

HIV Sequence Compendium 2010

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I

Preface

I-1 Introduction

This compendium is an annual printed summary of the data contained in the HIV sequence database. In these compendia we try to present a judicious selection of the data in such a way that it is of maximum utility to HIV researchers. Each of the alignments attempts to display the genetic variability within the different species, groups and subtypes of the virus.

This compendium contains sequences published before January 1, 2010. Hence, though it is called the 2010 Compendium, its contents correspond to the 2009 curated alignments on our website.

The number of sequences in the HIV database is still increasing exponentially. In total, at the time of printing, there were 339,306 sequences in the HIV Sequence Database, an increase of 45% since last year.

The number of near complete genomes (>7000 nucleotides) increased to 2576 by end of 2009, reflecting a smaller increase than in previous years. However, as in previous years, the compendium alignments contain only a small fraction of these. Included in the alignments are a small number of sequences representing each of the subtypes and the more prevalent circulating recombinant forms (CRFs) such as 01 and 02, as well as a few outgroup sequences (group O and N and SIV-CPZ). Of the rarer CRFs we included one representative each. A more complete version of all alignments is available on our website, <http://www.hiv.lanl.gov/content/sequence/NEWALIGN/align.html>

Reprints are available from our website in the form of both HTML and PDF files. As always, we are open to complaints and suggestions for improvement. Inquiries and comments regarding the compendium should be addressed to seq-info@lanl.gov.

I-2 Acknowledgements

The HIV Sequence Database and Analysis Project is funded by the Vaccine and Prevention Research Program of the AIDS Division of the National Institute of Allergy and Infectious Diseases (Dr. Geetha Bansal, Project Officer) through interagency agreement IAA Y1-AI-8309-1 “HIV/SIV Database and Analysis Unit” with the U.S. Department of Energy.

I-3 Citing the compendium or database

The LANL HIV Sequence Database may be cited in the same manner as this compendium:

HIV Sequence Compendium 2010. Carla Kuiken, Brian Foley, Thomas Leitner, Christian Apetrei, Beatrice Hahn, Ilene Mizrahi, James Mullins, Andrew Rambaut, Steven Wolinsky, and Bette Korber editors. 2010. Publisher: Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico. LA-UR 10-03684.

I-4 About the PDF

The complete *HIV Sequence Compendium 2010* is available in Adobe Portable Document Format (PDF) from our website, <http://www.hiv.lanl.gov/>. The PDF version is hypertext enabled and features ‘clickable’ table-of-contents, indexes, references and links to external web sites.

This volume is typeset using L^AT_EX.

I-5 About the cover

The cover (Figure I.1) of this compendium depicts the translation of sequence information into its biological context. Although the full sequence of HIV-1 has been known for over 20 years, atomic-level details of its biological context are still emerging. Recently, the structure of the gp41-interactive region of the HIV-1 gp120 envelope glycoprotein was solved (Pancera *et al.* 2010 PNAS 107, 1166–1171). The newly solved portions of gp120 involve the mature N- and C-termini, residues 31–82 and 493–511, respectively. These are depicted in red, with the previously determined gp120 core in black, shown binding to the CD4 receptor (yellow) and the antigen-binding fragment of a human antibody (blue). This structure has been fit into the electron-tomogram (gray) of the HIV-1 viral spike bound by CD4 and antibody (Liu *et al.* 2008 Nature 455, 109–113). Although the functional spike is a trimer of three gp120 and three gp41 envelope glycoproteins, only a single gp120 subunit has been shown for clarity. Shown as an overlay is the sequence of HIV-1 Env with the signal peptide starting at residue 1, the mature N-terminus of gp120 starting at residue 31, the N-terminus of gp41 starting at residue 512, and the newly determined structural regions highlighted in red.

Image provided by Jonathan Stuckey, Structural Biology Section, Vaccine Research Center, NIAID/NIH.

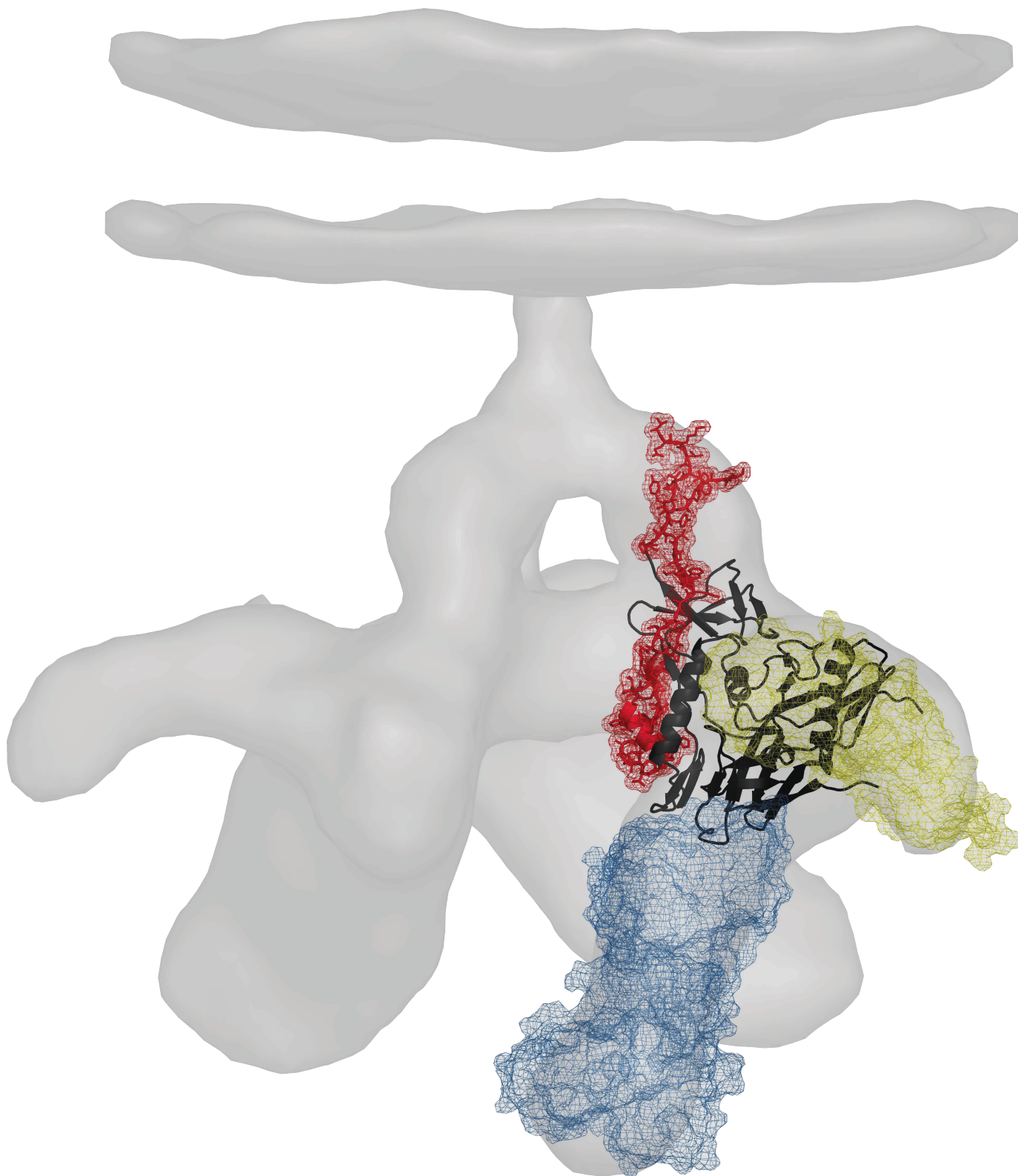
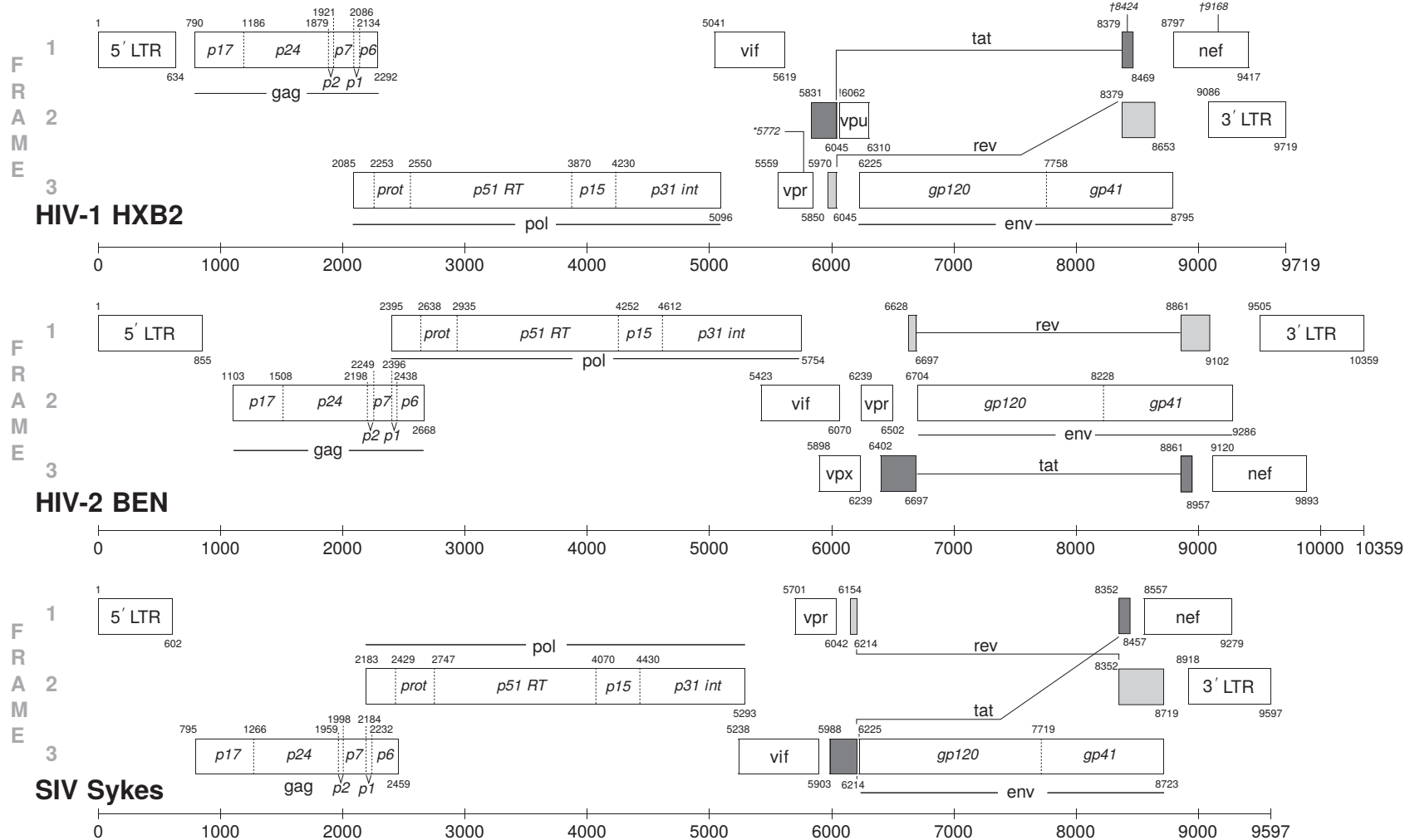


Figure I.1: Newly solved portions of gp120. These are depicted in red, with the previously determined gp120 core in black, shown binding to the CD4 receptor (yellow) and the antigen-binding fragment of a human antibody (blue). This structure has been fit into the electron-tomogram (gray) of the HIV-1 viral spike bound by CD4 and antibody.

I-6 Genome maps



Landmarks of the HIV-1, HIV-2, and SIV genomes. Open reading frames are shown as rectangles. The gene start, indicated by the small number in the upper left corner of each rectangle normally records the position of the **a** in the **atg** start codon for that gene, while the number in the lower right records the last position of the stop codon. For *pol*, the start is taken to be the first **t** in the sequence **tttttag**, which forms part of the stem loop that potentiates ribosomal slippage on the RNA and a resulting -1 frameshift and the translation of the Gag-Pol polypeptide. The *tat* and *rev* spliced exons are shown as shaded rectangles. In HXB2, *5772 marks the position of a frameshift in the *vpr* gene caused by an “extra” **t** relative to most other subtype B viruses; !6062 indicates a defective **acg** start codon in *vpu*; †8424 and †9168 mark premature stop codons in *tat* and *nef*. See Korber *et al.*, Numbering Positions in HIV Relative to HXB2CG, in *Human Retroviruses and AIDS*, 1998, p. 102. Available from <http://www.hiv.lanl.gov/content/sequence/HIV/REVIEWS/HXB2.html>

I-7 HIV/SIV proteins

Name	Size	Function	Localization
Gag			
MA	p17	membrane anchoring; env interaction; nuclear transport of viral core (myristylated protein)	virion
CA	p24	core capsid	virion
NC	p7	nucleocapsid, binds RNA	virion
	p6	binds Vpr	virion
Pol			
Protease (PR)	p15	Gag/Pol cleavage and maturation	virion
Reverse Transcriptase (RT)	p66, p51	reverse transcription, RNase H activity	virion
RNase H	p15		virion
Integrase (IN)	p31	DNA provirus integration	virion
Env	gp120/gp41	external viral glycoproteins bind to CD4 and secondary receptors	plasma membrane, virion envelope
Tat	p16/p14	viral transcriptional transactivator	primarily in nucleolus/nucleus
Rev	p19	RNA transport, stability and utilization factor (phosphoprotein)	primarily in nucleolus/nucleus shuttling between nucleolus and cytoplasm
Vif	p23	promotes virion maturation and infectivity	cytoplasm (cytosol, membranes), virion
Vpr	p10-15	promotes nuclear localization of preintegration complex, inhibits cell division, arrests infected cells at G2/M	virion nucleus (nuclear membrane?)
Vpu	p16	promotes extracellular release of viral particles; degrades CD4 in the ER; (phosphoprotein only in HIV-1 and SIVcpz)	integral membrane protein
Nef	p27-p25	CD4 and class I downregulation (myristylated protein)	plasma membrane, cytoplasm, (virion?)
Vpx	p12-16	Vpr homolog present in HIV-2 and some SIVs, absent in HIV-1	virion (nucleus?)
Tev	p28	tripartite tat-env-rev protein (also named Tnv)	primarily in nucleolus/nucleus

I-8 Landmarks of the genome

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 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 RNA forms a hairpin stem-loop structure with a side bulge; the bulge is necessary for Tat binding and function.

RRE Rev responsive element, 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-1, spanning the border of gp120 and gp41). The 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 site for Rev protein, while RXRE is the binding site for Rex protein. RRE (and RXRE) form complex secondary structures, necessary for specific protein binding.

PE Psi elements, a set of 4 stem-loop structures preceding and overlapping the Gag start codon which are the sites recognized by the cysteine histidine box, a conserved motif with the canonical sequence CysX2CysX4HisX4Cys, present in the Gag p7 MC protein. The Psi Elements are present in unspliced genomic transcripts but absent from spliced viral mRNAs.

SLIP An TTTTTT slippery site, followed by a stem-loop structure, is responsible for regulating the -1 ribosomal frameshift out of the Gag reading frame into the Pol reading frame.

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 Inhibitory/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-1. The INS elements have been defined by functional assays as elements that inhibit expression posttranscriptionally. Mutation of the RNA elements was shown to lead to INS inactivation and up regulation of gene expression.

Genes and gene products

GAG The genomic region encoding the capsid proteins (group specific antigens). The precursor is the p55 myristylated pro-

tein, which is processed to p17 (MAtrix), p24 (CApsid), p7 (NucleoCapsid), and p6 proteins, by the viral protease. Gag associates with the plasma membrane where the virus assembly takes place. The 55 kDa Gag precursor is called assemblin to indicate its role in viral assembly.

POL The genomic region encoding the viral enzymes protease, reverse transcriptase, RNase, and integrase. These enzymes are produced as a Gag-Pol precursor polypeptide, which is processed by the viral protease; the Gag-Pol precursor is produced by ribosome frameshifting near the 3' end of gag.

ENV Viral glycoproteins produced as a precursor (gp160) which is processed to give a noncovalent complex of the external glycoprotein gp120 and the transmembrane glycoprotein gp41. The mature gp120-gp41 proteins are bound by non-covalent interactions and are associated as a trimer on the cell surface. A substantial amount of gp120 can be found released in the medium. gp120 contains the binding site for the CD4 receptor, and the seven transmembrane domain chemokine receptors that serve as co-receptors for HIV-1.

TAT Transactivator of HIV gene expression. One of two essential viral regulatory factors (Tat and Rev) for HIV gene expression. Two forms are known, Tat-1 exon (minor form) of 72 amino acids and Tat-2 exon (major form) of 86 amino acids. 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 elongation from the LTR promoter, preventing the 5'LTR AATAAA polyadenylation signal from causing premature termination of transcription and polyadenylation. It is the first eukaryotic transcription factor known to interact with RNA rather than DNA and may have similarities with prokaryotic anti-termination factors. Extracellular Tat can be found and can be taken up by cells in culture.

REV The second necessary regulatory factor for HIV expression. A 19 kDa phosphoprotein, localized primarily in the nucleolus/nucleus, Rev acts by binding to RRE and promoting the nuclear export, stabilization and utilization of the unspliced viral mRNAs containing RRE. Rev is considered the most functionally conserved regulatory protein of lentiviruses. Rev cycles rapidly between the nucleus and the cytoplasm.

VIF Viral infectivity factor, a basic protein of typically 23 kDa. Promotes the infectivity but not the production of viral particles. In the absence of Vif the produced viral particles are defective, while the cell-to-cell transmission of virus is not affected significantly. Found in almost all lentiviruses, Vif is a cytoplasmic protein, existing in both a soluble cytosolic form and a membrane-associated form. The latter form of Vif is a peripheral membrane protein that is tightly associated with the cytoplasmic side of cellular membranes. In 2003, it was discovered that Vif prevents the action of the cellular APOBEC-3G protein which deaminates DNA:RNA heteroduplexes in the cytoplasm.

VPR Vpr (viral protein R) is a 96-amino acid (14 kDa) protein, which is incorporated into the virion. It interacts with the p6 Gag part of the Pr55 Gag precursor. Vpr detected in the cell is localized to the nucleus. Proposed functions for Vpr include the targeting the nuclear import of preintegration complexes, cell growth arrest, transactivation of cellular genes, and induction of cellular differentiation. In HIV-2, SIV-SMM, SIV-RCM, SIV-MND-2 and SIV-DRL the Vpx gene is apparently the result of a Vpr gene duplication event, possibly by recombination.

VPU Vpu (viral protein U) is unique to HIV-1, SIVcpz (the closest SIV relative of HIV-1), SIV-GSN, SIV-MUS, SIV-MON and SIV-DEN. There is no similar gene in HIV-2, SIV-SMM or other SIVs. Vpu is a 16 kDa (81-amino acid) type I integral membrane protein with at least two different biological functions: (a) degradation of CD4 in the endoplasmic reticulum, and (b) enhancement of virion release from the plasma membrane of HIV-1-infected cells. Env and Vpu are expressed from a bicistronic mRNA. Vpu probably possesses an N-terminal hydrophobic membrane anchor and a hydrophilic moiety. It is phosphorylated by casein kinase II at positions Ser52 and Ser56. Vpu is involved in Env maturation and is not found in the virion. Vpu has been found to increase susceptibility of HIV-1 infected cells to Fas killing.

NEF A multifunctional 27-kDa myristylated protein produced by an ORF located at the 3' end of the primate lentiviruses. Other forms of Nef are known, including nonmyristylated variants. Nef is predominantly cytoplasmic and associated with the plasma membrane via the myristyl residue linked to the conserved second amino acid (Gly). Nef has also been identified in the nucleus and found associated with the cytoskeleton in some experiments. One of the first HIV proteins to be produced in infected cells, it is the most immunogenic of the accessory proteins. The nef genes of HIV and SIV are dispensable *in vitro*, but are essential for efficient viral spread and disease progression *in vivo*. Nef is necessary for the maintenance of high virus loads and for the development of AIDS in macaques, and viruses with defective Nef have been detected in some HIV-1 infected long term survivors. Nef downregulates CD4, the primary viral receptor, and MHC class I molecules, and these functions map to different parts of the protein. Nef interacts with components of host cell signal transduction and clathrin-dependent protein sorting pathways. It increases viral infectivity. Nef contains PxxP motifs that bind to SH3 domains of a subset of Src kinases and are required for the enhanced growth of HIV but not for the downregulation of CD4.

VPX A virion protein of 12 kDa found in HIV-2, SIV-SMM, SIV-RCM, SIV-MND-2 and SIV-DRL and not in HIV-1 or other SIVs. This accessory gene is a homolog of HIV-1 vpr, and viruses with Vpx carry both vpr and vpx. Vpx function in relation to Vpr is not fully elucidated; both are incorporated into virions at levels comparable to Gag proteins through interactions with Gag p6. Vpx is necessary for efficient replication of SIV-SMM in PBMCs. Progression to AIDS and death

in SIV-infected animals can occur in the absence of Vpr or Vpx. Double mutant virus lacking both vpr and vpx was attenuated, whereas the single mutants were not, suggesting a redundancy in the function of Vpr and Vpx related to virus pathogenicity.

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. They modulate transcriptional and posttranscriptional steps of virus gene expression and are 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. 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. Their functional importance continues to be elucidated.

Complex retroviruses Retroviruses regulating their expression via viral factors and expressing additional proteins (regulatory and accessory) essential for their life cycle.

I-9 Amino acid codes

A	Alanine
B	Aspartic Acid or Asparagine
C	Cysteine
D	Aspartic Acid
E	Glutamic Acid
F	Phenylalanine
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
X	unknown or “other” amino acid
Y	Tyrosine
Z	Glutamic Acid or Glutamine
.	gap
-	identity
*	stop codon
#	incomplete codon

I-10 Nucleic acid codes

A	Adenine
C	Cytosine
G	Guanine
T	Thymine
U	Uracil
M	A or C
R	A or G
W	A or T
S	C or G
Y	C or T
K	G or T
V	A or C or G
H	A or C or T
D	A or G or T
B	C or G or T
N	unknown
.	gap
-	identity

II

HIV-1/SIVcpz Complete Genomes

Contents

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II-1 Introduction

While the “web-alignment” this year has grown to 1500 full-length genomes, the compendium alignment herein has strict page limitations. The selection here was made such that subtypes A-G, CRF’s 01 and 02, and CPZ were represented with one sequence from each country where the subtype has been sequenced. More recent sample were generally selected. For the rare subtypes H–K and groups N–P all sequences were included, and for CRF’s 03 and up, one representative was included. Unique recombinant forms and unclassified sequences were not included this year. This resulted in 192 sequences of HIV-1/CPZ from all over the world to display the genetic variation of this taxonomic cluster.

The HXB2 sequence was chosen as master sequence in this alignment. This is also the HIV Database genome coordinate standard sequence. The alignment was generated by an iterative process between automated alignments using HMMER and manual editing using MASE, BioEdit and Se-Al. As in previous years, the alignment presented is not suggested to be an “optimal alignment” with the absolute minimum number of gaps and mismatches. It is a compromise between optimal alignment, readability, and an attempt to keep insertions and deletions from altering the protein reading frame presentation. Most gaps have been introduced in multiples of 3 bases to maintain open reading frames when translated directly from the alignment.

Also part of this nucleotide alignment is a translation to protein sequence based on the HXB2 sequence; the HIV genome has many overlapping coding regions, and all are shown. For more complete annotation of functional domains, see the protein sequence alignments in Chapter V.

II-2 Annotated features

Features of HIV-1 annotated in the alignment that follows.

Feature	Location	Page
5' LTR U3 start	1	18
TCF-1 alpha	315-329	20
NF- κ -B-II	350-359	22
NF- κ -B-I	364-373	22
Sp1-III	375-386	22
Sp1-II	388-397	22
Sp1-I	398-408	22
TATA Box	427-431	24
TAR element start	453	24
5' LTR U3 end	455	24
+1 mRNA start site	456	24
5' LTR R repeat begin	456	24
TAR element end	513	24
Poly-A signal	527-532	24
5' LTR R repeat end	551	24
5' LTR U5 start	552	26
Extensive secondary structure	568-605	26
5' LTR U5 end	633	26
Lys tRNA primer binding site	634-653	26
Packaging loops begin	681	28
Packaging loops end	789	30
Gag and Gag-Pol start	790	30
Gag p17 Matrix end	1185	36
Gag p24 Capsid start	1186	36
Gag p24 Capsid end	1881	44
Gag p2 start	1882	44
Gag p2 end	1920	44
Gag-Pol fusion TF protein start	1921	44
Gag p7 nucleocapsid start	1921	44
Gag p7 nucleocapsid end	2085	46
Gag-Pol -1 ribosomal slip site	2085	46
Gag p1 start	2086	46
Gag p1 end	2133	48
Gag p6 start	2134	48
Gag-Pol TF end	2252	50
Pol protease start	2253	50
Gag p6 end	2292	50
Gag end	2292	50
Pol Protease end	2549	54
Pol p66 and p51 RT start	2550	54
p51 end and p66 RT continue	3869	70
Pol p15 RNase H start	3870	70
Pol p66 RT, Pol p15 RNase H end	4229	74
Pol p31 Integrase start	4230	74
Vif start	5041	84
Pol p31 integrase end	5096	84
Vpr start	5559	90
Vif end	5619	90

Feature	Location	Page
frameshift insert in HXB2	5772	92
Vpr premature end (HXB2 only)	5795	92
Tat exon 1 start	5831	94
Vpr end	5850	94
Rev exon 1 start	5970	94
Tat Rev exon 1 end	6045	96
intron start	6046	96
Vpu start (ACG in HXB2)	6062	96
Env start	6225	98
Vpu end	6310	100
Env signal peptide end	6314	100
Env gp120 start	6315	100
V1 loop start	6615	104
V1 loop end	6691	106
V2 loop start	6696	106
V2 loop end	6811	108
V3 loop start	7110	112
V3 loop end	7217	112
V4 loop start	7377	116
V4 loop end	7477	116
V5 loop start	7602	118
V5 loop end	7636	120
Rev Responsive Element (RRE) region	7710	120
Env gp120 end	7757	120
Env gp41 start	7758	120
RRE end	8061	124
Tat Rev intron end	8378	128
Tat Rev exon 2 start	8379	128
Tat premature stop in HXB2	8424	130
Tat end	8469	130
Rev end (TAA) in some lineages	8605	132
Rev end	8653	132
Env gp41, gp160 end	8795	134
Nef start	8797	134
3' LTR U3 start	9086	138
Nef premature end in HXB2	9168	140
TCF-1 alpha binding	9400-9414	142
Nef end	9417	142
NF- κ -B-II	9435-9444	144
NF- κ -B-I	9449-9458	144
Sp1-III	9462-9471	144
Sp1-II	9473-9482	144
Sp1-I	9483-9493	146
TATA box	9512-9516	146
TAR element start	9538	146
3' LTR U3 end	9540	146
3' LTR repeat start	9541	146
TAR element end	9599	146
Poly-A signal	9612-9617	146
3' LTR R repeat end	9636	146
3' LTR U5 start	9637	146
Extensive secondary structure in this region?	9646	148
3' LTR U5 end	9719	148

II-3 Sequences

Sequences included in the HIV-1/SIVcpz complete genome alignment.

Name	Accession	Country	Author	Reference
B.FR.83.HXB2	K03455	France	van Beveren, C.P.	(in) Weiss,RL, Teich,N, Varmus,H and Coffin,J(Eds); RNA TUMOR VIRUSES, SECOND EDITION, 2, Vol 2: 1102-1123; Cold Spring Harbor Laboratory, Cold Spring Harbor (1985)
A.CD.02.02CD_KTB035	AM000055	D.R.C.	Vidal, N.	ARHR 22(2):182-187 (2006)
A.SN.01.DDJ369	AY521631	Senegal	Meloni, S.T.	J Virol 78(22):12438-12445 (2004)
A1.AU.03.PS1044_Day0	DQ676872	Australia	Li, B.	J Virol 81(1):193-201 (2007)
A1.CY.06.CY171	FJ388950	Cyprus	Kousiappa, I.	ARHR 25(8); 727-40 (2009)
A1.GE.99.99GEMZ011	DQ207944	Georgia	Zarandia, M.	ARHR 22(5):470-476 (2006)
A1.IT.02.60000	EU861977	Italy	Riva, C.	ARHR 24(10); 1319-25 (2008)
A1.KE.02.ML1990	EU110092	Kenya	Land, A.M.	ARHR 24(6):865-872 (2008)
A1.RU.08.PokA1Ru	FJ864679	Russia	Bychenko, A.B.	Unpublished
A1.RW.93.93RW037A	AB287379	Rwanda	Sakamoto, Y.	Unpublished
A1.SE.95.SE8538	AF069669	Sweden	Carr, J.K.	AIDS 13(14):1819-1826 (1999)
A1.TZ.01.A341	AY253314	Tanzania	Arroyo, M.A.	ARHR 20(8):895-901 (2004)
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01_AE.JP.x.DR0492	AB253423	Japan	Sakamoto, Y.	Unpublished
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P.FR.09.RBF168	GU111555	France	Plantier, J.-C.	<i>Nat Med</i> 15 (8); 871-2 (2009)
CPZ.CD.90.ANT	U42720	D.R.C.	Vanden Haesevelde, M.M.	<i>Virology</i> 221 (2):346-350 (1996)
CPZ.CM.05.SIVcpzMT145	DQ373066	Cameroon	Keele, B.F.	<i>Science</i> 313 (5786):523-526 (2006)
CPZ.GA.88.GAB1	X52154	Gabon	Huet, T.	<i>Nature</i> 345 (6273):356-359 (1990)
CPZ.TZ.00.TAN1	AF447763	Tanzania	Santiago, M.L.	<i>J Virol</i> 77 (3):2233-2242 (2003)
CPZ.US.85.US_Marilyn	AF103818	United States	Gao, F.	<i>Nature</i> 397 (6718):436-441 (1999)

[illegible]

B.FR.83.HXB2	5' LTR U3 start	TGGAAGGGCTAATTCAC.TCCCAACGAAGA.CAAGATATCCTTGATCTGTGGATCTACCACACAAAGGCTACTTCCTGATTAGCAGAACTAC..ACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAA	166
H.BE.93.VI991			0
H.BE.93.VI997			0
H.CF.90.056			0
H.GB.00.00GBAC4001			0
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J.SE.93.SE9289.7897			0
J.SE.94.SE9173.7022			0
K.CD.97.97ZR.E0TB11			0
K.CM.96.96CM.MP535			0
01 AE.CF.90.90CF11697			0
01 AE.CN.07.07J5WX045			103
01 AE.HK.04.HK001			0
01 AE.JP.x.DR0492			0
01 AE.TH.04.BKM			166
01 AE.US.00.00US.MSC1164			111
01 AE.VN.98.98VND15			0
02 AG.CM.02.02CM.0013BBY			0
02 AG.CY.05.CY048			0
02 AG.ES.06.PI261			0
02 AG.FR.91.DJ263			0
02 AG.GH.03.03GH121AG			166
02 AG.LR.x.P044951			166
02 AG.NG.01.PL0710			0
02 AG.SE.94.SE7812			0
02 AG.SN.98.98SE.MP1211			0
02 AG.US.00.00US.MSC3083			0
02 AG.UZ.02.02UZ0683			0
03 AB.RU.97.KAL153_2			0
04 cpx.CY.94.94CY032_3			0
05 DF.BE.x.VI1310			0
06 cpx.AU.96.BFP90			166
07 BC.CN.98.98CN009			0
08 BC.CN.97.97CNGX.6F			0
09 cpx.GH.96.96GH2911			0
10 CD.TZ.96.96TZ.BF061			0
11 cpx.CM.95.95CM.1816			0
12 BF.AR.99.ARMA159			166
13 cpx.CM.96.96CM.1849			0
14 BG.ES.00.X605			0
15 01B.TH.99.99TH.MU2079			0
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17 BF.AR.99.ARMA038			0
18 cpx.CU.99.CU76			0
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20 BG.CU.99.CU103			0
21 A2D.KE.99.KER2003			0
22 01A1.CM.01.01CM.0001BBY			0
23 BG.CU.03.CB118			0
24 BG.CU.03.CB378			0
25 cpx.CM.02.1918LE			0
26 AU.CD.02.02CD.MBT0047			166
27 cpx.FR.04.04CD.FR.KZ5			166
28 BF.BR.99.BREPM12609			0
29 BF.BR.01.BREPM16704			0
31 BC.BR.04.04BR142			0
32 06A1.EE.01.EE0369			0
33 01B.MY.05.05MYKL007_1			0
34 01B.TH.99.01B2478P			0
35 AD.AF.05.05AF095			0
36 cpx.CM.00.00CMNYU830			0
37 cpx.CM.00.00CMNYU926			0
38 BF1.UY.03.UY03.3389			0
39 BF.BR.04.04BRRJ179			0
40 BF.BR.05.05BRRJ055			0
42 BF.LU.03.03BF.05.03			0
43 02G.SA.03.03J11223			0
N.CM.95.YBF30			0
N.CM.97.YBF106			0
N.CM.02.DJ00131			0
N.CM.04.04CM.1015_04			0
0 BE.87.ANT70			166
0 CM.x.BCF06			166
0 CM.91.MVP5180			166
0 CM.96.96CMA102			0
0 CM.97.97CMA6447			0
0 CM.98.98CMA104			0
0 CM.99.99CMU4122			0
0 FR.92.VAU			0
DO.FR.08.RBF208			0
0 SN.99.99SE.MP1299			166
0 US.x.I.2478B			166
0 US.97.97US08692A			0
0 US.99.99USTWLA			0
P.FR.09.RBF168			167
CPZ.CD.90.ANT			0
CPZ.CM.05.SIVcpzMT145			0
CPZ.GA.08.GAB			166
CPZ.TZ.00.TAN1			0
CPZ.US.85.US.Marilyn			166

