Subsequent Western blot analysis of peripheral blood cells showed HIV dual reactivity. Samples FT and ON cluster with the subtype B viruses.
NCBI gi: 532155
BASE COUNT 269 a 162 c 185 g 150 t
ORIGIN 111 bp downstream from the start of gag

```
        1 agtgaatgaa ttggacagat ttggattagc agagaccctg ttggagtcaa aagaaggatg
 gag cds ->
       61 tcacaaaatt cttacggtct tagctccatt agtaccaaca ggatcagaaa atttaaaaag
      121 ccttttttaat actgtctgcg tcattttctg cttgcacgca gaacagaaag tgaaagatac
      181 tgaggaagca aaaaagatag cacagagcca tctagtggtg gacgcagaaa aagtgccagc
      241 tacaagtaaa tcaacagcac cacctagtgg cagaaattat ccagtgcagc aggtagccgg
      301 caattatgtc cacgtgccgc taagcccccg aaccctaaat gcctgggtaa aattaataga
      361 agaaaagaag ttcggggcag aagtagtgcc aggattccaa gcactatcgg aagggtgcac
      421 cccttatgat attaatcaga tgctaaattg tgtaggagaá caccaggcag ccatgcaaat
      481 tattagggaa ataatcaatg aggaggcggc agactgggac cagcagcatc caataccagg
      541 cccactgcca gcaggacaac ttagggaccc cagagggtca gatatagcag gaaccaccag
      601 cacagtagag gaacaaatac agtggatgta caggcaacca aatcctgttc cggtagggaa
      661 catttacaga agatggatcc aaatagggct gcagaaatgt gtccggatgt acaatcccac
      721 taatatatta gatgtaaaac aagggccaaa ggaacccttc caaagc
                                                    gag cds ->
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HIV2PA1

```
LOCUS       HIV2PA1       781 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) p16/p28 gag sequence,
            sample PA, clone 1, partial cds.
ACCESSION   L33087
SOURCE      Human immunodeficiency virus type 2 PCR-amplified PBMC DNA recovered
            from a 35 year old asymptomatic male U.S. immigrant from rural
            Sierra Leone.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   J. Virol. 68, 7433-7447 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient PA was a 35 year old male U.S. immigrant from rural Sierra
            Leone who apparently acquired HIV-2 infection prior to his move to
            the United States, roughly twenty years ago, and thus represents a
            long-term survivor of HIV-2.  He had normal CD4 levels and was
            otherwise asymptomatic.  Sample PA defines a distinct subtype,
            which has been designated as subtype E [1].
            NCBI gi: 532169
BASE COUNT      276 a    167 c    194 g    144 t
ORIGIN      111 bp downstream from the start of gag
        1 agccagagaa ttagacagat ttggattggc agaaagcctg ttggaaaaca aggaaggatg
 gag cds ->
       61 tcacagaata ctgacagtac tagaaccatt aatgccaaca ggctctgaaa atttaaaaag
      121 cttgtttaac gctgtctgcg tagtttactg cctgcacgca gcagtgaaag tgaaagatac
      181 agaggaagcg aaaaaacatg tacagcagca ccacctagtg gcaggaggta aaactacaga
      241 gaaactgcct cctcagagta gaccaacagc gccacctagt ggaggtggag ggaattatcc
      301 agtgcaacag ataggaaata actatgtgca ctctccactg tccccaagaa cattgaatgc
      361 atgggtcaaa ttagtagaag aaaagaaatt tggagcagag gtagtgccag gcttccaggc
      421 attatcagaa ggatgcaccc cgtatgacat caaccagatg cttaattgcg tgggggaaca
      481 tcaggcagcc atgcaaatta tcagagagat aatcaatgaa gaagcagcag attgggacgt
      541 acagcatcca agagggcaac cgccagcaca gggcctaaga gacccatcag gatcagacat
      601 agcagggaca accagtaccc ccgcagaaca aatagagtgg atgtacagga atccaaatcc
      661 aatccctgtg ggagacatct atagaagatg gatccagcta gggctccaga aatgtgtcag
      721 aatgtataat ccaacaaaca ttctggacgt caaacagggg cccaaagaat cttttcagag
      781 c
  gag cds ->
```

```
LOCUS       HIV2PA2       995 bp ds-DNA             VRL       23-AUG-1994
DEFINITION  Human immunodeficiency virus type 2 (HIV-2) pol reverse
            transcriptase sequence, sample PA, partial cds.
ACCESSION   L33093
SOURCE      Human immunodeficiency virus type 2 PCR-amplified PBMC DNA recovered
            from a 35 year old asymptomatic male U.S. immigrant from rural
            Sierra Leone.
REFERENCE   1  (bases 1 to 995)
  AUTHORS   Gao,F., Yue,L., Robertson,D.L., Hill,S.C., Hui,H., Biggar,R.J.,
            Neequaye,A.E., Whelan,T.M., Ho,D.D., Shaw,G.M., Sharp,P.M. and
            Hahn,B.H.
  TITLE     Genetic diversity of human immunodeficiency virus type 2: Evidence
            for five distinct sequence subtypes with differences in virus
            biology
  JOURNAL   Unpublished (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the in vivo extent of HIV-2 genetic and biological variation.  Up
            to now, HIV-2 sequences have been derived almost solely from
            cultured isolates.  Since cultivation may select against viruses
            which can not grow in a particular cell type, Gao et al. argue that
            a greater variation may be elucidated by sequencing virus obtained
            from uncultured PBMCs.  With this aim in mind, peripheral blood
            samples were collected from 12 HIV-2 seropositive patients (2238,
            60415K, 60667K, 7312A, 7810A, 7924A, FA, FO784, FT, JA, ON, and PA)
            from six different West African countries, living in both urban and
            rural areas.  Uncultured PBMC DNA was PCR amplified, and the
            recombinant clones were manually sequenced.  Another portion of the
            cells was used for virus isolation.
            Patient PA was a 35 year old male U.S. immigrant from rural Sierra
            Leone who apparently acquired HIV-2 infection prior to his move to
            the United States, roughly twenty years ago, and thus represents a
            long-term survivor of HIV-2.  He had normal CD4 levels and was
            otherwise asymptomatic.  Sample PA defines a distinct subtype,
            which has been designated as subtype E [1].
            NCBI gi: 532171
BASE COUNT      392 a    182 c    218 g    203 t
ORIGIN      806 bp downstream from the start of pol
        1 agaaggaggg acaattagaa cgagcccctc ccactaatcc ttataataca ccaacctttg
 pol cds ->
       61 ctattaggaa aaaagataag agtaaatgga ggatgcttat agatttcagg gagctaaata
      121 aggcaacaca ggacttcaca gaagtccaac tgggtattcc acacccagca ggtctaaaag
      181 aaatggagca gataacagtg ttagatatag gggatgccta tttttcggta cccctagacc
      241 cagaatttag acagtataca gcattcacca taccctcggt aaataatcaa gaaccaggaa
      301 aaagatacat ctacaaggtc ctaccacaag ggtggaaggg atccccagca gtctttcagg
      361 agaccatgag acaggtacta gagcccttca gaaaagcaaa ttcggacgtt ctactcattc
      421 agtacatgga cgacttacta attggcagta acaggagcat gacagagcat gacaggatgg
      481 tagtacaatt aaaagacatg ctgaacaacc tggggttcag caccccagag gataagtttc
      541 agagagaacc acccttaaaa tggatggggt atttactata ccccaagaaa tggaaactac
      601 aaaaaataga gcttcctgaa aaagaaagat ggacagttaa tgacattcag aagttagtag
      661 gaatactaaa ttgggcagca caagtatatc caggaatcaa aacaaaaaat ttatgcaagc
      721 tcatcagagg aaaaatgacc ctaacagaag aggttcagtg gacagaattg tcagaggcag
      781 aattggcaga aaataagatt attctaagtc agggacagga gggaagatac tatagggaag
      841 aagaaaactt agaagcaaca gtactaaaga accaagataa tcagtggagc tataagattc
      901 atcagggaga cagaattctt aaagtaggaa aatttcccca aataaaaaat acccatacaa
      961 atggagtaag actattagct agtgtagtac agaaa
                                        pol cds ->
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SIVCPZGAB2

```
LOCUS       SIVCPZGAB2    280 bp ss-RNA             VRL       15-JUN-1994
DEFINITION  Simian immunodeficiency virus (SIVcpz) partial pol sequence, sample
            SIVcpzGAB2.
ACCESSION   U11495
SOURCE      Simian immunodeficiency virus from uncultured PCR-amplified PBMC
            DNA derived from a chimpanzee who lived in a tropical rainforest
            in northeastern Gabon.
REFERENCE   1  (bases 1 to 280)
  AUTHORS   Janssens,W., Fransen,K., Peeters,M., Heyndrickx,L., Motte,J.,
            Bedjabaga,L., Delaporte,E., Piot,P. and van der Groen,G.
  TITLE     Phylogenetic analysis of a new chimpanzee lentivirus SIVcpz-gab2
            from a wild-captured chimpanzee from Gabon
  JOURNAL   AIDS Res. Hum. Retroviruses 10, 1191-1192 (1994)
COMMENT     This is the third chimpanzee lentivirus that has been isolated and
            molecularly characterized.  The first isolated was derived from a
            chimpanzee from Gabon (SIVcpzGAB) and the second isolated was
            derived from a chimpanzee from Zaire (SIVcpzANT still under study).
            This 280 bp pol sequence was derived from a wild chimpanzee from
            the tropical rainforest of northeastern Gabon.  SIVcpzGAB2 clusters
            with the HIV-1 sequences and SIVcpzGAB.
BASE COUNT      117 a     47 c     60 g     56 t
ORIGIN      approximately 2588 bp downstream from beginning of pol cds
        1 ggtagtagaa tccatgaaca aagaattaaa aaagattata gggcaagtta gagaccaagc
 pol cds ->
       61 agaacactta aagacagcag tacaaatggc tgtattcatt cacaatttta aaagaaaagg
      121 ggggattggg gggtacactg caggagaaag aatagtagac atgctagcaa cagacttaca
      181 aacacaagaa ctacaaaaac aaattctaaa aattcaaaaa tttcgggttt attacagagg
      241 cagcagagac ccaatttgga aaggaccagc ctctctcctg
                                           pol cds ->
```

LOCUS SIVHUB670 228 bp ss-RNA VRL 17-FEB-1994
DEFINITION Simian immunodeficiency virus (SIVhu) envelope sequence, human isolate SIVhuB670, partial cds.
ACCESSION S67406
SOURCE Simian immunodeficiency virus from PCR-amplified DNA from cocultured PBMCs derived from an asymptomatic human laboratory worker.
REFERENCE 1 (bases 1 to 228)
AUTHORS Khabbaz,R.F., Heneine,W., George,J.R., Parekh,B., Rowe,T., Woods,T., Switzer,W.M., McClure,H.M., Murphey-Corb,M. and Folks,T.M.
TITLE Brief report: infection of a laboratory worker with simian immunodeficiency virus
JOURNAL N. Engl. J. Med. 330, 172-177 (1994)
COMMENT This partial envelope sequence was isolated from a human laboratory worker who had been working with SIV, specifically with the strain SIVsmB670. This strain was originally isolated from a sooty mangabey and subsequently introduced experimentally into a macaque. The researcher was seroreactive to both HIV-2 and SIV antibodies. However, the infecting virus was determined to be SIV. The researcher is asymptomatic with normal CD4 counts. Khabbaz et al. report difficulty in obtaining virus by both isolation and PCR and conclude that it may be due to a low viral burden or its distribution in tissue. Khabbaz et al. also report a premature termination in the nef gene (preliminary data) not present in the presumably infecting SIVB670 strain.
NCBI gi: 455953
BASE COUNT 107 a 36 c 48 g 37 t
ORIGIN 340 bp downstream from the start of envelope

```
        1 atgagatgca ataagacaga aacagacaaa tgggggttaa cagggaatgc aataacaaca
 env cds ->
       61 acagcaacaa cagcagcacc atcagcaaga acaccaaaag taacagcaaa cgttgtaaat
      121 gaaactagtt cttgtgtaaa aaacaataat tgtacaggct tagagcagga accaatggta
      181 agctgtaaat ttaacatgac agggttaaaa agggacaaaa agaaagaa
                                                    env cds ->
```

SIVSMCI2

```
LOCUS       SIVSMCI2      453 bp ss-RNA             VRL       06-OCT-1994
DEFINITION  Simian immunodeficiency virus (SIVsm) env sequence, sooty mangabey
            isolate SMCI2, partial cds.
ACCESSION   X78508
SOURCE      Simian immunodeficiency virus from PCR-amplified DNA extracted from
            cocultured PBMCs isolated from an asymptomatic sooty mangabey captured in
            its natural habitat in Cote d'Ivoire.
REFERENCE   1 (bases 1 to 453)
  AUTHORS   Peeters,M., Janssens,W., Fransen,K., Brandful,J., Heyndrickx,L.,
            Koffi,K., Delaporte,E., Piot,P., Gershy-Damet,G.M., and van der
            Groen,G.
  TITLE     Isolation of simian immunodeficiency viruses from two sooty mangabeys
            in Cote d'Ivoire: Virological and genetic characterization and
            relationship to other HIV type 2 and SIV sm/mac strains
  JOURNAL   AIDS Res. Hum. Retroviruses 10, 1289-1294 (1994)
COMMENT     This sequence, SMCI2, was obtained through a study designed to
            compare genetic isolates of HIV-2 and SIV from the same region of
            Africa, specifically Cote d'Ivoire.  It was isolated from a
            seropositive sooty mangabey in good health, with no signs of
            AIDS-like disease.  This animal was captured roughly ten years ago
            in its natural habitat in Cote d'Ivoire and subsequently housed in
            isolation at the University of Abidjan, Cote d'Ivoire.  PBMCs from
            the animal were cocultured with those from a healthy human donor,
            and the viral sequences were PCR amplified, cloned, and sequenced.
            Through phylogenetic analysis, Peeters et al. determined that the
            SMCI2 and SMCI8 sooty mangabey sequences were equidistant from both
            the HIV-2 sequences and from other SIVsm and SIVmac sequences.
            Peeters et al. also conclude from serological data that these SIVsm
            sequences are closer to some HIV-2s than SIVcpz is to HIV-1.  Based
            on several pieces of evidence, the evolutionary history of SIV and
            HIV-2 infection may be explained by cross-speciation from sooty
            managbeys to humans [1].  Both <SMCI2> and <SMCI8>, accession number
            X78509, are shown in alignment below.
BASE COUNT      159 a     71 c    108 g    115 t
ORIGIN      1861 bp downstream from the start of env
        1 gacgtggtca cgagacaaca agaactgttg cgactgaccg tctggggaac taaaaacctc
 env cds ->
 start
       61 cagactagag tcactgccat cgagaaatac ctaaaggatc aggcacggct aaatgcttgg
      121 ggatgtgcat ttagacaagt ctgccacact acggtacctt gggaaaataa cactttgcaa
      181 cctgattgga ataatatgac ttggcaagaa tgggaaataa agatcagaga tctggaggca
      241 aatatctcag aatcattgga ggaggcacaa atacaacaag aaaagaatat gtatgagttg
      301 caaaaattaa atagctggga tgtgtttggc aaccggtttg attttacctc ttgggtcaaa
      361 tatatctata taggatttta tgtagtagta ggaattatag ggttaagaat aatagtctac
      421 ttaatacaat tattaggtaa gcttaggaag ggc
                                 env cds end ->
```

```
CONSENSUS GACGTGGTCACGAGACAACAAGAACTGTTGCGACTGACCGTCTGGGGAACTAAAAACCTC     60
SMCI2     ------------------------------------------------------------     60
SMCI8     ------------------------------------------------------------     60

CONSENSUS CAGACTAGAGTCACTGCCATCGAGAAATACCTAAAGGATCAGGCACGGCTAAAT?CTTGG    119
SMCI2     -----------------------------------------------------G------    120
SMCI8     -----------------------------------------------------T------    120

CONSENSUS GGATGTGCATTTAGACAAGTCTGCCACACTACGGTACCTTGGGA?AAT?ACACTTTGCAA    177
SMCI2     ---------------------------------------------A---A-----------    180
SMCI8     ---------------------------------------------G---G-----------    180
```

```
CONSENSUS CCTGATTGGAATAATATGACTTGGCAAGAATGGGAAATAAAGATCAGAGATCTGGAGGCA   237
SMCI2     ------------------------------------------------------------   240
SMCI8     ------------------------------------------------------------   240

CONSENSUS AATATCTCAGAA??ATTGGAG?A?GCACAAATACAACAAGAAAAGAA?ATGTATGAGTTG   292
SMCI2     ------------TC-------G-G----------------------T------------   300
SMCI8     ------------AA-------A-C----------------------C------------   300

CONSENSUS CAAAA?TTAAATAGCTGGGATGTGTTTGGCAAC?GGTTTGATTTTACCTCTTGGGTCAAA   350
SMCI2     -----A-----------------------------C-------------------------   360
SMCI8     -----G-----------------------------T-------------------------   360

CONSENSUS TATATCTATATAGGATTTTATGTAGTAGTAGGAATTATAGG?TTAAGAATA?TAGTCTAC   408
SMCI2     ----------------------------------------G---------A--------   420
SMCI8     ----------------------------------------A---------G--------   420

CONSENSUS TTAATACAATTATT?GGTAAGC?TAGGAAGGGC    439
SMCI2     --------------A-------T----------    453
SMCI8     --------------G-------A----------    453
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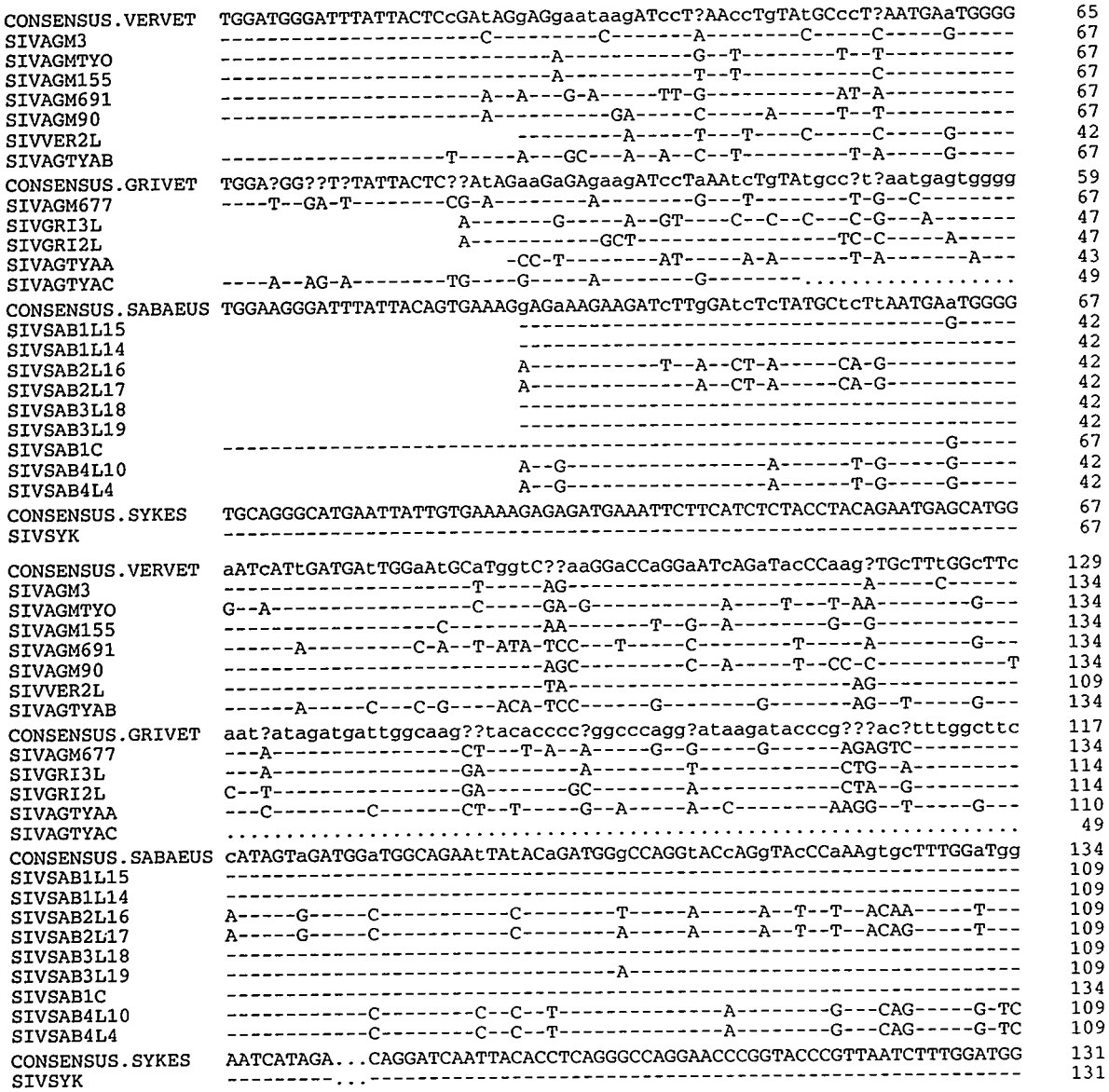
CONSENSUS.VERVET TGGATGGGATTTATTACTCcGAtAGgAGgaataagATccT?AAccTgTAtGCccT?AATGAaTGGGG 65
SIVAGM3 ----------C---------C-------A--------C-----C-----G----- 67
SIVAGMTYO ----------A----------G--T--------T--T---------- 67
SIVAGM155 ----------A----------T--T----------C---------- 67
SIVAGM691 ----------A--A---G-A-----TT-G----------AT-A---------- 67
SIVAGM90 ----------A----------GA-----C-----A-----T--T---------- 67
SIVVER2L ---------A-----T---T----C-----C-----G----- 42
SIVAGTYAB ----------T-----A---GC---A--A--C--T---------T-A-----G----- 67
CONSENSUS.GRIVET TGGA?GG??T?TATTACTC??AtAGaaGaGAgaagATccTaAAtcTgTAtgcc?t?aatgagtgggg 59
SIVAGM677 ----T--GA-T--------CG-A--------A--------G---T--------T-G--C-------- 67
SIVGRI3L A-------G-----A--GT----C--C--C---C-G---A------- 47
SIVGRI2L A----------GCT----------TC-C-----A----- 47
SIVAGTYAA -CC-T--------AT-----A-A------T-A-------A--- 43
SIVAGTYAC ----A--AG-A--------TG----G-----A--------G--------..... 49
CONSENSUS.SABAEUS TGGAAGGGATTTATTACAGTGAAAGgAGaAAGAAGATcTTgGAtcTcTATGCtcTtAATGAaTGGGG 67
SIVSAB1L15 ----------G----- 42
SIVSAB1L14 ---------- 42
SIVSAB2L16 A----------T--A--CT-A-----CA-G---------- 42
SIVSAB2L17 A----------A--CT-A-----CA-G---------- 42
SIVSAB3L18 ---------- 42
SIVSAB3L19 ---------- 42
SIVSAB1C ----------G----- 67
SIVSAB4L10 A--G----------A------T-G-----G----- 42
SIVSAB4L4 A--G----------A------T-G-----G----- 42
CONSENSUS.SYKES TGCAGGGCATGAATTATTGTGAAAAGAGAGATGAAATTCTTCATCTCTACCTACAGAATGAGCATGG 67
SIVSYK ---------- 67
CONSENSUS.VERVET aATcATtGATGAtTGGaAtGCaTggtC??aaGGaCCaGGaATcAGaTacCCaag?TGcTTtGGcTTc 129
SIVAGM3 ----------T-----AG----------A-----C------ 134
SIVAGMTYO G--A----------C-----GA-G----------A----T---T-AA--------G--- 134
SIVAGM155 ----------C--------AA-------T--G--A--------G--G---------- 134
SIVAGM691 ------A---------C-A--T-ATA-TCC---T-----C--------T-----A---------G--- 134
SIVAGM90 ----------AGC---------C--A-----T--CC-C----------T 134
SIVVER2L ----------TA----------AG---------- 109
SIVAGTYAB ------A-----C---C-G----ACA-TCC------G--------G-------AG--T-----G--- 134
CONSENSUS.GRIVET aat?atagatgattggcaag??tacacccc?ggcccagg?ataagatacccg???ac?tttggcttc 117
SIVAGM677 ---A----------CT---T-A--A-----G--G-----G------AGAGTC---------- 134
SIVGRI3L ---A----------GA--------A--------T----------CTG--A--------- 114
SIVGRI2L C--T----------GA-------GC--------A----------CTA--G--------- 114
SIVAGTYAA ---C---------C--------CT--T-----G--A-----A--C---------AAGG--T-----G--- 110
SIVAGTYAC 49
CONSENSUS.SABAEUS cATAGTaGATGGaTGGCAGAAtTAtACaGATGGgCCAGGtACcAGgTAcCCaAAgtgcTTTGGaTgg 134
SIVSAB1L15 ---------- 109
SIVSAB1L14 ---------- 109
SIVSAB2L16 A-----G-----C----------C---------T-----A-----A--T--T--ACAA-----T--- 109
SIVSAB2L17 A-----G-----C----------C---------A-----A-----A--T--T--ACAG-----T--- 109
SIVSAB3L18 ---------- 109
SIVSAB3L19 ----------A---------- 109
SIVSAB1C ---------- 134
SIVSAB4L10 ----------C---------C--C--T----------A--------G---CAG-----G-TC 109
SIVSAB4L4 ----------C---------C--C--T----------A--------G---CAG-----G-TC 109
CONSENSUS.SYKES AATCATAGA...CAGGATCAATTACACCTCAGGGCCAGGAACCCGGTACCCGTTAATCTTTGGATGG 131
SIVSYK ---------...---------- 131

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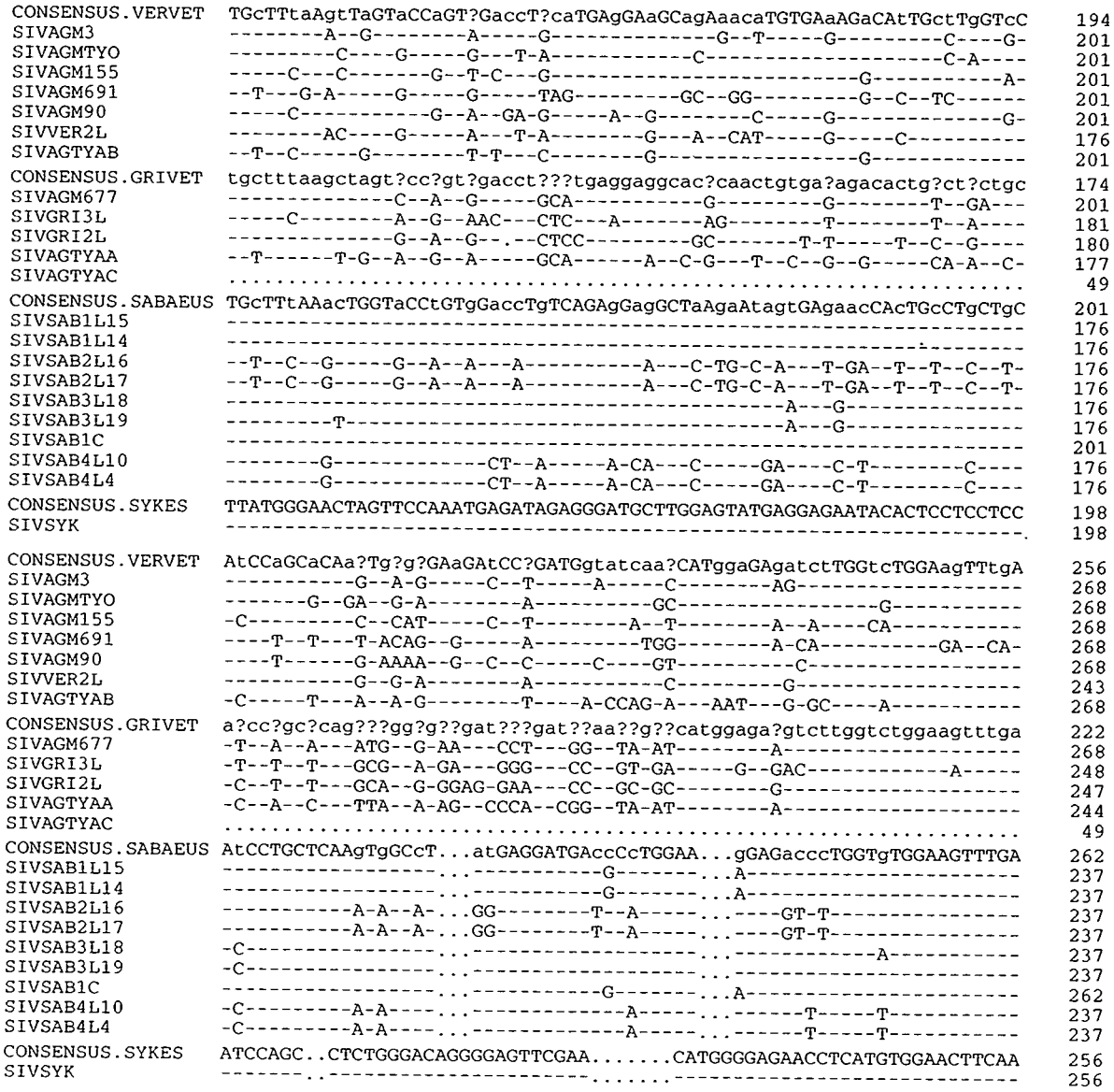
CONSENSUS.VERVET TGcTTtaAgtTaGTaCCaGT?GaccT?caTGAgGAaGCagAaacaTGTGAaAGaCAtTGctTgGTcC 194
SIVAGM3 --------A--G--------A-----G-----------G--T-----G---------C----G- 201
SIVAGMTYO ---------C----G-----G---T-A-----------C-----------------C-A---- 201
SIVAGM155 -----C---C-------G--T-C---G-----------------------G----------A- 201
SIVAGM691 --T---G-A-----G-----G-----TAG---------GC--GG---------G--C--TC------ 201
SIVAGM90 -----C----------G--A--GA-G-----A--G--------C-----G-------------G- 201
SIVVER2L --------AC----G-----A---T-A--------G---A--CAT-----G-----C---------- 176
SIVAGTYAB --T--C-----G--------T-T---C--------G----------------G------------ 201
CONSENSUS.GRIVET tgctttaagctagt?cc?gt?gacct???tgaggaggcac?caactgtga?agacactg?ct?ctgc 174
SIVAGM677 -------------C--A--G-----GCA----------G---------G--------T--GA--- 201
SIVGRI3L -----C--------A--G--AAC---CTC---A--------AG--------T--------T--A---- 181
SIVGRI2L -------------G--A--G--.--CTCC---------GC-------T-T-----T--C--G---- 180
SIVAGTYAA --T------T-G--A--G--A-----GCA------A--C-G---T--C--G--G-----CA-A--C- 177
SIVAGTYAC 49
CONSENSUS.SABAEUS TGcTTtAAacTGGTaCCtGTgGaccTgTCAGAgGagGCTaAgaAtagtGAgaacCAcTGcCTgCTgC 201
SIVSAB1L15 ---------- 176
SIVSAB1L14 ---------- 176
SIVSAB2L16 --T--C--G-----G--A--A---A----------A---C-TG-C-A---T-GA--T--T--C--T- 176
SIVSAB2L17 --T--C--G-----G--A--A---A----------A---C-TG-C-A---T-GA--T--T--C--T- 176
SIVSAB3L18 ----------A---G---------- 176
SIVSAB3L19 ---------T----------A---G---------- 176
SIVSAB1C ---------- 201
SIVSAB4L10 --------G-------------CT--A-----A-CA---C-----GA----C-T--------C---- 176
SIVSAB4L4 --------G-------------CT--A-----A-CA---C-----GA----C-T--------C---- 176
CONSENSUS.SYKES TTATGGGAACTAGTTCCAAATGAGATAGAGGGATGCTTGGAGTATGAGGAGAATACACTCCTCCTCC 198
SIVSYK ---------- 198
CONSENSUS.VERVET AtCCaGCaCAa?Tg?g?GAaGAtCC?GATGgtatcaa?CATggaGAgatctTGGtcTGGAagTTtgA 256
SIVAGM3 ----------G--A-G-----C--T-----A-----C--------AG---------- 268
SIVAGMTYO -------G--GA--G-A--------A----------GC----------G---------- 268
SIVAGM155 -C---------C--CAT-----C--T--------A--T--------A--A----CA---------- 268
SIVAGM691 ----T--T---T-ACAG--G-----A---------TGG--------A-CA----------GA--CA- 268
SIVAGM90 ----T------G-AAAA--G--C--C-----C----GT----------C---------- 268
SIVVER2L ----------G--G-A--------A----------C---------G---------- 243
SIVAGTYAB -C-----T---A--A-G--------T----A-CCAG-A---AAT---G-GC----A---------- 268
CONSENSUS.GRIVET a?cc?gc?cag???gg?g??gat???gat??aa??g??catggaga?gtcttggtctggaagtttga 222
SIVAGM677 -T--A--A---ATG--G-AA---CCT---GG--TA-AT--------A---------- 268
SIVGRI3L -T--T--T---GCG--A-GA---GGG---CC--GT-GA-----G--GAC----------A----- 248
SIVGRI2L -C--T--T---GCA--G-GGAG-GAA---CC--GC-GC--------G---------- 247
SIVAGTYAA -C--A--C---TTA--A-AG--CCCA--CGG--TA-AT--------A---------- 244
SIVAGTYAC 49
CONSENSUS.SABAEUS AtCCTGCTCAAgTgGCcT...atGAGGATGAccCcTGGAA...gGAGacccTGGTgTGGAAGTTTGA 262
SIVSAB1L15 ----------...----------G--------...A---------- 237
SIVSAB1L14 ----------...----------G--------...A---------- 237
SIVSAB2L16 ----------A-A--A-...GG---------T--A-----...----GT-T---------- 237
SIVSAB2L17 ----------A-A--A-...GG---------T--A-----...----GT-T---------- 237
SIVSAB3L18 -C----------...----------...----------A---------- 237
SIVSAB3L19 -C----------...----------...---------- 237
SIVSAB1C ----------...----------G--------...A---------- 262
SIVSAB4L10 -C---------A-A----...----------A-----...------T-----T---------- 237
SIVSAB4L4 -C---------A-A----...----------A-----...------T-----T---------- 237
CONSENSUS.SYKES ATCCAGC..CTCTGGGACAGGGGAGTTCGAA.....CATGGGGAGAACCTCATGTGGAACTTCAA 256
SIVSYK -------..----------.....---------- 256

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CONSENSUS.VERVET  tCCc?ATGtTaGCagt?Cagta?GaCCc?accaG?gagTa?tT?acaGACaTgcAT????ca?t?gg  310
SIVAGM3           ----.----------C--A--T-----T-A---AA-A--TC-C--T----------...GATC-T--  331
SIVAGMTYO         ---T.-----G---A-A-----C-----C-ATC-G-----C--T--T----------...GGGC-G-T  331
SIVAGM155         ---A.-----G--T--T-----C-----CT-A--G-----C--T------T-AT--TCAA--G-T--  334
SIVAGM691         ----.---C-----.-G--...A-G--ATG----.----G.--C-AT---------GCAA--G-G--  328
SIVAGM90          C---T----------G-----T-----A-A---AC----T--AGA----------...G--C-G-T  332
SIVVER2L          ----.----------C--A--C-----T--A--A--A--T--TGA----------TCAA--G-T--  309
SIVAGTYAB         ----.---C----....-T---A-G--TCG----G.G---.--C----------..........  317
CONSENSUS.GRIVET  ccc?.aagtt?gCaGTggAgTaccgcCC????atG?atA?ggatAtgcAcg?gcatgc???g???ta  273
SIVAGM677         ---G.-----G--G----------GGAC---TT--A---C-------AA-----AAA-CGC--  334
SIVGRI3L          ---T.-----A----------TTAAG--ATGG---C---AA----------G-ATG-AAAA-AAG--  314
SIVGRI2L          ---T.-----AA-------A-TTAAG--ATGG---C---GA--C-----T-AA-----CTGA...--  310
SIVAGTYAA         --GG.---C-G-----AC-A--------.....-G-G-T-TT--CTG--AT---C....G-CATGG  300
SIVAGTYAC         ...........--T---C----------.....-G-G-T-TT--C-G-TAT------.........   90
CONSENSUS.SABAEUS ccCa.?TacTAGCAGTGGACTATGttGCTTGGAGaCTGCACCCAGAgCAGGTGCCGtCAGtgtctG?  326
SIVSAB1L15        ----.C--------------------------G-------------------------CACAA-G  303
SIVSAB1L14        ----.C--------------------------G-------------------------CACAA-G  303
SIVSAB2L16        T---.G-GT----------------A-------------------------------------C  303
SIVSAB2L17        T---.G-GT----------------A-------------------------------------C  303
SIVSAB3L18        -T--.A--T----------------C--------------------A---------A---------A  303
SIVSAB3L19        ---T.G--T-----------------------------------A---------G---------A  303
SIVSAB1C          ----.C--------------------------G-------------------------CACAA-G  328
SIVSAB4L10        T---.A-----------------------------------------------------------C  303
SIVSAB4L4         T---.A-----------------------------------------------------------C  303
CONSENSUS.SYKES   CCCC...CACCTGGCCTATACACCAGGCTGGGAGATGGCCCGCTT.GCAGTTAGAGAGACAAACAGG  319
SIVSYK            ----...-----------------------------------.----------------------  319

                        <- nef
CONSENSUS.VERVET  ?Aa??ggaagtagc???accgcagGcttGcGGTTa?gc?cgTc?cc?aggaGatgACattaaaaacT  367
SIVAGM3           C--GA---------T.A----------T-----A--A-A--A--AT--T----------G----  397
SIVAGMTYO         G--GA---------CAG------A--C--------GAA.-A--A--AT-----------------  397
SIVAGM155         T-CAG-A--C----C.G---A----------TCCT.G--TG--T---------------G----  399
SIVAGM691         G--.................GTA----------G.-G----CGGG-CCT-TGT--CAACC-GCA-  376
SIVAGM90          G--GA---------T.A----------T-----A--.---TG--GG----------TG-----  397
SIVVER2L          T-CAG-A--C----C.T-A-CGCA-----T-----A--.---TG--T---------------G----  374
SIVAGTYAB         .--TGT----A--TA.GGAT-TG--T---------G--G-A--CGGG--CT-TGT--CAACC-TCA-  382
CONSENSUS.GRIVET  ?a?agc??????????g?t?a?c?ctT?g??c????.......??????????????????????  286
SIVAGM677         GTGTCAGCACTTTGCG-T-GGGACT--CCGC-A.....................................  367
SIVGRI3L          A-C---AAGAGGAAGT-G-TTC-G-C-A-CT-GGTT.......ACCATGGAGATGACATTAAGAACT  374
SIVGRI2L          A-C---AGGAGGAAGT-G-T-C-G-C-A-CT-GGTT.......ACCATGGAGATGACATTAAGAACT  370
SIVAGTYAA         C-A---.....GCTAACGC-G-A---T-TGGTT.....................................  328
SIVAGTYAC         ...........GCTGACGC-A-A---.-TGGTT.....................................  111
CONSENSUS.SABAEUS CTgACCACAAAACCACATCCTATgGAGTt.............GTCATGGTGATGACATTAAGAACT  379
SIVSAB1L15        --A-------------------------.............-------------------------  356
SIVSAB1L14        --A-------------------------.............-------------------------  356
SIVSAB2L16        ----------------------------.............-------------------------  356
SIVSAB2L17        ----------------------------.............-------------------------  356
SIVSAB3L18        ----------------------------.............-------------------------  356
SIVSAB3L19        ----------------------------.............-------------------------  356
SIVSAB1C          --A-------------------------.............-------------------------  381
SIVSAB4L10        ----------------------A-----.............-------------------------  356
SIVSAB4L4         ----------------------A----C.............-------------------------  356
CONSENSUS.SYKES   AAAACCACAAGAGC.....................................TGCAGTCAGCACTTAGTAAGAACA  357
SIVSYK            --------------.....................................-----------------------  357
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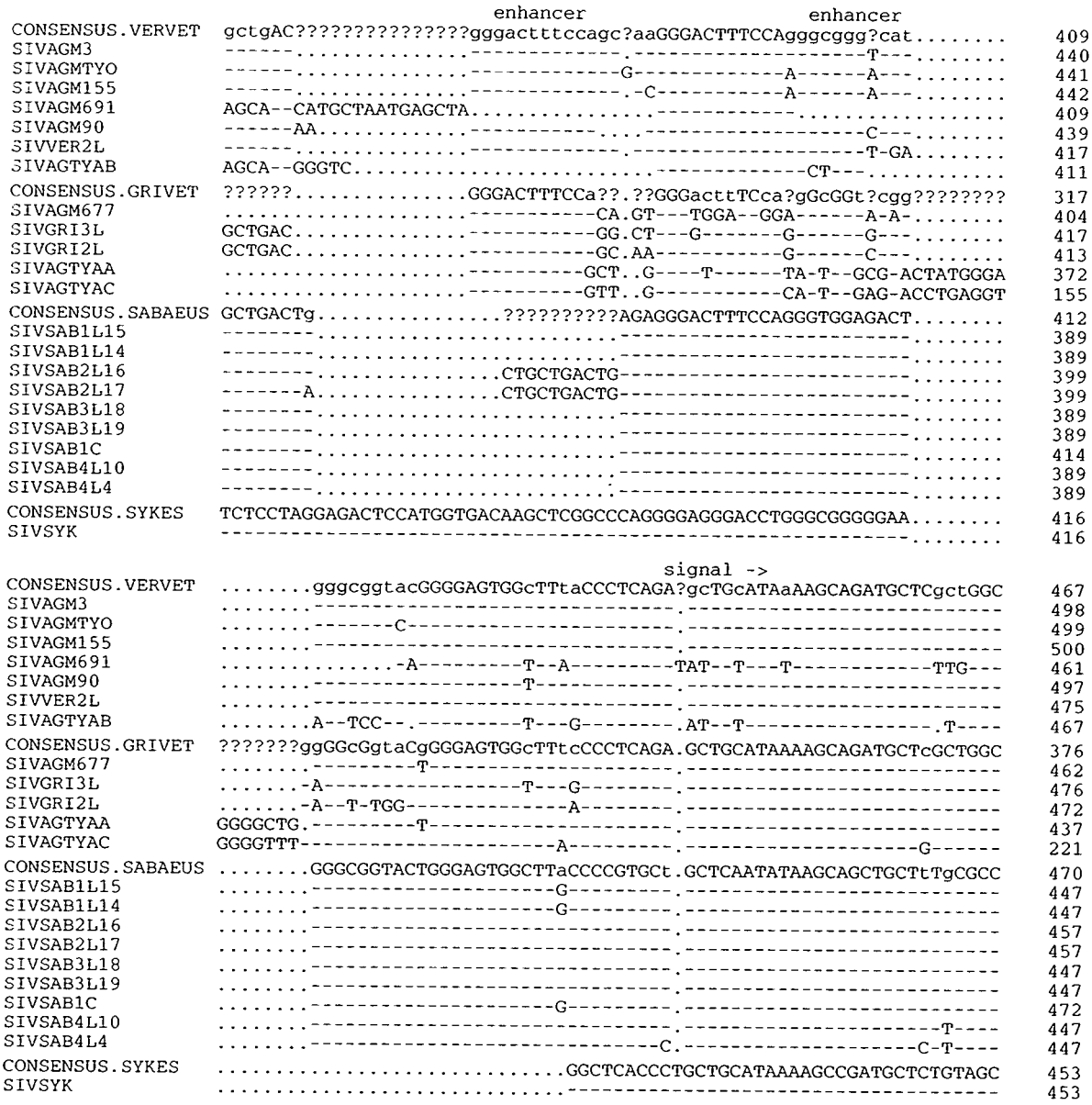
enhancer
enhancer
signal ->
CONSENSUS.VERVET
SIVAGM3
SIVAGMTYO
SIVAGM155
SIVAGM691
SIVAGM90
SIVVER2L
SIVAGTYAB
CONSENSUS.GRIVET
SIVAGM677
SIVGRI3L
SIVGRI2L
SIVAGTYAA
SIVAGTYAC
CONSENSUS.SABAEUS
SIVSAB1L15
SIVSAB1L14
SIVSAB2L16
SIVSAB2L17
SIVSAB3L18
SIVSAB3L19
SIVSAB1C
SIVSAB4L10
SIVSAB4L4
CONSENSUS.SYKES
SIVSYK

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      putative mRNA start  ->
CONSENSUS.VERVET  TTGTAACT?cAGt?CTCTTACT..AGGaGaCCAGCTtGAGCCTGGGTGTTCGCTGGTtAgCCTAACc  530
SIVAGM3           --------.----.--------..----------------------------------------  561
SIVAGMTYO         --------.----.--------..----------------------------------------  562
SIVAGM155         --------.----.--------..----------------------------------------  563
SIVAGM691         --------.----G--------..----- -----A--------------------.---------  523
SIVAGM90          --------.----.--------..----------------------------------------  560
SIVVER2L          --------C----.--------..----------------------------------------.  538
SIVAGTYAB         --------.T--GT--------..---G----------------------------G-A------T  531

CONSENSUS.GRIVET  TTGTAACT.CAGT.CTCTTACT..AGGAGACCAGCTaGAGCCTGGGTGTTCGCTGGTTAGCCTAACC  439
SIVAGM677         --------.----.--------..----------------------------------------  525
SIVGRI3L          --------.----.--------..----------------------------------------  539
SIVGRI2L          --------.----.--------..----------------------------------------  535
SIVAGTYAA         --------.----.--------..-----------T----------------------------  500
SIVAGTYAC         --------.----.--------..-----------T----------------------------  284

CONSENSUS.SABAEUS .TGtAAAA.CAGT.CTCTGcTTGGAGGCTgCCAGATTGAGCCtGGGTGTTCTCTGGTAAGtCTGAAC  534
SIVSAB1L15        .-------.----.----------------------------------------------------  511
SIVSAB1L14        .--G----.----.----------------------------------------------C------  511
SIVSAB2L16        .-------.----.----------------------------------------------------  521
SIVSAB2L17        .-------.----.----------------------------------------------------  521
SIVSAB3L18        .-------.----.--------------A-----------C------------------------  511
SIVSAB3L19        .-------.----.--------------A------------------------------------  511
SIVSAB1C          .-------.----.----------------------------------------------------  536
SIVSAB4L10        .-------.----.-----T----------------------------------------------  511
SIVSAB4L4         .-------.----.----------------------------------------------------  511

CONSENSUS.SYKES   TATCCGCGGAGTTGCAACTAGCTCTCTCCAGCGGCCTGGGAGCCCTGAGAGACTGGTAGAGCGGCCC  520
SIVSYK            ----------------------------------------------------------------  520

CONSENSUS.VERVET  TGgt?TGGCC?.......acCAgGGGTAAGga?CTCCttGGCTT?agaaagc?????.........  571
SIVAGM3           ----.-----.......--------------.-----------.-------..............  602
SIVAGMTYO         ----.-----.......--------------.-----------.-------..............  603
SIVAGM155         ----.-----.......--------------.-----------.-------..............  604
SIVAGM691         ---AC-----C.......T-----------AGC----AC-----..---T--T............  567
SIVAGM90          ----.-----.......--------------.-----------.G------..............  601
SIVVER2L          ----.-----.......--------------.-----------.-------..............  579
SIVAGTYAB         --ACT-----A.......GT--A-------AGC----AC-----G-ATGCTATGCTT.........  581

CONSENSUS.GRIVET  cGGT.TGGCC........ACCGGGGGTAAGGA.CTCCTTGGCTtcaTATAGCT.............  482
SIVAGM677         ----.-----.......--------------.--------------------..............  568
SIVGRI3L          .---.-----.......--------------.--------------------..............  581
SIVGRI2L          .---.-----.......--------------.--------------------..............  577
SIVAGTYAA         ----.-----.......--------------.-----------G--------..............  543
SIVAGTYAC         ----.-----.......--------------.----------CGG-------..............  327

CONSENSUS.SABAEUS CAGCTTGAGCCTGGGTGTTCGCTGGGGAAGGCaAGCCTaAGAGCACtCTGGTGAGGTCTtGGTAGAt  601
SIVSAB1L15        ----------------------------------------------------------------C  578
SIVSAB1L14        ----------------------------------------------------------------C  578
SIVSAB2L16        --------------------------------G-------------------------------  588
SIVSAB2L17        --------------------------------G-------------------------------  588
SIVSAB3L18        ----------------------------------------------------------C-------  578
SIVSAB3L19        ----------------------------------------------------------C-------  578
SIVSAB1C          ----------------------------------------------------------------C  603
SIVSAB4L10        -------------------------------------T-------A--------------------  578
SIVSAB4L4         -------------------------------------T-------A--------------------  578

CONSENSUS.SYKES   GGGAGCCCTTGCCAGTAAAGGCTAGTGAGGTCCGGGTTTGGCCGCC.....................  566
SIVSYK            ----------------------------------------------.....................  566
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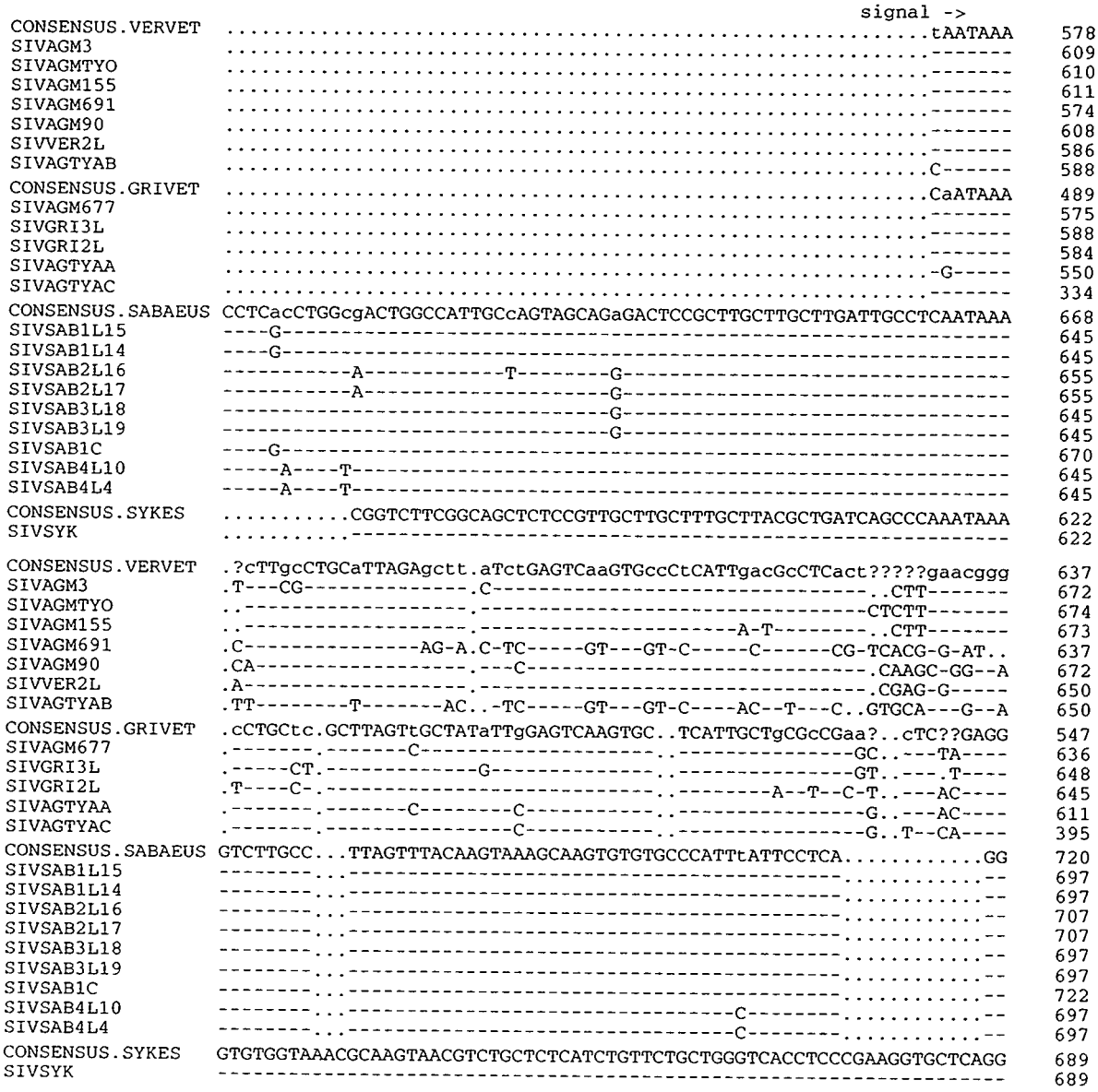
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CONSENSUS.VERVET .....tAATAAA 578
SIVAGM3 609
SIVAGMTYO 610
SIVAGM155 611
SIVAGM691 574
SIVAGM90 608
SIVVER2L 586
SIVAGTYAB .....C------ 588
CONSENSUS.GRIVET .....CaATAAA 489
SIVAGM677 575
SIVGRI3L 588
SIVGRI2L 584
SIVAGTYAA .....-G----- 550
SIVAGTYAC 334
CONSENSUS.SABAEUS CCTCacCTGGcgACTGGCCATTGCcAGTAGCAGaGACTCCGCTTGCTTGCTTGATTGCCTCAATAAA 668
SIVSAB1L15 ----G----------- 645
SIVSAB1L14 ----G----------- 645
SIVSAB2L16 ----------A----------T--------G----------- 655
SIVSAB2L17 ----------A----------G----------- 655
SIVSAB3L18 ----------G----------- 645
SIVSAB3L19 ----------G----------- 645
SIVSAB1C ----G----------- 670
SIVSAB4L10 -----A----T----------- 645
SIVSAB4L4 -----A----T----------- 645
CONSENSUS.SYKES ..........CGGTCTTCGGCAGCTCTCCGTTGCTTGCTTTGCTTACGCTGATCAGCCCAAATAAA 622
SIVSYK ....---------- 622
CONSENSUS.VERVET .?cTTgcCTGCaTTAGAgctt.aTctGAGTCaaGTGccCtCATTgacGcCTCact?????gaacggg 637
SIVAGM3 .T---CG----------.C----------..CTT------- 672
SIVAGMTYO ..----------.----------A-T---------..CTT------- 673
SIVAGM155 ..----------.----------CTCTT------- 674
SIVAGM691 .C----------AG-A.C-TC-----GT---GT-C-----C------CG-TCACG-G-AT.. 637
SIVAGM90 .CA----------.---C----------.CAAGC-GG--A 672
SIVVER2L .A----------.----------.CGAG-G----- 650
SIVAGTYAB .TT--------T-------AC..-TC-----GT---GT-C----AC--T---C..GTGCA---G--A 650
CONSENSUS.GRIVET .cCTGCtc.GCTTAGTtGCTATaTTgGAGTCAAGTGC..TCATTGCTgCGcCGaa?..cTC??GAGG 547
SIVAGM677 .-------.-------C----------..----------GC..---TA---- 636
SIVGRI3L .-----CT.----------G----------..----------GT..----.T---- 648
SIVGRI2L .T----C-.----------..--------A--T--C-T..---AC---- 645
SIVAGTYAA .-------.-------C--------C----------..----------G..---AC---- 611
SIVAGTYAC .-------.----------C----------..----------G..T--CA---- 395
CONSENSUS.SABAEUS GTCTTGCC...TTAGTTTACAAGTAAAGCAAGTGTGTGCCCATTtATTCCTCA.....GG 720
SIVSAB1L15 --------...----------..--- 697
SIVSAB1L14 --------...----------..--- 697
SIVSAB2L16 --------...----------..--- 707
SIVSAB2L17 --------...----------..--- 707
SIVSAB3L18 --------...----------..--- 697
SIVSAB3L19 --------...----------..--- 697
SIVSAB1C --------...----------..--- 722
SIVSAB4L10 --------...----------C--------..--- 697
SIVSAB4L4 --------...----------C--------..--- 697
CONSENSUS.SYKES GTGTGGTAAACGCAAGTAACGTCTGCTCTCATCTGTTCTGCTGGGTCACCTCCCGAAGGTGCTCAGG 689
SIVSYK ---------- 689

```
CONSENSUS.VERVET  ?????ctTcctTACTGGGtTcTCTCTc?gaCCCAGGcGAGAgAAA?CTCCAGCAGT              686
SIVAGM3           TAAAA----------.A----------.--------                              724
SIVAGMTYO         ..AAT----------T----------.--------                              725
SIVAGM155         .AGAAG---------AA----------.--------                              725
SIVAGM691         .....-C--AA----------.T-.------G--------.--------                 683
SIVAGM90          ACC..G---------T----------.--------                               723
SIVVER2L          TCCT.G---------.A----------.--------                              701
SIVAGTYAB         AT...-C-T-A-------G-T-----..--------A----A---C----------          701

CONSENSUS.GRIVET  TGAACCTCTCTTACTGgGTTCTCCTgT.?aCCCAGG?aGGAGAAActcCa???AGT          597
SIVAGM677         ----------..-------TG----------                                   682
SIVGRI3L          ----------A----------.T-------CG----------GCA                     700
SIVGRI2L          ----------.T-------C----------GCA                                 697
SIVAGTYAA         ----------T-..G------G--------.CT-GAGC---                         664
SIVAGTYAC         ----------T-..-------G--------.CT-CAGC---                         448

CONSENSUS.SABAEUS AaaACCCTGGTTACT.........AAGGATCCCTGttAgaAAAaaTCCTTAGCA            765
SIVSAB1L15        ----------.........----------A----------                           742
SIVSAB1L14        -C--------.........----------A----------                           742
SIVSAB2L16        ----------.........----------T.---------                           751
SIVSAB2L17        ----------.........----------T.---------                           751
SIVSAB3L18        ----------.........----------.---------                           741
SIVSAB3L19        --G-------.........----------A----------                           742
SIVSAB1C          -C--------.........----------A----------                           767
SIVSAB4L10        ----------.........----------G-AG-------                           742
SIVSAB4L4         ----------.........----------G-AG-------                           742

CONSENSUS.SYKES   GAGCGCGCCTTCAGTGGCGCCGAACAGGGACTTGACTAGGCCAGGGACCCGAGAGGAGGTGACGCCA  756
SIVSYK            ------------------------------------------------------------      756

CONSENSUS.SYKES   GTCAAAGGGAGTCCGGATCCAAGAGGGATCGGCTGTCCGTCCTAGGCCGACCGGTGCTGGTGGCTCG  823
SIVSYK            ------------------------------------------------------------      823

CONSENSUS.SYKES   TGGTGTACACACGAGACGAGGTAAGTGATCCAGCG                                858
SIVSYK            ---------------------------------                                 858
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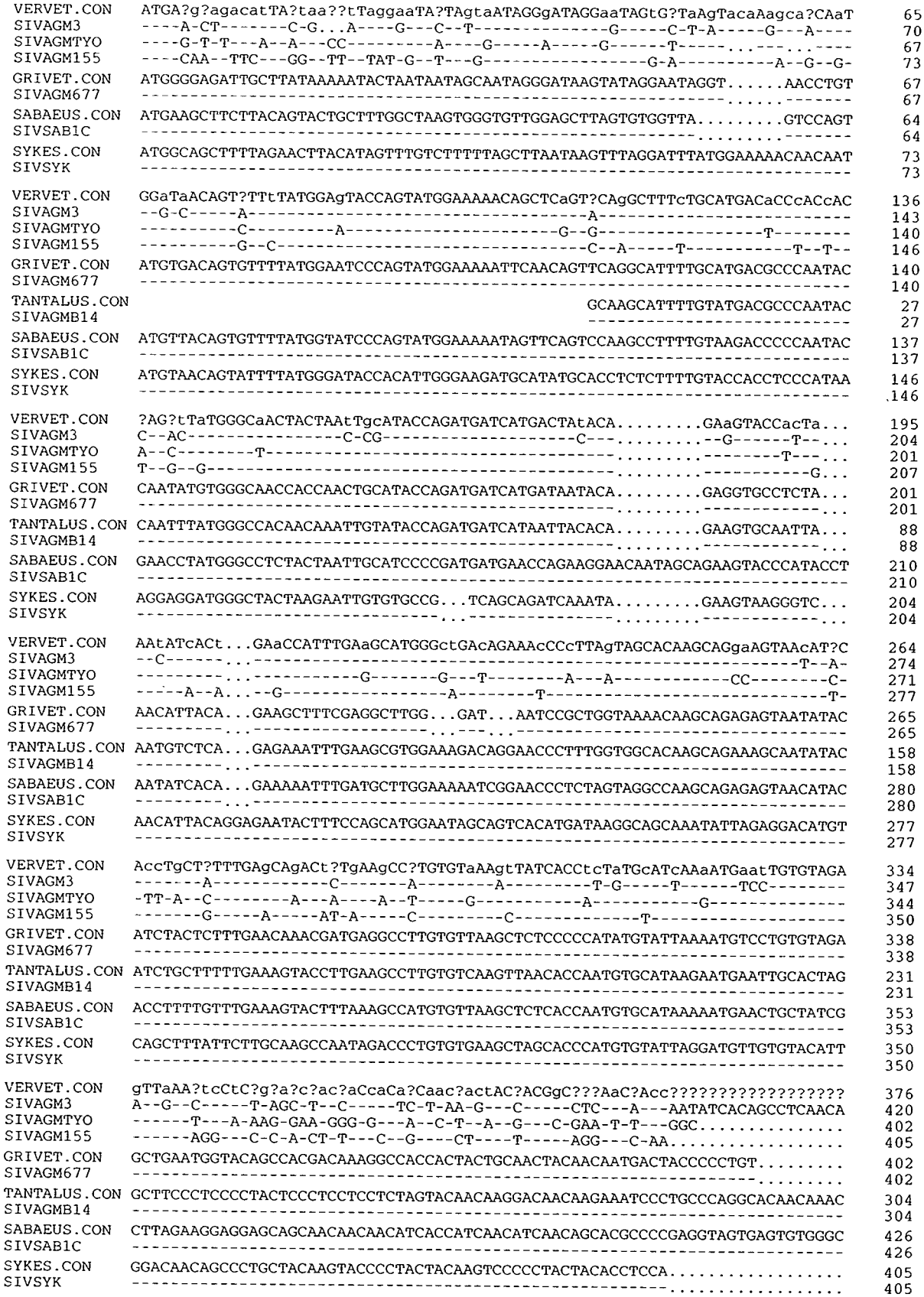

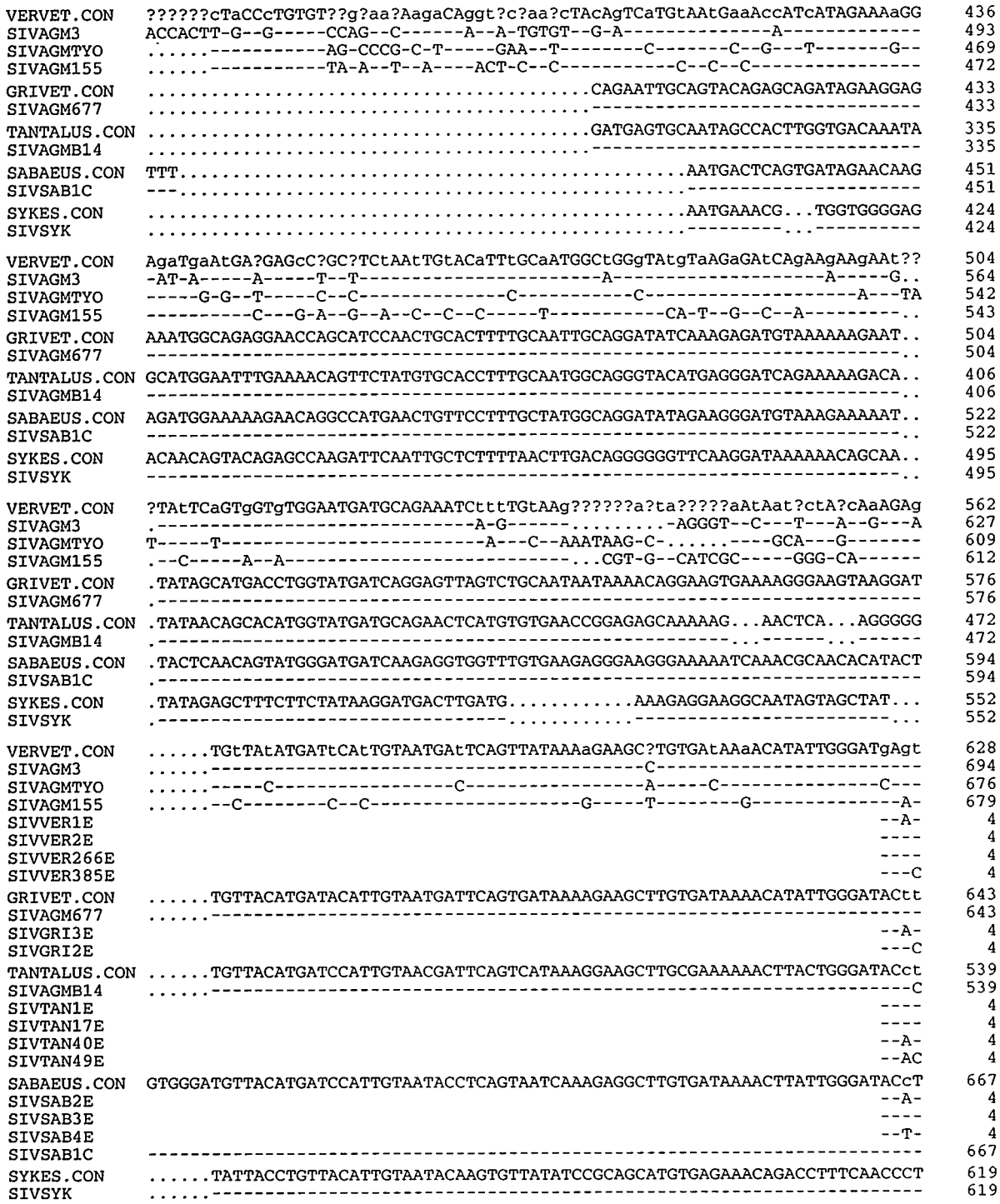

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VERVET.CON    TaAGatTaAGaTAcTGTGCtCCaGCAGGaTatGCttTgcTaAAATGtAAtGAt?a?gAtTATgatGGgTttaa   699
SIVAGM3       ----------G--------C--G-----G-T------AT-------C--C---T-T--------CA--------   767
SIVAGMTYO     -G--G-----G--T--------------T-----------------------G-A------A------A---   749
SIVAGM155     -----C-------T-----------------C--------T------------TGG-------CA--A-----   752
SIVVER1E      ----GC-------------A--T-----------------------C------AGAA-----ACA--C---GC    77
SIVVER2E      -------G-------------------------C---T-G----------CC-T------A------AC--    77
SIVVER266E    ----GC-------T-----C----------T---CC-----------------GCA-----------T-----    77
SIVVER385E    -------G--------------------G-TC--CC-AT-------------CT-T--C--------------    77

GRIVET.CON    TaAGAgTaAGATAcTGTGCACCAGCAGG?TaTGCTTTgtTaAaATGcaatGATAAGgATTATAa?GGCTTTGC   714
SIVAGM677     ----------------------------G---------C-------T----------------GA--------   716
SIVGRI3E      ----------------------------A--------A-------------------------T--------    77
SIVGRI2E      -T---T-G-----T--------------C-T---------G-G----TTA------A-------C--------    77

TANTALUS.CON  TaAGgtTaaGATAtTGTGCACCaGCaGgctTTGCTaTcTTaAAATGtAagGATACtAATTAtaCAGGcTtTGG   612
SIVAGMB14     -T-----------------------T-CTG----------G--------A-----------C-----------   612
SIVTAN1E      ----A--------C-------------------------------------------------A-----      77
SIVTAN17E     -G---C-T--------------T--------------T--------C--------A----------------    77
SIVTAN40E     ----A---C----------------T---------C-T--------C-G-------------G----------    77
SIVTAN49E     -----C-T-------------------------------------A-------------------A---      77

SABAEUS.CON   TTAG??TtAG?TATTGTGCTCCaGCaGGtTATGCtTTgcTAAGATGTgcAGATaCAGAtTAttcAGGaCATAA   737
SIVSAB2E      ----AT-G--A--------------T-------------------------------------------      77
SIVSAB3E      ----GC----G----------------------------T-----------------------------G-----   77
SIVSAB4E      ----AT-A--A-----------T-----C-----G--A---------AG----T----C--CAG---------    77
SIVSAB1C      ----GC----G-------------------------------------------------------------   740

SYKES.CON     TTCCGATTCAATACTGTGCTCCACCGGGTTACTCATTGTTGAAATGCAATGATACAAATTTTGAAGGAGACGA   692
SIVSYK        -------------------------------------------------------------------------   692

VERVET.CON    accaaa?TGttc?AATGT?tcaGTaGTgCAtTGtACagg?tTaATgAATACAACAGT?ActACaGG?tTgtT?   765
SIVAGM3       GA----C-----T-----T-----G-----------TAAC--G--A-----------G-----T--AC----G   840
SIVAGMTYO     --A---T--C--A-----A--------------------C----------------G--A-----G-----G   822
SIVAGM155     G---G-A-----T-----T--------------C---ACT----------------A--C--T--TC----A   825
SIVVER1E      T----GA---AGA-----TAGT-----------C-----G--G--------------C-G------C---C-A   150
SIVVER2E      --AG--C--C--T-----C-----------C--------G----------------A-----T--C-----G   150
SIVVER266E    -A----C--C--C-----A-----G--A--------CAACC----------------G--------G-----A   150
SIV2010E                                                                -G------AC-A--A    15
SIVVER385E    --A---T-----C-----A--------------------GC----------------A--------G---C-G   150

GRIVET.CON    TCCaAa?TGtAAGAATGTttCAGTagt?CAcTGtACTAGatTAATaAATACtACtaTAAccACAGG?ATAGGa   784
SIVAGM677     ------G--C----------------G--T-------------C--------------T-----G------   789
SIVGRI3E      ------A--------------------A----------G-------------------------A-----G   150
SIVGRI2E      ---T-GT-----------GA----TACT-----C------C----------A--AG---G------T------   150

TANTALUS.CON  ?...attTGTAgaAATGTtTCAGTaGTaAGcTGcACaGG?tTaATGAATACtACAgTaAGtTCaGCtTTTGG?   679
SIVAGMB14     C...-CA-----------G-----------T--------C--------------------C-----------T   682
SIVTAN1E      T...G----------------------T--T--T--T--A--G--------------G--C-----A-----C   147
SIVTAN17E     G...--------G----------G--------------GC-----------------------------C   147
SIVTAN40E     T...--------AC--------------------T--T--AC--------------A-------T--------G   147
SIVTAN49E     G...--A-----------A--------T-----------C-----------C--------------------A   147

SABAEUS.CON   G...??aTGTaagAATGTAaCAGTaTCAGCTTGCACTAGgtTaATaAATACTACtgTAAGcACAGG?ATAGGt   804
SIVSAB2E      -...GC-------------------------------------------------A----------G------   147
SIVSAB3E      -...AA-----------------------------------A-------------------------G------   147
SIVSAB4E      -...AAT---C-A------T----T---------------C-T--T--------A-----T-----A------   147
SIVSAB1C      -...GC-----G---------------------------------C--------------------A-----A   810

SYKES.CON     T...GTCTGTACAAATGTAACTGCAGTATCATGCACACAGGAATTCAATACATTGGCTAGCACATGGTTCCAA   762
SIVSYK        -...-------------------------------------------------------------------   762
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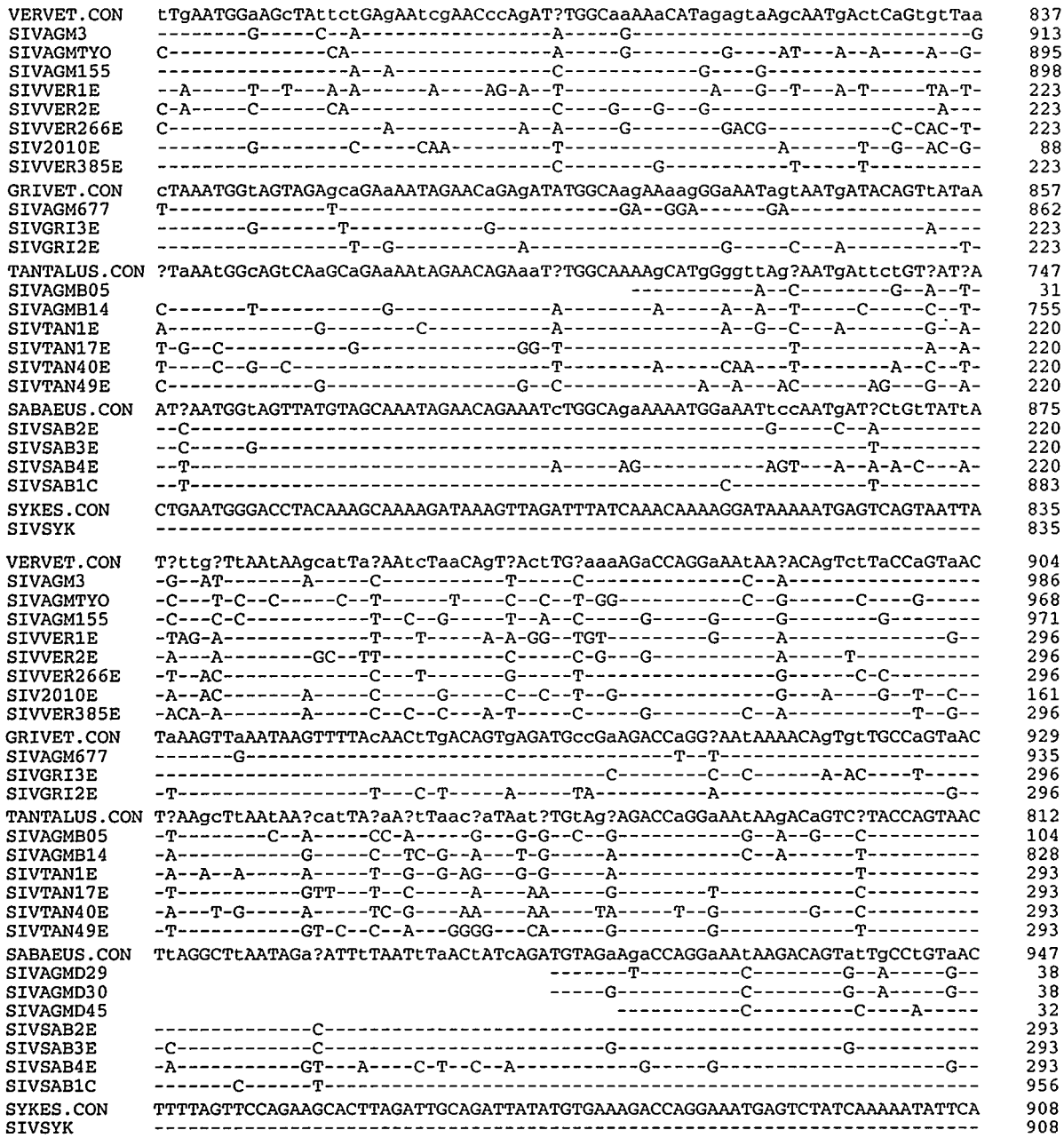

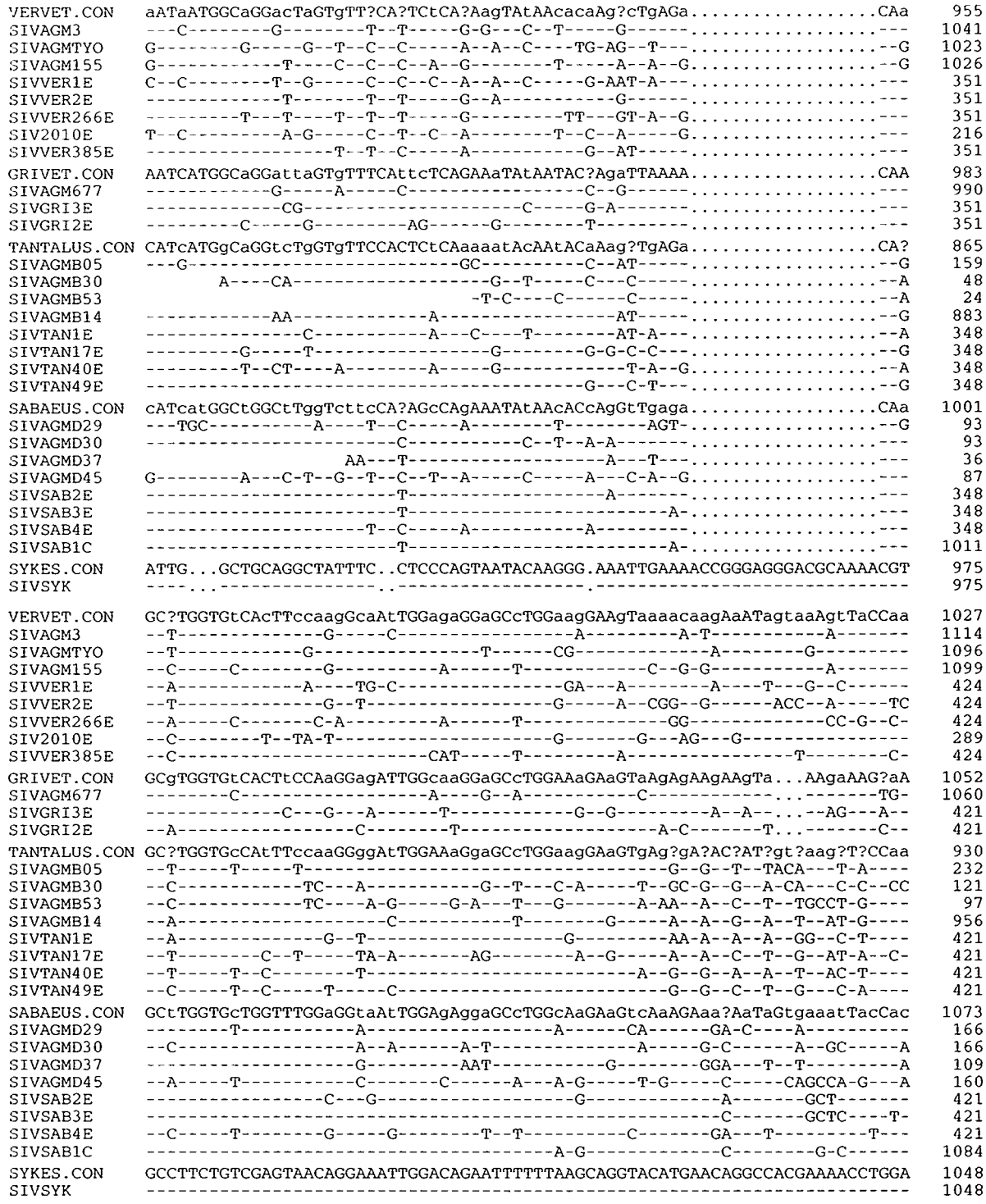

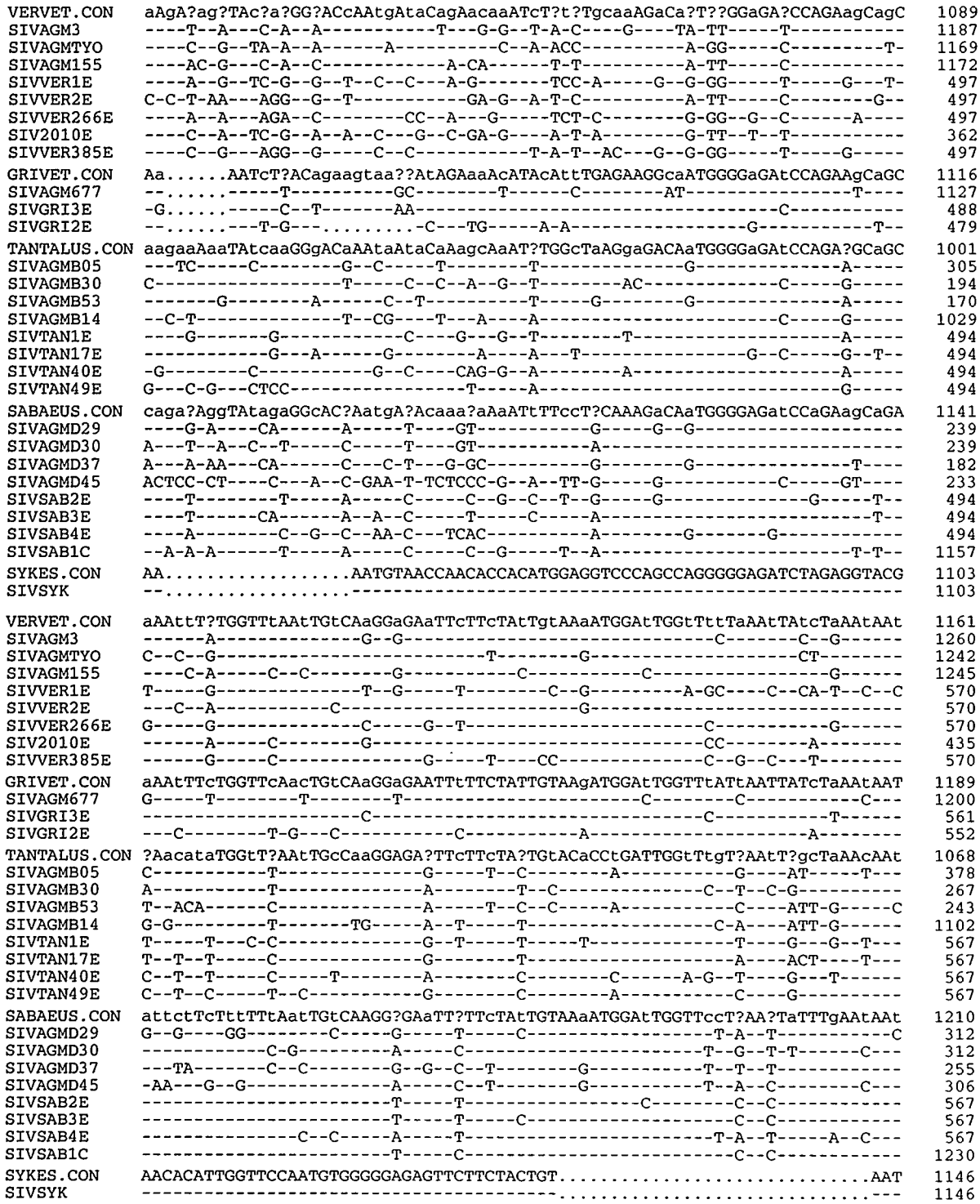

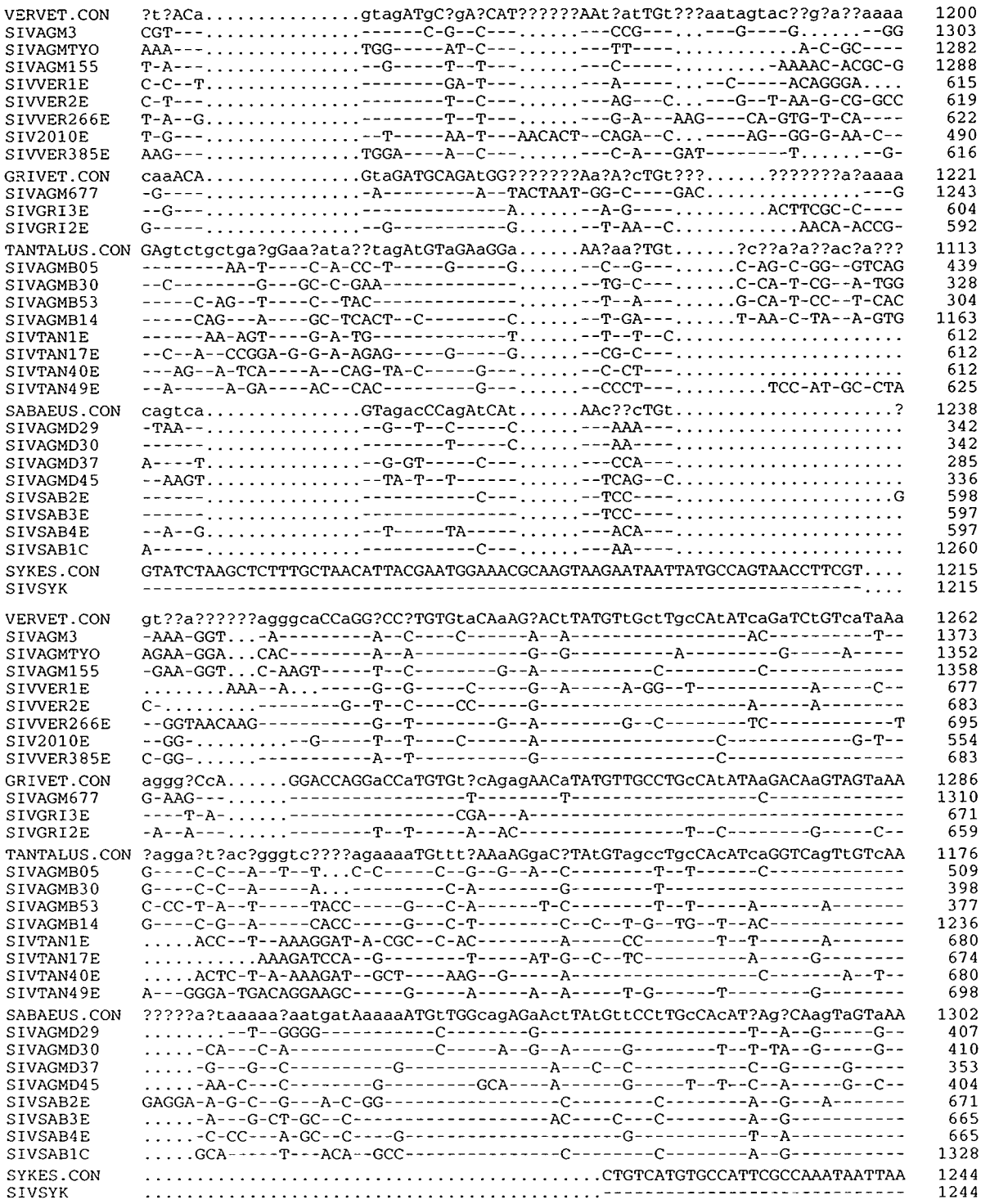

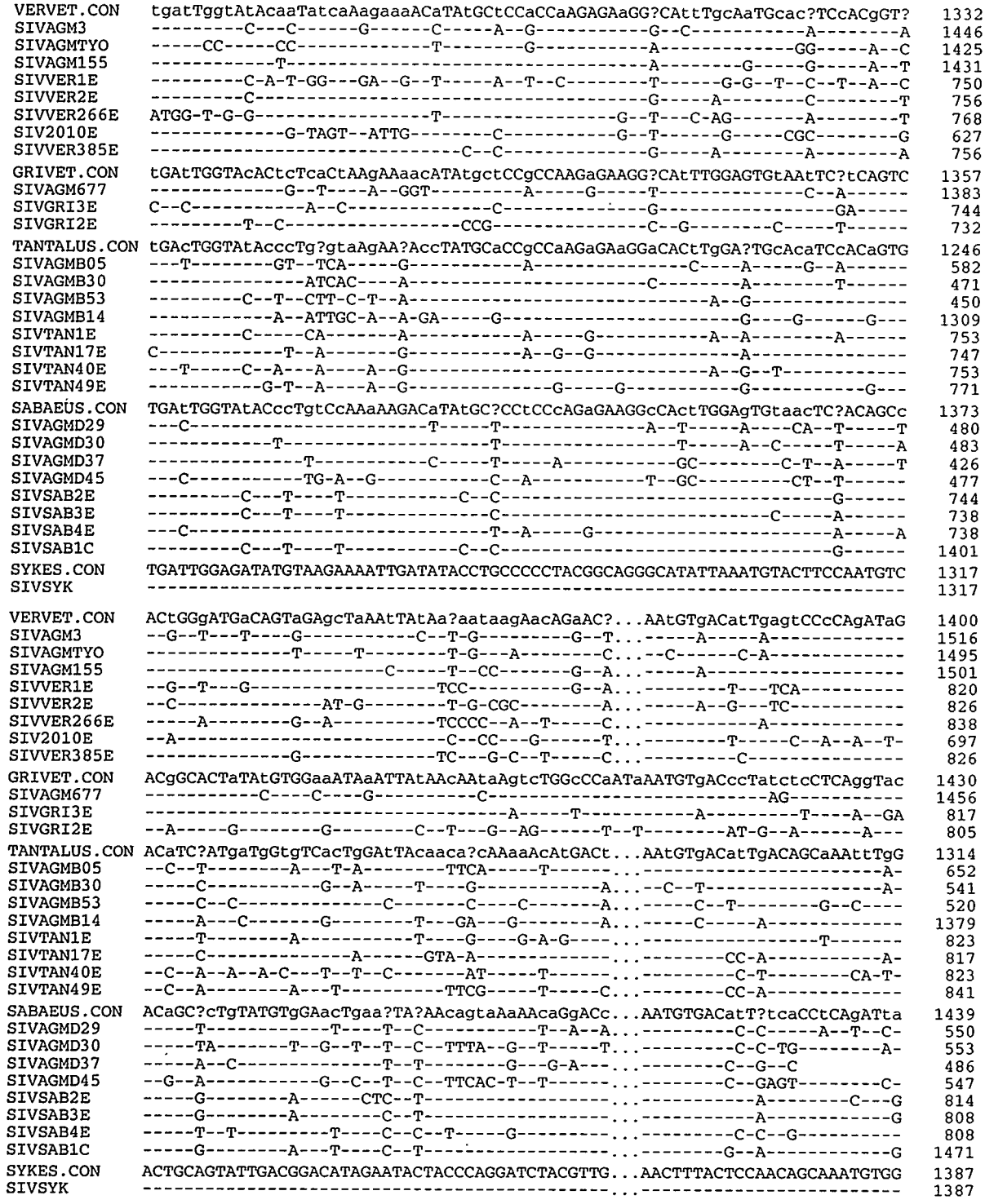

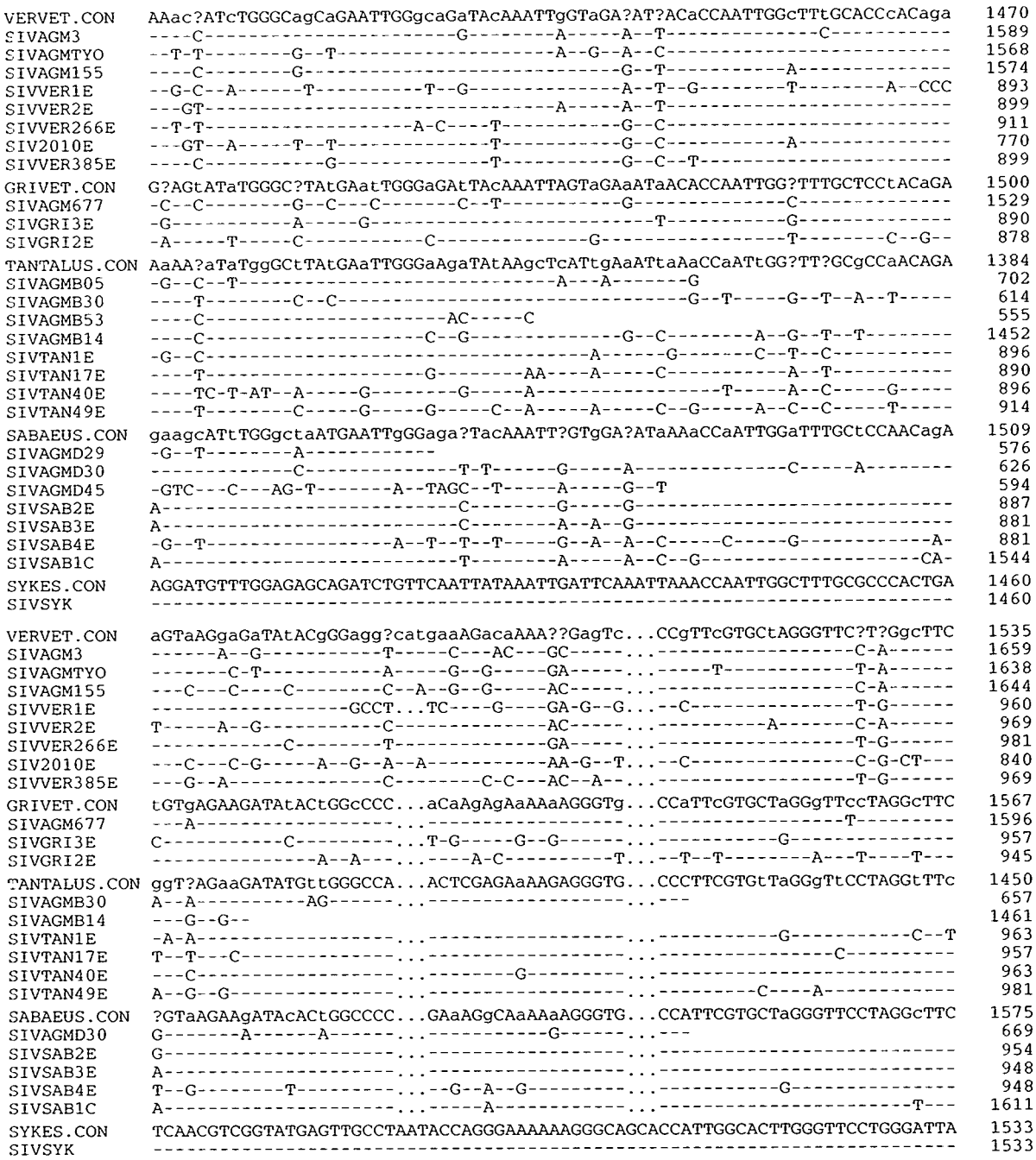

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VERVET.CON    TTgGGaGCtGCtGGaACTGCAATGGGAGCAgCGGCgAcagccCTGACGGTCCAGTCtCaGcATTT?CTTGCTG  1607
SIVAGM3       --A----------G-------------------------------------------------A-------  1732
SIVAGMTYO     -----G-------------------------------GCAG---------------C-G------G-------  1711
SIVAGM155     --------------G-----------------------------------------------A-------  1717
SIVVER1E      ----------A--C-------------------T--G--G----------------------G-------  1033
SIVVER2E      -----G-----------------------A-----------------------------------A-------  1042
SIVVER266E    -------------------------------------------------------------A-------  1054
SIV2010E      -----G--A--A--C-------------------------------------------G----G         906
SIVVER385E    -----------------------------------------------------------------G-------  1042

GRIVET.CON    TTgGGaGCtGCTGGaACTGCAATGGGCGCAGCgGCgACAgCgCTGACgGTCCAGTCTCGGCATTTgCTTGCTG  1640
SIVAGM677     ----------------------------------A---A-------A------------------------  1669
SIVGRI3E      --------------C-------------------------C----------------------A-------  1030
SIVGRI2E      --A--G--A-----------------------T-------------------------------------  1018

TANTALUS.CON  TTGGGacgAGCTGGAGCTGCAATGGGTGCaACAGcgACaG?GTTGACGGTCCAGTCtCAGCAATTACTTGCtG  1522
SIVTAN1E      -----GGC-----------------------------------C---------------C--------------A-  1036
SIVTAN17E     ------------------------------------------A-------------------------------  1030
SIVTAN40E     ----------------------------G----------C-------------------------------  1036
SIVTAN49E     ---------------------------------AA--G-A-------------------------------  1054

SABAEUS.CON   TTGGGAGCAGCTGGAGCTGCAATGGGTGCAGCGGCGACAGCCCTGACGGTCCAGTCTCAGCAgTTACT?GCTG  1647
SIVSAB2E      ------------------------------------------------------------------C----  1027
SIVSAB3E      ------------------------------------------------------------------T----  1021
SIVSAB4E      ------------------------------------------------------------A-----T----  1021
SIVSAB1C      ------------------------------------------------------------------C----  1684

SYKES.CON     CTCTCGGCTGCGGGCACTGCAATGGGGGGCGCTGCGACAGCGCTAACACTCCAGTCTCAGACTTTGTTGGCTG  1606
SIVSYK        ----------------------------------------------------------------------  1606

VERVET.CON    GGATAcTGCAGCAGCAgAAGAAtcTGCTGGCGGCtGTGGagGCTCAACAgCAgATGTTGAAGCTGACCATtTG  1680
SIVAGM3       ----------------------------------------------------------------------  1805
SIVAGMTYO     ----------------------------------------------------------------------  1784
SIVAGM155     -----T-----------------------------------GA-------------------------------  1790
SIVVER1E      -----T----------------CT----------A-------------A--A----------------A--  1106
SIVVER2E      ----------------A------T-------------------------A--------------------  1115
SIVVER266E    ----------------------------------------A-----------------------------  1127
SIVVER385E    ----------------------------------------------------------------------  1115

GRIVET.CON    GGATATTGCAGCAGCAGAaGAActTGCTGGcGGCTGTGGAgCAGCAaCAACAgcTGTTGAAGCTGACCATTTG  1713
SIVAGM677     ----------------------------------------A------------T-----------------  1742
SIVGRI3E      ------------------------------T---------------------------------------  1103
SIVGRI2E      ------------------G---TC----------------------G-----A-----------------  1091

TANTALUS.CON  GGATaTTGCAGCAGCAGAAGAATCTGCTGGCGGCaGT?GAGCAGCAGCAGCA?ATGCTAAAGCTCACCATTTG  1593
SIVTAN1E      ----G-----------------------------------T--------------G---------------  1109
SIVTAN17E     ---------------------------------------A--------------A---------------  1103
SIVTAN40E     ---------------------------------T--A--------------A---------------  1109
SIVTAN49E     ---------------------------------------T--------------G---------------  1127

SABAEUS.CON   GGATA?TGCAGCAGCAGAAAAATCTGCTTGCGGCTGTAGAGCAGCAGcagCAAATGCTAAAGCTCAC?ATtTG  1718
SIVSAB2E      -----C-------------------------------------...-----------------C-----  1097
SIVSAB3E      -----T-------------------------------------------------------------C-----  1094
SIVSAB4E      -----T-------------------------------------------------------T--C--  1094
SIVSAB1C      -----C-------------------------------------------------------T-----  1757

SYKES.CON     GGATAGTGCAGCAGCAGCAAAAGTTGCTGGAGGCAGTTGAGGCACAGCAACACCTCTTAGGCTTAACTGTCTG  1679
SIVSYK        ----------------------------------------------------------------------  1679

VERVET.CON    GGGTGTgAAAAACCTCAATGCCCGCGTCACAGCtCTTGAGAAGTACCTaGaGGAtCAGGCaCGgtTaAAcgCt  1753
SIVAGM3       ----------------------------------------------------C-----G-----G--T---  1878
SIVAGMTYO     ------T-------------------------C-------------------------AC-----T-C  1857
SIVAGM155     ------------------------------------------------G-C-------------------  1863
SIVVER1E      ----------                                                               1116
SIVVER2E      ----------                                                               1125
SIVVER266E    ----------                                                               1137
SIVVER385E    ----------                                                               1125

GRIVET.CON    GGGTGTgAAAAACCTCAATGCCCGCGTCACAGCTCTCGAGAAGTACCTAGAGGATCAGGCACGGCTAAATTCA  1786
SIVAGM677     ----------------------------------------------------------------------  1815
SIVGRI3E      ----------                                                               1113
SIVGRI2E      ------A---                                                               1101

TANTALUS.CON  GGGTGTGAAA                                                              1603
SIVTAN1E      ----------                                                               1119
SIVTAN17E     ----------                                                               1113
SIVTAN40E     ----------                                                               1119
SIVTAN49E     ----------                                                               1137

SABAEUS.CON   GGGTGT?AAaAACCTCAATGCCCGCGTCACTGCTCTTGAGAAATACCTAGAGGATCAGGCACGGTTGAACATT  1790
SIVSAB2E      ------G---                                                               1107
SIVSAB3E      ------A---                                                               1104
SIVSAB4E      ------G--G                                                               1104
SIVSAB1C      ------A-----------------------------------------------------------------  1830

SYKES.CON     GGGTGTCAAAAACCTTAACGCCCGGCTCACAGCTTTAGAGACGTATCTCAGAGACCAGGCCATCTTGTCAAAT  1752
SIVSYK        ----------------------------------------------------------------------  1752
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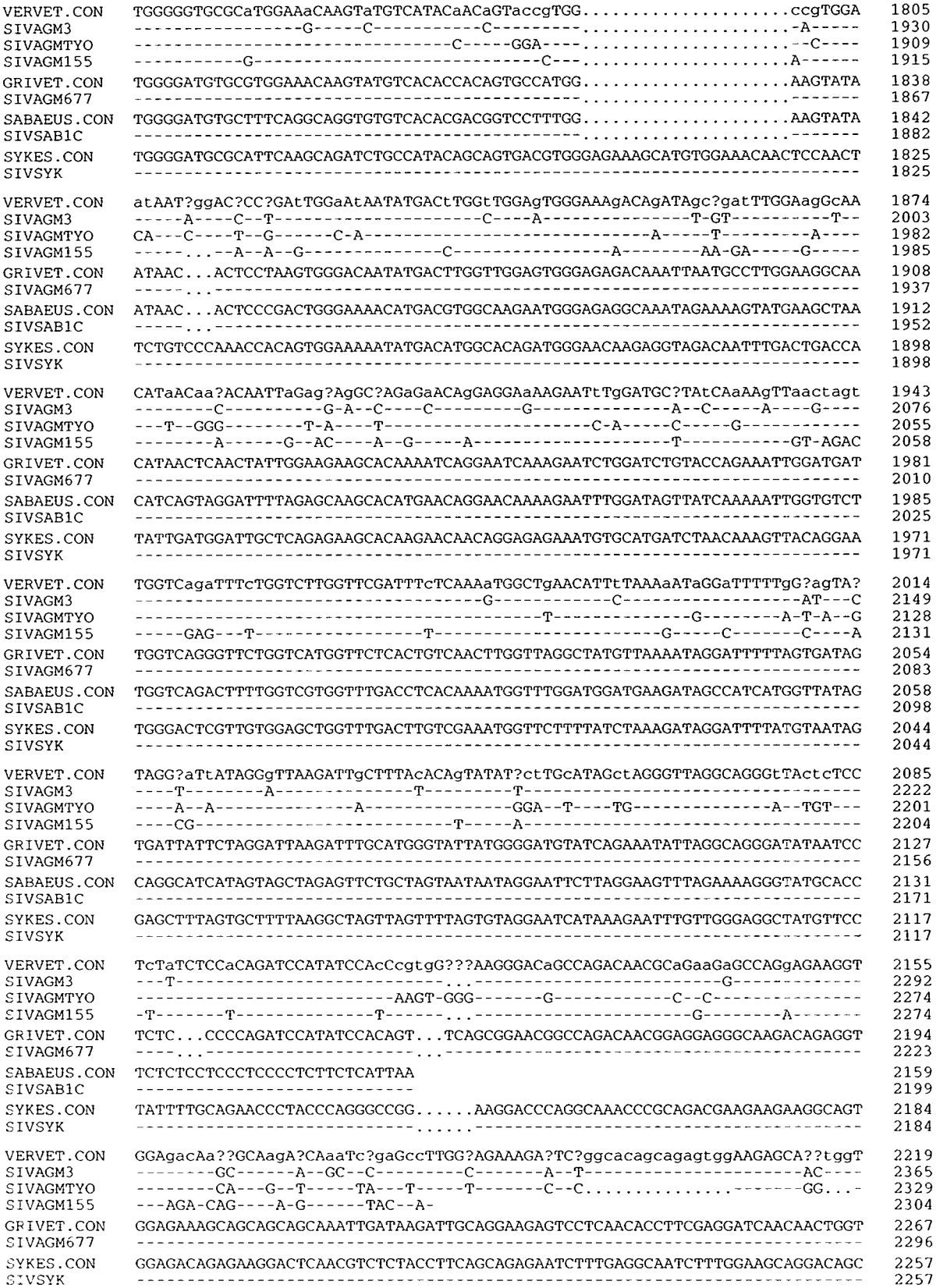

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VERVET.CON   G?A?GC??TTGACC???TGG????CGA????CA?CA??TGGCTATACAACAGTTGCCTGACCCTCCT??TTCA  2272
SIVAGM3      -C-A--GA------AAT---TGCT---TCAG--G--TC-----------------------------AG----  2438
SIVAGMTYO    -T-T--AG------GCC---CTGA---GGCT--A--CT-----------------------------CA----  2402
GRIVET.CON   GGCTCAACTTCAAGAGCTGCAGCTTGAGAATAAGGACTTGGTGTTACAACATCTGCCTGACCCTCCTCATATT  2340
SIVAGM677    ------------------------------------------------------------------------  2369
SYKES.CON    AGCTTTGGAGGACAGTC.........................TGCAGCAGCTTCAGATCTCTGATTAGACA  2303
SIVSYK       -----------------.........................----------------------------  2303

                 <- rev          nef cds ->
VERVET.CON   ?CTTAGGA??GCTTT?CA?TAC?T?CAATATGGGCT?G??GAACTCAAA?CCG??GCACAAGAA??A?T????  2325
SIVAGM3      T-------GC-----C--G---A-A-----------T-GG---------G---CA---------GC-G-TGTC  2511
SIVAGMTYO    G-------AA-----T--A---C-G-----------C-CA---------A---GC---------AT-C-CCAA  2475
GRIVET.CON   CATCAGGACAGCAGTGGGATACCTGCAGTATGGGCTCCAGCAACTCCAAGAGGCAGCAACAGGGCTTGCTCAA  2413
SIVAGM677    ------------------------------------------------------------------------  2442
SYKES.CON    GCTTACTATCACCTGGGGATTCATCAGCTATGGGTTCAACGAGCTCAAAATCGCAGCAGCTTCGCTCGGAAGG  2376
SIVSYK       ------------------------------------------------------------------------  2376

VERVET.CON   ?CT?TGGCA?GC?TTGCACAAAACGC??G??ACCAGATATGGCTTGCTTGCAGATCCGCTTATAGG???ATC?  2386
SIVAGM3      G--T-----C--C-------------GG-CT-----------------------------------GCA---A  2584
SIVAGMTYO    A--C-----G--G-------------AT-TC-----------------------------------AAC---G  2548
GRIVET.CON   GCTCTGGCGAGGGCTGCGAGGGAAGCCTGGGGCAGACTGGGTGCTATTGTCCGATCCGCTTATCGGGCAGTCA  2486
SIVAGM677    ------------------------------------------------------------------------  2515
SYKES.CON    GAAATACGCGATTGGGTGGCGGCTATTTGGCAAGCAATATACGCCGCTACCAGACGAGTTGTCGAGGCCGTTG  2449
SIVSYK       ------------------------------------------------------------------------  2449

VERVET.CON   TCAAC??TCCAAGAAGAGTGCGACAAGGCCTTGA?G?AATCCTTAAT                            2429
SIVAGM3      -----TC----------------------------A-G----------                            2631
SIVAGMTYO    -----AG----------------------------G-A-------                            2592
GRIVET.CON   TCAACAGTCCAAGAAGAGTGCGGCAAGGCCTTGAAAAAGTCCTGGGG                           2533
SIVAGM677    ---------------------------------------------                            2562
SYKES.CON    CAGCCTTGCCGCGGAGGCTTCGACAAGGCTTGGAGATCTACCTTAAC                            2496
SIVSYK       ---------------------------------------------                            2496
```

SIVSAB1C

```
LOCUS       SIVSAB1C    10036 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) complete genomic sequence,
            African green monkey isolate SIVagmSAB-1.
ACCESSION   U04005
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild female asymptomatic sabaeus
            African green monkey captured in its natural habitat of Senegal.
REFERENCE   1  (bases 1 to 10036)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus sab-1 was derived from a wild female asymptomatic sabaeus
            African green monkey.  She was caught in her natural habitat of
            Senegal and susequently exported to the United States.  From the
            point of capture and throughout the study, she was housed in an
            individual cage.
            Phylogenetic analysis suggests that each AGM species is infected
            with a distinct subtype of SIVagm.  Interestingly, the sabaeus viral
            genome seems to be a mosaic of many viruses infecting different
            primate species [1].  Virus sab-1 forms a distinct lineage in the 5'
            end of gag, clusters closest to the HIV2/SIVsm group in the 3' gag
            and 5' pol regions, and clusters closest to the other SIVagm
            lineages in the 3' pol, env and nef regions [1].  This feature
            was demonstrated for two viral sabaeus strains, sab-1 and sab-D37
            (sequenced only over the 5' end of the pol gene).  Jin et al.
            conclude that an ancestor of the sabaeus virus was a recombinant
            with two breakpoints: one roughly at codon 310 of gag and the other
            at 710 of pol.
            NCBI gi: 466229
BASE COUNT     3293 a   1975 c   2517 g   2251 t
ORIGIN
        1 tggaagggat ttattacagt gaaaggagaa agaagatctt ggatctctat gctcttaatg
       61 agtggggcat agtagatgga tggcagaatt atacagatgg gccaggtacc aggtacccaa
      121 agtgctttgg atggtgcttt aaactggtac ctgtggacct gtcagaggag gctaagaata
      181 gtgagaacca ctgcctgctg catcctgctc aagtggccta tgaggatgac gcctggaaag
      241 agaccctggt gtggaagttt gacccactac tagcagtgga ctatgttgct tggaggctgc
      301 acccagagca ggtgccgtca gcacaaggct aaccacaaaa ccacatccta tggagttgtc
      361 atggtgatga cattaagaac tgctgactga gaGGGACTTT CCAGGGTGGA GAcTGGGCGG
                                       NFkb ->       <--> Sp1   <- -> Sp1
      421 TACTGGGAGT GGcttgcccc gtgctgctca aTATAAgcag ctgctttgcg cctgtaaaac
           <--> Sp1  <-              signal ->
      481 agtctctgct tggaggctgc cagattgagc ctgggtgttc tctggtaagt ctgaaccagc
                             ->      TAR I             <-          ->
      541 ttgagcctgg gtgttcgctg gggaaggcaa gcctaagagc actctggtga ggtcttggta
            TAR II            <-
      601 gaccctcgcc tggcgactgg ccattgccag tagcagagac tccgcttgct tgcttgattg
      661 cctcAATAAA gtcttgcctt agtttacaag taaagcaagt gtgtgcccat ttattcctca
       signal ->
```

```
 721 ggacaaccct ggttactaag gatccctgat agaaaaaatc cttagcagtg gcgcccgaac
                                                      <- LTR end
 781 agggacttga ctaaagacgt cccggccgca gagtagacca gcctgaggac tcctttgact
 841 gagtaagacc ggacggaaga aaggcggacc gtgccggagt gcaggtaaga ggcgcctgcg
 901 gacccgagac accctcgggc tgtgtgtgtg tgagaagaga ggaaaaagag aagtcagaca
 961 gggctgacaa ggctggctta gcagtggcag aaggctaggt cgagcgggaa aggaaaATGg
                                                    gag cds start ->
1021 gtgcgagtaa ctcagtctta agtggtagga aactagatgc attcgaatca gtcaggttac
1081 ggcccaacgg aaagaagaag tataagttaa gacatctagt atgggcaagc aaggaactag
1141 atcgatttag cctttcagca aatctcttag agacaaagga aggggtcgtc aaaattctta
1201 gtgtactcct tcccctagtt cctacagggt cagagaattt aattgctctc tttaatttat
1261 gctgcgtgtt agcttgtatt cacgcagaaa taaaagtgaa agatacagag gaagcaaaag
1321 cgaaagtaaa agaggaagtg ccagcagaaa tgacagaaag tgccacagcg acatctagtg
1381 gccaaactaa ggaactgcag gcaaaaaaga aaaatgagcc aacagtgaca cctagtggtg
1441 gctcgcgaaa ttaccccatt gtcagtgtta ataatcaatg ggtccaccag ccattgtccc
1501 caaggacact taatgcttgg gtaaaagtga ttgaggaaaa gaagttcagt gcagaggtag
1561 tacccatgtt tagcgcccta gcagaaggag ctatccctta tgatatcaat caaatgctca
1621 atgcagtagg agaacaccag ggggcactac aaatagtgaa agatgttatc aatgaagaag
1681 cggcagattg ggaccttaga cacccgccgc cgcaacagcc cccagctcag ggagtgctaa
1741 gggacccaca agggtcagac atagcgggca ctactagcac aatacaagag caaatagaat
1801 ggaccaccag agcacagaat gctgtcaatg taggaaatat ttataaagga tggatcatcc
1861 tgggtctcca gaaatgtgtc aaaatgtaca acccagtaaa cattttagac attaaacaag
1921 ggcctaaaga acctttcaag gattatgtag atagattcta caaggctctg agagcagagc
1981 agacagaccc tgctgtaaag aactggatga cacagtctct gttgatccag aatgccaacc
2041 cagattgtaa gacagtgctc aaagggttag gcatgaatcc aaccctagaa gagatgctta
2101 ctgcatgcca aggcattgga ggagcacaac ataaggcacg tctaatggcg gaagctatga
2161 cagcggcctt tcagcaacaa acagttggga acatctttgt gcagcaaggg gcaagaccca
2221 ggggtccctt agggggaaga ggtagacctc tgaacccaaa tattaaatgt tacaattgtg
2281 gaaagcctgg tcacctggct agattttgta aggcccctag gagacaaggc tgctggaaat
2341 gtggcagccc agaccatcag atgaaagatt gtcaaaaaca ggtTAAtttt ttagggtttg
                                        pol orf start  -> (NH2 terminus
                                                           unknown)
2401 gcccctgggg cagagggaaa cccaggaatt tccctctgac ctccatcaga ccaacagctc
2461 ccccaatgga acgggattac agcaggccgg aggaaaattg gtatgcagac agacctccga
2521 ccagaggacc agggccagac gatccagcaa cagccctgtt aaagcagtat gctgttcagg
2581 ggaaacggca gaaacagcag tggcaaaacc actcgccaca acagagcccc tacgaggagg
2641 cttacagctc cctcaggtct ctctttggag aagaccaaTG Aaaactgtgt acatagaggg
                                                 <- gag cds end
2701 acagaaagtc actgctctat tagacacagg agcagatgac tcagtaatac agggtataga
2761 attaggagac aattggaaac caagaataat tggaggaata ggaggatgta ttaatgtaaa
2821 agcataccac aatcaggagg taaaaataga agataaaact tgtaaagcta ccattttggt
2881 aggagaaaca ccagttaata ttataggaag aaatgtctta gcacaattag gagttactct
2941 aaatttgaca caaagagaga tagaacctat aaaagtccac ttaaagccag gacaagatgg
3001 gccaaggata aggcaatggc ctttgtcaaa agaaaaaata gaggccttaa aggccatttg
3061 tgaagactta gaaaaacaag gacatttgga aagaataggg ccagaaaatc catataacac
3121 cccagtcttt gcaataagga agaaagataa aactcagtgg agaatactca tggacttcag
3181 gcagttaaat aaaagtactc aagactttca ggaagtccag ttagggatac cccacccagc
3241 aggcttacag caaagggagc agattacagt gttggacata ggagatgcct attttagctg
3301 ccctttagat ccagactttc agaaatatac agcattcacc atcccatcag tcaataatag
3361 ggagccaggc ataagatatc agtataaggt gctcccacag gggtggaaag gctcacccac
3421 aatttttcag acaacagcca acaaaattct gcaggaattt aggcaaaaga acccagatgt
3481 agatatatat caatacatgg atgatatgtt aatagccagt gataggccaa aggcagaaca
3541 tctagtaatg gtacagcagt taagagacta tctagaaact tgggggttta aaacccctga
3601 aaagaagttt caaaaggatc caccatacct ctggatgggg tatgaattgt atccaaagaa
3661 atggcaactg caggagatca ccctaccaga aagggaagaa tggacagtga atgatattca
3721 aaaattagta ggaaagttaa attgggcaag tcaaatttac acagggataa agactaaaca
3781 tttgtgtaga ctaattagag gagctagacc tttgacagag atagtccaat ggacagaaga
3841 ggcagaacta gaattagaag aaaatagaca gatcttaaga caaaagcagc agggacaata
3901 ttatgaccct gctcttcctt taagggctaa ggttcttaaa ctgggagatg gccaatgggg
```

SIVSAB1C

```
   3961 atatcagata taccagccag aaaataaaat actgaaggtt ggcaaatatg caaaaatcaa
   4021 aacagcacac accaatgaat taagaatgtt agcaggccta gtacagaaga taggaaagga
   4081 aagcatagtc atctggggac agatacctat tatggaactg ccagtagaaa gagagctctg
   4141 ggaacaatgg tggtctgact attggcaggt cacctggatc ccggaatggg aaatggtcag
   4201 tactcctcaa ttgattagat tgtggtacaa attagtaaaa gatcccatcc caggagaagc
   4261 agtctattat gtagatgggg cagctaatag aaattccaaa gaaggaaaag caggatactt
   4321 aacagataga ggggatcaaa aggtggtagc attagagaat actaccaacc agaaagcaga
   4381 gttagaggcc attctgttag ccttaagaga ctctggaagc aaagtaaata taataacaga
   4441 ctcacaatat gctatgggta ttatagcagg ggaacctaca gaatcagata ataacatagt
   4501 acaacaaatt atagaggaac taataaagaa ggaggcagtg tatatagcat gggtacctgc
   4561 ccataaagga gtaggtggca atgaggaaat tgataaacta gttagtcaag gaataagaca
   4621 agtactattc ctggacagaa ttgaagaagc acaagaagag catgataaat accatgccaa
   4681 ttggaggagt atgcaacaag aatttggctt acctgctata gtagcaaaag aaatagtagc
   4741 ggcatgtcct aaatgccaga taaaagggga gtctgtacat gggcaagtag atgctagtcc
   4801 aggagtgtgg caaatggatt gtacacacct agaaggaaaa atcatcatag tggctgttca
   4861 tgttgctagt ggatttatag aagcagaagt aatcccacag gaaacaggaa aagctacagc
   4921 acacttcctg ctgaagttag ccagcagatg gcccatcaca cagctgcata cagataatgg
   4981 taccaacttt actagccagc aagtagcagc tatttgctgg tggggaaaaa tagagcacac
   5041 atttggggta ccctacaacc cccaaagtca gggagtagta gaatctatga ataagcagtt
   5101 aaaagaaatc ataggacaaa ttagagatga tgcagaaaga ttggaaacag cagtcataat
   5161 ggcagtgcac attcacaatt ttaaaagaaa agggggggatt gggggtact ctgcagcaga
   5221 aagactaatc aatataatac atacagaact agaaaccaaa acacttcaac aaaaaatttc
   5281 aaaaattcaa aattttcggg tctattacag ggaaggcaga gaccctgtgt ggaaaggtcc
   5341 ggctaagctc atctggaaag gagaaggagc agtagttata caagaacagg gtgaattgaa
   5401 aacaatccca agaagaaaag ccaaaattat aaaagattAT Ggaaaagcat tggatagtca
                                  vif cds start ->
   5461 ggcccctctg gaaggtaacg ggcggacagc aggagaggtg gacTAGccta gtgaaatacc
                                                      <- pol cds end
   5521 acatgcatgt gtccaaacag tgtgttcatt ggcggtatac ccctcatact aaaataagat
   5581 ggaattggta ctcctatcaa gaatgggtca tacccctgaa ggatggagct ctaataaaag
   5641 ttactaatta ttggcattta accccagaga aaggatggtt agaaacctat gcaacaggaa
   5701 taggatacag taaaggggaa tggtttacag agcttgatcc ttggacagcg gaccatatta
   5761 ttcattggtc ctatttcccc tgttttacag atagagctgt ccaacaagcc atcaggggag
   5821 aaaagtatct ttggtgtaaa caccaggtgg gacatcagcc aacagggcaa gtaccatcat
   5881 tacagtattt agcacttagg gtatatacaa ATGgcctcag gagggtggct cccaccagta
                           vpX cds start ->
   5941 ggaggggatc ctcccaagga tccccccaag aatcccagag aagagatacc aggatggcta
   6001 gaaacatggg atttgcccag agagccgttc gacgaatggc tccgagacat gttacaggac
   6061 ctcaattcag aggcccagtg ccacttccca aggaatctcc ttttccgtct ttggtggaat
   6121 attgtggaag aaccagccat TGAtcatggg caaaccaggc tggaaggctg gtataaatat
                              <- vif cds end
   6181 tgtagaattc tgcaaaaggc tttatttgtg catatgaaag gtagatgttg taagccaaag
   6241 actcaccctg cgtATGgacc aggagcagga ggcccgcccc caggtctggg aggagcttca
        tat cds start ->
   6301 ggaggagctg catcggccgc tccaggcctg TGAtaatact tgcttctgca aagtttgctg
                                        <- vpX cds end
   6361 ctttcattgt attctctgct tccataaaaa ggccctaggc attcgctatt ATGtccctag
                                                rev cds start ->
   6421 gccaagaaga gcttctaaga agatttcgca taatcaagtt tctctacaca acTAGTaagt
                                                           5' sj /\
                                                              <- tat cds
   6481 ATGaagcttc ttacagtact gctttggcta agtgggtgtt ggagcttagt gtggttagtc
env cds ->
   6541 cagtatgtta cagtgtttta tggtatccca gtatggaaaa atagttcagt ccaagccttt
   6601 tgtaagaccc ccaatacgaa cctatgggcc tctactaatt gcatccccga tgatgaacca
   6661 gaaggaacaa tagcagaagt acccatacct aatatcacag aaaaatttga tgcttggaaa
   6721 aatcggaacc ctctagtagg ccaagcagag agtaacatac acctttttgtt tgaaagtact
   6781 ttaaagccat gtgttaagct ctcaccaatg tgcataaaaa tgaactgcta tcgcttagaa
   6841 ggaggagcag caacaacaac atcaccatca acatcaacag cacgccccga ggtagtgagt
```

```
6901 gtgggcttta atgactcagt gatagaacaa gagatggaaa aagaacaggc catgaactgt
6961 tcctttgcta tggcaggata tagaagggat gtaaagaaaa attactcaac agtatgggat
7021 gatcaagagg tggtttgtga agagggaagg gaaaaatcaa acgcaacaca tactgtggga
7081 tgttacatga tccattgtaa tacctcagta atcaaagagg cttgtgataa aacttattgg
7141 gataccttta ggcttaggta ttgtgctcca gcaggttatg ctttgctaag atgtgcagat
7201 acagattatt caggacataa ggcatgtagg aatgtaacag tatcagcttg cactaggtta
7261 atcaatacta ctgtaagcac aggaatagga attaatggta gttatgtagc aaatagaaca
7321 gaaatctggc agaaaaatgg caattccaat gattctgtta ttattaggct caatagatat
7381 tttaatttaa ctatcagatg tagaagacca ggaaataaga cagtattgcc tgtaaccatc
7441 atggctggct tggtcttcca tagccagaaa tataacacca ggttgaaaca agcttggtgc
7501 tggtttggag gtaattggag aggagcctgg aaggaagtca aagaaacaat agtgagacta
7561 ccaccaaaaa agtatagtgg cacaaatgac acaaacaaga tttttctaca aagacaatgg
7621 ggagatccag aatctgaatt cttctttttt aattgtcaag gtgaattctt ctattgtaaa
7681 atggattggt tcctcaacta tttgaataat aagtcagtag acccagacca taacaactgt
7741 gcaaaaaata atacaaagcc atgttggcag agaacctatg ttccctgcca cataaggcaa
7801 gtagtaaatg attggtacac cttgtctaaa aagacatacg cccctcccag agaaggccac
7861 ttggagtgta actcgacagc cacagcgctg tatgtagaat tgaactataa cagtaaaaac
7921 aggaccaatg tgacgttatc acctcagatt gaaagcattt gggctaatga attgggagat
7981 tacaaattag tggaaatcaa gccaattgga tttgctccaa ccaaagtaag aagatacact
8041 ggccccgaaa gacaaaaaag ggtgccattc gtgctagggt tcctaggttt cttgggagca
8101 gctggagctg caatgggtgc agcggcgaca gccctgacgg tccagtctca gcagttactc
8161 gctgggatac tgcagcagca gaaaaatctg cttgcggctg tagagcagca gcagcaaatg
8221 ctaaagctca ctatttgggg tgtaaaaaac ctcaatgccc gcgtcactgc tcttgagaaa
8281 tacctagagg atcaggcacg gttgaacatt tggggatgtg ctttcaggca ggtgtgtcac
8341 acgacggtcc tttggaagta taataacact cccgactggg aaaacatgac gtggcaagaa
8401 tgggagaggc aaatagaaaa gtatgaagct aacatcagta ggattttaga gcaagcacat
8461 gaacaggaac aaaagaattt ggatagttat caaaaattgg tgtcttggtc agacttttgg
8521 tcgtggtttg acctcacaaa atggtttgga tggatgaaga tagccatcat ggttatagca
8581 ggcatcatag tagctagagt tctgctagta ataataggaa ttcttaggaa gtttagaaaa
8641 gggtatgcac ctctctcctc cctcccctct tctcatTAAc AGatccatat ccacctggac
                                                  /\ 3' sj
                                              <- env cds end
8701 aagggacagc cagacaaaga agaagagcaa ggcagcggtg ggctaaacag cgacagcagg
8761 tcatacactt ggcagagaga attcttgaga cacctgtgtc acagattgat cacttggctc
8821 aggaatttga ccagttggtt ctcgacaatc ttcagcaacc tccatcgctg cctccaggac
8881 atccaacaga gaaccagaca gctaacagct catctTGAat ATGggtggca agagctcaaa
                                                 <- rev cds end
                                       nef cds start ->
8941 gcagcagcag cgtcactcac tgtggctgtg gtccaagctg cgacaagcgc cagtgattca
9001 gtacgacatg cttgcagatc cattgttagg gcagtcatcg cacatccaag aagaatgcgc
9061 caagagcttg agagatggtt taattaggca aggagactcc tctagaacag aagaaggtgt
9121 aaaaatgaaa catcaaggaa gacagccctc gtggtatgat gaggatgaag aagaagtagg
9181 ctttccagta aggccttgct taccactacg agcaatgaca tataagttgg caatagactt
9241 tggccacttt ttaaaagaaa agggggggact ggaagggatt tattacagtg aaaggagaaa
                                  LTR start ->
9301 gaagatcttg gatctctatg ctcttaatga gtggggcata gtagatggat ggcagaatta
9361 tacagatggg ccaggtacca ggtacccaaa gtgctttgga tggtgcttta aactggtacc
9421 tgtggacctg tcagaggagg ctaagaatag tgagaaccac tgcctgctgc atcctgctca
9481 agtggcctat gaggatgacg cctggaaaga gaccctggtg tggaagtttg acccactact
9541 agcagtggac tatgttgctt ggaggctgca cccagagcag gtgccgtcag cacaaggcTA
9601 Accacaaaac cacatcctat ggagttgtca tggtgatgac attaagaact gctgactgag
    <- nef cds end
9661 agggactttc cagggtggag actgggcggt actgggagtg gcttgccccg tgctgctcaa
9721 tataagcagc tgctttgcgc ctgtaaaaca gtctctgctt ggaggctgcc agattgagcc
9781 tgggtgttct ctggtaagtc tgaaccagct tgagcctggg tgttcgctgg ggaaggcaag
9841 cctaagagca ctctggtgag gtcttggtag accctcgcct ggcgactggc cattgccagt
9901 agcagagact ccgcttgctt gcttgattgc ctcaataaag tcttgcctta gtttacaagt
9961 aaagcaagtg tgtgcccatt tattcctcag gacaaccctg gttactaagg atccctgata
10021 gaaaaaatcc ttagca
```

SIV2010E

```
LOCUS       SIV2010E      906 bp    DNA             VRL       24-AUG-1994
DEFINITION  Simian immunodeficiency virus (SIVbab) partial envelope sequence,
            yellow baboon sample SIVbab2010.
ACCESSION   U10897
SOURCE      Simian immunodeficiency virus from PCR-amplified DNA extracted from
            uncultured leukocytes derived from an asymptomatic pregnant female
            yellow baboon from Tanzania.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Jin,M.J., Rogers,J., Allan,J.S., Desrosiers,R.C., Shaw,G.M.,
            Sharp,P.M. and Hahn,B.H.
  TITLE     Infection of a yellow baboon with SIV from African green monkeys:
            Evidence for cross-species transmission in the wild
  JOURNAL   J. Virol. (In press, 1994)
COMMENT     Two wild yellow baboons from Tanzania were identified in a previous
            study with strong SIV(agm) seroreactivity.  They lived in a
            national park where yellow baboons and African green monkeys share
            the same habitat.  In this study, molecular characterization was
            performed for virus derived from one of the SIVagm seroreactive
            yellow baboons (animal 2010) and from two vervet African green
            monkeys (animals ver266 and ver385).  With this aim in mind,
            uncultured leukocyte DNA was PCR-amplified, cloned and sequenced
            over a 672 bp region of gag and a 906 bp region of env for animal
            2010 (only the env region was analyzed for isolates ver266 and
            ver385).  Jin et al. note that the viral strain derived from
            the yellow baboon (animal 2010) clusters with SIV strains of the
            vervet subtype, including ver266 and ver385, and believe that this
            is the first evidence for simian-to-simian cross-species transmission
            of SIV in the wild.
BASE COUNT      308 a    163 c    220 g    215 t
ORIGIN      approximately 862 bp downtream from the start of env
        1 agtacaggac tattattgaa tgggagctat tccgagaaca aaacccagat ttggcaaaaa
 env cds ->
       61 catagagtaa acaatgattc ggtactgata ttacttaata aacattacaa tctgacagtc
      121 acctgtaaga gaccaggaaa taagacaatc ttgcctgtca ctatcatggc aggaatggtg
            ->              v3 loop equivalent
      181 ttccattccc aaaagtataa taccagactg aggcaagcct ggtgtcattt taatggcaat
                                                          <-
      241 tggagaggag cctgggagga agtgaaaaga gagatagtaa agttaccaaa agacagatat
      301 cagggaacaa acgatgcaca gaagatctat ttacaaagac agtttggtga tccagaagca
      361 gcaaatttat ggttcaattg tcagggagaa ttcttctatt gtaaaatgga ttggttccta
      421 aattatataa ataatttgac agttgatgca aatcataaca ctaacagatg caataagacg
      481 gggaaaacaa gtggagcgcc aggtccttgt gcacaaagaa cttatgttgc ttgccacatc
      541 agatctgtcg ttaatgattg gtatacagtt agtaaattga catatgcccc accaagagag
      601 ggtcatttgg aatgccgctc cacggtgaca gggatgacag tagagctaaa ttataacaac
      661 cagagcagaa ctaatgtgac tttgagccca caaattgaaa gtatatgggc tgctgaattg
      721 ggcagatata aattggtaga gatcacacca attggatttg cacccacaga agtcaggcgg
      781 tatacagggg gacaagaaag acaaaaaagg gttcccttcg tgctagggtt cctggctttc
      841 ttgggggcag caggcactgc aatgggagca gcggcgacag ccctgacggt ccagtctcag
      901 gatttg
        env cds ->
```

LOCUS SIV2010G 672 bp DNA VRL 24-AUG-1994
DEFINITION Simian immunodeficiency virus (SIVbab) partial gag sequence, yellow baboon sample SIVbab2010.
ACCESSION U10899
SOURCE Simian immunodeficiency virus from PCR-amplified DNA extracted from uncultured leukocytes derived from an asymptomatic pregnant female yellow baboon from Tanzania.
REFERENCE 1 (bases 1 to 672)
AUTHORS Jin,M.J., Rogers,J., Phillips-Conroy,J.E., Allan,J.S., Desrosiers,R.C., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
TITLE Infection of a yellow baboon with SIV from African green monkeys: evidence for cross-species transmission in the wild
JOURNAL J. Virol. (In press, 1994)
COMMENT Two wild yellow baboons from Tanzania were identified in a previous study with strong SIV(agm) seroreactivity. They lived in a national park where yellow baboons and African green monkeys share the same habitat. In this study, molecular characterization was performed for virus derived from one of the SIVagm seroreactive yellow baboons (animal 2010) and from two vervet African green monkeys (animals ver266 and ver385). With this aim in mind, uncultured leukocyte DNA was PCR-amplified, cloned and sequenced over a 672 bp region of gag and a 906 bp region of env for animal 2010 (only the env region was analyzed for isolates ver266 and ver385). Jin et al. note that the viral strain derived from the yellow baboon (animal 2010) clusters with SIV strains of the vervet subtype, including ver266 and ver385, and believe that this is the first evidence for simian-to-simian cross-species transmission of SIV in the wild.
BASE COUNT 245 a 141 c 161 g 125 t
ORIGIN approximately 304 bp downstream from the start of gag

```
        1 gtagcaacag taaggcaatg ctgccaccta gtgaaaaaag aaaaaagtgc agcagagaca
 gag cds ->
       61 tctagtggcc gccagaaaaa tgacaggtcc acagcgacat ctagtggaca gagtcagaat
      121 tttcccgcac aacaacaggg aaatacatgg gtacatgtac cactctctcc acgcacgttg
      181 aatgcgtggg taaaggcagt agaggagaaa aaatttggag cagaaatagt accaatgttc
      241 caagcattgt cagaaggctg tactccatat gacatcaatc aaatgttgaa tgtccttgga
      301 gatcatcagg gggcgctaca aatagtgaaa gaaatcatta atgaagaggc agcccaatgg
      361 gatatacaac acccgccccc agcagggccc ttaccagcag gacagcttag agacccaaga
      421 ggctcagacg tagcaggaac aactagtaca gtgcaagaac aattagaatg gatctacaca
      481 gctaacccaa gagtagatgt aggggctatc tatagaaggt ggataatcct tgggctgcaa
      541 aaatgtgtca aaatgtataa cccagtgtca atcctagaca tcaaacaggg accaaaagaa
      601 ccctttaagg attatgtaga tagattttac aggaccatca gagcagagca ggcctcagga
      661 gaagtaaaac aa
                gag cds ->
```

SIVGRI2E

```
LOCUS       SIVGRI2E     1101 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmGRI-2.
ACCESSION   U03995
SOURCE      Simian immunodeficiency virus from PCR-amplified DNA extracted from
            cocultured PBMCs derived from a grivet African green monkey from
            Ethiopia.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466209
BASE COUNT      375 a    182 c    268 g    276 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 actcttagat tgagatattg tgcaccagca ggctttgctt tgttgagatg cttagataag
 env cds ->
       61 aattataacg gctttgctcc tagttgtaag aatgtgacag ttactcactg cactagacta
      121 ataaatacaa cagtaagcac aggtatagga ctaaatggta gtagagctga gaatagaaca
      181 gaaatatggc aagaaaaggg gaatagcaat aatacagtta ttattaagtt aaataagttt
      241 tataacctta cagtaagatg tagaagacca ggaaataaaa cagtgttgcc agtgacaatc
                              ->          v3 loop equivalent
      301 atggccggat tggtgtttca tagtcagaag tataatacta gattaaaaca agcatggtgt
                                                                        <-
      361 cacttccaag gcgattggca tggagcctgg aaagaagtaa aacaagaagt taagaaagca
      421 aaaaatttga caacagatga cataaaattg agaaggcaat ggggggatcc agaagctgca
      481 aacttctggt ttagctgcca aggagaattc ttctattgta aaatggattg gtttattaat
      541 tatataaata atgaaacagt ggatgcagat gggaataaat gcaacaaacc gaaaggacca
      601 ggaccaggtc cttgtgtaca acgaacatat gttgcctgtc acataagaca ggtagtcaat
      661 gattggtata ccctcactaa gaaaacatac cgtccgccaa gagaaggcca gttggagtgc
      721 aattcttcag tcacagcact gtatgtggag ataaattaca ataatgagag tggccctatt
      781 aatgtgacat tgtcacctca gatacgaagt atttgggcct atgaattggg cgattacaaa
      841 ttagtggaaa taacaccaat tggttttgct cccacggatg tgagaagata tacaggaccc
      901 acaaaacaaa aaagggttcc ttttgtgcta ggattcttag gtttcttagg ggcagctgga
      961 actgcaatgg gcgcagctgc gacagcgctg acggtccagt ctcggcattt gcttgctggg
     1021 atattgcagc agcagaggaa tctgctggcg gctgtggagc agcagcaaca actgttgaag
     1081 ctgaccattt ggggtgtaaa a
                       env cds ->
```

```
LOCUS       SIVGRI2L      697 bp ss-RNA             VRL       28-MAR-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) LTR sequence, African green
            monkey isolate SIVagmGRI-2.
ACCESSION   U04007
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a grivet African green monkey from
            Ethiopia.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466239
BASE COUNT      172 a    162 c    197 g    166 t
ORIGIN      start of LTR
        1 aatagaagag aggctatcct aaatctgtat gctctcaatg aatggggcat tatagatgat
      LTR ->
       61 tggcaaggat acacccgcgg cccaggaata agatacccgc taacgtttgg cttctgcttt
      121 aagctagtgc cagtggactc tccgaggagg cagccaactg ttatagacat tgcctgctgc
      181 accctgctca ggcaggggag agtgaagatc caagcggcca tggagaggtc ttggtctgga
      241 agtttgaccc taagttaaca gtggaattta agccatggat gcatagagac atgcatgaac
      301 atgcctgata aacagcagga ggaagtggtt accgcctagc tcggttacca tggagatgac
      361 attaagaact gctgacGGGA CTTTCCagca aGGGACTTTC CAGGGCGGTC CggGAGGTGT
                       NFkb ->          NFkb ->       <--> Sp1   <-  -> Sp1
      421 GGCGGGGAGT GGCtttaccc tcagagctgc aTAAAAgcag atgctcgctg gcttgtaact
           <--> Sp1                    signal ->
      481 cagtctctta ctaggagacc agctagagcc tgggtgttcg ctggttagcc taaccggttg
                               ->        TAR I           <-
      541 gccaccgggg gtaaggactc cttggcttca tatagctcAA TAAAtctgcc cgcttagttg
                                          signal ->
      601 ctatattgga gtcaagtgct cattgctacg tcgcatctca cgaggtgaac ctctcttact
      661 gggttctcct gttacccagg caggagaaac tccagca
                                              <- LTR
```

SIVGRI3E

```
LOCUS       SIVGRI3E     1113 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmGRI-3.
ACCESSION   U03994
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a grivet African green monkey from
            Ethiopia.
REFERENCE   1  (bases 1 to 1113)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466207
BASE COUNT      395 a    188 c    271 g    259 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 acattaagag taagatactg tgcaccagca ggatatgctt tattaaaatg caatgataag
 env cds ->
       61 gattataatg gctttgctcc aaaatgtaag aatgtttcag tagtacactg tactaggtta
      121 ataaatacta ctataaccac aggaataggg ctaaatggga gtagagtaga aaatagaacg
      181 gagatatggc aagaaaaggg aaatagtaat gatacagtaa taataaagtt aaataagttt
      241 tacaacttga cagtgagatg ccgcagacca ggcaacaaaa caatactgcc tgtaacaatc
                              ->          v3 loop equivalent
      301 atggcaggac gagtgtttca ttctcagaaa tacaatacga aattaaaaca agcgtggtgt
                                                                        <-
      361 cactcccagg gaaattggct aggagcctgg aaggaggtaa gagaaaaaat aaaagaagaa
      421 aagaatctca ctgaagtaaa aatagaaaac atacatttga gaaggcaatg gggagaccca
      481 gaagcagcaa atttctggtt caactgtcac ggagaatttt tctattgtaa gatggattgg
      541 ttcattaatt atcttaataa tcagacagta gatgcagatg gaaaaagctg tacttcgcac
      601 aaaaagggtc aaggaccagg accatgtgcg aagaaaacat atgttgcctg ccatataaga
      661 caagtagtaa acgactggta cactctaacc aagaaaacat atgccccgcc aagagaaggg
      721 catttggagt gtaattcgac agtcacggca ctatatgtgg aaataaatta taacaataaa
      781 tctggtccaa taaatgtaac cctatcttct caagtgagga gtatatgggc atatgagttg
      841 ggagattaca aattagtaga aattacacca attgggtttg ctcctacaga cgtgagaaga
      901 tacactggcc cctcgagaga gaagagggtg ccattcgtgc tggggttcct aggcttcttg
      961 ggagctgctg gcactgcaat gggcgcagcg gcgacagccc tgacggtcca gtctcggcat
     1021 ttacttgctg ggatattgca gcagcagaag aacttgctgg tggctgtgga gcagcaacaa
     1081 cagctgttga agctgaccat ttggggtgtg aaa
                                    env cds ->
```

```
LOCUS       SIVGRI3L      700 bp ss-RNA              VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIV) LTR sequence, African green
            monkey isolate SIVagmGRI-3.
ACCESSION   U04006
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a grivet African green monkey from
            Ethiopia.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466238
BASE COUNT      177 a    155 c    204 g    164 t
ORIGIN      start of LTR
        1 aatagaaggg agaaaatgtt aaacctctac gccctgaata agtggggaat aatagatgat
      LTR ->
       61 tggcaaggat acaccccagg cccaggtata agatacccgc tgacatttgg cttctgcttc
      121 aagctagtac cggtaaccct ctctgaagag gcacagaact gtgatagaca ctgtctactg
      181 catcctgctc aggcgggagg agatggggat ccaagtggac atggggagac cttggtctgg
      241 aaatttgacc ctaagttagc agtggagttt aagccatgga tgcataaaga tatgcacggg
      301 atggaaaaga agtaaacagc aagaggaagt ggtttccgcc tagctcggtt accatggaga
      361 tgacattaag aactgctgac GGGACTTTCC aggctGGGGC TTTCCAGGGC GGTGCggGAG
                            NFkb ->         NFkb ->       <--> Sp1  <-  -> Sp1
      421 GCGGTACGGG GAGTGGTttt gccctcagag ctgcaTAAAA gcagatgctc gctggcttgt
        Sp1   <-->  Sp1  <-             signal ->
      481 aactcagtct cttactagga gaccagctag agcctgggtg ttcgctggtt agcctaaccg
                                  ->           TAR I         <-
      541 gttggccacc gggggtaagg actccttggc ttcatatagc tcAATAAAcc tgcctgctta
                                                 signal ->
      601 gttgctatgt tggagtcaag tgctcattgc tgcgccgagt ctctgaggtg aacctctctt
      661 actgagttct cctgttaccc aggcgggaga aactccagca
                                                    <- LTR
```

SIVSAB2E

```
LOCUS       SIVSAB2E     1107 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmSAB-2.
ACCESSION   U03996
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild female asymptomatic sabaeus
            African green monkey captured in its natural habitat of Senegal.
REFERENCE   1  (bases 1 to 1107)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus sab-2 was derived from a wild female asymptomatic sabaeus
            African green monkey.  She was caught in her natural habitat of
            Senegal and susequently exported to the United States.  From the
            point of capture and throughout the study, she was housed in an
            individual cage.
            Phylogenetic analysis suggests that each AGM species is infected
            with a distinct subtype of SIVagm.  Interestingly, the sabaeus viral
            genome seems to be a mosaic of many viruses infecting different
            primate species [1].  Virus sab-1 forms a distinct lineage in the 5'
            end of gag, clusters closest to the HIV2/SIVsm group in the 3' gag
            and 5' pol regions, and clusters closest to the other SIVagm
            lineages in the 3' pol, env and nef regions [1].  This feature
            was demonstrated for two viral sabaeus strains, sab-1 and sab-D37
            (sequenced only over the 5' end of the pol gene).  Jin et al.
            conclude that an ancestor of the sabaeus virus was a recombinant
            with two breakpoints: one roughly at codon 310 of gag and the other
            at 710 of pol.
            NCBI gi: 466211
BASE COUNT      362 a    206 c    265 g    274 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 acatttagat tgagatattg tgctccagct ggttatgctt tgctaagatg tgcagataca
 env cds ->
       61 gattattcag gacataaggc atgtaagaat gtaacagtat cagcttgcac taggttaata
      121 aatactacta taagcacagg gataggtatc aatggtagtt atgtagcaaa tagaacagaa
      181 atctggcaga aaaatggaaa tgccaatcat actgttatta ttaggcttaa tagacatttt
      241 aatttaacta tcagatgtag aagaccagga aataagacag tattgcctgt aaccatcatg
                          ->                v3 loop equivalent
      301 gctggcttgg tcttccatag ccagaaatat aacaccaagt tgagacaagc ttggtgctgg
                                                                        <-
      361 tttggcggtg attggagagg agcctggcag gaagtcaaag aaaaaatagt ggctttacca
      421 ccagataggt atagtggcac aaatgacaca aacaagatct ttctgcaaag gcaatgggga
      481 gatccggaag ctgaattctt ctttttaat tgtcaaggtg aatttttcta ttgtaaaatg
      541 gactggttcc tcaactattt gaataatcag tcagtagacc cagaccataa tccctgtgga
      601 ggaaatgaca agaataacag gaaatgttgg cagagaacct atgttccctg ccacataagg
      661 caaatagtaa atgattggta caccttgtct aaaaagacat acgcccctcc cagagaaggc
      721 cacttggagt gtaactcgac agccacagcg ctgtatgtag aactgctcta taacagtaaa
      781 aacaggacca atgtgacatt atcacctcac attgaaagca tttgggctaa tgaattggga
      841 gactacaaat tggtggagat aaaaccaatt ggatttgctc caacagaggt aagaagatac
```

```
 901 actggccccg aaaggcaaaa aagggtgcca ttcgtgctag ggttcctagg cttcttggga
 961 gcagctggag ctgcaatggg tgcagcggcg acagccctga cggtccagtc tcagcagtta
1021 ctcgctggga tactgcagca gcagaaaaat ctgcttgcgg ctgtagagca gcagcaaatg
1081 ctaaagctca ccatttgggg tgtgaaa
                          env cds ->
```

SIVSAB3E

```
LOCUS       SIVSAB3E     1104 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmSAB-3.
ACCESSION   U03997
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild female asymptomatic sabaeus
            African green monkey captured in its natural habitat of Senegal.
REFERENCE   1  (bases 1 to 1104)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus sab-3 was derived from a wild female asymptomatic sabaeus
            African green monkey.  She was caught in her natural habitat of
            Senegal and susequently exported to the United States.  From the
            point of capture and throughout the study, she was housed in an
            individual cage.
            Phylogenetic analysis suggests that each AGM species is infected
            with a distinct subtype of SIVagm.  Interestingly, the sabaeus viral
            genome seems to be a mosaic of many viruses infecting different
            primate species [1].  Virus sab-1 forms a distinct lineage in the 5'
            end of gag, clusters closest to the HIV2/SIVsm group in the 3' gag
            and 5' pol regions, and clusters closest to the other SIVagm
            lineages in the 3' pol, env and nef regions [1].  This feature
            was demonstrated for two viral sabaeus strains, sab-1 and sab-D37
            (sequenced only over the 5' end of the pol gene).  Jin et al.
            conclude that an ancestor of the sabaeus virus was a recombinant
            with two breakpoints: one roughly at codon 310 of gag and the other
            at 710 of pol.
            NCBI gi: 466213
BASE COUNT      371 a    205 c    255 g    273 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 acctttaggc ttaggtattg tgctccagca ggttatgctt tgttaagatg tgcagataca
 env cds ->
       61 gattattcag ggcataagaa atgtaagaat gtaacagtat cagcttgcac tagattaata
      121 aatactactg taagcacagg gataggtatc aatgggagtt atgtagcaaa tagaacagaa
      181 atctggcaga aaaatggaaa ttccaatgat tctgttatta tcaggcttaa tagacatttt
      241 aatttaacta tcagatgtag gagaccagga aataagacag tgttgcctgt aaccatcatg
                          ->             v3 loop equivalent
      301 gctggcttgg tcttccatag ccagaaatat aacaccaggt tgaaacaagc ttggtgctgg
                                                                      <-
      361 tttggaggta attggagagg agcctggcaa gaagtcaaag aaacaatagt ggctctacct
      421 ccagataggt atcaaggcac aaaagacaca aataaaatct tcctacaaag acaatgggga
      481 gatccagaag ctgaattctt ctttttaat tgtcaaggtg aatttttcta ctgtaaaatg
      541 gattggttcc tcaactattt gaataatcag tcagtagacc cagatcataa tccctgtaat
      601 aagactagcg acaaaaaatg ttggcagaga aactatgctc cctgccacat aaggcaagta
      661 gtaaatgatt ggtacacctt gtctaaaaag acatatgccc ctcccagaga aggccacttg
      721 gagtgcaact caacagccac agcgctgtat gtagaactga actataacag taaaaacagg
      781 accaatgtga cattatcacc tcagattgaa agcatttggg ctaatgaatt gggagactac
      841 aaattagtag agataaaacc aattggattt gctccaacag aagtaagaag atacactggc
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```
 901 cccgaaaggc aaaaaagggt gccattcgtg ctagggttcc taggcttctt gggagcagct
 961 ggagctgcaa tgggtgcagc ggcgacagcc ctgacggtcc agtctcagca gttacttgct
1021 gggatattgc agcagcagaa aaatctgctt gcggctgtag agcagcagca gcaaatgcta
1081 aagctcacca tttggggtgt aaaa
                        env cds ->
```

SIVSAB3L18

```
LOCUS       SIVSAB3L18    741 bp    DNA             VRL       28-MAR-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) LTR sequence, African green
            monkey isolate SIVagmSAB-3, clone 18.
ACCESSION   U04012
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild female asymptomatic sabaeus
            African green monkey captured in its natural habitat of Senegal.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus sab-3 was derived from a wild female asymptomatic sabaeus
            African green monkey.  She was caught in her natural habitat of
            Senegal and susequently exported to the United States.  From the
            point of capture and throughout the study, she was housed in an
            individual cage.
            Phylogenetic analysis suggests that each AGM species is infected
            with a distinct subtype of SIVagm.  Interestingly, the sabaeus viral
            genome seems to be a mosaic of many viruses infecting different
            primate species [1].  Virus sab-1 forms a distinct lineage in the 5'
            end of gag, clusters closest to the HIV2/SIVsm group in the 3' gag
            and 5' pol regions, and clusters closest to the other SIVagm
            lineages in the 3' pol, env and nef regions [1].  This feature
            was demonstrated for two viral sabaeus strains, sab-1 and sab-D37
            (sequenced only over the 5' end of the pol gene).  Jin et al.
            conclude that an ancestor of the sabaeus virus was a recombinant
            with two breakpoints: one roughly at codon 310 of gag and the other
            at 710 of pol.  An alignment of this LTR sequence and another one
            of its clones SIVSAB3L19 (U04013) is shown below.
            NCBI gi: 466244
BASE COUNT      184 a    165 c    209 g    183 t
ORIGIN      start of LTR
        1 gagaaagaag atcttggatc tctatgctct taatgaatgg ggcatagtag atggatggca
      LTR ->
       61 gaattataca gatgggccag gtaccaggta cccaaagtgc tttggatggt gctttaaact
      121 ggtacctgtg gacctgtcag aggaggctaa gaatagagag gaccactgcc tgctgcaccc
      181 tgctcaagtg gcctatgagg atgacccctg gaaggagacc ctggtatgga agtttgactc
      241 aatattagca gtggactatg ctgcttggag actgcaccca gaacaggtgc cgacagtgtc
      301 tgactgacca caaaaccaca tcctatggag ttgtcatggt gatgacatta agaactgctg
      361 actgagaGGG ACTTTCCAGG GTGGAGAcTG GGCGGTACTG GGAGTGGCtt accccgtgct
            NFkb ->       <--> Sp1   <- ->  Sp1  <-->  Sp1  <-
      421 gctcaaTATA Agcagctgct ttgcgcctgt aaaacagtct ctgcttggag gctaccagat
         signal ->                                                    ->
      481 tgagcccggg tgttctctgg taagtctgaa ccagcttgag cctgggtgtt cgctggggaa
            TAR I            <-            ->     TAR II            <-
      541 ggcaagccta agagcactct ggtgaggtct cggtagatcc tcacctggcg actggccatt
      601 gccagtagca gggactccgc ttgcttgctt gattgcctcA ATAAAgtctt gccttagttt
                                          signal ->
```

```
      661 acaagtaaag caagtgtgtg cccatttatt cctcaggaaa accctggtta ctaaggatcc
      721 ctgttagaaa aatccttagc a
                                <- LTR

CONSENSUS  GAGAAAGAAGATCTTGGATCTCTATGCTCTTAATGAATGGGGCATAGTAGATGGATGGCA     60
SIVSAB3L18 ------------------------------------------------------------     60
SIVSAB3L19 ------------------------------------------------------------     60

CONSENSUS  GAATTATACAGATGG?CCAGGTACCAGGTACCCAAAGTGCTTTGGATGGTGCTTTAAA?T    118
SIVSAB3L18 ---------------G-------------------------------------------C-    120
SIVSAB3L19 ---------------A-------------------------------------------T-    120

CONSENSUS  GGTACCTGTGGACCTGTCAGAGGAGGCTAAGAATAGAGAGGACCACTGCCTGCTGCACCC    178
SIVSAB3L18 ------------------------------------------------------------    180
SIVSAB3L19 ------------------------------------------------------------    180

CONSENSUS  TGCTCAAGTGGCCTATGAGGATGACCCCTGGAAGGAGACCCTGGT?TGGAAGTTTGAC?C    236
SIVSAB3L18 ---------------------------------------------A------------T-    240
SIVSAB3L19 ---------------------------------------------G------------C-    240

CONSENSUS  ??TATTAGCAGTGGACTATG?TGCTTGGAGACTGCACCCAGAACAGGTGCCG?CAGTGTC    292
SIVSAB3L18 AA------------------C------------------------------A-------    300
SIVSAB3L19 TG------------------T------------------------------G-------    300

CONSENSUS  TGACTGACCACAAAACCACATCCTATGGAGTTGTCATGGTGATGACATTAAGAACTGCTG    352
SIVSAB3L18 ------------------------------------------------------------    360
SIVSAB3L19 ------------------------------------------------------------    360

CONSENSUS  ACTGAGAGGGACTTTCCAGGGTGGAGACTGGGCGGTACTGGGAGTGGCTTACCCCGTGCT    412
SIVSAB3L18 ------------------------------------------------------------    420
SIVSAB3L19 ------------------------------------------------------------    420

CONSENSUS  GCTCAATATAAGCAGCTGCTTTGCGCCTGTAAAACAGTCTCTGCTTGGAGGCTACCAGAT    472
SIVSAB3L18 ------------------------------------------------------------    480
SIVSAB3L19 ------------------------------------------------------------    480

CONSENSUS  TGAGCC?GGGTGTTCTCTGGTAAGTCTGAACCAGCTTGAGCCTGGGTGTTCGCTGGGGAA    531
SIVSAB3L18 ------C-----------------------------------------------------    540
SIVSAB3L19 ------T-----------------------------------------------------    540

CONSENSUS  GGCAAGCCTAAGAGCACTCTGGTGAGGTCTCGGTAGATCCTCACCTGGCGACTGGCCATT    591
SIVSAB3L18 ------------------------------------------------------------    600
SIVSAB3L19 ------------------------------------------------------------    600

CONSENSUS  GCCAGTAGCAGGGACTCCGCTTGCTTGCTTGATTGCCTCAATAAAGTCTTGCCTTAGTTT    651
SIVSAB3L18 ------------------------------------------------------------    660
SIVSAB3L19 ------------------------------------------------------------    660

CONSENSUS  ACAAGTAAAGCAAGTGTGTGCCCATTTATTCCTCAGGAA?ACCCTGGTTACTAAGGATCC    710
SIVSAB3L18 ---------------------------------------A--------------------    720
SIVSAB3L19 ---------------------------------------G--------------------    720

CONSENSUS  CTG?TAGAAAAA?TCCTTAGCA    730
SIVSAB3L18 ---T--------.---------    741
SIVSAB3L19 ---A--------A---------    742
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SIVSAB4E

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LOCUS       SIVSAB4E     1104 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmSAB-4.
ACCESSION   U03998
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild female asymptomatic sabaeus
            African green monkey captured in its natural habitat of Senegal.
REFERENCE   1  (bases 1 to 1104)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus sab-4 was derived from a wild female asymptomatic sabaeus
            African green monkey.  She was caught in her natural habitat of
            Senegal and susequently exported to the United States.  From the
            point of capture and throughout the study, she was housed in an
            individual cage.
            Phylogenetic analysis suggests that each AGM species is infected
            with a distinct subtype of SIVagm.  Interestingly, the sabaeus viral
            genome seems to be a mosaic of many viruses infecting different
            primate species [1].  Virus sab-1 forms a distinct lineage in the 5'
            end of gag, clusters closest to the HIV2/SIVsm group in the 3' gag
            and 5' pol regions, and clusters closest to the other SIVagm
            lineages in the 3' pol, env and nef regions [1].  This feature
            was demonstrated for two viral sabaeus strains, sab-1 and sab-D37
            (sequenced only over the 5' end of the pol gene).  Jin et al.
            conclude that an ancestor of the sabaeus virus was a recombinant
            with two breakpoints: one roughly at codon 310 of gag and the other
            at 710 of pol.
            NCBI gi: 466215
BASE COUNT      368 a    194 c    262 g    280 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 acttttagat taagatattg tgctcctgca ggctatgcgt tactaagatg tagagattca
 env cds ->
       61 gactacagag gacataagaa ttgtcaaaat gtatcagttt cagcttgcac taggcttatt
      121 aatactacag taagtacagg aataggtatt aatggtagtt atgtagcaaa tagaacagaa
      181 atatggcaag aaaatggaaa tagtaataat acagctataa taaggcttaa taggtattat
      241 aatcttacca taagatgtag aaggccaggg aataagacag tattgcctgt gaccatcatg
                          ->         v3 loop equivalent
      301 gctggcttgg tctttcacag ccaaaaatat aacacaaggt tgagacaagc ctggtgttgg
                                                                       <-
      361 tttgggggta agtggagagg tgcttggcaa gaagccaaag aagaaattgt gaaattatca
      421 ccagaaaggt atagcgggac caaaaacaca tcacaaattt tcctacaaag acagtgggga
      481 ggtccagaag cagaattctt ctttttttaac tgccaaggag aatttttcta ttgtaaaatg
      541 gattggttct taaattattt aaacaatcaa tcggttgacc ctaatcataa cacatgtact
      601 ccaaaaagcg acaaaagatg ttggcagaga acttatgtgc cttgccacat tagacaagta
      661 gtaaatgact ggtataccct gtccaaaaag acatatgctc cacccaggga aggccacttg
      721 gagtgtaact caacagcaac agctctttat gtggaattga actacaatag taagaacagg
      781 accaatgtga cactctcgcc tcagattagg agtatttggg ctaatgaatt aggtgattat
      841 aaattggtag aaatcaaacc cattgggttt gctccaacaa atgtgagaag atatactggc
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 901 cccgagagac agaaaagggt gccattcgtg ctggggttcc taggcttctt gggagcagct
 961 ggagctgcaa tgggtgcagc ggcgacagcc ctgacggtcc agtctcagca attacttgct
1021 gggatattgc agcagcagaa aaatctgctt gcggctgtag agcagcagca gcaaatgcta
1081 aagctcacta tctggggtgt gaag
                        env cds ->
```

SIVSAB4L10

```
LOCUS       SIVSAB4L10    742 bp ss-RNA             VRL       17-SEP-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) LTR sequence, African green
            monkey isolate SIVagmSAB-4, clone 10.
ACCESSION   U04014
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild female asymptomatic sabaeus
            African green monkey captured in its natural habitat of Senegal.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Muller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic genome structure of simian immunodeficiency virus from west
            African green monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus sab-4 was derived from a wild female asymptomatic sabaeus
            African green monkey.  She was caught in her natural habitat of
            Senegal and susequently exported to the United States.  From the
            point of capture and throughout the study, she was housed in an
            individual cage.
            Phylogenetic analysis suggests that each AGM species is infected
            with a distinct subtype of SIVagm.  Interestingly, the sabaeus viral
            genome seems to be a mosaic of many viruses infecting different
            primate species [1].  Virus sab-1 forms a distinct lineage in the 5'
            end of gag, clusters closest to the HIV2/SIVsm group in the 3' gag
            and 5' pol regions, and clusters closest to the other SIVagm
            lineages in the 3' pol, env and nef regions [1].  This feature
            was demonstrated for two viral sabaeus strains, sab-1 and sab-D37
            (sequenced only over the 5' end of the pol gene).  Jin et al.
            conclude that an ancestor of the sabaeus virus was a recombinant
            with two breakpoints: one roughly at codon 310 of gag and the other
            at 710 of pol.  An alignment of this LTR sequence and another one
            of its clones SIVSAB4L4 (U04015) is shown below.
            NCBI gi: 466246
BASE COUNT      182 a    164 c    205 g    191 t
ORIGIN      start of LTR
        1 aaggaagaag atcttggatc tatatgcttt gaatgagtgg ggcatagtag atggctggca
      LTR ->
       61 gaactacact gatgggccag gtacaaggta cccgaagcag tttgggttct gctttaagct
      121 ggtacctgtg gctctatcag aagcagctca gaatgatgag catcactgcc tcctgcaccc
      181 tgctcaaata gcctatgagg atgacccatg gaaggagact ctggtttgga agtttgatcc
      241 aatactagca gtggactatg ttgcttggag actgcaccca gagcaggtgc cgtcagtgtc
      301 tgcctgacca caaaaccaca tcctatagag ttgtcatggt gatgacatta agaactgctg
      361 actgagaGGG ACTTTCCAGG GTGGAGAcTG GGCGGTACTG GGAGTGGCtt accccgtgct
            NFkb ->       <--> Sp1   <- -> Sp1   <--> Sp1   <-
      421 gctcaaTATA Agcagctgct tttcgcctgt aaaacagtct ctgtttggag gctgccagat
         signal ->                                                    ->
      481 tgagcctggg tgttctctgg taagtctgaa ccagcttgag cctgggtgtt cgctggggaa
             TAR I           <-            ->      TAR II           <-
      541 ggcaagcctt agagcacact ggtgaggtct tggtagatcc tcaactggtg actggccatt
      601 gccagtagca gagactccgc ttgcttgctt gattgcctcA ATAAAgtctt gccttagttt
                                          signal ->
```