	TCF-1 alpha										
B.FR.83.HXB2	GT	T	A	G	A	A	G	A	C	C	326
A.CD.02.02CD.KTB035	A	G	---	G	-	G	-	T	---	CTG	0
A.SN.01.DD3369	A	G	---	G	-	G	-	T	---	CTG	0
A1.AU.03.PS1044.Day0	A	G	---	G	-	G	-	T	---	CTG	0
A1.CY.06.01.CY171	A	G	---	G	-	G	-	T	---	CTG	0
A1.GE.09.99GEM2011	A	G	---	G	-	G	-	T	---	CTG	0
A1.IT.02.60800	A	G	---	G	-	G	-	T	---	CTG	0
A1.KE.02.ML1990	A	G	---	G	-	G	-	T	---	CTG	0
A1.RU.08.PokA1Ru	A	G	---	G	-	G	-	T	---	CTG	0
A1.RW.93.93RW037A	A	G	---	G	-	G	-	T	---	CTG	0
A1.SE.05.SE8538	A	G	---	G	-	G	-	T	---	CTG	0
A1.---.01.A341	A	G	---	G	-	G	-	T	---	CTG	0
A1.UA.01.01UADN139	A	G	---	G	-	G	-	T	---	CTG	0
A1.UG.99.99UGA07072	A	G	---	G	-	G	-	T	---	CTG	0
A1.ZA.04.04ZASK162B1	A	G	---	G	-	G	-	T	---	CTG	0
A2.CV.07.07CDKTB48	A	G	---	G	-	G	-	T	---	CTG	0
A2.CY.94.94CY017.41	A	G	---	G	-	G	-	T	---	CTG	0
B.AR.04.04AR143170	B	.	0	4	.	0	4	.	0	4	0
B.AU.04.PS1038.Day174	B	.	0	4	.	0	4	.	0	4	0
B.BO.99.BOL0122	B	.	0	9	.	0	9	.	0	1	0
B.BR.05.BREPM1081	B	.	0	5	.	0	5	.	0	8	0
B.CA.97.CANB3FULL	B	.	0	9	.	7	.	0	9	7	0
B.CN.05.05CNHB.hp3	B	.	0	5	.	0	5	.	0	5	0
B.CO.01.PCM001	B	.	0	1	.	0	1	.	0	1	0
B.CU.99.Cu19	B	.	0	9	.	0	9	.	0	9	0
B.CY.06.CY165	B	.	0	6	.	0	6	.	0	6	0
B.DE.86.D31	B	.	0	6	.	0	6	.	0	6	0
B.DK.04.PMYL.012	B	.	0	4	.	0	4	.	0	4	0
B.DO.05.05DO.160884	B	.	0	5	.	0	5	.	0	5	0
B.EC.89.EC003	B	.	0	9	.	0	9	.	0	9	0
B.ES.07.X2231	B	.	0	7	.	0	7	.	0	7	0
B.FR.92.92FR.BX08	B	.	0	9	.	0	9	.	0	9	0
B.GA.88.OY1	B	.	0	8	.	0	8	.	0	8	0
B.GB.86.G88.46R	B	.	0	6	.	0	6	.	0	6	0
B.GE.03.03GEMZ004	B	.	0	3	.	0	3	.	0	3	0
B.HT.05.05HT.129389	B	.	0	5	.	0	5	.	0	5	0
B.IN.x.11807	B	.	0	.	1	1	.	0	.	8	0
B.JM.05.05JM.KJ108	B	.	0	5	.	0	5	.	0	5	0
B.JP.05.DR6538	B	.	0	5	.	0	5	.	0	5	0
B.KR.04.04KR05	B	.	0	4	.	0	4	.	0	4	0
B.MM.99.MSTD101	B	.	0	9	.	0	9	.	0	9	0
B.NL.00.671.00T36	B	.	0	0	.	0	0	.	0	3	0
B.RU.04.04RU128005	B	.	0	4	.	0	4	.	0	4	0
B.TH.00.00TH.C3198	B	.	0	0	.	0	0	.	0	3	0
B.TT.01.01TV.CRC50069	B	.	0	1	.	0	1	.	0	6	0
B.TW.04.TWCYS	B	.	0	4	.	0	4	.	0	4	0
B.UA.01.01UAKV167	B	.	0	1	.	0	1	.	0	7	0
B.US.07.CR0027M	B	.	0	7	.	0	7	.	0	7	0
B.UY.01.01UYTRA1179	B	.	0	1	.	0	1	.	0	7	0
B.YE.02.02YES07	B	.	0	2	.	0	2	.	0	7	0
B.ZA.03.03ZAP5045MB2	B	.	0	3	.	0	3	.	0	5	0
C.AR.01.ARC4006	C	.	0	1	.	0	1	.	0	6	0
C.BR.04.04BR01	C	.	0	4	.	0	4	.	0	1	0
C.BW.00.00BW07621	C	.	0	0	.	0	0	.	0	7	0
C.CN.98.YNRL9840	C	.	0	9	.	0	9	.	0	8	0
C.CY.05.CY040	C	.	0	5	.	0	5	.	0	4	0
C.ES.07.X2118.2	C	.	0	7	.	0	7	.	0	2	0
C.ET.02.02ET.288	C	.	0	2	.	0	2	.	0	8	0
C.GE.03.03GEMZ033	C	.	0	3	.	0	3	.	0	3	0
C.IL.98.98I5002	C	.	0	9	.	0	9	.	0	2	0
C.IN.03.D24	C	.	0	3	.	0	3	.	0	4	0
C.KE.00.KER2010	C	.	0	0	.	0	0	.	0	1	0
C.MM.99.mIDU101.3	C	.	0	9	.	0	9	.	0	1	0
C.MM.93.93MM.965	C	.	0	3	.	0	3	.	0	5	0
C.SN.90.90SE.364	C	.	0	9	.	0	9	.	0	4	0
C.SO.89.89SM.145	C	.	0	8	.	0	8	.	0	5	0
C.TZ.02.C0178	C	.	0	2	.	0	2	.	0	7	0
C.US.98.98US.MSC3018	C	.	0	9	.	0	9	.	0	8	0
C.UY.01.TB4301	C	.	0	1	.	0	1	.	0	3	0
C.YE.02.02YES11	C	.	0	2	.	0	2	.	0	1	0
C.ZA.05.05ZAPSK240B1	C	.	0	5	.	0	5	.	0	2	0
C.ZM.02.02ZM108	C	.	0	2	.	0	2	.	0	8	0
D.CD.83.ELI	D	.	0	3	.	0	3	.	0	1	0
D.CM.01.01CM.0009BBY	D	.	0	1	.	0	1	.	0	9	0
D.CY.06.CY163	D	.	0	6	.	0	6	.	0	3	0
D.KE.97.ML15.2	D	.	0	9	.	0	9	.	0	2	0
D.KR.04.04KBH8	D	.	0	4	.	0	4	.	0	8	0
D.SN.x.SE365	D	.	0	.	x	.	0	.	0	5	0
D.TD.99.MN011	D	.	0	9	.	0	9	.	0	1	0
D.TZ.01.A280	D	.	0	1	.	0	1	.	0	8	0
D.UG.99.99UGK09958	D	.	0	9	.	0	9	.	0	9	0
D.YE.02.02YES16	D	.	0	2	.	0	2	.	0	1	0
D.ZA.90.R1	D	.	0	.	0	.	0	.	0	1	0
F1.A0.06.A0.06.ANG125	F	1	.	0	.	0	6	.	0	6	0
F1.AR.02.ARE933	F	1	.	0	.	0	2	.	0	3	0
F1.BE.93.VI850	F	1	.	0	.	0	3	.	0	5	0
F1.BR.07.07BR844	F	1	.	0	.	0	7	.	0	8	0
F1.ES.x.P1146	F	1	.	.	x	.	.	.	0	1	0
F1.FI.93.FIN0363	F	1	.	0	.	0	3	.	0	3	0
F1.FR.96.96FR.MP411	F	1	.	0	.	0	9	.	0	6	0
F1.JP.04.DR6082	F	1	.	0	.	0	4	.	0	8	0
F1.R0.96.BCI.R07	F	1	.	0	.	0	6	.	0	7	0
F1.RU.08.D88.845	F	1	.	0	.	0	8	.	0	8	0
F2.CM.97.CH53657	F	2	.	0	.	0	7	.	0	5	0
G.BE.96.DRCBL	G	.	0	6	.	0	9	.	0	6	0
G.CM.04.178.15	G	.	0	4	.	0	1	.	0	7	0
G.CU.99.Cu74	G	.	0	9	.	0	9	.	0	4	0
G.ES.05.P962	G	.	0	5	.	0	5	.	0	2	0
G.GH.03.03GH175G	G	.	0	3	.	0	3	.	0	7	0
G.KE.93.HH8793.12.1	G	.	0	9	.	0	3	.	0	1	0
G.NG.01.01NG.PL0669	G	.	0	1	.	0	1	.	0	6	0
G.PT.7695	G	.	0	.	0	.	7	.	0	6	0
G.SE.93.SE6165	G	.	0	3	.	0	3	.	0	6	0

		TCF-1 alpha	
B.FR.83.HXB2	GTTAGAAGAAGCC...AACAAAGGAGAGAACACCAGCTGTGTACACCTGTGAGCCTGCATGGA...ATGGATGACCCGGAGAGAGAAGTGTAGAGTGGAGGTTTGACAGCCGCTAGCATTTTCACATGCCCCGAGAGCTGCATCCGGAGTACTTCAAGAAC...	326	
H.BE.93.VI991		0	
H.BE.93.VI997		0	
H.CF.90.056		0	
H.GB.00.00GBAC4001		0	
J.CD.97.J.97DC.KTB147		0	
J.SE.93.SE9289.7897		0	
J.SE.94.SE9173.7022		0	
K.CD.97.97ZR.EQTB11		0	
K.CM.96.96CM.MP535		0	
01 AE.CF.90.90CF11697	AG---G---A-----AT-A-G-A-T-T-C-----CA-----AA-----G-A-----TGAA-A-----C-GAT---A-----TTC-----CGAAGA---A-----G-A-----A---AG-----	263	
01 AE.CN.07.07J5WX045		0	
01 AE.HK.04.HK001		0	
01 AE.JP.x.DR0492	AG---G---GAA-----A---G-T-C-----CA-A-A-----A-G---GAA-T-----C-GAT---A-----TC-----CGAAGA---A-----AAA-C-A-T-AT-AG-----	326	
01 AE.TH.04.BKM	AG---G---G-A-----A---G---C-----CA-A-A-----A-G---GAA-A-----C-GAT---A-----TGC-----CGAAGA---A-----AA-C-A-T-AT-A-----	271	
01 AE.US.00.00US.MSC1164		0	
01 AE.VN.98.98VND15		0	
02 AG.CM.02.02CM.0013BBY		0	
02 AG.CY.05.CY048		0	
02 AG.ES.06.P1261		0	
02 AG.FR.91.DJ263		0	
02 AG.GH.03.03GH121AG	AG---G---CTG-----G---T-A-----CA-C-T-AA-----A-G---GAA-C-----C-G-T-C---A-----TTA-G---AGA-C-A-TA-AAA-C---T-A-AG-----	326	
02 AG.LR.x.A-44951	G-----T-----A-----CA-CT-T-A-----A-G---GAA-C-C-C-----C-G-T-C---A-----TA-G---C-CA-A-AA-TA-AAA-C---T-A-AG-----	326	
02 AG.NG.01.PL0710		0	
02 AG.SE.94.SE7812		0	
02 AG.SN.98.98SE.MP1211		0	
02 AG.US.00.00US.MSC3083		0	
02 AG.UZ.02.02UZ0683		0	
03 AB.RU.97.KAL153_2		0	
04 cpx.CY.94.94CY032_3		0	
05 DF.BE.x.VI1310		0	
06 cpx.AU.96.BFP90	-G-----CTT...CT-----A-T-C-----CA-AT-A-----GCA-G-TGAA-A-----A-A-----TC-----AGGAGA---A-----AAA-----TT-A-AG-----	326	
07 BC.CN.98.98CN009		0	
08 BC.CN.97.97CNXG_6F		0	
09 cpx.GH.96.96GH1211		0	
10 CD.TZ.96.96TZ.BF061		0	
11 cpx.CM.95.95CM.1816		0	
12 BF.AR.99.ARMA159	-G---A-G-----TG-----A-T---C-----CA-----AA-----A-TGAA-C-----AC-GATA---A-----G-GC-AAGA---T-A-A-AAA---A---GG-AT-AG-----	326	
13 cpx.CM.96.96CM.1849		0	
14 BG.ES.00.X605		0	
15 01B.TH.99.99TH.MU2079		0	
16 A2D.KR.97.97KR004		0	
17 BF.AR.99.ARMA038		0	
18 cpx.CU.99.CU76		0	
19 cpx.CU.99.CU7		0	
20 BG.CU.99.CU103		0	
21 A2D.KE.99.KER2003		0	
22 01A1.CM.01.01CM.0001BBY		0	
23 BG.CU.03.CB118		0	
24 BG.CU.03.CB378		0	
25 cpx.CM.02.1918LE		0	
26 AU.CD.02.02CD.MBT047	-G-----T---T-G---A---A---C-AC-G-TG-A-----A-----G-TAGT--AG-----C-CAT---A-----T-AA-----CGGA-G---CA---C-----A---AG-----	326	
27 cpx.FR.04.04CD.FR.KZ5	-G---G---TG-----A---A---C-C---T-A-----G---GAA-A-----AT---A-----T-----C-AAGA-TG-A-----AAA-----T-A-AG-----	326	
28 BF.BR.99.BREPM12609		0	
29 BF.BR.01.BREPM16704		0	
31 BC.BR.04.04BR142		0	
32 06A1.EE.01.EE0369		0	
33 01B.MY.05.05MYKL007_1		0	
34 01B.TH.99.09R2478P		0	
35 AD.AF.05.05AF095		0	
36 cpx.CM.00.00CMNYU830		0	
37 cpx.CM.00.00CMNYU926		0	
38 BF1.UY.03.UY03_3389		0	
39 BF.BR.04.04BRRJ179		0	
40 BF.BR.05.05BRRJ055		0	
42 BF.LU.03.LuBF_05_03		0	
43 02G.SA.03.J11223		0	
N.CM.95.YBF30		0	
N.CM.97.YBF106		0	
N.CM.02.DJ00131		0	
N.CM.04.04CM.1015_04		0	
0 BE.87.ANT70	-GC---AG-CTAGGAG-T-C-T-T---GGG-T-ATC-CC-G-T-A-CAT-TGCC-----T-T-A-TA-AC-T-A---A-AC-GAT---A---T-ATCT---GCAACACC-TG-T-TATGATAACT-C-A---CT---C---G-----	329	
0 CM.x.BCF06	-GC---GAG-CTGGGT-T-C-AAT---G-TG-T-T-C-T---T-A-CTT-TAATT---T---TAT-G-TGAAC-C-AG---A-AC-A-A---CA---T-ATCAT---GCC-CACA-TG-A-T-TGC-AAA---C-A---CT---CCC-ATAAC-----	333	
0 CM.91.MVP5180	-GC---GAG-CTGGGT-T-C-AAT---AG-TG-T-T-C-T---T-A-CTT-TAAT-----GCT-G-TG-AC-CG-G-GA-AC-A-A---CA---T-ATCAT---GC-AACA-T-A---TGC-AAA---C-A---CT---CCC-G-----	329	
0 CM.96.96CM182		0	
0 CM.97.97CMAB6447		0	
0 CM.98.98CM104		0	
0 CM.99.99CMU4122		0	
0 FR.92.VAU		0	
DO.FR.08.RBF208		0	
0 SN.99.99SE.MP1299	-GC---G---CTAGGA-----GT-T---GGG-T---C-CC-G-T-A-CTT-AAC-----C---T-T-A---AACC-CG-GC---A-AC-GA-A---CA---T-ATCA---GCAGCACC-TG-T-TATG-TAACCA-C-A---CT---T-C-G-----	329	
0 US.x.I.2478B	-GC-A-AG-CTGGGA---TGTTG-T---GGG-TAATC-CC-G-T-A-CTT-TAAC-----C---T-T-A-T-AC-CG---GA-AC-GA-A---CA---T-ATCA---G-GCAACACC-TG-T-TAAGATAACC-C-A---T---CCC-GGAC-----	332	
0 US.97.97US08692A		0	
0 US.99.99USTWLA		0	
P.FR.09.RBF168	AG-T-G---ATGGGAG-TG-GCAG---AG-T-AGC-C---T-A-CCT-ACTT---GGATTCA---ATC-T-G-GA-C---AT---A---ATCA-G-G-GAAAGA-TG-T---TT-C-AAA---C---ACTG-T-CT-AGAC-----	333	
CPZ.CD.90.ANT		0	
CPZ.CM.05.SIVcpzMT145	-G---C-----TG-----T---A-T-C-----G-T-CA-AT-T-A---G---A-TGA-C-A-G-C-G-T-C---C---A-G-G-C-AAGA-T-T-A-A-AA-----A-AG-TGAC-----	330	
CPZ.GA.08.GAB		0	
CPZ.TZ.00.TAN1	AG---GCGG-----T-----C-A-TAC-C-G---CA-T-A-----A-TGAAC-TG-C---C---ATC-CA---CTGAA-G-TCGGAGA---GA-TAA-----A-----CG---T---	327	
CPZ.US.85.US_Marilyn		0	

	TCF-1 alpha		NF-κ-B-II		NF-κ-B-I		Sp1-III		Sp1-II		Sp1-I	
B. FR. 83. HXB2	TGCTGACAT.....		CGAGCTTGTACAAG.....		GGACTTTCCGCT.....		GGGGACTTTCCA.....		GGGAGCGCTGGCCTG.....		GGGACTGGG.....	401
A. CD. 02. 02CD KTB035	-C.....		A-AG---GAC-G.....		A-----G-----		-T---TT-----		GGC...-AGT---			403
A. SN. 01. DDJ369											0	
A1. AU. 03. PS1044_Day0											0	
A1. CY. 06. CY171											0	
A1. GE. 99. 99GEM2011											0	
A1. IT. 02. 68060	-CAGA.....		CTGCTGACAC.....		A-AA---GAC-----		GGGGACTTTCCAG.....		-T---TT-----		-AGT---	410
A1. KE. 02. ML1990											0	
A1. RU. 08. PokA1Ru											0	
A1. RW. 93. 93RW037A	-C.....		A-AG---GAC-AG.....				-G-----		-T---TT-----		-AGT---	403
A1. SE. 95. SE8538											0	
A1. TZ. 01. A341											0	
A1. UA. 01. 01UADN139											0	
A1. UG. 99. 99UGA07072											0	
A1. ZA. 04. 04ZASK162B1											0	
A2. CD. 97. 97CDKT848											0	
A2. CY. 94. 94CY017_41											0	
B. AR. 04. 04AR143170											0	
B. AU. 04. PS1030_Day174											0	
B. BO. 99. B0L0122											0	
B. BR. 05. BREPM1081											0	
B. CA. 97. CANB3FULL											0	
B. CN. 05. 05CNHB_hp3	-C.....		T---AT-----						-A-----		-C-----	401
B. CO. 01. PCM001											0	
B. CU. 99. Cu19											0	
B. CY. 06. CY165											0	
B. DE. 86. D31											0	
B. DK. 04. PMVL_012											0	
B. DO. 05. 05DO_160884											0	
B. EC. 89. EC003											0	
B. ES. 07. X2131											0	
B. FR. 92. 92FR_BX08											0	
B. GA. 88. OYI											0	
B. GB. 86. GB8_46R			CCGGA-T.....				-G-----				-C-----	399
B. GE. 03. 03GEMZ004											0	
B. HT. 05. 05HT_129389											0	
B. IN. x. 11807											0	
B. JM. 05. 05JM_KJ108											0	
B. JP. 05. DR6538											0	
B. KR. 04. 04KPM5	CTGAGCTAAG.....		GACTGCTGACAC.....		T---T---C-----		-T-A-G-----		-A-----			403
B. MM. 99. MST018											0	379
B. NL. 00. 671_00T36											0	
B. RU. 04. 04RU128005											0	
B. TH. 00. 00TH_C3198											0	
B. TT. 01. 01TT_CRC50069											0	
B. TW. 94. TWCY5	-Y-----						-G-----		-C-----		-R-----	400
B. UA. 01. 01UAKV167											0	
B. US. 07. CR0027M											0	
B. UY. 01. 01UYTRA1179											0	
B. YE. 02. 02YE507											0	
B. ZA. 03. 03ZAPS045MB2											0	
C. AR. 01. ARG4006											0	
C. BR. 04. 04BR013											0	
C. BW. 00. 00BW07621											0	
C. CN. 98. YNRL9840											0	
C. CY. 05. CY040											0	
C. ES. 07. X2118_2											0	
C. ET. 02. 02ET_288											0	
C. GE. 03. 03GEW033											0	
C. IL. 98. 98IS002											0	
C. IN. 03. D24	-T-CAGAA.....		G-GA---T-G-TGACACAG.....		AAG-----		CCGGGGCGTTCCA--G-A-----		-T-----			423
C. KE. 00. KER2010											0	
C. MM. 99. mIDU101_3											0	
C. MW. 93. 93MW_985											0	
C. SN. 90. 90SE_364											0	
C. SO. 89. 89SM_145											0	
C. TZ. 02. C0178											0	
C. US. 98. 98US_MSC3018											0	
C. UY. 01. TRA3011											0	
C. YE. 02. 02YE511											0	
C. ZA. 05. 05ZAP5K240B1	-CAGAA.....		G-GA---T-CG-TG-----		-ACT--C-CTGGGGCGTTCCAGG.....				-A---T-----		-G-----	401
C. ZM. 02. 02ZM108											0	
D. CD. 83. ELI											0	
D. CM. 01. 01CM_0009BBY											0	
D. CY. 06. CY163											0	
D. KE. 97. ML415_2											0	
D. KR. 04. 04KHB8	-C.....		T---T---T---G-----		GGGGACTTTCCAG.....				AA-----		-A-----	358
D. SN. x. SE365	-C.....		A-AG---GAC-----		-A-----		-T-----		-TT-----		-AGT---	400
D. TD. 99. MN011											0	
D. TZ. 01. A280											0	
D. UG. 99. 99UGK00958											0	
D. YE. 02. 02YE516											0	
D. ZA. 90. R1											0	
F1. A0. 06. A0_06_ANG125											0	
F1. AR. 02. ARE933											0	
F1. BE. 93. VI850	GAGAAC.....		CAGAGAA.....		TGCTGACAC.....		A-AGA-T-GA-G-----		CA---GCG---A-AAG-CGGGACT-G.....			167
F1. BR. 07. 07BR844											0	
F1. ES. x. P1146											0	
F1. FI. 93. FIN9363											0	
F1. FR. 96. 96FR_MP411											0	
F1. JP. 04. DR6082	-C.....		AGAAGATTAGAGATTGCTGACAT.....		T---T-----				-A-G-CG--CCAGA-----		-A-AA-----	401
F1. RO. 96. BCI_R07	ACCTCTGACACAGAGAT				A-AGA-T-A-G-----							444
F1. RU. 08. D88_845											0	
F2. CM. 97. CM53657											0	
G. BE. 96. DRCLB											0	
G. CM. 04. 178_15	-C.....		A-AG---GAC-AGGGGACTTTCCGCCT.....		-ACT--C-AG-----		-C-----		-A-----		-G-----	366
G. CU. 99. Cu74											0	
G. ES. 05. P962											0	
G. GH. 03. 03GH175G	CAGAAGGTGT.....		TGACTGCTGACAC.....		A-AG---GAC-AG.....		-C-----		-T-----		-G-----	424
G. KE. 93. HH070_12_1											0	
G. NG. 01. 01NGPL0669	-CAGC.....		TGCTGACAC.....		A-AG---GAC-AGG.....		-C-----		-T-----		-G-C-----	331
G. PT. x. PT2695											0	
G. SE. 93. SE6165											0	

	TCF-1 alpha	NF-κ-B-II	NF-κ-B-I	Sp1-III	Sp1-II	Sp1-I	
B.FR.83.HXB2	TGCTGACAT.....	CGAGCTTGCTACAAG.....	GGACTTTCCGCT.....	GGGACTTTCCA.....	GGGAGCGTGGCCTG.....	GGC.....GGGACTGGG	401
H.BE.93.VI991							0
H.BE.93.VI997							0
H.CF.90.056							0
H.GB.00.00GBAC4001							0
J.CD.97.J.97DC.KTB147							0
J.SE.93.SE9289.7897							0
J.SE.94.SE9173.7022							0
K.CD.97.97ZR.EQTB11							0
K.CM.96.96CM.MP535							0
01 AE.CF.90.90CF11697	G.....	A-AG-T--ACCA.....	G.....	T--TT--.....	AGT--		338
01 AE.CN.07.073SWX045							0
01 AE.HK.04.HK001							0
01 AE.JP.x.DR0492	A.....	A-AG-T--ACT--	G.....	T--T-G--	AGT--		401
01 AE.TH.04.BKM	A.....	A-AG-T--ACTA.....	G.....	T--T-G--	AGT--		345
01 AE.US.00.00US.MSC1164							0
01 AE.VN.98.98VNN015							0
02 AG.CM.02.02CM.0013BBY							0
02 AG.CY.05.CY048							0
02 AG.ES.06.P1261							0
02 AG.FR.91.DJ263	T--CAGAA.....	CTGCTGACG.....	G-GA--T-ACAGTTGCTGAC.....	AAG--	A--	AGT--	425
02 AG.GH.03.03GH121AG			A--C.....	A--	AGT--		401
02 AG.LR.x.P044951							0
02 AG.NG.01.PL0710							0
02 AG.SE.94.SE7812							0
02 AG.SN.98.98SE.MP1211							0
02 AG.US.00.00US.MSC3083							0
02 AG.UZ.02.02UZ0683							0
03 AB.RU.97.KAL153_2							0
04 cpx.CY.94.94CY032_3							0
05 DF.BE.x.VI1310							0
06 cpx.AU.96.BFP90	AGGC.....	TGCTGACAA.....	A-AG-T--ATG--		T-----	G-----	413
07 BC.CN.98.98CN009							0
08 BC.CN.97.97CNGX.6F							0
09 cpx.GH.96.96GH2911							0
10 CD.TZ.96.96TZ.BF061							0
11 cpx.CM.95.95CM.1816							0
12 BF.AR.99.ARMA159		AGACTGCTGACACAGA.....	GACTGCTGACAC.....	A-AGAAT--A-G--		A-G-CG-GCCAGA.....	421
13 cpx.CM.96.96CM.1849							0
14 BG.ES.00.X605							0
15 01B.TH.99.99TH.MU2079							0
16 A2D.KR.97.97KR004							0
17 BF.AR.99.ARMA038							0
18 cpx.CU.99.CU76							0
19 cpx.CU.99.CU7							0
20 BG.CU.99.CU103							0
21 A2D.KE.99.KER2003							0
22 01A1.CM.01.01CM.0001BBY							0
23 BG.CU.03.CB118							0
24 BG.CU.03.CB378							0
25 cpx.CM.02.1918LE							0
26 AU.CD.02.02CD.MBT0047	C.....	A-AG--GAC--	C.....	T-----G.....	T--TT--	AGT--	402
27 cpx.FR.04.04CD.FR.KZ5	C.....	A-AG--GAC-AAA.....	C.....	C-----A.....	C-----	GT-----	404
28 BF.BR.99.BREPM12609							0
29 BF.BR.01.BREPM16704							0
31 BC.BR.04.04BR142							0
32 06A1.EE.01.EE0369							0
33 01B.MY.05.05MYKL007_1					T-----	G-----	33
34 01B.TH.99.09R2478P							0
35 AD.AF.05.05AF095							0
36 cpx.CM.00.00CMNYU830							0
37 cpx.CM.00.00CMNYU926							0
38 BF1.UY.03.UY03.3389							0
39 BF.BR.04.04BRRJ179							0
40 BF.BR.05.05BRRJ055							0
42 BF.LU.03.1uBF.05.03							0
43 02G.SA.03.J11223							0
N.CM.95.YBF30							0
N.CM.97.YBF106							0
N.CM.02.DJ00131							0
N.CM.04.04CM.1015_04							0
0 BE.87.ANT70	GA--A-A-A.....	CTGCTGACCT.....	GA--A--GAC-CTGT.....	G-A--AGCAAAGACTGCTGACACTGC.....	T-G-AG-GACAGG.....	TT-G--	435
0 CM.x.BCF06	TAAGAC--A.....	TAAGTGC--TG.....	GA--A--GAC-CTGC.....	G-----AACTGC.....TGACACTGT.....	GC-----T-G-AG-GATAAG.....	TT-G--	432
0 CM.91.MVP5180		CGGACTTTCCAGACTGC.....	G-----	G-----T-G-AG-GATAAG.....	GC-----T-G-AG-GATAAG.....	TT-G--	408
0 CM.96.96CMA102							0
0 CM.97.97CMA8447							0
0 CM.98.98CMA104							0
0 CM.99.99CMU4122							0
0 FR.92.VAU							0
DO.FR.08.RBF208							0
0 SN.99.99SE.MP1299	GA--A-A-C.....	TGCTGACCT.....	GA--A--GAC-CTGC.....	G-----AGCAGAGACTGCTGACACGGC.....	G-----T-TG--A-G-A-AG.....	TT-G--	435
0 US.x.I.2478B	TAAAC--		GA--G--GAC-CTGT.....	G-----AACAAAGACTGCTGACATTGC.....	GC-----AT-G-AG-GACAAG.....	TT-G--	436
0 US.97.97US08692A							0
0 US.99.99USTWLA							0
P.FR.09.RBF168	TAAAG--	GCTACGACGCTACTAAGTTGCTGACA.....	CTGC-GGGA.....	GGAAAGTCC.....	C-AG--GAA-AA--GA--AG-A--		429
CPZ.CD.90.ANT							0
CPZ.CM.05.SIVcpzMT145	T--TTAGAC--GC--CATGCCACAAGA.....	ACTGCTGACTCTGCGGGA.....		AAGGGACTTTTCCGGG.....	A--T-GTCCGGA.....	GT--	421
CPZ.GA.08.GAR							0
CPZ.TZ.08.TAN1							0
CPZ.US.85.US_Marilyn	GATGGC--TAAC--GCGCAGGCGCAATAAAACTGCTGACTG.....	A-GA--T--AGG--		ACTT-CCAA-GGACGTTCCAAG.....	G--GTG--T-A--	A-A--	428

	Sp1-1	TATA Box	5' LTR U3 end	5' LTR R repeat begin	TAR element start	TAR element end	Poly-A signal	5' LTR R repeat end														
B.FR.83.HXB2	GAGTGGCGA...	GCCCTC...	AGATCCTGCATATAAGCAGCTGCTTTT	GCGTGTACTGGGTCTCTCTGGTTAGA...	CCAGATCTGAGCCTGGGAGCTCTCTGGCTAACT...	AGGGAACCCACTGCTCTTAAGCC...	TCAATAAAG...	CTTGCCTTGAGT...	GCTTCA	551												
H.BE.93.VI991										0												
H.BE.93.VI997										0												
H.CF.90.056										0												
H.GB.00.00GBAC4001						G			C-T	63												
J.CD.97.J.97DC.KTB147										0												
J.SE.93.SE9280.7887										0												
J.SE.94.SE9173.7022										0												
K.CD.97.97ZR.EQTB11										0												
K.CM.96.96CM.MP535										0												
01 AE.CF.90.90CF11697	T	A	G	A	C	C	T	T	A	G	C	AG	C	A	488							
01 AE.CN.07.07J5WX045															0							
01 AE.HK.04.HK001															0							
01 AE.JP.x.DR0492	T	A	G	A	C	C	T	T	G	C	G	A	G	AG	C	A	551					
01 AE.TH.04.BKM	T	A	G	A	C	C	T	T	G	C	A	G	A	AG	C	A	495					
01 AE.US.00.00US.MSC1164																0						
01 AE.VN.98.98VND15																0						
02 AG.CM.02.02CM.0013BBY																0						
02 AG.CY.05.CY048																0						
02 AG.ES.06.P1261																0						
02 AG.FR.91.DJ263																0						
02 AG.GH.03.03GH181AG	T	A	AG		C	C	C	T	C		T	G	G	G	G	A	575					
02 AG.LR.x.P044951	T	A	G		C	C	C	T	C	A	G	A	G	A	G	A	551					
02 AG.NG.01.PL0710																0						
02 AG.SE.94.SE7812																0						
02 AG.SN.98.98SE.MP1211																0						
02 AG.US.00.00US.MSC3083																0						
02 AG.UZ.02.02UZ0683																0						
03 AB.RU.97.KAL153_2																0						
04 cpx.CY.94.94CY032_3																0						
05 DF.BE.x.VI1310																0						
06 cpx.AU.96.BFP90	T	A	G	A	C	C	C	T	T	C		T	A	G	A	G	AT	563				
07 BC.CN.98.98CN009																0						
08 BC.CN.97.97CNGX_6F																0						
09 cpx.GH.96.96GH2911																0						
10 CD.TZ.96.96TZ.BF061																0						
11 cpx.CM.95.95CM.1816																0						
12 BF.AR.99.ARMA159	TC	A	G		C	C			A	G	TA		G				571					
13 cpx.CM.96.96CM.1849																0						
14 BG.ES.00.X605																0						
15 01B.TH.99.99TH.MU2079																0						
16 A2D.KR.97.97KR004																0						
17 BF.AR.99.ARMA038																0						
18 cpx.CU.99.CU76																0						
19 cpx.CU.99.CU7																0						
20 BG.CU.99.CU103																7						
21 A2D.KE.99.KER2003																0						
22 01A1.CM.01.01CM.0001BBY																0						
23 BG.CU.03.CB118																0						
24 BG.CU.03.CB378																0						
25 cpx.CM.02.1918LE																0						
26 AU.CD.02.02CD.MBT0047	T	A	G		C	C			T		A	G	A				551					
27 cpx.FR.04.04CD.FR.KZ5		A	G	A	C	C	C				G						554					
28 BF.BR.99.BREPM12609																0						
29 BF.BR.01.BREPM16704																0						
31 BC.BR.04.04BR142																8						
32 06A1.EE.01.EE0369	A	G	G	A	C	C	C	T	T	C		A	G	A	G	A	CT	183				
33 01B.MY.05.05MYK1007_1																	A	0				
34 01B.TH.99.00R2478P																	0					
35 AD.AF.05.05AF095																	0					
36 cpx.CM.00.00CMNYU830																	0					
37 cpx.CM.00.00CMNYU926																	0					
38 BF1.UY.03.UY03.3389																	0					
39 BF.BR.04.04BRRJ179																	28					
40 BF.BR.05.05BRRJ055																	29					
42 BF.LU.03.luBF_05_03																	83					
43 02G.SA.03.J11223																	67					
N.CM.95.YBF30																	AA	110				
N.CM.97.YBF106																	AA	110				
N.CM.02.DJ00131																	AA	22				
N.CM.04.04CM.1015_04																	AA	22				
0.BE.87.ANT70	T	A	AG	C	C	T	C		GG	TAGAG	G	C	C	CTCTA	GCT	G	CG	AG	582			
0.CM.x.BCF06	T	A	G	C	C	T	C		GG	TAGAGA	G	C	C	CTCTA	GCT	G	CG	AG	580			
0.CM.91.MVP5180	T	A	G	C	C	T	C		TAG	TAGAG	G	C	C	CTCTA	GCT	G	CG	AG	556			
0.CM.96.96CMA102																			15			
0.CM.97.97CMA0447																			15			
0.CM.98.98CMA104																			15			
0.CM.99.99CMA1122																			13			
0.FR.92.VAU																			96			
DO.FR.08.RBF208																			0			
0.SN.99.99SE.MP1299	T	A	G	C	ACC	T	C		GG	TAGAGA	G	C	C	CTCTA	GCT	G	CG	AG	583			
0.US.x.I.2478B	T	A	AG	C	C	T	C		GG	TAGAG	G	T	C	CTCTG	GCT	G	CG	AG	584			
0.US.97.97US08692A																			0			
0.US.99.99USTWLA																			10			
P.FR.09.RBF168	TTTACC	T	AGAGC		CAC	T			G	AC	TA			CTTAA	GCA		GGAAGC		AG	A	579	
CPZ.CD.90.ANT																				96		
CPZ.CM.05.SIVcpzMT145																				570		
CPZ.CD.98.GAB1	T	T	TG	CTCAG	C	G			T	CAC	G	T		A	C	GTG	A			TA	TT	570
CPZ.TZ.00.TAN1																					99	
CPZ.US.85.US_Marilyn	CGTG	TTTT	A		A	GA		A	C	C	C	T		C	TG	CTAA	CTG		AA	C		576

	5' LTR U5 start	Extensive secondary structure	5' LTR U5 end	Lys tRNA primer binding site	
B.FR.83.HXB2	..AGTAGTGTGTGCCGCTCTGTT.GTGTGA.....CTCTGGTAAGTCTAGAGATCCCTCAGACCCCTT...TTAGTCAGTGTGGAAAAT..CTCTAG...CAGTGGCGCCCGAACAGGGACCTGAAA.....				659
A.CD.02.02CD.KTB035	T.....C.....T.....AG.....C...C.....AAAGAA...A...T.....C...T.....A-C.....TC.....				659
A.SN.01.DDJ369					0
A1.AU.03.PS1044.Day0					0
A1.CY.06.CY171					0
A1.GE.99.99GEMZ011					0
A1.IT.02.68060	R.....		AC...C...A-T...AA...	TC	673
A1.KE.02.WL1990			AC...C...G-G...AA...TTC		3
A1.RU.08.PoKa1Ru			AC...C...A-T-A...AA...T	TC	162
A1.RW.93.93RW037A	A.....		AC...C...A-T-A...AA...T	TC	659
A1.SE.95.SE8538					0
A1.TZ.01.A341					0
A1.UA.01.01UADN139					0
A1.UG.99.99UGA07072					0
A1.ZA.04.04ZASK162B1	G.....		AC...C...A-T-A...A...T		83
A2.CD.97.97CDKT848					0
A2.CY.94.94CY017.41				TTGA-AA-CGAAAGT	21
B.AR.04.04AR143170					0
B.AU.04.PS1030.Day174					0
B.B0.99.B0L0122					0
B.BR.05.BREPM1081			A.....A-C.....		130
B.CA.97.CANB3FULL				TT	0
B.CN.05.05CNHB.hp3				GC	657
B.CO.01.PCM001			T-C.....		0
B.CU.99.Cu19					218
B.CY.06.CY165					0
B.DE.86.D31				GTK-CGC	196
B.DK.04.PMVL.012					17
B.DO.05.05D0.160884					0
B.EC.89.EC003					0
B.ES.07.X2231					109
B.FR.92.92FR.BX08					0
B.GA.88.OYI					196
B.GB.86.GB8.46R					657
B.GE.03.03GEMZ004					0
B.HT.05.05HT.129389					0
B.IN.x.11807					0
B.JM.05.05JM.KJ108					0
B.JP.05.05DR6538					661
B.KR.04.04KPMH5					637
B.MM.99.MSTD101					28
B.NL.00.071.00T36	A.....		AA.....AAA...T	T	172
B.RU.04.04RU128005				R	136
B.TH.00.00TH.C3198					0
B.TT.01.01TT.CRC50069					658
B.TW.94.TWCYS			A.....		0
B.UA.01.01UAKV167					0
B.US.07.CR0027M					0
B.UY.01.01UYTRA1179					0
B.YE.02.02YE507					0
B.ZA.03.03ZAP5045MB2					83
C.AR.01.ARG4006					0
C.BR.04.04BR013					111
C.BW.00.00BW07621					25
C.CN.98.YNRL9840					0
C.CY.05.CY040					0
C.ES.07.X2118.2					91
C.ET.02.02ET.288					0
C.GE.03.03GEW2033					0
C.IL.98.98IS002					0
C.IN.03.D24	C.....				680
C.KE.00.KER2010					0
C.MM.99.mIDU101.3					28
C.MW.93.93MW.95					0
C.SN.90.90SE.364					0
C.SO.89.89SM.145					0
C.TZ.02.C0178					0
C.US.98.98US.MSC3018					0
C.UY.01.TRA3011					0
C.YE.02.02YE511					0
C.ZA.05.05ZAP5K240B1	G.....				83
C.ZM.02.02ZM108					659
D.CD.83.ELI					196
D.CM.01.01CM.0009BBY					0
D.CY.06.CY163					0
D.KE.97.ML415.2					117
D.KR.04.04KBH8	A.....A.....A.....		TC...G...A...T	T	616
D.SN.x.SE365			TCG...T...AA...C	T	649
D.TD.99.MN011					0
D.TZ.01.A280					0
D.UG.99.99UGK00958					0
D.YE.02.02YE516					0
D.ZA.90.R1					0
F1.A0.06.A0.06.ANG125					0
F1.AR.02.ARE933					0
F1.BE.93.VI850					0
F1.BR.07.07BR844					416
F1.ES.x.P1146					0
F1.FI.93.FIN9363					0
F1.FR.96.96FR.MP411					0
F1.JP.04.DR6082	A.....				650
F1.R0.96.BCI.R07	T.....				693
F1.RU.08.D88.845					107
F2.CM.97.CM53657					0
G.BE.96.DRCBL					642
G.CM.04.178.15					193
G.CU.99.Cu74	G.....				270
G.ES.05.P962					126
G.GH.03.03GH175G					699
G.KE.93.HH070.12.1					48
G.WG.01.01WGPL0669					0
G.PT.x.PT2695					606
G.SE.93.SE6165					60

	5' LTR U5 start	Extensive secondary structure	5' LTR U5 end	Lys tRNA primer binding site	
B.FR.83.HXB2	..AGTAGTGTGTGCCGCTGTGTT.GTGTGA.....CTCTGGTAAGTACAGAGATCCCTCAGACCCCTT...T		..CTCTAG...CAGTGGCGCCGCAACAGGGACCTGAAA.....		659
H.BE.93.VI991			..AAA.....T.....		28
H.BE.93.VI997					0
H.CF.90.056					0
H.GB.00.00GBAC4001		W.....A.....Y.....			162
J.CD.97.J.97DC.KTB147					0
J.SE.93.SE9200.7897					0
J.SE.94.SE9173.7022					0
K.CD.97.97ZR.EQTB11					0
K.CM.96.96CM.MP535					0
01 AE.CF.90.90CF11697	..G.....G.A.AG.....	..AC...C...A.T.A..AA..T.....	..T....GCGAAAGTTAATAGGGAC.....		613
01 AE.CN.07.07J5WX045					0
01 AE.HK.04.HK001	..G.....G.T.AG.....	..AC...C...A.T.A..AA..T.....	..T....GCGAAAGTTAATAGGGAC.....		35
01 AE.JP.x.DR0492	..G.....G.T.TG.....	..AC...C...A.T.A..AA..T.....	..T....GTGAAAGTTAATAGGGAC.....		676
01 AE.TH.04.BKM			..T....GCGAAAGTTAATAGGGAC.....		620
01 AE.US.00.00US.MSC1164					0
01 AE.VN.98.98VNN015					0
02 AG.CM.02.02CM.0013BBY					0
02 AG.CY.05.CY048					0
02 AG.ES.06.P1261	..T.....	..AC...C...A.TTA..A.....	..G.A...G...G...CCGGAAGCTAATAGGGAC.....		100
02 AG.FR.91.DJ263		..AC...C...A.T...AA.....			21
02 AG.GH.03.03GH181	..T.....	..AC...C...A.T.A..AA..T.....	..T....G.....		683
02 AG.LR.x.P044951					658
02 AG.NG.01.PL0710					0
02 AG.SE.94.SE7812			..T....G.....		34
02 AG.SN.98.98SE.MP1211					0
02 AG.US.00.00US.MSC3083					0
02 AG.UZ.02.02UZ0683					0
03 AB.RU.97.KAL153_2			..T....GTGAAA.....		12
04 cpx.CY.94.94CY032_3					26
05 DF.BE.x.VI1310		..AT.....			688
06 cpx.AU.96.BFP90		..AC...C...A...AA..T.....	..T....GCGAAAGTTAATAGGGAC.....		0
07 BC.CN.98.98CN009					0
08 BC.CN.97.97CNGX_6F					0
09 cpx.GH.96.96GH2911			..T....TA.....		30
10 CD.TZ.96.96TZ.BF061		..CCT.....			29
11 cpx.CH.95.95CM.1816		..TAAAT.....			29
12 BF.AR.99.ARMA159	..A.T.....	..A...C.....	..T.....		679
13 cpx.CM.96.96CM.1849		..AAA.....T.....			28
14 BG.ES.00.X605	..T.....	..AC...C...AAT...AA..T.....	..T....GCGAAAGTTAACAGGGAC.....		106
15 01B.TH.99.99TH.MU2079		..TAATTCGCCCTT.....	..T....GTGAAAGTTAATAGGGAC.....		67
16 A2D.KR.97.97KR004			..GT....GTGAAA.....		12
17 BF.AR.99.ARMA038					0
18 cpx.CU.99.CU76					0
19 cpx.CU.99.CU7					0
20 BG.CU.99.CU103		..AC...C...A...AA..T.....	..T....GTGAAAGTTAAAAGGGAC.....		132
21 A2D.KE.99.KER2003					0
22 01A1.CM.01.01CM.0001BBY					0
23 BG.CU.03.CB118	..T.....	..AC...C...A...AA..T.....	..T....GCGAAAGTTAAAAGGGAC.....		106
24 BG.CU.03.CB378	..T.....	..AC...C...A.R...AA..T.....	..T....GTGAAAGTTAATAGGGAC.....		106
25 cpx.CM.02.1918LE					0
26 AU.CD.02.02CD.MBT047	..G.....	..AC...C...GT...AA..T.....	..T....GCGAAA.....		664
27 cpx.FR.04.04CD.FR.KZ5		..A.....	..T....		662
28 BF.BR.99.BREPM12609		..C.....TAG.....			21
29 BF.BR.01.BREPM16704					21
31 BC.BR.04.04BR142	..G.....	..TA.C...T.....	..T....ACGAAAGTTAATAGGGAC.....		107
32 06A1.EE.01.EE0369		..A.AC...A...AA..T.....	..T....ACGAAAGTTAATAGGGAC.....		308
33 01B.MY.05.05MYKL007_1					44
34 01B.TH.99.01B2478P					0
35 AD.AF.05.05AF095					0
36 cpx.CM.00.00CMNYU830					0
37 cpx.CM.00.00CMNYU926					0
38 BF1.UY.03.UY03_3389	..T.....	..AC.....			88
39 BF.BR.04.04BRRJ179		..A.....			136
40 BF.BR.05.05BRRJ055		..AY.....C.....			137
42 BF.LU.03.LuBF_05_03		..AC...C...A.G...AA..T.....	..T....GTGAAAGTTAATAGGGAC.....		182
43 02G.SA.03.J11223	..A.....	..AC...C...A.T.A..AA..T.....			192
N.CM.95.YBF30	..G.....A-CA..CG..A.....	..C.....	..T....S.....		208
N.CM.97.YBF106	..G.....A-CA..CG..A.....	..C.....	..T....		208
N.CM.02.DJ00131	..G.....A-CA..CG..A.....	..C.....	..T....		120
N.CM.04.04CM.1015_04	..G.....A-CA..CG..A.....	..C.....	..T....		120
O.BE.87.ANT70	..A...C...T.A.....CAA-C..GT.....	..T.AC...AGACTGAA-CA.....	..T....G.....		688
O.CM.x.BCF06	..C...T.A.....CAA-C..T.....	..T.AC...AGACTGAA-CA.....			676
O.CM.91.MVP5180	..C...T.A.....CAA-C..GT.....	..T.AC...AGACTGAA-CA.....	..GC.....		661
O.CM.96.96CMA102	..C...T.A.....CAA-C..GT.....	..T.ACG...AGACTGAA-C.A..T.....			112
O.CM.97.97CMA8447	..C...T.A.....CAA-C..G.....	..T.ACG...AGACTGAGCA-A.....			111
O.CM.98.98CMA104	..C...T.A.....CAA-C..G.....	..T.ACG...AGACTGAA-CA.....			110
O.CM.99.99CMU4122	..C...T.A.....CAA-C..T.....	..T.ACG...AGACTGAA-CA.....			109
O.FR.92.VAU	..C...T.A.....CAA-C..GT.....	..T.AC...AGACTGAA-CA-G...A.T.....			195
DO.FR.08.RBF208	..T.CATCTGTTCAA..C...T.....	..T.ACG...AGACTGAG-YA.....			84
O.SN.99.99SE.MP1299	..C...T.A.....CGA-C..T.....	..T.ACG...AGACTGAG-CA.....	..G.....		688
O.US.x.I.2478B	..C...T.A.....CAA-C..T.....	..T.AC...A.T.A..AG...AAT.....			681
O.US.97.97US08692A	..C...T.A.....CAA-C..T.....	..T.AC..TAGACT-AG..TSA..A.T.....			76
O.US.99.99USTWLA	..C...T.A.....CAA-C..GT.....	..T.AC...AGCCTGAA-CA.....			106
P.FR.09.RBF168	..C...T.A.....CA-AA.....	..G.AC...CTAG-C-A.....			677
CPZ.CD.90.ANT			..G.....		3
CPZ.CM.05.SIVcpzMT145	..C...T.A.....A-CA.....	..T.AA...ATA-TGA-AGAA..T.....			194
CPZ.GA.08.GAT	..G...C...TA-CA..ACAC.....	..T.AA...TAT-CAA.....	..G.....		678
CPZ.TZ.08.TAN1	..AC...TA-CA..ACCGG.....	..TTTG...AGT-G-TAA-AA..T.....	..C.....		208
CPZ.US.85.US_Marilyn	..AC...TA-CT-C..A.....	..A.TC...A-AAGTAG--A..T.....	..T....		682

[illegible]

Packaging loops begin										
B.FR.83.HXB2	GCGAAAGGAAACAGAGGAG.....CTCTCTCGACGC..AGGACT...CGGCTT.....GCTGAA.....GCGCGCACGGCAAGAGGCGAG...GGG...CGGCGA...CTG...GTG...AGTACGCCAAAA.....									758
H.BE.93.VI991	GACTTGAAA.....CA.....A.....									144
H.BE.93.VI997	TTGATA-T.....TA.....A.....A.....									85
H.CF.90.056	GACTTGAAA.....TA.....A.....T.....									105
H.GB.00.00GBAC4001	GACTTGAAA.....TA.....A.....T.....									278
J.CD.97.J.97DC KTB147										0
J.SE.93.SE9280 7887										81
J.SE.94.SE9173 7022										82
K.CD.97.97ZR E0TB11										0
K.CM.96.96CM MP535										0
01 AE.CF.90.90CF11697	TCGAAA.....TT.....A.....T.....									713
01 AE.CN.07.073SWX045	TCGAAA.....TT.....A.....T.....									0
01 AE.HK.04.HK001	TCGAAA.....TT.....A.....T.....									135
01 AE.JP.x.DR0492	TCGAAA.....TT.....A.....T.....									775
01 AE.TH.04.BKM	TCGAAA.....TT.....A.....T.....									719
01 AE.US.00.00US MSC1164										0
01 AE.VN.98.98VND15										22
02 AG.CM.02.02CM 0013BBY										0
02 AG.CY.05.CY048										0
02 AG.ES.06.P1261	TTAATAGGGAC.TCGAAA.....TT.....A.....A.....GACT.....									211
02 AG.FR.91.DJ263	TTAATAGGGAC.TCGAAA.....TT.....A.....A.....GACT.....									121
02 AG.GH.03.03GH181AG	TTAATAGGGAC.TCGAAA.....TT.....A.....T.....A-GACT.....									794
02 AG.LR.x.PDC44951	ATAATAGGGAC.TCGAAA.....TT.....G-A.....AGACT.....									768
02 AG.NG.01.L0710	TTAATAGGGAC.TCGAAA.....TT.....A.....A.....GACT.....									0
02 AG.SE.94.SE7812	TTAATAGGGAC.TCGAAA.....TT.....A.....A.....GACT.....									145
02 AG.SN.98.98SE MP1211										0
02 AG.US.00.00US MSC3083										0
02 AG.UZ.02.02UZ0683										0
03 AB.RU.97.KAL153_2										0
04 cpx.CY.94.94CY032_3	GTTAATAGGAC.TCGAAA.....TT.....A.....T.....									124
05 DF.BE.x.VI1310	GACTTGAAAA.....TAG.....A.....AA.....									134
06 cpx.AU.96.BFP90	TCGAAA.....TT.....A.....T.....									786
07 BC.CN.98.98CN009	TTGAAA.....TA-G.....A.....									105
08 BC.CN.97.97CNX 6F										0
09 cpx.GH.96.96GH2911										0
10 CD.TZ.96.96TZ BF061	C..CTGAAA.....TAG.....A.....									136
11 cpx.CM.95.95CM 1816	GACCCGAAA.....TA-G.....A.....T.....									134
12 BF.AR.99.ARMA159	TAG.....									778
13 cpx.CM.96.96CM 1849	GA..CGTGAAAGCG..A-CT.....A.....T.....									135
14 BG.ES.00.X605	TCGAAA.....TT.....A.....T.....									205
15 01B.TH.99.99TH MU2079	TCGAAA.....TT.....A.....T.....									166
16 A2D.KR.97.97KR004	GTAATAGGGAC.TTGAAA.....TT.....A.....A.....									124
17 BF.AR.99.ARMA038										0
18 cpx.CU.99.CU76										75
19 cpx.CU.99.CU7										0
20 BG.CU.99.CU103	TCGAAA.....TT.....A.....T.....									233
21 A2D.KE.99.KER2003										0
22 01A1.CM.01.01CM 0001BBY										0
23 BG.CU.03.CB118	TCGAAA.....G-TT.....A.....T.....									207
24 BG.CU.03.CB378	TCGAAA.....TT.....A.....T.....									207
25 cpx.CM.02.1918LE										0
26 AU.CD.02.02CD MBT047	GTAAAAGGGAC.TCGAAA.....G-TT.....A.....A.....									778
27 cpx.FR.04.04CD FR.KZ5										760
28 BF.BR.99.BREPM12609	GACTTGAAA.....TAG.....									127
29 BF.BR.01.BREPM16704	GACTTGTGA.....TTG.....T.....									129
31 BC.BR.04.04BR142	GACCGGAAA.....T-G.....A.....T.....									215
32 06A1.EE.01.EE0369	TCGAAA.....TT.....A.....T.....									408
33 01B.MY.05.05MYKL007_1	TCGAAA.....TT.....A.....T.....									143
34 01B.TH.99.09R2478P										0
35 AD.AF.05.05AF095										0
36 cpx.CM.00.00CMNYU830										0
37 cpx.CM.00.00CMNYU926										0
38 BF1.UY.03.UY03 3389	TAG.....A.....A.....									184
39 BF.BR.04.04BRRJ179	TAG.....A.....									232
40 BF.BR.05.05BRRJ055	TAG.....									241
42 BF.LU.03.LuBF 05_03	GACYTGAAA.....TAG.....									290
43 02G.SA.03.J11223	TCGAAA.....R-TT.....A.....T.....									292
N.CM.95.YBF30	GACTTGAAAA.....TAG.....G.....CTGA..A.....									312
N.CM.97.YBF106	GACTTGAAAA.....TAG.....G.....CTGA..A.....A-GACTCGGCT-G-TG.....									313
N.CM.02.DJ00131	GACTTGAAAA.....TAG.....G.....CTGA..A.....									219
N.CM.04.04CM 1015_04	GACTTGAAAA.....TAG.....G.....CTGAAA.....									226
O.BE.87.ANT70	GACTTGAAA.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..C..CT.....A-AACTCA.....A.....AG-GTG.....AT.....									787
O.CM.x.BCF06	GACTTGAAA.....T.....T.....G-G..AA..AA..CTC.....ACGGGCT.....AGCAG.....T-A..CT..CT.....A-AACTCA.....AA.....A.....G-GA-TA.....									786
O.CM.91.MVP5180	GACTTGAAA.....T.....T.....G-G..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..CT..CT.....A-AACTCA.....AA.....A.....G-GA-TA.....									762
O.CM.96.96CA182	CCGGAA..A.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..C..CT.....A-ACT-ACA..GGGTGAGTAA.....									217
O.CM.97.97CAAB6447	GACCAGAAA..A.....T.....T.....G-G..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..CT..CT.....A-AACTC.....A.....AG.....G-GA-TA.....									219
O.CM.98.98CA104	GACTTGAAA.....T.....T.....G-G..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..C..CT.....A-AACTCA.....A.....AG-GTG.....AA.....									219
O.CM.99.99CMU4122	GACCTGAAAAG..T.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..CT..CT.....A-ACT-A.....A.....AA.....G-GA-TA.....									218
O.FR.92.VAU	C.....T.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..C..CT.....A-AACTCA.....AA.....A.....G-GA-TA.....									295
DO.FR.08.RBF208	GACCGGAAA..A.....T.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..C..CT.....A-ACT-ACA..AGGG.....									191
O.SN.99.99SE MP1299	GACTTGAAA..A.....T.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..C..CT.....A-AACTCA.....A.....AG.....G-GA-TA.....									789
O.US.x.I 2478B	GACATGAAA..A.....T.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..CT..CT.....A-AACTCA.....A.....G-TGAGTA..A.....									789
O.US.97.97US08692A	GACTTGAAA..A.....T.....T.....T.....G-A..AA..AA..CTC.....ACGGGCT.....AGC-G.....T-A..CT..CT.....A-AACTCA.....A.....G.....T-AGTAA.....									184
O.US.99.99USTWLA	GACTT.....T.....T.....T.....T.....AG-A..AA..AA..CTC.....AC-GGCT.....AGC-G.....T-A..C..CT.....A-AACTCA.....GA.....AA.....G-GA-TA.....									210
P.FR.09.RBF168	GACTTG.....T.....T.....T.....T.....TCTGA..A..CTC.....C-GGCT.....AGC-G.....T-A..CT..CTG.....AGGA-AGCT-ACA-CGGTGA-TA.....									778
CPZ.CD.90.ANT	ACTTGAGGA..T-C..AA-CTGTG..C-CC.....TC.....C.....GTA..GA.....C-GA.....AG.....CTTC-TTTTGTGTTTGTGC.....									107
CPZ.CM.05.SIVcpzMT145	GACTTGAAA..T.....T.....T.....G.....CTGA..A.....C.....C-GACTCGGCTTGTCTGAGT.....									303
CPZ.CM.88.GAB1	TGA-G.....T.....T.....T.....G.....CTGA..A.....C.....C-GACTCGGCTTGTCTGAGT.....									771
CPZ.TZ.00.TAN1	AGC-GG..AACCGGGCCCTG.....T.....T.....T.....G.....CTGA..A.....TC.....G.....ACT.....C.....G.....T.....A-A..G.....C-GACTCCG.....AGA.....GT.....GAGTACAT.....									296
CPZ.US.85.US Marilyn	A-TAC.....CTGA..AA..TC.....G.....ACT.....C.....G.....T.....A-A..G.....C-GACTCCG.....AGA.....GT.....GAGTACAT.....									771

Packaging loops end_Gag and Gag-Pol start

	..ATTTTGACTAGC.....GGAGGCTAGAAG.....GAGAGAGATGGGTGCGAGAGCGTCAGTATTAAAGCGGGGAGAATTAGATCGATGGGAAAAAATTCGGTTAAGGCCAGGGGGAAGAAAAATATAAAATTAACATATAG	892
B.FR.83.HXB2		
Gag		
A.CD.02.02CD.KTB035	A.T.....A.....G.....A.....GC.....G.....CG.C.G.....T.....	889
A.SN.01.DDJ369	A.....AG.....GC.....G.....G.A.G.-G.-C.-A.....	99
A1.AU.03.PS1044_Day0	A.....AG.....GC.....G.....G.C.....T.....	103
A1.CY.06.CY171	A.....AG.....GC.....G.....G.A.....CC.T.....	97
A1.GE.99.99GEMZ011	A.....AG.....GC.....G.....G.C.....CC.....	903
A1.TT.02.60800	A.....AG.....GC.....G.....G.C.....CC.....	221
A1.KE.02.ML1990	A.....AG.....GC.....G.....G.A.G.....T.....	395
A1.RU.08.PokA1Ru	A.....AG.....GC.....G.....G.C.....CC.....	891
A1.RW.93.93RW037A	A.....AG.....GC.....G.....G.A.G.....T.....	97
A1.SE.95.SE8538	A.....AG.....GC.....G.....G.A.G.....T.....	97
A1.TZ.01.A341	A.....AG.....GC.....G.....G.A.G.....T.....	97
A1.UA.01.01UADN139	A.....AG.....GC.....G.....G.A.G.....T.....	97
A1.UG.99.99UGA07072	A.....AG.....GC.....G.....G.A.G.....T.....	97
A1.ZA.04.04ZASK162B1	A.....AG.....GC.....G.....G.A.G.....T.....	324
A2.CD.97.97CDKT848	A.....AG.....GC.....G.....G.A.G.....T.....	239
A2.CY.94.94CY017_41	A.....AG.....GC.....G.....G.A.G.....T.....	261
B.AR.04.04AR143170	A.....AG.....GC.....G.....G.A.G.....T.....	99
B.AU.04.PS1038_Day174	A.....AG.....GC.....G.....G.A.G.....T.....	103
B.BO.99.BOL0122	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.BR.05.BREPM1081	A.....AG.....GC.....G.....G.A.G.....T.....	381
B.CA.97.CANB3FULL	A.....AG.....GC.....G.....G.A.G.....T.....	172
B.CN.05.05CNHB_hp3	A.....AG.....GC.....G.....G.A.G.....T.....	888
B.CO.01.PCM001	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.CU.99.Cu19	A.....AG.....GC.....G.....G.A.G.....T.....	433
B.CY.06.CY165	A.....AG.....GC.....G.....G.A.G.....T.....	103
B.DE.86.D31	A.....AG.....GC.....G.....G.A.G.....T.....	438
B.DK.04.PMVL_012	A.....AG.....GC.....G.....G.A.G.....T.....	259
B.DO.05.05DO_160884	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.EC.99.EC093	A.....AG.....GC.....G.....G.A.G.....T.....	3
B.ES.07.X2231	A.....AG.....GC.....G.....G.A.G.....T.....	352
B.FR.92.92FR.BX08	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.GA.88.OYI	A.....AG.....GC.....G.....G.A.G.....T.....	438
B.GB.86.G88_46R	A.....AG.....GC.....G.....G.A.G.....T.....	891
B.GE.03.03GEMZ004	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.HT.05.05HT_129389	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.IN.x.11807	A.....AG.....GC.....G.....G.A.G.....T.....	242
B.JM.05.05JM.KJ108	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.JP.05.DR6538	A.....AG.....GC.....G.....G.A.G.....T.....	896
B.KR.04.04KRM5	A.....AG.....GC.....G.....G.A.G.....T.....	370
B.MM.99.mSTD101	A.....AG.....GC.....G.....G.A.G.....T.....	270
B.NL.00.671_00T36	A.....AG.....GC.....G.....G.A.G.....T.....	418
B.RU.04.04RU128005	A.....AG.....GC.....G.....G.A.G.....T.....	383
B.TH.00.00TH.C3198	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.TT.01.01TT.CRC50069	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.TW.94.TWCYS	A.....AG.....GC.....G.....G.A.G.....T.....	891
B.UA.01.01UAKV167	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.US.07.CR0027M	A.....AG.....GC.....G.....G.A.G.....T.....	117
B.UY.01.01UYTRA1179	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.YE.02.02YES07	A.....AG.....GC.....G.....G.A.G.....T.....	97
B.ZA.03.03ZAPS045MB2	A.....AG.....GC.....G.....G.A.G.....T.....	324
C.AR.01.ARG4006	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.BR.04.04BR013	A.....AG.....GC.....G.....G.A.G.....T.....	353
C.BW.00.00BW07621	A.....AG.....GC.....G.....G.A.G.....T.....	269
C.CN.98.YNRL9840	A.....AG.....GC.....G.....G.A.G.....T.....	103
C.CY.05.CY040	A.....AG.....GC.....G.....G.A.G.....T.....	103
C.ES.07.X2118_2	A.....AG.....GC.....G.....G.A.G.....T.....	335
C.ET.02.02ET_288	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.GE.03.03GEMZ033	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.IL.98.98IS002	A.....AG.....GC.....G.....G.A.G.....T.....	238
C.IN.03.D24	A.....AG.....GC.....G.....G.A.G.....T.....	913
C.KE.00.KER2010	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.MM.99.mIDU191_3	A.....AG.....GC.....G.....G.A.G.....T.....	271
C.MW.93.93MW_965	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.SN.90.90SE_364	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.SO.89.89SM_145	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.TZ.02.C0178	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.US.98.98US.MSC3018	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.UY.01.TRA3011	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.YE.02.02YES11	A.....AG.....GC.....G.....G.A.G.....T.....	97
C.ZA.05.05ZAPSK240B1	A.....AG.....GC.....G.....G.A.G.....T.....	326
C.ZM.02.02ZM108	A.....AG.....GC.....G.....G.A.G.....T.....	891
D.CD.83.ELI	A.....AG.....GC.....G.....G.A.G.....T.....	438
D.CM.01.01CM_0009BBY	A.....AG.....GC.....G.....G.A.G.....T.....	97
D.CY.06.CY163	A.....AG.....GC.....G.....G.A.G.....T.....	103
D.KE.97.ML415_2	A.....AG.....GC.....G.....G.A.G.....T.....	358
D.KR.04.04KBH8	A.....AG.....GC.....G.....G.A.G.....T.....	851
D.SN.x.SE365	A.....AG.....GC.....G.....G.A.G.....T.....	891
D.TD.99.MN011	A.....AG.....GC.....G.....G.A.G.....T.....	110
D.TZ.01.A200	A.....AG.....GC.....G.....G.A.G.....T.....	97
D.UG.99.99UGK09958	A.....AG.....GC.....G.....G.A.G.....T.....	97
D.YE.02.02YES16	A.....AG.....GC.....G.....G.A.G.....T.....	97
D.ZA.90.R1	A.....AG.....GC.....G.....G.A.G.....T.....	238
F1.A0.06.A0_06_ANG125	A.....AG.....GC.....G.....G.A.G.....T.....	1
F1.AR.02.ARE933	A.....AG.....GC.....G.....G.A.G.....T.....	201
F1.BE.93.VI850	A.....AG.....GC.....G.....G.A.G.....T.....	247
F1.BR.07.07BR844	A.....AG.....GC.....G.....G.A.G.....T.....	665
F1.ES.x.P1146	A.....AG.....GC.....G.....G.A.G.....T.....	190
F1.FI.93.FIN9363	A.....AG.....GC.....G.....G.A.G.....T.....	233
F1.FR.96.96FR.MP411	A.....AG.....GC.....G.....G.A.G.....T.....	103
F1.JP.04.DR6082	A.....AG.....GC.....G.....G.A.G.....T.....	889
F1.R0.96.BCI_R07	A.....AG.....GC.....G.....G.A.G.....T.....	931
F1.RU.08.08R_845	A.....AG.....GC.....G.....G.A.G.....T.....	348
F2.CM.97.CM53657	A.....AG.....GC.....G.....G.A.G.....T.....	97
G.BE.96.DRCBL	A.....AG.....GC.....G.....G.A.G.....T.....	877
G.CM.04.178_15	A.....AG.....GC.....G.....G.A.G.....T.....	428
G.CU.99.Cu74	A.....AG.....GC.....G.....G.A.G.....T.....	505
G.ES.05.P962	A.....AG.....GC.....G.....G.A.G.....T.....	375
G.GH.03.03GH175G	A.....AG.....GC.....G.....G.A.G.....T.....	355
G.KE.93.HH8793_12_1	A.....AG.....GC.....G.....G.A.G.....T.....	294
G.NG.01.01NGPL0669	A.....AG.....GC.....G.....G.A.G.....T.....	97
G.PT.x.PT2695	A.....AG.....GC.....G.....G.A.G.....T.....	843
G.SE.93.SE6165	A.....AG.....GC.....G.....G.A.G.....T.....	295

		Packaging loops end_Gag and Gag-Pol start			
B.FR.83.HXB2	..ATTTTGACTAGC.....GGAGGCTAGAAG.....	GAGAGAGATGGGTGCGAGAGCGTCA	TATTAAAGCGGGGAGAAATAGATCGATGGGAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAAAATATAAAATAAACATATAG	892	
Gag		M G A R A S V L S G G E L D R W E K I R L R P G G K K K Y K L K H I			
H.BE.93.VI991			GCT.....G.....	278	
H.BE.93.VI997			CG.....ACT-T.....G.....	219	
H.CF.90.056			C-A.....GCT.....G.....	239	
H.GB.00.00GBAC4001			GCT.....G.....	413	
J.CD.97.1.97DC.KTB147			G-A-AGC-T.....G-CC-AGC.....G.....	90	
J.SE.93.SF9280.7887			T.....G.....G.....	215	
J.SE.94.SF9173.7022			T.....G.....G.....	216	
K.CD.97.97ZR.EQTB11			T.....G.....G.....	103	
K.CM.96.96CM.MP535			T.....G.....G.....	103	
01 AE.CF.90.90CF11697			T.....G.....G.....	847	
01 AE.CN.07.07JSWX045			T.....G.....G.....	103	
01 AE.HK.04.HK001			T.....G.....G.....	269	
01 AE.JP.x.DR0492			T.....G.....G.....	910	
01 AE.TH.04.BKM			T.....G.....G.....	853	
01 AE.US.00.00US.MSC1164			T.....G.....G.....	97	
01 AE.VN.98.98VNN15			T.....G.....G.....	156	
02 AG.CM.02.02CM.0013BBY			T.....G.....G.....	97	
02 AG.CY.05.CY048			T.....G.....G.....	103	
02 AG.ES.06.P1261			T.....G.....G.....	345	
02 AG.FR.91.DJ263			T.....G.....G.....	255	
02 AG.GH.03.03GH181AG			T.....G.....G.....	928	
02 AG.LR.x.POC44951			T.....G.....G.....	902	
02 AG.NG.01.PL0710			T.....G.....G.....	97	
02 AG.SE.94.SF7812			T.....G.....G.....	279	
02 AG.SN.98.98SE.MP1211			T.....G.....G.....	104	
02 AG.US.00.00US.MSC3083			T.....G.....G.....	97	
02 AG.UZ.02.02UZ0683			T.....G.....G.....	97	
03 AB.RU.97.KAL153.2			T.....G.....G.....	124	
04 cpx.CY.94.94CY032.3			T.....G.....G.....	258	
05 DF.BE.x.VI1310			T.....G.....G.....	268	
06 cpx.AU.96.BFP90			T.....G.....G.....	920	
07 BC.CN.98.98CN009			T.....G.....G.....	239	
08 BC.CN.97.97CNX.6F			T.....G.....G.....	99	
09 cpx.GH.96.96GH2911			T.....G.....G.....	103	
10 CD.TZ.96.96TZ.BF061			T.....G.....G.....	271	
11 cpx.CM.95.95CM.1816			T.....G.....G.....	268	
12 BF.AR.99.ARMA159			T.....G.....G.....	912	
13 cpx.CM.96.96CM.1849			T.....G.....G.....	270	
14 BG.ES.00.X605			T.....G.....G.....	339	
15 01B.TH.99.99TH.MU2079			T.....G.....G.....	300	
16 A2D.KR.97.97KR004			T.....G.....G.....	259	
17 BF.AR.99.ARMA038			T.....G.....G.....	97	
18 cpx.CU.99.CU76			T.....G.....G.....	209	
19 cpx.CU.99.CU7			T.....G.....G.....	118	
20 BG.CU.99.CU103			T.....G.....G.....	367	
21 A2D.KE.99.KER2003			T.....G.....G.....	97	
22 01A1.CM.01.01CM.0001BBY			T.....G.....G.....	97	
23 BG.CU.03.CB118			T.....G.....G.....	341	
24 BG.CU.03.CB378			T.....G.....G.....	341	
25 cpx.CM.02.1918LE			T.....G.....G.....	97	
26 AU.CD.02.02CD.MBT047			T.....G.....G.....	912	
27 cpx.FR.04.04CD.FR.K25			T.....G.....G.....	895	
28 BF.BR.99.BREPM12609			T.....G.....G.....	261	
29 BF.BR.01.BREPM16704			T.....G.....G.....	263	
31 BC.BR.04.04BR142			T.....G.....G.....	349	
32 06A1.EE.01.EE0369			T.....G.....G.....	542	
33 01B.MY.05.05MYKL007.1			T.....G.....G.....	277	
34 01B.TH.99.09R2478P			T.....G.....G.....	97	
35 AD.AF.05.05AF095			T.....G.....G.....	97	
36 cpx.CM.00.00CMNYU830			T.....G.....G.....	97	
37 cpx.CM.00.00CMNYU926			T.....G.....G.....	97	
38 BF1.UY.03.UY03.3389			T.....G.....G.....	318	
39 BF.BR.04.04BRJ179			T.....G.....G.....	366	
40 BF.BR.05.05BRJ055			T.....G.....G.....	375	
42 BF.LU.03.1uBF.05.03			T.....G.....G.....	421	
43 02G.SA.03.J11223			T.....G.....G.....	426	
N.CM.95.YBF38			T.....G.....G.....	450	
N.CM.97.YBF106			T.....G.....G.....	451	
N.CM.02.DJ00131			T.....G.....G.....	362	
N.CM.04.04CM.1015_04			T.....G.....G.....	364	
0.BE.87.ANT70			T.....G.....G.....	943	
0.CM.x.BCF06			T.....G.....G.....	942	
0.CM.91.MVP5180			T.....G.....G.....	918	
0.CM.96.96CMA182			T.....G.....G.....	373	
0.CM.97.97CMA8447			T.....G.....G.....	375	
0.CM.98.98CMA184			T.....G.....G.....	375	
0.CM.99.99CMU4122			T.....G.....G.....	374	
0.FR.92.VAU			T.....G.....G.....	452	
DO.FR.08.RBF208			T.....G.....G.....	350	
0.SN.99.99SE.MP1299			T.....G.....G.....	945	
0.US.x.I.2478B			T.....G.....G.....	945	
0.US.97.97US08692A			T.....G.....G.....	340	
0.US.99.99USTWLA			T.....G.....G.....	366	
P.FR.09.RBF168			T.....G.....G.....	937	
CPZ.CD.90.ANT			T.....G.....G.....	256	
CPZ.CM.05.SG.CpZMT145			T.....G.....G.....	461	
CPZ.GA.88.GAB1			T.....G.....G.....	929	
CPZ.TZ.00.TAN1			T.....G.....G.....	455	
CPZ.US.85.US.Marilyn			T.....G.....G.....	934	