```
661 acaagtaaag caagtgtgtg cccattcatt cctcaggaaa accctggtta ctaaggatcc
721 ctgtgaagaa aaatccttag ca
                          <- LTR

CONSENSUS  AAGGAAGAAGATCTTGGATCTATATGCTTTGAATGAGTGGGGCATAGTAGATGGCTGGCA     60
SIVSAB4L10 ------------------------------------------------------------     60
SIVSAB4L4  ------------------------------------------------------------     60

CONSENSUS  GAACTACACTGATGGGCCAGGTACAAGGTACCCGAAGCAGTTTGGGTTCTGCTTTAAGCT    120
SIVSAB4L10 ------------------------------------------------------------    120
SIVSAB4L4  ------------------------------------------------------------    120

CONSENSUS  GGTACCTGTGGCTCTATCAGAAGCAGCTCAGAATGATGAGCATCACTGCCTCCTGCACCC    180
SIVSAB4L10 ------------------------------------------------------------    180
SIVSAB4L4  ------------------------------------------------------------    180

CONSENSUS  TGCTCAAATAGCCTATGAGGATGACCCATGGAAGGAGACTCTGGTTTGGAAGTTTGATCC    240
SIVSAB4L10 ------------------------------------------------------------    240
SIVSAB4L4  ------------------------------------------------------------    240

CONSENSUS  AATACTAGCAGTGGACTATGTTGCTTGGAGACTGCACCCAGAGCAGGTGCCGTCAGTGTC    300
SIVSAB4L10 ------------------------------------------------------------    300
SIVSAB4L4  ------------------------------------------------------------    300

CONSENSUS  TGCCTGACCACAAAACCACATCCTATAGAGT?GTCATGGTGATGACATTAAGAACTGCTG    359
SIVSAB4L10 --------------------------------T---------------------------    360
SIVSAB4L4  --------------------------------C---------------------------    360

CONSENSUS  ACTGAGAGGGACTTTCCAGGGTGGAGACTGGGCGGTACTGGGAGTGGCTTACCCCGTGC?    418
SIVSAB4L10 ------------------------------------------------------------T    420
SIVSAB4L4  ------------------------------------------------------------C    420

CONSENSUS  GCTCAATATAAGCAGCTGCT?TTCGCCTGTAAAACAGTCTCTG?TTGGAGGCTGCCAGAT    476
SIVSAB4L10 --------------------T----------------------T----------------    480
SIVSAB4L4  --------------------C----------------------C----------------    480

CONSENSUS  TGAGCCTGGGTGTTCTCTGGTAAGTCTGAACCAGCTTGAGCCTGGGTGTTCGCTGGGGAA    536
SIVSAB4L10 ------------------------------------------------------------    540
SIVSAB4L4  ------------------------------------------------------------    540

CONSENSUS  GGCAAGCCTTAGAGCACACTGGTGAGGTCTTGGTAGATCCTCAACTGGTGACTGGCCATT    596
SIVSAB4L10 ------------------------------------------------------------    600
SIVSAB4L4  ------------------------------------------------------------    600

CONSENSUS  GCCAGTAGCAGAGACTCCGCTTGCTTGCTTGATTGCCTCAATAAAGTCTTGCCTTAGTTT    656
SIVSAB4L10 ------------------------------------------------------------    660
SIVSAB4L4  ------------------------------------------------------------    660

CONSENSUS  ACAAGTAAAGCAAGTGTGTGCCCATTCATTCCTCAGGAAAACCCTGGTTACTAAGGATCC    716
SIVSAB4L10 ------------------------------------------------------------    720
SIVSAB4L4  ------------------------------------------------------------    720

CONSENSUS  CTGTGAAGAAAAAATCCTTAGCA     738
SIVSAB4L10 -----------------------     742
SIVSAB4L4  -----------------------     742
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SIVSABD37P

```
LOCUS       SIVSABD37P    651 bp ss-RNA             VRL       17-SEP-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) pol sequence, African green
            monkey isolate SIVagmSABD37, partial cds.
ACCESSION   U04018
SOURCE      Simian immunodeficiency virus, PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild sabaeus African green monkey
            captured in its natural habitat of Senegal.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Muller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic genome structure of simian immunodeficiency virus from west
            African green monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Phylogenetic analysis suggests that each AGM species is infected
            with a distinct subtype of SIVagm.  Interestingly, the sabaeus viral
            genome seems to be a mosaic of many viruses infecting different
            primate species [1].  Virus sab-1 forms a distinct lineage in the 5'
            end of gag, clusters closest to the HIV2/SIVsm group in the 3' gag
            and 5' pol regions, and clusters closest to the other SIVagm
            lineages in the 3' pol, env and nef regions [1].  This feature
            was demonstrated for two viral sabaeus strains, sab-1 and sab-D37
            (sequenced only over the 5' end of the pol gene).  Jin et al.
            conclude that an ancestor of the sabaeus virus was a recombinant
            with two breakpoints: one roughly at codon 310 of gag and the other
            at 710 of pol.
            NCBI gi: 466250
BASE COUNT      252 a     94 c    145 g    160 t
ORIGIN
        1 tctgttattc aggggttaga attaggggat aattggaagc caagaattat aggaggaata
 pol cds ->
       61 ggaggctgta ttaatgttag ggcatatcat aatcaagaag ttgaaataga aggaaaagga
      121 tgtaaagcaa ctattttagt gggagatact ccagtaaaca taataggaag aaatgtacta
      181 gctcaattag gagtaacttt aaacttagta gcaaaaacaa ttctcccaat aaaagtgcag
      241 ttaaagcctg gaaaagatgg tcccaggtta agacaatggc ctctatcaaa agaaaagatt
      301 gaagccctaa gaacaatttg tgagcaatta gaaaaggaag gacatctgga aaggataggg
      361 ccagaaaatc catacaacac tccagtcttt gcaattagaa agaaagataa atcacaatgg
      421 aggatgttga tggactttag ggaactcaat aaggcaactc aagactttca agaagtacaa
      481 ttaggtatac cacacccggc agggttacag caaagagaac agataacagt cttagatata
      541 gcagatgctt atttttcatg tcctttagat gaggattttc agaagtacac agcttttact
      601 attcctagtg taaataacaa ggaaccaggt atgagatttc agtacaaggt g
                                                              pol cds ->
```

```
LOCUS       SIVTAN17E    1113 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmTAN-17.
ACCESSION   U04000
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild asymptomatic tantalus African
            green monkey captured in its natural habitat of Uganda.
REFERENCE   1  (bases 1 to 1113)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus tan-17 was derived from a wild asymptomatic tantalus
            African green monkey.  This monkey was caught in its natural
            habitat of Uganda in the same region as tan-49.
            NCBI gi: 466219
BASE COUNT      369 a    191 c    282 g    271 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 accttgaggc ttagatattg tgcacctgca ggctttgcta ttttaaaatg caaggataca
 env cds ->
       61 aattatacag gctttgggat ttgtaggaat gtttcagtgg taagctgcac agggctaatg
      121 aatactacag taagttcagc ttttggcttg aacggcagtc aagcggaaaa tagaacagag
      181 gtttggcaaa agcatggggt tagtaatgat tctgtaataa ttaagcttaa taagttttat
      241 aacttaacaa taaaatgtag gagaccaggt aataagacag tcctaccagt aaccatcatg
                          ->              v3 loop equivalent
      301 gcgggtcttg tgttccactc tcaaaagtac aatacgaggc tcagacaggc ttggtgccac
                                                                      <-
      361 tttcaaggta aatggaaaga ggcctggaaa gaggtgagag aaaccattgt gaaattaccc
      421 aaagaaaaat atcgaggaac aaatgataca aagaaaatat ggttaaggag acaatggggg
      481 gacccagagg ctgctaatat ttggttcaat tgccaaggag agttcttcta ttgtacacct
      541 gattggtttg taaattactt aaataatgac tcagcccgga ggagaaaaga ggatgtggaa
      601 gggaacgact gtaaagatcc aaggaaatgt tttaaaagat cgtacgttcc ctgccacata
      661 aggtcggttg tcaacgactg gtataccttg agtaagaaga cctatgcacc accgagggaa
      721 ggacacttgg aatgcacatc cacagtgaca tccatgatgg tgtcactaga ttacgtaaac
      781 aaaaacatga ctaatgtgac cctaacagca aatttagaaa atatatgggc ttatgaattg
      841 gggagatata aaatcataga aatcaaacca attggatttg cgccaacaga tgttagacga
      901 tatgttgggc caactcgaga aaagagggtg cccttcgtgt tagggtccct aggtttcttg
      961 ggacgagctg gagctgcaat gggtgcaaca gcgacagagt tgacggtcca gtctcagcaa
     1021 ttacttgctg ggatattgca gcagcagaag aatctgctgg cggcagtaga gcagcagcag
     1081 caaatgctaa agctcaccat ttggggtgtg aaa
                                    env cds ->
```

SIVTAN1E

```
LOCUS       SIVTAN1E     1119 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmTAN-1.
ACCESSION   U03999
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild tantalus African green monkey
            captured in its natural habitat of Uganda.
REFERENCE   1  (bases 1 to 1119)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466217
BASE COUNT      382 a    187 c    280 g    270 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 accttaagat taagatactg tgcaccagca ggctttgcta tcttaaaatg taaggatact
 env cds ->
       61 aattatacag gatttggtgt ttgtagaaat gtttcagtag ttagttgtac tggattgatg
      121 aatactacag tgagctcagc atttggcata aatggcagtc aggcagaaaa cagaacagaa
      181 atatggcaaa agcatggagt gagcaataat tctgtgataa taaaactaaa taaacattat
      241 aagttgaaga tagtgtgtag aagaccagga aataagacag tcttaccagt aaccatcatg
                          ->            v3 loop equivalent
      301 gcaggtctcg tgttccactc acaacaatat aatacaaaat taagacaagc atggtgccat
                                                                      <-
      361 ttccagggtg attggaaagg agcctggagg gaagtgagaa aaacaatagt ggagcttcca
      421 aaagagaaat atcgagggac aaataacaca aggcagattt ggctaagtag acaatgggga
      481 gatccagaag cagctaacat ttggctcaat tgccaaggag agtttttcta ttgtactcct
      541 gattggtttg ttaattggct gaataatgag tctaatagtg gaagaaatgt agatgtagaa
      601 ggtaataatt gcaccactgg aaaggataaa cgctgctaca aaaggacata tgtcccctgc
      661 catattaggt caattgtcaa tgactggtac accctcagta agaaaaccta tgcaccacca
      721 agggaaggac acttagaatg cacatcaaca gtgacatcta tgatggtatc actggattat
      781 aacagcaaag aaaggactaa tgtgacattg acagctaatt tggagaacat atgggcttat
      841 gaattgggaa gatataagct catagaaatt gaaccaatcg gtttcgcgcc aacagagata
      901 agaagatatg ttgggccaac tcgagaaaag agggtgccct tcgtgttggg gttcctaggc
      961 tttttggggg cagctggagc tgcaatgggt gcaacagcga cagcgttgac ggtccagtcc
     1021 cagcaattac ttgcagggat gttgcagcag cagaagaatc tgctggcggc agttgagcag
     1081 cagcagcaga tgctaaagct caccatttgg ggtgtgaaa
                                        env cds ->
```

```
LOCUS       SIVTAN40E    1119 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmTAN-40.
ACCESSION   U04001
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild asymptomatic tantalus African
            green monkey captured in its natural habitat of Uganda.
REFERENCE   1  (bases 1 to 1119)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus tan-40 was derived from a wild asymptomatic tantalus
            African green monkey.  This monkey was caught in its natural
            habitat of Uganda.
            NCBI gi: 466221
BASE COUNT      383 a    194 c    268 g    274 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 acattaagat tacgatattg tgcaccagct ggctttgctc ttttaaaatg cagggatact
 env cds ->
       61 aattatgcag gctttggtat ttgtaacaat gtttcagtag taagctgtac tggactaatg
      121 aatactacaa taagttctgc ttttgggtta aacgggagcc aagcagaaaa tagaacagaa
      181 atttggcaaa aacatggcaa tagtaatgat tcagtcatta taaagttgaa taaacattat
      241 cagttaaaaa taaaatgtat aagacctggg aataagacgg tcctaccagt aaccatcatg
                          ->             v3 loop equivalent
      301 gctggcttgg tattccactc acaaaagtac aatacaaagt taaggcaagc ttggtgtcac
                                                                       <-
      361 ttccaaggtg attggaaagg agcctggaag gaagtaaggg agacaatagt taaacttcca
      421 aaggaaaaat accaagggac aaagaacaca acagagatat ggctaagaag acaatgggga
      481 gatccagaag cagccaatat ttggttcaat tgtcaaggag aattcttcta ctgtacaccc
      541 gattggatgg ttaattggct taacaatgag agtgattcag gaaaatcagt taacgtagag
      601 ggaaacactt gtactcctga gaaagatagg ctatgtaaga agaggacata tgtagcctgc
      661 cacatccggt cagtagttaa tgattggtac acactgagta aaaagaccta tgcaccgcca
      721 agagaaggac acttagagtg tacatccaca gtgacctcaa taatagcgtc tcttgactac
      781 aacaataaaa atatgactaa tgtgacactt acagcaaaca ttgaaaatct ttatgcatat
      841 gagttgggaa ggtataaact cattgaaatt aaacctattg gattcgcgcc gacagaggtc
      901 agaagatatg ttgggccaac tcgagagaag agggtgccct tcgtgttagg gttcctaggt
      961 ttcttgggac gagctggagc tgcaatgggt gcgacagcga cagcgttgac ggtccagtct
     1021 cagcaattac ttgctgggat attgcagcag cagaagaatc tgctggcggc tgtagagcag
     1081 cagcagcaaa tgctaaagct caccatttgg ggtgtgaaa
                                        env cds ->
```

SIVTAN49E

```
LOCUS       SIVTAN49E    1137 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmTAN-49.
ACCESSION   U04002
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from a wild asymptomatic tantalus African
            green monkey captured in its natural habitat of Uganda.
REFERENCE   1  (bases 1 to 1137)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.
            Virus tan-49 was derived from a wild asymptomatic tantalus
            African green monkey.  This monkey was caught in its natural
            habitat of Uganda in the same region as tan-17.
            NCBI gi: 466223
BASE COUNT      378 a    204 c    296 g    259 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 acactaaggc ttagatattg tgcaccagca ggctttgcta tcttaaaatg taaagatact
 env cds ->
       61 aattatacag gctatgggat atgtagaaat gtatcagtag ttagctgcac aggcttaatg
      121 aataccacag taagttcagc ttttggacta aatggcagtc aggcagaaaa tagaacagag
      181 atctggcaaa agcataggat taacaatgat agtgtgataa ttaagcttaa taagtactac
      241 aaattagggg taacatgtag gagaccaggg aataagacag tcttaccagt aaccatcatg
                          ->                v3 loop equivalent
      301 gcaggtctgg tgttccactc tcaaaaatac aatacgaagc ttagacaggc ctggtgtcac
                                                                       <-
      361 ttccatgggg actggaaagg agcctggaag gaagtgaggg agaccattgt gaagctacca
      421 agagacagat actccgggac aaataataca aatcaaatat ggctaaggag acaatgggga
      481 gatccagagg cagccaatat ctggtttaac tgccaaggag agttcttcta ctgtacacca
      541 gattggtttg tcaattggct aaacaatgaa tctgcaggag gaaactacac agatgtagag
      601 ggaaaccctt gttccaatag cactaaaggg ggaatgacag gaagcagaaa gtgtttaaaa
      661 agaacatatg ttggctgcca tatcaggtcg gttgtcaatg actggtatag cttgagtaaa
      721 aagacctatg caccgccgag agagggacac ttggagtgca catccacggt gacctcaatg
      781 atggtatcat tggattacaa ttcgaaaaat atgaccaatg tgaccctaac agcaaatttg
      841 gaaaatatat gggcctatga gttggggaga tacaaactca tagaaatcaa gccaataggc
      901 ttcgcgccta cagaagtgag gagatatgtt gggccaactc gagaaaagag ggtgcccttc
      961 gtgctaggat tcctaggttt cttgggacga gctggagctg caatgggtgc aacagaaacg
     1021 gagttgacgg tccagtctca gcaattactt gctgggatat tgcagcagca gaagaatctg
     1081 ctggcggcag ttgagcagca gcagcagatg ctaaagctca ccatttgggg tgtgaaa
                                                                env cds ->
```

```
LOCUS       SIVVER1E     1116 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmGRI-2.
ACCESSION   U04003
SOURCE      Simian immunodeficiency virus PCR-amplified DNA extracted from
            cocultured PBMCs derived from a vervet African green monkey from
            East Africa.
REFERENCE   1  (bases 1 to 1116)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466225
BASE COUNT      375 a    193 c    278 g    270 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 gaattaaggc taagatactg tgcacctgca ggatatgctt tgctaaaatg caatgataga
 env cds ->
       61 aattatacag gctttgctcc aagatgtaga aatgttagtg tagtgcattg cacagggttg
      121 atgaatacaa cagtcagtac aggcttgcta ttaaatggta gttatacaga gaatagaaca
      181 gaaatttggc aaaaacataa agtgagtaat aattcagtta ttattaggat taataagcat
      241 tataatttaa caataaggtg tgtaagacca gggaataaaa cagtcttacc agtgaccatc
                           ->              v3 loop equivalent
      301 atggcaggtc tggtgttcca ctcccaaaaa tacaacacga aattaagaca agcatggtgt
                                                                       <-
      361 cacttcaaag gtgactggag aggagcctgg agagaaataa aacaaaaaat tgtagagcta
      421 ccaaaagaaa ggtatcaggg gactaacgac acaaagcaaa tcttcctaca aaggcagtgg
      481 ggagatccag aggcatctaa tttgtggttt aattgtcatg gggaattttt ctattgcaag
      541 atggattgga tgctaaacta cattaacaac ctcactgtag atgcgaatca taataattgt
      601 aacagtacac agggaaaaag accagggccg tgtgtccaaa ggacatatgt agggtgtcat
      661 atcagatcag tcatcaatga ttggtacaaa ttggcaagaa agacttatgc acctcccaga
      721 gaaggtcatt tggagtgtac ctctacagtc acgggtatgg cagtagagct aaattatatc
      781 cataagaaca ggacaaatgt gactttgtca ccccagatag aagccatatg ggcatcagaa
      841 ttgggtaggt acaaattggt agaaattacg ccaattggtt ttgcaccaac cccagtaagg
      901 agatatacgg ggccttcaag agaaaagagg gtgcccttcg tgctagggtt cttgggcttc
      961 ttgggagctg caggcactgc aatgggagca gcggctacgg cgctgacggt ccagtctcag
     1021 catttgcttg ctgggatatt gcagcagcag aagaacttgc tggcggcagt ggaggctcaa
     1081 caacaaatgt tgaagctgac catatggggt gtgaaa
                                      env cds ->
```

SIVVER266E

```
LOCUS       SIVVER266E   1137 bp    DNA             VRL       24-AUG-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVver266.
ACCESSION   U10896
SOURCE      Simian immunodeficiency virus  from PCR-amplified DNA extracted from
            cocultured leukocytes derived from a vervet African green monkey from
            Kenya.
REFERENCE   1  (bases 1 to 1137)
  AUTHORS   Jin,M.J., Rogers,J., Allan,J.S., Desrosiers,R.C., Shaw,G.M.,
            Sharp,P.M. and Hahn,B.H.
  TITLE     Infection of a yellow baboon with SIV from African green monkeys:
            Evidence for cross-species transmission in the wild
  JOURNAL   J. Virol. (In press, 1994)
COMMENT     Two wild yellow baboons from Tanzania were identified in a previous
            study with strong SIV(agm) seroreactivity.  They lived in a
            national park where yellow baboons and African green monkeys share
            the same habitat.  In this study, molecular characterization was
            performed for virus derived from one of the SIVagm seroreactive
            yellow baboons (animal 2010) and from two vervet African green
            monkeys (animals ver266 and ver385).  With this aim in mind,
            uncultured leukocyte DNA was PCR-amplified, cloned and sequenced
            over a 672 bp region of gag and a 906 bp region of env for animal
            2010 (only the env region was analyzed for isolates ver266 and
            ver385).  Jin et al. note that the viral strain derived from
            the yellow baboon (animal 2010) clusters with SIV strains of the
            vervet subtype, including ver266 and ver385, and believe that
            is was the first evidence for simian-to-simian cross-species
            transmission of SIV in the wild.
BASE COUNT      381 a    210 c    270 g    276 t
ORIGIN      approximately 727 bp downstream from the start of env
        1 gagttaaggc taagatattg tgccccagca ggatttgccc tgctaaaatg taatgatgca
 env cds ->
       61 gattatgatg gttttaaaac aaactgctcc aatgtatcag tggtacattg taccaaccta
      121 atgaatacaa cagtgactac agggttgtta ctgaatggaa gctattctga aaatcgaacc
      181 caaatatggc agaaacatag gacgagcaat gactccgcac ttattttact taataagcat
      241 tacaatttaa cagtgacttg taaaagacca ggaaataaga cagtcctccc agtaacaata
                          ->            v3 loop equivalent
      301 atggctggat tagtttttca ttctcagaag tataacttaa ggttaaggca agcatggtgc
                                                                      <-
      361 cacttcccaa gcaattggaa aggagcttgg aaggaagtaa aggaagaaat agtaaacctg
      421 cccaaagaaa gatacagagg caccaatgac ccaaaacgaa tcttcttcca aagacagtgg
      481 ggggacccag aaacagcgaa tttgtggttt aattgtcacg gagagttttt ctattgtaaa
      541 atggattggt tcttaaatta tctgaataat ttaacggtag atgctgatca taatgaatgt
      601 aagaatacaa gtggtacaaa aagtggtaac aagagggcac cagggccttg tgtacagaga
      661 acttatgtgg cctgccatat tcgatctgtc ataatatggt tggagacaat atcaaagaaa
      721 acttatgctc caccaagaga gggtcatcta gaatgcacat ccacggttac tggaatgaca
      781 gtggaactaa attatatccc caaaaataga accaatgtga cattaagtcc ccagatagaa
      841 tctatctggg cagcagaatt ggaccgatat aaattggtag agatcacacc aattggcttt
      901 gcacccacag aagtaaggag atacacggga ggtcatgaaa gacaaaagag agtcccgttc
      961 gtgctagggt tcttgggctt cttgggagct gctggaactg caatgggagc agcggcgaca
     1021 gccctgacgg tccagtctca gcatttactt gctgggatac tgcagcagca gaagaatctg
     1081 ctggcggctg tggaagctca acagcagatg ttgaagctga ccatttgggg tgtgaaa
                                                              env cds ->
```

```
LOCUS       SIVVER2E     1125 bp ss-RNA             VRL       25-MAY-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVagmVER-2.
ACCESSION   U04004
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from vervet African green monkeys from East
            Africa.
REFERENCE   1  (bases 1 to 1125)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Mueller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic Genome Structure of Simian Immunodeficiency Virus from West
            African Green Monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466227
BASE COUNT      371 a    208 c    271 g    275 t
ORIGIN      approximately 727 bp downstream from beginning of env cds
        1 gagttaagat tgagatactg tgctccagca ggatatgcct tgttgaaatg taatgaccat
 env cds ->
       61 gattataatg ggtacaaaca gaactgctct aatgtctcag tagtgcactg tacagggtta
      121 atgaatacaa cagtaactac tggcttgttg ctaaatggca gctatcatga gaatcgaacc
      181 cagatctggc gaaagcatgg agtaagcaat gactcagtga taatattgat taataaggct
      241 tttaatctaa cagtcacttg cagaaggcca ggaaataaaa cagttttacc agtaacaata
                           ->               v3 loop equivalent
      301 atggcaggat tagtgtttca ttctcagaaa tataacacaa ggctgagaca agcttggtgt
                                                                        <-
      361 cacttccagg gtaattggag aggagcctgg gaggaaatac ggcaggaaat aaccaaatta
      421 cctccacata aatacagggg gactaatgat acagagaaga tatttctgca aagacaattt
      481 ggagacccag aagcggcaaa cttatggttt aattgccaag gagaattctt ctattgtaag
      541 atggattggt ttttaaatta tctaaataat cttacagtag atgctgacca taatagttgc
      601 aatggttcaa ggacgagccc tagggcaccg ggtccctgtg cccaaaggac ttatgttgct
      661 tgccatataa gatcagtcat aaatgattgg tacacaatat caaagaaaac atatgctcca
      721 ccaagagaag ggcatttaca atgcacctcc acggttaccg ggatgacagt agaattgaat
      781 tataatagtc gcaacagaac aaatgtaacg ttgtctcccc agatagaaag tatctgggca
      841 gcagaattgg gcagatacaa attagtagaa attacaccaa ttggctttgc acccacagat
      901 gtaagaaggt atacgggagg ccatgaaaga caaaaacgag tcccgttcgt gcaagggttc
      961 ctaggcttct tgggggctgc tggaactgca atgggagcaa cggcgacagc cctgacggtc
     1021 cagtctcagc atttacttgc tgggatactg cagcagcaaa agaatttgct ggcggctgtg
     1081 gaggctcaac agcaaatgtt gaagctgacc atttggggtg tgaaa
                                                  env cds ->
```

SIVVER2L

```
LOCUS       SIVVER2L      701 bp ss-RNA             VRL       17-SEP-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) LTR sequence, African green
            monkey isolate SIVagmVER-2.
ACCESSION   U04017
SOURCE      Simian immunodeficiency virus  PCR-amplified DNA extracted from
            cocultured PBMCs derived from vervet African green monkeys from East
            Africa.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Jin,M.J., Hui,H., Robertson,D.L., Muller,M.C., Barre-Sinoussi,F.,
            Hirsch,V.M., Allan,J.S., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Mosaic genome structure of simian immunodeficiency virus from west
            African green monkeys
  JOURNAL   EMBO J. 13, 2935-2947 (1994)
COMMENT     This sequence was obtained as part of a study designed to determine
            the breadth of genetic variation of SIV infecting African green
            monkeys.  With this aim in mind, Jin et al. PCR-amplified, cloned
            and sequenced the LTR and partial envelope region from 12 isolates
            (ver-1, ver-2, gri-2, gri-3, sab-1, sab-2, sab-3, sab-4, tan-1,
            tan-17, tan40, and tan-49).  These isolates were derived from
            different African green monkey species inhabiting various
            geographical regions.  Most of the vervet and grivet viruses and
            all of the sabaeus and tantalus viruses were derived from feral
            animals.
            NCBI gi: 466249
BASE COUNT      186 a    158 c    187 g    170 t
ORIGIN      start of LTR
        1 gaggaataaa atccttaact tgtacgccct caatgagtgg ggaatcattg atgattggaa
      LTR ->
       61 tgcatggtct aaaggaccag gaatcagata cccaaagtgc tttggcttct gctttaaact
      121 agtgccagta gacttacatg aggaggcaaa acattgtgag agacactgct tggtccatcc
      181 agcacaagtg ggagaagatc cagatggtat caaccatgga gaggtcttgg tctggaagtt
      241 tgatcccatg ttagcagtcc aatacgaccc tacaagagaa tattttgaag acatgcattc
      301 aacagttggt acaggaaact agcctaaccg cagcttgtgg ttaagccgtt gcctaggaga
      361 tgacattaag aactgctgac GGGACTTTCc agcaaGGGAC TTTCCAGGGC GGGTCgAGGG
                           NFkb ->      <-      ->NFkb   <--> Sp1   <- ->
      421 CGGTACGGGG AGTGGCttta ccctcagagc tgcaTAAAAg cagatgctcg ctggcttgta
        Sp1   <-->  Sp1  <-             signal ->
      481 actccagtct cttactagga gaccagcttg agcctgggtg ttcgctggtt agcctaactg
                                  ->       TAR I            <-
      541 gttggccacc aggggtaagg actccttggc ttagaaagct AATAAAactt gcctgcatta
                                                signal ->
      601 gagcttatct gagtcaagtg ccctcattga cgcctcactc gagggacggg tcctgttcct
      661 tactgggttc tctctcaacc caggcgagag aaactccagc a
                                                     <- LTR
```

```
LOCUS       SIVVER385E   1125 bp    DNA             VRL       24-AUG-1994
DEFINITION  Simian immunodeficiency virus (SIVagm) partial envelope sequence,
            African green monkey isolate SIVver385.
ACCESSION   U10898
SOURCE      Simian immunodeficiency virus from PCR-amplified DNA extracted from
            cocultured leukocytes derived from a vervet African green monkey from
            Kenya.
REFERENCE   1  (bases 1 to 1125)
  AUTHORS   Jin,M.J., Rogers,J., Phillips-Conroy,J.E., Allan,J.S.,
            Desrosiers,R.C., Shaw,G.M., Sharp,P.M. and Hahn,B.H.
  TITLE     Infection of a yellow baboon with SIV from African green monkeys:
            evidence for cross-species transmission in the wild
  JOURNAL   J. Virol. (In press, 1994)
COMMENT     Two wild yellow baboons from Tanzania were identified in a previous
            study with strong SIV(agm) seroreactivity.  They lived in a
            national park where yellow baboons and African green monkeys share
            the same habitat.  In this study, molecular characterization was
            performed for virus derived from one of the SIVagm seroreactive
            yellow baboons (animal 2010) and from two vervet African green
            monkeys (animals ver266 and ver385).  With this aim in mind,
            uncultured leukocyte DNA was PCR-amplified, cloned and sequenced
            over a 672 bp region of gag and a 906 bp region of env for animal
            2010 (only the env region was analyzed for isolates ver266 and
            ver385).  Jin et al. note that the viral strain derived from
            the yellow baboon (animal 2010) clusters with SIV strains of the
            vervet subtype, including ver266 and ver385, and believe that this
            is the first evidence for simian-to-simian cross-species transmission
            of SIV in the wild.
BASE COUNT      376 a    210 c    272 g    267 t
ORIGIN      approximately 727 bp downstream from the start of env
        1 gagctaagat tgagatactg tgctccagca gggttcgccc tattaaaatg taatgactat
 env cds ->
       61 gactatgatg ggtttaaaca aaattgttcc aatgtatcag tagtgcattg tacagggcta
      121 atgaatacaa cagtaactac agggttgctg ttgaatggaa gctattctga gaatcgaacc
      181 cagatctggc aaaagcatag agtaagtaat gattcagtgt taatacagat taataaacat
      241 tacaacctca caattacttg caaaaggcca ggaaacaaaa cagtcttacc tgtgacaata
                          ->               v3 loop equivalent
      301 atggcaggac tagtttttca ctctcaaaag tataacacga gattgagaca agcctggtgt
                                                                       <-
      361 cacttccaag gcaattggca tggagcttgg aaggaaataa aacaagaaat agttaagtta
      421 cccaaagaca ggtacagggg gaccaacgac acagaacaaa tttatttgac aaggcagtgg
      481 ggagatccag aggcagcaaa tttgtggttc aattgtcaag gagagttctt ttattccaaa
      541 atggattggt tcttgaacta tttaaataat aagacatgga atgcagacca taatcaatgt
      601 gataatagta ctaagactgg aagggcacca ggaccttgtg tacaaaggac ttatgttgct
      661 tgccacatca gatctgtcat aaatgattgg tatacaatat caaagaaaac atacgcccca
      721 ccaagagaag ggcatttaca atgcacatcc acggtaactg ggatgacagt ggagctaaat
      781 tatatcaatg acaatagaac caatgtgaca ctgagtcccc agatagaaac catctgggca
      841 gcggaattgg gcagatataa attggtagag atcactccaa ttggctttgc acccacagaa
      901 gtgagaagat atacgggagg ccatgaaagc ccaaaacgaa tcccgttcgt gctagggttc
      961 ttgggcttct tgggagctgc tggaactgca atgggagcag cggcgacagc cctgacggtc
     1021 cagtctcagc atttgcttgc tgggatactg cagcagcaga agaatctgct ggcggctgtg
     1081 gaggctcaac agcagatgtt gaagctgacc atttggggtg tgaaa
                                                 env cds ->
```

II

Amino Acid Alignments

The amino acid sequence alignments that follow were generated by the PIMA program ("pattern induced multiple alignment"; R.F.Smith and T.F.Smith, *PNAS* **87**:118, 1990 and *Protein Engineering* **5**:35, 1992). The alignments were also subject to some hand-editing performed with MASE (D.V. Faulkner and J. Jurka, *TIBS* **13**:321, 1988). For information concerning both these UNIX tools, contact Dr. Randall Smith, Institute of Molecular Genetics, Baylor College of Medicine, Houston, Texas, 713-798-4735.

With few exceptions (most notably with HIV-1 *env*), only full-length protein sequences have been included in this compilation. Sequences not ready for publication at this time, but which are reflected in the consensus sequences and patterns will usually be identified. Eight sequence subtypes have been identified for HIV-1s (see Part I and Part III). Five sequence subtypes exist for HIV-2s. Sequence subtypes have been defined by "cladistic" criteria applied to nucleotide sequences; it remains to be seen whether the amino acid sequence subtypes inferred from that classification are valid, or whether a "phenetic" classification would be preferable.

The reference sequences for the alignments are mixed case consensus sequences in which upper case letters refer to amino acid residues which are conserved 100% and lower case letters represent amino acid residues conserved in at least 50% of the sequences. Again, consensus sequences have been generated for each of the defined subtypes (see Parts I and III). The user should keep in mind that these subtypes have been "cladistically" defined, not "phenetically" defined (the number of phenotypes remains to be discovered).

Within the sequences, "-"'s are used to indicate residues conserved with respect to the reference sequence and "."'s represent actual gaps. Blank spaces within the alignment indicate lack of sequence information over that region. Annotation of the *env* amino acid sequences utilizes "*" for conserved cysteine residues and "^^^" for potential N-linked glycosylation sites. A summary of *env* cysteine and N-linked glycosylation sites is found in Part III.

PART II Amino Acid Sequences and their Variation

Introduction II-1
Contents(1994) II-2

A. HIV-1 Alignments and Consensus Sequences

GAG II-A-2
POL II-A-18
VIF II-A-26
VPR II-A-28
TAT II-A-29
REV II-A-31
VPU II-A-32
ENV II-A-34
NEF II-A-64

B. HIV-2/SIV Alignments and Consensus Sequences

GAG II-B-1
POL II-B-5
VIF II-B-12
VPX II-B-13
VPR II-B-14
TAT II-B-15
REV II-B-16
ENV II-B-18
NEF II-B-31

C. SIVAGM and SIVSYK Alignments and Consensus Sequences

GAG II-C-1
POL II-C-4
VIF II-C-9
VPX II-C-10
TAT II-C-11
REV II-C-12
ENV II-C-13
NEF II-C-21

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HIV1 GAG

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CONSENSUS.A mGARaSvLsggkLDawekIrLRPgGkKkYrlKHlvwAsreLerFaLnPslLeT?egcqqimeQlqsalkTg?e  71
HIVU455     ----------K---S----------N----------------K-T---G----A------LG---P--Q--T-  73
HIVUG266    ----V----E----- -------E-----K----- ------K----------T----R-L----P--Q--A-  71
HIVMAL      ------------------------------------------------G----G-----------T----S-  73
HIVVI32     ------------------------------M----------D----------K----------E------T-  73
HIVVI57     ------------------------------------------------T------L----P-----T-  73
HIVVI59     I--------E-----X----------Q-------X--K-------------T------I----P-----T-  73
HIVVI310    --------------K-----------Q-------------------------T------I----P-----T-  73
HIVVI354    ------I---------KR----------QI--I-----K--K-----G--K-A-----------------S-  73
HIVVI415    ------------------------R----M----------D------G----A------L----P-----T-  73
HIVK7       I----------Q--RX-------------------------------------T-R---------------T-  73
HIVK29      ----------------------------M----------------------T------I----P-----T-  73
HIVK88      ----------------------------M----------D----------A-----------------T-  73
HIVK89      --------------T-------------K----------------------T----------P-----T-  73
HIVK98      ----T-------------------N-R-K---I-------------G----T-------K------Q--T-  73
HIVK112     ----------------------------I----------K----------T-----------------T-  73
HIVK124     ------------------------------------------------T-----------S----T-  73
HIVCI4      ----------------------------M---I--G---------------T-------A---------T-  73
HIVCI20     ------------------------------------------------AG----L-----AH-R--S-  73
HIVCI32     ----------R-----------------K----------------S-----LI--F--T-G--S-  73
HIVCI51     ------I-------S----------R-Q----------------------A------I----------S-  73
HIVCI59     ------------------------------------------G----AD----L--------R--S-  73
HIVG141     --------------D----Q-----T-R-K---I-----------D------S---K--LG---P-----S-  73
HIVTN238    --------T----------------R---KI----------------G----V------I-----T----S-  73
HIVTN243    ------------------------R----M----------------G----A------I-----T----S-  73
HIVTN240    ------------------------R----------------------F---A------I-----T----S-  73
HIVTN245    ------------------------R---KM----------------G----A--R---IR----T----S-  73
HIVLBV105   --------------T---------------M----------------G----A------L----PSV---S-  73
HIVLBV23    ----------------R-----------M----------------G----A-------G---T--Q--T-  73
HIVLBV2310  --------------S-----------------------------G----A-----L--------R--S-  73
HIVIC144    ------------------------------------------GF---A-----L------T----S-  73
HIVDJ258    --------------S-----------------------------G----A-----L--------G-ESK  73

CONSENSUS.B MGARASVLSgGeLDrWekIRLRPgGKKkYkLKHiVWASReLERFAvnPgLLEtseGCRqIlgQLqPsLqTGsE  73
HIVSF2      --------------K-------------------------------------------------------  73
HIVBZ167    ----------------------------R---V------------------AA------------------  73
HIVBZ190    -----------K--K------------R-Q----------------------A------------------  73
HIVBZ200    --------------K------------A-----------------------------K-I------------  73
HIVPH136    ----------------R-----------------------------------G------E----A------  73
HIVPH153    -----------K-----------------Q-----------------------------------H-A----T-  73
HIVTB132    -----------Q----K------------R-------------------------------------------  73
HIVLAI      -------------------------------------------------------------------------  73
HIVHXB2R    -------------------------------------------------------------------------  73
HIVBH102    -------------------------------------------------------------------------  73
HIVPV22     -------------------------------------------------------------------------  73
HIVMN       ----------------N--------------V---------------------------------------  73
HIVJH3      ------------------------------------------S------------------------  73
HIVJRCSF    ----------------------------R----------------------S---------------K----  73
HIVOYI      --------------K--------------Q---------------I----------------------K----  73
HIVNY5CG    --------------K------------Q-R-----------------------------R-----------  73
HIVNL43     --------------K------------Q-------------------------------------------  73
HIVCDC4     ------------------------Q-R---------K-------------K------------------  73
HIVHAN      --------------K--------------Q-----------------------------M-----------  73
HIVCAM1     --------------K-------------------------------------------------------  73
HIVRF       -----------K--K--------R---R-------------------S----A-----------A------  73
HIVD31      ----------------------------R-------------------------------------------  73
HIVJRFL     -----------K--K--------------R----------------------S-----------L-A-K----  73
HIVUG280    -------------------------------------------------------------------A------  73
HIVYU2      ---------A----K------------Q-R----------------D------------------------  73
HIVBCSG3C   -----------K--K-----------------L-----------------A------------------  73
```

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CONSENSUS.C MGARASiLrGgKLD?WEkIrLrPGGkKhYMiKHLVWASRELerFALnpgLLETseGCkqIikqLqPalQTGTe  72
HIVUG268    ------V-------T----K-------C--M----------G-----S-----------M----------D  73
HIVSM145    --------------A--R-----------------------------------------M----------  73
HIVZAM18    --------K-----T-------------------------------------------------SI-----  73
HIVZAM19    --------X-----A-------------------------------------------------------  73
HIVZAM20    --------------K-----------------------------------AD------R--H--------  73
HIVDJ259    ----------E---A----K-----R-R--L-----------K-----S-----------R----------  73
HIVVI313    --------------T--R-K-K--------M---------------D-------Q--RE---K---------K  73

CONSENSUS.D MGARASVLsGGkLD?WEkIrLRPGgkKKY?LKHivWASRELeRfalNPGLLETseGCkQIigQLqPaiqtGse  71
HIVELI      --------------K--------------R-------------Y--------------------------T-  73
HIVNDK      --------------T--R-----------A---LI---------T----------------------S------  73
HIVZ2Z6     --------------A--------------R---L--------------------D-------------R----  73
HIVVI203    --------T-----S--------------R-------------------------------E----S----T-  73
HIVVI205    --------------Q---------KS---R-----------K---------------R---E----------K  73
HIVG109     -----------Q--A--R-----------Q----------------------A-------E--H-NL-S---  73
HIVK31      --------------E----Q-----H---K---------------I-------P------M---H--------  73
HIVUG274    --------------E----------N---K---------------I-------------M------LK----  73
HIVUG270    --------------E----------N---K---L--------------------------M-----S------  73
HIVSE365    -----------Q--R--------------K--------------------------R---------------  73

CONSENSUS.F MGARASVLSGGKLDaWEKIrLRPGGkKKYr?KHLvWASRELERFA??PgLLETsEGCrkIIgQLQpSLQTGSE  70
HIVVI174    -------------------Q----------M--------------ID------P-----------T-------  73
HIVVI69     -------------------------R---KM---I----------LD--------------------------  73
HIVBZ162    ------------------------------L--------------IN----------Q---------------  73
HIVVI325    --------------T----------S----L--------------LN-S----T----Q--R-----------  73

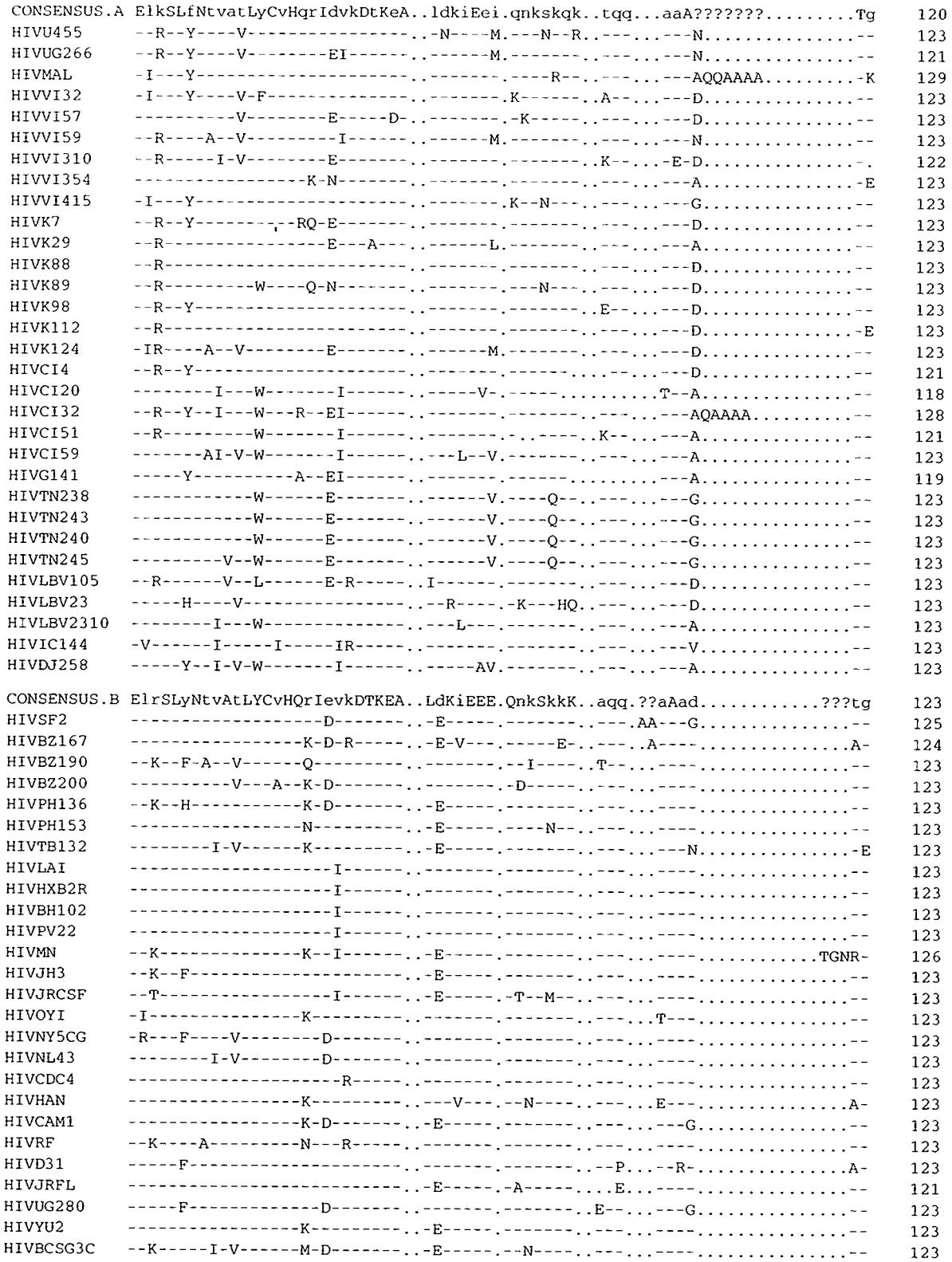
CONSENSUS.G MGARASVLSGGKLD?WEKIRLRPGGKK?YR?KHLVWASRELE?FALNPGLLETTEGCQQI??QLQP?LQTGTE  66
HIVVI191    --------------A------------Q--I-----------K-----------------MR----A------  73
HIVLBV217   --------------E------------K--M-----------R-----------------LQ----S------  73

CONSENSUS.H MGARASVLSGG?LDAWEKIRLRPGGKK?YRLKHLVWASRELERFALNP?LL?T?EGCLQ?IEQLQPALKTGTE  67
HIVVI525    -----------R--------------Q--------------------G--E-S-----I-------------  73
HIVVI557    -----------K--------------K--------------------D--D-A-----L-------------  73

CONSENSUS.O MGA?ASVLTGSKLDAWE?IRL?PGSKK?YRLKHLVWASRELER?ACNP?LLETAEG?E?LLQQLEPALKTGS?  64
HIVANT70    ---S-------------Q---K-----K---------------F----E-------N-K-------------D  73
HIVMVP51    ---R-------------R---R-----A---------------Y----G-------T-Q-------------E  73

SIVCPZGAB   MGARASVLTGGKLDRWEKVRLRPGGRKRYMMKHLVWASRELERFACDPGLMESKEGCTKLLQQLEPALKTGSE  73
```

HIV1 GAG


CONSENSUS.A ElkSLfNtvatLyCvHqrIdvkDtKeA..ldkiEei.qnkskqk..tqq...aaA???????.....Tg 120
HIVU455 --R--Y----V----------..-N----M.---N--R..---...---N.....-- 123
HIVUG266 --R--Y----V--------EI------..------M.-------..---...---N.....-- 121
HIVMAL -I---Y----------..-------.----R--..---...---AQQAAAA.....-K 129
HIVVI32 -I---Y----V-F----------..-------.K------..A--...---D.....-- 123
HIVVI57 ----------V--------E-----D-..-------.-K-----..---...---D.....-- 123
HIVVI59 --R----A--V---------I------..------M.-------..---...---N.....-- 123
HIVVI310 --R-----I-V--------E-------..-------.--------..K--...-E-D.....-. 122
HIVVI354 ----------K-N-------..-------.-------..---...---A.....-E 123
HIVVI415 -I---Y----------..-------.K--N---..---...---G.....-- 123
HIVK7 --R--Y--------,--RQ-E-------..-------.-------..---...---D.....-- 123
HIVK29 --R----------E---A---..------L.-------..---...---A.....-- 123
HIVK88 --R----------..-------.-------..---...---D.....-- 123
HIVK89 --R---------W----Q-N-------..-------.---N---..---...---D.....-- 123
HIVK98 --R--Y----------..-------.--------..E--...---D.....-- 123
HIVK112 --R----------..-------.-------..---...---D.....-E 123
HIVK124 -IR----A--V--------E-------..------M.-------..---...---D.....-- 123
HIVCI4 --R--Y----------..-------.------...---...---D.....-- 121
HIVCI20 --------I---W-------I------..-----V-.-----.....T--A.....-- 118
HIVCI32 --R--Y--I---W---R--EI------..-------.-------..---...---AQAAAA.....-- 128
HIVCI51 --R---------W--------I------..-------.-..-----..K--...---A.....-- 121
HIVCI59 -------AI-V-W-------I------..---L--V.-------..---...---A.....-- 123
HIVG141 -----Y----------A--EI------..-------.-------...---A.....-- 119
HIVTN238 ----------W------E-------..------V.----Q--..---...---G.....-- 123
HIVTN243 ----------W------E-------..------V.----Q--..---...---G.....-- 123
HIVTN240 ----------W------E-------..------V.----Q--..---...---G.....-- 123
HIVTN245 ---------V--W------E-------..------V.----Q--..---...---G.....-- 123
HIVLBV105 --R------V--L------E-R-----..I------.-------..---...---D.....-- 123
HIVLBV23 -----H----V----------..--R----.-K---HQ..---...---D.....-- 123
HIVLBV2310 --------I---W----------..---L---.-------..---...---A.....-- 123
HIVIC144 -V------I-----I-----IR-----..-------.-------..---...---V.....-- 123
HIVDJ258 -----Y--I-V-W-------I------..-----AV.-------..---...---A.....-- 123
CONSENSUS.B ElrSLyNtvAtLYCvHQrIevkDTKEA..LdKiEEE.QnkSkkK..aqq.??aAad.....???tg 123
HIVSF2 ----------D-------..-E-----.-------..---.AA---G.....-- 125
HIVBZ167 ----------K-D-R-----..-E-V---.-----E-..---..A----.....A- 124
HIVBZ190 --K--F-A--V------Q---------..-------.--I----..T--.....-- 123
HIVBZ200 ----------V---A--K-D-------..-------.-D-----..---.....-- 123
HIVPH136 --K--H----------K-D-------..-E-----.-------..---.....-- 123
HIVPH153 ----------N---------..-E-----.----N--..---.....-- 123
HIVTB132 --------I-V------K---------..-E-----.-------..---...---N.....-E 123
HIVLAI ----------I------..-------.-------..---..----.....-- 123
HIVHXB2R ----------I------..-------.-------..---..----.....-- 123
HIVBH102 ----------I------..-------.-------..---..----.....-- 123
HIVPV22 ----------I------..-------.-------..---..----.....-- 123
HIVMN --K----------K--I------..-E-----.-------..---..----.....TGNR- 126
HIVJH3 --K--F----------..-E-----.-------..---..----.....-- 123
HIVJRCSF --T----------I------..-E-----.-T--M--..---..----.....-- 123
HIVOYI -I----------K---------..-------.-------..---...T---.....-- 123
HIVNY5CG -R---F----V--------D-------..-------.-------..---..----.....-- 123
HIVNL43 --------I-V--------D-------..-------.-------..---..----.....-- 123
HIVCDC4 ----------R-----..-------.-------..---..----.....-- 123
HIVHAN ----------K---------..---V---.--N----..---...E---.....A- 123
HIVCAM1 ----------K-D-------..-E-----.-------..---.....-G.....-- 123
HIVRF --K----A---------N---R-----..-------.-------..---..----.....-- 123
HIVD31 -----F----------..-------.-------..--P....-R-.....A- 123
HIVJRFL ----------..-E-----.-A-----....E..----.....-- 121
HIVUG280 -----F----------D-------..-------.--------..E--.....---G.....-- 123
HIVYU2 ----------K---------..-E-----.-------..---..----.....-- 123
HIVBCSG3C --K-----I-V------M-D-------..-E-----.--N----..---..----.....-- 123

```
CONSENSUS.C ELrSL?NtVatLyCVH??IevrDTKEA..LDkieEE.QNK?QQK??Tqq..ak?AD.............?G   117
HIVUG268    -----Y----------KG---------..-------.---I---..-.....ET--.............K-   121
HIVSM145    -----F----------EK---------..-------.---S---..---..--A--.............-   123
HIVZAM18    --K--F---V--W---ED-T-------..--RL---.---S---TK---..--A--.............-   125
HIVZAM19    --K--H-A--V-----KX-T-------..--R----.---C---..----..--E--.............-   123
HIVZAM20    -----Y----------AG---------..-E----.---C---..----..--T--.............-   123
HIVDJ259    -----Y----------AR--IQ-----..-------.---C---..--K..-ET--.............K-   124
HIVVI313    --I--H----------EK--I------..----K--.---S---..----..-AA--.............N-   124

CONSENSUS.D elkSL?NTvATLYCVHerIeVkdTKEA..leKmEEE.qnKSKkK.?aQQ???atAD.............tr   120
HIVELI      --R--Y----------KG-D-------..-------.-------..---...-A--.............-G   123
HIVNDK      -IR--Y---------------------..V------.--------..T--...-A--.............    121
HIVZ2Z6     --R--F---------------------..-------.-----N-.K---...-A--.............AG   124
HIVVI203    -----F----------Q----------..-D-L---.-------..---...----.............--   123
HIVVI205    -I---F----------K----------..---L---.-------.R---...-A--.............-K   124
HIVG109     D----Y----------N----------..-------.-------..---AQQ----.............--   126
HIVK31      -I---Y----------AG-K-TN----..-D-I---.-T-----..---...E---.............--   123
HIVUG274    -I---F----------K-T------..-D-I---.-T-----..---...----.............--   123
HIVUG270    -V---F----------K-A------..-D-I---.-T-----..---...----.............--   123
HIVSE365    --R--Y--I--------K----------..V------.R------..V--...----.............SG   123

CONSENSUS.F ELrSL?NTv?vLYfVHQrvE?kDTKEA..L?KLEEE.QNKSqQK..tqQ...?aAd.............KG   115
HIVVI174    -----F--IV---Y------I-------..-E-----.-------..---...---.............--   122
HIVVI69     -----Y---A-------K--V-------..-E-----.--------..K---...V---.............--   123
HIVBZ162    -----Y---A----------V-------..-D-----.--------..-K-...A---.............--   123
HIVVI325    --K--F---VT--C----I-IR------..-D-----.----K---..A--...ET-N.............--   123

CONSENSUS.G E?KSL?N??A?L?C?HQRI?vKDTkEA..LeEVEKa.QknSQQK..tQq...????.............?kG   104
HIVVI191    -I---Y-TI-T-Y-V----EI---Q---..-Q-----.--K----..--T......E.............E-   120
HIVLBV217   -L---F-AV-V-W-I----G-------..------R.-------..I--...A..D.............--   121
HIVTAIG                        -------..-------.-R-----..---....AAS.............E--    30

CONSENSUS.H ELQSLFNLLA?LYCVHQRID?KDTKEA..L?K??E?.QN??Q??..TQQ...AT?D.............K?   105
HIVVI525    ----------V---------I-------..-S-IE-V.--NR-QK..---...--A-.............-E   123
HIVVI557    ----------T---------V-------..-E-LK-A.--KS-NR..---...--G-.............-G   123

CONSENSUS.O ?L?SLWNAI?VLWCVHNR??I?DTQQA..IQKLKEVM.?SRKSA..?AA....KE?.............TS   104
HIVANT70    S-Q------V--------YK-G-----..---------.G------..D--....--D.............--   122
HIVMVP51    D-K------A--------FD-R-----..---------.A-----..E--....--E.............--   122

SIVCPZGAB   GLRSLFNTLAVLWCIHSDITVEDTQKA..LEQLKR..HHG......EQQ..SKTESNSG............SR   122
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HIV1 GAG

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                          p17 \/ p24
CONSENSUS.A nss?????....kvSqNYPIVQNaQgQm?hQ?lSPrTLnAwVKviEekaFspEVIPmFsaLSEGATpQdLNmM  182
HIVU455     S.....------------PV--A-----------V-D-------------------------  183
HIVUG266    --N.....----------T-R--TY-A-------- ---V--------------------S------  184
HIVMAL      ---.....S---------------I--AI-----------------------------------  193
HIVVI32     --G.....----------------I--S-----------------------T---------------  187
HIVVI57     ---.....----------------I--AV----------------------------------  187
HIVVI59     --N.....---------------IV--A---K----X---V-------------E----------  187
HIVVI310    ---.....---H-----------V--S--------------R-----------------------  186
HIVVI354    ---.....----------------V--AM---------------G-------------------N--I-  187
HIVVI415    ---.....N---------------I--AI----------------------------------  187
HIVK7       ---.....-------------R--I--N--------X----------L-------------------V-  187
HIVK29      ---.....----------------T--S-----------------------------------  187
HIVK88      ---.....----------------I--T-----------------------------------  187
HIVK89      -N-.....----------------IL-T-----------------------------------  187
HIVK98      ---.....----------------I--N-----------------------------------V-  187
HIVK112     S--.....----------------I--N-----------------------------------  187
HIVK124     ---.....----------------I--S-----------------------------------  187
HIVCI4      --R.....Q---------------V--SI----------------------------------  185
HIVCI20     .--.....--------------T--SM-------------------------T----------  179
HIVCI32     .-N.....---------L----V--A--------------------------T----------T-  189
HIVCI51     .--.....--------------T--SI----------A---R-----------------------  182
HIVCI59     .-G.....--------------T--PM-------------------------T----------  184
HIVG141     SR-.....ST--------------V--AI----------------------------------  183
HIVTN238    S--.....----------------V--P------------V-K-G-N-----------------  187
HIVTN243    S--.....----------------V--P------------V---G-N-----------------  187
HIVTN240    S--.....----------------A--P------------V---G-N-----------------  187
HIVTN245    S--.....----------------A--P------------V---G-N-----------------  187
HIVLBV105   .--NKGSQ....N----------V----V--PV-----D---------G-N-------------  191
HIVLBV23    -G-.....----------------I--A----------A-------------T----------  187
HIVLBV2310  .--.....--------------T--PM----------------------------------  184
HIVIC144    .--.....--------------T--PI----------------------------------  184
HIVDJ258    .--.....--------------V--PM-------------------------T----------  184

CONSENSUS.B nss.....qVSqNYPIVQnlqGQMVHQaiSPRTLNAWVKVvEEKAFSPEVIPMFsALsEGATPQDLNTM  187
HIVSF2      ---.....-----------------------------------------------------  189
HIVBZ167    T--.....----------M-------------------I---------------------  188
HIVBZ190    -N-.....-------------------------------------------------A-----------  187
HIVBZ200    ---.....K-----------------------------------------------------  187
HIVPH136    -K-.....----------K---------L---------------------------------  187
HIVPH153    SC-.....----------I-----------------------------------------  187
HIVTB132    ---.....----------M-----------------------------------------  187
HIVLAI      H--.....----------I-----------------------------------------  187
HIVHXB2R    H-N.....----------I-----------------------------------------  187
HIVBH102    H--.....----------I-----------------------------------------  187
HIVPV22     H--.....----------I-----------------------------------------  187
HIVMN       ---.....----------IE----------------------------------------  190
HIVJH3      ---.....K---------I-----------------------------------------  187
HIVJRCSF    ---.....-------------------------------I---------------------  187
HIVOYI      ---.....-------------------P-----------------------------A-----------  187
HIVNY5CG    ---.....-----------------------------------------------------  187
HIVNL43     -N-.....-----------------------------------------------------  187
HIVCDC4     ---.....-------------------------------I------------A----------  187
HIVHAN      -RN.....-----------------------------------------------------  187
HIVCAM1     ---.....-----------------------------------------------------  187
HIVRF       -G-.....-----------------------------------------------------  187
HIVD31      -N-.....-------------------P---------------------------------  187
HIVJRFL     ---.....----------M-----------------------------------------  185
HIVUG280    ---.....----------I-----------------------------------------  187
HIVYU2      ---.....-----------------------------------------------------  187
HIVBCSG3C   ---.....---R-------I-----------------------------------------  187
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                          p17 \/ p24
CONSENSUS.C .............kVSQNyPIVQNLQGQMvHQaiSPRTLNAWVKVIEeKAfSpe?ipmftalsegatpqdlntm   177
HIVUG268    .............--------------------L--------------------V-------------------   182
HIVSM145    .............-------------------------------------------I-------------------   184
HIVZAM18    .............Q---------------I-----------------G------I-------------------   186
HIVZAM19    .............-----------------------------------X-----.....................   163
HIVZAM20    .............-----F-------------------------------L-QRI--------------------   184
HIVDJ259    .............-----F-------------PL--------------------V--------------------   185
HIVVI313    .............--------------------PM--------------------V--------------------   185

CONSENSUS.D nss.........QVSQNYPIVQNLQGQMVHQaiSPRTLNAWVkVIEEKaFsPEViPMFsALSEGATPQDLNtM   184
HIVELI      -N-.........-------------------------------------------------------------   187
HIVNDK      .--.........-------------------------------------------------------------   184
HIVZ2Z6     -N-.........-------------------------------------------------------------   188
HIVVI203    ---.........--------------------L-----------------N----------------------   187
HIVVI205    ---.........-----------------------------E-----------T------------------   188
HIVG109     --N.........--------------------L-----------------N-------A--------------   190
HIVK31      ---.........-------------------VM-----------------------------------------   187
HIVUG274    ---.........-------------------------------------------------T--------------   187
HIVUG270    ---.........-------------------------------------------------------------A-   187
HIVSE365    -N-.........--------------------L---------------D---------T--------------   187

CONSENSUS.F .............VSQNYPIVQNlQGQMVHQaiSPRTLNAWVKVIEEKAFSPEVIPMFSALseGATPQDLNTM   175
HIVVI174    .............-------------------------------------------------------------   182
HIVVI69     .............-------------------------------------------------------------   183
HIVBZ162    .............------------------S-----------------------------------------   183
HIVVI325    .............----------M-------PL---------------------------AD----------   183

CONSENSUS.G nsS.........QVSQNYPIVQnaQGQmvHQpisPRTLNAWVKVvEEKaFSPEVIPMFSALSEGATPQDLNtM   168
HIVVI191    ---.........--------------------LT----------I---N-----------------------   184
HIVLBV217   DN-.........-------------------------------------------------------------   185
HIVTAIG     ---.........----------xI---PI--A-------------------------------------I     93

CONSENSUS.H ???.........K?SQNYPIVQNAQGQ?VHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNAM   164
HIVVI525    KDK.........-V-------------M-----------------------------------------   187
HIVVI557    NGN.........-I-------------P-----------------------------------------   187

CONSENSUS.O .?R.........Q??QNYPIV?NAQGQMVHQAISPRTLNAWVKAVEEKAFNPEIIPMFMALSEGA??YDINTM   161
HIVANT70    .A-.........-AG------S-----------------------------------------IS------   185
HIVMVP51    .P-.........-TS------T-----------------------------------------VP------   185

SIVCPZGAB   EGGASQGASASAGISGNYPLVQNAQGQMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGALPQDVNTM   195
```

HIV1 GAG

```
CONSENSUS.A LNiVgGHQAAMQMLKdtINeEAAewDR?HPVhAgPippgQmREPrGSDIAGtTStlqEqigwmT...sNPPıP  251
HIVU455     --V----------------------L-------------------------V--------...G-----  253
HIVUG266    --V-E------------------ --L---Q-R--------------------V---VR --...------  252
HIVMAL      ----------------------D---V-----------------------------------...------  263
HIVVI32     ----------------A------G---L---------------------------P--------...------  257
HIVVI57     -------------------------L---------------------------P--------...------  257
HIVVI59     --V---------------------X--L-----R----------K---------------RX---...G-----  257
HIVVI310    -------------------------V---Q---V-----------------------------...----V-  256
HIVVI354    ----K---------------------I---Q------S-I--------------T---------...G-----  257
HIVVI415    -------------------------L---------------------------T----A---...G---N-  257
HIVK7       ----------------------X--L---------------------------P---LQ---...------  257
HIVK29      -------------------------L---------------------------P--------...G-----  257
HIVK88      -------------------------L---------------------------P--------...------  257
HIVK89      -------------------------L---------------------------P---L----...------  257
HIVK98      -------------------------L---------------------------P---LQ---...------  257
HIVK112     -------------------------L---------------------------P--------...------  257
HIVK124     --------------N----------L---------------------------P--------...------  257
HIVCI4      ------------------G-------V---------L-----------------------...----V-  255
HIVCI20     -------------------------V-----------------------------------...----V-  249
HIVCI32     --T---------------------V--------A---------------------A---...N-----  259
HIVCI51     -------------------------T---------------------V-----------...----T-  252
HIVCI59     -------------------------V---Q---------------------N---------...------  254
HIVG141     ----------------------D---T-------A---------------------------...------  253
HIVTN238    ---------------E----------V-----------------------------------...N-----  257
HIVTN243    ---------------E----------V-----------------------------------...N-----  257
HIVTN240    ---------------E----------V-----------------------------------...N-----  257
HIVTN245    ---------------E----------V-----------------------------------...N-----  257
HIVLBV105   -------------------------T---R-----------------------------I-...----V-  261
HIVLBV23    -------------------------V---Q---Y----L---------------A---Q---...------  257
HIVLBV2310  -------------------------V-----------------------N---------...------  254
HIVIC144    -------------------------V-----------------------N---$-----...------  253
HIVDJ258    -------------------------V-----------------------------------...------  254

CONSENSUS.B LNTVGGHQAAMQMLKeTINEEAAEwDRlHPvhAGPiaPGQMREPRGSDIAGTTSTLQEQIGWmT...nNPPiP  257
HIVSF2      -------------------------V-----------------------------------...------  259
HIVBZ167    ---------------D-----------------------------------------------...------  258
HIVBZ190    -----------------------------------------------------------------...------  257
HIVBZ200    ----------------------X-----------------------------------------...------  257
HIVPH136    ---------------------------------V-----------------------------...------  257
HIVPH153    -----------------------------------------------------------------...------  257
HIVTB132    -------------------------------------------------------------I-...H-----  257
HIVLAI      -------------------------V-----------------------------------...------  257
HIVHXB2R    -------------------------V-----------------------------------...------  257
HIVBH102    -------------------------V-----------------------------------...------  257
HIVPV22     -------------------------V-----------------------------------...------  257
HIVMN       ---------------------------------T-----------------------------...------  260
HIVJH3      ------------------------------AQ-------------------------------...S-----  257
HIVJRCSF    -----------------------------------------------------------------...------  257
HIVOYI      -----------------------------------------------------------------...------  257
HIVNY5CG    -----------------------------------------------------------------...H-----  257
HIVNL43     -----------------------------------------------------------------...H-----  257
HIVCDC4     -----------------------------------------------------------------...----T-  257
HIVHAN      -----------------------------------------------------------------...------  257
HIVCAM1     -----------------------------------------------------------------...------  257
HIVRF       -----------------------------------------------------------------...------  257
HIVD31      -----------------------------------------------------------------...------  257
HIVJRFL     -----------------------------------------------------------------...------  255
HIVUG280    -----------------------------------------------------------------...------  257
HIVYU2      -----------------------------------------------------------------...------  257
HIVBCSG3C   ------------------------------Q---V-----------------------------...------  257
```

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CONSENSUS.C lntvgghqaamqmlkdtineeaaewdrlhpvhagpvapgqmRePRGSDIAGTTStLQEQIaWMT...?NPPiP  246
HIVUG268    ------------------------------------------------------------N---...S-----  252
HIVSM145    --------------------------------Q----------D----------------...S-----  254
HIVZAM18    ----------------------------------N----L----------------------...N---V-  256
HIVZAM19    ..................................-----------------------------...N---V-  193
HIVZAM20    ---------------------------I-------------------------------------...A---V-  254
HIVDJ259    ----------------------------------I-----------------N----------...S-----  255
HIVVI313    --------------------------------Q--------I----------------------...N-----  255

CONSENSUS.D LNTvGGHqAAMQMLKETIneEAAEWDRlHPvHAGPiAPGQMREPRGSDIAGTTStLQEQi?WMT...sNPPIP  253
HIVELI      ------------------------------------------------------------A---...------  257
HIVNDK      ------------------D---------------V----------------------A---...------  254
HIVZ2Z6     ------------------------------------------------------------A---...------  258
HIVVI203    ------------------------------------------------------------G---...------  257
HIVVI205    -------H----------I-----------------------------------------A---...------  258
HIVG109     ---A--------------------------------------------------------A---...A-----  260
HIVK31      ------------------------------A-----------------------------G---...N-----  257
HIVUG274    --------------------------V-------------------------------G---...------  257
HIVUG270    ------------------------------------------------------I----VG---...------  257
HIVSE365    ------------------------------------------------------------G---...N-----  257

CONSENSUS.F LNTVGGHQAAMQMLKDTINEEAAEWDRLHPv?AGPiPPGQ?REPRGSDIAGTTSTLQEQIqWMT...sNPPvP  243
HIVVI174    --------------------------------Q--------I----------------------...N-----  252
HIVVI69     ------------------------------H---N----M----------------------...----I-  253
HIVBZ162    ------------------------------AQ--------I----------------------...------  253
HIVVI325    ------------------------------H--------M------------------T---...------  253

CONSENSUS.G lNTVGGHQAAMQMlKDTINEEAAEWDRIHPpQAGPIpPGQIRdPRGSDIAGTTSTLQEQIRWMT...SNPPIP  238
HIVVI191    ------------------------------------------E---------------------...------  254
HIVLBV217   --------------------------------Q-----------------------------...------  255
HIVTAIG     S------------S---------------------A---------------------------...------  163

CONSENSUS.H LN?VGGHQAAMQ?LKDTINEEAAEWDR?HPVHAGPIPPGQMREPRGSDIAGTTSTLQEQIAWMT...?NP?IP  229
HIVVI525    --T---------I--------------L-----------------------------------...G--A--  257
HIVVI557    --I---------M--------------V-----------------------------------...S--P--  257

CONSENSUS.O LNAIGGHQGALQVLKEVINEEA?EWDRTHPP??GPLPPGQIREPTGSDIAGTTSTQQEQI?WTT..R????IP  224
HIVANT70    ----------------------V--------PV--------------------------H---..-PNQP--  256
HIVMVP51    ----------------------A--------AM--------------------------I---..-GANS--  256

SIVCPZGAB   LNAVGGHQGAMQVLKEVINEEAAEWDRLHPTHAGPIAPGQLREPRGSDIAGTTSTLQEQIGWTT...ANPPIP  265
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HIV1 GAG

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CONSENSUS.A VGdIYkrwIiLGLNKIVRMYSPvSILDirQgPKEPFrdYVdrFfKtLRAeqAtQeVKnwMTeTLLvQNANPDC  324
HIVU455     -----R-----------------------------------------------D-----------------  326
HIVUG266    --E--R- ----------------------E-----KE---K-----------D--- --------------  323
HIVMAL      ------------------------------------------------------------------------  336
HIVVI32     ----------------------------K-------------------------G-----------------  330
HIVVI57     ----------------------------K----------------V------S-D-----------------  330
HIVVI59     -----R---------------------V--R-----K--------I-------------------------  330
HIVVI310    --E-----------------------------------------------------A-----------------  329
HIVVI354    --K---K$-------------------------------E--N--------K--------$-------------  328
HIVVI415    ----------------------T----VK----------------I-----------G---------------  330
HIVK7       ------------------------------R--------------A------S-D--GX--------------  330
HIVK29      ----------------------------K-----------------------G-------I-------  330
HIVK88      --------------------------VK-----------------------G---------------  330
HIVK89      ----------------------------K-----------------------D-----------------  330
HIVK98      ----------------------------K----------------A-----------G---------------  330
HIVK112     ----------------------------K-----------------------G---------------  330
HIVK124     ----------------------------K-----------------------G---------------  330
HIVCI4      --E--R-----------------------------------------C-------------------I-------  328
HIVCI20     --E------V------------------------------------------------------------  322
HIVCI32     --E-------------------------------------Y--------S-------------------  332
HIVCI51     --E---K---------------------------------------------------------------  325
HIVCI59     --E------V--------------------------------------X----------------------  327
HIVG141     --E-------------------------------------------------------------------  326
HIVTN238    ----------------------I--------------------Y-----------------------------  330
HIVTN243    ----------------------I--------------------Y-----------------------------  330
HIVTN240    ---------------------------------------------Y-----------------------------  330
HIVTN245    ---------------------------------------------Y-----------------------------  330
HIVLBV105   ----------------------------K-----------------------D------D-----------  334
HIVLBV23    -----RK---------------------------------------------D-----------------  330
HIVLBV2310  --E------V-----------------------------------V---------------------------  327
HIVIC144    --E------V---------------------------------------S-------------------  326
HIVDJ258    ------------------------------------------------------------------------  327

CONSENSUS.B VGeIYKRwIIlGLNKIVRMYSPtSILDIrQGPKEpFRDYvDRFYKTLRAEQAsQeVKNwmTETlLVqNaNPDC  330
HIVSF2      ---------------------------------------------------D-----------------  332
HIVBZ167    --K-------------------I-------------------------------D-----------------  331
HIVBZ190    ----------M-----------------K-----------------------------------------S----  330
HIVBZ200    -------X---------------------------------------------------------------  330
HIVPH136    ----------M-----------------K---------------------------------------------  330
HIVPH153    ---------------------------------------------------D-----------------  330
HIVTB132    ------------------------------------------------------------------P------  330
HIVLAI      ------------------------------------------------------------------------  330
HIVHXB2R    ------------------------------------------------------------------------  330
HIVBH102    ------------------------------------------------------------------------  330
HIVPV22     ---------------------------------------L--------------------------------  330
HIVMN       ----------------------S-----------------------------------RT-------------  333
HIVJH3      ----------------------S---------------------------------------------------  330
HIVJRCSF    ----------------------V-----------------------------T--------------------  330
HIVOYI      ---------------------------------------------------D-----------------  330
HIVNY5CG    ------------------------------------------------------------------------  330
HIVNL43     ------------------------------------------------------------------------  330
HIVCDC4     ----------------------I---------------------------------------------------  330
HIVHAN      ---------------------------K----------------------T--------------------  330
HIVCAM1     ------------------------------------------------------------------------  330
HIVRF       ----------------------I-------------------------------D--------F---------  330
HIVD31      ---------------------------------------------------T--------------------  330
HIVJRFL     ------------------------------------------------------------------------  328
HIVUG280    ---------------------------K-----------------------------------------S----  330
HIVYU2      ------------------------------------------------------------------------  330
HIVBCSG3C   ----------------------S-----------S-----------------------------------  330
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CONSENSUS.C VGdIYKRWIILGLNKIVRMYSPVSILDIkQGPKEPFRDYVDRFFKTLRAEQAtQDVKNWMTdTLLVQNANPDC  319
HIVUG268    --E-------------------------------------------------------------------  325
HIVSM145    -------------------------------------------------------------------  327
HIVZAM18    ----------------------------------------------------------E----------  329
HIVZAM19    ----------------------------R-----------------------------E----------  266
HIVZAM20    --E-------------------------R-----------------------------------------  327
HIVDJ259    ----------------------------R----------------------S-------------------  328
HIVVI313    -------------------------------------------------------------------  328

CONSENSUS.D VgeIYKrWIIlGLNKIVrMYSPVSILDIRQGPKePFRDYVDRFYKTLRAEQAsQdVKnWMTETLLVQNANPDC  326
HIVELI      ----------V-------------------------------------------------------------  330
HIVNDK      -------------------------------------------------------------------  327
HIVZ2Z6     ---------------------------------------------------E--G---------------  331
HIVVI203    ---------------------------------------------------T-E-----------------  330
HIVVI205    -KK--------------K---------------K-----------------------------------  331
HIVG109     ------K---M-------------------------------------------------------------  333
HIVK31      -------------------------------------------------------------------  330
HIVUG274    -------------------------------------------------------------------  330
HIVUG270    -------------------------------------------------------------------  330
HIVSE365    ---------------------------------------------------T-E-----------------  330

CONSENSUS.F VGeIYKRWIILGLNKIVRMYSPVSILDIrQGPKEpFRDYVDRFFKTLRAEqATQEVKgWMTDTLLvQNANPDC  316
HIVVI174    -------------------------------------------------------------------  325
HIVVI69     --D-----------------------------------------------E--------------I-------  326
HIVBZ162    -------------------------------------------------------------------  326
HIVVI325    ----------------------------K-----S----------------------N---------------  326

CONSENSUS.G VGeIYKRWIILGLNKIVRMYSPVSILDIRQGPKEPFRDYVDRFFKTLRAEQATQ?VK?WMTDTLLVQNANPDC  309
HIVVI191    --D---------------------------------------------------E--G---------------  327
HIVLBV217   ---------------------------------------------------D--N---------------  328
HIVTAIG     ----------------------                                                  185

CONSENSUS.H VGDIYKRWIILGLNKIVRMYSPVSILDI?QGPKEPFRDYVDRFFK?LRAEQATQ?VK?WMTDTLLVQNANPDC  298
HIVVI525    ----------------------------K----------------T--------D--N---------------  330
HIVVI557    ----------------------------R----------------A--------E--G---------------  330

CONSENSUS.O VGDIYRKWIVLGLNKMVKMYSPVSILDI?QGPKEPFRDYVDRFYKTLRAEQATQEVKNWMTETLLVQN?NPDC  295
HIVANT70    ----------------------------K---------------------------------------A----  329
HIVMVP51    ----------------------------R---------------------------------------S----  329

SIVCPZGAB   VGDVYRRWVILGLNKVVRMYCPVSILDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTDTLLVQNANPDC  338
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HIV1 GAG

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                                        p24 \/  \/  'p2'       \/ p7
CONSENSUS.A KsILraLg?gAtLeEMMTacQgVggPgHKArvLAEAmSqvq??n...???iMmQrGnf.?Gqkr?iKCFNCGk  385
HIVU455     --------P-------------------------------QTS.....--------.R-PR-.--------  391
HIVUG266    -------RPK-----------R-R--S---Q----------QTS.....--------.K----.--------  388
HIVMAL      -T--K---P-----------------S------------ATNST....AA--------.K----.--------  403
HIVVI32     --------P-------------------------------H--QA-.....-------I.R-GXKR--------  396
HIVVI57     --------T-----------------S--------------QP-.....--------.R--RG.--------  395
HIVVI59     ----KR-RVR-------------------K-----I----QTS.....--------.K----.--------  395
HIVVI310    ----K---T-----------------S----I-------A-HT-.....--I-----.K----.--------  394
HIVVI354    -T---G--A----K-------E--E---------------HNTS.....--------.K---K.--------  393
HIVVI415    -T------T---------------------------------HT-.....--------.K--R-.--------  395
HIVK7       ----K---T-----------------S---K--------A-QT-.....--------.K---T.--------  395
HIVK29      --------A----------S---------------------HT-.....--------.R----.--------  395
HIVK88      --------T---------------------------------HT-.....--------.R----.--------  395
HIVK89      --------T---------------------------------HT-.....--------.R----.--------  395
HIVK98      ----K---T---------------------------------QA-.....--------.R----.--------  395
HIVK112     -----G--T----------------------I---------HT-.....--------.R----.--------  395
HIVK124     --------A-----------------S------------ATNNI...NAAV-------.K-P-KI--------  399
HIVCI4      --------T---------------------------------HT-.....----K---.R----.--------  393
HIVCI20     --------P---------------------------------QS-.....--------.R--RT.--------  387
HIVCI32     ----K---P---------------------------------QS-.....--------.K--RKFV-------  398
HIVCI51     --------P---------S----------------------QS-.....--------.R--RT.--------  390
HIVCI59     --------P---------------------------------QS-.....--------.G--RT.--------  392
HIVG141     -T------P---------------------------------NA-.....----K---.K----.--------  391
HIVTN238    ----K---T-----------------S-----------HA-QAS.....--------.K---G.-------R  395
HIVTN243    ----K---T-----------------S-----------HA-HA-.....--------.K----.--------  395
HIVTN240    ----K---T-----------------S-----------HA-HAT.....--------.K----.-------R  395
HIVTN245    ----K---S-----------------S-----------HA-HA-.....--------.K----.-------R  395
HIVLBV105   -T------P--S-----------------------------HP-.....--------.K----I--------  400
HIVLBV23    -T------A---------------------------------HT-.....V-------.R----.--------  395
HIVLBV2310  --------PA--------------------------------QT-.....--------.R--RT.--------  392
HIVIC144    -T------P---------------------------------QS-.....--------.R--RT.--------  391
HIVDJ258    --------P---------S----------------------QS-.....------D-.R--RT.--------  392

CONSENSUS.B KTILKALGPaATLEEMMtACQGVGGPgHKARvLAEAMSqv..tn..?satiMmQrGnF.rnqrKtvKCFNCGK  397
HIVSF2      ----------------------------------------..--...P-N--------.--------------  399
HIVBZ167    ----------------------------------------..P-..S-------K---.-----I--------  399
HIVBZ190    ----------------------------------------..--...----------.--------------  397
HIVBZ200    -----------------S--------------------X-..--...--A--------.--------------  397
HIVPH136    ------------------------S-------------..--...---A-------.-----I--------  397
HIVPH153    -------------------------------------A..--...---M-L-----.--T-----------  397
HIVTB132    ----------------------------------------..--...-------K-K-.-----I--------  397
HIVLAI      ----------------------------------------..--...----------.-----I--------  397
HIVHXB2R    ----------------------------------------..--...----------.-----I--------  397
HIVBH102    ----------------------------------------..--...T---------.-----M--------  397
HIVPV22     ----------------------------------------..--...T---------.-----M--------  397
HIVMN       ----------------------------------------..--...----------.-----II-------  400
HIVJH3      ----------------------------------------..--...-T--------.-----II-------  397
HIVJRCSF    ----------------------------------------..--...P---------.-----N--------  397
HIVOYI      ----------------------------------------...-...-V-V---K---.K------------  396
HIVNY5CG    ----------------------------------------..--...P----I-----.---K---------  397
HIVNL43     ---------G------------------------------..--...P----I-K---.--------------  397
HIVCDC4     ----------------------------------------..--...----------.-R-G---------  397
HIVHAN      ----------------------------------------..-G...--A--------.--------------  397
HIVCAM1     ----------------------------------------..--...----------.--------------  397
HIVRF       ------------------------S----I--------..--...-----L-K---.-D---I--------  397
HIVD31      ----------------------------------------..--...---V-------.--------------  397
HIVJRFL     ----------------------------------------..--...P---------.-----I--------  395
HIVUG280    ----------------------------------------..--...PVN----N---.-----I--------  397
HIVYU2      ----------------------------------------..--...----------.--------------  397
HIVBCSG3C   ---------G------------------------------..--...----------.--------------  397
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                                        p24 \/  \/  'p2'       \/ p7
CONSENSUS.C KTILRALGPgAsLEEMMTACQGVGGPsHKARVLAEAMSQann?n......imMQrsNF.KGpkrivKCFNCGK    384
HIVUG268    -------------------------G--------------I-......--------.------I-------    391
HIVSM145    -------------------------A--------------I-......-L---G--.--S-----------    393
HIVZAM18    ---------A-T-------------------------------T-......-L------.-----S--------    395
HIVZAM19    ---------A-T-------------------------------STT......X-------.---RX---------    332
HIVZAM20    -----------T---------------------------T-SA-......V----G--.-----T--------    393
HIVDJ259    ----------------------------------------T-T-.....----K---.---RKTI-------    394
HIVVI313    -------------------------G--------------I-.....----K---.------I-------    394

CONSENSUS.D ktILKALGP?ATLeEMMTACQgVGgPsHKARVLAEAMSQa?.tn..s?taimMQrgNF.KGprkiiKCFNCGk    392
HIVELI      ---------Q-------------------------------..--..-V-TA-------.--------------    398
HIVNDK      ---------Q----------------G------------V..-G..-A--V-------.-----S--------    395
HIVZ2Z6     ---------Q-------------------------------..--..-AA-V-------.-----T--------    399
HIVVI203    ---------G-------------------------------..--..TNV---------.---KR---------    398
HIVVI205    ---------Q---K-------E-------------------..-S..-A--VI------.---K----------    399
HIVG109     ---------A-------------------------------..-S..-NA-----K---.-----VV------R    401
HIVK31      ---------G----------------G-------------N.G-....----------.--Q-----------    397
HIVUG274    R--------G-------------------------------..--..AN----------.--------------    398
HIVUG270    ---------A-------------------------------..S-..ANA------A--.---KRN--------    398
HIVSE365    -N-------G--------------E---------------..-S..-AA---------.--Q---V-------    398

CONSENSUS.F KTILKAlGPGAtLEEMMTACQGVGGPGHKARvLAEaMSQa..TN..??a?ImMQksNF.KGQRrivKCFNCGk    381
HIVVI174    ----------------------------------------..--..TA-A--------.--------------    393
HIVVI69     ------M-----------------------------T----..--.....-A--------.-----T--------    392
HIVBZ162    ----------------------------------------..--.....-T-L------.--------------    392
HIVVI325    -----------S-------------------I-------V..--.....TT----RG--.----K-I------R    392

CONSENSUS.G KTIL?ALGPGATLEEMMTACQGVGGP?HKARVLAEAMSQA..SG..?A?A?MMQK??F.KGP???IKCF?CGK    366
HIVVI191    ----R--------------------G-------------..--..V-A-M----SG-.---KRT----N---    395
HIVLBV217   ----K--------------------S-------------..--..T-T-I----GN-.---RKN----D---    396

CONSENSUS.H K?IL?ALG?GASIEEMMTACQGVGGP?HKA?VLAEAMSQV.?TN..??A??MMQKGNF.KGQRRI?KCFNCGK    356
HIVVI525    -N--K---T-----------------S---R---------..--..TH-AI-------.------V-------    398
HIVVI557    -T--R---Q-----------------G---K---------.N--....-VM-------.------I-------    397

CONSENSUS.Ó KQILK?LGP?ATLEEMMVACQGVGGPTHKA??LAEAMA?AQQDLKGGYTAVFMQRGQN.P?RKG?IKCFNCGK    360
HIVANT70    -----S---G--------------------RV------T-------------------.-I---T--------    401
HIVMVP51    -----A---E--------------------KI------S-------------------.-N---P--------    401

SIVCPZGAB   KQILKALGPGATLEEMMTACQGVGGPSHKARVLAEAMSMVQ.NQ..GRADVFFQKGQG.AGPKRKIKCFNCGK    407
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HIV1 GAG

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                                        pol cds ->
                                             p7 \/     'p1'      \/ p6
CONSENSUS.A EGHlArNCrAPrKkGCwKCgkEGHQmKdCT.?e.rQANFlgkiwpSsKG.RPgNFpQsRp.....    441
HIVU455     -----K-----------------------..-.-----------N--.----------.....    447
HIVUG266    --------K--K---- --K-----I----..-.------K--------.--R-------.....    443
HIVMAL      ------------------------------..-.------------H--.-----L----.....    459
HIVVI32     ------------------------------.N-.------------N--.----------.....    453
HIVVI57     ------------------------------..-.---------------.----------.....    451
HIVVI59     ----------------X--R----------..-.---------------.----------.....    451
HIVVI310    --------------------N---------..-.------------T--.-------N-L.....    450
HIVVI354    --------K---------------I-N--..K.------------N--.-----L-N--.....    449
HIVVI415    ------------------------------..-.----------S----.----------.....    451
HIVK7       ----------------X--R-----L----..-.------RR-X-----.----------.....    451
HIVK29      ------------------------------..D.--------L------.-------N-L.....    451
HIVK88      ------------------------------..-.G--------------.-------N-L.....    451
HIVK89      --------------------------E--..-.-------R-------.-------N-L.....    451
HIVK98      ------------------------------..-.-------R-------.----------.....    451
HIVK112     -------------R----------------..-.---------------.-------N-L.....    451
HIVK124     ---I-K-------R------R---------..-.------------H--.-----L----.....    455
HIVCI4      ------------------------------..-.---------------.----------.....    449
HIVCI20     --------K----R----------------..-.---------------.----------.....    443
HIVCI32     ---I-K-------------------------..-.-----I---------.----------.....    454
HIVCI51     --------K-----------R---------..-.---------------.----------.....    446
HIVCI59     --------K----R----------------..-.---------------.-------G--.....    448
HIVG141     ------------------------------..-.------------N--.----------.....    447
HIVTN238    ------------------------------..-.------------N--.----------.....    451
HIVTN243    --------------------R---------..-.------------N--.----------.....    451
HIVTN240    ------------------------------..-.------------N--.----------.....    451
HIVTN245    ------------------------------..-.------------N--.----------.....    451
HIVLBV105   ------------------------------..-.---------------.-----L---T.....    456
HIVLBV23    ------------------------------..-.---------------.----------.....    451
HIVLBV2310  --------K----R----------------..-.---------------.----------.....    448
HIVIC144    --------K---------------------..-.---------------.--R------T.....    447
HIVDJ258    --------K---------------------..-.------------T--.----------.....    448

CONSENSUS.B eGHiAkNCrAPRkkGCWkCGkEGHQMKdCt.?E?RQANFLGKIWPShKG.RpgNFlQsRp?????????..??    453
HIVSF2      -----------------R--R---------..-.------------Y--.----------.....    455
HIVBZ167    ----------------------------S..-.------------Y--.----------.....    455
HIVBZ190    ----------------------------S..-.---------------.----------.....    453
HIVBZ200    --------------------R---------..-.------------N--.-------N--.....    453
HIVPH136    --------------------R---------..-.---------------.----------.....    453
HIVPH153    -----R--K-----------R---------..-.---------------.----------.....    453
HIVTB132    -----------------R------------..-.---------------.----------.....    453
HIVLAI      -----R-------------------------..-.------------Y--.----------EPTAPPFLQ..SR    464
HIVHXB2R    ---T-R-------------------------..-.------------Y--.----------.....    453
HIVBH102    ---T-R-------------------------..-.------------Y--.----------EPTAPPFLQ..SR    464
HIVPV22     ---T-R-------------------------..-.------------Y--.----------EPTAPPFLQ..SR    464
HIVMN       -------------R----------------..-.------------C--.-.R--P---T.....    455
HIVJH3      ---L-R-----------------------N..-.------------S--.----------.....    453
HIVJRCSF    -----R---------------------E--..-.------------Y--.----------.....    453
HIVOYI      --------------------R---------..-.---------------.-------N--.....    452
HIVNY5CG    ------------------------------..-.---------------.----------.....    453
HIVNL43     ------------------------------..-.---------------.----------.....    453
HIVCDC4     -----R--K-----------R---------..-.---------------.----------.....    453
HIVHAN      -----R-------------------------..-.---------------.----------.....    453
HIVCAM1     V----------------------------N..-.---------------.----------.....    453
HIVRF       V--------------------------.N-G---------------.----------.....    455
HIVD31      ------------R----------------..-.------------Y--.-------R--.....    453
HIVJRFL     -----R-------------------------..-.------------Y--.----------.....    451
HIVUG280    V----------------------------N.N-.------------Y--.----------.....    454
HIVYU2      ------------------------------..-.---------------.----------.....    453
HIVBCSG3C   -----R--K----R----------------..-.---------------.-----P---L.....    453
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                                        pol cds ->
                                           p7 \/     'p1'      \/ p6
CONSENSUS.C EGHiArnCRAPRKKGCWKCG?EGHQMKDCT..E.RQANFLGKIWPs?KG.RPGNFLQsRPeptap????????   443
HIVUG268    ---L----------------R---------..-.-----------PN--.---------------PA......   454
HIVSM145    --------------------K---------..-.------------H--.-------N-------PAESFRVR   462
HIVZAM18    -----K--------------K---------..-.------------H--.---------------.......R   457
HIVZAM19    -----KI-------------X---------..-.------------H--.----------.............   388
HIVZAM20    --------------------R---------..-.------------Q--.-------N-------PAENFR..   460
HIVDJ259    ---L----------------R---------..-.------------N--.----------.............   450
HIVVI313    ---L----------------K---------..-.------------Y--.-------N--.............   450

CONSENSUS.D EGHiAkNCrAPrkkGCWkCGkEGHQmKdCT..e.RQANFLGkiWPShKG.rPGNFlQSRp.............   448
HIVELI      -----------------R-------L----..-.--------R-------.----------.............   454
HIVNDK      ---T----------------R---------..-.---------------.----------.............   451
HIVZ2Z6     ------------R------------L----..-.---------------.----------.............   455
HIVVI203    ---L--------------------------..-.---------------.----------.............   454
HIVVI205    -----------K--------R----I----..-.------------L--.----------.............   455
HIVG109     -------------R----------------..-.------------N--.----------.............   457
HIVK31      ---L----------------R---------..-.-------RL---R--.G---------.............   453
HIVUG274    --------------------------E--..-.---------------.---------L.............   454
HIVUG270    ---L------------ ---R----I----..-.---------------.----------.............   453
HIVSE365    -----R--K-----------Q---------..G.------------S--.-----P----.............   454

CONSENSUS.F eGHiAknCRAPRKKGCWKCGrEGHQMKDCT..E.rQANFLGKIWPSnKG.rPGNFLQsRP.............   437
HIVVI174    -----R-----------------------..-.---------------.----------.............   449
HIVVI69     ---V-------------------------..-.---------------.----------.............   448
HIVBZ162    T-----------------------------..-.G----------H--.-------N--.............   448
HIVVI325    ------H-------------K---------..-.---------------.K---------.............   448

CONSENSUS.G EGHLARNCRAPRK?GCWKCG?EGHQMKDCT..E.RQANFLG?IWPSHKG.RPGNFLQ?R?.............   417
HIVVI191    -------------K------R---------..-.-------R-------.-------I-T.............   451
HIVLBV217   -------------R------K---------..-.-------K-------.-------N-P.............   452

CONSENSUS.H EGH?ARNCRAPRKKGCWKCG?EGHQ?KDCT..E.RQANFLGKIW???KG.RPGNFLQSRP.............   406
HIVVI525    ---I----------------R----M----..-.----------PSS--.----------.............   454
HIVVI557    ---L----------------K----L----..-.----------SPN--.----------.............   453

CONSENSUS.O EGHIA?NCRAPRK?GCWKCGQEGHQMKDC?..NG?QANFLGKYWPPGGT.RPGNYVQ???.............   410
HIVANT70    -----R-------K---------------R..--K--------------.-------RPA.............   458
HIVMVP51    -----K-------R---------------K..--R--------------.-------KQV.............   458

SIVCPZGAB   EGHLARNCKAPRRKGCWRCGQEGHQMKDCT..G.RQVNFLGKGWPSRSG.RPGNFVQNRT.............   463
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HIV1 GAG

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                          \/ (minor)                \/ (minor)        / p6 terminus (80%)
CONSENSUS.A .EPtAPpAE?f?gmgeeit.s?...?pkqeqkd..??ke??ppl?SlKSLFGNDpLSQ                    483
HIVU455     .--------I-.----KM-.-P....A---L--....R-QT.--V-------------                    493
HIVUG266    .--------IL.R-K--M-.-P.....---K---.....--.QT--I-----                         480
HIVMAL      .--------S-.-F----K.PS....Q------.....--LY.--A---------Q---                  505
HIVVI32     .--S-----I-.------A.-P....-------....R-QSQ--V----                            491
HIVVI57     .--------L-.------A.-P....-------....RGQG---V----                            489
HIVVI59     .--------IL.RIRK-M-.-P....-----T..........-SI----                            483
HIVVI310    .--------S-.----D--.-S....Q-------....R-HP---V----                           488
HIVVI354    .--------S-.-F----A.PS....-RP-PRE.....--RY.--T----                           486
HIVVI415    .--------IV.---G--..-P....-------.....R-QA---V----                           486
HIVK7       .--------I-.RIE---A.-....P-------.....--QP.-SV----                           488
HIVK29      .--------I-.-------.-P....-------....R-QA---T----                            489
HIVK88      .--------IC.------A.-P....-----R-....R-QT---V----                            489
HIVK89      .--------IC.------A.-P....S------....R-Q..ASI----                            487
HIVK98      .--------I-.-------.-P....-------....R-QP.--V----                            488
HIVK112     .--------I-.-----MA.-P....-------....R-QT--SI----                            489
HIVK124     .--------S-.-F-----.PS....Q---P--....--LY.--A-V--                            492
HIVCI4      .--------LL.-------.-S....-----.....R-QP.-SI----                            484
HIVCI20     .--------S-.--R----.-S....----PR-....-GLY---A----                            481
HIVCI32     .--------S-.--E---A.-S....----PG-....-GLY---A----                            492
HIVCI51     .--------S-.-L-----.-S....LQ--PR-....-GLY---A----                            484
HIVCI59     .--------N-.--E-Q--.-S....----PR-....-GLY---T----                            486
HIVG141     .--S-----S-.-F-----.PS....Q------..KD--LY.--A----                            486
HIVTN238    .--------NW.-------.-L....L------....--HP---V----                            489
HIVTN243    .--------DW.-R---T-.-L....L------....--DP---V----------                      495
HIVTN240    .--------NW.-------.-L....-------....--HP---V----                            489
HIVTN245    .--------NW.-------.-L....L------....--HP---V----                            489
HIVLBV105   .--S-----S-.-F---V-.PS....-------....--LY---T----                            494
HIVLBV23    .--------MIF-------.-P....--K----....R-QPL-SV----                            490
HIVLBV2310  .--------S-.-------.-S....----PR-....-GLY---T----                            486
HIVIC144    .--------S-.--.--K-.TS...S-Q--PR-....--LY---T----                            485
HIVDJ258    .-----L--S-.-------.-P....----PRE....QGLY---T----                            486

CONSENSUS.B ?EPTAPpeesf.rfgeetttPs????qKQEpiD....kelY?plasLrsLFGnDPsSq                   500
HIVSF2      .----------.-----K----....-------....-----.--T-------------                  502
HIVBZ167    .--------I-.----------....----TK-....-----.-----K-                           493
HIVBZ190    .----------.----------....-----V-....Q-K-.---A---                           491
HIVBZ200    .------A---.G----M.---....P---QK-....EG--P-------                            491
HIVPH136    .----------.----------....-------....-----.-----K-                          491
HIVPH153    .----------.--R------P....-------....-----.-S---KL                          491
HIVTB132    .------A---.----------....----T--....-----.--TA-K-------                     497
HIVLAI      P----------.-S-V------....-------....-----.--T-------------                  512
HIVHXB2R    .----------.-S-V-----P....-------....-----.--T-------------                  500
HIVBH102    P----------.-S-V-----P....-------....-----.--T-------------                  512
HIVPV22     P----------.-S-V-----P....-------....-----.--T-------------                  512
HIVMN       .----------.---------YQKQEK---T--....-D--.-----K-------L--                  506
HIVJH3      .----------.----------....-----R-....-----.---------------P                 500
HIVJRCSF    .----------.------A---QKQE-------....-----.--T-------------                 504
HIVOYI      .------A---.G--------P....-------....-G--.--T-------------                  499
HIVNY5CG    .----------.----------....-------....-----.----------S-----                 500
HIVNL43     .----------.----------....-------....-----.----------S-----                 500
HIVCDC4     .----------.---D------....-----R-....-----.---------------                 500
HIVHAN      .----------.-----.A-A--....-------....-----.-----K----S-----                499
HIVCAM1     .----------.-----K----....-------....-----.---------------                 500
HIVRF       .----------.-----.----....----K--....-----.-----K----------                501
HIVD31      .----------.------A--F....-------....-----.---------------                 500
HIVJRFL     .-------K--.------A---....-------....--M-.--T-------------                 498
HIVUG280    .----------.--V-------....-----L-....-----.SS-----                         492
HIVYU2      .-----S---V.----------....-------....-----.----------S-----                500
HIVBCSG3C   .----------.---------P....----RE-....--M-.---------------                 500
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                          \/ (minor)                \/ (minor)        / p6 terminus (80%)
CONSENSUS.C ?ePtAppAESF.rF.EetT.Pa....pkQEpkd?????e???PLtsLkSLFGNDP                          482
HIVUG268    .----------.--.-G--.-P....-------.......RE--I----                               488
HIVSM145    P----------.--.----.--....----L-E.........-------                               495
HIVZAM18    P----------.--.----.--....-N-----....R-...-------                               492
HIVZAM19    .X-X-XX----.--.----.--....-N-----....R-...--------------                        428
HIVZAM20    ..----------.--.----.--....-----R-....SPTGE---A---                             496
HIVDJ259    .----------.G-.--P-.-P....Q---L--KEPYK-...---A-R-                              488
HIVVI313    .----------.--.-----.-S....--------....K-...-------                             484

CONSENSUS.D .EPTAPPAeSF.GFGEeit.Ps....qKQEqKd????kEly.PlasLkSLFGNDPlsQ                     494
HIVELI      .----------.-------.--....-------....----.--T-------------                     500
HIVNDK      .----------.-------.--....-------....----.-------------S--                     497
HIVZ2Z6     .----------.-------.--....-------....----.-STA----------L-                     501
HIVVI203    .----------.-----KA.--....A---P-E.....---.-V-----                             490
HIVVI205    .-------K--.-------.--....-------....---N.--T----                             492
HIVG109     .----------.-----M-.-P....-------KEKD----.--T--R-                             498
HIVK31      .----------.-------.--....-------....--M-.-------                             490
HIVUG274    .----------.----K--.--....-------....--PC.-------                             491
HIVUG270    .----------.-------.--....-------....----.-S-A---                             490
HIVSE365    .----------.-----T-.--....-------....----.-------                             491

CONSENSUS.F .EPtAPPAEsF.GF?EEIt.PS....PkQEqKd....eglypPLaSLKS                             474
HIVVI174    .----------.--G----.--....------G....------------                             487
HIVVI69     .--S-------.--R----.--....-------....---S--------                             486
HIVBZ162    .----------.--R---N.--....------E....------------                             486
HIVVI325    .--------N-.--G----.--....-R--T--....KEQGS--T----                             486

CONSENSUS.G .EP?APPAEsl.gfgEEI?.?S....PKQEPrd....KELYpPL?SLKS                             451
HIVVI191    .--T-----.....---T.S-....-------....-------V----                             484
HIVLBV217   .--S-------.------A.P-....-----.....----.--T----                             487

CONSENSUS.H .EPTAPPAESF.GFGEEMT.P?....PKQE??D....?E..?PL?SLKS                            436
HIVVI525    .----------.-------.-S....----PR-....K-..P--A----                             490
HIVVI557    .----------.-------.-P....----RK-....A-..S--T----                             489

CONSENSUS.O .?PSAPPME......E?VK.?Q....ENQ?QKG..???ELY.PFASLKSLFGTDQ                      443
HIVANT70    .H-------.....-E--.G-....---E---..GPN---.-------------                        498
HIVMVP51    .S-------.....-A--.E-....---S---..DQE---.-------------                        498

SIVCPZGAB   .EPTAPPIESY.GYQEEEK.SQ....EKKEG.....ESSLY.PPTSLKSLFGSDPSSQ                    508
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HIV1 POL

Sequence subtypes C and E are not currently represented in POL.

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CONSENSUS.A FFRE.NLAFQQGEAREF...........SSE..QTRANSPTSRNLWDGGKDD..LP...CETGAER..QG..    49
HIVU455     ----.-----------.....---..------------------..--...-------..--..    49

CONSENSUS.B FFRE.dLAFpQGkAref???????????sSe..QtRANSptrrElqVWgrdnnSlS????EAGadR..QG..    50
HIVLAI      ----.----L-------SSEQTRANSPTI---..---------------------...------..--..    62
HIVHXB2R    ----.----L-------.....---..--------------------P-...------..--..    50
HIVMN       ----.----L----.--.....---..-N--------------------EAGE---D--..--..    53
HIVJRCSF    ----.----L-------.....P--..------------------S----EAGA------..--..    54
HIVJRFL     ----.----L-------.....---..---------K--------S----...------..--..    50
HIVOYI      ----.-----------.....---..--------S---R--------P-...------..--..    50
HIVSF2      ----.----L-------.....---..----------------GE-----...------..--..    50
HIVNY5CG    ----.-----------.....---..----------------------...------..--..    50
HIVNL43     ----.-----------.....---..----------------------...------..--..    50
HIVCAM1     ----.N------E----.....---..----------------E-----...------..--..    50
HIVHAN      ----.-------E--K-.....---..----------------S.-S---...------..--..    49
HIVD31      ----.----L-------.....--A..----------------S----...------..--..    50
HIVRF       ----.N----------L.....---..----------------.----...---E--..--..    49
HIVYU2      ----.----------K-.....---..-------I---R---R-------...------..--..    50
HIVBCSG3C   ----.-----------.....---..------S---------G----P-.....---G-..--..    50

CONSENSUS.D FFRE.dLAFPQGKAGEl.....Sse..QTRANSPTSRELRVWGrD.NPLS....eTGAER..QG..    49
HIVELI      ----.N----------.....-PK..----------------.----....K-----..--..    49
HIVZ2Z6     ----.-----------.....---..----------------.----...------..--..    49
HIVNDK      ----.----------F.....---..---------------G-.----...------..--..    49

CONSENSUS.O FFRe.?LAsggheARql.....caE..ts?piSPT??????gGG??.??Segt?Esg?Erg??r..    39
HIVMAL      ----.N--FPQGK--EF.....PS-..QTRAN---SRELRVW--DK.TL-....-T-A--..QG..    49
HIVANT70    ---Q.I----------.....---..--T-----D....---....----G---T---PE-..    46
HIVMVP5180  ----.V----------.....---..--V-----N....---....----R--ES-G-SG-..    46

SIVCPZGAB   FFRE.RLAFPQREARQL.....CAE..QNRTNGPTDRELWVPGGRE.......EPGEERGREQ..    48
SIVCPZGAB2  ..........................................................................    0
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                    \/ protease  <- gag cds end
CONSENSUS.A .TDSFSFPQITLWQRPLVTVKIGGQLIEALLDTGADDTVLEDINLPGKWKPKIIGGIGGFIKVRQYDQILIEI  121
HIVU455     .--------------------------------------------------------------------------  121

CONSENSUS.B .tVSfsfPQiTLWQRPlVTikIGGQLKEALLDTGADDTVleeMnLPgrWKPKMIGGIGGFIKVrQYDQIlieI  122
HIVLAI      .----N-----------------------------------S----------------------------  134
HIVHXB2R    .----N---V-------------------------------S----------------------------  122
HIVMN       .P--------------I----------------------G-----R----------------------T-G-  125
HIVJRCSF    .I---N-----------------------------------D-D--------------------------P-D-  126
HIVJRFL     .N---N-----------------------------------D-D----------------------------  122
HIVOYI      .----NL---------I----------------------------------------------------------  122
HIVSF2      .----N--------------R-------------------------K----------------------PV--  122
HIVNY5CG    .----------------------------------------------------------------------------  122
HIVNL43     .-------------------------------------------------------------G----------  122
HIVCAM1     .--------------------------------------------------------------------P---  122
HIVHAN      .---L-L---------------------------------V---S--------------------------V--  121
HIVD31      .-----------------------------------------S----------------------------  122
HIVRF       .---------------I--V--------------------------K------------------------  121
HIVYU2      .--------------------------------------------------------------------P---  122
HIVBCSG3C   .N--L------------------------------------------------------------------P---  122

CONSENSUS.D .TVSFnfPQITLWQRPLVtIKIGGQLKEALLDTGADDTVLEEmNLPGKWKPKMIGGIGGFIKVRQYDQIlIEI  121
HIVELI      .-----------------A----------------------------------------------------P---  121
HIVZ2Z6     .-----C----------------------------------------------------------------------  121
HIVNDK      .----S-----------------------------------I----------------------------  121

CONSENSUS.O .avs?clPQIpLWdRPiVTarVGGhLcEaLLDTGADDTVLnnIqLeGkWkPKMIGGIGGFIKVkeYdnvtvEi  110
HIVMAL      .I--FSF---T--Q--V--V----Q-K-------------EE-N-P-----------------RQ--QILI--  121
HIVANT70    .-L-V-----------------------V-------------------------------------------  118
HIVMVP5180  .--PI---------------K-------------------------R-T----------------N-----V  118

SIVCPZGAB   .SISTNLPQITLWQRPLIPVKVEGQLCEALLDTGADDTVIERIQLQGLWKPKMIGGIGGFIKVKQFDNVHIEI  120
SIVCPZGAB2  ..............................................................................  0

                                        protease \/ p66, p51
CONSENSUS.A CGKKTIGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIETVPVKLKPEMDGPKVKQWPLTEEKIKALTEICNE  194
HIVU455     --------------------------------------------------------------------------  194

CONSENSUS.B CGHKAiGTVLVGPTPVNIIGRNLLTQiGCTLNFPISPIETVPVKLKPGMDGPKVKQWPLTEEKIKaLvEICTE  195
HIVLAI      --------------------------------------------------------------------------  207
HIVHXB2R    --------------------------------------------------------------------------  195
HIVMN       -------------------------L----------------------------------------I-----  198
HIVJRCSF    -----V-----------------------------------------------------------------------  199
HIVJRFL     --------------------------------------------------------------------------  195
HIVOYI      -------------------------L----------------------------------------V-I-----  195
HIVSF2      --------------------------------------------------------------------------  195
HIVNY5CG    --------------------------------------------------------------------------  195
HIVNL43     --------------------------------------------------------------------------  195
HIVCAM1     --------------------------------------------------------------------------  195
HIVHAN      -----------------------------------------------------------------I-----  194
HIVD31      --------------------------------------------------------------------------  195
HIVRF       --------------------------------------------------------------------------  194
HIVYU2      --------------------------------------------------------------------------  195
HIVBCSG3C   --------------------------------------------------------------------------  195

CONSENSUS.D CG?KAiGTVLVGPTPVNIIGRNLLTQIGCTLNFPISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALTEICTe  193
HIVELI      --Q-----------------------------------------------------------------------D  194
HIVZ2Z6     --H--------------------------------------------------------------------------  194
HIVNDK      --Y--M-----------------------------------------------------------------------  194

CONSENSUS.O ?GkevqGTvLVGPTPVNIiGRNiLTglGCTLNFPISPIapVPVKLKPGMDGPkVKQWPLs?EKIeALTaICqe  181
HIVMAL      C--KAI--I-------------M--QI-----------ET------------R------TE---K---E--KD  194
HIVANT70    E-R-------------------------------------------------------K------------  191
HIVMVP5180  Q-----------------L-----------------------------------------R------------  191

SIVCPZGAB   EGRKVVGTVLVGPTPVNIIGRNILTQLGCTLVFPISSIETVPVKLKPGMDGPKVKQWPLSAEKIKALTEICQE  193
SIVCPZGAB2  ..............................................................................  0
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HIV1 POL

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CONSENSUS.A MEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHTAGLKKKKSVTVLDVGD  267
HIVU455     ---------------------------------------------------------------------------  267

CONSENSUS.B MEKEGKISKiGPENPYNTPVFAIKKKDSTKWRKLVDFRELNkrTQDFWEVQLGIPHPAGLKkkKSVTVLDVGD  268
HIVLAI      ---------------------------------------------------------------------------  280
HIVHXB2R    ---------------------------------------------------------------------------  268
HIVMN       -------------------------------------------K-------------------------------  271
HIVJRCSF    -------------------------------------------R-------------------------------  272
HIVJRFL     -------------------------------------------K------------------R-------------  268
HIVOYI      ---------V-------------------------------------------------------------------  268
HIVSF2      ---------------------------------------------------------------------------  268
HIVNY5CG    ------------------------------------------------------------Q----------------  268
HIVNL43     ------------------------------------------------------------Q----------------  268
HIVCAM1     ---------------------------------------------------------------------------  268
HIVHAN      ---------------------------------------------------------------------------  267
HIVD31      ---------------------------------------------------------------------------  268
HIVRF       ---------------------------------------------------------------------------  267
HIVYU2      ---------------------------------------------------------------------------  268
HIVBCSG3C   ---------------------------------------------------------------------------  268

CONSENSUS.D MEKEGKISRiGPENPYNTPIFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGD  266
HIVELI      ---------------------------------------------------------------------------  267
HIVZ2Z6     ---------V-------------------------------------------------------------------  267
HIVNDK      ---------------------------------------------------------------------------  267

CONSENSUS.O MEqEGKIsrIGPENPYNTPiFAIKKKDsTKWRKLVdFRELNKRTQdFWEVQLGIPHPgGLKqkqSVTVLDVGD  254
HIVMAL      --K----LK----------V--------------N--------------------A---K-K---------  267
HIVANT70    ----------------------------G-----------------E--------------------------  264
HIVMVP5180  ---------------------------------------------------------R----------------  264

SIVCPZGAB   MEKEGKISKIGPENPYNTPIFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGD  266
SIVCPZGAB2  ...........................................................................    0

CONSENSUS.A AYFSVPLDESFRKYTAFTIPSINNETPGVRYQYNVLPQGWKGSPSIFQSSMTKILEPFRSQHPDIVIYQYMDD  340
HIVU455     ---------------------------------------------------------------------------  340

CONSENSUS.B aYFSVPLdkdFRKYTAFTIPSiNNETPgiRYQYNVLPQGWKGSPAIFQsSMTkILEPFrKQNPdivIYQYMDD  341
HIVLAI      --------E------------------------------------------------------------------  353
HIVHXB2R    --------E------------------------------------------------------------------  341
HIVMN       ---------------------------------------------------------------------------  344
HIVJRCSF    ------------------------------------------------------------I--------------  345
HIVJRFL     ------------------------------------------------------------I--------------  341
HIVOYI      ---------------------------------------------------------------------------  341
HIVSF2      ---------------------------------------------------------------------------  341
HIVNY5CG    ------------------------------------------------C------------------------  341
HIVNL43     ------------------------------------------------C------------------------  341
HIVCAM1     ----------------------T-----------------------------------------------------  341
HIVHAN      ---------------------------------------------------------------------------  340
HIVD31      --------E-------------------V----------------------------------------------  341
HIVRF       ---------E-----------------R-----------------------------K----E---------  340
HIVYU2      -------HE-------------------T----------------------T-----------L---------  341
HIVBCSG3C   R------------------------------------------------------------------------  341

CONSENSUS.D AYFSVPLDeDFRKYTAFTIpSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQNPEiVIYQYMDD  339
HIVELI      -------------------S-----------------------------------------M---------  340
HIVZ2Z6     --------K------------------------------------------------------------------  340
HIVNDK      ---------------------------------------------------------------------------  340

CONSENSUS.O AYFScPLDpDFRKYTAFTIPSvNNETPGiRYQYNVLPQGWKGSPAIFQSSMTKILdPFR??NPE?eIyQYmDD  324
HIVMAL      ----V---E------------I-------------------------------E---TK---IV--------  340
HIVANT70    ---------------------------------------------------------RD---L--C------  337
HIVMVP5180  ----------------------------V-------------------------------KS---V-----I--  337

SIVCPZGAB   AYFSCPLDKDFRKYTAFTIPSINNETPGVRYQYNVLPQGWKGSPSIFQSSMTKILEPFREKNPDITIYQYMDD  339
SIVCPZGAB2  ...........................................................................    0
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CONSENSUS.A LYVGSDLEIGQHRAKIEELRAHLLSWGFITPDKKHQKEPPFLWMGYELHPDKWTVQPIQLPEKDSWTVNDIQK  413
HIVU455     ------------------------------------------------------------------------  413

CONSENSUS.B LYVGSDLEIgQHRtKIEELRqHLLrWGfTTPDKKHQKEPPFLWMGYELHPDKWTVQPIvLPEKDSWTVNDIQK  414
HIVLAI      --------------------------L-------------------------------------------  426
HIVHXB2R    --------------------------L-------------------------------------------  414
HIVMN       ------------A------R-------------------------------------------------  417
HIVJRCSF    ----------------------K-------------------------------------------------  418
HIVJRFL     ------------A-------------------------------------------------------------  414
HIVOYI      ---------------------------------------------------------M--------------  414
HIVSF2      ---------------------------------------------------------M--------------  414
HIVNY5CG    ------------------------------------------------------------------------  414
HIVNL43     ------------------------------------------------------------------------  414
HIVCAM1     --------------------------L-----------------------------M--------------  414
HIVHAN      ---------E--------------K-------------------------------------------------  413
HIVD31      ---------------------------------------------------------T--------------  414
HIVRF       ------------I------E---K-------------------------------------------------  413
HIVYU2      ------------------------------------------------------------------------  414
HIVBCSG3C   ------------------------------------------------------------------------  414

CONSENSUS.D LYVGSDLEIGQHRTKIEeLREHLLRWGFTtPDKKHQKEPPFLWMGYELHPDKWTVQsIkLPEKESWTVNDIQk  412
HIVELI      -----------------K-----------R-----------------------------------------N  413
HIVZ2Z6     ------------------------------------------------------------------------  413
HIVNDK      ---------------------------------------------------------P-N--------------  413

CONSENSUS.O LYVGSDLpl?eHRkriElLREHLyqWGFTTPDKKHQKEPPFLWMGYELHPDKWTVQpIQLPdKevWTVNDIQK  396
HIVMAL      -------EIGQ--TK--E-----LK-------------------------------------S--------  413
HIVANT70    ---------T-------------------------------------------S----N-D---------  410
HIVMVP5180  ---------A-----V--------------------------------------------------------  410

SIVCPZGAB   LYVGSDLEIDQHRKKVEELRQHLLKWGFTTPDKKHQKEPPFLWMGYELHPDKWTVQPIQLPEKEVWTVNDIQK  412
SIVCPZGAB2  ........................................................................  0

CONSENSUS.A LVGKLNWASQIYAGIKVKQLCKLLRGAKALTDIVTLTEEAELELAENREI...LKDPVHGVYYDPSKDLVAEI  483
HIVU455     ----------------------------------------------...--------------------  483

CONSENSUS.B LVGKLNWASQIYaGIKVkqLCKLLRGtKALTEVipLTeEAELELAENREI...LKEPVHgVYyDPSKDLiaEi  484
HIVLAI      ------------P----R-------------------------------...--------------------  496
HIVHXB2R    ------------P----R-------------------------------...--------------------  484
HIVMN       ----------------------------------------------...-------------------V  487
HIVJRCSF    ---------------------------------K------------...-----------------V--  488
HIVJRFL     ----------------------------------------------...-------------------L  484
HIVOYI      ------------------N-------------------------...----------------V--L  484
HIVSF2      ----------------------------------------------...------E---------V---  484
HIVNY5CG    -----------------R--------I------V-----------...--------------------  484
HIVNL43     -----------------R---------------V-----------...--------------------  484
HIVCAM1     ---------------------------------V-----------...-------------------L  484
HIVHAN      -------------------------P----------K---------...---------C------V---  483
HIVD31      -----------------R--------A----------K---------...--------------------  484
HIVRF       ---------------------------------VQ--K---------...--------------------  483
HIVYU2      ------------------R-------------------------...--------------------  484
HIVBCSG3C   ------------S--------------------VT----------...--------------------  484

CONSENSUS.D LVgkLNWASQIYpGIKVrQLCKLLRGTKALTEViPLTEEAELELAENREI...LKEPVHGVYYDPSKDLIAEi  482
HIVELI      --ER----------------------------------------...--------------------  483
HIVZ2Z6     ----------------------------------------------...--------------------  483
HIVNDK      ------------A----K---------------V-----------...-------------------L  483

CONSENSUS.O LvGKLNWASQIYqGIrVkeLCKLiRGtKsLTevVPLs?EAELELeENRE?...LKePVHGVYYqPdKDLwv?I  463
HIVMAL      ------------P--K--Q----L--A-A--DI---TA------A----I...----------D-S---IAE-  483
HIVANT70    -I---------------R-------------------R-----------R...--Q---------------N-  480
HIVMVP5180  ---------------------------------------K-----------K...-------------------S-  480

SIVCPZGAB   LIGKLNWASQIYPGIKIKQLCKLIRGTKKLTDVVPLTPEAELELAENREI...VSTPVHGVYYDPDKELIAEI  482
SIVCPZGAB2  ........................................................................  0
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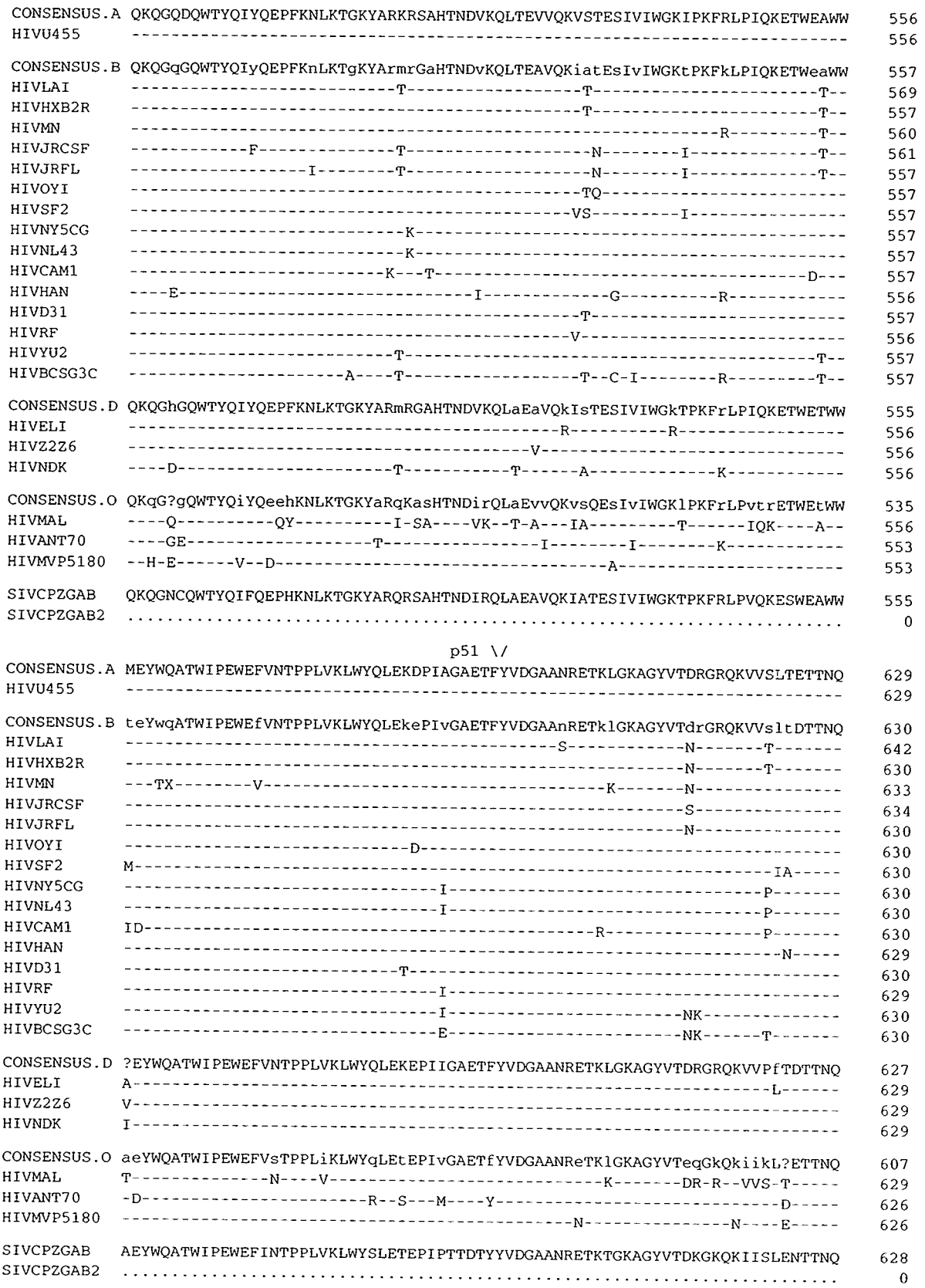
HIV1 POL


CONSENSUS.A QKQGQDQWTYQIYQEPFKNLKTGKYARKRSAHTNDVKQLTEVVQKVSTESIVIWGKIPKFRLPIQKETWEAWW 556
HIVU455 556
CONSENSUS.B QKQGqGQWTYQIyQEPFKnLKTgKYArmrGaHTNDvKQLTEAVQKiatEsIvIWGKtPKFkLPIQKETWeaWW 557
HIVLAI 569
HIVHXB2R 557
HIVMN 560
HIVJRCSF 561
HIVJRFL 557
HIVOYI 557
HIVSF2 557
HIVNY5CG 557
HIVNL43 557
HIVCAM1 557
HIVHAN 556
HIVD31 557
HIVRF 556
HIVYU2 557
HIVBCSG3C 557
CONSENSUS.D QKQGhGQWTYQIYQEPFKNLKTGKYARmRGAHTNDVKQLaEaVQkIsTESIVIWGkTPKFrLPIQKETWETWW 555
HIVELI 556
HIVZ2Z6 556
HIVNDK 556
CONSENSUS.O QKqG?gQWTYQiYQeehKNLKTGKYaRqKasHTNDirQLaEvvQKvsQEsIvIWGKlPKFrLPvtrETWEtWW 535
HIVMAL 556
HIVANT70 553
HIVMVP5180 553
SIVCPZGAB QKQGNCQWTYQIFQEPHKNLKTGKYARQRSAHTNDIRQLAEAVQKIATESIVIWGKTPKFRLPVQKESWEAWW 555
SIVCPZGAB2 0
p51 \/
CONSENSUS.A MEYWQATWIPEWEFVNTPPLVKLWYQLEKDPIAGAETFYVDGAANRETKLGKAGYVTDRGRQKVVSLTETTNQ 629
HIVU455 629
CONSENSUS.B teYwqATWIPEWEfVNTPPLVKLWYQLEkePIvGAETFYVDGAAnRETklGKAGYVTdrGRQKVVsltDTTNQ 630
HIVLAI 642
HIVHXB2R 630
HIVMN 633
HIVJRCSF 634
HIVJRFL 630
HIVOYI 630
HIVSF2 630
HIVNY5CG 630
HIVNL43 630
HIVCAM1 630
HIVHAN 629
HIVD31 630
HIVRF 629
HIVYU2 630
HIVBCSG3C 630
CONSENSUS.D ?EYWQATWIPEWEFVNTPPLVKLWYQLEKEPIIGAETFYVDGAANRETKLGKAGYVTDRGRQKVVPfTDTTNQ 627
HIVELI 629
HIVZ2Z6 629
HIVNDK 629
CONSENSUS.O aeYWQATWIPEWEFVsTPPLiKLWYqLEtEPIvGAETfYVDGAANReTKlGKAGYVTeqGkQkiikL?ETTNQ 607
HIVMAL 629
HIVANT70 626
HIVMVP5180 626
SIVCPZGAB AEYWQATWIPEWEFINTPPLVKLWYSLETEPIPTTDTYYVDGAANRETKTGKAGYVTDKGKQKIISLENTTNQ 628
SIVCPZGAB2 0

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CONSENSUS.A KTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRSESEIVNQIIEKLIEKEKVYLSWVPAHKGIGGNEQV  702
HIVU455     ------------------------------------------------------------------------  702

CONSENSUS.B KTELqAIhLALQDSGLEVNIVtDSQYAlGIIQAQPDkSESELVsQIIEqLIKKEKVYLaWVPAHKGIGGNEQV  703
HIVLAI      ----------------------------------------N-------------------------------  715
HIVHXB2R    -------Y---------------------------Q------N-------------------------------  703
HIVMN       ------------------------------------------------------------------------  706
HIVJRCSF    ------------------------------------------------------------------------  707
HIVJRFL     ------------------------------------------------------------------------  703
HIVOYI      ------------------------------------------------------------------------  703
HIVSF2      ------------------------------------------------------------------------  703
HIVNY5CG    ------------------------------------------------------------------------  703
HIVNL43     ------------------------------------------------------------------------  703
HIVCAM1     -------Y-----------------------------------------E------------------------  703
HIVHAN      ------------------------------------------------------------------------  702
HIVD31      ----------------------S-----I-----------------------------T--------------  703
HIVRF       ------------------------------------------------------------------------  702
HIVYU2      -------Y---------------------------R--------------------------------------  703
HIVBCSG3C   ----E---------------------------------------------------------------------  703

CONSENSUS.D KTELQAINLALQDSGLEVNIVTDSQYALGIIQAQPDKSESELVsQIIEQLIKKEKVYLAWVPAHKGIGGNEQV  700
HIVELI      ----------------------------------------N-------------------------------  702
HIVZ2Z6     ------------------------------------------------------------------------  702
HIVNDK      ------------------------------------------------------------------------  702

CONSENSUS.O KaELmAillALQDSke?VNIVTDSQYaLGiIssQPtqSeSpIVqQIIEeLtkKe?VYLtWVPAHKGIGGNEki  678
HIVMAL      -T--Q--H------GSE--------------QA--DK---E--N----Q-IQ-DK---S------------QV  702
HIVANT70    ----------------T------------V-------------------------Q------------------  699
HIVMVP5180  ------V-I-------Q---------V-----------D---------------R------------------  699

SIVCPZGAB   QAELKALLLALQDSDQQVNIVTDSQYVLGIIQSQPDHSESELVNQIIEELIKKEKIYLSWVPAHKGIGGNEQV  701
SIVCPZGAB2  ........................................................................    0

CONSENSUS.A DKLVSSGIRKVLFLDGIDKAQEDHEKYHCNWRAMASDFNLPPVVAKEIVASCNKCQLKGEAMHGQVDCSPGIW  775
HIVU455     ------------------------------------------------------------------------  775

CONSENSUS.B DkLVSaGiRKVLFLdGIDKAQeeHEKYHSNWrAMAsDFNLPPvVAKEIVASCDKCQLKGEAMHGQVDCSPGIW  776
HIVLAI      ----------------------D-------------------------------------------------  788
HIVHXB2R    ----------------------D-------------------------------------------------  776
HIVMN       ----------------------D-------------------I-----------------------------  779
HIVJRCSF    ----------------------D-------------------I-----------------------------  780
HIVJRFL     ----------------------D--------K----------------------------------------  776
HIVOYI      ------------------------------------------------------------------------  776
HIVSF2      --------------N---------------------------------------------------------  776
HIVNY5CG    ------------------------------------------------------------------------  776
HIVNL43     -G----------------------------------------------------------------------  776
HIVCAM1     ------------------------------------------------------------------------  776
HIVHAN      ----------------------D------------N-----------------------------------  775
HIVD31      ----------------------D-------------------------------------------------  776
HIVRF       -R---T---------------D-------------------------------------------------  775
HIVYU2      ------------------------------------------------------------------------  776
HIVBCSG3C   -------V----------------------------------------------------------------  776

CONSENSUS.D DKLVSQGIRKVLFLDGIDKAQEEHEKYHNNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAMHGQVDCSPGIW  773
HIVELI      ------------------------------------------------------------------------  775
HIVZ2Z6     ------------------------------------------------------------------------  775
HIVNDK      ------------------------------------------------------------------------  775

CONSENSUS.O DKLVSkdIRrVLFLeGIDqAQEdHEKYHSNWrAlASdFgLPPiVAKEIiASCpKChiKGEA?HGQVDcSPeiW  750
HIVMAL      -----SG--K----D---K---E----------M----N---------V---D--QL----M--------G--  775
HIVANT70    -------------------------------K----E-----V------------------I---------V-  772
HIVMVP5180  ------------------------------------------------------------T-----Y-----  772

SIVCPZGAB   DKLVSAGIRKVLFLDGIDRAQEEHERYHSNWKAMASDFNLPPIVAKEIVAHCDKCQVKGEAMHGQVDCSPGIW  774
SIVCPZGAB2  ........................................................................    0
```

HIV1 POL

```
CONSENSUS.A QLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYFILKLAGRWPVKVIHTDNGSNFTSAAVKAVCWWAN  848
HIVU455     ------------------------------------------------------------------------  848

CONSENSUS.B QLDCTHLEGKvILVAVHVASGYIEAEVIPaETGQETAYFlLKLAGRWPVktiHTDNGsNFtstTVkAACWWaG  849
HIVLAI      ------------------------------------------------------------------------  861
HIVHXB2R    ------------------------------------------------------------GA--R-------  849
HIVMN       ------------------------------------------------------P-------------T-  852
HIVJRCSF    ----------I-------------------------------------T----------------------  853
HIVJRFL     ----------I------------------------------------------------------------  849
HIVOYI      ----------I-----------------------------I------------------------------  849
HIVSF2      ----------I------------------------------------------------------------  849
HIVNY5CG    ------------------------------------------------V----------------------  849
HIVNL43     ------------------------------------------------V----------------------  849
HIVCAM1     ------------------------------------------------------G--I------------  849
HIVHAN      ----------I-----------------V--------------------V-----P---------------  848
HIVD31      ---------------------------------------I------------------------------  849
HIVRF       ----------I-----------------------------I----------V----------------------  848
HIVYU2      ------------------------------------------------T------------A----------  849
HIVBCSG3C   ----------I------------------------------------------------------------  849

CONSENSUS.D QLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYFlLKLAGRWPVKvVHTDNGSNFTSAaVKAACWWAG  846
HIVELI      ------------------------------------------------------------------------  848
HIVZ2Z6     ---------------------------------------I----------I----------------------  848
HIVNDK      ------------------------------------------------------------T---------  848

CONSENSUS.O Q?DCTHlEGKIIIVAVHVASgfIEAEVIPAETGQETAYFlLKLAaRWPVKViHTDNGpNFTSaamKAACWWan  822
HIVMAL      -L------------------Y-----------------I----G------V-----S------V--------  848
HIVANT70    -I----M-------------------------------------------------TT---------  845
HIVMVP5180  -M------------------D-------------------------------------------TG  845

SIVCPZGAB   QVDCTHLEGKVIIVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTIHTDNGPNFTSAAVKAACWWAD  847
SIVCPZGAB2  ........................................................................    0

CONSENSUS.A IQQEFGIPYNPQSQGVVESMNKELKKIIGQVREQAEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIATD  921
HIVU455     ------------------------------------------------------------------------  921

CONSENSUS.B iKQEFGIPYNPQSQGVvESMNkeLKkIIGQVRDQAEHLKtAVQMAVFIHNFKRKGGIGGYSAGERIvdIIATD  922
HIVLAI      ------------------------------------------------------------------------  934
HIVHXB2R    ------------------------------------------------------------------------  922
HIVMN       ----------------I---------------------R--------------------------G-----  925
HIVJRCSF    ------------------------------------------------------------------I------  926
HIVJRFL     ------------------------------------------------------------------------  922
HIVOYI      --------------------N---------------------------------------------------  922
HIVSF2      --------------------N---------------------------------------------------  922
HIVNY5CG    ----------------I---------------------------------------------------------  922
HIVNL43     ----------------I---------------------------------------------------------  922
HIVCAM1     --------------------N-----------------------------------------I------  922
HIVHAN      ------------------------------------------------------------------------  921
HIVD31      V-----------------------------------------------------------------------  922
HIVRF       --------------------Q--Q---------------------------------------------------  921
HIVYU2      ------------------------------------------------------------------------  922
HIVBCSG3C   ------------------------------------------------------------------------  922

CONSENSUS.D IKQEFGIPYNPQSQGVVESMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNFKRkgGIGGYSAGERIIDIIATD  919
HIVELI      ----------------------------------------------------RR------------------  921
HIVZ2Z6     ------------------------------------------------------------------------  921
HIVNDK      ------------------------------------------------------------------------  921

CONSENSUS.O IqhEFGIPYNPQSQGVVEaMNKELKsIIqQVRdQAEHLkTAVQMAVFvHNFKRKGGIGGYtAGERiIDilAsq  895
HIVMAL      -KQ---------------S------K--G---E--------------I------------S-------MI-TD  921
HIVANT70    ---------------------------------R--------------------------------------  918
HIVMVP5180  ------------------------------------------------------------L-------  918

SIVCPZGAB   IKQEFGIPYNPQSQGVVESLNKELKKIIGQVRDQAEHLKTAVQMAVFIHNFKRKGGIGGYTAGERIIDIIATD  920
SIVCPZGAB2  ..............----M-----------------------------------------V-ML---   58
```

```
                                                                                                  vif cds ->
CONSENSUS.A IQTKELQKQISKIQNFRVYYRDSRDPIWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRDYGKQMAGDDC    994
HIVU455     ------------------------------------------------------------------------------    994

CONSENSUS.B IQtKELQKQITKIQNFRVYYRDsrdPlWKGpAKLLWKGEGAVVIQDNsdIKVVPRRKaKiIRDYGKQmagDDC    995
HIVLAI      ------------------------------------------------------------------------------   1007
HIVHXB2R    ------------------------N-------------------------------------------------------    995
HIVMN       ------------------------------------------------N-----------V-------T-----      998
HIVJRCSF    ----------------------N---I-----------------------------V---------------          999
HIVJRFL     ------------------------E-----------------------------V---------------          995
HIVOYI      ------------------------E-------------------------------------------------------    995
HIVSF2      ----------------------NK-------------------------------------------------------    995
HIVNY5CG    --I----------------------V-------------------------------------------------------    995
HIVNL43     -------------------------V-------------------------------------------------------    995
HIVCAM1     ------------------------------------------------------------------------------    995
HIVHAN      ------------------------E-F---------------------------------------GS---           994
HIVD31      ------------------------------------------------E-----------------------          995
HIVRF       ------------------------------H-------------------------------------------------    994
HIVYU2      ------------------------------------------------------------------------------    995
HIVBCSG3C   ----------------------NK-------------------------------------------------------    995

CONSENSUS.D IQTkELQKQIiKIQNFRVYYRDSRDPIWKGPAKLLWKGEGAVVIQDnSDIKVVPRRKVKIIRDYGKQMAGDDC    992
HIVELI      ------------------------------------------K-------------------------          994
HIVZ2Z6     ----------T-------------------------------------------------------------          994
HIVNDK      ---R--------------------------------------------------------------------          994

CONSENSUS.O IQTtELQKQIlKi?nFRVYYRDsRDPIWKGPAqLLWKGEGAVVIQDkgDIKVVPRRKAKIIRdYGKQMAGtDs    967
HIVMAL      ---K------T--Q--------N---------K------------NS----------------------D-C    994
HIVANT70    ------------XHK-------------------------------------------------E----------    991
HIVMVP5180  -------------N-------------------------------------------------------------    991

SIVCPZGAB   IQTSELQKQILKVQKFRVYYRDSRDPIWKGPATLLWKGEGAVVIQDQGELKVVPRRKAKIIRDYGKQMAGDDC    993
SIVCPZGAB2  L--Q--------I--------G----------S--                                          93

CONSENSUS.A MAGRQDED                                                                     1002
HIVU455     --------                                                                     1002

CONSENSUS.B VAsRQDED                                                                     1003
HIVLAI      --------                                                                     1015
HIVHXB2R    --------                                                                     1003
HIVMN       --------                                                                     1006
HIVJRCSF    --------                                                                     1007
HIVJRFL     --------                                                                     1003
HIVOYI      --------                                                                     1003
HIVSF2      --------                                                                     1003
HIVNY5CG    --------                                                                     1003
HIVNL43     --------                                                                     1003
HIVCAM1     --------                                                                     1003
HIVHAN      --------                                                                     1002
HIVD31      --G-----                                                                     1003
HIVRF       --------                                                                     1002
HIVYU2      --G-----                                                                     1003
HIVBCSG3C   --------                                                                     1003

CONSENSUS.D VASRQDED                                                                     1000
HIVELI      --------                                                                     1002
HIVZ2Z6     --------                                                                     1002
HIVNDK      --------                                                                     1002

CONSENSUS.O mA?gQtEsES?EQP?EIP                                                            982
HIVMAL      V-G--D-D                                                                     1002
HIVANT70    --S-------V---S---                                                           1009
HIVMVP5180  --NR------M---G---                                                           1009

SIVCPZGAB   VASRQNED                                                                     1001
```

HIV1 VIF

```
                                <- pol cds
CONSENSUS.A MENRWQVMIVWQVDRMKIRTWNSLVKHHMYVSKKAQGWFYRHHYESRHSRVSSEVHIPLGE..ARLVVRTYWG   71
HIVU455     ------------------------------------------------------------..----------   71

CONSENSUS.B MENRwqVMiVWQvDRMRIrtWksLVKHHmYiS?KAkgwfYrHHYEShPriSSEVhIPlGd..arLViTTYWG   70
HIVLAI      ------------------------------V-G--R----------P--------------..----------   71
HIVHXB2R    ------------------------------V-G--R----------P--------------..----------   71
HIVMN       ----R-------A-------------------K----R-----------------------..----------   71
HIVJRCSF    --------------------N----------G-----I-K------N--V----Q-------..----------   71
HIVJRFL     ----------------------------T-G-----I-----------------------..----------   71
HIVNH52     --------V----------A-----------R-----------------------------..-K--------   71
HIVOYI      ------------------------------V-K-----------------------------..-T--V-----   71
HIVSF2      ---------------------------------K-----------------V----------..-K--------   71
HIVNY5CG    ------------------N---R---------R---D----------N-K-----------..-K--------   71
HIVNL43     ------------------N---R---------R---D----------N-K-----------..-K--------   71
HIVCAM1     ---------------------------------G---K-S--------------------E..----V-----   71
HIVHAN      -----A--------------N------I-C-R---N-V--------N--V---------E..-K--------   71
HIVD31      ------------------------------V-G--EK---K------N-----------..----------   71
HIVRF       --------------------------------R-------------------------P--..E---------   71
HIVYU2      ------------------A-----------G--R----------P--------------..-K--------   71
HIVBCSG3C   --------------------I----------R----------------K-----------..----------   71

CONSENSUS.D MENRWQVMIVWQVDRMRI?TWKSLVKhHMYVSKKAnRWFYRHHYdSpHPKISSEVHIPLGE..ArLVvkTYWG   70
HIVELI      ------------------K-------------------------E---------------..----I-----   71
HIVZ2Z6     ------------------R----------------S-------------------------..-M--------   71
HIVNDK      ------------------N-------Y-------------------H--------------..-----T----   71

CONSENSUS.O MENRWQVlIVWQvDRqkvkaWnSLVKyHkY?SkKa?NW?YRHHYESRnPkVSS?VyIPvg?..A??VVtTYWG   64
HIVMAL      -------M-------MRIRT-H----H-M-V----K--F--------H-----E-H--L-D..-RL--R----   71
HIVANT70    ------------------------------R-R-TE--W----------R---S------V..-HV-------   71
HIVMVP5180  ------------I----------------M----A--R--------------A-----AE..-DI-------   71

SIVCPZGAB   MENRWQVMIVWQVDRMRIKTWNSLVKYHIYRSKKARGWFYRHHYDHPNPKVASEIHIPFRDY.SKLIVTTYWA   72

CONSENSUS.A LHTGEKDWHLGHGVSIEWRLKRYSTQVDPDLADHLIHLHYFDCFSESAIRRAILGQIVRPRCEYQAGHNKVGS   144
HIVU455     ------------------------------------------------------------------------   144

CONSENSUS.B LHTgeRdWhLGqGvsiEWrkkrYsTQVDPdLADqLIHlyYFDCFSeSAIrnailG?ivSPrCEyqAGHnKvGs   142
HIVLAI      ----------------------------E--------------D----K-L--H-----------------   144
HIVHXB2R    ----------------------------E--------------D----K-L--H-----------------   144
HIVMN       --------------------------------H----H------D----K----HR---I--F--------P   144
HIVJRCSF    --------------M---TR-----------------------------------H----------S----   144
HIVJRFL     ---------------V-------N-------------------------------H-----------------   144
HIVNH52     ---$K----------V--K-R--------N--------H----------------R--------------I--   143
HIVOYI      ------E------A---------------G-------T----------------N--------P--------   144
HIVSF2      ------E-------A------K-------G--------H----------K-----YR----------------   144
HIVNY5CG    ------------------------------------H----------T---R-----------------    144
HIVNL43     ------------------------------------H----------T---R-----------------    144
HIVCAM1     ------------------T-G-N-------------------------K--V-RL-----------------   144
HIVHAN      -------------A------R--------N-------------------------R----------S----    144
HIVD31      --------Q--H----------------G-------------------------R-G--S---R--------   144
HIVRF       --------------------R-----------------------------KPS--H-----------------   144
HIVYU2      ------------------------------------------------K----YR-----------------   144
HIVBCSG3C   -----------H---V-----------------------------------H-----------------    144

CONSENSUS.D LHTGEreWHLGQGVSIEWRKRRYSTQVDPGLADQLIHMYYFDCFsEsAIRKAILGhIVSprCEYQAGHnKVGS   143
HIVELI      ------------------------------------------------------D-----------------   144
HIVZ2Z6     ------D-------------------------------------A----------H--------S----    144
HIVNDK      -----K-------------------------------------A--------------S-----------    144

CONSENSUS.O LmpGErdeHLGHGVSIEWryK?YkTQiDPetADrmIHLhYFtCFteSAiRkAILGqrVltkCeY?aGHsqVGt   135
HIVMAL      -QT--K-W----------Q-R-S--L--DL--QL---Y--D--S-----Q----HI-SPR-D-Q---NK--S   144
HIVANT70    --------------------K----------------------A--V---------------PT-------   144
HIVMVP5180  ------E----------Q--E-------------------------------------------L--------   144

SIVCPZGAB   LSPGERAWHLGHGVSIQWRLGSYVTQVDPFTADRLIHSQYFDCFAETAIRRAILGQLVAPRCEYKEGHRQVGS   145
```

```
                                    vpR cds ->
CONSENSUS.A LQYLAL.KAL...VTPTRAKPPLPSVKKLTEDRWNKPQKTRGHRGSRTLNRH  192
HIVU455     ------.---...--------------------------------------  192

CONSENSUS.B LQYLAL.aAL...itpKkiKPPLPsV?KLTEDRWNKPqKTKGHrGShTmnGH  189
HIVLAI      ------.---...-------------T-------------------------  192
HIVHXB2R    ------.---...-------------T-------------------------  192
HIVMN       ------.T--...-------------K--------------------I---  192
HIVJRCSF    ------.T--...-K-----------K-------------------------  192
HIVJRFL     ------.T--...-KS----------K-------------------------  192
HIVNH52     ------.---...-------------T----------R-----K--------  191
HIVOYI      ------.---...-K-----------T-------------------------  192
HIVSF2      ------.---...-----T-------K-------------------------  192
HIVNY5CG    ------.---...-K--Q--------R-------------------------  192
HIVNL43     ------.---...-K--Q--------R-------------------------  192
HIVCAM1     ------.T--...-A-----------R-------------------------  192
HIVHAN      ------.---...T----------I-T----------------------H--  192
HIVD31      ------.---...-------------A----------R--------------  192
HIVRF       ------.---...T------------K-------------------------  192
HIVYU2      ------.T--...-----T-------K------------------R-----  192
HIVBCSG3C   ------.---...----R--------T-------------------------  192

CONSENSUS.D LQYLAL.tAL...iAPKkIKPPLPSVRKLTEDRWNKPQkTkGhrGSHTMNGH  191
HIVELI      ------.---...----Q--------------------Q-R-----------  192
HIVZ2Z6     ------.---...V------------------------------K--------  192
HIVNDK      ------.A--...-------------------------------R---------  192

CONSENSUS.O LQ?LAL.?Av...vk?k??kPPLPSVqkLTEDRWNKp??irdqlgShsMNGH  176
HIVMAL      --Y---.T-L...IAP-KTR------R----------QQTKGHR---T----  192
HIVANT70    --L---.R--...--ARSR-----------------HLR-----K-P-----  192
HIVMVP5180  --F---.K--...--V-RN--------R---------WK-------------  192

SIVCPZGAB   LQFLAL.KAL...ISERRHRPPLPSVAKLTEDRWNKHQRTKVHQENLTRNGH  193
```

HIV1 VPR

Sequence subtypes C and E are not currently represented in VPR.

```
                              <- vif cds
CONSENSUS.A MEQAPEDQGPQREPYAEXALELLEELKHEDVRHFPRQWLHGLGQHIYNTYGDTWEGVEAIIRILQQLLFIHFR  73
HIVU455     -------------------------------------------------------------------------  73

CONSENSUS.B MEQaPEDQGPQRePyNeWtLELLeeLK?EAVRHFPRiWLh?LgQhIYETYGDTWaGVEAiiRiLQQLLFihFr  71
HIVLAI      --------------H-----------N-----------G-------------------------------  73
HIVHXB2R    --------------H-----------N-----------G-------------------------------Q  73
HIVMN       ----------------Q-A--------N-----------G-------------------------------  73
HIVSC       ----------------------RK--S-----------G-------------------------------  73
HIVJRCSF    --------------------------N-----------S---Y---------------------------  73
HIVJRFL     --------------------------N--------V---S---Y---------------------------  73
HIVNH52     --------------------------N-----------S---Y---------T-----------------  73
HIVOYI      --------------------------S-----------S-E-Y---------E-----------------  73
HIVSF2      --------------------------R--------P---S---Y---------------------------  73
HIVNY5CG    --------------------------S-----------N-------------------------------  73
HIVNL43     --------------------------S-----------N-------------------------------  73
HIVCAM1     ---T--------Q-------------S---------P--LA-------------P----L--S--------  73
HIVHAN      ----------------A----------S-----------S---Y---------------------------  73
HIVD31      --------------------------S-----------S-------------T----L--M----------  73
HIVRF       --------------------------S---------L---S-------------------------------  73
HIVYU2      --------------H-----------R---------P---G-------------------------------  73
HIVBCSG3C   --------------------------N-----------G---Y-------------LV-T------TL--  73

CONSENSUS.D MEQAPeDQGPQREPYNEWtLELLEELKSEAVRHFPRIWLHSLGQhIYETYGDTWaGVEAiIRILQQLLFIHFR  73
HIVELI      -----A-----------A-------------------------------V-----------------  73
HIVZ2Z6     ------------------------------------------Y-------------L-------------  73
HIVNDK      -------------------------------------------------------------------------  73

CONSENSUS.O MEQApenQGParEPfNEWtLELLEELK?EAVRHFPRpWLhalGQyIYETYGDTWeGVmAIIRiLQQLLFtHyR  72
HIVMAL      -----AD---Q---H-----------Q--------I---S---H-----------E----S------I-F-  73
HIVANT70    ----------K------A--------A-------------------------V-----------------  73
HIVMVP51    ----L----------------------E----------Q-C-----------------------------  73

SIVCPZGAB   MEQAPEDQGPPREPYQEWALETLEELKNEAVRHFPRPWLHQLGQFIYDTYGDTWVGVEAIIRILQHLLFIHFR  73

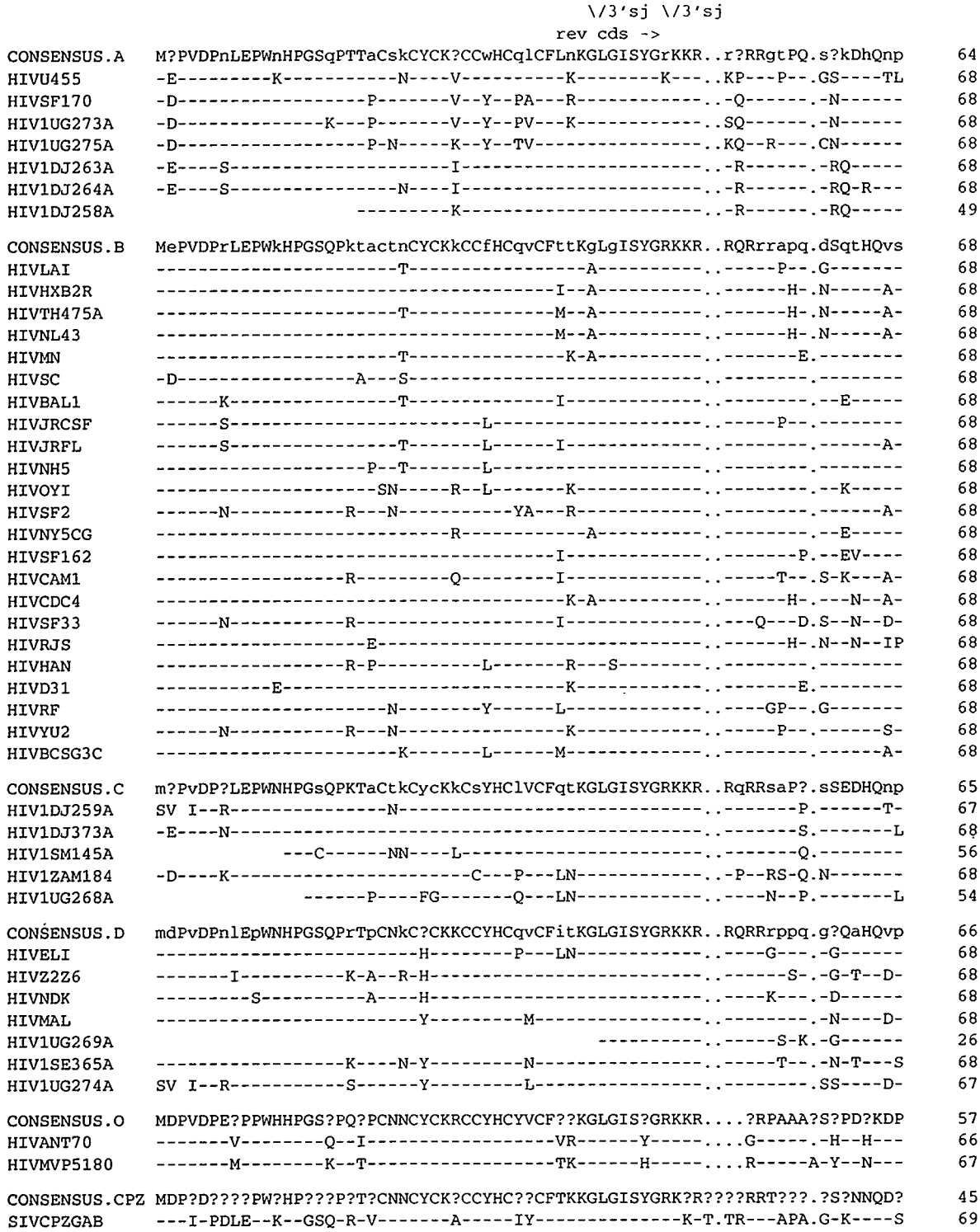
                        tat cds ->
CONSENSUS.A IGCQHSRIGIIP...GRRG.RNGASRS                                              96
HIVU455     ------------...----.-------                                               96

CONSENSUS.B igc?hSRiGitr...qRRa?RNGaSRS                                              93
HIVLAI      ---R-----V-Q...----.-------                                               96
HIVHXB2R    NWVST                                                                     78
HIVMN       ---R------I-...----.-------                                               96
HIVSC       ---R------IQ...---S.---S---                                               96
HIVJRCSF    ---R--------...----.-------                                               96
HIVJRFL     ---Q--------...----.-------                                               96
HIVNH52     ---Q---M---Q...R--T.-------                                               96
HIVOYI      ---Q--------...----.-------                                               96
HIVSF2      ---Q------IQ...----R-------                                               97
HIVNY5CG    ---Q------I-...----.-------                                               96
HIVNL43     ---R-----V--...----.-------                                               96
HIVCAM1     ---R------IQ...---S.-------                                               96
HIVHAN      ---R-------P...----.-------                                               96
HIVD31      ---Q--------...----.-------                                               96
HIVRF       ---Q--------...----.-------                                               96
HIVYU2      ---Q------IQ...----R-------                                               97
HIVBCSG3C   ---R-------Q...R---.-------                                               96

CONSENSUS.D IGCQHSRIgItR...QRRA.RNGSSRS                                               96
HIVELI      ----------I-...----.-------                                               96
HIVZ2Z6     ------------...----.-------                                               96
HIVNDK      --------S---...----.-------                                               96

CONSENSUS.O IGCQHSRIGI?p???rgRgrRNGSSRS                                               95
HIVMAL      ----------TR...QR-A.-------                                               96
HIVANT70    ----------N-...------------                                               97
HIVMVP51    ----------L-SNT------------                                              100

SIVCPZGAB   LGCQHSRIGILP...QRRR.SNGSNRS                                              96
```


\/3'sj \/3'sj
rev cds ->
CONSENSUS.A M?PVDPnLEPWnHPGSqPTTaCskCYCK?CCwHCqlCFLnKGLGISYGrKKR..r?RRgtPQ.s?kDhQnp 64
HIVU455 -E---------K----------N----V---------K--------K---..KP---P--.GS----TL 68
HIVSF170 -D-----------------P-------V--Y--PA---R----------..-Q------.-N------ 68
HIV1UG273A -D--------------K---P-------V--Y--PV---K----------..SQ------.-N------ 68
HIV1UG275A -D-----------------P-N-----K--Y--TV----------..KQ--R---.CN------ 68
HIV1DJ263A -E----S--------------------I----------..-R------.-RQ----- 68
HIV1DJ264A -E----S----------------N----I----------..-R------.-RQ-R--- 68
HIV1DJ258A --------K----------..-R------.-RQ----- 49
CONSENSUS.B MePVDPrLEPWkHPGSQPktactnCYCKkCCfHCqvCFttKgLgISYGRKKR..RQRrrapq.dSqtHQvs 68
HIVLAI ----------T----------A----------..-----P--.G------- 68
HIVHXB2R ----------I--A----------..------H-.N-----A- 68
HIVTH475A ----------T----------M--A----------..------H-.N-----A- 68
HIVNL43 ----------M--A----------..------H-.N-----A- 68
HIVMN ----------T----------K-A----------..-------E.-------- 68
HIVSC -D----------A---S----------..--------.-------- 68
HIVBAL1 ------K----------T----------I----------..--------.--E----- 68
HIVJRCSF ------S----------L----------..-----P--.-------- 68
HIVJRFL ------S----------T-------L------I----------..--------.------A- 68
HIVNH5 ----------P--T-------L----------..--------.-------- 68
HIVOYI ----------SN-----R--L-------K----------..--------.--K----- 68
HIVSF2 ------N----------R---N----------YA---R----------..--------.------A- 68
HIVNY5CG ----------R----------A----------..--------.--E----- 68
HIVSF162 ----------I----------..-------P.--EV---- 68
HIVCAM1 ----------R---------Q---------I----------..-----T--.S-K---A- 68
HIVCDC4 ----------K-A----------..------H-.---N--A- 68
HIVSF33 ------N----------R----------I----------..---Q---D.S--N--D- 68
HIVRJS ----------E----------..------H-.N--N--IP 68
HIVHAN ----------R-P----------L-------R---S---------..--------.-------- 68
HIVD31 ----------E----------K----------..-------E.-------- 68
HIVRF ----------N--------Y------L----------..----GP--.G------- 68
HIVYU2 ------N----------R---N----------K----------..-----P--.------S- 68
HIVBCSG3C ----------K-------L------M----------..--------.------A- 68
CONSENSUS.C m?PvDP?LEPWNHPGsQPKTaCtkCycKkCsYHClVCFqtKGLGISYGRKKR..RqRRsaP?.sSEDHQnp 65
HIV1DJ259A SV I--R----------N----------..-------P.------T- 67
HIV1DJ373A -E----N----------..-------S.-------L 68
HIV1SM145A ---C------NN----L----------..-------Q.-------- 56
HIV1ZAM184 -D----K----------C---P---LN----------..-P--RS-Q.N------- 68
HIV1UG268A ------P----FG-------Q---LN----------..----N--P.-------L 54
CONSENSUS.D mdPvDPnlEpWNHPGSQPrTpCNkC?CKKCCYHCqvCFitKGLGISYGRKKR..RQRRrppq.g?QaHQvp 66
HIVELI ----------H--------P---LN----------..----G---.-G------ 68
HIVZ2Z6 -------I----------K-A--R-H----------..------S-.-G-T--D- 68
HIVNDK ---------S----------A----H----------..----K---.-D------ 68
HIVMAL ----------Y---------M----------..--------.-N----D- 68
HIV1UG269A ----------..-----S-K.-G------ 26
HIV1SE365A ----------K----N-Y---------N----------..-----T--.-N-T---S 68
HIV1UG274A SV I--R----------S------Y---------L----------..--------.SS----D- 67
CONSENSUS.O MDPVDPE?PPWHHPGS?PQ?PCNNCYCKRCCYHCYVCF??KGLGIS?GRKKR....?RPAAA?S?PD?KDP 57
HIVANT70 -------V--------Q--I----------VR------Y-----....G-----.-H--H--- 66
HIVMVP5180 -------M--------K--T----------TK------H-----....R-----A-Y--N--- 67
CONSENSUS.CPZ MDP?D????PW?HP???P?T?CNNCYCK?CCYHC??CFTKKGLGISYGRK?R????RRT???.?S?NNQD? 45
SIVCPZGAB ---I-PDLE--K--GSQ-R-V-------A-----IY----------K-T.TR---APA.G-K----S 69

HIV1 TAT

```
                exon\/exon
CONSENSUS.A     ipKQplPqtqg??ptgpkESkKkVeSKteTDrf?                          95
HIVU455         --------S-RV.SA-QE---------AK----A                         101
HIVSF170        ----SI-----V.--------------A-----D                         101
HIV1UG273A      -----I-----I.S------Q------------A                         101
HIV1UG275A      -----I-----V.S---E--------------T                          101
HIV1DJ263A      V------T-R-D.--D------E-A------QGD                          101
HIV1DJ264A      VS-----T-R-N.---------E-----K--PCD                         101
HIV1DJ258A      V------T-G-NH--D------E-A---K--QYA                          83

CONSENSUS.B     LsKqP?sqprGD.PtgPkesKkkVErEtEtdP?dQ                         100
HIVLAI          -----T------.------ ------------F-                          100
HIVHXB2R        -----T------.------ ------------F-                          100
HIVTH475A       -----T--S---.------ ------------F-                          100
HIVNL43         -----T--S---.------ ------------F-                          100
HIVMN           -P---AP-F---.-----------------H-V-                          101
HIVSC           -P---A--A---.-------------------V-                          101
HIVBAL1         -----T-H----.----E--------------VH                          101
HIVJRCSF        -P---S--Q---.-------------------DN                          101
HIVJRFL         -----S------.-------------------D-                          101
HIVNH5          -----S-------.-DS----------------VH                         101
HIVOYI          -----A------.-------------------E-                          101
HIVSF2          -----A--S---.----T--------------F-                          101
HIVNY5CG        -----A------.-------------------DH                          101
HIVSF162        -P---A---Q--.-------------------VH                          101
HIVCAM1         -----A--FQ--.------------G----H-G-                          101
HIVCDC4         -----S--T---.------P--E----A----L-                          101
HIVSF33         -----S------.---------E---------L-                          101
HIVRJS          -P---A------.-------------------VH                          101
HIVHAN          -P---S--Q---.-DS--K----------A--F-                          101
HIVD31          -----A------.------------T------I-                          101
HIVRF           -----T------.--------E----------AV-                         102
HIVYU2          -----T--L---.----T--------------VH                          101
HIVBCSG3C       ---R-T------.-------------------V-                          101

CONSENSUS.C     IsKQpLpqtrgd.pTGpEeSKKkVESKtetDpfD                          98
HIV1DJ259A      ------------.----------------A-R--                          100
HIV1DJ373A      ------SR-Q--.---------------KA--L-                          101
HIV1SM145A      ------------.---S-----------K-----                          89
HIV1ZAM184      -P--S--H-QRV.S--------E----A---R--                          101
HIV1UG268A      --------P---.-----K------------ -                           86

CONSENSUS.D     iPkQPSSQpRGd?PTGPKeQKKKVESkAEtDpFDw                         100
HIVELI          ------------.-------------E----- -C                         101
HIVZ2Z6         ------------.------ ------E--------                         101
HIVNDK          --E-----S---.-----K ------E--------                         101
HIVMAL          L-E-----H---H------ ---------A-Q---                         102
HIV1UG269A      ------------.------ ---------A----                          58
HIV1SE365A      V-------H---.------ ----------Q---                          101
HIV1UG274A      -----------N.-----K ---------A-----                         100

CONSENSUS.O     VP?QS???T?RK.Q?RQEEQE??VEK??GP?G?P????SC??CTR?S?Q           85
HIVANT70        --K--PTI-K--.-E------EE---KA--G-Y-RRKG--HC---T-E-           114
HIVMVP5180      --E--LSH-G--.-K------KK---ET--S-Q-CHQD--NS---I-G-           115

CONSENSUS.CPZ   ??K?????SR??.?????KS?K?V??KT????G?C                         56
SIVCPZGAB       IP-QPLSQ--GN.KEGSE--T-E-AS--EADQ D                          101
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Sequence subtypes C and E are not currently represented in REV.