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FR.FR.83.HXB2
Gag
H.BE.93.VI991
H.BE.93.VI997
H.CF.90.856
H.GB.00.90GBAC4001
J.CD.97.J.97DC.KT8147
J.CD.97.J.97DC.KT8147
J.SD.94.SE91737822
K.CD.97.97ZTR.ET0T11
K.CM.96.96CM.MP535
01 AE.CF.90.90CF.F11697
01 AE.CN.97.97JSWK045
01 AE.HK.04.HK001
01 AE.JP.93.DR04921
01 AE.TH.74.8KM
01 AE.TX.97.03TUS.MSC1164
01 AE.VN.98.98VNDN15
02 AG.CM.02.02CM.00138BY
02 AG.CY.05.CY048
02 AG.ES.06.P1261
02 AG.FR.91.D1263
02 AG.GH.03.03GH181AG
02 AG.GN.95.P0C44951
02 AG.NG.01.PL0710
02 AG.SE.94.SE7812
02 AG.SN.98.98SE.MP1211
02 AG.US.00.00US.CSC3083
02 AG.VN.98.98VNDN2683
04 BR.RU.97.KAL153.2
04 cpx.CY.94.94CY032.3
05 DF.BE.x.VI1310
06 cpx.AU.96.BFP90
07 BC.CN.98.98CN009
08 BC.CN.97.97CNXG.6F
09 BG.CU.99.99BG29111
10 CD.TZ.96.96TZ.BF061
11 cpx.CM.95.95CM.1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM.1849
14 BG.ES.00.X605
15 1B.TH.99.99TH.MU2079
16 01B.KR.97.97KR004
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 02D.KE.99.KER2003
22 01A1.CM.01.01CM.0001B
23 BG.CU.03.CB178
24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02CD.MBTB047
27 cpx.FR.04.04CD.FR.KZ5
28 BF.BR.99.BREPM12609
29 BF.BR.01.BREPM16704
31 BC.BR.04.04BR142
32 06A1.EE.01.EE0369
33 01B.MY.05.05MYKL007.1
34 01B.TH.99.09UR2478P
35 AD.AF.05.05AF095
36 cpx.CM.00.00CMNYU830
37 cpx.CM.00.00CMNYU926
38 BF1.UY.03.UY03.3389
39 BF.BR.04.04BRJ1979
40 BF.BR.05.BABRRJ055
42 BF.LU.03.LU0F.05.03
43 02G.SA.03.J11223
N.CM.95.YBF30
N.CM.95.YBF196
N.CM.92.02D100.01
N.CM.04.04CM.1015.04
O.BE.87.ANT70
O.CM.x.BCF06
O.CM.91.MVP5180
O.CM.96.96CMA102
O.CM.97.97CMBAB447
O.CM.97.97CMA102
O.CM.99.99CMU4122
O.FR.92.VAU
OD.FR.08.RBF208
O.SN.99.99SE.MP1299
O.US.x.I.24788
O.US.97.97US08692A
O.US.99.99USTWLA
P.FR.09.RBF168
CPZ.CD.90.ANT
CPZ.CM.05.SIVcpzMT145
CPZ.CA.88.CA
CPZ.TZ.00.TAN1
CPZ.US.85.US.Marilyn

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FR. 83.HXBZ	ATAGACGATAAAAGACCACCAAGGAAGCTTTTAGACAAGATAGAGGAAGAGCAAACAAAGTAGAAGAAGACACAGCAGCAGCT.	GACACAGGCACAGCAATTCAG	1170
Gag	I E I K D T K E A L D K I E E E Q N S K K K A Q Q A A A	D T G H S N Q	
H.BE.93.VI991	-TG-G-	T-A-A-A-GGA-GCA	562
H.BE.93.VI997	-G-	A-T-A-A-AGAGA--CA	497
H.CF.90.056	-TG-G-	T-AG-A-A-AGA--CA	517
H.GB.00.00GBAC4001	-G-C-T-GT	RGT-A-AGA-GGA-GCA	691
J.CD.97.J.97DC.KTB147	-C-G-	T-A-AA-T-A-G	365
J.SE.93.SEG280.7887	-A-	A-AA-G-A-G	493
J.SE.94.SF9173.7022	-G-	A-AA-G-A-G	494
K.CD.97.97ZR.EQT811	-C-G-GG-	C-AGG-AA-GCTGA--AGG-	369
K.CM.96.96CM.MP535	-G-	C-AGA-C-GCTGA--AGG-	369
01.AE.CF.90.90CF.I1697	-TG-	G-AG-A-GCA-A	1125
01.AE.CN.07.07JSMX045	-C-	G-AG--GCA-A	381
01.AE.HK.04.HK001	-G-	G-AG-A-GCA-A	547
01.AE.JP.x.DR0492	-G-GG-	G-A--GCA-A	1188
01.AE.TH.04.BKM	-G-	G-AG-GCA-A	1131
01.US.00.00US.MSC1164	-G-	G-AG-GCA-A	375
01.AE.VN.98.98VNDND15	-G-	G-C-AG-GCA-A	434
02.AG.CM.02.02CM.0013BBY	-CT-	AG-C-	363
02.AG.CY.05.CY048	-G-	C-G-AG-	372
02.AG.ES.06.P1261	-A-	C-G-AG-	614
02.AG.FR.91.DJ263	-C-	C-AG-	524
02.AG.GH.03.03GH181AG	-A-	C-AGT-GC	1203
02.AG.LR.x.POC44951	T-A-C-	C-AG-	1171
02.AG.NG.01.PL0710	-TG-	C-GG-	360
02.AG.SE.94.SE7812	-C-	C-G-AG-	548
02.AG.SN.98.98SE.MP1211	-AG-	C-AG-	373
02.AG.US.00.00US.MSC3083	-A-	CTG-	372
02.AG.UZ.02.02UZ0683	-T-C-	C-AG-	366
03.AB.RU.97.KAL153_2	-G-	G-AG-GCA	402
04.cpx.CY.94.94CY032_3	-TG-C-	C-G-GGT-GCA-T	536
05.DF.BE.x.VI1310	-G-G-	G-G-AG-GC	549
06.cpx.AU.96.BFP90	-A-AG-C-	C-A-AG-G-A-T	1195
07.BC.CN.98.98CN009	-TG-CG-	CA-AG-AGCTGA-GGGA	508
08.BC.CN.97.97CNGX_6F	-AG-CG-	CA-A-A-GCTGAAG-GA	368
09.cpx.GH.96.96GH2911	-G-G-	A-A-A-A-GCA	381
10.CD.TZ.96.96TZ.BF061	-A-G-GC-	-A-GC	549
11.cpx.CM.95.95CM.1816	-G-G-	-A-GCA	546
12.BF.AR.99.ARMA159	-G-G-	A-G	1178
13.cpx.CM.96.96CM.1849	-G-	A-TGA-A-C-A	548
14.BG.ES.00.X605	-A-G-	GA-A-A-GC-A	614
15.01B.TH.99.99TH.MU2079	-G-	G-AG-GCAC	578
16.A2D.KR.97.97KR004	-G-G-	CAG-T-ACACAG-A-GCAGC	531
17.BF.AR.99.ARMA038	G-TG-G-	AGAC-GCAAGCGGCAGCTGACAAAAGGG	387
18.cpx.CU.99.CU76	-TG-	C-G-AG-GC	487
19.cpx.CU.99.CU7	-G-	A-AG-GC-C	396
20.BG.CU.99.CU103	-G-G-	GTGA-A-GC-A	645
21.A2D.KE.99.KER2003	-TG-	A-AG-GC	375
22.01A1.CM.01.01CM.0001BBY	-TG-	G-AG-GCA-C	375
23.BG.CU.03.CB118	-G-	GTGA-A-GCC-A	619
24.BG.CU.03.CB378	-G-G-	GTGA-A-GC-A	619
25.cpx.CM.02.1918LE	-TG-	-AGT-A-GCAGCCA	378
26.AU.CD.02.02CD.MBT0047	-A-TG-	A-AG-A	1181
27.cpx.FR.04.04CD.FR.KZ5	-TG-	-AGAG-AG-GC-A	1164
28.BF.BR.99.BREP.M12609	-G-	-G-A-GC-A	539
29.BF.BR.01.BREP.M16704	-T-	G-GCAGGAAATAGCAGACAGCAAGCAGCAGCTGGCAGCGG-AAACAG--C-G-	574
31.BC.BR.04.04BR142	-G-G-	CAG-G-CTGG--AAGGAA-T	624
32.06A1.EE.01.EE0369	-A-AG-GC-	C-A-A-G	811
33.01B.MY.05.05MYKL007_1	-G-	G-AG-A-GCA-A	555
34.01B.TH.99.00UR2478P	-TG-	G-AG-G-RGCA-A	375
35.AD.AF.05.05AF095	-CA-	T-AG-G	372
36.cpx.CM.00.00CMNYU830	-TG-	G-AG-GCAC	375
37.cpx.CM.00.00CMNYU926	-TG-G-	G-AG-TGCA	369
38.BF1.UY.03.UY03.3389	G-TG-G-T	A-G	584
39.BF.BR.04.04BRRJ179	G-G-	A-A-G	644
40.BF.BR.05.05BRRJ055	-G-	G-G-A-GCA	656
42.BF.LU.03.LuBF.05_03	-TG-G-	-A-C	699
43.02G.SA.03.J11223	-C-	AG-	695
N.CM.95.YBF30	-C-C-C-	GGG-CGGCAGCA-C-G-TAGCAAT	734
N.CM.97.YBF106	-CC-G-	GG--CGCGGGAGC-G-CAGCAT	735
N.CM.98.DRI11	-C-C-A-T-	GGG-CGGCAGGAGC-G-TAACAT	666
N.CM.04.04CM.1015_04	-CC-G-CTCA-T-	GGG-CGGCAGGAGC-G-TAACAT	648
O.BE.87.ANT70	TATA-A-TGG-T-	AGACAC-AG-GCA-GG-	1215
O.CM.x.BCF06	T-T-T-G-T-C-A-	GGGA-AC-AGTTCA-G-	1214
O.CM.91.MVP5180	T-T-T-C-CG-T-	AGGA-AC-AG-CCT-GG-	1190
O.CM.96.96CMA102	TATA-A-TG-T-	AGACAC-RG-CA-GG-	645
O.CM.97.97CMA8447	TATA-A-TGG-T-	A-CACTAG-TCA-G-	647
O.CM.98.98CML11	TATA-A-TG-T-	GTGACG-GC-GGACG	616
O.CM.99.99CMU4122	TATAGA-TG-T-	AGACAC-AGVGA-GG-	646
O.FR.92.VAU	TATA-A-TG-T-	A-ACAC-AG-TCA-G-	724
D.O.FR.08.RBF208	TATARAG-TG-	AGACAC-GG-GAA-GG-	622
O.SN.99.99SE.MP1299	-TA-AG-TG-	AGACAC-AG-GCA-GG-	1217
O.US.x.I.2478B	TATA-A-TGG-T-	AGACAC-AGTGCA-G-	1217
O.US.97.97US08692A	TATA-A-TGG-T-	AGACAC-AGTGCA-G-	612
O.US.99.99USTWLA	TATAGAG-T-	AGACAC-AR-CA-G	635
P.FR.09.RBF168	G-R-T--GT	GA-T	1200
CP2.CD.90.ANT	GA-A-	CTGTT-AAACA-ACAGTGGTGTCAAGCAGCATCTTAGT	779
CP2.CM.95.SIVcpzMT145	-AG-GG-	GA-A-CATG	509
CP2.CM.95.SIVcpzMT145	CA-C-A-C-	GAAGCCGTGAAGGGGAGCC	12
CP2.TZ.00.TAN1	GA-AGAG-CC-T-	-A-TG-CACTAGC-G-GCACAACAG. GAAACACAGGGGAGCA	187
CP2.US.85.US.Marilyn	G-GACAG-GG-T-	AGTGGCA-TA--TT	781

B. FR. 83. HXB2

Gag

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H.H.93.VI997
H.C.FF.90.056
H.GB.00.00GBAC4001
J.C.DJ.97.J 97DC KTB147
J.S.93.SE9280 7887
J.S.94.SE9173 7022
K.C.97.9727Z E081C
K.C.MN.96.CF9C.M535
01 AE.CF.96.CF911697
01 AE.CF.97.0735WX045
01 AE.HK.04.HK001
01 AE.JP.X.DR0492
01 AE.TH.04.BKM
01 AE.US.00.00US MSC1164
02 AG.97.01.97VWMD15
02 AG.CM.02.02CM 003BBY
02 AG.CY.05.CY048
02 AG.ES.06.P1261
02 AG.FR.91.DJ263
02 AG.GH.03.03GHI81AG
02 AG.LR.X.P044951
02 AG.LR.91.PL0710
02 AG.SE.94.SE7812
02 AG.SN.98.98SE MP1211
02 AG.US.00.00US MSC3083
02 AG.UZ.02.02UZ06683
03 AB.RU.97.KAL153 2
04 cp.xc.VY.94.KALY032_3
05 DF.BE.X.VI1130
06 CP.AU.96.BFP990
07 BC.CN.98.98CN0099
08 BC.CN.97.97CNCG 6F
09 cp.xc.GH.96.96GH9219
10 C.D.TZ.96.96TZ BF061
11 cp.xc.MN.95.95CM 1816
12 BF.FR.99.ARM159
13 cp.xc.ES.96.96CM 1849
14 BG.ES.00.X605
15 01B.TH.99.99TH MU2079
16 A2D.KR.97.97KR004
17 BF.FR.99.ARM038
18 cp.CU.99.CU76
19 cp.CU.99.CU77
20 BG.CU.99.CU103
21 A2L.CE.99.KER2003
22 01A1.KM.01.01CM 0001BBY
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 cp.CM.02.02181LE
26 AU.CD.02.02CD MBT0047
27 cp.FR.04.04CD FR.KZ5
28 BF.FR.99.BREP12609
29 BF.FR.01.BREP116704
30 01A1.EE.04.04BR142
32 06A1.EE.01.EE0369
33 01B.MY.05.05MY001007.1
34 01B.TH.99.09UR2478P
35 AD.AF.05.05AF095
36 cp.xc.CM.00.00CMNYU830
37 cp.xc.CM.00.00CMNYU326
38 BF1.UY.03.UY03 3389
39 BF.FR.04.04BRJR105
40 BF.BR.05.05BRBR9755
42 BF.LU.03.LuBf 05_03
43 02G.SA.03.J11223
N.CM.95.YBF30
N.CM.97.YBF106
N.CM.92.DJ00113
N.CM.94.04CM 1015_04
O.BE.87.ANT70
O.CM.X.BCF06
O.CM.91.MVP5180
O.CM.96.96CMA102
O.CM.97.97CMA8447
O.CM.98.98CM 1122
O.CM.99.99CMU4112
O.FR.92.VAU
DO.FR.08.RBF208
O.SN.99.99SE MP1299
O.US.X.I 2478B
O.US.97.97US08692A
O.US.99.99USTWLA
P.FR.09.RBF168
CPZ.CD.98.ANT
CPZ.CM.05.SVcpzMT145
CPZ.CD.98.GAB
CPZ.TZ.00.TAN1
CPZ.US.85.US Marilyn

Gag p17 Matrix end Gag p24 Capsid start

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FR. 83. HXB2
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H.BE. 93. VI991
H.BE. 93. VI997
H.CF. 90. 056
H.GB. 08. 006BAC4001
J.C. 97. J 97DC KTB147
J.C. 97. J 97DC KTB287
J.SE. 94. SE9173 7022
K.C. 97. 9727R EQTB11
K.M. 96. 96CM MP535
01 AE.CF. 90. 90CF11697
01 AE.CN. 97. 0773WSX045
01 AE.HK. 04. HK001
01 AE.JP. x. DR0492
01 AE.TH. 04. B0492
01 AG. 98. x. 0034181AG
01 AE.VN. 98. 98VUS MSC1164
02 AG.CM. 02. 02CM 0013BBY
02 AG.CY. 05. CY048
02 AG.ES. 06. P1261
02 AG.FR. 91. D1263
02 AG.GH. 03. P063181AG
02 AG.IG. x. x. PC044951
02 AG.NG. 01. PL0710
02 AG.SE. 94. SE7812
02 AG.SN. 98. 98SE MP1211
02 AG.US. 00. 96US MSC3083
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03 AB.RU. 97. KAL152 3
04 cpx.CY. 94. 94CY032 3
05 DF.BE. x. VI1310
06 cpx.AU. 96. BFP990
07 BC.CN. 98. 98CN0099
08 BC.CN. 97. 97CN6X 69
09 BF. 99. 96. 96GB21
10 CD.TZ. 96. 96TZ BF061
11 cpx.CM. 95. 95CM 1816
12 BF. AR. 99. ARMA159
13 cpx.CM. 96. 96CM 1849
14 BG.ES. 00. X605
15 01B.TH. 99. 99TH MU2079
16 AZD.KR. 97. 97KR004
17 BF. AR. 99. ARMA038
18 cpx.CU. 99. CU76
19 cpx.CU. 99. CU7
20 BG.CU. 99. CU103
21 AZD.KM. 99. KER2003
22 01A1.CE. 01. 01CM 0001BBY
23 BG.CU. 03. CB118
24 BG.CU. 03. CB378
25 cpx.CM. 02. 1918LE
26 AU. CD. 02. 02CD MBT0047
27 cpx.FR. 94. 04CD FR. KZS
28 BF. BR. 99. BREPM12609
29 BF. BR. 01. BREPM16704
31 BC. BR. 04. 04BR142
32 06A1.EE. 01. EE0369
33 01B.MY. 05. 05MYKU007 1
34 01B.TH. 99. 00UR2478P
35 AD. AF. 05. 05AF095
36 cpx.CM. 00. 00CMNYU830
37 cpx.CM. 00. 00CMNYU926
38 BF1.UY. 03. UY03 3389
39 BF. BR. 04. 04BRJR105
40 BF. BR. 05. 05BRBRJ055
42 BF. LU. 03. LU0F 05_03
43 02G.SA. 03. J11223
N.CM. 95. YBF30
N.CM. 97. YBF196
N.CM. 02. DJ0011311
N.CM. 04. 04CM 1015_04
O.BE. 87. ANT70
O.CM. x. BCF06
O.CM. 91. MVP5180
O.CM. 96. 96CMA102
O.CM. 97. 97CMA8B447
O.CM. 98. CM98
O.CM. 99. 99CMU4122
O.FR. 92. VAU
O.DR. 98. RBF208
O.SN. 99. 99SE MP1299
O.US. x. I 24788
O.US. 97. 97US08692A
O.US. 99. 99USUTLWA
P.FR. 09. RBF168
CPZ. CD. 90. ANT
CPZ. CM. 85. SV1cpxMT145
CPZ. CM. 85. GAB1
CPZ. TZ. 00. TAN1
CPZ. US. 85. US Marilyn

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H.BE.93.VI997
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H.GB.00.G0BCA4001
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J.S.E.93.SE9173 7022
K.C.D.97.9727R EOTB11
K.CM.96.96CM MP535
01 AE.CF.90.90CF11697
01 AE.CN.07.073WSX045
01 AE.HK.04.HK001
01 AE.JP.x.DR0492
01 AE.TH.04.BKM
01 AE.US.x.P0C4A951 MSC1164
01 AE.VN.98.98VNDND15
02 AG.CM.02.02CM 0013BBY
02 AG.CY.05.CY048
02 AE.ES.06.P1261
02 AG.FR.91.DJ263
02 AG.GH.03.03GH181AG
02 AG.IG.05.x.P0C4A951
02 AG.NG.01.P0710
02 AG.SE.94.SE7812
02 AG.SN.98.98SE MP1211
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02 AG.UZ.02.02UZ0663
03 AC.RU.97.KAL153 2
04 cp.x.CY.94.C94C502_3
05 DF.BE.x.VI1130
06 cp.x.VA.96.BFP990
07 BC.CN.98.98CNCN09
08 BC.CN.97.97CNCX 6F
09 cp.x.GH.96.96GH1211
10 CD.TZ.96.96TZ BF061
11 cp.x.CM.95.95CM 1816
12 BF.AR.99.ARMA159
13 cp.x.CM.96.96CM 1849
14 BG.ES.00.X065
15 01B.TH.99.99TH MU2079
16 AZD.KR.97.97KR R004
17 BF.AR.99.ARMA038
18 cp.x.CU.99.CU76
19 cp.x.CU.99.CU7
20 BG.CU.99.CU103
21 AZD.KM.99.KER2003
22 01A1.CE.01.01CM 0001BBY
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 cp.x.CM.02.1918LE
26 AU.CD.02.02CD MBT0847
27 cp.FR.04.04CD FR.KZS
28 BF.BR.99.BREP12609
29 BF.BR.01.BREP16704
31 BC.BR.04.04BR142
32 06A1.EE.01.EE0369
33 01B.MY.05.05MYK007_1
34 01B.TH.99.09UR2478P
35 AD.AF.05.05AF095
36 cp.x.CM.00.00CMNYU830
37 cp.x.CM.00.00CMNYU926
38 BF1.UY.03.UY03 3389
39 BF.BR.04.04BRJR105
40 BF.BR.05.05BRBJ075
42 BF.LU.03.LuBF 05_03
43 02G.SA.03.J11223
N.CM.95.YBF30
N.CM.97.YBF196
N.CM.02.DJ0011511
N.CM.04.04CM 1015_04
O.BE.87.ANT70
O.CM.x.BCF06
O.CM.91.MVP5180
O.CM.96.96CMA102
O.CM.97.97CMA8447
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O.FR.92.VAU
O.DR.08.RBF208
O.SN.99.99SE MP1299
O.US.x.I 24788
O.US.97.97US08692A
O.US.99.99USUTLWA
P.FR.09.RBF168
CPZ.CD.90.ANT
CPZ.CM.05.S1VcpzMT145
CPZ.CM.08.GAG
CPZ.TZ.00.TAN1
CPZ.US.85.US Marilyn

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 H. BE. 93. VI997
 H. CF. 90. 056
 H. GB. 00. 006BAC4001
 J. CD. 97. 1. 97DC KTB147
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 J. SE. 94. 5E9173 7022
 K. CD. 97. 972R EQTB11
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 01 AE. CN. 07. 07J5WX045
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 01 AE. TH. 04. BKM
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 02 AG. CY. 05. CY048
 02 AG. ES. 06. P1261
 02 AG. FR. 91. D3263
 02 AG. GH. 03. 03GHI181AG
 02 AG. LR. x. POC44951
 02 AG. NG. 01. PL0710
 02 AG. SE. 94. 5E7812
 02 AG. SN. 98. 98SE MP1211
 02 AG. US. 00. 00US MSC3083
 02 AG. UZ. 02. 02UZ0683
 03 AB. RU. 97. KAL153 2
 04 cpx. CY. 94. 94CY032 3
 05 DF. BE. x. VII1310
 06 cpx. AU. 96. BFP90
 07 BC. CN. 98. 98CNR09
 08 BC. CN. 97. 97CNGX 6F
 09 cpx. GH. 96. 96GH2911
 10 CD. TZ. 96. 96TZ BF061
 11 cpx. CM. 95. 95CM 1816
 12 BF. AR. 99. ARMA159
 13 cpx. CM. 96. 96CM 1849
 14 BG. ES. 00. X605
 15 01B. TH. 99. 99TH MU2079
 16 A2D. KR. 97. 97KR084
 17 BF. AR. 99. ARMA038
 18 cpx. CU. 99. CU76
 19 cpx. CU. 99. CU7
 20 BG. CU. 99. CU103
 21 A2D. KE. 99. KER2003
 22 01A1. CM. 01. 01CM 0001BBY
 23 BG. CU. 03. CB118
 24 BG. CU. 03. CB378
 25 cpx. CM. 02. 1918LE
 26 AU. CD. 02. 02CD MBT047
 27 cpx. FR. 04. 04CD FR K25
 28 BF. BR. 99. BREPM12609
 29 BF. BR. 01. BREPM16704
 31 BC. BR. 04. 04BR142
 32 06A1. EE. 01. EE0369
 33 01B. MY. 05. 05MYK1007 1
 34 01B. TH. 99. 09R2478P
 35 AD. AF. 05. 05AF095
 36 cpx. CM. 00. 00CMNYU830
 37 cpx. CM. 00. 00CMNYU926
 38 BF1. UY. 03. UY03 3389
 39 BF. BR. 04. 04BRJ179
 40 BF. BR. 05. 05BRJ055
 42 BF. LU. 03. 1uBF 05 03
 43 02G. SA. 03. J11223
 N. CM. 95. YBF38
 N. CM. 97. YBF106
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 O. BE. 87. ANT70
 O. CM. x. BCF06
 O. CM. 91. MVP5180
 O. CM. 96. 96CMA182
 O. CM. 97. 97CMA68447
 O. CM. 98. 98CMA184
 O. CM. 99. 99CMU4122
 O. FR. 92. VAU
 DO. FR. 08. RBF208
 O. SN. 99. 99SE MP1299
 O. US. x. I 2478B
 O. US. 97. 97US08692A
 O. US. 99. 99USTWLA
 P. FR. 09. RBF168
 CPZ. CD. 90. ANT
 CPZ. CM. 05. S1cpzMT145
 CPZ. GA. 88. GAB1
 CPZ. TZ. 00. TAN1
 CPZ. US. 85. US Marilyn

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 P K E P F R D Y V D R F Y K T L R A E Q A S Q E V K N W M T E T L L V Q N A N P D C K T I L K A L G P A A T L E E
 -A- -C- -T- -G- -GT- -T- -A- -T- -C- -G- -G- -T- -A- -G- -G- -T- -A- - 1215
 -A- - - - -A- -T- -T- -T- -CA- - -G- -G- -C- - -G- -A- -T- -C- - -G- -A- -G- -T- -A- - 1150
 -A- - - - -A- -T- -T- -T- -CA- -T- -G- -G- -A- -T- -C- - -A- -G- -A- -G- -T- -A- - 1170
 -A- - - - -A- -T- -T- -T- -CA- -C- -G- -G- -C- - -A- -T- -C- - -A- -G- -A- -G- -T- -A- - 1344
 -A- -T- - -G- -TA- -T- -G- -T- -A- -T- -C- - -A- -T- -C- -C- -G- -A- -G- -GA- - 1027
 -A- -T- - -A- -A- -T- -G- -T- -A- -T- -C- - -A- -T- -C- -C- -G- -A- -G- -GA- - 1026
 -A- -T- -C- - -A- -A- -T- -G- -T- -A- -T- -C- - -A- -T- -C- -C- -G- -A- -G- -GA- - 1147
 -A- - - - -TA- -T- -G- -GT- -T- -A- -CA- -A- -G- -C- - -C- -A- -G- -G- -T- -G- -T- - 1022
 -A- - - - -TA- -T- -C- -T- -A- -CA- -A- -G- -C- -C- -C- -A- -G- -G- -G- -T- -G- -T- - 1022
 -A- - -C- - -G- -TA- -T- -C- -G- -A- -A- - -AC- -A- -T- -C- -T- -C- - -A- -A- -G- -T- - 1778
 -A- - -C- - -TA- -A- -C- -A- -A- -A- -G- -C- -T- -C- -A- -T- -C- -T- -C- - -A- -A- -GA- -TT- - 1034
 -A- - -C- - -TA- -C- -G- -A- -A- -A- -A- -C- -A- -T- -C- -T- -C- - -A- -G- -GA- -TT- - 1200
 -A- - -C- - -TA- -C- -G- -A- -A- -A- -G- -C- -C- -A- -T- -C- -T- -C- - -A- -A- -GA- -TT- - 1841
 -A- -G- -C- -A- -TA- -C- -A- -A- -A- -G- -C- -C- -A- -T- -C- -G- -T- -C- - -A- -AG- -CC- -T- - 1784
 -A- -G- -C- -A- -TA- -C- -G- -A- -A- -A- -G- -C- -C- -A- -T- -C- -T- -C- - -A- -A- -GA- -T- -T- - 1028
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 -G- -A- -T- -TA- -T- -T- -G- -T- -A- -G- -C- -C- -T- -C- -T- -C- - -A- -G- -T- - 1823
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 -A- - - - -TA- -T- -T- -T- -A- -CA- -G- -T- -C- -C- -C- -G- -C- - -G- -A- -G- -T- - 1025
 -A- - - - -TA- -T- -T- -T- -G- -T- -A- -A- -G- -C- -C- -C- -G- -A- -G- -T- - 1019
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 -A- - -C- -T- -TA- -T- -TG- -C- -A- -A- -C- -G- -C- -C- -C- -A- -T- -C- -T- -C- - -A- -A- -G- -T- - 1189
 -A- - - - -TA- -T- -T- -T- -A- -A- -C- - -C- -A- - -C- - -A- -C- - -A- -A- -CA- - - 1202
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 -A- - - - -TA- -T- -T- -G- -T- -A- -G- -C- -C- -A- - -C- - -G- -A- -G- -T- - 1202
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 -A- - - - -TA- -T- -T- -C- -T- -A- -A- -A- -G- -C- -C- -C- -A- - -C- - -G- -A- -G- -T- - 1831
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 -A- -G- - -TA- -T- -C- -T- -A- -A- -GGG- -C- -C- -T- -AT- -C- -C- -G- -C- -A- -G- -ACA- -G- - 1040
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 -A- - - - -TA- -T- -TC- -T- -C- -T- -A- -A- -GGC- -C- -C- -C- -G- -A- -G- -T- - 1049
 -A- - -T- -TA- -T- -C- -T- -A- -A- -A- -G- -C- -C- -C- -G- -A- -G- -T- - 1298
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 -A- -G- -T- -TA- -A- -TC- -T- -C- -T- -A- -A- -A- -G- -C- -C- -G- -A- -G- -GT- - 1272
 -A- - -T- -TA- -T- -T- -T- -A- -A- -A- -G- -C- -C- -A- - -C- -C- -G- -A- -G- -T- - 1272
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 -A- - -T- -TA- -A- -T- -T- -A- -A- -A- -G- -C- -TC- - -T- -C- -C- -G- -G- -A- -G- -T- -T- -G- - 1834
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 -A- - -T- -TA- -T- -C- -T- -TG- -A- -A- -GG- -C- -C- -C- -G- - -G- -T- - 1192
 -A- - -T- -TA- -T- -C- -A- -TG- -A- -A- -GGG- -C- -C- -C- -G- - -G- -T- - 1227
 -A- - -T- -TA- -T- -A- -A- -G- -A- -C- -A- -G- -C- -C- -A- -A- -T- -C- -G- -A- -G- -T- - 1277
 -A- - -C- -TA- -T- -T- -T- -A- -A- -C- -T- -G- -C- -C- -C- -A- -A- -T- -C- -G- -A- -G- -T- - 1464
 -A- - -T- -TA- -C- -C- -G- -A- -AA- -C- -G- -G- -AC- -A- -A- -T- -C- -T- -C- - -A- -A- -GA- -T- -G- - 1208
 -A- - -C- -TA- -C- -G- -A- -A- -A- -C- -C- -C- -A- - -T- -C- -T- -C- - -A- -A- -GA- -T- - 1028
 -A- - -T- -T- -GT- -C- -T- -A- -A- -GGG- -A- -A- -T- -A- -T- -C- -C- -CC- -G- -G- -A- -A- -G- -T- - 1025
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 -A- - -T- -TA- -T- -GTG- -T- -T- -A- - -C- -A- -G- -C- -AC- - -T- -C- -T- -G- - -G- - 1237
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 -A- - -T- -TA- -T- -G- -CT- -T- -A- -A- -GGG- -C- -C- -C- -G- - -G- -T- - 1352
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 -A- -G- -TA- -C- -T- -A- -G- -AA- -T- -G- -AC- -C- -A- -A- -A- -ACAG- -CC- -A- -G- -GA- -CT- - 1388
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 -A- - -G- -T- -T- -C- -AT- -G- -A- -AAGT- -A- -A- -C- -T- -T- -G- -T- -A- -Y- -ACAA- -G- -T- -A- -G- -GA- -CT- -G- - 1301
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 -A- -G- -C- -T- -G- -TA- -A- -A- -A- -G- -CCT- -G- -GCC- -A- -A- -AA- -A- -C- -T- -C- -ACAC- -CC- -G- -G- -T- -A- -GA- -CT- -CT- - 1244
 -A- -G- -C- -G- -CT- -G- -T- -A- -A- -G- -C- -C- -A- -A- -G- -T- -C- -AC- -C- -G- -A- -G- -CT- -CT- - 1383
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[illegible]

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H.B.F. 03.VI971
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J.S.D. 93.SE9280 7887
J.S.E. 94.S91713 7022
K.C.D. 97.S97Z E0T811
K.M. 96.96CM MP535
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O1 AE. 98.90.90CF1
O1 AE. HK. 04.HK001
O1 AE. JP.x.DR0492
O1 AE. TH.04.BKM
O1 AE. US.00.00MS MSC1164
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O2 AG. ES.06.06E1261
O2 AG. FR.91.DJ263
O2 AG. GH.03.03GHIH181AG
O2 AG. LR.x.POC44951
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O7 BC. CN.98.98CN0099
O8 BC. CN.97.97CN0X 6F
O9 Cx. GH.96.96GZB911
O10 T.Z. 96.96ZT 0F61
O11 Cx. 95.95.95CM 1816
O12 Cx. 96.96.96CM 1849
O13 BG. ES.00.X605
O15 O1B. TH.99.99TH MU2079
O16 T.Z. 97.97.97KROA
O17 BF. AR.99.99ARMA038
O18 Cx. CU.99.CU78
O19 Cx. CU.99.CU7
O20 BG. CU.99.CU083
O21 AZD. KE.99.99KEZ003
O22 O1A1. CR.01.01CR 0001B
O23 BG. CU.03.CB118
O24 BG. CU.03.CB375
O25 Cx. CM.02.1918E
O26 AU. CD.02.02CD MBT047
O27 Cx. FR.04.04.04C FR. KZS
O28 BF. BR.04.BREPM12609
O29 BF. BR.01.BREPM16704
O30 BF. BR.04.04BRL12
O31 O1B. EE.01.EE0360
O32 O1B. EE.01.EE0360
O33 O1B. TH.99.09UR2478P
O35 AD. AF.05.05AF095
O36 Cx. CM.00.00CMNYU830
O37 Cx. CM.00.00CMNYU926
O38 BF1. UY.03.UY03 3389
O39 BF. BR.04.04BRJR179
O40 BF. BR.05.05BRJR3055
O42 BF. LU.03.Lu0F 05 03
O43 O2C. SA.03.J11223
N.C.M. 95.YBF30
N.C.M. 97.YBF106
N.C.M. 02.DJ1313
N.C.M. 04.04CM 0015 04
O.B.E. 87.ANT79
O.C.M. x.BC0F6
O.C.M. 91.MVP5180
O.C.M. 96.96CMKA182
O.C.M. 97.97CMBAB447
O.C.M. 98.98CMNYU830
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CPZ. GA.95.S1VCPMT145
CPZ. GA.98.GAB1
CPZ. TZ.00.TANI
CPZ. US.85.US Marilyn

[illegible]

		Gag-Pol -1 ribosomal slip site		Gag p7 nucleocapsid end*Gag p1 start			
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		C F N C G K E G H T A R N C R A P R K K G C W K C G K E G H Q M K D C T		E R Q A N F L G K I W P S Y K			
		C F N C G K E G H T A R N C R A P R K K G C W K C G K E G H Q M K D C T		F F R E D L A F L Q			
B. FR. 83. HXB2							
Gag							
Pol							
A. CD. 02. 02CD_KTB035							2108
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A1. AU. 03. PS1044_Day0							1322
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A1. GE. 99. 99GEM2011							1298
A1. IT. 02. 60000							2119
A1. KE. 02. ML1990							1437
A1. RU. 08. PokA1Ru							1602
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A1. SE. 95. SE0538							1313
A1. TZ. 01. A341							1316
A1. UA. 01. 01UADN139							1313
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A1. ZA. 04. 04ZASK162B1							1558
A2. CD. 97. 97CDKT848							1473
A2. CY. 94. 94CY017_41							1471
B. AR. 04. 04AR143170							1315
B. AU. 04. PS1038_Day174							1325
B. BO. 99. BOL0122							1331
B. BR. 05. BREPM1081							1618
B. CA. 97. CANB3FULL							1394
B. CN. 05. 05CNB hp3							2113
B. CO. 01. PCM001							1319
B. CU. 99. Cu19							1652
B. CY. 06. CY165							1328
B. DE. 86. D31							1660
B. DK. 04. PWVL_012							1481
B. DO. 05. 05DO_160884							1319
B. EC. 89. EC003							1227
B. ES. 07. X2231							1577
B. FR. 92. 92FR_BX08							1325
B. GA. 88. 0YT							1657
B. GB. 86. GB8_46R							2342
B. GE. 03. 03GEMZ004							1310
B. HT. 05. 05HT_129389							1318
B. IN. x. 11807							1461
B. JM. 05. 05JM_KJ108							1325
B. JP. 05. DR653							2118
B. KR. 04. 04KMH5							2092
B. MM. 99. mSTD101							1501
B. NL. 00. 671_00T36							1649
B. RU. 04. 04RU128005							1605
B. TH. 00. 00TH_C3198							1328
B. TT. 01. 01TT_CRC50069							1337
B. TW. 94. TWCYS							2113
B. UA. 01. 01UAKV167							1319
B. US. 07. CR0027M							1357
B. UV. 01. 01UVTRA1179							1319
B. YE. 02. 02YE507							1328
B. ZA. 03. 03ZAPS045MB2							1546
C. AR. 01. ARG4006							1310
C. BR. 04. 04BR013							1566
C. BW. 00. 00BW07621							1479
C. CN. 98. YNRL9840							1310
C. CY. 05. CY040							1316
C. ES. 07. X2118_2							1342
C. ET. 02. 02ET_288							1310
C. GE. 03. 03GEMZ033							1307
C. IL. 98. 98IS002							1448
C. IN. 03. D24							2138
C. KE. 00. KER2010							1307
C. MM. 99. mIDU101_3							1477
C. MW. 93. 93MW_965							1307
C. SN. 90. 90SE_364							1307
C. SO. 89. 89SM_145							1313
C. TZ. 02. C0178							1307
C. US. 98. 98US_MSC3018							1307
C. UY. 01. TRA3011							1298
C. YE. 02. 02YE511							1307
C. ZA. 05. 05ZAPSK240B1							1530
C. ZM. 02. 02ZM108							2110
D. CD. 83. ELT							1663
D. CM. 01. 01CM_0009BBY							1310
D. CY. 06. CY163							1325
D. KE. 97. ML415_2							1583
D. KR. 04. 04KBH8							2076
D. SN. x. SE365							2116
D. TD. 99. MH011							1335
D. TZ. 01. A280							1312
D. UG. 99. 99UGK09958							1316
D. YE. 02. 02YE516							1322
D. ZA. 90. R1							1463
F1. A0. 06. A0_06_ANG125							1211
F1. AR. 02. ARE933							1408
F1. BE. 93. V1850							1451
F1. BR. 07. 07BR844							1877
F1. ES. x. P1146							1397
F1. FI. 93. FIN9363							1443
F1. FR. 96. 96FR_MP411							1310
F1. JP. 04. DR6082							2102
F1. RO. 96. BCI_R07							1338
F1. RU. 08. D88_845							1573
F2. CM. 97. CM53657							1304
G. BE. 96. DRCLB							2081
G. CM. 04. 178_15							1638
G. CU. 99. Cu74							1730
G. ES. 05. P062							1600
G. GH. 03. 03GH175G							2154
G. KE. 93. HH8793_12_1							1518
G. NG. 01. 01NGPL0669							1322
G. PT. x. PT2695							2059
G. SE. 93. SE6165							1520

		Gag-Pol -1 ribosomal slip site		Gag p7 nucleocapsid end Gag p1 start			
B. FR. 83. HKB2		GTTTCAATTGTGGCAAAGAGGGCACACAGCCAGAAATTCAGGGGCCCTAGGAAAAAGGGCTGTGGAAATGTGGAAGGAGGACACCAATGAAGAGTTGTACT.....		GAGAGACAGGCTAATTTTATAGGAAGACTGGCCTTCTCTACAA.....		2114	
Gag		C F N C G K E G H T A R N C R A P R K K G C W K C G K E G H Q M K D C T		E R Q A N F L G K I W P S Y L Q			
Pol				F F R E D L A F L Q			
H. BE. 93. VI991	1509	-C	-C	-A	-T	-A	-G
H. BE. 93. VI997	1444	-C	-C	-G	-A	-T	-G
H. CF. 90. 056	1464	-C	-C	-G	-A	-T	-G
H. GB. 00. 00GBCA4001	1638	-C	-C	-T	-G	-A	-G
J. CD. 97. J. 97DC KTB147	1315	-C	-C	-T	-G	-A	-G
J. SE. 93. SE9280 7887	1434	-C	-C	-A	-T	-A	-G
J. SE. 94. SE9173 7022	1435	-C	-C	-A	-T	-A	-G
K. CD. 97. 97ZR EQTB11	1310	-C	-C	-A	-CT	-T	-G
K. CM. 96. 96CM MP535	1310	-C	-C	-A	-CT	-T	-G
01 AE. CF. 90. 90CF11697	2063	-C	-C	-G	-A	-CT	-T
01 AE. CN. 07. 07J5WX045	1319	-C	-C	-G	-A	-CT	-T
01 AE. HK. 04. HK001	1485	-C	-C	-GG	-A	-CT	-T
01 AE. JP. x. DR0492	2126	-C	-C	-G	-A	-CT	-T
01 AE. TH. 04. BKM	2069	-C	-C	-G	-A	-CT	-T
01 AE. US. 00. 00US MSC1164	1319	-C	-C	-G	-A	-CT	-T
01 AE. VN. 98. 98VND15	1369	-C	-C	-G	-A	-CT	-T
02 AG. CM. 02. 02CM 0013BBY	1301	-C	-C	-G	-A	-CT	-T
02 AG. CY. 05. CY048	1313	-C	-C	-G	-A	-CT	-T
02 AG. ES. 06. PI261	1552	-C	-C	-T	-A	-CT	-T
02 AG. FR. 91. 01263	1462	-C	-C	-T	-A	-CT	-T
02 AG. GH. 03. 03GH181AG	2138	-C	-C	-G	-A	-CT	-T
02 AG. LR. x. POC44951	2109	-C	-C	-G	-A	-CT	-T
02 AG. NG. 01. PL0710	1298	-C	-C	-G	-A	-CT	-T
02 AG. SE. 94. SE7812	1486	-C	-C	-G	-A	-CT	-T
02 AG. SN. 98. 98SE MP1211	1311	-C	-C	-G	-A	-CT	-T
02 AG. US. 00. 00US MSC3083	1310	-C	-C	-G	-A	-CT	-T
02 AG. UZ. 02. 02UZ0683	1304	-C	-C	-G	-A	-CT	-T
03 AB. RU. 97. KAL153 2	1340	-C	-C	-G	-A	-CT	-T
04 cpx. CY. 94. 94CY032 3	1483	-C	-C	-G	-A	-CT	-T
05 DF. BE. x. VI1310	1496	-C	-C	-T	-A	-CT	-T
06 cpx. AU. 96. BFP90	2136	-C	-C	-G	-A	-CT	-T
07 BC. CN. 98. 98CN009	1446	-C	-C	-G	-A	-CT	-T
08 BC. CN. 97. 97CNG 6F	1306	-C	-C	-G	-A	-CT	-T
09 cpx. GH. 96. 96GH2911	1319	-C	-C	-G	-A	-CT	-T
10 CD. TZ. 96. 96TZ BF061	1496	-C	-C	-G	-A	-CT	-T
11 cpx. CM. 95. 95CM 1816	1484	-C	-C	-G	-A	-CT	-T
12 BF. AR. 99. ARMA159	2119	-C	-C	-G	-A	-CT	-T
13 cpx. CM. 96. 96CM 1849	1498	-C	-C	-G	-A	-CT	-T
14 BG. ES. 00. X605	1555	-C	-C	-G	-A	-CT	-T
15 01B. TH. 99. 99TH MU2079	1513	-C	-C	-G	-A	-CT	-T
16 A2D. KR. 97. 97KR004	1477	-C	-C	-G	-A	-CT	-T
17 BF. AR. 99. ARMA038	1328	-C	-C	-G	-A	-CT	-T
18 cpx. CU. 99. CU76	1425	-C	-C	-G	-A	-CT	-T
19 cpx. CU. 99. CU7	1343	-C	-C	-G	-A	-CT	-T
20 BG. CU. 99. CU103	1592	-C	-C	-G	-A	-CT	-T
21 A2D. KE. 99. KER2003	1322	-C	-C	-G	-A	-CT	-T
22 01A1. CM. 01. 01CM 0001BBY	1322	-C	-C	-G	-A	-CT	-T
23 BG. CU. 03. CB118	1569	-C	-C	-G	-A	-CT	-T
24 BG. CU. 03. CB378	1566	-C	-C	-G	-A	-CT	-T
25 cpx. CM. 02. 1918LE	1325	-C	-C	-G	-A	-CT	-T
26 AU. CD. 02. 02CD MBT047	2125	-C	-C	-G	-A	-CT	-T
27 cpx. FR. 04. 04CD FR K25	2111	-C	-C	-G	-A	-CT	-T
28 BF. BR. 99. BREPM12609	1480	-C	-C	-G	-A	-CT	-T
29 BF. BR. 01. BREPM16704	1515	-C	-C	-G	-A	-CT	-T
31 BC. BR. 04. 04BR142	1568	-C	-C	-G	-A	-CT	-T
32 06A1. EE. 01. EE0369	1749	-C	-C	-G	-A	-CT	-T
33 01B. MY. 05. 05MYKL007 1	1493	-C	-C	-G	-A	-CT	-T
34 01B. TH. 99. 09UR2478P	1316	-C	-C	-G	-A	-CT	-T
35 AD. AF. 05. 05AF095	1310	-C	-C	-G	-A	-CT	-T
36 cpx. CM. 00. 00CMNU830	1319	-C	-C	-G	-A	-CT	-T
37 cpx. CM. 00. 00CMNU926	1310	-C	-C	-G	-A	-CT	-T
38 BF1. UY. 03. UY03 3389	1525	-C	-C	-G	-A	-CT	-T
39 BF. BR. 04. 04BRJ179	1582	-C	-C	-G	-A	-CT	-T
40 BF. BR. 05. 05BRJ055	1597	-C	-C	-G	-A	-CT	-T
42 BF. LU. 03. 03LUBF 05 03	1640	-C	-C	-G	-A	-CT	-T
43 02G. SA. 03. J11223	1642	-C	-C	-G	-A	-CT	-T
N. CM. 95. YBF30	1687	-C	-C	-G	-A	-CT	-T
N. CM. 97. YBF106	1685	-C	-C	-G	-A	-CT	-T
N. CM. 02. DJ00131	1605	-C	-C	-G	-A	-CT	-T
N. CM. 04. 04CM 1015 04	1598	-C	-C	-G	-A	-CT	-T
O. BE. 87. ANT70	2180	-C	-C	-G	-A	-CT	-T
O. CM. x. BCF06	2179	-C	-C	-G	-A	-CT	-T
O. CM. 91. MPV5180	2155	-C	-C	-G	-A	-CT	-T
O. CM. 96. 96CM0102	1610	-C	-C	-G	-A	-CT	-T
O. CM. 97. 97CMAB8447	1612	-C	-C	-G	-A	-CT	-T
O. CM. 98. 98CM104	1612	-C	-C	-G	-A	-CT	-T
O. CM. 99. 99CMU4122	1611	-C	-C	-G	-A	-CT	-T
O. FR. 92. VAU	1689	-C	-C	-G	-A	-CT	-T
DO. FR. 08. RBF208	1587	-C	-C	-G	-A	-CT	-T
O. SN. 99. 99SE MP1299	2179	-C	-C	-G	-A	-CT	-T
O. US. x. T. 2478B	2182	-C	-C	-G	-A	-CT	-T
O. US. 97. 97US08692A	1617	-C	-C	-G	-A	-CT	-T
O. US. 99. 99USTWLA	1600	-C	-C	-G	-A	-CT	-T
P. FR. 09. RBF168	2162	-C	-C	-G	-A	-CT	-T
CPZ. CD. 90. ANT	1553	-C	-C	-G	-A	-CT	-T
CPZ. CM. 05. SIVcpzMT145	1659	-C	-C	-G	-A	-CT	-T
CPZ. GA. 88. GAB1	2181	-C	-C	-G	-A	-CT	-T
CPZ. TZ. 00. TAN1	1770	-C	-C	-G	-A	-CT	-T
CPZ. US. 85. US_Marilyn	2175	-C	-C	-G	-A	-CT	-T

[illegible]

Alignments

HIV-1/SIVcpz Complete Genomes

[illegible]

Alignments

HIV-1/SIV cpz Complete Genomes

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L L D T G A D D T V L E E M S L P G R W K P K M I G G I G G F I K V R Q Y D Q I L I E I C G H K A I G T V L V	
B. FR. 83. HXB2	
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A. CD. 02. 02CD KTB035	-T- A-A-G- T- -G- 2478
A. SN. 01. DDJ369	-T- A-A-G- -G- C- 1685
A1. AU. 03. PS1044_Day0	-T- A-A-G- -G- -G- 1692
A1. CY. 06. CY171	-T- A-A-G- -C- T- -G- 1689
A1. GE. 99. 99GEMZ011	-T- A-A-G- -G- -G- 1668
A1. IT. 02. 60809	-T- A-A-G- -G- -G- 2489
A1. KE. 02. ML1990	-T- A-A-G- -G- -G- 1807
A1. RU. 08. PokA1Ru	-T- A-A-G- -G- -G- 1987
A1. RW. 93. 93RW037A	-T- A-A-G- -G- -G- 2477
A1. SE. 95. SE8538	-T- A-A-G- -G- -G- 1683
A1. TZ. 01. A341	-T- A-A-G- -G- -G- 1686
A1. UA. 01. 01UADN139	-T- A-A-G- -G- -G- 1683
A1. UG. 99. 99UGA07072	-T- A-A-G- -G- -G- 1683
A1. ZA. 04. 04ZASK162B1	-T- A-A-G- -G- -G- 1925
A2. CD. 97. 97CDKT848	-T- A-A-GG- A- C- -G- 1822
A2. CY. 94. 94CY017_41	-T- A-A-GG- -C- C- -G- 1841
B. AR. 04. 04AR143170	-T- A-A-G- -G- -G- 1683
B. AU. 04. PS1038_Day174	-T- A-A-G- -G- -G- 1695
B. BO. 99. BOL0122	-T- A-A-G- -G- -G- 1704
B. BR. 05. BREPM1081	-T- A-A-G- -G- -G- 1988
B. CA. 97. CANB3FULL	-T- A-A-G- -G- -G- 1773
B. CN. 05. 05CNHB_hp3	-T- A-A-G- -G- -G- 2483
B. CO. 01. PCW001	-T- A-A-G- -G- -G- 1689
B. CU. 99. Cu19	-T- A-A-G- -G- -G- 2031
B. CY. 06. CY165	-T- A-A-G- -G- -G- 1743
B. DE. 86. D31	-T- A-A-G- -G- -G- 2030
B. DK. 04. PMVL_012	-T- A-A-G- -G- -G- 1851
B. DO. 05. 05DO_160884	-T- A-A-G- -G- -G- 1695
B. EC. 89. EC093	-T- A-A-G- -G- -G- 1609
B. ES. 07. X2231	-T- A-A-G- -G- -G- 1947
B. FR. 92. 92FR_BX08	-T- A-A-G- -G- -G- 1692
B. GA. 88. OYI	-T- A-A-G- -G- -G- 2027
B. GB. 86. GB8_46R	-T- A-A-G- -G- -G- 1504
B. GE. 03. 03GEMZ004	-T- A-A-G- -G- -G- 1680
B. HT. 05. 05HT_129389	-T- A-A-G- -G- -G- 1685
B. IN. x. 11807	-T- A-A-G- -G- -G- 1831
B. JM. 05. 05JM_KJ108	-T- A-A-G- -G- -G- 1692
B. JP. 05. DR6538	-T- A-A-G- -G- -G- 2488
B. KR. 04. 04KRM5	-T- A-A-G- -G- -G- 1682
B. MM. 99. mSTD101	-T- A-A-G- -G- -G- 1871
B. NL. 00. 671_00T36	-T- A-A-G- -G- -G- 2049
B. RU. 04. 04RU128005	-T- A-A-G- -G- -G- 1975
B. TH. 00. 00TH_C3198	-T- A-A-G- -G- -G- 1698
B. TT. 01. 01TT_CRC50069	-T- A-A-G- -G- -G- 1704
B. TW. 94. TWY5	-T- A-A-G- -G- -G- 2483
B. UA. 01. 01UAKV167	-T- A-A-G- -G- -G- 1710
B. US. 07. CR0027M	-T- A-A-G- -G- -G- 1736
B. UY. 01. 01UYTRA1179	-T- A-A-G- -G- -G- 1689
B. YE. 02. 02YE507	-T- A-A-G- -G- -G- 1701
B. ZA. 03. 03ZAPS045MB2	-T- A-A-G- -G- -G- 1916
C. AR. 01. ARG4006	-T- A-A-G- -G- -G- 1668
C. BR. 04. 04BR013	-T- A-A-G- -G- -G- 1948
C. BW. 00. 00BW07621	-T- A-A-G- -G- -G- 1837
C. CN. 98. YNRL9840	-T- A-A-G- -G- -G- 1668
C. CY. 05. CY040	-T- A-A-G- -G- -G- 1689
C. ES. 07. X2118_2	-T- A-A-G- -G- -G- 1900
C. ET. 02. 02ET_288	-T- A-A-G- -G- -G- 1686
C. GE. 03. 03GEMZ033	-T- A-A-G- -G- -G- 1665
C. IL. 98. 98IS002	-T- A-A-G- -G- -G- 1818
C. IN. 03. D24	-T- A-A-G- -G- -G- 2520
C. KE. 00. KER2010	-T- A-A-G- -G- -G- 1665
C. MM. 99. mDDU101_3	-T- A-A-G- -G- -G- 1835
C. MW. 93. 93MW_965	-T- A-A-G- -G- -G- 1671
C. SN. 90. 90SE_364	-T- A-A-G- -G- -G- 1653
C. SO. 89. 89SM_145	-T- A-A-G- -G- -G- 1705
C. TZ. 02. C0178	-T- A-A-G- -G- -G- 1665
C. US. 98. 98US_MSC3018	-T- A-A-G- -G- -G- 1659
C. UY. 01. TRA3011	-T- A-A-G- -G- -G- 1656
C. YE. 02. 02YE511	-T- A-A-G- -G- -G- 1659
C. ZA. 05. 05ZAPS240B1	-T- A-A-G- -G- -G- 1888
C. ZM. 02. 02ZM108	-T- A-A-G- -G- -G- 2453
D. CD. 83. ELT	-T- A-A-G- -G- -G- 2030
D. CM. 01. 01CM_0009BBY	-T- A-A-G- -G- -G- 1683
D. CY. 06. CY163	-T- A-A-G- -G- -G- 1692
D. KE. 97. ML415_2	-T- A-A-G- -G- -G- 1950
D. KR. 04. 04KBH8	-T- A-A-G- -G- -G- 2443
D. SN. x. SE365	-T- A-A-G- -G- -G- 2501
D. TD. 99. MN011	-T- A-A-G- -G- -G- 1708
D. TZ. 01. A280	-T- A-A-G- -G- -G- 1685
D. UG. 99. 99UGK09958	-T- A-A-G- -G- -G- 1683
D. YE. 02. 02YE516	-T- A-A-G- -G- -G- 1695
D. ZA. 90. R1	-T- A-A-G- -G- -G- 1830
F1. A0. 06. A0_06_ANG125	-T- A-A-G- -G- -G- 1587
F1. AR. 02. ARE933	-T- A-A-G- -G- -G- 1778
F1. BE. 93. V1850	-T- A-A-G- -G- -G- 1821
F1. BR. 07. 07BR844	-T- A-A-G- -G- -G- 2265
F1. ES. x. P1146	-T- A-A-G- -G- -G- 1761
F1. FI. 93. FIN9363	-T- A-A-G- -G- -G- 1813
F1. FR. 96. 96FR_MP411	-T- A-A-G- -G- -G- 1686
F1. JP. 04. DR6082	-T- A-A-G- -G- -G- 2457
F1. RO. 96. BCI_R07	-T- A-A-G- -G- -G- 5008
F1. RU. 08. D88_845	-T- A-A-G- -G- -G- 1943
F2. CM. 97. CM53657	-T- A-A-G- -G- -G- 1674
G. BE. 96. DRICBL	-T- A-A-G- -G- -G- 2448
G. CM. 04. 178_15	-T- A-A-G- -G- -G- 2005
G. CU. 99. Cu74	-T- A-A-G- -G- -G- 2088
G. ES. 05. P962	-T- A-A-G- -G- -G- 1967
G. GH. 03. 03GH175G	-T- A-A-G- -G- -G- 2524
G. KE. 93. HH8793_12_1	-T- A-A-G- -G- -G- 1885
G. NG. 01. 01NGPL8669	-T- A-A-G- -G- -G- 1689
G. PT. x. PT2695	-T- A-A-G- -G- -G- 2426
G. SE. 93. SE6165	-T- A-A-G- -G- -G- 1881

[illegible]

Pol Protease end_Pol p66 and p51 RT start

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 AC - - - - - A - - - - - G - A - C - - - - - G - - - - - T - - - - - G - - - - - C - - - - - G - - - - - C - - - - - A - - - - - G - - - - - T - - - - - 2026
 AC - - - - - A - - - - - G - A - C - - - - - G - - - - - T - - - - - G - - - - - C - - - - - G - - - - - C - - - - - A - - - - - G - - - - - T - - - - - 2076
 AC - - - - - A - - - - - A - G - - - - - G - - - - - T - - - - - T - - - - - G - - - - - C - - - - - A - - - - - G - - - - - T - - - - - 2008
 AC - - - - - TG - - - - - A - - - - - T - - - - - T - - - - - G - - - - - G - - - - - C - - - - - A - - - - - G - - - - - C - - - - - 2020
 AC T - - - - - GAT - A - - - - - A - - - - - G - - - - - G - - - - - G - - - - - G - - - - - C - - - - - A - - - - - G - - - - - C - - - - - 2259
 AC C - - - - - C - - - - - A - - - - - A - - - - - G - - - - - G - - - - - G - - - - - G - - - - - G - - - - - C - - - - - A - - - - - G - - - - - C - - - - - 2169
 AC G - - - - - TT - A - - - - - A - - - - - G - - - - - A - - - - - A - - - - - G - - - - - G - - - - - C - - - - - A - - - - - G - - - - - C - - - - - 2845
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 AC C - - - - - G - - - - - A - - - - - A - - - - - G - - - - - G - - - - - A - - - - - T - - - - - G - - - - - A - - - - - G - - - - - C - - - - - 2193
 AC C - - - - - G - - - - - A - - - - - A - - - - - G - - - - - T - - - - - G - - - - - T - - - - - A - - - - - G - - - - - C - - - - - A - - - - - G - - - - - 2018
 AC - - - - - A - - - - - A - - - - - A - - - - - G - - - - - T - - - - - G - - - - - T - - - - - A - - - - - G - - - - - C - - - - - A - - - - - T - - - - - 2017
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 AC C - - - - - AG - - - - - A - 2047
 AC G - A - - - - - C - - - - - C - G - - - - - A - - - - - T - - - - - C - - - - - C - - - - - C - - - - - C - - - - - A - - - - - G - - - - - T - - - - - 2187
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[illegible]

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26 AU.CD.02.02CD MBT0047
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29 BF.BR.01.BREPM16704
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CPZ.US.85.UY Marilyn

[illegible]

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A.CD.02.02CD.KTB035	-A	A	3155
A.SN.01.D0J369	-A-A	G-W-G-K-V-G-S-P-A-I-F	2362
A1.AU.03.PS1044.Day0	-A	A	2369
A1.CY.06.CY171	-A	A	2366
A1.GE.99.99GEMZ011	-A	A	2345
A1.IT.02.60060		C	3166
A1.KE.02.ML1990		C	2484
A1.RU.08.PokaIRu	-C	A	2664
A1.RW.93.93RW037A		G-T	3154
A1.SE.95.SE8538		G	2360
A1.TZ.01.A341	-A	A	2363
A1.UA.01.01UADN139	-A	A	2360
A1.UG.99.99UGA07072		T	2360
A1.ZA.04.04ZASK162B1	-A	A	2602
A2.CD.97.97CDKTB48	-A	A	2499
A2.CY.94.94CY017_41	-A	A	2507
B.AR.04.04AR143170		R	2392
B.AU.04.PS1038.lay174		G	2381
B.BO.99.BOL0122		T	2381
B.BR.05.BREPMM1081	-C	A	2605
B.CA.97.CANB3FULL		T	2450
B-CN.05.05CNHB.hp3		T	3160
B.CO.01.PCM001		T	2466
B.CU.99.Cu19	-C	A	2708
B.CY.06.CY165	-C	A	2420
B.DE.86.D31		A	2707
B.DK.04.PMWL_012	-G	A	2528
B.DO.02.05DD_160884		G	2372
B.EC.89.EC003		T	2286
B.ES.07.X2231		G	2624
B.FR.92.92FR.BX08		T	2369
B.GA.88.OY1		G	2704
B.GB.86.GBB_46R		C	3181
B.GE.03.03GEMZ004	-G	A	2381
B-HT.05.05HT_129389	-K-W	A	2362
B.IN.x.11807		R	2508
B.JM.05.05JM.KJ108		G	2369
B.JP.05.DRE538		T	3165
B.KR.04.04KR05	-G	G	2339
B.MM.99.mSTD101		T	2551
B.NL.00.671_00T36	-A	A	2726
B.RU.04.04RU128005	-A	A	2652
B.TH.00.00TH.L198	-C	A	2375
B.TT.01.01TT_CRC50069	-C-T	A	2381
B.TW.94.TWCYS	-C	A	3160
B-UA.01.01UAKV167	-G	A	2387
B.US.07.CR0027M	-G	A	2413
B.UY.01.01UYTRA1179	-G	A	2366
B.YE.02.02YES01	-A	A	2378
B.ZA.03.03ZAP5045MB2	-A	A	2593
C.AR.01.ARG4006		T-G	2345
C.BR.04.04BR013	-T	A	2625
C.BW.00.00BW07621		G	2514
C-CN.98.YNRL9840		G	2345
C.CY.05.CY040	-A	A	2466
C-ES.07.X2118_2	-A	A	2577
C-ET.02.02ET_288	-C	A	2363
C-GE.03.03GEMZ033	-A	A	2342
C-IL.98.98IS002	-A	A	2495
C-IN.03.D24		T	3197
C-KE.00.KER2010		G	2342
C-MM.99.mIDU101_3		T	2512
C-MW.93.93MW_965	-C	A	2348
C-SN.98.98SE_364		T	2330
C-SO.89.89SM_145		G	2382
C-TZ.02.C0178		T	2342
C-US.98.98US_MSC3018		G	2336
C-UY.01.TRA3011		T	2333
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F1-ES.x.PI146		T	2438
F1-FI.93.FIN9363		T	2490
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G-BE.96.DRCBL	-A	A	3118
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G-GH.03.03GH175G	-C	A	3201
G-KE.93.HH8793_12_1		T	2562
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G-SE.93.SE6165		T	2555

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 16 A2D. KR. 97. 97KR004
 17 BF. AR. 99. ARMA038
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 19 cpx. CU. 99. CU7
 20 BG. CU. 99. CU103
 21 A2D. KE. 99. KER2003
 22 01A1. CM. 01. 01CM 0001BBY
 23 BG. CU. 03. CB118
 24 BG. CU. 03. CB378
 25 cpx. CM. 02. 1918LE
 26 AU. CD. 02. 02CD MBT047
 27 cpx. FR. 04. 04CD FR K25
 28 BF. BR. 99. BREPM12609
 29 BF. BR. 01. BREPM16704
 31 BC. BR. 04. 04BR142
 32 06A1. EE. 01. EE0369
 33 01B. MY. 05. 05MYK007 1
 34 01B. TH. 99. 09R2478P
 35 AD. AF. 05. 05AF095
 36 cpx. CM. 00. 00CMNYU830
 37 cpx. CM. 00. 00CMNYU926
 38 BF1. UY. 03. UY03 3389
 39 BF. BR. 04. 04BRJ179
 40 BF. BR. 05. 05BRJ055
 42 BF. LU. 03. 1uBF 05 03
 43 02G. SA. 03. J11223
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T-G.....C.....T-A-A-T-C-T.....A-G-G.....A- 2485
G-A.....C.....G.....T-A-G-T-C.....A-G.....A- 2508
G.....C.....G.....T-A-G-T-C.....A-G.....A- 2579
 -A-A.....GT.....A-A.....GC-A-C.....AG.....C-G.....T-G.....AA.....AG.....A- 2585
 -A-A.....T-GT.....A-A.....G-AG-C-A.....C-G.....G.....AA.....G.....A- 2475
 -A-A.....T-T.....C.....GGA-T.....T-G-T-A-C.....A-C-G.....A-G.....A- 2476
 -A-A.....CA.....C.....T-A.....A-G-T-A-C.....A-C-G.....A-C.....A- 2357
 -G.....G.....A-A-GC-A.....A-A.....C.....T.....A- 3110
 -A-A.....T-GT.....C.....G-A.....G-G.....C.....T.....C-GT.....A- 2360
 -G.....G.....A-C.....GC-A-C.....A-A.....C.....A.....C-GT.....T..... 2523
 -G.....G.....C.....A-C-A.....A-G.....C.....T.....C-G.....C-G..... 3173
 -G.....G.....C.....T-A.....A-G.....C.....T.....C-G.....C-G..... 3113
 -G.....G.....C.....T-A.....A-G.....C.....T.....C-A.....T.....C-G..... 2366
 -G.....G.....C.....T-A.....A-G.....C.....T.....C-A.....T.....C-G..... 2416
T-GGC.....C.....C-AG.....GG-G-A-T-C-T.....A.....C-G-AA.....G-G.....A- 2348
T-GGCA.....C.....C-A.....G-G-G-C-T.....A.....G-A.....G.....A- 2360
T-GGCA.....C.....C-A.....G-G-G-C-T.....A.....G-A.....G.....A- 2599
T-GGCA.....C.....C-A.....G-G-G-C-T.....A.....G-A.....G.....A- 2509
 -A-A.....C-T.....C.....C-C-C-A-C.....G-G-A-C-T.....A.....G-A.....G.....A- 3185
 -A-A.....T-GGCA.....C.....C-C-C-A-C.....G-G-G-C-T.....A.....G-A.....G.....C- 3156
T-GGCA-T.....C.....C-AGT-C.....G-G-G-C-T.....A.....G-A.....G..... 2345
T-GGCG.....C.....C-A.....G-G-G-C-T.....A.....A.....G-A.....G..... 2533
T-GGCA.....C.....C-A.....AT-G-A-C-T.....A.....G.....G.....G..... 2558
T-GGCA.....C.....C-A.....G-G-G-C-T.....A.....G.....G.....G..... 2357
T-GGCA.....C.....C-A.....G-G-G-C-T.....A.....G.....G.....G..... 2351
T.....G.....G.....G.....G.....G.....G.....G.....G.....A- 2387
C.....T.....C.....TTCA-C.....A-C-A-C-T.....G.....A.....G.....A- 2527
T.....C.....AG.....C.....A-A-GG.....A- 2543
 -A-A.....T-G.....T.....C.....T-A-C.....A-G-C.....A-G.....G.....A-G.....A- 3189
 -A-A.....T.....C.....T.....G.....A.....G.....A- 2493
 -A-A.....G.....C.....T-A.....A-C.....G.....A.....G.....A- 2501
 -A-A.....G.....C.....T-A.....A-C.....G.....A.....G.....A- 2363
 -A-A.....G.....C.....T-A.....A-C.....G.....A.....G.....A- 2540
 -A-A.....T-T-G.....C-A-A-C.....C-A-A-G.....C.....G.....A-A-GA-GG-A- 2525
 -G-A-C.....C.....G.....G.....G.....T.....T.....G.....GA-GG.....A- 3166
 -G-A-C.....GT.....G-A-A-C-A-C.....A-G-T.....CC-A-G.....G.....G.....A- 2566
 -G-A-C.....T.....A-C-A-A-G-C-T.....C-A.....G.....G.....A- 2599
 -G-A-C.....GT.....C.....A-G.....A-G.....C.....T.....C.....T.....C.....A- 2560
 -A-A.....G-C.....C.....G.....C.....T-G.....T.....T.....C.....A- 2524
C.....C.....G.....A-A-C.....A-G.....A.....G.....A.....A- 2375
G.....T.....C.....A.....A-C.....A.....G.....A.....A- 2466
G.....T.....C.....A.....A-C.....A.....G.....A.....A- 2387
G.....T.....C.....A.....A-C.....A.....G.....A.....A- 2627
G.....G.....G.....C.....GC-A.....A-G.....C.....A.....T.....A.....T.....C.....A- 2366
G.....T.....C.....A.....AT-T.....A.....T.....T.....G.....G.....C.....A- 2369
G.....T.....C.....A.....A-T.....A.....T.....A.....G.....G.....A- 2604
 -G-A-C.....T-G-C.....T-G-A-C-GGC-A.....A.....C.....C.....G.....G.....A- 2586
 -A-A.....T-G.....A-C-GGC-G.....A.....C.....C.....G.....G.....G.....G..... 3166
 -A-A.....GT.....A-A-C-C-A.....A.....G.....C.....G.....G.....G.....G..... 3152
C.....G.....A.....A.....A.....A.....A.....A.....A.....A.....A- 2527
C.....G.....A.....A.....A.....A.....A.....A.....A.....A.....A- 2562
T-G.....T.....C.....A-G-G.....A.....G.....A.....A.....GT.....A- 2633
 -G-A.....G.....C.....T-A.....A-G-C-T.....C.....T.....C.....T.....A- 2796
GT.....C.....A.....G.....G.....T.....C.....T.....A-T.....T.....A- 2540
 -A-A.....G.....G.....A.....A.....G.....T.....C.....T.....A-T.....T.....A- 2363
T-GGC.....C.....C-A.....G-G-T-C-T.....A.....C.....G.....G.....A- 2354
 -G-G.....GT.....C.....GGC.....A.....C.....T.....A.....A.....A.....G.....A- 2366
C-T.....C.....G.....A.....G.....G.....G.....A.....A.....A.....G.....A- 2351
C-T.....C.....G.....A.....G.....G.....G.....A.....A.....A.....G.....A- 2584
C-T.....C.....G.....A.....G.....G.....G.....A.....A.....A.....G.....A- 2638
 -A-A.....T-T.....T-C-C-GC-A.....AT.....C.....G.....G.....A.....A- 2644
 -A-A.....Y-C-T.....R-Y.....A.....A.....R.....T.....T.....A- 2699
 -G-A.....T-G.....A-C-C-A.....A-G-C-G-G.....A.....C-A.....A- 2686
 -G-A-C.....G.....T-G-CA.....TC-A-A-C-G-GA-C.....G-A-C-T-C-G.....CC-C-G.....C-CA-A-GAGG-G-A-C- 2755
 -T-A-A-G.....G.....T-TCA.....T-A-A-G-GA-C.....G-A-C-T-G.....CC-C-G.....C-CA-A-GAG-G-A- 2753
 -T-A-G.....G.....T-TCA.....T-A-A-G-GA-C.....G-A-C-T-G.....CC-C-G.....C-CA-A-GAG-G-A- 2667
 -T-A-G.....G.....T-TCA.....T-A-A-G-GA-C.....G-A-C-T-G.....CC-C-G.....C-CA-A-GAG-G-A- 2666
 -C-C-G-A.....T.....TCA.....TC-T-A-C-G-G-G-C-C.....AT-AA-T-G-G.....CC-A-A-T-CCCC-GACAG-A-A-GG-T-ATT- 3215
 -C-C-G-A-G.....C.....T-G-TCA.....T-G-TCA.....T-A-A-G-GC-C.....A-AA-T-G.....CC-A-A-T-CC-T-ACAG-A-A-GG-ATT- 3214
 -C-C-G-A-G.....C.....T-G-TCA.....T-G-TCA.....T-A-A-G-GC-C.....A-AA-T-G.....CC-A-A-T-CC-T-G-CAG-A-A-GG-GC-ATT- 3190
 -C-C-A.....G.....T.....TCA.....TC-T-A-C-G-G-C-C.....GT-AA-T-G-G.....C-A-A-T-CCCT-GACAG-A-A-GAG-GG-T-ATT- 2651
 -C-C-A.....G.....T.....TCA.....TC-T-A-C-G-G-C-C.....GT-AA-T-G-G.....C-A-A-T-CCCT-G-CAG-A-A-GAG-GG-T-ATCA- 2553
 -C-C-A.....G.....T.....TCA.....TC-T-A-C-G-G-C-C.....GT-AA-T-G-G.....C-A-A-T-CCCT-GACAG-A-A-GAG-GG-T-ATT- 2647
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 -T-C-A.....T-T.....TCA.....TC-T-A-C-G-G-C-C.....AT-AA-T-G.....CC-A-A-T-CC-C-G-CAG-A-A-GAG-GG-T-ACTA- 2727
 -C-C-G-A.....G.....T.....TCA.....T-T-A-G-G-C-C.....AT-AA-T-G-G.....CC-A-A-T-CCCC-GACAG-A-A-GAG-GG-T-ATT- 2622
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 -C-C-G-A.....T.....TCA-T-G-TCA.....T-A-G-G-C-C.....AT-CAA-T-G.....CC-A-A-T-CCCT-GACAG-A-A-GAG-GG-T-ATT- 2612
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[illegible]

B.FR.83.HXB2
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11 cpx .CM .95.95CM 1816
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13 CM .CN .96.96CM 1849
14 BG .ES .00.X605
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16 01B .KR .97.97KR004
17 BF .AR .99.ARMA038
18 cpx .CU .99.CU76
19 cpx .CU .99.CU
20 BG .CU .99.CU103
21 ADZ .KE .99.KER2003
22 01A1.CM .01.01CM 0001B
23 BG .CU .03.CB118
24 BG .CU .03.CB378
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29 BF .BR .01.BREPM16704
30 BF .BR .00.04BR142
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O.US .x.I 2478B
O.US .97.97US08692A
O.US .99.99USTWLA
P.FR .09.RBF168
CPZ .CD .90.ANT
CPZ .CM .95.SIVcpzMT145
CPZ .CN .98.GAB1
CPZ .TZ .00.TANI
CPZ .US .85.US Marilyn

[illegible]

[illegible]

65

[illegible]

HIV-1/SIV cpz Complete Genomes

Alignments

HIV-1/SIV cpz Complete Genomes

HIV-1/SIVcpz
Complete Genomes

[illegible]