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                \/ 3' sj              exon\/exon
CONSENSUS.A     MA?RSG??DE.?LLKA?RIIK?LYQSNP?P?P?G.SRQARKNRRRRWRARQRQIDS?SERILS?CLGRPAEP     59
HIVU455         --R---NP--.D----V----L------C-N-R-.---------------------L------D--------     70
HIVSF170        --G---DS--.E----I----I------Y-K-K-.---------------------I------T--------     70

CONSENSUS.B     MAGrsgdsde.ellktVRlIKfLYQSnPpPspeG.TrqARRNRRRRWReRQRqIrsiSewilstyLgRsaeP     70
HIVLAI          ----------.D---A----------N---.-------------------H----R------------     70
HIVHXB2R        ----------.--IR------L--------N---.-------------------H----R--G---------     70
HIVNL43         ----------.--IR------L--------N---.-------------------H----R------------     70
HIVMN           ----------.--------------------S--.----------------H-----A----N----P---     70
HIVBRVA                   -------V----------R---.------------A-----Q-L-G-----F-------     60
HIVSC           --------E-.--------------------K---.-----------------------G----N----L---     70
HIVJH3             KKRRQRR.RAAQA-----------------.-------------Q---------G--I-N----P---     67
HIVBAL1         ----------.------------------IL--.-----------------------R--GA--------     70
HIVJRCSF        ----------.D-------------------N--.--------------------T---R--------P---     70
HIVJRFL         ----------.----------L----------.--------------------T---R--------P---     70
HIVNH5          ----------.----------------------.-PT--------------R---------RN--D-P---     70
HIVOYI          ----------.------------------N---.--------------------K--G-------------     70
HIVSF2          ----------.---R------L----------.-----------------------G-------------     70
HIVNY5CG        ----------.----------------------.--------------------T--------H-------     70
HIVSF162        ----------.---Q---F---------L---K-.-------------------Q---A--I--H----T--     70
HIVCAM1         ----------.----A-----L------L--SK-.-----------------H--A--N-----H---P---     70
HIVCDC4         ----------.--I----I--H--------K---.----------------R-H---A-L---C--------     70
HIVSF33         ------G--R.---TA--I--I------H-----.-------------------H----R----V----S--     70
HIVRJS          ----------.--I----I----------N---.----------------------D-----H---PT--     70
HIVHAN          ----------.--------------------N--.-PT---------------------R----F---P---     70
HIVD31          ----------.----------------------.-------------Q-----Q----R--------PEQ-     70
HIVRF           ----R------.D---A-----S----------.--------------------RC-----D------VD-     70
HIVYU2          ----------.D--R------V---------S--.----------------------G-L--N----PT--     70
HIVBCSG3C       ----------.----------L----D---N---.----------------------R----F-------     70

CONSENSUS.D     MAGRSGDsDE.dLLkA?RLIK?LYQSNPPPspEG?TRQARRNRRRRWRARQRQIhsIgERIlsTyLGRpeEP     68
HIVELI          ----------.-----V----F----------.-------------------RE-A----G------A--     70
HIVZ2Z6         -------R--.-----V----I----------.--------------------------------S---     70
HIVNDK          ----------.N----I----F----------.-------------------------IC-F-------     70
HIVMAL          ----------.---R-I----I--------NT--T-------------------N----------------     71

CONSENSUS.O     MAGRSE?.D?.QLLQAIQIIKILYQSNP?P?P?G.SRNARKNRRRRWRRRQAQVD?LA?R?LATVVHG?Q?N     59
HIVANT70        ------D.-..----------------Q-S-R-.---------------------T--A-V-------P-N-     68
HIVMVP5180      ------E.-Q.----------------C-T-A-.---------------------S--T-I-------S-D-     69

SIVCPZGAB       MAGRSEPQDDARLLQAVKIIKILYQSNPYPSPEG.TRKARRNRRRRWRARQKQISEISGRVLATYLGRPPKP     71

CONSENSUS.A     VPLQLPP?ERL?LDCSE??GTS?TQQ?QG?ETGVG?PQ??VESSA?LGSGTK?                    100
HIVU455         -------I---R-----SC---G---P--T-----G--IS-----V------N                    123
HIVSF170        -------L---H-----DR---E---S--A-----R--VP-----I------K                    123

CONSENSUS.B     VplqLPPleRLtLdcseDCGtSGtq......?GVGsPqiLvESPavLesGtKE                    116
HIVLAI          ---------------N---------.......------------T--------                    116
HIVHXB2R        ---------------N---------.......------------T--------                    116
HIVNL43         ---------------N---------.......------------T--------                    116
HIVMN           --------.Q----------------.......------------T--------                    115
HIVBRVA         ---------------N---------.......------------T--------                    106
HIVSC           ---------------N---------.......------------T--------                    116
HIVJH3          ---------------N---------.......------------TI-------                    113
HIVBAL1         ---------------D--------S......R-----------T--------                    117
HIVJRCSF        ---------------N---------.......---N-E------T--------                    116
HIVJRFL         ---------------N---------.......-----E------T--------                    116
HIVNH5          ---------------N---------.......----------------------                    116
HIVOYI          ----------N----------------.....-----E----------P----                    116
HIVSF2          --------------------N--A-.......---------------D-----                    116
HIVNY5CG        -------------------------.......--------L------G-----                    116
HIVSF162        -----------N-------------.......------V-G------D-----                    116
HIVCAM1         ----------------K---------.....----------------------                    116
HIVCDC4         -------------------------.......----------------------                    116
HIVSF33         --------D-----------------.....----------------------                    116
HIVRJS          -------------------------.......------V--------D                        111
HIVHAN          --------------------N----.....------V----------P----                    116
HIVD31          ---P----------------------.....----------------------                    116
HIVRF           -Q------------S----------.....------V-----------A--                    116
HIVYU2          --F------------N---------.....------------P--D-----                    116
HIVBCSG3C       -----------N-G-N---------.....------V-----T---P----                    116

CONSENSUS.D     VPLQLPPLERLnLNCsEDCgtSGTQ.......GVGsPQIsVEsP?vLeSGTEEQC                  115
HIVELI          ------------------R-----.....---H--------T----------                    118
HIVZ2Z6         --------------------A----.....------------T----------                    118
HIVNDK          -------------------------.....-------P--P-A--------                      116
HIVMAL          -----------T---N---------.....------------AI-G-----                    117

CONSENSUS.O     N?VDLPPLEQL?IRDPE?D?L??????????????????????T????????N                   78
HIVANT70        -I---------S-----G-Q-SEAWTVDPRAEDN$CLQNLCSCN-ILATRIAE                    120
HIVMVP5180      -L---------N-----A-R-PGTG.....................-V.DPGTKD-                103

SIVCPZGAB       GDLELPELDKLSLQCVETTQDVGTSNTSQPQTATGETVPAGGNYSILGKGAKN                    124
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HIV1 VPU

Sequences of the A, C, and E subtypes are not currently available for the VPU.

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                                                                                                                  env cds ->
CONSENSUS.B mqslqi?aivalvvaaiiaIvvWt.iv?ieyrKilRQr......?kidRl?idrireraeDsGNeSeGdqee.      61
HIVLAI      --PI--.--A-----I-------S.--I----------.....-----.---LI-----------...-.      59
HIVMN       --P-V-A--------G------ S.--F------R---.....-----.----S---------------.      62
HIVSC       --P---LS---------------S.--F-X--------.....-----.--------X--------IRK-.      63
HIVBRVA     --P---S----------------S.-ALL----L----.....-----.--------------------.      63
HIVJH3      ---- -A-------V--------S.--F----------.....-----.--------------------.      62
HIVBAL1     --A---S---G------------.--F----------.....-----.----T----------D-----.      63
HIVCDC4     ----E-V---E------------.--F----------.....----VNX------E--N----------.      64
HIVOYI      IY----L-------VT-------.--LL---------.....-----.-------------D-------.      63
HIVSF33     - --T-L----I--VT-----I--.--L-K--------.....-----.--------------------.      62
HIVSF2      ------L---S---V---------.--L----------.....X----.------K--------------.      63
HIVNY5      -L-X.............X-----.--F-----V----.....-V--I.--------------------.      49
HIVNL43     --PIIV.--------I-------S.--I----------.....-----.---LI-----------E....      59
HIVCAM1     -LP---X-------V---------.--F------R--K.....QV---.----I----------------.      63
HIVJRCSF    --P---L--------G----I--S.--L----------.....-----.--K----------------.      63
HIVJRFL     ----Y-L--------I-------S.--L----------.....-----.--------------------.      63
HIVSF162    --P---L-----------------.--Y----------.....-----.----T----------------.      63
HIVHAN      -L----A----------V-----.--V-----L----.....--N--.---LT----------------.      63
HIVD31      -----VA-------V---------.--F---------.....-----.----I----------------.      63
HIVRF       ----E-L----------L------.--G--I--T---K......X-----.--------------D--E--.      64
HIVBCSG3C   --PI--A-------VG-------.......X-----.....-----.-K--SK---------------.      56

CONSENSUS.D MQPl?IIAIAALVVAiIiAIVVWT.IVfIEYRRIKrQR.......kIDCl.iDRIrERAEDSGNESEGdREe.      62
HIVELI      ----G------------L------.----------K--.......R----.L---T--------------K.      63
HIVZ2Z6     ---SQ----------A--------.----------.....----I.--------------------.      63
HIVNDK      ----V-------------------.--Y----------.....-----.----------------E---.      63

CONSENSUS.O mh???lLAiialsall?Inv??W?fi????lRkyl?Qr?qdr?e?eIler.lrRIrEirdDSdyESngeeeqe      57
HIVMAL      IQPLVI---V--VVT-I-AIVV-T.-VFIEI--IRR--.......K-DRL.ID----RAE--GN--E-DT-E.      63
HIVANT70    --HRD-----II----F---IL-G--....-----E-KE---K-R-----.--------------------      68
HIVMVP5180  --QEN---L------CL---LI-L-N....--I--V--K---R-Q-----.----K----------E--Q--      68

SIVCPZGAB   MTLLVGL.VLILVGLIAWNICIWGYIIKWGYRRYKRHR....LETEIERL.NLILRERAEDSGNESNGEEEER      67

CONSENSUS.B lSaL????vem?GH?Apwd?dDl                                                       77
HIVLAI      I---VEMG---.--H----I---                                                       81
HIVMN       ----....-G-.--D---VIN--                                                       80
HIVSC       ----....---.--D--G-I---                                                       81
HIVBRVA     ----....---G--D----I---                                                       82
HIVJH3      ----....---.--D----I---                                                       80
HIVBAL1     ----....---.--H----IN--                                                       81
HIVCDC4     ----....---.--H---NV---                                                       82
HIVOYI      ----....---.--H----V--M                                                       81
HIVSF33     --V-....---.--D----VN--                                                       80
HIVSF2      ----....---.--L----V---                                                       81
HIVNY5      ----....---.--D----VN--                                                       67
HIVNL43     V---VEMG---.--H----I---                                                       81
HIVCAM1     ----....M--.--N----VN--                                                       81
HIVJRCSF    ----....--R.--L----IN--                                                       81
HIVJRFL     --V-....--R.--L----IN--                                                       81
HIVSF162    ----....--R.--L----V---                                                       81
HIVHAN      ----....--R.--L----VN-Q                                                       81
HIVD31      ----....---.--H----V---                                                       81
HIVRF       ----....---.--H----V---                                                       82
HIVBCSG3C   ----....---.--H-L--I---                                                       74

CONSENSUS.D LSKL....VEM.GHHAPWDiDDL                                                      80
HIVELI      ----....---.-----------                                                       81
HIVZ2Z6     ----....---.-----------                                                       81
HIVNDK      ----....---.-------V---                                                       81

CONSENSUS.O vm?L....v?shGfdnPm?fe?l                                                       72
HIVMAL      LSK-....-EM.-H-A-WDVDD-                                                       81
HIVANT70    --D-....-L--------.--.P                                                       85
HIVMVP5180  --E-....IH----A---.--.-                                                       85

SIVCPZGAB   LEQLIHNYNHNNHFANPM.FD.L                                                       88
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                                        <- vpU cds
                                   signal peptide/gp120
                                                *                                *
CONSENSUS.A     Mrvmgi.q?nyq?lwr????....Wgtmilg??iIcna??e??lWVtVyYGVPVWkdaeTTLfcASdAk     52
HIVSF1703       ------.-M-C-N-L-.....-------ML---S-.TS.K-------------------------     58
HIVU455         ------.-R--PC---.....-------LI-----..Q.Q---------------V----------     57
HIVZ321         -K-K--.-G-W-NW-K.....---L---LV---S-.A-.N-------------------------     58
HIVRW020          -R--.-TSW-N---.....-------MLV-YS-.A-.N---A---------------G-----     56
HIVUG031fr        -R--.-R-W-H-L-.....--I----MI---S-RTD.K-------------E------------     57
HIVNI           ------.-K--PL---.....---N-FWIM-----..-.Q-------------T------------     57
HIVRW009          ---T.LM---N---.....-------ML---S-.AN.N------------------LG-----     56
HIVUG275A       -KA--T.-M-C-NW--.....-------ML---ST.A-.D------------R-------------     58
HIVUG273A       ---K--.-R-W-H-L-.....---I---LIT--ST.AK.N------------R-------------     58
HIVVI191A       ---K--.-M-W-H--K.....---L---LG-----..-.N-----F--------------------     57
HIVDJ264A       ------.-R--PLF-K.....--MI-FWIM-----..-.K------------R-------------     57
HIVDJ263A       -----M.-R--PL--K.....---I-FWTM-----..-.K------------RNT-----------     57
HIVDJ258A       ------.-K--PL---.....---I-F IM-----..K.EM-----------R--K----------     56
HIVCARGAN       ------.-K---H-L-.....-----F-LI--SCV.AD.Q-------------N-D-------N-R     58
HIVCARSAS       ---K-T.-K--SP---.....--I----LI---S-.T-.K---------------K----------     58
HIVCAR4054      ---KET.-R-WHN--K.....-RL--F-MLM----.K-.N------------RE-N----------     58
HIVCAR286Afr    ---K-T.-R-W-N---.....--L--F-MLM----.TN.N-------------R-----------     58
HIVCAR4023      ---KE...K.--H---WGWK....--S-L--ILM----.DKDK----------R--N----------     60
HIVCAR423A      ---KE...K.--H---WGWK....--S-L--ILM----.SD.K----------R--N----------     59
HIVKENYA        -----T.-R-C-H-L-.....-------MI---S-.A-.N-------------N------------     58
                                                *                                *
CONSENSUS.B     ??mrvkgi.rknyqhlwr????????wGtmLlGmlMicsa??e.?lWVTvYYGVPVWkeatTTLFcASdak     56
HIVJRCSF          ------.--------K.....G-IL---T------.V-.K--------------T-----------     58
HIVJRFL           ------.--S--Y--K.....G--L---I------.V-.K-------------------------     58
HIVALA1           ------.-R---R---.....--I----I------.T-.K-------------------------     58
HIVBRVA           ------.K--------W.....G-M----I------.TD.K---------------N----------     59
HIVJH3            ------.---------.....-------I------.A-.Q--------------A----------     58
HIVBAL1           ---TE-.--S---W--.....--I----I----N-.E-.K-----------------------R-     58
HIVYU2            --ATE-.---------K.....G--L----------.A-.Q-------------------------     58
HIVMN             ------.-R----W-G.....-------L------.T-.K-------------------------     58
HIVHXB2R          ----E...-.------WGWR....-------------.T-.K-------------------------     59
HIVLAI            ----E...-.------WGWK....-------I------.T-.K-------------------------     59
HIVNL43           ----E...-.------WGWK....-------I------.T-.K-------------------------     59
HIVMFA            ----E...-.------WGWK....--I----I------.T-.N-------------------------     59
HIVCAM1           --A---.---C-R---.....-------------.AD.K-------------------------     58
HIVNY5CG          --A--T.---------.....-------------.A-.Q-------------------------     58
HIVADA            -K----.--------K.....--I----------.V-.N-------------------------     58
HIVJFL            ----E-.---C-----.....-------------.AG.K-------------------------     58
HIVSIMI84         ------.---C-----.....-------------.V-.Q-------------------------     58
HIVD31            -K--E-.---------.....-------------.T-.K-------------------------     58
HIVSF162          ------.---------.....G--L----------.V-.K-------------------------     58
HIVBCSG3C         ----E-.---------.....-----F-I---Y--.AG.N-------------------------     58
HIVOYI            -TAR-T.-----R---.....-------------.A-.N-----------------------R     58
HIVSF33           --ARET.-----C---.....-------------.A-.N----------D------------     58
HIVCDC4         MA--A---.---C-----.....-------------.AA.N-------------------------     60
HIVSF2            -K---T.-R-------.....---L----------.T-.K-----------------------R     58
HIVSF2B13         -K--ET.---------.....--IL----------.K-.K-----------------------R     58
HIVHAN            -K--ET.-----R---.....G--L-------S-V.AG.N-------------------------     58
HIVRF             ---MEM.---C----K.....-------------.A-.D----------------------E--     58
HIVWMJ2           ------.MR-C----I.....-----F--W-----.V-.Q-------------------------     58
HIVTB132          ----E-.---C-----.....---L---I---S--.A-.N-------------------------     58
HIVBR020           X--EM.--HW--W-K.....G-IL----------.KD.N-------------------G-----     58
HIVTH014           X-T--.-----RQ---.....-------I------.A-.K-------------------------     58
HIVUS711fr         X---T.--------K.....-------------.A-.N--------------I----------     58
HIVUS712           X-TE-.---C--W--.....--I-------T-NN.A-.ES-------------------------     58
HIVUS715           X-T--.---C--W-K.....--I----I----N-.T-.K--------------N----------     58
HIVUS716           X-T--.---C--W-K.....--M----I----NT..-.N-------------------------     57
HIVHA593           XA-EM.--HC------.....R-I-------T---.A-.N-------------------------     58
HIVHA594           X-T--.---------K.....--I----------.V-.Q-------------------------     58
HIVHA596           X-T--.---------K.....--I----------.V-.Q-------------------------     58
HIVHA599           X----.---C-----.....--M----L------.T-.RF-----------D-I----------     58
HIVHA651           XA-EM.--HW----T.....-------I------..S-.Q-------------------------     57
HIVRJS          --ARE-.-T-W-----.....-------------.T-.N-------------------------     58
HIVGUNfr                                                A-.K-------------------------     29
HIVSC             -----S.GR-------.....-------I------.A-.Q-------------------------     58
HIVBR014           XA---.---C--WCW.....R--I----------.T-.K-------------------------     59
HIVTH026           X-T--.---------.....-------------.AN.N-------------------G-----     58
HIVBR021          ------.---C-R---.....--I-------T---EED.K-------------------------     59
HIVACH9                                                                 ----------     18
HIVACP1                                                                 ----------     18
HIVJM                                                                   ----------     18
HIVWM                                                                   ----------     18
HIVMA208          ---R--.-R-------WGTMLLGI-------------.AD.N-------------------------     66
HIVP896           ----E-.---W---.-.....G-IL----------AK-.KT---I-------R-------------     58
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                                        <- vpU cds
                                    signal peptide/gp120
                                                *                                *
CONSENSUS.C     mrVrgi.lrNwqqWwi........wGILGFWmlmicnv??g.nLWVTVYYGVPVWkeAkttLFCASDaK      57
HIVMA959         X----.P---------.........--------F---S-.W-.--------------D-----------      58
HIVMA960         X----.S---------.........-----------YS-.L-.--------------------------      58
HIVZAM20A       ------.---C-----.........-------------G.V-.D--------------------------      58
HIVD1024        ------.---Y---G-.........--------------.V-.--------------------------      58
HIVBR025                                                E.K--------------------------      28
HIVSM145A       ------.---------.........------------SG.G-.-------------R----------S-      58
HIVZAM18A       ----E-.---------.........--------V-NY--VGD.--------------------------      59
HIVDJ259A       -K-M-T.Q---PR--V.........---------L---G....--------------D-NPP--------      56
HIVDJ373A       ---M--.QM-C-----.........G---------LM--G.M-.-------------Q--NP---------      58
HIVSE364A       ---T-M.---C-P---.........--------RL-Y--.G-.--------------------------      58
HIVUG268A       ---M--.Q--C-----.........-------I-------.M-.----------------T----------      58

                                                *                                *
CONSENSUS.D     mrvrei.erNyQhlw????????WGtmlLgmlmtcs??ae.?lWVTVYYGVPvWKeAtTTLFcASDAK      55
HIVJY1          ---MG-.RM------K.........--I----I-----V.--.D--------------------------      58
HIVNDK          --A--K.---C-N--K.........--I----------A.--.D----------I---------------      58
HIVMAL          ------.Q----NW-R.........--M----------I.--.D--------------------------      58
HIVELI          --A-G-.---C-NW-K.........--I----I-----A.-D.N--------------------------      58
HIVZ2Z6         ----G-.---C-N--K.........--I----I-----N.-D.N--------------------------      58
HIVUG024        -----M.Q-------K.........--I-------I--GTE-.QS-------------------------      59
HIVUG021         X---M.R--C----G.........---L--E---IY-T.TG.N--------------------------      58
HIVUG038        ---M--.M----S--R.........-------L-----S.--..K--------------N----------      57
HIVUG046        ---MG-.---------ERNQHSLWR--I-------I-K..G-..--------------------------      64
HIVUG266A       ---KG-.P----N-LR.........---II---III--T.-D.N-------------D-E----G-----      58
HIVUG269Afr     ------.---------R.........----------I-RV.TG.E--------------------------      58
HIVUG274Afr     ------.---------I.........----------Y-V.--.Q--------------------------      58
HIVSE365A       --A--M.K-------R.........-------------V.--.K--------------------------      58
HIVCAR4020      ----G-.---------R.........-------I-----V.--.K----------------E----------      58

                                                *                                *
CONSENSUS.E     mrVket.qmnwpnlWk????....WGtliLGlviicsA.Sd.NLWVTvYYGVPvWrDAdTtLfcASDAK      58
HIVTH966         X----.---------.........--I-----------.--.--------------------------      58
HIVTH975         X----.---------.........--------------.--.--------------------------      58
HIVTH022         X----.---------.........------------N-.--.-------------K------------      58
HIVTN243        ------.---------.........--------------.--.--------------------------      58
HIVTH006         X----.---------.........--------------.--.-----G---------------G-----      58
HIVTH011fr      ------.---------.........-----------x--.-N.--------------------------      58
HIVCARELO       ----G-.-----H---.........------------R-.-E.-----------A----E----------      58
HIVCAR4017      -----...K.YQH--RWGWK....--SML--ILM----.--.-----------A-K------------      59
HIVCAR4039      ---RG-.-K-------.........---------M----.--.----------------K-N--------      58
HIVCAR4071      ----G-.---------.........----------M---.--.--------------------------      58
HIVCARMBA       ----G-.--T---W--.........------------N-.-N.-------------K------C------      58

                                                *                                *
CONSENSUS.F     MRVRGM.QRNWQHLGK........WGLLFLGIL?ICNA..E.nlwVTVYYGVPVWKeATTTLFCASDAK      56
HIVBRA7944                                                -.EFG------------------------      28
HIVBZ163Afr     ------.---------.........---------L----..-.--------------D------------      57
HIVBZ126Afr     ------.---------.........---------I----..-.--------------------------      57

                                                *                                *
CONSENSUS.G     MRvkGI.qrNWQhLWk........WGtLILGLVIIcsA.sn.nLWVTVYYGVPvWEDadtpLFCASDAk      58
HIVVI525A       ---R--.-T---N--N.........-----------S--.--.--------------E----------      58
HIVLBV217       --A---.L--------.........--I---------N-.-G.-----------A------T--------      58
HIVCAR4067      ------.---------.........--------------.T-.S--------------R-A--------R      58

                                                *                                *
CONSENSUS.O     MtvtMK.aM?KrNrKlw.......?lylamALiiPCL??S??QLYATVYsGVPVWEdA?PvLFCASDAN      54
HIVANT70        -I----.--E---K---.......T---------T---..-LR-------A--------T----------      59
HIVMVP5180      -------.V-K-N---S-.......S--I----L----SY-K.--------------E-A----------      60
HIVVAU          --AI--.--G------G.......IWC-IL--------..-CN----------------K-T--------      59

                                                                                 *
CONSENSUS.CPZ   M?????.?????????.......???????I??????T.?E.???VTV?YGVPVW??A?P?LFCA??A?      20
SIVCPZGAB       -KVMEK.KKRDWNSLS.......IITIITI-LLTPCL-.S-..LW---Y------HD-D-V----SD-K      58

                      *                         *                                *
CONSENSUS.U     MrVm?i.qrNcq?lw?........wgililgmi?ICna.???nlWVTVYYGVPVW?dAeTTLFCASDAK      51
HIVZAM184       ---RG-.PK-W-QW-I.........----GFW-LM--SV.VG.-------------RE-K----------      58
HIVCAR4081      -K--ET.----PRS-R.........--------LVI-----.SDN-------------K------------      59
HIVK124A        ----G-.-----L-LG.........G--M-----I----.A..-------------R------------      57
HIVZ3fr         ---KE-.---Y-H--K.........-SLI-----M--K-.IE.KS-----------K------------      58
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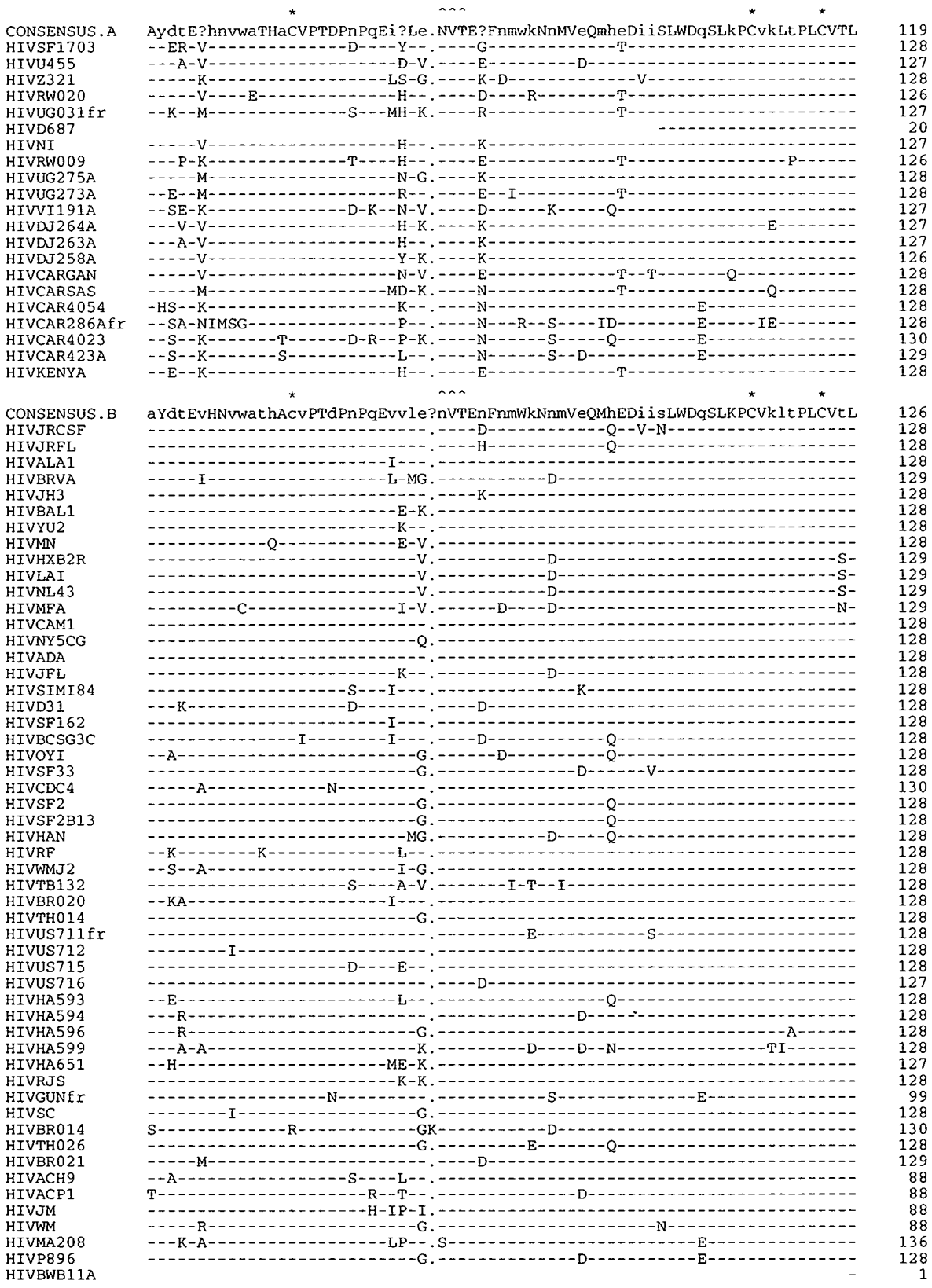
HIV1 ENV


CONSENSUS.A AydtE?hnvwaTHaCVPTDPnPqEi?Le.NVTE?FnmwkNnMVeQmheDiiSLWDqSLkPCvkLtPLCVTL 119
HIVSF1703 --ER-V----------D----Y--.----G----------T---------- 128
HIVU455 ---A-V----------D-V.----E---------D---------- 127
HIVZ321 -----K----------LS-G.----K-D----------V---------- 128
HIVRW020 -----V----E----------H--.----D----R--------T---------- 126
HIVUG031fr --K--M----------S---MH-K.----R----------T---------- 127
HIVD687 ---------- 20
HIVNI -----V----------H--.----K---------- 127
HIVRW009 ---P-K----------T----H--.----E----------T----------P------- 126
HIVUG275A -----M----------N-G.----K---------- 128
HIVUG273A --E--M----------R--.----E--I----------T---------- 128
HIVVI191A --SE-K----------D-K--N-V.----D------K-----Q---------- 127
HIVDJ264A ---V-V----------H-K.----K----------E-------- 127
HIVDJ263A ---A-V----------H--.----K---------- 127
HIVDJ258A -----V----------Y-K.----K---------- 126
HIVCARGAN -----V----------N-V.----E----------T--T-------Q---------- 128
HIVCARSAS -----M----------MD-K.----N----------T----------Q-------- 128
HIVCAR4054 -HS--K----------K--.----N----------E---------- 128
HIVCAR286Afr --SA-NIMSG----------P--.----N---R--S----ID--------E-----IE-------- 128
HIVCAR4023 --S--K-------T------D-R--P-K.----N------S-----Q--------E---------- 130
HIVCAR423A --S--K-------S----------L--.----N------S--D----------E---------- 129
HIVKENYA --E--K----------H--.----E----------T---------- 128
CONSENSUS.B aYdtEvHNvwathAcvPTdPnPqEvvle?nVTEnFnmWkNnmVeQMhEDiisLWDqSLKPCVkltPLCVtL 126
HIVJRCSF ----------.----D----------Q--V-N---------- 128
HIVJRFL ----------.----H----------Q---------- 128
HIVALA1 ----------I---.---------- 128
HIVBRVA -----I----------L-MG.----------D---------- 129
HIVJH3 ----------.----K---------- 128
HIVBAL1 ----------E-K.---------- 128
HIVYU2 ----------K--.---------- 128
HIVMN ----------Q----------E-V.---------- 128
HIVHXB2R ----------V.----------D----------S- 129
HIVLAI ----------V.----------D----------S- 129
HIVNL43 ----------V.----------D----------S- 129
HIVMFA ---------C----------I-V.------D----D----------N- 129
HIVCAM1 ----------. 128
HIVNY5CG ----------Q. 128
HIVADA ----------. 128
HIVJFL ----------K--.----------D---------- 128
HIVSIMI84 ----------S---I---.----------K---------- 128
HIVD31 ---K----------D-------.----D---------- 128
HIVSF162 ----------I---.---------- 128
HIVBCSG3C ----------I--------I---.----D----------Q---------- 128
HIVOYI --A----------G.------D----------Q---------- 128
HIVSF33 ----------G.----------D------V---------- 128
HIVCDC4 -----A----------N---------.---------- 130
HIVSF2 ----------G.----------Q---------- 128
HIVSF2B13 ----------G.----------Q---------- 128
HIVHAN ----------MG.----------D----Q---------- 128
HIVRF --K--------K----------L--.---------- 128
HIVWMJ2 --S--A----------I-G.---------- 128
HIVTB132 ----------S----A-V.-------I-T--I---------- 128
HIVBR020 --KA----------I---.---------- 128
HIVTH014 ----------G.---------- 128
HIVUS711fr ----------.---------E----------S---------- 128
HIVUS712 --------I----------. 128
HIVUS715 ----------D----E--.---------- 128
HIVUS716 ----------.----D---------- 127
HIVHA593 --E----------L--.----------Q---------- 128
HIVHA594 ---R----------. 128
HIVHA596 ---R----------G.----------A------ 128
HIVHA599 ---A-A----------K.---------D----D--N----------TI------- 128
HIVHA651 --H----------ME-K.---------- 127
HIVRJS ----------K-K.---------- 128
HIVGUNfr ----------N---------.----------S----------E---------- 99
HIVSC --------I----------G.---------- 128
HIVBR014 S----------R----------GK----------D---------- 130
HIVTH026 ----------G.---------E-------Q---------- 128
HIVBR021 -----M----------.----D---------- 129
HIVACH9 --A----------S----L--.---------- 88
HIVACP1 T----------R--T--.----------D---------- 88
HIVJM ----------H-IP-I.---------- 88
HIVWM -----R----------G.----------N---------- 88
HIVMA208 ---K-A----------LP--.S----------E---------- 136
HIVP896 ----------G.----------D----------E---------- 128
HIVBWB11A - 1

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                          *                ^^^                                  *      *
CONSENSUS.C   AYe?EvHNVWAThACVPTdPnPQEmvle.NVTenFNMWkNdmVdQMHeDiIslWdqsLKPCVklTPLCvtL  126
HIVMA959      ---R-------------------I-W-.------------I---------------------------  128
HIVMA960      ---Q-------------------V--G.-------------------V---------------------  128
HIVD757                                                        --------------------  20
HIVD747             -------------------G.---------R----N-----V---------------------  63
HIVD760           ------Y-----G-D---I---.---G----------------V---------------------  64
HIVNOF                                                                  V--------  9
HIVZAM20A     ---T----------------S------A.-----------------------------------M--------  128
HIVD1044                                                                -------  7
HIVD1024      ---E-----------------------.--------------N-----V---------------------  128
HIVD744                                                      RV---T---------------  20
HIVD766                                                                    ----  4
HIVD808                                                     -----P---------------  21
HIVD868                                                       --P---------------  18
HIVBR025      --DT-----------------------.---------E----E---Q------G---------------  98
HIVSM145A     ---R----------------S----L-G.-----------------------------------------  128
HIVZAM18A     ---R-------------------I--G.----------------------R-------------------  129
HIVDJ259A     --KV----------------S---LA--.-----------G------Q---------------------  126
HIVDJ373A     ---T----------------S---L-M-.-----------G------Q-------EG-------------  128
HIVSE364A     ---R-G-------------------W-.----Y-----------------------------------  128
HIVUG268A     ---T-------------------I---.----S-------------Q-V-------------------  128

                          *                ^^^                                  *      *
CONSENSUS.D   sY??eaHNiWATHACVPTDPnPrEiele.NVtEnFnmWkNnMVEqMHeDiISLwdqsLKPCVKLtPLCVTL  123
HIVJY1        --EP--------------------M-.-----------------------------N-------------  128
HIVNDK        A-KK----------------Q-----.-----------------------------------------  128
HIVMAL        --ET-V--------------Q-----.----G-------------------------------------  128
HIVELI        --ET----------------Q--A--.-----------------------------------------  128
HIVZ2Z6       --KT----------------Q-----.---------R---------------------------------  128
HIVUG024      A KA----------------Q--.--------------------V---------------------  128
HIVUG021      --EA----------------Q--V--.-------I----------D----------------P------  128
HIVUG038      --IK-----------------------.-----------------------------------------  127
HIVUG046      --EP--------------------K--.-----------D--------V---------------------  134
HIVUG266A     A-DT-V--V----------------K--.---------------R---------E---------------  128
HIVUG269Afr   --KKG----------------xK--.-------------------------E---------------  128
HIVUG274Afr   --IA--------------D----R--.------D-----------------------------------  128
HIVSE365A     --ET-K--------------Q----A.-----------------------------------------  128
HIVCAR4020    --KA----------------Q-M--K.--S-----------------------------------------  128

                          *                ^^^                                  *      *
CONSENSUS.E   AHeTEvHNvWATHACVPtdpnPqeiyle.nvtenfnmwknnmveqmqedvIsLWDqsLKPCVkLTPLCVtL  128
HIVTH966      ------------------------H--.-I-----------------------------------------  128
HIVTH975      ------------------------H--.-----------------------------------------  128
HIVTH022      ----------------E---------.-----------------------------------------  128
HIVTN243      -------------------------.---------N-----------------------------------  128
HIVTH006      -----M------------------H--.-----------------------------------------  128
HIVTH011fr    ----------------------.....................x-T----R-----R--------  102
HIVCARELO     -------------------------M-.----H-------------------------------------  128
HIVCAR4017    --K---------------------M-.-------------A------I-----ER--------------  129
HIVCAR4039    --K---------------------M-.-----------------------------------------I-  128
HIVCAR4071    --------I---------------F--.-----------------------------------------  128
HIVCARMBA     --V--M-----------.HTQ---V-M-.-----------------H--I-----E---------------  127

                          *                ^^^                                  *      *
CONSENSUS.F   SYErEVHNVWATHACVPTDPnPQEVvLe.NVTENFDMWKNnMVEQMHTDIISLWDQSLKPCVKLTPLCVTL  126
HIVBRA7944    --------------------D----E-K.-----------------------------------------  98
HIVBZ163Afr   -------------------------.----------S-------------------------------  127
HIVBZ126Afr   ---K----------------------.-----------------------------------------  127

                          *                ^^^                                  *      *
CONSENSUS.G   sYSTEsHNVWATHACVPTDPNPQEIsLe.NVTENFNMWKNnMVEQMHEDIISLWDESLkPCVkLTPLCVTL  128
HIVVI525A     -------------------------.----------K--------------------E--------  128
HIVLBV217     A-----------------------N.-----------------------------------------  128
HIVCAR4067    -----K----------------V--.-----------------------------E------------  128

                          *                ^^^                                  *      *
CONSENSUS.O   LTSTEqHNIWAsQACVPTDP?P?EypL?.NVTd?FnIWKNYmVdQMhEDIIsLWdQSLKPCvqMTFLCVQM  120
HIVANT70      -----K----------T-Y----H.----D---------E--Q----------------------  129
HIVMVP5180    ----------------N-H-F--G.----N-D-----------------E------EK--------  130
HIVVAU        ----------T--------S-N--E-K.---GK-------I---------D-----------------  129

                          *                                                     *      *
CONSENSUS.CPZ ??STE?HN?WAT??CVP?DP?P??V?L?.N????FN??KN?MV??M?ED???L??QS?KPCVKLTP?C???  58
SIVCPZGAB     AH---A--I---QA---T--S-QE-F-P.-VIES--MW--N--DQ-H--IIS-WD--L--------L-VTL  128

                          *                ^^^                                  *      *
CONSENSUS.U   aYetE?HNVWATHACVPtDPnPQEivLe.NVTEnFNMWKNnMVeQMHeDIISLWDqSLKPCVKLTpLCVTL  120
HIVZAM184     ---R-V--------------------.----------D--D-----------------------------  128
HIVCAR4081    S-S--K--------------------L--.----K--------------------E---------------  129
HIVK124A      --K--M--------------------H--.------------------T----------------------  127
HIVZ3fr       ---K-S----------S--S---L--G.----------K-----------------------F-----  128
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                 *                          ^^^       ^^^
CONSENSUS.A      ?C???????????n????????????n?t???????n?t??...?????m??????.......??e..ikN   130
HIVSF1703        N-SH.........-ITTH........-I-TNNP...-I-........KY-E............G-..---   156
HIVU455          D-H.........-ITI.........-N-N......-N-.....NITD.GVR...........E-..M--   153
HIVZ321          S-H.........................-I-IKD....-N-.....NVDTE-.K...........E-..---   152
HIVRW020         D-N..........ATAS.........-V-N.....................................-..MR-   141
HIVUG031fr       N-T.........TVD..........-T-NV.....-IS........KD-I............G-..---   150
HIVD687          N-S.........DVT..........-N-FS.....-VS........YD-.K............G-..---    43
HIVNI            D-HNX........-NSYS........-SS.......-L-........SD-.N...........G-..---   152
HIVRW009         E-N.........-ITNV........-N-V......-I-........DD-.K............G-..---   150
HIVUG275A        N-SDVN.......-VTVT........-HSI..............SSD-.K............G-..---   153
HIVUG273A        N-TNA........-LTNA........-KNAKVNSAT-G-.......IQS-E............R-..---   161
HIVVI191A        E-H.........................-S-TPD....-N-.......TQSTII...........D-..TT-   150
HIVDJ264A        D-HN........................-V-SN.....-R-......ISRD-.Q...........G-..V--   150
HIVDJ263A        D-HNV........-SS..........-SSTSI....-R-......IDSK-.Q...........E-..---   155
HIVDJ258A        E-H..........-VSNS........-TSSYR....-IS........SE-.R...........E-..---   152
HIVCARGAN        E-H..........KP...........-T-DSTK...-NSAE...NMT..FEGI..........G-..-T-   157
HIVCARSAS        D-T..........-VA..........-DST.....................................N-..LR-   143
HIVCAR4054       N-TDVKK.......-ST.....................................LEGQ...........V-..M--   147
HIVCAR286Afr     N-TDAKIDCTNGR-NSAGGQTCTGVQ-S-A.....................EVGQ...........V-..M--   167
HIVCAR4023       N-TDVK........-ITV.........-S-S.TGNSA-TI.....NRT..VDSQ...........VG..---   164
HIVCAR423A       N-T..........-VTVT........-SSN......-V-KT...NSSQSSKYNIDG.......KE-..---   164
HIVKENYA         N-SNV........................-V-AT.....SG-........THGGR...........GR..M--   151
                 ^*^                        ^^^
CONSENSUS.B      nCtd????????.????????...??n?t???????n????????????mek?...........ge..ikN   141
HIVJRCSF         --K-V.....................-A-.......-TTSSS....EGM--R.............--..---   153
HIVJRFL          --K-V.....................-A-.......-TTNDS....EGT--R.............--..---   153
HIVALA1          H-I-YL....................-A-.......-TTSSN....GTK--R.............--..---   154
HIVBRVA          --H-F.....................-A-.......-ATSNS....GKM--G.............--..M--   154
HIVJH3           --I-WG.......NDTSP........-A-.......-TTSSG....GEK---.............--..M--   159
HIVBAL1          ----LR.......NATNG........-D-.......-TTSSS....RGMVGG............--..M--   159
HIVYU2           ----LR....................-A-.......-TTSSS....WET---.............--..---   154
HIVMN            ----LR.......NTTNTN.......-S-AN.....-NSNS.....EGTIKG............--..M--   161
HIVHXB2R         K---LK....................-D-NT.....-SSSG.....RMI---.............--..---   156
HIVLAI           K---LG.......NATNT........-SSNT.....-SSSG.....EMM---.............--..---   161
HIVNL43          K---LK....................-D-NT.....-SSSG.....RMI---.............--..---   156
HIVMFA           K---LK....................-D-NT.....-SSNG.....RMI---.............--..---   156
HIVCAM1          I--NV.....................-N-RT.....-SSDWDRR..EGEKM-.............--..---   157
HIVNY5CG         ----LT....................-A-YA.....-GSS.........E-R.............--..-R-   151
HIVADA           ----LR....................-V-NI.....-NSS......EG.-.R.............--..---   152
HIVJFL           --INLK....................-V-NI.....-NS.......WGK--E.............--..---   153
HIVSIMI84        ---NWKSA..................-S-SNT....-SS.........LE--.............--..---   154
HIVD31           ----LK....................-A-NTN....-SSWTM....TGE-.-.............--..---   156
HIVSF162         H--NLK....................-A-.......-TKSSN....WKE-DR............--..---   154
HIVBCSG3C        ----ELK...................-A-.......-TTSTNTPSGSWKKMER...........--..---   160
HIVOYI           D---V........NTTSSSLR.....-A-.......-TTSSS....WET---.............--..L--   161
HIVSF33          ----YLG...................-A-NT.....-NSSGG......TV--............E-..---   155
HIVCDC4          ----LNTN..................-T-.......-TTELSIIVVWEQRG-.............--..MR-   162
HIVSF2           ----LG....................KA-NT.....-SSNWK......EEI-............--..---   154
HIVSF2B13        ----LG....................KA-T......-SNNWK......EEI-............--..---   153
HIVHAN           K---YN....................-A-.......-SSWGR.......---.............--..-Q-   151
HIVRF            ----ANL...................-G-.......-VTSSSG...GTM--N............--..---   156
HIVWMJ2          --I-K.....................-I-DWK....-TTI.........IGG.............--..V--   151
HIVTB132         ---NLR....................-D-.....................................S-..M--   142
HIVBR020         --I-LN.......NSTN.......NN-SS..............GVKTGID-.............--..---   156
HIVTH014         ----LR....................-A-NT.....SST.........--G.............--..---   150
HIVUS711fr       ----KL....................I-A-YS.....-IS.......LEGEI-............-D..---   154
HIVUS712         ----LS....................-A-NTN....ATTTTNSS.AGMM-DR............--..---   160
HIVUS715         ---NLR....................-D-NTT...R-AT..NTTSSETM--E............--..---   160
HIVUS716         K---LG....................-A-NTT............SSGRM--G............--..---   152
HIVHA593         E-H-VNVNGTAN.NGT.........T-V-ESGVNSSDVTSNNVTNSNWGTMEK.............--..---   176
HIVHA594         ----VE....................-S-NAT....-SS.......GGIID-............--..---   154
HIVHA596         ----VK....................-S-NVT....-SS.......GGII-G............--..---   154
HIVHA599         H---AR....................-S-NVT....IEV........EKV--.............-D..---   153
HIVHA651         ---AAE....................RNDTG...SS-SS.......G.ID.-............--..-Q-   152
HIVRJS           ---NWK....................-D-DT.....-TT..NSSS.GEK--E............--..---   157
HIVGUNfr         ---NLV....................-A-YS.....-SS.......WEK-DR............--..-Q-   124
HIVSC            ---NLR.......NDTST........-A-.......-TTSSN....RGK--G.............--..MT-   159
HIVBR014         ----V........NVTNT........-N-....TST-SS......RLEE---.............-G..---   161
HIVTH026         ----LR....................-A-.......-TSST........--G.............--..M--   150
HIVBR021         ---NVNT......NST..........-T-.......-STNAT..SSWEN-.-............E-..---   160
HIVACH9          ----NL....................-S-NLG....-NT.........DI.-............--..---   111
HIVACP1          ----DLR...................-D.....................WEQ---.............--..---   108
HIVJM            --N-ASR......NVTKR........-D-NENATDS-NGTATSGN.KTM---Y...........A-..---   131
HIVWM            ----CVTS..................-C-NLR....-VTNTKSSS.KEI---.............--..---   122
HIVMA208         ----ATIR..........TNT.....-T-NT.....-SS.......GEVK-R...........E-..---   166
HIVP896          ---NL........NITK.........-T-.......-PTSSS....WGM---.............--..---   157
HIVBWB11A        ---NDLG......DATNT........-SS..............SEGM--I.............--..---    28
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CONSENSUS.C      nC?????.....n?t????.....N?t???????n?t?????????????.....?e..ikN  138
HIVMA959         --S.........-AN.........-TATN.....-V-ATNNVT.....................SD..M--  153
HIVMA960         --A.....................-V-IS.....-E-Y.........................K-..V--  145
HIVD757          --T.........-A..........-V-YDNG...-Y-..........................E-..---   40
HIVD747          H-T.........-A-YS.......-S-Y......-S-YN........................E-..---   85
HIVD760          E-GNV.......-A-........-I-NNGEN..-P-NITNNR.....................E-..---   94
HIVNOF           --TDVKV.................-A-SNSN...-M-..........................G-..---   31
HIVZAM20A        E-G.........-V-VPKD.....-S-YNGDINS-T-MK........................E-..MR-  158
HIVD1044         E-RQA.......-F-.........-A-NAN....-A-..........................E-..-R-   29
HIVD1024         E-GKV.......-A-.........-I-NNG..................................E-..---  147
HIVD744          K-D.........A-S.........-A-SSG..................................E-..V--   37
HIVD766          E-R.........-V-SNG......-G-YNETY..-ESV.........................K-..---   30
HIVD808          E-R.........-VSSNG......-G-YNETY..-ESV.........................K-..---   47
HIVD868          E-REV.......-D-RNGV.....-V-NNG..................................E-..---   41
HIVBR025         H-S.........-R-IDYN.....-R-D.....-MG...........................G-..---  120
HIVSM145A        --TE........ANI.........-I-SVG....-V-SNDNK.....................E-..---  154
HIVZAM18A        E-G.........-V..........-V-HE.....-S-K..........................G-..M--  148
HIVDJ259A        --S.........-VQS........-A-YE.....-S-K..........................E-..M--  147
HIVDJ373A        --S.........-KVTATG.....-GSVTY....-S-E..........................KD..MR-  153
HIVSE364A        --R.........-V-TSN......-A-S.....-DNPN..........................G-..---  151
HIVUG268A        --T.........-VNV........-I-NNA....-A-NSPYEN.GKLMEQ.............G-..---  161
                 ^*^         ^^^          ^^^        ^^^
CONSENSUS.D      nCt??????....n?t??????....N?t??????.n?t????.?????????????????.?e..mkn  136
HIVJY1           ---NAGG.................-K-TNGN...-T-N....QEEQMMEK.............G-..---  159
HIVNDK           ---DELR.................-SKG.....-GKVEEE.......................EK..R--  151
HIVMAL           ---NV........-G-AV......-G-NAGS...-R-NA.....ELKMEI.............G-..V--  161
HIVELI           --SDELRN................-G-MGN....-V-TEE........................KG..---  153
HIVZ2Z6          --IDEVME................-V-MKNN...-V-EE.........................IR..---  153
HIVUG024         --IEWKNE.....-E-KG......-K-VDPDKD..............................IG..---  155
HIVUG021         ---EWK..................-A-T.....-A-.........N.EG.............IG..---  149
HIVUG038         H--DV........-S-........-I-STNV...-N-........SI.EK.............G-..---  154
HIVUG046         H--EYKAP.....-A-I.......-A-DRDI.................................G..---  157
HIVUG266A        --SEGRV......TD-.......-G-IG.....-G-.........I.................GD..-R-  152
HIVUG269Afr      ---EAKF......-V-RATNGK....-TVR.....-A-.........KG.G.............L-..--D  159
HIVUG274Afr      ---EWK..................-T-EQEK...-TA........VPGSTTSD.........TD..-R-  157
HIVSE365A        --RDISS......DA-SNTIS.....-V-GIP................MMGK.............G-..-Q-  158
HIVCAR4020       H--RLENIA....-SSLTN.....-ASARS....-D-......DNNHTNSTNTRWVYDGME.K-..-T-  175
                 ^*^                      ^^^                ^^^
CONSENSUS.E      nCt?a?????...??????.....N?t??.....n????????ignit.?????????????de..VrN  145
HIVTH966         --IN-........NLTNVN.....-II.....HGP....NI-----.....................--..---  157
HIVTH975         ---.........TLTKV.......-I-.....-FS.....K-----.....................--..---  153
HIVTH022         ---N-........NLINVN.....-I-.....-VS....NI-----.....................--..---  157
HIVTN243         I--N-KLTNA...NLTNVN.....-I-.....-VS....NI-----.....................--..---  162
HIVTH006         ---N-KVT.....NVS........-TI.....-AP.....D-----.....................--..---  156
HIVTH011fr       ---Yx........NLTNVK.....-I-.....-VP....NK-----.....................-G..---  131
HIVCARELO        R--N-.....................-F-.....-ATDA......-V-.NATAKFNATKEMENT..-K-  162
HIVCAR4017       ---K-.....................-F-KA.....-STEAAL....-GS.....YSNETAEMEN-..---  163
HIVCAR4039       H--R-.....................-F-NS.....-YTKG......-E-.........VEMEN-..-S-  155
HIVCAR4071       D--K-DF...................-T-KF.....-TTEK......PEI........EISEMQK-..-S-  159
HIVCARMBA        ---R-NL...................-S-NA.....-ST.......NAN-.........LKMEN-..-K-  155
                 ^*^          ^^^
CONSENSUS.F      nCT?At?......NAT.........??........???.........a?Q?g?tLKEeP...Ga..IQN  148
HIVBRA7944       ---D--A.....---.........TT........NDT...........-HS.------...-E..---  127
HIVBZ163Afr      ---N-.I.....---.....................................-I-D-.D---G-...--..---  152
HIVBZ126Afr      H--S--P.....---.....................................-T-N-T------...--..---  154
                 ^*^          ^^^          ^^^
CONSENSUS.G      NCT?v??......N?T???.....N?ss??...??????.?????N????s??.....Ee..MkN  144
HIVVI525A        ---K-TY......-S-AAN.....-R--TV....TTP...TSTVT-NSTV-GK.....--..-T-  168
HIVLBV217        ---NAIA......-V-NS......-KT-.....NNSSLG.....-STVS-I.....--..---  162
HIVCAR4067       ---E-NN......-C-RD......-N-TV..............-CEE..........-K..---  154
                 ^*^          ^^^          ^^^
CONSENSUS.O      nCtd?????....N?t???l??....n?T?.....................nE??mk?  133
HIVANT70         E--.........-IA.........G-T.....................--NL--K  145
HIVMVP5180       --V-LQT.....-K-..G-L.....-E-I.....................--..-RN  152
HIVVAU           ----IKNSI....-T-NSP-NS....-N-.....................K-..V-Q  155
                  *           ^^^
CONSENSUS.CPZ    ?C?????????.............N?T??????????T???.?????????.....??..???   62
SIVCPZGAB        Q-SKANFSQAK.............-L-.....NQ-SS.....PP.....LE..MKN  154
                 ^*^          ^^^          ^^^
CONSENSUS.U      nCsdv?????...N?T??.....nste??..??????.....????.....ee..ikN  136
HIVZAM184        ----ATSTNS...-T-.....................--..---  146
HIVCAR4081       T-T.........-I-K.....----V...NNNSTV.....DNK.....--..---  155
HIVK124A         ---N-.....-G-GG.....---TGN....NIT.....RED.....IG..M--  154
HIVZ3fr          --I--K.....-S-N.....-N--E.....AT..-T-  148
```

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                                    peptide T region
                 *  ^^^                                                  *^^^
CONSENSUS.A      CsfNmTtelrdkkqkvyslFYrLDvVqi????????n??????...?n?????????YrLInCntSaitqA   174
HIVSF1703        --Y-----------------K----P-DK.......-NG.........-NN...IRTQ--------------   210
HIVU455          ------------------------I---.........-KTD.......-NS.....----------T----   202
HIVZ321          --Y---------QR-I--------I-P-GG.................-SS.NGDSSK--------------   205
HIVRW020         ----I----K----Q------K------NE.....K-ET.....DK--------------------------   191
HIVUG031fr       --Y-----------I----------P-.........-ES.........-SS..DNFSE--------------   203
HIVD687          -------------R-IFT.---------D.....................-SS.....SE--------------    90
HIVNI            ----I---V----K-MHA----------.........-EN.........-GS......Q--------------   201
HIVRW009         --------------R---------I---NS.......-SN.........-SS....HNQ--------------   203
HIVUG275A        ------------Q--IHP--------P-.........-GSN........-RQ.....----------------   202
HIVUG273A        ------------TRR------K------K........-SSE.....-------------------------   208
HIVVI191A        -TY---------V---H----------NGI......-GTSN......-NS.....AQ--------------   205
HIVDJ264A        --------------Q-SA----------.........-ESS.......-SS......Q----------K--   200
HIVDJ263A        ----------------SA----------.........-ESSNSQ.....------------K-          204
HIVDJ258A        ------------Q--MSA----------SES.....-NSQ.....-------------------------   201
HIVCARGAN        ----------------------K------DEN.....-GTR.......-NS.....EL--------------   211
HIVCARSAS        --Y----K-N--R---H----K--I-P-NKINDASG-ISENN.....-SSSGNITKQ----S----T----   209
HIVCAR4054       ----I---IN-R-K-EHA----------NS....NS-ISN.........AN...YND-------V-TAK--   202
HIVCAR286Afr     ----I---I-NR-K-E-A--------PTNN....DD-STD........-YTHN.....-------A-T-K--   222
HIVCAR4023       ------S-I--R-K-E-A------I-P-NN....NN-NT.........-NTND..YND-M-----V--VK--   221
HIVCAR423A       ----T---II--RKQE-A------I-P-NN.....N-NTNE.....------IA-TVK--              214
HIVKENYA         .--Y-I------RR-------------P-NEN.....-SSNNE.....--------------------     202
                 *  ^^^                                                  *^^^
CONSENSUS.B      cSFnittsirdkvqkeyAlfykldvvpid????...???????????n?????????yrlisCntsvitQa   185
HIVJRCSF         ------K----------------------NK.................-NT......K--------------   202
HIVJRFL          ----------E-----------------N.................-NT......S------D--------   201
HIVALA1          ------------M---S---H--------N.................-NT......S-I------------   202
HIVBRVA          ------------M-----------I----NDKT..............-T.......R--------------   204
HIVJH3           ----------------H-----H-----N.......NSTKDNIKND.-ST......R--------------   216
HIVBAL1          -------N--G----------.---IA---.................-NS....NNR--------------   208
HIVYU2           ---------------------N-------.................-AS.....----------------   200
HIVMN            ------------M------L----I-S--.................-DS.....TS--------------   209
HIVHXB2R         -----S----G-------F-----II---.................-DT.....TS-K-T----------   204
HIVLAI           -----S----G-------F-----II---.................-DT.....TS-T-T----------   209
HIVNL43          -----S------------F-----I----.................-TS.....----------------   202
HIVMFA           -----S----N-------F-----IR---.................-TT.....----------------   202
HIVCAM1          ----V-----N--R----------------KA..............-TS.....-T--H----------   205
HIVNY5CG         ----V--I--N-I--------R--I----KD..............-TS.....-T--N-D-------   199
HIVADA           ------------K-D-----R-------ND..............-TS.....----N----T----   200
HIVJFL           ----T----KN-M-R--------------KD..............-TS.....-T--N----T----   201
HIVSIMI84        ----V----KN---T----------M--EDD..............-TS.....-T--N----------   202
HIVD31           ------------------H----------ND..............-TS.....----------------   204
HIVSF162         ---KV-----N-M----------------ND..............-TS.....-K--N----------   202
HIVBCSG3C        ----V...LG--K--A--------------NDK.............-ST.....K----------T---   207
HIVOYI           ----T-------M-EQ---------L---KN.............DTK.....F---H----T----   209
HIVSF33          -------G-------A--Y----------DD.....NT.....-TS.....----H--S-----T   205
HIVCDC4          --------------R----------E---DNK....NTT.....-NT.....K----N----------   215
HIVSF2           ------------I---N---RN-------.....NASTTT.....-YT.....N----H--R------   207
HIVSF2B13        ---Y--------I---N---RN-------.....NASTTT.....-YT.....N----H--R------   206
HIVHAN           ---KV--N--------S-----T------N.....NKTSNRD....-TT.....S-M--H--R------   206
HIVRF            ---QV---R---T--K------------EKG.....NISPK..NNTS-NT...SYGN-T--H--S------   217
HIVWMJ2          --------R----H--------------KGD.....N.....-SS.....R----N----------   201
HIVTB132         ---K--------L-----------I---NND.............-TS.....---------I----   190
HIVBR020         ----T---VK--EK-------N----Q-G.............-DN.....TS---T----------   204
HIVTH014         ---------KT--K.D-------------N.............D-TS.....----N----------   197
HIVUS711fr       -------------K-------S-N-I--G.............GD-TS.....--MVK----------   202
HIVUS712         ----V-A-----M-R----------IQ--.............-TS.....----------------   206
HIVUS715         ----------------F-----------E.............-DT.....TS----------L---   208
HIVUS716         ------------M------L-----I---.............-DN.....NS--------------   200
HIVHA593         -------N----M---T-Q-----I---E.............DQN.KTNNTL----N----------   228
HIVHA594         ----V----K--TT--H-----------..............GNN.SSKNGS-I-------T----   206
HIVHA596         R---V-A--K--TT--H-----------..............SKNN.SSKNGN-I-------T----   207
HIVHA599         -------N-KG-I-------S----L---.............N-TG.SSNSSR-I------T-VK--   206
HIVHA651         ----V----K---T-QS----R------Q.............E-ND....NSS----N----------   202
HIVRJS           ----------N-L--G-----------...............ND-TS.....-T--N----------   205
HIVGUNfr         -------RK-N----Q---LNR--I----.............KTS.....-T--x----------   170
HIVSC            ----------S-----------------..............-TS.....-T--N----------   205
HIVBR014         ----V-----N-M---------P------.............KT......R-M--H----------   207
HIVTH026         ---------ST--.-D------S------.............-NT.....IS----N----------   197
HIVBR021         ---------KN--K-D----NR-------.............-DN.....TS-M--N----------   208
HIVACH9          --------RGG-M------L-----I---.....NST.....SN-YT.....S--------------   163
HIVACP1          ---Y---N--N-M--Q----DR-----T-.............DD-TS.....-K--N----------   156
HIVJM            -------NMGG-MK------NT-----V-NSN....NN.....SN-DS.....-I-T----------   184
HIVWM            ---Y------N-R-----T-----I----.....NDKD.....-TS.....--------------   172
HIVMA208         -------N-K-RM--A--T-----I---G.....NDSTS.NNNTS-NYT.....S------D-------   224
HIVP896          ---Y------N--K------NR------ENT.............-NT.....K--NHR---------   206
HIVBWB11A        -------R-------K----------A--GS.............-TS.....--------------    76
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                                                peptide T region
                 *  ^^^                                          ^^^                 *^^^
CONSENSUS.C      CsFnaTTe?rDkkqkvyAlFYrlDiVpl?????..?n????......n?s??.????YrLinCnTSaiTQA  182
HIVMA959         --------L---R--------K------N.......EKD........-S-S....GE------S--TV---  205
HIVMA960         --------I----H--------------N.......ENEN.......-N-.....---------T----  195
HIVD757          ----T---L--Q----A----K--V---DG......-D.........-S-.....--------------   89
HIVD747          ----T---L-------Q----K--V---........-TTD.......-S-.....--------------  134
HIVD760          -P------I--RQ---------------D.......-NN........-ST.....--------------  143
HIVNOF           ---YT---IG-----------KP-V---........-ER.................N-I--H----T----   77
HIVZAM20A        -------VIN--TS--H-----V-----NDENS...-KTNA......-ST...KPTK-I-------T----  217
HIVD1044         -T------I--R----H----K------D.......-ESK.......-D-....SRN-------------   82
HIVD1024         --------I--R--T-------------D.......SN.........-K-.....K--------------  196
HIVD744          --------I--R--T---X---------D.......DRNER......-S-.....KY-------------   90
HIVD766          --------L--R--R------T----L-N.......KKNS.......-D-.....Y--------------   81
HIVD808          --------V--R--T------------FN......KK.........-S-.....EY-------------   97
HIVD868          --------I--R--T-------------D.......-KKK.......-N-....SEY-------------   94
HIVBR025         ----M---V---RE--H-----------K.......-ESS.......-T-.....GD---V----------  172
HIVSM145A        --------LS------------------NEGE....-NSRK..............---------------  205
HIVZAM18A        --------LK----R------K------NEN....N-SSE.......DS-.....E--------------  202
HIVDJ259A        ----V---L---R--A------------NE......-NSE.....---------------------------  195
HIVDJ373A        ----I---L------K-----K------G.......-GNEE..............---------S----  201
HIVSE364A        ----I---L---RRNE------------SGSK....-SS........-S-.....E--------------  204
HIVUG268A        ----V---I-----TAH----K--V-S-EGNS....-T..................---------------  209
                 *  ^^^                                          ^^^                 *^^^
CONSENSUS.D      CsFnitt??rDKkkqvyalFYkLDvVqid???????n?s????....n??......?YRLinCntSaItQa  180
HIVJY1           -------VIS------H----R----P--DDNS..A-T-NT......-YT.....N--------------  216
HIVNDK           ----V....---RE----------I-P--NN.....-RT.....-ST.....N------D--T----  199
HIVMAL           ------PVGS--R.-E--T--N--L----DSD.............-SS.....---------V----  209
HIVELI           ----V--VLK---Q-------R--I-P--.....-D-ST.....-ST.....N--------------  205
HIVZ2Z6          -------VV---T---H----R--I-P--ND.....-ST.....-ST.....N--------------  205
HIVUG024         ----V--EV------E----------MND.....-NT.....-TS.....-------------E  205
HIVUG021         ---...-EV------A----------MNDD.....-ST.....-TS.....-------A-T----  197
HIVUG038         -----S-IV---Q-EIN-I--R-----MT.....-N-ND.............----H----T----  202
HIVUG046         ----V--KVI-----EH----------M-.....DN-T.....-TN.....---------V----  207
HIVUG266A        -------EI----------------P--D.....N-ST.....-TS.....----------T  203
HIVUG269Afr      -Y--V--EI-------R----------MNNSES..I-T-..............-------S------  210
HIVUG274Afr      -------EL----E--------------D.....N-ST.....-ST.....N---V--T-------  209
HIVSE365A        -------EI---RQN--S---R--L-P-GNSNK...-ST.....-YT.....S---------V-K--  212
HIVCAR4020       ----V--VI-------H-------I-P-EDEDNIKG-T-DNTK....-IT.....R----------S  236
                 *  ^^^                                          ^^^                 *^^^
CONSENSUS.E      CsFNmTTelrDkkqkvhAlFYklDlV?i??????.?NsSe????.............YrLIncntSVIKqA  190
HIVTH966         --------I----------------Q-EDK.....----.....--------------  206
HIVTH975         --------II---------------QMEG......-T--.....--------------  201
HIVTH022         -T------I---Q--------R--I-QMHNE.....----.....--------------  206
HIVTN243         ------------------------I-Q-GDK.....----.....--------------  211
HIVTH006         ------------------------I-QV.....----.....--------------  202
HIVTH011fr       ----I--V-K--E----------I-P-GD.....N-G-SEYSE.....----------R-  184
HIVCARELO        ---------G--H---S---------P-DGNIDG..-N--.....-I--H--------  214
HIVCAR4017       ----V------R----Y-----T-I-S-D.....---SD.....-M-----N------  211
HIVCAR4039       ----I--K----TKEAY-P---H---P-KE.....---SE.....-V--LVIH------  204
HIVCAR4071       ----I-------E-E-Y----RS---P-ERNSGE.N-G-S.....----H---------  212
HIVCARMBA        ----------------S-I--VS---SMNA.....-N-.....--------------  202
                 *  ^^^                                          ^^^                 *^^^
CONSENSUS.F      CSFNmttEVxdKQqKVHaLFyrLDIVPISn??....NnS??e.....YRLInCnTSTITQA  196
HIVBRA7944       ---------R---L---S----------.....---.G-.....--------------  175
HIVBZ163Afr      ----V-M----------x---------GR....-G-GDY.....--------------  204
HIVBZ126Afr      -----S----N----------K--------SS....---.R-.....----H-D-------  205
                 *  ^^^                                          ^^^                 *^^^
CONSENSUS.G      CSFNiTTE?RDK?K?EYALFYrLDVVPIn?n?....NsS.....???YRLInCNvSTIKQA  188
HIVVI525A        ----V---L---Q-A------K------DN-R....-D-.....----H---------  217
HIVLBV217        --------V---S-K----------G-E....---.....TTD-------A------  214
HIVCAR4067       --------I---R-T----------EDQ....---.....T--------------  204
                 *  ^^^                  ^^^     ^^^                 *^^^
CONSENSUS.O      C?FNVTTVlkDKkEkKQALFYVsDL?k?N?ts??..N?T???.....mY?LtNCNSTtI?QA  176
HIVANT70         -E------I----------MEL-E--ST..-K-NSK.....--T---------T--  200
HIVMVP5180       -S-------T----Q----------S-V-DSNAV..-G-.....T-M-------I-K--  204
HIVVAU           -D----------Q---------T--V-I-A--....-E-.....--R-I-------R--  205
                 *                                    ^^^                 *^^^
CONSENSUS.CPZ    C?FN??T???DKK??????FY??D??????.....N?.....N?T.....??Y????CNTT?ITQ?   83
SIVCPZGAB        -S--VT-ELR---KQVYSL--VE-VVNLG.....-E.....-N-.....-RIIN----A---A  202
                 *  ^^^                  ^^^^                ^^^^                *^^^
CONSENSUS.U      CSfnitTEl?Dk?ktvyaLFYkLDvV?in?n??..?Nnss????...???.....?YRLInCNTSaItQA  181
HIVZAM184        --YRT----K--TLR--S--------Q-DP.....S--TM.....----S------A--  195
HIVCAR4081       --------IR--K--A-----R----P--D-N....--N.....S----------K--  205
HIVK124A         --------VR-RK-Q---------I-QM-E-QD...-S--GEYR.....----------  209
HIVZ3fr          ---KVP---K--TE--HT--------PL-VT.....----I.....SST.....---------T----  201
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HIV1 ENV

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                *           *         *     ^^^   * ^^^   *                ^^^
CONSENSUS.A     CPKvsFEPIPIhYCaPAgFAILkC?dk?FnGtG.pckNvStVQCThG?ikPvvsTQLLLNGSLAe?ev?Ir    239
HIVSF1703       ------------------------N-AE-----.-------------.-R--I------------GR-K--    279
HIVU455         ------------------------K-PE---K-.--R----------.-----------------R-IR--    271
HIVZ321         ------------------------R-EE-E-K-.--R----------.-R---------------G--R--    274
HIVRW020        ------------------------K-TE-----.-------------.-R--I------------EGIQ--    260
HIVUG031fr      ----T-----------------R-NEDD-----.L------------X-----------------KG-R--    273
HIVD687         ------------------------KG-K-----.S.S----------.-----------------E-IV--    158
HIVNI           ------------------------K--G-----.-------------.-----------------G--V--    270
HIVRW009        ----------N-------------K--K-----.-------------.-----------------E-II--    272
HIVUG275A       ------------------------N-QE-----.I-N----------.-----------------GK-K--    271
HIVUG273A       ------------------------N--E-----.L-----S------.-R---------------T--K-K    277
HIVVI191A       ------------------------R--E-----.--R---S------.-----------------EKIM--    274
HIVDJ264A       ----T-------------------N--K-----.-------------.-----------------E--V--    269
HIVDJ263A       ----T-------------------N--K-----.L------------.-----------------E--V--    273
HIVDJ258A       ----T-------------------N--K-----.-------------.---A-------------G--V--    270
HIVCARGAN       ----T---------T---------NE-K-----.--R---S------.-----T-----------E--I--    280
HIVCARSAS       ------------------------K-TE-K---.-------------.-R---------------GKIM--    278
HIVCAR4054      ------------------------N-TK-----.-----------Y-.-----------------E--M--    271
HIVCAR286Afr    ----T------------X------R--E-----.----X---------.X----------------GG-I--    291
HIVCAR4023      ---IT------------------N-TK-S---.-------------.-----------------EG-M--    290
HIVCAR423A      ------------------------R-EK-----.--N----------.-----------------G--K--    283
HIVKENYA        ----T-------------------K--K-----.--T----------.-----------------G--M--    271
                *           *         *     ^^^   * ^^^   *                ^^^
CONSENSUS.B     CPkvsFePIPiHyCapagfailkCndkkFnGtG.pCtNVSTVQCTHG.IrPvVStqLLlNGSLaeeevviR    254
HIVJRCSF        ------------------------N-T---K-.Q-K----------.------------------K----    271
HIVJRFL         ---I--------------------T---K-.--K----------.----------------------    270
HIVALA1         ------Q-----------------K------K-.T-K----------.----------------------    271
HIVBRVA         ----T-------------------N-------.-------------.----------------------    273
HIVJH3          ---I-----------------I----------.-------------.-K--------------------    285
HIVBAL1         ------------------------K------K-.-------------.----------------------    277
HIVYU2          ------------------------------------.-------------.------------------I---    269
HIVMN           ---I-------------------------S-K-.S-K----------.----------------------    278
HIVHXB2R        ------------------------N-T-----.-------------.----------------------    273
HIVLAI          ------------------------N-T-----.-------------.----------------------    278
HIVNL43         ------------------------N-T-----.-------------.------------------D----    271
HIVMFA          ---------------------------T-----.-------------.------------------G---    271
HIVCAM1         -------------T----------------K-.-------------.-----------------K-----    274
HIVNY5CG        ------------------------------.-------------.-K---------------G-----    268
HIVADA          -------------T---------K--------.--K----------.----------------------    269
HIVJFL          -------------T----------------K-.--K----------.-------H---------G-----    270
HIVSIMI84       -------------T-----------------.--K----------.-K--------S----S-G-----    271
HIVD31          -------------T-----M---K--R---K-.Q-K----------.----------------------    273
HIVSF162        ------------------------------S-.-------------.------------------G----    271
HIVBCSG3C       ---I--------------------K--------.S-K----------.-K--------------------    276
HIVOYI          ---I------M---T-----------------.-------------.-K------------------I--    278
HIVSF33         ------------------------N---S-K-.Q-----------.-K--------------------    274
HIVCDC4         -------------T-T---L------------.-------------.----------------------    284
HIVSF2          -------------T----------N-T---K-.-------------.---I------------------    276
HIVSF2B13       ------------------------N-T---K-.-------------.-K--------------------    275
HIVHAN          ----------------------------K-.--K----------.-----------------K-----    275
HIVRF           -------------T------------------.--K----------.----------------------    286
HIVWMJ2         ------------------------------.-------------.------------------I---    270
HIVTB132        ------------------------R----S-N-.--K----------.-K-----------------X--    259
HIVBR020        ----T---------T---Y------G-------.-------------.-K----------------DI---    273
HIVTH014        -------------T-------Q--N-------.-------------.----------------------    266
HIVUS711fr      --R---------F-T----------N-T---K-.-------------.----------------------    271
HIVUS712        ------------------------------.--K----------.------S-----------G----    275
HIVUS715        ------------F-----------K--------.-------------.-K--------------------    277
HIVUS716        ---I--------------------------.S------------.------------------I---    269
HIVHA593        -------------T-----------RN-----.--K----------.-K----------------A-----    297
HIVHA594        ------------------------N-T-----.-------------.----------------------    275
HIVHA596        ------------------------N-T-----.-------------.----------------------    276
HIVHA599        ----------------------------S-.--K----------.---A----------------I--    275
HIVHA651        ----------------------R-P--K---.-------------.-K------------------I--    271
HIVRJS          -------------------V----K--N-----.-------------.-----------------G-----    274
HIVGUNfr        -------------T-----L------------.--K----------.-----------------G-I---    239
HIVSC           ---------------RW.----N--N-------.-------------.-------H-------------L-    273
HIVSBA                                                                 ----------          20
HIVSBB                                                                 ----------          20
HIVSBC                                                                 ----------          20
HIVBR014        -------------T----V-----N-M-----.-------------.--------------------L-    276
HIVTH026        -------------T------I------------.-------------.----------------------    266
HIVBR021        ----T---------T-----------N-T-K-.T-K----------.----------------------    277
HIVACH9         ------------------------K--------.--K----------.----------------------    232
HIVACP1         ------------------------K--------.--K----------.----------------------    225
HIVJM           ---I--------------------R-EQ---K-.T-----------.-----------------K---V-    253
HIVWM           ------------F-----------N-T-S-K-.-------------.----------------------    241
HIVMA208        -------------T-----L-----T------.--K----------.-----------------K------    293
HIVP896         ------Q-------V-----M----N-T---S-.-------------.------------------DI---    275
HIVBWB11A       ---------------------------------.--R----------.-----------------G-----    145
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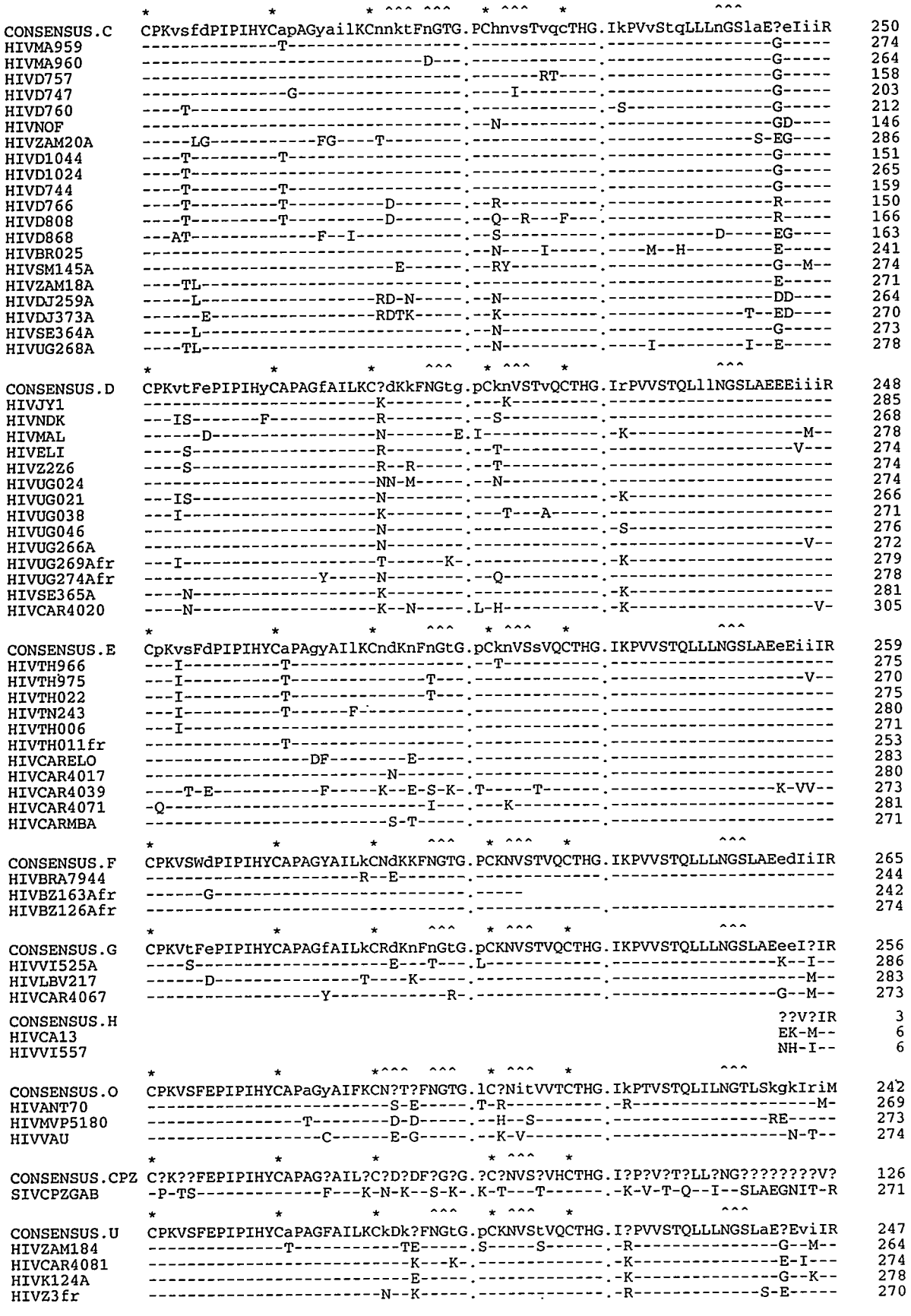

HIV1 ENV

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                                 <-          V3 neutralization loop          ->
                    ^^^          ^*^    ^^^
CONSENSUS.A     SenitnNaktiivql??pv?inctrp.?nntr.ks???vri???gpgq??afya.tgdi.....igdirqa    290
HIVSF1703       ---------------NKT-E------.N----.--...---..----..----.----.....-------    334
HIVU455         ---F-----------VN--K---S--.Y.---.-N...I-RYSI-S--..---V.--K-.....-------    328
HIVZ321         ---F-D---I-----VK--N-T-M--.N----.--...IS-...---R..--F-.----.....-------    329
HIVRW020        ---------------DKA-K------.N----.-G...---..----..----.--G-.....-------    315
HIVUG031fr      ----S-----K.....................................................          284
HIVD687         --------R------VK--R------.G---N.-N...-H-..-----..----.R-R-.....-----K-    213
HIVNI           ---------------AN--K------.N----.-G...-H-..-----..----.----.....-------    325
HIVRW009        --------H------NET-L---S--.N----.--...-H-..-----..----.---V.....-------    327
HIVUG275A       ---------N-L- -TT--T------.N----.T-...---..-----..S---.----.....----K--    325
HIVUG273A       ----SD----L----TT--K------.G----.T-...---..-----..----.----.....-------    332
HIVVI191A       ---F-D-G-------VE--K------.S----.-G...IH-...---R..----.--Q-.....T------    329
HIVDJ264A       ---------N-----VT--G------.N----.--...---..-----..T---.----.....-----K-    324
HIVDJ263A       --------QN-----VA--R------.N----.--...---..-----..T---.----.....-------    328
HIVDJ258A       ---------N-----VT--R---S--.G----.--...---..-----..T---.----.....-------    325
HIVCARGAN       ---------------VK--N-T-I--.SRT--.-R...WH-...-S--..----.IDG-.....T----K-    335
HIVCARSAS       ---FS----------NQS-E------.N----.RR...MH-...---R..--I-.-DA-.....V------    333
HIVCAR4054      ---F-D---------KN--R------.G----.-G...IH-...---PGQ-I--.----.....-------    328
HIVCAR286Afr    ---------------DS--G------.G----.--...I--MHI---R..S---.K-V.....-------    348
HIVCAR4023      ---------------DS--I------.N----.R-...M--..-----..T---.---.....T------    345
HIVCAR423A      ---F-----------DS--R------.N-Y--.-M...IPT..----GQVI--.--K-.....----K-    340
HIVKENYA        ---------N----FAE--K------.N----.M-...I--..----..----.---.....--N----    326
                  ^^^          ^^^   ^*^    ^^^
CONSENSUS.B     senftdnaktIivqlnesveiNCtRp?nnntr.ks???i?i??.gpgr..afyt.tg?i???..igdirqa    307
HIVJRCSF        -D----------------K------.S----.--...-H-..-----..----.--E-.....-------    326
HIVJRFL         -D---N---------K----------.-----.--...-H-..-----..----.--E-.....-------    325
HIVALA1         -D------------------------.-IYRK.GR...-H-..-----..--H-.-RQ-.....-EN----    326
HIVBRVA         -----N-V-----------------.-----.-R...-TM..-----..VY--.--Q-.....-----R-    328
HIVJH3          ---------------K-P-V------.SKT--.RR...-H-..-----..-----.-KQ-.....A--L---    340
HIVBAL1         -A--A----V----------------.-----.--...-H-..-----..----.--E-.....-------    332
HIVYU2          -----N-------------V------.-----.--...-N-..-----..-L--.--E-.....-------    324
HIVMN           -------------H-----Q------.-Y-K-.-R...-H-..-----..----.-KN-.....--T----    333
HIVHXB2R        -V--------------T---------.-----.-R...-R-QR.----..--V-.I-K.....--NM---    329
HIVLAI          -A--------------Q---------.-----.--...-R-QR.----..--V-.I-K.....--NM---    334
HIVNL43         -A--------------T---------.-----.--...-R-QR.----..--V-.I-K.....--NM---    327
HIVMFA          -A--------------T---------.-----.--...-R-QR.----..--V-.I-K.....--NM---    327
HIVCAM1         -----N---------K-P-------L.-----.--...-A-..-----..TV-A.-DR-.....-------    329
HIVNY5CG        -----N-V-----------------.-----.-G...-A-..-----..TL-A.REK-.....-------    323
HIVADA          -S--------N-----K----------.-----.--...-H-..-----..----.--E-.....-------    324
HIVJFL          ----M----------K-IA------.-----.--...-TL..-----..----.--D-.....-------    325
HIVSIMI84       ---------------K--V------.--SK-.-T...LHM...--K-..---A.--D-GGY..T-Y----    329
HIVD31          -D-------------K----------.--Y-S.-R...-R-...-AR-..-----.K-K-.....-------    328
HIVSF162        ---------------K----------.-----.--...-T-..-----..---A.--D-.....-------    326
HIVBCSG3C       -A--S----------K-A--------.-KK--.-R...-TT..-----..VY--.--E-.....V------    331
HIVOYI          -S---N---I------K---------.-----.NR...-S-..-----..--H-.-KQ-.....-------    333
HIVSF33         -D---N-----L----V---------.---R-.RR...-TS..---K..VL--.--E-.....-----K-    329
HIVCDC4         -----N----------V---------.--H--.-R...VTL..-----..VW--.--E-.....L-N----    339
HIVSF2          -D---N-------------A------.-----.--...-Y-..-----..--H-.--R-.....-----K-    331
HIVSF2B13       -D-----------------A------.-----.-G...-H-..-----..-V--.--R-.....-----K-    330
HIVHAN          -D-----T-----H-----------.-----.-G...-H-..-----..-V--.--R-.....V----L-    330
HIVRF           -------V--------A--Q------.-----.--...-TK..-----..VI-A.--Q-.....-----K-    341
HIVWMJ2         -------------H-----------.Y--V-.R-...LS-..-----..--.R.-RE-.....--I----    324
HIVTB132        ---------------K-P--------.--Y--.-X...-XM..-----..XX--.--E-.....-----R-    314
HIVBR020        ---L-N---------KDP-D------.-----.--...-H-..-----..---A.--D-.....-------    328
HIVTH014        -S------RV-----------------.-----.--...-HL..-----..-W--.--Q-.....-------    321
HIVUS711fr      -----N---------K-A--------.-----.--...-HL..-----..---A.--E-.....-------    326
HIVUS712        -A-LS----I----------M--I--.-----.--...-H-..-----..----.--D-.....-----K-    330
HIVUS715        -A-LS--------------QM-----.-----.--...-H-..-----..----.--E-.....-------    332
HIVUS716        -----N---------K----M-----.-----.--...-H-..-----..----.--Q-.....-------    324
HIVHA593        -----N------I----T--------.----S.-R...-S-..-----..--RA.-.K-.....--N----    351
HIVHA594        -----N------I-PK---V------.--S--.-R...-S-..-----..VW--.--Q-.....-----K-    330
HIVHA596        -----N------I--K---V------.-----.-R...-S-..-----..VW--.--Q-.....--N--K-    331
HIVHA599        A---SN----------KA-L------.-----.R-VHSGH-...-G---..TLF-.-.H-.....V----K-    332
HIVHA651        ----------------T-IQ------.-----.---...-N-..-----..-W-A.-.N-.....-------    325
HIVRJS          -----N------------IV------Y-TKKI.RH...-H-..-----..---V.--G-.....M------    330
HIVGUNfr        -----N------------IV------.-----.--...-T-...-S---..--HA.IEK-.....--N----    294
HIVSC           ---------------K-A--------.----T.R-...-H-..-----..---A.--D-.....-------    328
HIVSBA          -D---N---------K-A--------.-----.R-...-N-..-----..-----.--D-.....-------     75
HIVSBB          -----N-----------T--------.----S.-R...-S-..-----..--VA.ARE-.....-----K-     75
HIVSBC          -D---N------------Q---I--.-----.--...-S-..-----..----.--E-.....-------     75
HIVBR014        ----MN----------------N--IQ-.RI...-H-..-----..--HA.--G-.....K-N--.P    331
HIVTH026        YS---N---I----------.-----.--...-PL.....-Q..-W--.--Q-.....--N----    321
HIVBR021        ---------I-------T--------.-----.--...-HM...-W--..---A.--E-.....--N----    332
HIVACH9         -----N--R----------------.-----.--...-P-..-----..----.--D-.....-------    287
HIVACP1         -----N---I------K--K---I--.------.-G...-G-..-----..TV--.AEK-.....-------    280
HIVJM           -D---N----------KT-V------.-----.--...-H-...A---..-----.--D-.....-----K-    308
HIVWM           -----N---------K-P-Q---I--.-----.-G...-H-...---K..----.--E-.....--N----    296
HIVMA208        -----E-H-I-----K-P--------.GH---.--...-PM...-----..--FA.--D-.....-----K-    348
HIVP896         -------------------V------.------.RR...LS-..-----..---A.RRN-.....-------    330
HIVBWB11A       --------R--T-----------I--.------.-G...-NV...-----..-L--.--D-.....-------    200
```

```
                                <-              V3 neutralization loop              ->
                    ^^^         ^^^    *     ^^^
CONSENSUS.C     SenltnNvktIivhln?sveivctRp.nNNTR.ks...iRi...GPGQ..tfya.tgdI.....IGdIRqA   304
HIVMA959        ----------------E---------.------.R-...---...-----..V---.NN--.....-------   329
HIVMA960        -------AQ-----F-E---------.------.--...---...-----..-----.-NE-.....--N--E-   319
HIVD757         ----A----------Q--R-------.------.--...---...-----..-----.----.....-------   213
HIVD747         ----------------Q-----Y---.------.-G...V--...-----..-----.----.....-------   258
HIVD760         -----D----------Q---V-----.------.--...---...-----..-----.----.....-------   267
HIVNOF          -------I---V----K--D------.------.-R...--V...-----..-V--.-NA-.....-------   201
HIVZAM20A       -------AQ----Q--K-I----A--.G------.--...---...-----..--F-.--A-.....-------   341
HIVD1044        ---P---A--------Q----M----.------.--...---...-----..-----.----.....-------   206
HIVD1024        ----------------Q---------.------.--...---...-----..-----.----.....-----R-   320
HIVD744         ----------------Q----E----.S------.--...---...-----..-----.--E-.....-------   214
HIVD766         ----------L----Q---------.------.--...L---...-----..-----.----.....-----R-   205
HIVD808         ---------------YQ---------.------.--...T---...-----..-----.----.....-------   221
HIVD868         -------A-I-----DQP----R---.------.--...---...-----..-----.----.....-----R-   218
HIVBR025        -K---D----------E---TN-----.------.--...---...-----..A---.--E-.....-------   296
HIVSM145A       -------A--------Q----R---Y.A------.--...V---...-----..---..-N--.....-------   328
HIVZAM18A       -------A--------E---------.S------.--...---...-----..A---.--G-.....--N----   326
HIVDJ259A       -------A-I---Q--E--A-N----.------.E-...---...-----..-----.----.....-------   319
HIVDJ373A       -------A-I---Q--Q----N----.------.Q-...---...-----..-----.----.....-------   325
HIVSE364A       -------A--------E-I----A--.------.--...M---...-----..-----.----.....-------   328
HIVUG268A       -------A-I---Q--K----N-A--.------.E-...---...-----..-----.----.....-------   333
                  ^^^         ^^^   ^*^
CONSENSUS.D     SENltnNaKtIIvqlnesv?InCtRP?y?n?r?qr..?tpi...glgq..alyt?t?????...?g?i?qA   294
HIVJY1          -------V-----H-----E------DNKIT-.-S...---...-----..-----.-R.I.....K-D-R--   340
HIVNDK          -------V--------A-IV-------.-KYT-.--...-S-...--R-..S---I-GKKKK...T-Y-G--   326
HIVMAL          -----D-T-N-------T-T-------.GN-T-.RG...IHF...-P--..-----.-.GI.....V-D-RR-   332
HIVELI          ---------N--AH-----K-T-A--.-Q-T-.--...---...-----..S---.-.RS.....RSI-G--   328
HIVZ2Z6         ---------I---------A-------.-R-I-.--...-S-...-----..----.-.KT.....RSI-G--   328
HIVUG024        ---I------I---H-----V-------.-N-I-.--...---...-----..-----.-.RR.....IED-RR-   328
HIVUG021        ---------I---H-----P-------.-DKVS.Y-...---...-V-R..-S--.-.RI.....K-D-R--   320
HIVUG038        ---IS--------------T-S-A--.FYAIE.RQ..R---...-Q---..V---.-.KK.....I-R-G--   326
HIVUG046        --------------------P---S--.-E-K-.R-...---...-----..-Y--.-.KL.....K-Y-RP-   330
HIVUG266A       ---------I---------I-------.-N-IKI--...---...-R---..--F..-TRR.....K-IKG--   327
HIVUG269Afr     ---------I------A--T-T-----.-TKT-.H-.........AQ-R..-WW-.-.GI.....T-D-R--   330
HIVUG274Afr     ---------I----------T-D-A--.-E-I-.--...---...-T--..-----.-QGRKK...I-K-G--   335
HIVSE365A       --------------F----M-------.-N-K-.--...---...-----..V-H..-TRV.....K-D-R--   335
HIVCAR4020      -----D---------K---N-S-----.NNYK-.-G...---...-----..-----.-.RV.....I-D-RK-   359
                  ^^^         ^^^   ^*^     ^^^
CONSENSUS.E     SENltnNAktIIVhLnksVeINCTRP.snntr.tS...?ri...GPGq..VFYr.TGdi.....iGdIrkA   313
HIVTH966        -------------------------.------.--...TT-...----..----.----.....T-N----   330
HIVTH975        --------Q--------------------.------.--...V--...-----..----.----.....-------   325
HIVTH022        -------------------------.------.--...IT-...-----..----.----.....-----R-   330
HIVTN243        -----D-------------G------.----X.P-...ITX...-----..----.----.....----XR-   335
HIVTH006        -------------Y------------.------.--...IT-...-----..----.----.....-----Q-   326
HIVTH011fr      ---------I----------------.------.--...IA-...-----..----.----.....--N----   308
HIVCARELO       --------R----------------.YK---.--...A---...-----..---K.--S-.....T------   338
HIVCAR4017      ----------------A--------.-KKI-.--...V---...-----..---K.---L.....-------   335
HIVCAR4039      ---I---------Q-VTP-Q------.---I-.--...V---...-----..---K.--S-.....T------   328
HIVCAR4071      -------------------------.FKKM-.--...V---...---R..---K.--S-.....T------   336
HIVCARMBA       ----A------------P--------.------.--...V---...-----..---G.--E-.....-----R-   326
                  ^^^         ^^^   ^*^     ^^^
CONSENSUS.F     SeNIsdNtKtIIVqlN?sveINCTRP.nnntR.ks...Iri...GpGr..?fya.tg?i.....iGDIRkA   317
HIVBRA7944      -Q-----A-----H--E--Q------.------.--...-HL...---Q..A--T.--E-.....-------   299
HIVBZ126Afr     -Q-----A-----HF-E--Q------.--Y--.--...-YF...-----..A-HT.A-K-.....-------   329
                  ^^^         ^^^   ^*^     ^^^
CONSENSUS.G     SEnfTdNaKvIIVQlN?sieInCtRP.NNNTR.KS...I??...gpGq..afYA.TGdI.....IGdIRQA   308
HIVVI525A       -----N----------ETV-------.-----.--...-KF...-T-R..VL--.--A-.....--N----   341
HIVLBV217       -----N---N----F-K--D-V----.-----.--...-HI...-----..-L--.--A-.....-------   338
HIVCAR4067      ---L-N---I------K-V--I----.-----.--...-SF...-----..----.----.....-------   328
                  ^^^               ^*^     ^^^
CONSENSUS.H     S?NITDNTKNIIVQLK?PV?INCTRP.NNNTR.?S??.I?I...G?GQ..?F?A.?G?I.....IGDIR?A    47
HIVCA13         -E--------------N--V-------.------.R-MR.-G-...-R--..T-H-.I-A-.....-----Q-    63
HIVVI557        -K--------------S--P-------.------.K-...-S-...-P--..A-Y-.T-D-.....-----K-    61
                                  *     ^^^
CONSENSUS.O     gknI?dsgkNIivTLN??i?mtCeRp.gn?tv.Qe...i?i...GPma...WyS.Mgl????n?k??sR?A   287
HIVANT70        A-D-LEG---------STLN------.QI.DI.--...MR-...----..----.--IGG..TAGNS--A-   325
HIVMVP5180      ----TE-A--------TP-N---I-E.-IAE-.-D...-YT...---R...-R-.-T-KRSN-TSPR--V-   332
HIVVAU          ----S---E--LI---TN-TIA----.--Q-I.-K...-MA...----..----.-A-S...-T-GDT-A-   330
                                  *
CONSENSUS.CPZ ???K?????V??????E?????C?RPGN???R.??...?QI...GPGM..TFYN.?E??.....?GDTR?A   151
SIVCPZGAB       VEN-SKNTD-WIVQLV-AVSLN-H----.NT-.GE...V--...----..----.I-NV.....V----S-   326
                  ^^^               ^*^     ^^^
CONSENSUS.U     SeNiT?NAKtIIVqlnepV?InCTRP??nntr?kS...iRi...GPGq..aFya.tgdi.....iGdirQA   299
HIVZAM184       -----D---N----FT---Q-S----.S----.R-...--F...---..----..-N--.....-------   318
HIVCAR4081      -----D---I---H---S-E------.N----.--...V--...-----..T---.----.....-------   329
HIVK124A        -Q-L-N---------VK--R------.N--I-.--...---...-----..--F-.----.....--N----   333
HIVZ3fr         -----N----------T-K------GSDKKIRQ-...---...---K..V---....K.....G-ITG--   324
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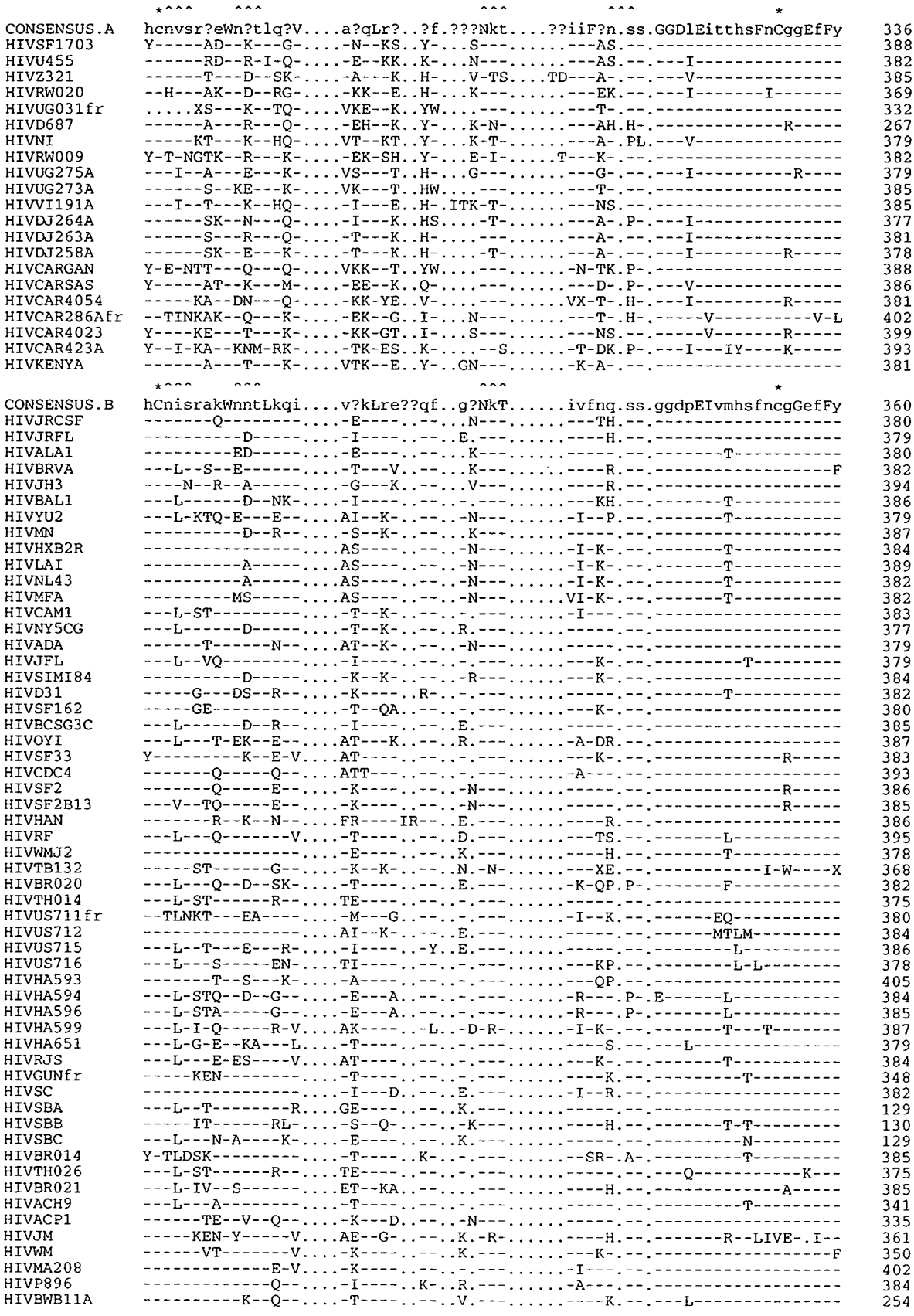

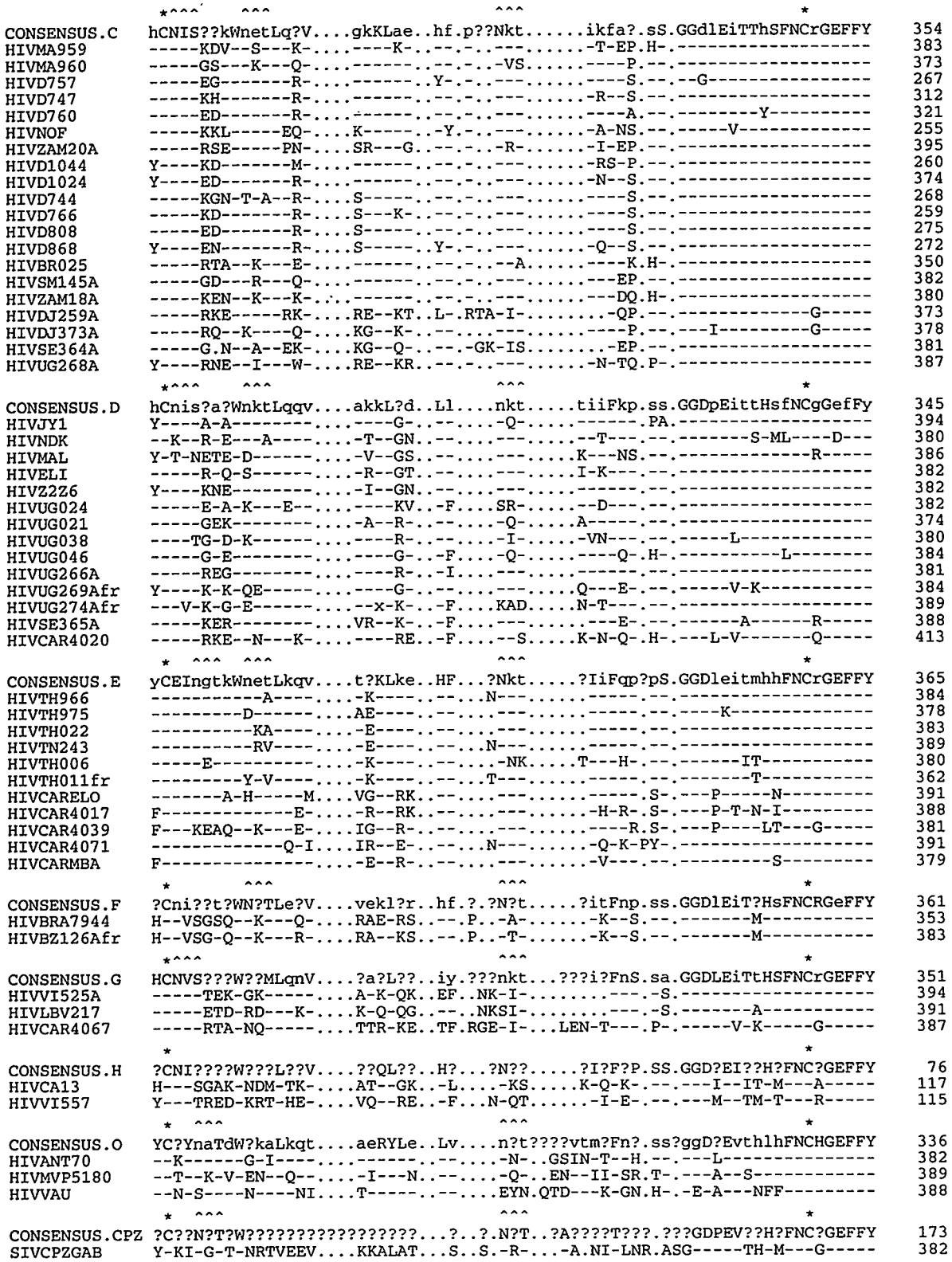

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CONSENSUS.A     cnts?LFNstW??????.....N?t???????..?n?t????????ndtit?????lq.CrIkqIvnmwQr    369
HIVSF1703       -D--G------GG.........-S-.DSIQES...-S-......ES----I.....-P.------I-----    434
HIVU455         ----G----I-...........-GS.....MS...-DM......GP-G---.....--.------I-----    422
HIVZ321         ----G---G--L..........-G-......S...-N-..WKIDTV----I.....-P.------------    429
HIVRW020        ----G------ES.........-S-.....ES...-N-......TS----.....-T.------I----K    411
HIVUG031fr      ----G----I-WE.........-G-...NNMP...-S-......ET-G---.....-P.-K----I-----    376
HIVD687         ----N------D..........-S-.....WD...-N-.......A--N--.....H-.-----------K    307
HIVNI           ----K------DNS........-S-......A...-H-......GS-----.....--.-----------K    421
HIVRW009        ----G------SKR........-G-....WQS...-G-........ELN--.....-P.------I--C--    424
HIVUG275A       -D--G------NG.........-TSKQE......SSS-ES......-GN--.....--.------I-----    423
HIVUG273A       ---AG------NK.........-DSIKS.......-D-KS.....--I--.....--.------I-----    428
HIVVI191A       -S--G------E..........-G-QVA.......-D-GS.....----.....-P.-------R----    427
HIVDJ264A       ----E------DNSL.......-H-ES.........-H-E.........-N--.....--.-----------K    419
HIVDJ263A       ----E------...........-S-WD.........-SSNHIESNHTEGN--.....--.-----------K    427
HIVDJ258A       ----S------...........-SSSIHT......-YSS....NDTD.N--.....--.-----------K    421
HIVCARGAN       ----G----S-KNE........-D-KSMKGL....KG-...........--.....--.------------    430
HIVCARSAS       ----G---K--WGP........-S-TN.........-Q-IG.....-----.....-P.-------R----    429
HIVCAR4054      ---TD------YNI........-G-.........G-N-Q.....ET-G---.....--.------IR----    424
HIVCAR286Afr    LQYIS----S-TDT........-S-..........-SSR.....TG---DIIT...-P.--------I---    446
HIVCAR4023      -D--R----I-K..........-D-.........G-I-GNITGWE.-FNDSII...-P.------------    446
HIVCAR423A      ----K------K..........-G-.....................TEE---ESEDPIV-P.-------H----    435
HIVKENYA        --S-G------TNMQES.....-S-ESN.....................----------P.----.-I-----    421
                *^^^   ^^^             ^^^           ^^^                  *
CONSENSUS.B     Cn?tqLfnstW??????????..n?T????????..n?t???????????tit??...Lp.CrIkqiinmWQe    391
HIVJRCSF        --S---------...........-D-.....EKS..SG-......EGND--I.....--.------------    421
HIVJRFL         --S---------N..........-N-.....EGS..-N-......EGN.---.....--.------------    420
HIVALA1         --S---------...........-S-..EGPKGS..-N-......EE..N--.....--.------V-----    422
HIVBRVA         --T---------YR.........-T-.......G..-I-......EGNSP--.....--.------------    423
HIVJH3          --S---------LS.........-S-W.NDTEGS..-N-......GGND---.....--.------------    441
HIVBAL1         --S---------...........-V-.....EES..-N-......VENN---.....--.------------    427
HIVYU2          --S-----.--...........-D-.....RKL..-N-......GR..N--.....--.------------    416
HIVMN           --TSP------NG.........-N-.....WN...-T-......GSNNN--.....-Q.-K----------    429
HIVHXB2R        --S---------.F........-S-W..STEGS..-N-......EGSD---.....--.-----------K    429
HIVLAI          --S---------.F........-S-W..STEGS..-N-......EGSD---.....--.-----F------    434
HIVNL43         --S---------.F........-S-W..STEGS..-N-......EGSD---.....--.-----F------    427
HIVMFA          --S---------.F........-S-W..STEGS..-N-......EGSD---.....--.-----F------    427
HIVCAM1         --T-----T--LF.........-G-W.........-D-..EGLNNTERN--.....--.--------R---    428
HIVNY5CG        -KT---------LF........-S-W.........-D-..ERS.DNNE--I.....--.--------R---    421
HIVADA          --S---------NF........-G-W.........-L-QSNGT.EGND---.....--.------------    425
HIVJFL          --S---------LS........-G-W.........-D-..EESKDTREP-I.....--.--------R---    424
HIVSIMI84       --S-K------...........-D-.....STW..-D-....TGSNKGN--.....-L.--------R---    427
HIVD31          --SA--------..........-D-.....KES..-N-........NG---.....--.------------    421
HIVSF162        --S---------..........-N-.....IGP..-N-........NG---.....--.--------R---    419
HIVBCSG3C       -KS---------AG........-N-W.........-SSA.ERSDDTGGN--.....--.------------    431
HIVOYI          --TS--------..........-D-.....TRA..-S-........EV---.....--.------V-----    426
HIVSF33         --T-K------NE.........-S-W.........-A-.......GND---.....--.------------    423
HIVCDC4         --S------A-...........-V-...SNGTW..SV-..RKQKDTGDI--.....--.--------R--V    440
HIVSF2          --T-----N--RL.........-H-.....EGT..KG.........ND--I.....--.------------    426
HIVSF2B13       --TA-------NP.........-N-.....EGN..-T.........DP-I.....--.------------    424
HIVHAN          --S-K------...........-N-...STWND..-G.........ND--I.....--.------------    426
HIVRF           --T---------..........-S-.....EGS..-N-......GGND---.....--.------V-----    436
HIVWMJ2         --S---------..........-G-D.IKGDNK..-S-..........L--.....--.-----------G    419
HIVTB132        --T-K------...........-S-.....EGN..DDG.......EERN--.....--.------V-----    408
HIVBR020        --T---------T.........-N-....EGTS..-T-.......GND---.....--.------VD----    424
HIVTH014        --T---------..........-D-...STWN...-N-.......GNG---.....--.------V-----    416
HIVUS711fr      --T---------TTL.......-N-.....GKS..-S-........AGN--.....--.---R----V--K    422
HIVUS712        --S---------..........-S-.....QLV..-D-........GGN--.....-Q.------------    423
HIVUS715        --S-K------...........-G-.....ES..-N-.......GDDP-V.....--.-----V------    425
HIVUS716        --S---------YN........-G-..........-S-.....EGNNTI--.....-Q.-----------Q    419
HIVHA593        --T---------..........-S-.....EES..-S-.......EEG---.....--.------------    445
HIVHA594        --TSK-------..........-D-.....KRS..-ID.........G---.....--.------V-----    422
HIVHA596        --TSK------...........-D-.....KRS..........SDIDGI-I.....--.------V-----    424
HIVHA599        --TSK------EF........-S-W....NGT...EGLDETNNGTGGN--.....--.------V----R    436
HIVHA651        --T-K------...........-S-.....EES..........KYNESN--LT...--.------------    420
HIVRJS          --S---------MS........-S-.......G..-D-.......TGLN--.....--.--------R---    424
HIVGUNfr        --T---------LV........-G-W.........-N-.....KRSND---.....-Q.--------S---    390
HIVSC           --S----S---...........-G-.....EGS..-N-......GGND---.....--.----E-------    423
HIVSBA          --T-K------TW........-S-W.........-G-.....EGNNTN--.....--.------V-----    171
HIVSBB          --T-K------ND........SS-W.........-V.ERSSKAEENDIL-.....-Q.------V-----    176
HIVSBC          --S---------YS........-N-W.........-G-.......GGEN--.....--.------------    169
HIVBR014        --T------A-ML.........-G-W....TGS..-N-.........KN--.....--.--------R---    426
HIVTH026        --TS-------NN.........-G-W.........-G-......TGYS---.....--.------V-----    416
HIVBR021        --T---------LSN.......-D-..........-V-H.....---.....--.---------T---    423
HIVACH9         --S-K------...........-V-.....EET..-SN.EGDSTIGND--V.....--.------------    387
HIVACP1         -KTR--Y----SD.........-S-W.........-D-.......GGDN--.....--.------------    375
HIVJM           -DS----D---QLNKSDGNW..-S-....SSIW..-N-.EG..NITGD.--.....-Q.------V-----    414
HIVWM           --A------I-...........-G-..........-G-.EGS.NNTGDS--.....--.------------    392
HIVMA208        --T---------TWN.......-G-....GESN..-V-....GTEGNS---.....-Q.-----F--L--K    449
HIVP896         --TA--------..........-V-.....GGT..-G-......EGNDI--.....-Q.-----------K    425
HIVBWB11A       --S---------..........-N-GEFNNIEG..-N-........GKN--.....--.------------    298
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                *^^^   ^^^            ^^^                                *
CONSENSUS.C     CnTs?LFnsty?????p?....ngt???.......??????.???????IT.....lp.crIkQiiNmwqe    384
HIVMA959        ----G----NF..........-D-EG........NST.........LS--......--.------------    420
HIVMA960        ----R------....N-.....---VS.......NDTE......SNST--......--.------------    415
HIVD757         ----N------....M-.....---KG.......NS.........NST--......IQ.------------    306
HIVD747         ----D---G--....M-.....---KS.......NSS.........ST--......I-.------------    351
HIVD760         ----G---G--....M-.....---KS.......NL.........NST--......I-.------V-L---    360
HIVNOF          ---TD--SA.............-A-KF.......NES......DPNAT--......--.------------    293
HIVZAM20A       ----I---RSHLG..LF.....---E........NNS........PQN--......I-.---N--------    436
HIVD1044        ----N------...........-S-YML.......NGTT....SNSTLN--......I-.------------    303
HIVD1024        ----N------....M-.....---.....................KSNSNST--.....IL.-S----V-----    413
HIVD744         ----N----A-....M-.....---YMF.....NGTYMF.NSTSNAT--.....I-.---------C--    316
HIVD766         ----G---G--....MH.....---.....................KSNSSSI--.....I-.------------    298
HIVD808         ----G---G--....M-.....---.....................KSNSSSI--.....I-.------------    314
HIVD868         ----N---G--....M.....---.....................KSNSSST--.....IL.-----VV-----    310
HIVBR025        ----S------....T-.....-S-                                                     366
HIVSM145A       ----G------....N-.....-N-.....................GSESNNN--.....-Q.------------    421
HIVZAM18A       ----N------....K-.....-D-.........NST.....YNPNDT--.....--.-----------G    421
HIVDJ259A       ----D---..............-QSIT..................NEN--.....-Q.------------    405
HIVDJ373A       ----A---DSITN..A-I....-NSST..................DAN--.....-Q.------------    418
HIVSE364A       -D--K---G-THT.........ANS.....................N--.....IQ.-----------G    414
HIVUG268A       ----S----SDNN.........-S-.....................I--.....--.-----------G    420
                *^^^   ^^^            ^^^          ^^^          ^^^          *
CONSENSUS.D     CntS?LFNstw????.......n?t???????...nst?.??????n?tit.....lp.CrIkQIinmwq?    377
HIVJY1          ----R------...........-SSTWN.......-D-.....LNSEG--K.....--.----------G    436
HIVNDK          ----R------...........-Q-.....------.....GFN-G-V-.....--.------V-L--R    419
HIVMAL          ----K------Q..........-NGARLS.....---.....ESTGS--.....--.-----------K    429
HIVELI          ----G------...........-ISA..WN.....-I-..ESNNST-TN--.....-Q.-------K-VAG    427
HIVZ2Z6         ----G------...........DISKSEWA.....---..ESDDK...P--.....-Q.----------G    426
HIVUG024        ----K---HSVGE.........-N-LS.......I-N.....GV.-TN--.....--.-K----V--C-G    424
HIVUG021        ----G---NSVWTS........-S-I.....................GA.-G---.....--.-----------G    413
HIVUG038        ----Q------.GS........-D-S.....---Y.......-N--K.....I-.---R----L--E    420
HIVUG046        -DA-R---R-Y...........-TSG.....---.....GVN-S--K.....--.----------G    423
HIVUG266A       ----G---NSVWR.........-DYPS.....---.....GVNESV--.....--.-K------L--G    424
HIVUG269Afr     -D--R---DSY...........-TSALNSTQG...-ES.........EN--.....--.-----------E    426
HIVUG274Afr     ----R---NSGWENY.......-IS.....---.....GG.-E--R.....-Q.----------E    431
HIVSE365A       ----G------KT.........KSG.....................DN--.....--.--------L--R    422
HIVCAR4020      ----Q---HK-...........-D-TGEMSEQ...-NNT.ES.....EN--.....--.---R---R---R    458
                *^^^   ^^^            ^^^          ^^^                *
CONSENSUS.E     CNTt?LFn?t????........NeTm....???..N?t.......????It.....LP.CkIkQiinMwQg    395
HIVTH966        ----R---N-CIG.........---I....GGC..-D-.....-I.....--.------------    423
HIVTH975        ----K---S-WIG.........-G-....EGR..-SS.....DTP-V.....--.------------    420
HIVTH022        ----R--SN-CIK.....----....AGC..-G-.....-I.....--.------------    422
HIVTN243        ----R---N-CIG.....----....NGC..-G-.....-.....--.------------    428
HIVTH006        ---PK---G-MEGP.....-N-E....GPN..-T-.....-I.....--.------V--C--    420
HIVTH011fr      ----Q---N-CIG.....----....KGC..-D-.....-I.....--.------------    401
HIVCARELO       ----N---S-WEI.....-K--....KS..-D-.....NLSN--.....--.-R----G-----    433
HIVCAR4017      ----Q---S-WRI.....----....EKV..-G-.....NSNM--.....--.-R-R--V----R    431
HIVCAR4039      ----R---S-WGT.....---I.....ES..-V-.....NPRN--.....--.---R-NV----R    423
HIVCAR4071      ----R---IST.....-G-.....T..-G-.....-.....--.-R---V-K---E    425
HIVCARMBA       ----K---S-WEM.....-K-I....EEL..-G-.....-.....--.-R----V-----    418
                *^^^           ^^^                                *
CONSENSUS.F     cNTskLFnd?????........Nnt???????.............???????....Lp?CrIrQfVNMWQr    387
HIVBRA7944      ---------                                                                     362
HIVBZ126Afr     ----G----TGS.....-G-.....IT.....-L.-----I-----E    414
                *^^^   ^^^            ^^^                                *
CONSENSUS.G     CnTSgLFN?s????.......?N?t????????..n????.....????i?t??..Lp.CrIKQIVrMWQr    379
HIVVI525A       -K--E---STWLF.....-S-GLVNSTW...-DTR.....KD-T.....-Q.-K----------    439
HIVLBV217       --------S-ILS.....-NNAPS.....-SS.....KN-T.....--.------------    431
HIVCAR4067      --------S.....-S-KTTNDTKT..-DT.....-T.....-Q.-------K----    426
                *      ^^^                  ^^^                *
CONSENSUS.H     CNT?KLFNSTW????.......N?????.N???..NGT.....????...L?.CRIKQI??MWQR    102
HIVCA13         ---T-------TTNT.......-GSYVS.-NTE..---.....IT.....-Q.------VS----    161
HIVVI557        ---S-------V.....-STS...-DIS..---.....TIIE...-P.------IN----    156
                *^^^   ^^^  *         ^^^   *      ^^^          ^^^          *
CONSENSUS.O     CNTs?mFNytFsc?????????N?t???c??????N?tn?.....?NgT??.....iP.CrLrQvVRsWmr    371
HIVANT70        ---AK--------.....-G-..T-...SVS-VSQG.....N---.....L-.-K---------I-    426
HIVMVP5180      ----G------I.....-C-KSG-QEIKGS-E--.....K---.....--.-K---L-----K    436
HIVVAU          ---NRL--H----KKNMTNNKI-C-.....-IS-N.....S---QA.....--.---------D---    438
                *                                                                  *
CONSENSUS.CPZ   C?????F???????.....?IT.....NG??I.....??.CRI?QIV??W??    187
SIVCPZGAB       -NTSQI-TD.....N--.....--II-.....LP.---R---SS-MR    413
                *^^^                 ^^^                *
CONSENSUS.U     CNTS?LFns?w??.....ns?????????..n?t???????????it.....LP.C?IkQi??mWQ?    369
HIVZAM184       ----N----TYNP.....--T...ESNS.....DLNIT.....--.-R----IN---R    411
HIVCAR4081      ----R----S-KG.....KYSGHES.....-D-.....--.-K-R--VR---K    423
HIVK124A        ----K----V-G.....---S.....-V-KV.NGTKVKET--.....--.-K----IN---E    431
HIVZ3fr         ----E--TGI-.....-GT...WD..K..-C-STESNCT..GN--.....--.-R---VVRT--G    423
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                  CD4
                -binding-
                           *  ^^^                                ^^^
CONSENSUS.A     vgq.AmYapPIq.g?irc?sNITGllLTRDGg??.....n????.....???net.FrPgGgdmrdNWrsE    416
HIVSF1703       ---.--------.-V-K-I-------------D......-NSA.............---.---T--N--------  487
HIVU455         ---.--------.-V---E-------------T......-NTK.............---.------------K--  475
HIVZ321         ---.-------K.-V-K-V-----I------VG......-NTS.............---.--------------  482
HIVRW020        ---.---P----.-V---E-------------.......-NST...........--I.------N--------  463
HIVUG031fr      -E-.---P----.-I---D-------------G......DANS......TNG---.------N--------  432
HIVD687         ---.-------E.-EL--E-------------.......-TSN......TNET--.--------------  362
HIVNI           ---.--------.-I---D-------------.......-NST.............---.--------------  473
HIVRW009        T--.--------.-V-S-V-------------N......-NTT.........T--.---------------  477
HIVUG275A       A-K.-I-----K.-V---V------I------GN.....-SE.............---.-----R---------  476
HIVUG273A       --R.-------K.-V---E-------------NG.....SNT.............---.------------N-  481
HIVVI191A       ---.--------.-M---E------I-----VGN.....-ST.............---.--------------  480
HIVDJ264A       --R.-------P.-E---E-------------SN.....-ST.............---.--------------  472
HIVDJ263A       --L.-------S.-E---K-------------SN.....-ST.............---.-S------------  480
HIVDJ258A       --K.-I-----S.-E---E------I------SN.....-ST...........--I.---------------  474
HIVCARGAN       A--.-------T.-I---E-------------FN.....-RT........NDT--.---------------  485
HIVCARSAS       --K.-------K.-A-N-R-------------G......-NRS.........---.---E--NT-------  482
HIVCAR4054      ---.--------.-EL--D-------------V......-NT.........Q-D-.---T--N-K------  477
HIVCAR286Afr    ---.--------.RV---E-------------L......-ST.........Q---.---T-----N-----  499
HIVCAR4023      ---.----S--P.-E-S-N-----X-------DD.....-ST...........--I.---T-----N-----  499
HIVCAR423A      ---.---T----.-E-K-E-------------K......-TT..........-K-.---I-----------  487
HIVKENYA        A--.--------.-I-K-V------I------DN.....-SE..........S--.---------------  474
                           *  ^^^                ^^^
CONSENSUS.B     Vgk.AmyapPi?.GqircsSnITGLlLTrDgG??????.n?t?......????Ei.FRpgGGdMrdNWRse  439
HIVJRCSF        ---.-------K.------------------K.......-ES.........EI--.---------------  474
HIVJRFL         ---.-------R.--------------------INE....-G-...........--.---------------  473
HIVALA1         ---.-------E.-------------------.......-SS.........NNT--.---------------  475
HIVBRVA         ---.-------R.---K--------------NN.....-E-.........TDT--.------N--------  478
HIVJH3          ---.-------E.------------------DNQ....-E-...........-T.------N--------  494
HIVBAL1         --R.-------R.------------------PED....-K-...........-V.---------------  480
HIVYU2          ---.-------R.------------------KDT....-G-...........--.---------------  469
HIVMN           ---.-------E.------------------KDT.DT.-D-...........--.---------------  484
HIVHXB2R        ---.-------S.------------------NSN....-ES..........--.---------------  482
HIVLAI          ---.-------S.------------------NNN....-GS..........--.---------------  487
HIVNL43         ---.-------S.------------------NNN....-GS..........--.---------------  480
HIVMFA          ---.-------S.------------------KNT....-ES...........-V.---------------  480
HIVCAM1         ---.-------T.-T-S--------------RGE....-E-...........-T.---------------  481
HIVNY5CG        ---.-------S.------------------DKE....-S-..........T--.---------------  475
HIVADA          ---.-------R.-------------I------T......-SS.........GS--.---------------  478
HIVJFL          ---.-------N.------------------KE.....-GA..........--.------N-------K  476
HIVSIMI84       ---.-------E.-H----------------K......-ES........ETT-T.---------------  481
HIVD31          ---.-------S.------------------KNKD...-E-...........-T.------N--------  475
HIVSF162        ---.-------R.------------------KEIS...-T-...........--.---------------  473
HIVBCSG3C       ---.-------S.-----T------------TSDT...-T-...........-T.---------------  485
HIVOYI          ---.-------S.-------K----------K......-T-........NGI--.---A-----------  480
HIVSF33         ---.-------E.------------------GDK....-S-..........T--.---A--N-K------  477
HIVCDC4         ---.----L--K.-L----------------GE.....-Q-..........T--.---------------  493
HIVSF2          ---.-------G.---S--------------T......-V-........NDT-V.---------------  480
HIVSF2B13       ---.-------G.---S--------------I......-G-........NDT-V.---------------  478
HIVHAN          ---.-------G.-L----------I------ND.....-SS.........TT--.------N------N-  480
HIVRF           ---.-------S.---K-I------------EDTT...-T-...........--.--L---N--------  490
HIVWMJ2         ---.-------Q.------------------.......-SS.........SRE--.------N--------  472
HIVTB132        -X-.-L-D---G.-----T------------NQ.....-G-........NET--.------N--------  463
HIVBR020        ---.--SV---K.-K-KS-------------.......-NE.......MNTT--.---------------  478
HIVTH014        ---.-------R.------------------.......-SE.......NKTT-T.---------------  470
HIVUS711fr      ---.-------R.-L----------------S......-KN.........ET-T.---------------  475
HIVUS712        ---.-------R.------------------IN.....KSE........NGT--.---------E-----  478
HIVUS715        ---.-------R.------------------NS.....-E-........NTT--.------N-K------  480
HIVUS716        ---.-------R.---K--------------T......-A-..........N-T.------N--------  471
HIVHA593        ---.-------E.------------------NN.....-K-........NGT--.---------------  500
HIVHA594        ---.-------S.------------------EN.....-E-...........-T.---------------  474
HIVHA596        ---.-------S.------------------EN.....-G-E......NNET-T.---------------  481
HIVHA599        ---.------AS.---S---K----------NV.....-ES........KDN-T.--------K------  491
HIVHA651        ---.-------E.------------------NN.....-D-........TET-T.---------------  475
HIVRJS          ---.-------E.------------------I......-G-N........DT-T.---------------  478
HIVGUNfr        ---.-------Q.------------------.......-GSE.......NT--.---------------  443
HIVSC           ---.-------K.--VK--------------NSK....-GSK......NENT--.---------------  481
HIVSBA          ---.-------R.-------------I------KNT....-E-...........--.---------------  224
HIVSBB          ---.-------R.-L----------------NNNNNT.-NN..........T--.---A-----------  233
HIVSBC          ---.-------R.-------------I------...NNT.-V-...........--.---------------  222
HIVBR014        ---.-------D.-----L-H----------.......-T-........NRTE--.---------------  480
HIVTH026        ---.-------K.-------H----------.......-NE........NTT--.--------K-----K  469
HIVBR021        ---.-------S.---S--------------.......-IS........ADN-T.---------------  476
HIVACH9         ---.-------R.---N---K----------N......-E-T.......DT-T.---------------  441
HIVACP1         ---.-------N.------------------DE.....-EIT........NI-T.------N--------  430
HIVJM           ---.-------R.------------------NSNS...-D-N........KT-T.------N-K------  471
HIVWM           ---.-------A.------------------IN.....-N-N.......NDT--.---------------  448
HIVMA208        ---.-------Q.-N-S--------------IN.....-ASK.......DN-T.---------------  504
HIVP896         ---.-------T.------------------.......-S-E......T.ET--.---------------  479
HIVBWB11A       ---.-------R.------------------SSS....-ES                               334
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                  CD4
                 -binding-
                          ^^^*  ^^^                ^^^
CONSENSUS.C      VGr?amYaPPi?.gnItCkSNiTGlLL?RdgG???????n?t???????????Et.FrPGGgdMrdNWRse   431
HIVMA959         ---.-------E.--------------T-G--PT.....-TK........T..--.---------------   473
HIVMA960         ---.-------A.--------------L----HT.....-T.......NNT..--.---------------   469
HIVD757          ---.-------E.-----E--------V----TES....-N-...........--.---------N-----   359
HIVD747          ---.-------A.-----------I--V----IEL....-D-.......KT..--.------E--------   406
HIVD760          ---.------FA.R-------------V----EDT....-D-..........-I.-S-------------   413
HIVNOF           ---TS------E.-----N--------T----NA.....-T-.....NNTT..-I.------N-K----N-   350
HIVZAM20A        --K.---P---A.-----I--------T----IDT....-S-KITHETNGTRN--.---------------   500
HIVD1044         ---.-------E.-----T--------E----PD.....-N-..........-I.---------N-----   355
HIVD1024         ---.-------E.-------------V----TE....S-T-...........--.---------N-----   466
HIVD744          ---.-------E.-------------V----RG..QES-T-..........-I.---------N-----   371
HIVD766          ---.-------E.-------------V----TE....S-N-ET.........--.---------------   353
HIVD808          ---.-------E.-------------V----TE....S-N-...........--.---------N-----   367
HIVD868          ---.-------E.-------------A----TE....S-H-..........-I.---------N-----   363
HIVSM145A        --Q.-------K.-----T--------L----NDPK...RTEE....QNNT..-R.---------------   480
HIVZAM18A        --Q.-------A.-------------T----S......-D-T.....NT...--.---------------   475
HIVDJ259A        ---.-------K.-I------V-----T----T.....-T-.....TEG..-I.---------------   459
HIVDJ373A        ---.-------Q.-I-A----------T----T.....-S-D.........--.---------------   470
HIVSE364A        ---.-I-----A.-------------T----TTN....-N-..........-I.---------------   467
HIVUG268A        ---.-------K.-K---R--------T----ETSET..-S-..........--.---------------   475
                          *  ^^^                ^^^          ^^^
CONSENSUS.D      vgk.AmYaPPie.g?I?CsSnITGLlLtRDGG???...?N?s???.??????net.fRPGGGdmrDNwrsE   425
HIVJY1           ---.---------.-L-K-T------------VN.....-ST.........---.--------K----N-   489
HIVNDK           ---.---------.-L-K--------------AN.....-S-.........H--.I-------------   472
HIVMAL           T--.-------A.-V-N-L------I------.......-S-DNS......D---.L-----------I--   484
HIVELI           .R-.-I-------.RN-L-------------IN.....-ST.........---.---------------   479
HIVZ2Z6          ---.---------.-Q-N-------------TN.....-S-.........---.---------------   479
HIVUG024         ---.-------Q.-L-R-------------.......-T-Q.........---.---------------   476
HIVUG021         ---.---T----.-Q-N---T----------VK.....-N-Q.........---.-------------N-   467
HIVUG038         ---.------N-.-L-N-T------------IGK.....-N-Q.....N-D-.---------------   476
HIVUG046         ---.---------.-L-K--------------.....N-TRQ.........---.---------------   476
HIVUG266A        --T.---------.-L-K--------------V.....-N-Q.........---.---------------   477
HIVUG269Afr      ---.---------.-I-R--------------IT.....-N-.........---.------N---------   479
HIVUG274Afr      ---.-------I.-Q-K--------------V.....-N-S...NETSSK--I.---------------   490
HIVSE365A        ---.---------.-V-S----------L----IH.....-T-....NET....--.---------------   477
HIVCAR4020       --Q.---------.-V-N-T------------NTK....-G-.......KNDI-I.---------------   515
                          *  ^^^                ^^^          ^^^
CONSENSUS.E      vGq.AMYaPPis.g?iNCVSNITGiLLtRDGG???...?n?t??........nET.FRPGGGnikDNWRsE   444
HIVTH966         A-L.---------.-R-----------------A.....N-TS.........---.---------------   476
HIVTH975         A--.---------.-K-----------------D.....N-S-T........---.---------------   474
HIVTH022         A--.-------R.-R-----------------.......ANNA.........---.---------------   474
HIVTN243         A--.---------.-K-----------------A.....-T-T.........---.---------------   481
HIVTH006         A--.---------.-R-----------------A.....-N-T.....:...---.---------------   473
HIVTH011fr       ---.---------.-R-----------------D.....IDKT........---.---------------   454
HIVCARELO        --R.---------.ELV---------------P.....-TA.........---.-------M-------   485
HIVCAR4017       ---.---------.-VV----------I----.......-E-HE.........---.--------------   484
HIVCAR4039       --K.---------.-V---------L-------.....SNSGE........P--.------DMR------   476
HIVCAR4071       ---.-------D.EA------------V----KIE....-E-.........I--.-------M-------   479
HIVCARMBA        ---.---N--V-.-V----------------ML.....-N-Q.........---.-------------N-   472
                          *
CONSENSUS.F      VGr.AMYApPIa.G?IqCnS?ITGllLTRDGg????...N????........?eT.lRPGGGdMrDNWRSE   433
HIVBZ126Afr      ---.----A--E.-N-T---N----------QNS....-QT...........--.F-----N-K------   467
                          ^^^*  ^^^          ^^^^         ^^^
CONSENSUS.G      vGQ.AMYaPPIA?GNItC?SnITGLiLTRDGG.....?nNsT??.......?nET.FRPgGGDMRdNWRSE   430
HIVVI525A        ---.---------A---E-R-S-----------.....N--N-.........---.---------G-----   493
HIVLBV217        ---.---------.-----K-------------.........--NG.........---.---A-----------   484
HIVCAR4067       T--.---N----.-----I------L-------.........----EN.......RT--.--------------   481
                          *  ^^^                ^^^
CONSENSUS.H      ?GQ.AMYAPPI?.GKITC?SNITGLILTSDHV.......N?SAE?.......?VT.FRPGGGDMRDNWRSE   150
HIVCA13          A--.-------N.-----V-------------.......-R---........E--.---------------   214
HIVVI557         V--.-------K.-----E-------------.......-.---S.......N--.---------------   209
                          ^^^*  ^^^          ^^^^         ^^^
CONSENSUS.O      GgS.glYAPPI?.GNLtC?SnITGMIlQlD?pW......Nss??.......?n?T.lRP?GGDMkDIWRTe   418
HIVANT70         -Q-.-------K.-----M---------M-NT-.....---NN.........-V-.F--I-----------   480
HIVMVP5180       -E-.RI-----P.-----H----------Q--.....--TGE.........-.-.---V----------K   489
HIVVAU           ---.-------P.---V-R----------T--.....-KTHP.......NST-.---G----------Q   493
                          *
CONSENSUS.CPZ    V??.GIY??P?R.GN??C?S?ITG??L???????.....N???.........???.??P??????D?WR?E   207
SIVCPZGAB        -GR.---AP-I-.--IT-N-N---LL-TSDTPVT.....-NSG.........NLT.FR-TGGNMK-I--S-   467
                          *  ^^^                ^^^
CONSENSUS.U      VG?.AMYAPPIe.GvIrCsSNITGl?LtRDGGn??...?Nstq?......???ET.FRPGGGDMrDNWRSE   419
HIVZAM184        --R.-------A.---K-T-----II-S-----SG....---.........NGT--.---------------   467
HIVCAR4081       --Q.-------P.-----E------I------.....N-K-NN.........T--.---------------   477
HIVK124A         --R.---------.-L-N--------L------E.....N--S-.........N--.---------------   485
HIVZ3fr          --Q.---------.-T----------L-------Gx....-A--.........N--.---------K------   478
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                                                gp120/gp41
CONSENSUS.A   LYkYKvVkieplgvaPtr.AkrRVV.....eREKRA??vg.lGavflgFLGaAGSTmGAaSiTLtvQARqL    478
HIVSF1703     ----------------P.------.....Q-----..--.I----I----------------------    549
HIVU455       ----------------.------.....------..--.---I------------------------    537
HIVZ321       ----------------K.------.....A------..I-.M--F----------------------R-    544
HIVRW020      ----------------S-.------.....------..--.I----------------------A-----    525
HIVUG031fr    ----------------.------.....------..I-.M----I----------------M------    494
HIVD687       -----D----------.------.....------..--.------------------------------    424
HIVNI         ----------------.------.....------..--.----------------R------------    535
HIVRW009      ----------------.------.....------..--.-----I----------------------    539
HIVUG275A     ----------------.-R-----.....------..--.V----------------------------    538
HIVUG273A     -------Q---------P.------.....Q-----..--.-----I----------------------    543
HIVVI191A     ----------------S-.------.....A-----..--.--------------------L---------    542
HIVDJ264A     -------------I---H.--G---.....------..--.-----F----------------------    534
HIVDJ263A     ----------------.------.....------..--.------------------------------    542
HIVDJ258A     ----------------.------.....------..--.---F----------------------------    536
HIVCARGAN     --------LT.TRIR---                                                      502
HIVCARSAS     -------------I----                                                       500
HIVCAR4054    -------E-K---I----                                                       495
HIVCAR286Afr  -------E-N--------                                                      517
HIVCAR4023    -------E----------                                                       517
HIVCAR423A    --R----E----------                                                       505
HIVKENYA      ----------------K.------.....------..--.I----------------------------    536

CONSENSUS.B   LYKYKVvkIEplGvAPTk.akrRvv.....QrekRa..vg?iGamflGfLGaAGSTMgaasmtLtVqaRql    501
HIVJRCSF      ----------------.------.....------..--.---L--------------R------------    536
HIVJRFL       ----------------.------.....------..--.---V----------------------L-    535
HIVALA1       ----------------R.------.....------..--.L--L--------------R------------    537
HIVBRVA       ----------------.------.....------..--.L--L----------------L-------L-    540
HIVJH3        ----------L-------.------.....------..--.---V---------------.---------L-    555
HIVBAL1       ----------------.------.....------..--.---V---------------A--------L-    542
HIVYU2        ----------------.------.....------..--.L--L----------------I---------    531
HIVMN         -------T---------.------.....------...A.---L----------------V-------L-    545
HIVHXB2R      ----------------.------.....------..--.---L----------------------------    544
HIVLAI        ----------------.------.....------..--.---L--------------R------------    549
HIVNL43       ----------------.------.....------..--.---L-------------CT-----------    542
HIVMFA        ----------T-------.------.....------..--.---L----------------------------    542
HIVCAM1       ----------------.------.....------..--A---L--------------VAL-----T---    544
HIVNY5CG      ----------------.------.....------..--AL--L-----------------A----T---    538
HIVADA        ----------------.------.....------..--T----------------------I-------L-    541
HIVJFL        ----------------.------.....--K---..--T----------------------------L-    539
HIVSIMI84     ----------------.------.....------..--L---L----------------------------    544
HIVD31        ----------------.------.....------..--LL--V--------------R--A---------    538
HIVSF162      ----------------.------.....------..-.TL----------------R-L----------    535
HIVBCSG3C     ----------------T.------.....------..--.---L----------------------------    547
HIVOYI        ----------------.-R----.....------..--ML-----------------R------------    543
HIVSF33       ----------------.------.....------..--V--------------------I-------K-    540
HIVCDC4       ----------------.------.....------..--ML----------------T--A---------    556
HIVSF2        ------I------I----.------.....------..--IV----------------V-L---------    543
HIVSF2B13     ----------I----.------.....------..--I-----------------R---------K-    541
HIVHAN        ----------------.------.....------..--ML----------------R-L---------    543
HIVRF         -------R---------R.------.....------..--T----------------G-I-------H-    553
HIVWMJ2       -------R---------.------.....------..--T----------------G-L---------    535
HIVTB132      ----------------X.------.....------..--.---ASP----------X--PT-----P---    525
HIVBR020      -------R-----I---R.------.....------..--TL--------------------VA---------    541
HIVTH014      ----------------.P-----.....------..--T----------T---------I---------    533
HIVUS711fr    ----------I----.------.....------..--.---V---------------A--------L-    537
HIVUS712      ----------------.------.....------..--.F----------------------------L-    540
HIVUS715      -------R-----I---R.------.....------..A-.L-V----------------IA---------    542
HIVUS716      ----------------R.------.....------..--.--------------------L-------L-    533
HIVHA593      ----------------.------.....------..--IV-----------------------------L-    563
HIVHA594      ----------------R.------.....------..--AL-----------------------------    537
HIVHA596      ----------------.--K---.....------..--VL-----------------------------    544
HIVHA599      ----------------.--S---.....------..--VL------L----------------------    554
HIVHA651      ----------------.------.....------..--TL-------------------------L-    538
HIVRJS        ----------------.------.....------..--V--------------------A--------    541
HIVGUNfr      ----------I-----.------.....------..--T--V----------------I---------    506
HIVSC         ----------------.------.....------..--T----------------T---------L-    544
HIVSBA        -------R-----I----.------.....------..--.--------------------I-------L-    286
HIVSBB        ------IQ----------.------.....------..--.---VLF--------------L---------    295
HIVSBC        ----------------.------.....------..--.---V----------------I-------L-    284
HIVBR014      ----------------R.------.....---R--..--AL------------------L---------    543
HIVTH026      ----------------R.------.....------..--T--------------------I--M------    532
HIVBR021      -------R---------.------.....------..--T--------------------I----PV-RI    539
HIVACH9       ----------------R.------.....------..--T----------                      484
HIVACP1       ----------------R.------.....-------..I-T---L------                      473
HIVJM         ----------------R.------.....-------..-T.M--L------                      513
HIVWM         ----------------R.------.....-------..--.L---------                      490
HIVMA208      ----------------T.-----M.....-----                                       533
HIVP896       -------R---I-----R.----T-.....------..--.---V--------------R-V-------L-    541
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                                                gp120/gp41
CONSENSUS.C   LYKYKVVEiKPlGvaPT?.aKRRVV??...ereKRA..vg?igAvfLGFLGaAGsTmgAASitlTvqaRQl   492
HIVMA959      ----------------K.------.....------..--.--------------------V---------   535
HIVMA960      ----------------E.------.....------..--.----------------------------   531
HIVD757       ----------------T.------.....------..--.--------------------M---------   421
HIVD747       ----------------T.------.....------..--.--------------------M-V-------   468
HIVD760       ----------------T.------.....------..--L----------------------------   475
HIVNOF        ------------I---G.S-----.....------..--.----L-----------A-----------   412
HIVZAM20A     ------------I---G.P-----EK...QI----..--.----------------------L--------V  564
HIVD1044      ----------------T.P-----.....------..--.-------------------------PL     414
HIVD1024      ----------------A.------.....------..--.-------------------------      523
HIVD744       ----------------A.------.....--G---..--.L--------------                418
HIVD766       ------------I---A.------.....------..--.L--------------                400
HIVD808       ----------------T.------.....------..--.-------------------------      424
HIVD868       ----------V--T.------.....------..--.M----------T-                    410
HIVSM145A     ------------I---G.------.....------..--.----------------------------   542
HIVZAM18A     ------------I---A.------E....T-----..--.----------------------A----V  538
HIVDJ259A     ----------V-I---K.------.....G-----...A.L--M-------------------------  520
HIVDJ373A     ------------L---K.------.....------...A.LA-----------------------    531
HIVSE364A     ------------I---K.------.....------..--.----------------------------   529
HIVUG268A     --------V--------K.------.....------..--.----------------------------   537

CONSENSUS.D   LYKYKVvriePlG?APT?.akRRVV.....eREkRA..IG.LGa?FLGFLGaAGSTMGAasltLTvQARql  484
HIVJY1        ------------I---R.------.....------..--.---V--------------V-VA--G-----  551
HIVNDK        -------K---I-V---K.-R----.....------..--.---V----------------V---------  534
HIVMAL        ------------V---K.------.....------..--.---M----------------------     546
HIVELI        -------Q-----V---R.------.....------..--.---M--------------R-V---------  541
HIVZ2Z6       -------K-----V---R.------.....------..--.---M--------------R-----------  541
HIVUG024      ------IK-----L---R.------.....A-----..--.---V----------------------     538
HIVUG021      ------------L---K.-R----.....------..--.---L----------------------      529
HIVUG038      ------------I---M.S-----.....------..--.---L----------------T-----      533
HIVUG046      ------------L---E.------.....------..--.---M----------------M----      533
HIVUG266A     ------I-L----L---R.------.....------..--.---V----------------------L-  539
HIVUG269Afr   ------------L---T.------.....------..--.---L----------------------V  541
HIVUG274Afr   ------------R---R.------.....------..--.---L------T---------M--------V  552
HIVSE365A     --------L----V---T.------.....K-----..--.--VM----------------MA-------  539
HIVCAR4020    ---------K---I---R                                                     533

CONSENSUS.E   LYKYKVVQIEPlGiAPTR.AKRRVV.....EREKRA..VG.IGAMIFGFLGAAGSTMGAaSITLTVQARQL  506
HIVTH966      ----------------.------.....------..--.-----------------------------   538
HIVTH975      ----------------.------.....------..--.-----------------------------   536
HIVTH022      ----------------.------.....------..--.-----------------------------   536
HIVTN243      ----------------.------.....------..--.-----------------------------   543
HIVTH006      ----------------.------.....------..--.-----------------------------   535
HIVTH011fr    ----------------.------.....------..--.------------------P------      511
HIVCARELO     ----------------                                                      503
HIVCAR4017    ----------V----                                                        502
HIVCAR4039    ----------I-V----                                                     494
HIVCAR4071    ----------------                                                      497
HIVCARMBA     ----------------                                                      490

CONSENSUS.F   LYKYKVVkIEPLGVAPTr.AkRqVV.....kRekRA.?VG.iGAvflGFLgaAGSTMGAASITLTVQArQL  495
HIVBZ126Afr   -------E----------.------.....------.V--.---L-----S--------------------  530

CONSENSUS.G   LYKYKViKIKpLGvAPTr.ARRRVV.....?REKRA..I?.?GAVFLGFLGAAGSTMGAAS??LTVQVRQL  487
HIVVI525A     ------V---S-------.------.....E-----..-G.L--------------------IT--------  555
HIVLBV217     ----------------K.------.....G-----..-..T------------------LA---------  545
HIVCAR4067    ----------I----                                                        499

CONSENSUS.H   LYKYKVV??EPLG?APT?.A?RRVV.....?REKRA..VG.L?AVFLGFLGAAGSTMGAAS?TLTVQARQL  204
HIVCA13       -------KI----V---K.-K----.....G-----..--.-G------------------I---------  276
HIVVI557      -------RV----L---R.-R----.....E-----..--.-E------------------V---------  271

CONSENSUS.O   LfkYKVVrvKPFSVAPTk.iaRP?Igt?t?HREKRA..vG.LgMLFLGvLSAAGSTMGAAATaLtVqthtl  482
HIVANT70      --N----------------R.----V-S-R-.------..--.----------------------T-A------  546
HIVMVP5180    -YN----QI----------.MS--I-NIH-P------..--.-----------------------R--SV  556
HIVVAU        ----------------.----T---RS.------..A-.-A-----I-----------------R-QH-  559

CONSENSUS.CPZ L??Y?VV?I?PLSVAPT?.??R?????Q?.?RQKR?.??G.?G??FLG?L?AAGSTMGAA???LT?Q?R?L  245
SIVCPZGAB     -YK-K--R-E-------K.AR-HTVAR-K.D----A.AF-.L-AL---F-G---------AVT--V-A-Q-  534

CONSENSUS.U   LYKYKVVKiEPLGvAPTr.akRRVV.....EREKRA..vG.lGA?FLGFLGAAGSTMGAASmtLTvQARQL  480
HIVZAM184     --------L--------K.PR----.....------..--.---V----------------I---------  529
HIVCAR4081    ----------------                                                        495
HIVK124A      ------------L---S.------.....-------..I-.---M-------------------------  547
HIVZ3fr       ----------------.------.....------..--.M--L----------------A--A-----   540
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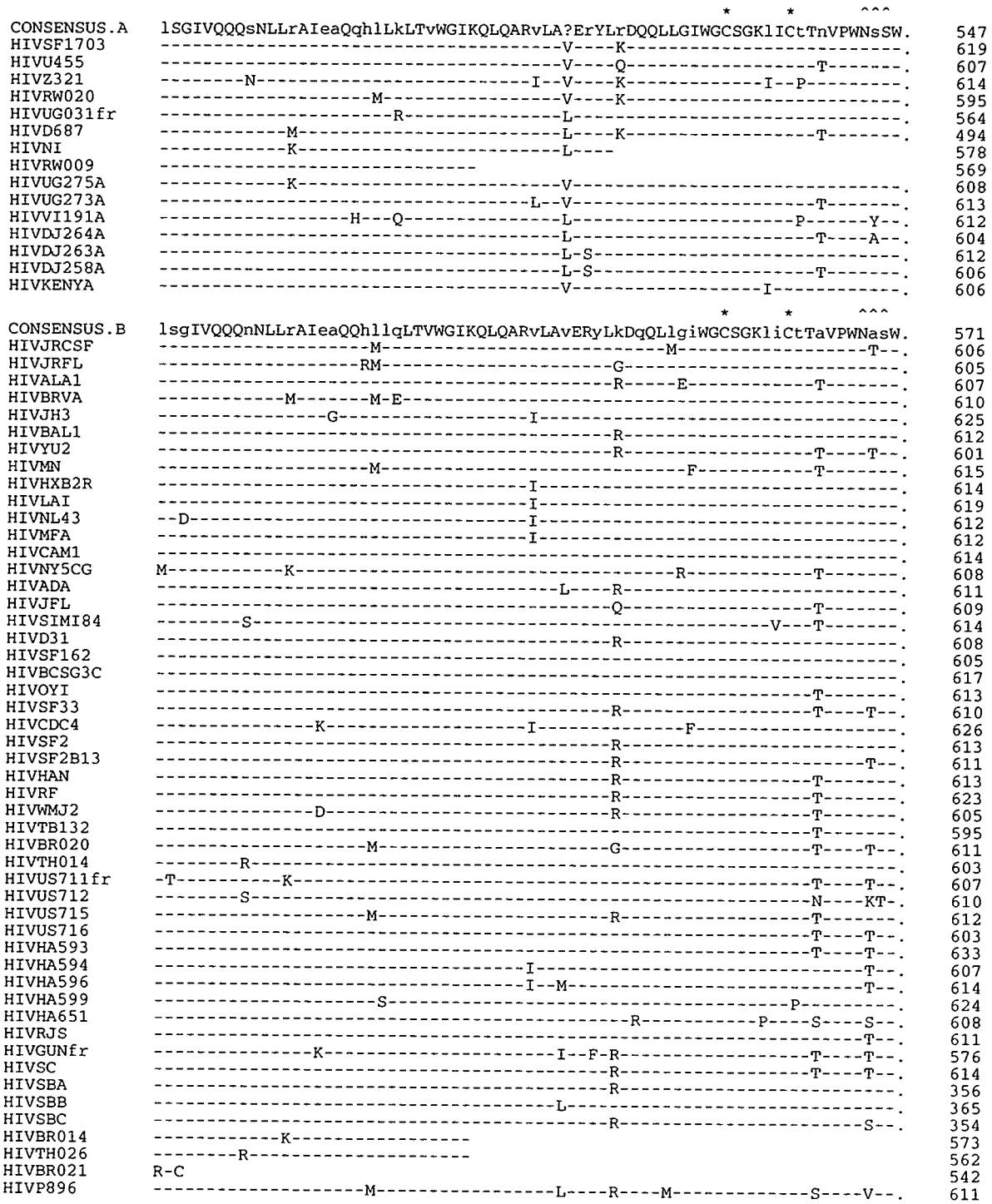

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                                                                                                  *     *      ^^^
CONSENSUS.C   LsGIVQqqsNLLrAIEaqqHmLQLTvWGIKQLqtRVLAiERYLkdQQLLGiWGcSGKLICTTaVpWNsSW.    562
HIVMA959      -F----------------H-L-------------------------------------------------A-----.    605
HIVMA960      ----------------R---------------A---------Q------L-----------T-------.    601
HIVD757       --------------------L-------------------------------R--------N-------.    491
HIVD747       --------------------L----I-------A----------E-----------------T-------.    538
HIVD760       --------------------L-------------------------------M--------------------.    545
HIVNOF        ------------------------------------------                                    458
HIVZAM20A     --------------------I------------A-----------------------------------------.    634
HIVSM145A     ---------------------------------RA---------E-------------------------.    612
HIVZAM18A     --------------------L-----------------M-------------------------S------.    608
HIVDJ259A     ------------------------------------------------------------N----A--.    590
HIVDJ373A     ------------K---VH-----------------------------------------------------.    601
HIVSE364A     ------------------------------------------------------------------------.    599
HIVUG268A     --------N-----------------------------------Q-----------------------------.    607
                                                                                  *     *      ^^^
CONSENSUS.D   lSGIVqQQNNLLrAIeAQQHlLQLTVWGIKqlQARvLAVErYLkDQqLLGiWGCSGkhICtT?VPWNSSW.    553
HIVJY1        --------------------M-------------------S---------------------T-------.    621
HIVNDK        M----H-----------------------------------------R------------R-----N-------.    604
HIVMAL        ------------------------------------------Q--R---M-----------F-------.    616
HIVELI        M-----------------------------------I-------------------------N-------.    611
HIVZ2Z6       -----------------------------------I---------------------L----T-------.    611
HIVUG024      M-------------------------------------S---------------R---P-Q-------.    608
HIVUG021      ----------------------------                                                  559
HIVUG266A     ------------M-------------------------S---------------------S-------.    609
HIVUG269Afr   ------------------------------------S--G------------R-----N-------.    611
HIVUG274Afr   ----------------K-------------------I-------------------------T-------.    622
HIVSE365A     ---------------------------------I-------R------------R-----N-------.    609
                                                                              *     *      ^^^
CONSENSUS.E   lSGIVQQqSNLLRAiEAQQHlLQLTVWGikQLQARVlAVERYLKDQKflGLWgCSGKIICTTAVPWNSTW.    576
HIVTH966      V-------------------------------------------------------------------------.    608
HIVTH975      ------------------------------------------------------------------------.    606
HIVTH022      --------------------M---------------------------------------------------.    606
HIVTN243      -------X------X-------------XX------X----------LX---X-----------------.    613
HIVTH006      ------------------------------------------------------------------------.    605
                                                                                  *     *      ^^^
CONSENSUS.F   lSgIVQQQnNLLkAIEAQQHLLQLTVWGIKQLQARVLAVERYLQDQQLLGLWGCSGKLICTTNVPWNSSW.    565
HIVBZ126Afr   --E---------R-------------------------------------------------------------.    600
                                                                                  *     *      ^^^
CONSENSUS.G   LSGIVQQQ?NLLRAIEAQQHLLQLTVWGIKQLQARVLAVER?L?DQQ?LGIWGCSGKLICTTNVPWNTSW.    553
HIVVI525A     --------S-------------------------------F-K---P---------------------.    625
HIVLBV217     --------N---------------------------------Y-Q---L----------------------.    615
CONSENSUS.H   LSGIVQQQSNLL?AI?AQQH?LKLT                                                    226
HIVCA13       ------------R--E----L----                                                    301
HIVVI557      ------------Q--Q----M----                                                    296
                                                                                  *     *      ^^^
CONSENSUS.O   ?KGIVQQQDNLLRAIQAQQ?LLRlSvWGIRQLRARLlALETliQNQQlLnLWGCKgkLiCYTSVKWN?tW?    549
HIVANT70      L------------------Q-----X----------------L------S--------V--------R--I    617
HIVMVP5180    L------------------H----------------Q----------R-------------------TS-S    627
HIVVAU        I------------------H---P----------------F-------------NR----------K--G    630
                                                                                  *     *      ^^^
CONSENSUS.CPZ ??GIVQQQ?NLL?AIE?QQHLLQLS?WGVKQLQAR?LAVE?YL?DQQ?L?LWGC??K??C?TTVPWNNSW?    299
SIVCPZGAB     LS------N---K---A--------I---------L----R--Q---I-G----SG-AV-Y---------P    605
                                                                                  *     *      ^^^
CONSENSUS.U   lSGIVQQQnNLLrAIeAQQHLLqLTVWGIKQLQARvLAvErYL?dQQLLGiWGCSGKlICTTtVPWNSSW.    549
HIVZAM184     --------S---K---------K------------A--M----Q-------------------------.    599
HIVK124A      M--------------D-----------------------S--K-------------H----N-------.    617
HIVZ3fr       ------------------------------------------ES-----L--------------------.    610
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                    ^^^       ^^^          ^^^
CONSENSUS.A  ........SNks?sdIWdnMTWLqWdKEisnYT?iIY?LiEesqnQQEkNEqdLLALDkWanLWnWFdIsn  607
HIVSF1703    .........--RTQ-E--N--------------D---N------I-------E----------------K  682
HIVU455      .........----QE---N-------E----S--G---Q-----------L----------- ---N---  669
HIVZ321      .........----Q-----K----E----V----QV--N------T---I--R-----------------  677
HIVRW020     .........----MNE-----------------Q---N----------------------S--------R  658
HIVUG031fr   ...........----Y-E--------------N---EL--S---D-------------------------  627
HIVD687      ...........---TY-------------------K---A-----A---------------TS--S----TK  557
HIVUG275A    ...........----Q----------------N---EL--R-L--------------------------G---  671
HIVUG273A    ...........----Q-E----------------N---D----A-----------------S--S------  676
HIVVI191A    ...........----YD---N----------D---QL--G----------------------S--S------  675
HIVDJ264A    ...........---TYN---E--------------D---N-------------K--------ES-----N-TK  667
HIVDJ263A    ...........---TYN--------------V----D---N--------------------Q--------G-TK  675
HIVDJ258A    ...........---TFN----------------D---T----------------------G--S--G-T-  669
HIVKENYA     ...........----Q-E--E------------D---N-L-------------------------------  669
                    ^^^       ^^^          ^^^
CONSENSUS.B  ........SNksl??iW?nmTWmeWerEIdnYT?lIytLieesQnQQekNeqeLLeLdkWasLWnWf?Itn  629
HIVJRCSF     ........-----DS--N--------K--E---NT---------I----------------------G--K  669
HIVJRFL      ........-----DR--N--------------SE-------------------------------D--K  668
HIVALA1      ........-----NQ--D--------------S-------------------------------N---  670
HIVBRVA      ........-----SD--D--------------N---S---D--I------K--------------N---  673
HIVJH3       ........-----EE--D--------------S--------------------G----------T---  688
HIVBAL1      ........-----NK--D----I--D---N---SI--S-----------------------------D--K  675
HIVYU2       ........-----NE--D-----K---------HI--S---Q------------A----------D--K  664
HIVMN        ........-----DD--N-----Q---------S---S-L-K--T---------------------D---  678
HIVHXB2R     ........-----EQ--NHT-----D---N---S--HS-----------------------------N---  677
HIVLAI       ........-----EQ--N-------D---N---S--HS-----------------------------N---  682
HIVNL43      ........-----EQ--N-------D---N---S--HS-----------------------------N---  675
HIVMFA       ........-----EQF-N-------D---N---S--HS--D--------------------------N---  675
HIVCAM1      ........-----DK--N--------------N-----------------KD-----T--------D---  677
HIVNY5CG     ........-----DK--D--------------G----------I---------------------D--K  671
HIVADA       ........---T-DM--D----------E---G-----------------D--A----------D-S-  674
HIVJFL       ........-----DE- N-----Q-----S---S-----------------L----------- ---D---  670
HIVSIMI84    ........-----NQ--D--------------G---R----------Q---D--K--T--------S--K  677
HIVD31       ........----MDM--N--------------S---------------------N--EN--S--D-S-  671
HIVSF162     ........-----DQ--N--------------N-------------------------------D-SK  668
HIVBCSG3C    ........-----NQ--D-----Q-----E---D---N----------------------------T---  680
HIVOYI       ........-----NE--D-----Q---------H--------------------------G--S--S---  676
HIVSF33      ........-----DK--N--------------S-----L-------------------------S---  673
HIVCDC4      ........---T-DQ--N-------D-------H----------------Q----Q--------T-SD--K  689
HIVSF2       ........-----ED--D-----Q---------NT----L--------------------------S---  676
HIVSF2B13    ........----MED--D-----Q--K------NT----L--------------------------N---  674
HIVHAN       ........---T-DQ--N--------------S-------Q---------------------S-YD-S-  676
HIVRF        ........-----NM--N-----Q---------GI--N-L--------------------N-----D--Q  686
HIVWMJ2      ........----MNQ--D-L-------------SI--S---------G------------------D---  668
HIVTB132     ........-----DE--N----------N---G----------X------LD-------------D---  658
HIVBR020     ........-----DD--T-------K-------S----------R--------------D------T-SK  674
HIVTH014     ........-----DK--N--------------RE---------------L---------------D--K  666
HIVUS711fr   ........-----DK--G--------------G--------------------------------T---  670
HIVUS712     ........-----DQ--Q-----Q------K--DV-----G--------------------------D--Q  673
HIVUS715     ........----HDQ--Q-----Q--K------S---N---V--------------------------D---  675
HIVUS716     ........-----DQ--G-----Q---------G--------------------------------N---  666
HIVHA593     ........-----SE--D-----Q---------S--------------------------G-----E---  696
HIVHA594     ........-----EK--N--------------G---S-------------D--------------N--K  670
HIVHA596     ........-----EK--N--------------G---S--G----------D--------------N--K  677
HIVHA599     ........--R--QY--N----I----------DI--S---K---------------Q--------S--K  687
HIVHA651     ........-----EQ--N----L----------S---S--K--------------------------N--E  671
HIVRJS       ........-----EE--D----------N---G-------Q------------A--T--------S-S-  674
HIVGUNfr     ........-----KQ--D-L------------GI-FN----A---------D--------G-----S---  639
HIVSC        ........-----DK--G--------------S--------------------------------N---  677
HIVSBA       ........-----DQ--D-----Q-----E---S---N-------------D-----------S--S---  419
HIVSBB       ........-----ND--D-----Q-D---NK--DS--Q-------------D--K--E--------S-SK  428
HIVSBC       ........-----DQ--N-----Q-----E---S---N--------------------------S---  417
HIVP896      ........----VDD--N--------------DY--D-L-K--T------K--------------D---  674
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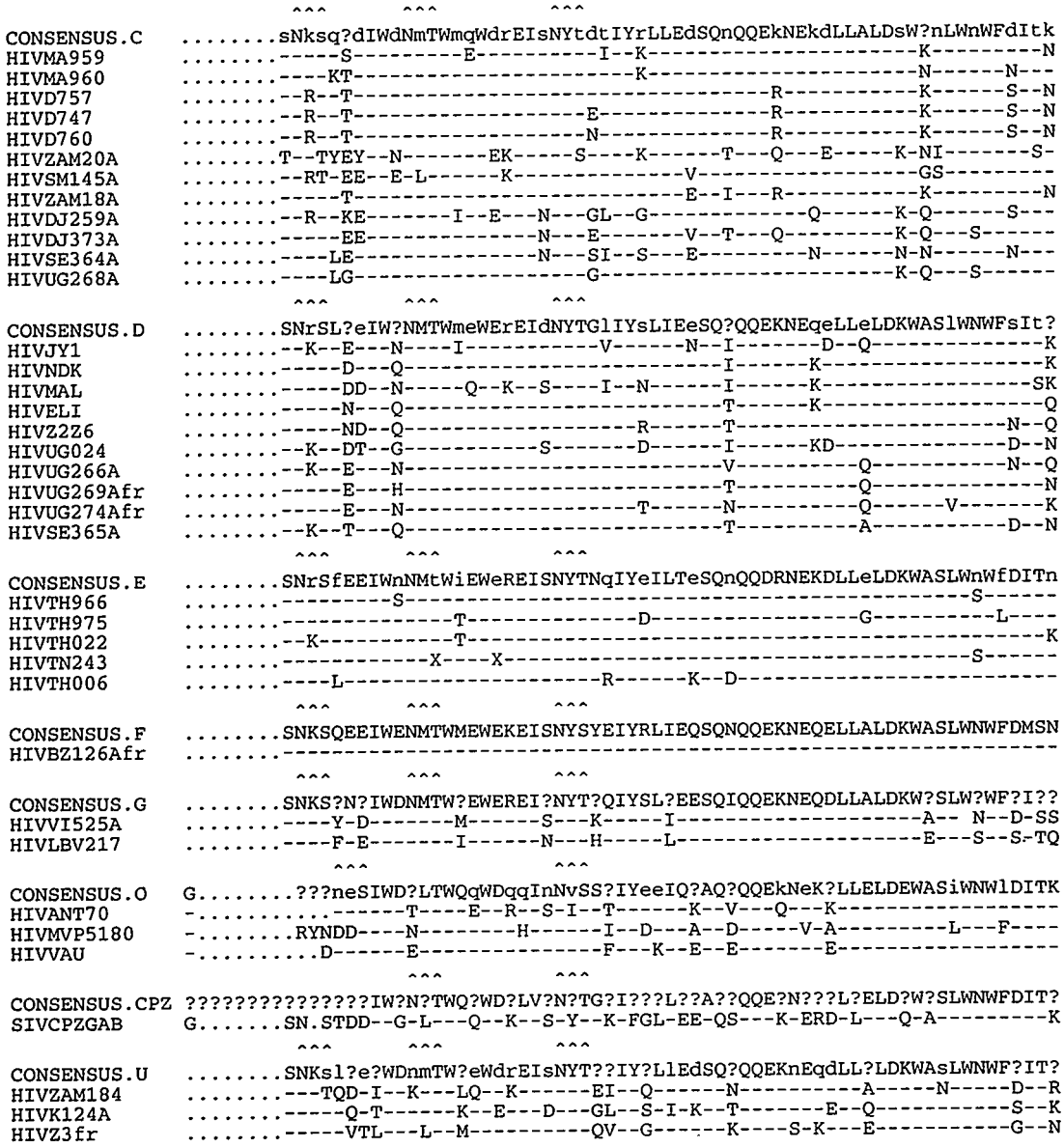

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                                                                \/3' sj       <- tat cds
CONSENSUS.A   WLWYIriFimIVGGLIGLRIvfaVlsiInRVRqGYSPlSFQtltp?pr??pdRperIeeeGG.eQdrdRSi   674
HIVSF1703     ----------------------------------------IH--N--G.------------.--G-----   751
HIVU455       ------L-VI------------T--------------------A-I-EG.LG--G-------.--GK----   738
HIVZ321       -----K----------------------------------HHQ-E.---------G--.--------   746
HIVRW020      -----K--------------------V--------------IR--N-KE.---LG--DG---.--------   727
HIVUG031fr    -----K--------------I--------------------H--N--G.L---G-------.--G-----   696
HIVD687       ------------------------N--------------------HQ-E.----G----G--.-------V   626
HIVUG275A     ------L-----------------V---------------H--N--G.L---G-------.K-------   740
HIVUG273A     ------L--------------L--F-V-----K----V----H--N--D.L------A----.--------   745
HIVVI191A     ----------------------------------------PHHQ-E.-----G---G--.----G---   744
HIVDJ264A     -----K---------------L---TV-K---------------HHQ-E.---------G--.---K---V   736
HIVDJ263A     -----K-----------------T-----------------HHQ-G.---------G--.-------G   744
HIVDJ258A     ---------I---------------T-----------------HHW-EP---------G--.---K----   739
HIVKENYA      -----K----------------T--------------------H--A--G.L-----------.--------   738

CONSENSUS.B   wLWyIkiFImIvgGLvGLrivFavLSiVNrvRQGYSPlSfQT?lPaprg.pdrPegieeeGG.erdRdrSg   697
HIVJRCSF      ---------------I------S--------------------L---T--.------------.--------   738
HIVJRFL       ------------------L--T--------------------L-------.------------.--------   737
HIVALA1       ----------------------S-------------------R---R-E.------------.--------   739
HIVBRVA       ---------------I--------------------------R--GR--.------------.-------S   742
HIVJH3        -----R----------------T--------------------R-------.------------.D-------   757
HIVBAL1       ---------------I------S--------------------H--SS--.----G-------.--------   744
HIVYU2        ---------------I------V--------------------H---Q--.----D-------.--------   733
HIVMN         ------------------------------------------L--RP-V---.------------.-----T--   747
HIVHXB2R      ------L-----------------------------------H--T---.------------.-------I   746
HIVLAI        ------------------------------------------H--T---.------------.-------I   751
HIVNL43       ------L-----------------------------------H--I---.------------.-------I   744
HIVMFA        ----------------------------------------H--NRG-.------------.-------V   744
HIVCAM1       -----------I---I------TI--L---------------RF-V---.------------.G----T--   746
HIVNY5CG      ---------------I------T--------------------R---Q--.------------.--------   740
HIVADA        ---------------I------T--------------------H-------.------------.D------V   743
HIVJFL        ---S---------A--------------------------R--T---.----G-------.--------   739
HIVSIMI84     ---------------I----I----------------------L-------.------------.--------   746
HIVD31        ------------------------S------------R-------.------------.D------N   740
HIVSF162      ----------------------T--------------------RF------.------------.-------S   737
HIVBCSG3C     ---------------I------T--------------------H--T---.------------.--------   749
HIVOYI        -----R---I-----------------------------------R--TQ--.------------.--------   745
HIVSF33       -----R---------I----I----------------------LI--Q--.---------G--.-------T   742
HIVCDC4       ---------------I--------------------------L--N---.------T--G--.--G--G-T   758
HIVSF2        ----------------------------------------R--V---.----D-------.-------V   745
HIVSF2B13     ------------------------V---------------R--T---.----D-------.-------V   743
HIVHAN        ---------------I--------------------------L---T--.-RQ--E-------.----G--V   745
HIVRF         -----R------------K----------------------H-------.--------G---.--------   755
HIVWMJ2       ---------------I------T--------------------H--T---.------------.-------V   737
HIVTB132      X-------------------I-T--------------------H--X---.----G-------.-----T--   727
HIVBR020      ------------A----------------K--------V----R---Q--.-----E-------.D-E-E---   743
HIVTH014      ----------------------------------------L--RF--Q--.-GG---------.-Q-----E   735
HIVUS711fr    ---------------I--------------------------R-------.------------.--Q-x---   739
HIVUS712      ----------------------S--------------------R---A--.------------.--------   742
HIVUS715      ---------------I------I--------------------H---R--.------------.--------   744
HIVUS716      ------------A------V--I--------------------HH--L--.------------.--------   735
HIVHA593      ------------------------------------V----H-------.------------.----G--V   765
HIVHA594      ---------------I--------------------------L---Q--.----G-------.----G--E   739
HIVHA596      ----------------------------------------L---Q--.----G-------.----G--E   746
HIVHA599      ------L--------I-------I-------A-----------L-------.L------G----.----GT--   756
HIVHA651      ----------------------T--------------------R-------.------------.-------S   740
HIVRJS        -----R-----------------------------------R--T---.------------.--------   743
HIVGUNfr      ---------------I--------------------------H--T---.------TG----.--------   708
HIVSC         ----------------------T--------------------R--SQ--.------------.--------   746
HIVSBA        -----R---------I---------                                                  444
HIVSBB        ------------------------                                                   453
HIVSBC        ---------I-----I---------                                                  442
HIVP896       -----RL--------I--------------------------L---S--.------T-----.--------   743
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                                                        \/3' sj       <- tat cds
CONSENSUS.C    WLWYIkIFImIVGGLIGLrIiFaVLsIVNRVrqGYSPLSFQTLtPnprG?pDRlgrIEeeGG.EQD?drSi   691
HIVMA959       ----------------------------------------------------.----------.---K----   737
HIVMA960       ----------------------------------------------------.L---------.---K-S--   733
HIVD757        ----------------K---------------------------G-.----E---GG--.---K----     623
HIVD747        ---------I---------------C-----KA-----------                              646
HIVD760        ------------------------------------------                                650
HIVZAM20A      -----R-------------------------------------------I--E----------.---R----   767
HIVSM145A      ---------I-----------V-------------------------.----------.---K----     744
HIVZAM18A      -------------------S-------------------------.----------.---R-K--       740
HIVDJ259A      ----------------------------------------------.---P-G------.---RG---     722
HIVDJ373A      ----------------------------------------------I-----.---PRG------.---KG--T  733
HIVSE364A      ----------------------------------------------I-----.----------.---R----  731
HIVUG268A      --------------------------------K----------T---.---P-E------.---R---V    739

CONSENSUS.D    WLWYIkifImivgGLIGLRIvFaVlSlVNRVRQGYSPLSfQTLLPaPRg?PDRPegiEEEGG.EqGR?RSi   680
HIVJY1         ---------------------T-------------------------.----------.----D---     753
HIVNDK         ------L-----------------V----------------V---.-----E------.-R--D---     736
HIVMAL         -----R---IV---------I-----------------L-----T---P----------.----G---     749
HIVELI         -----------I-----------------------------------.------T-----.-R--D--V    743
HIVZ2Z6        ----------------------------------------------.----------.-R--D---       743
HIVUG024       -----RL--I-----------------------------------T---.----GET-----.----G---   740
HIVUG266A      ------------------------------------L---------.------T-----.----G---     741
HIVUG269Afr    -----R-S----------------F-----------------------.----------.----G---     743
HIVUG274Afr    -----R-------------------------------------------E.-----E------.----G---   754
HIVSE365A      ----------V-E-------I-------------------------.----------.----D---       741

CONSENSUS.E    WLWYIKIFIMIVGGLIGLRIIFAvLSIVNRVRQGYSPLSfQtp?HhQrE.pDRPERIEEgGG.eQGRdRSV   707
HIVTH966       ---------------------------------------------I-Q---.----------.--------   740
HIVTH975       ---------------------------------------------Y-----.---------E--.--------  738
HIVTH022       ------------------------------------------I-P-----.----------.--------    738
HIVTN243       ----------------------X---------------L---T------.L----------.----E---     745
HIVTH006       ------------------------------------------LT---G-.----------.A-------    737

CONSENSUS.F    WLWYIKIFIMIVGGLIGLRIVFAVLSIVNRVRKGYSPLSLQTHIPSPRE.PDRPEGIEEGGG.EQGNERSV   697
HIVBZ126Afr    ----------------------------------------------------.----------.--------  732

CONSENSUS.G    WLWYIKIFIM?VGGLIGL?IVFAVLSIVNRVRQGYSPLSFQTL?HHQ?E.PDR?ERIEEGGG.E?DR?RS?   666
HIVVI525A      ----------V-------R-----------------------T---G-.---L---------.-H--T--T   756
HIVLBV217      ----------I-------K-----------------------A---R-.---P---------.-Q--D--V   747

CONSENSUS.O    WLWYIKIAIIIVGALiGvRViMIvLNlVKNIRQGYQPLSLQIP??hq?E.agTPGrTGegGG.eedRprWt   670
HIVANT70       ----------------V----------I----------------NH--E-.---------G---.--G----I  746
HIVMVP5180     -----------------I-----I------------------VP-RQ-.-E-------E--.-G---K--     759
HIVVAU         --------------------V----------------------IQQ-A-.V----G------.D---R---   760

CONSENSUS.CPZ  WLWYIKIF?M?VG?I?GLRI?????S??R?VRQGY?PLS?Q?????Q??.?????EI?E?GG.??DR?R??   369
SIVCPZGAB      --------L-A--G-I----IMTVF-VV-R-----S---L-TLIPV-RE.QGRLG--D-G--.EQ--S-SV   737

CONSENSUS.U    WLWYIKIFimIVGGLIGLRIVfa??S?vNRVRQGYSPLSFQtllP?PrG.pDRPgriEEeGG.EqgrdRSi   667
HIVZAM184      ---------I-----------I-II-V-------------IPT-H-E-.L---------G--.---------  731
HIVK124A       --------V--------------ML-L-----------------A---.----EG------.---------  749
HIVZ3fr        ----------------------TVF-II----------------T---.------T------.-EDNN--V   742
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CONSENSUS.A   rLVsGFLalAWDDLRsLCLFsYHrLRDfilIa.artVelLghsslkglrlg.......weglkYL.wN.Ll   735
HIVSF1703     ------------------------------.-------KR---R-----.................---.--   812
HIVU455       --------I------N-----------A--V.--A-----R---------.....-------.--.--   799
HIVZ321       -------P-----------C------CA---.--I--T-.......I-R-.........--T----.G-.-V   800
HIVRW020      ----------------------------S--.-------------------.....-------.--.--   788
HIVUG031fr    ------------------------------.-------E-N--------.....-------.G-.--   757
HIVD687       ---------------N----                                                     646
HIVUG275A     H-----------------------------.--------Q.....------.--.--               790
HIVUG273A     ----------------------------V.----K----R.....-.---------I---.--.--     799
HIVVI191A     ----------------------------V.--I--T--RR.....-.---------A----.--.--     798
HIVDJ264A     ----------------------H----V---.V-A---------------.....-GA----.G-.--     797
HIVDJ263A     -----------------------------V---.V-A---------------.....--A-Q--.G-.--   805
HIVDJ258A     ----------------------Q----V---.V-A---------------.....--A-Q--.G-.--     800
HIVKENYA      ---T-----------------------------.TE----------R-----.....-------.--.--   799

                                 *
CONSENSUS.B   rlv?GfLaliWdDLrsLclFsYhrlrdLlLiv.ariVElLg?.....?rrG.......WeaLkYw.wn.LL   750
HIVJRCSF      Q--N-------V-----F------------T-.T-------.....-----.....--I----.--.--   792
HIVJRFL       ---N-------V-----------------T-.T-------.....-----.....--V----.--.--     791
HIVALA1       ---D-L-----V--------------------.T-------.....-----.....--V----.--.--     793
HIVBRVA       P--D-----F-V-----F--------------.T-------.....-----.....--V----.--.--     796
HIVJH3        Q--D-L--I--V--------------------.T-------.....-----.....-------.--.--     811
HIVBAL1       P--N-------V-----F--------------.M-------......LAG-.....--V----.--.--     799
HIVYU2        P--D----I--V--------------------.T-------.....---.....-GV----.--.--       787
HIVMN         ---H----I--V-----F-----H.------A.--------.....---.....--V----.--.--       800
HIVHXB2R      ---N-S--------------------------.T-------.....---.....-------.--.--       800
HIVLAI        ---N-S--------------------------.T-------.....---.....-------.--.--       805
HIVNL43       ---N-S--------------------------.T-------.....---.....-------.--.--       798
HIVMFA        ---N-S--------------------------.T-------.....---.....-------.--.--       798
HIVCAM1       ---T-----------------------------.--------.....---.....-------.--.--     800
HIVNY5CG      P--N-------V--------------------.--------.....---.....------C.--.--       794
HIVADA        ---D-----F----------------------.--------.....---.....--V----.--.--       797
HIVJFL        Y--T-------E--W-----------------.T-------.....---.....-------.--.--       793
HIVSIMI84     Q--T---PI--G-----F--------------.--------.....---.....--I----.--.--       800
HIVD31        ---K----------S-----L----------A.--------.....---.....--V----.--.--       794
HIVSF162      P--H-L----------------------I--A.--------.....---.....-------.G-.--       791
HIVBCSG3C     ---N-----F------------------I-V-.T-------.....---.....-------.-S.--       803
HIVOYI        ---D-----------------------I---.--------.....---.....--V----.--.--       799
HIVSF33       ---N-----F---------------T------.--------.....---.....--V----.--.--       796
HIVCDC4       ---H-----V----------------------.--------.....---.....--V----.--.--       812
HIVSF2        ---D-------E----------R--------A.--T--I--.....H--.....-------.-S.--       799
HIVSF2B13     ---D-------E----------R--------A.V-T--I--.....H--.....--V---G.-S.--       797
HIVHAN        ---S-----F------------R----------.-K---T--.....---.....--V----.--.--     799
HIVRF         GA-N---T------WT--S-------------.V-------.....---.....-------.--.--       809
HIVWMJ2       ---H----------------------------.K-------.....---.....-------.--.--       791
HIVTB132      ---D----IF-V---N--------------V-.T------X.....---.....-------.--.--       781
HIVBR020      ---T-L-EI--------F----R----------.--------.....---.....-------.--.--     797
HIVTH014      ---S-L-T---E--------------------.--------.....---.....----R--.--.--       789
HIVUS711fr    ---N---T-F-N--------------------.-----I--.....---.....--L----.--.--       793
HIVUS712      Q--D----I--V----------Y----------.T-------.....---.....-------.--.--     796
HIVUS715      Q--T----I--V--------------------.--------.....---.....--I----.--.--       798
HIVUS716      Q--D---TI--V--------------------.T-------.....---.....--V----.--.--       789
HIVHA593      ---N----------------------------I.--------.....---.....-------.--.--     819
HIVHA594      -I-N----------------------------.--------.....---.....-------.-S.--       793
HIVHA596      -I-N----------------------------A.--------.....---.....-------.-S.--     800
HIVHA599      ---N----------------------------.-------I.....---.....------G.--.--       810
HIVHA651      P-AH----------------------------I.--------.....---.....-------.--.--     794
HIVRJS        P--T----------------------------.--------.....---.....-------.--.--     797
HIVGUNfr      ---H-------------F--------------.--------.....---.....--V---L.--.--     762
HIVSC         ---D----I--V-                                                           759
HIVP896       P--N-----F-V---N----L--L--N-----.T-------R.....--.....-------.--.--     797
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                                 *
CONSENSUS.C   RLvsGFLalaWDDlrslclfSYhrLRDfiLia.ARavELLgrsslrglQrG.......WealKYL.Gs.Lv    752
HIVMA959      ------------------------------V-.---------------K-........-D------.-N.-G    798
HIVMA960      ---N-----F-------------Q---LL-V-.--V---------------.......--------.-N.--    794
HIVD757       ---N----------.CGA-AS                                                      642
HIVZAM20A     ---N-----V--------R----Q----T---.------------------.......--------.--.--    828
HIVSM145A     ---N--------------------------V-.-------------E----.......--------.-N.-G    805
HIVZAM18A     ---D-----F-----------------------.---A-------------.......--------.--.--    801
HIVDJ259A     ----------------------R----L----.--------.......---.........T----.--.--    776
HIVDJ373A     -----------------F---------L---V.--V-----.......---.........T----.--.--    787
HIVSE364A     -------SI----------------------V.-------I.......---.........I----.--.-A    785
HIVUG268A     --I-------------------R----LL---.------------------.......--------.--.--    800
                                 *
CONSENSUS.D   RLvnGfsALiWDdLRnLCLFsYhrLRDliLIA.aRIVelLGR.......RG.......WealKYl.Wn.LL    734
HIVJY1        ---------F----------------------.T--------.......--.........---I---.-S.--    807
HIVNDK        -----LF--F-----------------S----.---------.......--.......--------.--.--    790
HIVMAL        ---------------------------L---.T--------.......--.......--------.--.--    803
HIVELI        --L------------S----------------.V--------.......--.......-DI----.--.--    797
HIVZ2Z6       --------------------------------.---------.......--.......--------.--.--    797
HIVUG024      --L--L--------------R--H---------.----A----.......--.........---I---.--.--    794
HIVUG266A     ---S--L--A-----S------------L---.T--------.......--.........------W.--.--    795
HIVUG269Afr   ---S-------------------------.T--------.......--.........---I---.--.--    797
HIVUG274Afr   ----------------------R-----L---.-----I---.......--........-K-I---.--.--    808
HIVSE365A     ------------G------------------.---------.......--.........--V----.-S.--    795
                                 *
CONSENSUS.E   RLVsGFLALaWdDLRSLCLFsYhRLRDFIlIA.ARtvELLGhSSLKGLRRG.......WEGLKYL.GN.LL    768
HIVTH966      ---T-------------------------S--.--------R---------.......--------.--.--    801
HIVTH975      ---------I-E--------L-----------.---L--------------.......--------.--.--    799
HIVTH022      --------------------------------.------------------.......--------.--.--    799
HIVTN243      ----------------------------S--.--A---------------.......--------.--.--    806
HIVTH006      ----------------------R---------.--------------                            783
                                 *
CONSENSUS.F   RLVNGFLALVWDDLRNLCLFSYRHLRDLILIA.ARIV.......NRGLRRG.......WEALKLL.GN.LT    751
HIVBZ126Afr   --------------------------------.----.......-------.......--------.--.--    786
                                 *
CONSENSUS.G   R???GFL???WDDL?SLCLFSY??LRD??LIV.?RTVELLGR????????G.......WE?LKYL.WN.LL    706
HIVVI525A     -SAN---PLV----W-------RL---LL---.A--------.......R-.........--A-----.--.--    810
HIVLBV217     -LVS---SIA----R-------HQ---FI---.T--------NSLKGLRL-.........--G-----.--.--    808
                                                                          *  *
CONSENSUS.O   plPqGFL?lLYTDLRTIILWtYHLLSNLaSgI.........qklI?yLgLGLWIlGQktIeaCRlc?A.v?    727
HIVANT70      -S-----P-------------------------.........--V-S--R---------I-NV--I-A-.-T    807
HIVMVP5180    A--P---QQ-------------------I---.........RR--D--------------------G-.-M    820
HIVVAU        -------H------------I---------E-.........----RH-------I--R-------FK-.II    821
                                        *                                 *
CONSENSUS.CPZ ?L??G???L?WDDLRNLGIWSYQSLTSLACNV.WRQLKTLGHLILHSLRLL.......RERLCLL.GG.II    423
SIVCPZGAB     R-VE-CLP-I----------------------.------------------.......--------.--.--    798
                                 *
CONSENSUS.U   RLVnGFlALaWdDLRsLClFSYHRLRDlILIa.?r?VelLgr???????rG.......WEaLKyL.gN.Ll    719
HIVZAM184     ---S----------------------C-----.A-T-----HSSLKGLRL-.........--G--H-.W-.--    792
HIVK124A      ------S--I-----D----------------.T-I------.......--.........-------.--.--    803
HIVZ3fr       -----------E------I------------V....-KG-.-.......--.......--------.--.-V    792
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                <- rev cds
CONSENSUS.A     lyWGrELK?SAinLlDtiAiavAgwtDRvIEigQrigRAilnIPrRIRQGlEraLl   790
HIVSF1703       --------N-----------------------A-C-------------F-----   867
HIVU455         --------I---T---AV-V-----I--------T---------------------   855
HIVZ321         I---Q---N--------V-----D-------VV--A---F----------------   856
HIVRW020        --------T--V--V---------R------V----F----------------G--   844
HIVUG031fr      --------T-----F-----------------------I---------F-----   813
HIVUG275A       A-------I---S-F----VVI---------L---LC----H--------F-----   846
HIVUG273A       -F------I-------------------------------F----------F-----   855
HIVVI191A       --------I---T---AT-----R----I-------V-------------A-K--Q   854
HIVDJ264A       T---Q---N--------------N-----------V----R---V-----------   853
HIVDJ263A       ----Q---N----------L---N-----------V---------------------   861
HIVDJ258A       ----Q---N--V--------V--N----------EV---------------------   856
HIVKENYA        ----Q---I--S--V-----V-----------A-G------H--------F-----   855
                          ^^^
CONSENSUS.B     qYWsqElknsavsllnatAiaVaEgTDRvievvqra?RailhiprRiRQGleraLl   805
HIVJRCSF        ----------------------------I------VY-------T-----------   848
HIVJRFL         ----------------------------I--AL--TY-------T-----------   847
HIVALA1         -------------------------------L---F-------------F-----   849
HIVBRVA         ---------------------G-R---A-------F-----------------Q   852
HIVJH3          --------------F--I-----------LKIL---F-------T-----------   867
HIVBAL1         -------------------V------------L---V---------------------   855
HIVYU2          ---I----------------------------IL---F--V----V-----------   843
HIVMN           --------S-----------------------L---G-------T-----------   856
HIVHXB2R        ---------------------------------G-C---R------------I--   856
HIVLAI          ---------------------------------G-C---R------------I--   861
HIVNL43         ------------N--------------------L-A-Y---R------------I--   854
HIVMFA          ---------------------------------G-Y---R------------I--   854
HIVCAM1         -------R------FDTI-----------------C----------------L--   856
HIVNY5CG        ---G-------I-------V------------A--IC-G--------------L--   850
HIVADA          -------R-------------------------IY-------T---------L--   853
HIVJFL          ----------------------------I------IG-------V-----------   849
HIVSIMI84       ----------------T---V--------------IG--V----------F-----   856
HIVD31          ------------------------------------W-------V-----------   850
HIVSF162        ---I----------FD-I----------I---A--IG--F----------F-----   847
HIVBCSG3C       ------------N---V-----------------TY----------------L--   859
HIVOYI          ----------VI-------------------I----Y--F-N--------------   855
HIVSF33         L-----------------------------------VG-------T-----F-----   852
HIVCDC4         --------------V-V-----------------IY--F----------F-----   868
HIVSF2          ---I---------W--------T---------A---Y------H---------L--   855
HIVSF2B13       ---I---R-------------------------Y----------------L--   853
HIVHAN          --------------F-TI-----------------C---------V---------   855
HIVRF           ----------------T-----------I---A--IL--F----------------   865
HIVWMJ2         ----K-------G----I----------------IC---I---------------   847
HIVTB132        --------------------------------L--VY----N--T------KGR   835
HIVBR020        --------S----------V--------I--IA--FF-GF--------------Q   853
HIVTH014        ---I-------------------------------Y-------T-----------   845
HIVUS711fr      --------H--------------------------Y---I---T-----------   849
HIVUS712        --------S----------------------L--IG-------T-----------   852
HIVUS715        --------SG---------------------L---G-------------F-----   854
HIVUS716        --------S-----------V----------L---W-------T-----------   845
HIVHA593        ------------N--D------------I----R--F-------T-----------   875
HIVHA594        ------I--N-----S---------------II--IG-----V-T-----------   849
HIVHA596        ------I-----------------------II--IG-----V-T-----------   856
HIVHA599        ---------------------------I--G-RGVC------------------   866
HIVHA651        ---------------------------I--I----V--L-N--T-----------   850
HIVRJS          ---I                                                     801
HIVP896         ------------------------------KI----C---RN--T-----------   853
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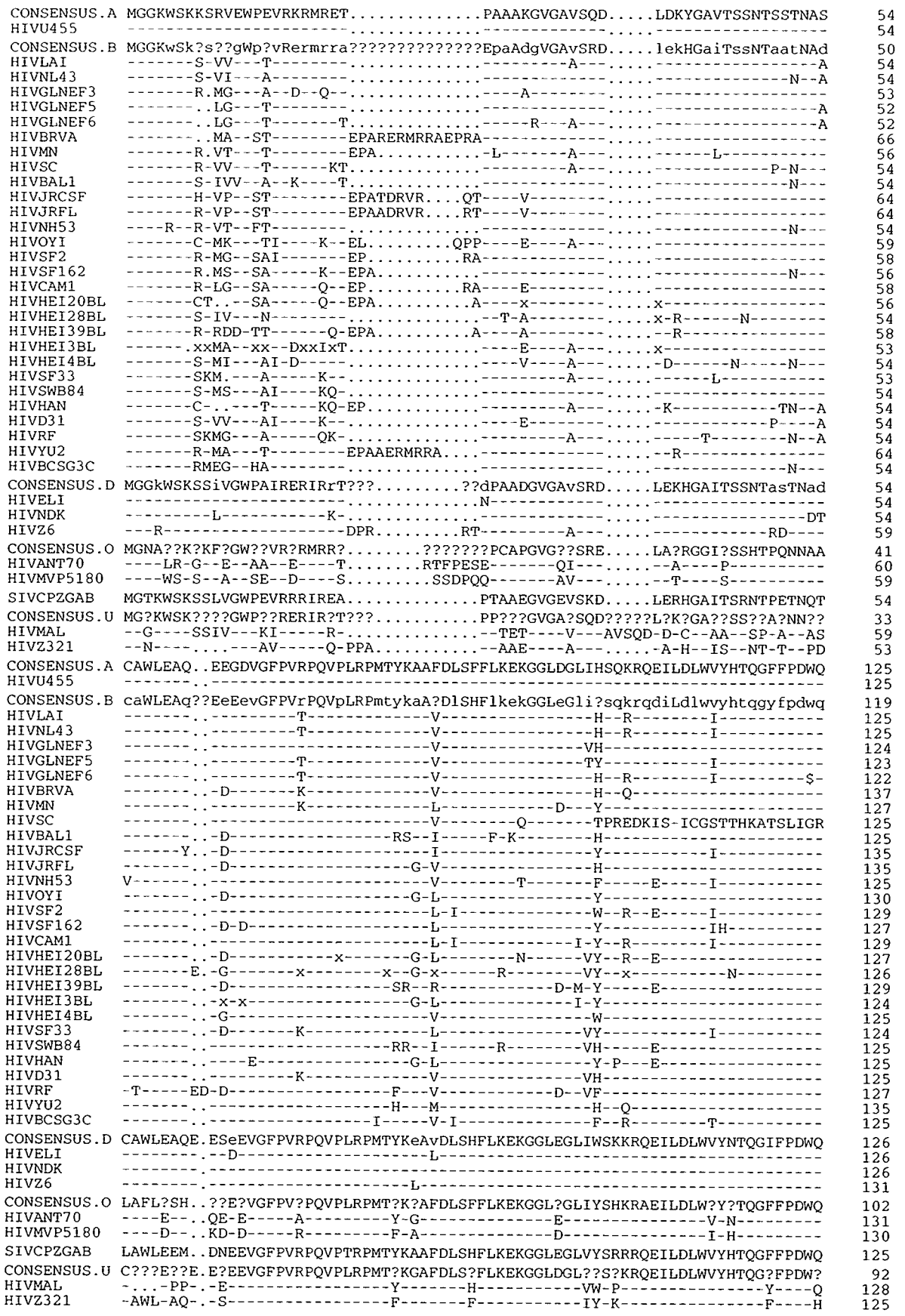
                <- rev cds
CONSENSUS.C     qYWGlElKKSAiSlldtiAIaVaEGTDRIie??Qri?Rai?nIPrRIRQGFEAALq   804
HIVMA959        L-----I------IV--L----------L-SL---G---R---A----------L   854
HIVMA960        L-----I-------V---------------LI--LG---Y--------------L   850
HIVZAM20A       ------------------------------LV---C---R------            875
HIVSM145A       --------------------T----------LA---C-GVR---T----------L   861
HIVZAM18A       --------------V-A---T----------FI---C---R------            848
HIVDJ259A       --------------N-T--T---------KFI-GLW---C----------------   832
HIVDJ373A       -----------V-----T------------II---W--FC----------------   843
HIVSE364A       ------I------------T----------LV---C---S----------------   841
HIVUG268A       ----Q-----------------S--------VG-G-G---LH--------------   856

CONSENSUS.D     qYWiqeLkNSaisL?dt?AIaVAEgTDRvIeivqRa?RA?L?iP?RiRQGlERaLL   784
HIVJY1          ---T------F---LNAT----------I--LIR--F--V-H--R-V---------   863
HIVNDK          ---S---R---S--L--I------R------V----C--I-NV-R--------L--   846
HIVMAL          ---G----------LN-T------C-------G--FG--I-H--R-----F-----   859
HIVELI          ---S---R---S--F-AI--------------I---C--V-N--R--------S--   853
HIVZ2Z6         ---SR------S--L--I---------------R--C--V-H--T--------L--   853
HIVUG024        --------------FN-T--V-------I--L---IG--I-N--T--------L--   850
HIVUG266A       ------------N-FN-T----------A-------V--I-N--T-----F-----   851
HIVUG269Afr     K-------------F--I--V----------VI---V--V-H--R-----F-----   853
HIVUG274Afr     --------------F--T----------I-------V--V-N--T-----------   864
HIVSE365A       -----K--------L--I----------I-DV----C--I-H--T-----------   851
                     ^^^
CONSENSUS.E     lYWgQELKISAISLlNATAIAVAGWTDrvIEVAQgaWRAILHIPRRIRQGLERALL   824
HIVTH966        ------------------------------------I--------------------   857
HIVTH975        V--S----------------------------------------------------   855
HIVTH022        --------------F-------------I-----R--------------------   855
HIVTN243        ----------------------------K-------------                 847
                     ^^^
CONSENSUS.F     LYWGQELKNSAISLLNTTAIVVTEGTDRIIAALQRIGRAILNIPTRIRQGFERALL   807
HIVBZ126Afr     ----------------------------------------------------------   842
                                                      *
CONSENSUS.G     ?YWGQELKNSAI?LL?T?AIA?A??TDRVIE??Q?ACRA?L?IPRRIRQG?ERALL   749
HIVVI525A       Q-----------H--N-T---V-EG------IV-I----V-H--------F-----   866
HIVLBV217       L-----------N--D-V---T-NW------VA-R----I-N--------L-----   864
                          ^^^
CONSENSUS.O     QYWLQELqnSATnLLDT?AVaVANWTDgiIlGiQrIG?GilnIPRRIRQGlER?Ll   780
HIVANT70        ------------S----L------------A------T--R-----------S--   863
HIVMVP5180      -------K---------I--S-----------L----Q-F-H--------A--I-V   876
HIVVAU          --------T--------V---------ST-----S--R--------------L--   877

CONSENSUS.CPZ   QYWGKELKISAISLLDATAIAVAEGTDRIIEAFQVTLRIIRNIPRRIRQGLERALL   479
SIVCPZGAB       ----------------------------------------------------------   854
                                                      *
CONSENSUS.U     lYWgqELKNSAISLldtiAivVAewTDrIIeiGQR?cRAilnIPrRIRQGFERALL   774
HIVZAM184       --------------------A--------------A----R---T-----------   848
HIVK124A        Q--TR---------V----V---G---S--K----LG--F-H--------------   859
HIVZ3fr         ---------------NAT------G------V---I--------------------   848
```



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CONSENSUS.A NYTPGPGIRYPLTFGWCYKLVPVDPAEVE.EATGGENNSLLHPICQHGVDDEEKEVLMWKFDSTLALKHRAYE 197
HIVU455     ----------------------------.---------------------------------------- 197
CONSENSUS.B nytpGpG?ryPLtfGWCfKLVPvepekvE.eanegennsLlHPmslHGmddpe?evL?WrFDsrlAfhHmARe 188
HIVLAI      -------V---------Y-------D---.---K---T-----V---------R---E----------V--- 197
HIVNL43     -------V---------Y-------D---.---K---T-----V---------R---E----------V--- 197
HIVGLNEF3   ---S---V-F---------------D---.---K---T-----V---------RG--E----------V--- 196
HIVGLNEF5   KD-----V-------------------I-.---K---------------E-A-G---E-K----------- 195
HIVGLNEF6   -------V---------Y-------D---.---K---T-----V---------R---E----------V--- 194
HIVBRVA     -------V-------------------I-.---------------Q-------R---Q--------------- 209
HIVMN       -------I-------------------I-.---K----C------Q--WMTRREKC                  182
HIVSC       TTHQ-Q-SDI--C----------K---I-.--------------------E---R---E----N---------D 197
HIVBAL1     -------T-F-----------------.--------C-S-----------K---A-K---S-----V--- 197
HIVJRCSF    ---A---V-F-------------D-----.--------C------Q-------K---V-K---K--L--V--- 207
HIVJRFL     -------I-F-----------------.--------C------Q--IE---K---E-----K-----V--- 207
HIVNH53     -------I---------------G-DE--.......-S-----A----TE-T-R---K-----H---------- 191
HIVOYI      -------I----C---------MD-DQ--.-------------I---------K---V-K-------R----- 202
HIVSF2      -------I-------------------.------------------E-A-K---V-----K--------- 201
HIVSF162    -------I---------------D-DY--.---A-----------Q-------K---V--------------- 199
HIVCAM1     -------I-------------------Q--.---KR--A-------Q-------K---M-K------------- 201
HIVHEI20BL  -------I---------------D--Q--.K-------C------Q---x---K-x-M-K----x-xx----- 199
HIVHEI28BL  -------V-W-------------A-----.--------K---------x----R---V-K------Y------ 198
HIVHEI39BL  -------T---------------D-D---.-D-K----C------Q-------K---Q-K---Q-----V--- 201
HIVHEI3BL   -------V-----------------xE--.K-----R-C----x-----E-T-G---R-K---x-----V--- 196
HIVHEI4BL   -------V-F-------------x---x-.-------x------I-----E---N---E------------- 197
HIVSF33     -------V-F-------------------.-------------------E---K---V-K---H---R----- 196
HIVSWB84    -------T-W---P---------------.-------------------E---K---V-K---S-----K--- 197
HIVHAN      -------V-----------------D..-.-.....-S-----A----TE-T-R---K-K---H-----K--- 191
HIVD31      -------T-F-------------K--Q--.---------------------R---V---------K----- 197
HIVRF       -------T-----------------D---.--T----------IC--------K---V-K---------V--- 199
HIVYU2      -----.-T-W-----------------I-.---A----C------Q-------R-G-E----------V--- 206
HIVBCSG3C   -------I---------------D---I-.---------------Q-------R---E--------------- 197
CONSENSUS.D NYTPGPGIRYPLTFGWCfeLVPVDPqEVE.EaTEgEtNcLLHP?CQhGMEDpERqVLkWRFNSRLAfEHKARE 197
HIVELI      ----------------Y-----------.-D------S----I---------------------------- 198
HIVNDK      ----------------Q----------.----R-D------M--Q----------M--------L------ 198
HIVZ6       ------------------------R---.-------------V-------T--E---------------- 203
CONSENSUS.O ?YTPGPG?RFPLTFGWLFKLVPVS?EEAERLGNT?E?A?LLHPAC?HG?ED?H?EIL?W?FDRSLG?TH?A?? 159
HIVANT70    N------T---------------E---------C-R-N------A--F--T-K---M-K------N--V-MI 204
HIVMVP5180  C------P---------------A---------N-D-S------N--A--A-G---K-Q------L--I-LQ 203
SIVCPZGAB   NYTTGPGTRFPLCFGWCFKLVPLTEEQVE.QANEGDNNCLLHPICQHGMEDEDKEVLVWRFDSRLALRHIARE 197
CONSENSUS.U NYTPGPG?R?PL?FGWCFKLVP??P?EVE.EAN?GENNCLLHP?SQHGM?D?EREVL?WKFDSSLA??H?ARE 150
HIVMAL      -------I-F--T---------MS-E---.---E---------I-----E-A-----K---------LR-R--- 200
HIVZ321     -------T-Y--C---------VD-R---.---T---------M-----D-D-----M--------RK-L--- 197
CONSENSUS.A LHPEFY.KD                                                               205
HIVU455     ------.--                                                               205
CONSENSUS.B lHpEyy.KdcLTSMCLQGTFRWGISREARLGGTGEWRALRCCI                             230
HIVLAI      -----F.-N-                                                              206
HIVNL43     -----F.-N-                                                              206
HIVGLNEF3   -----F.-N-                                                              205
HIVGLNEF5   K----F.-N-                                                              204
HIVGLNEF6   -----F.-N-                                                              203
HIVBRVA     ------.-N-                                                              218
HIVSC       ------.-------------------------------------                           239
HIVJRCSF    ------.---                                                              216
HIVJRFL     ------.---                                                              216
HIVNH53     ------.---                                                              200
HIVOYI      V-----.---                                                              211
HIVSF2      ------.---                                                              210
HIVSF162    ------.---                                                              208
HIVCAM1     K---F-.---                                                              210
HIVHEI20BL  x---F-.---                                                              208
HIVHEI28BL  --x---.---                                                              207
HIVHEI39BL  ------.---                                                              210
HIVHEI3BL   ------.-                                                                203
HIVHEI4BL   ------.---                                                              206
HIVSF33     ------.---                                                              205
HIVSWB84    ------.---                                                              206
HIVHAN      ------.---                                                              200
HIVD31      ------.-N                                                               205
HIVRF       K-----.---                                                              208
HIVYU2      ------.-N                                                               214
HIVBCSG3C   ------.-NR                                                              206
CONSENSUS.D mHPEFY.KdC                                                              206
HIVELI      ------.-N                                                               206
HIVNDK      L-----.---                                                              207
HIVZ6       ------.---                                                              212
CONSENSUS.O ?HPELF?KD                                                               166
HIVANT70    T-----Q--                                                               213
HIVMVP5180  K-----P-                                                                211
SIVCPZGAB   QHPEYY.KD                                                               205
CONSENSUS.U ?HPE?Y.KDC                                                              157
HIVMAL      Q---Y-.---                                                              209
HIVZ321     M---F-.--                                                               205
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CONSENSUS.A MGArNSVLRGKKADELEkiRLRPgGKKkYrLKHiVWAANeLDrFGLaESLLESKEGCQkIltVLdPlVPTGSE     73
HIV2ROD     ----------------R--------------------K-------------------------M------     73
HIV2NIHZ    ---------------------------K-------------------------------------------     73
HIV2ISY     ---K-----------------------------------------T-------------IS--E--------     73
HIV2ST      ---------------------------------------------------------------------------     73
HIV2BEN     ------------------V----------------------K-----------------R-----------     73
HIV2CAM2    ------------------V----------K-------------------------R--K-----------     73
HIV2D194    ------------------V----N---R-----V-------------------------K--E--------     73
HIV2GH1     ----------------------S-------------------K-------------------------------     73
HIV27924A                                          ---------------------R-IS-----------     36
HIV260415K                                         ----------------------R-------------     36
HIV2FA                                             ----------------------I---N--------     36
CONSENSUS.B MGAR?SVLSGKKTDELEKVRLRPGGKK?Y?LKH??WAvNELdRFGLAE?LLeSKEGChKILtvLaPLvPTGSE     67
HIV2D205    ----G----------------------K-M---VV-------------S--------Q---K-----------     73
HIV2UC1     ----S----------------------R-C---II-------------S-------------------------     73
HIV260667K                                         ----E------N--G---------A--E--------     36
HIV2JA                                             ----------S-------------------------     36
HIV27312A                                          A----------N--------Q---------M-----     36
HIV2FT                                             ----------T-------------------------     36
HIV27810A                                          A----------T--G----------A----------     36
HIV2ON                                             ----------R-------------------------     36
CONSENSUS.C                                        ANELDRFALAESLLETKEGCQKILTVLEPLVPTGSE     36
HIV22238                                           ----------------------------------------     36
CONSENSUS.D MGaRnSVLSGKkADELEKiRLRPgGKKkYmLKHvVWAANELDRFGLAESLLenKEGCQKIlsVLaPLVPTGSE     73
SIVMM251    ---------------------------------------------------------------------------     73
SIVMM32H    ---------------------------------------------------------------------------     73
SIVMM1A11   ----------------------N----------------------------------------------------     73
SIVMM142    ---------------------------------------------------------------------------     73
SIVMM239    --V--------------------N----------------------------------------------------     73
SIVMNE      ---------------------------------------------------------------------------     73
SIVSMMH4    -----------E------V----N-------------------------D--------------------------     73
SIVSMMH9    --V-----------------------------I---------------------------------------------     73
SIVSMMPBJ   ----------------------------R-Q---I---------------------------------------------     73
SIVSTM      ----S-------------V-----------------------------------S--------IT--E--------     73
SIVSTM22579 ----S-------------V-----------------------------------S---------T--E--------     73
HIV2FO784                                          ----------------------------------------     36
CONSENSUS.E                                        ARELDRFGLAESLLENKEGCHRILTVLEPLMPTGSE     36
HIV2PA                                             ----------------------------------------     36

                                                                                p16 \/ p28
CONSENSUS.A NLkSLfNTvCViWCiHAEEKvKDTEeAk?ivq.RHLvAETgTaEKMPntSRPTAPpSgkggNfPVQq?gG?NY    142
HIV2ROD     ------------------------G--Q--R.--------------S-------S-E----Y---HV--.--    144
HIV2NIHZ    ------------------------G--Q---.-------------------------..------VA-.--    142
HIV2ISY     -----Y--T-----L-------------R--G.-------E--------I-----------------I--.--    144
HIV2ST      --------------------A--------QK--.-------K-T----S----------N--------VA-.--    144
HIV2BEN     --------------L-------------KLA-.--------------------------R--Y----A--.--    144
HIV2CAM2    ----------------------------R-AL.---A----------D--------------Y---SI--.--    144
HIV2D194    --------------L-------------KLA-.----------------I------------------A--.--    144
HIV2GH1     --------------L-------------KL--.---G----------S----------R-R------T--G--    145
HIV27924A   -----------V----------------K---.-----------------------------Y---SI--.--    107
HIV260415K  -----------A-------------G--Q---.--------------S----------E-------HV--.--    107
HIV2FA      --Q-----------L------------RKL--.-------------------------S--------T--G--    108
CONSENSUS.B NLKSLFNtVCViyCLHAeeKVKDTEEAKKiAQ.sHL?v...dtEKmPats?ptAppSG..rNYPVQQvAG.NY    131
HIV2D205    -------I----F-------------------.R--AA...--------NK--------..G------L--.--    139
HIV2UC1     ----------------------------------.R--AA...---------R--------..G------I--.--    139
HIV260667K  ----------------G--------------.R--VG...N--------R----S--..G------I--.--    102
HIV2JA      -----------V---------------------.---A-...N---T----R--------..----------.--    102
HIV27312A   ------------W-----K----------L--.---V-...----T-TADK-A-TS--..----------.--    102
HIV2FT      ------------F-----Q-------------.---V-...-A--V----KS------..----------.--    102
HIV27810A   -----------V---------------------.---AA...N--------K--------..----------.--    102
HIV2ON      --------------------------M--.---V-...-A--T----R--------..----------.--    102
CONSENSUS.C NLKSLYNTTCVIWCLHAEQKVKHTEERNEVVE.RHLAAETKNAEKMPATSRPTAPSSGGRGNYPVQQVAG.NY    107
HIV22238    ----------------------------.----------------------------------------.--    107
CONSENSUS.D NLKSLyNTVcViWCiHAEEKVKhTEeAKQiVq.RHLVvETGTae?MPkTSRPTAPpSgrGgNYPVQQ?GG.NY    142
SIVMM251    ---------------------------------.----------T----------S----------I--.--    144
SIVMM32H    ---------------------------------.----------T----------S----------I--.--    144
SIVMM1A11   ---------------------------------.----------I----------S----------I--.--    144
SIVMM142    ---------------------------------.----M------T----------F----------I--.--    144
SIVMM239    ---------------------------------.---------T-T----------S----------I--.--    144
SIVMNE      ---------------------------------.----------T----------S----------V--.--    144
SIVSMMH4    ---------------------------------.----------DR--A------------------V--.--    144
SIVSMMH9    ---------R-L--------------------.----------DK--A------------------V--.--    144
SIVSMMPBJ   ----------L--------------------.----------DK--A----------K--------I--.--    144
SIVSTM      -----F----------------------V-K.----------NK--A------------------V--.--    144
SIVSTM22579 -----F----------------------V-K.----------DK--A------------------V--.--    144
HIV2FO784   ---------------L-------D--G------.----------DK--S---------D--R------V--.--    107
CONSENSUS.E NLKSLFNAVCVVYCLHAAVKVKDTEEAKKHVQQHHLVAGGKTTEKLPPQSRPTAPPSGGGGNYPVQQIGN.NY    108
HIV2PA      ---------------------------------------------------------------------.--    108
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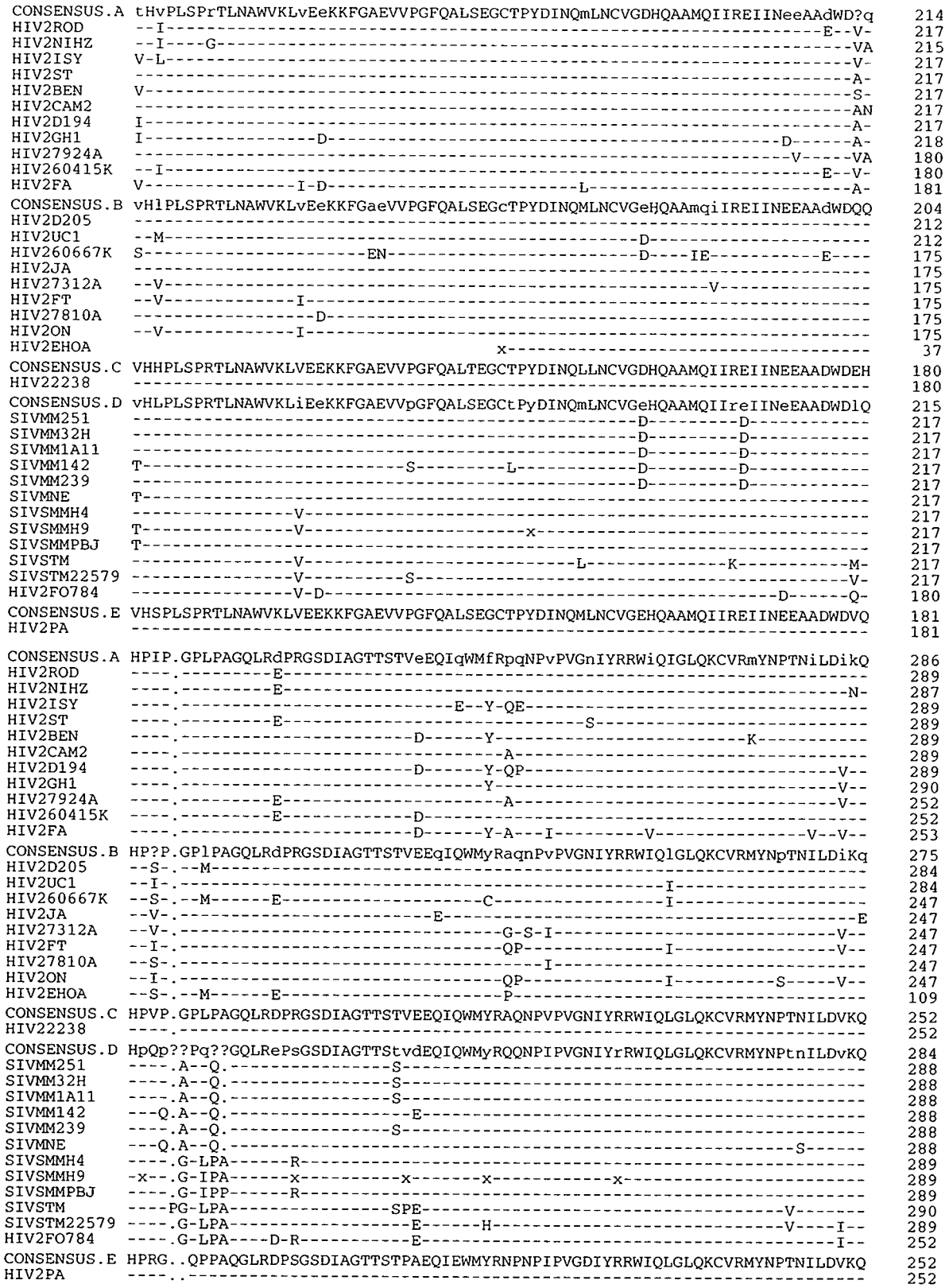
HIV2/SIV GAG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HIV2ROD --I---------- 217
HIV2NIHZ --I----G---------- 215
HIV2ISY V-L---------- 217
HIV2ST ---------- 217
HIV2BEN V---------- 217
HIV2CAM2 ---------- 217
HIV2D194 I---------- 217
HIV2GH1 I----------D---------- 218
HIV27924A ---------- 180
HIV260415K --I---------- 180
HIV2FA V----------I-D----------L---------- 181
CONSENSUS.B vHlPLSPRTLNAWVKLvEeKKFGaeVVPGFQALSEGcTPYDINQMLNCVGeHQAAmqiIREIINEEAAdWDQQ 204
HIV2D205 ---------- 212
HIV2UC1 --M----------D---------- 212
HIV260667K S----------EN----------D----IE----------E---- 175
HIV2JA ---------- 175
HIV27312A --V----------V---------- 175
HIV2FT --V----------I---------- 175
HIV27810A ----------D---------- 175
HIV2ON --V----------I---------- 175
HIV2EHOA x---------- 37
CONSENSUS.C VHHPLSPRTLNAWVKLVEEKKFGAEVVPGFQALTEGCTPYDINQLLNCVGDHQAAMQIIREIINEEAADWDEH 180
HIV22238 ---------- 180
CONSENSUS.D vHLPLSPRTLNAWVKLiEeKKFGAEVVpGFQALSEGCtPyDINQmLNCVGeHQAAMQIIreIINeEAADWDlQ 215
SIVMM251 ----------D---------D---------- 217
SIVMM32H ----------D---------D---------- 217
SIVMM1A11 ----------D---------D---------- 217
SIVMM142 T----------S---------L----------D---------D---------- 217
SIVMM239 ----------D---------D---------- 217
SIVMNE T---------- 217
SIVSMMH4 ----------V---------- 217
SIVSMMH9 T----------V----------x---------- 217
SIVSMMPBJ T---------- 217
SIVSTM ----------V----------L----------K----------M- 217
SIVSTM22579 ----------V----------S----------V- 217
HIV2FO784 ----------V-D----------D------Q- 180
CONSENSUS.E VHSPLSPRTLNAWVKLVEEKKFGAEVVPGFQALSEGCTPYDINQMLNCVGEHQAAMQIIREIINEEAADWDVQ 181
HIV2PA ---------- 181
CONSENSUS.A HPIP.GPLPAGQLRdPRGSDIAGTTSTVeEQIqWMfRpqNPvPVGnIYRRWiQIGLQKCVRmYNPTNiLDikQ 286
HIV2ROD ----.---------E---------- 289
HIV2NIHZ ----.---------E----------N- 287
HIV2ISY ----.----------E--Y-QE---------- 289
HIV2ST ----.---------E----------S---------- 289
HIV2BEN ----.----------D------Y----------K---------- 289
HIV2CAM2 ----.----------A---------- 289
HIV2D194 ----.----------D------Y-QP----------V-- 289
HIV2GH1 ----.----------Y----------V-- 290
HIV27924A ----.---------E----------A----------V-- 252
HIV260415K ----.---------E----------D---------- 252
HIV2FA ----.----------D------Y-A---I---------V----------V--V-- 253
CONSENSUS.B HP?P.GPlPAGQLRdPRGSDIAGTTSTVEEqIQWMyRaqnPvPVGNIYRRWIQlGLQKCVRMYNpTNILDiKq 275
HIV2D205 --S-.--M---------- 284
HIV2UC1 --I-.----------I---------- 284
HIV260667K --S-.--M------E----------C----------I---------- 247
HIV2JA --V-.----------E----------E 247
HIV27312A --V-.----------G-S-I----------V-- 247
HIV2FT --I-.----------QP----------I----------V-- 247
HIV27810A --S-.----------I---------- 247
HIV2ON --I-.----------QP----------I----------S-----V-- 247
HIV2EHOA --S-.--M------E----------P---------- 109
CONSENSUS.C HPVP.GPLPAGQLRDPRGSDIAGTTSTVEEQIQWMYRAQNPVPVGNIYRRWIQLGLQKCVRMYNPTNILDVKQ 252
HIV22238 ---------- 252
CONSENSUS.D HpQp??Pq??GQLRePsGSDIAGTTStvdEQIQWMyRQQNPIPVGNIYrRWIQLGLQKCVRMYNPtnILDvKQ 284
SIVMM251 ----.A--Q.----------S---------- 288
SIVMM32H ----.A--Q.----------S---------- 288
SIVMM1A11 ----.A--Q.----------S---------- 288
SIVMM142 ---Q.A--Q.----------E---------- 288
SIVMM239 ----.A--Q.----------S---------- 288
SIVMNE ---Q.A--Q.----------S------ 288
SIVSMMH4 ----.G-LPA------R---------- 289
SIVSMMH9 -x--.G-IPA------x----------x-------x----------x---------- 289
SIVSMMPBJ ----.G-IPP------R---------- 289
SIVSTM ----PG-LPA----------SPE----------V------- 290
SIVSTM22579 ----.G-LPA----------E------H----------V----I-- 289
HIV2FO784 ----.G-LPA----D-R----------E----------I-- 252
CONSENSUS.E HPRG..QPPAQGLRDPSGSDIAGTTSTPAEQIEWMYRNPNPIPVGDIYRRWIQLGLQKCVRMYNPTNILDVKQ 252
HIV2PA ----..---------- 252

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CONSENSUS.A GPKEpFQSYVDRFYKSLRAEQTDpAVKNWMTQTLL?QnaNPDCKLVLKGLGmNPTLEEMLTaCQGvGGPgQKA  358
HIV2ROD     ------------------------------------V-------------------------------------  362
HIV2NIHZ    ------------------------------------I-----------------------T-------------  360
HIV2ISY     ----S-------------------A-----------V-.S---------------------------I-------  361
HIV2ST      ------------------------------------V---------------I---------------------  362
HIV2BEN     ------------------------------------I-------------------------------------  362
HIV2CAM2    ----S-------------------------------V-------------------------------------  362
HIV2D194    ----S-------------------------------I---------------------------------S---  362
HIV2GH1     ------------------------------------I-------------------------------------  363
HIV27924A   ----S---                                                                     260
HIV260415K  --------                                                                     260
HIV2FA      ----S---                                                                     261
CONSENSUS.B GPKEPFQsYVDRFYKSLRAEQTDPAVKNWMTQTLLIQNANPDCKLVLKGLGMNPTLEEMLTACQGIGGPGQKA  348
HIV2D205    ------------------------------------------------------------------------  357
HIV2UC1     ------------------------------------------------------------------------  357
HIV260667K  -------N                                                                     255
HIV2JA      --------                                                                     255
HIV27312A   --------                                                                     255
HIV2FT      --------                                                                     255
HIV27810A   --------                                                                     255
HIV2ON      --------                                                                     255
HIV2EHOA    ------------------------------------------------------------------------  182
CONSENSUS.C GPKEPFQS                                                                     260
HIV22238    --------                                                                     260
CONSENSUS.D GPKEpFQSYVDRFYKSLRAEQtDpavKNWMTqTlLIQNANPDCKLVLKGLg?NPTLEEMLTACQGVgGPGQKa  356
SIVMM251    ----------------------A---------------------------V---------------------  361
SIVMM32H    ----------------------A---------------------------V---------------------  361
SIVMM1A11   ----------------------A---------------------------V---------------------  361
SIVMM142    ------------------------------------------------T---------------------  361
SIVMM239    ----------------------A---------------------------V---------------------  361
SIVMNE      ------------------------------------------------M---------------------  361
SIVSMMH4    ------------------------------------------------M---------------------  362
SIVSMMH9    ----S-------------------x-----------------------xI--------------x-----x  362
SIVSMMPBJ   ------------------------------------------------I---------------------  362
SIVSTM      ----T----------------A--S------R-----------------M---------------------  363
SIVSTM22579 --------------------A-----------P-----------------M---------------------  362
HIV2FO784   ----T---                                                                     260
CONSENSUS.E GPKESFQS                                                                     260
HIV2PA      --------                                                                     260

          p28 \/       p2       \/ p8                                      pol cds ->
CONSENSUS.A RLMAEALKEam?PaPIPFAAAQQ....r?aikcWNCGKEGHSArQcrAPRRQGCWKCGK?GHiManCP?RQAG  423
HIV2ROD     ---------VIG-----------....-K-F-----------------------------P----T---D----  431
HIV2NIHZ    ---------V-A-----------....-KTF--------------WS------------S--V-----D----  429
HIV2ISY     ----------R-----------....KR-------------------------------S--------D----  430
HIV2ST      ----------A-----------....-RT-----------------------------A-----K--E----  431
HIV2BEN     ----------G-S----------....-K--RY--------------------------P--------E----  431
HIV2CAM2    ----------G-P----------....-RT-----------------------------P----T---D----  431
HIV2D194    ----------LT-----------....-R--R-----------K---------------S--------E----  431
HIV2GH1     ----------LT-P---------....-KV-R-------------------------T--V--K--E----  432
CONSENSUS.B RLMAEALKEALTPapiPFAAaQqkAGkrgTVTCWNCGK?GHTArQCrAPRRQGCWKCGkqGHIMSKCPERQAG  420
HIV2D205    -------------------V-----------------Q-------------------T-------------  430
HIV2UC1     ----------------------------------V----K-----------------------------  430
HIV2EHOA    -------------STN------PR--.KR---------A-------K-----------Q-------------  254
CONSENSUS.D RLMAEALKealap?plPFaAaQq?Gp?rkpikCwNCgKeGHsArQcraPRRqGCWKCGkmgHvMAKCP?RQaG  425
SIVMM251    -------------V-I------KR--.-------------------------------D-------D----  433
SIVMM32H    -------------V-I-------R--.-------------------------------D-------D----  433
SIVMM1A11   -------------V-I-------R--.-------------------------------D-------D----  433
SIVMM142    -------------A-I-------K--.-------------------------------D-------N----  433
SIVMM239    -------------V-I-------R--.-------------------------------D-------D----  433
SIVMNE      -------------G---------K--.-----------------T----------Q---------D----  433
SIVSMMH4    -----------R-DQ-----V--K-.Q--T-------------K---------------T--------E----  434
SIVSMMH9    --------D--TQG----x-V--K-.Qx-I-x-x--x--------F-----x-------A--------E----  434
SIVSMMPBJ   --------D--TQG------V--K-.Q--I-----------------------------A--------E----  434
SIVSTM      ---------VFQ-D---------Q-..-RTV-------A--T-K--KG----------QQ--Q-----E--V-  434
SIVSTM22579 ----------FQ-G---------Q-..-RTV----------T-K--K-----------P--Q-----E--V-  433
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HIV2/SIV GAG

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        p8 \/     p1     \/ p6                                  \/ HIV2s only
CONSENSUS.A FLGlGpwGKkpRNFPvaq?pqGL.................tPTAPP?DPavdLLEkYMQQG?rQRE.Q...R    471
HIV2ROD     ------------------V----.................------V--------------K----.-...-    482
HIV2NIHZ    ---I-H----A----A--V----.................------L--------------K----.-...-    480
HIV2ISY     ----------------VPSS---.................------M--------------RK---.-...-    481
HIV2ST      ------------------I----.................------I--VE----------K----.-...-    482
HIV2BEN     ------R---------T-A----.................I-----A---AE---R-----RK---.-...-    482
HIV2CAM2    ---I--------------V----.................------L--------------K----.-...-    482
HIV2D194    ---M--R--Q-----A--A----.................I-----I--------------RK---.-...-    482
HIV2GH1     ---M--------------A-P--.................I-----A--------R-----RE---.-...-    483
CONSENSUS.B FLGlGPWGKKPRNFPmtQvPQGvtPSAPPMnPAeGMTPrGAtPSAPPADPAvEMLKsYMqmGrqqre????sR    489
HIV2D205    ------------------------------------------------------------------....--    499
HIV2UC1     ----------------------------D-------------------------K-------....--    499
HIV2EHOA    ---F-----------.V-A---IV---------F----Q--I---------E----N---L-K....KQKEN-    322
CONSENSUS.D FLGlGPWGKKPrNFPMAQ?hQGL?????????.........tpTApPedPAvDLLknYMqlGkqQRE????sr    475
SIVMM251    ------------------V----.................-------------------------....--    484
SIVMM32H    ------------------V----.................-------------------------KQRE--    488
SIVMM1A11   ------------------V----.................-------------------------KQRE--    488
SIVMM142    ------------------V----.................-------E----------H-------....--    484
SIVMM239    ------------------V----.................M-------------------------KQRE--    488
SIVMNE      ---F--------------M----.................-------------------------....-K    484
SIVSMMH4    ------------------MP---.................I----------------KM-RK---....N-    485
SIVSMMH9    ------------------MP---.................----x------------KV-RR---....N-    485
SIVSMMPBJ   ------------------MP---.................----------------KM-RR---....N-    485
SIVSTM      ---F-------H------IP---.................----------A---RS------K---....--    485
SIVSTM22579 ---F--------------IP---TPTAPPEMP.....----V---A---RS------K---....--    491

                        \/ HIV2s only          /p6
CONSENSUS.A eRPYKEVTEDlLhlEqgetPhRe?tTEDLLHLNSLFGkDQ                                  510
HIV2ROD     --------------------Y--PP---------------                                  522
HIV2NIHZ    ------------RF--A---C--.----------------                                  519
HIV2ISY     Q----------------------.-------------N--                                  520
HIV2ST      ----------F-Q--KQ---C--.-----------------                                 521
HIV2BEN     ---------------R-------.E---------------                                  521
HIV2CAM2    Q-----------------A-C--.----------------                                  521
HIV2D194    ----------------------G.A---------------                                  521
HIV2GH1     -----------------KA----.A---------------                                  522
CONSENSUS.B ERPYKEV.................TEDLLHLNSLFGEDQ                                  511
HIV2D205    -------.................---------------                                  521
HIV2UC1     -------.................---------------                                  521
HIV2EHOA    -------.................---------------                                  344
CONSENSUS.D ekPYKEv.................TEDLlHLNSLFG?DQ                                  496
SIVMM251    -------.................------------G--                                  506
SIVMM32H    -------.................------------G--                                  510
SIVMM1A11   ------M.................------------G--                                  510
SIVMM142    G------.................------------G--                                  506
SIVMM239    -------.................------------G--                                  510
SIVMNE      R------.................------------E--                                  506
SIVSMMH4    -R-----.................------------E--                                  507
SIVSMMH9    -R-----.................------------E--                                  507
SIVSMMPBJ   -R-----.................------------E--                                  507
SIVSTM      KT-----.................------------E--                                  507
SIVSTM22579 KT-----.................----V--------                                   510
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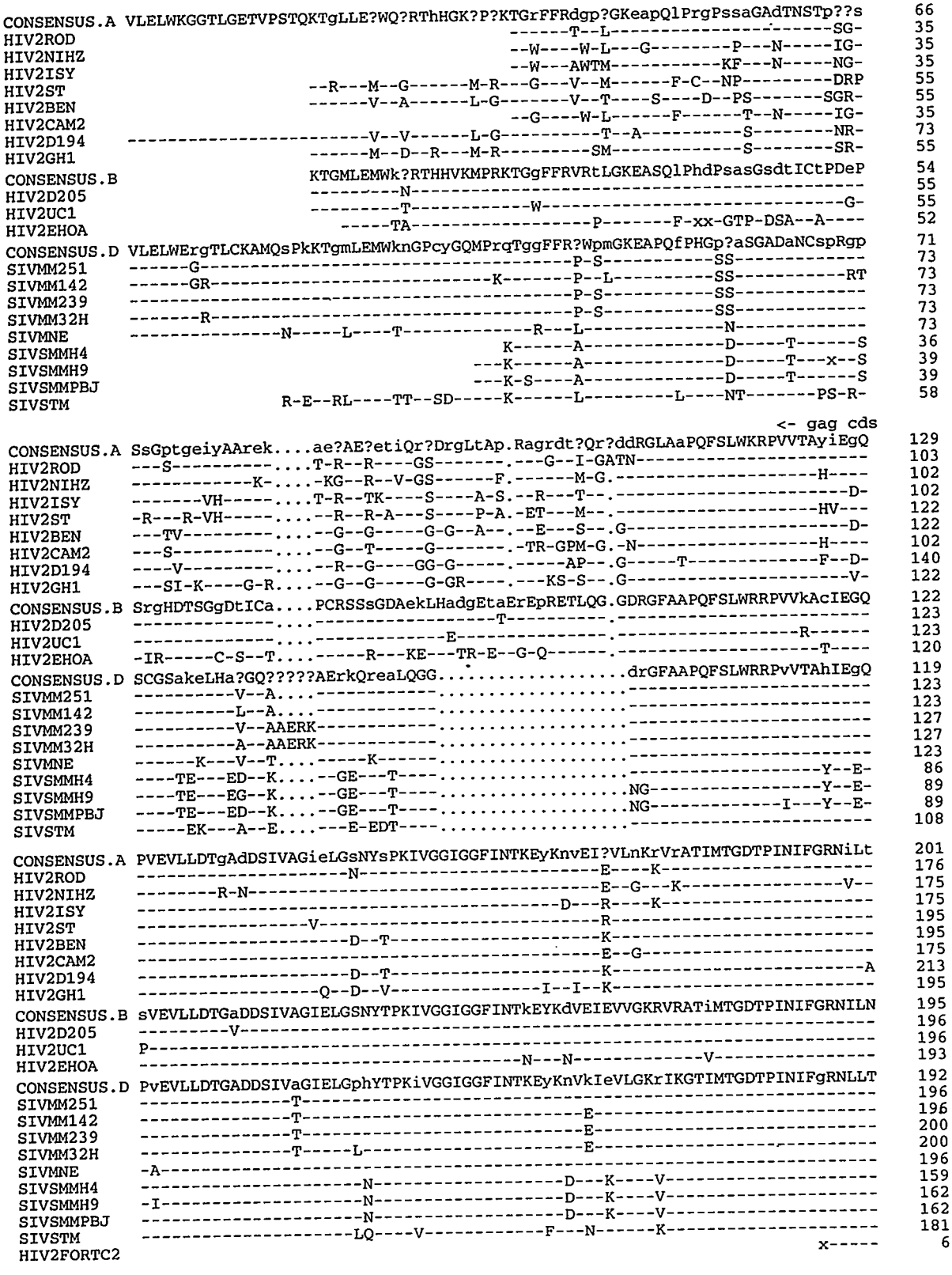
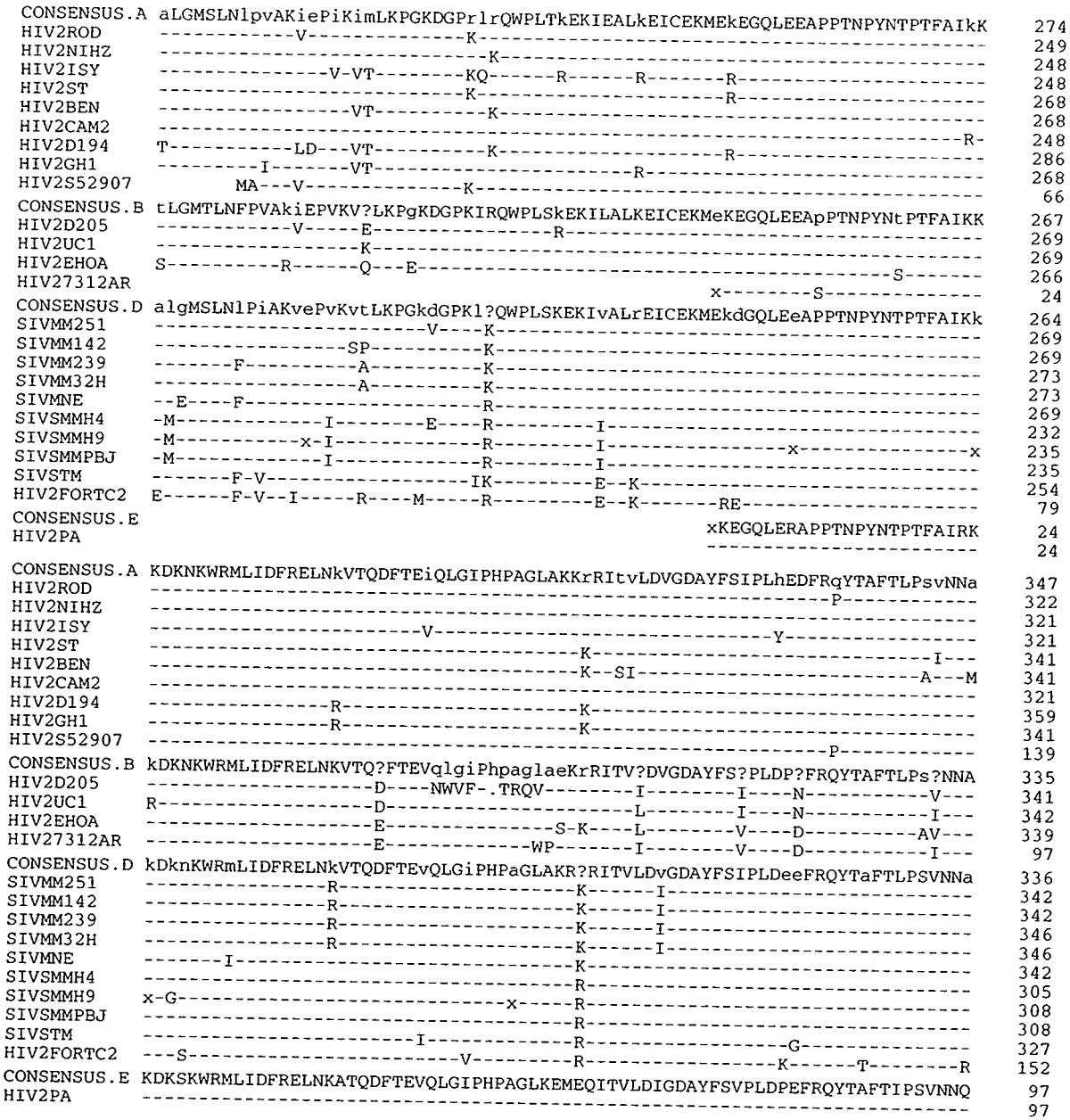


HIV2/SIV POL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HIV2ROD ----------V----------K---------- 249
HIV2NIHZ ----------K---------- 248
HIV2ISY ----------V-VT--------KQ------R------R-------R---------- 248
HIV2ST ----------K----------R---------- 268
HIV2BEN ----------VT----------K---------- 268
HIV2CAM2 ----------R- 248
HIV2D194 T----------LD---VT----------K----------R---------- 286
HIV2GH1 ---------I-------VT----------R---------- 268
HIV2S52907 MA---V----------K---------- 66
CONSENSUS.B tLGMTLNFPVAkiEPVKV?LKPgKDGPKIRQWPLSkEKILALKEICEKMeKEGQLEEApPTNPYNtPTFAIKK 267
HIV2D205 ----------V-----E----------R---------- 269
HIV2UC1 ----------K---------- 269
HIV2EHOA S----------R------Q---E----------S------- 266
HIV27312AR x--------S---------- 24
CONSENSUS.D algMSLNlPiAKvePvKvtLKPGkdGPKl?QWPLSKEKIvALrEICEKMEkdGQLEeAPPTNPYNTPTFAIKk 264
SIVMM251 ----------V----K---------- 269
SIVMM142 ----------SP----------K---------- 269
SIVMM239 -------F----------A----------K---------- 273
SIVMM32H ----------A----------K---------- 273
SIVMNE --E----F----------R---------- 269
SIVSMMH4 -M----------I--------E----R---------I---------- 232
SIVSMMH9 -M----------x-I----------R---------I----------x----------x 235
SIVSMMPBJ -M----------I----------R---------I---------- 235
SIVSTM -------F-V----------IK---------E--K---------- 254
HIV2FORTC2 E------F-V--I-----R----M-----R---------E--K-------RE---------- 79
CONSENSUS.E xKEGQLERAPPTNPYNTPTFAIRK 24
HIV2PA ---------- 24
CONSENSUS.A KDKNKWRMLIDFRELNkVTQDFTEiQLGIPHPAGLAKKrRItvLDVGDAYFSIPLhEDFRqYTAFTLPsvNNa 347
HIV2ROD ----------P---------- 322
HIV2NIHZ ---------- 321
HIV2ISY ----------V----------Y---------- 321
HIV2ST ----------K----------I--- 341
HIV2BEN ----------K--SI----------A---M 341
HIV2CAM2 ---------- 321
HIV2D194 ----------R----------K---------- 359
HIV2GH1 ----------R----------K---------- 341
HIV2S52907 ----------P---------- 139
CONSENSUS.B kDKNKWRMLIDFRELNKVTQ?FTEVqlgiPhpaglaeKrRITV?DVGDAYFS?PLDP?FRQYTAFTLPs?NNA 335
HIV2D205 ----------D----NWVF-.TRQV--------I--------I----N----------V--- 341
HIV2UC1 R----------D----------L--------I----N----------I--- 342
HIV2EHOA ----------E----------S-K----L--------V----D----------AV--- 339
HIV27312AR ----------E----------WP-------I--------V----D----------I--- 97
CONSENSUS.D kDknKWRmLIDFRELNkVTQDFTEvQLGiPHPaGLAKR?RITVLDvGDAYFSIPLDeeFRQYTaFTLPSVNNa 336
SIVMM251 ----------R----------K------I---------- 342
SIVMM142 ----------R----------K------I---------- 342
SIVMM239 ----------R----------K------I---------- 346
SIVMM32H ----------R----------K------I---------- 346
SIVMNE -------I----------K---------- 342
SIVSMMH4 ----------R---------- 305
SIVSMMH9 x-G----------x-----R---------- 308
SIVSMMPBJ ----------R---------- 308
SIVSTM ----------I----------R----------G---------- 327
HIV2FORTC2 ---S----------V---------R----------K------T--------R 152
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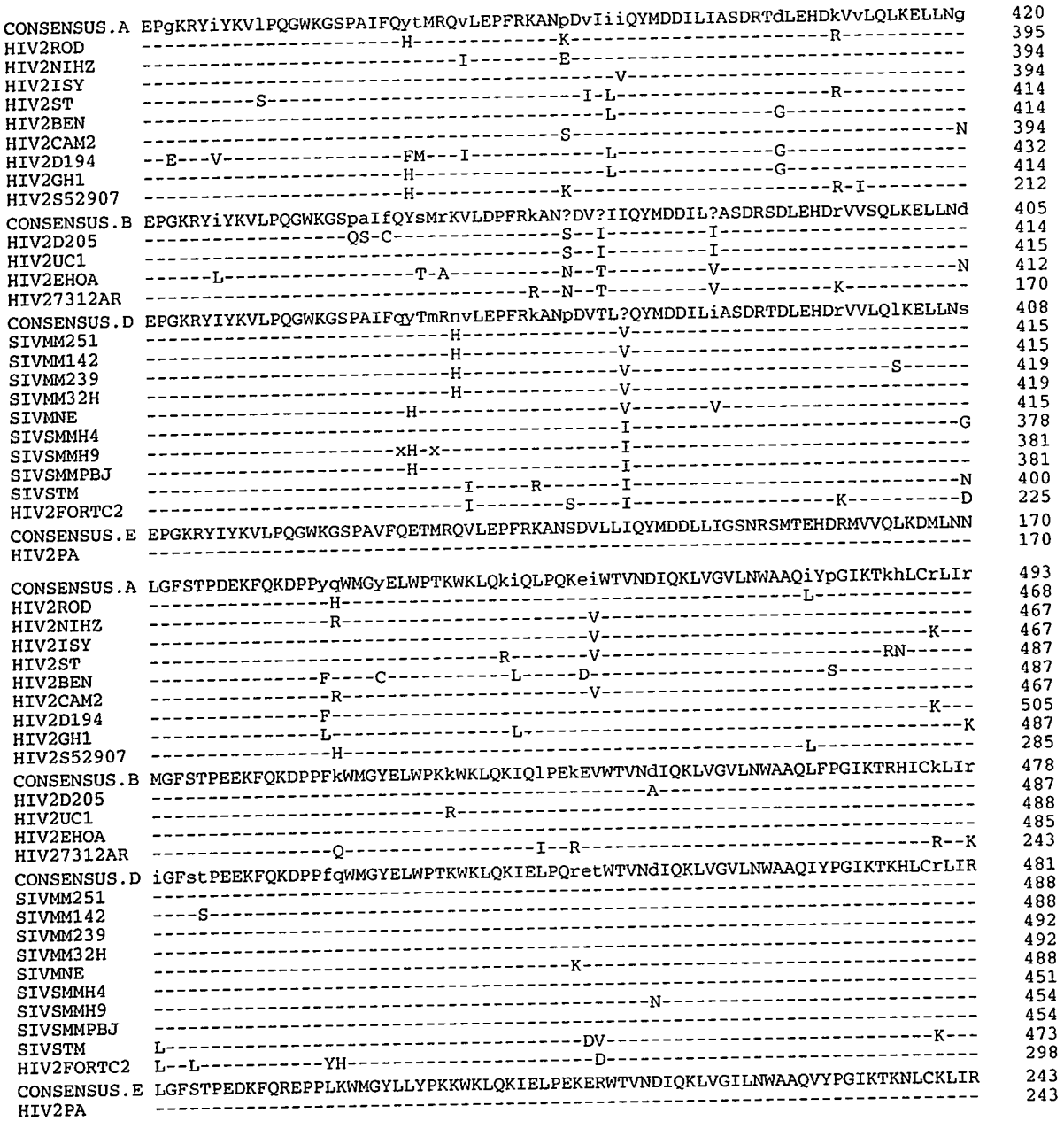
HIV2PA ---------- 97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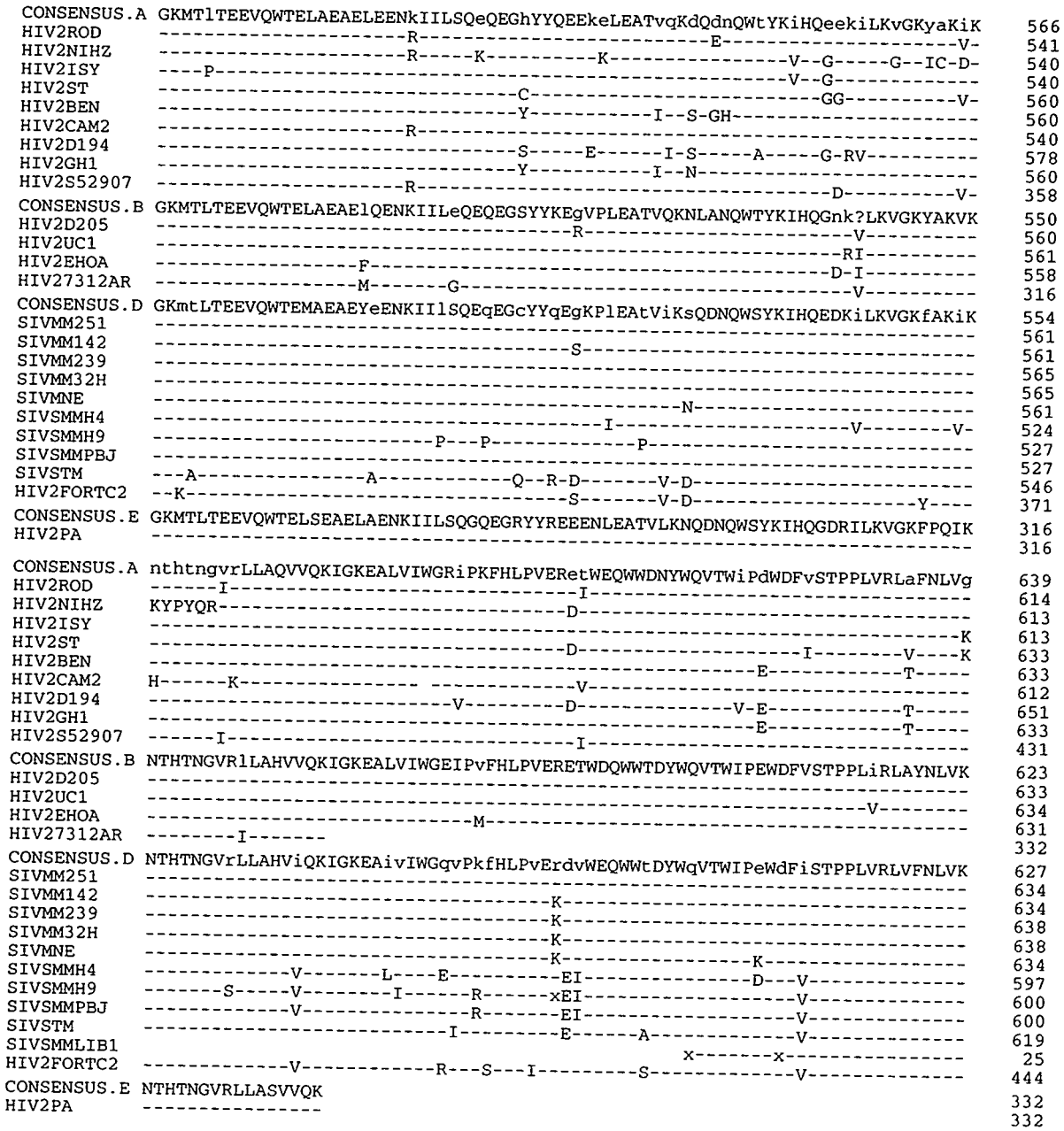
HIV2ROD ----------H----------K----------R---------- 395
HIV2NIHZ ----------I--------E---------- 394
HIV2ISY ----------V---------- 394
HIV2ST ----------S----------I-L----------R---------- 414
HIV2BEN ----------L----------G---------- 414
HIV2CAM2 ----------S----------N 394
HIV2D194 --E---V----------FM---I----------L----------G---------- 432
HIV2GH1 ----------H----------L----------G---------- 414
HIV2S52907 ----------H----------K----------R-I--------- 212
CONSENSUS.B EPGKRYiYKVLPQGWKGSpaIfQYsMrKVLDPFRkAN?DV?IIQYMDDIL?ASDRSDLEHDrVVSQLKELLNd 405
HIV2D205 ----------QS-C----------S--I---------I---------- 414
HIV2UC1 ----------S--I---------I---------- 415
HIV2EHOA ------L----------T-A----------N--T---------V----------N 412
HIV27312AR ----------R--N--T---------V----------K---------- 170
CONSENSUS.D EPGKRYIYKVLPQGWKGSPAIFqyTmRnvLEPFRkANpDVTL?QYMDDILiASDRTDLEHDrVVLQlKELLNs 408
SIVMM251 ----------H----------V---------- 415
SIVMM142 ----------H----------V----------S------ 419
SIVMM239 ----------H----------V---------- 419
SIVMM32H ----------H----------V----------V---------- 415
SIVMNE ----------H----------I----------G 378
SIVSMMH4 ----------I---------- 381
SIVSMMH9 ----------xH-x----------I---------- 381
SIVSMMPBJ ----------H----------I----------N 400
SIVSTM ----------I-----R-------I----------D 225
HIV2FORTC2 ----------I--------S----I----------K---------- 170
CONSENSUS.E EPGKRYIYKVLPQGWKGSPAVFQETMRQVLEPFRKANSDVLLIQYMDDLLIGSNRSMTEHDRMVVQLKDMLNN 170
HIV2PA ---------- 170
CONSENSUS.A LGFSTPDEKFQKDPPyqWMGyELWPTKWKLQkiQLPQKeiWTVNDIQKLVGVLNWAAQiYpGIKTkhLCrLIr 493
HIV2ROD ----------H----------L---------- 468
HIV2NIHZ ----------R----------V---------- 467
HIV2ISY ----------V----------K--- 467
HIV2ST ----------R-------V----------RN------ 487
HIV2BEN ----------F----C----------L-----D----------S---------- 487
HIV2CAM2 ----------R----------V---------- 467
HIV2D194 ----------F----------K--- 505
HIV2GH1 ----------L----------L----------K 487
HIV2S52907 ----------H----------L---------- 285
CONSENSUS.B MGFSTPEEKFQKDPPFkWMGYELWPKkWKLQKIQlPEkEVWTVNdIQKLVGVLNWAAQLFPGIKTRHICkLIr 478
HIV2D205 ----------A---------- 487
HIV2UC1 ----------R---------- 488
HIV2EHOA ---------- 485
HIV27312AR ----------Q----------I--R----------R--K 243
CONSENSUS.D iGFstPEEKFQKDPPfqWMGYELWPTKWKLQKIELPQretWTVNdIQKLVGVLNWAAQIYPGIKTKHLCrLIR 481
SIVMM251 ---------- 488
SIVMM142 ----S---------- 488
SIVMM239 ---------- 492
SIVMM32H ---------- 492
SIVMNE ----------K---------- 488
SIVSMMH4 ---------- 451
SIVSMMH9 ----------N---------- 454
SIVSMMPBJ ---------- 454
SIVSTM L----------DV----------K--- 473
HIV2FORTC2 L--L----------YH----------D---------- 298
CONSENSUS.E LGFSTPEDKFQREPPLKWMGYLLYPKKWKLQKIELPEKERWTVNDIQKLVGILNWAAQVYPGIKTKNLCKLIR 243
HIV2PA ---------- 243

HIV2/SIV POL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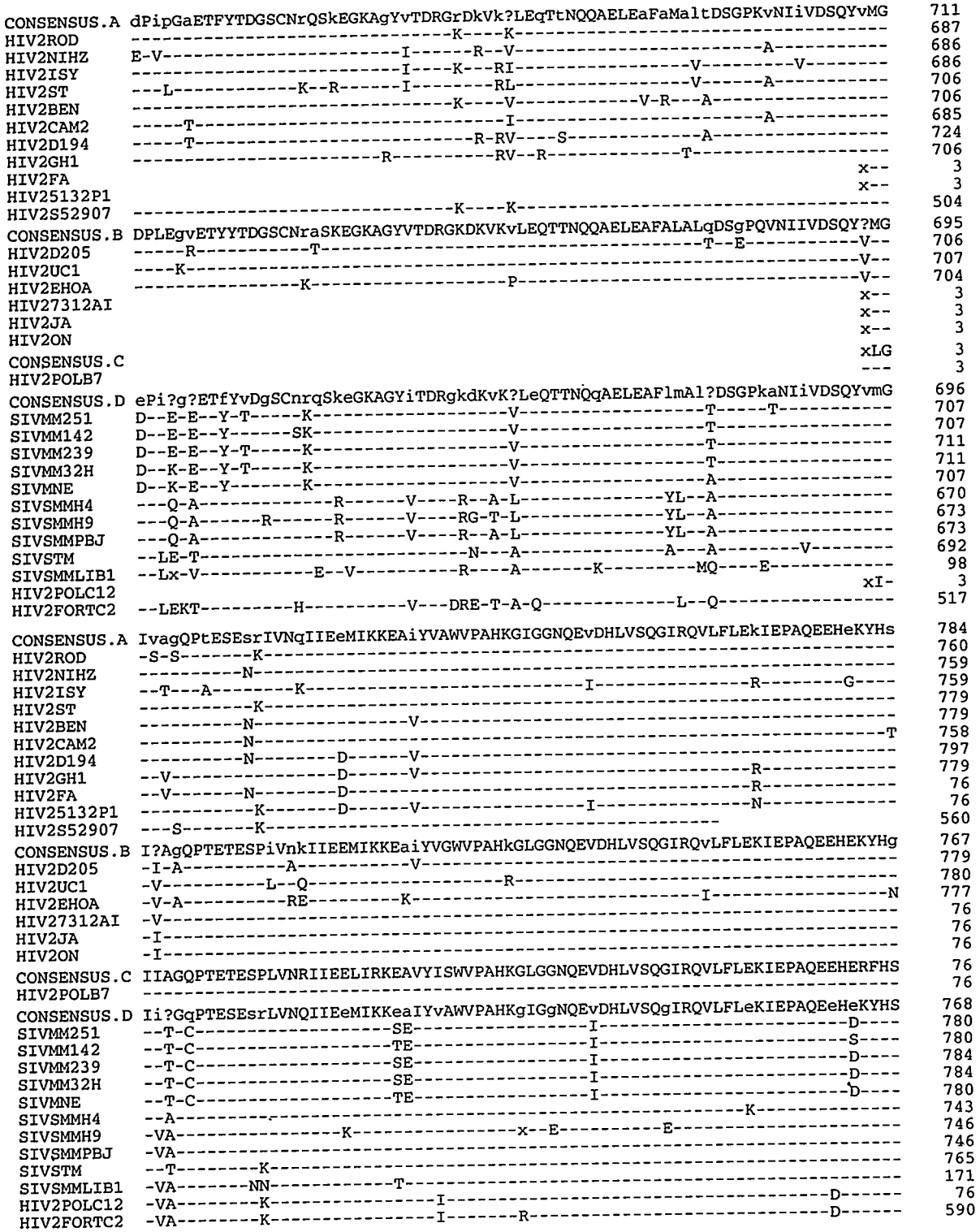
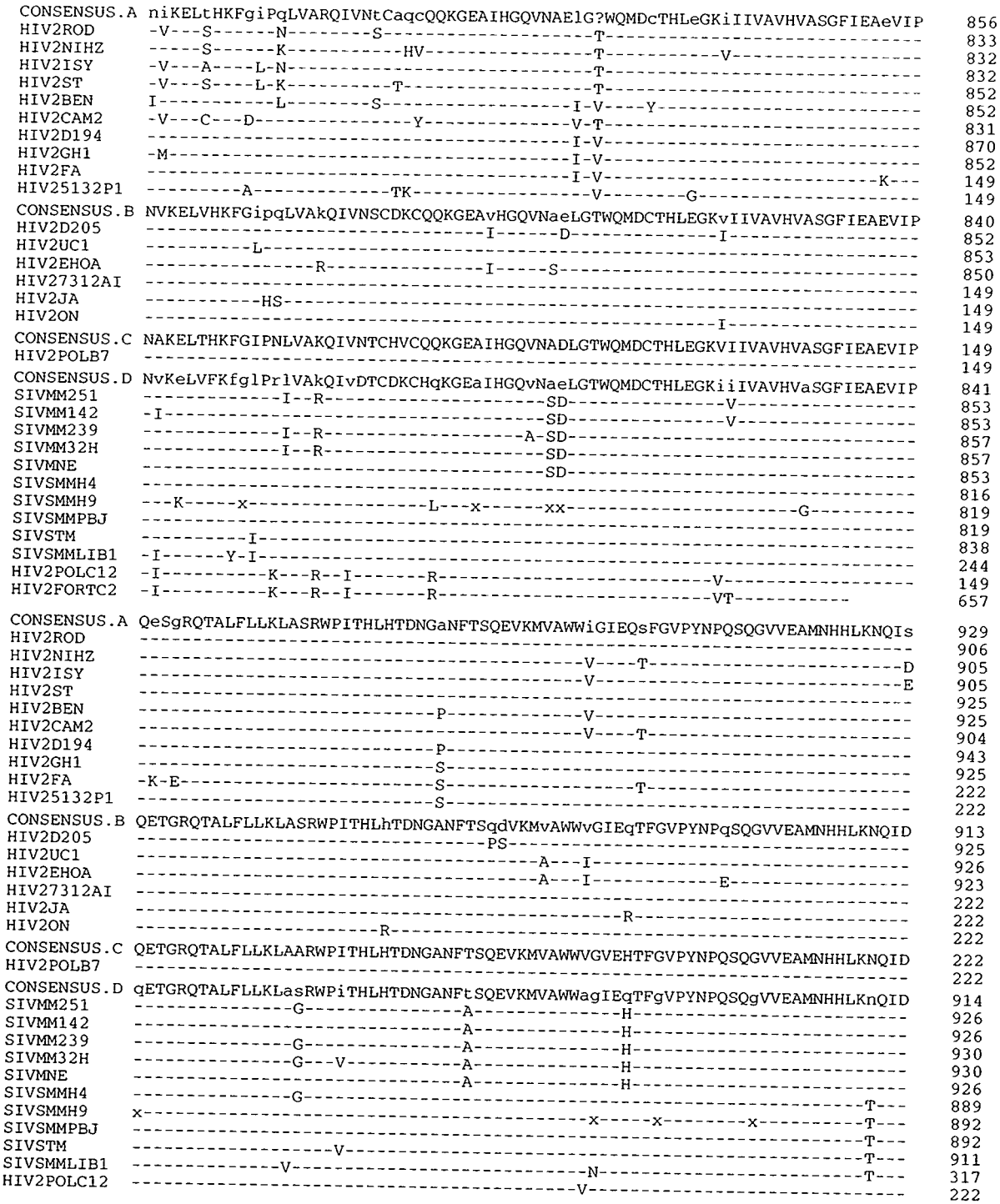
HIV2ROD ----------R----------E----------V- 541
HIV2NIHZ ----------R-----K----------K----------V--G-----G--IC-D- 540
HIV2ISY ----P----------V--G---------- 540
HIV2ST ----------C----------GG----------V- 560
HIV2BEN ----------Y----------I--S-GH---------- 560
HIV2CAM2 ----------R---------- 540
HIV2D194 ----------S-----E------I-S-----A-----G-RV---------- 578
HIV2GH1 ----------Y----------I--N---------- 560
HIV2S52907 ----------R----------D----------V- 358
CONSENSUS.B GKMTLTEEVQWTELAEAElQENKIILeQEQEGSYYKEgVPLEATVQKNLANQWTYKIHQGnk?LKVGKYAKVK 550
HIV2D205 ----------R----------V---------- 560
HIV2UC1 ----------RI---------- 561
HIV2EHOA ----------F----------D-I---------- 558
HIV27312AR ----------M-------G----------V---------- 316
CONSENSUS.D GKmtLTEEVQWTEMAEAEYeENKIIlSQEqEGcYYqEgKPlEAtViKsQDNQWSYKIHQEDKiLKVGKfAKiK 554
SIVMM251 ---------- 561
SIVMM142 ----------S---------- 561
SIVMM239 ---------- 565
SIVMM32H ---------- 565
SIVMNE ----------N---------- 561
SIVSMMH4 ----------I----------V--------V- 524
SIVSMMH9 ----------P---P----------P---------- 527
SIVSMMPBJ ---------- 527
SIVSTM ---A----------A----------Q--R-D-------V-D---------- 546
HIV2FORTC2 --K----------S-------V-D----------Y---- 371
CONSENSUS.E GKMTLTEEVQWTELSEAELAENKIILSQGQEGRYYREEENLEATVLKNQDNQWSYKIHQGDRILKVGKFPQIK 316
HIV2PA ---------- 316
CONSENSUS.A nthtngvrLLAQVVQKIGKEALVIWGRiPKFHLPVERetWEQWWDNYWQVTWiPdWDFvSTPPLVRLaFNLVg 639
HIV2ROD ------I----------I---------- 614
HIV2NIHZ KYPYQR----------D---------- 613
HIV2ISY ---------- 613
HIV2ST ----------D----------I--------V----K 633
HIV2BEN ----------E----------T----- 633
HIV2CAM2 H------K---------- ----------V---------- 612
HIV2D194 ----------V---------D----------V-E----------T----- 651
HIV2GH1 ----------E----------T----- 633
HIV2S52907 ------I----------I---------- 431
CONSENSUS.B NTHTNGVRlLAHVVQKIGKEALVIWGEIPvFHLPVERETWDQWWTDYWQVTWIPEWDFVSTPPLiRLAYNLVK 623
HIV2D205 ---------- 633
HIV2UC1 ----------V-------- 634
HIV2EHOA ----------M---------- 631
HIV27312AR --------I------- 332
CONSENSUS.D NTHTNGVrLLAHViQKIGKEAivIWGqvPkfHLPvErdvWEQWWtDYWqVTWIPeWdFiSTPPLVRLVFNLVK 627
SIVMM251 ---------- 634
SIVMM142 ----------K---------- 634
SIVMM239 ----------K---------- 638
SIVMM32H ----------K---------- 638
SIVMNE ----------K----------K---------- 634
SIVSMMH4 ----------V--------L----E----------EI----------D---V---------- 597
SIVSMMH9 -------S-----V--------I------R------xEI----------V---------- 600
SIVSMMPBJ ----------V----------R-------EI----------V---------- 600
SIVSTM ----------I---------E------A----------V---------- 619
SIVSMMLIB1 x-------x---------- 25
HIV2FORTC2 ----------V----------R---S---I---------S----------V---------- 444
CONSENSUS.E NTHTNGVRLLASVVQK 332
HIV2PA ---------- 332



HIV2/SIV POL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HIV2ROD -V---S------N--------S--------------------T------------------------------ 833
HIV2NIHZ -----S------K----------HV---------------T----------V------------------ 832
HIV2ISY -V---A----L-N-------------------------T------------------------------ 832
HIV2ST -V---S----L-K----------T-----------------T------------------------------ 852
HIV2BEN I-----------L--------S------------------I-V----Y------------------------ 852
HIV2CAM2 -V---C---D--------------Y-------------V-T------------------------------ 831
HIV2D194 --I-V------------------------------ 870
HIV2GH1 -M--I-V------------------------------ 852
HIV2FA --I-V-------------------------K--- 149
HIV25132P1 ---------A------------TK----------------V--------G---------------------- 149
CONSENSUS.B NVKELVHKFGipqLVAkQIVNSCDKCQQKGEAvHGQVNaeLGTWQMDCTHLEGKvIIVAVHVASGFIEAEVIP 840
HIV2D205 ----------------------------------I------D-------------I------------------ 852
HIV2UC1 ----------L-- 853
HIV2EHOA ----------------R---------------I-----S---------------------------------- 850
HIV27312AI -- 149
HIV2JA -----------HS-- 149
HIV2ON --I------------------ 149
CONSENSUS.C NAKELTHKFGIPNLVAKQIVNTCHVCQQKGEAIHGQVNADLGTWQMDCTHLEGKVIIVAVHVASGFIEAEVIP 149
HIV2POLB7 -- 149
CONSENSUS.D NvKeLVFKfglPrlVAkQIvDTCDKCHqKGEaIHGQvNaeLGTWQMDCTHLEGKiiIVAVHVaSGFIEAEVIP 841
SIVMM251 ------------I--R--------------------SD--------------V------------------ 853
SIVMM142 -I---------------------------------SD--------------V------------------ 853
SIVMM239 ------------I--R-----------------A-SD---------------------------------- 857
SIVMM32H ------------I--R---------------------SD---------------------------------- 857
SIVMNE ----------------------------------SD---------------------------------- 853
SIVSMMH4 -- 816
SIVSMMH9 ---K-----x----------------L---x------xx--------------------G---------- 819
SIVSMMPBJ -- 819
SIVSTM ----------I-- 838
SIVSMMLIB1 -I------Y-I-- 244
HIV2POLC12 -I----------K---R--I-------R-------------------------V------------------ 149
HIV2FORTC2 -I----------K---R--I-------R-------------------------VT----------- 657
CONSENSUS.A QeSgRQTALFLLKLASRWPITHLHTDNGaNFTSQEVKMVAWWiGIEQsFGVPYNPQSQGVVEAMNHHLKNQIs 929
HIV2ROD -- 906
HIV2NIHZ --V----T----------------------D 905
HIV2ISY --V----------------------------E 905
HIV2ST -- 925
HIV2BEN ----------------------------P-------------V------------------------------ 925
HIV2CAM2 --V----T------------------------ 904
HIV2D194 ----------------------------P-- 943
HIV2GH1 ----------------------------S-- 925
HIV2FA -K-E-------------------------S-----------------T------------------------ 222
HIV25132P1 ----------------------------S-- 222
CONSENSUS.B QETGRQTALFLLKLASRWPITHLhTDNGANFTSqdVKMvAWWvGIEqTFGVPYNPqSQGVVEAMNHHLKNQID 913
HIV2D205 ---------------------------------PS---------------------------------- 925
HIV2UC1 --A---I------------------------- 926
HIV2EHOA --A---I-----------E------------- 923
HIV27312AI -- 222
HIV2JA --R------------------------------ 222
HIV2ON ----------------------R-- 222
CONSENSUS.C QETGRQTALFLLKLAARWPITHLHTDNGANFTSQEVKMVAWWVGVEHTFGVPYNPQSQGVVEAMNHHLKNQID 222
HIV2POLB7 -- 222
CONSENSUS.D qETGRQTALFLLKLasRWPiTHLHTDNGANFtSQEVKMVAWWagIEqTFgVPYNPQSQgVVEAMNHHLKnQID 914
SIVMM251 ---------------G---------------A-------------H------------------------ 926
SIVMM142 ----------------------------------A-------------H------------------------ 926
SIVMM239 ---------------G---------------A-------------H------------------------ 930
SIVMM32H ---------------G---V-----------A-------------H------------------------ 930
SIVMNE ----------------------------------A-------------H------------------------ 926
SIVSMMH4 ---------------G---T--- 889
SIVSMMH9 x--x-----x--------x----------T--- 892
SIVSMMPBJ ---T--- 892
SIVSTM -------------------V---T--- 911
SIVSMMLIB1 --------------V----------------------------N----------------------T--- 317
HIV2POLC12 --V------------------------------ 222

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CONSENSUS.A rIREQANTiETIVLMAvHCMNFKRRGGIGDMTPaERliNMiTtEQEIQFLQaKNSklknFrVYfREGRdQLWk   1002
HIV2ROD     ----------------I----------------S----------------------D-------------    979
HIV2NIHZ    --------V---------------------------I-----------------------------------    978
HIV2ISY     --------M-------------------------V---V-----------------------------N---Q    978
HIV2ST      --------V---------------------------------V-A--------------Q---------------    998
HIV2BEN     ------------------------------------------------R---NF---Q--Y---------    998
HIV2CAM2    --------V-----------------------S-----------------------------------------    977
HIV2D194    ------------------------------------------------R---NF-K-Q--Y---------   1016
HIV2GH1     ------------------------------------------------R---NF---Q--Y---------    998
HIV2FA      --------------                                                              236
HIV25132P1  K-------------                                                             236
CONSENSUS.B RiRDQAVSiETVVLMAtHCMNFKRRGGIGDMTPAERlVNMITTEQEIQFfQaKNLKFQNFqVYYREGRDQLWK    986
HIV2D205    -L-------------------------------------------------------------------------    998
HIV2UC1     ----------------A-------------------------------------------------------    999
HIV2EHOA    ------------------------------------I-----------L-T--------R------------    996
HIV27312AI  --------------                                                             236
HIV2JA      --------------                                                             236
HIV2ON      --------L-----                                                             236
CONSENSUS.C RIREQANTMETIVL                                                             236
HIV2POLB7   --------------                                                             236
CONSENSUS.D rIReQANsvETiVLMAvHCmNFKrRGGiGDMTPAERLvNMITTEQEIQFQQSKNSKFKNFRVYYREGRDQLWK    987
SIVMM251    ------------------------------------I-----------------------------------    999
SIVMM142    ------------------------------------I-----------------------------------    999
SIVMM239    ------------------------------------I-----------------------------------   1003
SIVMM32H    ------------------------------------I-----------------------------------   1003
SIVMNE      --------M---------------------------L-----------------------------------    999
SIVSMMH4    --------I-------------------------------------------------------------    962
SIVSMMH9    --------I-------I--I-------------------------------------------------------    965
SIVSMMPBJ   --------I-------------------------------------------------------------    965
SIVSTM      ---D---T---V----------K---L-------------------------------------------    984
SIVSMMLIB1  K--D----I-------T-------------------------------------------------------    390
HIV2POLC12  K--D----------                                                             236

                                        vif cds ->
CONSENSUS.A GPGELLWKGdGAViVKVGtdIKviPRRKAKIIrDYGgRQE?DSgshLEGARE?dGE?ACPCQVPEIQNKRPRG   1072
HIV2ROD     ---------E---L--------I----------------M----------.---M-                 1036
HIV2NIHZ    -------------------E---V--------K-------M----------.---M-                 1035
HIV2ISY     ------------------------------------P---M----------.---M-                 1035
HIV2ST      ------------------A---I---------K-------M----N------.---V-                 1055
HIV2BEN     ---------E-------------V----------------L--SP--------.---M----------------   1070
HIV2CAM2    ---------------------I----------------L--S---------.N--V-                 1034
HIV2D194    ------------------A----V----------------L--S---------.---V-                 1073
HIV2GH1     ------------------A--------------------L--.--------E---V-                 1055
CONSENSUS.B GPGeLLWKGEGAViIKVGTEIKViPRRKAKIIRhYGGGKeLDCsaDmEDTrQ?aremaqs?QVPEA          1050
HIV2D205    ----------------------V---------------G------------.-------D             1058
HIV2UC1     -------------L-----------------------------GT-------.-------G-----       1064
HIV2EHOA    ---D--------------------------N------------V---M-AREVAQSN                 1056
CONSENSUS.D GPGELLWKGEGAVilKVGTdIKVVPRRKAKIIKDYGGGKEvDSsSHmEDTgE.ArEVA                1044
SIVMM251    ------------------------------------------------------.-----             1056
SIVMM142    ------------------------------------M-----------.-----                    1056
SIVMM239    ------------------------------------------------------.-----             1060
SIVMM32H    ------------------------------------------------------.-----             1060
SIVMNE      -------------V-----------------------------------------.-----             1056
SIVSMMH4    -------------------E--------------------L--G--L-----.-----                1019
SIVSMMH9    -------------------E--------------------L--G--L-----.-----                1022
SIVSMMPBJ   -------------------E--------------------L--G--L-----.-----                1022
SIVSTM      --------------V---------------------------G--L---R-.-G---                 1041
SIVSMMLIB1  ------                                                                      396

CONSENSUS.A GALCSPPQGGMGMVDLQQGNIPTTRKKSSRNTGILEPNTRKRMALLSCSKINLVYRKVLDRCYPRLCRHPNT   1144
HIV2BEN     ------------------------------------------------------------------------   1142
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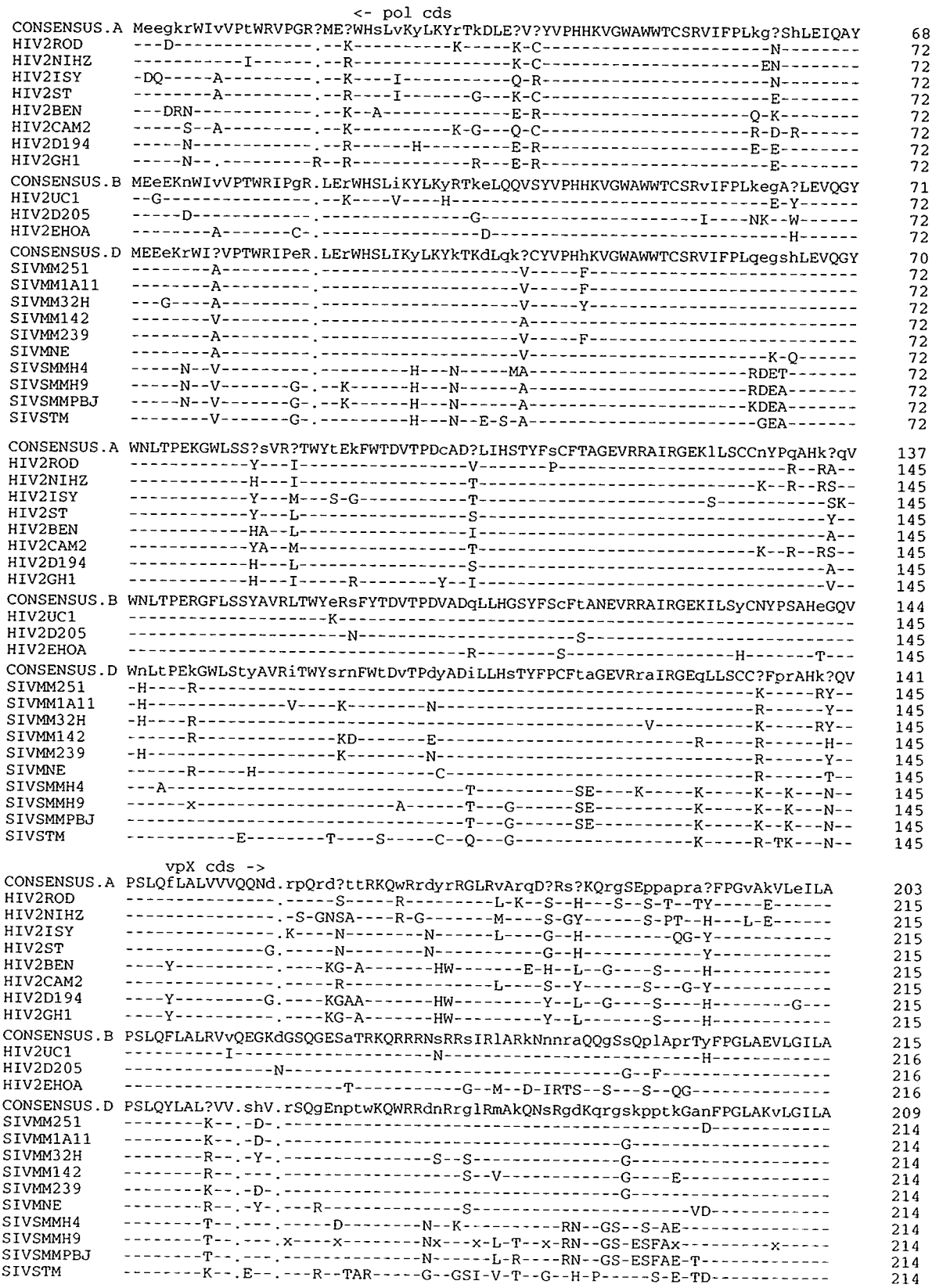
HIV2/SIV VIF


<- pol cds
CONSENSUS.A MeegkrWIvVPtWRVPGR?ME?WHsLvKyLKYrTkDLE?V?YVPHHKVGWAWWTCSRVIFPLkg?ShLEIQAY 68
HIV2ROD ---D----------.--K----------K-----K-C----------N-------- 72
HIV2NIHZ ----------I------.--R----------K-C----------EN-------- 72
HIV2ISY -DQ-----A---------.--K----I----------Q-R----------N-------- 72
HIV2ST --------A---------.--R----I-------G---K-C----------E-------- 72
HIV2BEN ---DRN----------.--K--A----------E-R----------Q-K-------- 72
HIV2CAM2 -----S--A---------.--K----------K-G---Q-C----------R-D-R------ 72
HIV2D194 -----N----------.--R------H---------E-R----------E-E------- 72
HIV2GH1 -----N--.---------R--R----------R---E-R----------E-------- 72
CONSENSUS.B MEeEKnWIvVPTWRIPgR.LErWHSLiKYLKyRTkeLQQVSYVPHHKVGWAWWTCSRvIFPLkegA?LEVQGY 71
HIV2UC1 --G----------.--K----V----H----------E-Y------ 72
HIV2D205 -----D----------.----------G----------I----NK--W------ 72
HIV2EHOA --------A-------C-.----------D----------H------ 72
CONSENSUS.D MEEeKrWI?VPTWRIPeR.LErWHSLIKyLKYkTKdLqk?CYVPHhKVGWAWWTCSRVIFPLqegshLEVQGY 70
SIVMM251 --------A---------.----------V-----F---------- 72
SIVMM1A11 --------A---------.----------V-----F---------- 72
SIVMM32H ---G----A---------.----------V-----Y---------- 72
SIVMM142 --------V---------.----------A---------- 72
SIVMM239 --------A---------.----------V-----F---------- 72
SIVMNE --------A---------.----------V----------K-Q------ 72
SIVSMMH4 -----N--V---------.---------H---N-----MA----------RDET------- 72
SIVSMMH9 -----N--V-------G-.--K------H---N------A----------RDEA------- 72
SIVSMMPBJ -----N--V-------G-.--K------H---N------A----------KDEA------- 72
SIVSTM --------V-------G-.---------H---N--E-S-A----------GEA------- 72
CONSENSUS.A WNLTPEKGWLSS?sVR?TWYtEkFWTDVTPDcAD?LIHSTYFsCFTAGEVRRAIRGEKlLSCCnYPqAHk?qV 137
HIV2ROD ----------Y---I----------V-------P----------R--RA-- 145
HIV2NIHZ ----------H---I----------T----------K--R--RS-- 145
HIV2ISY ----------Y---M---S-G----------T----------S----------SK- 145
HIV2ST ----------Y---L----------S----------Y-- 145
HIV2BEN ----------HA--L----------I----------A-- 145
HIV2CAM2 ----------YA--M----------T----------K--R--RS-- 145
HIV2D194 ----------H---L----------S----------A-- 145
HIV2GH1 ----------H---I-----R--------Y--I----------V-- 145
CONSENSUS.B WNLTPERGFLSSYAVRLTWYeRsFYTDVTPDVADqLLHGSYFScFtANEVRRAIRGEKILSyCNYPSAHeGQV 144
HIV2UC1 ----------K---------- 145
HIV2D205 ----------N----------S---------- 145
HIV2EHOA ----------R--------S----------H-------T--- 145
CONSENSUS.D WnLtPEkGWLStyAVRiTWYsrnFWtDvTPdyADiLLHsTYFPCFtaGEVRraIRGEqLLSCC?FprAHk?QV 141
SIVMM251 -H----R----------K-----RY-- 145
SIVMM1A11 -H----------V----K--------N----------R------Y-- 145
SIVMM32H -H----R----------V----------K-----RY-- 145
SIVMM142 ------R----------KD-------E----------R------R------H-- 145
SIVMM239 -H----------K--------N----------R------Y-- 145
SIVMNE ------R-----H----------C----------R------T-- 145
SIVSMMH4 ---A----------T----------SE----K-----K-----K--K---N-- 145
SIVSMMH9 ------x----------A------T---G------SE----------K-----K--K---N-- 145
SIVSMMPBJ ----------T---G------SE----------K-----K--K---N-- 145
SIVSTM ----------E--------T----S-----C--Q---G----------K-----R-TK---N-- 145
vpX cds ->
CONSENSUS.A PSLQfLALVVVQQNd.rpQrd?ttRKQwRrdyrRGLRvArqD?Rs?KQrgSEppapra?FPGvAkVLeILA 203
HIV2ROD ----------.-----S-----R---------L-K--S--H---S--S-T--TY-----E------ 215
HIV2NIHZ ----------.-S-GNSA----R-G-------M-----S-GY------S-PT--H---L-E------ 215
HIV2ISY ----------.K----N--------N------L----G--H---------QG-Y---------- 215
HIV2ST ----------G.-----N--------N----------G--H----------Y---------- 215
HIV2BEN ----Y----------.----KG-A-------HW-------E-H--L--G----S----H---------- 215
HIV2CAM2 ----------.-----R----------L----S--Y------S---G-Y---------- 215
HIV2D194 ----Y---------G.----KGAA-------HW---------Y--L--G----S----H--------G--- 215
HIV2GH1 ----Y----------.----KG-A-------HW---------Y--L-------S----H---------- 215
CONSENSUS.B PSLQFLALRVvQEGKdGSQGESaTRKQRRRNsRRsIRlARkNnnraQQgSsQplAprTyFPGLAEVLGILA 215
HIV2UC1 ----------I----------N----------H---------- 216
HIV2D205 ----------N----------G--F---------- 216
HIV2EHOA ----------T----------G--M--D-IRTS--S---S--QG---------- 216
CONSENSUS.D PSLQYLAL?VV.shV.rSQgEnptwKQWRRdnRrglRmAkQNsRgdKqrgskpptkGanFPGLAKvLGILA 209
SIVMM251 --------K--.-D-.----------D---------- 214
SIVMM1A11 --------K--.-D-.----------G---------- 214
SIVMM32H --------R--.-Y-.----------S--S----------G---------- 214
SIVMM142 --------R--.---.----------S--V----------G----E---------- 214
SIVMM239 --------K--.-D-.----------G---------- 214
SIVMNE --------R--.-Y-.---R----------S----------VD---------- 214
SIVSMMH4 --------T--.---.-----D--------N--K----------RN--GS--S-AE---------- 214
SIVSMMH9 --------T--.---.x----x--------Nx---x-L-T--x-RN--GS-ESFAx---------x----- 214
SIVSMMPBJ --------T--.---.----------N------L-R----RN--GS-ESFAE-T---------- 214
SIVSTM --------K--.E--.---R--TAR-----G--GSI-V-T--G--H-P-----S-E-TD---------- 214

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                                                                                                                <- vif cds
CONSENSUS.A MtdPREtvPPGNSGEETIgEAFeWLdRTvEAiNREAVNHlPRELIFQVWQRSWrYWHDeQGMS?SYTKYRYLC      72
HIV2ROD     ----------------------A--N-----------------------------------------E---------  73
HIV2NIHZ    ------------------E---A----------------H-----------------------T---------  73
HIV2ISY     --N----I----------E---D-----------------------------------------R---------  73
HIV2ST      -AG----I-------------------------------------------------------I---------  73
HIV2BEN     ------R-----------------E--I--L-------------------------------A---------  73
HIV2CAM2    ------------------E---A-----------------------------------------Q---------  73
HIV2D194    -A----R---------------------I--L---------------------A---------T---------  73
HIV2GH1     ------R---------------------I--L--------------------------D----P---------  73
CONSENSUS.B M.DPRERVPPGNSdEETvGEAF?WLErTiteLNRVAVNHLPRELIFQVWQrsWAYWREEQGMSiSYTKYRYLl  71
HIV2UC1     -.---------------I----D---------------------------C-----------S---------  72
HIV2D205    -.--------------------A-------------------------------------------------  72
HIV2EHOA    -.------------G--------E---T-LEH-------------------K---------------------C  72
CONSENSUS.D MsdPRErIPPGNSGEEtigeaFeWLnRTvEeINReAVNHLpRELIFQVWqRsWEYWHDEqGMs?SYvKyRYLC  72
SIVMM251    ------------------------------------------------------------------Q---------  73
SIVMM1A11   ------------------------------------------------------------------P---------  73
SIVMM32H    -----------------V-----------------------------------------------Q---------  73
SIVMM142    ------------------------------------------------------------------Q--T------  73
SIVMM239    ------------------------------------------------------------------P---------  73
SIVMNE      ------------------------------------------------------------------Q---------  73
SIVSMMH4    -------------------K--------------A--------------R---------M---E--T------  73
SIVSMMH9    -xx---x---------xx--x-D--H--x-----A-----x--------R-x-------M---V--T-x----  73
SIVSMMPBJ   ----------------------D--D--------A--------------R---------M---V--T------  73
SIVSTM      ----------------A-E------H----D-------------------R------------PG---------  73

CONSENSUS.A lmQkAvfiHfkrgcTClGgghGpgGw?r?GPPPPPPPGLV                                    110
HIV2ROD     II----YM-VRK------R--------.-P-----------                                   112
HIV2NIHZ    -I-M-MYM-A--DG------M-QK-G.DQ-----------                                   112
HIV2ISY     -------M---K----R-E--------.-S-----------                                   112
HIV2ST      -----M---S-----------------.-S-----------                                   112
HIV2BEN     -----I-T--------W-EDM-RE-LEDQ-----------                                   113
HIV2CAM2    --------------------------.-P-----------                                   112
HIV2D194    I-----Y----K------R--------.-P-----------                                   112
HIV2GH1     --------------------------.-S-----------                                   112
CONSENSUS.B LMQKAMFvHytKGCrCLqEGHGPGGW.RSGPPPPPPPGLA                                   110
HIV2UC1     -------------------------.-------------                                   111
HIV2D205    -------------------------.-------------                                   111
HIV2EHOA    -------I-FA---G--R--------.-------------                                   111
CONSENSUS.D LiQKAlFmHcKkGCRCLGegHGAGGW.RpGPPPPPPPGLA                                   111
SIVMM251    -M-----------------------.-------------                                   112
SIVMM1A11   -------------------------.-------------                                   112
SIVMM32H    -------------------------.-------------                                   112
SIVMM142    -------------------------.-------------                                   112
SIVMM239    -------------------------.-------------                                   112
SIVMNE      -------------------------.-------------                                   112
SIVSMMH4    -------V-----------E-------.-T-----------                                   112
SIVSMMH9    ------------------GE-------.-------------                                   112
SIVSMMPBJ   -----M------------GE-------.-------------                                   112
SIVSTM      ---------S-R--------------.-------------                                   112
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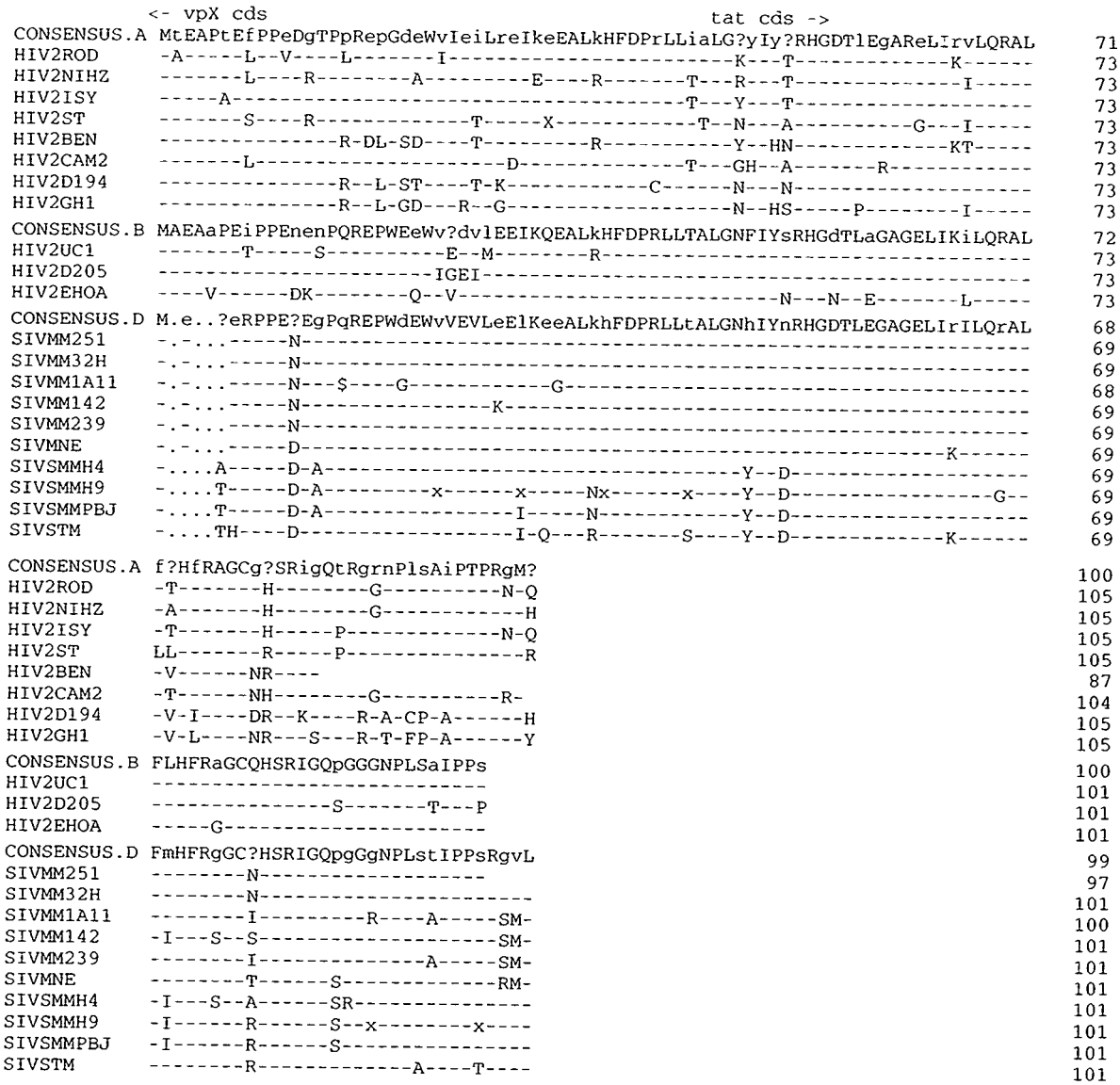
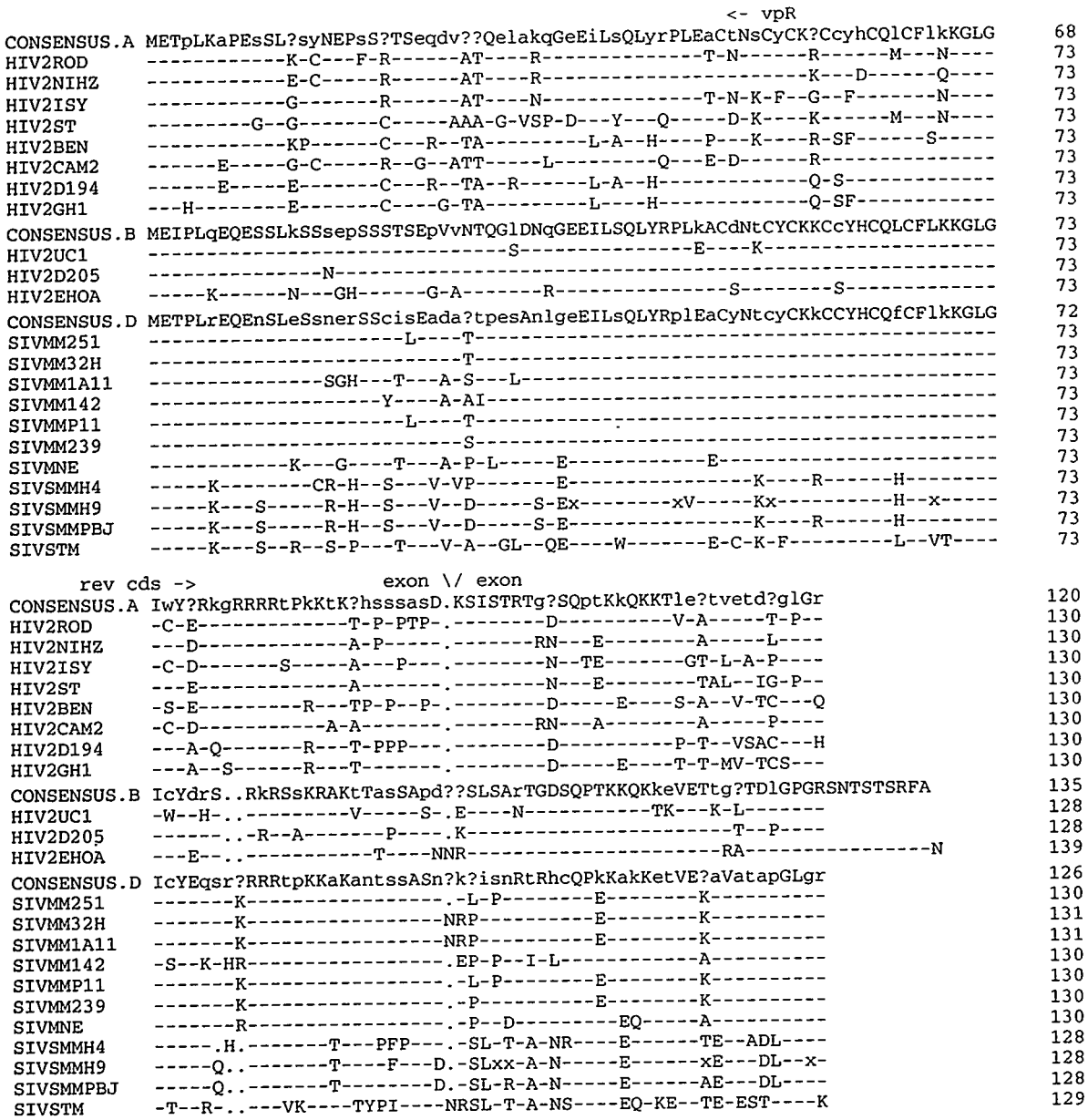
HIV2/SIV VPR


<- vpX cds
tat cds ->
CONSENSUS.A MtEAPtEfPPeDgTPpRepGdeWvIeiLreIkeEALkHFDPrLLiaLG?yIy?RHGDTlEgAReLIrvLQRAL 71
HIV2ROD -A-----L--V----L-------I----------K---T----------K------ 73
HIV2NIHZ -------L----R--------A---------E----R-------T---R---T----------I----- 73
HIV2ISY -----A----------T---Y---T---------- 73
HIV2ST -------S----R----------T-----X----------T--N---A----------G---I----- 73
HIV2BEN ---------------R-DL-SD---T---------R----------Y--HN----------KT----- 73
HIV2CAM2 -------L----------D----------T---GH--A-------R---------- 73
HIV2D194 ---------------R--L-ST----T-K----------C------N---N---------- 73
HIV2GH1 ---------------R--L-GD---R--G----------N--HS-----P--------I----- 73
CONSENSUS.B MAEAaPEiPPEnenPQREPWEeWv?dvlEEIKQEALkHFDPRLLTALGNFIYsRHGdTLaGAGELIKiLQRAL 72
HIV2UC1 -------T-----S----------E--M--------R---------- 73
HIV2D205 ----------IGEI---------- 73
HIV2EHOA ----V------DK--------Q--V----------N---N--E-------L----- 73
CONSENSUS.D M.e..?eRPPE?EgPqREPWdEWvVEVLeElKeeALkhFDPRLLtALGNhIYnRHGDTLEGAGELIrILQrAL 68
SIVMM251 -.-...-----N---------- 69
SIVMM32H -.-...-----N---------- 69
SIVMM1A11 -.-...-----N---$----G----------G---------- 68
SIVMM142 -.-...-----N----------K---------- 69
SIVMM239 -.-...-----N---------- 69
SIVMNE -.-...-----D----------K------ 69
SIVSMMH4 -....A-----D-A----------Y--D---------- 69
SIVSMMH9 -....T-----D-A---------x------x-----Nx------x----Y--D----------G-- 69
SIVSMMPBJ -....T-----D-A----------I-----N----------Y--D---------- 69
SIVSTM -....TH----D----------I-Q---R-------S----Y--D----------K------ 69
CONSENSUS.A f?HfRAGCg?SRigQtRgrnPlsAiPTPRgM? 100
HIV2ROD -T-------H--------G----------N-Q 105
HIV2NIHZ -A-------H--------G----------H 105
HIV2ISY -T-------H-----P----------N-Q 105
HIV2ST LL-------R-----P----------R 105
HIV2BEN -V------NR---- 87
HIV2CAM2 -T------NH--------G----------R- 104
HIV2D194 -V-I----DR--K----R-A-CP-A------H 105
HIV2GH1 -V-L----NR---S---R-T-FP-A------Y 105
CONSENSUS.B FLHFRaGCQHSRIGQpGGGNPLSaIPPs 100
HIV2UC1 ---------- 101
HIV2D205 ----------S-------T---P 101
HIV2EHOA -----G---------- 101
CONSENSUS.D FmHFRgGC?HSRIGQpgGgNPLstIPPsRgvL 99
SIVMM251 --------N---------- 97
SIVMM32H --------N---------- 101
SIVMM1A11 --------I---------R----A-----SM- 100
SIVMM142 -I---S--S----------SM- 101
SIVMM239 --------I----------A-----SM- 101
SIVMNE --------T------S----------RM- 101
SIVSMMH4 -I---S--A------SR---------- 101
SIVSMMH9 -I------R------S--x--------x---- 101
SIVSMMPBJ -I------R------S---------- 101
SIVSTM --------R----------A----T---- 101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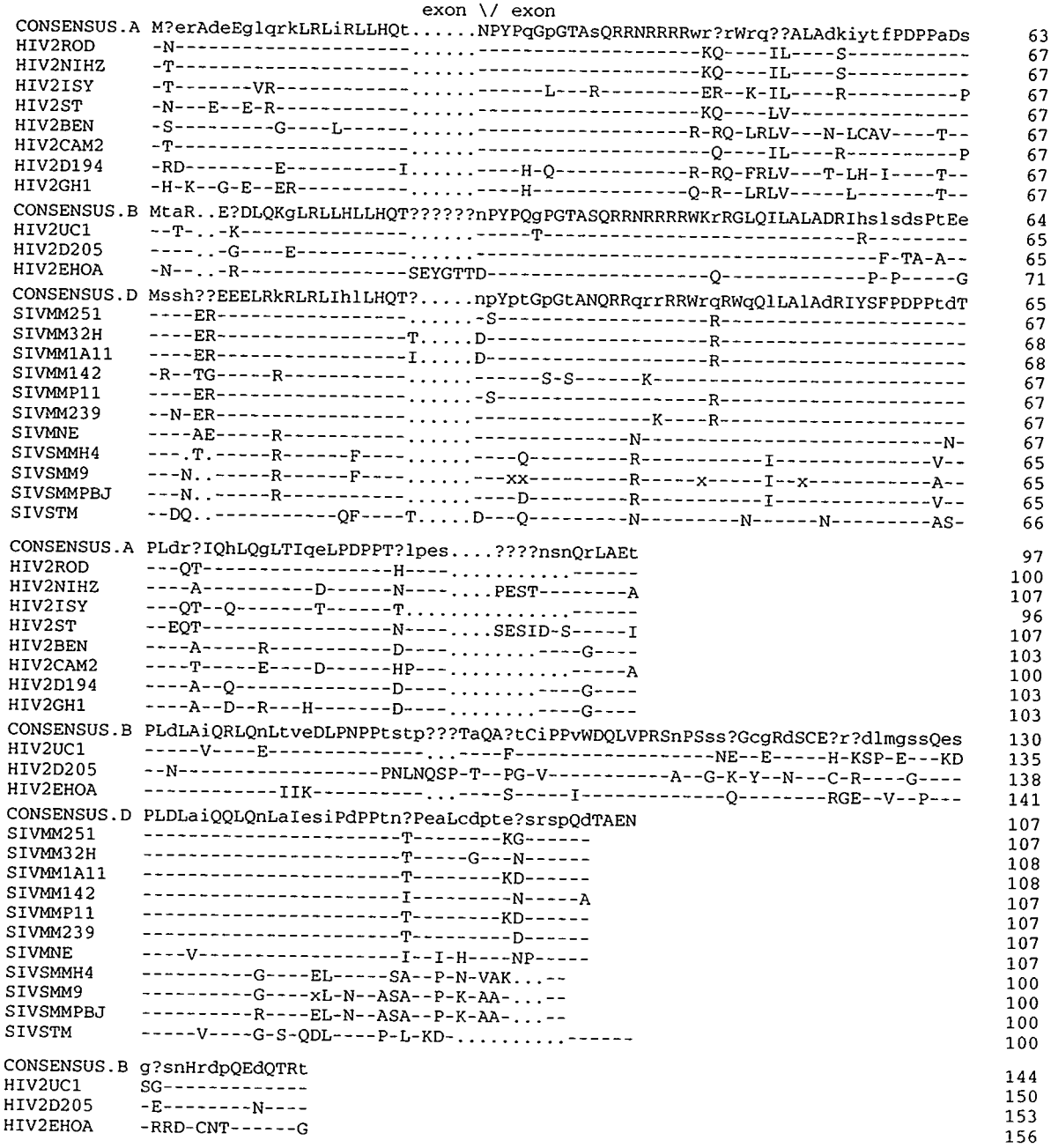
HIV2/SIV REV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CONSENSUS.A M?erAdeEglqrkLRLiRLLHQt.....NPYPqGpGTAsQRRNRRRRwr?rWrq??ALAdkiytfPDPPaDs 63
HIV2ROD -N----------.....----------KQ----IL----S---------- 67
HIV2NIHZ -T----------.....----------KQ----IL----S---------- 67
HIV2ISY -T-------VR----------.....------L---R---------ER--K-IL----R----------P 67
HIV2ST -N---E--E-R----------.....----------KQ----LV---------- 67
HIV2BEN -S---------G----L------.....----------R-RQ-LRLV---N-LCAV----T-- 67
HIV2CAM2 -T----------.....----------Q----IL----R----------P 67
HIV2D194 -RD--------E----------I.....----H-Q----------R-RQ-FRLV---T-LH-I----T-- 67
HIV2GH1 -H-K--G-E--ER----------.....----H----------Q-R--LRLV-----L-------T-- 67
CONSENSUS.B MtaR..E?DLQKgLRLLHLLHQT??????nPYPQgPGTASQRRNRRRRWKrRGLQILALADRIhslsdsPtEe 64
HIV2UC1 --T-..-K----------.....-----T----------R--------- 65
HIV2D205 ----..-G----E----------.....----------F-TA-A-- 65
HIV2EHOA -N--..-R----------SEYGTTD----------Q----------P-P-----G 71
CONSENSUS.D Mssh??EEELRkRLRLIhlLHQT?.....npYptGpGtANQRRqrrRRWrqRWqQlLAlAdRIYSFPDPPtdT 65
SIVMM251 ----ER----------.....-S----------R---------- 67
SIVMM32H ----ER----------T.....D----------R---------- 68
SIVMM1A11 ----ER----------I.....D----------R---------- 68
SIVMM142 -R--TG-----R----------.....------S-S------K---------- 67
SIVMMP11 ----ER----------.....-S----------R---------- 67
SIVMM239 --N-ER----------.....----------K----R---------- 67
SIVMNE ----AE-----R----------.....----------N----------N- 67
SIVSMMH4 ---.T.-----R------F----.....----Q---------R----------I----------V-- 65
SIVSMM9 ---N..-----R------F----.....---xx---------R-----x-----I--x----------A-- 65
SIVSMMPBJ ---N..-----R----------.....----D---------R----------I----------V-- 65
SIVSTM --DQ..----------QF----T.....D---Q---------N---------N------N---------AS- 66
CONSENSUS.A PLdr?IQhLQgLTIqeLPDPPT?lpes....????nsnQrLAEt 97
HIV2ROD ---QT----------H----.....------ 100
HIV2NIHZ ----A----------D------N----....PEST--------A 107
HIV2ISY ---QT--Q-------T------T.....------ 96
HIV2ST --EQT----------N----....SESID-S-----I 107
HIV2BEN ----A-----R----------D----.....----G---- 103
HIV2CAM2 ----T-----E----D------HP---.....-----A 100
HIV2D194 ----A--Q----------D----.....----G---- 103
HIV2GH1 ----A--D--R---H-------D----.....----G---- 103
CONSENSUS.B PLdLAiQRLQnLtveDLPNPPtstp???TaQA?tCiPPvWDQLVPRSnPSss?GcgRdSCE?r?dlmgssQes 130
HIV2UC1 -----V----E----------...----F----------NE--E-----H-KSP-E---KD 135
HIV2D205 --N----------PNLNQSP-T--PG-V----------A--G-K-Y--N---C-R----G---- 138
HIV2EHOA ----------IIK----------...----S-----I----------Q--------RGE--V--P--- 141
CONSENSUS.D PLDLaiQQLQnLaIesiPdPPtn?PeaLcdpte?srspQdTAEN 107
SIVMM251 ----------T--------KG------ 107
SIVMM32H ----------T-----G---N------ 108
SIVMM1A11 ----------T--------KD------ 108
SIVMM142 ----------I---------N-----A 107
SIVMMP11 ----------T--------KD------ 107
SIVMM239 ----------T---------D------ 107
SIVMNE ----V----------I--I-H----NP----- 107
SIVSMMH4 ----------G----EL-----SA--P-N-VAK...-- 100
SIVSMM9 ----------G----xL-N--ASA--P-K-AA-...-- 100
SIVSMMPBJ ----------R----EL-N--ASA--P-K-AA-...-- 100
SIVSTM -----V----G-S-QDL----P-L-KD-.....------ 100
CONSENSUS.B g?snHrdpQEdQTRt 144
HIV2UC1 SG---------- 150
HIV2D205 -E--------N---- 153
HIV2EHOA -RRD-CNT------G 156