B. FR. 83. HXB2
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H. BE. 93. VI091
H. BE. 93. VI097
H. CF. 96. 056
H. GB. 00. 00GBCA4001
J. CD. 97. J 97DC KTB147
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J. SE. 94. SE9173 7022
K. CD. 97. 97ZR EDTB11
K. CM. 96. 96CM MP535
01 AE. CF. 90. 90CF11697
01 AE. CM. 97. 97SCW045
01 AE. BA. 04. HK001
01 AE. JP. x. DR042
01 AE. TH. 04. 8KM
01 AE. US. 00. 00US MSC1164
01 AE. VN. 98. 98VNN150
02 AG. CM. 02. 02CM 0013BBY
02 AG. FR. 91. 91F010 01
02 AG. ES. 96. P1261
02 AG. FR. 91. DJ263
02 AG. GH. 03. 03GHI81AG
02 AG. LR. x. POC44951
02 AG. IT. 01. 01F010 01
02 AG. SE. 94. SE7812
02 AG. SN. 98. 98SE MP1211
02 AG. US. 00. 00US MSC3083
02 AG. UZ. 02. 02UZ06683
03 AB. RU. 97. KAL153 2
04 cpv. CY. 94. 94CY032 3
05 DF. BE. x. VI1130
06 cpv. AU. 96. BFP90
07 BC. CN. 98. 98CNC09
08 BC. CN. 97. 97CNC67 6F
09 cpv. GH. 96. 96GHI2911
10 CD. TZ. 96. 96TZ BF061
11 cpv. CM. 95. 95CM 1816
12 BF. AR. 99. ARMA159
13 cpv. CM. 96. 96CM 1849
14 BG. ES. 00. X605
15 01B. TH. 99. 99TH MU2079
16 AZD. KR. 97. 97KRA04
17 BF. AR. 99. ARMA038
18 cpv. CU. 99. CU76
19 cpv. CU. 99. CU77
20 BG. CU. 99. CU103
21 AZD. KE. 99. KER2003
22 01A. CM. 01. 01CM 0001BBY
23 BG. CU. 03. CB178
24 BG. CU. 03. CB38
25 cpv. CM. 02. 1918LE
26 AU. CD. 02. 02CD MBT0047
27 cpv. FR. 04. 04CD FR. KZ5
28 BF. BR. 99. BREPM12609
29 BF. BR. 01. BREPM16704
31 BC. BR. 04. 04BR1242
32 AE. BR. 01. E03669
33 01B. MY. 05. 05MYK1007. 1
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35 AD. AF. 05. 05AF095
36 cpv. CM. 00. 00CMNYU830
37 cpv. CM. 00. 00CMNYU926
38 BF1. UY. 03. UY03 3389
39 BF. BR. 04. 04BRJR175
40 BF. BR. 05. 05BRBR1095
42 BF. LU. 03. LuBf 05_03
43 02G. SA. 03. J11223
N. CM. 95. YBF30
N. CM. 97. YBF106
N. CM. 02. DJ0071
N. CM. 04. 04CM 0115_04
O. BE. 87. AN770
O. CM. x. BCF66
O. CM. 91. MVP5180
O. CM. 96. 96CMA102
O. CM. 97. 97CMA8B447
O. CM. 98. 98CMA102
O. CM. 99. 99CMU4122
O. FR. 92. VAU
O. DR. 08. RBF208
O. SN. 99. 99SE MP1299
O. US. x. I 24788
O. US. 97. 97US08692A
O. US. 99. 99USUTLWA
P. FR. 09. RBF168
CPZ. CD. 00. ANT
CPZ. CD. 95. SITcpvMT145
CPZ. CD. 98. GAD1
CPZ. TZ. 00. TAN1
CPZ. US. 85. US Marilyn

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FR. 83. HXB2
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H.BE. 93. VI991
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H.CF. 90. 056
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J.S. 93. SE9280 7887
J.S. 93. SE9173 7022
K.C.D. 97. 97ZTR EOTB11
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01 AE. CF. 89. 90CF11697
01 AE. CN. 87. 87J5WXX045
01 AE. HK. 04. HK001
01 AE. JP. x. DR0492
01 AE. TH. 04. BKM
01 AE. TH. 98. 98THM55 MSC1164
01 AE. CN. 98. 98VNNDD15
02 AG. CM. 02. 02CM 0013BBY
02 AG. CY. 05. CY048
02 AE. ES. 06. P1261
02 AG. FR. 91. DJ263
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02 AG. NG. 01. PL0710
02 AG. SE. 94. SE7812
02 AG. SN. 98. 98SE MP1211
02 AG. US. 00. 000US MSC3083
02 AG. UZ. 02. 02UZ0663
03 AB. RU. 97. KAL153 2
04 cpx. CY. 94. 94CY032 3
05 DF. BE. x. VF1130
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08 BC. CN. 97. 97CNGX 6F
09 cpx. GH. 96. 96GH2911
10 CM. TZ. 96. 96TZ BF061
11 cpx. CM. 95. 95CM 1816
12 BF. AR. 99. ARMA159
13 cpx. CM. 96. 96CM 1849
14 BG. ES. 00. X605
15 01B. TH. 99. 99TH MU2079
16 AZD. KR. 97. 97KR004
17 BF. AR. 99. ARMA038
18 cpx. CU. 99. CU76
19 cpx. CU. 99. CU7
20 BG. CU. 99. CU103
21 AZD. KE. 99. KER2003
22 01A. CM. 01. 01CM 0001BBY
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24 BG. CU. 03. CB378
25 AU. CM. 02. 1918LE
26 AU. CD. 02. 02CD MBT0847
27 cpx. FR. 04. 04CD FR. KZ5.
28 BF. BR. 99. BREPM12609
29 BF. BR. 01. BREPM16704
31 BC. BR. 04. 04BR142
32 01B. ME. 01. EE0369
33 01B. ME. 05. 05MYK1007. 1
34 01B. TH. 99. OUR2478P
35 AD. AF. 05. 05AF095
36 cpx. CM. 00. 00CMNYU830
37 cpx. CM. 00. 00CMNYU926
38 BF1. UY. 03. UY03 3389
39 BF. BR. 04. 04BRJR175
40 BF. BR. 05. 05BRJR105
42 BF. LU. 03. LuBf 05_03
43 BG. SA. 03. J11223
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N.CM. 97. YBF106
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N.CM. 04. 04CM 0015 04
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O.CM. 97. 97CMA8B447
O.CM. 98. 98CMA104
O.CM. 99. 99CMA1122
O.FR. 92. VAU
O.DN. 88. RBF208
O.SN. 99. 99SE MP1299
O.US. x. I 24788
O.US. 97. 97US08692A
O.US. 99. 99USTWLA
P.FR. 09. RBF168
CPZ. CD. 90. ANT
CPZ. CM. 85. SV1cpxMT145
CPZ. GA. 88. GAB
CPZ. Z. 00. TAN1
CPZ. US. 85. PU5 Marilyn

[illegible]

[illegible]

Alignments

HIV-1/SIVcpz Complete Genomes

[illegible]

Pol. 83. HXB2	GCAGGATTTGGGGATAGAAGTAAATAGTAACAGCTCACAATATGCATTAGGAATCATTC	CAAGCAACAGATCAAGGTGAATCAGAGTTAGTCAATCAAAATAAGACAGTAAATAAAAAAGGAAAGVCTTCT	TGGCATGGGTACGACACACAAGGAATTG	4176
A. CD. 02. 02CD KTB035	A - A - A - A - T - G - G - G - CAGG - G - A - C - G - A - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4170
A. SN. 01. DDJ369	A - A - A - C - T - G - G - G - CAGG - A - A - C - G - G - A - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3377
A1. AU. 03. PS1044 Day0	A - A - A - C - G - G - G - CAG - A - A - T - G - A - AC - GG - A - C - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3384
A1. CY. 06. CY171	A - A - A - C - T - G - G - G - CAGT - A - A - A - A - AC - G - A - GA - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3381
A1. GE. 99. 99GEMZ011	A - A - A - C - T - G - G - G - CAGG - G - G - G - A - AC - G - A - GA - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3360
A1. IT. 02. 60900	A - A - A - C - T - G - G - G - CAG - A - A - A - A - AC - G - A - GA - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4181
A1. KE. 02. ML1999	A - A - A - C - T - G - G - G - CAG - A - A - A - A - AC - G - A - GA - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4199
A1. RU. 08. Poka1Ru	A - A - A - C - T - G - G - G - CAGG - A - A - A - A - AC - G - A - GA - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3679
A1. RW. 93. 93RW037A	A - A - A - C - G - T - G - G - G - CAG - A - A - C - A - AC - GG - C - A - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4169
A1. SE. 95. SE5838	A - A - A - C - G - T - G - G - G - CAGC - A - A - A - A - AC - GG - C - A - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3375
A1. TZ. 01. A341	A - A - A - C - T - G - G - G - CAG - A - A - A - A - AC - GG - C - A - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3375
A1. UA. 01. 01UADN139	A - A - A - C - T - G - G - G - CAG - A - A - A - A - AC - GG - C - A - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3375
A1. UC. 99. 99UGA07072	A - A - A - C - T - G - G - G - CAG - A - A - A - A - AC - GG - C - A - A - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3375
A1. ZA. 04. 04ZASK162B1	A - A - A - C - T - G - G - G - CAGG - G - A - A - A - AC - G - A - G - C - T - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3617
A2. CD. 97. 97CDKT848	A - A - A - G - C - T - G - G - G - AGC - A - A - A - A - AC - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3511
A2. CY. 94. 94CY017 41	A - A - A - G - G - T - G - G - G - AAGG - A - A - A - A - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3553
B. AR. 04. 04AR143170	A - A - A - A - T - G - G - G - AGG - G - G - G - G - G - C - A - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3387
B. AU. 04. PS1038 Day174	A - A - A - C - C - M - AGG - A - G - G - A - A - C - A - A - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3396
B. BO. 99. BOL0122	A - A - A - C - C - GG - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3680
B. BR. 05. BREPM1081	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3465
B. CA. 97. CANB3FULL	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4175
B. CN. 05. 05CNHB hp3	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3381
B. CO. 01. PCN001	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3723
B. CU. 99. CU19	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3435
B. CY. 06. CY165	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3435
B. DE. 86. D31	A - A - A - T - A - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3722
B. DK. 04. PMVL 012	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3543
B. DO. 05. 05DO 160884	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3387
B. EC. 89. EC003	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3301
B. ES. 07. X2231	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3639
B. FR. 92. 92FR BX08	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3384
B. GA. 88. OY1	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3719
B. GB. 86. G88 46R	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4196
B. GE. 03. 03GEMZ004	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3372
B. HT. 05. 05HT 129389	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3639
B. IN. x. 11807	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3377
B. JM. 05. 05JM KJ108	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3523
B. JP. 05. DR6538	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3384
B. KR. 04. 04KWS	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4180
B. MM. 99. mSTD101	A - A - A - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3566
B. NL. 00. 671 00T36	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3667
B. RU. 04. 04RU128005	A - A - A - C - T - G - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3390
B. TH. 00. 00TH 8198	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3396
B. TT. 01. 01TT CRC50069	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4176
B. TW. 94. TWCYS	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3402
B. UA. 01. 01UAKV167	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3428
B. US. 07. CR0027M	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3391
B. UY. 01. 01UYTRA1179	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3608
B. YE. 02. 02YES9	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3360
B. ZA. 03. 03ZAPS045MB2	A - A - A - C - G - AG - G - G - T - A - A - C - C - G - C - A - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3640
C. AR. 01. ARG4006	A - A - A - A - G - G - G - T - G - G - C - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3529
C. BR. 04. 04BR013	A - A - A - C - C - G - G - G - C - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3360
C. BW. 00. 00BW07621	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3381
C. CN. 98. YNRL9840	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3392
C. CS. 05. CY040	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3378
C. CS. 07. X2118 2	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3357
C. ET. 02. 02ET 288	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3510
C. GE. 03. 03GEMZ033	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3357
C. IL. 98. 98IS002	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3510
C. IN. 03. D24	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3357
C. KE. 00. KER2010	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3527
C. MM. 99. mIDU101 3	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3363
C. MW. 93. 93MW 965	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3345
C. SN. 98. 98SE 364	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3397
C. SO. 89. 89SM 145	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3357
C. SZ. 02. C0178	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3351
C. US. 98. 98US MSC3018	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3348
C. UY. 01. TRA3011	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3351
C. YE. 02. 02YES17	A - A - A - C - C - T - G - G - G - G - G - G - G - G - G - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3351
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D. CD. 83. ELT	A - A - A - G - C - T - G - G - G - AG - G - A - G - G - T - C - A - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3722
D. CM. 01. 01CM 0009BBY	A - A - A - G - C - T - G - G - G - AG - G - A - G - G - T - C - A - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3375
D. CY. 06. CY163	A - A - A - C - C - G - G - G - T - A - G - G - G - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3384
D. KE. 97. ML415 2	A - A - A - C - C - G - G - G - T - A - G - G - G - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3642
D. KR. 04. 04KRBH	A - A - A - C - C - G - G - G - T - A - G - G - G - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		4135
D. SN. x. SE365	A - A - A - C - C - G - G - G - T - A - G - G - G - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3383
D. TD. 99. MN011	A - A - A - C - C - G - G - G - T - A - G - G - G - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3400
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D. YE. 02. 02YES16	A - A - A - C - C - G - G - G - T - A - G - G - G - G - G - C - AT - G - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3387
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F1. AR. 02. ARE933	A - A - A - C - C - G - G - G - T - G - G - G - G - G - A - C - G - C - T - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3470
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F1. BR. 07. 07BR844	A - A - A - C - C - G - G - G - T - G - G - G - G - G - A - C - G - C - T - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3957
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G. CU. 99. Cu74	A - A - A - C - C - G - G - G - T - G - G - G - G - G - A - C - G - C - T - G -	G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G - G -		3780
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Pol p66 RT, Pol p15 RNase H end, Pol p31 Integrase start

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HIV-1/SIVcpz Complete Genomes

HIV-1/SIVcpz
Complete Genomes

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02 AG.UZ.02.02UZ0683-----G-----C-G-C-----T-----A-----A-G-----A-T-----A-G-----C-----3906

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05 DF.BE.x.VI1310-----G-----C-A-A-----GTG-----C-A-----T-----A-G-A-AA-A-----AAAT--CA-A-----T-----4708

06 CPX.AU.96.BFP90-----A-G-----C-A-AC-----C-----GT-----A-----T-----A-A-G-A-A-A-----A-T--C-A-----G-----4012

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09 CPX.GH.96.96GH2911-----C-A-A-----GT-----A-----A-TA-AA-A-----A-AT--C-A-----G-C-----G-----4044

10 CD.TZ.96.96TZ.BF061-----A-----C-C-CA-AC-----G-----CC-----T-A-C-T-----A-A-----A-T--C-A-----C-----4685

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16 A2D.KR.97.97KR004-----C-CC-AC-----GT-----C-A-----CC-----A-G-A-A-A-A-T-----AAAT--T-CA-A-----C-----3985

17 BF.AR.99.ARMA038-----G-----C-GC-----C-----GGT-----C-A-----TCC-----A-C-G-A-AA-A-----AAATG-C-A-A-----G-----G-----3906

18 CPX.CU.99.CU76-----C-A-AC-----T-----G-----G-----GT-----A-----CC-----T-A-G-A-A-A-A-----AAAT--CA-A-----C-----4146

19 CPX.CU.99.CU7-----C-T-A-----GC-----GT-----A-----GCC-----T-A-AG-A-----C-----A-T-----A-----G-----T-----3885

20 BG.CU.99.CU103-----G-----C-A-AC-----G-----GT-----C-A-----T-----C-----A-C-G-A-G-AA-A-----A-A-----C-A-----T-----3888

21 A2D.KE.99.99KER2003-----C-A-AC-----T-----G-----G-----GT-----A-----Y-----CC-----T-A-G-A-A-A-A-----A-AT--CA-A-----C-----4123

22 01A1.CM.01.01CM.0001BBY-----C-A-AC-----T-----G-----G-----GT-----A-----CC-----T-A-G-A-A-A-A-----A-AT--CA-A-----C-----4105

23 BG.CU.03.CB118-----A-G-----C-A-AC-----T-----G-----GT-----A-----CC-----A-CG-----A-----A-T-----C-----3888

24 BG.CU.03.CB378-----A-G-----C-CA-AC-----GGGTGG-----A-----A-C-G-A-C-A-----AAAT--C-A-----4685

25 CPX.CM.02.1918LE-----C-C-A-----GT-----C-A-----A-G-AA-G-A-A-----A-TG-T-A-A-----G-----4671

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39 BF.BR.04.04BRJ179-----A-----C-C-CA-AC-----T-----A-----R-T-----Y-A-A-GT-----A-----C-----G-----C-----4218

40 BF.BR.05.05BRJ1055-----C-----C-A-A-----GT-----C-A-----C-----A-----G-A-A-A-A-----AA-TG-CA-A-----C-----4205

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O.BE.87.ANT70-----A-----G-----T-----C-----G-----C-----T-----TA-----T-----A-----ACCT-----T-AA-A-----CA-G-AA-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----C-----A-----4710

O.CM.x.BCF06-----A-----G-----T-----C-----G-----C-----T-----TA-----T-----A-----ACCT-----T-AA-A-----CA-G-AA-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----C-----A-----4710

O.CM.91.MVP5180-----A-----G-----T-----C-----G-----C-----T-----TA-----T-----A-----ACCT-----T-AA-A-----CA-G-AA-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----C-----A-----4710

O.CM.96.CMA182-----A-----G-----T-----C-----G-----C-----T-----TA-----T-----A-----ACCT-----T-AA-A-----CA-G-AA-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----C-----A-----4710

O.CM.97.97CMA8447-----A-----G-----T-----C-----G-----C-----T-----TA-----T-----A-----ACCT-----T-AA-A-----CA-G-AA-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----C-----A-----4710

O.CM.98.98CMA184-----A-----T-----C-----C-----G-----C-----C-----T-----T-----GT-----A-----C-----GCCT-----T-AA-A-----CA-G-AA-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----A-----4166

O.CM.99.99CMU4122-----A-----T-----C-----C-----G-----C-----C-----T-----T-----GT-----A-----C-----GCCT-----T-AA-A-----CA-G-AA-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----A-----4165

O.FR.92.VAU-----A-----T-----C-----C-----G-----C-----C-----T-----T-----GT-----A-----C-----GCCT-----T-AA-A-----AG-CA-G-AA-----T-A-----AAAC--AC-A-----T-----G-----A-----A-----T-----A-----G-----4246

DO.FR.08.RBF208-----A-----T-----C-----C-----G-----C-----C-----T-----T-----GGT-----A-----C-----GCCT-----T-AA-A-----CA-G-A-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----A-----4141

O.SN.99.99SE.MP1299-----T-----C-----C-----G-----C-----C-----T-----T-----GGT-----A-----C-----GCCT-----T-AA-A-----AG-CA-G-A-----T-A-----CAAC--AC-A-----T-----G-----A-----A-----T-----A-----4733

O.US.x.I.2478B-----T-----T-----C-----G-----C-----C-----T-----T-----GT-----A-----C-----GCCT-----T-AA-A-----TA-G-A-----T-A-----A-TAAC--AC-A-----T-----G-----A-----A-----T-----A-----4736

O.US.97.97US08692A-----T-----T-----C-----G-----C-----C-----T-----T-----GT-----A-----C-----GCCT-----T-AA-A-----TA-G-A-----T-A-----A-TAAC--AC-A-----T-----G-----A-----A-----T-----A-----4131

O.US.99.99USTWLA-----R-----T-----Y-----G-GC-C-----G-----C-----T-----GTG-----C-----A-----GCCT-----C-Y-----TA-Y-----G-A-----A-----AR-A-----CTTAAT--A-----CT-----T-----G-----G-----A-----G-----G-----4163

P.FR.09.RBF168-----A-AAGT-----C-----C-----G-----C-----C-----A-C-----G-----T-----C-----A-----AGCT-----T-AA-A-----AG-A-AA-A-----G-A-----TAAT--C-----A-----A-----C-----A-----4716

CPZ.CD.90.ANT-----A-----T-----C-----G-----C-----C-----T-----G-----T-----C-----A-----AGCT-----T-AA-A-----AG-A-AA-A-----G-A-----TAAT--C-----A-----A-----C-----A-----4119

CPZ.CM.05.SIVcpzMT145-----A-----T-----C-----G-----C-----C-----T-----G-----T-----C-----A-----AGCT-----T-AA-A-----AG-A-AA-A-----G-A-----TAAT--C-----A-----A-----C-----A-----4722

CPZ.GA.88.GAB1-----A-----T-----C-----G-----C-----C-----T-----G-----T-----C-----A-----AGCT-----T-AA-A-----AG-A-AA-A-----G-A-----TAAT--C-----A-----A-----C-----A-----4741

CPZ.TZ.00.TAN1-----AGA-----C-----T-----C-----CA-CC-----G-----G-----T-----G-----A-----A-----T-----ACCA-----T-AA-A-----AG-A-AA-A-----G-A-----ACA--TC-A-----T-----G-----A-----T-----T-----4741

CPZ.US.85.US.Marilyn-----A-----G-----C-----A-----C-----T-----GTG-----T-----T-----ATCT-----C-----T-----AA-AG-----A-----A-----A-----T-----C-----A-----C-----AC-A-----A-----G-----A-----T-----A-----4740

[illegible]

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J.SD.96.SE1173 7022
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K.CA.96.96CM MP535
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02 AG.SN.98.98SE MP1211
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09 cpx.GH.96.96GH9211
10 CD.TZ.96.96TZ BF061
11 cpx.CM.95.95CM 1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM 1849
14 BG.ES.00.X065
15 01B.TH.99.99TH MU2079
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17 BF.AR.99.ARMA038
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19 cpx.CU.99.CU7
20 BG.CU.99.Cu103
21 AZD.KE.99.KER2003
22 01A1.CM.01.01CM 0001BBY
23 BG.CU.03.CB118
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25 cpx.CM.02.1918LE
26 AU.CD.02.02CD MBT047
27 cpx.FR.04.04CD FR.KZ5
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CPZ.US.85.US Marilyn

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V E S M N K E L K K I I G Q V R D Q A E H L K T A V Q M A V F I H N F K R K R G G # I G G G Y S A G E R I V D I I A T D	
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02 AG. NG. 01. PL0710
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40 BF. BR. 05. 05BRBR075
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CPZ. US. 85. US Marilyn

[illegible]

[illegible]

Alignments

HIV-1/SIV cpz Complete Genomes

[illegible]

[illegible]

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 G-C - - - - - G - A - C - - - - - C - - - - - C - G - A - G - - - - - C - G - - - - - T 4742
 G - - - - - T - - - - - G - A - T - - - - - C - - - - - C - G - A - G - - - - - GCT - G - - - - - 4677
 G - - - - - T - A - A - - - - - G - A - C - - - - - C - - - - - A - A - C - - - - - ACTG - A - G - - - - - G - - - - - G - G - - - - - 4700
 G - - - - - T - T - - - - - A - - - - - G - A - C - - - - - T - C - - - - - C - G - A - G - - - - - C - G - - - - - T 4871
 -G - C - - - - - T - ATG - - - - - GA - C - A - G - - - - - A - - - - - T - - - - - CTG - A - G - - - - - A - - - - - GC - G - - - - - 4547
 -G - - - - - T - A - G - - - - - T - A - G - - - - - A - - - - - T - C - - - - - C - G - A - G - - - - - C - G - - - - - 4667
 - - - - - A - G - - - - - T - A - G - - - - - A - - - - - T - C - - - - - CGG - A - G - C - A - - - - - GC - G - - - - - 4668
 - - - - - AGA - A - GG - - - - - CT - AG - C - A - - - - - G - A - C - - - - - CTG - A - G - C - A - - - - - T - GC - G - - - - - 4545
 - - - - - AGAG - A - G - - - - - T - - - - - G - - - - - CTG - A - G - C - A - - - - - A - C - - - - - 4549
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 -G - - - - - G - - - - - A - G - - - - - T - A - G - G - - - - - G - - - - - AG - A - - - - - T - - - - - C - G - A - AT - - - - - AC - T - C - - - - - 4552
 G - C - - - - - A - G - - - - - T - A - G - - - - - A - - - - - G - - - - - AG - A - - - - - T - - - - - AC - G - GA - AC - - - - - A - T - - - - - G - - - - - 4715
 GG - G - - - - - T - - - - - A - G - - - - - C - A - G - - - - - G - - - - - AG - A - - - - - T - - - - - C - G - GA - C - - - - - A - T - C - - - - - 5365
 GG - - - - - T - A - G - - - - - C - A - G - - - - - G - - - - - AG - A - - - - - T - - - - - C - GA - A - - - - - GA - T - C - - - - - 5305
 GG - - - - - A - T - - - - - A - G - - - - - T - C - A - G - - - - - GG - - - - - AG - - - - - T - - - - - C - G - GA - AC - A - - - - - A - T - C - - - - - 4558
 GG - - - - - T - A - G - - - - - T - A - G - - - - - G - - - - - AG - A - - - - - T - - - - - C - G - GAGA - A - - - - - A - T - C - - - - - 4608
 -C - - - - - T - - - - - A - - - - - G - - - - - G - - - - - C - T - G - - - - - AC - GGA - - - - - A - T - - - - - T - - - - - 4540
 -G - - - - - G - - - - - A - - - - - A - G - G - - - - - C - - - - - C - T - G - - - - - A - C - G - A - - - - - A - T - C - - - - - T - - - - - 4552
 -G - - - - - T - A - G - - - - - A - - - - - A - - - - - A - - - - - C - T - G - A - - - - - A - C - G - A - - - - - A - T - C - - - - - 4791
 -G - - - - - T - A - G - - - - - A - - - - - A - - - - - A - - - - - G - - - - - ATTG - GA - C - - - - - A - A - - - - - GC - G - - - - - 4701
 -G - - - - - T - - - - - C - A - G - - - - - G - - - - - T - - - - - T - - - - - C - G - A - - - - - A - - - - - T - C - G - - - - - 5377
 -G - - - - - T - - - - - C - A - G - - - - - G - - - - - T - - - - - T - - - - - C - G - A - - - - - A - - - - - T - C - - - - - 5348
 GG - - - - - T - - - - - A - G - G - G - - - - - C - - - - - C - - - - - T - G - - - - - AC - G - A - - - - - A - T - C - - - - - 4537
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 - - - - - T - - - - - A - - - - - A - - - - - A - - - - - C - - - - - C - - - - - A - - - - - A - - - - - A - C - - - - - 4579
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 - - - - - A - C - - - - - A - C - - - - - G - - - - - A - - - - - AA - - - - - A - A - C - - - - - C - - - - - G - - - - - AGC - G - - - - - 4735
 - - - - - A - T - AAG - - - - - GA - A - - - - - A - - - - - AA - - - - - A - A - C - - - - - C - - - - - TTG - GA - - - - - A - - - - - AGTA - G - - - - - 5381
 -G - - - - - G - A - G - - - - - A - A - - - - - A - - - - - GT - A - - - - - T - - - - - ATTG - GA - - - - - C - A - A - - - - - GC - G - - - - - 4685
 - - - - - A - G - - - - - A - - - - - A - - - - - GT - A - - - - - T - - - - - C - - - - - ATTG - GA - C - - - - - A - A - - - - - GC - A - - - - - 4531
 - - - - - G - A - C - - - - - GA - A - G - G - - - - - G - - - - - A - A - - - - - T - - - - - CTG - A - G - C - G - - - - - C - A - G - - - - - 4555
 -G - - - - - A - A - - - - - TC - A - - - - - A - C - - - - - A - - - - - T - - - - - ACTG - A - - - - - T - - - - - A - - - - - GC - G - - - - - 4732
 -G - C - - - - - CC - - - - - A - C - A - GG - T - - - - - G - - - - - A - G - - - - - CTG - A - G - C - A - - - - - AGC - G - - - - - 4717
 -G - - - - - A - A - A - - - - - GA - A - - - - - C - - - - - GC - - - - - C - - - - - C - GGG - G - - - - - G - - - - - A - - - - - GC - G - - - - - 5358
 - - - - - A - A - G - G - - - - - A - A - - - - - A - A - - - - - A - G - - - - - T - - - - - CTG - A - - - - - C - A - - - - - GC - G - - - - - 4758
 -G - - - - - T - A - - - - - A - C - A - GG - G - - - - - A - - - - - A - T - - - - - T - G - - - - - C - G - GA - - - - - T - A - T - - - - - CT - - - - - 4791
 GG - C - C - - - - - T - AA - G - - - - - A - - - - - A - - - - - G - - - - - AG - T - - - - - T - - - - - C - G - GAG - - - - - A - T - - - - - 4749
 -G - - - - - G - - - - - G - - - - - A - A - AA - G - A - - - - - C - - - - - CC - - - - - A - - - - - C - - - - - G - - - - - C - G - A - - - - - T - G - G - - - - 4716
 -G - - - - - A - C - - - - - A - A - G - - - - - C - - - - - G - - - - - CC - - - - - A - - - - - T - C - A - - - - - C - G - G - - - - - GC - G - - - - - 4567
 -G - C - - - - - G - - - - - C - A - G - - - - - A - - - - - A - - - - - T - G - - - - - CTG - GA - G - C - A - - - - - A - - - - - T - C - G - - - - - 4658
 GG - - - - - A - A - G - A - - - - - A - A - G - A - - - - - A - - - - - C - - - - - T - G - - - - - C - G - GA - - - - - A - T - C - - - - - T - - - - - 4579
 -G - C - - - - - G - - - - - A - C - - - - - A - C - AA - G - G - - - - - A - - - - - T - - - - - Y - T - G - T - - - - - A - C - G - GAGA - - - - - A - T - C - - - - - 4819
 -G - G - - - - - T - G - - - - - A - - - - - C - C - AA - G - G - - - - - CT - G - - - - - AG - - - - - C - G - T - G - - - - - AC - G - A - - - - - T - - - - - T - G - - - - - 4558
 -G - - - - - A - - - - - A - G - G - - - - - G - - - - - A - - - - - C - - - - - T - G - - - - - C - G - A - - - - - T - - - - - T - C - G - - - - - 4561
 G - - - - - C - - - - - A - - - - - A - - - - - A - - - - - AG - - - - - T - - - - - C - - - - - CTG - - - - - - - - - - - - - - - - GC - - - - - 4796
 -G - C - - - - - G - - - - - A - A - - - - - A - AA - G - G - - - - - A - - - - - T - - - - - T - G - - - - - A - C - G - GAGA - - - - - A - T - C - - - - - 4778
 - - - - - A - - - - - A - - - - - GA - A - G - - - - - A - - - - - A - - - - - G - - - - - ACTG - - - - - C - G - - - - - GT - G - - - - - 4561
 -G - - - - - C - A - G - - - - - C - A - G - - - - - G - A - G - - - - - A - - - - - T - G - - - - - ACT - GA - - - - - T - - - - - GC - - - - - 5358
 - - - - - GA - A - G - - - - - A - - - - - A - - - - - C - - - - - G - - - - - TTG - A - G - C - A - - - - - GC - G - - - - - 5344
 -G - - - - - A - A - G - T - T - - - - - G - - - - - G - - - - - G - - - - - G - - - - - G - - - - - G - - - - - C - - - - - 4719
 -G - - - - - T - - - - - A - A - - - - - GAT - AATT - G - A - - - - - C - - - - - G - - - - - T - - - - - C - A - - - - - GG - AG - - - - - G - - - - - GC - G - - - - - 4757
 - - - - - A - - - - - A - - - - - A - - - - - AT - A - A - - - - - T - - - - - C - - - - - G - - - - - ACTG - GAG - - - - - T - - - - - GT - G - - - - - 4825
 - - - - - AAG - - - - - GA - A - - - - - AA - - - - - A - - - - - C - - - - - C - - - - - TTG - A - - - - - AA - C - A - - - - - AGT - G - - - - - 4988
 GG - - - - - T - A - - - - - A - A - C - - - - - G - - - - - G - - - - - AG - - - - - T - - - - - C - G - A - A - - - - - A - T - C - - - - - 4732
 -G - - - - - A - G - - - - - C - A - - - - - CG - - - - - G - - - - - AG - T - - - - - AC - - - - - T - - - - - C - G - GA - AC - - - - - A - T - C - - - - - 4555
 -G - - - - - G - - - - - T - - - - - A - A - AA - G - G - - - - - A - - - - - T - - - - - T - - - - - CT - - - - - A - - - - - A - T - - - - - TG - G - - - - - 4546
 -G - - - - - T - - - - - A - - - - - A - - - - - G - - - - - T - - - - - T - - - - - AAC - G - GA - A - C - - - - - A - - - - - T - C - - - - - 4558
 -G - - - - - A - - - - - T - G - A - G - G - - - - - A - - - - - GC - G - - - - - C - - - - - T - G - - - - - CTG - GA - A - - - - - A - - - - - T - C - - - - - T - - - - - 4543
 -G - - - - - CAA - A - - - - - A - A - - - - - C - - - - - G - - - - - T - - - - - C - A - - - - - A - - - - - AC - GGG - - - - - C - G - - - - - T - - - - - 4776
 - - - - - A - - - - - A - - - - - G - - - - - C - - - - - A - - - - - A - - - - - G - - - - - C - A - - - - - A - - - - - T - - - - - 4830
 - - - - - GC - A - G - - - - - A - - - - - A - - - - - A - - - - - A - - - - - A - - - - - GA - A - - - - - A - - - - - C - - - - - 4836
 - - - - - RG - A - A - - - - - A - - - - - A - - - - - A - - - - - A - - - - - A - - - - - A - - - - - A - - - - - A - C - - - - - 4891
 -G - - - - - M - R - - - - - C - AR - R - R - - - - - R - G - - - - - G - Y - - - - - A - C - T - G - - - - - R - C - G - A - - - - - T - - - - - C - - - - - 4878
 - - - - - C - AR - R - R - - - - - R - G - - - - - G - Y - - - - - A - C - T - G - - - - - R - C - G - A - - - - - T - - - - - C - - - - - 4878
 G - C - - - - - R - - - - - T - G - - - - - TC - G - - - - - A - - - - - A - G - C - GTC - T - - - - - G - - - - - AAC - - - - - CAGTCT - - - - - C - A - A - T - - - - - A - - - - - ACT - GA - A - - - - - C - AG - - - - - T - - - - - A - G - - - - - 4947
 - - - - - T - - - - - T - G - - - - - TC - G - - - - - A - - - - - A - G - A - - - - - GTC - T - - - - - A - - - - - CAGCTT - - - - - C - A - A - T - - - - - A - - - - - ACT - GA - A - - - - - C - AG - - - - - T - - - - - A - G - - - - - 4945
 - - - - - T - G - - - - - TC - G - - - - - A - - - - - A - G - A - - - - - GTC - T - - - - - A - - - - - CAGCTT - - - - - C - A - A - T - - - - - A - - - - - ACT - GA - A - - - - - C - AG - - - - - T - - - - - A - G - - - - - 4859
 - - - - - T - G - - - - - TC - G - - - - - A - - - - - A - C - A - G - - - - - GTC - T - - - - - A - - - - - CAGCTT - - - - - C - A - A - T - - - - - A - - - - - ACT - GA - A - - - - - C - AG - - - - - G - T - - - - - A - G - - - - - 4858
 -G - T - - - - - AGT - T - T - T - - - - - TG - - - - - CCATG - A - G - G - C - - - - - AT - - - - - ATGC - G - - - - - TGAA - - - - - A - T - G - TAGT - - - - - C - TT - T - - - - - AG - AA - - - - - GA - T - - - - - AC - - - - - 5407
 -G - C - - - - - TT - T - T - T - G - CA - A - - - - - GATA - AA - GG - T - C - - - - - AT - - - - - AATGC - G - - - - - GGAA - - - - - A - T - TAGT - - - - - CAAT - C - - - - - AG - A - - - - - GA - T - - - - - AC - - - - - 5406
 -G - C - - - - - G - G - GT - T - T - G - CA - A - - - - - GATA - A - GG - C - C - - - - - AT - - - - - AATGC - G - - - - - GGAA - - - - - A - T - G - TAGT - - - - - CAAT - C - - - - - GAG - AA - - - - - GA - T - - - - - AC - - - - - 5382
 -G - C - - - - - GT - T - T - T - G - CTA - - - - - T - TR - A - G - G - C - - - - - AT - - - - - ATGC - G - - - - - GGA - - - - - G - A - T - TAGT - - - - - CA - T - C - - - - - AG - A - - - - - GA - T - - - - - AC - - - - - 4843
 -G - C - - - - - T - C - - - - - T - - - - - TACA - - - - - ATA - A - GG - G - T - - - - - AT - - - - - AATG - G - - - - - TGA - - - - - A - - - - - AGT - - - - - CAAT - C - - - - - A - - - - - GA - T - - - - - AC - - - - - 4845
 -G - C - - - - - GT - T - T - T - G - C - G - - - - - T - TA - A - G - G - C - - - - - AT - - - - - AATGC - G - - - - - GGAT - G - A - T - TAGT - - - - - CA - T - C - - - - - AG - A - - - - - GA - T - - - - - AC - - - - - TA 4839
 -GCC - - - - - GT - T - T - T - G - ATG - - - - - T - TG - A - G - G - C - C - - - - - AT - - - - - ATGC - G - - - - - G - - - - - TGA - - - - - A - T - G - TAGT - - - - - CA - T - C - - - - - AG - CA - - - - - GA - T - - - - - AC - - - - - 4838
 GG - C - - - - - AGG - T - T - T - G - TCCA - - - - - T - TA - AA - GG - G - - - - - AT - - - - - AATGC - G - - - - - GGA - - - - - G - A - T - AGT - - - - - CA - TGC - G - - - - - AG - TA - - - - - GA - T - - - - - AC - - - - - 4919
 -G - C - - - - - AGT - T - T - T - G - AATG - - - - - T - GG - A - G - G - C - C - - - - - AT - - - - - ATGC - G - - - - - A - - - - - TGAA - - - - - A - T - G - TAGT - - - - - CA - T - C - - - - - A - - - - - CA - - - - - AC - - - - - 4814
 -G - C - - - - - GT - T - T - T - G - - - - - C - T - GA - A - G - G - C - - - - - AT - - - - - ATGC - G - - - - - TGAA - - - - - A - T - G - TAGT - - - - - T - C - - - - - AG - AA - - - - - GA - T - - - - - AC - - - - - 5406
 -C - - - - - AGT - T - T - T - A - CCG - - - - - TTTA - A - G - G - C - - - - - AT - - - - - ATGC - G - - - - - TGAA - - - - - A - - - - - T - G - TAGT - - - - - CA - T - C - - - - - AG - GCA - - - - - GA - T - - - - - AC - - - - - 5409
 -C - S - - - - - WAGT - T - T - T - A - CCG - - - - - TTTA - A - G - G - C - - - - - AT - - - - - ATGC - G - - - - - R - - - - - TGAA - - - - - A - - - - - T - G - TAGT - - - - - CA - T - C - - - - - AG - GCA - - - - - GA - T - - - - - AC - - - - - 4804
 -C - - - - - GT - CT - T - T - G - A - GA - - - - - C - TGA - A - GG - - - - - T - - - - - AT - - - - - AATGC - G - - - - - TGA - - - - - C - A - A - T - G - TAGT - - - - - GA - T - C - - - - - AT - - - - - AA - - - - - GA - T - - - - - AC - - - - - 4836
 G - T - - - - - G - - - - - TT - T - T - G - A - CA - - - - - A - CCA - T - TG - G - T - T - - - - - G - - - - - TATGC - T - G - - - - - AGAA - A - A - A - T - - - - - CAAGTG - G - - - - - AC - - - - - GGT - A - - - - - C - C - - - - - GA - - - - - A - - - - - 5389
 G - A - G - AGA - - - - - T - - - - - CCAACATTGGGATAAA - - - - - G - G - - - - - GTG - TC - - - - - AT - A - ATGT - - - - - C - CCA - - - - - C - A - A - T - T - GAG - - - - - ATTGGGA - AG - - - - - T - - - - - A - - - - - T - - - - - 4708
 G - GGC - - - - - C - GA - T - T - A - AATC - G - - - - - AGC - AA - TG - C - - - - - A - AATG - - - - - C - A - A - T - - - - - C - A - - - - - G - - - - - AG - A - - - - - T - C - G - - - - - AC - - - - - T - - - - - 4895
 G - TGC - - - - - T - - - - - A - TT - CA - A - - - - - TA - TT - A - - - - - AA - G - G - C - - - - - C - - - - - C - - - - - AGCC - - - - - G - C - - - - - A - C - T - - - - - TC - - - - - CT - GGA - TCT - - - - - GT - - - - - G - G - T - CTTAC - - - - - TA 5417
 -G - GCAGGG - - - - - A - - - - - A - T - ACA - A - - - - - AGAT - A - A - - - - - GG - TTT - CAT - - - - - AGCCTGT - - - - - CCA - - - - - C - A - - - - - T - CA - AGGAT - - - - - AC - - - - - GGA - C - - - - - C - T - - - - - A - - - - - 5000
 -G - A - - - - - T - - - - - TA - ATA - A - - - - - A - A - A - A - G - T - T - G - - - - - GT - A - A - - - - - CA - C - - - - - C - A - G - T - - - - - A - - - - - AC - - - - - GGA - CT - C - AG - - - - - A - - - - - T - - - - - GA - G - - - - - 5413