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                                *   *                ^^^     *           *
CONSENSUS.A M??grnqLliaillLaSacliyC???qyVTVfYgiPaWrNAsIPLfCATkNRDTWGTIQClPDNDDYQEi?LNV  67
HIV2ROD     -.M..--------------V--T..--------V-T-K--T-------R-------------------T---  68
HIV2NIHZ    -KGSK-------V----Y--H-K..-F-----------------------------------------T---  71
HIV2ISY     -.S-KI---V-F--T-------T..K-------V-V-K-------------------------------P---  70
HIV2ST      -.C-----FV-S----------V..--------V-V---------------------------------A---  70
HIV2BEN     -EP-----FVV---T----V--S..------------K-------------------------------I---  71
HIV2CAM2    -ER------------------RQ.--------V---K-------------------------------P---  72
HIV2D194    -EP------V----T-------K..-----------------------------------------T---  71
HIV2GH1     -.C-KSL-CV-S-----Y-V--T..--------V-V-----------------------K---------T---  70
HIV2U07104  -...GA----T---T--------..R-----S----G--------V-----------------------A---  68
HIV2U07106  -TRR-A----S---T--------..K-N--------------------T-------------------T---  71
HIV2U07107  -APQKT----S---T--------..E-------A--------------R-------------------A---  71
HIV2U07108  -ARE-T--I--T-------R--..Q------------K-------------------------------A---  71
HIV2CBL21   -.CS--L--V-S----I------..T--------V-----------------------------------A---  70
HIV2CBL22   -.S-KI---V----T----V--..T--------V-----------------------------------LT---  70
HIV2CBL23   -MG------V------T------..TN-----------------------------------------T---  71
HIV2CBL24   -.C------VTT--------S-..TK---------------------R-------------------A---  70
HIV2CAM1    -AYK----------T-------KRK-------------------------------------------P---  73
HIV2CAM2BR  -GC-------------------.KQ--------V---K-------------------------------P---  72
HIV2CAM3    -TRKG-----------Y----.RQ--------------T---------------------------S---  72
HIV2CAM4    -AC-KS--------T-T------..A-----------------------------------------P---  71
HIV2CAM5    -TC-----------T--Y-VH-..K--------V-V-----------------------------A---  71
HIV2CAM6    -GRK--------I-T---I----..K-------------------------------------------P---  71
HIV2ALI     -MSS-----VT--------V--..K--------V---K-------------------------------A---  71
                                                ^^^     *           *
CONSENSUS.B MAh?sn?L?i?LLLIsiyGf?gk??nyVTVFYGIPAWrNAtvPLfCATtNRDTWGTVQCLPDNgDYTEI?lNI  65
HIV2UC1     ---T--H-F-L-----V---L-HKK---------------------------------------SV--  73
HIV2D205    --YF-SR-P-A----G-S--VC-..Q------------------I-----------------R---  71
HIV2EHOA    ---VN-Y-LVT--------YM--..-F----------K--SI------R--------------D-----Q---  71
              *                 *                 ^^^     *           *
CONSENSUS.D MgClGNQLLIAilllSvygiyC?..qYVTVFYGvPAWrNATiPLFCaTkNRDTWGTTQCLPDNgDYSElAlNv  70
SIVMM251    ----------------------T..-------------------------------------------  71
SIVMM32H    ----------------------T..----------------------E--------------------  71
SIVMM1A11   ----------------------T..L------------------------------------------  71
SIVMM142    ----------------------I..-----------------------------------D---------  71
SIVMM239    ----------------------T..L-----------------------------------------V----  71
SIVMNE      -------------F--A-----I..--------------------V-R--------------D--------I  71
SIVSMMH4    -----------L--V--LE-C-V..------------K-----------------------D------I--  71
SIVSMMH9    -----------LS-x-AS----V..----------------V------R--------------------I--  71
SIVSMMPBJ   -----------L----AS----V..--------I--------V---------------------------I--  71
SIVP209C19  -----------L--V-ALK---V..------------K----------R--------------N------V-I  71
SIVSTM      -A-P------------ACLT--T..-------------------------------------------I--  71
```

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                    ^^^                     *       *     *
CONSENSUS.A TEAFDAW?nNtvTeQAiEDVWnLFETSiKPCVKLTPLCvaM?C??????????t?????????????....??    109
HIV2ROD     -------.-------------H-------------------K-SSTESSTGNN-.................TS    123
HIV2NIHZ    -------.--------V-----------------------N-TR......NM-...................     118
HIV2ISY     -------.D-I-----V----------------------T-N-........NAS.................T    116
HIV2ST      -------.--------V----S-------------------R-........NS-.................TA    117
HIV2BEN     -------.--------V----H-------------------N-SRVQG...NT-.........TPNP......    125
HIV2CAM2    -------.D--I-------------------------------K-........NIS.................TS    119
HIV2D194    -------.D------------R-------------------N-........NI-...................     116
HIV2GH1     -------.D-------V----S--------------------S-........NS-.................T    116
HIV2U07104  -------.--------------------T-------------T-..RKSSGNTS-.................G    120
HIV2U07105                                           -T-..SKNSGNTSI...................     12
HIV2U07106  -------.--------------------T-------------N-..SKNSGNTS-...................    122
HIV2U07107  -------.--------------------T-------------N-SKNYNNTSAGNTTTPTAESM..........    133
HIV2U07108  -------.--------------------T-------------N-..SKDSSNTS-...................    122
HIV2CBL21   -------.D-------V----S-----------------T-N-...TTMKNIS-...................    120
HIV2CBL22   -------.D------------H-------------------N-..TKTRRNMTI...................    121
HIV2CBL23   -------.D--------------------------------R-..NNTDARNT-...................    122
HIV2CBL24   -------.D-------V----S-------------------K-..NNT...AT.................TP    119
HIV2CAM1    -------.----------------------------------K-....DGNITS-...................    122
HIV2CAM2BR  -------.D--I-----------------------------K-.....NISTSD...................    120
HIV2CAM3    -------.-------------S-------------------K-..NNTQSSNTA...................    123
HIV2CAM4    -------.---I-----------------------------K-..KRMTGNTT-...................    122
HIV2CAM5    -------N-----D--V---------------------IK-E-...KKLGNAT-...................    122
HIV2CAM6    -------.D-------V-----------------------N-SRSRPS..NS-.................GN    124
HIV2ALI     -------.D-------V----R-----------------I--K-SNISTESTTTS...................    124
                                        *       *    *^^^
CONSENSUS.B TEAFDAW.dNTVT?QAvdDVWsLFETSIKPCVKLTPLCVaM?CnkT?t???n??...................    110
HIV2UC1     -------.N----E---------------------------R--N-G-...-TT...................    123
HIV2D205    -------.-----Q--------R-------------------N-S--E-NPG-AS...................    124
HIV2EHOA    -------.-----D--TK--------------------T-K----WSS.........................    119
                                        *       *    *         ^^^
CONSENSUS.D TEsFDAW.?NTVTEQAIEDVW?LFETSIKPCVKLtPLCItMrC........NKsEtdrWGLTks????????t    124
SIVMM251    -------.E------------Q------------S--------.....-------------S.......-    128
SIVMM32H    -------.E------------Q------------S--------.....------K------L.......-    128
SIVMM1A11   -------.E------------Q----------------------.....-------------S.......-    128
SIVMM142    -------.E------------Q------------S--------.....------K------S.......-    128
SIVMM239    -------.N------------Q------------S--------.....-------------I.......-    128
SIVMNE      -------.E------------H-------------------K-.....------K------S.......-    128
SIVSMMH4    --A----.D------------N-----------------A---.....--T--------GNA......G-    129
SIVSMMH9    --A----.D------------N----------------------.....----xx-----.....GxPAP-    130
SIVSMMPBJ   --A----.D------------N----------------------.....----------...GTPAPTT-    132
SIVP209C19  --A----.N------------N-----------------A---.....--T--------.....RG      126
SIVSMB670                                            ---.....--T---K----GNA......I-     19
SIVSTM      --A----.D------------N-----------------A---.....--N---K----GKT.......V    128
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                                        *    ^*^          *  ^^^          ^^^       *
CONSENSUS.A ???????t???????????ine?spcir??nCs?Gl?eEemv?CqFnMtGLerDkkk?YnetWYs?DVVCe??  154
HIV2ROD     KSTSTTT-TPTD...QEQE-S-DT--A-AD---.--G---TIN-------------Q-------K-----T.  191
HIV2NIHZ    TWTGRTD-Q......NITI--DT-H.A-AD--T.--K----ID---S--------R-Q-T-A---K----D..  181
HIV2ISY     ESAVATTSPS.....GPDM--DTD---QLN---.--R--D--E---------L----Q-S-----K-----S.  182
HIV2ST      KNTTSTP-TTTTA..NTT.-G-N-S---TD--T.--G-----D--------------L-------K-----S.  185
HIV2BEN     RTSSSTTSRPPTS..AASI---T-N--ENNT-A.--GY---MQ-E---K---Q---RR-KD---LE----D..  193
HIV2CAM2    DTTMIRT-TPSTA..KEAP-SDN-----TN---.--E--KI-K-H------------Q-------S----D..  187
HIV2D194    SGTTATPSPP.....NITI-D-N-T--GDN--T.--GK--V-E-E-------Q---RK--DA---R----DK.  182
HIV2GH1     NNTTTTGSTT.....GMSE---T--SY.SD--T.--GK--I-N---Y----------Q-------K-----S.  181
HIV2U07104  NATTSTP.....MINETSI---T-----TN---.--R-----S--------A---P-G-------S-----T.  186
HIV2U07105  .....GS-TTTTD..AAMV---T-Q---AN---.--R---L-S---D----T---P-R-------S----DA.   76
HIV2U07106  .....GS-TTPA...AISM---T-----TD---.--R-----S---S----T---P-R-------S-----TT  186
HIV2U07107  ..................---N-S---AN---.--E---I-N-----A--P---P-W-------R-----N.  185
HIV2U07108  .....GN-PTST...ASYV---T-S--HTDT--.--R---I-S---S----A---P-R-------S-----AT  186
HIV2CBL21   .....TARPTTGISNTESILK-N-S--STDT-A.--EQ--T-D--------------Q-T-----K-----S.  186
HIV2CBL22   ......AQSITTTAKAVVINDTD.---KTN--T.--G--DI-N-E-D----V--QS-R-------A-----..  184
HIV2CBL23   ..TPTTASPRTIKPVTE..-S-N-S---AN---.--G---V-N--------------Q-------K-----..  188
HIV2CBL24   EGEAQATSTTAATATGAME---T---VSTN--T.--GD---IS-E------Q-----L-------K----D.S  190
HIV2CAM1    ....GNT-TSTRARITSEE-K-N-S--SAD--P.--K-----M--------------Q-------N----K..  188
HIV2CAM2BR  .TTMIRT-TPSTAKEAPISDKFP-----AN---.-IG--KI-R-H------------Q-------S----DN.  190
HIV2CAM3    .......-ESPAKSMEINE---T---M-TD---.--K-----S-------------RR-T-S---T-----A.  187
HIV2CAM4    .....AT-ASTTLLNDTTLL--S-T--GAN--T.--E---LME--------Q---V-R-------K----DT.  188
HIV2CAM5    ..LSNKT-TSSTANLAIDDNT...---KNDT-P.--ED-D--T-H------AL--P-R-------T----D..  187
HIV2CAM6    VTTTIPS-TAATTTPGMTV---T---M-AD---.--QR----E---S-A--A---P-Q-------Q-----..  194
HIV2ALI     .........PSPGSTLKPL---SD---KAD--PR--GD----N-R------Q---P-Q-------K-----..  186
                              ^^^  *  ^^^*          *                          *
CONSENSUS.B ????Ttp?tts???????llNetspCIkNDsC?.GiGlEe??dC?F?MTGLrRDE?KQYKDTWY??DLeC???  159
HIV2UC1     TKPI---I--TKP..SEN---D--------T-P.-----NTV--Y-N--------K--------EK----N..  191
HIV2D205    STTT-K-T---R...GLKTI---D--------T.-L-E--IMQ-N-S--------L--------SE----...  190
HIV2EHOA    ASKE--TSSA-LRSSTQT----D-K--Q----A.------MI--Q-K----K---S--------KQ--V-EKG  191
                              ^^^  *    ^*^          *  ^^^          ^^^       *
CONSENSUS.D tt?tta?t?a?????k??vvNets?Ci??nnCt.GLEqEpmisCKFnMTGLkRDkkkEYNETWYS?DLvCEQ?  181
SIVMM251    -IT-A-P-S-PVS.E-IDM-----S--AQ----.-----Q------T--------T---------T------.  198
SIVMM32H    --AP--P-A-S....-IDM-----S--THD---.-----Q--G-----------T---------T------.  195
SIVMM1A11   --T.A-PKAMSE...-INMI----S--VHD---.-----Q--G----------------------A------.  195
SIVMM142    --AS-TT-TTAKSVETRDI-----P-VVHD---.----------------------------A------.  199
SIVMM239    --AS-TS-T-SA...-VDM-----S--AQD---.-----Q------------------------A------.  196
SIVMNE      --AP--IPTKAE...AIK----N-P--NHD---.--------------------RR--------A------.  196
SIVSMMH4    --TAITT-ATPSV..AEN-I--SNP--KN-S-A.--------G--------N-------------R--I---S  199
SIVSMMH9    --Q-STTPP...SPIIAK---DSDP--RS----.-------V--------------R--------R------N  199
SIVSMMPBJ   Q-T--QASTTPTSPITAK---DSDP--KI----.-------V--------------R--------R------N  204
SIVP209C19  AET---T-P-GTPSG-EK-I--GDP--RN-S-A.--------G-----------RR---------R--I---S  198
SIVSMB670   --A---APS-RTPKVTAN------S-VKN----.-------V----------------                  76
SIVSTM      --V-PTAAA-AT...-PEL-----S-VSN----.---E-SLVG-------------R--------S--I---.  196
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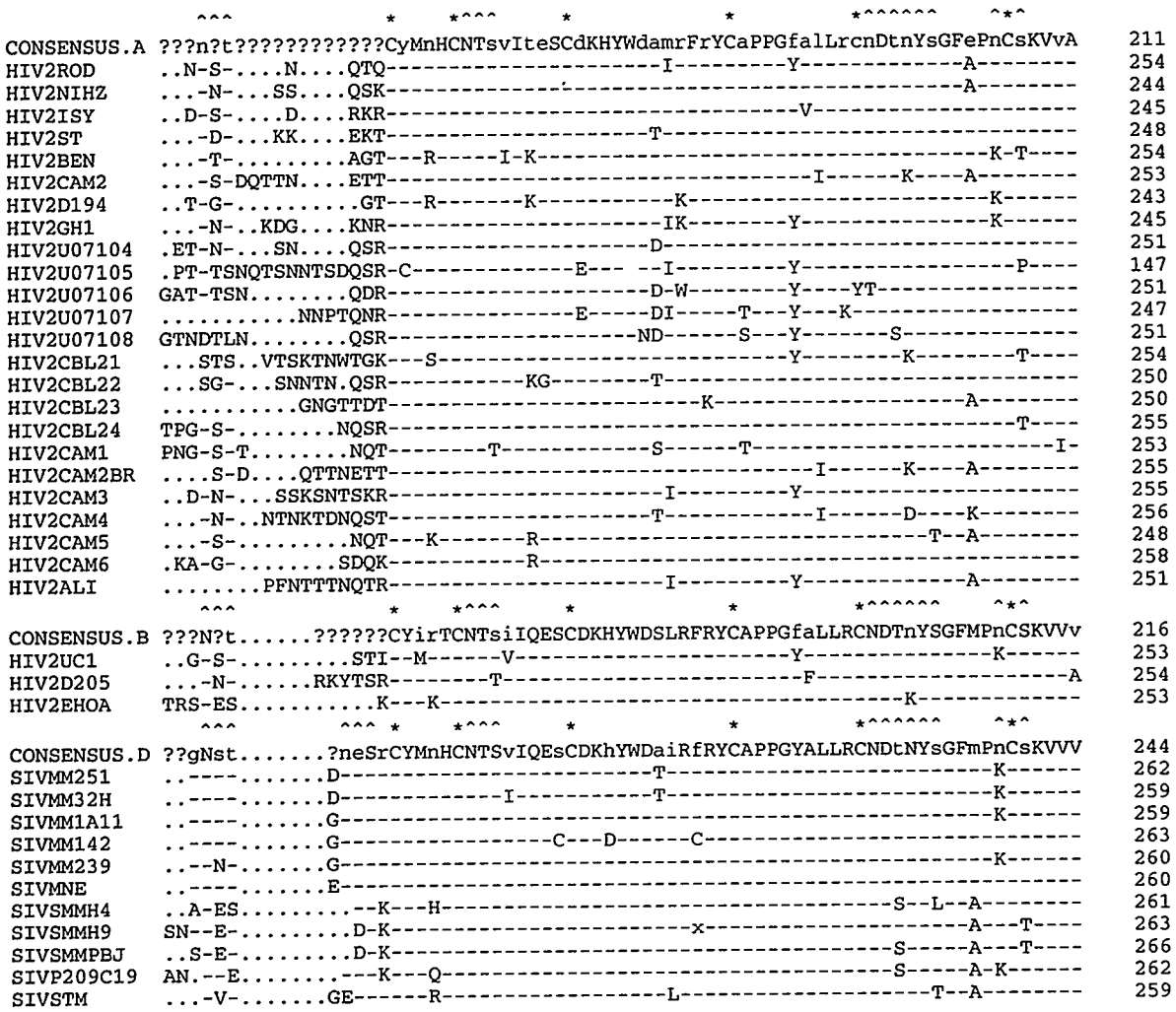
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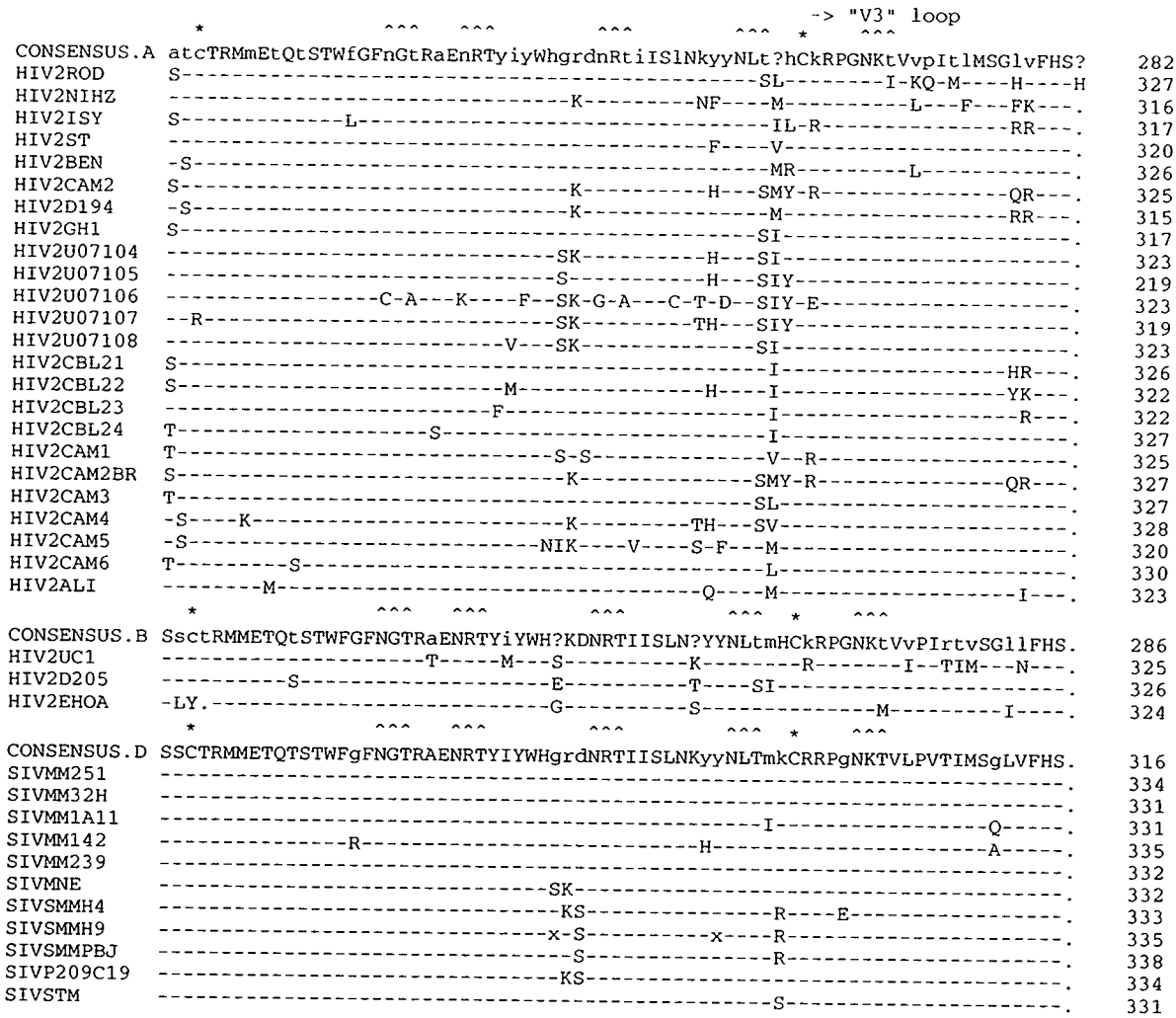
HIV2ROD ..N-S-....N....QTQ----------I---------Y----------A-------- 254
HIV2NIHZ ...-N-...SS....QSK----------.----------A-------- 244
HIV2ISY ..D-S-....D....RKR----------V---------- 245
HIV2ST ...-D-...KK....EKT----------T---------- 248
HIV2BEN ...-T-.....AGT---R-----I-K----------K-T---- 254
HIV2CAM2 ...-S-DQTTN....ETT----------I------K----A-------- 253
HIV2D194 ..T-G-.....GT---R-------K----------K----------K------ 243
HIV2GH1 ...-N-..KDG....KNR----------IK--------Y----------K------ 245
HIV2U07104 .ET-N-...SN....QSR----------D---------- 251
HIV2U07105 .PT-TSNQTSNNTSDQSR-C----------E--- --I---------Y----------P---- 147
HIV2U07106 GAT-TSN.....QDR----------D-W--------Y----YT---------- 251
HIV2U07107 .....NNPTQNR----------E-----DI-----T---Y---K---------- 247
HIV2U07108 GTNDTLN.....QSR----------ND------S---Y-------S---------- 251
HIV2CBL21 ...STS..VTSKTNWTGK---S----------Y--------K--------T---- 254
HIV2CBL22 ...SG-...SNNTN.QSR----------KG--------T---------- 250
HIV2CBL23 .....GNGTTDT----------K----------A-------- 250
HIV2CBL24 TPG-S-.....NQSR----------T---- 255
HIV2CAM1 PNG-S-T.....NQT--------T----------S------T----------I- 253
HIV2CAM2BR ....S-D....QTTNETT----------I------K----A-------- 255
HIV2CAM3 ..D-N-...SSKSNTSKR----------I---------Y---------- 255
HIV2CAM4 ...-N-..NTNKTDNQST----------T----------I------D----K-------- 256
HIV2CAM5 ...-S-.....NQT---K-------R----------T--A-------- 248
HIV2CAM6 .KA-G-.....SDQK----------R---------- 258
HIV2ALI .....PFNTTTNQTR----------I---------Y----------A-------- 251
CONSENSUS.B ???N?t.....??????CYirTCNTsiIQESCDKHYWDSLRFRYCAPPGfaLLRCNDTnYSGFMPnCSKVVv 216
HIV2UC1 ..G-S-.....STI--M------V----------Y----------K------ 253
HIV2D205 ...-N-.....RKYTSR--------T----------F----------A 254
HIV2EHOA TRS-ES.....K---K----------K---------- 253
CONSENSUS.D ??gNst.....?neSrCYMnHCNTSvIQEsCDKhYWDaiRfRYCAPPGYALLRCNDtNYsGFmPnCsKVVV 244
SIVMM251 ..----.....D----------T----------K------ 262
SIVMM32H ..----.....D----------I----------T----------K------ 259
SIVMM1A11 ..----.....G----------K------ 259
SIVMM142 ..----.....G----------C---D------C---------- 263
SIVMM239 ..--N-.....G----------K------ 260
SIVMNE ..----.....E---------- 260
SIVSMMH4 ..A-ES.....--K---H----------S--L--A-------- 261
SIVSMMH9 SN--E-.....D-K----------x----------A---T---- 263
SIVSMMPBJ ..S-E-.....D-K----------S-----A---T---- 266
SIVP209C19 AN.--E.....---K---Q----------S-----A-K------ 262
SIVSTM ...-V-.....GE------R----------L----------T--A-------- 259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CONSENSUS.A atcTRMmEtQtSTWfGFnGtRaEnRTyiyWhgrdnRtiISlNkyyNLt?hCkRPGNKtVvpItlMSGlvFHS? 282
HIV2ROD S---------- 327
HIV2NIHZ ---------- 316
HIV2ISY S---------- 317
HIV2ST ---------- 320
HIV2BEN -S---------- 326
HIV2CAM2 S---------- 325
HIV2D194 -S---------- 315
HIV2GH1 S---------- 317
HIV2U07104 ---------- 323
HIV2U07105 ---------- 219
HIV2U07106 ---------- 323
HIV2U07107 --R---------- 319
HIV2U07108 ---------- 323
HIV2CBL21 S---------- 326
HIV2CBL22 S---------- 322
HIV2CBL23 ---------- 322
HIV2CBL24 T---------- 327
HIV2CAM1 T---------- 325
HIV2CAM2BR S---------- 327
HIV2CAM3 T---------- 327
HIV2CAM4 -S----K---------- 328
HIV2CAM5 -S---------- 320
HIV2CAM6 T---------S---------- 330
HIV2ALI --------M---------- 323
CONSENSUS.B SsctRMMETQtSTWFGFNGTRaENRTYiYWH?KDNRTIISLN?YYNLtmHCkRPGNKtVvPIrtvSGllFHS. 286
HIV2UC1 ----------T-----M---S----------K--------R-------I--TIM---N---. 325
HIV2D205 ----------S----------E----------T----SI---------- 326
HIV2EHOA -LY.----------G----------S----------M---------I----. 324
CONSENSUS.D SSCTRMMETQTSTWFgFNGTRAENRTYIYWHgrdNRTIISLNKyyNLTmkCRRPgNKTVLPVTIMSgLVFHS. 316
SIVMM251 ---------- 334
SIVMM32H ---------- 331
SIVMM1A11 ----------I----------Q-----. 331
SIVMM142 ----------R----------H----------A-----. 335
SIVMM239 ---------- 332
SIVMNE ----------SK---------- 332
SIVSMMH4 ----------KS----------R----E---------- 333
SIVSMMH9 ----------x-S----------x----R---------- 335
SIVSMMPBJ ----------S----------R---------- 338
SIVP209C19 ----------KS---------- 334
SIVSTM ----------S---------- 331

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            "V3" loop <-
                     *                                ^^^                              *
CONSENSUS.A ?qpi?N?rPrQAwCwfkG?WkeAMqEVkqTlakHPRYkg.?tn?t????inf?aPgkgSDpEvayMWtnCRGE   343
HIV2ROD     Y---.-K----------K--D------E--------R-..--D-R..N-S-A-------------------   395
HIV2NIHZ    .--VI-KK--------E-Q---------E----------...-RSRTEN-K-K---R------T---------   385
HIV2ISY     .-K-I-KK------R---E-R----------V--------..--D-N..K---T----D--------------   385
HIV2ST      .---.-R----------E-----K---L----------..--D-E..K-R-I---ER---------------   387
HIV2BEN     .---.-T-------R-G-R-R----------VQ------..I-D-G..K---TK--A-------F--------   393
HIV2CAM2    .R--I-K----------N-T----------E------.TK-I-...D-T-K--ER------T---S-----   393
HIV2D194    .R-VY-KK-G------Q-N-I---R----------G-..--D-G..K---TK--I------T---------   383
HIV2GH1     .---.-T----------K-R----------I--------..--D-K..N---TK--R---------------   384
HIV2U07104  .---.-N----------K----------V-----E-..--K-E..D-H-A---------A----------   390
HIV2U07105  .---.-T-----S--L--Q--------------------..--N-G..K---T----S----A-----I----   286
HIV2U07106  .---.-N---------T-T-R----------V-----R-..--E-R..K---T---------A----------   390
HIV2U07107  .---.-N----------R---------E--T-----R-..--D-G..K---A---------A----------   386
HIV2U07108  .---.-R---------T-K-----R--R--I-E----R-..--N-G..N-K-V---------A----------   390
HIV2CBL21   .R-VI-RK-M------E-K-R----------V-----R-..--K-E..N-T-AG--E----------------   394
HIV2CBL22   .R-VL-TK--------Q-R--------------------..--N-E..S-T-T---R------T---------   390
HIV2CBL23   .--VI-K----------E--G------E----------..--E-K..N---T--------------------   390
HIV2CBL24   .---.-N----------K--------------------..--D-S..K---IG-------------------   394
HIV2CAM1    .---.-R----------N-T----------V-----R-..--D-G..N---T--------------------   392
HIV2CAM2BR  .R--I-K----------N-T----------E-------..-KNIT..D-T-K--ER------T---S-----   395
HIV2CAM3    .---.-T----------K---------E----------..--D-K..K---A---R----------------   394
HIV2CAM4    .---.-M----------E--G--K------LE-------..ATNIN..N-RLAE-------------------   395
HIV2CAM5    .---.-K----------N-R---E-----VV-----R-..EPNKT...V--I--------------------   386
HIV2CAM6    .---.-R--K--------Q-R---E------KE-----K..F-V-N..N-T-E---R----------------   397
HIV2ALI     .---.-K----------E-R-------E--V--------..--D-N..Q---TK--R---A-EV---------   390
                       *    ^^^                      ^^^                          *
CONSENSUS.B .QPi.NkRPrQAWCWFKGNWtEAI?EVKeTIikHPRYkG??tN?t????irl?eh??gSDPEvryMWTNCRGE   346
HIV2UC1     .--L.-T-------------I---R--------------..--N-E..R---VGPSA-------H--------   392
HIV2D205    .---.--------------------K---R----------GAK-I-SV.KL.VS--GK-----TT---------   395
HIV2EHOA    .---.----K--------------Q------KN----S-.T--...ISQ---A--ARS----------------   391
                       *                                ^^^     ^^^              *
CONSENSUS.D .QPi.NeRPKQAWCwFgG?Wk?AIkEvKqtiVKHPRYtG..TNntd..kInltAPgGG.DPEVTFMWTNCRGE   380
SIVMM251    .---.-D----------K--D----------------..-----..----------.--------------   400
SIVMM32H    .---.-D----------N--D----M------------..-----..-------R--.--------------   397
SIVMM1A11   .---.-D---------R-K--D----------------..-----..----------.--------------   397
SIVMM142    .--V.---------R---N--E----------------..---S-..-------R--.--------------   401
SIVMM239    .---.-D----------K--D----------------..-----..----------.--------------   398
SIVMNE      .---.-D--------R-E-N--E----------------..-----..----------.--------------   398
SIVSMMH4    .---.----------E-S--K--Q---E-L--------..--D-R..-------A--.--------------   399
SIVSMMH9    .---.-------------E--E--R---xxL------K-..--xxx..Q-K-------.--------------   401
SIVSMMPBJ   .---.-------------E--K--Q---E-L--------..--K-E..Q-K-------.--------------   404
SIVP209C19  .---.---------R---N-SE--Q---E-L--------..--D-K..-------A--.--------------   400
SIVSTM      .---.-------------E-RG------E-L--------..--D-A..--RIV-----.--------------   397
SIVSTM22579                                                                 --------     8
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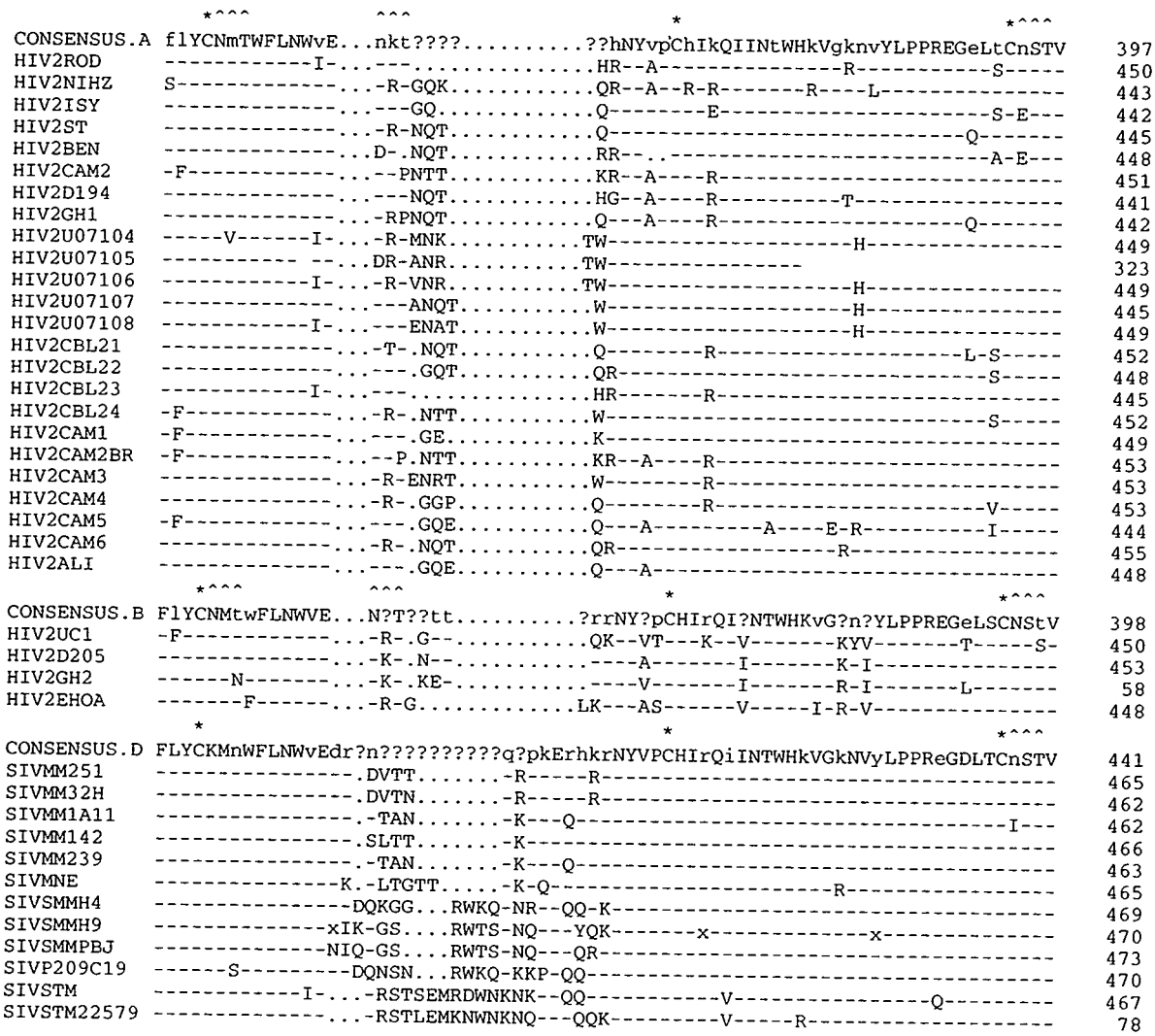
HIV2/SIV ENV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HIV2ROD ----------I-...---.....HR--A----------R----------S----- 450
HIV2NIHZ S----------...-R-GQK.....QR--A--R-R-------R----L---------- 443
HIV2ISY ----------...---GQ.....Q--------E---------S-E--- 442
HIV2ST ----------...-R-NQT.....Q----------Q------- 445
HIV2BEN ----------...D-.NQT.....RR--..----------A-E--- 448
HIV2CAM2 -F----------...--PNTT.....KR--A----R---------- 451
HIV2D194 ----------...---NQT.....HG--A----R----------T---------- 441
HIV2GH1 ----------...-RPNQT.....Q---A----R----------Q------- 442
HIV2U07104 -----V------I-...-R-MNK.....TW----------H---------- 449
HIV2U07105 ---------- --...DR-ANR.....TW---------- 323
HIV2U07106 ----------I-...-R-VNR.....TW----------H---------- 449
HIV2U07107 ----------...---ANQT.....W----------H---------- 445
HIV2U07108 ----------I-...---ENAT.....W----------H---------- 449
HIV2CBL21 ----------...-T-.NQT.....Q--------R----------L-S----- 452
HIV2CBL22 ----------...---.GQT.....QR----------S----- 448
HIV2CBL23 ----------I-...---.....HR-------R---------- 445
HIV2CBL24 -F----------...-R-.NTT.....W----------S----- 452
HIV2CAM1 -F----------...---.GE.....K---------- 449
HIV2CAM2BR -F----------...--P.NTT.....KR--A----R---------- 453
HIV2CAM3 ----------...-R-ENRT.....W--------R---------- 453
HIV2CAM4 ----------...-R-.GGP.....Q--------R----------V----- 453
HIV2CAM5 -F----------...---.GQE.....Q---A---------A----E-R----------I----- 444
HIV2CAM6 ----------...-R-.NQT.....QR----------R---------- 455
HIV2ALI ----------...---.GQE.....Q---A---------- 448
CONSENSUS.B FlYCNMtwFLNWVE...N?T??tt.....?rrNY?pCHIrQI?NTWHKvG?n?YLPPREGeLSCNStV 398
HIV2UC1 -F----------...-R-.G--.....QK--VT---K--V-------KYV-------T-----S- 450
HIV2D205 ----------...-K-.N--.....----A-------I-------K-I---------- 453
HIV2GH2 ------N--------...-K-.KE-.....----V-------I-------R-I-------L------- 58
HIV2EHOA -------F-------...-R-G.....LK---AS------V-----I-R-V---------- 448
CONSENSUS.D FLYCKMnWFLNWvEdr?n??????????q?pkErhkrNYVPCHIrQiINTWHkVGkNVyLPPReGDLTCnSTV 441
SIVMM251 ----------.DVTT.....-R-----R---------- 465
SIVMM32H ----------.DVTN.....-R-----R---------- 462
SIVMM1A11 ----------.-TAN.....-K---Q----------I--- 462
SIVMM142 ----------.SLTT.....-K---------- 466
SIVMM239 ----------.-TAN.....-K---Q---------- 463
SIVMNE ----------K.-LTGTT.....-K-Q----------R---------- 465
SIVSMMH4 ----------DQKGG...RWKQ-NR--QQ-K---------- 469
SIVSMMH9 ----------xIK-GS....RWTS-NQ---YQK-------x----------x---------- 470
SIVSMMPBJ ----------NIQ-GS....RWTS-NQ---QR---------- 473
SIVP209C19 ------S---------DQNSN...RWKQ-KKP-QQ---------- 470
SIVSTM ----------I-...-RSTSEMRDWNKNK--QQ----------V----------Q--------- 467
SIVSTM22579 ----------...-RSTLEMKNWNKNQ---QQK---------V-----R---------- 78

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                          ^^^  ^^^                                  SU \/ TM ?
CONSENSUS.A TSiiANId?????nqt??nITFSAevaeLYrLelGDYkLvEiTpigFAPT?ekRyss.ap?R?krgvfVLGfL  459
HIV2ROD     --------.WQNN---..--------------------------------K------.-HG-HT---------  519
HIV2NIHZ    --------...AGD--..-------A----------------------SV------.-HQ-HT---------  510
HIV2ISY     --------.VDGD-R-..----------------------V--------A------.--G-H----L-----  511
HIV2ST      --------..GGE---..---------------------I-V--------PV-----.--V-N----------  513
HIV2BEN     --------..IDK-R-HT---------------------I----------DQR----.T-V-N----------  518
HIV2CAM2    --------.ERD.---T.------D-------------------------SQ----P.-HG-P---A------  520
HIV2D194    --------..SDG---..----------------------I-V---P----K------.--V-N----------  509
HIV2GH1     --------.VNS.---..----------------------I-V--------R------.--V-N----------  510
HIV2U07104  --------..GG.---..---------------------------------SV-----.-HG-HT         507
HIV2U07106  --------..GG.---..-------------------N------------S-N----.-HG-HT-         508
HIV2U07107  --------..GG.---..--------G-----GI---------S------S---D--.-HG-HRE         504
HIV2U07108  --------..GG.---..--------------------------F-----P------.-HR-HP-x        509
HIV2CBL21   --------.TYG.---..D---------------------------------SV-----.--G-N----P-----  520
HIV2CBL22   ---L----.VNG.---..---------------------------------T------.T-M-N----M-----  516
HIV2CBL23   --------.ANG.-N-..D---------------------------------A------.T-M-N----------  513
HIV2CBL24   --------.VKN.---..---------------------------------S-Q--L-.S-K-N----------  520
HIV2CAM1    --------TDM..-G-ET---------------------------------T------.-HG-Q----------  519
HIV2CAM2BR  --------.ERD.---T.------D-------------------------SQ----P.-HG-P---A------  522
HIV2CAM3    --------.VEA.---..---------------------------------S------.-HK-HT---------  521
HIV2CAM4    --L-----...MR-DST.----------------------I-V--------DQ----P.--T-S----------  521
HIV2CAM5    -------ETNMHKT--..---------D--K--------------------S------.--G-N----------  514
HIV2CAM6    -------N.VD..---S.--------G-----------------------EQ-----.DHG-Q----------  523
HIV2ALI     --L-----TDG..---..---------------------------------S-R----.T-R-N--------L-  516
HIV2GB1222                                                                   --L-----    8
                          ^^^
CONSENSUS.B TSlIANI???sd?N?T??NI?vSAEVsELYrLElGDYKLVEITPIGFAPTe?kRYSS.vtPRNKRGV?VLGFL  460
HIV2UC1     -------DVYY-G-D-KT--TM----G-------------------------I-----.T--------M-----  522
HIV2D205    -------N..--.-S-T.--S-----------------------------DVR----.-K-------M-----  521
HIV2GH2     --I----N..-AN-A-..--S------------P-----------------V-----.-N-------L-----  126
HIV2EHOA    -------D.WI-K-L-..--T---------K--------------------SI-----.---------L-----  517
                          ^^^  ^^^
CONSENSUS.D TSlIAnId.W??gNqT..nITmSAEVAELYRLELGDYKLvEITPIglAPT?VkRYTTggtSRnKRGVFVLGFL  508
SIVMM251    --------.-TD----..S---------------------------------D----------------------  535
SIVMM32H    --------.-TD----..---------------------------------D----------------------  532
SIVMM1A11   --------.-TD----..-------------------------------N-R----------------------  532
SIVMM142    -------N.-TD----..S-------------------------------N----------------------  536
SIVMM239    --------.-ID----..---------------------------------D----------------------  533
SIVMNE      --------.-ID----..---------------------------------N----------------------  535
SIVSMMH4    -----E--.-INS-E-..---------------------I----------S-R----T-A-------------  539
SIVSMMH9    -----E--.-IN--K-..--------------------------F---S------T-A-------------  540
SIVSMMPBJ   -----E--.-IN--E-..-------------------------AF---S------T-A-------------  543
SIVP209C19  -----E--.-INN-E-..---------------------------------D-R----T-A-------------  540
SIVSTM      --I-----.-TNN-E-..---A---------------------------N------.S---T----------  536
SIVSTM22579 --I-----.-TNN-E-..---A---------------------------N------.S---T----------  147
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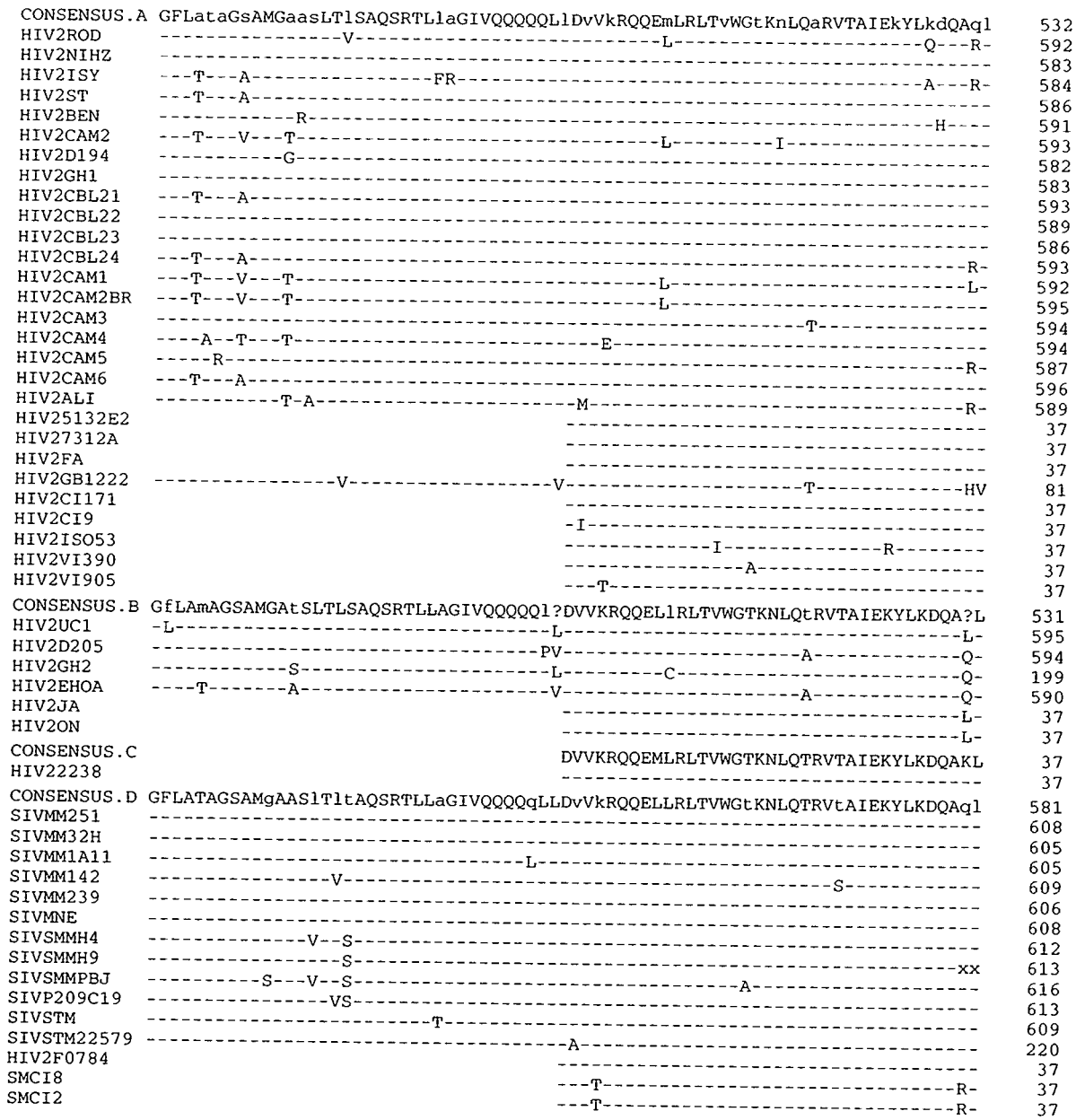
CONSENSUS.A GFLataGsAMGaasLTlSAQSRTLlaGIVQQQQQLlDvVkRQQEmLRLTvWGtKnLQaRVTAIEkYLkdQAql 532
HIV2ROD ----------V----------L----------Q---R- 592
HIV2NIHZ ---------- 583
HIV2ISY ---T---A----------FR----------A---R- 584
HIV2ST ---T---A---------- 586
HIV2BEN ----------R----------H---- 591
HIV2CAM2 ---T---V---T----------L---------I---------- 593
HIV2D194 ----------G---------- 582
HIV2GH1 ---------- 583
HIV2CBL21 ---T---A---------- 593
HIV2CBL22 ---------- 589
HIV2CBL23 ---------- 586
HIV2CBL24 ---T---A----------R- 593
HIV2CAM1 ---T---V---T----------L----------L- 592
HIV2CAM2BR ---T---V---T----------L---------- 595
HIV2CAM3 ----------T---------- 594
HIV2CAM4 ----A--T---T----------E---------- 594
HIV2CAM5 -----R----------R- 587
HIV2CAM6 ---T---A---------- 596
HIV2ALI ----------T-A----------M----------R- 589
HIV25132E2 ---------- 37
HIV27312A ---------- 37
HIV2FA ---------- 37
HIV2GB1222 ----------V----------V----------T----------HV 81
HIV2CI171 ---------- 37
HIV2CI9 -I---------- 37
HIV2ISO53 ----------I----------R--------- 37
HIV2VI390 ----------A---------- 37
HIV2VI905 ---T---------- 37
CONSENSUS.B GfLAmAGSAMGAtSLTLSAQSRTLLAGIVQQQQQl?DVVKRQQELlRLTVWGTKNLQtRVTAIEKYLKDQA?L 531
HIV2UC1 -L----------L----------L- 595
HIV2D205 ----------PV----------A----------Q- 594
HIV2GH2 ----------S----------L---------C----------Q- 199
HIV2EHOA ----T-------A----------V----------A----------Q- 590
HIV2JA ----------L- 37
HIV2ON ----------L- 37
CONSENSUS.C DVVKRQQEMLRLTVWGTKNLQTRVTAIEKYLKDQAKL 37
HIV22238 ---------- 37
CONSENSUS.D GFLATAGSAMgAASlTltAQSRTLLaGIVQQQQqLLDvVkRQQELLRLTVWGtKNLQTRVtAIEKYLKDQAql 581
SIVMM251 ---------- 608
SIVMM32H ---------- 605
SIVMM1A11 ----------L---------- 605
SIVMM142 ----------V----------S---------- 609
SIVMM239 ---------- 606
SIVMNE ---------- 608
SIVSMMH4 ----------V--S---------- 612
SIVSMMH9 ----------S----------xx 613
SIVSMMPBJ ----------S---V--S----------A---------- 616
SIVP209C19 ----------VS---------- 613
SIVSTM ----------T---------- 609
SIVSTM22579 ----------A---------- 220
HIV2F0784 ---------- 37
SMCI8 ---T----------R- 37
SMCI2 ---T----------R- 37

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                  *     *        ^^^       ^^^              ^^^
CONSENSUS.A NSWGCaFRQVChTtVPwvNdsLtPdWnNMTWQeWe?qvryLeANIS?sLEqAQiQQEKNmYELQkLNsWDvfg  603
HIV2ROD     ---------------------A---D--------K----------K----------------------I--  665
HIV2NIHZ    -------------S------T--------------QK---------Q-----------------------T  656
HIV2ISY     --------------------T---E----------HKI-F------E-------------------------  657
HIV2ST      --------------------T--------------QRI-N------E-------------------------  659
HIV2BEN     ---------------------S---K--------K----------Q---E-------------------IL-  664
HIV2CAM2    -----------------A-E---------------QK---------Q---E--L-------------N----T  666
HIV2D194    ------------------------------------KR-H-------Q-------------------------  655
HIV2GH1     ----------------------S------------K----------Q-------------------------  656
HIV2CBL21   ---------------------T-Q---------K--Q-I--------T-------------------------  666
HIV2CBL22   ------------------------R-D--------Q-I--------GQ------------------------  662
HIV2CBL23   --------------------T---E----------GKI-D------QQ------------------------  659
HIV2CBL24   ----------------------Q---------Q--H----------EL------------------------  666
HIV2CAM1    -------------------------A--------QK---------Q-----------------R--------  665
HIV2CAM2BR  -----------------A-E---------------QK---------Q---E--L-------------N----T  668
HIV2CAM3    ------------------------------------QK-H-------EM--------------------I--  667
HIV2CAM4    -----V------------------N----------LRT---D----QL------------------------S  667
HIV2CAM5    -----------------T-----------------HKI-D------D------------------------S  660
HIV2CAM6    ------------------------------------QK---------Q-------------------------  669
HIV2ALI     -------------------N--K---D--------Q----------EQ----------T------------T  662
HIV25132E2  -------------------------D--------ER---------Q-------------------------  110
HIV27312A   -------------------------D-----Q--K-I-D------E-------------------------  110
HIV2FA      ---------------------------------Q--Q-I--------E-------------------------  110
HIV2GB1222  ------------------------------------Q----------ER------------------------  154
HIV2CI171   ----------------L---------K--------M----------QQ------------------------S  110
HIV2CI9     ----------------------A------------E----------EI------------------------  110
HIV2ISO53   -----------Y--------T-----------Q--H-I--------EQ------------------------  110
HIV2VI390   ---------------------K-----------AK---F------QQ------------------------  110
HIV2VI905   --------------------T---N-Q-----Q--Q-I--------A---------------------- -I--  109
                  *     *        ^^^       ^^^              ^^^
CONSENSUS.B NSWGCAFRQVCHTTVPWpNetl?PdWnNMTWQQWEkqVnfLdANITaLLEEAQIQQEkNMYELQKlN?WDvFg  602
HIV2UC1     ----------------------T---E---------R--------------------R---------S-----  668
HIV2D205    ----------------------T-N------------H--------------------------I-S-----  667
HIV2GH2     -------------------D--K---Q--------------E-------------------------S-----  272
HIV2EHOA    -----------------V--S-K------------R--R-------K--------------------Q--I-S  663
HIV2JA      ---------------------H-N-Q--------QK--Y------Q--------------------Q-----  110
HIV2ON      ----------------------IE-----------AK-Q-------Q--------------------Q----S  110
                  *     *        ^^^       ^^^              ^^^
CONSENSUS.C NSWGCAFRQVCHTTVPWVNDSMQPEWQNMTWQQWEKQIAFLEDNITELLEQAQIQQEKNMYELQKLNSWDVFG  110
HIV22238    ------------------------------------------------------------------------  110
                  *     *        ^^^       ^^^              ^^^
CONSENSUS.D NsWGCAFRQVCHTtVpwpN?sLtPdWnNmtWQeWErkvdfLEaNIt?lLEeAQiQQEkNmyELQKLNswDvfG  652
SIVMM251    -A-----------------A--------D-------------E---A-------------------------  681
SIVMM32H    -A-----------------A--------D-------------E---A-------------------------  678
SIVMM1A11   -A-----------------A----K---E-------------E---A-------------------------  678
SIVMM142    -A-----------------A--------E-----------------A-------------------------  682
SIVMM239    -A-----------------A----K---E-------------E---A-------------------------  679
SIVMNE      -A-----------------AN---N---E-------------E---A-------------------------  681
SIVSMMH4    -------------------ET-V-N-----------Q---------Q-----------------------I--  685
SIVSMMH9    -------------x------DT---x----x-----KQ-N-------xx---------x---------xx-xx-  686
SIVSMMPBJ   ----------------R--DT---N----------KQ-N-------QS-----------T----------I--  689
SIVP209C19  -------------------D--V-I-D-----Q---Q--S------Q-------------F---------I--  686
SIVSTM      -------------------D--V-----------------------Q------V-------------------  682
SIVSTM22579 -------------------D--V-----------------------Q------V-------------------  293
HIV2F0784   ---------------E---ST---------------Q---------Q-------------------N--I--  110
SMCI8       -----------------E-DT-Q------------I-IRD-----SEK--N----------------------  110
SMCI2       -A---------------E-NT-Q------------I-IRD-----SES------------------------  110
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HIV2/SIV ENV

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                                                                                                / early stop
CONSENSUS.A NWfDltsWikYiqYGVyivvgiiaLRiviYvvQmlsRlRkGYRPVFSspPgYiQQiHIHkd?eQpareeTEeD    675
HIV2ROD     --------V-------L-I-AV-------------------------------------RG---N------    738
HIV2NIHZ    --L-F---VR-------V----V-------I-------------------------------Q----------    729
HIV2ISY     ----------------M-----V-------------------------------------W---D-------    730
HIV2ST      ----------------------V-------------------------A-F--------R----------    732
HIV2BEN     --------V-------H----------A-----L---F--------------L--------RG---N-G----    737
HIV2CAM2    ---------S-------------V-------------------------S------------P----S------    739
HIV2D194    ----------------------G---A--I--L-----------------L------T-RG---N------    728
HIV2GH1     ---------------------V-V---A--I--L-----------------L------T-RG---N-G----    729
HIV2CBL21   ---------R-----------------I---------F---------P--A-L--V----HRG--PS------    739
HIV2CBL22   ----------------F--I-VV-----------------------------V--------W---D--G----    735
HIV2CBL23   -------------------II--VV------I---------------------L--------W----------    732
HIV2CBL24   -----A-----------VII-------IV-----------------------L------RHW---D-G-----    739
HIV2CAM1    ----------------------V------I-----------------------------L--L--------    738
HIV2CAM2BR  ---------S-------------V-------------------------------P----S------    741
HIV2CAM3    ---------R-------------V---A---I-----F----------------------Q---D-------    740
HIV2CAM4    ---------R------------VV------I---I-----------------L------T-K-----G-----    740
HIV2CAM5    ---------R------F-II-VV-------------------------------------W----NG---G-    733
HIV2CAM6    --------L--V----C--A---V-------------------------------------L----N-G----    742
HIV2ALI     --L---A-V---------I---V-------------------------------------Q---T-G-----    735
HIV25132E2  -------------------A-V-----A--I---------                                    150
HIV27312A   -----A--V-------------V---VI------IG---R                                    150
HIV2FA      --------V-------------V----I-----------R                                    150
HIV2GB1222  --L-----V---H---V-----VV-------------------------------------Q---T-------    227
HIV2CI171   - ----- --------F-----VV--------------R-                                    149
HIV2CI9     ----------------L-II-V-V---A--I--L-------                                   151
HIV2ISO53   -------------------IA---V-----------G---R-                                  151
HIV2VI390   -------------------A-V-----A---------F---                                   151
HIV2VI905   ---------G------C--------------L--IG---R-                                  150
CONSENSUS.B NWFDfTSWmayirLGLYvVaGliVLRIviYI?QMLArLRKGYRPVFSSPPSYTQQIPIRKdRGQPANEETEeg    674
HIV2UC1     ------------------------------M-------------------------H----------DE    741
HIV2D205    ----L---IK--H----I----V-----V--V-------------------------------------    740
HIV2GH2     ----L---IK--H---------------V--V----------------------------G----------    345
HIV2EHOA    -----------------I-I-IV----A---I-------------------------------------    736
HIV2JA      ------------K-----------------I----K---                                   150
HIV2ON      ----------HL---------I---------M--------                                  150
CONSENSUS.C NWLDLTSWVKYIYLGFYIVAGVIVLRIAIYVVQMLMRLRKG                                  151
HIV22238    ----------------------------------------                                   151
CONSENSUS.D NwfDltsWikYIqyGvyivvGvi?LRiviY?vQmLaklrqGYRPVFSSPPsyfqq?hiqq?q?lpTkEG?egd    719
SIVMM251    -----A---------I-V-----L------I---------------------- T-T--DPA---R--K---    753
SIVMM32H    -----A-----------------L------I-----------------------T----DPA---R--K---    751
SIVMM1A11   -----A-----------------L------I---------------------- T----D-A---R--K---    750
SIVMM142    ---------------I--I----L------I-----R----------------- T-T--DPA------KK--    754
SIVMM239    -----A-----------------L------I-----------------------T----DPA---R--K-R-    752
SIVMNE      -----A---R-------------L------I----------------------XT--R-D-A------T---    754
SIVSMMH4    ---------R------L--L---G------V-----R-------------A-V--IP-HKG-EP-----E---    758
SIVSMMH9    --x---x---------L--L---G------V-----R-------------AxVx-IP-xTG-E------E---    759
SIVSMMPBJ   ----------------L--L---G------V-----R-------------A-V--IP--TG-E------E---    762
SIVP209C19  ---------R------L--L--VG------V-----R-------------A-V--IP-HKG-EP-----E--E    759
SIVSTM      --------VR-------L-I-LVM--VA--IM-L--R--K-----------CR--IP-HKG-EQ-----T-EG    755
SIVSTM22579 -----A--VR-------L-I-IVM--VA--V-----R--K-----------H--IL-HKG-EQL----T-EG    366
HIV2F0784   ---------------F----I-L---I--V-------SK                                    150
SMCI8       ----F---V---YI-F-V---I-G----V-LI-L-G-H-K                                   150
SMCI2       -R--F---V---YI-F-V---I-G---IV-LI-L-G---K                                   150
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                                                                                                  nef start ->
                                <- tat cds                  *                                        <- rev cds
CONSENSUS.A vg?n?Gdr?WPWpiayihflirllirlltglyniCRdLlSr?f?tlqpi?q?l????t??RDWlRlkaAyLQY    735
HIV2ROD     G-S-G---Y------------Q------R--S--------S-L---L-Y-N-.....------RT-F---    804
HIV2NIHZ    --S-G---S-------------------------------ISPI----F-S-QRAL-AI-------------    802
HIV2ISY     --NDV-S-S-----E--------------R---S-------....-YL-L-P-.....-------------    792
HIV2ST      --NSV--NW-----R-------Q-----NR-----------S-Q---L-S-S-RRAL-AV-----FNT-----    805
HIV2BEN     --GDS-YDL-----N-VQ---H--T---I-----------KNSP-RRL-S-S-....-AI---------Q---    806
HIV2CAM2    --G-G---S---Q-E-------Q-------------N----I-Q-----L-N-.....-----P-V-F---    805
HIV2D194    A-DDS-FGL----LN--Q---H--T--------S--G---KNSP-RRL-S-S-....-AI-------------    797
HIV2GH1     DRDDD-YDL ----N------H--T-------K-------TNSP-HRL-S-N-....-AI-------------    797
HIV2CBL21   --DSV--SS-- ----------------I-------T-I-KS-Q-----S-G-QRAL-AI-----PG------    811
HIV2CBL22   --D-A-SSS-- --R-------Q-V----W--SS-------S-LI--A-.....-------------------    796
HIV2CBL23   --N-V--SL ----R------HQ-------------N----ISL--R-VF-S-QRAL-AI-----TD------    804
HIV2CBL24   --D-V-TSL-------------------I------------SSLI----L-S-QRAL-AI------E------    812
HIV2CAM1    --S-V---F-------------------R---S-------I-L-----L-N-.....-----AST-F---    804
HIV2CAM2BR  --G-G---S---Q-E.....------N----I-Q-----L-N-.....-----P-V-F---    789
HIV2CAM3    --I-G---S-------T------------R---S-------S-L-----F-N-.....------RT-F---    806
HIV2CAM4    --D-V--SL-------L------------R--SS-------S-P---RA.....L-AI-------------    806
HIV2CAM5    G-N-A--NS---Q-R-------Q----------S--N---KS-L---L-.....------NT-F---    795
HIV2CAM6    --N-G-Y-S--------------------R--SS-------S-L-----L-N-.....------RT-F---    808
HIV2ALI     --D-V---L-------L----H--A---I---S--------I-SI----F-S-QRAL-TI-----------    808
HIV2GB1222  --S-V---F---------------S---I----S--N----I-L-----F-N-.....---P--RT-F---    293
                                          *
CONSENSUS.B GGndggYRSWPWQIEYiHFl?RQlRnLLIWLYngCrtLLlKTfq?Lqpi???lq.....pLRLpvAYLqY    734
HIV2UC1     ---E-A----------A---I--------------N-----S-I---A...--.....----SL-----    803
HIV2D205    -----D-------------L----------------------I-HQ-STN--.....----------    805
HIV2GH2     --E----------------L--P---------S-S-------RT----LQP.....---L------    407
HIV2EHOA    ---NE--------------PI----D------S------S----T---V...--.....-----P---R-    798
              ^^^                .   *
CONSENSUS.D GG??GGnsSWPwQIEYiHFLIRQLiRLLTWLfsncRtlLsR?yQiLqPilQrlS?tLqRiREVlR?eltYLQY    787
SIVMM251    --EG-------------------------------------A----------A--R-V-----T-------    826
SIVMM32H    --EG-------------------------------------A----------AA---------T-------    824
SIVMM1A11   --EG-----------------------------------V----------A--R-------T-------    823
SIVMM142    --GS-----------------------------------A-------F----A--R-------L-------    827
SIVMM239    --EG-----------------------------------V----------A----------T-------    825
SIVMNE      --GS-----------------------------------A-------F--F-T----------T-------    827
SIVSMMH4    --DR--SR-----------------------S--DW-L-S------V--S--T----V---I-I-IA----    831
SIVSMMH9    --xR---R---x-------------------S--DW-L-xC-----V--S--R----A---I-V-I-----    832
SIVSMMPBJ   --GR---R-----------------------S--DW-L-NC-T---V--S--R----A---I-VQIA----    835
SIVP209C19  --DR--SR-----------------------S--DW-L-S------V-----T----V---I-I-I-----    832
SIVSTM      --DR--IN--------T-------V------YN-F-AC---I--T-H-TF--I-RI-------V-LGAA----    828
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HIV2/SIV ENV

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                 *
CONSENSUS.A GceWIQeAfqAfaratrETlagawr?lwg?l?riGRgILavPRRIRQGAEiaLL  786
HIV2ROD     ----------A----------C-G--RV-E--------------------    858
HIV2NIHZ    ----------L--T--------G-D--RA-Q-----------------L---  856
HIV2ISY     ----------L--V-----TS-G-S---A-G--------------------    846
HIV2ST      -G-------R------G---TN---GF--T-GQ-------------------    859
HIV2BEN     --------------T---------GW--EAAR-----------------L---  860
HIV2CAM2    ----------A---A-------C-DV--M-Q-----------------L---  859
HIV2D194    ---------R----TA---I-----G-CEAAQ-------------------    851
HIV2GH1     -G----------KT------S--GG-CAAVQ-V------------------    851
HIV2CBL21   --------L----------TSV--NFC-TMGQ-------I---------L---  865
HIV2CBL22   ---------R---KF----------D---G-G----E-----------------  850
HIV2CBL23   ------G---------------T--D---A-Q-------------------    858
HIV2CBL24   --------L--LT-----------N---A-Q-----------------L---  866
HIV2CAM1    ------------G--AK---TS-C-S--RT-G-----------------L---  858
HIV2CAM2BR  ----------A---A-------C-D--EV-Q-------V----------L---  843
HIV2CAM3    -RQ----------------TS-C-G--RT-DNF-----SI-------------  860
HIV2CAM4    --------------TA---------N--EAMG-L---------------L---  860
HIV2CAM5    --------------------TS-G-S---T-G-----------------L---  849
HIV2CAM6    --------------FA-----S-C-S---T-G--------I-------------  862
HIV2ALI     --------------IA----TNT--D---AMQWV--R----------------  862
HIV2GB1222  ----------A----------C-G---T-G------------------T--   347
CONSENSUS.B GIsWFQEA??AAaRa??ETLAsag?tlWeaLRRaAgaIiAIPRRIRQglELaLL  783
HIV2UC1     --------IQ--T--AR----NT-RA--K----T-E----------------  857
HIV2D205    --------LR-----TG-------E----------R--------------T--  859
HIV2GH2     --D-----LR----VTR-------E-F--I---M----V--------R------  461
HIV2EHOA    --------IQ-----AG------AR-S-GV------E----------A-----  852
CONSENSUS.D GwsyfqEAvqa?wrsatETLAgAwgdlWEtLgRvGRwIlAIprRiRQGLELtLL  840
SIVMM251    -----H-----G----------R------R-G--------------------  880
SIVMM32H    ----------VG-------------------R-G--------------------  878
SIVMM1A11   --N--H----VD--------------- -A-R-G--------------------  876
SIVMM142    ----------AQ-----------E---A-Q-G--------------------  881
SIVMM239    -----H-----V--------------------R-G------------------  879
SIVMNE      ----------VA-----------------------------------------  881
SIVSMMH4    --R--------W-KL-R----S----I---------G----------------  885
SIVSMMH9    --R-L---AxxW-KFxR----S--R----------G----xx-----------  886
SIVSMMPBJ   --R-L---A--W-KFVR----S--R----------G----------------  889
SIVP209C19  ----------W-KF-R----S--R-I---------G-------V------A--  886
SIVSTM      -CIWI---A--A--A-G----S-GR----------R-G---------------  882
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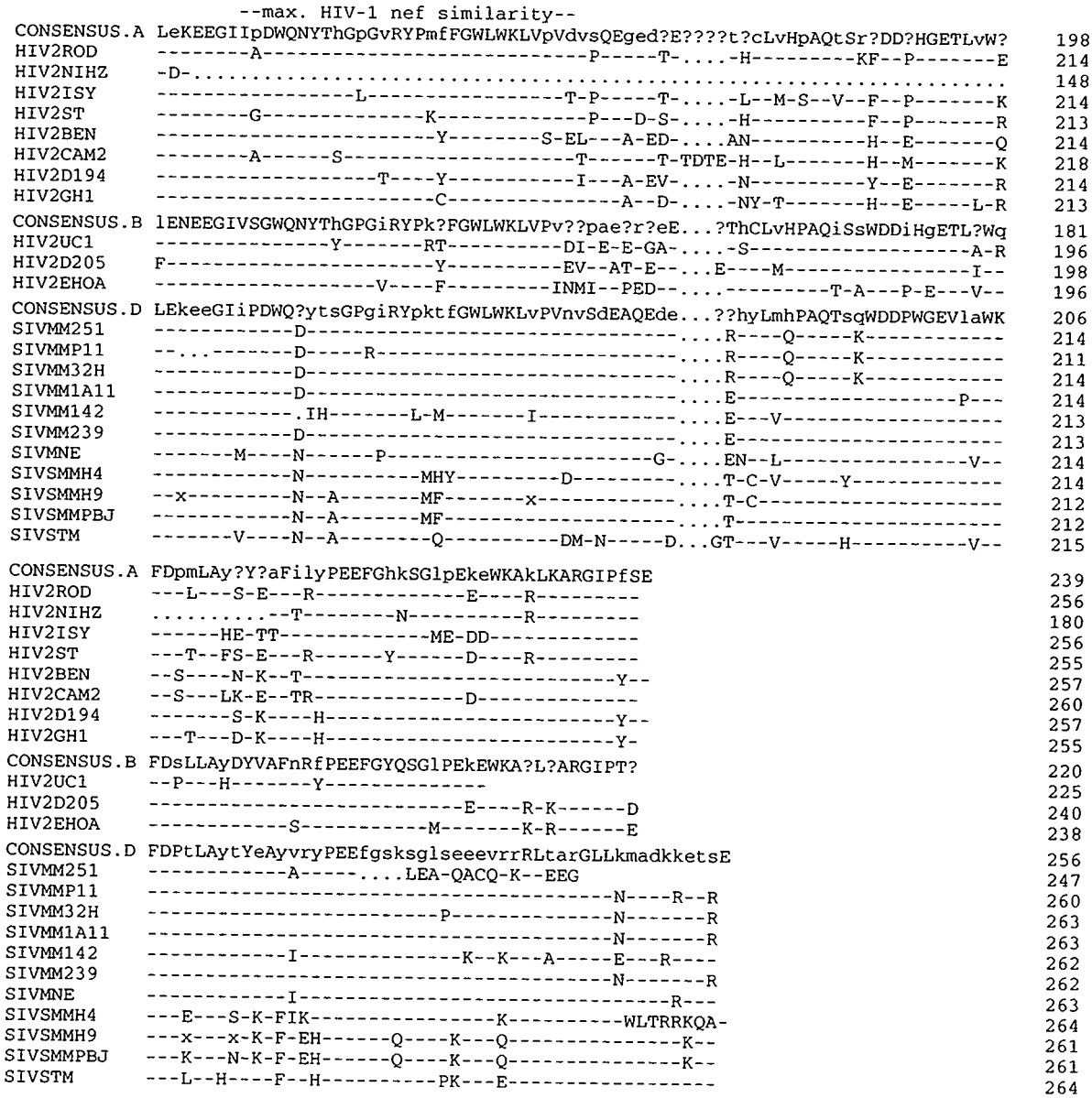
HIV2/SIV NEF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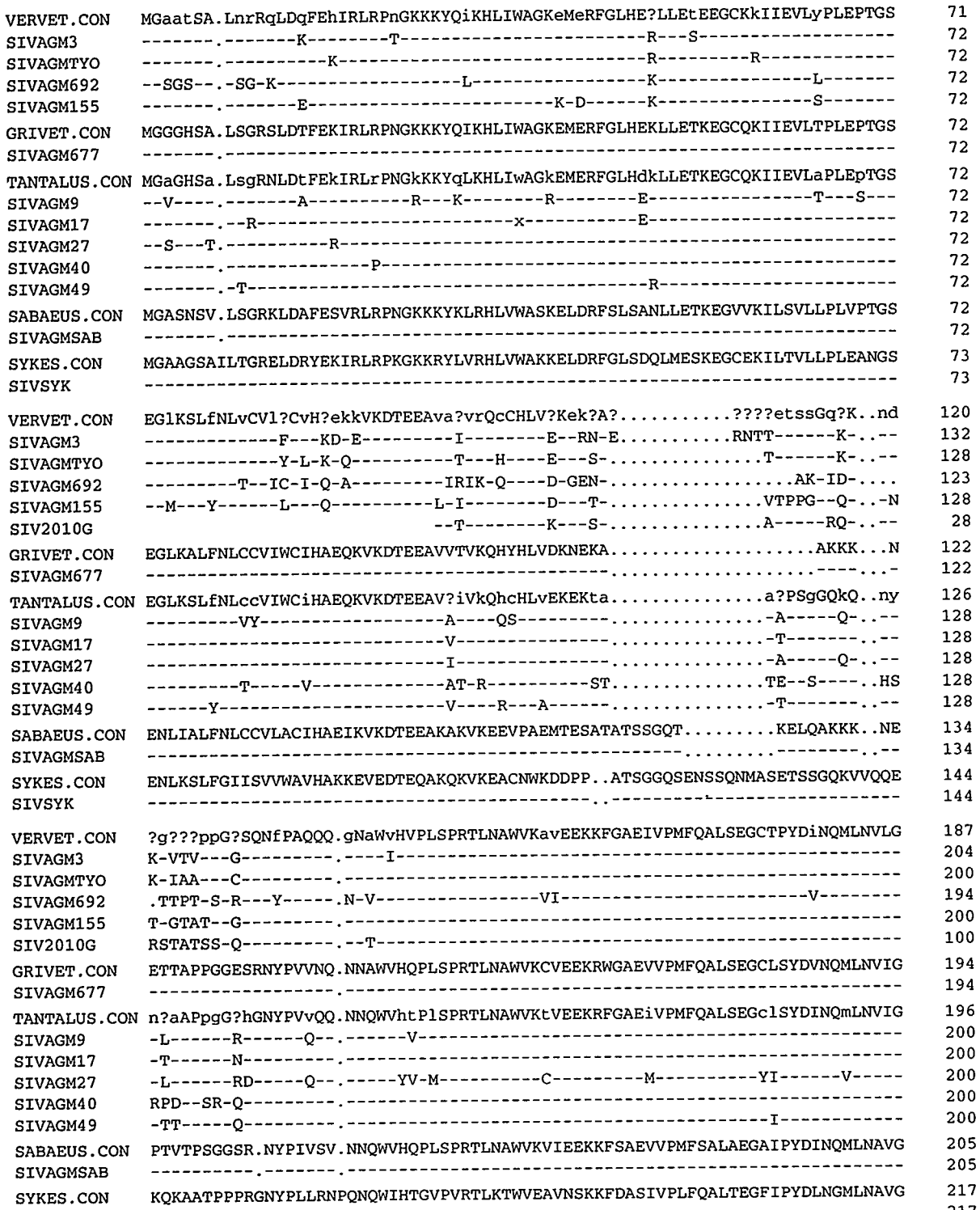
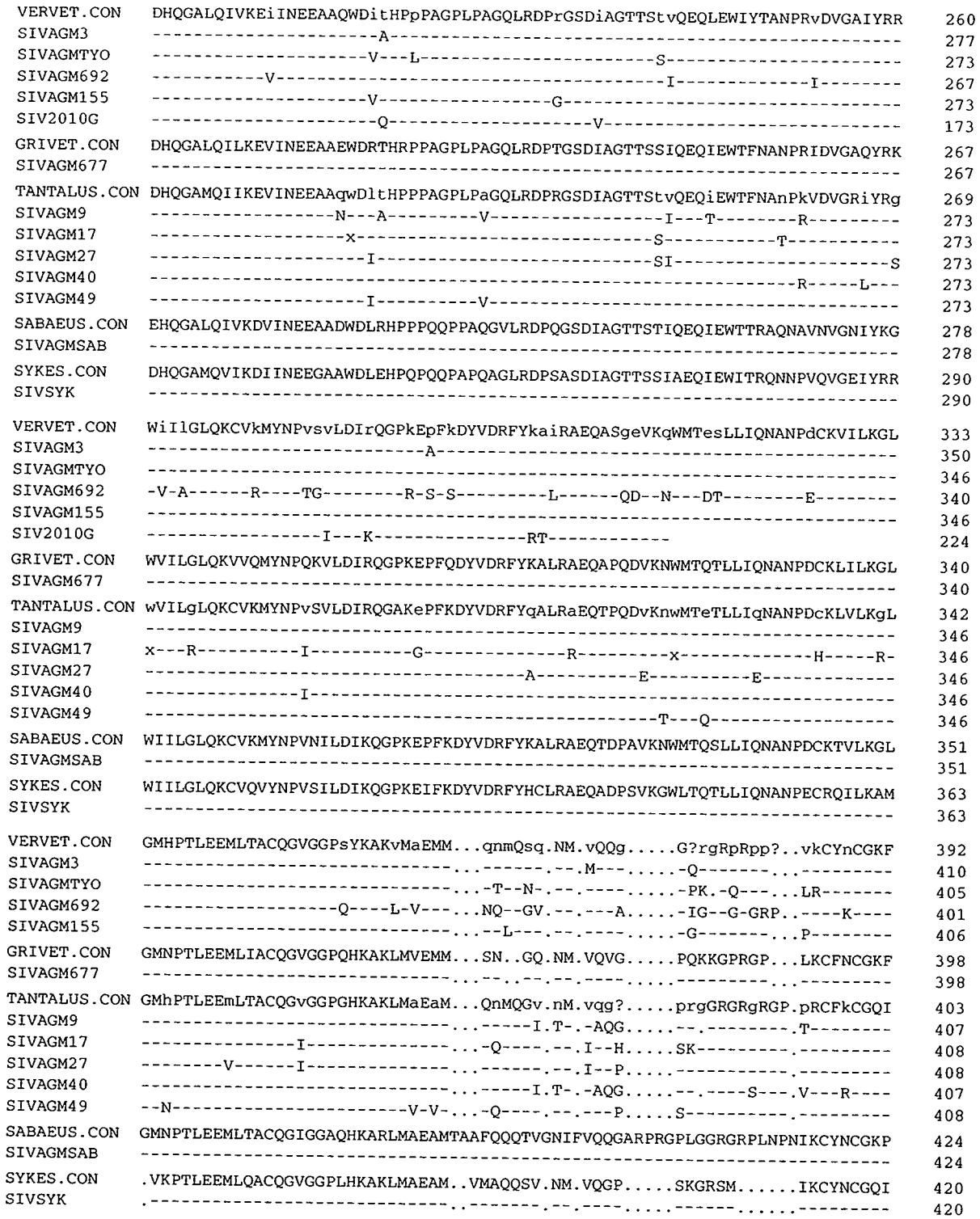
CONSENSUS.A LeKEEGIIpDWQNYThGpGvRYPmfFGWLWKLVpVdvsQEged?E????t?cLvHpAQtSr?DD?HGETLvW? 198
HIV2ROD --------A----------P-----T-....-H---------KF--P-------E 214
HIV2NIHZ -D-.....-- 148
HIV2ISY ----------L----------T-P-----T-....-L--M-S--V--F--P-------K 214
HIV2ST --------G----------K----------P---D-S-....-H----------F--P-------R 213
HIV2BEN ----------Y--------S-EL---A-ED-....AN----------H--E-------Q 214
HIV2CAM2 --------A------S----------T------T-TDTE-H--L-------H--M-------K 218
HIV2D194 ----------T----Y----------I---A-EV-....-N---------Y--E-------R 214
HIV2GH1 ----------C----------A--D-....-NY-T-------H--E-----L-R 213
CONSENSUS.B lENEEGIVSGWQNYThGPGiRYPk?FGWLWKLVPv??pae?r?eE...?ThCLvHPAQiSsWDDiHgETL?Wq 181
HIV2UC1 ----------Y-------RT----------DI-E-E-GA-....-S----------A-R 196
HIV2D205 F----------Y----------EV--AT-E--...E----M----------I-- 198
HIV2EHOA ----------V----F---------INMI--PED--....---------T-A---P-E---V-- 196
CONSENSUS.D LEkeeGIiPDWQ?ytsGPgiRYpktfGWLWKLvPVnvSdEAQEde...??hyLmhPAQTsqWDDPWGEVlaWK 206
SIVMM251 ----------D----------....R----Q-----K---------- 214
SIVMMP11 --...--------D-----R----------....R----Q-----K---------- 211
SIVMM32H ----------D----------....R----Q-----K---------- 214
SIVMM1A11 ----------D----------....E----------P--- 214
SIVMM142 ----------.IH-------L-M-------I----------....E---V---------- 213
SIVMM239 ----------D----------....E---------- 213
SIVMNE -------M----N------P----------G-....EN--L----------V-- 214
SIVSMMH4 ----------N----------MHY---------D---------....T-C-V-----Y---------- 214
SIVSMMH9 --x---------N--A-------MF-------x----------....T-C---------- 212
SIVSMMPBJ ----------N--A-------MF----------....T---------- 212
SIVSTM -------V----N--A--------Q----------DM-N-----D...GT---V-----H----------V-- 215
CONSENSUS.A FDpmLAy?Y?aFilyPEEFGhkSGlpEkeWKAkLKARGIPfSE 239
HIV2ROD ---L---S-E---R----------E----R--------- 256
HIV2NIHZ ....--T--------N----------R--------- 180
HIV2ISY ------HE-TT----------ME-DD---------- 256
HIV2ST ---T--FS-E---R------Y------D----R--------- 255
HIV2BEN --S----N-K--T----------Y-- 257
HIV2CAM2 --S---LK-E--TR----------D---------- 260
HIV2D194 -------S-K----H----------Y-- 257
HIV2GH1 ---T---D-K----H----------Y- 255
CONSENSUS.B FDsLLAyDYVAFnRfPEEFGYQSGlPEkEWKA?L?ARGIPT? 220
HIV2UC1 --P---H-------Y---------- 225
HIV2D205 ----------E----R-K------D 240
HIV2EHOA ----------S----------M-------K-R------E 238
CONSENSUS.D FDPtLAytYeAyvryPEEfgsksglseeevrrRLtarGLLkmadkketsE 256
SIVMM251 ----------A-----....LEA-QACQ-K--EEG 247
SIVMMP11 ----------N----R--R 260
SIVMM32H ----------P----------N-------R 263
SIVMM1A11 ----------N-------R 263
SIVMM142 ----------I----------K--K---A-----E---R---- 262
SIVMM239 ----------N-------R 262
SIVMNE ----------I----------R--- 263
SIVSMMH4 ---E---S-K-FIK----------K----------WLTRRKQA- 264
SIVSMMH9 ---x---x-K-F-EH------Q----K---Q----------K-- 261
SIVSMMPBJ ---K---N-K-F-EH------Q----K---Q----------K-- 261
SIVSTM ---L--H----F--H----------PK---E---------- 264


VERVET.CON MGaatSA.LnrRqLDqFEhIRLRPnGKKKYQiKHLIWAGKeMeRFGLHE?LLEtEEGCKkIIEVLyPLEPTGS 71
SIVAGM3 -------.-------K--------T----------R---S---------- 72
SIVAGMTYO -------.----------K----------R---------R---------- 72
SIVAGM692 --SGS--.-SG-K----------L----------K----------L------- 72
SIVAGM155 -------.-------E----------K-D------K----------S------- 72
GRIVET.CON MGGGHSA.LSGRSLDTFEKIRLRPNGKKKYQIKHLIWAGKEMERFGLHEKLLETKEGCQKIIEVLTPLEPTGS 72
SIVAGM677 -------.---------- 72
TANTALUS.CON MGaGHSa.LsgRNLDtFEkIRLrPNGkKKYqLKHLIwAGkEMERFGLHdkLLETKEGCQKIIEVLaPLEpTGS 72
SIVAGM9 --V----.-------A----------R---K--------R--------E----------T---S--- 72
SIVAGM17 -------.--R----------x----------E---------- 72
SIVAGM27 --S---T.----------R---------- 72
SIVAGM40 -------.----------P---------- 72
SIVAGM49 -------.-T----------R---------- 72
SABAEUS.CON MGASNSV.LSGRKLDAFESVRLRPNGKKKYKLRHLVWASKELDRFSLSANLLETKEGVVKILSVLLPLVPTGS 72
SIVAGMSAB -------.---------- 72
SYKES.CON MGAAGSAILTGRELDRYEKIRLRPKGKKRYLVRHLVWAKKELDRFGLSDQLMESKEGCEKILTVLLPLEANGS 73
SIVSYK ---------- 73
VERVET.CON EGlKSLfNLvCVl?CvH?ekkVKDTEEAva?vrQcCHLV?Kek?A?.....????etssGq?K..nd 120
SIVAGM3 ----------F---KD-E---------I---------E--RN-E.....RNTT------K-..-- 132
SIVAGMTYO ----------Y-L-K-Q----------T---H----E---S-.....T------K-..-- 128
SIVAGM692 ---------T--IC-I-Q-A---------IRIK-Q----D-GEN-.....AK-ID-.... 123
SIVAGM155 --M---Y------L---Q----------L-I---------D---T-.....VTPPG--Q-..-N 128
SIV2010G --T--------K---S-.....A-----RQ-..-- 28
GRIVET.CON EGLKALFNLCCVIWCIHAEQKVKDTEEAVVTVKQHYHLVDKNEKA.....AKKK...N 122
SIVAGM677 ----------.....----...- 122
TANTALUS.CON EGLKSLfNLccVIWCiHAEQKVKDTEEAV?iVkQhcHLvEKEKta.....a?PSgGQkQ..ny 126
SIVAGM9 ---------VY----------A----QS---------.....-A-----Q-..-- 128
SIVAGM17 ----------V----------.....-T-------.-- 128
SIVAGM27 ----------I----------.....-A-----Q-..-- 128
SIVAGM40 ---------T-----V----------AT-R----------ST.....TE--S-----..HS 128
SIVAGM49 ------Y----------V----R---A------.....-T-------.-- 128
SABAEUS.CON ENLIALFNLCCVLACIHAEIKVKDTEEAKAKVKEEVPAEMTESATATSSGQT.....KELQAKKK..NE 134
SIVAGMSAB ----------.....---------.-- 134
SYKES.CON ENLKSLFGIISVVWAVHAKKEVEDTEQAKQKVKEACNWKDDPP..ATSGGQSENSSQNMASETSSGQKVVQQE 144
SIVSYK ----------..---------- 144
VERVET.CON ?g???ppG?SQNfPAQQQ.gNaWvHVPLSPRTLNAWVKavEEKKFGAEIVPMFQALSEGCTPYDiNQMLNVLG 187
SIVAGM3 K-VTV---G---------.----I---------- 204
SIVAGMTYO K-IAA---C---------.---------- 200
SIVAGM692 .TTPT-S-R---Y-----.N-V----------VI----------V--------- 194
SIVAGM155 T-GTAT--G---------.---------- 200
SIV2010G RSTATSS-Q---------.--T---------- 100
GRIVET.CON ETTAPPGGESRNYPVVNQ.NNAWVHQPLSPRTLNAWVKCVEEKRWGAEVVPMFQALSEGCLSYDVNQMLNVIG 194
SIVAGM677 ----------.---------- 194
TANTALUS.CON n?aAPpgG?hGNYPVvQQ.NNQWVhtPlSPRTLNAWVKtVEEKRFGAEiVPMFQALSEGclSYDINQmLNVIG 196
SIVAGM9 -L------R------Q--.------V---------- 200
SIVAGM17 -T------N---------.---------- 200
SIVAGM27 -L------RD-----Q--.-----YV-M----------C---------M----------YI------V----- 200
SIVAGM40 RPD--SR-Q---------.---------- 200
SIVAGM49 -TT-----Q---------.----------I---------- 200
SABAEUS.CON PTVTPSGGSR.NYPIVSV.NNQWVHQPLSPRTLNAWVKVIEEKKFSAEVVPMFSALAEGAIPYDINQMLNAVG 205
SIVAGMSAB ----------.-------.---------- 205
SYKES.CON KQKAATPPPRGNYPLLRNPQNQWIHTGVPVRTLKTWVEAVNSKKFDASIVPLFQALTEGFIPYDLNGMLNAVG 217
SIVSYK ---------- 217

AGM GAG


VERVET.CON DHQGALQIVKEiINEEAAQWDitHPpPAGPLPAGQLRDPrGSDiAGTTStvQEQLEWIYTANPRvDVGAIYRR 260
SIVAGM3 ----------A---------- 277
SIVAGMTYO ----------V---L----------S---------- 273
SIVAGM692 ----------V----------I----------I-------- 267
SIVAGM155 ----------V----------G---------- 273
SIV2010G ----------Q----------V---------- 173
GRIVET.CON DHQGALQILKEVINEEAAEWDRTHRPPAGPLPAGQLRDPTGSDIAGTTSSIQEQIEWTFNANPRIDVGAQYRK 267
SIVAGM677 ---------- 267
TANTALUS.CON DHQGAMQIIKEVINEEAAqwDltHPPPAGPLPaGQLRDPRGSDIAGTTStvQEQiEWTFNAnPkVDVGRiYRg 269
SIVAGM9 ----------N---A---------V----------I---T--------R--------- 273
SIVAGM17 ----------x----------S----------T---------- 273
SIVAGM27 ----------I----------SI----------S 273
SIVAGM40 ----------R-----L--- 273
SIVAGM49 ----------I----------V---------- 273
SABAEUS.CON EHQGALQIVKDVINEEAADWDLRHPPPQQPPAQGVLRDPQGSDIAGTTSTIQEQIEWTTRAQNAVNVGNIYKG 278
SIVAGMSAB ---------- 278
SYKES.CON DHQGAMQVIKDIINEEGAAWDLEHPQPQQPAPQAGLRDPSASDIAGTTSSIAEQIEWITRQNNPVQVGEIYRR 290
SIVSYK ---------- 290
VERVET.CON WiIlGLQKCVkMYNPvsvLDIrQGPkEpFkDYVDRFYkaiRAEQASgeVKqWMTesLLIQNANPdCKVILKGL 333
SIVAGM3 ----------A---------- 350
SIVAGMTYO ---------- 346
SIVAGM692 -V-A------R----TG--------R-S-S---------L------QD--N---DT--------E--------- 340
SIVAGM155 ---------- 346
SIV2010G ----------I---K----------RT---------- 224
GRIVET.CON WVILGLQKVVQMYNPQKVLDIRQGPKEPFQDYVDRFYKALRAEQAPQDVKNWMTQTLLIQNANPDCKLILKGL 340
SIVAGM677 ---------- 340
TANTALUS.CON wVILgLQKCVKMYNPvSVLDIRQGAKePFKDYVDRFYqALRaEQTPQDvKnwMTeTLLIqNANPDcKLVLKgL 342
SIVAGM9 ---------- 346
SIVAGM17 x---R----------I----------G----------R---------x----------H-----R- 346
SIVAGM27 ----------A----------E----------E---------- 346
SIVAGM40 ----------I---------- 346
SIVAGM49 ----------T---Q---------- 346
SABAEUS.CON WIILGLQKCVKMYNPVNILDIKQGPKEPFKDYVDRFYKALRAEQTDPAVKNWMTQSLLIQNANPDCKTVLKGL 351
SIVAGMSAB ---------- 351
SYKES.CON WIILGLQKCVQVYNPVSILDIKQGPKEIFKDYVDRFYHCLRAEQADPSVKGWLTQTLLIQNANPECRQILKAM 363
SIVSYK ---------- 363
VERVET.CON GMHPTLEEMLTACQGVGGPsYKAKvMaEMM...qnmQsq.NM.vQQg.....G?rgRpRpp?..vkCYnCGKF 392
SIVAGM3 ----------...-------.--.M---.....-Q-------...--------- 410
SIVAGMTYO ----------...-T--N-.--.----.....-PK.-Q---...LR------- 405
SIVAGM692 ----------Q----L-V---...NQ--GV.--.---A.....-IG--G-GRP..----K---- 401
SIVAGM155 ----------...--L---.--.----.....-G-------...P--------- 406
GRIVET.CON GMNPTLEEMLIACQGVGGPQHKAKLMVEMM...SN..GQ.NM.VQVG.....PQKKGPRGP...LKCFNCGKF 398
SIVAGM677 ----------...--.-.--.--.----.....---------...--------- 398
TANTALUS.CON GMhPTLEEmLTACQGvGGPGHKAKLMaEaM...QnMQGv.nM.vqg?.....prgGRGRgRGP.pRCFkCGQI 403
SIVAGM9 ----------...-----I.T-.-AQG.....--.---------.T-------- 407
SIVAGM17 ----------I----------...-Q----.--.I--H.....SK---------.--------- 408
SIVAGM27 --------V------I----------...-------.--.I--P.....----------.--------- 408
SIVAGM40 ----------...-----I.T-.-AQG.....--.----S---.V---R---- 407
SIVAGM49 --N----------V-V-...-Q----.--.---P.....S----------.--------- 408
SABAEUS.CON GMNPTLEEMLTACQGIGGAQHKARLMAEAMTAAFQQQTVGNIFVQQGARPRGPLGGRGRPLNPNIKCYNCGKP 424
SIVAGMSAB ---------- 424
SYKES.CON .VKPTLEEMLQACQGVGGPLHKAKLMAEAM..VMAQQSV.NM.VQGP.....SKGRSM......IKCYNCGQI 420
SIVSYK .----------..-------.--.----.....------.....--------- 420

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VERVET.CON    GHmQrqCpeprk?kCLKCGKpGHlAkDCR.........GqVNFLGYG.RWMGaKPrNFp...aatlgaePsA   450
SIVAGM3       -----------MR--------------.........---------.-----------...-----V--T-   469
SIVAGMTYO     -----------T-------L--------.........---------.-----------...----------   464
SIVAGM692     --V-KN-TQKGPVV---------F-R---.........-A-------.-------K--....LEHRA-V---   459
SIVAGM155     -----------I----------------.....................----T------...----------   465
GRIVET.CON    GHMQRECKAPRQIKCFKCGKIGHMAKDCKN.........GQANFLGYG.HWGGAKPRNFVQYRGDTVGLEPTA   461
SIVAGM677     ----------------------------.........---------.------------------------   461
TANTALUS.CON  GHiQKDCprgGPiKCLKCGKPgHmAkDCRs.........GQANFLgRMptPwGSKPRNF....LEQgGaVPTA   463
SIVAGM9       -----------N----------L-R---T.........---------.----------....---D------   466
SIVAGM17      --V-----------------R-------G.........------R---A-x-------....----------   468
SIVAGM27      -------Q-A--T-----------------.........---------------------...-----R----   468
SIVAGM40      --------K----------------------.....---------.----------....----------   466
SIVAGM49      --V----------------------------.....---------------------...----------   468
SABAEUS.CON   GHLARFCKAPRRQGCWKCGSPDHQMKDCQK.........QVNFLGFG.PWGRGKPRNF.....PLTSIRPTA   481
SIVAGMSAB     ----------------------------.........--------.----------.....---------   481
SYKES.CON     GHMQKDCKKPLKAKCFNCGKTGHLARACRQPKRNQGPPVAQANFLGKGWGVSRRPPANF......PVRSEPSA   487
SIVSYK        ------------------------------------------------------------.....--------   487

VERVET.CON    PPPPs.................n?tpYDpAkkLLqqYaekGkQlReq?r?.ppa?npdwtEgYSLnSLFGEDQ   501
SIVAGM3       -----.................-----------D--------RKK.---V-------------------   521
SIVAGMTYO     -----.................GT----------------------K-N.---M-------------------   519
SIVAGM692     ----H.................-PGA--E-TR--EK-TQE-A-Q-RKVEK..SSQAGREE-D---K-------   513
SIVAGM155     ----N.................-S-------------------M-N-N-N.---N----N-------------   520
GRIVET.CON    PPMET...................AYDPAKKLLQQYAEKGQRLREEREQ.TRKQKEKEVEDVSLSSLFGGDQ   513
SIVAGM677     -----...................-----------------------.----------------------   513
TANTALUS.CON  pp?paH........gfptGpp?a?GAYDPAkRLLeQYaKKgdQLrkQKE........KELEDYSLSSLFGEDQ   517
SIVAGM9       --L---.........ETSV--T.-R-------------------------.----------------   522
SIVAGM17      --IA--.........--------.VA----------G----------R---.........----------   518
SIVAGM27      KKM---.........V----L-.-A------R---------E---K----.........----------   524
SIVAGM40      --M-T-.........--------.-Q----------------------R---.........----------   522
SIVAGM49      -RL-T-.........-V----SDWR-------------T---E-------.........----------   525
SABAEUS.CON   PPMERDYSRPEENWYADRPPTRGPGPDDPATALLKQYAVQGKRQKQQWQNHSPQQSPYEEAYSSLRSLFGEDQ   554
SIVAGMSAB     ----------------------------------------------------------------------   554
SYKES.CON     PPLED....IEDGPWLTWSAQMSQQAQAKAQNSPSKKPPTNREVLSPKE..SSGKEETKSLYPSLSSLFGEDQ   554
SIVSYK        -----....-------------------------------------..----------------------   554
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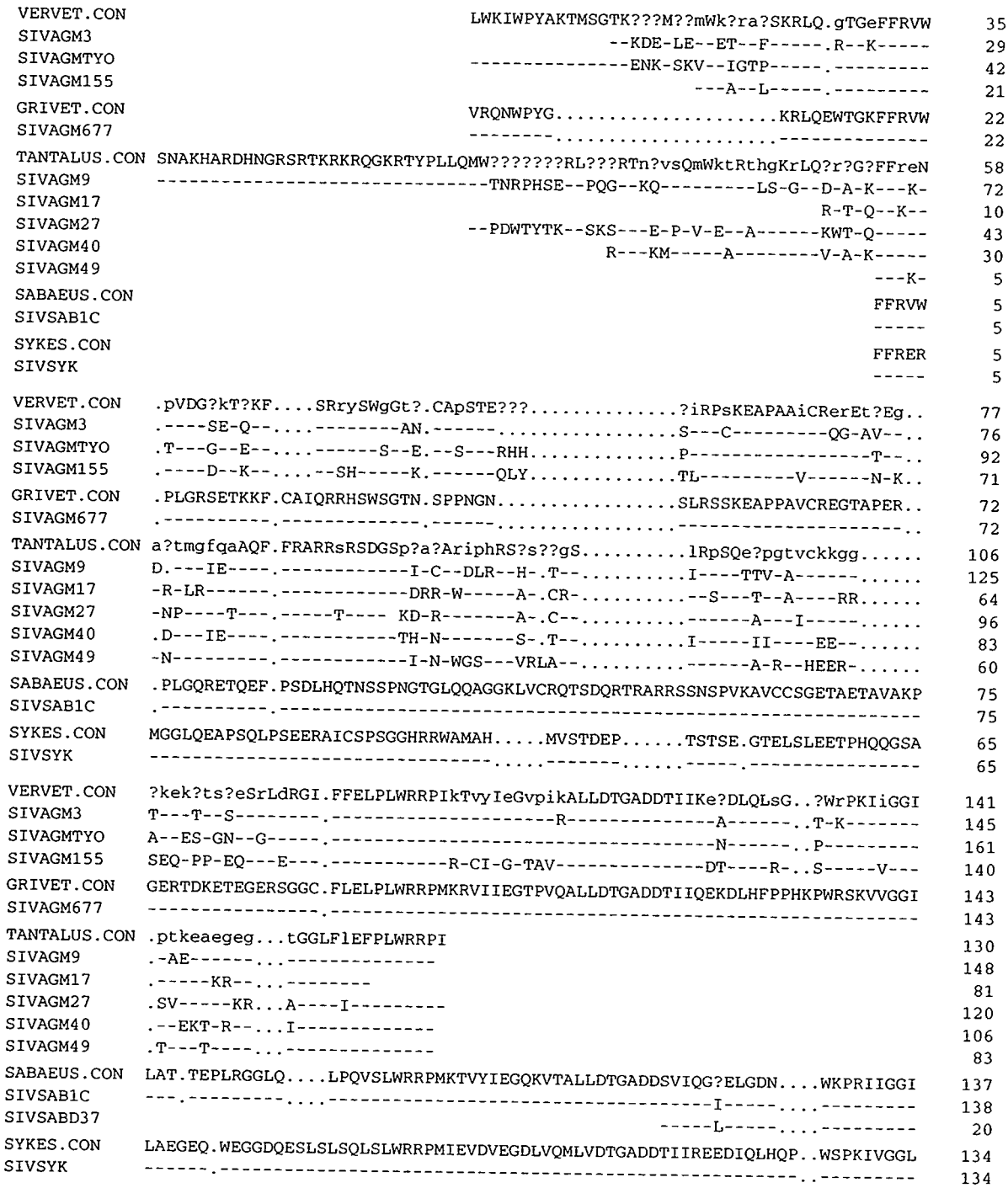
AGM POL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SIVAGM9
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SABAEUS.CON
SIVSAB1C
SYKES.CON
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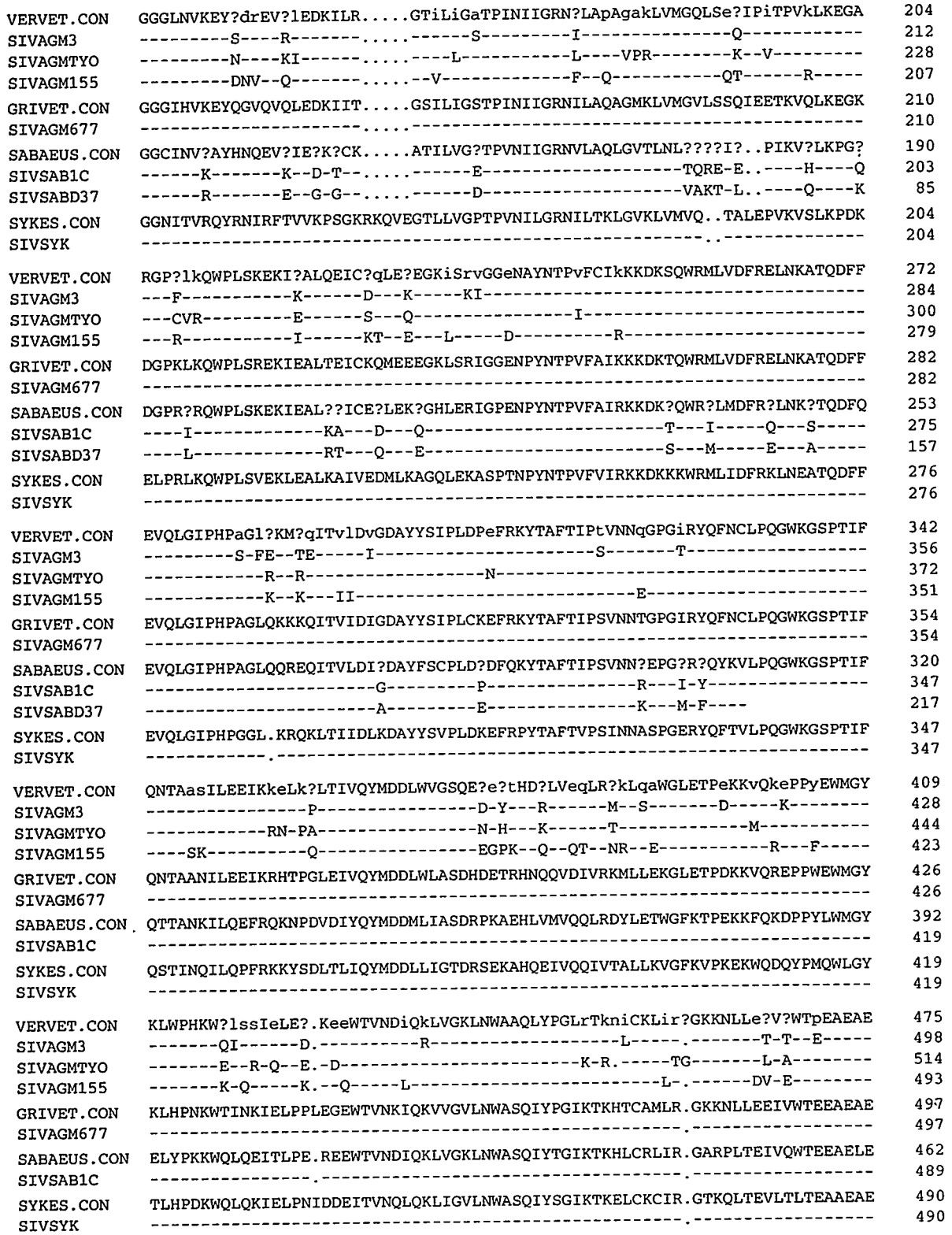
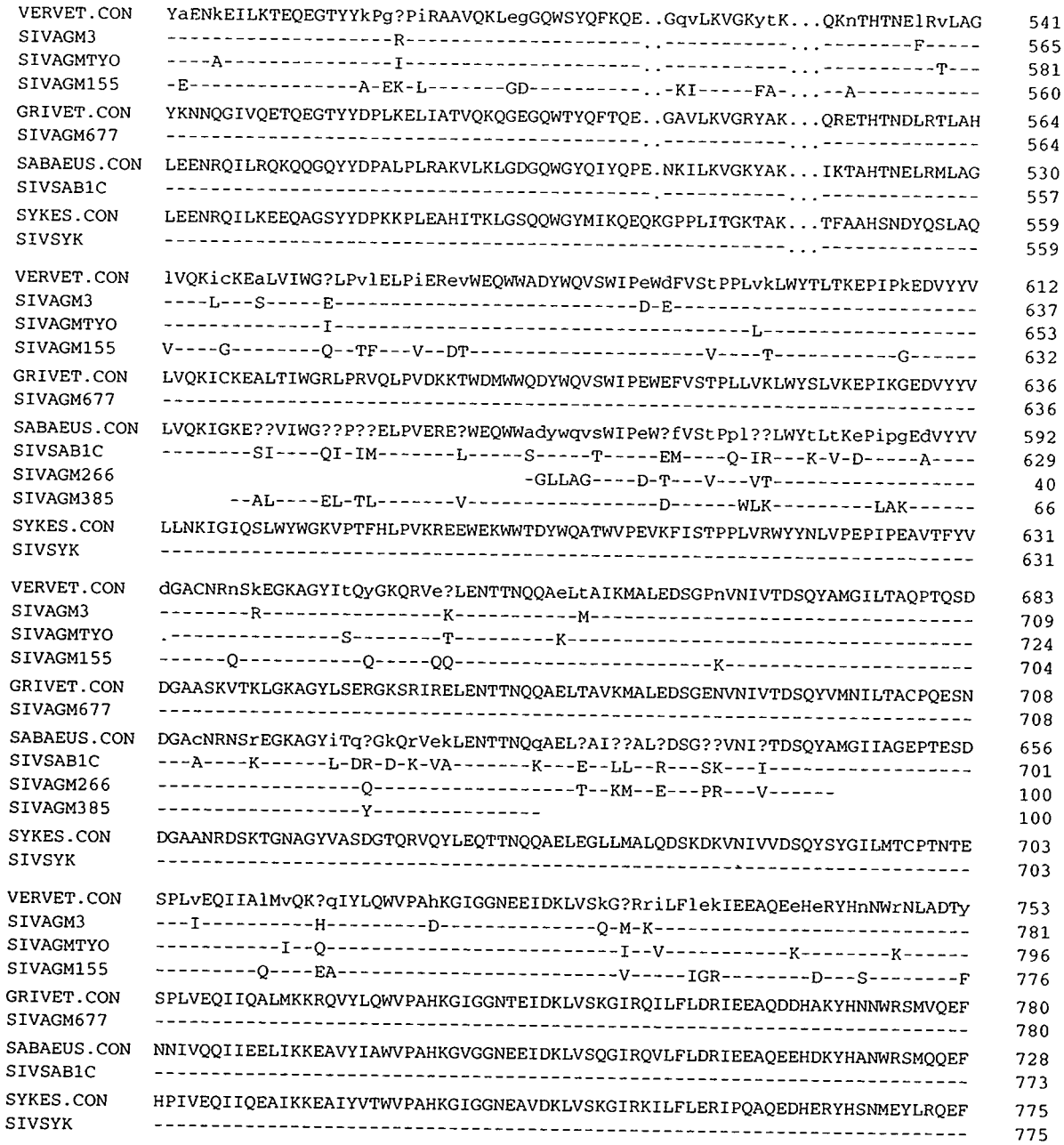

VERVET.CON GGGLNVKEY?drEV?lEDKILR.....GTiLiGaTPINIIGRN?LApAgakLVMGQLSe?IPiTPVkLKEGA 204
SIVAGM3 ---------S----R-------.....------S---------I----------Q---------- 212
SIVAGMTYO ---------N----KI------.....----L----------L----VPR--------K--V--------- 228
SIVAGM155 ---------DNV--Q-------.....--V----------F--Q----------QT------R----- 207
GRIVET.CON GGGIHVKEYQGVQVQLEDKIIT.....GSILIGSTPINIIGRNILAQAGMKLVMGVLSSQIEETKVQLKEGK 210
SIVAGM677 ----------.---------- 210
SABAEUS.CON GGCINV?AYHNQEV?IE?K?CK.....ATILVG?TPVNIIGRNVLAQLGVTLNL????I?..PIKV?LKPG? 190
SIVSAB1C ------K-------K--D-T--.....------E----------TQRE-E..----H----Q 203
SIVSABD37 ------R-------E--G-G--.....------D----------VAKT-L..----Q----K 85
SYKES.CON GGNITVRQYRNIRFTVVKPSGKRKQVEGTLLVGPTPVNILGRNILTKLGVKLVMVQ..TALEPVKVSLKPDK 204
SIVSYK ----------..---------- 204
VERVET.CON RGP?lkQWPLSKEKI?ALQEIC?qLE?EGKiSrvGGeNAYNTPvFCIkKKDKSQWRMLVDFRELNKATQDFF 272
SIVAGM3 ---F----------K------D---K-----KI---------- 284
SIVAGMTYO ---CVR---------E------S---Q----------I---------- 300
SIVAGM155 ---R----------I------KT--E---L-----D----------R---------- 279
GRIVET.CON DGPKLKQWPLSREKIEALTEICKQMEEEGKLSRIGGENPYNTPVFAIKKKDKTQWRMLVDFRELNKATQDFF 282
SIVAGM677 ---------- 282
SABAEUS.CON DGPR?RQWPLSKEKIEAL??ICE?LEK?GHLERIGPENPYNTPVFAIRKKDK?QWR?LMDFR?LNK?TQDFQ 253
SIVSAB1C ----I----------KA---D---Q----------T---I-----Q---S----- 275
SIVSABD37 ----L----------RT---Q---E----------S---M-----E---A----- 157
SYKES.CON ELPRLKQWPLSVEKLEALKAIVEDMLKAGQLEKASPTNPYNTPVFVIRKKDKKKWRMLIDFRKLNEATQDFF 276
SIVSYK ---------- 276
VERVET.CON EVQLGIPHPaGl?KM?qITvlDvGDAYYSIPLDPeFRKYTAFTIPtVNNqGPGiRYQFNCLPQGWKGSPTIF 342
SIVAGM3 ---------S-FE--TE-----I----------S-------T---------- 356
SIVAGMTYO ----------R--R----------N---------- 372
SIVAGM155 ----------K--K---II----------E---------- 351
GRIVET.CON EVQLGIPHPAGLQKKKQITVIDIGDAYYSIPLCKEFRKYTAFTIPSVNNTGPGIRYQFNCLPQGWKGSPTIF 354
SIVAGM677 ---------- 354
SABAEUS.CON EVQLGIPHPAGLQQREQITVLDI?DAYFSCPLD?DFQKYTAFTIPSVNN?EPG?R?QYKVLPQGWKGSPTIF 320
SIVSAB1C ----------G---------P----------R---I-Y---------- 347
SIVSABD37 ----------A---------E----------K---M-F---- 217
SYKES.CON EVQLGIPHPGGL.KRQKLTIIDLKDAYYSVPLDKEFRPYTAFTVPSINNASPGERYQFTVLPQGWKGSPTIF 347
SIVSYK ----------.---------- 347
VERVET.CON QNTAasILEEIKkeLk?LTIVQYMDDLWVGSQE?e?tHD?LVeqLR?kLqaWGLETPeKKvQkePPyEWMGY 409
SIVAGM3 ----------P----------D-Y---R------M--S-------D-----K--------- 428
SIVAGMTYO ----------RN-PA----------N-H---K------T----------M---------- 444
SIVAGM155 ----SK----------Q----------EGPK--Q--QT--NR--E----------R---F----- 423
GRIVET.CON QNTAANILEEIKRHTPGLEIVQYMDDLWLASDHDETRHNQQVDIVRKMLLEKGLETPDKKVQREPPWEWMGY 426
SIVAGM677 ---------- 426
SABAEUS.CON QTTANKILQEFRQKNPDVDIYQYMDDMLIASDRPKAEHLVMVQQLRDYLETWGFKTPEKKFQKDPPYLWMGY 392
SIVSAB1C ---------- 419
SYKES.CON QSTINQILQPFRKKYSDLTLIQYMDDLLIGTDRSEKAHQEIVQQIVTALLKVGFKVPKEKWQDQYPMQWLGY 419
SIVSYK ---------- 419
VERVET.CON KLWPHKW?lssIeLE?.KeeWTVNDiQkLVGKLNWAAQLYPGLrTkniCKLir?GKKNLLe?V?WTpEAEAE 475
SIVAGM3 -------QI------D.----------R----------L-----.-------T-T--E----- 498
SIVAGMTYO -------E--R-Q--E.-D----------K-R.-----TG-------L-A-------- 514
SIVAGM155 -------K-Q-----K.--Q-----L----------L-.------DV-E-------- 493
GRIVET.CON KLHPNKWTINKIELPPLEGEWTVNKIQKVVGVLNWASQIYPGIKTKHTCAMLR.GKKNLLEEIVWTEEAEAE 497
SIVAGM677 ----------.---------- 497
SABAEUS.CON ELYPKKWQLQEITLPE.REEWTVNDIQKLVGKLNWASQIYTGIKTKHLCRLIR.GARPLTEIVQWTEEAELE 462
SIVSAB1C ----------.----------.---------- 489
SYKES.CON TLHPDKWQLQKIELPNIDDEITVNQLQKLIGVLNWASQIYSGIKTKELCKCIR.GTKQLTEVLTLTEAAEAE 490
SIVSYK ----------.---------- 490

AGM POL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SIVAGM3 ----------R----------..----------...--------F----- 565
SIVAGMTYO ----A----------I----------..----------...----------T--- 581
SIVAGM155 -E----------A-EK-L-------GD----------..-KI-----FA-...--A---------- 560
GRIVET.CON YKNNQGIVQETQEGTYYDPLKELIATVQKQGEGQWTYQFTQE..GAVLKVGRYAK...QRETHTNDLRTLAH 564
SIVAGM677 ----------..----------...---------- 564
SABAEUS.CON LEENRQILRQKQQGQYYDPALPLRAKVLKLGDGQWGYQIYQPE.NKILKVGKYAK...IKTAHTNELRMLAG 530
SIVSAB1C ----------.----------...---------- 557
SYKES.CON LEENRQILKEEQAGSYYDPKKPLEAHITKLGSQQWGYMIKQEQKGPPLITGKTAK...TFAAHSNDYQSLAQ 559
SIVSYK ----------...---------- 559
VERVET.CON lVQKicKEaLVIWG?LPvlELPiERevWEQWWADYWQVSWIPeWdFVStPPLvkLWYTLTKEPIPkEDVYYV 612
SIVAGM3 ----L---S-----E----------D-E---------- 637
SIVAGMTYO ----------I----------L---------- 653
SIVAGM155 V----G--------Q--TF---V--DT----------V----T----------G------ 632
GRIVET.CON LVQKICKEALTIWGRLPRVQLPVDKKTWDMWWQDYWQVSWIPEWEFVSTPLLVKLWYSLVKEPIKGEDVYYV 636
SIVAGM677 ---------- 636
SABAEUS.CON LVQKIGKE??VIWG??P??ELPVERE?WEQWWadywqvsWIPeW?fVStPpl??LWYtLtKePipgEdVYYV 592
SIVSAB1C --------SI----QI-IM-------L-----S-----T-----EM----Q-IR---K-V-D-----A---- 629
SIVAGM266 -GLLAG----D-T---V---VT---------- 40
SIVAGM385 --AL----EL-TL-------V----------D------WLK---------LAK------ 66
SYKES.CON LLNKIGIQSLWYWGKVPTFHLPVKREEWEKWWTDYWQATWVPEVKFISTPPLVRWYYNLVPEPIPEAVTFYV 631
SIVSYK ---------- 631
VERVET.CON dGACNRnSkEGKAGYItQyGKQRVe?LENTTNQQAeLtAIKMALEDSGPnVNIVTDSQYAMGILTAQPTQSD 683
SIVAGM3 --------R----------K----------M---------- 709
SIVAGMTYO .----------S--------T---------K---------- 724
SIVAGM155 ------Q----------Q-----QQ----------K---------- 704
GRIVET.CON DGAASKVTKLGKAGYLSERGKSRIRELENTTNQQAELTAVKMALEDSGENVNIVTDSQYVMNILTACPQESN 708
SIVAGM677 ---------- 708
SABAEUS.CON DGAcNRNSrEGKAGYiTq?GkQrVekLENTTNQqAEL?AI??AL?DSG??VNI?TDSQYAMGIIAGEPTESD 656
SIVSAB1C ---A----K------L-DR-D-K-VA-------K---E--LL--R---SK---I---------- 701
SIVAGM266 ----------Q----------T--KM--E---PR---V------ 100
SIVAGM385 ----------Y---------- 100
SYKES.CON DGAANRDSKTGNAGYVASDGTQRVQYLEQTTNQQAELEGLLMALQDSKDKVNIVVDSQYSYGILMTCPTNTE 703
SIVSYK ---------- 703
VERVET.CON SPLvEQIIAlMvQK?qIYLQWVPAhKGIGGNEEIDKLVSkG?RriLFlekIEEAQEeHeRYHnNWrNLADTy 753
SIVAGM3 ---I----------H---------D----------Q-M-K---------- 781
SIVAGMTYO ----------I--Q----------I--V----------K--------K------ 796
SIVAGM155 ---------Q----EA----------V-----IGR--------D---S--------F 776
GRIVET.CON SPLVEQIIQALMKKRQVYLQWVPAHKGIGGNTEIDKLVSKGIRQILFLDRIEEAQDDHAKYHNNWRSMVQEF 780
SIVAGM677 ---------- 780
SABAEUS.CON NNIVQQIIEELIKKEAVYIAWVPAHKGVGGNEEIDKLVSQGIRQVLFLDRIEEAQEEHDKYHANWRSMQQEF 728
SIVSAB1C ---------- 773
SYKES.CON HPIVEQIIQEAIKKEAIYVTWVPAHKGIGGNEAVDKLVSKGIRKILFLERIPQAQEDHERYHSNMEYLRQEF 775
SIVSYK ---------- 775

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VERVET.CON    GLPQIVAKEIVAMCPKCQiKGEPvHGQVDASPGvWQMDCTHlEgKvvIVAVHVASGFIEAEVIPRETGKETA   825
SIVAGM3       ----------------------------------------------I------------------------   853
SIVAGMTYO     --------------------------------T---------K----------------------------   868
SIVAGM155     ------------------V----I----------------I---I--------------------------   848

GRIVET.CON    GLPNIVAKEIVAACPKCQIRGEPKHGQVDASIETWQMDCTHLEGKVIIVAVHVASGFIEAEVIPRETGKETA   852
SIVAGM677     ------------------------------------------------------------------------   852

SABAEUS.CON   GLPAIVAKEIVAACPKCQIKGESVHGQVDASPGVWQMDCTHLEGKIIIVAVHVASGFIEAEVIPQETGKATA   800
SIVSAB1C      ------------------------------------------------------------------------   845
SIVAGM381                                                             -------------      13
SIVAGM384                                                             -------------      13
SIVAGM386                                                             -------------      13
SIVAGM385A                                                            -------------      13
SIVAGM385B                                                            -------------      13
SIVAGM385C                                                            -------------      13
SIVAGM385D                                                            -------------      13

SYKES.CON     HLPRQVAKAIIQQCPKCQNRGEPKHGQVDVDIYNWQMDCTHEEGKVICVAVNTASGYIETKILKRETGDETA   847
SIVSYK        ------------------------------------------------------------------------   847

VERVET.CON    KFLLKIlsRWPITqLHTDNGPNFTSQEVAAmCWWGKiEHTTGvPYNPQSQGSIESMNKQLKEIIGKIRDDCQ   897
SIVAGM3       ------------------------------------------------------------------------   925
SIVAGMTYO     ----------------------------I-----------I----------------------------   940
SIVAGM155     ------IG-----H----------------------V--------------------------------   920

GRIVET.CON    HFLLKLLARWPVKHLHTDNGPNFTSQNVAAVCWWGNIEHTTGIPYNPQSQGSVESMNRQLKEIISQIRDDCE   924
SIVAGM677     ------------------------------------------------------------------------   924

SABAEUS.CON   hFLLKLASRWPItkLHTDNGtNFTSQQVAAIcWWgKIEHT?GVPYNPQSQGVVESMNKQLKEIIGQIRdDAE   871
SIVSAB1C      -------------Q--------------------------F------------------------------   917
SIVAGM381     Q-----------A--------P-------------------F--------------------------E---   85
SIVAGM384     -------------Q--------------------------F------------------------------   85
SIVAGM386     -------------H--------------------------F------------------------------   85
SIVAGM385A    ------------------------------Y- E-----Y------------------------------   84
SIVAGM385B    ----------------------------------------Y------------------------------   85
SIVAGM385C    ----------------------------------------Y------------------------------   85
SIVAGM385D    ----------------------------------------Y------------------------------   85

SYKES.CON     LFLMQIASRWPIKQIHTDNGPNFVSDKFKAACWWCGIEHTTGIPYNPQSQGIVESKNRYLKEAISQIRDDVT   919
SIVSYK        ------------------------------------------------------------------------   919

VERVET.CON    YTEtAVLMAChiHNFKRKGGIGGlT?AERLINmITTQLEiqhLQTKIQKILNFRVYYREGRDPVWKGPaqLI   968
SIVAGM3       -------------------------P-------------L----------------------------G---   997
SIVAGMTYO     ---A------IL-----------Q-S------I-------------------------------------  1012
SIVAGM155     -------------------------A--------------NT---------------------------R--   992

GRIVET.CON    RLETAVQMATHIHNFKRKGGIGGISSAERLVNMLTTQLELNTLQNQIQKILNFKVYYREGRDPVWKGPARLI   996
SIVAGM677     ------------------------------------------------------------------------   996

SABAEUS.CON   RLETAVlMAVHIHNFKRKGGIGGYSAAERLINIIHTELETKTLQQKISKIQNFRVYYREGRDPVWKGPAKLI   943
SIVSAB1C      ------I-----------------------------------------------------------------   989
SIVAGM381     -------                                                                      92
SIVAGM384     ------I                                                                      92
SIVAGM386     ------I                                                                      92
SIVAGM385A    -------                                                                      91
SIVAGM385B    -------                                                                      92
SIVAGM385C    -------                                                                      92
SIVAGM385D    -------                                                                      92

SYKES.CON     HLQTAVAMATFILNFKRKGGIGGISPGERYINMLYTELQLQ.QNTTSPKFSNFRVYYRQGKNE.WKGPARLL   989
SIVSYK        ----------------------------------------.---------------------.--------   989
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AGM POL

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VERVET.CON    WKGEGA.VVlK?G?eLKvvPRRKAKIIKDYEPrkr?GdE??lEGagGsDnQMAGDS      1018
SIVAGM3       ------.--I-G-V---EY----------------M---SN------A--           1046
SIVAGMTYO     ------.----D-SD-----------------KQ-V-N-GDV--TR----            1061
SIVAGM155     ------.----E-E--------------------TL---TH--------H------      1047
GRIVET.CON    WKGEGA.VVIKEGEDIKVVPRRKAKIIKDYGERKTMDSEGSMEGVREANKQMEGDSDLQDQE 1057
SIVAGM677     ------.------------------------------------------------------ 1057
SABAEUS.CON   WKGEGA.VVIQEQGELKTIPRRKAKIIKDYG..KALDSQAPLEGNGRTAGEVD          993
SIVSAB1C      ------.------------------------..--------------------          1039
SYKES.CON     WKGEGAVVVQTEEGDIFAVPRRKAKIITDHG..ERMDSGSHVENDPKTD             1036
SIVSYK        --------------------------------..----------------            1036
```

In this, and several of the AGM alignments that follow, only one consensus sequence was generated, as several of the species have only one representative. SIVSYK was not included in this consensus, although its similarity to the consensus sequence is shown.

```
CONSENSUS M??eK?WvmRvtWkV?e??itkWqgiVrYwmr??r?l??W?Y?mHyqitWawytmsryvIPl???g?I?Vd?Ywh   56
SIVAGMTYO -NPN-E---------PGDL-------------.Q-N-K.-N-Y------------------IGKH-E-C--L---   73
SIVAGM155 -SQ--H----L----Q-EV------------N.K-N-K.-E-K-------------------PGS-E-H--I---   73
SIVAGM3   -NQ--E---------P-EL-------------.T-K-D.-K-R---------------E---GQH-S-H--L---   73
SIVAGM677 -ER--Q-IV--V-R-S-RQ-SR-R---T-KI-.NKQ-P.-E-RH-W-VQ-QFW-Y-QFI---SKDDY-E-NI-HN   73
SIVSAB1C  -..--H-IV-PL---TGGQQER-TSL-K-H-HVSKQCVH-R-TP-TK-R-N--SYQEW----KDGAL-K-TN---   73

SIVSYK    -..--E-IVVP--RMTPRQ-DRL-H-IKTHKYKSKE-EKAT-KH----E-Q---YCQWT--VG.D-T-WITF-HN   72

CONSENSUS LtPe?GWLstyavGiqY?s??????yrTElDP?TADs?IH?hYF?CFtdRAiqqAlrG?rf?.fCqfpeGHk?tG  115
SIVAGMTYO ----Q------------V-NLESK.-------A----I--G---N--KE---------H--V.---------S--  146
SIVAGM155 -A-KQ------------V-LVNDK.-------N----M--C---T-------------N--I.-----G---L--  146
SIVAGM3   ----K--------E----L-NRDPW.-------A----L--T---T---E---RK--L-Q--T.---------K--  146
SIVAGM677 ----R----SHG--LS-YH..QKG.-K--V--G---RM--LY--N----------I--EKYT.W-T-K----..-  142
SIVSAB1C  ----K---E---T--G-....SKGEWF-----W---HI--WS--P------V---I--EKYL.W-KHQV--QP--  143

SIVSYK    -A--R---HMQGIR---....QWNQWN-D-T-AV--RL--NF--P---A--VN--V--ELLTSH-WT-..-TD..  139

CONSENSUS QVpSLQyLALlah.qNGlR?rs?r??.trr?rnlGs?Qgav???grMA?r???r?q??sq?Afw?rtp?psmell  169
SIVAGMTYO -------------.-----E--K-GK.---S-----K----...-Q--K-YVT-S-PGGEA---E---V------  216
SIVAGM155 -------------.-----K--Q-GE.---T-----Q----...----Q-YGR-N-QR--T---P---I------  216
SIVAGM3   -------------.-----Q--Q-SK.-GGT--M-FE----...----K-HAR-Y-SG--D---A-A-V------  216
SIVAGM677 --Q---L---V-Y.T--I-K--K-TF.--MAG----R---M...----T-HAQGSKRR--K-L-NEHAN------  212
SIVSAB1C  ----------RVY.T----RVAPT...S--GSSQ--P-ESQRRDT---RNMGFAQRAVRRM-PRHV-GPQFRGPV  214

SIVSYK    ----------QVYLKD-GGFLQSLPACA-NTMV-H-KKCR-DPKRDQCHCKGRTGSDR-IQ--YSSRNIW-L-SI  214

CONSENSUS sgg???t??sh?gkgl???H                                                        180
SIVAGMTYO ---RRK-WY--D----QIL                                                         235
SIVAGM155 ---RGE-GKT-S---I                                                            232
SIVAGM3   ---GRKESH--AR---                                                            232
SIVAGM677 CR-GKE-                                                                     219
SIVSAB1C  PLPKESPFP-LVEYCGRTS-                                                        234

SIVSYK    LKRRGRD                                                                     221
```

AGM VPX

```
CONSENSUS MASG?????????????????rdPRE?rPG?lEiWDLsREPwDeWLrDMl?dlN?EA??HFgrelLfqvWnycqEE?      53
SIVAGMTYO ----.............-----A---EV----------K------Q---Q--RL----------------.      59
SIVAGM155 ----.............-----E---G-----------------VEEI-N--KL-------Y---------.      59
SIVAGM3   ----.............-----A---E-------------------E-I-Q--KM----------------.      59
SIVAGM677 ----.....................-----PL--W------D--------Q---R---E--RR---MNM-IR-----V--.      59
SIVSAB1C  ----GWLPPVGGDPPKDPPKN---EI--W--T---P---F--------Q---S--QC--P-N---RL-WNIV--P      75

CONSENSUS gerhgtp??EraYKYyrlvQKalFVHfrcgCrrrqpfepYeerr?GqggGragrvppgl?AAPGL              114
SIVAGMTYO -------MM-----------------------------------D-------N------E                  119
SIVAGM155 ---Q-R-IA-----------------------------------N------P-------D                  119
SIVAGM3   ---NR--ML-------K---------------------------D-------------D                  119
SIVAGM677 -R--N--WN-IG-----I---SM----------G--S------N-----.-PPP----A                    118
SIVSAB1C  AID--QTRL-GW---C-IL-------MKGR-CKPKTHPA-GPGAG-PPP-LG-ASGGAAS-----             140
```

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CONSENSUS       MDkge?eq???hqdL?e????PLq?CtNkCfCKkCCyHCqlCFlqKgLGvtYhapR?R?rkki?s?n??     53
SIVAGMTYO       -----A--IVS----S-DYQK---T-K----------------------------T-.----R-L-LA     68
SIVAGM155       -----ED-DVS----IKQYRK--ET---------------F---R----I----F-T-.----A-ADRI     68
SIVAGM3         -----D--GAY----I-QLKA--KR-----Y--C----------------------I-.----APLDRF     68
SIVAGM677       ---E-.-PHPLL---....HR---P-----Y--------E----------R--VS-K-.--TSTQD-QD     63
SIVSAB1C        --QEQEARPQVWEE-Q-ELHR---A-D-T----V--F--I---HK-A--IR-YV--P-RAS-KI-H-QV     69

SIVSYK    MSSTDQICQTQRVPPSFLEGTFL.EKG-PTP-.------N--------------I--AR--K-AARS-SEDDSA     73

CONSENSUS p???QSIStr?gRd?QTTqe?qekVEt?A??n????RKNL????????GA?                          82
SIVAGMTYO -LQH-----KW---G---PTS------T-GS-                                            100
SIVAGM155 -VPQ----I-.---S-----S-K---EQ-KA-LRIS----GDETRGPV--G                         118
SIVAGM3   -EQK------.---S----KG------S-RTAPSLG----AQQSGRAT--S                         118
SIVAGM677 -IRQ-----V.Q-NG---E-GKTE--                                                   88
SIVSAB1C  SLHN                                                                         73

SIVSYK    -TGTLPRAG-TQANP--K...KKA---EKDSTSLPSAE--                                    110
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AGM REV

```
CONSENSUS MpLG?EErr?lrlI??ly??npypp??eGTARQRRRARrRWr?qq?Qi??laeRil?t??????qlvqa?dqLvl     55
SIVAGMTYO ----P----FV---WL--ST-----SG---------------Q--D--RV-V--.-......QE-.-Y-V-R-AD     67
SIVAGM155 ----P----L----AF--RS----SV.--------------KNR-K--YA-----WG-R..QED-----I-----     72
SIVAGM3   ----S----L----AF-NKN-----V.---------------QA-E-LRA-----WHSR..VEE-----I-----     72
SIVAGM677 -S--K--KQA-KI-KT--GS----QFS.----------Q---K--Q--DKI-G-V-N-F..EDQ---AQLQE-Q-     72
SIVSAB1C  -S--Q--LLRRFR-IKFLYTTNPY-PGQ----------Q--AK-RQ-VIH------E-PVSQIDH-A-EF-----     75

SIVSYK    --DQGS-QLAVF-RMIAHLQE---GP.--PRQT---R--Q--QRRT-RLY-QQ--FEAIFGSRTAALE..-S-..     70

CONSENSUS d?qhl??QqlPdpP???PTENQTANSSS                                                  77
SIVAGMTYO EA---AI-------HSA                                                             84
SIVAGM155 -T---VT-------SQA                                                             89
SIVAGM3   -Q---AI-------SSS                                                             89
SIVAGM677 ENKD-VL-H-----HIH                                                             89
SIVSAB1C  -N....L--P-SL-PGH----------                                                   99

SIVSYK    .........---QISD                                                              77
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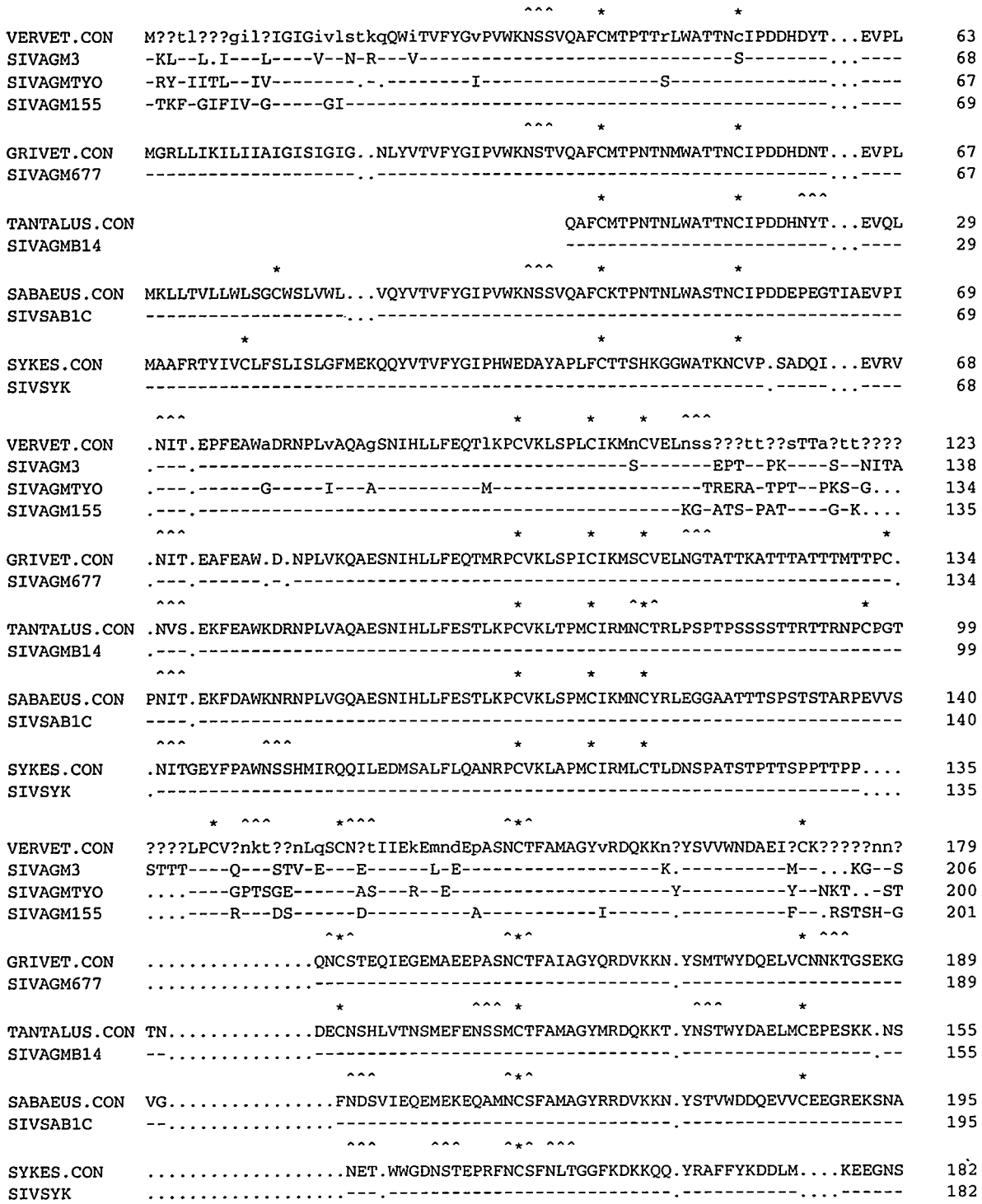
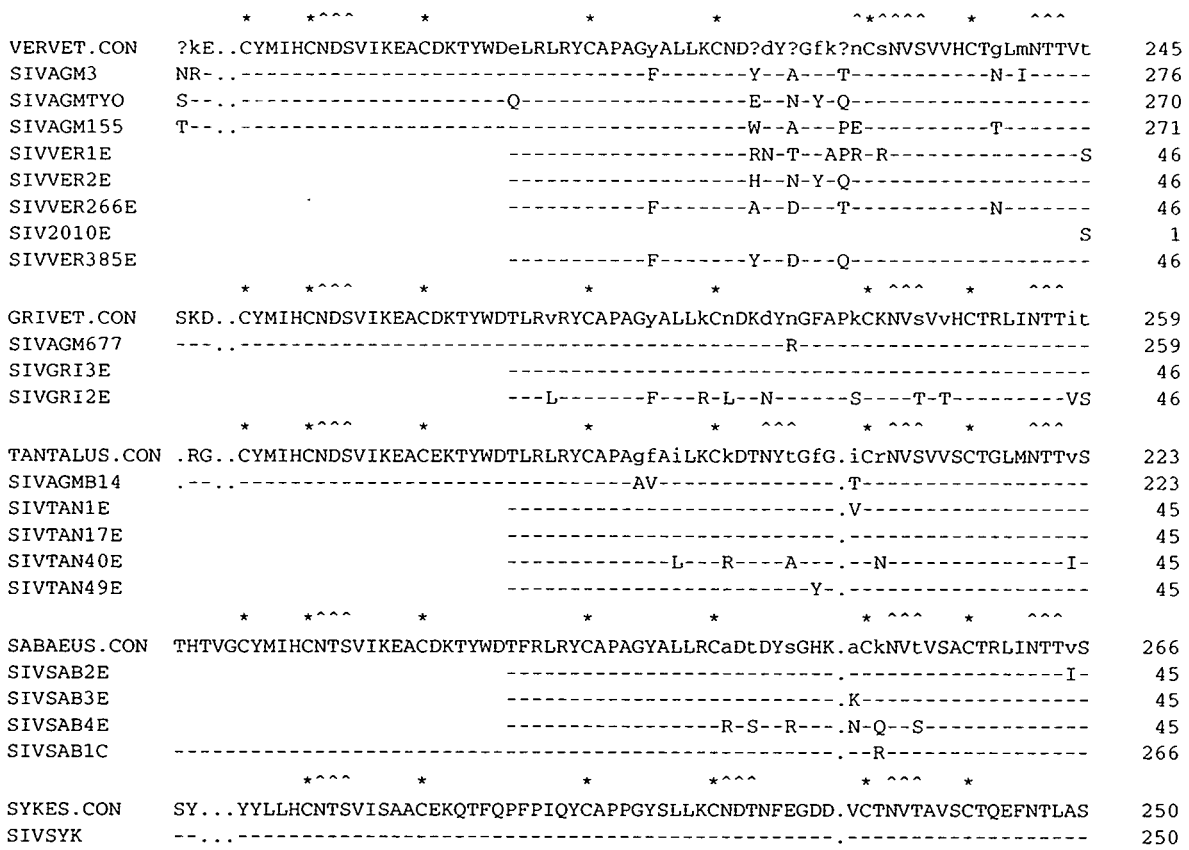


AGM ENV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SIVAGM3 276
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SIVAGM155 271
SIVVER1E 46
SIVVER2E 46
SIVVER266E 46
SIV2010E 1
SIVVER385E 46
GRIVET.CON 259
SIVAGM677 259
SIVGRI3E 46
SIVGRI2E 46
TANTALUS.CON 223
SIVAGMB14 223
SIVTAN1E 45
SIVTAN17E 45
SIVTAN40E 45
SIVTAN49E 45
SABAEUS.CON 266
SIVSAB2E 45
SIVSAB3E 45
SIVSAB4E 45
SIVSAB1C 266
SYKES.CON 250
SIVSYK 250

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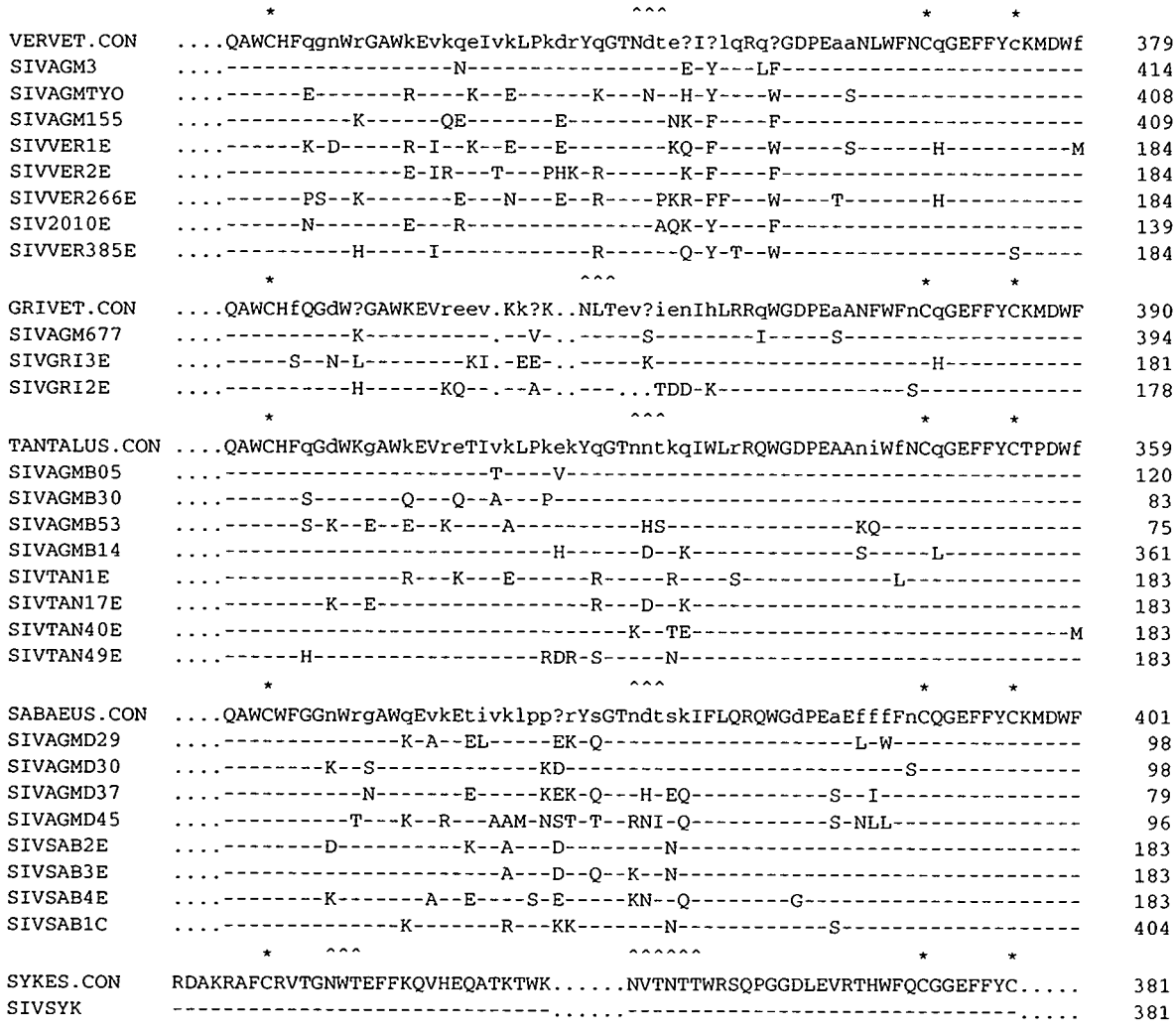
                 ^^^   ^^^          ^^^          ^^^  *    ^^^
VERVET.CON       TGLLLNGSYsENrTqIWqKHrvsNdsvlil?NKhyNLtvtCkRPGNKTvLPVTIMAGlVFHSQkYNtrLR..    314
SIVAGM3          ----------------------------V-F-------------------------------R------..    346
SIVAGMTYO        ---------H------------N-NT----F------S---R-----------------------MK--..    340
SIVAGM155        --------------------G---------L-----------------------------------------..    341
SIVVER1E         ---------T----E-----K---N--I-RI-------IR-V-------------------------K--..    116
SIVVER2E         ---------H-------R--G------I--I--AF------R-------------------------------..    116
SIVVER266E       ----------------------T----A---L-----------------------------------L---..    116
SIV2010E         ------------K---------N-------L-----------------I--------M------------..     71
SIVVER385E       ----------------------------QI--------I-------------------------------..    116
                 ^^^   ^^^          ^^^          ^^^  *    ^^^
GRIVET.CON       TGIGLNGSR?ENRTEIWQekGNsNdTVIIKLNKFYNLTVRCRRPGNKTvLPVTIMAGlVFHSQKYNTrLK..    328
SIVAGM677        ---------S--------KG--D-----------------------------------------------..    329
SIVGRI3E         ---------V-------------------------------------I--------R---------K--..    116
SIVGRI2E         ---------A--------------N-----------------------------------------------..    116
                 ^^^   ^^^          ^^^              *    ^^^
TANTALUS.CON     SAFGlNGSQAENRTEiWQKHgvsNdSVIIKLNKhY?Lti?CrRPGnKTVLPVTiMaGlVFHSQkyNTkLR..    291
SIVAGMB05                     -----------------Q---V-----K-------M---------Q-------..     52
SIVAGMB30                                                          T-M------------..     15
SIVAGMB53                                                                 IH------..      7
SIVAGMB14        ----------------------------------N---L----------------M------------..    293
SIVTAN1E         ----I-------------------N----------K-K-V----------------------Q-------..    115
SIVTAN17E        ---------------V-----------------F-N---K--------------------------R--..    115
SIVTAN40E        ---------------------N-------------Q-K-K-I--------------------------..    115
SIVTAN49E        --------------------RIN----------Y-K-GVT-------------------------------..    115
                 ^^^   ^^^                  ^^^  *    ^^^
SABAEUS.CON      TGIGINGSYVANRTEIWQkNGNsNd?vIIRLNR?fNLTIRCRrPGNKTVLPVTImAGLvfHSQKYNTrlr..    334
SIVAGMD29                                          --I----------A---I----------V..     30
SIVAGMD30                                          ----------------------------K--..     30
SIVAGMD37                                                             N-------KF-..     11
SIVAGMD45                                            ----------------------------..     28
SIVSAB2E         ----------------------A-HT-------H---------------------------------K--..    115
SIVSAB3E         -------------------------S-------H---------------------------------K..    115
SIVSAB4E         ------------------E-----NTA------YY----------------------------------..    115
SIVSAB1C         -------------------------S-------Y---------------------------------K..    336
                 ^^^                ^^^              *    ^^^
SYKES.CON        TWFQLNGTYKAKDKVRFIKQKDKNESVIILVPEALRLQIICERPGNESIKNIQL.AAGYFLPVIQG.KLKTG    320
SIVSYK           ----------------------------------------------------.-----------.-----    320
```

AGM ENV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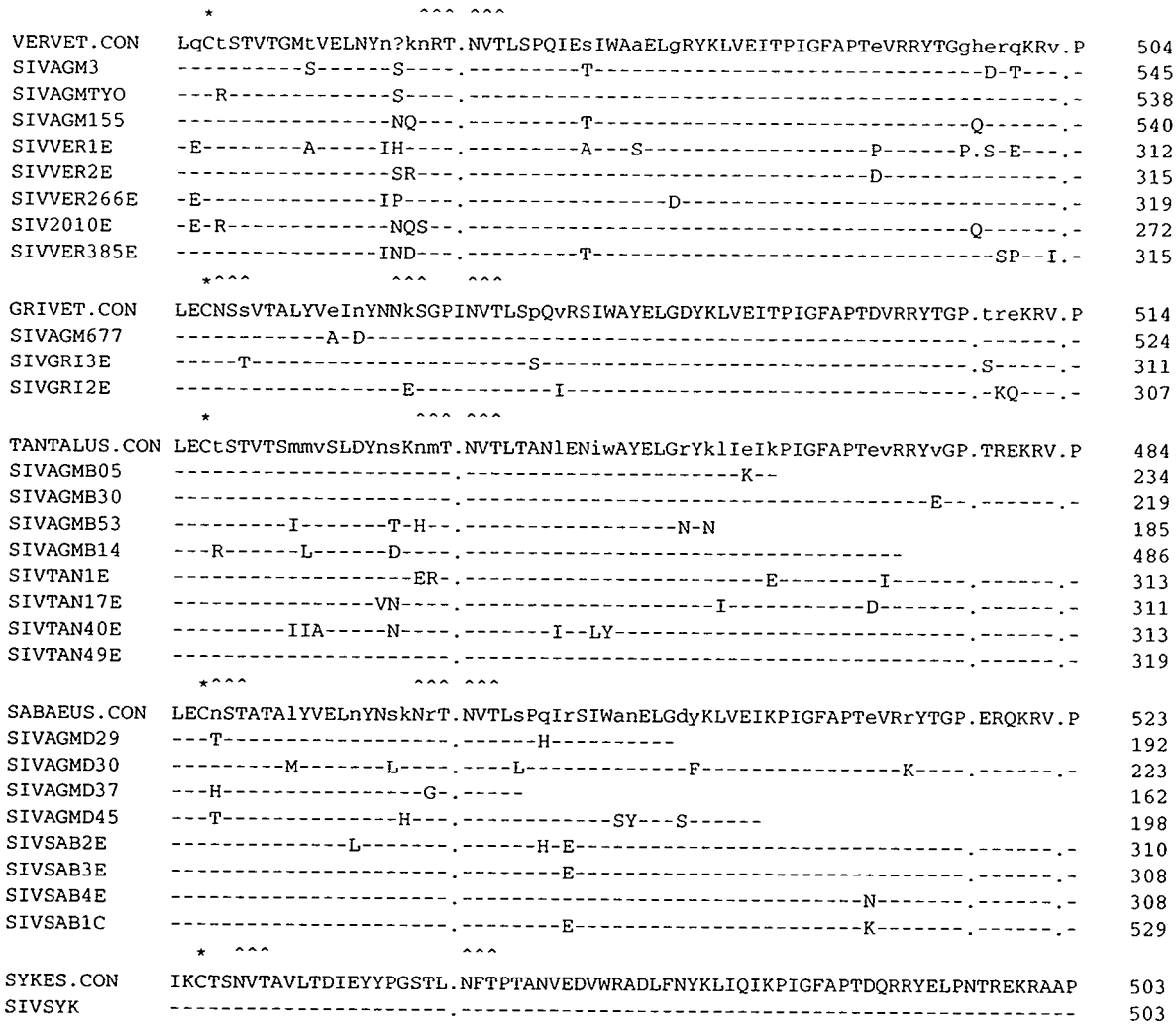
SIVAGM3 ....----------N----------E-Y---LF---------- 414
SIVAGMTYO ....------E-------R----K--E------K---N--H-Y----W-----S---------- 408
SIVAGM155 ....----------K------QE-------E--------NK-F----F---------- 409
SIVVER1E ....------K-D-----R-I--K--E---E--------KQ-F----W-----S------H----------M 184
SIVVER2E ....--------------E-IR---T---PHK-R------K-F----F---------- 184
SIVVER266E ....------PS--K-------E---N---E--R----PKR-FF---W----T-------H---------- 184
SIV2010E ....------N-------E---R--------------AQK-Y----F---------- 139
SIVVER385E ....----------H-----I----------R------Q-Y-T--W----------S----- 184
GRIVET.CON ....QAWCHfQGdW?GAWKEVreev.Kk?K..NLTev?ienIhLRRqWGDPEaANFWFnCqGEFFYCKMDWF 390
SIVAGM677 ....----------K----------.--V-..-----S--------I-----S---------- 394
SIVGRI3E ....-----S--N-L--------KI.-EE-..-----K----------H---------- 181
SIVGRI2E ....----------H------KQ--.--A-..---...TDD-K----------S---------- 178
TANTALUS.CON ....QAWCHFqGdWKgAWkEVreTIvkLPkekYqGTnntkqIWLrRQWGDPEAAniWfNCqGEFFYCTPDWf 359
SIVAGMB05 ....----------T----V---------- 120
SIVAGMB30 ....------S-------Q---Q--A---P---------- 83
SIVAGMB53 ....------S-K--E--E--K----A----------HS----------KQ---------- 75
SIVAGMB14 ....----------H------D--K----------S-----L---------- 361
SIVTAN1E ....----------R---K---E------R-----R----S----------L---------- 183
SIVTAN17E ....--------K--E----------R---D--K---------- 183
SIVTAN40E ....----------K--TE----------M 183
SIVTAN49E ....------H----------RDR-S-----N---------- 183
SABAEUS.CON ....QAWCWFGGnWrgAWqEvkEtivklpp?rYsGTndtskIFLQRQWGdPEaEfffFnCQGEFFYCKMDWF 401
SIVAGMD29 ....----------K-A--EL-----EK-Q----------L-W---------- 98
SIVAGMD30 ....--------K--S----------KD----------S---------- 98
SIVAGMD37 ....----------N-------E-----KEK-Q---H-EQ----------S--I---------- 79
SIVAGMD45 ....----------T---K--R---AAM-NST-T--RNI-Q----------S-NLL---------- 96
SIVSAB2E ....--------D----------K--A---D--------N---------- 183
SIVSAB3E ....----------A---D--Q--K--N---------- 183
SIVSAB4E ....--------K-------A--E----S-E-----KN--Q--------G---------- 183
SIVSAB1C ....----------K-------R---KK-------N----------S---------- 404
SYKES.CON RDAKRAFCRVTGNWTEFFKQVHEQATKTWK.....NVTNTTWRSQPGGDLEVRTHWFQCGGEFFYC..... 381
SIVSYK ----------.....----------..... 381

VERVET.CON LNYlNNlT.....vdadH??N?C?n?t??k????raPGPCvQRTYVacHIRSVindwytiskkTYAPPREGH 435
SIVAGM3 ------R-.....--P--..-P-.-G-..-GKG.K-----A----------L-R---------- 475
SIVAGMTYO ------K-.....W--Y-..-F-....SS-KKG.H----------Y--------S--L---------- 468
SIVAGM155 --------.....-----..-H-...KNNAGKG.-S---------- 470
SIVVER1E ---I----.....---N-..-N-.-S-QG....K-.----------G----------KLAR---------- 243
SIVVER2E --------.....-----..-S-.-GSRTSP...------A---------- 245
SIVVER266E --------.....-----..-E-K-TSGT-SGNK----------IWLE---------- 249
SIV2010E ---I----.....---N-NT-R-.-K-GKTSG...-----A----------V-----V--L---------- 202
SIVVER385E ------K-.....WN---..-Q-D-S-..-TG..---------- 245
GRIVET.CON INYlNN?T.....vDAdG????C?..???kkgp..GPGPCvqrTYVACHIRQVVNDWYTltKKtYaPPREGh 444
SIVAGM677 ------R-.....E--E-TNRT-D.....-GK-..----------VS--V-------- 454
SIVGRI3E ------Q-.....-----..KS-...TSH---Q..-----AKK---------- 241
SIVGRI2E ---I--E-.....-----..NK-....NKP---..----------R-----Q 237
TANTALUS.CON vN?LNNeSa?g???dVEG..N?C..???t??gltgs?rkClKRtYVacHIRSvVNDWYtLskKtYAPPREGH 415
SIVAGMB05 --Y------N-TNL----..-K-..PDR-SG-----.---------- 187
SIVAGMB30 --W---D--E-AQK----..-D-..PNT-MG-----.----------Q---------- 150
SIVAGMB53 --Y-----ED-TLL----..-K-..ANT-TPP----T------S--------I-------FH---------- 143
SIVAGMB14 L-Y-----SE-SFT----..-R-..SNI-SG-----T---------GL----------LQ-R-------- 429
SIVTAN1E --W-----NS-RNV----..-N-.....T--KDKR-Y-----P-----I---------- 244
SIVTAN17E --Y---D--RRRKE----..-D-.....KDP---F--S--P---------- 242
SIVTAN40E --W-----DS-KSVN---..-T-.....TPEKD-L-K---------- 244
SIVTAN49E --W------G-NYT----..-P-...SNSTK-GMTGS---------G----------S---------- 250
SABAEUS.CON LNyLNNqs.....VdPdH..N?C.....???k?ndkkCWqRtYvPCHIrQvVNDWYTLsKKTYAPPREGh 454
SIVAGMD29 ------LT.....------..-K-.....NKG---------- 153
SIVAGMD30 --F-----.....------..-N-.....T-Q----------I---------- 154
SIVAGMD37 ------K-.....-G---..-P-.....S-N---R----N----------Q 135
SIVAGMD45 --------.....-N---..-Q-.....KTN------A-N----------A----------Q 152
SIVSAB2E --------.....------..-P-.....GGNDK-NR----------I---------- 241
SIVSAB3E --------.....------..-P-.....N-TS-------N-A---------- 239
SIVSAB4E --------.....---N-..-T-.....TPKS--R---------- 239
SIVSAB1C ------K-.....-----..-N-.....A-N-T-P---------- 460
SYKES.CON .....NVSKLFANITNGNASKNNYASNLR.....LSCAIRQIINDWRYVRKLIYLPPTAGH 432
SIVSYK .....---------- 432

AGM ENV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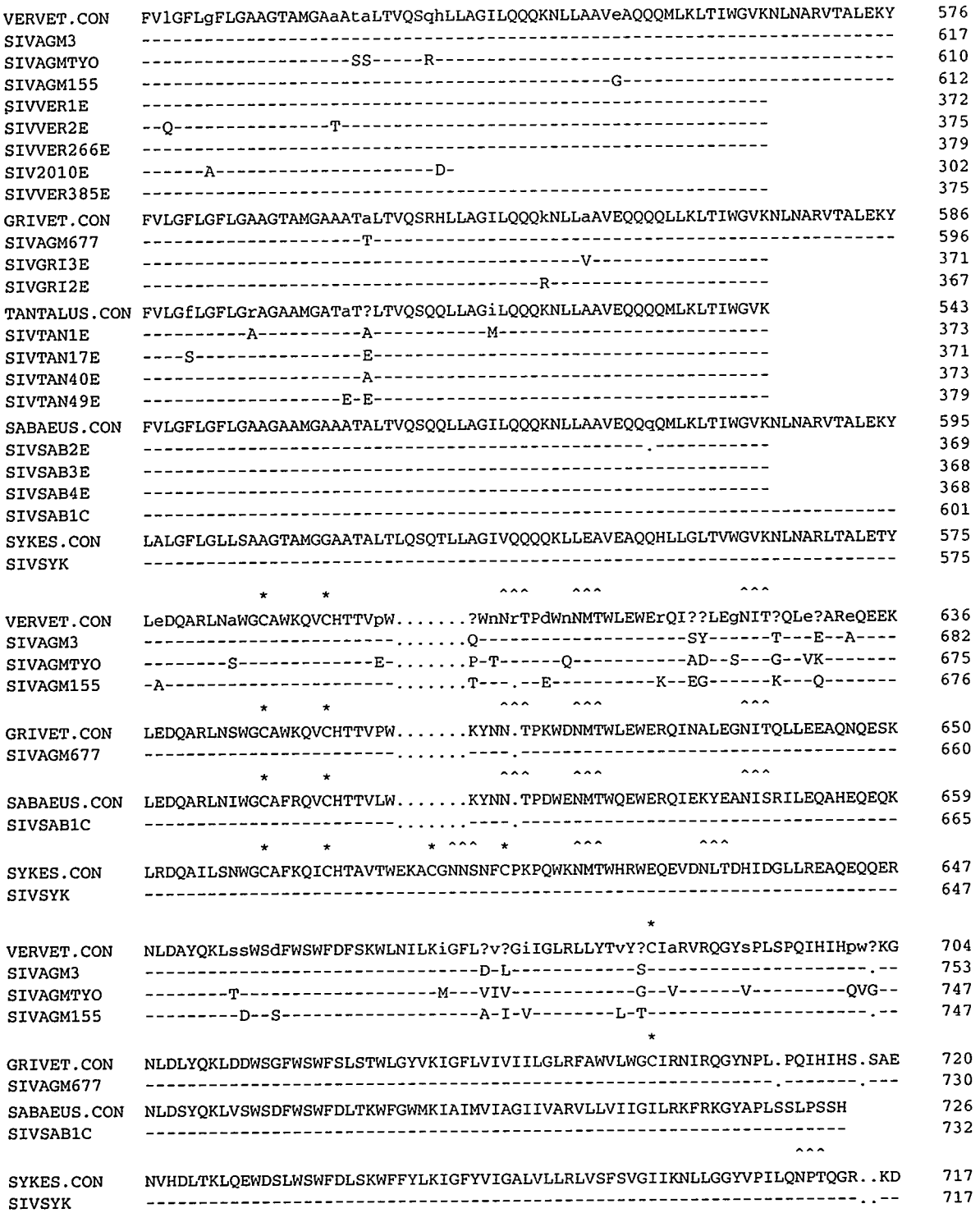
SIVAGMTYO ---R----------S----.----------.- 538
SIVAGM155 ----------NQ---.---------T----------Q------.- 540
SIVVER1E -E--------A-----IH----.---------A---S----------P------P.S-E---.- 312
SIVVER2E ----------SR---.----------D----------.- 315
SIVVER266E -E----------IP----.----------D----------.- 319
SIV2010E -E-R----------NQS--.----------Q------.- 272
SIVVER385E ----------IND---.---------T----------SP--I.- 315
GRIVET.CON LECNSsVTALYVeInYNNkSGPINVTLSpQvRSIWAYELGDYKLVEITPIGFAPTDVRRYTGP.treKRV.P 514
SIVAGM677 ----------A-D----------.------.- 524
SIVGRI3E -----T----------S----------.S-----.- 311
SIVGRI2E ----------E----------I----------.-KQ---.- 307
TANTALUS.CON LECtSTVTSmmvSLDYnsKnmT.NVTLTANlENiwAYELGrYklIeIkPIGFAPTevRRYvGP.TREKRV.P 484
SIVAGMB05 ----------.----------K-- 234
SIVAGMB30 ----------.----------E--.------.- 219
SIVAGMB53 ---------I-------T-H--.----------N-N 185
SIVAGMB14 ---R------L------D----.---------- 486
SIVTAN1E ----------ER-.----------E--------I------.------.- 313
SIVTAN17E ----------VN----.----------I----------D-------.------.- 311
SIVTAN40E ---------IIA-----N----.-------I--LY----------.------.- 313
SIVTAN49E ----------.----------.------.- 319
SABAEUS.CON LECnSTATAlYVELnYNskNrT.NVTLsPqIrSIWanELGdyKLVEIKPIGFAPTeVRrYTGP.ERQKRV.P 523
SIVAGMD29 ---T----------.------H---------- 192
SIVAGMD30 ---------M-------L----.----L----------F----------K----.------.- 223
SIVAGMD37 ---H----------G-.----- 162
SIVAGMD45 ---T----------H---.----------SY---S------ 198
SIVSAB2E ----------L-------.------H-E----------.------.- 310
SIVSAB3E ----------.--------E----------.------.- 308
SIVSAB4E ----------.----------N-------.------.- 308
SIVSAB1C ----------.--------E----------K-------.------.- 529
SYKES.CON IKCTSNVTAVLTDIEYYPGSTL.NFTPTANVEDVWRADLFNYKLIQIKPIGFAPTDQRRYELPNTREKRAAP 503
SIVSYK ----------.---------- 503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SIVAGM3 617
SIVAGMTYO 610
SIVAGM155 612
SIVVER1E 372
SIVVER2E 375
SIVVER266E 379
SIV2010E 302
SIVVER385E 375
GRIVET.CON FVLGFLGFLGAAGTAMGAAATaLTVQSRHLLAGILQQQkNLLaAVEQQQQLLKLTIWGVKNLNARVTALEKY 586
SIVAGM677 596
SIVGRI3E 371
SIVGRI2E 367
TANTALUS.CON FVLGfLGFLGrAGAAMGATaT?LTVQSQQLLAGiLQQQKNLLAAVEQQQQMLKLTIWGVK 543
SIVTAN1E 373
SIVTAN17E 371
SIVTAN40E 373
SIVTAN49E 379
SABAEUS.CON FVLGFLGFLGAAGAAMGAAATALTVQSQQLLAGILQQQKNLLAAVEQQqQMLKLTIWGVKNLNARVTALEKY 595
SIVSAB2E 369
SIVSAB3E 368
SIVSAB4E 368
SIVSAB1C 601
SYKES.CON LALGFLGLLSAAGTAMGGAATALTLQSQTLLAGIVQQQQKLLEAVEAQQHLLGLTVWGVKNLNARLTALETY 575
SIVSYK 575
VERVET.CON LeDQARLNaWGCAWKQVCHTTVpW.....?WnNrTPdWnNMTWLEWErQI??LEgNIT?QLe?AReQEEK 636
SIVAGM3 682
SIVAGMTYO 675
SIVAGM155 676
GRIVET.CON LEDQARLNSWGCAWKQVCHTTVPW.....KYNN.TPKWDNMTWLEWERQINALEGNITQLLEEAQNQESK 650
SIVAGM677 660
SABAEUS.CON LEDQARLNIWGCAFRQVCHTTVLW.....KYNN.TPDWENMTWQEWERQIEKYEANISRILEQAHEQEQK 659
SIVSAB1C 665
SYKES.CON LRDQAILSNWGCAFKQICHTAVTWEKACGNNSNFCPKPQWKNMTWHRWEQEVDNLTDHIDGLLREAQEQQER 647
SIVSYK 647
VERVET.CON NLDAYQKLssWSdFWSWFDFSKWLNILKiGFL?v?GiIGLRLLYTvY?CIaRVRQGYsPLSPQIHIHpw?KG 704
SIVAGM3 753
SIVAGMTYO 747
SIVAGM155 747
GRIVET.CON NLDLYQKLDDWSGFWSWFSLSTWLGYVKIGFLVIVIILGLRFAWVLWGCIRNIRQGYNPL.PQIHIHS.SAE 720
SIVAGM677 730
SABAEUS.CON NLDSYQKLVSWSDFWSWFDLTKWFGWMKIAIMVIAGIIVARVLLVIIGILRKFRKGYAPLSSLPSSH 726
SIVSAB1C 732
SYKES.CON NVHDLTKLQEWDSLWSWFDLSKWFFYLKIGFYVIGALVLLRLVSFSVGIIKNLLGGYVPILQNPTQGR..KD 717
SIVSYK 717

AGM ENV

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                                                *                   *
VERVET.CON   qPDNA?ePgEGGd??k?kse?WQK?SgtaewKS?wC??LT?W??????WLYNSCLTLL??LR?AFQY?QYGL    756
SIVAGM3      -----EG------KR-NS--P---E--------N--KR--N-CSISSI----------VH--S----I----    825
SIVAGMTYO    R----D-------NSRI-L-S- -D-.....--R.-MQ--A-LTRLNT----------IQ--K----L----    812
SIVAGM155    -----G--E---RTG-S--TH                                                      768
                                                      *       *   *
GRIVET.CON   RPDNGGGQDRGGESSSSKLIRLQEESSTPSRINNWWLNFKSCSLRIRTWCYNICLTLLIFIRTAVGYLQYGL    792
SIVAGM677    ----------------------------------------------------------------------    802
                          ^^^                             *
SYKES.CON    PGKPADEEEGSGDREGLNVSTFSRESLRQSLEAGQQLWRTV.........CSSFRSLIRQLTITWGFISYGF    780
SIVSYK       ----------------------------------------.........----------------------    780
                                      *
VERVET.CON   ?ELK??AQE????LA??AQNA??QIWLACRSAYR?I?NSPRRVRQGLE?ILN                      794
SIVAGM3      G---AA---AVVA--RL----GY-----------A-I-----------G---                      877
SIVAGMTYO    A---TG---ILQT--GV----CH-----------N-V-----------E--                      863
GRIVET.CON   QQLQEAATGLAQALARAAREAWGRLGAIVRSAYRAVINSPRRVRQGLEKVLG                      844
SIVAGM677    ------------------------------------------------------                   854
SYKES.CON    NELKIAAASLGREIRDWVAAIWQAIYAATRRVVEAVAALPRRLRQGLEIYLN                      832
SIVSYK       ------------------------------------------------------                   832
```

```
CONSENSUS MG??nSKpqhkk?l?lW?aLh?t??tryglLaDPLiGqSSt?QEECdKaLrkslirk?ng?mTpegrrlqegd?w  63
SIVAGMTYO --SQ----A---YSK--Q---K-HV----------T---V----------Q--N--E-E-------T-      75
SIVAGM155 --LGS-------Q-TI-R---A-RH----------L------G--------R--N---------D--Q-      75
SIVAGM3   --LG--------Q-S--H---K-RA----------L--------KE-----R--K------K-----K-      75
SIVAGM677 --SS---R-QQGL-K--RG-RGKPGADWV--S---------V----G---K--W.G-..-K---D--------TF  72
SIVSAB1C  --GKS--Q-QRHS-W--SK-RQAPVIQ-DM-----L----HI----A-S--DG---QGDSSR-E--VKMKHQGRQ  75

SIVSYK    --STS--S-QLRSEGKYAIGWRLFGKQ-TP-P-E-SRPLQPCRGGF---W-ST-TEPIDPHGPDRDWGHSG-QKF  75

CONSENSUS deW?sddEeE....VGFPVrPrvPLRqmTYKLAvDFsHFLKeKGGLdGIYYSdRRnkILnLYALNEWGIiDdWna 133
SIVAGMTYO E--.------....---------------------------------------------------------- 145
SIVAGM155 ---.--E-D-....-------------I---------------------------------------------- 145
SIVAGM3   ---.--E-D-....-----------------------------------------Q------------------ 145
SIVAGM677 ---.D-----....-----Q---------------------S----------E--E----------------Q- 142
SIVSAB1C  PS-YDE----....-------CL---A------I--G---------E-----E--K---D---------V-G-QN 146

SIVSYK    SPGDIVQD-GDTGL-----C-QT---TL-----I-L---I-N----Q-MN-CEK-DE--H--LQ--H----RI-. 149

CONSENSUS ws?GPGiRyPrcFGfCFKLVPVdLhEEA?tcErHCLvHPAQ......??edpDgi?hgE?LvWKFDPmLAvqYdp 196
SIVAGMTYO --K-----F-K-----------------Q------------.....MG------S---I----------I---- 214
SIVAGM155 --K-------------------A-----E------------.....LH------N---I-A-------------- 214
SIVAGM3   --E-------------------------E------------.....VR------N---V---------------- 214
SIVAGM677 Y-P--------V----------------RN------M----.....MG------D---V-------K---E-R- 211
SIVSAB1C  YTD---T---K---W---------S---KNS-N---L----.....VAYED-AWK..-T-------L---D-VA 213

SIVSYK    YTS---T---LI--WLWE---NEIEGCLEYE-HTL-L---SGQGSSSMG-.-HVELQPPPGYTPGWE-ARL-LER 223

CONSENSUS ?r?yftdmh???gkrk                                                          207
SIVAGMTYO N-E------GLV.---                                                          229
SIVAGM155 S-E----LYSTV-TGN                                                          230
SIVAGM3   N-K-L----DL.----                                                          229
SIVAGM677 ..DM-K---EH.A--                                                           223
SIVSAB1C  W-LHPEQVPSAQ-                                                             226