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15 TB.TH.99.99TH.MU2079
16 AZD.KR.97.97KR004
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 AZD.KE.99.99KE2003
22 01AI.CM.01.01CM.0001BE
23 BG.CU.03.CB118
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29 BF.FR.01.BREPM16704
31 BC.BR.04.04BR142
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38 BF1.UY.03.UY03.3389
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40 BF.FR.05.05BRU1055
42 BF.LU.03.LUBF.05.03
43 02G.SA.03.J11223
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N.CM.97.YBF106
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CPZ.US.85.US.Marilyn

[illegible]

[illegible]

Alignments

HIV-1/SIVcpz Complete Genomes

[illegible]

V.FR.83.HXB2
 Vpr (frameshifted)
 Vpr
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 H.BE.93.VI997
 H.BE.98.856
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 J.SE.93.SE9280 7887
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[illegible]

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 Tat exon 1
 Rev exon 1

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HIV Sequence Compendium 2010

[illegible]

Alignments

HIV-1/SIVcpz Complete Genomes

HIV-1/SIVcpz
Complete Genomes

[illegible]

FR.33.HXB2	ATAATAGCAATAGTTGTGGTCCATAGTAATCATGAAATATAGGAAATATTAAGACAA	AGAAAAATAGACAGGTGAATGTATAGACTA	ATAGAAAGACGAGAAGACAGTGGCA	ATGAGAGTGAAGGAG	AAA	6242
Vpu	I A I I V V V S I V I I E Y R K I L R Q	R K I D R L I D R L	I E R A E D S G	#N E S E G	E	K
A.CD.02.02CD KTB035	-C- -T- -A- -A- -T- -T- -T- -C- GAG- AG-					
A.SN.01.DD3369	-CT- - - -A- -A- -T- -GGG- -A- -T- GAG- AG- G-					
A1.AU.03.PS1044 Day0	-C- - - -A- -A- -T- -GGT- -A- -T- GC- AG-					
A1.CY.06	-C- - - -A- -A- -T- -GGT- -A- -T- GCA- A-					
A1.GE.99.99GEM2011	G-C- - - -A- -A- -T- -GGT- -A- -T- GC- A-					
A1.IT.02.60000	-C- - - -A- -A- -T- -GGT- -A- -T- GC- A-					
A1.KE.02.ML1990	-CT- -G- -A- -A- -C- -A- -TT- -GGT- -A- -T- GC- A-					
A1.RU.08.PoKa1Ru	-C- - - -A- -A- -T- -GGT- -A- -T- GC- AG-					
A1.RW.93.93R0378	-C- - - -A- -A- -T- -GGT- -A- -T- GC- AG-					
A1.SE.95.SE338	-CC- - - -A- -A- -T- -GGT- -A- -T- GC- AG-					
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A1.UG.99.99UGA07072	-CC- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
A1.ZA.04.04ZASK162B1	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
A2.CD.97.97CDK148	-TT- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
A2.CY.94.94CY017_41	-CT- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.AR.04.04AR143170	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.AU.04.PS1038 Day174	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.BO.99.BOL0122	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.BR.05.BREPM1081	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.CA.97.CANB3FULL	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.CN.05.05CNBH hp3	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.CO.01.PC0001	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.CU.99.Cu19	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.CY.06.CY165	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.DE.86.D31	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.DK.04.PMVL 012	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.DO.05.05DO 160884	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.EC.89.EC003	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.ES.07.X2231	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.FR.92.92FR BX08	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.GA.88.OY1	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.GB.86.GB8 46R	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.GE.03.03GENZ004	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.HT.05.05HT 129389	-M-R- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.IN.x.11807	-T- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.JM.05.05JM KJ108	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.JP.05.DR6538	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.KR.04.04KMS	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.MM.99.MST0101	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.NL.00.671 00T36	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.RU.04.04RU128005	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.TH.00.00TH C3198	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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B.UA.01.01UAKV167	G- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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B.UY.01.01UYTRA1179	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.YE.02.02YES07	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
B.ZA.03.03ZAPSO45MB2	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
C.AR.01.ARC4006	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
C.BR.04.04BR013	G-CT- - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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C.CN.98.YNRL9840	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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C.ES.07.X2118_2	-CC- -A- -A- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
C.ET.02.02ET 288	-CT- - - -A- -A- -C- -A- -T- -GGT- -A- -T- G- AG- AG-					
C.GE.03.03GENZ033	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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C.MW.93.93MW 965	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
C.SN.96.90SE 364	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
C.SO.89.89SM 145	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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C.ZA.05.05ZAPSK240B1	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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D.CY.06.CY163	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
D.DE.97.ML413_2	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
D.KR.04.04KBH8	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
D.SN.x.SE365	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
D.TD.99.MN011	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
D.TZ.01.A280	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
D.UG.99.99UGK09958	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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F1.BE.93.VI850	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
F1.BR.07.07BR844	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
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F1.JP.04.DR6082	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
F1.R0.96.BCI R07	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
F1.RU.08.D88 845	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
F2.CM.97.97CM3657	-C- - - -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.BE.96.DRCLB	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.CM.04.178_15	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.CU.99.Cu74	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.ES.05.P962	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.GH.03.03GH175G	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.KE.93.HH8793 12_1	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.NG.01.01NG09669	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.PT.x.PT2695	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.SE.93.SE6165	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.BE.96.DRCLB	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.CM.04.178_15	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.CU.99.Cu74	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.ES.05.P962	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.GH.03.03GH175G	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.KE.93.HH8793 12_1	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.NG.01.01NG09669	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.PT.x.PT2695	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					
G.SE.93.SE6165	-GC- -C- -A- -A- -T- -GGT- -A- -T- G- AG- AG-					