SIVSYK    QTGKPQELQSALS-NIS                                                         240
```

III

Analysis

PART III Analysis

Contents III-1

A. Gag Proteins (Robert J. Gorelick and Louis E. Henderson) 2

B. HIV-1 Tat: Structure and Function (Kuan-Teh Jeang) 11

C. HIV-1 and HIV-2 Sequence Subtypes (Gerald Myers) 23

HIV-1 Phylogenetic Trees 23

HIV-1 Subtype Summary 31

HIV-2 Phylogenetic Trees 32

D. HIV Synonymous and Nonsynonymous Substitution Frequencies (G. Myers) . 34

HIV-1 and HIV-2 *gag* and *env* Substitution Frequencies 34

HIV-1 Intersubtype Comparisons 36

E. Global Variation in the HIV-1 V3 Region (Bette Korber) 37

Introduction 37

Subtype consensus sequences 39

Amino acids found in the V3 loop of each subtype(1994) 40

Analyses of variation at the immunogenic tip of the V3 loop 44

Country codes 47

Alignments of sequences by subtype 52

Brief descriptions and references for all sequences included in the study . 66

Phenetic relationships of the tip of the V3 loop 84

F. Mutations in HIV-1 RT and Protease (John Mellors, Raymond Schinazi, Brendan Larder; Simon Wain-Hobson) 93

Gag Proteins

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INTRODUCTION

All retroviruses utilize a *gag* gene to encode a precursor polyprotein (Gag precursor) that is initially incorporated in the budding particle and ultimately cleaved by a viral protease (encoded by a *pol* gene) into structural proteins of the mature virus collectively referred to as Gag proteins (See Figure 1 for biosynthesis of HIV-1 virion proteins). Gag precursors are self-associating proteins capable of assembling into virion-like particles without the requirement of other viral factors. For most members of the retrovirus family, including lentiviruses, assembly takes place on the cytoplasmic side of the cell membrane and nascent virion-like particles bud through the membrane into extracellular space. During normal viral replication the self-associating Gag precursors selectively bind viral RNA and package two plus strands of the genome inside the particle. They also form associations with viral Env proteins such that the budding particle is encapsulated within a lipid envelope containing viral Env proteins. All retroviruses express viral encoded enzymes from a *pol* gene as Gag-Pol fusion proteins and the self-associating properties of the Gag portion directs assembly of the Gag-Pol fusion protein into the budding particle. Thus, the Gag precursor orchestrates assembly of the nascent virion by forming the core structure and interacting with all other viral components (RNA, Pol proteins, envelope lipid and Env proteins) to facilitate their incorporation into the budding viral particle. The term "Gag precursor" was originally adopted to indicate that the major antigenic protein (capsid antigen, CA; [1]) or "Group antigen" (Gag) was synthesized as a precursor. The term does little to convey the important biological properties of the protein and a more descriptive name such as "Assemblin" might be more appropriate.

HIV-1 GAG PRECURSOR (ASSEMBLIN)

HIV-1 *gag* genes are generally about 500 codons in length. Figure 2 is a composite diagram indicating posttranslational modifications, proteolytic cleavages and sites for various interactions that are known for the HIV-1 Gag precursor (Assemblin, $Pr55^{gag}$). The upper panel in Figure 2 indicates the posttranslationally modified form of the protein that participates in the assembly of the immature virion particle. During or shortly after assembly, the viral protease (PR; product of the *pol* gene) is activated and the Gag precursor is cleaved (middle panel) into the proteins found in the mature virus (lower panel). The Gag precursor is thought to be organized into domains that roughly correspond to the final proteolytic cleavage products [matrix antigen (MA), capsid antigen (CA), nucleocapsid (NC), and p6] that make up the core of the mature virus.

During or shortly after translation, the initiator Met residue is removed leaving Gly-2 as the new N-terminal residue. Cellular myristoyltransferases catalyze the covalent attachment of a myristoyl group [$CH_3(CH_2)_{12}COO^-$] (Myr) to the amino group of Gly-2 via an amide bond and cellular kinases phosphorylate at least two sites on the protein in the CA domain (one serine and one threonine residue, but the exact sites have not been identified). The protein also binds two zinc ions to form zinc-fingers in the NC domain. As indicated in Figure 2, these posttranslational modifications carry through to the Gag proteins found in the mature virus. Thus MA is myristoylated at the N-terminal end, CA is phosphorylated at two sites and the NC protein contains two zinc fingers.

The myristoyl group and the first 31 N-terminal amino acid residues of the MA domain are necessary for targeting the Gag precursor to the cell membrane [2, 3]. The MA domain of the Gag precursor has also been implicated in binding and assembly of the *env* gene products into mature virus [4, 5]. Presumably the interactions with the *env* gene products involve the cytoplasmic domain of the transmembrane (TM) protein associating with the MA domain, however this has not been directly demonstrated.

The CA domain of the precursor appears to be involved in self-association or Gag/Gag interactions [6]. These interactions have been narrowed down to amino acid residues ~240–430 (see Figure 2, upper panel; [7, 8]). Located within the CA domain is a region called the major homology region (MHR) which is required for efficient viral replication and particle production [9]. The MHR includes residues 285–304 in the HIV-1 (IIIB) CA domain. Amino acid residues, 287/Q, 291/E, 296/Y, and 299/R (in the sequence of IIIB) are completely conserved in the MHR region of all primate lentiviruses.

A region between residues 178 and ~300 in the CA domain of the Gag precursor has been shown to bind Cyclophilin A [10]. Cyclophilin A is a peptidyl-prolyl cis-trans isomerase thought to play a role in immune regulation and has been found in preparations of purified HIV-1 (Henderson, unpublished). Other protein-protein interactions of the HIV-1 Gag precursor include interactions of the p6 domain with the viral encoded Vpr protein [11, 12].

Gag protein-protein interactions also play a significant role in packaging the viral enzymes encoded by the *pol* gene. The *pol* gene products are expressed as a Gag-Pol fusion protein which results from synthesis initiating as for the Gag precursor and progressing in the *gag* frame to a site just past the NC domain (Gag-Pol frameshift site, Figure 2) where a –1 ribosomal frameshift event occurs followed by synthesis continuing in the *pol* frame [13]. The resulting fusion protein is referred to as the Gag-Pol precursor (Pr160Gag-Pol) and contains the Gag sequences required for association with Gag precursors and incorporation into virion particles. The fusion protein is ultimately cleaved by the activated viral PR to the mature Pol products (PR; reverse transcriptase, RT; and integrase, IN) and the corresponding Gag proteins (MA, CA, p2, NC) and peptides derived from the *pol* reading frame preceding the codon for the N-terminal residue of PR. The "transframe" peptide isolated directly from whole virus [HIV-1 (MN)] has the sequence FLREDLAF [14], where the first two residues (FL) are encoded by the *gag* gene and correspond to the first two residues of the p1 peptide (lower panel, Figure 2) and the remainder of the transframe peptide is encoded by the *pol* gene.

In addition to the various protein-protein interactions involved in the assembly, the Gag precursor also binds and packages the viral genomic RNA. The NC domain of the Gag precursor is directly involved in the nucleic acid binding properties of the protein. The NC domain (Figure 2, upper panel) is rich in basic residues (Lys and Arg) and contains two copies of a zinc binding sequence [$Cys(X)_2Cys(X)_4His(X)_4Cys$] referred to as a retroviral CCHC zinc finger [see Figure 3; 15]. The basic residues confer a nucleic acid binding property to the domain and the CCHC zinc fingers are involved in the specificity for the viral RNA [16–18]. Apparently, during viral assembly, the NC domain of the Gag precursor specifically binds to a site near the 5′ end of the genomic RNA referred to as the Psi site. If either of the two zinc fingers in the NC domain are disrupted by site directed mutagenesis, or the Psi sequence in the RNA is deleted, noninfectious particles are produced with reduced levels of packaged viral genome [16–19]. Mutants with the first finger replaced by the second finger also package reduced levels of viral RNA, but a mutant with the second finger replaced by the first (i.e., NC domain with two identical copies of the first finger) packages normal levels of viral RNA [20]. Thus, even though both zinc fingers are required for specific RNA packaging, they are not functionally equivalent in this regard.

MATURE GAG PROTEINS

After the Gag precursor assembles into the immature virion, the activated viral protease cleaves the protein into the mature Gag proteins found in the infectious virus (Figure 2). Based on *in vitro* analysis, the order of cleavage is as follows: p2/NC > MA/CA = p1/p6 > CA/p2 > NC/p1. The MA/CA and p1/p6 sites are cleaved approximately 12-fold slower and the CA/p2 cleavage proceeds about 400-fold slower than the initial p2/NC cleavage [21–23]. Following proteolytic cleavage (Figure 2) the mature Gag proteins rearrange to form the core structure of the mature infectious virus. The mature MA protein remains associated with the inner side of the lipid envelope while the CA protein forms the outer shell of the capsid structure which contains the NC protein bound to the genomic RNA. During the infection process, RT and IN together with the MA protein, NC

protein and the genomic RNA are taken into the cell as the "pre-integration complex" [24]. It has been suggested that proviral DNA synthesis takes place within the pre-integration complex. The mature MA protein plays a role in transport of the viral nucleoprotein complex into the nucleus for integration of provirus into the host genome [24, 25]. The MA protein detected in the nucleus is phosphorylated [26], whereas the MA protein in the virus is not. Thus, the phosphorylation of MA occurs during or after the viral infectious event. Within the MA protein there is a nuclear localization signal (NLS) [25] that is similar to other nuclear targeting sequences. The signal is located between residues 14–36 and 107–116 of the HIV-1 p17 MA protein (see Figure 2) and mutants lacking the signal accumulate proviral DNA in the cytoplasm. The NC protein may also play a role in the infection process. Mutants of the NC protein which still package RNA but have alterations within the zinc-finger structures have reduced infectivity [20] suggesting that a role is performed by the NC protein which may be at the level of the preintegration complex. The NC protein has additional functions in the virus life cycle. These include strong nucleic acid annealing and melting activities [27, 28]. It has been suggested that the NC protein is involved in annealing of the primer tRNA to the primer binding site of the viral genome. These activities may also have implications in strand transfer reactions that occur after the first strong stop synthesis of the proviral DNA, to complete synthesis of the provirus for subsequent integration. The NC protein has also been shown to catalyze the formation of the genomic RNA dimer found in virion particles [29]. A recent report showed that HIV-1 with a defective protease had an RNA dimer structure that was different from that found in wild-type HIV-1 [30]. This indicates that dimer formation is probably catalyzed by the mature NC protein and not by the Gag precursor.

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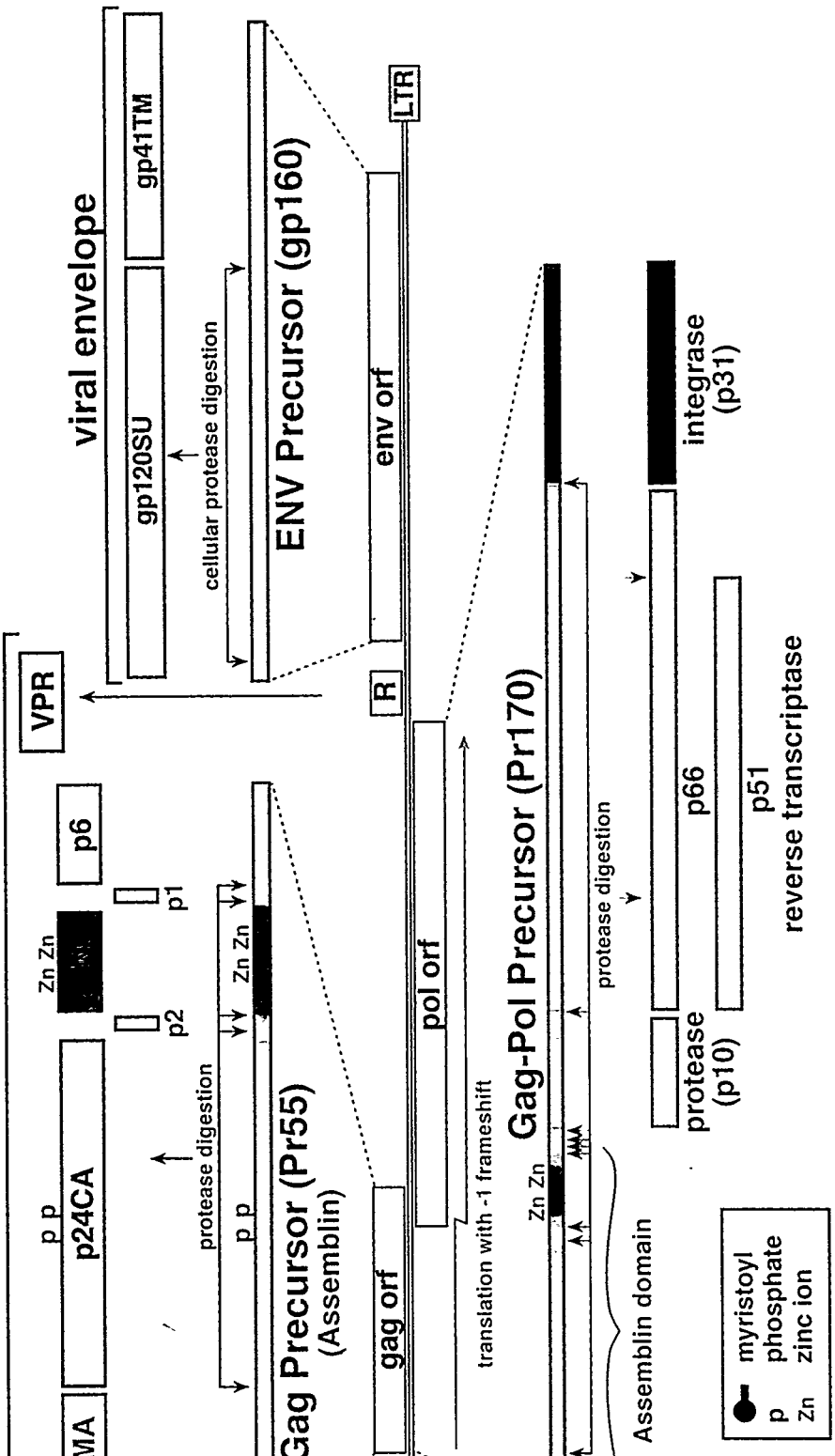

Figure 1. Biosynthesis of HIV-1 Virion Proteins. Steps in the biosynthesis of proteins found in mature infectious HIV-1 virion particles are outlined in a schematic diagram. Proteins are indicated in color and designated according to convention. Naturally occurring proteolytic cleavage sites are indicated by red arrows and some posttranslational modifications are indicated (glycosylation sites in gp120 and gp41 are omitted).

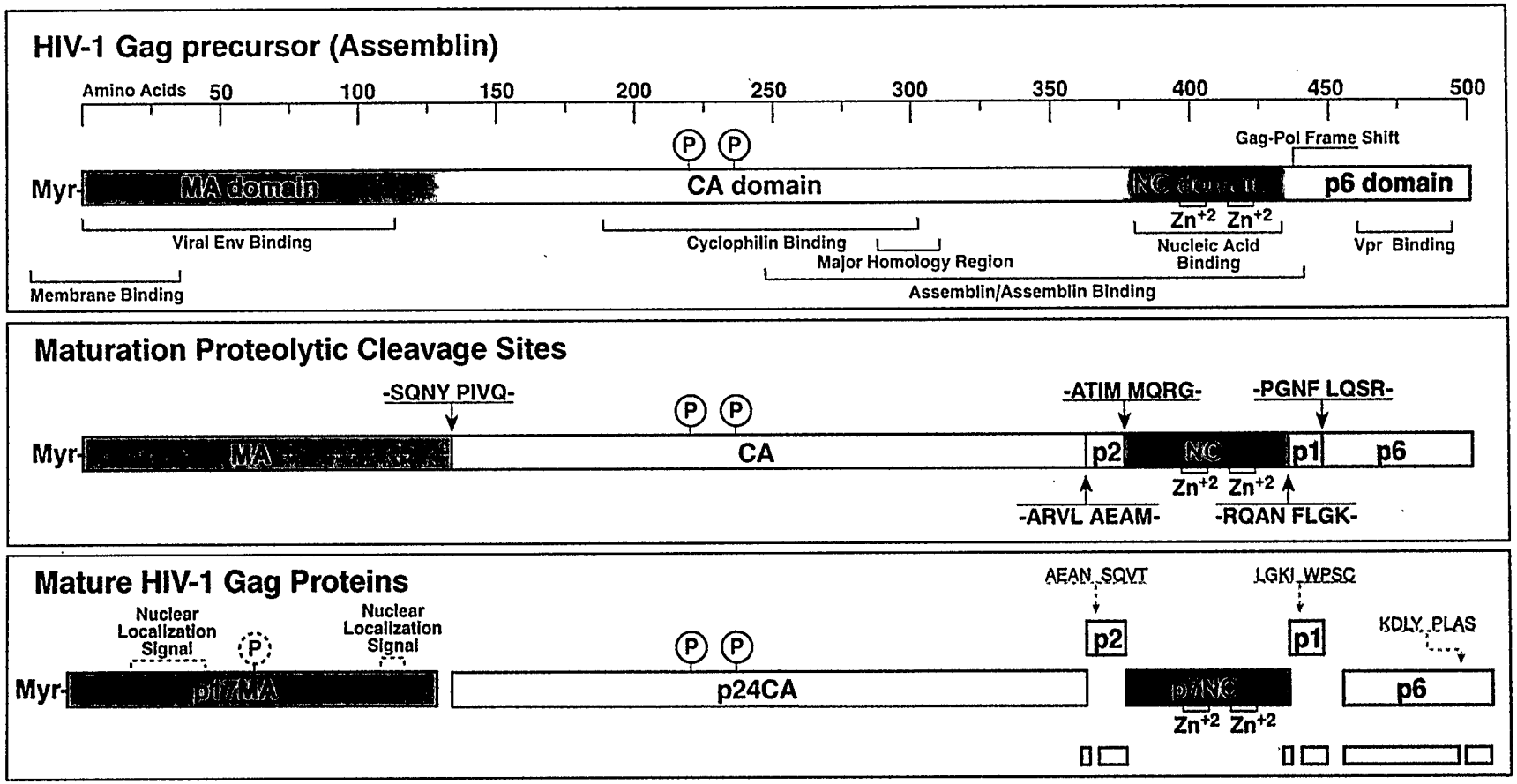

Figure 2. Biosynthetic Processing of HIV-1 Gag Proteins. The biosynthetic processing of the HIV-1 Gag precursor (Assemblin) and its natural proteolytic cleavage products is indicated in the schematic diagram. The upper panel shows the posttranslationally modified Gag precursor that participates in assembly and budding of the immature viral particle. The protein is depicted as organized into domains that correspond to final cleavage products, matrix antigen (MA), capsid antigen (CA), nucleocapsid (NC) protein and p6 (lower panel) found in the mature virus. The Gag precursor and MA are myristoylated (Myr-) on the N-terminal amino group of glycine (Gly-2). The precursor and CA are phosphorylated at two sites (one serine and one threonine residue). The NC domain of the Gag precursor and the NC protein bind two zinc ions to form zinc-fingers. The MA protein is not phosphorylated in the virus but is phosphorylated during the infectious process (indicated in the lower panel). The middle panel indicates the sites for proteolytic attack by the viral protease during the normal maturation process. The lower panel indicates the mature Gag proteins and also the products of partial proteolysis of p1, p2, and p6 found in the infectious virus.

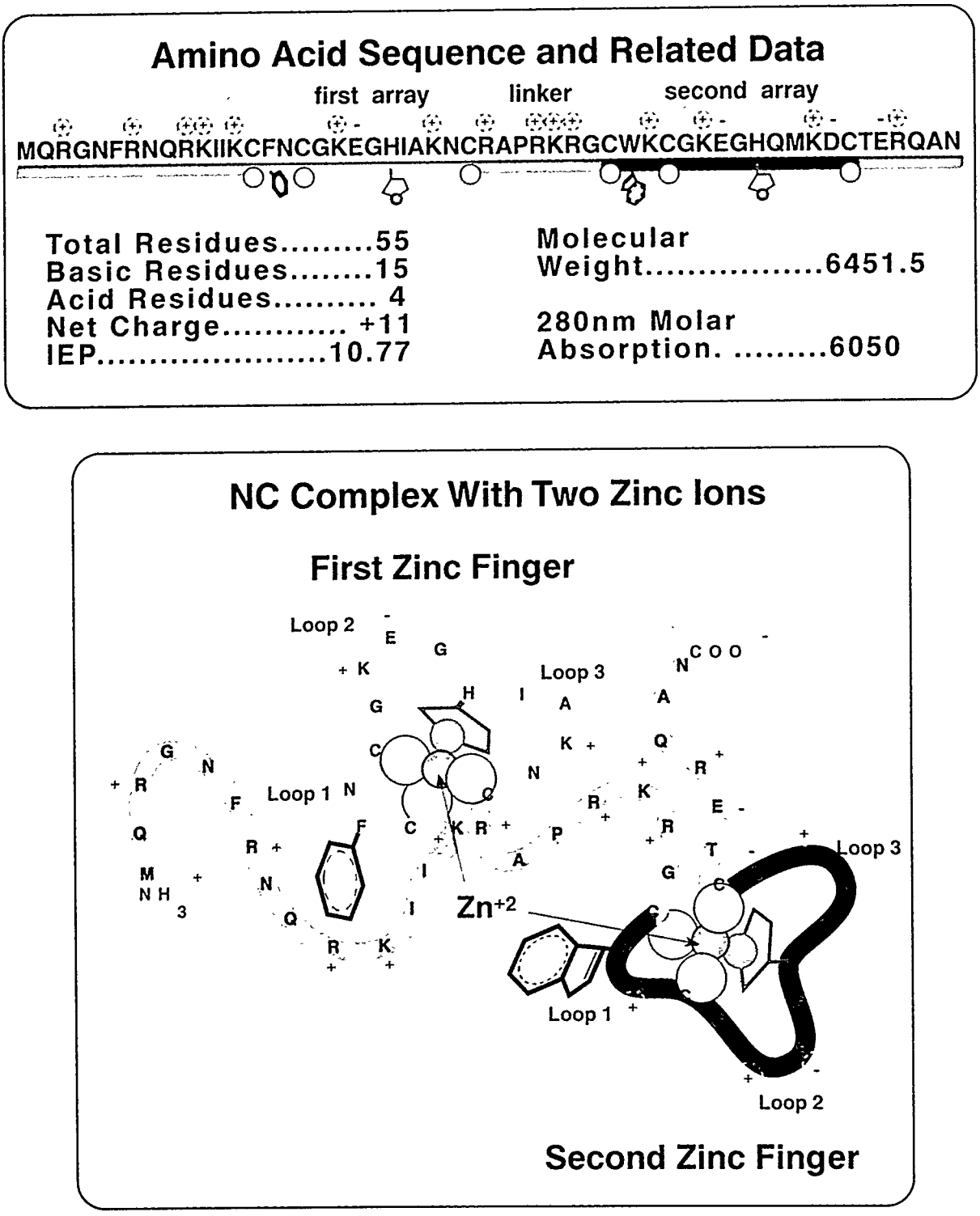

Figure 3. HIV-1_{MN} Nucleocapsid (NC) Protein. The upper panel shows the amino acid sequence of the NC protein and indicates the distribution of charged residues. Amino acid side chains that coordinate with zinc ions are indicated as well as aromatic residues that are required for specific RNA binding. The panel also lists fundamental molecular data for the protein. The lower panel is a cartoon to indicate the zinc-finger structures formed by binding metal ions.

HIV-1 Gag Consensus Sequences

```
CONSENSUS.A mGARaSvLsggkLDawekIrLRPgGkKkYrlKHlvwAsreLerFaLnPslLeT?egcqqimeQlqsalkTg?e   71
CONSENSUS.B ----------e--r-------------k---i----------v--g---ts---R--lg---Ps-q--s-   73
CONSENSUS.C ------i-r-----?------r-----h-Mi---------------pg----s---k--ikq--P--Q--T-   72
CONSENSUS.D --------------?---------g----?---i---------f-l--G----s---k--ig---P-iqt-s-   71
CONSENSUS.F ------------------------------?-------------??-g----s---rk-Ig---pS-Q--S-   70
CONSENSUS.G --------------?------------?--?----------?-----G----T------??---P?-Q--T-   66
CONSENSUS.H ----------?---------------?-------------------?--?-----L-?I----P-----T-   67
CONSENSUS.O ---?----T-S------?---?--S--?---------------?-C--?----A--?E?LLQ--EP-----S?   64

CONSENSUS.A ElkSLfNtvatLyCvHqrIdvkDtKeA..ldkiEei.qnkskqk..tqq...aaA???????.........Tg  120
CONSENSUS.B --r--y-------------e-------..------E.-----k-..a--.??--ad.............???t-  123
CONSENSUS.C --r--?----------??-e-r-----..-----e-E.---?Q--??---..ak?-D..............?-  117
CONSENSUS.D e----?----------e--e--d----..-e-m--E.-----k-.?a--???-t-D..............tr  120
CONSENSUS.F --r--?---?v--f----vE?------..-?-L--E.----q--..---...?--d..............K-  115
CONSENSUS.G -?---?-??-?-?-?----?----k--..-eEV-Ka.-kn-Q--..---...???-..............?k-  104
CONSENSUS.H --Q----LL-?---------?------..-?-??-?.--??Q??..---...-T?D..............K?  105
CONSENSUS.O ?-?--W-AI?V-W---N-??I?--QQ-..IQ-LK-VM.?SR-SA..?AA....KE-..............-S  104

                    p17 \/ p24
CONSENSUS.A nss?????....kvSqNYPIVQNaQgQm?hQ?lSPrTLnAwVKviEekaFspEVIPmFsaLSEGATpQdLNmM  182
CONSENSUS.B ---.........q---------nlq---V--ai----------v---------------s---------T-  187
CONSENSUS.C ............-----y-----L----v--ai---------------f--e?ip-ft-lsegat-q-lntm  177
CONSENSUS.D ---.........Q----------L----V--ai---------k-----------i---------------t-  184
CONSENSUS.F ............----------l----V--ai----------------------------se--------T-  175
CONSENSUS.G ---.........Q---------n-----v--pis----------v-------------------------t-  168
CONSENSUS.H ???.........-?-------------?V--AI-----------V-------------------------A-  164
CONSENSUS.O .?R.........Q??------?------V--AI----------AV-----N--I----M------??Y-I-T-  161

CONSENSUS.A LNiVgGHQAAMQMLKdtINeEAAewDR?HPVhAgPippgQmREPrGSDIAGtTStlqEqigwmT...sNPPiP  251
CONSENSUS.B --T-----------e----------l--v-----a-------------------------...n-----  257
CONSENSUS.C lntv-ghqaamqmlk--in-eaa--drlhpv-a-pva--q--e-----------------a---...?-----  246
CONSENSUS.D --Tv---q-------E--n--------l--v-----A----------------------?---...------  253
CONSENSUS.F --T----------------------L--v?--------?------------------q---...----v-  243
CONSENSUS.G l-T----------l-------------I--pQ--------I-d----------------R---...------  238
CONSENSUS.H --?---------?-----------------------------------------------A---...?--?--  229
CONSENSUS.O --AI----G-L-V--EV-----?----T--P??--L----I---T----------Q----?-T-..R????--  224

CONSENSUS.A VGdIYkrwIiLGLNKIVRMYSPvSILDirQgPKEPFrdYVdrFfKtLRAeqAtQeVKnwMTeTLLvQNANPDC  324
CONSENSUS.B --e-------l-----------t-----------p----v---Y--------s------m---l--q-a----  330
CONSENSUS.C ---------------------------k-------------------------D------d-----------  319
CONSENSUS.D -ge-------l------r---------------e---------Y--------s-d-----------------  326
CONSENSUS.F --e-------------------------------p----------------------g---D-----------  316
CONSENSUS.G --e-------------------------------------------------?--?---D-----------  309
CONSENSUS.H ------------------------?----------------?---------?--?---D-----------  298
CONSENSUS.O -----RK--V-----M-K----------?--------------Y-----------------------?----  295

                                      p24 \/  \/  'p2'       \/ p7
CONSENSUS.A KsILraLg?gAtLeEMMTacQgVggPgHKArvLAEAmSqvq??n...???iMmQrGnf.?Gqkr?iKCFNCGk  385
CONSENSUS.B -T--K---Pa-------t----------------------..t-..?sat---------.rn-rKtv-------  397
CONSENSUS.C -T------P--s--------------s------------ann--.....-m---s--.K-p--iv-------  384
CONSENSUS.D kt--K---P?----------------s------------a?.t-..s-ta-m---g--.K-prki--------  392
CONSENSUS.F -T--K-l-P-------------------------a---a..T-..?-a--m--ks--.K--R-iv-------  381
CONSENSUS.G -T--?---P-----------------?------------A..SG..?A-A?---K??-.K-P??-----?---  366
CONSENSUS.H -?--?------SI-------------?---?----------.-T-..?-A-?---K----.K--R-I?-------  356
CONSENSUS.O -Q--K?--P?-------V--------T---??-----A?A-QDLKGGYTAVF----QN.P?R-G---------  360
```

```
                                        pol cds ->
                                             p7 \/      'p1'       \/ p6
CONSENSUS.A EGHlArNCrAPrKkGCwKCgkEGHQmKdCT.?e.rQANFlgkiwpSsKG.RPgNFpQsRp.............    441
CONSENSUS.B e--i-k------k----k----------t.--?-----------h--.-p---l----?????????..??    453
CONSENSUS.C ---i--n-------------?---------..-.-----------s?--.-----L----eptap????????    443
CONSENSUS.D ---i-k------k----k----------..-.-----------h--.r----l----.............    448
CONSENSUS.F e--i-kn-------------r---------..-.-----------n--.r----L----.............    437
CONSENSUS.G -------------?------?---------..-.-------?----H--.-----L-?-?.............    417
CONSENSUS.H ---?----------------?----?----..-.----------???--.-----L----.............    406
CONSENSUS.O ---I-?-------?------Q--------?..NG?-------Y--PGGT.----YV-???.............    410

                        \/ (minor)                \/ (minor)        / p6 terminus (80%)
CONSENSUS.A .EPtAPpAE?f?gmgeeit.s?...?pkqeqkd..??ke??ppl?SlKSLFGNDpLSQ                   483
CONSENSUS.B ?------ees-.rf---t-tPs???-q---pi-....--lY?--as-rs---n--s-q                   500
CONSENSUS.C ?e---p---S-.rF.--t-.Pa....----p--??--?---?--ts-k-------                     482
CONSENSUS.D .--------eS-.-F-----.Ps....q------??----ly.--as-k-------ls-                 494
CONSENSUS.F .---------s-.-F?----.PS....--------....egly---a----                         474
CONSENSUS.G .--?-----sl.-f----?.?S....----Pr-....--LY--------                           451
CONSENSUS.H .--------S-.-F---M-.P-....----??-....?-..?-------                           436
CONSENSUS.O .?-S---M-.......-?VK.?Q....EN-?--G..--?-LY.-FA-------T-Q                   443
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HIV-2/SIV Gag Consensus Sequences

```
CONSENSUS.A MGArNSVLRGKKADELEkiRLRPgGKKkYrLKHiVWAANeLDrFGLaESLLESKEGCQkIltVLdPlVPTGSE     73
CONSENSUS.B ----?---S---T-----V--------?-?---??--v---d------?--e-----h----v-a--v-----     67
CONSENSUS.C                                  -------A-------T----------E--------     36
CONSENSUS.D --a-n---S--k-----------------m---v----------------en--------s--a--------     73
CONSENSUS.E                                  -R-------------N----HR-----E--M-----     36

                                                                          p16 \/ p28
CONSENSUS.A NLkSLfNTvCViWCiHAEEKvKDTEeAk?ivq.RHLvAETgTaEKMPntSRPTAPpSgkggNfPVQq?gG?NY    142
CONSENSUS.B -------t----y-L--ee---------K-A-.s--?v...dt--m-a-s?pt-p---..r-Y----vA-.--    131
CONSENSUS.C -----Y--T-----L---Q---H---RNEV-E.---A---KN-----A-------S--GR--Y----VA-.--    107
CONSENSUS.D -----y---c----------h-----Q---.----v-----e?--k----------r---Y-------.--    142
CONSENSUS.E -------A---VY-L--AV---------KH--QH----GGK-T--L-PQ---------G---Y----I-N.--    108

CONSENSUS.A tHvPLSPrTLNAWVKLvEeKKFGAEVVPGFQALSEGCTPYDINQmLNCVGDHQAAMQIIREIINeeAAdWD?q    214
CONSENSUS.B v-l--------------------ae-----------c-------------e----mqi------------Q-    204
CONSENSUS.C V-H------------------------------T----------L--------------------------EH    180
CONSENSUS.D v-L-------------i----------p---------t-y----------e--------re----------l-    215
CONSENSUS.E V-S-----------------------------------------------E-------------------V-    181

CONSENSUS.A HPIP.GPLPAGQLRdPRGSDIAGTTSTVeEQIqWMfRpqNPvPVGnIYRRWiQIGLQKCVRmYNPTNiLDikQ    286
CONSENSUS.B --?-.--l----------------------q----y-a-n----------l----------p-------q    275
CONSENSUS.C --V-.------------------------------Y-A--------------L----------------V--    252
CONSENSUS.D -pQp??-q??----e-s----------tvd------y-Q---I------r----L-----------tn---v--    284
CONSENSUS.E --RG..QP--QG----S----------PA---E--Y-NP--I---D-------L----------------V--    252

CONSENSUS.A GPKEpFQSYVDRFYKSLRAEQTDpAVKNWMTQTLL?QnaNPDCKLVLKGLGmNPTLEEMLTaCQGvGGPgQKA    358
CONSENSUS.B -------s---------------------------I-----------------------------I-------    348
CONSENSUS.C --------                                                                    260
CONSENSUS.D ---------------------t--av-----q-l-I--------------g?--------------g-----a    356
CONSENSUS.E ----S---                                                                    260

          p28 \/       p2       \/ p8                                      pol cds ->
CONSENSUS.A RLMAEALKEam?PaPIPFAAAQQ....r?aikcWNCGKEGHSArQcrAPRRQGCWKCGK?GHiManCP?RQAG    423
CONSENSUS.B ----------LT--pi----a-qkAGk-gTVT------?--T----------------kq----SK--E----    420
CONSENSUS.D --------e-lap?pl--a-a-q?Gp?-kp---w--g-e--s-----a---q------kmg-v--K-----a-    425

        p8 \/     p1     \/ p6                                    \/ HIV2s only
CONSENSUS.A FLGlGpwGKkpRNFPvaq?pqGL.................tPTAPP?DPavdLLEkYMQQG?rQRE.Q...R    471
CONSENSUS.B --------------mt-v---vtPSAPPMnPAeGMTPrGA--S---A----EM-Ks--qm-rqqre????s-    489
CONSENSUS.D -----------r---M---h---?????????.........-p--p-ed------kn--ql-kq---????sr    475

CONSENSUS.A eRPYKEVTEDlLhlEqgetPhRe?tTEDLLHLNSLFGkDQ                                   510
CONSENSUS.B -------.....................-----------E--                                511
CONSENSUS.D -k----v.....................----l-------?--                                496
```

HIV-1 Tat: Structure and Function

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INTRODUCTION

Most viruses encode functions used to regulate genome transcription. Examples include the SV40 T-antigen, the adenovirus E1a protein, and the herpes virus immediate-early proteins. For the human immunodeficiency viruses (HIV), Tat functions similarly, though not identically, to those above. Over the past decade, we have learned much about Tat, both in structure and in function. While a goal of this Los Alamos database is to completely compile relevant tat sequences, the intent of this brief accompanying overview is not similarly archival, but rather to "add flavor" to raw data. It is written for the purpose of apprising, in a short format, the readers on some of the current thoughts about Tat. For more in-depth discussions, complete subject reviews can be found elsewhere (e.g. Felber and Pavlakis, 1993; Jeang and Gatignol, 1994).

TAT FUNCTION

Tat is a small nuclear protein of 86 to 101 amino acids in size (depending on the viral strain) which is encoded from two separate exons (see Section I). Analyses of "full-length" Tat have been performed commonly using the 86 amino acid version. However, it should be noted that while many laboratory strains (e.g. HXB2 and NL4-3) have the smaller Tat (86 aa) most HIV-1s have the 101 aa protein (see compendium Part II).

A. Transcription. Despite intensive efforts, the mechanism of Tat action remains incompletely understood. It is, however, accepted that Tat is required for optimal HIV viability (Fisher et al., 1986; Dayton et al., 1986). Tat's role in critically directing transcription (Peterlin et al., 1986; Rice and Mathews, 1988; Laspia and Mathews, 1989) from the HIV LTR is one indispensable function suggested for this protein. However, increasingly there is evidence that Tat has other important effects on the virus and on the host cell (see Concluding Perspectives, below).

In activating transcription from the LTR, Tat differs from other prototypic viral transcription trans-activators in requiring a bipartite responsive element consisting of DNA and RNA. To our knowledge, Tat is the first characterized eukaryotic transcription factor that binds to a nascent leader RNA, TAR (Berkhout et al., 1989; Dingwall et al., 1989; Cordingley et al., 1990; Roy et al., 1990; Calnan et al., 1991), and then influences formative events at the TATAA-enhancer-promoter (Berkhout et al., 1990; Selby and Peterlin, 1990; Southgate et al., 1990; reviewed in Jeang et al., 1991; see Fig. 1A). TAR RNA has extensive secondary structure containing a stem, a bulge, and a loop (Muesing et al.,1987; Berkhout and Jeang, 1989; Roy et al., 1990c; see Fig. 1B). Earlier, studies have indicated that the specific UCU sequence of the bulge is critical for binding by Tat (Dingwall et al. 1989,; Roy et al. 1990a, Calnan et al., 1991; Cordingley et al., 1990). In comparison, the structure of the stem, but not its specific sequence, was proposed to be important for function. However, more recent findings reveal that both for Tat binding and for transcription there are sequence specific requirements for the immediate stem nucleotide pairs that flank the bulge (Weeks and Crothers, 1991; Berkhout and Jeang, 1991; Churcher et al., 1993). The loop of TAR RNA is an important binding site for cellular factor(s) that cooperate with Tat in the activation of the LTR (Sheline et al., 1991; Wu et al., 1991). A more extensive discussion of the role of cellular factors that bind TAR RNA (Gatignol et al., 1989; Gaynor et al., 1989; Gatignol et al., 1991) is presented in the compendium Part IV.

While it is clear that Tat binds TAR RNA and interacts with enhancer-promoter-binding factors (Berkhout and Jeang, 1992), the mechanism by which these physical events influence transcription

are not wholly evident. A number of models that attempt to explain the transcription function of Tat have been proposed. These include i) anti-terminating (Kao et al., 1987) stalled RNA polymerase II (RNAP II), ii) increasing processivity/elongation of transcribing RNAPII complex (Laspia et al., 1989; Marciniak et al., 1990), and iii) facilitating initiation of RNAPII complexes at the promoter (Laspia et al., 1989, Jeang and Berkhout, 1992; Jeang et al., 1993a; reviewed in Cullen, 1993). Currently, there are conflicting findings that support each of the models. It is possible that Tat, like basal transcription factor TFIIF (Buratowski, 1994), functions simultaneously as an initiation and as an elongation factor. Alternatively, conflicting attributions could arise from differences in the rate-limiting events (Jeang et al., 1993a) for the various experimental systems used to define Tat action.

A couple of observations indicate that Tat is not a typical transcriptional trans-activator. First, unlike other activators (Tjian and Maniatis, 1994), a modular activation domain has been difficult to define for HIV-1 Tat (see below, Activity domains of Tat). Second, in different settings, neither Tat nor Tat-chimera, in contrast to modular activators, is able to directly activate transcription from a minimal TATA-promoter (Southgate and Green, 1991; Berkhout and Jeang, 1992; Kamine and Chinnadurai, 1992). Instead for physiological activity, Tat requires the presence of an upstream enhancer-binding factor such as Sp1 (Harrich et al., 1989; Kamine et al., 1991;; Southgate and Green, 1991; Zimmermann et al., 1991; Jeang and Berkhout, 1992; Jeang et al., 1993b). Thus it appears that Tat is more aptly classified with transcriptional co-activators (Dynlacht et al., 1991) in bridging conformationally a stereospecific architecture (Tjian and Maniatis, 1994) between Sp1 (Jones and Tjian, 1985; Jones et al., 1986) and TATA-binding protein (TBP; Jeang et al., 1993b; Huang et al., 1993; Kashanchi et al., 1994).

B. Translation. There is evidence that Tat also functions in regulating translation (Rosen et al., 1986; Cullen, 1987). Indeed there are findings that TAR RNA can inhibit translation (Parkin et al., 1988; SenGupta and Silverman, 1989) of HIV-1 mRNAs, most likely through activation of double-stranded RNA-dependent protein kinase and 2-5A synthetase (SenGupta and Silverman, 1989; Edery et al., 1989). Addition of Tat was found to reverse this translational inhibition (SenGupta et al., 1990; Braddock et al., 1990).

ACTIVITY DOMAINS IN TAT

Tat is synthesized from an mRNA joined from two coding exons. The first exon codes for amino acids 1–72, while (in most strains of HIV-1) the second exon codes for amino acids 73–101 (see Fig. 2). In most functional assays, the first 72 amino acids of Tat fully effect transcriptional trans-activation of the LTR. In fact, a truncated 58 amino acid form of Tat is virtually completely active in co-transfection assays (Seigel et al., 1986; Garcia et al., 1988; Kuppusway et al., 1989).

A. First coding exon. The combined results from many laboratories have permitted an arbitrary demarcation of "domains" in Tat (Kuppuswamy et al., 1989). For instance, the N-terminus of Tat (domain 1; Fig. 2) has 13 amino acids with amphipathic characteristics. Mutations that alter the acidic composition of this region were felt originally to affect trans-activation (Rappaport et al., 1989); however, results from a later study conflicted with this interpretation (Tiley et al., 1990).

Amino acids 22 to 37 (domain 2, Fig. 2) contain seven cysteines and are highly conserved between different isolates of HIV-1s, group O as well as group M. Individual mutation in six of the seven cysteines abolish Tat function (see Table I). Although originally proposed as a metal-chelating dimerization domain (Frankel et al., 1988), this region was recently shown to be used for intramolecular disulfide bond formation in monomeric Tat proteins found within cells (Koken et al., 1994). Currently, it is believed that Tat is active functionally as a monomer rather than a dimer (Rice and Chan, 1991; Koken et al., 1994).

Domain 3 (amino acids 40 to 48) contains a RKGLGI motif that is conserved between HIV-1, HIV-2 and SIV Tat. This region, in conjunction with the amino terminus and the cysteine domain, has been suggested to circumscribe the minimal activation domain of HIV-1 Tat (Carroll et al., 1991; Derse et al., 1991). Domain 4 (amino acids 49-72) contains a basic RKKRRQRRR motif. These amino acids confer TAR RNA-binding properties to Tat (Dingwall et al., 1989; Roy et al., 1990;

Weeks et al., 1990; Chang and Jeang, 1992) and are important for nuclear localization of the protein (Ruben et al., 1989; Hauber et al., 1989). However, recent studies suggest that this short basic domain is insufficient in determining the entire specificity of Tat-TAR binding since amino acids outside of the domain also contribute to this interaction (Churcher et al., 1993; Luo et al., 1993).

Table I summarizes 75 point mutations in the first coding exon of Tat collated from the work of eight laboratories (Garcia et al., 1988; Sadaie et al., 1989; Kuppuswamy et al., 1989; Ruben et al., 1989; Hauber et al., 1989; Meyerhans et al., 1989; Rice and Carlotti, 1990a; Rice and Carlotti, 1990b; Siderovski et al., 1992). As alluded to above, since the first 58 amino acids of Tat recapitulate well the trans-activation function of the whole protein, it is not surprising that most of the mutations are clustered within amino acids 1 to 58. In many cases, individual amino acids have been changed to more than one counterpart. This heightens the validity of the resulting phenotype. Examination of these mutants reveals that the region spanning amino acids 1–21 is remarkably tolerant of changes. In contrast, changes in amino acids 22 through 40 were generally deleterious for trans-activation. Finally, although the basic domain (amino acids 49–57) as a unit is necessary for Tat function, individual amino acid changes do not significantly affect activity.

B. Second coding exon. Less information is available about the second coding exon of Tat. It is clear that in routine transfection assays of HIV-1 Tat, absence of the second exon does not alter greatly Tat activity. However, findings from HIV-2 and SIV Tat are quite clear in demonstrating that this exon contributes towards optimal trans-activation (Viglianti and Mullin, 1988; Tong-Starksen et al., 1993). Recently, there have been suggestions that the second exon of HIV-1 Tat, in specific assays, is important for trans-activation (Jeang et al., 1993b) and for trans-repression (Howcroft et al., 1993).

There are two short motifs in the second exon of HIV-1 Tat that could have functional importance (see Fig. 2). The first is an RGD sequence that is used as a cell adhesion signal for binding to cellular integrins (Brake et al., 1990). This RGD motif is not found, however, in HIV-2 or SIV Tat proteins. In addition, a ESKKKVE motif is conserved across different HIV-1 Tat proteins and is partially preserved in HIV-2 and SIV Tats. However, because this motif falls beyond amino acid 86, commonly regarded as the C-terminal boundary of full-length Tat, its functional significance has not been examined.

CONCLUDING PERSPECTIVES

While research on Tat has been narrowly focused upon its trans-activation properties for the HIV LTR-promoter, there is increasing evidence that Tat has other pleiotropic effects on cellular genes, host cell metabolism, and viral infectivity/pathogenesis (see e.g. Drysdale and Pavlakis, 1991). For instance, Tat is reported to function as a secreted growth factor in stimulating the growth of Kaposi-like cells (Ensoli et al., 1990; Ensoli et al., 1993; Barillari et al., 1993). It can affect the organization of neurons and astrocytes (Kolson et al., 1993) and is neurotoxic at low concentrations (Sabatier et al., 1991). Some of these findings are partly explained by the ability of Tat to modulate expression of cellular genes (Roy et al., 1990b; Buonaguro et al., 1994; Scala et al., 1994), to perturb ambient levels of cytokines (Rautonen and Rautonen, 1992), and to protect cells from programmed cell death (Zauli et al., 1993).

Because the viral functions of Tat have been largely extrapolated from subgenomic experiments, one is unsure whether these findings reflect well the complete role of Tat in the setting of the whole virus. The limited number of experiments performed on Tat function in the context of infectious virions suggests that Tat has additional roles, beyond transcription, in affecting viral pathogenicity (Cheng-Mayer et al., 1991; Sakai et al., 1992; Huang et al., 1994).

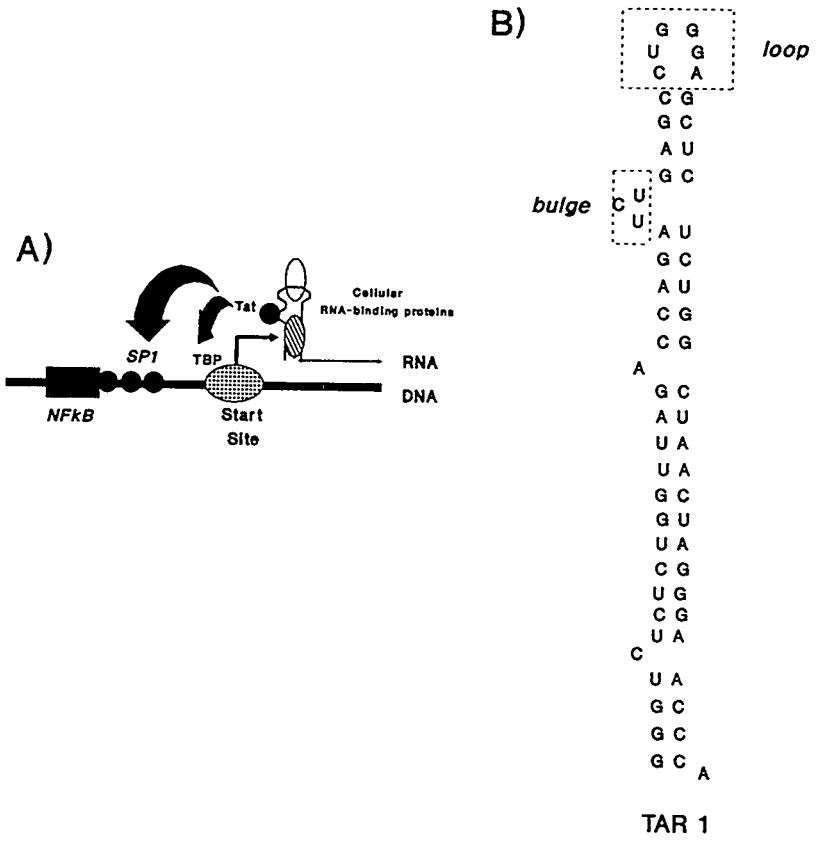

Fig. 1. Interaction of Tat with DNA and RNA targets in the HIV-1 LTR. A) A schematic representation of the functional interactions between Tat, TAR-RNA-binding proteins and promoter elements. Biochemical evidence exists that Tat contacts directly SP1 (Jeang et al., 1993b) and TATAA-binding protein (TBP; Kashanchi et al., 1994). B) Secondary structure of TAR RNA. The crucial trinucleotide bulge and hexanucleotide loop elements are boxed.

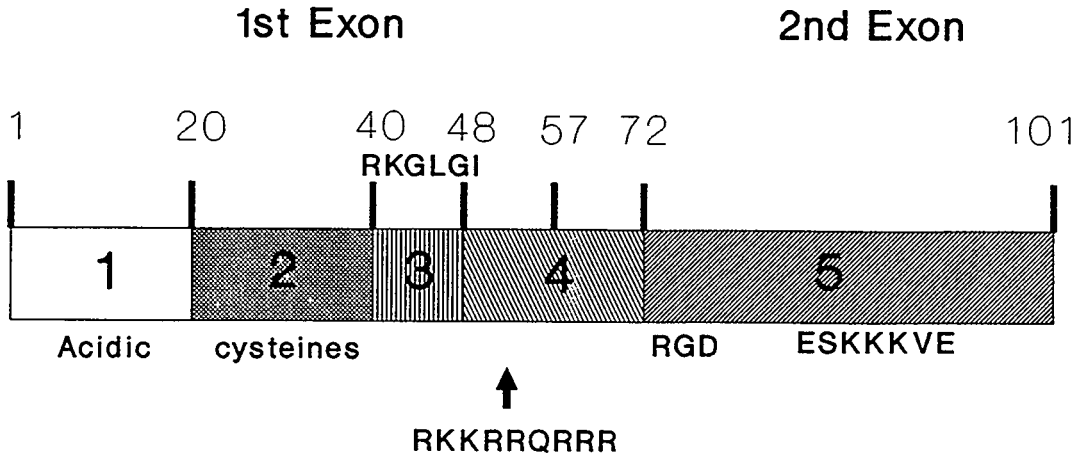

Fig. 2. Domain classifications of Tat protein. The demarcation of domains is somewhat arbitrary. The first exon includes amino acids 1–72, while the second exon includes 73-101. Motifs and characteristics of each "domain" are indicated above or below each region.

Table I. Point mutations in Tat

Original Amino Acids(s) and Their Position(s)	Mutant Amino Acid(s)	Resulting Activity	Consensus Amino Acid(s)
Q2	A	++	E
P3	A	++	P
P3	Q	++	P
V4	A	++	V
D5	A	+	D
P6	A	++	P
P6	S	++	P
Δ3–6		+	
P6P10	LL	++	
R7	A	++	R
L8	A	++	L
E9	A	++	E
P10	A	++	P
P10P13	LL	++	
W11	A	++	W
K12	A	++	K
K12	N	++	K
P18	A	++	P
K19	R	++	K
A21	D	++	A
A21T23	VA	+	
T23	A	++	T
C22	S	–	C
C22	G	–	C
N23	T	++	T
N24	A	++	N
N24	K	++	N
C25	R	–	C
C25	G	–	C
Y26	A	+	Y
Y26	F	++	Y
C27	S	–	C
C27	G	–	C
K28K29	AA	+	KK
K28K29	EA	–	KK
C30	G	–	C
C31	S	++	C
C31	E	–	C
C31	G	++	C
F32	A	+	F
H33	A	–	H
C34	G	–	
C34	S	–	C
G35	A	+	Q

Key: Column 3, ++ > 50% wild type activity; + > 10% wild type activity; +/– or – indicate <10% wild type activity.

Table I. (cont.) Point mutations in Tat

Original Amino Acids(s) and Their Position(s)	Mutant Amino Acid(s)	Resulting Activity	Consensus Amino Acid(s)
C37	G	–	C
C37	S	–	C
F38	A	–	F
F38	L	++	F
K40	D	–	T
K40	T	++	T
K41	A	–	K
K41*	T	–	K
K41*	T	++	K
L43	F	+	L
G44	S	++	G
S46	A	++	S
S46	P	–	S
Y47	H	++	Y
Y47	A	++	Y
G48	S	++	G
G48R49†	SG	++	
R49	T	++	R
K50	stop	–	K
K50K51	Y50Y51	+	KK
K50K51	S50G51	+/+	
K50	E	++	K
K50	T	++	K
R52	E	++	R
R53	I	++	R
Q54	N	++	Q
R55	G	+	R
R55R56	L55T56	+	
R56	E	++	R
R57Q63	SE	++	RQ
L69	I	++	L

Key: Column 3, ++ > 50% wild type activity; + > 10% wild type activity; +/– or – indicate <10% wild type activity.

* Different results reported for the same mutation from Kuppuswamy et al., 1989, and Myerhans et al., 1989.

† Amino acids beyond position 59 completely changed.

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HIV-1 Tat Consensus Sequences

```
                                                  \/3'sj \/3'sj
                                                rev cds ->
CONSENSUS.A   M?PVDPnLEPWnHPGSqPTTaCskCYCK?CCwHCqlCFLnKGLGISYGrKKR..r?RRgtPQ.s?kDhQnp    64
CONSENSUS.B   -e----r----k------kt-ctn----k--f---v--tt-g-g--------..-Q-rrapq.dSqt--vs    68
CONSENSUS.C   m--v--?--------s--K---t--yc-k-sY--lV--qt----------..-q--sa-?.-SE-----    65
CONSENSUS.D   md-v---l-p--------r-p-N--?--K--Y---v--it----------..-Q--rppq.g-Qa--v-    66
CONSENSUS.O   -D----E?P--H----?-Q?P-NN----R--Y--YV--??------?-----....?-PAAA?--P-?KD-    57
CONSENSUS.CPZ -D-?-????--?--???-?-?-NN-------Y--??--TK----------?-???---T???.?S?NN-D?    45

             exon\/exon
CONSENSUS.A   ipKQplPqtqg??ptgpkESkKkVeSKteTDrf?                                        95
CONSENSUS.B   Ls-q-?s-pr-D.-----es-k---rE--tdP?dQ                                      100
CONSENSUS.C   -s----p--r-d.----Ee----------t-p-D                                       98
CONSENSUS.D   --k--SS-pR-d------eQ------kA-t-p-Dw                                      100
CONSENSUS.O   V-?-S???-?RK.Q?RQE-QE??--K??GP?G?P????SC??CTR?S?Q                       85
CONSENSUS.CPZ ??-?????SR?-.?????K-?-?-??--????G-C                                      56
```

HIV-2/SIV Tat Consensus Sequences

```
                                                                  <- vpR
CONSENSUS.A METpLKaPEsSL?syNEPsS?TSeqdv??QelakqGeEiLsQLyrPLEaCtNsCyCK?CcyhCQlCFlkKGLG    68
CONSENSUS.B --I--qEQ----k-Ssep--S---pV-NT-G-DN-------------k--d-t----K---------------    73
CONSENSUS.D -----rEQ-n--e-sner--cis-a-a-tp-s-nlg---------pl---y-tc---k------f--------    72

      rev cds ->                exon \/ exon
CONSENSUS.A IwY?RkgRRRRtPkKtK?hsssasD.KSISTRTg?SQptKkQKKTle?tvetd?glGr                  120
CONSENSUS.B -c-drS..-k-Ss-RA-tTa---pd??-L-Ar--D--------keV-T-g?--l-P--SNTSTSRFA         135
CONSENSUS.D -c-Eqsr?----p--a-ant----n?k?isn-tRhc--k-ak-etV--a-a-ap--g-                  126
```

HIV-1 and HIV-2 Sequence Subtypes

1. Introduction

In addition to the six HIV1 sequence subtypes A through F recognized in the 1993 database compendium (III-2 of APR 94), there are now two new subtypes to be considered, G and H, for what is now being called the M group of HIV-1 sequences (see Janssens et al., *AIDS Res. Hum. Retroviruses* **10**:877–879, 1994). Furthermore, we are aware of several sequences that don't fit at this time into any of the defined sequence subtypes of group M. And, as the cover of this compendium reveals, the O group of HIV-1s includes sequences that are as different from one another as M group subtypes. (The O group CA9 and VI686 sequences have not been made public, but were kindly provided to us for the use in the cover figure by the Institute of Tropical Medicine, Antwerp.) Together, the M and O group sequences of HIV-1s appear to constitute a "double star" phylogeny (Myers, *AIDS Res. Hum. Retroviruses* **10**:1317–1322, 1994).

Heretofore, the database has recognized two subtypes of HIV-2s, A and B. A recent study by Hahn's group at the University of Alabama argues for the existence of at least five HIV-2 sequence subtypes, A through E (Gao et al., *J. Virol.* **68**:7433–7447, 1994; the criteria used were virtually identical to those used for defining HIV-1 group M sequence subtypes).

Both HIV-1 and HIV-2 data sets present some evidence for hybrid viruses (see Sharp et al., *AIDS* **8** (suppl 1):S27–S42, 1994).

2. HIV-1 Phylogenetic Trees

The availability of many new HIV-1 *env* gp120 and gp160 coding sequences (Part I) permits us to generate new phylogenetic trees that can be compared to i) HIV-1 *gag* cds trees and ii) partial *env* cds trees. Since the publication of the 1993 compendium, we have been experimenting with asymmetrically-weighted parsimony analysis (as implemented by Hillis et al., *Science* **264**:671–677, 1994) as a way to reduce effects of homoplasy. The first step in this process is to run ordinary parsimony analysis in order to determine the substitution biases; all things being equal, the biases will tend to follow the base composition of the sequences. We use Macintosh versions of PAUP and MacClade to accomplish this step. A resulting substitution frequency matrix (for HIV-1 *env* gp120 sequences) is shown below:

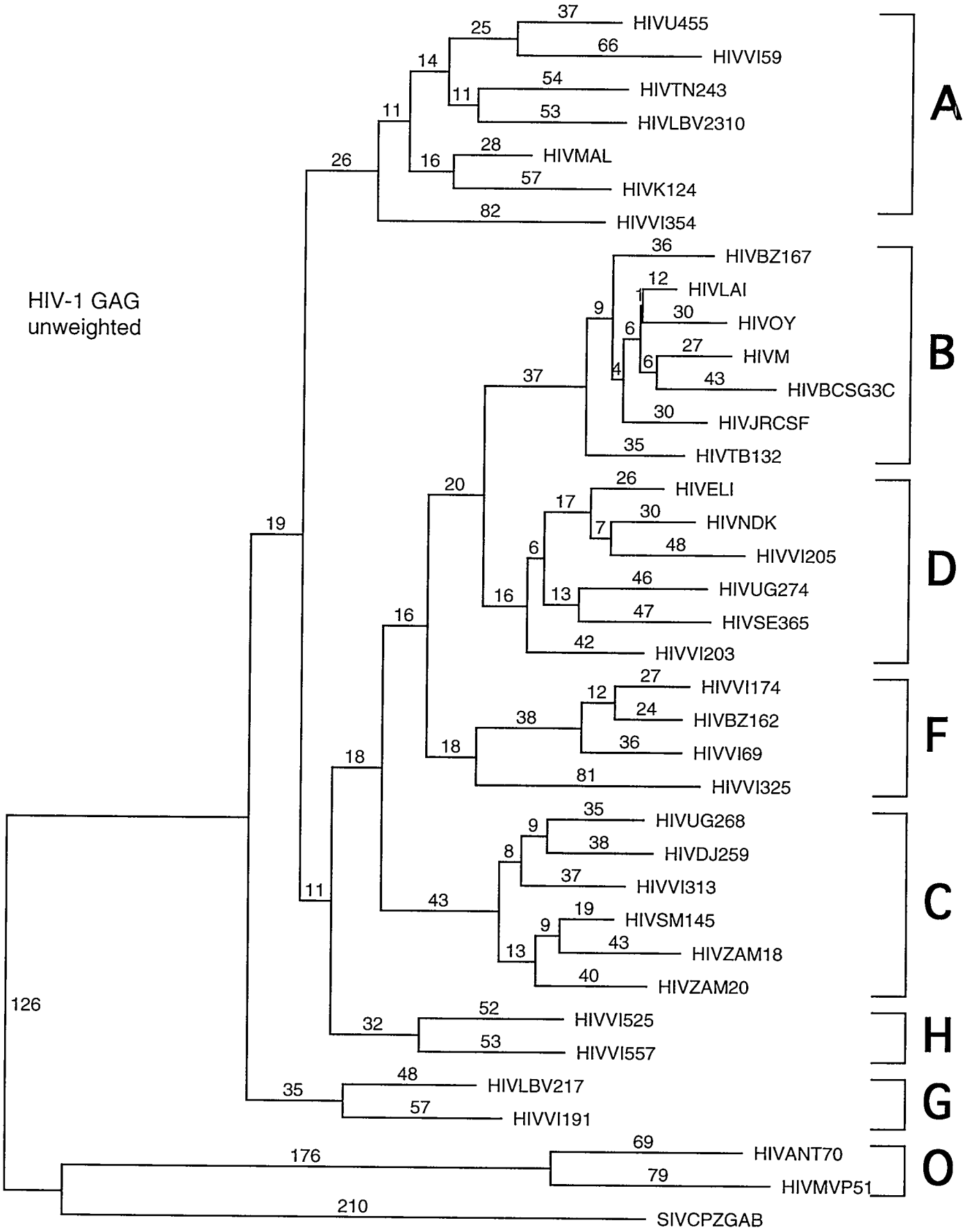
	to:	A	C	G	T
from:	A		0.104	0.222	0.074
	C	0.060		0.023	0.095
	G	0.163	0.027		0.022
	T	0.052	0.112	0.046	

We see from this table that some transversions (e.g., A to C) are as frequent as some transitions (e.g., C to T). Purine-purine transitions occur at almost twice the frequency of pyrimidine-pyrimidine transitions. These appear to be consequences of the unusual base composition of HIVs and SIVs.

The next step in the analysis is to re-execute the parsimony algorithm (PAUP) using an inverse weighting table generated from the substitution matrix. Hence, the least common changes (G to T) are given the greatest weight and the most common substitutions (A to G) are given the least weight. In applying the inverse weighting rule, it may be necessary to truncate values in order that the triangle inequality relationship be preserved (see Maddison and Maddison: MacClade:Analysis of Phylogeny and Character Evolution. Sinauer Associates, Sunderland MA, 1992). Because the branch lengths in the newly generated tree are derived from weighted terms, they are no longer indicative of the minimal number of base changes, as they would be in ordinary parsimony. However, the lengths do provide accurate relative distances. We continue to employ maximum likelihood analysis, neighbor-joining, and bootstrapping in order to strengthen inferences based upon parsimony tree analyses.

When the signal to noise ratio is sufficiently high, the weighted approach won't drastically change the tree analysis; however, it will invariably change one or two individual relationships, attachments to a major trunk. Weighted parsimony is especially warrented when analyzing "deeper" phylogenetic relationships that have attained "mutational saturation" (III.D).

In the following analyses, both unweighted and weighted trees are shown for HIV-1 *gag*, *env* and *tat* coding sequences in that order.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HIVVI59
HIVTN243
HIVLBV2310
HIVMAL
HIVK124
HIVVI354
HIVBZ167
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HIVOY
HIVM
HIVBCSG3C
HIVJRCSF
HIVTB132
HIVELI
HIVNDK
HIVVI205
HIVUG274
HIVSE365
HIVVI203
HIVVI174
HIVBZ162
HIVVI69
HIVVI325
HIVUG268
HIVDJ259
HIVVI313
HIVSM145
HIVZAM18
HIVZAM20
HIVVI525
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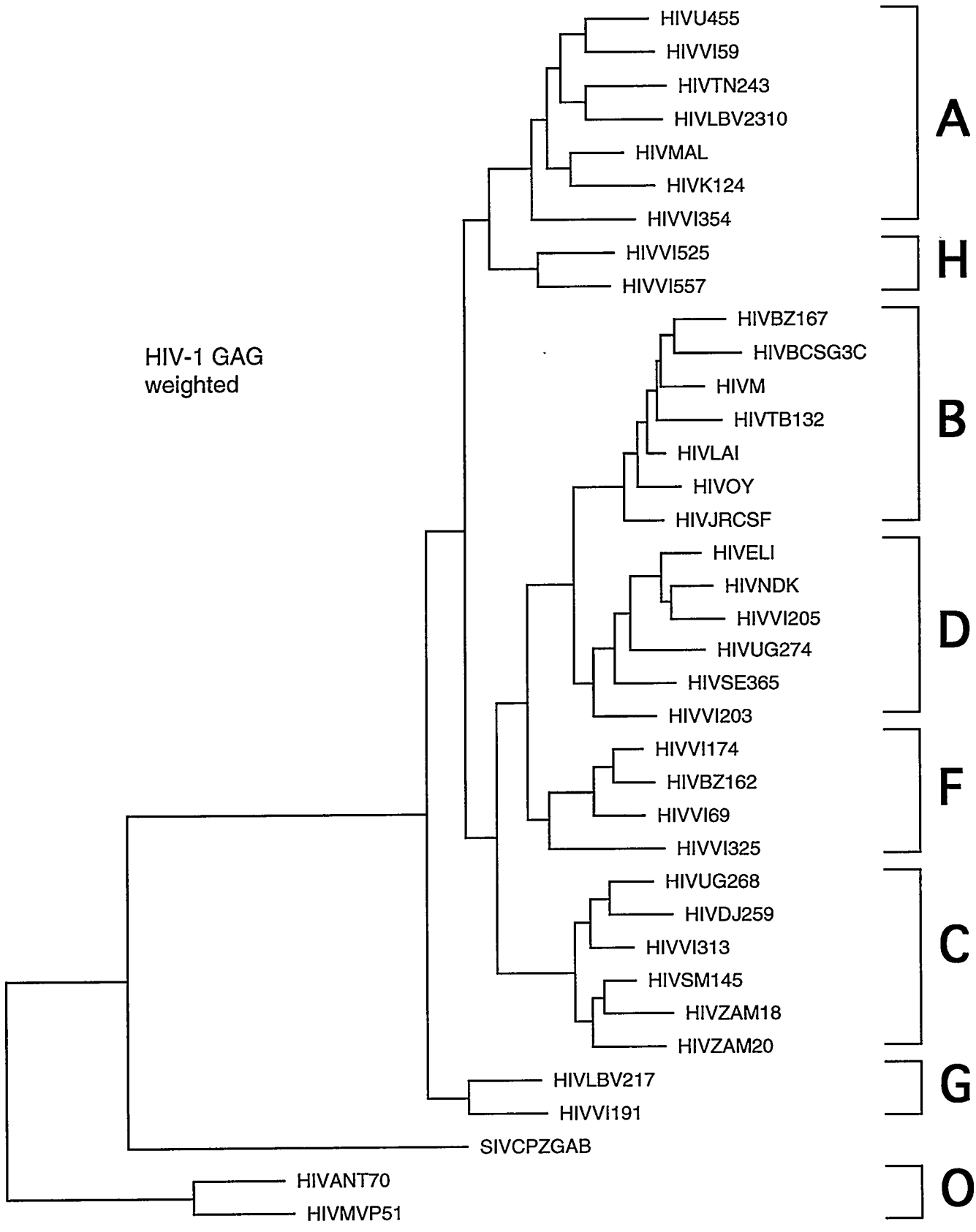
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HIVVI59
HIVTN243
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HIVBCSG3C
HIVM
HIVTB132
HIVLAI
HIVOY
HIVJRCSF
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HIVNDK
HIVVI205
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HIVVI174
HIVBZ162
HIVVI69
HIVVI325
HIVUG268
HIVDJ259
HIVVI313
HIVSM145
HIVZAM18
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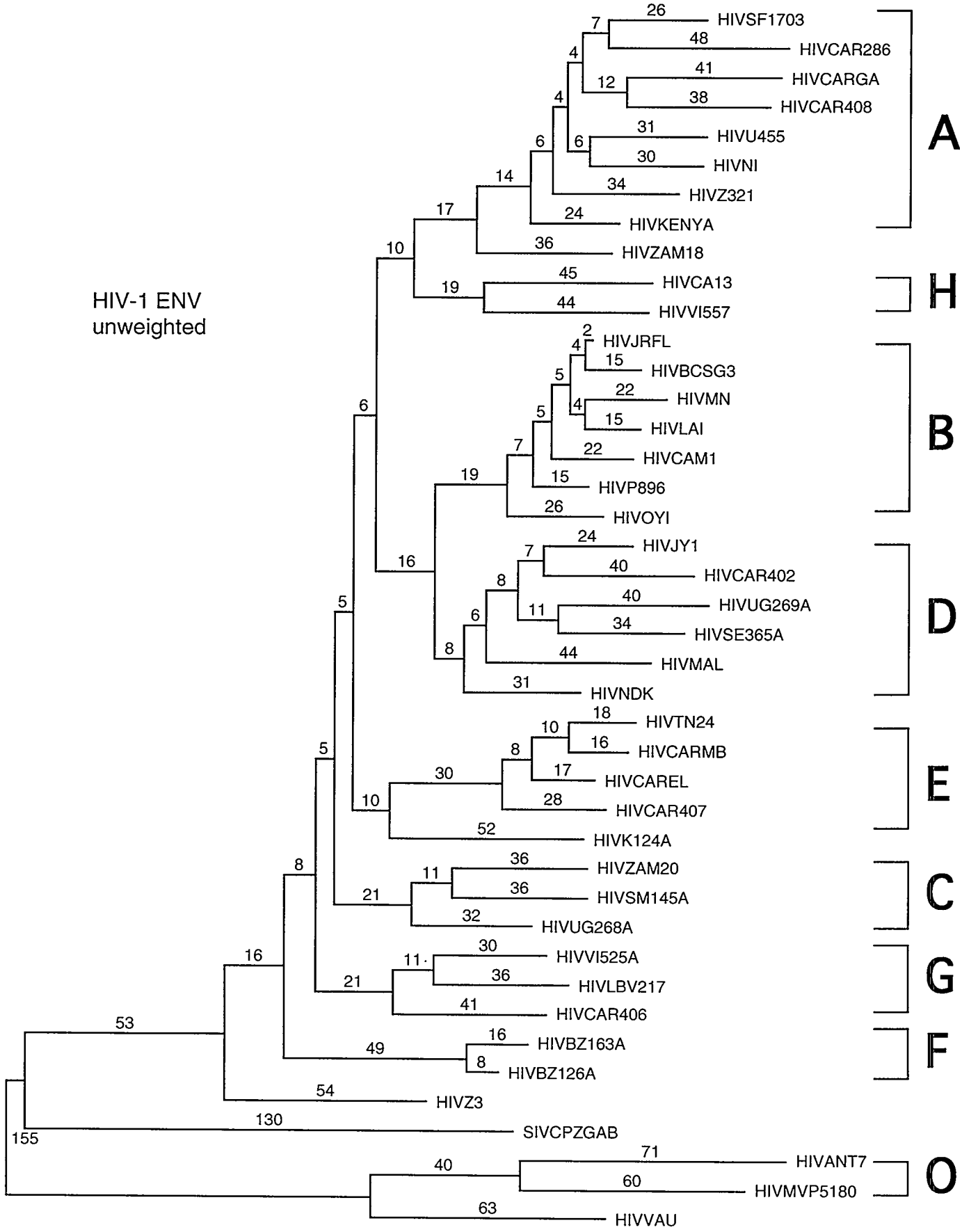
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HIVBCSG3
HIVMN
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HIVCAM1
HIVP896
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HIVNDK
HIVTN24
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HIVCAREL
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B
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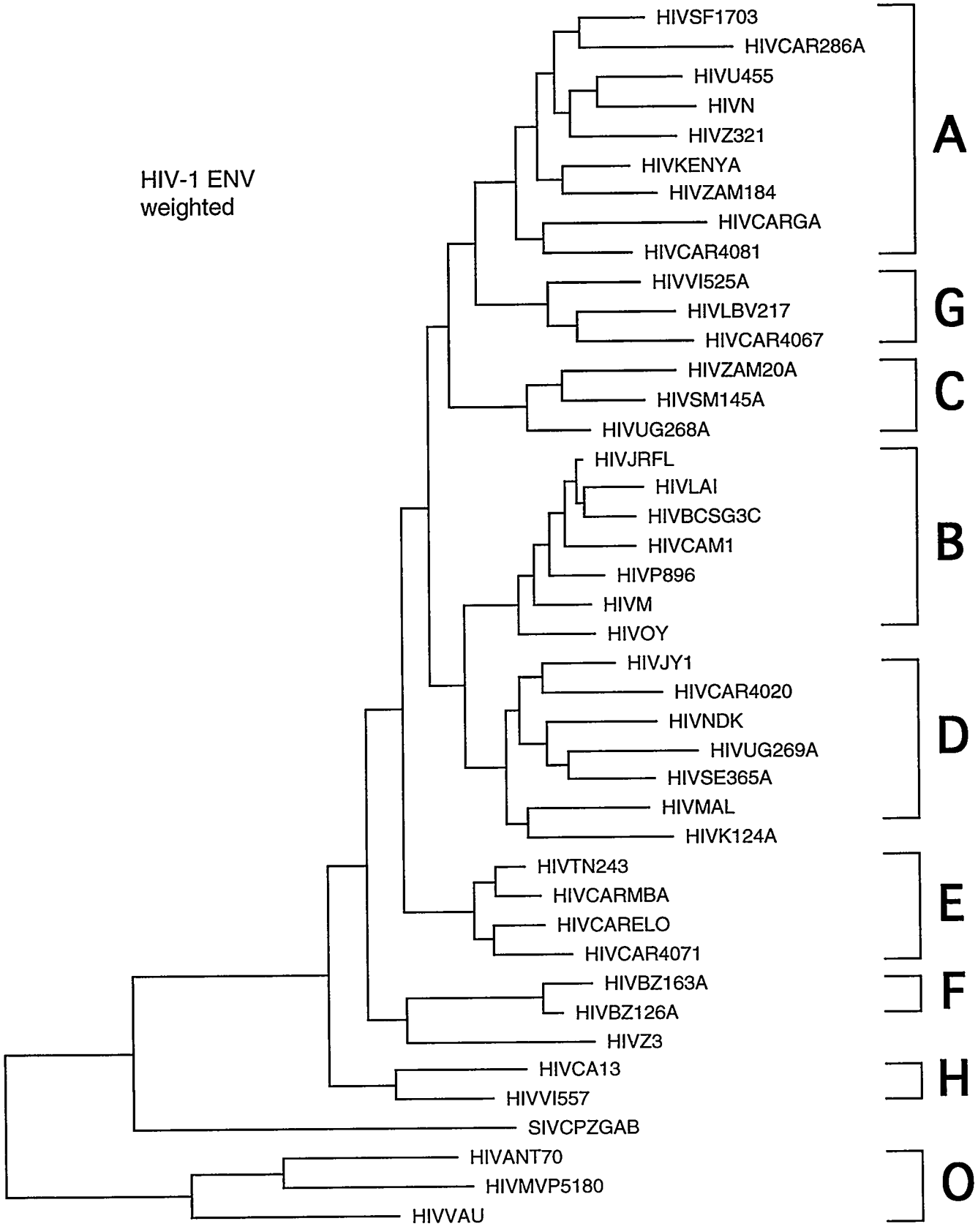
E
C
G
F
O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HIVLBV217
HIVCAR4067
HIVZAM20A
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HIVBCSG3C
HIVCAM1
HIVP896
HIVM
HIVOY
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HIVCAR4020
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HIVCAR4071
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HIVZ3
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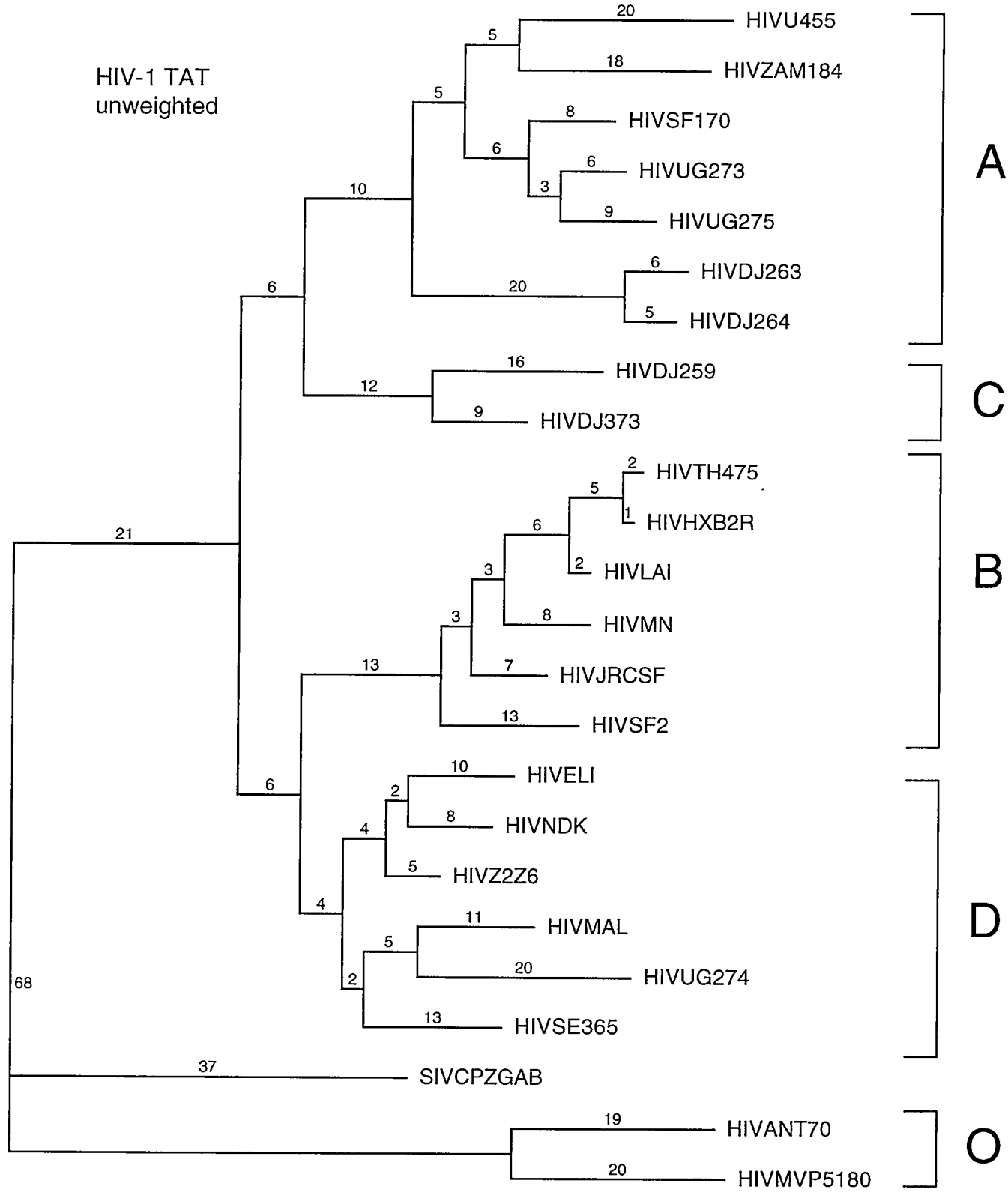
HIV-1 TAT
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HIVELI
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HIVANT70
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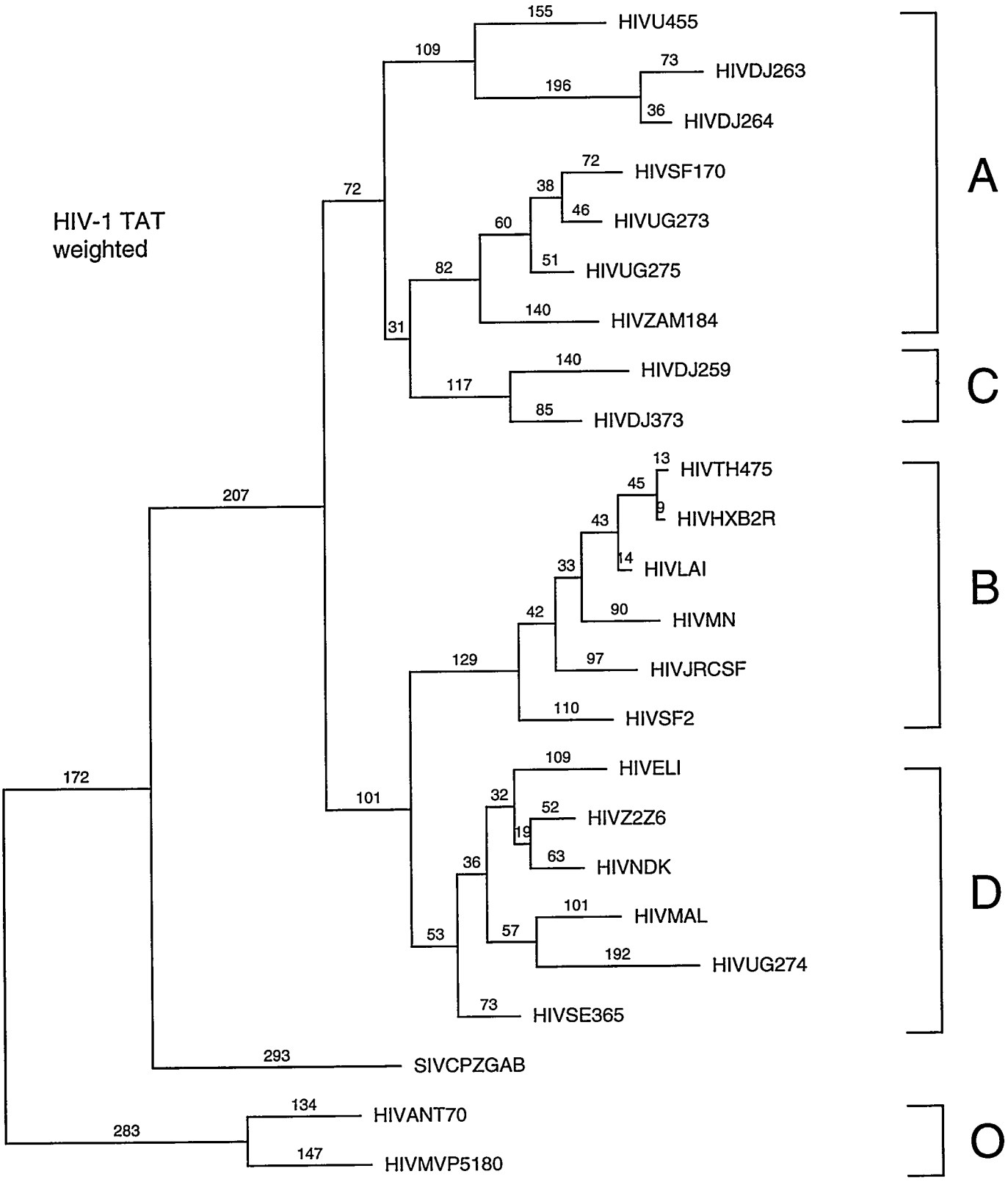
A
C
B
D
O


HIV-1 TAT
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HIVU455
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109
73
196
36
72
38
46
60
51
82
140
31
140
117
85
13
45
9
43
14
33
42
90
129
97
110
109
172
32
52
101
19
63
36
101
53
57
192
73
293
134
283
147
A
C
B
D
O

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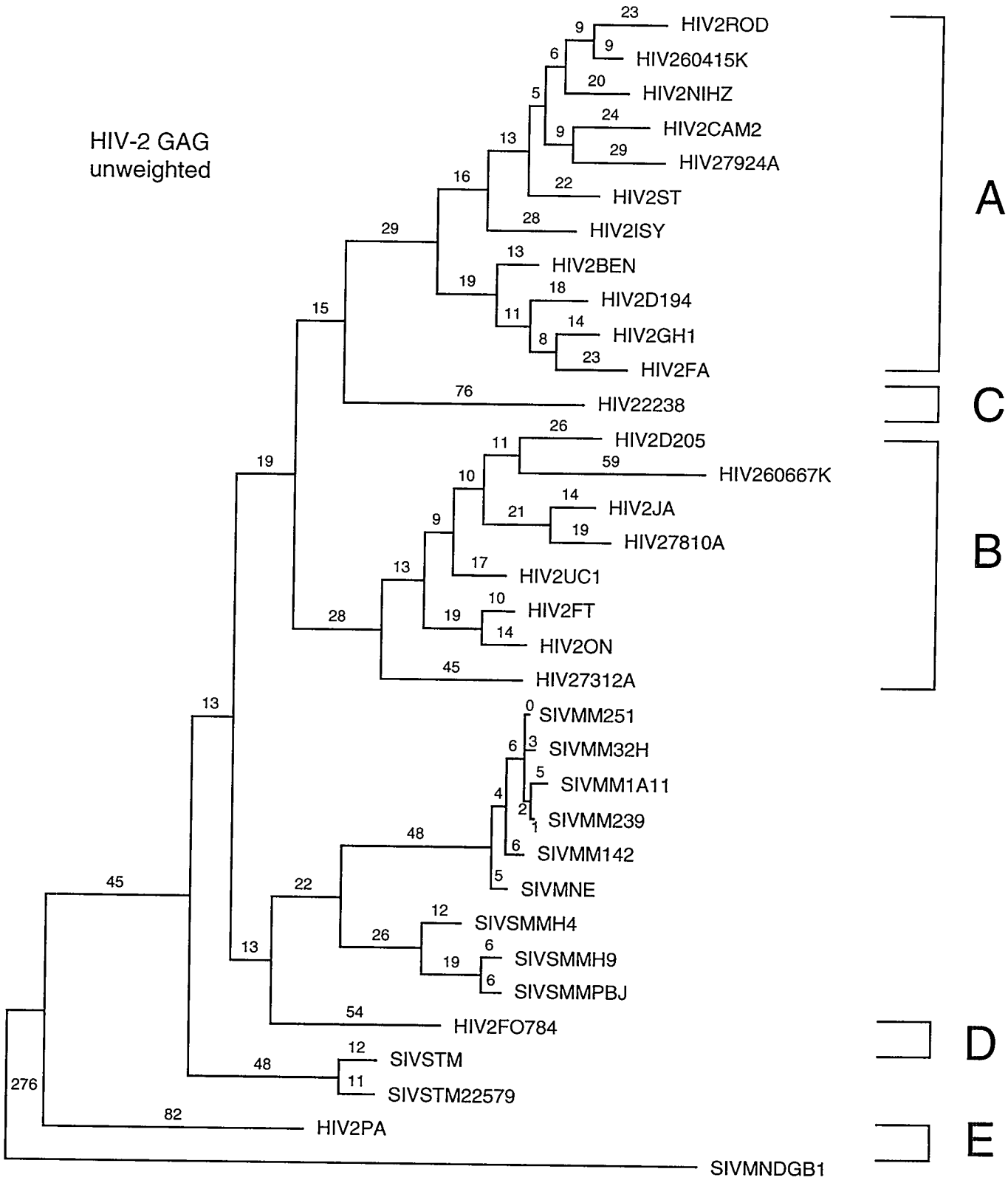
3. HIV-1 Subtype Summary

From various phylogenetic analyses, including those shown on the previous pages of this section, we can update the table of HIV-1 sequence subtype representatives originally presented on page III-2 of APR 94. Not all sequences are listed in the table; this table emphasizes complete *env* and *gag* coding sequences and concordant and discordant *env-gag* pairs. Subtype assignments derived from V3 coding sequences, which in a few instances may not agree with the following assignments, are summarized in III.E. The subtype A sequences are particularly diverse, leading to uncertainties (The designation 'U' indicates uncertainty). Group O sequences have not been subtyped. HIV-2 *gag* subtypes are shown in the following phylogenetic trees, first an unweighted then a weighted tree.

TABLE I. HIV-1 Subtypes

env Subtype	*gag* Subtype	Sample Locale(s)
A U455, DJ258 DJ264, Z321, SF170, UG031, RW009, RW020, CAR423, CAR4054	**A** U455, DJ258 K112, K29, K88, VI32, CI20, K7, K98, CI59, LBV2310, CI51, CI44, CI32	Central Africa
A VI191	**G** VI191	Central Africa
D K124(?), UG266	**A** K124, UG266	Central Africa
E TN243 (CM243), CAR4017, CAR4071, TH011, TH006	**A** TN243 (CM243)	Thailand, Central African Republic
B LAI, JRCSF, D31, SF2 TB132, BR014, TH014	**B** LAI, JRCSF, D31, SF2 TB132, PHI136, PHI153	North America, Europe, South America, Asia
C ZAM18, SM145, UG268 NOF, D747, BR025, DJ373	**C** ZAM18, SM145, UG268 DJ259, VI131, SE364	Central and Southern Africa, India, Brazil
D ELI, NDK, SE365, UG274 UG038, UG021, CAR4020	**D** ELI, NDK, SE365, UG274 VI120, G109, K31, G270	Central Africa
F BZ163, BZ126, BR7944	**F** VI174, BZ162, VI325	South America, Central Africa, Europe
G LBV217 CAR4067, CAR4081	**G** LBV217	Central Africa, Taiwan Russia
G VI525	**H** VI525	Central Africa
H VI557 (partial)	**H** VI557	Central Africa
U ZAM184, Z3	**U**	Central and Southern Africa
O Group ANT70, MVP5180, VAU	**O Group** ANT70, MVP5180	West Africa, France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HIV260415K
HIV2NIHZ
HIV2CAM2
HIV27924A
HIV2ST
HIV2ISY
HIV2BEN
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HIV2GH1
HIV2FA
HIV22238
HIV2D205
HIV260667K
HIV2JA
HIV27810A
HIV2UC1
HIV2FT
HIV2ON
HIV27312A
SIVMM251
SIVMM32H
SIVMM1A11
SIVMM239
SIVMM142
SIVMNE
SIVSMMH4
SIVSMMH9
SIVSMMPBJ
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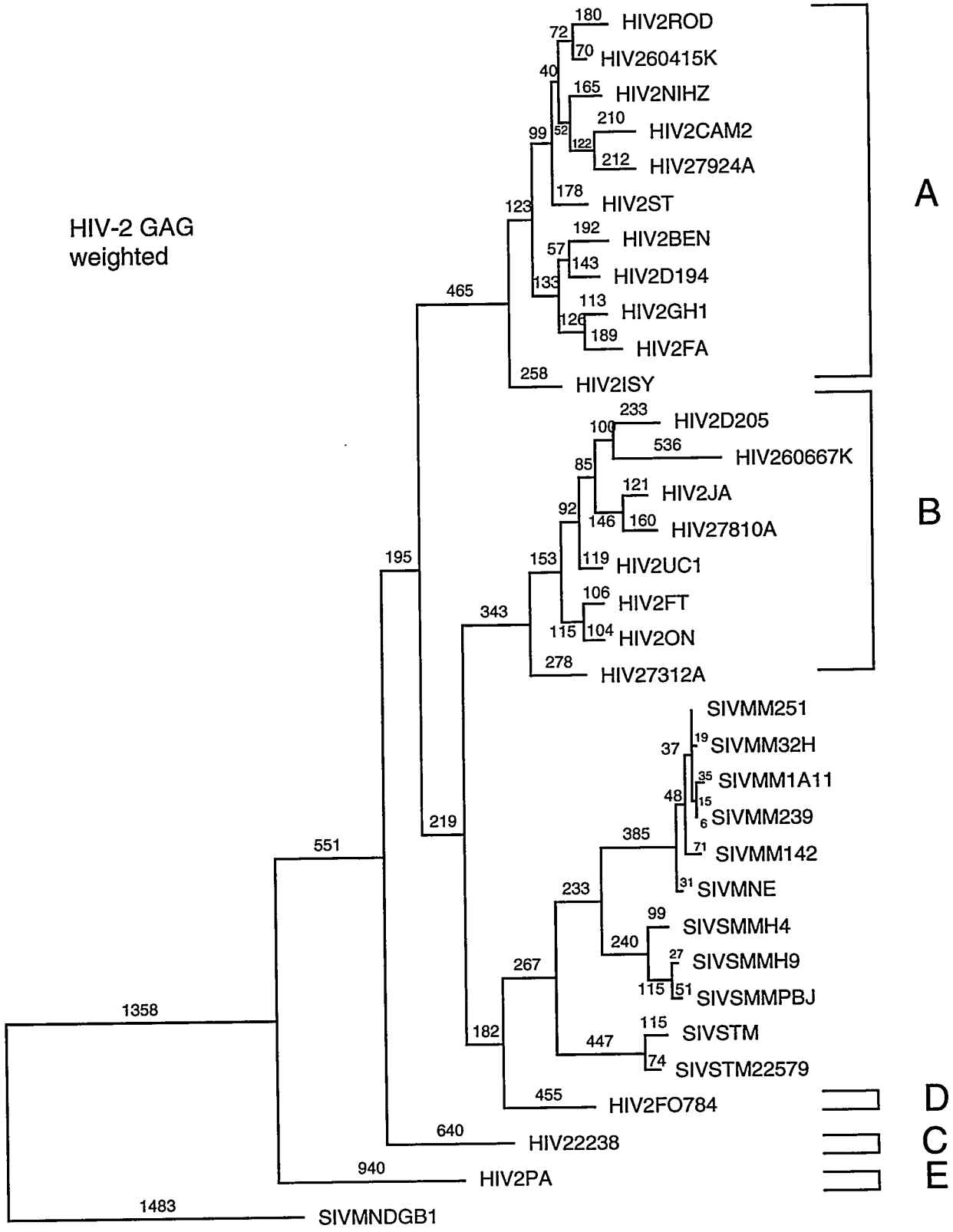
SIVSTM
SIVSTM22579
HIV2PA
SIVMNDGB1
A
C
B
D
E


HIV-2 GAG
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HIV2BEN
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HIV2FA
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HIV2D205
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HIV2JA
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SIVSMMH9
SIVSMMPBJ
SIVSTM
SIVSTM22579
HIV2FO784
HIV22238
HIV2PA
SIVMNDGB1
A
B
D
C
E

HIV Synonymous and Nonsynonymous Substitution Frequencies

1. HIV-1 and HIV-2 *gag* and *env* substitution frequencies.

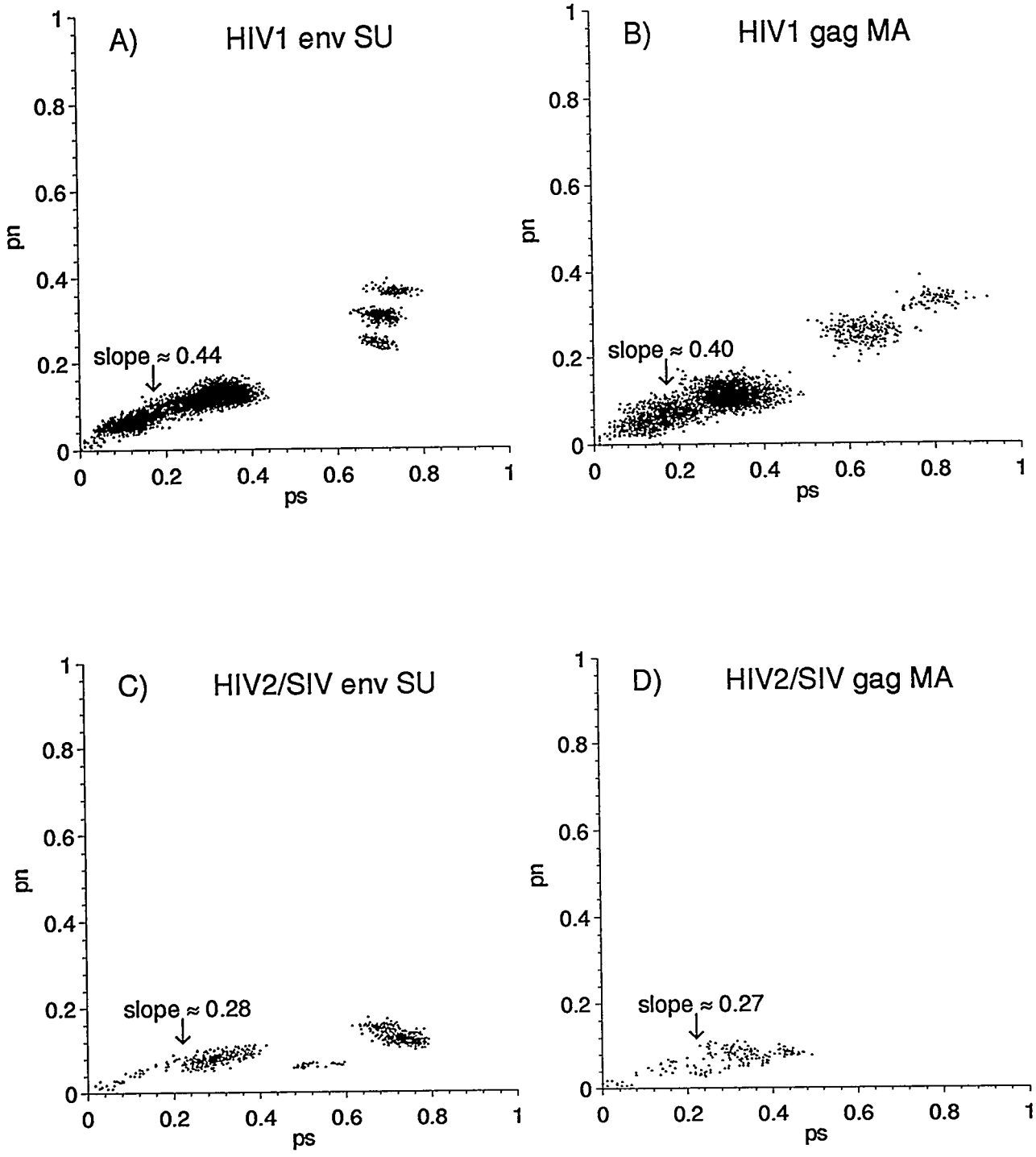
Of the possible kinds of nucleotide substitutions in a typical viral coding sequence, synonymous (or so-called "silent") substitutions are the most commonly observed. If "mutational saturation" has not been reached for any of the pairwise relationships in a homologous set of sequences, synonymous substitution frequencies can provide a linear measure of genetic variation under conditions of minimal selection pressure. Nonsynonymous substitutions (generating amino acid replacements) tell us something about negative and positive Darwinian selection; under certain circumstances, they also serve as a metric. We should keep in mind the possibility that subtle selective pressures may be exerted upon synonymous substitutions (we have seen in the previous section that base composition is a factor in this regard), as well as the possibility that amino acid replacements may be unselected (Kimura's neutral theory). The majority of sites in a coding sequence will be nonsynonymous targets, however the majority of changes observed will be synonymous, because these produce the least negative effects.

Nonsynonymous (pn) and synonymous (ps) substitution frequencies are shown in the accompanying plots for a large number of pairwise relationships over a) HIV-1 *env* SU, b) HIV-1 *gag* MA, c) HIV-2/SIV *env* SU, and d) HIV-2/SIV *gag* MA coding sequences. The Nei-Gojobori algorithm was used to determine these frequencies [1]. "Initial" slopes have been calculated, using a least-squares program, over the range of ps and pn values of 0.0 to 0.3; multiple hits are likely to be encountered for values greater than 0.3. Synonymous substitution frequencies approach saturation in the range of 0.6 to 0.8; the saturation levels for nonsynonymous substitutions are less certain due to the very nature of positive selection effects.

Of note in these plots is first, the uncanny similarity of *env* SU slopes to *gag* MA slopes—0.44 and 0.40 for HIV-1s, 0.28 and 0.27 for HIV-2s. Equivalently measured slopes for *gag* CA coding sequences (not shown)—0.15 for HIV-1s and 0.09 for HIV-2/SIVs—clearly indicate that the near-identities needn't have been the case. We don't have an explanation for this phenomenon at this time: it seems to suggest that either *env* SU and *gag* MA are "co-selected" in some sense, or that they are both demonstrating some fixed level of neutral mutation not seen in *gag* CA coding sequences. Synonymous substitution frequencies at the scale of complete coding sequences are generally uniform across the viral genomic molecule; that is to say no gradient of intrinsic base substitution has been observed for HIVs.

A second finding is that HIV-1s possess higher slopes of pn to ps than do HIV2/SIVs for *env* and *gag* coding sequences. This result is consistent with a study conducted by Shpaer and Mullins [2], which was based upon a smaller data set and a different method for determining substitution frequencies.

Finally, the extent of synonymous changes are approximately equivalent for the majority of HIV-1, HIV-2, and SIV sequence relationships—ps of 0.4—although this cannot be taken as evidence of identical ages of the sequence sets. The clusters of more mutated sequence relationships, ps greater than 0.4, come about through comparison of HIV-1 M group sequences to O group sequences, and through comparison of HIV-2 sequences of one subtype to those of another subtype and to SIVs. The former effect—the nearly identical extents of synonymous substitution in HIV-1s and HIV-2s—is probably merely a consequence of sampling: sequences tend to be reported for individuals who have been recently infected and therefore haven't diverged that much from other recently infected (and sampled) sources.


A)
HIV1 env SU
slope ≈ 0.44
B)
HIV1 gag MA
slope ≈ 0.40
C)
HIV2/SIV env SU
slope ≈ 0.28
D)
HIV2/SIV gag MA
slope ≈ 0.27
pn
ps
0
0.2
0.4
0.6
0.8
1

2. HIV-1 Intersubtype Comparisons

As new HIV-1 *env* coding sequences have become available, phylogenetic tree analyses (III-C) have pointed toward a "star" relationship among the M group of HIV-1s and separately among the O group of HIV-1s [3]. An analysis of synonymous and nonsynonymous substitution frequencies provides some corroboration of the hypothesis that HIV-1s are part of two star phylogenies, which are suggestive of two separate introductions of virus at about the same time into the human population.

In the following analysis, 340 nt from the C2-V3 coding regions of HIV-1 subtypes A through H (of the M group) were analyzed using the Nei-Gojobori algorithm [1]. The average frequencies of ps (synonymous substitutions) and pn (nonsynonymous substitutions) were determined for members of a given sequence subtype (e.g., A) in relation to all other subtype sequences (e.g., B through H). Ideally, such a study would involve equal numbers of each subtype; however, that is not possible with the current data sets. Notwithstanding this limitation, the averages are remarkably identical as shown in the schematic summary below. Preliminary results based upon unpublished O group sequences (not shown) point to highly similar averages among these viral sequences—moreover, values that are similar to the average value shared by group M subtype sequences [3].

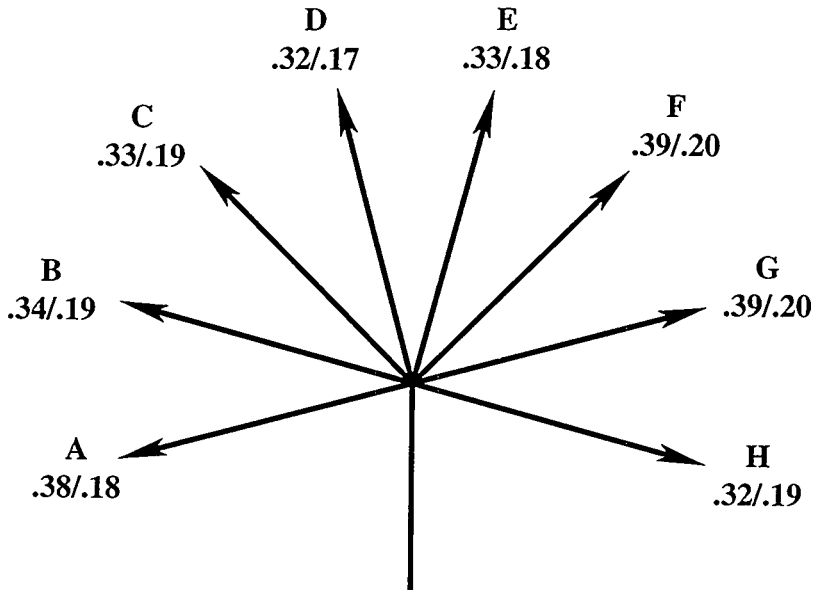
Average intersubtype synonymous and nonsynonymous substitution frequencies are given for each subtype set relative to all other subtype sequences; thus '.38/.18' gives the average ps and pn values respectively for A group sequences. Although these averages were calculated over a shorter coding stretch and involved more sequences, they are comparable to the ones reported in refs 1 and 3 (slightly higher in every case as is to be expected for C2-V3 relative to *env* gp120, hence average pn to ps ratios closer to 0.5 than to 0.4, as shown in the previous section).

References

[1] Korber et al., *J. Virol.* **68**:6730–6744, 1994.

[2] Shpaer, G and Mullins, J., *J. Mol. Evol.* **37**:57–65, 1993).

[3] Myers, *AIDS Res. Hum. Retroviruses* **10**:1317–1323, 1994.



Global Variation in the HIV-1 V3 Region

Introduction

Due to the immunogenicity and functional importance of the V3 loop, there has been a great deal of interest in the V3 region of the envelope protein, resulting in a large international effort to obtain V3 region sequences. This section, which includes sequences taken from 707 individuals and references, provides an overview of the variation of sequences that span this region.

Sequences

To best summarize the spectrum of international HIV-1 variants, only one representative viral sequence was included per infected individual. A complete set of references accompanies the sequence alignments, and nomenclature was preserved from the original papers so individuals and isolates can be clearly identified. HIV-1 was deleted from the sequence names in this section, as all sequences included here are HIV-1. Included with the references when available are brief descriptions of critical features of the sequences. This includes the health status of the individual from whom the virus was derived, whether or not the virus was cultured, and the year the blood sample was taken. All sequences are prefaced by a two letter country code to identify the country that the individual resided in at the time that the blood sample was taken. If the person was a recent immigrant and this information was available, we included the country of origin in the references. The two letter code was developed for Internet (Copyright 1992, Lawrence H. Landwater and the Internet Society), and incorporated here based on a suggestion made by Dr. Francine McCutchan. The key to the country codes follows this introduction.

Sometimes only one viral sequence was available from a person: a clone from an isolate, or a direct sequence of PCR amplified peripheral blood DNA. For other individuals, up to 80 viral sequences from PCR amplified DNA or RNA from blood samples were available. Consequently, nearly 2000 sequences are represented by the 707 included in this section. When two sequences were available from a person, one of the two was randomly selected. When three or more sequences were generated from a person, all available sequences were aligned (without regard to different time points of sampling) and a consensus of the most common base found in each position in the alignment was generated. If there was a tie (e.g., 10 A's, 10 T's), the top base or amino acid in the alignment was used. If a set of sequences from two or more individuals was epidemiologically linked, and genetically very similar, only one sequence from the set was included. In the sequence description and references section, the short hand "PCR-direct, peripheral blood DNA" is used to signify that viral DNA was amplified from PBMCs, without culturing, and a single "direct" sequence was obtained from the amplification reaction products. The short hand "Consensus, PCR-clones, peripheral blood DNA" signifies that viral DNA was amplified from PBMCs and a set of clones was generated and sequenced from the PCR amplification products. The cloned sequences were aligned and a consensus was generated. In a handful of cases, a particular gp160 clone from an isolate was shown to be expressed and functional using a vaccinia virus T7 expression system. In these cases, the clone rather than the consensus of all sequences from a particular individual was included.

Phylogenetic clustering

Sequences have been organized according to their phylogenetic subtype association (A–H). These sequence subtypes (A–H) have been defined based on the phylogenetic relationships determined by using both *gag* and *env* genes (when possible), are approximately genetically equidistant in envelope, and have multiple members. The phylogenetic subtype designations and associations have generally been adopted by the HIV research community, and are now often presented with the publication of new sequences. We have either determined the subtype designations here at Los Alamos, if they were not specified in the original manuscript, or else confirmed the subtype designations of the

original manuscripts, and then used the subtypes to organize this section. Generally, confirmations were done by aligning a set HIV-1 V3 region sequences with longer *env* gene sequences (Part IIIC) that have clear subtype associations, and then using parsimony or neighbor joining trees to determine associations. Some of the shorter gene fragments from this region were given a subtype designation based on Hamming distances, using the similarity function of the MASE program (Faulkner DV, and Jurka *J. TIBS* 13:321–322 (1988)); these sequences have ".sh" appended to their name to indicate that they were too short for phylogenetic analysis. Parsimony trees were generated using PAUP (David Swofford, Illinois Natural History Survey), and neighbor-joining trees were generated with Kimura distances using PHYLIP (Joseph Felsenstein, University of Washington). All available nucleotide sequence information was used for phylogenetic analysis; longer protein sequences were trimmed to be approximately the same length as the majority of the PCR fragments in this region, for the purposes of presentation. Some sequences were difficult to classify, and are included in the "U", or unclassified, section.

The set of sequences used to help resolve subtype associations were selected based on being "typical" of the subtype they represent. Included were: A_2RW020W, A_UG273, B_W2BR020, B_D2US711, C_D3MA959, C_D760, D_D2UG021, D_HIVELI, E_W2TH006, E_ELOENV1, F_BZ126, F_BZ163, G_VI525, G_LBV21-7, H_CA13, H_VI557, O_MVP5180, and O_VAU (see references for more information about these sequences.)

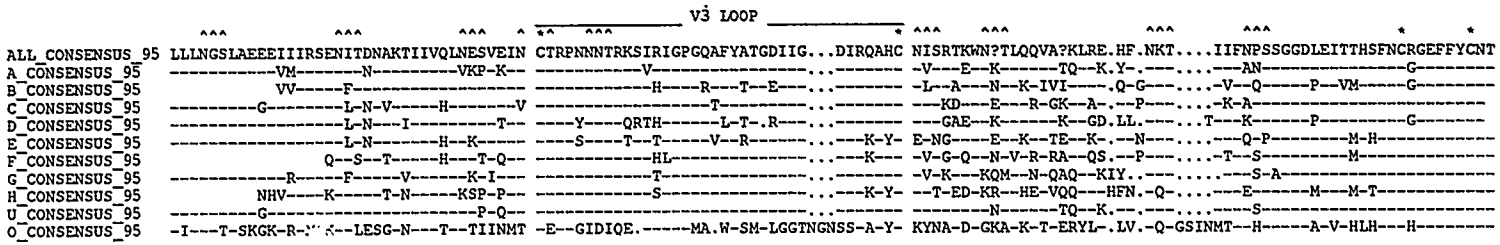
Limitations of phylogenetic analyses

Most of the PCR derived sequences contain a sub-optimal length for phylogenetic analyses, given the level of variability in this region – typically on the order of 250 to 300 nucleotides. Due to this limitation, some of the classifications in this section are uncertain and are our best estimate given the available information. Control studies were performed to compare the phylogenetic clustering of the V3 region using available longer sequences, however, and these studies indicate that our subtype designations based on the V3 region are generally reliable. For 146 sequences, we had an approximately 700 base region of *env* available representing all of the subtypes A–H. (The limitation in length was due to including the H subtype sequences, which did not cover all of gp120.) After removing positions in the alignment which included gaps, 519 bases were left. When a 298 base V3 region fragment was excised from this set, and neighbor joining trees were constructed using both the 519 base and 298 base long sequences, the phylogenetic subtype designations were consistent in each case. Further, when a subset of longer gp120 sequences was analyzed (92 of the 146), including 935 bases after removing positions in the alignment which included gaps, the subtype designations were again clear in neighbor-joining trees. This indicates that the limited V3 region PCR fragments are adequate for subtype determination.

Without detailed analysis, genetic recombination between subtypes may obscure phylogenetic relationships between sequences. A characteristic of recombination is an indeterminate place in phylogenetic analyses, and some of the "Uncertain" category sequences may prove to be recombinant genomes on further inspection. Also, while a subtype designation based on a gene or gene fragment may be correct, recombination events outside the region examined may have occurred. Therefore, care should be taken to not overinterpret the subtype designations.

Limitations of V3 amino acid consensus sequences

The V3 amino acid consensus sequences generated for each subtype have interesting features; however, one should be wary about assuming that any of the consensus sequences may broadly represent their subtype. Certainly many V3 loop variants in each of the subtypes are extremely divergent from the consensus sequences. These divergent forms may have very different biological and immunological characteristics from viruses which are similar to the consensus. Additionally, because of the relatively small sample size of most of the subtypes, consensus sequences can be dominated by a small group of highly similar sequences, which may in turn be a sampling artifact. Hence, these consensus sequences are "evolving" as new sequences from each subtype become available.



Subtype consensus sequences. This V3 region alignment shows a consensus sequence generated for each of the nine subtypes. The nine subtype consensus sequences indicate the most common amino acid found in each position among the sequences associated with each subtype. The sequences are aligned to a consensus based on the most common amino acid in the subtype consensus sequences, which approximates a "global" consensus. It was generated in this way (rather than by using all 707 sequences) to avoid over-representation of the B subtype, which has by far the largest number of available sequences. As is the convention in this compendium, a dash (-) indicates concurrence with the top sequence in the alignment; a period (.) indicates a deletion. The carets show where the N-linked glycosylation sites are found in the consensus. The V3 loop is set off from the surrounding sequence by a space on either side to facilitate viewing. Interesting features of the consensus alignment are: 1) Only in the B subtype is GPGR the most common tip of the V3 loop; globally, GPGQ is more prevalent. 2) A highly conserved N-linked glycosylation site is constitutively absent in the C subtype, proximal to the first cysteine (C) in loop. 3) The D subtype consensus has 34 amino acids from cysteine (C) to cysteine (C) rather than the more common 35; at the point where the deletion occurs, it is not uncommon to find insertions of 2 to 4 amino acids, as can be observed in the sequence alignments. 4) The D subtype has two arginine (R) residues in the V3 loop that are uncharacteristic relative to the other consensus sequences; positively charged amino acids in these positions may result in a syncytia inducing, non-monocytropic phenotype (Fouchier RAM, et al., J. Virol. 66:3183-3187 (1992)). 5) A higher degree of variation is seen in the region just downstream of the V3 loop than within it. This difference is also observed internally among the sequences of the different subtypes. 6) The A, C, G and H consensus seuqences have very similar V3 loop sequences.

V3 loop amino acids – following 4 pages. The "global" consensus sequence for all of the subtypes is shown at the top. Directly beneath the global consensus are shown aligned the subtype alternative amino acids that can be found in the six subtype consensus sequences at each position. For each subtype, the number of sequences which are currently available is indicated. The V3 loop consensus sequences (the most common amino acid found in each position among the sequences associated with each subtype), are shown. Written just above each consensus is the percentage of sequences that had the most common amino acid at each position (if a particular amino acid is perfectly conserved in a given position in a subtype, the 100% is not shown). Directly beneath the most common amino acid in each position are the other amino acids found in that position, listed from most common to least common. A dash (-) indicates a deletion; unusual insertions are not shown.

V3 consensus for subtypes A - O

N C T R P N N N T R K S I R I G P G Q A F Y A T G D I I G D I R Q A H C N I S

A subtype (124 sequences)

89		76		98	71	98	96	97	96	60	82	56	48	93	98	96		89	60	94	98	94	86	88	65	94	90		78			80	99	80		87	87	86
N	C	T	R	P	N	N	N	T	R	K	S	V	R	I	G	P	G	Q	A	F	Y	A	T	G	D	I	I	G	D	I	R	Q	A	H	C	N	I	S
T		I		H	G	K	Y	I	L	R	G	I	H	L	A	S		R	T	I	H	T	R	D	E	V	T		N	T	K	R	V	Y		T	V	N
D		S		L	S	R	K	K	N	Q	R	M	P	M		R		K	S	L	I	-	-	-	A	M	V		S	E		E	A	F		E	I	K
S		A			T		T	R	S	E	N	A	G	T				S	V	S	F	G	A	S	N	N	K		V	D		R	Q	Q		D	L	S
I		M			X		-	V		M	M	W	N	F					I		H	K	I	N	-	R	L			N		K	A					T
		V			Y					X		L	S						P		I	V			G	K				S		E	V					
												Y	C								F	-				S					V		Q	H					
																					Q	L				-								Y					
																																		F					
																																		Q					

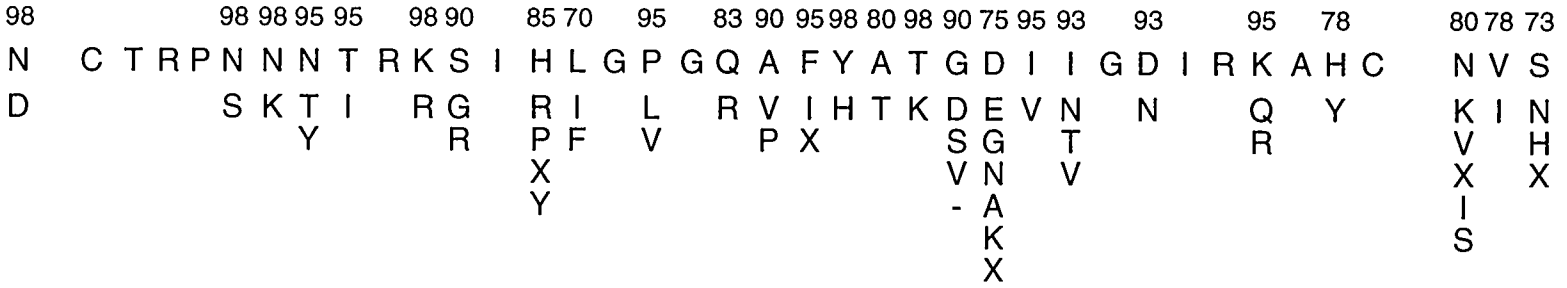
B subtype (338 sequences)

94		94		99	86	96	95	97	94	83	68	96	61	75	97	88	99	83	89	83	89	55	94	86	43	97	90		84	97	99	88	92		94	56	94
N	C	T	R	P	N	N	N	T	R	K	S	I	H	I	G	P	G	R	A	F	Y	T	T	G	E	I	I	G	D	I	R	Q	A	H	N	L	S
T	S	I	S	L	S	K	-	K	S	R	G	L	P	M	A	W	K	K	T	W	F	A	A	-	D	V	V		N	T	S	K	P	Y	T	I	N
D		E			G	D	Y	R	G	E	R	V	T	L		L	R	Q	V	L	H	R	I	E	Q	-	T		E	M		E		Q	I	V	D
H		S			H	E	I	I	I	G	X	G	N	V		G	S	S	G	V	V	T	R	R	K	K	A		A	V		L		F	S		T
I		L			F	I	K	V	K	N	H	K	S	T		Q	A	G	S	I	I	D	-	S	D	L	G		H	L		K		Y	K		
K		V			Y	S	S		T	Q	T	M	Q	K		S	F	R	X	X	R	T		T	N	-			I					Q			
Y						-	H		X	S		L	R	S		F	T	S							S													
						H	T			T		V	A	Y		V		G							T													
												M	G	G											R													
													X	X											-													
													I	K											N													
													K												Y													

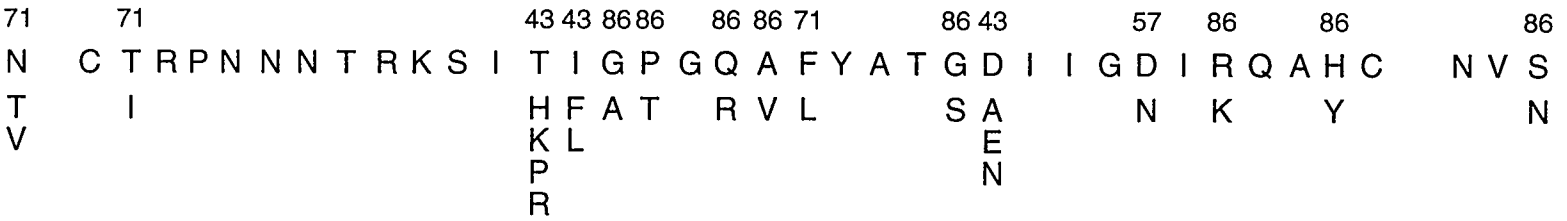
C subtype (40 sequences)

| | 91 | 98 | 81 | | | 83 | 95 | 69 | 93 | 91 | | | 67 | 98 | 93 | 98 | 98 | 71 | 78 | | | 78 | | | 88 | | 85 | | |

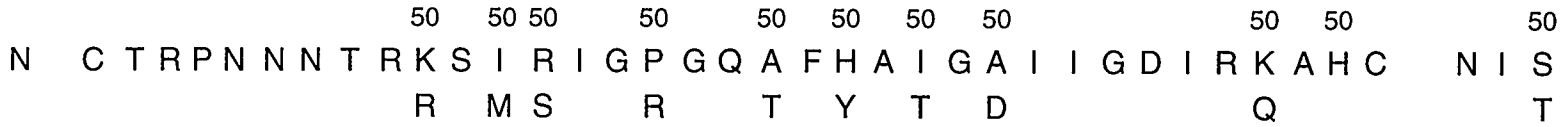
F Subtype (41 sequences)



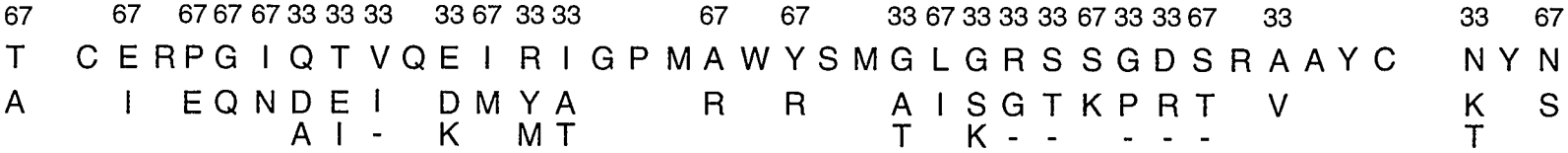
G Subtype (8 sequences)



H Subtype (2 sequences)



O Sequences (3 sequences)



Unclassified Sequences (13 sequences)

94	94	99	90	97	89	98	96	87	72	96	64	77	99	88	99	84	92	87	91	57	95	91	48	96	92	83	97	98	92	92	95	58	94
N	C	T	R	P	N	N	N	T	R	K	S	I	R	I	G	P	G	Q	A	F	Y	A	T	G	D	I	I	G	D	I	R	Q	A	H	C
S				G	S	D	I	K	R	R	M	H	F		S		R	T	I	F	T	I	-	G	V	T		N	-	-	K		Y	
T				S		I	K	N	I		T	N	L				K	V					K	N	K	-	-				Q			
V						T	R		T		V		V										-	S	-							I		
						Y																									S		
																															T		

Summary of variations in the tetrameric tip of the V3 loop. This table is a tally of the 38 different tetramers observed at the tip of the V3 loop among the viruses found in the 707 individuals analyzed. This tip is thought to form a turn, and is the focal point of the potent neutralizing antibody epitopes that have been mapped to the V3 loop, as well as of T cell epitopes. Each column shows the number of occurences of a given tetramer in either the entire 707 sequences (combined), or in subsets consisting of subtypes A-O, the unclassified sequences (U). Underneath the column heading is the number of sequences in each category. The most common form found in each subtype is highlighted by bold lettering. In the B subtype, GPGR is the predominant form, however globally GPGQ tends to be more common.

	Combined	A	B	C	D	E	F	G	H	O	U
	707	124	338	40	73	65	41	8	2	3	13
GPGR	341	9	**235**		15	10	6				4
GPGQ	289	**105**	11	**40**	**19**	**50**	**33**	**6**	1		**7**
GPGK	33	2	22								1
GWGR	22		22								
GLGQ	17				17						
GPGS	13	1	10								
GSGQ	12	3			6						1
APGR	11	1	10								
GPGG	8		7								
GQGQ	6		1		5						
GPMA	6									**2**	
GLGR	6		5				1				
GRGQ	5	1			3				1		
GVGR	4		1		1		1				
GQGR	4		2		1	1					
GTGQ	3				3						
GSGR	3	1	2								
GPGH	3					3					
GPLS	2										
GGGR	2		2								
APGQ	2	1						1			
GLGS	1		1								
AQGR	1				1						
GTGR	1							1			
GTGG	1		1								
GPMS	1										
GPMR	1									1	
GPLR	1										
GPLA	1										
GPKR	1		1								
GPGA	1				1						
GLRQ	1				1						
GGGQ	1					1					
GQRK	1		1								
GFGR	1		1								
GARR	1		1								
GAGR	1		1								
APGS	1		1								

Summary of octameric variation (cont.)

	Combined	A	B	C	D	E	F	G	H	O	U
	707	124	338	40	73	65	41	8	2	3	13
QRGPGRAF	2		2								
HMGPGKTF	2	1	1								
HMGPGKAF	2		2								
YIGPGRAV	2		2								
TRGPGHVF	2					2					
TMGPGRVW	2		2								
TMGPGQVF	2					2					
TMGPGKVF	2		2								
TIGPGQIF	2					2					
SIGQGQAL	2				2						
SIGPGRVW	2		2								
SIGLGQAL	2				2						
RIGPGQSF	2	2									
RIGPGQAL	2				2						
RFGPGQAF	2										2
PIGRGQAL	2				2						
PIGPGKAF	2		2								
PIGLGQAY	2				2						
NTGPGRAF	2		2								
NIGPGQAF	2	2									
HMGPGRAL	2				2						
HMGLGRAF	2		2								
HLGPGRAW	2		2								
HLGPGQAL	2				2						
HIGSGRAF	2	1	1								
HIGSGQAY	2				2						
HIGPGRTF	2		2								
HIGPGRSF	2	1	1								
HIGPGQAI	2				2						
HIGGGRTL	2		2								
AIGPGRTV	2		2								
unique	140	16	62	3	26	10	8	5	2	3	5

Summary of variations in the octameric tip of the V3 loop. This table is a tally of the 207 different octamers found at the tip of the V3 loop among the 707 individuals analyzed here. The table is structured the same as the tetramer table on the previous page. Amino acid changes proximal to the tip can influence the specificity of anti-V3 neutralizing antibodies. The 140 forms that were only found once in the entire data set are not shown here, to save space, and are summarized in the row called "unique."

	Combined	A	B	C	D	E	F	G	H	O	U
	707	124	338	40	73	65	41	8	2	3	13
HIGPGRAF	116	3	**110**		1		2				
RIGPGQTF	55	26		**27**							2
RIGPGQAF	37	25		8		1		1			2
HIGPGQAF	32	**27**	1				4				
HLGPGQAF	28	2					**26**				
PIGPGRAF	27	1	26								
TIGPGQVF	23					**23**					
NIGPGRAF	17		16								1
RIGPGQVF	15	2		2		10	1				
SIGPGRAF	14	1	13								
PIGLGQAL	11				**11**						
HMGWGRAF	10		10								
HIAPGRAF	10	1	9								
HIGPGKAF	9	1	8								
TIGPGRAF	9		9								
HIGPGRAY	9				9						
HIGPGQAL	8				7			1			
RIGPGRVF	7					7					
PIGPGQAF	6	2			1	2		1			
HIGPGSAF	5		5								
HLGWGRAF	5		5								
HLGPGQAW	5		5								
HIGPGQTF	5	5									
PLGPGQAW	4		4								
PMGPGRAF	4		4								
NMGPGRAF	4		4								
QIGPGRAF	3		3								
HIGPGRAV	3		3								
HIGPGGAF	3		3								
PMGPGKAF	3		3								
HMGPGRAF	3	1	2								
PIGPGQVF	3					3					
NIGPGQVF	3					3					
HMGWGRTF	3		3								
HLGPGRAF	3	1	1								1
GIGPGQTF	3	3									

COUNTRY CODES

It is becoming increasingly useful to name viral isolates and samples with a country code. The following code was captured from an Internet file.

This is a list based on the International Organization for Standardization (ISO) 3166:1988 standard, updated from a list prepared by Mark Horton. Note that the original standard has this same information sorted into about 6 different orders, both in English and French, therefore this is an abbreviated version not to be taken as the entire standard. While it has been checked against the standard, it may possibly contain errors; the standard and registration newsletters should be verified for any critical application.

This copy has been updated through registration Newsletter III-13 and is believed to be current through at least January 1991.

Table of Country Codes from ISO 3166

Country	A 2	A 3	Number
AFGHANISTAN	AF	AFG	004
ALBANIA	AL	ALB	008
ALGERIA	DZ	DZA	012
AMERICAN SAMOA	AS	ASM	016
ANDORRA	AD	AND	020
ANGOLA	AO	AGO	024
ANGUILLA	AI	AIA	660
ANTARCTICA	AQ	ATA	010
ANTIGUA AND BARBUDA	AG	ATG	028
ARGENTINA	AR	ARG	032
ARUBA	AW	ABW	533
AUSTRALIA	AU	AUS	036
AUSTRIA	AT	AUT	040
BAHAMAS	BS	BHS	044
BAHRAIN	BH	BHR	048
BANGLADESH	BD	BGD	050
BARBADOS	BB	BRB	052
BELGIUM	BE	BEL	056
BELIZE	BZ	BLZ	084
BENIN	BJ	BEN	204
BERMUDA	BM	BMU	060
BHUTAN	BT	BTN	064
BOLIVIA	BO	BOL	068
BOTSWANA	BW	BWA	072
BOUVET ISLAND	BV	BVT	074
BRAZIL	BR	BRA	076
BRITISH INDIAN OCEAN TERRITORY	IO	IOT	086
BRUNEI DARUSSALAM	BN	BRN	096
BULGARIA	BG	BGR	100
BURKINA FASO	BF	BFA	854
BURUNDI	BI	BDI	108
BYELORUSSIAN SSR	BY	BYS	112
CAMBODIA	KH	KHM	116
CAMEROON	CM	CMR	120
CANADA	CA	CAN	124
CAPE VERDE	CV	CPV	132

CAYMAN ISLANDS	KY	CYM	136
CENTRAL AFRICAN REPUBLIC	CF	CAF	140
CHAD	TD	TCD	148
CHILE	CL	CHL	152
CHINA	CN	CHN	156
CHRISTMAS ISLAND	CX	CXR	162
COCOS (KEELING) ISLANDS	CC	CCK	166
COLOMBIA	CO	COL	170
COMOROS	KM	COM	174
CONGO	CG	COG	178
COOK ISLANDS	CK	COK	184
COSTA RICA	CR	CRI	188
COTE D'IVOIRE	CI	CIV	384
CUBA	CU	CUB	192
CYPRUS	CY	CYP	196
CZECHOSLOVAKIA	CS	CSK	200
DENMARK	DK	DNK	208
DJIBOUTI	DJ	DJI	262
DOMINICA	DM	DMA	212
DOMINICAN REPUBLIC	DO	DOM	214
EAST TIMOR	TP	TMP	626
ECUADOR	EC	ECU	218
EGYPT	EG	EGY	818
EL SALVADOR	SV	SLV	222
EQUATORIAL GUINEA	GQ	GNQ	226
ETHIOPIA	ET	ETH	230
FALKLAND ISLANDS (MALVINAS)	FK	FLK	238
FAROE ISLANDS	FO	FRO	234
FIJI	FJ	FJI	242
FINLAND	FI	FIN	246
FRANCE	FR	FRA	250
FRENCH GUIANA	GF	GUF	254
FRENCH POLYNESIA	PF	PYF	258
FRENCH SOUTHERN TERRITORIES	TF	ATF	260
GABON	GA	GAB	266
GAMBIA	GM	GMB	270
GERMANY	DE	DEU	276
GHANA	GH	GHA	288
GIBRALTAR	GI	GIB	292
GREECE	GR	GRC	300
GREENLAND	GL	GRL	304
GRENADA	GD	GRD	308
GUADELOUPE	GP	GLP	312
GUAM	GU	GUM	316
GUATEMALA	GT	GTM	320
GUINEA	GN	GIN	324
GUINEA-BISSAU	GW	GNB	624
GUYANA	GY	GUY	328
HAITI	HT	HTI	332
HEARD AND MC DONALD ISLANDS	HM	HMD	334
HONDURAS	HN	HND	340
HONG KONG	HK	HKG	344
HUNGARY	HU	HUN	348
ICELAND	IS	ISL	352

INDIA	IN	IND	356
INDONESIA	ID	IDN	360
IRAN (ISLAMIC REPUBLIC OF)	IR	IRN	364
IRAQ	IQ	IRQ	368
IRELAND	IE	IRL	372
ISRAEL	IL	ISR	376
ITALY	IT	ITA	380
JAMAICA	JM	JAM	388
JAPAN	JP	JPN	392
JORDAN	JO	JOR	400
KENYA	KE	KEN	404
KIRIBATI	KI	KIR	296
KOREA, DEMOCRATIC PEOPLE'S REPUBLIC OF	KP	PRK	408
KOREA, REPUBLIC OF	KR	KOR	410
KUWAIT	KW	KWT	414
LAO PEOPLE'S DEMOCRATIC REPUBLIC	LA	LAO	418
LEBANON	LB	LBN	422
LESOTHO	LS	LSO	426
LIBERIA	LR	LBR	430
LIBYAN ARAB JAMAHIRIYA	LY	LBY	434
LIECHTENSTEIN	LI	LIE	438
LUXEMBOURG	LU	LUX	442
MACAU	MO	MAC	446
MADAGASCAR	MG	MDG	450
MALAWI	MW	MWI	454
MALAYSIA	MY	MYS	458
MALDIVES	MV	MDV	462
MALI	ML	MLI	466
MALTA	MT	MLT	470
MARSHALL ISLANDS	MH	MHL	584
MARTINIQUE	MQ	MTQ	474
MAURITANIA	MR	MRT	478
MAURITIUS	MU	MUS	480
MEXICO	MX	MEX	484
MICRONESIA	FM	FSM	583
MONACO	MC	MCO	492
MONGOLIA	MN	MNG	496
MONTSERRAT	MS	MSR	500
MOROCCO	MA	MAR	504
MOZAMBIQUE	MZ	MOZ	508
MYANMAR	MM	MMR	104
NAMIBIA	NA	NAM	516
NAURU	NR	NRU	520
NEPAL	NP	NPL	524
NETHERLANDS	NL	NLD	528
NETHERLANDS ANTILLES	AN	ANT	532
NEUTRAL ZONE	NT	NTZ	536
NEW CALEDONIA	NC	NCL	540
NEW ZEALAND	NZ	NZL	554
NICARAGUA	NI	NIC	558
NIGER	NE	NER	562
NIGERIA	NG	NGA	566
NIUE	NU	NIU	570
NORFOLK ISLAND	NF	NFK	574

NORTHERN MARIANA ISLANDS	MP	MNP	580
NORWAY	NO	NOR	578
OMAN	OM	OMN	512
PAKISTAN	PK	PAK	586
PALAU	PW	PLW	585
PANAMA	PA	PAN	590
PAPUA NEW GUINEA	PG	PNG	598
PARAGUAY	PY	PRY	600
PERU	PE	PER	604
PHILIPPINES	PH	PHL	608
PITCAIRN	PN	PCN	612
POLAND	PL	POL	616
PORTUGAL	PT	PRT	620
PUERTO RICO	PR	PRI	630
QATAR	QA	QAT	634
REUNION	RE	REU	638
ROMANIA	RO	ROM	642
RWANDA	RW	RWA	646
ST. HELENA	SH	SHN	654
SAINT KITTS AND NEVIS	KN	KNA	659
SAINT LUCIA	LC	LCA	662
ST. PIERRE AND MIQUELON	PM	SPM	666
SAINT VINCENT AND THE GRENADINES	VC	VCT	670
SAMOA	WS	WSM	882
SAN MARINO	SM	SMR	674
SAO TOME AND PRINCIPE	ST	STP	678
SAUDI ARABIA	SA	SAU	682
SENEGAL	SN	SEN	686
SEYCHELLES	SC	SYC	690
SIERRA LEONE	SL	SLE	694
SINGAPORE	SG	SGP	702
SOLOMON ISLANDS	SB	SLB	090
SOMALIA	SO	SOM	706
SOUTH AFRICA	ZA	ZAF	710
SPAIN	ES	ESP	724
SRI LANKA	LK	LKA	144
SUDAN	SD	SDN	736
SURINAME	SR	SUR	740
SVALBARD AND JAN MAYEN ISLANDS	SJ	SJM	744
SWAZILAND	SZ	SWZ	748
SWEDEN	SE	SWE	752
SWITZERLAND	CH	CHE	756
SYRIAN ARAB REPUBLIC	SY	SYR	760
TAIWAN, PROVINCE OF CHINA	TW	TWN	158
TANZANIA, UNITED REPUBLIC OF	TZ	TZA	834
THAILAND	TH	THA	764
TOGO	TG	TGO	768
TOKELAU	TK	TKL	772
TONGA	TO	TON	776
TRINIDAD AND TOBAGO	TT	TTO	780
TUNISIA	TN	TUN	788
TURKEY	TR	TUR	792
TURKS AND CAICOS ISLANDS	TC	TCA	796
TUVALU	TV	TUV	798

UGANDA	UG	UGA	800
UKRAINIAN SSR	UA	UKR	804
UNITED ARAB EMIRATES	AE	ARE	784
UNITED KINGDOM	GB	GBR	826
UNITED STATES	US	USA	840
UNITED STATES MINOR OUTLYING ISLANDS	UM	UMI	581
URUGUAY	UY	URY	858
USSR	SU	SUN	810
VANUATU	VU	VUT	548
VATICAN CITY STATE (HOLY SEE)	VA	VAT	336
VENEZUELA	VE	VEN	862
VIET NAM	VN	VNM	704
VIRGIN ISLANDS (BRITISH)	VG	VGB	092
VIRGIN ISLANDS (U.S.)	VI	VIR	850
WALLIS AND FUTUNA ISLANDS	WF	WLF	876
WESTERN SAHARA	EH	ESH	732
YEMEN, REPUBLIC O	YE	YEM	887
YUGOSLAVIA	YU	YUG	890
ZAIRE	ZR	ZAR	180
ZAMBIA	ZM	ZMB	894
ZIMBABWE	ZW	ZWE	716

List of changes applied, as specified in registration newsletters:
Newsletter III-1, 1989-12-5:
Burma deleted, Myanmar added (same numeric value, change of country name)
Newsletter III-2, 1990-07-16
Namibia, changing information not included in this file
Newsletter III-3, 1990-08-14
Afghanistan, changing information not included in this file
Newsletter III-4, 1990-08-14
Ethiopia, changing information not included in this file
Newsletter III-5, 1990-08-14
Fiji, changing information not included in this file
Newsletter III-6, 1990-08-14
Hungary, changing information not included in this file
Newsletter III-7, 1990-08-14
Unification of Yemen, under new numeric code
Newsletter III-8, 1990-08-14
Romania, changing information not included in this file
Newsletter III-9, 1990-08-14
Poland, changing information not included in this file
Newsletter III-10, 1990-08-14
Kampuchea deleted, Cambodia added (same numeric value, change of name)
Newsletter III-11, 1990-08-14
Benin, changing information not included in this file
Newsletter III-12, 1990-12-04
Czechoslovakia, changing information not included in this file
Newsletter III-13, 1990-10-30
Germany unified (DDR deleted, new name and numeric code for unified Germany)

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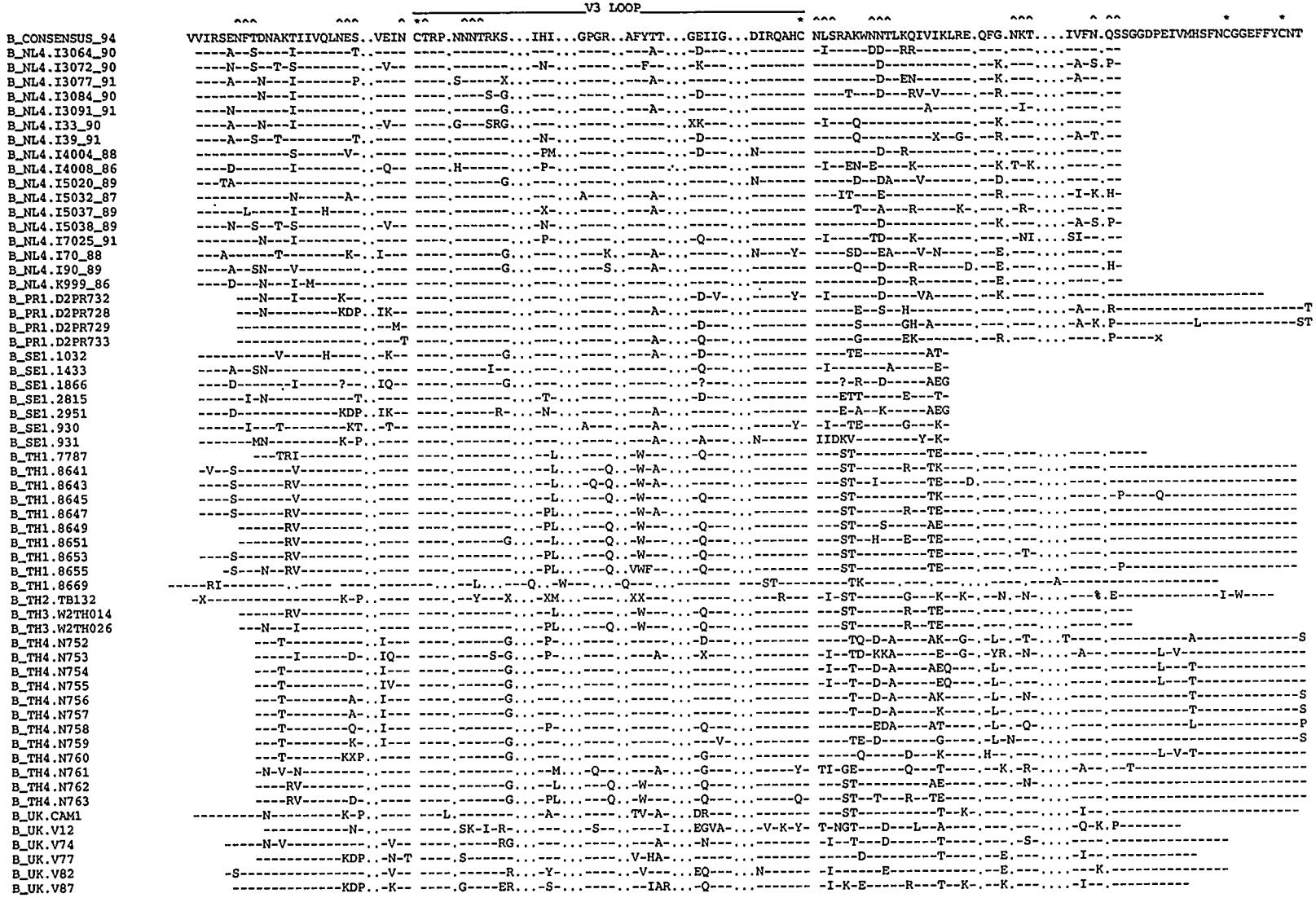
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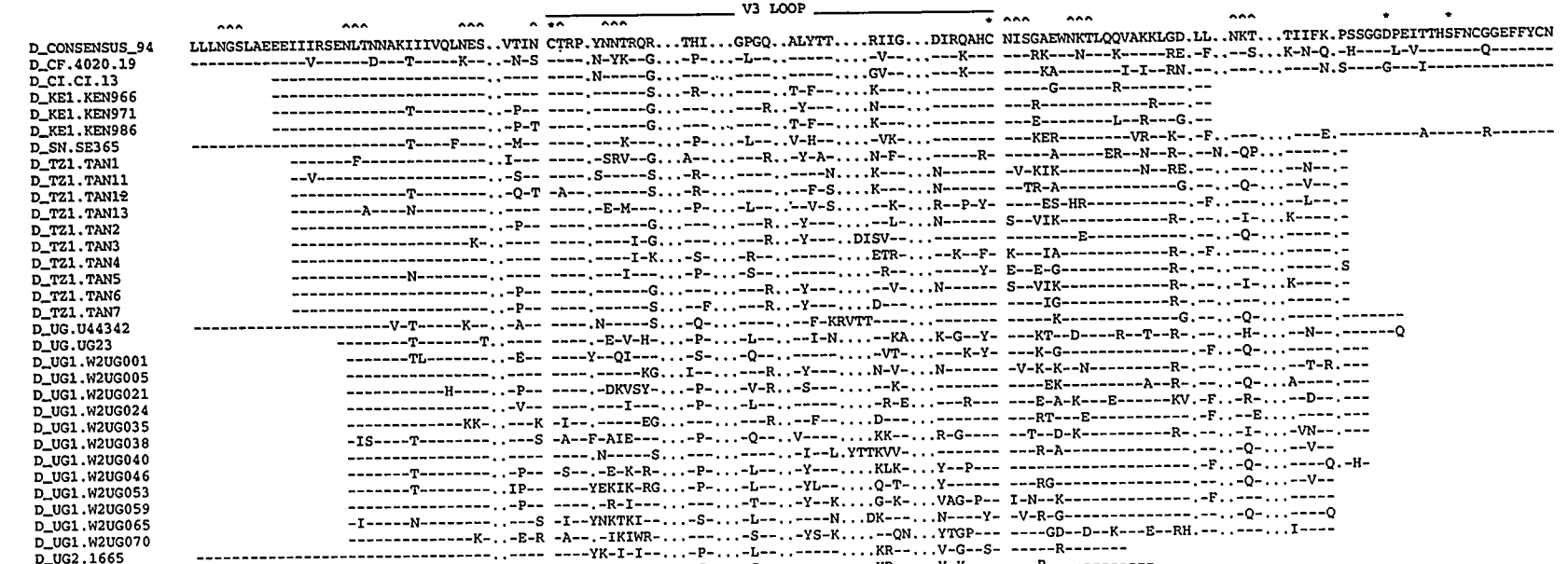
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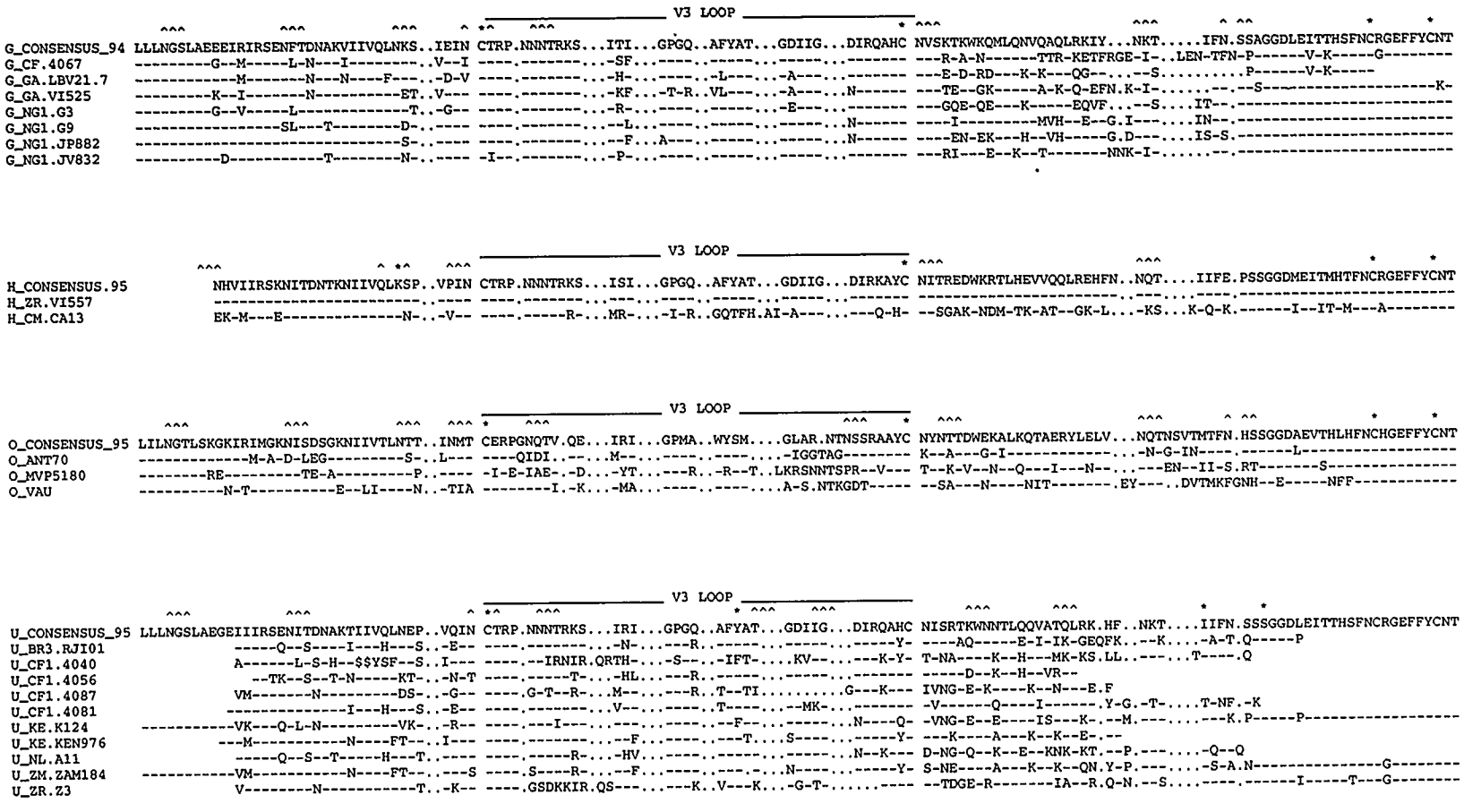
B_CONSENSUS_94 LLLNGSLAEEEIIRSENLTNNAKTIIVHLNKS..VEIN CTRP.SNNTRTS..ITI...GPGQ..VFYAT...GDIIG...DIRKAYC EINGTKWNETLKQVTEKLKE.HFN.NKT....IIFQ.PPSGGDLEITMHHFNCRGEFFYCNT
B_CF1.1697 QNNQIS----------.I---- ----.FKV-I-...AR-...---R..--HK-...-A-N-...-------- K-D---------R--I--R-.. --- ----.-LYRP
B_CF1.4002 ----------D---------- ----.FKRV---...VR-...---K..--HK-...-A-L-...------F- ---K-R--D--NK---------...K----..-L--P
B_CF1.4013 D---------- ----.FKK--I-...AR-...---R..--HK-...-A-L-...------F- K--E---------E--K--R--K.. --- ----P
B_CF1.4031 ---------- ----.VR-...---K..--E---...------F- K--E---------E--K--R--K.. --- ----P
B_CF1.4069 G---------AD---------E-..---- ----.FKK--I-...AR-...---R..--HK-...-A-L-...------F- ---K-R--D--NK---------...K----..-L--P
B_CF1.4084 N------D---------P..---- Y---.VR-...---K..--E---...------F- K--E---------E--K--R--K.. --- ----P
B_CF1.4017 ---------- ----.-KI---...VR-...---K..--A-M-...------F- ---------E-VK--RK.. --- ----.-H-RP
B_CF1.4039 -VV------I---------Q-VTP..-Q-- ----.---I---...VR-...---K..--S-T-...------F- --KEAQ--K---E-IG--R-.. --- ----R
B_CF2.4071TG2 ---------- ----.FKKM---...VR-...---R..--K-...-S-T-...---------- ---------Q-IIR--E-.. --- ----.-NK...T-Q-KP-Y----------
B_CF2.ELO ---------R---------- ----.YK-----...AR-...---K..--K-...-S-T-...---------- ----A-H-----MVG--RK.. --- ----.---S----P-----N----------
B_CF2.MBA ---------A---------P..---- ----.---------...VR-...---G..--E---...---R-F- ---------R-.. --- ----.-V---.----------S----------
B_CM.CA10 ---------- ----.-TTI---...SR-...---.A--KI .EG-S-...N--A--- ---------F----K--R--Y-.. --- ----.-K---.-SP--P----S----------
B_TH1.8639 ---------- ----.---------R..---.---...I---...------...------ ---------A---------- --- ----.---.----L----------
B_TH1.8657 ---------- ----.---------...---.---...---...------...------ ---------A---------- --- ----.---.----------
B_TH1.8659 ---------- ----.---------...---.---...---...------...------ ---------V---------- --- ----.---.----------
B_TH1.8663 ---------- ----.---------...---.---...---...------...------ ---------KV--------- --- ----.---.----VV-----S----------
B_TH1.8671 ---------- ----.---------...---.---...---...------...------ ---------A----AG----- --- ----.---.----H.-----VV----------
B_TH1.8673 ---------- ----.---------...---.---...---...------...------ ---------A-R--------- --- ----.---.----------
B_TH1.8683 ---------- ----.---------...-P-...---.---...------...------ ---------N--------- --- ----.---.----------
B_TH1.TA10671 ---------- ----.---------...--M-...---.---...------...------ ---R------ ----K---KA---------- --- ----.-I--K-...----.---.----------
B_TH1.TA7792 ---------- ----.---------...---P-...---.---...------...------ ---------KA---------- --- ----.---.----C-.-----P-
B_TH1.TA7794 ---------- ----.---------...---.---...---...------...---K-...------...------ ---------A---------- --- ----.---.----------
B_TH1.TA8173 ---------- ----.---------...---.---...-P-...---.---...------...------ ---------A---------- --- ----.---.----------T--
B_TH1.TA8176 ---------- ----.---------...---.---...-P-...---.---...A-----...------...------ ---------V---------- --- ----.---.----------
B_TH2.TN235 ---------- ----.---------...---.---...---...---.---...------...------ ---------V-T-------- --- ----.---.----------X----------
B_TH2.TN239 ---------- ----.---------...---.---...---...---.---...------...------ ---------A---------- --- ----.---.----------
B_TH2.TN241 -----K---------- ----.---------...---.---...---...---.---...------...------ ---------V------GE- --- ----.---.----------
B_TH2.TN242 ---------- ----.---------...---.---...---...---.---...------...---X--- ---R------A-----K---------- --- ----.---.----L----------
B_TH2.TN243 ---------- ----.---------...-G-...---.---...---...---.---...------...---X--- ---------RV--------- --- ----.---.----------
B_TH2.TN244 ---------- ----.---------...-V-...---.---...---...---.---...------...------ ----E--KA---------- --- ----.---.----P----------
B_TH3.W2TH001 ---------- ----.---------...---.---...-N-...---.---...---.---...------...------ ---------V-R-------- --- ----.---.----I--R----------
B_TH3.W2TH003 ---------- ----.---------...---.---...--V-...---.---...---.---...------...------ ---------V---------- --- ----.---.----------
B_TH3.W2TH005 ---------- ----.---------...---.---...-P-...---.---...---.---...------...---Q--- ---E------KV--------- --- ----.---.----X----------
B_TH3.W2TH006 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---R------KV--------- --- ----.---.----M----------
B_TH3.W2TH007 ---------- ----.---------...---.---...-N-...---.---...---.---...------...------ ---R------A-----K--E- --- ----.---.----------
B_TH3.W2TH009 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---R------Y-V-----K--- --- ----.---.----T----------
B_TH3.W2TH011 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------KV---X----- --- ----.---.----------
B_TH3.W2TH015 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------A---------- --- ----.---.----K----------
B_TH3.W2TH018 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------A----K----- --- ----.---.----------
B_TH3.W2TH019 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------A---------- --- ----.---.----------
B_TH3.W2TH020 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------KA--------- --- ----.---.----------
B_TH3.W2TH021 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------KA--------- --- ----.---.----------
B_TH3.W2TH022 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------V---K------ --- ----.---.----------
B_TH3.W2TH023 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------KV--------- --- ----.---.----------
B_TH3.W2TH024 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------A----K----- --- ----.---.----------
B_TH4.D3TH966 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------D---------A --- ----.---.----K----------
B_TH4.D3TH975 ---------- ----.---------...---.---...---...---.---...---.---...------...------ ---------AK--N---K.. --- ----.---.----VV----------
B_TH.N764 ---------- ----.---------...---K---...---...---.---...---.---...------...------ ---------- --- ----.---.----H----------

V3 LOOP
F_CONSENSUS_94
F_BR.7944
F_BR2.BZ126
F_BR2.BZ163
F_BR3.RJ103
F_CM.CA16
F_CM.CA20
F_CM.CA4
F_GA.VI354
F_RO1.14018
F_RO1.14020
F_RO1.14024
F_RO1.14027
F_RO1.14028
F_RO1.14034
F_RO1.14036
F_RO1.14041
F_RO1.14046
F_RO2.RM53002
F_RO2.RM53011
F_RO2.RM53012
F_RO2.RM53013
F_RO2.RM53014
F_RO2.RM53015
F_RO2.RM53018
F_RO2.RM53021
F_RO2.RM53022
F_RO2.RM53023
F_RO2.RM53024
F_RO2.RM53027
F_RO2.RM53029
F_RO2.RM5303
F_RO2.RM53031
F_RO2.RM53032
F_RO2.RM53034
F_RO2.RM53035
F_RO2.RM53037
F_RO2.RM53040
F_RO2.RM53043
F_RO2.RM5306
F_RO2.RM5307
F_RO2.RM5308


V3 LOOP
G_CONSENSUS_94 LLLNGSLAEEEIRIRSENFTDNAKVIIVQLNKS..IEIN CTRP.NNNTRKS...ITI...GPGQ..AFYAT...GDIIG...DIRQAHC NVSKTKWKQMLQNVQAQLRKIY...NKT.....IFN.SSAGGDLEITTHSFNCRGEFFYCNT
G_CF.4067 ---------G--M-----L-N---I---------..V--I ----.--------...-SF...-----..-----...-----...-------- ---R-A-N------TTR-KETFRGE-I-..LEN-TFN-P------V-K-----G---------
G_GA.LBV21.7 ----------M-------N---N----F----..-D-V ----.--------...-H-...-----..-L---...-A---...-------- ---E-D-RD---K-K---QG--...--S..........P------V-K-----
G_GA.VI525 ---------K--I-------N----------ET..V--- ----.--------...-KF...-T-R..VL---...-A---...N------ ---TE--GK-----A-K-Q-EFN.K-I-.....---.--S--------------------K-
G_NG1.G3 ---------G--V-----L----------T..-G-- ----.--------...-R-...-----..-----...-E---...------- ---GQE-QE---K-----EQVF...--S....IT--.----------------------
G_NG1.G9 ----------------SL---T--------D-..---- ----.--------...-L...-----..-----...------...N------ ----I---------MVH--E--G.I---....IN--.----------------------
G_NG1.JP882 ----------------------------S-..---- ----.--------...--F...A---...-----...------...N------ ----EN-EK---H--VH-----G.D---....IS-S.----------------------
G_NG1.JV832 ----------D----------T--------N-..---- -I--.--------...-P-...----..-----...-----...------- ---RI---E--K--T-------NNK-I-.....---.----------------------
V3 LOOP
H_CONSENSUS.95 NHVIIRSKNITDNTKNIIVQLKSP..VPIN CTRP.NNNTRKS...ISI...GPGQ..AFYAT...GDIIG...DIRKAYC NITREDWKRTLHEVVQQLREHFN..NQT....IIFE.PSSGGDMEITMHTFNCRGEFFYCNT
H_ZR.VI557 ----------.---- ----.-------...---...-----..------...-----...------- ----------.---....-----.----------
H_CM.CA13 EK-M---E----------N-..-V-- ----.-----R-...MR-...-I-R..GQTFH.AI-A---...---Q-H- --SGAK-NDM-TK-AT--GK-L...-KS...K-Q-K.------I--IT-M---A--------
V3 LOOP
O_CONSENSUS_95 LILNGTLSKGKIRIMGKNISDSGKNIIVTLNTT..INMT CERPGNQTV.QE...IRI...GPMA..WYSM....GLAR.NTNSSRAAYC NYNTTDWEKALKQTAERYLELV...NQTNSVTMTFN.HSSGGDAEVTHLHFNCHGEFFYCNT
O_ANT70 ----------M-A-D-LEG---------S-..L--- ----QIDI..--...M--...-----..----....-IGGTAG-------- K--A---G-I-----------...-N-G-IN----.------L----------
O_MVP5180 --------RE---------TE-A---------P..---- -I-E-IAE-.-D...-YT...---R..-R--T..LKRSNNTSPR--V--- T--K-V--N--Q---I---N--...---EN--II-S.RT-------S----------
O_VAU ----------N-T----------E--LI----N..-TIA --------I.-K...-MA...-----..----....A-S.NTKGDT----- --SA---N----NIT--------.EY---..DVTMKFGNH--E-----NFF----------
V3 LOOP
U_CONSENSUS_95 LLLNGSLAEGEIIIRSENITDNAKTIIVQLNEP..VQIN CTRP.NNNTRKS...IRI...GPGQ..AFYAT...GDIIG...DIRQAHC NISRTKWNNTLQQVATQLRK.HF..NKT....IIFN.SSSGGDLEITTHSFNCRGEFFYCNT
U_BR3.RJI01 -----Q--S----I---H---S..-E-- ----.--------...-N-...---R..------...------...-----Y- ----AQ-----E-I-IK-GEQFK..--K....-A-T.Q-----P
U_CF1.4040 A------L-S-H--$$YSF--S..I--- ----.--IRNIR.QRTH-...-S--..-IFT-....KV--...---K-Y- T-NA----K--H---MK-KS.LL..---...T----.Q
U_CF1.4056 --TK--S--T-N-----KT-..-N-T ----.-----T-...-HL...---R..------...-------...------- -----D--K--H--VR--
U_CF1.4087 VM-------N---------DS-..-G-- ----.G-T--R-...M--...---R..T--TI.........G---K--- IVNG-E-K----K--N---E.F
U_CF1.4081 --------------I---H---S..-E-- ----.--------...V--...-----..T----...--MK-...-------- -V------Q----I-------.Y-G.-T-....T-NF.-K
U_KE.K124 ----------VK---Q-L-N---------VK-..-R-- ----.---I---...---...------..--F--...------...N----Q- -VNG-E--E----IS---K-.--M.---....---K.P-----P----------
U_KE.KEN976 ---M----------N----FT---..I--- ----.--------...--F...-----..---T....S----...------Y- ---K----A---K--K--E-.--
U_NL.A11 -----Q--S--T-----H---T..---- ----.-----R-...-HV...-----..-----...------...N--K--- D-NG-Q--K--E--KNK-KT.--P.---....-Q--Q
U_ZM.ZAM184 ----------VM---------N----FT---..---S ----.S----R-...--F...-----..---.-...N----...------Y- S-NE----A---K--K--QN.Y-P.---....-S-A.N--------------G--------
U_ZR.Z3 V--------N----------T..-K-- ----.GSDKKIR.QS---...---K..V---K...-G-T-.....----- --TDGE-R-------IA--R.Q-N.--S....----.------I-----T---G--------

A Subtype

At this time there are viral sequences from 124 HIV-1 infected individuals associated with HIV-1 subtype A. The A subtype consensus sequence (A_CONSENSUS_94) generated from these sequences was based on the most common amino acid found in each position in an alignment of these sequences. 105 of these sequences have been published and/or have been made available for printing in the database by their authors.

1. **CF1.ID#:** These twelve sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990-1991. Consensus, PCR-clones, cell culture, DNA. Murphy E, et al., AIDS Res. and Human Retroviruses 9:997-1006 (1993). GenBank accession numbers L11457-L11458, L11461-L11463, L11469-L11471, L11474-L11475, L11477-L11479, L11484-L11496, L11498, L11518, and L11523-L11524,
2. **CF2.GAN and SAS:** These sequences were kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg, France. They are a part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny.
3. **CI2.CI-ID#:** These sequences are from 11 of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-14 and CI-20 were symptomatic, and the others were asymptomatic. CI-14, CI-45 and CI-47 were serologically dually reactive for HIV-1 and HIV-2. The C2V3 region is part of a 900 bp sequence. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3-4 clones were sequenced, and the consensus of those clones is presented here. Janssens W, et al. AIDS 8:21-26 (1994). GenBank accession numbers X72024-X72027, X72030-X72039, X72043-X72056, and X72059-X72065.
4. **CM1.CA-ID#:** These sequences are 11 of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic (CA7, CA11, CA15, CA17, CA18, and CA21) and symptomatic (CA1, CA2, CA6, CA19 and CA22) individuals. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. Nkengasong JN, et al., AIDS 8:1405-12 (1994). GenBank accession numbers for the entire set of 17 envelope sequences: X80438-X80454.
5. **DJ.DJ-ID#:** These three sequences from Djibouti were from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession numbers L22939, L22941, and L23064.
6. **GA.VI191:** This sequence from Gabon was from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession number L22952.
7. **GH.D687:** A single sequence from an individual from Ghana, provided by Georg-Speyer Haus, Frankfurt, Germany (Dr. Ursula Dietrich). GenBank accession number L07652.
8. **KE.K89:** This sequence is named "KENYA" in the GenBank entry, but is identified as K89 in the original manuscript. It is a Kenyan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession number L22943.
9. **KE.KEN-ID#:** These 19 sequences were derived from patients who were part of a 1990-1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. Janssens W et al., in press AIDS Res. Hum. Retroviruses (1994). GenBank accession numbers for the entire set of 23 patients surveyed in this study: U12984-U13006.
10. **NG.NI:** A full gp120 envelope sequence from Nigeria was kindly provided by Dr. Tom Howard from the University of Southern California (USC) Howard et al. AIDS Res. and Hum. in press (1994).
11. **RW.SF1703:** This sequence is from Rwandan isolate sf170, a biologically active clone reported to be macrophage-tropic. Cheng-Mayer C, Homsy J, Evans LA, and Levy J. Proc. Natl. Acad. Sci. USA, 85:2815-19 (1988); and, Evans, L, Higgins, D, Cheng-Mayer C and Levy J. Unpublished (1990). GenBank accession number M66533.

12. **RW.W2RW-ID#:** Eight sequences from asymptomatic individuals from Rwanda sampled in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are in press: de Wolf F, et al. AIDS Res. and Human Retroviruses (1994); Osmanov S, et al. AIDS Res. and Human Retroviruses (1994); Gao F, et al. AIDS Res. and Human Retroviruses (1994), all in the November issue. GenBank accession numbers U08630-U08641, U08647-U08665, U08763-U08766, and U08793-U08794.
13. **TZ.TAN-ID#:** These four sequences are from a set of 14 Tanzanian samples from symptomatic individuals, using serum samples taken in 1988 to generate PCR clones from viral RNA for sequencing. Zwart G, et al., AIDS 7:467-474 (1993). GenBank accession numbers L01313, L01315-L01316, L01335, L01337-L01339.
14. **UG.1033:** This sequence is a consensus sequence of blood and CSF samples taken from a Ugandan patient 1033, CDC class IV-A. sequences which compose this consensus are: Z23182-Z23184, Z23220 Keys et al., Virology 196:475-483 (1993). GenBank accession numbers Z23177, Z23182-Z23184, and Z23220-Z23223.
15. **UG.U455:** This sequence is from the 1985 Ugandan isolate U455; the complete genomic sequence is available. Oram JD, et al., AIDS Res. and Human Retroviruses 6:1073-1078 (1990). GenBank accession number M62320.
16. **UG.UG06:** This sequence is from a Ugandan isolate. Atkin A, et al., AIDS Res. Human Retroviruses 9:351-356 (1993). GenBank accession number M98503.
17. **UG1.W2UG-ID#:** Three sequences from asymptomatic individuals from Uganda in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are in press: de Wolf F, et al. AIDS Res. and Human Retroviruses (1994); Osmanov S, et al. AIDS Res. and Human Retroviruses (1994); Gao F, et al. AIDS Res. and Human Retroviruses, November issue (1994). GenBank accession numbers U08666-U08669 and U08767-U08770, U08788-U08792 and U08795.
18. **UG2-ID#:** These 11 sequences are part of a set of sequences derived from 22 Ugandans who were attending an AIDS clinic, sampled in 1990. Consensus, PCR-clones, peripheral blood DNA. Albert J, et al., Virology 190:674-681 (1992). GenBank accession numbers M98902-M98905, M98908-M98910, M98914-M98917, M98919, M98924-M98928, M98938-M98941, M98946-M98966, and M98976-M98978,
19. **UG4.UG-ID#:** Two Ugandan sequences from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession numbers L22957 and L22951.
20. **ZR.Z321:** This sequence is from the 1976 Zairean isolate Z321. Srinivasan A, et al., AIDS Res. and Human Retroviruses 5:121-9 (1989). GenBank accession number M15896.
21. **ZR1.ID#:** These ten sequences are part of a set of 14 A and D sequences from women from Zaire; 8 were healthy, 4 showed minor signs of illness, and 2 had AIDS. PCR-direct, peripheral blood DNA. Potts KE, et al., AIDS Res. and Human Retroviruses 9:613-618 (1993). GenBank accession numbers L19624-L19626, L19628-L19630, L19632-L19634, and L19636.

The A subtype sequences which are not yet published, and for which the authors have not yet given permission for release, are from the following set:

1. **CI1.ID#:** Ten sequences from individuals from the Cote d'Ivoire. PCR-direct, peripheral blood DNA. These sequences were provided by the Centers for Disease Control, Atlanta GA, USA (Dr. Chin-Yih Ou and Dr. Marcia Kalish).
2. **UG3.ID#:** Six sequences from individuals from Uganda. PCR-clone, peripheral blood DNA. These sequences were provided by the Centers for Disease Control, Atlanta GA, USA (Dr. Chin-Yih Ou and Dr. Marcia Kalish).
3. **ZR2.ID#:** Three sequences from individuals from Zaire, provided by the LTCB, NCI, NIH, Bethesda, MD, USA (Dr. Marvin Reitz).

B Subtype

At this time we have included viral sequences from 338 HIV-1 infected individuals associated with HIV-1 subtype B. The B subtype consensus sequence (B_CONSENSUS_94) generated from these sequences was based on the most common amino acid found in each position in an alignment of these sequences. Please note that none of the studies which have published sequences of only the V3 loop sequences are included here, as the DNA sequences were deemed too short for phylogenetic analyses. (For example, LaRosa G, et al., Science 249:932-935 (1990) and Fouchier RAM, et al., J. Virol. 66:3183-3187 (1992).) 328 of these sequences have been published and/or have been made available for printing in the database by their authors.

1. **BE.SIMI84** One of two cloned env sequences from a patient with AIDS from Belgium. A vaccinia construct that expresses this gene was created to vaccinate the patient's non-infected brother with the goal of immune therapy by adoptive transfer of lymphocytes. Bex F, C Vanhulle, S Sprecher, M Geissendorfer, H Rubsamen-Waigmann and A Burny. Unpublished (1992). GenBank accession number L07421.
2. **BR1.ID#:** These 21 sequences represent the B env subtype sequences found among 22 Brazilian outpatients with varying degrees of disease progression. Consensus, PCR clones, peripheral blood PBMC DNA. Potts KE, et al., AIDS 7:1191-1197 (1993). GenBank accession numbers for 20 of the 56 clones from which consensus sequences were calculated: L19225-L19236, L19240-L19246 and L20963.
3. **BR2.W2BR-ID#:** 14 sequences from individuals from Brazil. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are in press: de Wolf F, et al. AIDS Res. and Human Retroviruses (1994); Osmanov S, et al. AIDS Res. and Human Retroviruses (1994); Gao F, et al. AIDS Res. and Human Retroviruses, November issue (1994). GenBank accession numbers U08670-U08714, U08771-U08778, U08780-U08782, U08792, U08796, U08797-U08798 and U08800,
4. **BR3.RJ- or SP-ID#:** These sequences came from the Brazilian cities Rio de Janeiro and Sao Paulo. The sequences that are very short, containing V3 loop fragments insufficient for phylogenetic analysis, are not included here (5 of the 26). The included 21 viral sequences are of the B subtype. An F subtype and a B-F recombinant were also observed in this set. Year of isolation for the sequences range from 1990-1992 for Rio de Janeiro, and 1992 for Sao Paulo. The only two with CD4+ cells < 200 were RJ636 and RJ27. The CDC clinical class ranged from II-IV. DNA extracted from PBMCs of HIV infected individuals was amplified, and the PCR product was directly sequenced. Morgado et al., AIDS Res. and Human Retroviruses 10:569-576 (1994) and Sabino EC et al. J. Virol. 68:6340-6346 (1994). GenBank accession numbers U00400-U00401, U00403, U00405, U00407-U00414, U00416-U00418, U00421, U00424-U00425, and U00427.
5. **CI.CI-22:** A single B subtype sequence from a set of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-22 was symptomatic. The C2V3 region is part of a 900 bp fragment that was sequenced for each individual. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3-4 clones were sequenced, and the consensus of those clones is presented here. Janssens W, et al. AIDS 8:21-26 (1994). GenBank accession numbers X72040-X72042.
6. **CM.CA5:** A single B subtype sequence from a set of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals, specifically, patient CA-5 was asymptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. Nkengasong JN, et al., AIDS 8:1405-12 (1994). GenBank accession numbers for the full set of 17 sequences which includes CA5 are X80438-X80454.
7. **DE.D31:** This sequence is from isolate D31. Kreutz A, et al., AIDS Res. and Hum. Retroviruses 8:1619-1629 (1992). GenBank accession number X61240.
8. **DE.HAN:** This sequence is from an infectious clone from the German isolate DE.HAN-2. Sauermann U, et al., AIDS Res. and Hum. Retroviruses 6:813-823 (1990)
9. **FR.J61:** This sequence is from one of the JBB clones from the French patient Bru. Wain-Hobson S, et al. Science 252:961-64 (1991) and Guo et al. Nature 349:745-6 (1991).
10. **FR.LAI:** This sequence is from the French isolate LAI (formerly BRU). Wain-Hobson S, Sonigo P, Danos O, Cole S, and Alizon M. Cell 40:9-17 (1985). Also see: Alizon M, Wain-Hobson S, Montagnier L, and Sonigo P, Cell 46:63-74 (1986) and Wain-Hobson S, et al. Science 252:961-964 (1991). GenBank accession number K02013.

11. **GA.OYI:** This sequence is from the Gabonese isolate OYI (designated elsewhere as isolate 397), isolated from a healthy HIV-1 infected individual. GA.OYI appears to have been the first viral sequence from Africa that phylogenetically clustered with North American viruses. Huet T, et al., AIDS 3:707-715 (1992). GenBank accession number M26727.

12. **HT.RF:** This sequence is from the clone HAT-3, from Haitian isolate RF. Starcich BR, et al., Cell 45:637-648 (1986). GenBank accession number M17451.

13. **HT.WMJ22:** This sequence is from the isolate WMJ22, isolated from a person of Haitian descent living in the U.S. Hahn BH, et al., Science 232:1548-1553 (1986). GenBank accession number M12507.

14. **HT1.D-ID#:** These seven sequences are from Haitians, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratories of Dr. Beatrice Hahn at the University of Alabama, and Dr. Marcia Kalish at the the Centers for Disease Control, Atlanta, GA. Except for D2HA590, the full gp160 was sequenced from clones derived from expanded culture stocks. D2HA590 is a direct sequence from PCR amplified DNA from expanded culture. The sequence ID numbers are abbreviated, for example D2HA590 can be read as DAIDS sequence (D), isolated in 1992 (2), Haitian (HA), patient 301590 (590). GenBank accession numbers: U08441-U08447, U04900. Both U08441 and U08442 are sequences from patient HT1.D1HA651 and are identical over the region of interest. GenBank accession numbers for additional clones derived from these patients: U04905-U04906, U04901 U04902 U04903 U04904

15. **HT2.H-ID#:** These 25 sequences are from Haitians. All sequences were PCR amplified from the infected individuals PBMCs, and this set includes direct sequences of PCR amplification products, consensus sequences of multiple clones of PCR products plus one direct sequence, and single clones of PCR products. These sequences were provided by the Centers for Disease Control, Atlanta, GA USA (Dr. Chin-Yih Ou), and John Hopkins University School of Hygiene and Public Health, Balimore, MD USA (Dr. Neal Halsy), and the Centers for Development and Health, Complexe Medico Sociale de la Cite Soleil, Port-au-Prince, Haiti (Dr. Reginald Boulos). GenBank accession numbers L07145-L07161, L07163-L07165, L07167-L07207, L07209-L07239, L07241-L07246.

16. **IN1.ID#:** These four sequences were isolated in Hyderabad, Andhra Pradesh, in southern India. The C2V3 region of env was amplified by nested priming from DNA from PBLs from fresh blood samples. Date of sampling and health status of HIV-1 infected individuals is unknown. Baskar PV, et al., AIDS Res. and Human Retroviruses 10:1039-1041 (1994). GenBank accession numbers L29091-L29094.

17. **JP.GUNA:** A Japanese 1989 isolate HIVGUN, infectious to T cells, was adapted to growth on fibroblast-like BT cells. A single amino acid change at the tip of the V3 loop was shown to be responsible for the change in tropism, GPGR to GSGR. Takeuchi Y, Akutsu M, Murayama K, Shimizu N, and Hoshino H. J. Virol. 65:1710-1718 (1991). GenBank accession number M59192.

18. **JP.JH32:** This is a sequence from a lambda clone of Japanese isolate JH3. Komiyama N, et al., AIDS Res. Hum. Retroviruses 5:411-419 (1989). GenBank accession number M21138.

19. **MFA:** This sequence is from the isolate MFA derived from an asymptomatic patient with hemophilia. Stevenson M, et al., J. Virol. 64:3792-3803 (1990). GenBank accession number M33943.

20. **NL1.ID#:** These nine sequences are part of a study of presumed donor-recipient pairs from an HIV-1 transmission study conducted in the Netherlands. If pairs were extremely close or identical, only the "recipient" is included here. Recipient samples were from the first sample to be antibody positive, and are numbers 1,3,5,7,9, and 13. These sequences are consensus sequences of multiple clones from PCR amplified serum RNA. Wolfs TFW, Zwart G, Bakker M, and Goudsmit J. Virology 189:103-110 (1992). GenBank accession numbers M91819-M91827, M91829, M91831-M91832, M91839, M91857-M91870, M91872, M91874, M91881-M91884, M91891, M91893, 91895-M91908, M91910, M91911-M91926.

21. **NL2.ID#:** These two sequences are part of a Dutch study of mutations occurring over a five year period (starting in 1985) in two patients. Serum RNA was PCR amplified and multiple clones were sequenced. The consensus for each patient is shown. Wolfs TFW, Zwart G, Bakker M, Valk M, Kuiken CL, and Goudmsit J. Virology 185:195-205 (1991). GenBank accession numbers M74591-M74684.

22. **NL3.NET-ID#:** These six consensus sequences from the Netherlands are samples from AIDS patients, using serum samples to generate PCR clones from viral RNA for sequencing. Zwart G, et al., AIDS 7:467-474 (1993). GenBank accession numbers L01282-L01297.

23. **NL4.ID#:** These 74 sequences represent a study of early seroconverters from different times with different risk factors for transmission during the AIDS epidemic in the Netherlands. The year the sample was taken is indicated in the last part of the sequence name. The risk group of the individual from whom the virus is derived is indicated in the first letter of the sequence name (D, B and H for IVDUs, hemophiliacs, and

homosexuals, respectively). Viral genomic RNA from sera was PCR amplified and amplification product was direct sequenced. Kuiken CL, et al., Proc. Natl. Acad. Sci. USA 90:9061-9065 (1993). GenBank accession numbers ZZ29219-Z29225, Z29256-Z29258, and Z29262-Z29325.

24. **PR1.D-ID#:** These four sequences are from Puerto Rico, and were generated as part of the DAIDS variation program in the laboratory of Dr. Marcia Kalish at the the Centers for Disease Control, Atlanta, GA. The C2V3 region was directly sequenced from PCR amplification of DNA from viral culture. The sequence ID numbers are abbreviated; for example D2PR732 can be read as DAIDS sequence (D), isolated in 1992 (2), Puerto Rico (PR), patient 301732 (732). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. GenBank accession numbers U04926-U04929.
25. **SE1.ID#:** Seven sequences that are consensus sequences of blood and CSF samples taken from each patient. The CDC disease stage class for the patients are as follows: II pts 930, 2815; III pt 931; IV-E pt 2951; IV-A pt 1032; and IV-C2 pts 1433, 1866. Keys et al., Virology 196:475-483 (1993). GenBank accession numbers Z23178-Z23181, Z23185-Z23187, Z23192-Z23194, Z23200-Z23219, Z23224-Z23227, Z23232-Z23235, and Z23240-Z23255.
26. **TH1.ID#:** These ten sequences are from individuals from Thailand. PCR-direct, peripheral blood PBMC DNA. Referred to as Thai subtype B in Ou et al. Ou C-Y et al., AIDS Res. and Human Retroviruses 8:1471-1472 (1992) and Ou C-Y et al. Lancet 341:1171-1174 (1993). (Published erratum appears in Lancet 342:250 (1993).) GenBank accession numbers L07442, L07449-L07456 and L07460.
27. **TH2.TB132:** This sequence is from a set of isolates from HIV seropositive individuals from Thailand. PCR, PBMC co-culture, DNA. Full env sequence is available. McCutchan FE, et al., AIDS Res. and Human Retroviruses 8:1887-1895 (1992). Please note: the TB132 locus name in the database corresponds to the McCutchan et al.'s "BK132" isolate. GenBank accession number L03697.
28. **TH3.W2TH-ID#:** 2 sequences from Thailand from asymptomatic individuals. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are in press: de Wolf F, et al. AIDS Res. and Human Retroviruses (1994); Osmanov S, et al. AIDS Res. and Human Retroviruses (1994); Gao F, et al. AIDS Res. and Human Retroviruses, November issue (1994). GenBank accession numbers U08715-U08718, U08801-U08802, and U08783-U08784.
29. **TH4.ID#:** These twelve sequences are B subtype sequences from Thailand. Ten were genetically most similar to HIV1 found in the Americas and Europe; these sequences were derived from people infected prior to 1988 (diagnosed in 1986 or 1987). The other two (N762 and N763) were designated B' and were isolated from people with more recent infections, 1988 and 1992. The sequences were obtained from PCR amplified PBMC DNA. The naming of the sequences submitted to GenBank does not correspond with the naming of the sequences in the paper. Kalish ML, et al, AIDS Res. and Human Retroviruses Nov., in press (1994). GenBank accession numbers for the entire set of thirteen sequences studied in this publication: U15576-U15588.
30. **UK.CAM1:** This sequence is from the British isolate CAM1. McIntosh A, and Karpas A, Thesis (1991), Cambridge University, England. GenBank accession number D10112.
31. **UK.V-ID#:** A set of six sequences from a study of hemophiliacs from Scotland who were originally thought to have been infected by the same batch of factor VIII. (ScV12 is a sequence from a hemophiliac from the U.S., included as a control). All are consensus sequences of multiple direct PCR sequences obtained from limiting dilution of PBMCs. The Scottish hemophiliacs were infected in 1984 and the PBMCs were obtained for analysis in 1989. Although the samples were potentially related, they were deemed sufficiently divergent in this region for inclusion in this set. Simmonds P, Balfe P, Ludlam CA, Bishop JO, and Leigh Brown, AJ. J. Virol. 64:5840-5850 (1990), and Balfe P, Simmonds P, Ludlam CA, Bishop JO, and Leigh Brown, AJ. J. Virol. 64:6221-6233 (1990). GenBank accession numbers M61327-M61346 and M61391-M61407.
32. **US.ACP1:** This virus was cultured from a seronegative man with Kaposi's sarcoma. (See: Ho D, The American J. of Med., 86:349-351 (1989). ACP1 was the sequenced after one passage in PBMCs. The sequence ACH9 was also derived from this patient. Ashkanazi, A, et al., Proc. Natl. Acad. Sci., USA 88:7056-7060 (1990). GenBank accession number M80660.
33. **US.ADA:** This sequence is from the monocytropic U.S. isolate ADA. Westervelt P, Gendelman HE, and Ratner L, Proc. Natl. Acad. Med. Sci. U.S.A. 88:3097-3101 (1991). GenBank accession number M60472.
34. **US.ALA1:** This sequence is from an infectious clone of the 1985 U.S. isolate AL-1, taken from a patient with AIDS. Buckler-White A, Theodore T, et al., Unpublished (1988). GenBank accession number M38430.
35. **US.BAL1:** This sequence is from the macrophage tropic U.S. isolate BAL, harvested from lung alveolar tissue. Reitz M, et al., Unpublished (1990). GenBank accession number M68893.

36. **US.BCSG3:** This is a fragment of a full genomic sequence from the provirus SG3, cloned as a single proviral unit. This clone replicates more efficiently in chimpanzeee than in human lymphocytes, and is extremely cytopathic in immortalized human T-cell lines. Ghosh SK, et al., Virology 194: 858-864 (1993). GenBank accession number L02317.

37. **US.BRVA:** This sequence is from U.S. isolate BRVA, which was taken from the brain tissue of a AIDS patient with neurological disorders. Anand R, et al., Virology 168:79-89 (1989). GenBank accession number M21098.

38. **US.BWB11A:** This sequence is from a study of variation in brain derived HIV-1 isolates by Monken CE, B Wu and A Srinivasan, and is part of a 32 sequence set, GenBank Accession L17097. A clone of proviral DNA was sequenced. (Manuscript in preparation, 1994).

39. **US.CDC42:** This sequence is from an infectious clone of the U.S. isolate CDC-451. Desai SM, et al., Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986). GenBank accession number M13137.

40. **US.JFL:** This sequence is from a non-infectious clone from the monocytropic U.S. isolate JFL. McNearney T, et al., Proc. Natl. Acad. Sci. U.S.A. 87:1917-21 (1990). GenBank accession number M31451.

41. **US.JM:** This sequence, along with B_US.WM, came from viral isolates after short term culture in PBMCs, PCR amplification, and cloning of PCR products. Both are from asymptomatic, seropositive individuals. Ashkanazi, A, et al., Proc. Natl. Acad. Sci., USA 88:7056-7060 (1990). GenBank accession number M80662.

42. **US.JRCSF:** This sequence is from an infectious clone of the 1986 U.S. isolate JRCSF, derived from from the CSF of a patient who died with Kaposi's sarcoma and severe AIDS encephalopathy. The infectious clone JRFL was isolated from the brain of the same patient. O'Brien WA, et al., Nature 348, 69-73 (1990). Also see: Pang S, Vinters HV, Akashi T, O'Brien WA, and Chen ISY, J AIDS 4:1082-1092 (1991). GenBank accession number M38429.

43. **US.MA:** This is a consensus of 35 sequences obtained either after viral culture or from PCR amplification products from patient PBMCs. Patient MA, from the US, was infected in 1984 or 1985, and had been experiencing neurological disorders prior to 1989 when the sample was taken. Kusumi K, et al., J. Virol. 66:875-885 (1992). GenBank accession numbers M79342-M79354 and M90025-M90046.

44. **US.MN:** This sequence is from 1984 U.S. isolate MN, taken from a pediatric AIDS patient. Gurgo C, et al., Virology 164:531-536 (1988). GenBank accession number M17449.

45. **US.NY5CG:** This sequence is from the 1984 U.S. isolate NY5. Willey R.W., et al., Proc. Natl. Acad. Sci. U.S.A. 83:5038-5042 (1986). GenBank accession number M38431.

46. **US.P896:** This sequence represents a molecular clone from an primary isolate derived from a Jamaican man who immigrated to Philidelphia 15 years earlier. At the time of viral isolation, he had no antiviral therapy, but was an AIDS patient with < 10 CD4 cells per mm3. The infectious molecular clone from which this sequence was derived is both macrophage-tropic and extremely cytopathic in lymphocytes. Collman R, et al. J. Virol. 66:7517-21 (1992). GenBank accession number M96155.

47. **US.RJS:** This is a consensus of six biologically characterized clones from isolate RJS, isolate 4. The HIV-1 infected individual had been infected for five years at the time of isolation. Complete env sequence is available. Daniels RS, Smith MH, and Fisher AG. J. Virol. 65:5574-5578 (1991) and Fisher AG et al., Nature 334:444-447 (1988). GenBank accession numbers M37491 and M37573-M37577.

48. **US.SB(A-C):** These three sequences are from 1988 U.S. isolates taken from a woman, her daughter and her sexual partner. The three viruses are epidemiologically linked, however the amino acids sequences appeared sufficiently divergent in this region to merit the inclusion of all three samples. Sequences were directly sequenced from PCR amplification products after the virus was briefly cultured. Burger H, et al., Proc. Natl. Acad. Sci. U.S.A. 88:11236-11240 (1991). GenBank accession numbers M77228-M77230.

49. **US.SC:** This sequence is from the 1984 U.S. isolate SC, from an AIDS patient. Gurgo C, et al., Virology 164:531-536 (1988). GenBank accession number M17450.

50. **US.SF162:** This sequence is from an infectious clone from the U.S. isolate SF162, cultured from cerebrospinal fluid. Cheng-Mayer C, Quiroga M, Tung JW, Dina D, and Levy J, J. Virol. 64:4390-4398 (1990). GenBank accession number M38428.

51. **US.SF2:** This sequence is from an infectious clone from the U.S. isolate ARV-2. Sanchez-Pescador R, et al., Science 227:484-492 (1985). HIVSF13 is a more infectious virus taken from the same patient (C. Cheng-Mayer, UCSF, San Francisco, CA, USA). GenBank accession number K02007.

52. **US.SF33:** This sequence is from an infectious clone from the 1984 U.S. isolate SF33. York-Higgins D, Cheng-Mayer C, Bauer D, Levy JA, and Dina D, J. Virol. 64:4016-4020 (1990). GenBank accession number M38427.

53. **US.WM:** This sequence, along with B_US.JM, came from viral isolates after short term culture in PBMCs, PCR amplification, and cloning of PCR products. Both are from asymptomatic, seropositive individuals. Ashkanazi, A, et al., Proc. Natl. Acad. Sci., USA 88:7056-7060 (1990). GenBank accession number M80663.
54. **US.YU:** This is a consensus sequence of eight lambda phage clones and 12 PCR amplified clones derived from the uncultured brain tissue of a patient with AIDS dementia complex. A macrophage tropic clone (YU-2) is almost identical to the consensus sequence of YU in this region, with only a single amino acid change (K to N) 10 amino acids from the carboxy-terminal end of the sequence. Li Y, et al., J. Virol. 65:3973-3985 (1991). Complete genomic sequences are available for two of the HIV1YU clones, along with biological characterizations of four of the HIV1YU clones: Li Y, et al., J. Virol. 66:6587-6600 (1991). The GenBank accession numbers for the YU-10 and YU-2 complete genomes are M93259 and M93258, respectively.
55. **US1.HC-ID#:** These are forty 1990-1991 U.S. samples, from the study of the dentist who was thought to have been the source of HIV-1 infection of six of his patients. Only the dentist's viral sequence and the Florida control sequences are shown here; the six epidemiologically and genetically linked patients are excluded from this alignment as their viral sequences were very similar to the dentist's. All sequences were PCR amplified from patient PBMCs. Most are direct sequences from the amplification products, although some are consensus sequences of multiple clones of PCR products and one direct sequence, Ou, C-Y, et al., Science 256:1165-1171 (1992). GenBank accession numbers for 70 of 75 sequences in this set: M90847-M90853, M90881-M90886, M90894-M90900, M90914-M90956, and M90958-M90964.
56. **US2.D-ID#:** These 15 sequences are from the USA, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratory of Dr. Marcia Kalish at the the Centers for Disease Control, Atlanta, GA. The C2V3 region was directly sequenced from PCR amplification products of DNA from viral culture. The sequence ID numbers are abbreviated, for example D2US711 can be read as DAIDS sequence (D), isolated in 1992 (2), United States (US), patient 301711 (711). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. GenBank accession numbers U04907-U04915, U04918 and U04921-U04925.
57. **US3.D-ID#:** These four sequences are from the US, and are part of a set of sequences generated as part of the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. gp160 sequences of clones from expanded culture stocks are available. The sequence ID numbers are abbreviated, for example D2US711 can be read as DAIDS sequence (D), isolated in 1992 (2), United States (US), patient 301711 (711). A full description of these sequences can be found in the April 1994 supplement to the HIV database, part III. GenBank accession numbers U08448-U08449 and U08451-U08452. GenBank accession numbers for additional clones from these patients: U04916-U04917 and U04919-U04920,
58. **US4.ZhuPt-ID#:** Sequences from five primary seroconverters. Consensus, PCR-clones, peripheral blood PBMC DNA. Although sequences were also available from two of the donors, only sequences from five recipients are shown here. Zhu et al., Science 261:1179-1181 (1993). GenBank accession numbers L21224-L21324, L21372-L21373, L21376-L21377, L21380-L21381, L21384-L21389, L21393-L21394, L21397-L21398, L21400-L21401, L21404, L21405, L21408, L21410-L21411, L21414, L21417-L21418, L21426-L21427, L21430-L21432, L21434-L21437, L21440-L21442, L21445, L21447, L21449-L21450, L21453-L21454, L21457, L21459, L21462-L21463, L21519-L21520, L21522-L21523, L21525-L21526, L21528-L21533, L21535-L21536, L21538-L21539, L21541, L21543, L21545-L21546, L21548, L21550-L21551, L21553-L21554, L21556, L21558-L21559, L21561-L21569, L21571-L21578, L21580, L21582, L21584, L21586, L21588, and L21590.
59. **US5.pt-ID#:** A consensus of PCR-clones, peripheral blood DNA. These sequences were part of a study of blood sequences compared to brain sequences from six individuals. Korber BTM, et al., J. Virol. 68:7467-7481 (1994). GenBank accession numbers U05360-U05568.

The 10 B subtype sequences which are not yet published, and for which the authors have not yet given permission for release, are from the following sets:

1. **PE:** A single envelope sequence from Peru, provided by the Centers for Disease Control, Atlanta, GA, USA, and the Walter Reed Research Institute.
2. **US:** A sequence from the United States, provided by Dr. Marvin Reitz of the NIH.
3. **US:** Six consensus consensus of PCR-clones, from peripheral blood DNA. These sequences were provided by Dr. Steven Wolinsky of Northwestern University Medical School, Chicago, IL, USA.
4. Two sequences of unspecified origin provided by Dr. Karen Coates Fryer, Macfarlane Burnet Centre for Medical Research, Fairfield, Victoria, Australia.

C Subtype

At this time there are viral sequences from 40 HIV-1 infected individuals associated with HIV-1 subtype C. The C subtype consensus sequence (C_CONSENSUS_94) generated from these sequences was based on the most common amino acid found in each position of an alignment. 38 of these sequences have been published and/or have been made available for printing in the database by their authors.

1. **BR.W2BR025:** This sequence is part of a gp160 sequence from an asymptomatic individual from Brazil, sampled in 1992. A clone was derived from an expanded viral culture, expressed and sequenced. This sequence was provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences from this patient can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are in press: de Wolf F, et al. AIDS Res. and Human Retroviruses (1994); Osmanov S, et al. AIDS Res. and Human Retroviruses (1994); Gao F, et al. AIDS Res. and Human Retroviruses (1994). GenBank accession number U15121.
2. **CF1.15166:** A single sequence from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990-1991. Consensus, PCR clones, cultured virus, DNA. Murphy E, et al., AIDS Res. and Human Retroviruses 9:997-1006 (1993). GenBank accession number L11525.
3. **DJ1.DJ-ID#:** These two sequences from Djibouti were from a a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession numbers L22940 and L23065.
4. **IN1.D-ID#:** These four sequences are from samples from high risk patients in India, PCR clones, DNA, PBMC culture. Dietrich U et al., AIDS 7:23-27 (1993). GenBank accession numbers L07651 and L07653-L07655.
5. **IN2.D-ID#:** These five sequences are from samples from high risk patients in India, primarily stage I. They were nested PCR amplified from DNA obtained from uncultured PBMC from patients serologically defined as HIV-1/HIV-2 mixed infections. Grez M et al., J Virol 68: 2161-8 (1994). GenBank accession numbers U07098 and U07100-U07103.
6. **MW1.ID#:** These 15 sequences are from pregnant women with risk factors from Malawi. PCR-direct, peripheral blood DNA. Orloff GM et al., AIDS Res. and Human Retroviruses 9:705-706 (1993). GenBank accesssion numbers L07427-L07441, L15721-L15733 and L15735.
7. **MW2.D-ID#:** These two sequences are from individuals from Malawi, generated as part of the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. The C2V3 was excised from full gp160 sequences, derived from clones from expanded culture stocks. The sequence ID numbers are abbreviated, for example D3MA959 can be read as DAIDS sequence (D), isolated in 1993 (3), Malawi (MA), patient 301959 (959). GenBank accession numbers U08453-U08454.
8. **SN.SE364:** A Senegalese sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession number L22944.
9. **SO.1574:** This sequence is a consensus sequence of blood and CSF samples taken from the Somalian patient 1574, CDC classification II. Keys et al., Virology 196:475-483 (1993). GenBank accession numbers Z23188, Z23190-Z23191, and Z23228-Z23231.
10. **SO.SM145:** A Somalian sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession number L22946.
11. **UG.UG268:** A Ugandan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession number L22948.
12. **ZA.NOF:** This sequence is from a South African individual, Dietrich U et al., AIDS 7:23-27 (1993). GenBank accession number L07426.

13. **ZM1.ZAM-ID#:** Two sequences from Zambia, from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession numbers L22954 and L22956.
14. **ZW.2647:** This sequence is a consensus sequence taken from blood and CSF samples taken from Zimbabwe patient 2647, CDC classification II. Keys et al., Virology 196:475-483 (1993). GenBank accession numbers Z23196-Z23199 and Z23236-Z23239.

The two C subtype sequences which are not yet published, and for which the authors have not yet given permission for release, are from S. Africa, and Zambia, provided by the Dept. of Med. Virology, University of Stellenbosch, Tygerberg, South Africa (Dr. Michael Becker).

D Subtype

At this time there are viral sequences from 73 HIV-1 infected individuals associated with HIV-1 subtype D. The D subtype consensus sequence (D_CONSENSUS_94) generated from these sequences was based on the most common amino acid found in each position of an alignment. All but 7 of these sequences have been published and/or have been made available for printing in the database by their authors.

1. **CF.4020:** This sample was the only D subtype from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990-1991. Consensus, PCR-clones, cell culture, DNA. Murphy E, et al., AIDS Res. and Human Retroviruses 9:997-1006 (1993). A full gp120 sequence from this isolate was kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg, France. It is a part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. GenBank accession numbers L11472-L11473.
2. **CI.CI-13:** A single D subtype sequence from a set of 13 isolates from individuals from Abidjan, Cote d'Ivoire. CI-13 was symptomatic, and serologically dually reactive for HIV-1 and HIV-2. The C2V3 region is part of a 900 bp fragment that was sequenced for each individual. Samples were collected between May 1990 and Sept. 1991. Virus was cultured with donor PBMCs, nested PCR amplified, 3-4 clones were sequenced, and the consensus of those clones is presented here. Janssens W, et al. AIDS 8:21-26 (1994). GenBank accession numbers X72028-X72029.
3. **KE1.KEN-ID#:** These three patients were part of a 1990-1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. W Janssens et al., in press AIDS Res. Hum. Retroviruses (1994). GenBank accession numbers for sequences from the entire set of 23 patients studied in this publication: U12984-U13006.
4. **SN.SE365:** A Senegalese sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession number L22945.
5. **TZ.TAN-ID#:** These ten sequences are from from a set of 14 Tanzanian samples from symptomatic individuals, using serum samples taken in 1988 to generate PCR clones from viral RNA for sequencing. Zwart G, et al., AIDS 7:467-474 (1993). GenBank accession numbers L01298-L01339.
6. **UG.U44342:** This sequence is from a Ugandan. Consensus of PCR-clones, peripheral blood DNA. Intact env sequences are available from this sample. Bruce C, C Clegg, A Featherstone, J Smith and J Oram. AIDS Res. and Human Retroviruses 9:357-368 (1992). GenBank accession numbers M98408-M98416.
7. **UG.UG23:** This sequence is from a Ugandan isolate. Atkin A, et al. and Pestano G, et al., unpublished. Andrew Atkin is at CUNY, NY, NY, USA. GenBank accession number M98504.
8. **UG1.W2UG-ID#:** Twelve sequences from asymptomatic individuals from Uganda in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are in press: de Wolf F, et al. AIDS Res. and Human Retroviruses (1994); Osmanov S, et al. AIDS Res. and Human Retroviruses (1994); Gao F, et al. AIDS Res. and Human Retroviruses (1994). GenBank accession numbers HU08721-U08741, HU08786-U08787, U08803-U08809 and U08821-U08824.
9. **UG2.ID#:** These twelve sequences are from 1986-1987 Ugandan samples. Consensus, PCR-clones, peripheral blood DNA. Oram JD, et al., AIDS Res. and Hum. Retroviruses 7:605-614 (1991). GenBank accession number for one of the 161 sequences used: M62320.
10. **UG3.ID#:** These 11 sequences are part of a set of sequences derived from 22 Ugandans who were attending an AIDS clinic, obtained in 1990. Consensus, PCR-clones, peripheral blood DNA. Albert J, et al., Virology 190:674-681 (1992). GenBank accession numbers L00614-L00618, L00733-L00737, M98894-M98899, M98901, M98906-M98907, M98911-M98913, M98918, M98920-M98923, M98929-M98937, M98942-M98945, and M98967-M98975.
11. **UG5.UG-ID#:** Three Ugandan sequences from a set of HIV-1 viral isolates from Africa. Health status of the individuals from which the virus was cultured was unspecified, and the year of viral isolation was probably

between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession numbers L22947 and L22949-L22950.

12. **US.AMK:** This sequence comes from a student living in Alabama, who moved from Zaire to the US in 1988. Virus was isolated from the patients PBMCs; this isolate was PCR amplified, and amplification products from both gag and env were subcloned and sequenced. His CD4 count was < 5 cells/mm3, and he was symptomatic at the time of viral isolation. Gao F, et al., AIDS Res. and Human Retroviruses (1994). GenBank accession number U08193.
13. **ZR.ELI:** This sequence is from the Zairean isolate ELI. Alizon M, Wain-Hobson S, Montagnier L, and Sonigo P. Cell 46:63-74 (1986). The complete genomic sequence and an infectious clone are available. GenBank accession number M27949.
14. **ZR.JY1:** This sequence is from Zairean isolate Z-84, clone JY1. Yourno J, et al., AIDS Res. and Human Retroviruses 4:165-173 (1988). GenBank accession number J03653.
15. **ZR.MAL:** This sequence is from a non-infectious clone of the Zairean isolate MAL. Alizon M, Wain-Hobson S, Montagnier L, and Sonigo P. Cell 46:63-74 (1986). The complete genomic sequence and an infectious clone from the isolate MAL are available. GenBank accession number K03456.
16. **ZR.NDK:** This sequence is from an infectious clone of the Zairean isolate NDK. The molecular clone is highly cytopathic in vitro. Spire B, et al., Gene 81:275-284 (1989). The complete genomic sequence is available. GenBank accession number M27323.
17. **ZR.Z2Z6:** This sequence is from an infectious clone of Zairean isolate Z2. Theodore T, and Buckler-White A, unpublished, and Srinivasan A, et al., Gene 52:71-82 (1987). The complete genomic sequence is available. GenBank accession number M22639.
18. **ZR1.ID#:** These four sequences are part of a set of 14 A and D sequences from women from Zaire. 8 were healthy, 4 showed minor signs of illness, and 2 had AIDS. PCR-direct, peripheral blood DNA. Potts KE, et al., AIDS Res. and Human Retroviruses 9:613-618 (1993). GenBank accession numbers L19623, L19627, L19631 and L19635.

The seven D subtype sequences which are not yet published, and for which the authors have not yet given permission for release, are from the following set:

UG4.ID#: Seven sequences from individuals from Uganda. PCR-direct, peripheral blood DNA. These sequences were provided by the Centers for Disease Control, Atlanta GA, USA (Dr. Chin-Yih Ou).

E Subtype

At this time there are viral sequences from 65 HIV-1 infected individuals associated with HIV-1 subtype E. The E subtype consensus sequence (E_CONSENSUS_94) generated from these sequences was based on the most common amino acid found in each position of an alignment. All but 17 these sequences have been published and/or have been made available for printing in the database by their authors.

1. **CF1.ID#:** These eight sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990-1991. Consensus, PCR-clones, cell culture, DNA. Murphy E, et al., AIDS Res. and Human Retroviruses 9:997-1006 (1993). GenBank accession numbers L11459-L11460, L11463-L11468, L11476, L11480-L11481, L11505-L11504, L11511-L11513 and L11519-L11521.
2. **CF2.ID#:** These three sequences were kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg Cedex, France. It is a part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny.
3. **CM.CA10:** A single E subtype sequence from a set of 17 sequences from a very diverse set of isolates from from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals, specifically, CA10 was symptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. Nkengasong JN, et al., AIDS 8:1405-12 (1994). GenBank accession numbers for the entire set of 17 sequences in this publication: X80438-X80454.
4. **TH1.ID#:** These twelve sequences are from a set of 23 individuals from Thailand. PCR-direct, peripheral blood PBMC DNA. Referred to as Thai subtype A in Ou et al. Ou C-Y et al., AIDS Res. and Human Retroviruses 8:1471-1472 (1992) and Ou C-Y et al. Lancet 341:1171-1174 (1993). (Published erratum appears in Lancet 342:250 (1993).) GenBank accession numbers L07443-L07445, L07447-L07448, L07457-L07459 and L07461-L07464.
5. **TH2.ID#:** These six sequences are from 16 isolates from HIV seropositive individuals from Thailand. PCR, PBMC co-culture, DNA. Full env sequence is available. McCutchan FE, et al., AIDS Res. and Human Retroviruses 8:1887-1895 (1992). Please note: the "TN-ID#" locus names in the database correspond to the McCutchan et al.'s "CM-ID#" isolates. GenBank accession numbers L03698-L03701 and L03703-L03704.
6. **TH3.W2TH-ID#:** Fifteen sequences from asymptomatic individuals from Thailand in 1992. Consensus, PCR-clones, cell-culture DNA and RNA. These sequences were provided by the WHO Global Programme on AIDS Vaccine Development Study. The complete set of C2V3 region WHO sequences can be found in the April supplement to the Human Retroviruses and AIDS 1993 database. Relevant papers are in press: de Wolf F, et al. AIDS Res. and Human Retroviruses in press (1994); Osmanov S, et al. AIDS Res. and Human Retroviruses in press (1994); Gao F, et al. AIDS Res. and Human Retroviruses, in press (1994). GenBank accession numbers U08810-U08811, U08825-U08836 and U08742-U08761.
7. **TH4.D-ID#:** These two sequences are are part of a set of sequences generated for the DAIDS variation program in the laboratory of Dr. Beatrice Hahn at the University of Alabama. They are clones from expanded culture stocks, and are excised from full gp160 sequences. The sequence ID numbers are abbreviated, for example D3TH966 can be read as DAIDS sequence (D), isolated in 1993 (2), Thai (TH), patient 301966 (966). GenBank accession numbers U08456 and U08457.
8. **TH.N764** This sequence is a E subtype sequence from Thailand (THP13). 12 of 13 sequences from Thai prisoners were of subtype B; N764 represents the only subtype E sequence identified in this set, from a prisoner infected in 1989. The sequences were obtained from PCR amplified PBMC DNA. Kalish ML, et al, AIDS Res. and Human Retroviruses Nov., in press (1994). GenBank accession number U15588.

The seventeen E subtype sequences not yet published, and for which the authors have not yet given permission for release, were provided by Dr. Xiao-Fang Yu of John Hopkins University, Dept. of Med. Microbiology, Baltimore, Maryland. The sequences from these individuals were consensus of clones derived from PCR amplified primary isolate DNA from Thai AIDS patients.

NOTE:

1. While the sequences in this subtype were distinct over this region of env from the other four env subtypes, in the gag gene it is not possible to make a distinction between this subtype and subtype A. What this means is that the isolates for which both gag and env are sequenced which cluster together as the "A" subtype in gag, are very distinctive in env and are broken down into two subtypes. env "A" and env "E". This holds true for the E subtypes sequences that originated in Thailand, as well as the E subtype isolate from the Central African Republic for which gag sequence was obtained. McCutchan FE, et al., AIDS Res. and Human Retroviruses 8:1887-1895 (1992); McCutchan FE, et al., AIDS 7:769-780 (1993); and Murphy E, et al., AIDS Res. and Human Retroviruses 9:997-1006 (1993).
2. The relative lack of diversity in the Thai sequences in this subtype relative to the other subtypes is likely to be a consequence of the short time span of the HIV-1 Subtype E epidemic in Thailand. McCutchan FE, et al., AIDS Res. and Human Retroviruses 8:1887-1895 (1992), and Ou C-Y et al., AIDS Res. and Human Retroviruses 8:1471-1472 (1992).

F Subtype

At this time there are viral sequences from 41 HIV-1 infected individuals associated with HIV-1 subtype F. The F subtype consensus sequence (F_CONSENSUS_94) generated from these sequences was based on the most common amino acid found in each position of an alignment. All of these sequences have been published.

1. **BR1.7944:** This sequence represents a single env F subtype sequence found among 22 Brazilian outpatients with varying degrees of disease progression. It was identified by Potts et al. as the single sequence which did not cluster with North American sequences in phylogenetic analysis. Consensus, PCR clones, peripheral blood PBMC DNA. Potts KE, et al., AIDS 7:1191-1197 (1993). GenBank accession number L19237.
2. **BR2.BZ-ID#:** Two sequences from Brazil of the F subtype. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994); Louwagie J, E Delwart, JI Mullins, FE McCutchan, G Eddy, and DS Burke Unpublished (1993). GenBank accession numbers L22085 and L22082.
3. **BR3.RJI03:** An F subtype sequence from Rio de Janeiro, Brazil. 26 additional B and a B-F recombinant were also observed in this set. Year of isolation for was 1993, from an individual of CDC clinical stage II. Morgado et al., AIDS Res. and Human Retroviruses 10:569-576 (1994). DNA was amplified directly PBMCs of HIV infected individual, and the PCR product was directly sequenced. GenBank accession number U00422.
4. **CM.CA-ID#:** These sequences are 3 of 17 sequences from a very diverse set of isolates from Yaounde and Douala, Cameroon. The sequences were derived from asymptomatic and symptomatic HIV infected individuals; specifically patients CA16 and CA20 were asymptomatic and patient CA4 was symptomatic. Virus was isolated by culture with donor PBMCs, and nested PCR amplified. A single clone was sequenced representing each HIV-1 isolate. The F subtype designation of these sequences is tentative. Although the F subtype sequences from Cameroon and Brazil consistently form a clade in phylogenetic analyses, the branch lengths between isolates from the two countries are typical of inter-subtype distances, and sequences from the two countries each form their own distinct clade within the F subtype (HIV database and Wouter Janssens, personal communication). Nkengasong JN, et al. AIDS 8:1405-12 (1994). GenBank accession numbers for the entire set of 17 sequences studied in this publication: X80438-X80454.
5. **RO1.ID#:** These nine sequences are from isolates from Romanian children, in different clinical stages. All isolates showed cytopathic properties in peripheral blood mononuclear cells. They are also known as RM(A-J). Dumitrescu O, ML Kalish, SC Kliks, CI Bandea, JA Levy. J Infect Dis 169: 281-8 (1994). GenBank accession numbers L19571-L19579.
6. **RO2.RM-ID#:** These 24 sequences are from isolates from Romanian children. Unpublished: Holm-Hansen C, G Grothues, B Rosok, S Rustad, R Pascu and B Asjo, University of Bergen, Norway. GenBank accession numbers X77964-X77987..

G Subtype

At this time there are viral sequences from 8 HIV-1 infected individuals associated with HIV-1 subtype G. The G subtype consensus sequence (G_CONSENSUS_94) generated from these 8 sequences was based on the most common amino acid found in each position of an alignment. 7 of these sequences have been published and/or have been made available for printing in the database by their authors.

1. **CF.4067:** This sequence was associated with the C subtype in first analysis of the C2V3 region (Murphy E, et al., AIDS Res. and Human Retroviruses 9:997-1006 (1993), but when a full gp120 sequence became avaliable from this isolate, and phylogenetic analysis was performed including some of the new subtype G sequences, it was more closely associated with G. The full length sequence was kindly provided prior to publication by Dr. MP Kieny of Transgene, Strasbourg Cedex, France. It is a part of a set of 14 HIV-1 gp120 isolates from Bangui, Central African Republic. The gp120 proteins have been expressed in a hybrid gp160 vaccinia virus expression system. Year of isolation and health status of individuals from which the virus was isolated were not provided. Viruses were isolated in the CAR by C Mathiot and B You (Pasteur Inst., Bangui), grown by F Barre-Sinoussi and A Deslandres (Pasteur Inst., Paris), and cloned and sequenced by D Schmitt and MP Kieny. GenBank accession numbers L11499 and L11500.
2. **GA.LBV21-7:** A sequence from Gabon from a set of HIV-1 viral isolates from Africa. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a full length env sequence. Janssens W, et al. AIDS Research and Human Retroviruses 10:877-878 (1994). GenBank accession number U09664.
3. **GA.VI525:** A sequence from Gabon from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al (in press, 1994), and Janssens W, et al. AIDS Research and Human Retroviruses 10:877-878 (1994). GenBank accession number L22953.
4. **NG1.ID#:** These four sequences represent G subtype sequences from Nigeria. Abimiku AG, et al., in press, AIDS Res. Hum. Retroviruses (1994). JP882 and JV832 were derived from AIDS patients, and G3 and G9 from healthy women. G9 was cultured on the T cell line CEM-SS, and the other three isolates were cocultured with uninfected donor PBMCs. DNA from viral cultures was PCR amplified, cloned and sequenced. GenBank accession numbers U13208-U13209, U13211 and U13213.

A G subtype sequence from Ghana was provided by Jaap Goudsmit's laboratory at the Dept. of Virology, Academic Medical Center, Amsterdam, The Netherlands. This sequence is not yet published (manuscript in preparation, 1994).

H Subtype

At this time there are viral sequences from 2 HIV-1 infected individuals associated with HIV-1 subtype H. The H subtype consensus sequence (H_CONSENSUS_94) generated from these 2 sequences was based on the most common amino acid found in each position of an alignment. Both of these sequences have been published and/or have been made available for printing in the database by their authors. Eight sequences that are too short for classification are closer to H than to other subtypes. The locus names (ID's) and sources of the sequences are:

1. **CM.CA13:** A sequence from Cameroon from a set of HIV-1 viral isolates from Africa used to define the prototype G and H env sequences. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a 900 base pair sequence. Janssens W, et al. AIDS Research and Human Retroviruses 10:877-878 (1994) and Nkengasong JN, et al., AIDS 8:1405-12 (1994). The H subtype association is not always clearly apparent using some sets of background sequences for comparison, and neighbor joining trees (HIV database, Wouter Janssens, personal communication), although parsimony trees confirmed the original association documented in Janssens W, et al. AIDS Research and Human Retroviruses 10:877-878 (1994). GenBank accession number U09667.
2. **ZR.VI557:** A sequence from Zaire from a set of HIV-1 viral isolates from Africa used to define the prototype G and H env sequences. This sequence was derived from a clone of PCR amplified DNA from cultured PBMCs. It represents a fragment of a 900 base pair sequence. Janssens W, et al. AIDS Research and Human Retroviruses 10:877-878 (1994). GenBank accession number U09666.

O Sequences

At this time there are viral sequences 3 HIV-1 infected individuals associated with HIV-1 subtype O that have been published and/or have been made available for printing in the database by their authors. The O subtype consensus sequence (O_CONSENSUS_94) generated from these 3 sequences was based on the most common amino acid found in each position of the alignment; when there was no consensus in a position the amino acid from ANT70 was used. These sequences represent a set of sequences that are extremely divergent relative to other HIV-1's. The subtypes A-H have been grouped together under the heading "M" for main. "O" sequences are as different from one another as are sequences from different "M" subtypes.

1. **CM.ANT70:** The complete viral genome has been sequenced from this viral isolate derived from a symptomatic Cameroonian, CDC stage III. R De Leys, et al., J. Virol. 64:1207-1216 (1990) and V Haesevelde J. Virol., 68:1586-1596 (1994). GenBank accession number L20587.
2. **CM.MVP5180:** The complete viral genome has been sequenced from an isolate derived from a Cameroonian woman, sampled in 1991; the donor died of AIDS in 1992. The viral isolate MVP-5180 was grown in several human T-cell lines and the monocytic U937 line. Gurtler L, et al. J. Virol., 68:1581-5 (1994). GenBank accession number L20571.
3. **FR.VAU:** This sequence was derived from an isolate from a French woman who died of AIDS in 1992. DNA was extracted from VAU infected PBMCs, PCR amplified, cloned, and gp160 env was sequenced. The viral isolate was highly cytopathic. P Charneau et al., Virology, in press (1994). GenBank accession number X80020.

Uncertain Classification

At this time there are viral sequences from 13 HIV-1 infected individuals that are not clearly associated with any of the HIV-1 genetic subtypes A through H. They either appeared distinct from the subtypes A-H in phylogenetic analysis, or else the subtype association was unclear, with different associations in different analyses. For some of the shorter gene fragments, subtype associations might have been established if more sequence information was available or if a different set of sequences was included in the background set used to define subtype associations. Some of these sequences may be representatives of subtypes as divergent as A-H, but only a single limited sample is yet available. Still others may represent recombinant genomes.

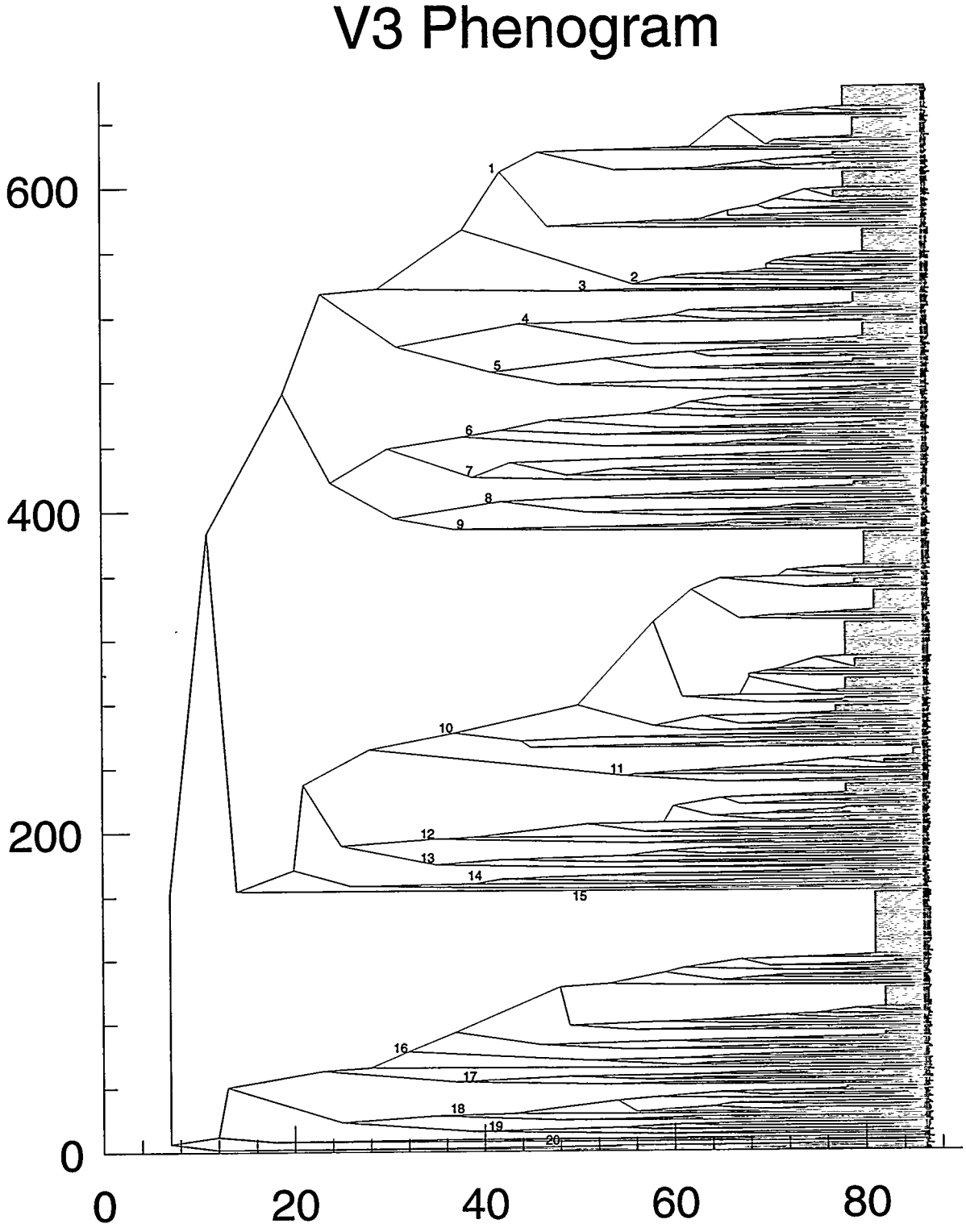
1. **BR3.RJI01** This sequence is B-F recombinant in the V3 region. DNA was amplified directly PBMCs of HIV infected individual, and the PCR product was directly sequenced. Sabino EC et al. J. Virol. 68:6340-6346 (1994). GenBank accession number U00420.
2. **CF.ID#:** These four sequences are from a set of sequences obtained from 27 symptomatic patients from the Central African Republic, from whom blood was drawn in 1990-1991. Consensus, PCR-clones, cell culture, DNA. Murphy E, et al., AIDS Res. and Human Retroviruses 9:997-1006 (1993). GenBank accession numbers L11482-L11483, L11497, L11508-L11510 and L11514-L11515.
3. **KE.K124:** A Kenyan sequence from a set of HIV-1 viral isolates from Africa. Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). This isolate is not clearly associated with D subtype, however Louwagie and colleagues found that it associated with the D subtype in env, and the A subtype in gag. Using parsimony analysis, we found that it was difficult to determine a clear association, and this observation was confirmed by Wouter Janssens (personal communication). GenBank accession number L22942.
4. **KE.KEN976** This is a single unclassified sequence from a set of patients who were part of a 1990-1992 cohort study of maternal risk factors in mother to child transmission, including 22 pregnant women and an infant from Kenya. The C2V3 region was sequenced. W Janssens et al., in press AIDS Res. Hum. Retroviruses (1994). GenBank accession number U12992.
5. **NL.A11:** This sequence is from a Dutch study of presumed HIV-1 donor-recipient pairs. This sequence is from a recipient at the time of seroconversion; the donor was a Zairean woman living in the Netherlands. The sequences from both donor and recipient were extremely similar, so only the recipient is shown here. This sequence is a consensus sequences of multiple clones from PCR amplified serum RNA. Wolfs TFW, G Zwart, M Bakker, and J Goudmsit. Virology 189:103-110 (1992). GenBank accession numbers M91849-M91856.
6. **ZM.ZAM184:** This Zambian sequence is an outlier, though in some phylogenetic analysis is appears most closely associated with the A subtype. In particular it is closely associated with A_CF.SAS (100/100 replicates in parsimony analysis of gp120). Health status of the individual from which the virus was cultured was unspecified, and the year of viral isolation was probably between 1989-1992. Viruses were cultured with donor PBMCs for 2 to 3 weeks. Full length env (gp160) was amplified, cloned and sequenced. Louwagie J, et al. in press (1994). GenBank accession number L22955.
7. **ZR.Z3:** This sequence is from the 1983 Zairean isolate Z-3 (non-infectious, possibly due to frame-shift). Willey RW, et al., Proc. Natl. Acad. Sci. USA 83:5038-5042 (1986). GenBank accession number K03347.

The three sequences which are not associated with any subtype and are not yet published, and for which the authors have not yet given permission for release, are from the following sets:

1. **ZR:** Two sequences from individuals from Zaire, provided by the LTCB, NCI, NIH, Bethesda, MD, USA (Dr. Marvin Reitz).
2. **GA:** A sequence provided by Dr. Wouter Janssens of the Prince Leopold Institute of Tropical Medicine, Antwerp, Belgium. It is a Gabonese isolate that is phylogenetically linked to F subtype sequences, but the relationship is distant.

Phenogram of the 14 amino acid tip of the V3 loop.

The immunogenic tip of the V3 loop has been the focus of a large number of serological studies. Here we have organized the 14 amino acid tip of the V3 sequences according to their amino acid similarities. The four amino acid tip of the loop (the GPGR motif) plus the 5 amino acids on either side were clustered using maximum linkage based on pairwise distance scores using the STR matrix (S. Henikoff and J. G. Henikoff, *Proteins: Structure, Function and Genetics* **17**: 49–61 (1993)). The resulting phenogram (B. T. M. Korber et al., *J. Virol.* **68**:6730–6744 (1994)) of all 660 non-embargoed sequences (660/707) is shown, with related sequences grouped into 20 clusters. The y-axis represents the number of sequences included in the phenogram, and the x-axis indicates the level of similarity between amino acids; the higher the score, the more similar the sequences. The twenty clusters were grouped so that the sequences within a cluster all are related by scores greater than 35. The alignment of these sequences corresponding to the phenogram is included, with a consensus from each cluster heading each group. The order of the sequences in the alignment corresponds to the order that the sequences appear in the phenogram, from top to bottom. There are two things worth noting in the alignment. First is the intermixing of amino acid sequences from different clades—often sequences from phylogenetically distinct subtypes have identical or nearly identical sequences in this region. Second is the diversity of the D subtype sequences. The two letter country codes can be used to follow geographic associations of similar sequences, or alternatively, the range of variation of a given subtype in a country of interest.


V3 Phenogram
600
400
200
0
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20

HIV-1 V3 Region

ALL_CONSENSUS	KSIHIGPGRAFYAT
CONSENSUS.1	---R----QT----
C_SO.1574	--VR----QT----
U_CF1.4081	--VR----QT----
C_MW1.6508	--VR----QT----
C_MW1.12229	--VR----QT----
C_MW1.12225	--VR----QT----
A_ZR1.6657	--VR----QT----
A_ZR1.6563	--VR----QT----
A_UG2.117	--VR----QT----
A_DJ.DJ264	--VR----QT----
A_DJ.DJ263	--VR----QT----
A_DJ.DJ258	--VR----QT----
A_CM1.CA2	--VR----QT----
A_CM1.CA19	--VR----QT----
A_CI2.CI45	--VR----QT----
A_CF1.4081	--VR----QT----
A_UG1.W2UG037	R-VR----QT----
A_UG2.78	R-VR----QT----
A_CM1.CA15	R-VR----QT----
A_CM1.CA17	--VR----QT---A
C_IN2.D808	--TR----QT----
C_MW2.D3MA960	---R----QT----
C_ZW.2647	---R----QT----
C_MW1.6518	---R----QT----
C_MW1.6510.sh	---R----QT----
C_MW1.12213	---R----QT----
C_IN2.D868	---R----QT----
C_IN2.D744	---R----QT----
C_IN2.D1024	---R----QT----
C_IN1.D760	---R----QT----
C_IN1.D757	---R----QT----
C_IN1.D1044	---R----QT----
C_CONSENSUS_94	---R----QT----
A_CI2.CI20	---R----QT----
C_ZM1.ZAM20	---R----QT-F--
C_DJ1.DJ259	E--R----QT----
C_UG.UG268	E--R----QT----
C_DJ1.DJ373	Q--R----QT----
A_KE.KEN985	---R----QT---G
C_SO.SM145	--VR----QT--TN
A_UG2.84	---G----QT---A
A_CI2.CI47	VRTG----QT----
A_UG4.UG273	T-VR----Q-----
A_ZR1.6663	T-VR----Q-----
A_UG2.82	T-VR----Q-----
A_CM1.CA21	T-VR----Q-----
A_KE.KEN977	T--R----Q-----
A_KE.KEN981	T--R----Q-----
A_RW.W2RW024	T-VR----QT----
A_RW.W2RW025	T-VR----QT----
A_KE.KEN88	T--R----QT----
A_UG4.UG275	T-VR----QS----
A_RW.W2RW008	T--R----QS-H--
A_KE.KEN979	T--C----QT---G
G_NG1.G3	---R----Q-----
U_CONSENSUS_94	---R----Q-----
C_ZM1.ZAM18	---R----Q-----
C_MW1.1227	---R----Q-----

ALL_CONSENSUS	KSIHIGPGRAFYAT
C_MW1.12215	---R----Q-----
C_MW1.12203	---R----Q-----
C_MW1.12199	---R----Q-----
C_BR.W2BR025	---R----Q-----
A_ZR1.6653	---R----Q-----
A_CF1.4055	---R----Q-----
A_CF1.4054	---R----Q-----
A_CF1.4033	---R----Q-----
A_RW.W2RW021	--VR----Q-----
A_UG1.W2UG031	--VR----Q-----
A_RW.SF1703	--VR----Q-----
A_CONSENSUS_94	--VR----Q-----
A_CI2.CI330	--VR----Q-----
A_CI2.CI3	--VR----Q-----
A_KE.KEN967	R--R----Q-----
A_RW.W2RW026	R--R----Q-----
A_CF1.4050	R-VR----Q-----
A_CM1.CA18	R-VR----Q-----
A_ZR1.6557.sh	Q-VR----Q-----
C_MW1.6512	Q-VR----Q-----
A_KE.K89	M--R----Q-----
A_ZR1.6655.sh	---R----QV----
F_CM.CA4	---R----QV----
C_MW1.12205	Q--R----QV----
C_MW1.12209	Q--R----Q--F--
U_KE.K124	---R----Q--F--
B_BR3.RJ626	---R----S-----
A_CM1.CA22	R-VR----Q-I---
A_CI2.CI21	--VN----Q-----
A_KE.KEN982	--AN----Q-----
A_KE.KEN965	T--R----Q---GR
E_CM.CA10	T-SR----Q---KI
CONSENSUS.2	T--T----QV--R-
E_TH3.W2TH019	T--T----QV--R-
E_TH3.W2TH022	T--T----QV--R-
E_TH3.W2TH011	T--T----QV--R-
E_TH3.W2TH009	T--T----QV--R-
E_TH3.W2TH006	T--T----QV--R-
E_TH2.TN244	T--T----QV--R-
E_TH2.TN242	T--T----QV--R-
E_TH2.TN241	T--T----QV--R-
E_TH2.TN239	T--T----QV--R-
E_TH1.TA8176	T--T----QV--R-
E_TH1.8673	T--T----QV--R-
E_TH1.8671	T--T----QV--R-
E_TH1.8663	T--T----QV--R-
E_TH1.8659	T--T----QV--R-
E_TH.N764	T--T----QV--R-
E_CONSENSUS_94	T--T----QV--R-
E_TH1.8657	T--T----QI--R-
E_TH3.W2TH018	T--T----QI--R-
E_TH3.W2TH020	T-LT----QV--R-
E_TH3.W2TH021	T-LT----QV--R-
E_TH1.8639	TR-T----QV--R-
E_TH3.W2TH015	TG-T----QV--R-
E_TH3.W2TH007	T--N----QV--R-
E_TH3.W2TH023	T--N----QV--R-

ALL_CONSENSUS	KSIHIGPGRAFYAT
E_TH3.W2TH001	T--N----QV--R-
E_TH1.TA10671	T--TM---QV--R-
E_TH3.W2TH003	T--TV---QV--R-
E_TH4.D3TH966	T-TT----QV--R-
E_TH1.TA7794	T--T----QV--K-
E_TH3.W2TH024	T--T----QVL-K-
E_TH1.TA8173	T--P----QV--R-
E_TH3.W2TH005	T--P----QV--R-
E_TH1.8683	T--P----QV--R-
E_TH2.TN235	T--P----Q---R-
E_TH1.TA7792	P--T----QV--R-
E_TH2.TN243	P--TX---QV--R-
CONSENSUS.3	---R----QTS---
A_CM1.CA7	R--R--S-QTS---
A_TZ.TAN15CON	--V-----QTS---
C_ZA.NOF	-R-RV---QTV---
CONSENSUS.4	---P----------
B_US1.HC44	---P----------
B_US2.D2US725	---P----------
B_US1.HC24	---P----------
B_NL4.H186_85	---P----------
B_NL2.Wolfsh1	---P----------
B_HT2.H6012	---P----------
B_HT2.H6010	---P----------
B_HT1.D1HA652	---P----------
B_NL4.I1025_89	R--P----------
A_RW.W2RW016	--VP----------
B_UK.V91	---P-------I--
B_US.MA	---PM---------
F_BR3.RJI03	---PL---------
B_TH1.8647	---PL-----W---
A_CI2.CI14	--VP----Q-----
A_KE.KEN978	--VP----Q-----
G_NG1.JV832	---P----Q-----
B_US1.HC09	Q--P----K-----
B_BR3.RJ636	---P-A--S-WF--
B_TH4.N758	---P--------T-
B_US4.ZhuPtA	---P--------T-
B_NL4.I7025_91	---P--------T-
B_NL4.I4008_86	---P--------T-
B_NL4.I1057_87	---P--------T-
B_NL4.H495_85	---P--------T-
B_NL4.H188_90	---P--------T-
B_NL4.H164_90	---P--------T-
B_NL4.H1091_90	---P--------T-
B_NL2.Wolfsh495	---P--------T-
B_US4.ZhuPtR	R--P--------T-
B_HT2.H6018	---P-------FT-
B_NL1.A7	R--P----K--FT-
B_NL4.H1112_90	R--P--L-S---T-
CONSENSUS.5	----L---Q---T-
G_CONSENSUS_94	---T----Q-----
H_ZR.VI557	---S----Q-----
C_CF1.15166	---SL---Q-----
G_NG1.G9	---TL---Q-----

ALL_CONSENSUS	KSIHIGPGRAFYAT
C_CF1.4067.CON	---GF---Q-----
C_CF1.4068.CON	---GF---Q-----
U_CF.4067	---SF---Q-----
G_NG1.JP882	---TFA--Q-----
F_RO2.RM53024	----L---Q---T-
F_RO2.RM5308	----L---Q---T-
F_RO2.RM53023	----L---Q---T-
F_RO1.14034	----L---Q---T-
F_RO2.RM53014	---XL---Q---T-
A_KE.KEN973	---R----Q---T-
U_KE.KEN976	---RF---Q---TS
U_ZM.ZAM184	R--RF---Q---TN
B_TH2.TB7787	----L-----W-T-
B_TH3.W2TH014	----L-----W-T-
B_TH1.8645	----L---Q-W-T-
B_TH1.8669	----L---Q-W-T-
B_TH1.8651	-G--L---Q-W-T-
B_TH4.N762	-G--L---Q-W-T-
B_TH1.8641	----L---Q-W---
B_TH1.8643	----L-Q-Q-W---
B_TH1.8653	---PL---Q-W-T-
B_TH3.W2TH026	---PL---Q-W-T-
B_TH1.8649	---PL---Q-W-T-
B_TH4.N763	-G-PL---Q-W-T-
B_TH1.8655	---PL---QVWFT-
CONSENSUS.6	-G------Q-----
B_NL4.H23_82	-G------K---T-
B_US.WM	-G------K---T-
B_NL4.I70_88	-G------K-----
A_NG.NI	-GV-----Q-----
A_UG2.118	-GV-----Q-----
A_KE.KEN983	-G------QS----
B_BR1.8625	--------S-----
B_BR2.W2BR018	--------S-----
B_NL4.I90_89	-G------S-----
A_CM1.CA1	-G------S-I---
B_HT2.H5996	-G------G-----
B_HT2.H6022	-G------G---T-
B_NL4.H434_85	--------G-----
B_BR1.10561	-G--M---ST----
B_NL1.A2	-G--L---GT----
A_CM1.CA11	TG------QT----
B_BR1.10581	-G-------T-F--
B_US1.HC19	-G-P--------T-
B_US1.HC40	-G-P--------T-
B_TH4.N752	-G-P--------T-
B_TH4.N753	-G-P----------
B_HT2.H6008	-G-T----------
B_BR2.W2BR004	-G-P----GS----
A_RW.W2RW020	-GVR----Q-----
C_IN1.D747	-GVR----QT----
F_GA.VI354	-G-R-----VI---
B_NL4.H187_90	-G-R-------I-A
A_UG2.111	T-V-----Q----R
A_UG2.115	--------Q----R
A_KE.KEN29	TG------Q----R
A_CI2.CI327	-GV-----Q----R

HIV-1 V3 Region

ALL_CONSENSUS	KSIHIGPGRAFYAT
A_GH.D687	-NV-----Q----R
A_ZR1.6559	QGV-----QV---R
A_CF1.1189	RIM------P---R
CONSENSUS.7	----M---K-----
B_US1.HC08	---PM-------T-
B_US2.D2US665	---PM-------T-
B_NL4.I4004_88	---PM-------T-
B_HT2.H5986	---PM---K---T-
B_US1.HC05	R--PM---K---T-
B_HT2.H6004	---PM---K-----
B_US2.D2US660	---PM---K-M---
B_US1.HC07	---TM---KV---G
B_US4.ZhuPtV	---TM---KV--V-
B_HT2.H5994	----M---K---T-
B_NL4.H135_90	----M---KT--T-
B_BR1.10591	-G--M---G---T-
B_US1.HC27	-G--M-------T-
B_CI.CI22	----M---S-I---
B_HT2.H6016	----M---S-----
A_CF1.11699	--V-M---------
B_TH4.N761	----M-Q-------
B_BE.SIMI84	-TL-M--K------
A_CM1.CA6	R---F---QTL---
A_ZR1.6569	RG--M---QIL---
A_CF1.4018	T-V-M---KT----
CONSENSUS.8	T-VR----QV--K-
E_CF1.4039	T-VR----QV--K-
E_CF1.4084	T-VR----QV--K-
E_CF1.4031	T-VR----QV--K-
E_CF1.4017	T-VR----QV--K-
E_TH4.D3TH975	T-VR----QV--R-
E_CF2.MBA	T-VR----QV--G-
E_CF1.1697	T-AR----QV--K-
E_CF2.ELO	T-AR----QV--K-
E_CF1.4013	T-VR-----V-HK-
E_CF2.4071TG2	T-VR-----V--K-
E_CF1.4002	I-AR-----V-HT-
E_CF1.4069	I-AR-----V-HK-
C_MW1.6506	--MR----QT----
C_SN.SE364	--MR----QT----
A_CF1.4023	R-MR----QT----
A_CI2.CI329	--LR----QT----
C_IN2.D766	--LR----QT----
C_MW1.12233	--MR----QP----
U_CF1.4087	R-MR-----T--TI
A_ZR1.6571.sh	---R----QV--TN
C_MW2.D3MA959	R--R----QV---N
U_ZR.Z3	Q--R----KV---K
CONSENSUS.9	-R-TM----VL-T-
B_NL1.A13	-RVTM----VW-T-
B_US.CDC42	-RVTL----VW-T-
B_US.BRVA	-R-TM----VY-T-
B_US1.HC13	-R-TM----VL-T-
B_US.BCSG3	-R-TT----VY-T-
B_NL4.BN132_84	-RMTL---KV--T-

ALL_CONSENSUS	KSIHIGPGRAFYAT
B_US.SF33	RR-TS---KVL-T-
B_HT.RF	---TK----VI---
G_GA.VI525	---KF-T--VL---
CONSENSUS.10	--------------
B_US2.D2US664	--------------
F_CM.CA20	--------------
B_US2.D2US656	--------------
B_US1.HC39	--------------
B_US1.HC34	--------------
B_US1.HC26	--------------
B_SE1.931	--------------
B_PR1.D2PR733	--------------
B_PR1.D2PR728	--------------
B_NL4.I3064_90	--------------
B_NL4.I3008_88	--------------
B_NL4.I1020_86	--------------
B_NL4.H594_85	--------------
B_NL4.H552_90	--------------
B_NL4.H17_82	--------------
B_NL4.H169_85	--------------
B_NL4.BN18_84	--------------
B_NL4.BN130_85	--------------
B_HT2.H6024	--------------
B_BR2.W2BR020	--------------
B_BR2.W2BR017	--------------
A_UG.1033	----L---------
B_US3.D2US711	----L---------
B_US.SC	R------------
B_US1.HC29	R-------------
B_HT2.H6020	R-------------
B_US2.D2US714	R---M---------
U_CF1.4056	T---L---------
B_US1.HC20	-----A--------
B_US1.HC41	-----A--------
B_US1.HC16	-----A--------
B_SE1.930	-----A--------
B_NL4.I5032_87	-----A--------
B_US1.HC30	R----A--------
A_CF1.4044	T----A--------
B_US1.HC46	-G------------
F_BR2.BZ163	-G------------
B_US1.HC42	-G------------
B_US1.HC18	-G------------
B_US1.HC01	-G------------
B_SE1.1032	-G------------
B_NL4.I3091_91	-G------------
B_NL4.I142_87	-G------------
B_NL4.H450_85	-G------------
B_NL4.H228_90	-G------------
B_NL3.NET4	-G------------
B_BR2.W2BR030	-G------------
B_BR1.8633	-G------------
A_GA.VI191	-G------------
B_UK.V74	RG------------
B_NL4.I117_90	IG------------
B_NL4.I3077_91	-X------------
B_US.RJS	RH------------

ALL_CONSENSUS	KSIHIGPGRAFYAT
B_IN1.20023	RR---------F--
B_IN1.30008	R----------F--
F_RO2.RM5306	----L---Q-----
F_RO2.RM5307	----L---Q-----
F_RO2.RM53035	----L---Q-----
F_RO2.RM53034	----L---Q-----
F_RO2.RM53032	----L---Q-----
F_RO2.RM53031	----L---Q-----
F_RO2.RM5303	----L---Q-----
F_RO2.RM53029	----L---Q-----
F_RO2.RM53027	----L---Q-----
F_RO2.RM53022	----L---Q-----
F_RO2.RM53018	----L---Q-----
F_RO2.RM53013	----L---Q-----
F_RO2.RM53011	----L---Q-----
F_RO2.RM53002	----L---Q-----
F_RO1.14046	----L---Q-----
F_RO1.14041	----L---Q-----
F_RO1.14036	----L---Q-----
F_RO1.14028	----L---Q-----
F_RO1.14027	----L---Q-----
F_RO1.14024	----L---Q-----
F_RO1.14020	----L---Q-----
F_RO1.14018	----L---Q-----
F_CONSENSUS_94	----L---Q-----
F_RO2.RM53040	--------Q-----
F_RO2.RM53043	--------Q-----
F_RO2.RM53037	--------Q-----
F_RO2.RM53015	--------Q-----
A_KE.KEN31	--------Q-----
A_KE.KEN112	--------Q-----
A_CF1.4010	--------Q-----
U_NL.A11	R---V---Q-----
A_KE.KEN980	X-------Q-----
B_BR1.8623	T-------Q-----
A_KE.KEN968	R-------Q----S
A_KE.KEN984	--------Q----S
A_UG2.124	--V-----Q-----
A_ZR1.6649	--V-----Q-----
A_UG2.116	--V-----Q-----
A_TZ.TAN81	--V-----Q-----
A_TZ.TAN142	--V-----Q-----
A_RW.W2RW009	--V-----Q-----
A_KE.KEN98	--V-----Q-----
A_KE.KEN970	--V-----Q-----
A_CI2.CI42	--V-----Q-----
A_TZ.TAN9CON	R-V-----Q-----
A_UG2.72	R-V-----Q-----
G_GA.LBV217	--------Q-L---
B_NL1.A1	--------K-----
B_NL4.H1_85	--------K-----
B_BR2.W2BR023	--------K-----
B_US1.HC32	R-------K-----
A_UG2.119	Q-V-----K-----
B_US2.D2US705	---N----------
B_US5.pt6bl	---N----------
B_NL4.H748_90	---N----------
B_HT2.H5998	---N----------

ALL_CONSENSUS	KSIHIGPGRAFYAT
B_HT2.H5990	---N----------
B_BR3.RJI01	---N----------
B_HT1.D1HA651	---N------W---
B_BR2.W2BR026	---T----------
B_US.SF162	---T----------
B_BR1.10593	---S----------
B_NL3.NET3	---S----------
B_NL4.I5037_89	---X----------
A_ZR.Z321	---S-------F--
B_SE1.2951	R--N----------
B_US1.HC28	R--T----------
B_BR2.W2BR014	R--I----------
B_NL3.NET2	R--G------I---
B_US.SF2	---Y-------HT-
B_US2.D2US704	----------HT-
F_BR2.BZ126	---YF------HTA
B_GA.OYI	NR-S-------HT-
B_US.ALA1	GR---------HT-
B_US1.HC37	----LA---G-H--
B_US2.D2US726	R----A-----H--
B_UK.V77	---------V-H--
B_US1.HC25	--------K--D--
B_JP.GUNA	---T--S----H-I
CONSENSUS.11	----M-W-------
B_BR2.W2BR021	----M-W-------
B_BR3.SPB1	----M-W-------
B_BR2.W2BR003	----M-W-------
B_BR1.8635	----M-W-------
B_BR1.7936	----M-W-------
B_BR1.7932	----M-W-------
B_BR2.W2BR019	R---M-W-------
B_BR3.RJ59	----L-W-------
B_BR3.RJ62	----L-W-------
B_BR2.W2BR024	----L-W-------
B_BR1.8621	----L-W-------
B_BR1.8629	----M-W--T----
B_BR2.W2BR028	----M-W--T----
B_BR1.7930	-G--M-W--T----
B_BR3.RJ12	------W---I---
B_BR3.RJ484	-G----W-------
B_BR3.RJ478	----M-W----HTN
B_BR3.RJ49	----M-W-----T-
B_BR3.SPB2	----M-W-----T-
B_BR3.RJ64	----L-W-----T-
B_BR3.RJ14	----V-W---L-T-
B_BR1.7934	----V-W--SLFT-
CONSENSUS.12	---N--------T-
B_NL4.I5038_89	---N--------T-
B_US2.D2US706	---N--------T-
B_NL4.I39_91	---N--------T-
B_NL4.I1035_87	---N--------T-
B_NL4.H29_82	---N--------T-
B_NL1.A3	---N--------T-
B_BR1.7942	---N--------T-
B_NL4.I3072_90	---N-------FT-
B_US.YU	---N------L-T-

HIV-1 V3 Region

ALL_CONSENSUS	KSIHIGPGRAFYAT
B_US1.HC11	R--NM-------T-
B_US1.HC21	R--NM-------T-
B_US.SBA	R--N--------T-
B_US2.D2US717	R--N--------T-
B_NL4.I138_89	---NT-------T-
B_SE1.2815	---T--------T-
B_US1.HC22	---T--------T-
B_NL4.I221_90	---T--------T-
B_BR1.8615	R--T--------T-
B_US.SBC	---S--------T-
B_US.JFL	---TL-------T-
B_BR1.10553	---Q--------T-
B_NL4.B63_84	---Q--------T-
F_BR.7944	---QL-------T-
B_NL4.I141_91	-G-Q--------T-
B_BR1.10575	--LSL-------T-
B_HT1.D2HA594	-R-S-----VW-T-
B_HT1.D2HA596	-R-S-----VW-T-
B_HT2.H13962	-R-S------W-T-
B_HT2.H13960	-R-S------S-T-
B_BR3.SPB4	-RKS--------T-
B_BR1.7940	-R-Y------V-T-
B_UK.V82	-R-Y------V-T-
B_US5.pt5bl	-R-A------V-T-
B_TH2.TB132	-X-XM----XX-T-
B_UK.CAM1	---A-----TV---
B_US1.HC38	-G-A-----TV---
B_US.NY5CG	-G-A-----TL--R
B_US.ACP1	-G-G-----TV-TA
CONSENSUS.13	RR-S-------V--
B_HT1.D2HA593	-R-S-------R--
B_HT2.H13958	-R-S-------R--
B_US.SBB	-R-S-------V-A
B_US1.HC06	-RLS-------V--
B_US.P896	RRLS---------R
B_US1.HC31	RR-S-------T-R
B_UK.V87	ER-S-------I-R
A_CF2.SAS	RRM--------I--
B_IN1.20016	RR-K-------V--
B_HT.WMJ22	R-LS-------XR-
B_HT2.H5992	R--T-------D-Y
B_US2.D2US724	R--SM------RTG
B_FR.LAI	IR-QR------VTI
B_MFA	IR-QR------VTI
B_IN1.30005	SRLQV------V-A
CONSENSUS.14	------L-----T-
B_BR1.7946	----L-L-----T-
B_NL1.A9	------L-----T-
B_US4.ZhuPtF	R---M-L-----T-
B_NL1.A4	RG----L--R--TR
A_CF1.4058	R-----S-----II
B_UK.V12	R-----S-----TI
B_BR1.10565	-G--L-F---L---
B_BR3.RJ483	-G--M-L-------
B_BR3.RJI02	----V-V---I---
F_RO2.RM53012	GIHI--V--P--R-

ALL_CONSENSUS	KSIHIGPGRAFYAT
CONSENSUS.15	-R-R--??------
B_DE.D31	-R-R--AR----TK
F_CM.CA16	RR-R--L--V----
B_BR3.RJ19	---QY-T-GGAFYA
CONSENSUS.16	----------T-
B_US3.D2US715	----------T-
B_US3.D2US716	----------T-
B_US3.D2US712	----------T-
B_US2.D2US662	----------T-
B_US1.HC45	----------T-
B_US1.HC35	----------T-
B_US1.HC33	----------T-
B_US.JRCSF	----------T-
B_US.BAL	----------T-
B_US.ADA	----------T-
B_SE1.1433	----------T-
B_PR1.D2PR732	----------T-
B_PR1.D2PR729	----------T-
B_NL4.K999_86	----------T-
B_NL4.I3048_89	----------T-
B_NL4.I3007_86	----------T-
B_NL4.I257_91	----------T-
B_NL4.I1164_90	----------T-
B_NL4.H724_81	----------T-
B_NL4.H557_82	----------T-
B_NL4.H466_82	----------T-
B_NL4.H457_85	----------T-
B_NL4.H36_82	----------T-
B_NL4.H35_80	----------T-
B_NL4.H339_82	----------T-
B_NL4.H293_85	----------T-
B_NL4.H153_82	----------T-
B_NL4.BN93_85	----------T-
B_NL4.BN90_85	----------T-
B_NL4.BN152_84	----------T-
B_NL4.BN142_84	----------T-
B_NL4.BA206_84	----------T-
B_NL4.BA1_84	----------T-
B_NL3.NET1	----------T-
B_NL1.A5	----------T-
B_HT2.H6014	----------T-
B_HT2.H6006	----------T-
B_HT2.H6002	----------T-
B_CONSENSUS_94	----------T-
B_BR3.RJ54	----------T-
B_BR3.RJ379	----------T-
B_US2.D2US727	--V---------T-
D_UG3.109	Q-V---------T-
B_NL4.I1083_87	R----------T-
B_US1.HC43	R----------T-
B_NL3.NET6	R----------T-
B_US1.HC12	R---------W-T-
A_CI2.CI326	R-W---------T-
B_JP.JH32	RR----------T-
B_US.MN	-R----------T-

ALL_CONSENSUS	KSIHIGPGRAFYAT
A_UG.UG06	RR-------S--TS
B_HT1.D2HA590	----------TG
B_HT2.H13954	----------TG
B_US.JM	-----A------T-
B_NL1.A10	--------S---T-
B_US1.HC36	--------S---T-
B_HT2.H5988	---------T-FT-
B_HT2.H6000	---------S--T-
B_BR3.RJ623	R---L---G---T-
B_US1.HC10	R-V-----S-L-T-
B_US2.D2US657	-G----------T-
B_US4.ZhuPtL	-G----------T-
B_TH4.N760	-G----------T-
B_TH4.N759	-G----------T-
B_TH4.N757	-G----------T-
B_TH4.N756	-G----------T-
B_TH4.N755	-G----------T-
B_TH4.N754	-G----------T-
B_SE1.1866	-G----------T-
B_NL4.I5020_89	-G----------T-
B_NL4.I3084_90	-G----------T-
B_NL4.BN29_85	-G----------T-
B_NL4.BA65_85	-G----------T-
B_CM.CA5	-G----------T-
B_NL4.I33_90	RG----------T-
B_US1.HC23	RG----------T-
B_NL4.H43_90	RG----------T-
D_UG1.W2UG005	-G--------Y-T-
B_NL3.NET5	RG--------V-T-
B_NL4.I3057_91	RG--------V-T-
B_DE.HAN	-G--------V-T-
B_US.BWB11A	-G-NV-----L-T-
D_ZR.MAL	RG--F---Q-L-T-
D_ZR1.6651.sh	-G------Q-L-TS
D_ZR1.6565.sh	--------Q-I-T-
F_RO2.RM53021	--------Q-X-T-
B_NL4.H490_85	----L---K-V-T-
D_UG3.120	--------Q-LFTI
D_TZ1.TAN3	QGT-------Y-T-
D_TZ1.TAN6	QGT-------Y-T-
D_TZ1.TAN2	QGT-------Y-T-
D_KE1.KEN971	QGT-------Y-T-
D_UG3.110	QGT-------YWT-
D_TZ1.TAN7	Q-T-F-----Y-T-
D_TZ1.TAN1	QGA-------Y---
D_UG3.114	QG--------Y-TD
D_CI.CI13	QGT-----Q-L-T-
D_KE1.KEN986	QGT-----QTLFT-
D_UG1.W2UG035	EGT-------LFT-
D_UG3.74	QGT-M-----L-TI
D_UG3.121	Q-T-----Q-L-T-
D_UG3.79	Q-T-----Q-L-T-
D_ZR1.6555	Q-T-L---Q-L-T-
D_UG3.122	Q-V-L---Q-L-T-
D_UG3.71	Q-------Q-L-T-
D_UG1.W2UG040	Q-T-----Q-I-TL
D_TZ1.TAN11	Q-TR----Q-L-TN
D_TZ1.TAN12	Q-TR----Q-LFTS

ALL_CONSENSUS	KSIHIGPGRAFYAT
D_KE1.KEN966	Q-TR----QTLFT-
D_UG.U44342	Q-TQ----Q-LFTK
B_HT1.D2HA599	H-G---G--TLFT-
B_HT2.H13968	H-G---G--TLFT-
CONSENSUS.17	QRT---S-Q-?-T-
D_CONSENSUS_94	QRT-----Q-L-T-
D_UG2.G1	QRT---S-Q-L-T-
U_CF1.4040	QRT---S-Q-IFT-
D_UG2.2999	QRT---T-Q-LHT-
D_UG1.W2UG059	QRT---T-Q-Y-TK
D_UG1.W2UG070	RRT---S-Q-YSTK
D_UG2.4133	IRT---S-Q-Y-R-
A_CF2.GAN	-RW---S-Q----I
A_UG1.W2UG029	RR----R-Q-----
A_UG.U455	RRYS--S-Q---V-
CONSENSUS.18	QRTP--L-Q-L-T-
D_UG2.1665	QRTP--L-Q-L-T-
D_UG2.31	QRTP--L-Q-L-T-
D_UG1.W2UG024	QRTP--L-Q-L-T-
D_ZR.ELI	QRTP--L-QSL-T-
D_UG2.5055	Q-TP--L-Q-L-T-
D_ZR.JY1	Q-TP--L-Q-L-T-
D_CF.402019	QGTP--L-Q-L-T-
D_UG1.W2UG046	RRTP--L-Q-Y-T-
D_UG3.83	RRTP--L-Q-L-T-
D_UG3.70	QRTP--R-Q-LFT-
D_UG5.UG266	QRTP--R-Q-LFT-
D_UG1.W2UG038	QRTP--Q-QVL-T-
D_UG2.G2	QRTP--Q-Q-L-T-
D_TZ1.TAN5	QRTP--S-Q-L-T-
D_UG5.UG274	QRTP--T-Q-L-T-
D_ZR1.6659.sh	QRTP----Q---T-
D_SN.SE365	QRTP--L-QVLHT-
D_UG1.W2UG021	YRTP--V---S-T-
D_TZ1.TAN13	QRTP--L-Q-LVTS
D_UG.UG23	HRTP--L-Q-LITN
D_UG2.5059	RTTP--L-Q-LITS
D_UG1.W2UG053	RGTP--L-Q-YLT-
CONSENSUS.19	QRTS--Q-Q-L-T-
D_UG1.W2UG001	QRTS--Q-Q-L-T-
D_UG2.4132	QRTS--Q---L-T-
D_TZ1.TAN4	QKTS--R-Q-L-T-
D_UG2.1685	QRTS--S-Q-L-T-
D_UG2.462	RRTS--Q-Q-Y-T-
D_US.AMK	LKTS--Q-Q-L-T-
D_UG1.W2UG065	QRTS--L-Q-L-TN
D_ZR.Z2Z6	QRTS--L-Q-L-T-
D_ZR.NDK	QRTS--LRQSL-TI
H_CM.CA13	R-MR--I--GQTFH
H_CONSENSUS_94	R-MR--I--GQTFH
D_UG2.653	SIRR-----WQTYY
A_CF1.11423	-M-PT---QGQVIY

HIV-1 V3 Region

ALL_CONSENSUS	KSIHIGPGRAFYAT
CONSENSUS.20	QE-R---MAWYSMG
O_ANT70	QEMR---MAWYSMG
O_CONSENSUS_94	QE-R---MAWYSMG
O_VAU	QK-MA--MAWYSMA
O_MVP5180	QD-YT--M-WRSM-

Mutations in HIV-1 Reverse Transcriptase and Protease Associated with Drug Resistance

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INTRODUCTION

The knowledge of HIV-1 drug resistance continues to increase at an exponential rate. This is particularly true for resistance to HIV-1 protease inhibitors, for which the first resistant variants were described less than two years ago (Otto et al., *PNAS* **90**:7453–7457, 1993). Now resistance to virtually all classes of protease inhibitors has been documented. To keep our readership informed of newly described mutations, we have updated the tables below, which first appeared in IAVN in May 1994 (Vol 2; No 5). Following the tables is a list of abbreviations used. We hope that the tables' revised content will be useful to virologists and clinicians active in the field. We urge all investigators to provide additions or amendments of the table to any of the authors. Data formatted as in the table with an appropriate reference (abstract, manuscripts or paper) would be welcomed.

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NUCLEOSIDE RT INHIBITORS

Compound	Amino Acid Change	Codon Change	In Vitro	In Vivo	Comments	Confirmed by Site-directed Mutagenesis	Refs.
AZT	M41L	ATG to TTG	n.d	Yes	M41L: 4-fold resistance; M41L/T215Y:	Yes	[1, 2, 3]
	D67N	GAC to AAC	Yes	Yes	60- to 70-fold; K67N/K70R/T215Y/	Yes	
	K70R	AAA to AGA	Yes	Yes	K219Q: 120-fold; M41L/K67N/	Yes	
	T215Y	ACC to TAC	Yes	Yes	K70R/T215Y: 180-fold. Effect of	Yes	
	T215F	ACC to TTC	n.d.	Yes	T215Y is reversed by a ddI resis-	Yes	
	K219Q	AAA to CAA	n.d.	Yes	tance mutation (L74V), NNRTI	Yes	
	K219E	AAA to GAA	n.d.	No	mutations (L100I; Y181C) or a (-)-FTC/3TC mutation (M184V)	Yes	
ddI	L74V	TTA to GTA	No	Yes	5- to 10-fold resistance; cross-resistance to ddC; can reverse the effect of the T215Y AZT resistance mutation	Yes	[4]
	V75T	GTA to ACA	Yes	No	observed with D4T selection; cross-resistance to ddI/ddC	Yes	[5]
	M184V	ATG to GTG	Yes	Yes	3- to 4-fold resistance; cross-resistance to ddC	Yes	[6]
ddC	K65R	AAA to AGA	Yes	Yes	4- to 10-fold resistance; observed in pts on receving ddI or ddC therapy	Yes	[7, 8]
	T69D	ACT to GAT	No	Yes	5-fold resistance	Yes	[9]
	L74V	TTA to GTA			observed with ddI therapy	Yes	[2]
	V75T	GTA to ACA			observed with D4T selection in vitro	Yes	[4]
	M184V	ATG to GTG			observed with ddI, 3TC therapy	Yes	[6]
	Y215C	TTC to TGC	No	Yes	4-fold resistance; arises on background of T215YAZT resistance mutation	Yes	[10]
D4T	I50T	ATT to ACT	Yes	?	30-fold resistance	Yes	[11]
	V75T	GTA to ACA	Yes	Yes	7-fold resistance; cross-resistance to ddI, ddC, d4C, and (-)-FTC	Yes	[5]
3TC or (-)-FTC	M184V	ATG to GTG or GTA	Yes	Yes	>100-fold resistance; M184V and M184I can suppress effects of	Yes	[12–14]
	M184I	ATG to ATA	Yes	Yes	AZT resistance mutations	Yes	[12–14]
Foscarnet	W88S	TGG to TCG	No	Yes	4-fold resistance	Yes	[15]
	E89G	GAA to GGA	Yes	No	isolated by screening RT clones for ddGTP resistance; 14-fold viral resistance	Yes	[16]
	E89K	GAA to GGA	Yes	No	E89K and L92I cause increased		[17]
	L92I	TTA to ATA	Yes	No	susceptibility to AZT		[17]
	S156A	TCA to GCA	Yes	No	and HIV-1 specific RTI		[17]
	Q161L	CAA to CTA	Yes	Yes	10-fold resistance	Yes	[15]
	H208Y	CAT to TAT	Yes	Yes	2-fold resistance	Yes	[15]
					Q161L + H208Y cause increased susceptibiltity to AZT (100-fold), nevirapine (20-fold) and TIBO R82150 (30-fold)		
1592U89	K65R	AAA to AGA	Yes	No	3-fold resistance	Yes	[18]
	L74V	TTA to GTA	Yes	No	4-fold resistance	Yes	
	Y115F	TAT to TTT	Yes	No	2-fold resistance	Yes	
	M184V	ATG to GTG	Yes	No	3-fold resistance	Yes	
					K65R/M184V: 8-fold resistance		
					L74V/M184V: 9-fold resistance		
					L74V/Y115F/M184V: 11-fold resistance		

HIV-1-SPECIFIC RT INHIBITORS

Compound	Amino Acid Change	Codon Change	In Vitro	In Vivo	Comments	Confirmed by Site-directed Mutagenesis	Ref.
Nevirapine	A98G	GCA to GGA	No	Yes		Yes	[19]
	L100I	TTA to ATA	No	Yes		Yes	[20]
	K103N	AAA to AAC	No	Yes		Yes	[20]
	V106A	GTA to GCA	Yes	Yes	~100-fold resistance; no effect on AZT resistance	Yes	[19–22]
	V108I	GTA to ATA	No	Yes		Yes	[20]
	Y181C	TAT to TGT	Yes	Yes	>100-fold resistance; cross-resistance to other NNRTI; can suppress effects of AZT resistance mutations	Yes	[19, 23–25]
	Y181I	TGT to ATT	No	Yes	High-level resistance		[26]
	Y188C	TAT to TGT	No	Yes		Yes	[20]
	G190A	GGA to GCA	No	Yes		Yes	[19]
TIBO R82150	L100I	TTA to ATA	Yes	?	>100-fold resistance; can reverse effects of AZT resistance mutations	Yes	[27–29]
TIBO R82913	L100I	TTA to ATA	Yes	?		Yes	[21]
	K103N	AAA to AAC	Yes	?	>100-fold resistance	Yes	[22]
	V106A	GTA to GCA	Yes	?	~100-fold resistance	Yes	[21]
	E138K	GAG to AAG	Yes	?			[28]
	Y181C	TAT to TGT	Yes	?	>100-fold resistance	Yes	[21]
	Y188H	TAT to CAT	Yes	?		Yes	[28]
	Y188L	TAT to TTA	No	Yes		Yes	[30]
L'697,593	K103N	AAA to AAC	Yes	?	20-fold resistance	Yes	[23]
	Y181C	TAT to TGT	Yes	?	>100-fold resistance	Yes	[23]
L'697,661	A98G	GCA to GGA	No	Yes	8-fold resistance	Yes	[31]
	L100I	TTA to ATA	Yes	No	2-fold resistance	Yes	[31]
	K101E	AAA to GAA	No	Yes	8-fold resistance	Yes	[31]
	K103N	AAA to AAC	Yes	Yes	8-fold resistance	Yes	[31]
	K103Q	AAA to CAA	No	Yes	8-fold resistance	Yes	[32]
	V108I	GTA to GCA	Yes	Yes	4-fold resistance	Yes	[31]
	V179D	GTT to GAT	No	Yes	4-fold resistance	Yes	[31]
	V179E	GTT to GAG	No	Yes	8-fold resistance	Yes	[31]
	Y181C	TAT to TGT	Yes	Yes	>30-fold resistance	Yes	[31]
BHAP U-90152 (delaviridine)	P236L	CCT to CTT	Yes	?	P236L sensitizes RT ~10-fold to Nevirapine, TIBO R82193, and L'697,661	Yes	[33]
BHAP U-87201 (ateviridine)	K101E	AAA to GAA	No	Yes	K103N and Y181C observed with U-87201 monotherapy; K101E, Y188H, E233Y and K238T observed with U87201/AZT combination therapy		[34]
	K103N	AAA to AAC	No	Yes			
	Y181C	TAT to TGT	No	Yes			[34]
	Y188H	TAT to CAT	No	Yes			[34]
	E233V	GAA to GTA	No	Yes			[34]
	P236L	CCT to CTT	Yes	No		Yes	[33]
	K238T	AAA to ACA	No	Yes			[34]
BHAP U 88204	L100I	TTA to ATA	Yes	?			[22, 35]
	V106A	GTA to GCA	Yes	?		Yes	[35]
	Y181C	TAT to TGT	Yes	?		Yes	[35]
	Y181I	TGT to ATT	Yes	Yes	High-level resistance to BHAP, Nevirapine, and TIBO. Observed in one Nevirapine-treated patient		[36]
HEPT	Y188C	TAT to TGT	Yes	?			[37]
E-EBU	Y181C	TAT to TGT	Yes	?			[37]
E-EBU-dM	Y106A	GTA to GCA	Yes	?			[37]

HIV-1-SPECIFIC RT INHIBITORS (cont.)

Compound	Amino Acid Change	Codon Change	In Vitro	In Vivo	Comments	Confirmed by Site-directed Mutagenesis	Ref.
E-EPU and	Y181C	TAT to TGT	Yes	?	Y188C is the predominant mutation	Yes	[38]
E-EPSeU	Y188C	TAT to TGT	Yes	?	for E-EPSeU; Y188C confers greater resistance to E-EPSeU/E-EPU than Y181C	Yes	[38]
α-APA R18893	Y181C	TAT to TGT	Yes	?		Yes	[39]
S-2720	G190E	GGA to GAA	Yes	?	Mutation decreases RT activity and viral replication competency	Yes	[40]
TSAO	E138K	GAG to AAG	Yes	?	>100-fold resistance	Yes	[41, 42]
BM+51.0836	Y181C	TAT to TGT	Yes	?		Yes	[43]

PROTEASE INHIBITORS

Compound	Amino Acid Change	Codon Change	In Vitro	In Vivo	Comments	Confirmed by Site-directed Mutagenesis	Refs.
A-77003	R8Q	CGA to CAA	Yes	?	10-fold viral resistance	Yes	[44, 45]
	R8K	CGA to AAA	Yes	?	10-fold viral resistance	Yes	[44]
	V32I	GTA to ATA	Yes	?	7-fold enzyme resistance	Yes	[45]
	M46I	ATG to ATA	Yes	?	No affect on susceptibility but restores replication kinetics of R8Q mutant	Yes	[44]
	M46L	ATG to TTG	Yes	?	2–3-fold enzyme resistance	Yes	[45]
	M46F	ATG to TTC	Yes	?	4-fold enzymee resistance	Yes	[45]
	G48V	GGG to GTG	Yes	?	R8K/M46I/G48V: 20-fold viral resistance		[46]
	V82I	GTC to ATC	Yes	?	no resistance alone but V32I and V82I are synergistic mutations yielding 20-fold enzyme resistance	Yes	[45]
	V82A	GTC to GCC	Yes	?	rare; seen with M46F		[47]
	I82T	ATC to ACC	Yes	?	G48V/I82Tcombined produce 100-fold viral resistance		[47]
A75925	V32I	GTA to ATA	Yes	?	40-fold viral resistance		[48]
ABT-538	V82F	GTC to TTC	Yes	?	V82F/I84V: 8- to 10-fold viral resistance	Yes	[49]
	I84V	ATA to GTA	Yes	?	M46I/L63P/A71V/V82F/I84V: 27-fold resistance	Yes	
BILA 1906 BS	V32I	GTA to ATA	Yes	?			[50]
	M46L	ATG to TTG	Yes	?	V32I/A71V: 3-fold viral resistance		
	A71V	GCT to GTT	Yes	?	V32I/A71V/M46I/I84V: 5-fold		
	I84V	ATA to GTA	Yes		V32I/A71V/M46I/I84V: 1000-fold (mutation also detected in p6/p7 cleavage site)		
BMS 186,318	A71T	GCT to ACT	Yes	?	A71T/V82A: 15-fold viral resistance;	Yes	[51]
	V82A		Yes	?	4-fold cross resistance to A77003	Yes	
L-735, 524	L10R	CTC? to CGC?	No	Yes	M46I/L63P/V82T: 4-fold viral resistance	Yes	[52]
	M46I	ATG to ATA	No	Yes	L10R/M46I/L63P/V82T: 4-fold viral resistance		
	L63P	CTC? to CCC?	No	Yes	L10R/M46I/L63P/V82T/I84V: 8-fold viral		
	V82T	GTC to ACC	No	Yes	resistance; cross resistance to XM-323 (15-		
	I84V	ATA to CTA	No	Yes	fold], A-80987 (4-fold), Ro-31-8959 (8-fold), VX-478 (8-fold), SC-52151 (8-fold)		
	V32I	GTA to ATA	Yes	?	V32I/M46L/V82A: 3-fold viral resistance		[46]
	M46I	ATG to ATA	Yes	?	V32I/M46L/A71V/V82A: 14-fold viral resistance		
	A71V	GCT to GTT	Yes	?			
	V82A	GTC to GCC	Yes	?			
P9941	V82A	GTC to GCC	Yes	?	6–8-fold resistance	Yes	[53]
Ro 31-8959	G48V	GGG to GTG	Yes	Yes		Yes	[54]
	I84V	ATA to GTA	Yes	?			[46]
	L90M	TTG to ATG	Yes	Yes	G48V/L90M combined yield >100-fold enzyme resistance, but double mutant rare in vivo; L90M most common in vivo		[54]
					G48V/I84V/L90M: 90-fold viral resistance		[46]
RPI-312	I84V	ATA to GTA	Yes	?	5-fold viral resistance	Yes	[55]
SC-52151	L24V	TTA to GTA	Yes	?	N88D: 10-fold viral resistance		[56, 57]
	G48V	GGG to GTG	Yes	?	G48V/V82A: 15-fold viral resistance		
	A71V	GCT to GTT	Yes	?	G48V/A71V/V75I/P81T: 20- to 30-fold		
	V75I	GTA to ATA	Yes	?	A71V/V75I/P81T: 30-fold viral resistance		
	P81T	CCT to ACT	Yes	?	L24V/G48V/A71V/V75I/P81T: 1000-fold		

PROTEASE INHIBITORS (cont.)

Compound	Amino Acid Change	Codon Change	In Vitro	In Vivo	Comments	Confirmed by Site-directed Mutagenesis	Refs.
	V82A	GTC to GCC	Yes	?	viral resistance; some cross resistance		
	N88D	AAT to GAT	Yes	?	to SC55389a and Ro31-8959, but not to L-735,524		
SC-55389	L10F	CTC to CGC	Yes	?	N88S seen alone with L10F;		[56, 57]
	N88S	AAT to AGT	Yes	?	10- to 20-fold viral resistance		
VB 11,328	L10F	CTC to GGC	Yes	?	L10F/I84V: 10-fold viral resistance		[58]
	M46I	ATG to ATA	Yes	?	I50V/M46I/I47V: 20-fold viral resiestance	Yes	[46, 58]
	I47V	ATA to CTA	Yes	?			
	I50V	ATT to GTT	Yes	?	3-fold viral resistance	Yes	[46]
	I84V	ATA to GTA	Yes	?			
XM323	L10F	CTC to CGC			L10F/V82A: 2.0-fold viral resistance;	Yes	[59]
	K45I	AAA to ATA			L10F/K45I/I84V: 50-fold		[46]
	G48V	GGG to GTG	Yes	?		Yes	[59]
	V82A	GTC to GCC	Yes	?	V82A/M46L: 7-fold resistance V82A/M46L/L97V: 11-fold resistance	Yes	[59]
	V82I	GTC to ATC	Yes	?	<2-fold viral resistance	Yes	[59]
	V82F	GTC to TTC	Yes	?	see below	Yes	[59]
	I84V	ATA to GTA	Yes	?	12-fold resistance alone; V82F/I84V: 92-fold resistance; cross resistant to P9941, but not A77003 or Ro 31-8959	Yes	[46, 59]
	L97V	TTA to GTA	Yes	?	no resistance alone; V82A/L97V: 3.0 fold resistance	Yes	[59]

ABBREVIATIONS

n.d.: not determined ?: unknown

Amino acids: A, alanine; C, cysteine; D, aspartate; E, glutamate; F, phenyalanine; G, glycine, H, histidine; I, isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; Y, tyrosine.

1592U89:	(1S, 4R)-4-[2-amino-6-cyclopropylamino)-9H-purin-9-yl]-2-cyclopentene-1-methanol succinate
3TC:	(-)-β-L-2′,3′-dideoxy-3′-thiacytidine
α-APA 18893:	alpha-nitroanilino-phenylacetamide
A-77003:	C2 symmetry-based protease inhibitor (Abbott)
A-75925:	C2 symmetry-based protease inhibitor (Abbott)
ABT-538:	C2 symmetry-based protease inhibitor (Abbott)
BM+51.0836:	thiazolo-isoindolinone derivative
AzddU:	3′-azido-2′,3′-dideoxyuridine
AZT-p-DDI:	3′-azido-3′-deoxythymidilyl-(5′,5′)-2,3,-dideoxy-5′-inosinic acid
AZT:	3′-azido-2′,3′-dideoxythymidine
BHAP:	bisheteroarylpiperazine
BILA 1906:	protease inhibitor (Boehringer-Ingelheim)
BMS 186,318	aminodiol derivative HIV-1 protease inhibitor (Bristol-Myer-Squibb)
d4C:	2′,3′-didehydro, 2′,3′-deoxycytidine
d4T:	2′,3′-didehydro,3′-deoxythymidine
ddC:	2′,3′-dideoxycytidine
ddI	2′,3′-dideoxyinosine
EBU-dM:	5-ethyl-1-thioxymethyl-6-(3,5-dimethylbenzyl)-uracil
E-EBU:	5-ethyl-1-ethoxymethyl-6-benzyluracil
E-EPSeU:	1-(ethoxy-methyl)-(6-phenyl-selenyl)-5-ethyl-uracil
E-EPU:	1-(ethoxy-methyl)-(6-phenyl-thio)-5-ethyluracil
(-)-FTC:	(-)-β-L-2′,3′-dideoxy-5-fluoro-3′-thiacytidine
HEPT:	1-[(2-hydroxyethoxy)methyl]6-(phenylthio)-thymine
L′697,593:	5-ethyl-6-methyl-3-(2-phthalimido-ethyl)pyridin-2(1H)-one
L′735,524:	hyrdoxyaminopentane amide HIV-1 protease inhibitor (Merck)
L′697,661:	3-{[(-4,7-dichloro-1,3-benzoxazol-2-yl)methyl]amino}-5-ethyl-6-methylpyridin-2(1H)-one
L-FDDC:	(-)-β-L-5-fluoro-2′,3′-dideoxycytidine
L-FDDC:	(-)-β-L-5-fluoro-dioxolane cytosine
Nevirapine:	11-cyclopropyl-5,11-dihydro-4-methyl-6H-dipyridol[3,2-b;2′,3′-e] diazepin-6-one
NNRTI:	nonnucleoside reverse transcriptase inhibitor
P9941:	protease inhibitor (Dupont Merck); [2-pyridylacetyl-IIePheAIa-Ψ(CHOH)]2
PFA:	phosphonoformate (foscarnet)
PMEA:	9-(2-phosphonyl-methoxyethyl)adenine
Ro 31-8959:	hydroxyethylamine derivative HIV-1 protease inhibitor (Roche)
RPI-312:	peptidly protease inhibitor; 1-[(3s)-3-(N-alpha-benzyloxycarbonyl)-L-asparginyl) amino-2-hydroxy-4-phenylbutyryl]-N-tert-butyl-L-proline amide
S-2720:	6-chloro-3,3-dimethyl-4-(isopropenyloxycarbonyl)-3,4,-dihydroquinoxalin-2(1H)thione
SC-52151	hydroxyethylurea isostere protease inhibitor (Searle)
SC-55389A	hydroxyethylurea isostere protease inhibitor (Searle)
TIBO R82150:	(+)-(5S)-4,5,6,7,-tetrahydro-5-methyl-6-(3-methyl-2-butenyl)imidazo[4,5,1-jk][1,4]-benzo-diazepin-2(1H)-thione
TIBO 82913:	(+)-(5S)-4,5,6,7,-tetrahydro-9-chloro-5-methyl-6-(3-methyl-2-butenyl)imidazo[4,5,1jk]-[1,4]benzodiazepin-2(1H)-thione
TSAO-m3T:	[2′,5′-bis-O-(tert-butyldimethylsilyl)-3′-spiro-5′-(4′-amino-1′,2′-oxathiole-2′,2′-dioxide)]-b-d-pentofuranosyl-N3-methyl-thymine
U90152:	1-[3-[(1-methylethyl)-amino]-2-pyridinyl]-4-[[5-[(methylsulfonyl)-amino]-lH-indol-2yl] carbonyl]-piperazine
VB 11,382:	hydroxyethylsulphonamide protease inhibitor (Vertex)
VX-478:	hydroxyethyl-sulphonamide protease inhibitor (Vertex)
XM 323:	cyclic urea protease inhibitor (Dupont Merck)

Table 2. Combinations of HIV-1 RTase mutations that confer multi-drug resistance

RTase genotype	AZT	ddI	Nevirapine	3TC
Single drug resistance				
M41L/T215Y	R	S	S	S
L74V	S	R	Sensitive	S
Y181C or V106A	S	S	Resistant	S
Double drug resistance				
M41L/T215Y/L74V	R	R	S	S
M41L/T215Y/V106A	R	S	R	S
L74V/Y181C	S	R	R	S
M184V	S	R	S	R
Triple drug resistance				
M41L/T215Y/L74V/V106A	R	R	R	S
M41L/T215Y/L74V/V106A/M184V	S	R	R	R

From Larder J Gen Virol 75, 951-957 (1994)

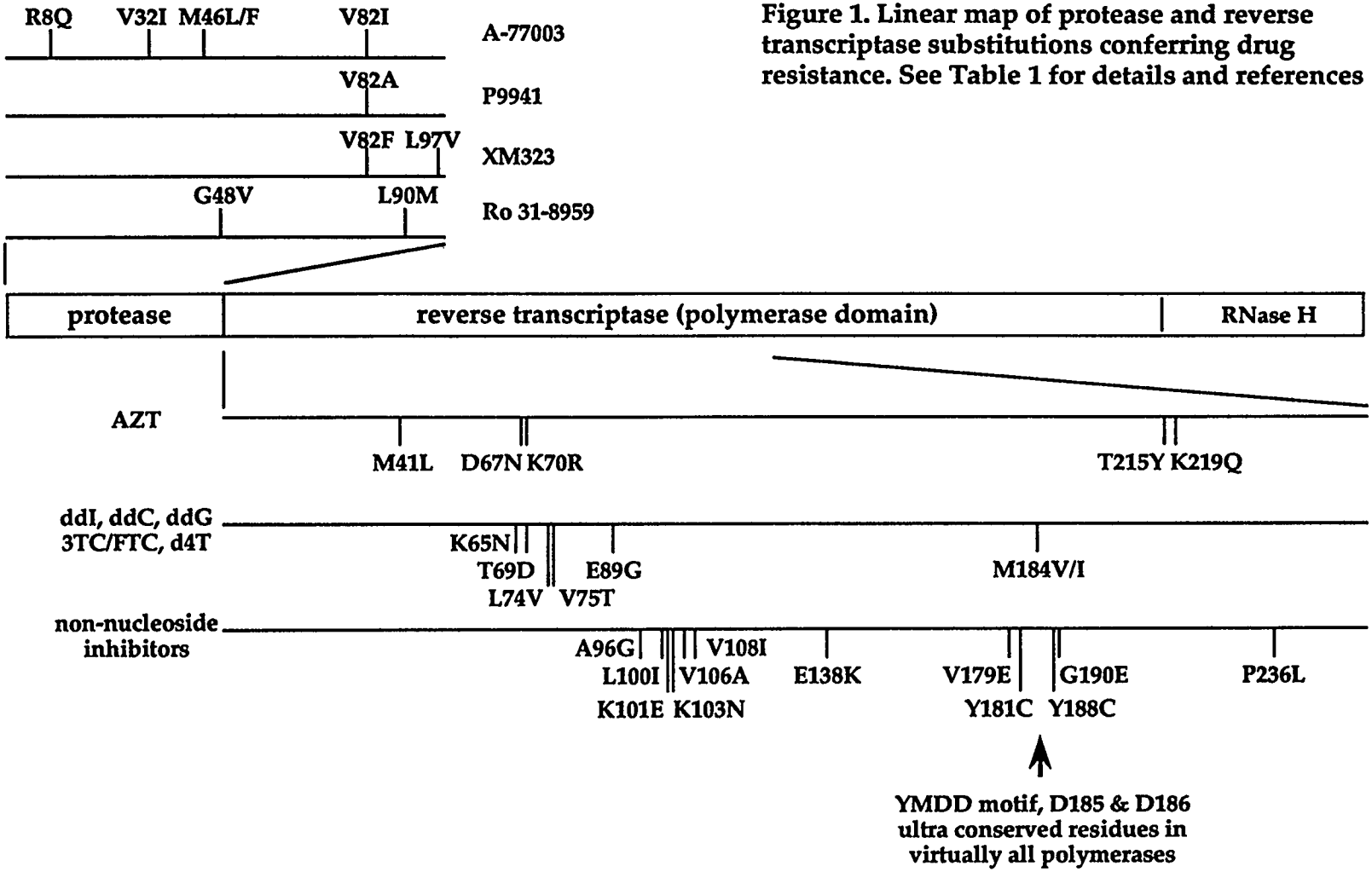

Figure 1. Linear map of protease and reverse transcriptase substitutions conferring drug resistance. See Table 1 for details and references

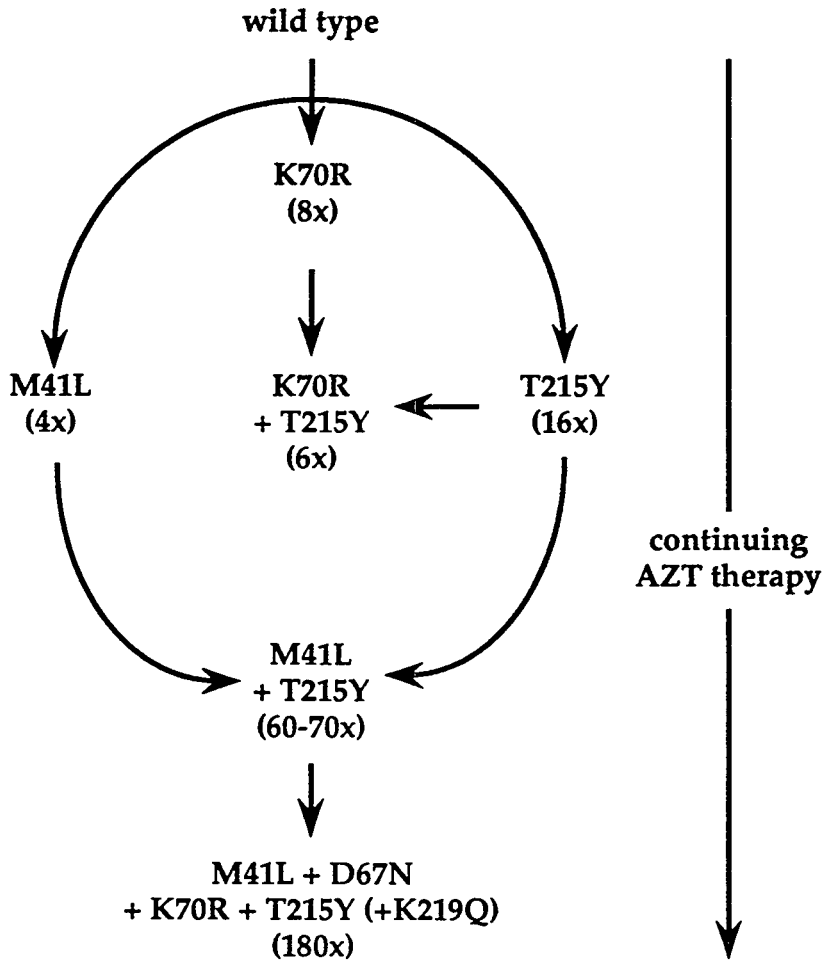

Figure 2. Temporal order of the emergence of mutations conferring AZT resistance

From Larder J Gen Virol 75, 951-957 (1994)

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IV

Related Sequences

This section of the compendium has typically featured HIV related viral sequences—of non-primate lentiviruses and human T-cell lymphotropic viruses I and II. Beginning in 1993, Part IV entries included, with greater emphasis, coding sequences for cellular proteins involved with HIV and SIV pathogenesis. In 1994, Part IV is completely devoted to cellular proteins; however, this does not imply that HIV related viral sequences will not be included in future updates. Kuan-Teh Jeang, one of the database editors, has written a summary for this year's section.

PART IV Related Sequences

Introduction IV-1
Contents(1994) 2
HIV and Cellular Factors (Kuan-Teh Jeang) 3
CEIF5A (M99499) 13
HIVEP1 (J05011) 14
HSCOUPTF (X16155, X58241) 15
HUMCOUPII (M62760) 16
HUMCYP (Y00052) 17
HUMCYPB (M60857) 18
HUMHIP116 (L34673) 19
HSIL02 (V00564) 21
HUMIL6 (M18403) 22
HUMIni1 (U04847) 23
HUMKUP70 (J04611) 24
HUMKUP86 (J04977) 25
HUMLA (J04205, M11108) 27
HUMLCK (M36881) 28
HUMMSS1 (D11094) 29
HUMNB23 (M26697) 30
HNFAT (U08015) 31
HUMNFKB (M58603) 33
HUMP65NFKB (M62399) 35
HUMP68K (M35663) 36
HSZFPBF1 (X51435) 38
HUMSF2P32 (M69039) 41
HUMSP1TF (J03133) 42
HUMTBP1 (M34079) 44
HUMTFIIDA (M34960) 45
HSTGFB1 (X02812, J05114) 46
HUMTRBP (M60801) 48
HSUSF (X55666) 49
HUSFII (S50537) 50
HUMYC1A (L11289) 51
YY1 (M77698) 52
Hcfos (K00650, M16287) 53
HINTAV (U07375) 56
HUMINTB5A (J05633) 57
MMLEF1 (X58636) 59
RNBCOP (X57228) 61
SCSUG1 (X66400) 63

HIV and Cellular Factors

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INTRODUCTION

Viruses are obligatory parasites of cells. Thus it is expected that host cell factors contribute importantly to the life-cycle of viruses. In this section, we survey four types of virus-cell interactions involving HIV-1. These four areas include: 1) DNA-binding proteins that recognize target motifs in proviral LTR; 2) RNA-binding proteins that bind HIV-1 RNAs; 3) cellular factors that form protein-protein complexes with HIV-1 regulatory proteins; and 4) cellular genes which are modulated upon viral infection. With rapid increases in knowledge in the area of virus-cell interactions, we anticipate that this initial survey would be expanded extensively in future editions of the data base. Additional discussions on HIV-cell interactions are found elsewhere (Jones and Peterlin, 1994; Jeang and Gatignol, 1994; Garcia and Gaynor, 1994).

I. DNA-BINDING PROTEINS

The promoter-enhancers of the human immunodeficiency virus (HIV) are contained in the U3 of the viral long terminal repeat (LTR). HIV-1 U3 is 454 nucleotides long and has binding sites for many transcription factors. Some of these are diagrammed in Figure 1. With the exception of NF-kB and Sp1 (Ross et al., 1991; Kim et al., 1993; Huang and Jeang, 1993; Huang et al., 1994), direct verification of the importance of the various sequences in viral contexts has not been performed.

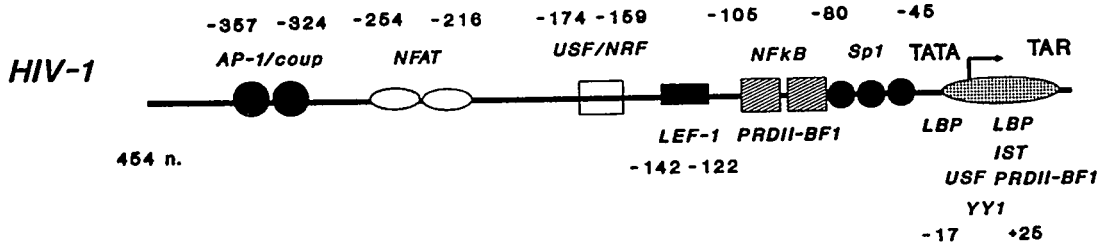

Fig. 1. Diagrammatic representation of the positions in U3 and R for some of the DNA-binding proteins that recognize the HIV-1 LTR.

Subgenomic assays in cultured cells indicate that the primary contributors to HIV-promoter activity are the NF-kB, Sp1, and TATAA (sequences from +1 to –105; Berkhout and Jeang, 1992). Nonetheless, it is likely that other DNA-binding factors also contribute in vivo. Beginning directionally from the 5′ end of U3, binding sites for AP-1 (a fos/jun hetero-complex; van Straaten et al., 1983; Hattori et al., 1988) and COUP (a member of the steroid/thyroid receptor superfamily; Cooney et al., 1991) are found between –324 and –357. Both COUP and AP-1 are expressed in human T-cells, and thus could compete with each other for the same proviral DNA sites during HIV-1 infection.

More proximally, between –216 and –254 are binding motifs for nuclear factor from activated T-cells (NFAT; Shaw et al., 1988). NFAT is an intermediating transducer of signals initiated at the

T-cell antigen receptor. Recent evidence suggests that NFAT binding activity is composed of three discrete polypeptides, NFATp (McCaffrey et al., 1993), Fos and Jun (Yaseen et al., 1993).

In the region between –159 and –174 is a binding consensus sequence for USF (Gregor et al., 1990). USF was characterized initially as a positive activator of adenovirus major-late-promoter transcription. In the HIV context, there is conflicting information on whether this factor has moderating (and thus be regarded as a negative regulatory factor; NRF; Lu et al., 1990) or stimulating (Maekewa et al., 1991) effects. Interestingly, USF also binds a second unrelated sequence (–5 to +11) that surrounds the HIV-1 initiator (Hu et al., 1993). USF interaction at the initiator-proximal site strongly activates expression from the TATAA-promoter (Hu et al., 1993). Of note, a factor distinct from USF, which binds the same DNA-sequence, has been cloned and characterized (TFE3; Bechmann and Kadesch, 1991).

LEF-1 is a T-cell specific transcription factor (Waterman and Jones, 1990). Once bound to its cognate site, LEF-1 bends DNA and thereby facilitates the assembly of nucleoprotein complexes at the promoter (Giese et al., 1992; reviewed in Jones and Peterlin, 1994). A high affinitiy LEF-1 binding site is present at –122 to –143. Two low affinity binding sites exist at –37 to –51 and +17 to +32 (Waterman and Jones, 1990).

NF-kB (Nabel and Baltimore, 1987) and Sp1 (Jones and Tjian, 1985; Jones et al., 1986) motifs are perhaps the best characterized sequence elements in the HIV-1 LTR. These sequences directly impact viral replication (Ross et al, 1991; Kim et al., 1993; Huang and Jeang, 1993; Huang et al., 1994), viral transcription (Harrich et al., 1990; Berkhout and Jeang, 1992; and references cited therein), and Tat transactivation (reviewed in Jones and Peterlin, 1994; Jeang and Gatignol, 1994). For more extensive discussions of the biochemical and functional properties of NF-kB (Ghosh et al., 1990; Kieran et al., 1990; Nolan et al., 1991; Liou et al., 1991; and references cited therein) and Sp1 (Dynan and Tjian, 1983; Briggs et al., 1986; Kadonaga et al., 1987; and references cited therein), readers should consult elsewhere.

PRDII-BF1 is a 300 kDa zinc-finger containing protein (Baldwin et al., 1990; Seeler et al., 1994). PRDII-BF1 recognizes and binds the NF-kB motif; however, it also binds a divergent sequence in R (+27 to +52; Seeler et al., 1994).

Positioned at the junction of U3 and R are sites for LBP (Yoon et al., 1994) and YY1 (Useheva and Shenk, 1994; Seto et al., 1991). While the role for LBP in HIV-1 transcription is not wholly understood (Jones et al., 1988; Kato et al., 1991), binding of YY1 to the LTR has been shown to repress HIV-1 expression and production of virions (Margolis et al., 1994). Besides LBP and YY1, a DNA-mediated activity for the induction of short transcripts (IST) has also been mapped to the same general vicinity (–5 to +26; Sheldon et al., 1993). The cDNA for the cellular factor that mediates IST-activity has not been isolated, and thus the authentic identity of this factor is unknown. HIP 116 is another newly cloned cDNA that binds to the TATA/initiator of the HIV-1 promoter (K.A. Jones, pers. communication).

II. RNA-BINDING PROTEINS

In recent years, it has become evident that RNA-binding proteins play important roles in gene regulation (see reviews, Keene and Query, 1991; Mattaj, 1993; Burd and Dreyfuss, 1994). For HIV-1, cellular proteins that bind viral regulatory RNAs have been studied in detail. In particular, at least eight host cell factors have been described to bind TAR RNA. Similarly, two RRE-binding factors have been characterized. There are also biologically compelling reasons as to why TAR- and RRE-binding proteins are meaningful contributors to the HIV-1 lifecycle.

The HIV-1 leader RNA, TAR, forms a stem-bulge-loop structure of approximately 60+ nucleotides (Muesing et al., 1987; Berkhout and Jeang, 1989). Early, it was reported that many human cellular proteins bound TAR RNA (Gatignol et al., 1989; Gaynor et al., 1989). Since then, some of these factors have been defined further. Tabulating from extant studies, eight proteins associate with either the bulge, loop, or stem of TAR RNA (see Figure 2). TAR loop-binding proteins include p68 (Marciniak et al., 1990), and TRP1/TRP185 (185 kDa; Sheline et al., 1991; Wu et al., 1991), while TRP2 (70-110 kDa; Sheline et al., 1991) binds to TAR-bulge. Proteins that complex with the

double-stranded stem of TAR RNA consist of P1/dsI (newly renamed as PKR; McCormack et al., 1992; Roy et al., 1991), SBP (140 kDa; Rounseville and Kumar, 1992), and TRBP (Gatignol et al., 1991; Gatignol et al., 1993). Finally, two human autoantigens recently have been identified as TAR RNA-binding factors. Lupus antigen Ku (Kaczmarski and Khan, 1993) binds to the loop of TAR, while La (Chang et al., 1994; Svitkin et al., 1994) recognizes U-residues within the overall context of the TAR secondary structure.

RRE-binding proteins have been studied less extensively. We know that TRBP also can bind RRE (Park et al., 1994), and that a 56 kDa factor has been described as a specific RRE-binding protein (Vaishnav et al., 1992). It is expected that other RRE-factors will emerge from future studies.

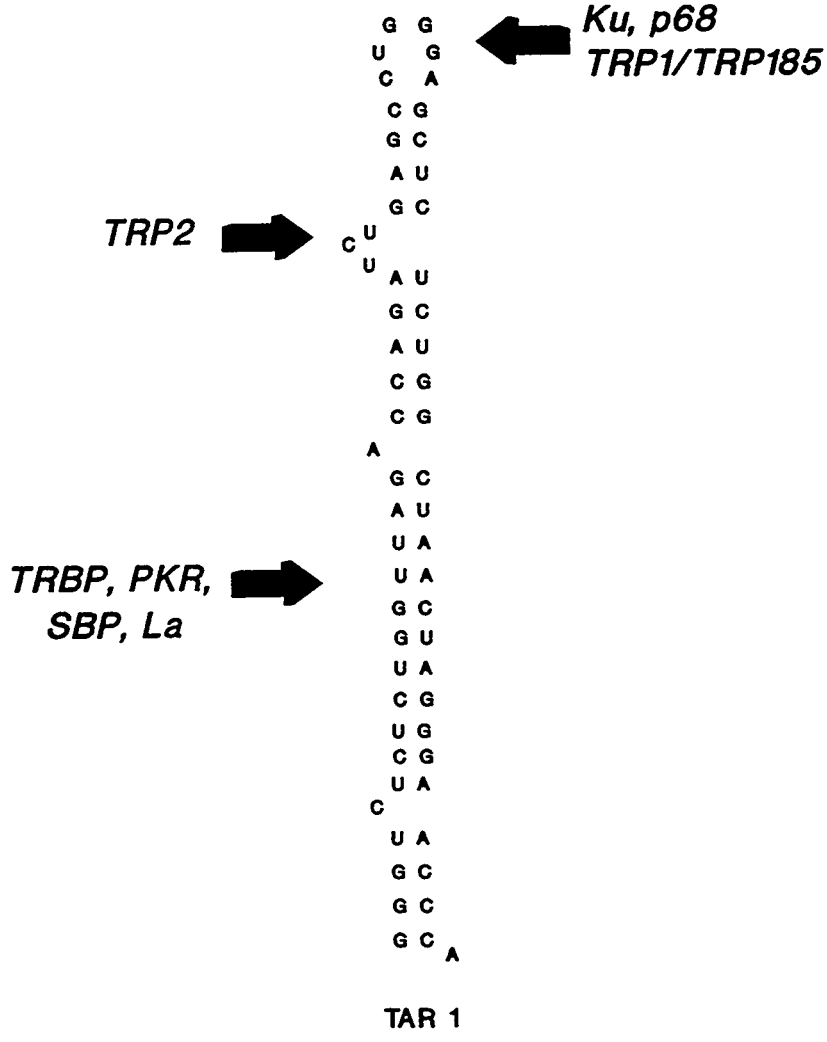

Fig. 2. Structure of the HIV-1 TAR RNA. Identities of the different proteins that bind to the loop, bulge or stem of the TAR hairpin are indicated.

III. PROTEIN-PROTEIN INTERACTIONS

Protein-protein interactions are well-documented to be important in gene regulation (see reviews, Lewin, 1990; Greenblatt, 1991). Recent studies suggest that many HIV-1 proteins complex with host cell factors. We describe below, in a non-exhaustive fashion, some examples pertaining to Tat, Rev, Gag, and Nef.

Although Tat is best known for transcription, it has other functions (Huang et al., 1994) and has been reported to be a secretable factor that promotes the growth of Kaposi-like cells (Ensoli et al., 1990). There is evidence that Tat can be taken up actively into cells (Frankel and Pabo, 1988) through binding to a cell-surface protein (Weeks et al., 1993) implicated to be avb5 integrin (Vogel et al., 1993). Once inside cells, Tat interacts with multiple partners in activating transcription.

Two factors that bind Tat are themselves critical components of the eucaryotic polII transcription machinery. Genetic evidence supports a critical role for Sp1 in HIV-1 Tat-mediated transactivation (Harrich et al., 1989; Kamine et al., 1991; Southgate and Green, 1991; Berkhout and Jeang, 1992). Interestingly, a direct interaction between Tat and Sp1 (Jeang et al., 1993) has been documented and perhaps reflects observed virus-cell biology. In addition, there is evidence that Tat also contacts TFIID (Kashanchi et al., 1994) and that Tat-Sp1-TFIID could be a multiprotein complex (Huang et al., 1993) inside cells.

A large family of proteins related to the 26S protease from human erythrocytes (Dubiel et al., 1994) are Tat-binding polypeptides. Members of this family include TBP-1 (Nelbock et al., 1990; Ohana et al., 1993), TBP-7 (Ohana et al., 1993; Shaw and Ennis, 1993), MSS1 (Shibuya et al., 1992), and SUG1 (Swaffield et al., 1992). The exact role of this family of proteins in cellular metabolism is not wholly clear; however, the 26S protease seems to regulate the degradation of some cyclins and in this manner has been implicated in modulating the stability of oncoproteins such as c-Mos, c-Myb, c-Myc and p53 (Dubiel et al., 1994).

Two other cellular proteins, a 36 kDa protein (Desai et al., 1991) and a cellular protein kinase (Hermann and Rice, 1993), have been reported to bind Tat. The biological roles of these two factors remain to be defined.

There are at least three cellular factors that bind Rev. Rev localizes to the nucleolus, and work by Laemmli and colleagues (Fankhauser et al., 1991) has demonstrated a tight association between Rev and nucleolar B23 protein. This protein-protein complex likely directs the subcellular localization of Rev.

At the functional level Rev transactivation could be modulated by associations with cellular factors. Two additional proteins have been shown to bind Rev, translation factor eIF-5A (Ruhl et al., 1993), and a p32 protein (YL2; Luo et al., 1994) originally characterized by Krainer and colleagues (Krainer et al., 1991) as a splicing factor-SF2-associated polypeptide. YL2 was identified as a Rev-binding factor through random screening using the yeast-two-hybrid assay; however, in the same assay YL2/p32 also binds HIV-1 and HIV-2 Tat proteins (Trinh and Jeang, unpublished observation; B.R. Cullen, pers. communication).

In addition to Tat and Rev, both HIV Gag and Nef also have cellular partners. p55 and p24 Gag bind cyclophilin A and cyclophilin B proteins (Luban et al., 1993). The cyclophilins are cellular polypeptides originally characterized for their specific binding to cyclosporin A. Nef has been found to bind b-COP, a coat protein from non-clathrin-coated vesicles (R. Benarous, pers. communication). This interaction may be important in promoting the intracellular sequestration of CD4. Another group of investigators has found that Nef binds directly to the lck-kinase in vitro (D. McPhee, pers. communication).

IV. CELLULAR GENES MODULATED BY HIV

Infection of cells by HIV most likely results in activation and repression of many cellular genes. Because of the ambient complexity of gene expression inside cells, it is logistically difficult to dissect those genes that are upregulated from those that are downregulated from those that remain unperturbed. Nevertheless, several examples of genes that respond to HIV infection are known. These include IL-2 (Westendorf et al., 1994), IL6 (Scala et al., 1994), and TGF-b (Buonaguro et al., 1994), among others. The identification of these genes has been based on classical approaches; however, we anticipate that with the advent of mRNA differential display technology (Liang and Pardee, 1992) the exhaustive characterization of cellular genes that respond to infection by HIV should be accomplished soon.

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```
LOCUS       CEIF5A       1792 bp ss-mRNA            VRT       06-APR-1994
DEFINITION  Chicken initiation factor 5A cDNA sequence, complete cds.
ACCESSION   M99499
SOURCE      Gallus gallus embryo whole tissue mRNA.
REFERENCE   1  (bases 1 to 1792)
  AUTHORS   Rinaudo,M.S., Joe,Y.A. and Park,M.H.
  TITLE     Cloning and sequencing of a chick embryo cDNA encoding the 20-kDa
            hypusine-containing protein, eIF-5A
  JOURNAL   Gene 137, 303-307 (1993)
COMMENT     Translation factor eIF-5A has been shown to bind Rev (Ruhl et al.
            J. Cell. Biol. 123: 1309-1320 1993).  At the functional level
            Rev transcription could be modulated by associations with eIF-5A.
            NCBI gi: 289799
BASE COUNT      542 a    347 c    391 g    511 t      1 others
ORIGIN
        1 gaattccgga tgccctaaag cacgtgcaac tcgtcgcaca cgtctcgccc cgcagccgcc
       61 gccATGgccg acgagttgga cttcacgacg ggcgacgccg gcgcctcgtc cacctatccc
     IF cds ->
      121 atgcagtgct cggcgctgcg taagaacggc ttcgtggtac tgaaggggcg cccgtgtaag
      181 atcgtggaga tgtccacctc caagacggga aagcacggcc acgccaaggt ccacctggtt
      241 ggtattgata tcttcaacgg gaaaaaatac gaagatattt gcccatcaac tcataacatg
      301 gatgtcccaa atataaagag gaacgactac cagctgatag ggattcagga tgggtacctc
      361 tccctgctga cagaaagtgg cgaagttcgt gaggatctaa agctgccaga aggtgatctg
      421 ggaaaagaaa tagaaggaaa gttcaatgcc aatgaagatg tgcagatatc cgtcataagt
      481 gcaatgaatg aagaatgtgc tgtagccata aagccttgca aaTAAagagg atcgccaggc
                                                      <- IF cds end
      541 acgggcaact gctcaggtct ggataaacca cagatcttta aatttggttc tgattgtcac
      601 caaagctctg gccttcacaa gcaacctcat ttctttttg aattgttaca aagcagtgct
      661 ggattctgga ttagtgttgc aggctaactg gcagttttca aaatcactga gattttaatt
      721 ccttaattgt aactatttta acattcctgt gggtttcagc tatggatctg agaaaccgtt
      781 caggtgttac tagtggatat atttttatt tgcttgagca aaacagtgtt tgtctgtatg
      841 aacagacaaa atacagtatt caggggcttt tagataagct agtaggtatc taggattata
      901 aagtgaccta gagcacaaat agtatttttc ttgacatgtt tagatagaac tgacaataaa
      961 agtagctttt ttttttttt aaagcttaaa tattttgtgg attgggactc ttgcagaact
     1021 gtaggtacca atcacaaatt ttagaccaag aaactcaagt gatcaaaaat gccagctggc
     1081 ttgagcaagc cccagtggcc atgtgcaact taactgtatt acctctgtat tctttttgc
     1141 caacttgttg gcttattgta acgttaaaat ggtgtcaaag cctacctgtg gtttaggcag
     1201 gcagttgagt tttgagtaga tgagacatag atwggtcaag gtgagaatgg atgctaaagc
     1261 tatagacttt cactcgaggc ctttgtcaga cttaaaggaa aaaaaaaaaa agaaaaaaaa
     1321 aaaacacagt tcaattgctt tcctttgtta tatttatctt aaactataaa agggtgacaa
     1381 actccgcggg aatctgttgc agtgcttcca gctttaggtt tcaatcttca ggttcagacc
     1441 atatttttgt agcacaatga ccacgtggtt tttcaaaaag tgggacaaat tgtagcattg
     1501 agcctaaact aaatgcatgt gtggattgtt gtgttgtttt ttttttttta atagaacaat
     1561 tgtcttttcc aaatacagac ttgacaaaca attctgaaca accatggctt cactataaaa
     1621 ataactagag agttgaaaaa gttagctcct atccacagga gtttggagtc attgaaacac
     1681 acatgcacgc ctctaactat ttagtagctt aatggtcaaa cacaaagctt tacagagcta
     1741 gtcatggaag gatacctagc ttactcttgt ttatagcact caactagaat tc
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HIVEP1

```
LOCUS       HIVEP1       1035 bp ss-RNA             PRI       28-SEP-1994
DEFINITION  Human immunodeficiency virus enhancer-binding protein (HIV-EP1)
            sequence, partial cds.
ACCESSION   J05011
SOURCE      Human B-cell lambda gt11 library.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Maekawa,T., Sakura,H., Sudo,T. and Ishii,S.
  TITLE     Putative metal finger structure of the human immunodeficiency virus
            type 1 enhancer binding protein HIV-EP1
  JOURNAL   J. Biol. Chem. 264, 14591-14593 (1989)
COMMENT     HIV-EP1, also referred to as MBP-1 or PRDII-BF1, is a cellular
            transcription factor which activates HIV-1 gene expression.  The
            protein contains two zinc finger domains, each of which can bind to
            either of the two NF-kappa B binding motifs in the HIV-1 enhancer
            or to the TAR transactivation response element.  Gaynor et al.
            (Genomics 9: 758-61, 1991) have mapped the gene which encodes
            HIV-EP1 to human chromosome 6p22.3-p24.
            NCBI gi: 326842
BASE COUNT      328 a    247 c    236 g    224 t
ORIGIN
        1 agtgagcaag ataaagaaaa ttccttaatc aaaagtgaac caagaagaat taaaatattt
 HIV-EP1 ->
       61 gatggaggat ataagtcaaa tgaagagtat gtatatgtcc gaggcagggg aagaggaaaa
      121 tacatttgtg aagaatgtgg aatacgttgt aagaaaccta gcatgttaaa gaaacacata
      181 cgaacccata cagatgtccg cccctaccac tgcacttact gtaacttctc ctttaagact
      241 aaaggaaatc tgacaaaaca catgaagtcc aaggcacata gcaagaaatg tgtggattta
      301 ggcgtctcag taggtttaat agatgaacag gatacagaag aatcagatga aaaacagaga
      361 ttcagttatg agcgatctgg atatgatctt gaagaatctg atggcccaga tgaggatgac
      421 aatgaaaatg aagacgatga tgaggacagc caggctgaat cagtcctgtc agccacaccc
      481 tcagtcacag ctagcccgca gcaccttcca tctagaagta gccttcagga ccctgtgagt
      541 actgacgagg atgtcaggat caccgattgc ttttctgggg tacacacgga cccaatggac
      601 gttctgccca gggcgctgct caccagaatg actgtcctga gcacagcaca gtctgactac
      661 aataggaaga cactctctcc ggggaaggcc aggcagcata ctgcgagaga tgaaaacgac
      721 acaattccgt ctgtagacac ttccaggtcc ccgtgtcatc agatgtctgt ggactaccct
      781 gagtcagaag aaattctgag aagttctatg gcaggaaaag ctgttgctat aacacagagc
      841 ccatcatctg taagacttcc tcctgctgca gctgagcaca gcccccagac agcagcgggg
      901 atgccttctg tggcctcacc acatcctgac cctcaagaac agaagcagca aataactcta
      961 cagccgactc caggcttgcc ttctccccac actcatttgt ttagccacct tcctttgcat
     1021 tcccagcagg aattc
                  HIV-EP1 ->
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LOCUS       HSCOUPTF     1513 bp    RNA             PRI       29-MAR-1991
DEFINITION  Human chicken ovalbumin upstream promoter transcription factor
            (COUP-TF) sequence, partial cds.
ACCESSION   X16155 X58241
KEYWORDS    DNA-binding protein; steroid receptor; transcription factor.
SOURCE      Human mRNA from cell line Hela s3.
REFERENCE   1  (bases 1 to 1513)
  AUTHORS   Wang,H., Tsai,Y., Cook,G., Beattie,G., Tsai,M.J. and O'Malley,W.
  TITLE     COUP transcription factor is a member of the steroid receptor
            superfamily
  JOURNAL   Nature 340, 163-166 (1989)
COMMENT     The promoter-enhancers of HIV are contained in the U3 region of
            the viral long terminal repeat.  Binding sites for COUP are
            present from -324 to -357 within the U3 region of the LTR of
            HIV-1. A negative role for this element is suggested by mutational
            analysis (Garcia et al. AIDS 8: S3-S17 1994).
            NCBI gi: 30139
BASE COUNT      319 a    520 c    451 g    223 t
ORIGIN
        1 agcagctggc gagatccgca ggacgacgtg gccgggggca accccggcgg ccccaacccc
 COUP-TF ->
       61 gcagcgcagg cggcccgcgg cggcggcggc ggcgccggcg agcagcagca gcaggcgggc
      121 tcgggcgcgc cgcacacgcc gcagaccccg ggccagcccg gagcgcccgc caccccggc
      181 acggcggggg acaagggcca gggcccgccc ggttcgggcc agagccagca gcacatcgag
      241 tgcgtggtgt gcggggacaa gtcgagcggc aagcactacg gccaattcac ctgcgagggc
      301 tgcaaaagtt tcttcaagag gagcgtccgc aggaacttaa cttacacatg ccgtgccaac
      361 aggaactgtc ccatcgacca gcaccaccgc aaccagtgcc aatactgccg cctcaagaag
      421 tgcctcaaag tgggcatgag gcgggaagcg gttcagcgag gaagaatgcc tccaacccag
      481 cccaatccag gccagtacgc actcaccaac ggggaccccc tcaacggcca ctgctacctg
      541 tccggctaca tctcgctgct gctgcgcgcc gagccctacc ccacgtcgcg ctacggcagc
      601 cagtgcatgc agcccaacaa cattatgggc atcgagaaca tctgcgagct ggccgcgcgc
      661 ctgctcttca gcgccgtcga gtgggcccgc aacatccccc tcttcccgga tctgcagatc
      721 accgaccagg tgtccctgct acgcctcacc tggagcgagc tgttcgtgct caacgcggcc
      781 cagtgctcta tgccgctgca cgtggcgccg ttgctggccg ccgccggcct gcatgcctcg
      841 cccatgtctg ccgaccgcgt cgtggccttc atggaccaca tccgcatctt ccaggagcag
      901 gtggagaagc tcaaggcgct acacgtcgac tcagccgagt acagctgcct caaagccatc
      961 gtgctgttca cgtcagacgc ctgtggcctg tcggatgcgg cccacatcga gagcctgcag
     1021 gagaagtcgc agtgcgcact ggaggagtac gtgaggagcc agtaccccaa ccagcccagc
     1081 cgttttggca aactgctgct gcgactgccc tcgctgcgca ccgtgtcctc ctccgtcatc
     1141 gagcagctct tcttcgtccg tttggtaggt aaaaccccca tcgaaactct catccgcgat
     1201 atgttactgt ctgggagcag cttcaactgg ccttacatgt ccatccagtg ctccTAGacc
                                                                  <-COUP-TF
     1261 ttgggcgctt cccacctgcc ccgtcccccc agagactcag aggacccacc tgggccaagg
     1321 actccaaagc cgcggggaca ccgggaagtg cagcgggcca ggcaggctgg gtgggaggga
     1381 ggagggccga gacaggagca gcccacccag cagaaataca atccgagcta caaagcatgg
     1441 gaaaaagaga ctcttttagg atcagatctg tgagcacgtt ggcgaggaaa aacaaaaaaa
     1501 caaaaaaaaa ccg
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HUMCOUPII

```
LOCUS       HUMCOUPII    2268 bp ss-mRNA            PRI       14-SEP-1992
DEFINITION  Homo sapiens chick ovalbumin upstream promoter transcription factor
            II (COUP-TFII) cDNA sequence, 5' end.
ACCESSION   M62760
SOURCE      Human female mRNA from HeLa S3 cell line.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Wang,L.-H., Ing,N.H., Tsai,S.Y., O'Malley,B.W. and Tsai,M.-J.
  TITLE     The COUP-TF compose a family of functionally related transcription
            factors
  JOURNAL   Gene Expression 1, 207-216 (1991)
COMMENT     The promoter-enhancers of HIV are contained in the U3 region of the
            viral long terminal repeat.  Binding sites for COUP are present
            from -324 to -357 within the U3 region of the LTR of HIV-1.
            A negative role for this element is suggested by mutational
            analysis (Garcia et al. AIDS 8: S3-S17 1994).
BASE COUNT      410 a    833 c    656 g    369 t
ORIGIN
        1 cgggccgtac tgccttttt cccctctttc attctttctc tccgtctttt tctcccccct
       61 ctgcgcacga aggatgtgct tctaggtggt gatctgccct cctctctctc ttttatcatt
      121 tctccccctc gccggcgagt tgactctttc cctatgtgtg tgaggcggcg gcggcagcag
      181 cagcagcagc ggctccggcg gcggcagcag cggcagcagc gacttcagcg gcggcggcgg
      241 cgctagacgc agcggctccg ggcccgaccc ggcggcttcg gcggcggctc cggcggcagc
      301 ggcggcccgg gcggcccgca gggaacggcg agcggcctcc acccacgact gcgggcggcg
      361 gcggccggag agagcgaggc gcgcgccgga cgcccggggc aggcggcggc ggcggcggcc
      421 cagcgccagg acgacgccgc gcagcgcccg acgcggacca ctttcatgct gattcccccg
      481 gacccgggca gcgctccggc cactccgcgg cgccggcctc cgccccggcc tgcctggctc
      541 cctgggctgc ccgcacccgg cgcctcagat ctcctagtcc tcctgatttc gatggctttc
      601 ctgaatggct gactgtgggc tgccctggac ttggcccccg gacagtcgcc tctcctcctc
      661 ctctacctcc tccttcacca ccacctcctc ttcctcctcc tcctcctccg ccaactcctc
      721 ggctgcacac cagctctaag agcgagagtg aacgagagag ggagggagag agtgagagcg
      781 agcgagatct ttggagagat ttttttttt gcctcctact tctgtcttga agccagacaa
      841 tcgacttcag ctctccctcc cctccctctt tctccacgtt ctgctcccac tcgctctcct
      901 gtccccttcc cctcccctcc cggcggaaag ccccccgaaa ccaacaaagc tgagccgaga
      961 gaaacaaaca aaacaaacac accgggccag acaagccatc gacaaaactt tgcaaaagca
     1021 aaaacaaaaa aggaaaaact aaccaacctc aaccaaccag cccccgagcc acccggggcg
     1081 ccctcccgcg ccctcttgca ccctcgcaca cacaaaaggc ggcgcgccgg agcccgagac
     1141 ccggggagtc gccgccgccc cgccgccgcc cgcagccagg ggagcaggaa gtccggacgc
     1201 agcccccata gatATGgcaa tggtagtcag cacgtggcgc gacccccagg acgaggtgcc
    COUP-TFII cds start ->
     1261 cggctcacag ggcagccagg cctcgcaggc gccgcccgtg cccggcccgc cgcccggcgc
     1321 cccgcacacg ccacagacgc ccggccaagg gggcccagcc agcacgccag cccagacggc
     1381 ggccggtggc cagggcggcc ctggcggccc gggtagcgac aagcagcagc agcagcaaca
     1441 catcgagtgc gtggtgtgcg gagacaagtc gagcggcaag cactacggcc agttcacgtg
     1501 cgagggctgc aagagcttct tcaagcgcag cgtgcggagg aacctgagct acacgtgccg
     1561 cgccaaccgg aactgtccca tcgaccagca ccatcgcaac cagtgccagt actgccgcct
     1621 caaaaagtgc ctcaaagtgg gcatgagacg ggaagcggtg cagaggggca ggatgccgcc
     1681 gacccagccg acccacgggc agttcgcgct gaccaacggg gatcccctca actgccactc
     1741 gtacctgtcc ggatatattt ccctgctgtt gcgcgcggag ccctatccca cgtcgcgctt
     1801 cggcagccaa tgcatgcagc ccaacaacat catgggtatc gagaacattt gcgaactggc
     1861 cgcgaggatg ctcttcagcg ccgtcgagtg ggcccggaac atccccttct tccccgacct
     1921 gcagatcacg gaccaggtgg ccctgcttcg cctcacctgg agcgagctgt ttgtgttgaa
     1981 tgcggcgcag tgctccatgc ccctccacgt cgccccgctc ctggccgccg ccggcctgca
     2041 tgcttcgccc atgtccgccg accgggtggt cgcctttatg gaccacatac ggatcttcca
     2101 agagcaagtg gagaagctca aggcgctgca cgttgactca gccgagtaca gctgcctcaa
     2161 ggccatagtc ctgttcacct cagatgcctg tggtctctct gatgtagccc atgtggaaag
     2221 cttgcaggaa aagtctcagt gtgctttgga agaatacgtt aggagcca
                                                    COUP-TFII ->
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LOCUS       HUMCYP        723 bp    RNA             PRI       07-JUN-1987
DEFINITION  Human T-cell cyclophilin cDNA sequence.
ACCESSION   Y00052
KEYWORDS    cyclophilin; cyclosporin A-binding protein.
SOURCE      Human mRNA from Jurkat cell library.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   Haendler,B., Hofer-Warbinek,R. and Hofer,E.
  TITLE     Complementary DNA for human T-cell cyclophilin
  JOURNAL   EMBO J. 6, 947-950 (1987)
COMMENT     The cyclophilins are cellular polypeptides originally characterized
            for their specific binding to cyclosporin A.  Subsequent studies
            have shown that both cyclophilin A and cyclophilin B bind to
            p55 gag and to the p24 capsid proteins (Luban et al. Cell 73:
            1067-78 ,1993).
            NCBI gi: 30308
BASE COUNT      179 a    165 c    176 g    203 t
ORIGIN
        1 gtgtactatt agccATGgtc aaccccaccg tgttcttcga cattgccgtc gacggcgagc
   cyclophilin cds start ->
       61 ccttgggccg cgtctccttt gagctgtttg cagacaaggt cccaaagaca gcagaaaatt
      121 ttcgtgctct gagcactgga gagaaaggat ttggttataa gggttcctgc tttcacagaa
      181 ttattccagg gtttatgtgt cagggtggtg acttcacacg ccataatggc actggtggca
      241 agtccatcta tggggagaaa tttgaagatg agaacttcat cctaaagcat acgggtcctg
      301 gcatcttgtc catggcaaat gctggaccca acacaaatgg ttcccagttt ttcatctgca
      361 ctgccaagac tgagtggttg gatggcaagc atgtggtgtt tggcaaagtg aaagaaggca
      421 tgaatattgt ggaggccatg gagcgctttg ggtccaggaa tggcaagacc agcaagaaga
      481 tcaccattgc tgactgtgga caactcgaaT AAgtttgact tgtgttttat cttaaccacc
                                        <- cyclophilin cds end
      541 agatcattcc ttctgtagct caggagagca cccctccacc ccatttgctc gcagtatcct
      601 agaatctttg tgctctcgct gcagttccct ttgggttcca tgttttcctt gttccctccc
      661 atgcctagct ggattgcaga gttaagttta tgattatgaa ataaaaacta aataacaatt
      721 gtc
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HUMCYPB

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LOCUS       HUMCYPB       851 bp ss-mRNA            PRI       27-MAR-1991
DEFINITION  Human cyclophilin B cDNA sequence, complete cds.
ACCESSION   M60857
KEYWORDS    cyclophilin B; cyclosporin A-binding protein;
            peptidyl-prolyl isomerase.
SOURCE      Human mRNA.
REFERENCE   1  (bases 1 to 851)
  AUTHORS   Price,E.R., Zydowsky,L.D., Jin,M., Hunter,C.H., McKeon,F.D. and
            Walsh,C.T.
  TITLE     Human cyclophilin B: A second cyclophilin gene encodes a peptidyl
            isomerase with a signal sequence
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907 (1991)
COMMENT     The cyclophilins are cellular polypeptides originally characterized
            for their specific binding to cyclosporin A.  Subsequent studies
            have shown that both cyclophilin A and cyclophilin B bind to
            p55 gag and to the p24 capsid proteins (Luban et al. Cell 73:
            1067-78 ,1993).
            NCBI gi: 181334
BASE COUNT      222 a    210 c    240 g    179 t
ORIGIN
        1 cgggaacgca acATGaaggt gctccttgcc gccgccctca tcgcggggtc cgtcttcttc
     cyclophilin B cds ->
       61 ctgctgctgc cgggaccttc tgcggccgat gagaagaaga aggggcccaa agtcaccgtc
                        mature peptide ->
      121 aaggtgtatt ttgacctacg aattggagat gaagatgtag gccgggtgat ctttggtctc
      181 ttcggaaaga ctgttccaaa aacagtggat aattttgtgg ccttagctac aggagagaaa
      241 ggatttggct acaaaaacag caaattccat cgtgtaatca aggacttcat gatccagggc
      301 ggagacttca ccaggggaga tggcacagga ggaaagagca tctacggtga gcgcttcccc
      361 gatgagaact tcaaactgaa gcactacggg cctggctggg tcagcatggc caacgcaggc
      421 aaagacacca acggctccca gttcttcatc acgacagtca agacagcctg gctagatggc
      481 aagcatgtgg tgtttggcaa agttctagag ggcatggagg tggtgcggaa ggtggagagc
      541 accaagacag acagccggga taaacccctg aaggatgtga tcatcgcaga ctgcggcaag
      601 atcgaggtgg agaagccctt tgccatcgcc aaggagTAGg gcacagggac atctttcttt
                                              <- mature peptide
                                                 <- cyclophilin B cds end
      661 gagtgaccgt ctgtgcaggc cctgtagtcc gccacagggc tctgagctgc actggccccg
      721 gtgctggcat ctggtggagc ggacccactc ccctcacatt ccacaggccc atggactcac
      781 ttttgtaaca aactcctacc aacactgacc aataaaaaaa aatgtgggtt ttttttttt
      841 ttaataaaaa a
```

```
LOCUS       HUMHIP116    3418 bp ss-mRNA            PRI       22-AUG-1994
DEFINITION  Human ATPase, DNA-binding protein (HIP116) cDNA sequence.
ACCESSION   L34673
KEYWORDS    ATPase; DNA-binding protein; SNF2/SWI2-related protein;
            transcription factor.
SOURCE      Homo sapiens mRNA.
REFERENCE   1  (bases 1 to 3418)
  AUTHORS   Sheridan,P.L., Schorpp,M., Voz,M.L. and Jones,K.A.
  TITLE     Cloning of a SNF2/SWI2-related protein that binds specifically to
            the HIV-1 promoter and to the SPH motifs of the SV40 enhancer
  JOURNAL   Unpublished (1994)
COMMENT     HIP 116 is a newly cloned cDNA whose protein binds to the
            TATA/initiator of the HIV-1 promoter (K.A. Jones, personal
            communication).
            NCBI gi: 531195
BASE COUNT     1135 a    602 c    744 g    937 t
ORIGIN
        1 attcccgggg tctgactgga ctcgcggcga cttacctttc agtcgtgcgc tcctgatccg
       61 gcgctcggaa tttgtccccg gcttcagggc tgcggggcct ggaaggaggc gtatcgaggc
      121 ggctcgaaaa cgatccaggg gagccgaggc gctcctcttg tcatcccact cagcgccATG
                                                              HIP116 cds start ->
      181 tcctggatgt tcaagaggga tccagtttgg aagtacttgc agactgtcca gtatggagtt
      241 catggaaatt ttccacgcct ctcatatcca actttctttc cacgttttga attccaagat
      301 gttatccctc cagatgactt tctaactagt gatgaagaag tagattccgt tttatttgga
      361 agtttgagag gtcatgtggt tggactacgc tattacacgg gagtagttaa taataatgaa
      421 atggttgcat tacaacgaga tcctaataac ccttatgata agaatgcaat taaagtaaac
      481 aatgtgaatg gaaatcaagt tggccattta aagaaagagc ttgcaggtgc tttggcctat
      541 atcatggaca acaaattggc acaaattgaa ggggtagttc cttttggtgc aaacaatgct
      601 tttaccatgc ctctgcatat gacttttgg ggaaaagaag aaaatagaaa agcggtttca
      661 gatcagttga agaaacatgg atttaaattg ggtcctgcac caaaaacttt aggattcaat
      721 ttggaaagtg gttggggctc tggaagagct ggaccaagct atagtatgcc agtgcatgct
      781 gcagtacaga tgacaactga acagcttaaa acagaatttg acaaattgtt tgaagattta
      841 aaagaagatg ataaaaccca tgaaatggaa ccagctgagg ctattgaaac accactgctt
      901 ccacatcaaa aacaagctct agcttggatg gtgtcacggg aaaatagcaa agaacttcca
      961 ccattctggg aacagcgaaa tgacttatac tataacacaa taacaaattt ttctgagaag
     1021 gaccgaccag aaaatgtcca tggaggaatt ttagctgatg atatgggttt gggtaaaact
     1081 cttacagcca ttgcagtaat ccttaccaac ttccatgatg gcagacctct tcctattgaa
     1141 agagttaaaa agaatctact gaagaaggaa tataatgtta acgatgactc tatgaaactt
     1201 ggaggaaaca ataccagtga aaaggcagat ggactaagca aagacgcatc tagatgtagt
     1261 gaacaaccca gtatttcaga tatcaaggag aagagtaagt ttcgcatgtc agaattgtct
     1321 acgtcccgcc ccaaaagaag aaaaactgct gtccagtaca tagaaagcag tgattcagag
     1381 gaaattgaaa caagtgaatt gccgcagaaa atgaaaggca aactgaaaaa tgtacagtct
     1441 gaaactaaag gcagggcgaa agcaggatct tctaaggtta tagaagatgt ggcatttgca
     1501 tgtgcattaa cttcatctgt tcctacaaca aaaaagaaaa tgttgaaaaa gggagcttgt
     1561 gcagtggagg ggtcaaagaa aactgatgtt gaggagagac caagaacaac actgatcatc
     1621 tgtccgcttt ctgtgttaag caactggatt gaccagtttg gacaacatat aaaatcagat
     1681 gtacacttga atttttatgt ttattatggt cctgatcgta ttagagaacc ggccttactt
     1741 tcaaaacagg atattgtttt gactacgtat aatattttaa ctcatgacta tggaactaaa
     1801 ggagatagtc cattacatag cataaggtgg ctaagagtga tcctggatga aggacatgcc
     1861 atacgaaatc caaatgctca gcagacaaaa gctgtacttg acttagaatc agaaagaaga
     1921 tgggttttga caggtactcc aatccagaat tctttaaagg acttgtggtc tcttctttcc
     1981 ttttttaaaac ttaaaccatt tattgataga gaatggtggc atagaacaat acagcgtcct
     2041 gtcacaatgg gagatgaagg aggacttagg cgtttacagt ccctaattaa aaatattaca
     2101 cttagaagaa caaagacaag caaaattaaa ggaaaacctg ttttggagtt accagaacgt
     2161 aaagtattta ttcagcacat tacactttca gatgaagaga gaaagattta tcagtctgtg
     2221 aaaaatgaag gcagagccac tattggaagg tattttaatg aagggactgt cctggcacat
     2281 tatgcagatg tcctgggtct tttgcttaga ctgcggcaaa tttgttgcca tacttacctt
     2341 cttacaaatg cagtgtcttc caatggcccc tcaggaaatg atacacctga agaactgaga
     2401 aagaagttaa taaggaagat gaagttaatt ctgagctcag gttcagatga ggaatgtgca
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HUMHIP116

```
2461 atttgcctgg attctttaac agttcctgtg ataacacatt gtgcacatgt attttgtaaa
2521 ccctgtattt gccaagtcat tcagaatgag cagccacatg ctaaatgccc tttatgcaga
2581 aatgatatac atgaagataa tttattagaa tgtcctccag aagaattagc acgtgacagt
2641 gagaaaaagt ctgatatgga atggacatcc agttcaaaga ttaatgcgct aatgcacgca
2701 ttgactgact taagaaagaa gaatcccaac ataaaaagtt tggttgtttc tcagtttaca
2761 acattcctgt ctttaataga aataccactt aaagcctctg gatttgtgtt tactcgtttg
2821 gatggttcca tggcccaaaa gaaaagagtt gaatcaattc agtgttttca aaacactgaa
2881 gcaggatctc caactataat gcttctgtcc ttaaaagcag gtggagttgg tttgaatctg
2941 tctgcagctt ctcgagtgtt tttaatggat ccagcctgga atcctgctgc tgaagatcag
3001 tgctttgaca gatgccatag acttggtcag aagcaagaag ttatcatcac aaaattcatt
3061 gtaaaggact ctgttgaaga aaatatgctg aaaatacaaa acaaaaagag agaacttgca
3121 gcaggagcct ttggaactaa aaaaccaaat gctgacgaaa tgaaacaagc caaaattaat
3181 gaaatcagaa cattaattga cttaTAAttt gtgggatttt agtaagaaga ctactatatg
                                <- HIP116 cds end
3241 tgagaggcgt gatatctgga tggaagttgg gctggatgat ctccaaagtc gtttcaactc
3301 ttaaagacat cttaatcctg aatgtaaaca attgttatgt gtttagaatc agaatttgat
3361 tttgaacttg agtaattcat ccttacagct atctgtagaa ttagtcatct tttttctt
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LOCUS       HSIL02          801 bp    RNA             PRI       09-MAR-1993
DEFINITION  Human interleukin-2 (IL-2) cDNA sequence.
ACCESSION   V00564
KEYWORDS    interleukin; signal peptide; lymphocyte regulatory molecule.
SOURCE      Human mRNA.
REFERENCE   1  (bases 1 to 801)
  AUTHORS   Taniguchi,T., Matsui,H., Fujita,T., Takaoka,C., Kashima,N.,
            Yoshimoto,R. and Hamuro,J.
  TITLE     Structure and expression of a cloned cDNA for human interleukin-2
  JOURNAL   Nature 302, 305-310 (1983)
REFERENCE   2  (bases 1 to 801)
  AUTHORS   Devos,R., Plaetinck,G., Cheroutre,H., Simons,G., Degrave,W.,
            Tavernier,J., Remaut,E. and Fiers,W.
  TITLE     Molecular cloning of human interleukin 2 cDNA and its expression in
            E. coli
  JOURNAL   Nucleic Acids Res. 11, 4307-4323 (1983)
COMMENT     IL-2 is a cytokine which has been shown to induce HIV gene
            expression (Matsuyama et al. AIDS 5: 1405-1417, 1991).  It may
            mediate this affect by altering the activity of cellular
            transcription factors (Garcia et al. AIDS 8: S3-S17, 1994).
            NCBI gi: 33780
BASE COUNT      282 a    147 c    114 g    258 t
ORIGIN
        1 atcactctct ttaatcacta ctcacagtaa cctcaactcc tgccacaATG tacaggatgc
                                                 IL-2 cds start ->
       61 aactcctgtc ttgcattgca ctaagtcttg cacttgtcac aaacagtgca cctacttcaa
      121 gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta cagatgattt
      181 tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca tttaagtttt
      241 acatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa gaactcaaac
      301 ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga cccagggact
      361 taatcagcaa tatcaacgta atagttctgg aactaaaggg atctgaaaca acattcatgt
      421 gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg attacctttt
      481 gtcaaagcat catctcaaca ctaactTGAt aattaagtgc ttcccactta aaacatatca
                                        <- IL-2 cds end
      541 ggccttctat ttatttaaat atttaaattt tatatttatt gttgaatgta tggtttgcta
      601 cctattgtaa ctattattct taatcttaaa actataaata tggatctttt atgattcttt
      661 ttgtaagccc taggggctct aaaatggttt cacttattta tcccaaaata tttattatta
      721 tgttgaatgt taaatatagt atctatgtag attggttagt aaaactattt aataaatttg
      781 ataaatataa aaaaaaaaaa c
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HUMIL6

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LOCUS       HUMIL6       1125 bp ss-mRNA            PRI       11-JUN-1993
DEFINITION  Human hybridoma growth factor (interleukin 6) cDNA sequence,
            complete cds, clone HGF15.
ACCESSION   M18403
KEYWORDS    hybridoma growth factor; interferon-beta-2; interleukin 6.
SOURCE      Human monocyte mRNA.
REFERENCE   1  (bases 1 to 1125)
  AUTHORS   Brakenhoff,J.P., De Groot,E.R., Evers,R.F., Pannekoek,H. and
            Aarden,L.A.
  TITLE     Molecular cloning and expression of hybridoma growth factor in
            Escherichia coli
  JOURNAL   J. Immunol. 139, 4116-4121 (1987)
COMMENT     IL-6 is a cytokine which has been shown to induce HIV gene
            expression (Matsuyama et al. AIDS 5: 1405-1417, 1991).  It may
            mediate this affect by altering the activity of cellular
            transcription factors (Garcia et al. AIDS 8: S3-S17, 1994).
            Draft entry and computer readable copy of sequence [1] kindly
            provided by J.Brakenhoff 20-SEPT-88.
            NCBI gi: 184631
BASE COUNT      339 a    246 c    233 g    307 t
ORIGIN      10 bp upstream of AvaI site; Chromosome 7p21.
        1 ttctgccctc gagcccaccg ggaacgaaag agaagctcta tctcgcctcc aggagcccag
       61 ctATGaactc cttctccaca agcgccttcg gtccagttgc cttctccctg gggctgctcc
   IL-6 cds ->
      121 tggtgttgcc tgctgccttc cctgccccag tacccccagg agaagattcc aaagatgtag
      181 ccgccccaca cagacagcca ctcacctctt cagaacgaat tgacaaacaa attcggtaca
      241 tcctcgacgg catctcagcc ctgagaaagg agacatgtaa caagagtaac atgtgtgaaa
      301 gcagcaaaga ggcactggca gaaaacaacc tgaaccttcc aaagatggct gaaaaagatg
      361 gatgcttcca atctggattc aatgaggaga cttgcctggt gaaaatcatc actggtcttt
      421 tggagtttga ggtataccta gagtacctcc agaacagatt tgagagtagt gaggaacaag
      481 ccagagctgt gcagatgagt acaaaagtcc tgatccagtt cctgcagaaa aaggcaaaga
      541 atctagatgc aataaccacc cctgacccaa ccacaaatgc cagcctgctg acgaagctgc
      601 aggcacagaa ccagtggctg caggacatga caactcatct cattctgcgc agctttaagg
      661 agttcctgca gtccagcctg agggctcttc ggcaaatgTA Gcatgggcac ctcagattgt
                                                    <- IL-6 cds end
      721 tgttgttaat gggcattcct tcttctggtc agaaacctgt ccactgggca cagaacttat
      781 gttgttctct atggagaact aaaagtatga gcgttaggac actattttaa ttatttttaa
      841 tttattaata tttaaatatg tgaagctgag ttaatttatg taagtcatat ttatattttt
      901 aagaagtacc acttgaaaca ttttatgtat tagttttgaa ataataatgg aaagtggcta
      961 tgcagtttga atatcctttg tttcagagcc agatcatttc ttggaaagtg taggcttacc
     1021 tcaaataaat ggctaactta tacatatttt taaagaaata tttatattgt atttatataa
     1081 tgtataaatg gtttttatac caataaatgg cattttaaaa aattc
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LOCUS       HUMIni1      1857 bp    mRNA            PRI       11-JAN-1994
DEFINITION  Human Ini1 cDNA sequence, complete cds.
ACCESSION   U04847
SOURCE      Human mRNA from HL60 cell line.
REFERENCE   1  (bases 1 to 1857)
  AUTHORS   Kalpana,G.V. and Goff,S.P.
  TITLE     The HIV-1 integrase binds to a novel human protein with sequence
            similarity to the yeast transcription factor SNF5
  JOURNAL   Unpublished
COMMENT     ;
BASE COUNT      457 a    524 c    476 g    400 t
ORIGIN
        1 gccccggccc cgccccagcc ctcctgatcc ctcgcagccc ggctccggcc gcccgcctct
       61 gccgccgcaA TGatgatgat ggcgctgagc aagaccttcg ggcagaagcc cgtgaagttc
    Ini1 cds start ->
      121 cagctggagg acgacggcga gttctacatg atcggctccg aggtgggaaa ctacctccgt
      181 atgttccgag gttctctgta caagagatac ccctcactct ggaggcgact agccactgtg
      241 gaagagagga agaaaatagt tgcatcgtca catggtaaaa aaacaaaacc taacactaag
      301 gatcacggat acacgactct agccaccagt gtgaccctgt taaaagcctc ggaagtggaa
      361 gagattctgg atggcaacga tgagaagtac aaggctgtgt ccatcagcac agagcccccc
      421 acctacctca gggaacagaa ggccaagagg aacagccagt gggtacccac cctgtccaac
      481 agctcccacc acttagatgc cgtgccatgc tccacaacca tcaacaggaa ccgcatgggc
      541 cgagacaaga agagaacctt ccccctttgc tttgatgacc atgacccagc tgtgatccat
      601 gagaacgcat ctcagcccga ggtgctggtc cccatccggc tggacatgga gatcgatggg
      661 cagaagctgc gagacgcctt cacctggaac atgaatgaga agttgatgac gcctgagatg
      721 ttttcagaaa tcctctgtga cgatctggat ttgaacccgc tgacgtttgt gccagccatc
      781 gcctctgcca tcagacagca gatcgagtcc taccccacgg acagcatcct ggaggaccag
      841 tcagaccagc gcgtcatcat caagctgaac atccatgtgg gaaacatttc cctggtggac
      901 cagtttgagt gggacatgtc agagaaggag aactcaccag agaagtttgc cctgaagctg
      961 tgctcggagc tggggttggg cggggagttt gtcaccacca tcgcatacag catccgggga
     1021 cagctgagct ggcatcagaa gacctacgcc ttcagcgaga accctctgcc cacagtggag
     1081 attgccatcc ggaacacggg cgatgcggac cagtggtgcc cactgctgga gactctgaca
     1141 gacgctgaga tggagaagaa gatccgcgac caggacagga acacgaggcg gatgaggcgt
     1201 cttgccaaca cgggcccggc ctggTAAcca gcccatcagc acacggctcc cacggagcat
                                       <- Ini1 cds end
     1261 ctcagaagat tgggccgcct ctcctccatc ttctggcaag gacagaggcg aggggacagc
     1321 ccagcgccat cctgaggatc gggtgggggt ggagtggggg cttccaggtg gcccttcccg
     1381 gtacacattc catttgttga gccccagtcc tgccccccac cccaccctcc ctacccctcc
     1441 ccagtctctg gggtcaggaa gaaaccttat tttaggttgt gttttgtttt tgtataggag
     1501 ccccaggcag ggctagtaac agtttttaaa taaaaggcaa caggtcatgt tcaatttctt
     1561 aaatctagtg tctttatttc ttctgttaca atagtgttgc ttgtgtaagc aggttagagt
     1621 gcacagtgtc cccaattgtt cctggcactg caaaaccaaa ttaaacaatc ccacaaagaa
     1681 ttctgacatc aatgtgtttt cctcagtcag gtctatttca agattctaga agttcctttt
     1741 gtaaaacttg cctttaaaac tcttcctcct aatgccatca gatctcttaa cattggctca
     1801 ctgtgggatc tttcctctta ggttgaattt ctacgtgaat atcaaagtgc ctttttc
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HUMKUP70

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LOCUS       HUMKUP70     2086 bp ss-mRNA            PRI       15-DEC-1989
DEFINITION  Human lupus p70 (Ku) autoantigen protein cDNA sequence, complete
            cds.
ACCESSION   J04611
KEYWORDS    Ku; autoantigen; p70 autoantigen.
SOURCE      Human mRNA from hepatoma G2 cell line.
REFERENCE   1  (bases 1 to 2086)
  AUTHORS   Reeves,W.H. and Sthoeger,Z.M.
  TITLE     Molecular cloning of cDNA encoding the p70 (Ku) lupus autoantigen
  JOURNAL   J. Biol. Chem. 264, 5047-5052 (1989)
COMMENT     The HIV-1 leader RNA, TAR, forms a stem-bulge-loop structure
            of approximately 60+ nucleotides.  Since TAR RNA binds many
            cellular proteins, it is thought to play a role in gene
            regulation.  Recently, it has been reported that the human
            lupus autoantigen Ku binds to the loop of HIV-1 TAR ( Kaczmarski
            and Khan, Biochem. Biophys. Res. Communications 196:935-942).
            Draft entry and computer-readable sequence [1] kindly submitted by
            W.H.Reeves, 21-FEB-1989.
            NCBI gi: 178649
BASE COUNT      589 a    461 c    550 g    486 t
ORIGIN
        1 cgcttccctg cgccaaagtg agcagtagcc aacATGtcag ggtgggagtc atattacaaa
              Lupus autoantigen Ku cds start ->
       61 accgagggcg atgaagaagc agaggaagaa caagaagaga accttgaagc aagtggagac
      121 tataaatatt caggaagaga tagtttgatt tttttggttg atgcctccaa ggctatgttt
      181 gaatctcaga gtgaagatga gttgacacct tttgacatga gcatccagtg tatccaaagt
      241 gtgtacatca gtaagatcat aagcagtgat cgagatctct tggctgtggt gttctatggc
      301 accgagaaag acaaaaattc agtgaatttt aaaaatattt acgtcttaca ggagctggat
      361 aatccaggtg caaaacgaat tctagagctt gaccagttta aggggcagca gggacaaaaa
      421 cgtttccaag acatgatggg ccacggatct gactactcac tcagtgaagt gctgtgggtc
      481 tgtgccaacc tctttagtga tgtccaattc aagatgagtc ataagaggat catgctgttc
      541 accaatgaag acaaccccca tggcaatgac agtgccaaag ccagccgggc caggaccaaa
      601 gccggtgatc tccgagatac aggcatcttc cttgacttga tgcacctgaa gaaacctggg
      661 ggctttgaca tatccttgtt ctacagagat atcatcagca tagcagagga tgaggacctc
      721 agggttcact ttgaggaatc cagcaagcta gaagacctgt tgcggaaggt tcgcgccaag
      781 gagaccagga agcgagcact cagcaggtta aagctgaagc tcaacaaaga tatagtgatc
      841 tctgtgggca tttataatct ggtccagaag gctctcaagc ctcctccaat aaagctctat
      901 cgggaaacaa atgaaccagt gaaaaccaag acccggacct ttaatacaag tacaggcggt
      961 ttgcttctgc ctagcgatac caagaggtct cagatctatg ggagtcgtca gattatactg
     1021 gagaaagagg aaacagaaga gctaaaacgg tttgatgatc caggtttgat gctcatgggt
     1081 ttcaagccgt tggtactgct gaagaaacac cattacctga ggccctccct gttcgtgtac
     1141 ccagaggagt cgctggtgat tgggagctca accctgttca gtgctctgct catcaagtgt
     1201 ctggagaagg aggttgcagc attgtgcaga tacacacccc gcaggaacat ccctccttat
     1261 tttgtggctt tggtgccaca ggaagaagag ttggatgacc agaaaattca ggtgactcct
     1321 ccaggcttcc agctggtctt tttacccttt gctgatgata aaaggaagat gccctttact
     1381 gaaaaaatca tggcaactcc agagcaggtg ggcaagatga aggctatcgt tgagaagctt
     1441 cgcttcacat acagaagtga cagctttgag aaccccgtgc tgcagcagca cttcaggaac
     1501 ctggaggcct tggccttgga tttgatggag ccggaacaag cagtggacct gacattgccc
     1561 aaggttgaag caatgaataa aagactgggc tccttggtgg atgagtttaa ggagcttgtt
     1621 tacccaccag attacaatcc tgaagggaaa gttaccaaga gaaaacacga taatgaaggt
     1681 tctggaagca aaaggcccaa ggtggagtat tcagaagagg agctgaagac ccacatcagc
     1741 aagggtacgc tgggcaagtt cactgtgccc atgctgaaag aggcctgccg ggcttacggg
     1801 ctgaagagtg gtctgaagaa gcaggagctg ctggaagccc tcaccaagca cttccaggac
     1861 TGAccagagg ccgcgcgtcc agctgccctt ccgcagtgtg gccaggctgc ctggccttgt
           <- Lupus autoantigen Ku cds end
     1921 cctcagccag ttaaaatgtg tttctcctga gctaggaaga gtctacccga cataagtcga
     1981 gggactttat gtttttgagg ctttctgttg ccatggtgat ggtgtagccc tcccactttg
     2041 ctgttcctta ctttactgcc tgaataaaga gccctaagtt tgtact
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LOCUS HUMKUP86 3052 bp ss-mRNA PRI 11-JUN-1993
DEFINITION Human lupus p86 (Ku) autoantigen cDNA sequence, complete cds.
ACCESSION J04977
KEYWORDS Ku antigen; nonhistone DNA binding protein; nuclear protein.
SOURCE Human fetal liver mRNA.
REFERENCE 1 (bases 1 to 3052)
AUTHORS Yaneva,M., Wen,J., Ayala,A. and Cook,R.
TITLE cDNA derived amino acid sequence of the 86kDa subunit of the Ku antigen
JOURNAL J. Biol. Chem. 264, 13407-13411 (1989)
COMMENT The HIV-1 leader RNA, TAR, forms a stem-bulge-loop structure of approximately 60+ nucleotides. Since TAR RNA binds many cellular proteins, it is thought to play a role in gene regulation. Recently, it has been reported that the human lupus autoantigen Ku binds to the loop of HIV-1 TAR (Kaczmarski and Khan, Biochem. Biophys. Res. Communications 196:935-942).
Draft entry and computer-readable sequence for [1] kindly submitted by M.Yaneva, 02-JUN-1989.
NCBI gi: 186791
BASE COUNT 906 a 592 c 708 g 846 t
ORIGIN 58 bp upstream of PvuII site.

```
        1 ggcgggcgac caaagcgcct gaggaccggc aacATGgtgc ggtcggggaa taaggcagct
                  Lupus autoantigen Ku cds start ->
       61 gttgtgctgt gtatggacgt gggctttacc atgagtaact ccattcctgg tatagaatcc
      121 ccatttgaac aagcaaagaa ggtgataacc atgtttgtac agcgacaggt gtttgctgag
      181 aacaaggatg agattgcttt agtcctgttt ggtacagatg gcactgacaa tccccttttct
      241 ggtggggatc agtatcagaa catcacagtg cacagacatc tgatgctacc agattttgat
      301 ttgctggagg acattgaaag caaaatccaa ccaggttctc aacaggctga cttcctggat
      361 gcactaatcg tgagcatgga tgtgattcaa catgaaacaa taggaaagaa gtttgagaag
      421 aggcatattg aaatattcac tgacctcagc agccgattca gcaaaagtca gctggatatt
      481 ataattcata gcttgaagaa atgtgacatc tccctgcaat tcttcttgcc tttctcactt
      541 ggcaaggaag atggaagtgg ggacagagga gatggcccct ttcgcttagg tggccatggg
      601 ccttcctttc cactaaaagg aattaccgaa cagcaaaaag aaggtcttga gatagtgaaa
      661 atggtgatga tatctttaga aggtgaagat gggttggatg aaatttattc attcagtgag
      721 agtctgagaa aactgtgcgt cttcaagaaa attgagaggc attccattca ctggccctgc
      781 cgactgacca ttggctccaa tttgtctata aggattgcag cctataaatc gattctacag
      841 gagagagtta aaaagacttg gacagttgtg gatgcaaaaa ccctaaaaaa agaagatata
      901 caaaaagaaa cagtttattg cttaaatgat gatgatgaaa ctgaagtttt aaaagaggat
      961 attattcaag ggttccgcta tggaagtgat atagttcctt tctctaaagt ggatgaggaa
     1021 caaatgaaat ataaatcgga ggggaagtgc ttctctgttt tgggattttg taaatcttct
     1081 caggttcaga gaagattctt catgggaaat caagttctaa aggtctttgc agcaagagat
     1141 gatgaggcag ctgcagttgc actttcctcc ctgattcatg ctttggatga cttagacatg
     1201 gtggccatag ttcgatatgc ttatgacaaa agagctaatc ctcaagtcgg cgtggctttt
     1261 cctcatatca agcataacta tgagtgttta gtgtatgtgc agctgccttt catggaagac
     1321 ttgcggcaat acatgttttc atccttgaaa aacagtaaga aatatgctcc caccgaggca
     1381 cagttgaatg ctgttgatgc tttgattgac tccatgagct tggcaaagaa agatgagaag
     1441 acagacaccc ttgaagactt gtttccaacc accaaaatcc caaatcctcg atttcagaga
     1501 ttatttcagt gtctgctgca cagagcttta catccccggg agcctctacc cccaattcag
     1561 cagcatattt ggaatatgct gaatcctccc gctgaggtga caacgaaaag tcagattcct
     1621 ctctctaaaa taaagaccct ttttcctctg attgaagcca agaaaaagga tcaagtgact
     1681 gctcaggaaa ttttccaaga caaccatgaa gatggaccta cagctaaaaa attaaagact
     1741 gagcaagggg gagcccactt cagcgtctcc agtctggctg aaggcagtgt cacctctgtt
     1801 ggaagtgtga atcctgctga aaacttccgt gttctagtga aacagaagaa ggccagcttt
     1861 gaggaagcga gtaaccagct cataaatcac atcgaacagt ttttggatac taatgaaaca
     1921 ccgtatttta tgaagagcat agactgcatc cgagccttcc gggaagaagc cattaagttt
     1981 tcagaagagc agcgctttaa caacttcctg aaagcccttc aagagaaagt ggaaattaaa
     2041 caattaaatc atttctggga aattgttgtc caggatggaa ttactctgat caccaaagag
     2101 gaagcctctg gaagttctgt cacagctgag gaagccaaaa agtttctggc ccccaaagac
     2161 aaaccaagtg gagacacagc agctgtattt gaagaaggtg gtgatgtgga cgatttattg
```

```
2221 gacatgataT AGgtcgtgga tgtatgggga atctaagaga gctgccatcg ctgtgatgct
                <-  Lupus autoantigen Ku cds end
2281 gggagttcta acaaaacaag ttggatgcgg ccattcaagg ggagccaaat tctcaagaaa
2341 ttcccagcag gttacctgga ggcggatcat ctaattctct gtggaatgaa tacacacata
2401 tatattacaa gggataattt agaccccata caagtttata aagagtcatt gttattttct
2461 ggttggtgta ttatttttc tgtggtctta ctgatctttg tatattacat acatgctttg
2521 aagtttctgg aaagtagatc ttttcttgac ctagtatatc agtgacagtt gcagcccttg
2581 tgatgtgatt agtgtctcat gtggaaccat ggcatggtta ttgatgagtt tcttaaccct
2641 ttccagagtc ctcctttgcc tgatcctcca acagctgtca cagcttgtgt tgagcaagca
2701 gtagcatttg cttcctccca acaagcagct gggttaggaa aaccatgggt aaggacggac
2761 tcacttctct ttttagttga ggccttctag ttaccacatt actctgcctc tgtatatagg
2821 tggttttctt taagtggggt gggaagggga gcacaatttc ccttcatact ccttttaagc
2881 agtgagttat ggtggtggtc tcatgaagaa aagacctttt ggcccaatct ctgccatatc
2941 agtgaacctt tagaaactca aaaactgaga aatttactac agtagttaga attatatcac
3001 ttcactgttc tctacttgca agcctcaaag agagaaagtt tcgttatatt gg
```

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LOCUS       HUMLA        1620 bp ss-mRNA            PRI       14-MAY-1991
DEFINITION  Human lupus autoantigen La cDNA sequence, clones
            lambda-La[2.1,26.2], complete cds.
ACCESSION   J04205 M11108
KEYWORDS    La antigen; La protein; SS-B antigen; autoantigen.
SOURCE      Human (adult) liver mRNA.
REFERENCE   1  (bases 223 to 391)
  AUTHORS   Chambers,J.C. and Keene,J.D.
  TITLE     Isolation and analysis of cDNA clones expressing human lupus La
            antigen
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119 (1985)
REFERENCE   2  (bases 1 to 1620)
  AUTHORS   Chambers,J.C., Kenan,D., Martin,B.J. and Keene,J.D.
  TITLE     Genomic structure and amino acid sequence domains of the human La
            autoantigen
  JOURNAL   J. Biol. Chem. 263, 18043-18051 (1989)
COMMENT     The HIV-1 leader RNA, TAR, forms a stem-bulge-loop structure
            of approximately 60+ nucleotides.  Since TAR RNA binds many
            cellular proteins, it is thought to play a role in gene
            regulation.  Recently, it has been reported that the human
            lupus autoantigen La recognizes U-residues within the overall
            context of the TAR secondary structure [Chang et al. J. Virol.
            68, 7008 (1994); Svitkin et al. J. Virol. 68, 7001 (1994)].
            Draft entry and computer-readable sequence for [2] kindly provided
            by J.D.Keene, 28-FEB-1989.
            NCBI gi: 178686
BASE COUNT      620 a    227 c    363 g    410 t
ORIGIN      Chromosome 2.
        1 ccggcggcgc tgggaggtgg agtcgttgct gttgctgttt gtgagcctgt ggcgcggctt
       61 ctgtgggccg gaaccttaaa gatagccgta ATGgctgaaa atggtgataa tgaaaagatg
            lupus La autoantigen cds start ->
      121 gctgccctgg aggccaaaat ctgtcatcaa attgagtatt attttggcga cttcaatttg
      181 ccacgggaca agtttctaaa ggaacagata aaactggatg aaggctgggt acctttggag
      241 ataatgataa aattcaacag gttgaaccgt ctaacaacag actttaatgt aattgtggaa
      301 gcattgagca aatccaaggc agaactcatg gaaatcagtg aagataaaac taaaatcaga
      361 aggtctccaa gcaaacccct acctgaagtg actgatgagt ataaaaatga tgtaaaaaac
      421 agatctgttt atattaaagg cttcccaact gatgcaactc ttgatgacat aaaagaatgg
      481 ttagaagata aaggtcaagt actaaatatt cagatgagaa gaacattgca taaagcattt
      541 aagggatcaa tttttgttgt gtttgatagc attgaatctg ctaagaaatt tgtagagacc
      601 cctggccaga agtacaaaga aacagacctg ctaatacttt tcaaggacga ttactttgcc
      661 aaaaaaaatg aagaaagaaa acaaaataaa gtggaagcta aattaagagc taaacaggag
      721 caagaagcaa aacaaaagtt agaagaagat gctgaaatga aatctctaga agaaaagatt
      781 ggatgcttgc tgaaattttc gggtgattta gatgatcaga cctgtagaga agatttacac
      841 atacttttct caaatcatgg tgaaataaaa tggatagact tcgtcagagg agcaaaagag
      901 gggataattc tatttaaaga aaaagccaag gaagcattgg gtaaagccaa agatgcaaat
      961 aatggtaacc tacaattaag gaacaaagaa gtgacttggg aagtactaga aggagaggtg
     1021 gaaaaagaag cactgaagaa aataatagaa gaccaacaag aatccctaaa caaatggaag
     1081 tcaaaaggtc gtagatttaa aggaaaagga aagggtaata aagctgccca gcctgggtct
     1141 ggtaaaggaa aagtacagtt tcagggcaag aaaacgaaat ttgctagtga tgatgaacat
     1201 gatgaacatg atgaaaatgg tgcaactgga cctgtgaaaa gagcaagaga agaaacagac
     1261 aaagaagaac ctgcatccaa acaacagaaa acagaaaatg gtgctggaga ccagTAGttt
                                                                    <- lupus
                                                                  La autoantigen
     1321 agtaaaccaa ttttttattc attttaaata ggttttaaac gacttttgtt tgcggggctt
     1381 ttaaaaggaa aaccgaatta ggtccacttc aatgtccacc tgtgagaaag gaaaaatttt
     1441 tttgttgttt aacttgtctt tttgttatgc aaatgagatt tctttgaatg tattgttctg
     1501 tttgtgttat ttcagatgat tcaaatatca aaaggaagat tcttccatta aattgccttt
     1561 gtaatatgag aatgtattag tacaaactaa ctaataaaat atatactata tgaaaagagc
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HUMLCK

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LOCUS       HUMLCK       2032 bp ss-mRNA            PRI       23-APR-1992
DEFINITION  Human lymphocyte-specific protein tyrosine kinase (lck) cDNA
            sequence, complete cds, clones HK[28,8.2,5].
ACCESSION   M36881
KEYWORDS    lymphocyte-specific protein tyrosine kinase.
SOURCE      Human adult peripheral blood lymphocyte mRNA.
REFERENCE   1  (bases 1 to 2032)
  AUTHORS   Perlmutter,R.M., Marth,J.D., Lewis,D.B., Peet,R., Ziegler,S.F. and
            Wilson,C.B.
  TITLE     Structure and expression of lck transcripts in human lymphoid cells
  JOURNAL   J. Cell. Biochem. 38, 117-126 (1988)
COMMENT     A group of investigators has found that HIV-1 Nef binds directly to
            the lck-kinase in vitro (D. McPhee personal communication).
            NCBI gi: 187033
BASE COUNT      450 a    576 c    584 g    422 t
ORIGIN
        1 cgcctggacc atgtgaatgg ggccagaggg ctcccgggct gggcagggac cATGggctgt
                                              lck kinase cds start ->
       61 ggctgcagct cacacccgga agatgactgg atggaaaaca tcgatgtgtg tgagaactgc
      121 cattatccca tagtccgact ggatgggaag ggcaggctgc tcatccgaaa tggctctgag
      181 gtgcgggacc cactggttac ctacgaaggc tccaatccgc cggcttcccc actgcaagac
      241 aacctggtta tcgctctgca cagctatgag ccctctcacg acggagatct gggctttgag
      301 aaggggggaac cactccgcat cctggagcag agcggcgagt ggtggaaggc gcagtccctg
      361 accacgggcc aggaaggctt catccccttc aattttgtgg ccaaagcgaa cagcctggag
      421 cccgaaccct ggttcttcaa gaacctgagc cgcaaggacg cggagcggca gctcctggcg
      481 cccgggaaca ctcacggctc cttcctcatc cgggagagcg agagcaccgc cgggtccttt
      541 tcactgtcgg tccgggactt cgaccaaaac cagggagagg tggtgaaaca ttacaagatc
      601 cgtaatctgg acaacggtgg cttctacatc tcccctcgaa tcacttttcc cggcctgcat
      661 gaactggtcc gccattacac caatgcttca gatgggctgt gcacacggtt gagccgcccc
      721 tgccagaccc agaagcccca gaagccgtgg tgggaggacg agtgggaggt tcccagggag
      781 acgctgaagc tggtggagcg gctgggggct gcacagttcg gggaggtgtg gatggggtac
      841 tacaacgggc acacgaaggt ggcggtgaag agcctgaagc agggcagcat gtccccggac
      901 gccttcctgg ccgaggccaa cctcatgaag cagctgcaac accagcggct ggttcggctc
      961 tacgctgtgg tcacccagga gcccatctac atcatcactg aatacatgga gaatgggagt
     1021 ctagtggatt ttctcaagac cccttcaggc atcaagttga ccatcaacaa actcctggac
     1081 atggcagccc aaattgcaga aggcatggca ttcattgaag agcggaatta tattcatcgt
     1141 gaccttcggg ctgccaacat tctggtgtct gacaccctga gctgcaagat tgcagacttt
     1201 ggcctagcac gcctcattga ggacaacgag tacacagcca gggagggggc caagtttccc
     1261 attaagtgga cagcgccaga agccattaac tacgggacat tcaccatcaa gtcagatgtg
     1321 tggtcttttg ggatcctgct gacggaaatt gtcacccacg gccgcatccc ttacccaggg
     1381 atgaccaacc cggaggtgat tcagaacctg gagcgaggct accgcatggt gcgccctgac
     1441 aactgtccag aggagctgta ccaactcatg aggctgtgct ggaaggagcg cccagaggac
     1501 cggcccacct ttgactacct gcgcagtgtg ctggaggact tcttcacggc cacagagggc
     1561 cagtaccagc ctcagcctTG Agaggaggcc ttgagaggcc ctggggttct ccccctttct
                             <- lck kinase cds end
     1621 ctccagcctg acttggggag atggagttct tgtgccatag tcacatggcc tatgcacata
     1681 tggactctgc acatgaatcc cacccacatg tgacacatat gcaccttgtg tctgtacacg
     1741 tgtcctgtag ttgcgtggac tctgcacatg tcttgtgcat gtgtagcctg tgcatgtatg
     1801 tcttggacac tgtacaaggt acccctttct ggctctccca tttcctgaga ccaccagaga
     1861 gaggggagaa gcctgggatt gacagaagct tctgcccacc tacttttctt tcctcagatc
     1921 atccagaagt tcctgaaggg ccaggacttt atctaatacc tctgtgtgct cctccttggt
     1981 gcctggcctg gcacacatca ggagttcaat aaatgtctgt tgatgactgc cg
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LOCUS       HUMMSS1      1478 bp ss-mRNA            PRI       24-JUL-1992
DEFINITION  Human MSS1 cDNA sequence, complete cds.
ACCESSION   D11094
KEYWORDS    mammalian suppressor of sgv1; transactivation factor.
SOURCE      Human.mRNA from Hela cell line.
REFERENCE   1  (bases 1 to 1478)
  AUTHORS   Shibuya,H., Irie,K., Ninomiya-Tsuji,J., Goebl,M., Taniguchi,T. and
            Matsumoto,K.
  TITLE     New human gene encoding a positive modulator of HIV Tat-mediated
            transactivation
  JOURNAL   Nature 357, 700-702 (1992)
COMMENT     MSS1 is part of a large family of proteins related to the 26S
            protease from human erythrocytes.  Each of these proteins has
            Tat-binding activity [1]. MSS1 positively affects gene expression
            through its interaction with Tat [1].
            NCBI gi: 219930
BASE COUNT      439 a    287 c    375 g    377 t
ORIGIN
        1 ccattgtgct ctaaagggaa ggtgctgtgt aatcattaag gagcggaggc ttttggagct
       61 gctaaaATGc cggattacct cggtgccgat cagcggaaga ccaaagagga tgagaaggac
 MSS1 cds start ->
      121 gacaagccca tccgagctct ggatgagggg gatattgcct tgttgaaaac ttatggtcag
      181 agcacttact ctaggcagat caagcaagtt gaagatgaca ttcagcaact tctcaagaaa
      241 attaatgagc tcactggtat taaagaatct gacactggcc tggccccacc agcactctgg
      301 gatttggctg cagataagca gacactccag agtgaacagc ctttacaggt tgccaggtgt
      361 acaaagataa tcaatgctga ttcggaggac ccaaaataca ttatcaacgt aaagcagttt
      421 gccaagtttg tggtggacct tagtgatcag gtggcaccta ctgacattga agaagggatg
      481 agagtgggcg tggatagaaa taaatatcaa attcacattc cattgcctcc taagattgac
      541 ccaacagtta ccatgatgca ggtggaagag aaacctgatg tcacatacag tgatgttggt
      601 ggctgtaagg aacagattga gaaactgcga gaagtagttg aaaccccatt acttcatcca
      661 gagaggtttg tgaaccttgg cattgagcct cccaagggcg tgctgctctt tggtccaccc
      721 ggtacaggca agacactctg tgcgcgggca gttgctaatc ggactgatgc gtgcttcatt
      781 cgagttattg gatctgagct tgtacagaaa tacgtcggtg agggggctcg aatggttcgt
      841 gaactctttg aaatggccag aacaaaaaaa gcctgcctta tcttctttga tgaaattgat
      901 gctattggag gggctcgttt tgatgatggt gctggaggtg acaatgaagt gcagagaaca
      961 atgttggaac tgatcaatca gcttgatggt tttgatcctc gaggcaatat taaagtgctg
     1021 atggccacta acagacctga tactttggat ccagcactga tgaggccagg gagattggat
     1081 agaaaaattg aatttagctt gcccgatcta gagggtcgga cccacatatt taagattcac
     1141 gctcgttcaa tgagtgttga aagagatatc agatttgaac tgttagcacg actgtgtcca
     1201 aatagcactg gtgctgagat tagaagcgtc tgcacagagg ctggtatgtt tgccatcaga
     1261 gcacggcgaa aaattgctac cgagaaggat ttcttggaag ctgtaaataa ggtcattaag
     1321 tcttatgcca aattcagtgc tactcctcgt tacatgacat acaacTGAac cctgaaggct
                                                          <- MSS1 cds end
     1381 ttcaagtgaa aactttaaat tggaatccta accttatata gacttgttaa taaccaattc
     1441 ataaacaaat aaatggcttc aactttagag cacaatgg
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HUMNB23

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LOCUS       HUMNB23      1293 bp ss-mRNA            PRI       26-OCT-1992
DEFINITION  Human nucleolar protein (B23) cDNA sequence, complete cds,
            clone lambda-Zap.
ACCESSION   M26697
KEYWORDS    B23 protein; nucleolar phosphoprotein; nucleolar protein;
            numatrin.
SOURCE      Human amnion mRNA from cell line U.
REFERENCE   1  (bases 1 to 1293)
  AUTHORS   Zhang,X.T., Thomis,D.C. and Samuel,C.E.
  TITLE     Isolation and characterization of a molecular cDNA clone of a human
            mRNA from interferon-treated cells encoding nucleolar protein B23,
            numatrin
  JOURNAL   Biochem. Biophys. Res. Commun. 164, 176-184 (1989)
COMMENT     Rev localizes to the nucleolus, and work by Laemmli and colleagues
            (Fankhauser et al. Mol. Cell. Biol. 11:2567-2575) has demonstrated
            a tight association between Rev and the nucleolar B23 protein.
            This protein-protein complex likely directs the subcellular
            localization of Rev.
            Draft entry and computer-readable copy of sequence [1] kindly
            submitted by C.E.Samuel, 03-AUG-1989.
            NCBI gi: 189311
BASE COUNT      422 a    223 c    310 g    337 t      1 others
ORIGIN
        1 cgggattccg tcctgcgcgg ttgttctctg gagcagcgtt cttttatctc cgtccgcctt
       61 ctctcctacc taagtgcgtg ccgccacccg ATGgaagatt cgatggacat ggacatgagc
           nucleolar protein B23 cds start ->
      121 cccctgaggc cccagaacta tcttttcggt tgtgaactaa aggccgacaa agattatcac
      181 tttaaggtgg ataatgatga aaatgagcac cagttatctt taagaacggt cagtttaggg
      241 gctggtgcaa aggatgagtt gcacattgtt gaagcagagg caatgaatta cgaaggcagt
      301 ccaattaaag taacactggc aactttgaaa atgtctgtac agccaacngt ttcccttggg
      361 ggctttgaaa taacaccacc agtggtctta aggttgaagt gtggttcagg gccagtgcat
      421 attagtggac agcacttagt agctgtggag gaagatgcag agtcagaaga tgaagaggag
      481 gaggatgtga aactcttaag tatatctgga aagcggtctg cccctggagg tggtagcaag
      541 gttccacaga aaaaagtaaa acttgctgct gatgaagatg atgacgatga tgatgaagag
      601 gatgatgatg aagatgatga tgatgatgat tttgatgatg aggaagctga agaaaaagcg
      661 ccagtgaaga aatctatacg agatactcca gccaaaaatg cacaaaagtc aaatcagaat
      721 ggaaaagact caaaaccatc atcaacacca agatcaaaag gacaagaatc cttcaagaaa
      781 caggaaaaaa ctcctaaaac accaaaagga cctagttctg tagaagacat taaagcaaaa
      841 atgcaagcaa gtatagaaaa aggtggttct cttcccaaag tggaagccaa attcatcaat
      901 tatgtgaaga attgcttccg gatgactgac caagaggcta ttcaagatct ctggcagtgg
      961 aggaagtctc ttTAAgaaaa tagtttaaac aatttgttaa aaaattttcc gtcttatttc
                      <- nucleolar protein B23 cds end
     1021 atttctgtaa cagttgatat ctggctgtcc tttttataat gcagagtgag aactttccct
     1081 accgtgtttg ataaatgttg tccaggttct attgccaaga atgtgttgtc caaaatgcct
     1141 gtttagtttt taaagatgga actccaccct ttgcttggtt ttaagtatgt atggaatgtt
     1201 atgataggac atagtagtag cggtggtcag acatggaaat ggtggggaga caaaaatata
     1261 catgtgaaat aaaactcagt attttaataa agt
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LOCUS       HNFAT         2743 bp    mRNA            PRI       08-JUL-1994
DEFINITION  Human NF-AT cDNA sequence, complete cds.
ACCESSION   U08015
SOURCE      Human cDNA from Jurkat cell library.
REFERENCE   1  (bases 1 to 2743)
  AUTHORS   Northrop,J.P., Ho,S.N., Chen,L., Thomas,D.J., Timmerman,L.A.,
            Nolan,G.P., Admon,A. and Crabtree,G.R.
  TITLE     NF-AT components define a family of transcription factors targeted
            in T-cell activation
  JOURNAL   Nature 369, 497-502 (1994)
COMMENT     NFAT, nuclear factor from activated T cells, is an intermediating
            transducer of signals initiated at the T-cell antigen receptor.
            Within the U3 region of the HIV-1 LTR, there are NFAT binding
            motifs present from -216 to -254. Recent evidence suggests that
            NFAT binding activity results from the interaction of three
            discrete polypeptides, NFATp (McCaffrey et al. Science 262:
            750-754), Fos and Jun (Yaseen et al. J. Biol. Chem. 268:
            14285-14293).
            NCBI gi: 500631
BASE COUNT      529 a    959 c    788 g    467 t
ORIGIN
        1 gaattccgca gggcgcgggc accggggcgc gggcagggct cggagccacc gcgcaggtcc
       61 tagggccgcg gccgggcccc gccacgcgcg cacacgcccc tcgatgactt tcctccgggg
      121 cgcgcggcgc tgagcccggg gcgagggctg tcttcccgga gacccgaccc cggcagcgcg
      181 gggcggccac ttctcctgtg cctccgcccg ctgctccact ccccgccgcc gccgcgcggA
                                                          NFAT cds start ->
      241 TGccaagcac cagctttcca gtcccttcca agtttccact tggccctgcg gctgcggtct
      301 tcgggagagg agaaactttg gggcccgcgc cgcgcgccgg cggcaccatg aagtcagcgg
      361 aggaagaaca ctatggctat gcatcctcca acgtcagccc cgccctgccg ctccccacgg
      421 cgcactccac cctgccggcc ccgtgccaca accttcagac ctccacaccg ggcatcatcc
      481 cgccggcgga tcacccctcg gggtacggag cagctttgga cggtgggccc gcgggctact
      541 tcctctcctc cggccacacc aggcctgatg gggcccctgc cctggagagt cctcgcatcg
      601 agataacctc gtgcttgggc ctgtaccaca acaataacca gtttttccac gatgtggagg
      661 tggaagacgt cctccctagc tccaaacggt ccccctccac ggccacgctg agtctgccca
      721 gcctggaggc ctacagagac ccctcgtgcc tgagcccggc cagcagcctg tcctcccgga
      781 gctgcaactc agaggcctcc tcctacgagt ccaactactc gtacccgtac gcgtcccccc
      841 agacgtcgcc atggcagtct ccctgcgtgt ctcccaagac cacggacccc gaggagggct
      901 ttccccgcgg gctgggggcc tgcacactgc tgggttcccc gcagcactcc ccctccacct
      961 cgccccgcgc cagcgtcact gaggagagct ggctgggtgc ccgctcctcc agacccgcgt
     1021 ccccttgcaa caagaggaag tacagcctca acggccggca gccgccctac tcaccccacc
     1081 actcgcccac gccgtccccg cacggctccc cgcgggtcag cgtgaccgac gactcgtggt
     1141 tgggcaacac cacccagtac accagctcgg ccatcgtggc cgccatcaac gcgctgacca
     1201 ccgacagcag cctggacctg ggagatggcg tccctgtcaa gtcccgcaag accaccctgg
     1261 agcagccgcc ctcagtggcg ctcaaggtgg agcccgtcgg ggaggacctg ggcagccccc
     1321 cgcccccggc cgacttcgcg cccgaagact actcctcttt ccagcacatc aggaagggcg
     1381 gcttctgcga ccagtacctg gcggtgccgc agcaccccta ccagtgggcg aagcccaagc
     1441 ccctgtcccc tacgtcctac atgagcccga ccctgcccgc cctggactgg cagctgccgt
     1501 cccactcagg cccgtatgag cttcggattg aggtgcagcc caagtcccac caccgagccc
     1561 actacgagac ggagggcagc cgggggccg tgaaggcgtc ggccggagga caccccatcg
     1621 tgcagctgca tggctacttg gagaatgagc cgctgatgct gcagcttttc attgggacgg
     1681 cggacgaccg cctgctgcgc ccgcacgcct tctaccaggt gcaccgcatc acagggaaga
     1741 ccgtgtccac caccagccac gaggctatcc tctccaacac caaagtcctg gagatcccac
     1801 tcctgccgga gaacagcatg cgagccgtca ttgactgtgc cggaatcctg aaactcagaa
     1861 actccgacat tgaacttcgg aaaggagaga cggacatcgg gaggaagaac acacgggtac
     1921 ggctggtgtt ccgcgttcac gtcccgcaac ccagcggccg cacgctgtcc ctgcaggtgg
     1981 cctccaaccc catcgaatgc tcccagcgct cagctcagga gctgcctctg gtggagaagc
     2041 agagcacgga cagctatccg gtcgtgggcg ggaagaagat ggtcctgtct ggccacaact
     2101 tcctgcagga ctccaaggtc attttcgtgg agaaagcccc agatggccac catgtctggg
     2161 agatggaagc gaaaactgac cgggacctgt gcaagccgaa ttctctggtg gttgagatcc
```

HNFAT

```
2221 cgccatttcg gaatcagagg ataaccagcc ccgttcacgt cagtttctac gtctgcaacg
2281 ggaagagaaa gcgaagccag taccagcgtt tcacctacct tcccgccaac ggtaacgcca
2341 tctttctaac cgtaagccgt gaacatgagc gcgtggggtg ctttttcTAA agacgcagaa
                                                        <- NFAT cds end
2401 acgacgtcgc cgtaaagcag cgtggcgtgt tgcacattta actgtgtgat gtcccgttag
2461 tgagaccgag ccatcgatgc cctgaaaagg aaaggaaaag ggaagcttcg gatgcatttt
2521 ccttgatccc tgttgggggt ggggggcggg ggttgcatac tcagatagtc acggttattt
2581 tgcttcttgc gaatgtataa cagccaaggg gaaaacatgg ctcttctgct ccaaaaaact
2641 gagggggtcc tggtgtgcat ttgcacccta aagctgctta cggtgaaaag gcaaataggt
2701 atagctattt tgcaggcacc tttaggaata aactttgctt tta
```

```
LOCUS       HUMNFKB      3625 bp ss-mRNA            PRI       20-FEB-1991
DEFINITION  Human nuclear factor kappa-B (NF-kappa-B) DNA binding subunit
            sequence, complete cds.
ACCESSION   M58603
KEYWORDS    nuclear factor kappa-B DNA binding subunit.
SOURCE      Human premyeloid mRNA.
REFERENCE   1  (bases 1 to 3625)
  AUTHORS   Meyer,R., Hatada,E.N., Hohmann,H.-P., Haiker,M., Bartsch,C.,
            Roethlisberger,U., Lahm,H.-W., Schlaeger,E.J., van Loon,A.P. and
            Scheidereit,C.
  TITLE     Cloning of the DNA-binding subunit of human nuclear factor kappa-B:
            The level of its mRNA is strongly regulated by phorbol ester or
            tumor necrosis factor alpha
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88, 966-970 (1991)
COMMENT     NF-kappa-beta motifs are perhaps the best characterized sequence
            elements in the HIV-1 LTR (Nabel and Baltimore Nature 326:711-
            713). NF-kappa-beta directly impacts viral replication (Ross et
            al. J. Virol. 65:4350-4358; Kim et al. J. Virol. 67:1658-1662;
            Huang and Jeang J. Virol. 67:6937-6944; Huang et al. EMBO J. 13:
            2886-2896), viral transcription (Harrich et al. J. Virol. 63:
            2585-2591; Berkhout and Jeang J. Virol. 63:5501-5504), and Tat
            transactivation (reviewed in Jones and Peterlin Annu. Rev. Biochem.
            63:717-743). For more extensive discussions of the biochemical and
            functional properties of NF-kappa-beta (Ghosh et al. Cell 62:
            1019-1029; Kieran et al. Cell 44: 261-272; Nolan et al. Cell 64:
            961-969; Liou et al. EMBO J. 11: 3003- 3009).
            NCBI gi: 189177
BASE COUNT      933 a    937 c    956 g    799 t
ORIGIN
        1 ggccaccgga gcggcccggc gacgatcgct gacagcttcc cctgcccttc ccgtcggtcg
       61 ggccgccagc cgccgcagcc ctcggcctgc acgcagccac cggccccgct cccggagccc
      121 agcgccgccg aggccgcagc cgcccggcca gtaaggcggc gccgcccgcg gccaccgcgg
      181 gccctgccgt tccctccgcc gcgctgcgcc atggcgcggc gctgactggc ctggcccggc
      241 cccgccgcgc tcccgctcgc cccgacccgc actcgggccc gcccgggctc cggcctgccg
      301 ccgcctcttc cttctccagc cggcaggccc cgccgcttag gagggagagc ccacccgcgc
      361 caggaggccg aacgcggact cgccacccgg cttcagaATG gcagaagatg atccatattt
      NF-kappa-beta DNA binding subunit cds start ->
      421 gggaaggcct gaacaaatgt ttcatttgga tccttctttg actcatacaa tatttaatcc
      481 agaagtattt caaccacaga tggcactgcc aacagatggc ccataccttc aaatattaga
      541 gcaacctaaa cagagaggat ttcgtttccg ttatgtatgt gaaggcccat cccatggtgg
      601 actacctggt gcctctagtg aaaagaacaa gaagtcttac cctcaggtca aaatctgcaa
      661 ctatgtggga ccagcaaagg ttattgttca gttggtcaca aatggaaaaa atatccacct
      721 gcatgcccac agcctggtgg gaaaacactg tgaggatggg atctgcactg taactgctgg
      781 acccaaggac atggtggtcg gcttcgcaaa cctgggtata cttcatgtga caaagaaaaa
      841 agtatttgaa acactggaag cacgaatgac agaggcgtgt ataaggggct ataatcctgg
      901 actcttggtg caccctgacc ttgcctattt gcaagcagaa ggtggagggg accggcagct
      961 gggagatcgg gaaaaagagc taatccgcca agcagctctg cagcagacca aggagatgga
     1021 cctcagcgtg gtgcggctca tgtttacagc ttttcttccg gatagcactg gcagcttcac
     1081 aaggcgcctg gaacccgtgg tatcagacgc catctatgac agtaaagccc ccaatgcatc
     1141 caacttgaaa attgtaagaa tggacaggac agctggatgt gtgactggag gggaggaaat
     1201 ttatcttctt tgtgacaaag ttcagaaaga tgacatccag attcgatttt atgaagagga
     1261 agaaaatggt ggagtctggg aaggatttgg agatttttcc cccacagatg ttcatagaca
     1321 atttgccatt gtcttcaaaa ctccaaagta taaagatatt aatattacaa aaccagcctc
     1381 tgtgtttgtc cagcttcgga ggaaatctga cttggaaact agtgaaccaa aacctttcct
     1441 ctactatcct gaaatcaaag ataaagaaga agtgcagagg aaacgtcaga agctcatgcc
     1501 caatttttcg gatagtttcg gcggtggtag tggtgccgga gctggaggcg gaggcatgtt
     1561 tggtagtggc ggtggaggag ggggcactgg aagtacaggt ccagggtata gcttcccaca
     1621 ctatggattt cctacttatg gtgggattac tttccatcct ggaactacta aatctaatgc
     1681 tgggatgaag catggaacca tggacactga atctaaaaag gaccctgaag gttgtgacaa
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```
1741 aagtgatgac aaaaacactg taaacctctt tgggaaagtt attgaaacca cagagcaaga
1801 tcaggagccc agcgaggcca ccgttgggaa tggtgaggtc actctaacgt atgcaacagg
1861 aacaaaagaa gagagtgctg gagttcagga taacctcttt ctagagaagg ctatgcagct
1921 tgcaaagagg catgccaatg ccctttttcga ctacgcggtg acaggagacg tgaagatgct
1981 gctggccgtc cagcgccatc tcactgctgt gcaggatgag aatggggaca gtgtcttaca
2041 cttagcaatc atccaccttc attctcaact tgtgagggat ctactagaag tcacatctgg
2101 tttgatttct gatgacatta tcaacatgag aaatgatctg taccagacgc ccttgcactt
2161 ggcagtgatc actaagcagg aagatgtggt ggaggatttg ctgagggctg gggccgacct
2221 gagccttctg gaccgcttgg gtaactctgt tttgcaccta gctgccaaag aaggacatga
2281 taaagttctc agtatcttac tcaagcacaa aaaggcagca ctacttcttg accaccccaa
2341 cggggacggt ctgaatgcca ttcatctagc catgatgagc aatagcctgc catgtttgct
2401 gctgctggtg gccgctgggg ctgacgtcaa tgctcaggag cagaagtccg ggcgcacagc
2461 actgcacctg gctgtggagc acgacaacat ctcattggca ggctgcctgc tcctggaggg
2521 tgatgcccat gtggacagta ctacctacga tggaaccaca cccctgcata tagcagctgg
2581 gagagggtcc accaggctgg cagctcttct caaagcagca ggagcagatc ccctggtgga
2641 gaactttgag cctctctatg acctggatga ctcttgggaa aatgcaggag aggatgaagg
2701 agttgtgcct ggaaccacgc ctctagatat ggccaccagc tggcaggtat ttgacatatt
2761 aaatgggaaa ccatatgagc cagagtttac atctgatgat ttactagcac aaggagacat
2821 gaaacagctg gctgaagatg tgaagctgca gctgtataag ttactagaaa ttcctgatcc
2881 agacaaaaac tgggctactc tggcgcagaa attaggtctg gggatactta ataatgcctt
2941 ccggctgagt cctgctcctt ccaaaacact tatggacaac tatgaggtct ctgggggtac
3001 agtcagagag ctggtggagg ccctgagaca aatgggctac accgaagcaa ttgaagtgat
3061 ccaggcagcc tccagcccag tgaagaccac ctctcaggcc cactcgctgc ctctctcgcc
3121 tgcctccaca aggcagcaaa tagacgagct ccgagacagt gacagtgtct gcgacacggg
3181 cgtggagaca tccttccgca aactcagctt taccgagtct ctgaccagtg gtgcctcact
3241 gctaactctc aacaaaatgc cccatgatta tgggcaggaa ggacctctag aaggcaaaat
3301 tTAGcctgct gacaatttcc cacaccgtgt aaaccaaagc cctaaaattc cactgcgttg
       <- NF-kappa-beta DNA binding subunit cds end
3361 tccacaagac agaagctgaa gtgcatccaa aggtgctcag agagccggcc cgcctgaatc
3421 attctcgatt taactcgaga ccttttcaac ttggcttcct ttcttggttc ataaatgaat
3481 tttagtttgg ttcacttaca gatagtatct agcaatcaca acactggctg agcggatgca
3541 tctggggatg aggttgctta ctaagctttg ccagctgctg ctggatcaca gctgctttct
3601 gttgtcattg ctgttgtccc tctgc
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LOCUS       HUMP65NFKB   1767 bp ss-mRNA            PRI       02-DEC-1991
DEFINITION  Human NF-kappa-B transcription factor p65 DNA binding subunit cDNA
            sequence, complete cds.
ACCESSION   M62399
KEYWORDS    NF-kappa-B transcription factor.
SOURCE      Human mRNA.
REFERENCE   1  (bases 1 to 1767)
  AUTHORS   Ruben,S.M., Dillon,P.J., Schreck,R., Henkel,T., Chen,C.-H.,
            Maher,M., Baeuerle,P.A. and Rosen,C.A.
  TITLE     A novel rel-related human cDNA that potentially encodes the 65 kDa
            subunit of NF-kappaB
  JOURNAL   Science 251, 1490-1493 (1991)
COMMENT     NF-kappa-beta motifs are perhaps the best characterized sequence
            elements in the HIV-1 LTR (Nabel and Baltimore Nature 326:711-
            713).  NF-kappa-beta directly impacts viral replication (Ross et
            al.  J. Viorl. 65:4350-4358; Kim et al. J. Virol. 67:1658-1662;
            Huang and Jeang J. Virol. 67:6937-6944; Huang et al. EMBO J. 13:
            2886-2896), viral transcription (Harrich et al. J. Virol. 63:
            2585-2591; Berkout and Jeang J. Virol. 63:5501-5504), and Tat
            transactivation (reviewed in Jones and Peterlin Annu. Rev. Biochem.
            63:717-743).  For more extensive discussions of the biochemical and
            functional properties of NF-kappa-beta (Ghosh et al. Cell 62:
            1019-1029; Kieran et al. Cell 44: 261-272; Nolan et al. Cell 64:
            961-969; Liou et al. EMBO J. 11: 3003- 3009).
            NCBI gi: 189503
BASE COUNT      354 a    626 c    470 g    317 t
ORIGIN
        1 gaattccggc gaatggctcg tctgtagtgc acgccgcggg cccagctgcg accccggccc
       61 cgcccccggg accccggccA TGgacgaact gttccccctc atcttcccgg cagagccagc
   NFkb p65 subunit cds start ->
      121 ccaggcctct ggcccctatg tggagatcat tgagcagccc aagcagcggg gcatgcgctt
      181 ccgctacaag tgcgaggggc gctccgcggg cagcatccca ggcgagagga gcacagatac
      241 caccaagacc caccccacca tcaagatcaa tggctacaca ggaccaggga cagtgcgcat
      301 ctccctggtc accaaggacc ctcctcaccg gcctcacccc cacgagcttg taggaaagga
      361 ctgccgggat ggcttctatg aggctgagct ctgcccggac cgctgcatcc acagtttcca
      421 gaacctggga atccagtgtg tgaagaagcg ggacctggag caggctatca gtcagcgcat
      481 ccagaccaac aacaacccct tccaagttcc tatagaagag cagcgtgggg actacgacct
      541 gaatgctgtg cggctctgct tccaggtgac agtgcgggac ccatcaggca ggcccctccg
      601 cctgccgcct gtccttcctc atcccatctt tgacaatcgt gcccccaaca ctgccgagct
      661 caagatctgc cgagtgaacc gaaactctgg cagctgcctc ggtggggatg agatcttcct
      721 actgtgtgac aaggtgcaga aagaggacat tgaggtgtat ttcacgggac caggctggga
      781 ggcccgaggc tcctttcgc aagctgatgt gcaccgacaa gtggccattg tgttccggac
      841 ccctccctac gcagacccca gcctgcaggc tcctgtgcgt gtctccatgc agctgcggcg
      901 gccttccgac cgggagctca gtgagcccat ggaattccag tacctgccag atacagacga
      961 tcgtcaccgg attgaggaga aacgtaaaag gacatatgag accttcaaga gcatcatgaa
     1021 gaagagtcct ttcagcggac ccaccgaccc ccggcctcca cctcgacgca ttgctgtgcc
     1081 ttcccgcagc tcagcttctg tccccaagcc agcaccccag ccctatccct ttacgtcatc
     1141 cctgagcacc atcaactatg atgagtttcc caccatggtg tttccttctg ggcagatcag
     1201 ccaggcctcg gccttggccc cggcccctcc ccaagtcctg ccccaggctc cagcccctgc
     1261 ccctgctcca gccatggtat cagctctggc ccaggcccca gcccctgtcc cagtcctagc
     1321 cccaggccct cctcaggctg tggccccacc tgcccccaag cccacccagg ctggggaagg
     1381 aacgctgtca gaggccctgc tgcagctgca gtttgatgat gaagacctgg gggccttgct
     1441 tggcaacagc acagacccag ctgtgttcac agacctggca tccgtcgaca actccgagtt
     1501 tcagcagctg ctgaaccagg gcatacctgt ggccccccac acaactgagc ccatgctgat
     1561 ggagtaccct gaggctataa ctcgcctagt gacaggggcc cagaggcccc ccgacccagc
     1621 tcctgctcca ctgggggccc cggggctccc caatggcctc ctttcaggag atgaagactt
     1681 ctcctccatt gcggacatgg acttctcagc cctgctgagt cagatcagct ccTAAggggg
                                                                <- NFkb p65

     1741 tgacgcctgc cctccccaga gcactgg
```

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LOCUS       HUMP68K      2562 bp ss-mRNA            PRI       29-JAN-1991
DEFINITION  Human p68 kinase complete cDNA sequence.
ACCESSION   M35663
KEYWORDS    p68 kinase.
SOURCE      Human mRNA from interferon-treated Daudi cell.
REFERENCE   1  (bases 1 to 2562)
  AUTHORS   Meurs,E., Chong,K., Galabru,J., Thomas,N.S., Kerr,I.M.,
            Williams,B.R. and Hovanessian,A.G.
  TITLE     Molecular cloning and characterization of the human double-stranded
            RNA-activated protein kinase induced by interferon
  JOURNAL   Cell 62, 379-390 (1990)
COMMENT     Human p68 kinase, also referred to as P1/dsI, DAI, and PKR,
            complexes with the double-stranded stem of TAR RNA (McCormack et
            al.  Virology 188:47-56; Roy et al. J. Virol. 65:632-640).  It is
            thought that TAR activates this kinase and results in the
            phosyphorylation and down-regulation of eIF-2 (Garcia and Gaynor
            AIDS 8:S3-S17).
            Draft entry and computer-readable sequence for [1] kindly submitted
            by E.Meurs, 22-JUN-1990.
            NCBI gi: 189505
BASE COUNT      843 a    478 c    500 g    741 t
ORIGIN
        1 cagtttctgg agcaaattca gtttgccttc ctggatttgt aaattgtaat gacctcaaaa
       61 ctttagcagt tcttccatct gactcaggtt tgcttctctg gcggtcttca gaatcaacat
      121 ccacacttcc gtgattatct gcgtgcattt tggacaaagc ttccaaccag gatacgggaa
      181 gaagaaATGg ctggtgatct ttcagcaggt ttcttcatgg aggaacttaa tacataccgt
 p68 kinase cds ->
      241 cagaagcagg gagtagtact taaatatcaa gaactgccta attcaggacc tccacatgat
      301 aggaggttta catttcaagt tataatagat ggaagagaat ttccagaagg tgaaggtaga
      361 tcaaagaagg aagcaaaaaa tgccgcagcc aaattagctg ttgagatact taataaggaa
      421 aagaaggcag ttagtccttt attattgaca acaacgaatt cttcagaagg attatccatg
      481 gggaattaca taggccttat caatagaatt gcccagaaga aaagactaac tgtaaattat
      541 gaacagtgtg catcgggggt gcatgggcca gaaggatttc attataaatg caaaatggga
      601 cagaaagaat atagtattgg tacaggttct actaaacagg aagcaaaaca attggccgct
      661 aaacttgcat atcttcagat attatcagaa gaaacctcag tgaaatctga ctacctgtcc
      721 tctggttctt ttgctactac gtgtgagtcc caaagcaact ctttagtgac cagcacactc
      781 gcttctgaat catcatctga aggtgacttc tcagcagata catcagagat aaattctaac
      841 agtgacagtt taaacagttc ttcgttgctt atgaatggtc tcagaaataa tcaaaggaag
      901 gcaaaaagat ctttggcacc cagatttgac cttcctgaca tgaaagaaac aaagtatact
      961 gtggacaaga ggttttggcat ggattttaaa gaaatagaat taattggctc aggtggattt
     1021 ggccaagttt tcaaagcaaa acacagaatt gacggaaaga cttacgttat taaacgtgtt
     1081 aaatataata acgagaaggc ggagcgtgaa gtaaaagcat tggcaaaact tgatcatgta
     1141 aatattgttc actacaatgg ctgttgggat ggatttgatt atgatcctga gaccagtgat
     1201 gattctcttg agagcagtga ttatgatcct gagaacagca aaaatagttc aaggtcaaag
     1261 actaagtgcc ttttcatcca aatggaattc tgtgataaag ggaccttgga acaatggatt
     1321 gaaaaaagaa gaggcgagaa actagacaaa gttttggctt tggaactctt tgaacaaata
     1381 acaaaagggg tggattatat acattcaaaa aaattaattc atagagatct taagccaagt
     1441 aatatattct tagtagatac aaaacaagta aagattggag actttggact tgtaacatct
     1501 ctgaaaaatg atggaaagcg aacaaggagt aagggaactt tgcgatacat gagcccagaa
     1561 cagatttctt cgcaagacta tggaaaggaa gtggacctct acgctttggg gctaattctt
     1621 gctgaacttc ttcatgtatg tgacactgct tttgaaacat caaagttttt cacagaccta
     1681 cgggatggca tcatctcaga tatatttgat aaaaaagaaa aaactcttct acagaaatta
     1741 ctctcaaaga aacctgagga tcgacctaac acatctgaaa tactaaggac cttgactgtg
     1801 tggaagaaaa gcccagagaa aaatgaacga cacacatgtT AGagcccttc tgaaaaagta
                                                  <- p68 kinase cds end
     1861 tcctgcttct gatatgcagt tttccttaaa ttatctaaaa tctgctaggg aatatcaata
     1921 gatatttacc ttttatttta atgtttcctt taatttttta ctatttttac taatctttct
     1981 gcagaaacag aaaggttttc ttctttttgc ttcaaaaaca ttcttacatt ttacttttttc
     2041 ctggctcatc tctttatttt ttttttttt ttttaaagac agagtctcgc tctgttgccc
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2101 aggctggagt gcaatgacac agtcttggct cactgcaact tctgcctctt gggttcaagt
2161 gattctcctg cctcagcctc ctgagtagct ggattacagg catgtgccac ccacccaact
2221 aatttttgtg tttttaataa agacagggtt tcaccatgtt ggccaggctg gtctcaaact
2281 cctgacctca agtaatccac ctgcctcggc ctcccaaagt gctgggatta cagggatgag
2341 ccaccgcgcc cagcctcatc tctttgttct aaagatggaa aaaccacccc caaattttct
2401 ttttatacta ttaatgaatc aatcaattca tatctattta ttaaatttct accgctttta
2461 ggccaaaaaa atgtaagatc gttctctgcc tcacatagct tacaagccag ctggagaaat
2521 atggtactca ttaaaaaaaa aaaaaaaaag tgatgtacaa cc
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HSZFPBF1

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LOCUS       HSZFPBF1     9020 bp    RNA             PRI       14-MAR-1990
DEFINITION  Human PRDII-BF1 sequence, clone PRDII-BF1.
ACCESSION   X51435
SOURCE      Human lambda gt11 library.
REFERENCE   1  (bases 1 to 9020)
  AUTHORS   Fan,C.M. and Maniatis,T.
  TITLE     A DNA-binding protein containing two widely separated zinc finger
            motifs that recognize the same DNA sequence
  JOURNAL   Genes Dev. 4, 29-42 (1990)
COMMENT     Human PRDII-BF1, also referred to as HIV-EP1 or MBP-1, is a
            cellular transcription factor which activates HIV-1 gene
            expression.  The protein contains two zinc finger domains, each of
            which can bind to either of the two NF-kappa B binding motifs in
            the HIV-1 enhancer or to the TAR transactivation response element.
            Gaynor et al. (Genomics 9: 758-61, 1991) have mapped the gene which
            encodes HPRDII-BF1 to human chromosome 6p22.3-p24.
            NCBI gi: 38017
BASE COUNT     2745 a   2164 c   1930 g   2181 t
ORIGIN
        1 cgctgctggg cggcggcagg gtggcggacg gagcggggga ccggggagcg gcggccgcga
       61 ggaggttatg tttgtgtttg gggttgtcaa gtgaaggagg gatcccaggc gccgccgccg
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9001 tgtttactga cctttaaaaa
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LOCUS       HUMSF2P32    1240 bp ss-mRNA            PRI       13-JAN-1993
DEFINITION  Human pre-mRNA splicing factor SF2p32 complete sequence.
ACCESSION   M69039
KEYWORDS    SF2p32.
SOURCE      Homo sapiens Female cDNA.
REFERENCE   1  (bases 1 to 1240)
  AUTHORS   Krainer,A.R., Mayeda,A., Kozak,D. and Binns,G.
  TITLE     Functional expression of cloned human splicing factor sf2: Homology
            to RNA-binding proteins, U1 70K, and drosophila splicing regulators
  JOURNAL   Cell 66, 383-394 (1991)
COMMENT     SF2p32 is a polypeptide from HeLa cells that copurifies with the
            essential pre-mRNA splicing factor SF2. It may be a subunit of SF2,
            although its function is presently unknown.
            SF2p32 is 92% identical to the mouse YL2 protein and is thought
            to be the human homolog.  Recently, YL2 has been shown to bind
            to the basic domain of the HIV-1 Rev protein and through this
            binding helps mediate its role (Luo et al. J. Virol. 68:3850-3856).
            It is hypothesized that Rev either inhibits RNA splicing or
            directly transports singly and unspliced HIV-1 transcripts out of
            the nucleus.
            Purification of this protein from HeLa cells is described in
            Krainer, A.R., Conway, G.C., and Kozak, D. (1990) Purification and
            Characterization of  SF2, a Human Pre-mRNA Splicing Factor. Genes
            Dev. 4, 1158-1171.
            NCBI gi: 338042
BASE COUNT      326 a    297 c    299 g    318 t
ORIGIN
        1 ctgcgctgcg tgccccgtgt gctgggctcc tccgtcgccg gcctccgcgc tgccgcgccc
  SF2p32 ->
       61 gcctcgcctt tccggcagct cctgcagccg gcaccccggc tgtgcacccg gcccttcggg
      121 ctgctcagcg tgcgcgcagg ttccgagcgg cggccgggcc tcctgcggcc tcgcggaccc
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      721 gaccgagggg tggacaacac ttttgcagat gagctggtgg agctcagcac agccctggag
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                                                                  <- SF2p32
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     1201 ataataatcc ctcgagttta caaaacaaaa aaaaaaaaaa
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HUMSP1TF

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LOCUS       HUMSP1TF     2655 bp ss-mRNA            PRI       30-SEP-1988
DEFINITION  Human transcription factor SP1 cDNA sequence, 3' end, clone Sp1-1.
ACCESSION   J03133
KEYWORDS    transcription factor SP1.
SOURCE      Human mRNA from HeLa cell line (library of C.Hauser).
REFERENCE   1  (bases 1 to 2655)
  AUTHORS   Kadonaga,J.T., Carner,K.R., Masiarz,F.R. and Tjian,R.
  TITLE     Isolation of cDNA encoding transcription factor Sp1 and functional
            analysis of the DNA binding domain
  JOURNAL   Cell 51, 1079-1090 (1987)
COMMENT     The Sp1 motifs are perhaps the best characterized sequence elements
            in the HIV-1 LTR.  These sequences directly impact viral
            replication (Ross et al. J. Virol. 65:4350-4358; Kim et al. J.
            Virol. 67:1658-1662; Huang and Jeang J. Virol. 67:6937-6944; Huang
            et al. EMBO J. 13:2886-2896), viral transcription (Harrich et al.
            J. Virol. 63:2585-2591; Berkhout and Jeang J. Virol. 63:5501-5504),
            and Tat transactivation (reviewed in Jones and Peterlin Annu. Rev.
            Biochem. 63:717-743).  For more extensive discussions of the
            biochemical and functional properties of Sp1 (Dynan and Tjian Cell
            32:669-680; Briggs et al. Science 234:47-52; Kadonaga et al. Cell
            51:1079-1090).
            Draft entry and computer-readable sequence for [1] kindly provided
            by J.T.Kadonaga, 17-NOV-1987.
            NCBI gi: 339517
BASE COUNT      717 a    726 c    630 g    582 t
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Sp-1 cds ->
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     1561 aaagacagtg aaggaagggg ctcgggggat cctggcaaaa agaaacagca tatttgccac
     1621 atccaaggct gtgggaaagt gtatggcaag acctctcacc tgcgggcaca cttgcgctgg
     1681 catacaggcg agaggccatt tatgtgtacc tggtcatact gtgggaaacg cttcacacgt
     1741 tcggatgagc tacagaggca caaacgtaca cacacaggtg agaagaaatt tgcctgccct
     1801 gagtgtccta agcgcttcat gaggagtgac cacctgtcaa aacatatcaa gacccaccag
     1861 aataagaagg gaggcccagg tgtagctctg agtgtgggca ctttgcccct ggacagtggg
```

```
1921 gcaggttcag aaggcagtgg cactgccact ccttcagccc ttattaccac caatatggta
1981 gccatggagg ccatctgtcc agagggcatt gcccgtcttg ccaacagtgg catcaacgtc
2041 atgcaggtgg cagatctgca gtccattaat atcagtggca atggcttcTG Agatcaggca
                                                        <- Sp-1 cds end
2101 cccggggcca gagacatatg ggccataccc cttaaccccg ggatgcaagg tagcatgggt
2161 ccaagagaca tggaagagag agccatgaag cattaaaatg catggtgttg agaagaatca
2221 ggagagggat acaagagagg agatggggtc ccggcaccca tctgtatcat cagtgcctct
2281 ttgaaggtgg gaaacattag tgaaaattct gttggtgcca cgctttgatg agcatttgtt
2341 tgaccccagt ttcttcttac acttcttacc ccagcctacc cttcctgcat ttctcttctc
2401 agctcttcca tgatggattc cccccccttt cctaaagcca tcatgccttg ataaatatat
2461 atgatcattg aaatactttt taacaaaaaa cagattctat attattatat atatatatat
2521 atataaagat atatagagat gcattcacag ggttggctgg agaggaagac cattctgtga
2581 ccaaaatacc ttggtcattt tttttatatt gccttatttc cctatggctg agccttgttg
2641 tgacacatca agctt
```

HUMTBP1

```
LOCUS       HUMTBP1      1341 bp ss-mRNA            PRI       14-MAY-1990
DEFINITION  Human immunodeficiency virus tat transactivator binding protein-1
            (tbp-1) cDNA sequence, complete cds.
ACCESSION   M34079
KEYWORDS    Tat-binding protein.
SOURCE      Human mRNA from Jurkat T-cell line.
REFERENCE   1  (bases 1 to 1341)
  AUTHORS   Nelbock,P., Dillion,P.J., Perkins,A. and Rosen,C.A.
  TITLE     A cDNA corresponding to a protein that interacts with the human
            immunodeficiency virus Tat transactivator
  JOURNAL   Science 248, 1650-1653 (1990)
COMMENT     TBP1 is part of a large family of proteins related to the 26S
            protease from human erythrocytes.  Each of these proteins has
            Tat-binding activity [1]. The exact role of this family of
            proteins in cellular metabolism is not wholly clear; however,
            the 26S protease seems to regulate the degradation of some
            cyclins and in this manner has been implicated in modulating
            the stability of oncoproteins such as c-Mos, c-Myb, c-Myc,
            and p53 (Dubiel et al. Biol. Chem. Hoppe-Seyler 375: 237-240).
            Draft entry and computer-readable [or printed] sequence for [1]
            kindly submitted by C.A.Rosen, 08-MAY-1990.
            NCBI gi: 338699
BASE COUNT      350 a    337 c    412 g    242 t
ORIGIN
        1 gaattccggc gaccgtgtgg gatgaggccg agcaagatgg aattggggag gaggtgctca
       61 agATGtccac ggaggagatc atccagcgca cacggctgct ggacagtgag atcaagatca
  TBP-1 cds ->
      121 tgaagagtga agtgttgaga gtcacccatg agctccaagc catgaaggac aagataaaag
      181 agaacagtga gaaaatcaaa gtgaacaaga ccctgccgta ccttgtctcc aacgtcatcg
      241 agctcctgga tgttgatcct aatgaccaag aggaggatgg tgccaatatt gacctggact
      301 cccagaggaa gggcaagtgt gctgtgatca aaacctctac acgacagacg tacttccttc
      361 ctgtgattgg gttggtggat gctgaaaagc taaagccagg agacctggtg ggtgtgaaca
      421 aagactccta tctgatcctg gagacgctgc ccacagagta tgactcgcgg gtgaaggcca
      481 tggaggtaga cgagaggccc acggagcaat acagtgacat tgggggtttg gacaagcaga
      541 tccaggagct ggtggaggcc attgtcttgc caatgaacca caaggagaag tttgagaact
      601 tggggatcca acctccaaaa ggggtgctga tgtatgggcc cccagggacg gggaagaccc
      661 tcctggcccg ggcctgtgcc gcacagacta aggccacctt cctaaagctg gctggccccc
      721 agctggtgca gatgttcatt ggagatggtg ccaagctagt ccgggatgcc tttgccctgg
      781 ccaaggagaa agcgccctct atcatcttca ttgatgagtt ggatgccatc ggcaccaagc
      841 gctttgacag tgagaaggct ggggaccggg aggtgcagag gacaatgctg gagcttctga
      901 accagctgga tggcttccag cccaacaccc aagttaaggt aattgcagcc acaaacaggg
      961 tggacatcct ggaccccgcc ctcctccgct cgggccgcct tgaccgcaag atagagttcc
     1021 cgatgcccaa tgaggaggcc cgggccagaa tcatgcagat ccactcccga aagatgaatg
     1081 tcagtcctga cgtgaactac gaggagctgg cccgctgcac agatgacttc aatggggccc
     1141 agtgcaaggc tgtgtgtgtg gaggcgggca tgatcgcact ggccaggggt gccacggagc
     1201 tcacccacga ggactacatg gaaggcatcc tggaggtgca ggccaagaag aaagccaacc
     1261 tacaatacta cgccTAGgca cacaggccag ccccagtctc acggctgaag tgcgcaataa
                          <- TBP-1 cds end
     1321 aagatggttt agggggaatt c
```

```
LOCUS       HUMTFIIDA    1035 bp ss-mRNA            PRI       15-SEP-1990
DEFINITION  Human transcription factor IID cDNA sequence, complete cds.
ACCESSION   M34960
KEYWORDS    transcription factor IID.
SOURCE      Human mRNA from Hela fibroblast cell line.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Kao,C., Lieberman,P., Schmidt,M., Zhou,Q., Pei,R. and Berk,A.J.
  TITLE     Cloning of the human TATA binding factor: Expression of a
            transcriptionally active TFIID protein
  JOURNAL   Science 248, 1626-1626 (1990)
COMMENT     There is evidence that Tat contacts TFIID (Kashanchi et al.
            Nature 367:295-299) and that Tat-Sp1-TFIID could be a
            multiprotein complex inside cells (Huang et al. EMBO J.
            13:2886-2896).
            Draft entry and computer-readable sequence kindly submitted by
            C.C.Kao, 05-JUN-1990.
            NCBI gi: 339493
BASE COUNT      304 a    275 c    236 g    220 t
ORIGIN
        1 ATGgatcaga acaacagcct gccaccttac gctcagggct tggcctcccc tcagggtgcc
TFIID cds ->
       61 atgactcccg gaatccctat ctttagtcca atgatgcctt atggcactgg actgacccca
      121 cagcctattc agaacaccaa tagtctgtct attttggaag agcaacaaag gcagcagcag
      181 caacaacaac agcagcagca gcagcagcag cagcagcaac agcaacagca gcagcagcag
      241 cagcagcagc agcagcagca gcagcagcag cagcagcagc aacaggcagt ggcagctgca
      301 gccgttcagc agtcaacgtc ccagcaggca acacagggaa cctcaggcca ggcaccacag
      361 ctcttccact cacagactct cacaactgca cccttgccgg gcaccactcc actgtatccc
      421 tcccccatga ctcccatgac ccccatcact cctgccacgc cagcttcgga gagttctggg
      481 attgtaccgc agctgcaaaa tattgtatcc acagtgaatc ttggttgtaa acttgaccta
      541 aagaccattg cacttcgtcg ccgaaacgcc gaatataatc ccaagcggtt tgctgcggta
      601 atcatgagga taagagagcc acgaaccacg gcactgattt tcagttctgg gaaaatggtg
      661 tgcacaggag ccaagagtga agaacagtcc agactggcag caagaaaata tgctagagtt
      721 gtacagaagt tgggttttcc agctaagttc ttggacttca agattcagaa catggtgggg
      781 agctgtgatg tgaagtttcc tataaggtta gaaggccttg tgctcaccca ccaacaattt
      841 agtagttatg agccagagtt atttcctggt ttaatctaca gaatgatcaa acccagaatg
      901 atcaaaccca gaattgttct ccttattttt gtttctggaa aagttgtatt aacaggtgct
      961 aaagtcagag cagaaattta tgaagcattt gaaaacatct accctattct aaagggattc
     1021 aggaagacga cgTAA
                      <- TFIID cds end
```

HSTGFB1

```
LOCUS       HSTGFB1      2745 bp    RNA             PRI       06-JUL-1989
DEFINITION  Human transforming growth factor-beta (TGF-beta) sequence.
ACCESSION   X02812 J05114
KEYWORDS    signal peptide; transforming growth factor-beta.
SOURCE      Human.
REFERENCE   1  (bases 1 to 2745)
  AUTHORS   Derynck,R., Jarrett,J.A., Chen,E.Y., Eaton,D.H., Bell,J.R.,
            Assoian,R.K., Roberts,A.B., Sporn,M.B. and Goeddel,D.V.
  TITLE     Human transforming growth factor-beta complementary DNA sequence
            and expression in normal and transformed cells
  JOURNAL   Nature 316, 701-705 (1985)
COMMENT     TGF-beta is a cellular cytokine which has been shown to inhibit
            HIV-1 gene expression (Garcia and Gaynor AIDS 8:S3-S17).
            The sequence downstream from the translational stop codon
            (2015-2017) was taken from a genomic clone.
            NCBI gi: 37092
BASE COUNT      527 a    938 c    801 g    479 t
ORIGIN
        1 acctccctcc gcggagcagc cagacagcga gggccccggc cgggggcagg ggggacgccc
       61 cgtccggggc acccccccgg gctctgagcc gcccgcgggg ccggcctcgg cccggagcgg
      121 aggaaggagt cgccgaggag cagcctgagg ccccagagtc tgagacgagc cgccgccgcc
      181 cccgccactg cggggaggag ggggaggagg agcgggagga gggacgagct ggtcgggaga
      241 agaggaaaaa aacttttgag acttttccgt tgccgctggg agccggaggc gcggggacct
      301 cttggcgcga cgctgccccg cgaggaggca ggacttgggg accccagacc gcctcccttt
      361 gccgccgggg acgcttgctc cctccctgcc ccctacacgg cgtccctcag gcgccccccat
      421 tccggaccag ccctcgggag tcgccgaccc ggcctcccgc aaagactttt ccccagacct
      481 cgggcgcacc ccctgcacgc cgccttcatc cccggcctgt ctcctgagcc cccgcgcatc
      541 ctagaccctt tctcctccag gagacggatc tctctccgac ctgccacaga tcccctattc
      601 aagaccaccc accttctggt accagatcgc gcccatctag gttatttccg tgggatactg
      661 agacaccccc ggtccaagcc tcccctccac cactgcgccc ttctccctga ggagcctcag
      721 ctttccctcg aggccctcct acctttgcc gggagacccc cagcccctgc aggggcgggg
      781 cctccccacc acaccagccc tgttcgcgct ctcggcagtg ccgggggggcg ccgcctcccc
      841 cATGccgccc tccgggctgc ggctgctgcc gctgctgcta ccgctgctgt ggctactggt
  TGF-beta ->
      901 gctgacgcct ggcccgccgg ccgcgggact atccacctgc aagactatcg acATGgagct
                                            alternative cds start ->
      961 ggtgaagcgg aagcgcatcg aggccatccg cggccagatc ctgtccaagc tgcggctcgc
     1021 cagccccccg agccaggggg aggtgccgcc cggcccgctg cccgaggccg tgctcgccct
     1081 gtacaacagc acccgcgacc gggtggccgg ggagagtgca gaaccggagc ccgagcctga
     1141 ggccgactac tacgccaagg aggtcacccg cgtgctaatg gtggaaaccc acaacgaaat
     1201 ctatgacaag ttcaagcaga gtacacacag catatatatg ttcttcaaca catcagagct
     1261 ccgagaagcg gtacctgaac ccgtgttgct ctcccgggca gagctgcgtc tgctgaggag
     1321 gctcaagtta aaagtggagc agcacgtgga gctgtaccag aaatacagca acaattcctg
     1381 gcgatacctc agcaaccggc tgctggcacc cagcgactcg ccagagtggt tatcttttga
     1441 tgtcaccgga gttgtgcggc agtggttgag ccgtggaggg gaaattgagg gctttcgcct
     1501 tagcgcccac tgctcctgtg acagcaggga taacacactg caagtggaca tcaacgggtt
     1561 cactaccggc cgccgaggtg acctggccac cattcatggc atgaaccggc ctttcctgct
     1621 tctcatggcc accccgctgg agagggccca gcatctgcaa agctcccggc accgccgagc
                                                    TGF-beta mature cds ->
     1681 cctggacacc aactattgct tcagctccac ggagaagaac tgctgcgtgc ggcagctgta
     1741 cattgacttc cgcaaggacc tcggctggaa gtggatccac gagcccaagg gctaccatgc
     1801 caacttctgc ctcgggccct gcccctacat ttggagcctg gacacgcagt acagcaaggt
     1861 cctggccctg tacaaccagc ataacccggg cgcctcggcg gcgccgtgct gcgtgccgca
     1921 ggcgctggag ccgctgccca tcgtgtacta cgtgggccgc aagcccaagg tggagcagct
     1981 gtccaacatg atcgtgcgct cctgcaagtg cagcTGAggt cccgccccgc cccgccccgc
                                                  <- TGF-beta cds end
     2041 cccggcaggc ccggccccac cccgccccgc ccccgctgcc ttgcccatgg gggctgTATT
                                                              signal ->
     2101 TAAggacacc gtgccccaag cccacctggg gccccattaa agatggagag aggactgcgg
```

```
2161 atctctgtgt cattgggcgc ctgcctgggg tctccatccc tgacgttccc ccactcccac
2221 tccctctctc tccctctctg cctcctcctg cctgtctgca ctattccttt gcccggcatc
2281 aaggcacagg ggaccagtgg ggaacactac tgtagttaga tctatttatt gagcaccttg
2341 ggcactgttg aagtgcctta cattaatgaa ctcattcagt caccatagca acactctgag
2401 atggcaggga ctctgataac acccatttta aaggttgagg aaacaagccc agagaggtta
2461 agggaggagt tcctgcccac caggaacctg ctttagtggg ggatagtgaa gaagacAATA
                                                          signal ->
2521 AAagatagta gttcaggcca ggcggggtgc tcacgcctgt aatcctagca cttttgggag
2581 gcagagatgg gaggatactt gaatccaggc atttgagacc agcctgggta acatagtgag
2641 accctatctc tacaaaacac ttttaaaaaa tgtacacctg tggtcccagc tactctggag
2701 gctaaggtgg gaggatcact tgatcctggg aggtcaaggc tgcag
```

HUMTRBP

```
LOCUS       HUMTRBP      1368 bp ss-mRNA            PRI       03-MAY-1991
DEFINITION  Human TAR RNA binding protein (TRBP) cDNA sequence, complete cds.
ACCESSION   M60801
KEYWORDS    TAR RNA binding protein.
SOURCE      Human mRNA from HeLa D98/AH-2 cell line.
REFERENCE   1  (bases 1 to 1368)
  AUTHORS   Gatignol,A., Buckler-White,A.J., Berkhout,B. and Jeang,K.-T.
  TITLE     Characterization of a human TAR RNA-binding protein that activates
            the HIV-1 LTR
  JOURNAL   Science 251, 1597-1600 (1991)
COMMENT     Human TRBP complexes with the double-stranded stem of TAR RNA
            (Gatignol et al.  Science 251:1597-16003; Gatignol et al. Mol. Cell.
            Biol. 13:2193-2202).
            NCBI gi: 339908
BASE COUNT      279 a    405 c    395 g    289 t
ORIGIN
        1 gctcttgggt tctgtagttt tctcgcgatc caaaaggctc cgtgcccaaa gcaaATGctg
                                                    TRBP cds start ->
       61 gccgccaacc caggcaagac cccgatcagc cttctgcagg agtatgggac cagaataggg
      121 aagacgcctg tgtacgacct tctcaaagcc gagggccaag cccaccagcc taatttcacc
      181 ttccgggtca ccgttggcga caccagctgc actggtcagg gccccagcaa gaaggcagcc
      241 aagcacaagg cagctgaggt ggccctcaaa cacctcaaag gggggagcat gctggagccg
      301 gccctggagg acagcagttc tttttctccc ctagactctt cactgcctga ggacattccg
      361 gtttttactg ctgcagcagc tgctacccca gttccatctg tagtcctaac caggagcccc
      421 gccatggaac tgcagccccc tgtctccccc cagcagtctg agtgcaaccc cgttggtgct
      481 ctgcaggagc tggtggtgca gaaaggctgg cggttgccgg agtacacagt gacccaggag
      541 tctgggccag cccaccgcaa agaattcacc atgacctgtc gagtggagcg tttcattgag
      601 attgggagtg gcacttccaa aaaattggca aagcggaatg cggcggccaa aatgctgctt
      661 cgagtgcaca cggtgcctct ggatgcccgg gatggcaatg aggtggagcc tgatgatgac
      721 cacttctcca ttggtgtggg cttccgcctg gatggtcttc gaaaccgggg cccaggttgc
      781 acctgggatt ctctacgaaa ttcagtagga gagaagatcc tgtccctccg cagttgctcc
      841 ctgggctccc tgggtgccct gggccctgcc tgctgccgtg tcctcagtga gctctctgag
      901 gagcaggcct ttcacgtcag ctacctggat attgaggagc tgagcctgag tggactctgc
      961 cagtgcctgg tggaactgtc cacccagccg gccactgtgt gtcatggctc tgcaaccacc
     1021 agggaggcag cccgtggtga ggctgcccgc cgtgccctgc agtacctcaa gatcatggca
     1081 ggcagcaagT GAagccccag ctggactcat ggatgtgcac cctttgctcc ctgctctttc
                  <- TRBP cds end
     1141 tgcctctggg ctcatgtatc tgcgcagctc tggtaccctc tgtgggtgcc atctctacct
     1201 ctgacacaga ctgcctgcct tgaagctgag aaggcacagg gcaaggagcc aaggaccaca
     1261 gagcctcagc cagcccagga tccgtcctca ttttattggt gatgatgaat gggaatgaaa
     1321 tcaggggggct gtctactaga gcctggaata aatatgctgc tttgtgga
```

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LOCUS       HSUSF        1739 bp    RNA              PRI       15-FEB-1991
DEFINITION  Human usf sequence for late upstream transcription factor,
            clone dI2.
ACCESSION   X55666
KEYWORDS    DNA-binding protein; helix-loop-helix domain;
            transcription factor; upstream stimulatory factor.
SOURCE      Human mRNA from lambda-Zap library.
REFERENCE   1  (bases 1 to 1739)
  AUTHORS   Gregor,P.D., Sawadogo,M. and Roeder,R.G.
  TITLE     The adenovirus major late transcription factor USF is a member of
            the helix-loop-helix group of regulatory proteins and binds to DNA
            as a dimer
  JOURNAL   Genes Dev. 4, 1730-1740 (1990)
COMMENT     USF was characterized initially as a positive activator of the
            adenovirus major-late-promoter transcription. Within the LTR of
            HIV-1, a consensus binding sequence for USF is present from -159 to
            -174.  However, there is conflicting information on whether this
            factor has moderating (and thus be regarded as a negative
            regulatory factor; Lu et al.  J. Virol. 64: 5226-5229 1990) or
            stimulating (Maekewa et al. Nucl.  Acids Res. 19: 4689-4694)
            effects.  Interestingly, USF binds a second sequence near the HIV-1
            intitiator (-5 to +11).  USF interaction at the initiator-proximal
            site strongly activates HIV-1 expression from the TATAA-promoter.
            Of note, a factor distinct from USF binds the same DNA sequence
           (TFE3; Bechmann and Kadesch Genes Dev 5:1057-1066).
            NCBI gi: 37614
BASE COUNT      426 a    435 c    491 g    387 t
ORIGIN
        1 ggaattcctt gaaaattttc cttggatagg aaaggactta gcactcaggc ctgtgaatct
       61 aggagataca aagacctcca aaaaaggacc agttcctcgg atgtgccccc tcacagagag
      121 ATGaaggggc agcagaaaac agctgaaacg gaagagggga cagtgcagat tcaggaaggt
  USF cds ->
      181 gcagtggcta ctggggaaga cccaaccagt gtggctattg ccagcatcca gtcagctgcc
      241 accttccctg accccaacgt caagtacgtc ttccgaactg agaatggggg ccaggtgatg
      301 tacagggtga tccaggtgtc tgaggggcag ctggatggcc aaactgaggg aactggcgcc
      361 atcagtggct accctgccac tcaatccatg acccaggcgg tgatccaggg tgctttcacc
      421 agtgatgatg cagttgacac ggaggggaca gctgctgaga cgcactatac ttacttcccc
      481 agcacggcag tgggagatgg ggcagggggt accacatcgg ggagtacagc tgctgttgtt
      541 actacccagg gctcagaggc actgctgggg caggcgaccc ctcctggcac tggtcaattc
      601 tttgtgatga tgtcaccaca agaagtactg cagggaggaa gccagcgctc aattgccccc
      661 aggactcacc cttattcccc gaagtcagaa gctccccgga cgactcggga tgagaaacgc
      721 agggctcagc ataatgaagt ggagcgtcgc cgccgagaca agatcaacaa ctggatcgtg
      781 cagctctcca agataatccc agactgctct atggagagca ccaagtctgg ccagagtaaa
      841 ggtgggattc tatccaaagc ttgtgattat atccaggagc ttcggcagag taaccaccgc
      901 ttgtctgaag aactgcaggg acttgaccaa ctgcagctgg acaatgacgt gcttcgacaa
      961 caggtggaag atcttaaaaa caagaatctg ctgcttcgag ctcagttgcg gcaccacgga
     1021 ttagaggtcg tcatcaagaa tgacagcaac TAActatggg gattcagggg ctttgggccc
                                          <- USF cds end
     1081 aagaactgca gatagcccag gagcaacagc ctaatcccgt gccccttcc ttcactgccc
     1141 cacttctggc atgggacagg gggaagttca gaaggtgtgt ccttgaactg aggccctgtg
     1201 atatggcggc ctgcagtggt gtgaagcaca caatgtggaa cgtgcactga cagccttgcc
     1261 caccccacc atgcagcccc tgggccttgt gctcctctcg cacaatgcat gtgctgtctc
     1321 catgctggat actggacaca ctaaactctg gggcttgtcc tgtgcttgct tagagtgccc
     1381 agcagaggtt tgctgacagg tgatgctctg gcttgcccca ggactctggc acttccattg
     1441 gttcttcctt tccctggagc tgaggtttag atgtgcaacc tgtggctcag gggagcaagc
     1501 ttacacaaga agtgagggaa ggatgtttag cagtggctgg tgcccatgaa gaggagattg
     1561 gccagtgaga agctgaggcc tatgcagaca tctctggagc cagagagaac aacaggcagg
     1621 ggcccacttg gggccttccc ccttgtgggg ggtcgttttt ttttttttctt ttctttttt
     1681 ttttttttt ttttttttt aagataaaat tgttcaaagc caaaaaaaaa aggaattcc
```

HUSFII

```
LOCUS       HUSFII       1299 bp    mRNA            PRI       11-MAR-1993
DEFINITION  Human upstream stimulatory factor II cDNA sequence.
ACCESSION   S50537
SOURCE      Human mRNA from Namalwa B cell line.
REFERENCE   1  (bases 1 to 1299)
  AUTHORS   Sirito,M., Walker,S., Lin,Q., Kozlowski,M.T., Klein,W.H. and
            Sawadogo,M.
  TITLE     Members of the USF family of helix-loop-helix proteins bind DNA as
            homo- as well as heterodimers
  JOURNAL   Gene Expr. 2, 231-240 (1992)
COMMENT     USF was characterized initially as a positive activator of the
            adenovirus major-late-promoter transcription. Within the LTR of
            HIV-1, a consensus binding sequence for USF is present from -159 to
            -174.  However, there is conflicting information on whether this
            factor has moderating (and thus be regarded as a negative
            regulatory factor; Lu et al.  J. Virol. 64: 5226-5229 1990) or
            stimulating (Maekewa et al. Nucl.  Acids Res. 19: 4689-4694)
            effects.  Interestingly, USF binds a second sequence near the HIV-1
            intitiator (-5 to +11).  USF interaction at the initiator-proximal
            site strongly activates HIV-1 expression from the TATAA-promoter.
            Of note, a factor distinct from USF binds the same DNA sequence
            (TFE3; Bechmann and Kadesch, Genes Dev 5:1057-1066).
            NCBI gi: 261070
BASE COUNT      339 a    369 c    367 g    224 t
ORIGIN
        1 ggcggcggca cgagcggtgg ccgaggcagc gggatccaga cccgggtcca gcatgtccag
   USFII ->
       61 taccagttcc gcacagagac aaatggagga caggctgtga tccaaaatcc cttcagcaat
      121 ggtggcagtc cggcggccga ggctgtcagc ggggaggcac gatttgccta tttcccagcg
      181 tccagtgtgg gagatactac ggctgtgtcc gtacagacca cagaccagag cttgcaggct
      241 ggaggccagt tctacgtcat gatgacgccc caggatgtgc ttcagacagg aacacagagg
      301 acgatcgccc cccggacaca cccttactct ccaaaaattg atggaaccag aacaccccga
      361 gatgagagga gaagagccca gcacaacgaa gtggagcgga ggcggaggga caagatcaac
      421 aactggatcg tccagctttc gaaaatcatt ccagactgta acgcagacaa cagcaagacg
      481 ggagcgagta aaggagggat cctgtccaag gcctgcgatt acatccggga gttgcgccag
      541 accaaccagc gcatgcagga gaccttcaaa gaggccgagc ggctgcagat ggacaacgag
      601 ctcctgaggc agcagatcga ggagctgaag aatgagaacg ccctgcttcg agcccagctg
      661 cagcagcaca acctggagat ggtgggcgag ggcacccggc agTGAcgccc gccaccacca
                                                      <- USFII cds end
      721 cgcagccgcc gccgcccacg ccggcctctg ctgccccctt ccccagccct tagcacagag
      781 agggacacat gcccctcccc cagctgcgtt tttttatagt agatttttaa caaaaaacgg
      841 ggagaaataa tgcatttctg tggatacagt gcccaccgcc ctcctccact tggaaacggt
      901 atcctccctg cccatccgtc tgtctgtcgc ccttctcccg gccctcgcta agccccggca
      961 cttctagtgg tctcacctgg caagagggag ggtacagagc ctctgccaac gtcccgctgg
     1021 tgcctcctgc tctctggagg tactgagaca gggtgctgat gggaaggagg ggagcctttg
     1081 gggggccac ccggggcctg gacctatgca gggaggccac gtcccacccc acctcttgtt
     1141 tctgggtccc tgctcccctt tggggtgtgt gtgtgtgttt taattttctt tatggaaaaa
     1201 ttgacaaaaa aaaaatagag agagaggtat ttaactgcaa taaactggcc ccatgtggaa
     1261 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa
```

```
LOCUS       HUMYC1A      1520 bp ss-mRNA            PRI       17-MAR-1994
DEFINITION  Human YC1 cDNA sequence.
ACCESSION   L11289
SOURCE      Homo sapiens mRNA from lambda gt11 library.
REFERENCE   1  (bases 1 to 1520)
  AUTHORS   Lu,Y., Ueberla,K., Touzjian,N. and Haseltine,W.A.
  TITLE     YC1: A human repressor of HIV-1 and IL2R alpha promoter
            transcription
  JOURNAL   Unpublished (1993)
COMMENT     ;
BASE COUNT      459 a    382 c    311 g    368 t
ORIGIN
        1 gaattcgggc cgagacttgg aaaccccaaa gtgtccgcga ccctgcacgg cagctccctt
       61 ccagcttcAT Gggcaaagtg tggaaacagc agatgtaccc tcagtacgcc acctactatt
    YC1 cds start ->
      121 acccccagta tctgcaagcc aagcagtctc tggtcccagc ccaccccatg gcccctccca
      181 gtcccagcac caccagcagt aataacaaca gtagcagcag tagcaactca ggatgggatc
      241 agctcagcaa aacgaacctc tatatccgag gactgcctcc ccacaccacc gaccaggacc
      301 tggtgaagct ctgtcaacca tatgggaaaa tagtctccac aaaggcaatt ttggataaga
      361 caacgaacaa atgcaaaggt tatggttttg tcgactttga cagccctgca gcagctcaaa
      421 aagctgtgtc tgccctgaag gccagtgggg ttcaagctca aatggcaaag caacaggaac
      481 aagatcctac caacctctac atttctaatt tgccactctc catggatgag caagaactag
      541 aaaatatgct caaaccattt ggacaagtta tttctacaag gatactacgt gattccagtc
      601 ctacaagtcg tggtgttggc tttgctagga tggaatcaac agaaaaatgt gaagctgtta
      661 ttggtcattt taatggaaaa tttattaaga caccaccagg agtttctgcc cccacagaac
      721 ctttattgtg taagtttgct gatggaggac agaaaaagag acagaaccca aacaaataca
      781 tccctaatgg aagaccatgg catagagaag gagaggtgag acttgctgga atgacactta
      841 cttacgaccc aactacagct gctatacaga acggatttta tccttcacca tacagtattg
      901 ctacaaaccg aatgatcact caaacttcta ttacacccta tattgcatct cctgtatctg
      961 cctaccaggt gcaaagtcct tcgtggatgc aacctcaacc atatattcta cacgaccctg
     1021 gtgccgtgtt aactccctca atggagcaca ccatgtcact acagcccgca tcaatgatca
     1081 gccctctggc ccagcagatg agtcatctgt cactaggcag caccggaaca tacatgcctg
     1141 caacgtcagc tatgcaagga gcctacttgc cacagtatgc acatatgcag acgacagcgg
     1201 ttcctgttga ggaggcaagt ggtcaacagc aggtggctgt cgagacgtct aatgaccatt
     1261 ctccatatac ctttcaacct aataagTAAc tgtgagatgt acagaaaggt gttcttacat
                                        <- YC1 cds end
     1321 gaagaaggtg tgaaggctga acaatcatgg atttttctga tcaattgtgc tttaggaaat
     1381 tattgacagt tttgcacagg ttcttgaaaa cgttatttat aatgaaatca actaaaacta
     1441 tttttgctat aagttctata aggtgcataa aacccttaaa ttcatctagt agctgttccc
     1501 ccgaacaggt ttattttagt
```

```
LOCUS       YY1          2353 bp ss-mRNA            PRI       25-MAY-1993
DEFINITION  Homo sapiens GLI-Krupple related protein (YY1) cDNA sequence,
            complete cds.
ACCESSION   M77698
KEYWORDS    GLI-Krupple related protein.
SOURCE      Homo sapiens mRNA.
REFERENCE   1  (bases 1 to 2353)
  AUTHORS   Shi,Y., Seto,E., Chang,L.-S. and Shenk,T.
  TITLE     Transcriptional repression by YY1, a human GLI-Krupple related
            protein, and relief of repression by adenovirus E1a protein
  JOURNAL   Cell 67, 377-388 (1991)
COMMENT     Positioned at the junction of U3 and R in the HIV-1 genome, is a
            binding site for YY1 (Useheva and Shenk Cell 76:1115-1121; Seto et
            al. Nature 354:241-245).  Binding of YY1 to the LTR has been shown
            to repress HIV-1 expression and production of virions (Margolis et
            al. J. Virol. 68:905-910).
BASE COUNT      625 a    598 c    608 g    522 t
ORIGIN
        1 cgccgagacg agcagcggcc gagcgagcgc gggcgcgggc gcaccgaggc gagggaggcg
       61 gggaagcccc gccgccgccg ccccgcccgc cccttccccc gccgcccgcc ccctctcccc
      121 ccgcccgctc gccgccttcc tccctctgcc ttccttcccc acggccggcc gcctcctcgc
      181 ccgcccgccc gcagccgagg agccgaggcc gccgcggccg tggcggcgga gccctcagcc
      241 ATGgcctcgg gcgacaccct ctacatcgcc acggacggct cggagatgcc ggccgagatc
  YY1 cds ->
      301 gtggagctgc acgagatcga ggtggagacc atcccggtgg agaccatcga gaccacagtg
      361 gtgggcgagg aggaggagga ggacgacgac gacgaggacg gcggcggtgg cgaccacggc
      421 ggcgggggcg gccacgggca cgccggccac caccaccacc accatcacca ccaccaccac
      481 ccgcccatga tcgctctgca gccgctggtc accgacgacc cgacccaggt gcaccaccac
      541 caggaggtga tcctggtgca gacgcgcgag gaggtggtgg gcggcgacga ctcggacggg
      601 ctgcgcgccg aggacggctt cgaggatcag attctcatcc cggtgcccgc gccggccggc
      661 ggcgacgacg actacattga acaaacgctg gtcaccgtgg cggcggccgg caagagcggc
      721 ggcggcggct cgtcgtcgtc gggaggcggc cgcgtcaaga agggcggcgg caagaagagc
      781 ggcaagaaga gttacctcag cggcggggcc ggcgcggcgg gcgggcgcgg cgccgacccg
      841 ggcaacaaga agtgggagca gaagcaggtg cagatcaaga ccctggaggg cgagttctcg
      901 gtcaccatgt ggtcctcaga tgaaaaaaaa gatattgacc atgagacagt ggttgaagaa
      961 cagatcattg gagagaactc acctcctgat tattcagaat atatgacagg aaagaaactt
     1021 cctcctggag gaatacctgg cattgacctc tcagatccca aacaactggc agaatttgct
     1081 agaatgaagc caagaaaaat taaagaagat gatgctccaa gaacaatagc ttgccctcat
     1141 aaaggctgca caaagatgtt cagggataac tcggccatga gaaaacatct gcacacccac
     1201 ggtcccagag tccacgtctg tgcagaatgt ggcaaagctt ttgttgagag ttcaaaacta
     1261 aaacgacacc aactggttca tactggagag aagccctttc agtgcacgtt cgaaggctgt
     1321 gggaaacgct tttcactgga cttcaatttg cgcacacatg tgcgaatcca taccggagac
     1381 aggccctatg tgtgcccctt cgatggttgt aataagaagt ttgctcagtc aactaacctg
     1441 aaatctcaca tcttaacaca tgctaaggcc aaaaacaacc agTGAaaaga agagagaaga
                              <-                          <- YY1 cds end
     1501 cccttctcga ccacgggaag catcttccag aagtgtgatt gggaataaat atgcctctcc
     1561 tttgtatatt atttctagga agaattttaa aaatgaatcc tacacaccta agggacatgt
     1621 tttgataaag tagtaaaaat taaaaaaaaa aaactttact aagatgacat tgctaagatg
     1681 ctctatcttg ctctgtaatc tcgtttcaaa aacacagtgt ttttgtaaag tgtggtccca
     1741 acaggaggac aattcatgaa cttcgcatca aaagacaatt ctttatacaa cagtgctaaa
     1801 aatgggactt cttttcacat tcttataaat atgaagctca cctgttgctt acaatttttt
     1861 taatttttga ttttccaagt gtgcatattg tacacttttt tggggatatg cttagtaatg
     1921 ctacgtgtga tttttctgga ggttgataac tttgcttgca gtagattttc tttaaaagaa
     1981 tgggcagtta catgcatact tcaaaagtat tttcctgtaa aaaaaaaaaa agttatatag
     2041 gttttgtttg ctatcttaat tttggttgta ttctttgatg ttaacacatt ttgtataatt
     2101 gtatcgtata gctgtattga atcatgtagt atcaaatatt agatgtgatt taatagtgtt
     2161 aatcaattta aacccatttt agtcactttt tttttccaaa aaaatactgc cagatgctga
     2221 tgttcagtgt aatttctttg cctgttcagt tacagaaagt ggtgctcagt tgtagaatgt
     2281 attgtacctt ttaacacctg atgtgtacat cccatgtaac agaaagggca acaataaaat
     2341 agcaatccta aag
```

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LOCUS       Hcfos         6210 bp ds-DNA              PRI       15-MAR-1990
DEFINITION  Human fos proto-oncogene (c-fos) sequence, complete cds,
            clone pc-fos(human)-1.
ACCESSION   K00650 M16287
KEYWORDS    c-myc proto-oncogene; fos oncogene; proto-oncogene.
SOURCE      Human DNA from lymphoblastic cell line (CCRF-CM).
REFERENCE   1  (bases 1 to 4165)
  AUTHORS   van Straaten,F., Mueller,R., Curran,T., van Beveren,C.P. and
            Verma,I.M.
  TITLE     Complete nucleotide sequence of a human c-onc gene: Deduced amino
            acid sequence of the human c-fos protein
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 80, 3183-3187 (1983)
REFERENCE   2  (sites)
  AUTHORS   Treisman,R.
  TITLE     Transient accumulation of c-fos RNA following serum stimulation
            requires a conserved 5' element and c-fos 3' sequences
  JOURNAL   Cell 42, 889-902 (1985)
REFERENCE   3  (bases 4166 to 6210)
  AUTHORS   Verma,I.M., Deschamps,J., van Beveren,C.P. and Sassone-Corsi,P.
  TITLE     Human fos gene
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 51, 949-958 (1986)
COMMENT     Between -216 and -254 of the HIV-1 LTR are binding sites for NFAT,
            nuclear factor from activated T cells (Shaw et al. Science 244:202-
            205).  Recent evidence suggests that NFAT binding activity results
            from the interaction of three discrete polypeptides, NFATp
            (McCaffrey et al. Science 262: 750-754), Fos and Jun (Yaseen et al.
            J. Biol. Chem. 268:14285-14293).
BASE COUNT     1497 a   1571 c   1619 g   1523 t
ORIGIN      Chromosome 14q24.3-q31.
        1 gcaggaacag tgctagtatt gctcgagccc gagggctgga ggttagggga tgaaggtctg
       61 cttccacgct ttgcactgaa ttagggctag aattggggat gggggtaggg gcgcattcct
      121 tcgggagccg aggcttaagt cctcggggtc ctgtactcga tgccgtttct cctatctctg
      181 agcctcagaa ctgtcttcag tttccgtaca agggtaaaaa ggcgctctct gccccatccc
      241 ccccgacctc gggaacaagg gtccgcattg aaccaggtgc gaatgttctc tctcattctg
      301 cgccgttccc gcctcccctc ccccagccgc ggcccccgcc tccccccgca ctgcaccctc
      361 ggtgttggct gcagcccgcg agcagttccc gtcaatccct ccccccttac acaggatgtc
                                                      -> transactivator region
      421 catattagga catctgcgtc agcaggtttc cacggccttt ccctgtagcc ctgggggggag
                                          <-
      481 ccatccccga aacccctcat cttgggggggc ccacgagacc tctgagacag gaactgcgaa
      541 atgctcacga gattaggaca cgcgccaagg cgggggcagg gagctgcgag cgctggggac
      601 gcagccgggc ggccgcagaa gcgcccaggc ccgcgcgcca cccctctggc gccaccgtgg
      661 ttgagcccgt gacgtttaca ctcattcata aaacgcttgt tataaaagca gtggctgcgg
      721 cgcctcgtac tccaaccgca tctgcagcga gcaactgaga agccaagact gagccggcgg
      781 ccgcggcgca gcgaacgagc agtgaccgtg ctcctaccca gctctgcttc acagcgccca
      841 cctgtctccg cccctcggcc cctcgcccgg ctttgcctaa ccgccacgAT Gatgttctcg
                                          cfos exon 1 start ->
      901 ggcttcaacg cagactacga ggcgtcatcc tcccgctgca gcagcgcgtc cccggccggg
      961 gatagcctct cttactacca ctcacccgca gactccttct ccagcatggg ctcgcctgtc
     1021 aacgcgcagg taaggctggc ttcccgtcgc cgcggggccg ggggcttggg gtcgcggagg
              <- cfos exon 1 end
     1081 aggagacacc gggcgggacg ctccagtaga tgagtagggg gctcccttgt gcctggaggg
     1141 aggctgccgt ggccggagcg gtgccggctc gggggctcgg gacttgctct gagcgcacgc
     1201 acgcttgcca tagtaagaat tggttccccc ttcgggaggc aggttcgttc tgagcaacct
     1261 ctggtctgca ctccaggacg gatctctgac attagctgga gcagacgtgt cccaagcaca
     1321 aactcgctaa ctagagcctg gcttcttcgg ggaggtggca gaaagcggca atccccccctc
     1381 ccccggcagc ctggagcacg gaggagggat gagggaggag ggtgcagcgg gcgggtgtgt
     1441 aaggcagttt cattgataaa aagcgagttc attctggaga ctccggagcg gcgcctgcgt
     1501 cagcgcagac gtcagggata tttataacaa acccccctttc aagcaagtga tgctgaaggg
```

Hcfos

```
  1561 ataacgggaa cgcagcggca ggatggaaga gacaggcact gcgctgcgga atgcctggga
  1621 ggaaaagggg gagacctttc atccaggatg agggacattt aagatgaaat gtccgtggca
  1681 ggatcgtttc tcttcactgc tgcatgcggc actgggaact cgccccacct gtgtccggaa
  1741 cctgctcgct cacgtcggct ttccccttct gttttgttct aggacttctg cacggacctg
                                  cfos exon 2 start ->
  1801 gccgtctcca gtgccaactt cattcccacg gtcactgcca tctcgaccag tccggacctg
  1861 cagtggctgg tgcagcccgc cctcgtctcc tctgtggccc catcgcagac cagagcccct
  1921 cacccttttcg gagtccccgc cccctccgct ggggcttact ccagggctgg cgttgtgaag
  1981 accatgacag gaggccgagc gcagagcatt ggcaggaggg gcaaggtgga acaggtgagg
                                                                <- cfos exon
                                                                   2 end
  2041 aactctagcg tactcttcct gggaatgtgg gggctgggtg ggaagcagcc ccggagatgc
  2101 aggagcccag tacagaggat gaagccactg atggggctgg ctgcacatcc gtaactggga
  2161 gccctggctc caagcccatt ccatcccaac tcagactctg agtctcaccc taagaagtac
  2221 tctcatagtt tcttccctaa gtttcttacc gcatgctttc agactgggct cttctttgtt
  2281 ctcttgctga ggatcttatt ttaaatgcaa gtcacaccta ttctgcaact gcaggtcaga
  2341 aatggtttca cagtggggtg ccaggaagca gggaagctgc aggagccagt tctactgggg
  2401 tgggtgaatg gaggtgatgg cagacacttt tactgaatgt cggtcttttt ttgtgattat
  2461 tctagttatc tccagaagaa gaagagaaaa ggagaatccg aagggaaagg aataagatgg
cfos exon 3 ->
start
  2521 ctgcagccaa atgccgcaac cggaggaggg agctgactga tacactccaa gcggtaggta
                                                                 <- cfos exon
                                                                    3 end
  2581 ctctgtgggt tgctcctttt taaaacttaa gggaaagttg gagattgagc ataagggccc
  2641 ttgagtaaga ctgtgtctta tgctttcctt tatccctctg tatacaggag acagaccaac
                                     cfos exon 4 start ->
  2701 tagaagatga gaagtctgct ttgcagaccg agattgccaa cctgctgaag gagaaggaaa
  2761 aactagagtt catcctggca gctcaccgac ctgcctgcaa gatccctgat gacctgggct
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  3061 tggacctatc tgggtccttc tatgcagcag actgggagcc tctgcacagt ggctccctgg
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  3301 tcagctcacc cacgctgctg gccctgTGAg ggggcaggga aggggaggca gccggcaccc
                                   <- cfos cds end
  3361 acaagtgcca ctgcccgagc tggtgcatta cagagaggag aaacacatct tccctagagg
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  3901 catgcattgt tgaggtggtc tgaatgttct gacattaaca gttttccatg aaaacgtttt
  3961 attgtgtttt taatttattt attaagatgg attctcagat atttatattt ttatttttatt
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  4081 ttgtttgctt attgttccaa gacattgtca ataaaagcat ttaagttgaa tgcgaccaac
  4141 cttgtgctct tttcattctg gaagtcttgt aagtttctga aaggtattat tggagaccag
  4201 tttgtcaaga agggtagctg ctggaggggg acacaccctc tgtctgatcc cttatcaaag
  4261 aggacaagga aactatagag ctgattttag aatattttac aaatacatgc cttccattgg
  4321 aatgctaaga ttttctactg cttctgggga cgggaaaccg ctgtgtaaca gcttttgtgg
  4381 gaatacattt tttctgtttc agtactcgca gggggaaata tttaaatttt gttgtgctaa
  4441 tattaaattc agatgttttg atcttaaagg aacccttaa gcaaacagaa cctagctttg
  4501 tacagactat tttaactttt tattctcaca aaatcacgtg gagggttatt ctacttcaaa
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```
4561 gatgagcaaa ttgaagaatg gttagaataa acaactttct tgatattccg ttatcggcat
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4681 aaaaaaattt tcaggccggg cgcggtggcc catgcctgta atcctagcac tttgggaggc
4741 cgaggcaggc ggatcacctg aggtcgggag ttcgagacca gcctgaccaa catggagaaa
4801 ccccgtcttt actaaaaata caaaattagc ctggtgtggt ggtgcatgcc tgtaatccta
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4921 actgagattg cgccattgca ctccagcctg ggcaacaaga ttgaaactct gtttaaaaaa
4981 aaaagttttc actaatgtgt acatttttt gtactctttt attctcgaaa gggaaggagg
5041 gctattgccc tatcccttat taataaatgc attgtggttt ctggtttctc taataccata
5101 tgcccttcat tcagtttata gtgggcggaa gtgggggaga aaaagttgct cagaaatcaa
5161 aagatatctc aaacagcaca aataatggct gatcgttctg caaacaaaaa gttacataat
5221 agctcaagaa ggagaagtca acatgactct gaacaagctt taacttagaa actttatcat
5281 cttaaggaag aacgtgacct ttgtccagga cgtctctggt aatggggcac ttacacacac
5341 atgcacacgt acaaaccaca gggaaaggag accgcccttc tgcctctgct cgcgagtatc
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5521 tcgagttaaa agttttaatt caaaatgaca gttttactga ggttgatgtt ctcgtctatg
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5641 ctcctatatc acacaccact tggggtgctg tttctgctag acttgtgatg acagtggcct
5701 taggatccct gtttgctgtt caaagggcaa atattttata gcctttaaat atacctaaac
5761 taaatacaga attaatataa ctaacaaaca cctggtctga aataacaagg tgatctaccc
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6061 ccagcctggg tgacacagca aaaccctatc tcaaaaaaaa aaaaaaaaaa aaggaaccca
6121 gctggttcct gtaggtgtgc aataataaca accagaggaa gaaaaggaag acgatttccc
6181 agatgaagaa gggcagctgg accttcggac
```

HINTAV

```
LOCUS       HINTAV       1074 bp    DNA             PRI       30-MAR-1994
DEFINITION  Human integrin alpha v sequence, promoter region and partial cds.
ACCESSION   U07375
SOURCE      Human.
REFERENCE   1  (bases 1 to 1074)
  AUTHORS   Donahue,J.P., Sugg,N. and Hawiger,J.
  TITLE     The integrin alphav gene: Identification and characterization of
            the promoter region
  JOURNAL   Unpublished
COMMENT     There is evidence that HIV-1 Tat can be taken up actively into
            cells through binding to a cell-surface protein (Weeks et al. J.
            Biol.  Chem. 268:5279-5284) implicated to be alpha-v-beta-5
            integrin (Vogel et al. J. Cell.. Biol. 121:461-468).  Once
            inside cells, Tat interacts with multiple partners in activating
            transcription.
            NCBI gi: 466371
BASE COUNT      143 a    394 c    328 g    209 t
ORIGIN
        1 agctttcctc atttttaaac aacagtcgca cggaagttcc cggcgggaca agggaacgtg
       61 ggtgcccttg ctactcccgt ggacgcgggt agattgggac gctggaccgt atctccccgc
      121 ccccgccccc acgcctcctc aggtgctcag cctgaggcct tcgtccagga gcgctgccgc
      181 tgacccaggc tcaggagctg ggggcccctg cacagacgcc caggtctcgg gacaggcggc
      241 gactgcactc acggaagtac gctgagctct cccctgtaga agggcgcctc tcctccccca
      301 cttcctcctc cagctccaca gcagcctccc gggccggctc ctcctccttc caggtctcct
      361 ccagtgccgc cgcggctctc aggcctgagg tgcggcgctc accccggcag tccccagcct
      421 cagacgctgc gtggagcggc ggagccggag ggaagcaaag gaccgtctgc gctgctgtcc
      481 ccgccccgcg cgctctgcgc ccctcgtccc tggcggtcgc tccgaagctc agccctcttg
      541 cctgccccgg agctgtcccg ggctagccga gaagagagcg gccggcaagt ttgggcgcgc
      601 gcaggcggcg ggccgcgggc actgggcgcc tcgctggggc gggggaggt ggctaccgct
      661 cccggcttgg cgtcccgcgc gcacttcggc gATGgctttt ccgccgcggc gacggctgcg
            vitronectin alpha subunit cds start ->
      721 cctcggtccc cgcggcctcc cgcttcttct ctcgggactc ctgctacctc tgtgccgcgc
      781 cttcaaccta gacgtggaca gtcctgccga gtactctggc cccgagggaa gttacttcgg
      841 cttcgccgtg gatttcttcg tgcccagcgc gtcttcgtaa gtggccgcac ttggaactgg
      901 agctggcccc ctcccccacc gcgcgcaccc acccagcgtt tctccattgg gattgatttc
      961 cattgggatt gatttccgag agatcccggc gtctgtctgt ctcacccatc ctacctctca
     1021 gagtggttta tatcctgggt ggaggaaata tttggggaaa tgaactccct ttgg
                                          vitronectin alpha subunit <-
```

```
LOCUS       HUMINTB5A    3117 bp ss-mRNA            PRI       30-JUL-1991
DEFINITION  Human integrin beta-5 subunit cDNA sequence, complete cds, clone
            10.
ACCESSION   J05633
KEYWORDS    integrin beta-5 subunit.
SOURCE      Human epithelial lung adenocarcinoma mRNA.
REFERENCE   1  (bases 1 to 3117)
  AUTHORS   McLean,J.W., Vestal,D.J., Cheresh,D.A. and Bodary,S.C.
  TITLE     cDNA sequence of the human integrin beta-5 subunit
  JOURNAL   J. Biol. Chem. 265, 17126-17131 (1990)
COMMENT     There is evidence that HIV-1 Tat can be taken up actively into
            cells through binding to a cell-surface protein (Weeks et al. J.
            Biol.  Chem. 268:5279-5284) implicated to be alpha-v-beta-5
            integrin (Vogel et al. J. Cell. Biol. 121:461-468).  Once
            inside cells, Tat interacts with multiple partners in activating
            transcription.
            Draft entry and computer-readable sequence for [J. Biol. Chem.
            (1990) In press] kindly submitted
            by J.W.McLean, 20-JUL-1990.
            NCBI gi: 186504
BASE COUNT      718 a    819 c    892 g    688 t
ORIGIN
        1 ccgcggagtg cagcgaccgc gccgccgctg agggaggcgc cccaccATGc cgcgggcccc
                          integrin beta-5 subunit cds start ->
       61 ggcgccgctg tacgcctgcc tcctggggct ctgcgcgctc ctgccccggc tcgcaggtct
                                  integrin beta-5 subunit mature peptide ->
      121 caacatatgc actagtggaa gtgccacctc atgtgaagaa tgtctgctaa tccacccaaa
      181 atgtgcctgg tgctccaaag aggacttcgg aagcccacgg tccatcacct ctcggtgtga
      241 tctgagggca aaccttgtca aaaatggctg tggaggtgag atagagagcc cagccagcag
      301 cttccatgtc ctgaggagcc tgcccctcag cagcaagggt tcgggctctg caggctggga
      361 cgtcattcag atgacaccac aggagattgc cgtgaacctc cggcccggtg acaagaccac
      421 cttccagcta caggttcgcc aggtggagga ctatcctgtg gacctgtact acctgatgga
      481 cctctccctg tccatgaagg atgacttgga caatatccgg agcctgggca ccaaactcgc
      541 ggaggagatg aggaagctca ccagcaactt ccggttggga tttgggtctt ttgttgataa
      601 ggacatctct cctttctcct acacggcacc gaggtaccag accaatccgt gcattggtta
      661 caagttgttt ccaaattgcg tcccctcctt tgggttccgc catctgctgc ctctcacaga
      721 cagagtggac agcttcaatg aggaagttcg gaaacagagg gtgtcccgga accgagatgc
      781 ccctgagggg ggctttgatg cagtactcca ggcagccgtc tgcaaggaga agattggctg
      841 gcgaaaggat gcactgcatt tgctggtgtt cacaacagat gatgtgcccc acatcgcatt
      901 ggatggaaaa ttgggaggcc tggtgcagcc acacgatggc cagtgccacc tgaacgaggc
      961 caacgagtac actgcatcca accagatgga ctatccatcc cttgccttgc ttggagagaa
     1021 attggcagag aacaacatca acctcatctt tgcagtgaca aaaaaccatt atatgctgta
     1081 caagaatttt acagccctga tacctggaac aacggtggag attttagatg gagactccaa
     1141 aaatattatt caactgatta ttaatgcata caatagtatc cggtctaaag tggagttgtc
     1201 agtctgggat cagcctgagg atcttaatct cttctttact gctacctgcc aagatggggt
     1261 atcctatcct ggtcagagga agtgtgaggg tctgaagatt ggggacacgg catcttttga
     1321 agtatcattg gaggcccgaa gctgtcccag cagacacacg gagcatgtgt ttgccctgcg
     1381 gccggtggga ttccgggaca gcctggaggt gggggtcacc tacaactgca cgtgcggctg
     1441 cagcgtgggg ctggaaccca acagcgccag gtgcaacggg agcgggacct atgtctgcgg
     1501 cctgtgtgag tgcagccccg gctacctggg caccaggtgc gagtgccagg atggggagaa
     1561 ccagagcgtg taccagaacc tgtgccggga ggcagagggc aagccactgt gcagcgggcg
     1621 tggggactgc agctgcaacc agtgctcctg cttcgagagc gagtttggca agatctatgg
     1681 gcctttctgt gagtgcgaca acttctcctg tgccaggaac aagggagtcc tctgctcagg
     1741 ccatggcgag tgtcactgcg gggaatgcaa gtgccatgca ggttacatcg gggacaactg
     1801 taactgctcg acagacatca gcacatgccg gggcagagat ggccagatct gcagcgagcg
     1861 tgggcactgt ctctgtgggc agtgccaatg cacggagccg ggggcctttg gggagatgtg
     1921 tgagaagtgc cccacctgcc cggatgcatg cagcaccaag agagattgcg tcgagtgccc
     1981 gctgctccac tctgggaaac ctgacaacca gacctgccac agcctatgca gggatgaggt
     2041 gatcacatgg gtggacacca tcgtgaaaga tgaccaggag gctgtgctat gtttctacaa
```

```
2101 aaccgccaag gactgcgtca tgatgttcac ctatgtggag ctccccagtg ggaagtccaa
2161 cctgaccgtc ctcagggagc cagagtgtgg aaacaccccc aacgccatga ccatcctcct
2221 ggctgtggtc ggtagcatcc tccttgttgg gcttgcactc ctggctatct ggaagctgct
2281 tgtcaccatc cacgaccgga gggagtttgc aaagtttcag agcgagcgat ccagggcccg
2341 ctatgaaatg gcttcaaatc cattatacag aaagcctatc tccacgcaca ctgtggactt
2401 caccttcaac aagttcaaca aatcctacaa tggcactgtg gacTGAtgtt tccttctccg
                                                    <- integrin beta-5
2461 aggggctgga gcggggatct gatgaaaagg tcagactgaa acgccttgca cggctgctcg
2521 gcttgatcac agctccctag gtaggcacca cagagaagac cttctagtga gcctgggcca
2581 ggagcccaca gtgcctgtac aggaaggtgc ctggccatgt cacctggctg ctaggccaga
2641 gccatgccag gctgcgtccc tccgagcttg ggataaagca aggggacctt ggcgctctca
2701 gctttccctg ccacatccag cttgttgtcc caatgaaata ctgagatgct gggctgtctc
2761 tcccttccag gaatgctggg cccccagcct ggccagacaa gaagactgtc aggaagggtc
2821 ggagtctgta aaaccagcat acagtttggc ttttttcaca ttgatcattt ttatatgaaa
2881 taaaaagatc ctgcatttat ggtgtagttc tgagtcctga gacttttctg cgtgatggct
2941 atgccttgca cacaggtgtt ggtgatgggg ctgttgagat gcctgttgaa ggtacatcgt
3001 ttgcaaatgt cagtttcctc tcctgtccgt gtttgtttag tacttttata atgaaaagaa
3061 acaagattgt ttgggattgg aagtaaagat taaaaccaaa agaatttgtg tttgtca
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LOCUS       MMLEF1       2460 bp    RNA              ROD       16-DEC-1993
DEFINITION  Mouse lymphoid enhancer binding factor 1 LEF1 sequence.
ACCESSION   X58636
SOURCE      Mus musculus RNA.
REFERENCE   1  (bases 1 to 2460)
  AUTHORS   Travis,A., Amsterdam,A., Belanger,C. and Grosschedl,R.
  TITLE     LEF-1, a gene enconding a lymphoid-specific DNA-binding protein
            with an HMG domain, regulates T cell receptor alpha enhancer
            function
  JOURNAL   Genes Dev. 5, 880-894 (1991)
COMMENT     LEF-1, lymphoid enhancer-binding factor, is a T-cell specific
            transcription factor.  It is capable of binding the minor groove of
            a DNA helix through its high mobility group (HMG) domain, a domain
            characteristic of other eukaryotic regulatory proteins.  This
            interaction results in a bending of the DNA helix and thereby
            facilitates the assembly of nucleoprotein complexes at the promoter
            (Giese et al. Cell 69: 185-195 1992, Jones and Peterlin Annu. Rev.
            Biochem.  63: 717-743 1994).  Within the LTR of HIV-1, one high
            affinity LEF-1 binding site exists at -122 to -143 and two low
            affinity binding sites are present; one located from -37 to -51 and
            another from +17 to +32 (Waterman and Jones New Biol. 2: 621-636
            1990).
            NCBI gi: 52887
BASE COUNT      603 a    768 c    629 g    460 t
ORIGIN
        1 cggaggagcc gaggggccac cggcagctct ttgctttgac cgaggggagg cggggagaga
       61 ggcgagccag gcagaaactc gagccgggaa caaagaggga tcgggctcga gtgtgtgtgt
      121 gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtaagtgtgt gtatcggccc gagctgcggg
      181 ctgggacatt tgggcccgaa gctcctgctg tgactcccca agactccgcc gtgccagcca
      241 ccgccgattc ccagcgctca tcatcacaaa ctttattctt ggcaaacttc tctttttctc
      301 ccctcccccc ccagcagatt aaatgctcct ccagaaggaa aaccgaagcg aaagggaagg
      361 aaagaagctc taacgcggac gtctgcagcc cggtggctct ttattgttta ctctgaagga
      421 agtggacttt tcggtatttt ctgattcttc tcgtacctcc gctggggcaa agggagcctc
      481 ttggccagct ctcctcttct caaaaacaaa acaaaacaaa accccaaatc accgaaatca
      541 gcatccgagg aatccgtgga gaggttttgc acggtgacgc accacgggac cctcgtttgc
      601 actttggcaa gtcgtgtccc ctccggaacc ggtgtcctcg aagcacagac cccagcaacg
      661 agtgcggcgt ggggtggcca cccagccctg gcagcctagc ctagtgcacg cggagcgcgt
      721 agacgctctc agaggcgccg gcgtgccgcc ctcgcagtct ggtgcccttc gccccaggcc
      781 ggggcgccgg cgtccttcta agtgggaaag cgcggcaatc gcagaggctc ctgcagctgc
      841 tccagccgtg ggccccctcgc ttgcccaccc ggcttccatt cacagtcctc ccgcactcag
      901 tcttccaact ccccccacctc acatcgaccc tcccttcttg ctgtctcgga gtgctcccgc
      961 agcggagcgg agattacaca gccgccgggA TGccccaact ttccggagga ggcggcgggg
                          LEF1 cds start ->
     1021 gggacccgga actctgcgcc accgatgaga tgatcccctt caaggacgaa ggcgatcccc
     1081 agaaggagaa gatcttcgcc gagatcagtc atcccgaaga ggagggcgac ttagccgaca
     1141 tcaagtcatc tttggttaac gagtccgaaa tcatcccagc cagcaacggg catgaggtgg
     1201 tcagacaagc cccgtcctct caggagccct accacgacaa ggccagagaa caccctgatg
     1261 aaggaaagca tccagacgga ggcctgtaca acaagggacc ctcctactcc agttactctg
     1321 gctacataat gatgcccaat atgaacagcg acccgtacat gtcaaatggg tccctttctc
     1381 cacccatccc gaggacatca aataaagtgc ccgtggtgca gccctctcac gcggtccacc
     1441 cgctcacccc cctcatcacc tacagcgacg agcacttttc tccgggatcc cacccgtcac
     1501 acatcccgtc agatgtcaac tccaagcaag gcatgtccag acaccctcca gctcctgaaa
     1561 tccccacctt ctacccccctg tctccgggcg gcgttggaca gatcacccca cccattggct
     1621 ggcaaggtca gcctgtttat cccatcacgg gtggattcag gcaaccctac ccatcctcac
     1681 tgtcaggcga cacttccatg tccaggtttt cccatcatat gattcctggt ccccctggcc
     1741 cccacacaac tggcatccct catccagcta ttgtaacacc tcaggtcaaa caggagcacc
     1801 cccacacgga cagtgaccta atgcacgtga agcctcaaca cgaacagaga aaggagcagg
     1861 agcccaaaag acctcatatt aagaagcctc tgaatgcttt catgttatat atgaaagaaa
     1921 tgagagcgaa tgtcgtagct gagtgcacgc taaaggagag tgcagctatc aaccagatcc
```

MMLEF1

```
1981 tgggcagaag atggcacgcc ctctcccggg aagagcaggc caaatactat gaactagcac
2041 ggaaagagag acagctacac atgcagcttt atccaggctg gtcagcgcga gacaattatg
2101 gcaagaagaa gaagaggaag agagagaagc tacaggagtc gacttcaggt acaggtccca
2161 gaatgacagc tgcctacatc TGAaacatgg tggtaagaga agctccttcc caacgtgcaa
                          <- LEF1 cds end
2221 agccaaggca gcgaccccag gccctcttct ggagatggaa gcttgttgaa accccagact
2281 gtctccacag cttgcccggc tgaccccaag gaacactgac agcaacctta ccctgaggtc
2341 actgctagcg ctgacccgaa gacacagtca ctgccacctc ttccttctgt cgtctactgc
2401 aagcgccgac ttccaaaaag aaagccgaaa acggttgttt cggaaaaaaa aaaaaaaaaa
```

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LOCUS       RNBCOP       3073 bp    RNA              ROD       07-FEB-1991
DEFINITION  Rat beta COP sequence.
ACCESSION   X57228
SOURCE      Rat mRNA.
REFERENCE   1  (bases 1 to 3073)
  AUTHORS   Duden,R., Griffiths,G., Frank,R., Argos,P. and Kreis,T.E.
  TITLE     beta COP, a 110kD protein associated with non-clathrin coated
            vesicles and the Golgi complex shows homology to beta adaptin
  JOURNAL   Cell 64, 649-665 (1991)
COMMENT     HIV-1 nef has been found to bind beta-COP, a coat protein from
            non-clathrin-coated vesicles.  This interaction may be important
            in promoting the intracellular sequestration of CD4.
            beta COP shows significant sequence homology to beta adaptin
            (clathrin-coated protein).
            NCBI gi: 55818
BASE COUNT      893 a    643 c    691 g    846 t
ORIGIN
        1 cttcccgacc cccacccccа cggagccaga tttacctggc acctttcgtc cttttcatct
       61 tgttttgagt tggttataaa caggaaccAT Gaccgcagct gagaacgtgt gctatacgtt
                  beta COP cds start ->
      121 aattaacgtg ccaatggact cagaaccccc ttctgaaatc agcttaaaaa atgacctgga
      181 gaaaggcgat gtgaagtcaa agactgaagc tttgaagaaa gtgatcatta tgattctgaa
      241 tggggaaaag cttcctggac tcctgatgac gatcattcgt ttcgtgctgc ctcttcagga
      301 tcacaccatc aaaaagttgc ttctggtctt ctgggaaatt gttccgaaaa caactccaga
      361 tgggaggctc ttacatgaaa tgattcttgt gtgtgatgca tacagaaagg atctccagca
      421 tcctaatgag tttattcgtg gatctactct tcgtttcctt tgcaaattga aggaagcaga
      481 attgctggaa cctctgatgc ctgctatccg tgcttgtttg gaacatcgtc acagctatgt
      541 taggagaaac gctgttttgg ccatctacac catctacaga aattttgaaa atcttatacc
      601 tgatgctcct gagctgatac atgattttct ggtaaacgag aaggatgcaa gctgcaaaag
      661 aaatgcattt atgatgctca ttcatgcaga tcaggatcga gctttggatt atttaagtac
      721 atgtattgat caagttcaga catttggaga cattctacag ttggttattg ttgaactaat
      781 ttataaggtc tgtcatgcta atccatcaga gagggcccgt ttcattcgct gtatctataa
      841 cttactgcag tcatctagtc ctgctgtaaa atacgaagct gctgggacac tggtgacact
      901 gtcaagtgct ccaactgcaa taaaggctgc tgctcagtgt tacattgatt taattattaa
      961 ggaaagtgat aacaatgtaa agctcattgt cctggaccga ttggtagaac taaaagagca
     1021 tcctgctcac gagcgagtcc tccaagatct ggtcatggac atcctacgag tactgagtac
     1081 accagaccta gaagtgcgca agaaaacgct gcagttagca ctggatcttg tctcatctag
     1141 gaatgttgaa gagttggtta ttgtcttgaa gaaggaagta attaaaacaa ataacgtgtc
     1201 tgagcatgaa gacactgaca aataccgaca gcttctcgtg cgaacactgc attcctgctc
     1261 tgtccgattt ccagatatgg ctgcaaatgt tattcctgtg ctaatggaat ttctcagtga
     1321 cagtaatgaa gcagcagctg ctgatgtctt ggagtttgtg cgtgaagcca ttcagcgctt
     1381 tgacaacctg agaatgctga ttgttgagaa gatgctggaa gtcttccatg ctattaagtc
     1441 tgtcaagatt tatcgaggag cactgtggat cctgggcgag tactgcagta ctaaggaaga
     1501 cattcagagt gtgatgactg aagtccgcag gtcccttggg gagatcccaa tcgtagaatc
     1561 agaaataaag aaagaagctg gcgagttaaa accagaagaa gaaataactg ttgggcccgt
     1621 tcagaaattg gttacagaga tgggcaccta tgctactcag agtgcactca gcagctctag
     1681 acctaccaag aaagaagagg acagaccacc cttgagagga ttcctcctgg atggagattt
     1741 ctttgttgct gcctcccttg ccacaactct gaccaagatt gcattacgct atgtagcatt
     1801 ggttcaggag aagaaaaagc aaaactcttt tgttgctgag gctatgttgc ttatggcaac
     1861 catccttcat ttgggaaaat cctctcttcc taagaagcca atcactgatg atgatgtaga
     1921 ccgaatttcc ctgtgcctca aggtcttatc tgaatgctca cctttaatga atgacatttt
     1981 taataaggag tgcagacagt ctctttccca aatgttgtct gccaaactcg aagaagagaa
     2041 actatcccaa aagaaagaat ctgaaaagag gaatgtaaca gtacagcctg atgaccccat
     2101 ttccttcatg caactaactg ctaagaatga gatgaactgc aaggaggatc agttccagct
     2161 gagtttgttg gcagcgatgg gtaacactca gaggaaagag gcagcagacc ccctggcgtc
     2221 caaactcaac aaggtcactc agttgacagg tttctctgat ccagtgtatg cagaagctta
     2281 tgttcatgtc aatcagtatg atattgtcct ggatgttctt gttgtaaacc aaaccagtga
     2341 tactttgcag aactgcacat tagagttagc tactctaggg gatctgaaac tcgtggaaaa
     2401 accatctcct ttgactcttg ctcctcatga ctttgcgaat attaaagcca atgtcaaagt
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```
2461 agcatcaaca gaaaatggaa taattttcgg caatatagtt tatgatgtct ctggagcagc
2521 aagtgacaga aactgtgtgg tcctcagtga catccacatt gacatcatgg actatatcca
2581 gcctgcaact tgcactgatg ctgagttccg tcagatgtgg gccgaatttg aatgggaaaa
2641 taaagtgaca gttaacacca acgtgactga cctgaatgat tatttacagc acatcctcaa
2701 gtccaccaac atgaagtgcc tgactccaga gaaggccctt tctggctact gtggcttcat
2761 ggcagccaac ctatatgctc gctctatatt tggagaggat gcacttgcaa atgtcagcat
2821 tgagaagcca gttcaccagg gaccagatgc tgctgttact ggccatataa gaattcgtgc
2881 aaaaagtcag ggaatggcct tgagccttgg agataaaatc aacctgtctc aaaagaagac
2941 tagtctcTAA gaatgaacaa acggtcctcg aaagtgtaag gttaaaattt aggtgtgggc
            <- beta-COP cds end
3001 tgattggact ccgacgtttt tgtactcttt catgctttat gtttgtagaa tttgagttca
3061 tgctgaattc att
```

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LOCUS       SCSUG1       1671 bp    DNA              PLN       09-JUL-1992
DEFINITION  S.cerevisiae SUG1 sequence, complete cds.
ACCESSION   X66400
KEYWORDS    ATPase; sug1 gene.
SOURCE      S.cerevisiae DNA.
REFERENCE   1  (bases 1 to 1671)
  AUTHORS   Swaffield,J.C., Bromberg,J.F. and Johnston,S.A.
  TITLE     Alterations in a yeast protein resembling HIV Tat-binding protein
            relieve requirement for an acidic activation domain in GAL4
  JOURNAL   Nature 357, 698-700 (1992)
COMMENT     SUG1 is part of a large family of proteins related to the 26S
            protease from human erythrocytes.  Each of these proteins has
            Tat-binding activity [1].  The exact role of this family of
            proteins in cellular metabolism is not wholly clear; however,
            the 26S protease seems to regulate the degradation of some
            cyclins and in this manner has been implicated in modulating
            the stability of oncoproteins such as c-Mos, c-Myb, c-Myc,
            and p53 (Dubiel et al. Biol. Chem. Hoppe-Seyler 375: 237-240).
            NCBI gi: 4590
BASE COUNT      529 a    289 c    366 g    487 t
ORIGIN
        1 gaattcgctt tggaaatggc accgttgccc cacacgtaac aaaaagagcc ttttcttcaa
       61 taatacccat tgtttgaaag agctggcttc tgactcgttt gtttaacctc tttttgcgac
      121 tgaaaacttg ttttttctatt tccctttttc ttcggttggg ttttttaata tgaaatcata
      181 ttttgcatac ttctctaccc ttattcttgt tcggaaattt tcgtatttta aaactgtcaa
      241 aatgcgagcg aggtggcaaa agttgtaata tcagtaacag ttaggttagg ttttatgtaa
      301 acggaacaac agtatagtgg gatactatca cgacaATGac agctgctgta acatcctcca
                              yeast SUG1 cds start ->
      361 atatagtatt agaaacccac gaaagtggta tcaaaccata ttttgaacag aagatccaag
      421 aaacagaatt aaagatccgc tccaaaacag aaaatggtcg cagactggaa gctcaaagga
      481 atgcattgaa tgacaaagta cgttttatca aggacgaact gcgtctatta caggaacctg
      541 gatcttatgt gggtgaagtt ataaagatcg tgtctgacaa aaaagttctc gttaaagtgc
      601 aacctgaggg aaaatacatc gtggatgttg caaaagatat aaacgtgaag gacttaaagg
      661 catctcaaag agtttgtcta aggagtgact cttatatgtt gcataaagtt cttgagaata
      721 aggctgaccc actagtttcg ttgatgatgg tggaaaaagt tcctgattcc acatacgata
      781 tggttggtgg tttgacaaag caaataaagg agattaaaga agttattgaa ttgcccgtaa
      841 aacatcctga acttttgaa agtttgggta ttgcgcaacc aaagggtgtc atcttatatg
      901 gccccccctgg tacagggaaa accttattgg caagagctgt cgcacatcac actgattgta
      961 aattcatcag ggtcagtggt gcggaactgg tacaaaagta tatcggcgaa ggttcccgta
     1021 tggtccgtga gctgtttgtg atggctagag aacatgctcc ctcaattatc tttatggatg
     1081 aaatcgattc cattggctct actcgtgtag aaggttctgg tggtggtgat tcagaagttc
     1141 aaagaacaat gttagaacta ctaaaccaat tggacgggtt tgaaacttct aaaaatatca
     1201 agatcataat ggccacgaat agactagata ttctagatcc agcacttttg agacccggta
     1261 gaatagatag gaagattgaa tttccacctc caagtgtcgc agctagagct gaaatttttaa
     1321 gaatccattc cagaaaaatg aatctaactc gtggtatcaa cttgagaaag gttgctgaaa
     1381 agatgaacgg ttgttctggt gccgatgtca aaggtgtctg tacagaagct ggtatgtatg
     1441 ctttaagaga aagaagaata cacgttactc aagaagactt cgaactcgct gtgggtaagg
     1501 ttatgaacaa gaaccaagaa acggccattt ctgtcgccaa gctgttcaag TGAtgtattc
                                                              <- yeast SUG1
     1561 gtttcacttg gctcattgta tatgttactt agtgtatgtg tataatatca tagtttagca
     1621 ttaactaaga ggcaaaatta taccgctgga tatacaggat ataacggtac c
```

V

Communications

The enclosed diskettes comprise the electronic portion of Part V, providing HIV and SIV nucleic acid and protein sequences in ASCII characters. As a general rule, American and non-European users receive nucleic acid files in GenBank format with protein translations of coding sequences given in the features tables. European users receive nucleic acid files in EMBL format and protein files in Swiss-Prot format. Both PC-DOS and Apple Macintosh formatted diskettes are available; which format you receive depends upon what you have requested. If you wish to change the diskette format or the file formats, simply contact us at 505-665-1356 or fax a message to us at 505-665-3493. If you wish to contact us via the postal service, our address is: HIV Sequence Database, T-10, MS K710, LANL, Los Alamos, NM, 87545, U.S.A. The diskettes contain READ.ME files to provide you with the most recent information regarding their contents. No alignments are included on the diskettes in this release of the Compendium.

Sequences and alignments are also available electronically from a server here at Los Alamos called "atlas." In the following instructions for accessing atlas, what you actually type at your terminal is shown in **boldface** type [with an explanation shown in square brackets]. What the server responds with is shown indented in *italic* type.

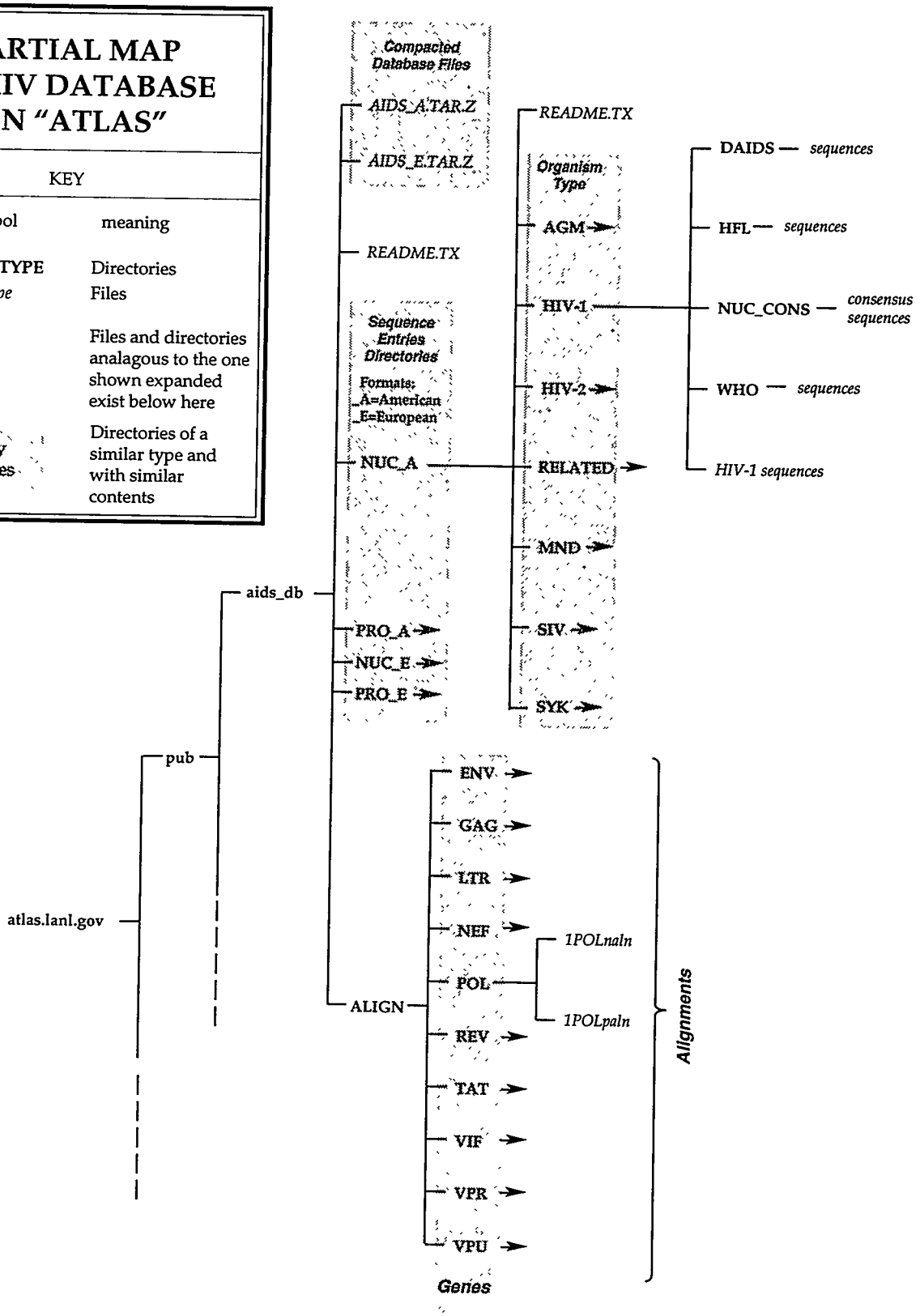
ftp atlas.lanl.gov [this ftp command connects your computer to atlas]
Name (atlas.lanl.gov): [atlas asks for your user name]
anonymous [for offsite users anonymous is the only name that works]
Guest login ok, send ident as password.
Password:
[enter your e-mail address or your name as ident]
Guest login ok. access restrictions apply.
cd pub [change to the directory called pub]
CWD command successful
cd aids-db
ls [this lists the files and directories inside of aids-db]
AIDS_A.TAR.Z, AIDS_E.TAR.Z, NUC_A, PRO_A, ALIGN, NUC_E, PRO_E, PROGS, README.TXT, ROADMAP
pwd [to show your location in the file hierarchy]
"/pub/aids-db" is current directory.
cd NUC_A/HIV_1 [move down 2 directories]
ls [all the GenBank format files are listed]
get hivr1s4 [this copies the file hivr1s4 to your home computer]
mget *.nf [this copies all files in the current directory with the suffix .nf to your home computer]
bye [this disconnects you from the server]

A map of the aids-db directories and files on atlas is reproduced on the following page. Many of the directories contain ReadMe files that describe the contents.

PARTIAL MAP OF HIV DATABASE ON "ATLAS"

KEY

symbol	meaning
BOLD TYPE	Directories
italic type	Files
→	Files and directories analagous to the one shown expanded exist below here
gray boxes	Directories of a similar type and with similar contents



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