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J.CD.97.SF2980 7887
J.CD.94.SE9173 7022
K.SE.97.97ZR E0T1B1
K.CM.96.96CM MP535
01 AE.CF.90.90CF11697
01 AE.CN.97.97JSW0X45
01 AE.HK.04.HK001
01 AE.JP.04.DR0232
01 AE.TH.04.BKM
01 AE.US.00.000US MSC1164
01 AE.VN.98.98NVND15
02 AG.CM.02.02ZCM 0013BBY
02 AG.CY.05.CY048
02 AG.ES.06.P1261
02 AG.ES.06.P1263
02 AG.GH.03.03GHB181AG
02 AG.LR.04.P0C44951
02 AG.NG.01.PL0710
02 AG.SE.94.SE7812
02 AG.SI.04.040SE MP1211
02 AG.US.00.000US MSC3083
02 AG.UZ.02.02UZ06683
04 BR.ARU.97.KAL153 2
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05 DF.BE.04.VI1310
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07 BC.CN.98.98CN009
08 BC.CN.97.97CNXG 6F
09 cpx.GH.96.96GH2911
10 CD.TZ.96.96TZ BF061
11 cpx.CM.95.95CM 1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM 1849
14 BG.ES.00.X605
15 01B.TH.99.99TH MU2079
16 AZD.KR.97.KR004
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 AZD.KR.99.KER2003
22 01A1.CM.01.0101_0001B
23 BG.CU.03.CB18
24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02ZCD MBT047
27 cpx.FR.04.04CD FR KZ5
28 BF.BR.99.BREPM12609
29 BF.BR.01.BREPM16704
31 BC.BE.04.04BR412
32 06A1.EE.01.EE0369
33 01B.MY.05.05MYKL007_1
34 01B.TH.99.09UR2478P
35 AD.AF.05.05AF095
36 cpx.CM.00.00CMNYU830
37 cpx.CM.00.00CMNYU926
38 BF1.UY.03.UY03 3389
39 BF.BR.04.04BRR1179
40 BF.BR.05.05BRR1055
42 BF.LU.03.LUBF 05_03
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O.US.99.99USTWLA
P.FR.09.RBF168
CPZ.CD.09.ANT
CPZ.CM.05.SIVcpzMT145
CPZ.CA.08.GAB
CPZ.TZ.00.TAN1
CPZ.US.85.US Marilyn

```

[illegible]

Alignments

HIV-1/SIV cpz Complete Genomes

		Vpu end		Env signal peptide end Env gp120 start												
B. FR. 83. HXB2		TATCAGCAGCTTGTGGAGATGGGGTGGAGATGG		GGCACCAGTCTCTTGGGATGTTGATGATCTGTAGTGCTACAGAAAA												
Vpu		I S A L V E M G V E M		G H H A P W D V D D L C												
Env		Y O H L W R W G W R W		G T M L L G M L M T I C S A T E K												
H.BE.93.VI991		CAAG	T-AA	T-G	C	T-GT	G	C		A	G	A	AG	T	C	5775
H.BE.93.VI997		CA-A-G	G	T-T	A	TT-G	T	C	T-A	G	G	C		T	A	5702
H.CF.90.056		CAAG	A	T-G	T	C	G	C		T	A	G	A	AA	C	5737
H.GB.00.00GBCA4001		CA	T	CG	T-AA	T-G	T	C	G	A	GG	C		T	AA	5905
J.CD.97.J.97DC KTB147		GGA-AA	A	CT	A	T	A	A	T	A	G	G	C		A	5597
J.SE.93.5E9280 7887		GG-AC	G	CT	A	T	A	A	T	AG	A	A	G	C		5716
J.SE.94.5E9173 7022		GG-T-AG		CT	A	T	A	A	T	G	C		A	GA	T	5717
K.CD.97.97ZR EQTB11		GG	G	A	C	T	T	AT	T-G	A	A	A	C	G	A	5592
K.CM.96.96CM MP535		GG-ACA	G	AC	T	T	AT	T-G	A	A	A	CAA	G	A	C	5596
01 AE.CF.90.90CF11697		GG-CA	AG	G	TT	A	T	G	A	T	CT	C	CC		T	6346
01 AE.CN.07.07J5WX045		GG-TAA	A	G	TT	A	A	T	G	A	T	CT	C	C		5596
01 AE.HK.04.HK001		GG-CAA	A	G	TT	A	T	G	A	T	CT	C	C		T	5767
01 AE.JP.x.DR0492		GG-CAA	A	G	TT	AA	T	G	A	T	CT	C	C		T	6408
01 AE.TH.04.BKM		GG-AA	A	G	TT	A	T	G	A	T	CT	A	C	C		6358
01 AE.US.00.00US MSC1164		GG-CAA	A	G	TT	A	T	G	A	T	CT	C	C		T	5602
01 AE.VN.98.98VND15		GG-CAA	A	G	TT	AA	T	G	A	T	CT	C	C		T	5652
02 AG.CM.02.02CM 0013B8Y		CA-T	A	G	TG	T	A	TT	TT	T	AA	A	T	A	GACA	5587
02 AG.CY.05.CY048		CA-T	A		GGTG	AA	AT	G	AA	A	T	A	CA	T		5599
02 AG.ES.06.P1261		CA-T	CA	A	G	TG	AA	AT	AA	CA	T	AA	GA	A	T	5839
02 AG.FR.91.01263		CA-T	A		T	G	CA	AT	T	AA	A	T	A	GA	A	5748
02 AG.GH.03.03GH181AG		T-ACA	C	GT	A	T	GA	AT	T	AA	A	T	AG	GA	T	6423
02 AG.LR.x.P0C44951		CA-T	A	T	T	G	A	A	AT	T	AA	A	T	A	ACA	6392
02 AG.NG.01.PL0710		G-CA	C	A	A	T	TG	AA	AT	T	CAA	A	T	A	GAT	5584
02 AG.SE.94.SE7812		CA-T	A		T	TG	AA	AT	T	AA	CA	T	A	GG	A	5772
02 AG.SN.98.98SE MP1211		G-CA	C	T	ATG	A	T	G	A	A	T	A	GA	A	T	5603
02 AG.US.00.00US MSC3083		CA-T	T		T	TG	AGG	T	TT	A	A	T	A	CA	A	5596
02 AG.UZ.02.02UZ0683		CA-C	A		T	G	AA	AT	T	AA	A	T	AG	CA	T	5590
03 AB.RU.97.KAL153_2		C-C	TTA	G	A	AT	G									5610
04 cpx.CY.94.94CY032_3		CA			A	TT	A	T	G	A			CT	A	C	5767
05 DF.BE.x.VI1310		GG-C		G	AG	CTTT	AT	G	A	A	A		C			5785
06 cpx.AU.96.BFP90		GG-A		A	A	G	TT	A	T	G	A	T	CT	TA	G	6433
07 BC.CN.98.98CN009		G		T	A								GT	G	C	5728
08 BC.CN.97.97CNGX_6F		A	A	G		T							GT	T	AGG	5570
09 cpx.GH.96.96GH2911		GG-AA		A	G	CT	A	T	A	T	A	G	C			5608
10 CD.TZ.96.96TZ BF061		G-CA	A	G		T	A	T	AGG	T	T	A	T	A	AG	5794
11 cpx.CM.95.95CM 1816		GG-CA		A		CT	A	T	A	A	A		C	C		5766
12 BF.AR.99.ARMA159		GG		T	G	AC	TT	T	AT	G	A	A	A			6398
13 cpx.CM.96.96CM 1849		GG-AA		A	A	TT	A	T	T	G	A	T	CT	A	T	5807
14 BG.ES.00.X605		GG-ATC		A	G	TT	A	T	T	G	A	T	CT	A	TG	5841
15 01B.TH.99.99TH MU2079		GG-CAA		A	G	T	A	T	T	G	A	T	G			5793
16 A2D.KR.97.97KR004		A		A	A	T	T	A	TT	G	C	A	TA	AA	G	5763
17 BF.AR.99.ARMA038		A		A	A	T	A	A	TT	G	C	A	TA	AA	G	5607
18 cpx.CU.99.CU76		CAAG	A	A	A											5696
19 cpx.CU.99.CU7		CA-C	A	AT	G	TT	A	A	T	G	A	G	CTTT	C	C	5619
20 BG.CU.99.CU103		GG		TG	C	G	TT	A	A	T	GG	A	T	CT	A	5870
21 A2D.KE.99.KER2003		G-AA		A									G	GC	T	5598
22 01A1.CM.01.01CM 0001BBY		GG-AA		A	A	TT	A	T	G	A	A	T	CCA	A	T	5803
23 BG.CU.03.CB118		GG		G	C	G	TT	A	A	T	GG	A	T	CT	T	5846
24 BG.CU.03.CB378		GG-A		C		G	TT	A	A	T	GG	A	T	CT	A	5834
25 cpx.CM.02.1918LE		CA-T	A		G	TTT	A	G	T	G	A	T	CT	C		5611
26 AU.CD.02.02CD MBT047		G			T	A	G	AA	G	TA	A	T	T	A	G	6397
27 cpx.FR.04.04CD FR_K25		GG-AGG				CT	A	T	G	A	A	A	T	T	CA	6393
28 BF.BR.99.BREPM12609		GGA		G	C	CT	T	T	T	G	A	A	A	T	A	5759
29 BF.BR.01.BREPM16704						TGGCAC	C	T	G							5791
31 BC.BR.04.04BR142		GGA-A	A	G		A	T	T	AGG	T	T		CC	T	A	5886
32 06A1.EE.01.EE0369		GGTCA		A		A	TT	A	T	T	G	A	T	A	CT	6038
33 01B.MY.05.05MYK1007_1		GG-CAA		A		G	TT	A	T	T	G	A	A	G	CT	5782
34 01B.TH.99.09UR2478P		GG-TAA		A		A	TT	A	AT	G	A	T	CT	C	C	5599
35 AD.AF.05.05AF095		GG-AA		A		A	T	A	T	G	A	A	A	T	GT	5596
36 cpx.CM.00.00CMNU830		G-TA		A		G	TT	A	A	T	G	A	T	CT	CTTG	5612
37 cpx.CM.00.00CMNU926		CA-C		A	AT	G	TT	A	T	T	G	A	T	A	ACA	5594
38 BF1.UY.03.UY03 3389		GG				GA	AG	C					A	TTGT	AT	5823
39 BF.BR.04.04BRR179		GG				G							CTTT	AT	T	5880
40 BF.BR.05.05BRR1055		G		A	C	A							A	C	GA	5906
42 BF.LU.03.luBF 05_03				K		A							A			5931
43 02G.SA.03.J11223		GG-AT				C	AT						T	G	SYT	5928
N.CM.95.YBF30		GG				AT	G	GAT	AA	A	TG	T	TTACTCTTCATCTTC	AG	AGCTT	5984
N.CM.97.YBF186		GG											CAAT	T	TGT	5869
N.CM.02.DJ00131		GG											CAAT	T	TGT	5868
N.CM.04.04CM 1015_04		GG											CAAT	T	TGT	5868
O.BE.87.ANT70		A-G				TTA	G	ACCTTG					TA	T	AGC	6444
O.CM.x.BCF06		A-G				TCA	G	ATCTTG					TG	AGC	A	6455
O.CM.91.MVP5180		A-G				TCA	G	ATCTTG					TA	AGC	A	6455
O.CM.96.96CM102		A-G				TCA	G	ATCTTG					TA	AGC	A	6455
O.CM.97.97CMA8447		ARG				TTA	G	ATCTTG					TG	AG	A	5889
O.CM.98.98CMA1804		AGG				TTA	G	ATCTTG					TA	AG	A	5885
O.CM.99.99CMU4122		C-G				TTAGG	ATCTT	G					TA	AG	A	5884
O.FR.92.VAU		A-G				TTAGG	ATCT	G					TG	T	A	5968
DO.FR.08.RBF208													GGCATG	TGC	C	5857
O.SN.99.99SE MP1299		A-G				TTAGG	ATCTTG						TG	AG	T	6455
O.US.x.I 2478B		A-G				TTAGG	ATCTTG						TG	AG	T	6455
O.US.97.97US98692A		A-G				TTAGG	ATCTTG						TG	AG	T	6455
O.US.99.99USTWLA		A-G				TTAGG	ATCTTG						TG	AG	T	6455
P.FR.09.RBF168		AGC				TTAGG	AACTTG						G	AATTTGCTTG	CTTTGG	6448
CPZ.CD.90.ANT													TG	G	GT	5823
CPZ.CM.05.SIVcpzMT145													GGTG	AG	TT	5942
CPZ.GA.88.GAB1													AGAG	CTGGAACA	CTT	6461
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CPZ.US.85.US_Marilyn													AGA	T	G	6468

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12.BF.AR..99.ARMA159
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17.BF.AR..99.ARMA038
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19.cpx.CU..99.CU7
20.BG.CU..99.CU103
21.AZ.KE..99.KER2003
22.01A.CM..01.01CM.0001BE
23.BG.CY..03.CB118
24.BG.CY..03.CB378
25.cpx.CM..02.1918LE
26.AU.CD..02.02CD.MBTB047
27.cpx.FR..04.04CD.FR.KZ5
28.BF.BR..99.BREP12609
29.BF.BR..01.BREPM16704
31.BC.BE..04.04BR1421
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34.01B.TH..99.09UR.2478P
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37.cpx.CM..00.00CMNYU926
38.BF1.UY..03.UY03.3389
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43.02G.SA..03.11223
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0.CM..97.97CMA8447
0.CM..98.98CMA1904
0.CM..98.98CMA4122
0.FR..92.VAU
DO.FR..08.RBF208
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O.US..97.97US08692A
P..99.99USU70
P.FR..09.RBF168
CPZ.CD..05.ANT
CPZ.CM..05.SIVcpzMT145
CPZ.CM..05.GAB1
CPZ.TZ..00.TANI
CPZ.US..85.US.Marilyn

[illegible]

V1 loop start

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J.S.E.93.SE9173 7022
K.C.D.97.9727R EQT11
K.CM.96.96CMT535
01 AE.CF.09.90CF11697
01 AE.CN.07.0735WX045
01 AE.HK.04.HK001
01 AE.JP.X.DR0492
01 AE.TH.04.BKM
01 AE.US.98.98US MSC1164
01 AE.VN.98.98VNDN15
02 AG.CM.02.02CM 0013BBY
02 AG.CY.05.CY048
02 AG.ES.06.P1261
02 AG.FR.91.DJ263
02 AG.GH.03.03GHI81AG
02 AG.IL.95.X.P0C44951
02 AG.NG.01.PL0710
02 AG.SE.94.SE7812
02 AG.SN.98.98SE MP1211
02 AG.US.00.000US MSC3083
02 AG.UZ.02.02UZ0663
03 AC.RU.97.KAL153 2
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05 DF.BE.X.VI1130
06 cpx.AU.96.BFP990
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08 BC.CN.97.97CNCX 6F
09 cpx.GH.96.96GH1211
10 CD.TZ.96.96TZ BF061
11 cpx.CM.95.95CM 1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM 1849
14 BG.ES.00.X065
15 01B.TH.99.99TH MU2079
16 AZD.KR.97.97KR004
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 AZD.KM.99.KER2003
22 01A1.KM.01.01CM 0001BBY
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02CD MBT0847
27 cpx.FR.04.04CD FR.KZS
28 BF.BR.09.BREP12609
29 BF.BR.01.BREP16704
31 BC.BR.04.04BR142
32 06A1.EE.01.EE0369
33 01B.MY.05.05MYK007_1
34 01B.TH.99.00R2478P
35 AD.AF.05.05AF095
36 cpx.CM.00.00CMNYU830
37 cpx.CM.00.00CMNYU926
38 BF1.UY.03.UY03 3389
39 BF.BR.04.04BRJR105
40 BF.BR.05.05BRBR1075
42 BF.LU.03.LuBf 05_03
43 02G.SA.03.J11223
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O.CM.91.MVP5180
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O.CM.97.97CMA8447
O.CM.98.CMA1122
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A1. IT. 02. 60000	-G- -C- C- G- G- CG- A- TG- G- AG- A- C- AG- A- -	-G- -	G- A- C- -	-T- G- AC- A- T- C- -	7398
A1. 02. ML1000	-G- C- C- G- G- CG- A- TG- G- AG- A- C- AG- A- -	-G- -	G- A- C- -	-T- G- AC- A- T- C- -	6689
A1. RU. 08. P0Ka1Ru	-G- C- C- A- G- C- A- AC- AG- GAA- G- A- T- C- T- C- A- -	-G- -	G- A- CCA- -	-T- G- AC- A- T- C- -	6884
A1. RW. 93. 93RW037A	-G- T- -C- G- G- G- C- CAC- A- C- AAG- C- A- -	-G- -	G- TA- -	-T- G- AC- A- T- C- -	7359
A1. SE. 95. SE8538	-G- -A- A- GC- TG- G- C- AAC- AC- T- C- AAT- C- A- -	-G- -	CTA- C- -	-T- AC- A- T- C- G- -	6589
A1. TZ. 01. A341	-G- T- -C- G- G- T- G- A- ATC- A- T- C- AAT- C- A- -	-G- -	CTA- C- -	-T- AC- A- T- C- G- -	6532
A1. UA. 01. 01UADN139	-T- GC- -A- C- A- AG- TAC- A- T- C- AAT- C- A- -	-G- -	CTA- C- -	-T- G- AC- A- T- C- -	6587
A1. UC. 99. 99UGA07072	-G- -A- A- GC- G- G- C- CTA- C- G- A- C- -	-G- -	GCTA- C- A- -	-T- AAC- A- T- C- -	6587
A1. ZA. 04. 04ZASK162B1	AGG- TG- AGT- C- G- G- T- A- A- GG- A- C- A- -	-G- -	G- TA- TC- -	-T- AC- T- T- -	6818
A2. CD. 97. 97CDKTB48	-G- -GC- C- A- G- G- T- GAAC- C- CCCT- G- A- -	-G- -	TAGC- -	-T- AC- A- T- -	6691
A2. CY. 94. 94CY017 41	-TT- -GC- C- A- G- G- GAAC- GA- CCCT- G- A- -	-C- -	CTA- C- -	-T- AC- A- TT- -	6744
B. AR. 04. 04AR143170	-T- G- -C- C- GC- -A- -T- TA- G- -T- AAT- A- -	-G- -	G- T- C- -	-T- A- T- T- C- -	6579
B. TU. 05. P51038 Day174	-C- -C- GC- -A- -AG- G- -	-G- -	G- T- C- -	-T- A- T- T- C- -	6579
B. B0. 99. B0L0122	-G- C- C- G- G- -A- -A- GCA- G- -	-G- -	TC- CA- -	-T- A- T- T- C- -	6561
B. BR. 05. BREPM1081	-G- C- C- G- G- -A- -A- GCA- G- -	-G- -	AAG- C- A- -	-T- A- T- T- C- -	6851
B. CA. 97. CANB3FULL	-G- C- C- G- G- -A- -A- GCA- G- -	-G- -	TG- AA- -	-T- A- T- T- C- -	6651
B. CN. 05. 05CNHB hp3	-C- -G- G- A- C- G- G- T- G- A- -	-G- -	T- G- A- -	-T- T- G- -	7388
B. CM. 00. 00CM001	-C- -G- G- A- C- G- G- T- G- A- -	-G- -	T- G- A- -	-T- T- G- -	6549
B. CU. 99. CU19	-G- G- -C- G- G- GG- A- -T- GCA- C- AC- A- A- G- A- -	-T- -	-	-T- T- G- -	6939
B. CY. 06. CY165	-A- G- T- -G- G- -AGAG- TT- GTA- G- -	-G- -	T- C- -	-T- T- -	6627
B. DE. 86. D31	-G- -G- -G- -T- AA- -G- -G- C- A- -	-G- -	T- C- -	-T- T- -	6908
B. DK. 04. PMVL 012	-G- -G- -G- -T- AA- -G- -G- C- A- -	-G- -	T- C- -	-T- T- -	6730
B. DO. 05. 05D00 160884	-A- -G- -G- -T- AA- -G- -G- C- A- -	-G- -	T- C- -	-T- T- -	6552
B. EC. 89. EC003	-G- -T- C- T- C- G- A- T- C- A- -	-G- -	GTA- -	-T- AC- T- T- C- -	6498
B. ES. 07. X2231	-G- -T- C- T- C- GG- G- T- AA- -G- -	-G- -	T- GA- A- -	-T- T- -	6807
B. FR. 92. 92FR BX08	-C- -C- G- G- -AG- G- -	-G- -	GAA- -	-T- T- -	6546
B. GA. 88. 0Y1	-C- -G- G- A- -T- CA- -G- -	-G- -	T- GA- A- -	-T- T- -	6920
B. GB. 86. G8B 46R	-C- -G- G- A- -T- CA- -G- -	-G- -	T- GA- A- -	-T- T- -	7360
B. GE. 03. 03GEMZ004	-C- -G- G- A- -T- CA- -G- -	-G- -	T- GA- A- -	-T- T- -	6807
B. HT. 05. 05HT 129389	-G- -G- A- G- TG- GGG- A- G- -	-G- -	T- GA- A- -	-T- T- -	6596
B. IN. x. 11807	-G- -G- G- -T- AA- -G- -	-G- -	T- GA- A- -	-T- T- -	6715
B. JM. 05. 05JM KJ108	-C- -C- G- G- -G- -G- -	-G- -	T- GA- A- -	-T- T- -	6585
B. JP. 05. DR6538	-A- -G- -G- -T- AA- -G- -	-G- -	T- GA- A- -	-T- T- -	7408
B. KR. 04. 04KMH5	-A- -G- -G- -T- AA- -G- -	-G- -	T- GA- A- -	-T- T- -	7334
B. MM. 99. mSTD101	-A- -T- C- -T- G- A- GAA- -G- -	-G- -	T- GA- A- -	-T- T- -	6797
B. NL. 00. 671 00T36	-G- -G- -G- -T- AA- -G- -	-G- -	T- GA- A- -	-T- T- -	6936
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K.CM. 96. 96CM MP535
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23 BG. CU. 03. CB118
24 BG. CU. 03. CB378
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28 BF. BR. 04. BRPMD12609
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31 BC. BR. 01. 04BRE141
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CPZ. TZ. 00. TANI
CPZ. US. 85. US Marilyn

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13 cpx.CM.96.96CM 1849
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29 BF.BR.01.BREP16704
31 BC.BR.04.04BR142
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CPZ.CD.00.ANT
CPZ.CM.05.S1VcpzMT145
CPZ.CM.08.GAR
CPZ.TZ.00.TAN1
CPZ.US.85.US Marilyn

[illegible]

Alignments

HIV-1/SIVcpz Complete Genomes

V5 loop end													Rev Responsive Element (RRE) region													Env gp120 end													Env gp41 start																																																																																										
B. FR. 83. HXB2													CTCTGGAGGAGGAGATATGAGGCAAAATTGGGAGAAGTGAATTATATATAAATATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCCAAAGAGA													AGAGTGGTG													CAGAGAGAAAAAAGAGCAGTGGGA													ATAGGAGCTTT																																																																													
Env													P G G G G D M R D N W R S E L Y K V K V V K I E P L G G V A P T K C K G													R V V													Q R E K R A V G													I G A L																																																																													
A. CD. 02. 02CD KTB035													G													GG													C													G													G													7776																																																			
A. SN. 01. 00J369													A													A													C													C													G													G													6999																																						
A1. AU. 03. PS1044 Day0													A													A													G													C													G													G													7015																																						
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A2. CD. 97. 97CDKT848													A													G													C													A													T													G													A													GC													7144												
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B. C. 97. C97CANB3FULL													A													A													T													G													G													GC													7793																																						
B. CN. 05. 05CNHB_hp3													A													A													T													G													G													GC													6960																																						
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B. CU. 99. Cu19													A													A													T													G													G													GC													7001																																						
B. CY. 06. CY165													A													A													T													G													G													GC													7117																																						
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123

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02 AG.NG.01.PL0710
02 AG.SE.94.SE7812
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09 cpx.GH.96.96GH1211
10 CD.TZ.96.96TZ BF061
11 cpx.CM.95.95CM 1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM 1849
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17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 AZD.KM.99.KER2003
22 01A1.KM.01.01CM 0001BBY
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02CD MBT047
27 cpx.FR.04.04CD FR.KZS
28 BF.BR.09.BREP12609
29 BF.BR.01.BREP16704
31 BC.BR.04.04BR142
32 06A1.EE.01.EE0369
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 12 BF.AR.99.ARMA159
 13 cpx.CM.96.96CM 1849
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 20 BG.CU.99.CU103
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 23 BG.CU.03.CB118
 24 BG.CU.03.CB378
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 CPZ.US.85.US Marilyn

Alignments

HIV-1/SIV cpz Complete Genomes

HIV-1/SIVcpz
Complete Genomes

[illegible]

FR.FR.83.HXB2
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01 AE.CN.07.07JSWX045
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01 AE.JP.03.DR0492
01 AE.TH.04.BKM
01 AE.VN.98.090US MSC116
01 AE.VN.98.98VND015
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02 AG.FR.01.D1263
02 AG.GH.03.03GH181AG
02 AG.HK.94.0C44951
02 AG.NG.01.PL0710
02 AG.SE.94.SE7812
02 AG.SN.98.98SE MP1211
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02 AG.UZ.02.020Z0683
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07 BC.CN.98.98CN009
08 BC.CN.97.GF7CNGX
09 cpx.GH.96.96GH2911
10 CD.TZ.96.96TZ BF061
11 cpx.CM.95.95CM 1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM 1849
14 BG.ES.00.X605
15 01B.TH.99.99TH MU2079
16 AZD.KR.97.97KR004
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19 cpx.CU.99.CU7
20 BG.CU.99.CU103
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22 01AI.KM.01.01CM 0001B
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24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02CD MBT0047
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28 BF.BR.99.BREPM12609
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31 BC.BR.04.04BR142
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36 cpx.CM.00.00CMNYU830
37 cpx.CM.00.00CMNYU926
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O.US.99.99USTWLA
P.FR.09.RBF168
CPZ.CD.00.ANT
CPZ.CM.05.SIVcpzMT145
CPZ.CA.88.CA101
CPZ.TZ.00.TAN1
CPZ.US.85.US Marilyn

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rev.FR.83.HXB2
 Rev exon 2
 Tat exon 2
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 H.BE.93.VI997
 H.BE.98.056
 CB.98.00CBAC4001
 J.CD.97.13.97DC.TB1747
 J.SE.93.SE9280.7887
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 06 cpx.AU.96.BFP90
 07 BC.CN.98.98CN009
 08 BF.CN.97.97CNX.GF
 09 cpx.GH.96.96GHZ911
 10 CD.TZ.96.96TZ.BF061
 11 cpx.CM.95.95CM.1816
 12 BF.AR.99.ARM159
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 14 BG.ES.00.X605
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 16 02A.KR.97.97KR004
 17 BF.AR.99.ARM038
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 19 cpx.CU.99.CU7
 20 BG.CU.99.CU103
 21 02A.KE.99.KEP2003
 22 01AI.CM.01.01CM.0001B
 23 BG.CU.03.CB118
 24 BG.CU.03.CB378
 25 cpx.CM.02.1918LE
 26 AU.CD.02.02CD.MBTB047
 27 cpx.FR.04.04CD.FR.KZ5
 28 BF.BR.99.BREPM12609
 29 BF.BR.01.BREPM16704
 31 BC.BR.04.04BR141
 32 06A1.EE.01.EE0369
 33 01B.MY.05.05MYKL007.1
 34 01B.TH.99.00R2478P
 35 AD.AF.05.05AF095
 36 cpx.CM.00.00CMNYU830
 37 cpx.CM.00.00CMNYU926
 38 BF1.BY.03.00BY3.3389
 40 BF.BR.05.05BRJ055
 42 BF.LU.03.LU0F.05.03
 43 02G.SA.03.11223
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 CPZ.CD.95.SIVcpzMT145
 CA.88.GA
 CPZ.TZ.00.TAN1
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[illegible]

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FR. 83.HXB2
Rev ex 2
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08 BC.CN. 97.97CNXG 6F
09 cpx.GH. 96.96GH2911
10 CD.TZ. 96.96TZ BF061
11 cpx.CM. 95.95CM 1816
12 BF.AR. 99.ARMA159
13 cpx.CM. 96.96CM 1849
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17 BF.AR. 99.ARMA038
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19 cpx.CU. 99.CU7
20 BG. 99.CU.9C103
21 AZD.CE. 99.KER2003
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23 BG.CY. 03.CB118
24 BG.CY. 03.CB378
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26 AU.CD. 02.02CD MBTB047
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28 BF.BR. 09.BREP12609
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37 cpx.CM. 00.00CMNYU926
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CPZ.CM. 05.SIVcpzMT145
CPZ.CM. 05.GAB1
CPZ.TZ. 00.TANI
CPZ.US. 85.US Marilyn

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A.CD.02.02CD

[illegible][illegible]

Alignments

HIV-1/SIVcpz Complete Genomes

[illegible]

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A. CD. 02. 02CD KTB035	CAG.....	AG-A-A-.....T-A-T-G-.....T-CT-A-A-.....	8983
A. SN. 01. DDJ369	AA.....	ACTCCTCCAGCAG-AAAA-.....AG-A-A-.....T-A-T-G-.....G-.....GAA-.....A-A-G-.....AG-CA-.....	8206
A1. AU. 03. PS1044_Day0	A-A-A-.....	AG-A-A-.....CCTA-.....AA-T-A-T-.....G-.....C-.....TA-ATC-CC-AG-CA-.....	8216
A1. CY. 06. CY171	A-.....	GCTC-CT-.....AGAG-A-A-.....C-T-A-T-.....T-G-.....G-.....C-T-.....T-.....AC-C-.....	8210
A1. GE. 99. 99GEMZ011	T-A-.....	GCTC-CT-.....CCAG-A-A-.....C-T-A-T-.....T-G-.....G-.....C-T-.....T-.....AC-C-.....	8162
A3. IT. 02. 68090	A-.....	GCTCCTGCT-.....AGAG-A-A-.....C-T-A-T-.....T-G-.....G-.....C-T-.....T-.....AC-C-.....	8013
A1. KE. 02. ML1990	A-.....	A-CTT-.....CAG-A-A-.....C-T-A-T-.....T-G-.....G-.....G-T-.....ATA-ATC-CC-AGC-CA-.....	8307
A1. RU. 08. PokA1Ru	A-.....	GCTC-CT-.....CCAG-A-A-.....C-T-A-T-.....T-G-.....G-.....C-T-.....T-.....AC-C-.....	8490
A1. RW. 93. 93RW037A	A-A-A-.....	ACTCCTCCAGGACAAA-.....CCTA-.....AG-A-A-.....T-A-T-.....T-G-.....A-.....T-C-.....A-ATC-CC-AG-CA-.....	8974
A1. SE. 95. SE8538	A-A-G-A-.....	A-CTT-.....AG-A-A-.....T-A-T-.....T-G-.....C-T-.....A-ATC-CC-AG-CA-.....	8174
A1. TZ. 01. A341	A-.....	A-CTT-.....CCAG-A-A-.....C-T-A-T-.....T-G-.....G-.....C-T-.....T-.....AC-C-.....	8152
A1. UA. 01. 01UADN139	A-.....	GCT-.....CCTGCTCCAGCAGCAG-CT-.....ACAG-A-A-.....C-T-A-T-.....T-G-.....G-.....C-T-.....A-ATC-CC-AG-CA-.....	8198
A1. UG. 99. 99UGA07072	G-A-.....	A-CTT-.....AG-A-A-.....T-A-T-.....T-G-.....G-.....C-T-.....A-ATC-CC-AG-CA-.....	8184
A1. ZA. 04. 04ZASK162B1	A-AG-.....	A-CTT-.....AG-A-A-.....T-A-T-.....T-G-.....G-.....C-T-.....A-ATC-CC-AG-CA-.....	8424
A2. CD. 97. 97CDKT848	G-.....	A-CTCCTCCA-.....GCAGCAGAAGGAGTAAGACCAA-CTT-.....AG-A-A-.....T-G-.....A-TT-A-CC-.....G-.....C-T-.....A-ATC-CC-AG-CA-.....	8324
A2. CY. 94. 94CY017_41	A-.....	A-CTCCTCCA-.....ACAGCACAAAGAACAGAGCA-TGTCT-.....CCAG-A-A-.....T-G-.....A-TT-A-CT-CT-.....G-.....C-T-.....A-ATC-CC-AG-CA-.....	8386
B. AR. 04. 04AR143170	C-A-.....	A-.....T-.....T-.....CGG-.....G-.....AT-.....A-AT-.....A-.....	8139
B. AU. 04. PS1038_Day174	R-.....	CR-.....G-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8152
B. BO. 99. BOL0122	AA-.....	AA-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8158
B. BR. 05. BREPM1081	AA-.....	AA-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8406
B. CA. 97. CANB3FULL	CT-.....	CT-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8233
B. CN. 05. 05CNHB_hp3	GA-.....	GA-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8146
B. CO. 01. PCW001	GA-.....	GA-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8530
B. CU. 99. CU19	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8232
B. CY. 06. CY165	A-.....	A-CTGAG-.....CCAGCAGAAAAGGAAAGAA-.....AT-G-.....T-.....G-.....G-.....C-.....T-.....	8490
B. DE. 86. D31	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8350
B. DK. 04. PMVL_012	A-.....	A-CT-.....AGGGAACAGCAGAA-.....ACAG-.....T-.....A-.....C-.....G-.....G-.....A-AT-CC-CA-CT-.....	8143
B. DO. 05. 05DO1_160884	T-.....	GCT-.....GAGCCAGCAAGGCCAGCAAG-.....G-G-.....AG-.....G-.....A-.....C-.....T-.....	8083
B. EC. 89. EC093	G-A-.....	G-A-.....AG-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8404
B. ES. 07. X2231	A-A-.....	A-A-.....AG-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8126
B. FR. 92. 92FR_BX08	A-A-.....	A-A-.....AG-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8517
B. GA. 88. OYI	AG-.....	AG-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8954
B. GB. 86. GB8_468	CA-.....	CA-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8199
B. GE. 03. 03GEMZ004	GA-.....	GA-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8275
B. HT. 05. 05HT_129389	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8999
B. IN. x. 11807	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8373
B. JM. 05. 05JM_KJ108	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8518
B. JP. 05. DR6538	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8432
B. KR. 04. 04KRM05	R-.....	R-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8164
B. MM. 99. mSTD101	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8164
B. NL. 00. 671_00T36	CA-.....	CA-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8221
B. RU. 04. 04RU128005	GA-.....	GA-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8283
B. TH. 00. 00TH_C3198	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8221
B. TT. 01. 01TT_CRC50069	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8194
B. TW. 94. TWYS	A-A-.....	A-A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8379
B. UA. 01. 01UAKV167	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8178
B. US. 07. CR0027M	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8475
B. UY. 01. 01UYTRA1179	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8319
B. YE. 02. 02YES07	AA-.....	AA-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8152
B. ZA. 03. 03ZAPSO45MB2	CA-A-G-.....	CA-A-G-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8191
C. AR. 01. ARG4006	GCTCCTCT-.....	GGTGTAGGAGACAGMAGGAGACAA-CT-.....T-.....GG-A-A-.....C-T-A-.....T-A-T-G-.....G-.....T-G-.....C-T-.....C-CT-AT-AC-.....	8369
C. BR. 04. 04BR013	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8189
C. BW. 00. 00BW07621	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8312
C. CN. 98. YNRL9840	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	9049
C. CY. 05. CY040	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8173
C. ES. 07. X2118_2	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8107
C. ET. 02. 02ET_268	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8108
C. GE. 03. 03GEMZ033	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8210
C. IL. 98. 98IS002	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8186
C. IN. 03. D24	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8161
C. KE. 00. KER2010	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8212
C. MM. 99. mCD001_3	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8363
C. MW. 93. 93MW_965	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	9027
C. SN. 90. 90SE_364	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8499
C. SO. 89. 89SM_145	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8194
C. TZ. 02. C0178	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8456
C. US. 98. 98US_MSC3018	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8861
C. UY. 01. TRA3011	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8961
C. YE. 02. 02YES11	C-.....	C-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8151
C. ZA. 05. 05ZAPSK240B1	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8137
C. ZM. 02. 02ZM108	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8317
D. CD. 83. ELT	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8026
D. CM. 01. 01CM_0009BBY	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8233
D. CY. 06. CY163	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8240
D. KE. 97. ML415_2	T-.....	T-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8762
D. KR. 04. 04KBH8	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8303
D. SN. x. SE365	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8262
D. TD. 99. MN011	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8130
D. TZ. 01. A200	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8965
D. UG. 99. 99UGK09958	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8032
D. YE. 02. 02YES16	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8481
D. ZA. 90. R1	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8134
F1. A0. 06. A0_06_ANG125	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8923
F1. AR. 02. ARE933	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8508
F1. BE. 93. V1850	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8603
F1. BR. 07. 07BR844	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8473
F1. ES. x. P1146	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8137
F1. FI. 93. FIN9363	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8360
F1. FR. 96. 96FR_MP411	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8189
F1. JP. 04. DR6082	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8995
F1. RO. 96. BCI_R07	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8032
F1. RU. 08. 08R_845	T-.....	T-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8481
F2. CM. 97. CM53657	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8134
G. BE. 96. DRCLB	C-A-.....	C-A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8923
G. CM. 04. 178_15	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8508
G. CU. 99. CU74	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8603
G. ES. 05. P962	G-.....	G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8473
G. GH. 03. 03GH175G	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8137
G. KE. 93. H8073_12_1	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8360
G. NG. 01. 01NGPL8669	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8189
G. PT. x. PT2695	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8995
G. SE. 93. SE6165	A-.....	A-.....G-.....A-.....C-T-.....G-.....Y-.....CG-.....G-.....AT-.....A-AT-.....A-.....	8402

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H.CF.90.056		T-A	G	TA				AG	T	C				AA	T	C	GG	8607
H.GB.00.006BAC4001														A	T	C	GG	8796
J.CO.97.1.97DC KTB147		G	TA	T				C	G	A	G			T	GGG	AG	AG	8449
J.SE.93.5E9280 7887		G-TC	TA	T				C	G	A				T	AGCG	AG	G	8582
J.SE.94.5E9173 7022		G-TC	TA	T				C	G	A				T	AGCG	AG	G	8592
K.CO.97.97ZTR EOTB11		G-T	T	T				G	A					T	AGAG	AG	G	8467
K.CM.96.96CM MP535		G-T	T	T				G	A					T	CAG	AG	A	8471
01 AE.CF.90.90CF11697		CT-A	G	T	T			G	A					T	A	AG	AG	9251
01 AE.CN.07.07J5WX045		CT-A	G	T	TA	C		G	C					T	A	AG	AG	8377
01 AE.HK.04.HK001		CT-A	G	T	TA			G	C					T	A	AG	AG	8666
01 AE.JP.x.DR0492		CT-A	G	TA	T			G	A					T	A	AG	AG	9322
01 AE.TH.04.BKM		CT-A	G	T	T			G	C					T	A	AG	AG	9287
01 AE.US.00.00US MSC1164		T-A	G	TA	T			G	C					T	A	AG	AG	8395
01 AE.VN.98.98VND15		CT-A	G	TA	T			G	C					T	A	AG	AG	8575
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02 AG.CY.05.CY048																		8146
02 AG.ES.06.P1261		G	T		A	T			G	A				T	A	GA	G	8744
02 AG.FR.91.DJ263		G	T		A	T			A	AC	C			T	A	GA	G	8680
02 AG.GH.03.03GH181AG		G	T		A	T			A	AACT	C			T	A	GA	G	9352
02 AG.LR.x.POC44951		G	T		A	T			A	CCT	TC			T	A	GA	G	9285
02 AG.NG.01.PL0710		G	T		A	T			A	AACT	TC			T	A	GA	G	8468
02 AG.SE.94.5E7812		G	T		A	T			A	AACT	TC			T	A	GA	G	8674
02 AG.SN.98.98SE MP1211		G	T		A	T			A	AACT	TC			T	A	GA	G	8519
02 AG.US.00.00US MSC3083		G	T		A	T			A	AACT	TC			T	A	GA	G	8401
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04 cpX.CY.94.94CY032 3		G	T						A	AG	TC			T	A	GA	G	8696
05 DF.BE.x.VI1310		T	G	A						AG	TC			T	A	GA	G	8693
06 cpX.AU.96.BFP90		G	T							AG	TC			T	A	GA	G	9329
07 BC.CN.98.98CN009		T	G	T						AGG	TC			T	A	GA	G	8627
08 BC.CN.97.97CNX 6F		T	G	T						AGG	TC			T	A	GA	G	8459
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12 BF.AR.99.ARMA159										AGG	TC			T	A	GA	G	8709
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14 BG.ES.00.XG605		C	G	T	TA	T				AGG	TC			T	A	GA	G	8659
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19 cpX.CU.99.CU7		T	G	T						AGG	TC			T	A	GA	G	8730
20 BG.CU.99.CU103		C	G	TA	T					AGG	TC			T	A	GA	G	8479
21 A2D.KE.99.KER2003										AGG	TC			T	A	GA	G	8372
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25 cpX.CM.02.1918LE										AGG	TC			T	A	GA	G	9296
26 AU.CO.02.02CD MBT0047		C	G	TA	T					AGG	TC			T	A	GA	G	9307
27 cpX.FR.04.04CD FR KZ5		T	G	TA	T					AGG	TC			T	A	GA	G	8697
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-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8932
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8879
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8946
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9007
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8950
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8892
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8861
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9517
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9578
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9526
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9024
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8960
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9022
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9898
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9091
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8561
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9581
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9647
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9003
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9992
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9561
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-8878
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-892
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9487
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9107
-CA-CT-T-A-A-A-G-GAA-C-A-C-G-TA-A-AAA-G-ACAAGA-A-A-T-A-T-A-AG-9469

B. FR. 83. HXB2	NF-κ-B-II		NF-κ-B-I		Spl-III		Spl-II	
	CATCGAGCTTGCTACAAG	GGACTTTCCGCT	GGGGACTTTCCAGGGAGG	CTGGGC	CTGGCGGG	9480		
A. CD. 02. 02CD KTB035	CA-AG	GAC	AAA	A- GAAG	TAA	T T A	A	9502
A. SN. 01. DDJ369	CTGACTGA	CA-AG	G	G	T T	A	A	8738
A1. AU. 03. PS1044 Day0								8667
A1. CY. 06. CY171								8210
A1. GE. 99. 99GEMZ011	CACAACTGC	GAC		GA				9570
A1. IT. 02. 6080	ACTGCTGA	CA-AG		GA- G	T T T	A	A	9573
A1. KE. 02. ML1990	CA-AG	GACT		GA- G	T T T	A	A	8828
A1. RU. 08. PokA1Ru	GACTGCTGACAT	AG- GAC- AG		GA- G	T T T	A	A	9019
A1. RW. 93. 93RW037A	GCA-AG	GAC- A	G	GA- G	T T T	A	A	9493
A1. SE. 95. SE8538	CA-AG	GAC		GA- G	T T T	A	A	8692
A1. TZ. 01. A341	CA- AA	GAC	A	GA- G	T T T	A	A	8670
A1. UA. 01. 01UADN139	GGCTGCTGACAT	AG- GAC	G	GA- G	T T T	A	A	8727
A1. UG. 99. 99UGA07072	CA-AG	GAC		GA- G	T T T	A	A	8702
A1. ZA. 04. 04ZASK162B1	ACTGCTGA	CA-AG	GAC- GGACTTTCTGC	TGG	TGT- GTT	A	A	8974
A2. CD. 97. 97CDKTB48	GATGCTGA	CA-AG	GAC		T T GA	A	A	8855
A2. CY. 94. 94CY017 41	GATGCTGA	CA-AG	GACG		T T G	A	A	8906
B. AR. 04. 04AR143170	C- T- T							8656
B. AU. 04. PS1038 Day174								8603
B. BO. 99. BOL0122	AGTGCTGA	GA- T T		GA- G	A			8703
B. BR. 05. BREPM1081	C- A- T T				T- G			8923
B. CA. 97. CANB3FULL								8687
B. CN. 05. 05CNHB hp3	C- A- T				A- A			9490
B. CO. 01. PCW001	C- A- TG			GA- G	A- A			8664
B. CU. 99. CU19	- - - TG- TT		A					9047
B. CY. 06. CY165								8232
B. DE. 86. D31	ACTGCTGA	T T						9015
B. DK. 04. PMVL 012	C- T- A- CT							8846
B. DO. 05. 05DO0 160884								8330
B. EC. 89. EC093								8310
B. ES. 07. X2231								8921
B. FR. 92. 92FR BX08			AG					8644
B. GA. 88. OYI								9034
B. GB. 86. GB8 46R	CG- AG	T						9470
B. GE. 03. 03GEMZ004	TG			A	GA- G	C		8682
B. HT. 05. 05HT 129389								8398
B. IN. x. 11807								8782
B. JM. 05. 05JM KJ108								8360
B. JP. 05. DR6538								9517
B. KR. 04. 04KRM5	ACTGCTGA	CT- T C			A- G			9488
B. MM. 99. mSTD101	TGA					C- A		8890
B. NL. 00. 671 00T36	AATGCTGA	C- T	AG					9060
B. RU. 04. 04RU128005	ACCGCTGA	A- T			GA- G	T- A		8980
B. TH. 00. 00TH C3198								8394
B. TT. 01. 01TT CRC50069								8390
B. TW. 94. TWY5	Y- T		AG		G	C		9455
B. UA. 01. 01UAKV167	C- T				GA- G	T		8739
B. US. 07. CR0027M	C- T				A- G			8801
B. UY. 01. 01UYTRA1179	C- T					T- G		8738
B. YE. 02. 02YES07	A- T		A		G			8714
B. ZA. 03. 03ZAPS045MB2								8896
C. AR. 01. ARG4006	CACAG- AG- GA- T- CG	TG	A- A	G- G	G	A- T		8699
C. BR. 04. 04BR013	CACAG- AG- GA- T- CG	TG	A- A	G- G	G	A- T		8992
C. BW. 00. 00BW07621	CACAG- AG- GA- T- CG	TG	A- A	G- G	AG	A- T		8837
C. CN. 98. YNRL9840								8152
C. CY. 05. CY040								8191
C. ES. 07. X2118 2	CACAG- AG- GA- T- T	TGCTGACACAG	AA	GRSRS- W	G- YTS- SS- K			8891
C. ET. 02. 02ET 288	CACAG- AG- GA- T- TC	TGCTGACACAG	AAGGACTTTCTGTG	CA- AA				8732
C. GE. 03. 03GEMZ033	CACAG- AG- GA- T- CG			A- G- G	GAG- T			8712
C. IL. 98. 98IS002	CACAG- AG- GA- T- CG	TG	A- A	G- G	A- T			8832
C. IN. 03. D24	CACAG- AG- GA- T- TGCT- ACACAGAAGGGACTTTCCGC	TG	A- A	G- G	G	T		9592
C. KE. 00. KER2010	CACAG- AG- GA- T- T- G	CG	A- A	G- G	AG	T		8694
C. MM. 09. mID01 3	CACAG- AG- GA- T- CG	GG	A- A	G- G	AG	T		8804
C. MW. 93. 93MW 965	CACAG- AG- GA- T- CG	TG	A- A	G- G	AG	T		8680
C. SN. 90. 90SE 364	CACAG- AG- GA- T- CG	TG	A- A	G- G	AG	T		8629
C. SO. 89. 89SM 145	CACAG- AG- GA- T- CG	TG	A- A	G- G	AG	T		8731
C. TZ. 02. C0178								8637
C. US. 98. 98US MSC3018								8337
C. UY. 01. TRA3011	CTGACACAG- AG- GA- T- C	TG	A- C	G- G	AG	A- GA- T		8705
C. YE. 02. 02YES11	CACAG- AG- GA- T- CG	TG	T	G- G	AG	T- T		8733
C. ZA. 05. 05ZAPSK240B1	CACAG- AG- GA- T- CG	TG	A	G- G	AG	A- T		8885
C. ZM. 02. 02ZM108	CACAG- AG- GA- T- CG	TG	A	G- G	AG	A- T		9545
D. CD. 83. ELT	TGACACCG- G	T	G					9019
D. CM. 01. 01CM 0009BBY								8421
D. CY. 06. CY163								8143
D. KE. 97. ML415 2	CACCTG- GT	CACACTGTGGACA	CTGATGTTACTACAAG	A	ACTA- G	T- T T		8998
D. KR. 04. 04KBH8	CACCTG- G		TTTTCTACAGG	G	AAGA- GC	T- A		9382
D. SN. x. SE365	CA- AG	GAC				T- T T		9481
D. TD. 99. MN011	CACCG- GTA- A	GACTGCTGACACCA	AG- CCTTCTACAAG	A	GA- GT			8691
D. TZ. 01. A280	CATCG	GACTGCTGACACCA	AGTTTGTCTACAAG		G- GA- GC	AA- AG		8686
D. UG. 99. 99UGK09958	AAC- GCT- ACACAAG	ATTGCTGACACG	AG- CTGTCTACAAG					8660
D. YE. 02. 02YES16	A- GTTTT- ACAAG			A	G- G	GA- G		8674
D. ZA. 90. R1	CACCG- GTTTTG- ACAAG				GA- G	GTGT- GT		8837
F1. A0. 06. A0 06 ANG125								8146
F1. AR. 02. ARE933	CACAG- GATT	GA- ACAG- AGAATCTAAAAG		A				8338
F1. BE. 93. V1850								8778
F1. BR. 07. 07BR844	AATGCTGA	CA- AGAAT- GA			A- G	GTC- AGA		9209
F1. ES. x. P114	ATCCA- G- GATT	GA- ATAG- AGATTCTAAAG				GTC- AGA		8848
F1. FI. 93. FIN9363	CACAG- GATT	GA- ACAG- AGAATCTAA		A		GTC- AGA		8800
F1. FR. 96. 96FR MP411	GGACACA- G- GATT	GA- ACAG- AG						8614
F1. JP. 04. DR6082	CT	T	TGCTGACATAG	AA- GATTCTAAA	G			9482
F1. RO. 96. BCI R07	ATTGCTGA	A- AGA- TAG- G- T			A- G	GTC- AGA		9505
F1. RU. 08. 08R 845	ATCGCTGA	CA- A- GACACAGAAGATTTA				GTC- AG		9033
F2. CM. 97. CM53657	GA- A- T- GATACAG- AGATTCTAAAAG				A- G	TC- AGA		8659
G. BE. 96. DRCLB	CACAG- AGTT	GA- A- GGGACTTTAAGTTGCTGACA	AA	C	GA- G	C- A		9467
G. CM. 04. 178 15	CA- AG	GAC- CAGATGTTGCTGACAA	GG	A- C	G	C- A		9045
G. CU. 99. CU74	CACAG- AGTT	GA- A						9098
G. ES. 05. P962	CACAG- AGTT	GA- ACAG- TGTTGCTGACAAGG			G- TG	C- A		9011
G. GH. 03. 03GH175G	CTGACACAG- AGTT	GA- A- G			G- GA- G	C- A		9573
G. KE. 93. HB84733 12 1	CACAG- AGTT	GA- A- G						8882
G. NG. 01. 01NGPL8669	CACAG- AGTT	GA- ACAGAGTTTGTGACAA	GG		GA- G	C- A		8726
G. PT. x. PT2695	CACAG- AGTT	GA- A	GG		G- GA- G	C- T		9529
G. SE. 93. SE6165	CACAG- AGTT	GA- A	GG	A- C	G- GA- G	C- A		8924

B. FR. 83.HXB2	NF-κ-B-II		NF-κ-B-I		Spl-III		Spl-II	
	CATCGAGCTTGCTACAAG	GGACTTTCCGCT	GGGGACTTTCCAGGGAGG	CTGTGC	CTGGCGGG	9480		
H.BE.93.VI991	CACAG-AGTT--GA-ACAG-AGATTCTATACA	G	T	TG	GA-G	T	T	8898
H.BE.93.VI997	TACAG-AGATT--GA	CAG	T	G	GA-G	C	T	8797
H.CF.98.056	CACAG-AGATT--GAA	AG	T	G	GA-G	AT		8798
H.GB.00.00GAC4001	ACTGCTGA--CA-AG--GAC-C	GGAAGATCTGA	CAAGACGT	TG		T	T	9008
J.CD.97.1.97DC KTB147	AA-AG-T-A	AGG	T		GA-G	T	C-T	8657
J.SE.93.5E9280 7887	AA-AG-T-A	CGG	T		GA-G	T		8779
J.SE.94.5E9173 7822	AA-AG-T-G		T		GA-G	T		8789
K.CD.97.97ZR E0TB11								8600
K.CM.96.96CM MP535								8604
01 AE.CF.98.90CF11697	GA-AG-T-ACC	A	C-GCT		GA-G	T	T	A 9447
01 AE.CN.97.07J5WX045								8377
01 AE.HK.04.HK001	AA-AG-T-ACT	A	C-GCT		GA-G	T	G	A 8862
01 AE.JP.x.DR0492	AA-AG-T-ACT	G	C-GCT		GA-G	T	G	A 9318
01 AE.TH.04.BKM	A-AG-T-ACT	A	C-GCT		GA-G	T	G	A 9482
01 AE.US.00.00US MSC1164								8395
01 AE.VN.98.98VND15	AA-AG-T-ACTA		C-GCT		GA-G	T	G-T	A 8771
02 AG.CM.02.02CM 0013BBY								8419
02 AG.CY.05.CY048	CA-AA--GAC	ATCT	A	G		T	T-TG	A 8146
02 AG.ES.06.P1261	CA-AG--GAC-A	G	A	G		T	T-T	A 8941
02 AG.FR.91.DJ263	CA-AG--GAC-A	G	A	G		T	T-T	A 8977
02 AG.GH.03.03GH181AG	CTGCTGA--CGG-GA-T-AGAT	TGCTGACAA	G	G-AGG		TGT-GTG	A	A 9572
02 AG.LR.x.POC44951	CA-AG--GAC	G	A-C			TGT-T	A	A 9481
02 AG.NG.01.PL0710	CA-AG--GGAC-AG	A				T-T-T	A	A 8665
02 AG.SE.94.5E7812	ACTGCTGA--CA-AG--GAC-A	TGCTGACAG	GGACTTTCTGACAG	A		TGT-GTT	A	A 8905
02 AG.SN.98.98SE MP1211	CA-AG--GAC-A	G					A	A 8706
02 AG.US.00.00US MSC3083	CA-AG--GAC-A	G	A					8401
02 AG.UZ.02.02UZ0683	CA-AG--GAC-A	G	A			T-T-T	A	A 8692
03 AB.RU.97.KAL153_2	GACTGCTGACAT--AG--GAC		G		GA-G	T	T-T	A 8657
04 cpx.CY.94.94CY032_3	CA-AG--GAC-AAG		C		GA-G	C	A	A 8895
05 DF.BE.x.VI1310	AGTGCTGA--CA-AGC-TTCTAC-A	G					A	8926
06 cpx.AU.96.BFP90	GCTGCTGA--AA-AG-T-ATG							9537
07 BC.CN.98.98CN009	CA-AGGA--TTCC-CG	G	A	G-G	T-AG	T	T	8824
08 CA.CN.97.97CNX 6F	CA-AGGA--TTCC-CG		A-C		GA-G	T		8680
09 cpx.GH.96.96GH2911	CA-AG--T-GC-G		AA					8653
10 CD.TZ.96.96TZ BF061	CA-AGGA--TTCC-CTGG		AA	G-G	AG	A	T	A 8835
11 cpx.CM.95.95CM 1816	ACTGCTGA--CA-AG--GAC		Y		GA-G	T		8895
12 BF.AR.99.ARMA159	ACTGCTGA--CA-AC--GAC-CAGAAGAATCTAAG			A-G-C		G-GCCA-GA	T	9465
13 cpx.CM.96.96CM 1849	AGAGAT--T	A-C-GTT		C				8895
14 BG.ES.00.X605	GCTGCTGA--CA-AG--GAC-AGG		C	T	G	C	A	8962
15 01B.TH.99.99TH MU2079	AA-AG-T-ACT	C-GCT			GA-G	T	G	A 8855
16 A2D.KR.97.97KR004	GCTGCTGA--CA-AG--GAC		A-C		TAG	T	CAA	A 8910
17 BF.AR.99.ARMA038	TGCTGA--CA-A	GAC-CAGAAGAATCTAA	G	A	G-C	G-GCCA-GA		8682
18 cpx.CU.99.CU76	CA-AG--GAC		C		GA-G	C		8810
19 cpx.CU.99.CU7	C-A-T-T		G					8512
20 BG.CU.99.CU103	CA-AG--GAC-AGG	G-ACT-C-GC		G		AA	A	8928
21 A2D.KE.99.KER2003	GCTGCTGA--CT-T-GT	A		G	AG	A	G	8695
22 01A1.CM.01.01CM 0001BBY	CA-AG--GAC-AGG	G-ACT-C-GC		G		TA	A	8937
23 BG.CU.03.CB118	CA-AG--GAC-AAG	G-ACT-C-GC		G		AA	A	8997
24 BG.CU.03.CB378								8425
25 cpx.CM.02.1918LE	CA-AG--GAC		C	T	GA-G	T	T-T	A 9493
26 AU.CD.02.02CD MBT047	CA-AG--GAC-AAA		C		GA-G	C		9506
27 cpx.FR.04.04CD FR K25	ACTGCTGA--A-T-G		C	T	G	A		8886
28 BF.BR.99.BREPM12609								8938
29 BF.BR.01.BREPM16704								8938
31 BC.BR.04.04BR142	CA-AGGA--TTCC-C	TG	A	G-G	AGA	T	T	8999
32 06A1.EE.01.EE0369	AA-AG-T-ACG				GA-G	T		9106
33 01B.MY.05.05MYK1007_1	AA-AG-T-ACTA	A	C-GCT		GA-G	T	G	A 8871
34 01B.TH.99.09R2478P	AA-AG-T-ACTA		C-GCT		GA-G	T	G	A 8634
35 AD.AF.05.05AF095	CA-AG--AC				GA-G	T	T-T	A 8662
36 cpx.CM.00.00CMNYU830								8410
37 cpx.CM.00.00CMNYU926								8396
38 BF1.UY.03.UY03 3389	ATTGCTGA--CA-AGAA--A-G			G	A-G-C	G-GTCA-A	T	8910
39 BF.BR.04.04BRR1379	CT--T				GA-G			8958
40 BF.BR.05.05BRR1055	T--C				A	T-G		A 8995
42 BF.LU.03.1uBF 05 03	C-A-T-T							8930
43 02G.SA.03.J11223	GCTGCTGA--CA-AG--GAC-CAGATGTTGTGACAAAG		C	T	G	C	A	A 9034
N.CM.95.YBF38	AG-GA--T	ACTGCTGACAA	GGGACTTTATACCTGGG	ACT	C-GC		A-T-T	9079
N.CM.97.YBF106	AG-GA--TAC			A	G	A	A-T-T	9001
N.CM.02.DJ00131	AG-GA--TACTA-T				C-GC			8938
N.CM.04.04CM 1015_04	AG-GA--T	ACTGCTGACAA	GGGACTTTACACATGGG	ACT	C-GT			8926
O.BE.87.ANT70	CTGA-GATT--GA-ACGTG		GGAAC	C-A-AA		AGACTGCTGACACTGC	T-GAGG	GACA GG
O.CM.x.BCF06	GA-A	GAC-C	TGC			AAACTGCTGACACTGT	C-T-G	A-G-ATAAG
O.CM.91.MVP5180						AGACTGCTGACACTGC	C-T-GA	G-GATA-AG
O.CM.96.96CMA102	A-GATT-T	GA-ACGT				AGACTGCTGACACTGC	T-T-GAGG	GA-A-AG
O.CM.97.97CMA06447	A-GA-T	GA-ACGTG				AGACTGCTGACACTGC	C-GA	G-GAT-AA
O.CM.98.98CMA184	A-A					AGACTGCTGACACTGC	CAT-GA	G-GAT-AG
O.CM.99.99CMA1122	A-GA-T	GA-ACGTG				AGACTGCTGACACTGC	T-T-GA	G-GAT-AG
O.FR.92.VAU	A-GACT	GA-GCT-C				AGACTGCTGACACTGC	C-T-GA	G-GAC-AG
DO.FR.08.RBF208								8561
O.SN.99.99SE MP1299	A-GATT	GA-ACGTG				AGACTGCTGACACGGC	T-T-GA	G-GAC-AG
O.US.x.I 24788	A-GGTT	GA-ACGTG				AGACTGCTGACATTGC	C-T-G	A-G-A-AAG
O.US.97.97US080692A	A-GGTT	GA-ACGTG				AGACTGCTGACATTGC	C-T-GA	G-GACA-AG
O.US.99.99USTWLA	A-GATT	GA-A-GC				TGCTGACACGGCA	C-T-GA	G-GATA-AG
P.FR.09.RBF168	GCTACTAA					ACACTGCA	G	C-GAAAGTCCCGAGGG
CPZ.CD.98.ANT	CGCTGACAG-G-AGA	TGGTCT				GTGACTATGGGCGGGCAG		A 9631
CPZ.CM.05.SIVcpzMT145	ACTGCTGAT	A-CA-TGTC-AAG						8943
CPZ.GA.88.GAB1		TAG-TG-CGCAATGCGGCAAGAATGCT	TGACTCTGC					9573
CPZ.TZ.00.TAN1	ACTGCTGA--GA-GA--TTGGACT					TG-TTA		9166
CPZ.US.85.US Marilyn	GGCGAATA-AACT--GA-G		AG-ACT	CTA		A	A	9545

	Sp1-II	Sp1-I	TATA box			TAR element start		TAR element end		Poly-A signal		3' LTR R repeat end	3' LTR U5 start
B.FR.83.HXB2	ACT.GGGGAGTGGCGA.GCCCTCAGA	TCC.TGCATATAAGCAGCTGCTTTTTCCTG.TACTGG	GTCTCTCTGGTT	AGACCAGATCTGAGCCTGGGAGCTCTCTGG	CTAACCAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCCTTGAGTGCTTCAAG	9638							
A.CD.02.02CD.KTB035	GT-AA	T-A	G	GCTGC	CTG-T.GTACTAA	TAG	A	A	A	C-G-AA		9660	
A.SN.01.DDJ369			G				A	A	A	G-A		8861	
A1.AU.03.P51044.Day0												8667	
A1.CY.02.CY171												8210	
A1.GE.99.99GEMZ011	GT	T-A	G			T	A			G-G		8792	
A1.IT.02.60000	GT	T-A	G				A			G		9700	
A1.KE.02.ML1990	GT	T-A	G			T				G-G		8943	
A1.RU.08.PokaIRu	GT	T-A	G				G	A		G		9168	
A1.RW.93.93RW037A	GT	T-A	C			T-C				CTG		9644	
A1.SE.95.5E8538	GT	T-A	G			T-A				G-A		8816	
A1.TZ.01.A341	GT	T-A	G			T		GAGC-T				8758	
A1.UA.01.01UADN139	GT	T-A	G							G		8852	
A1.UG.99.99UGA07072	GT	C-A	G			T-G	T			G-A		8824	
A1.ZA.04.04ZASK162B1	GT	T-A	AG			CTTG	T-GA-CAGATA			G-A	AG-CTC-AT	9109	
A2.CD.97.97CDKTB48	GT	T-A	C			CTTG	T-GA-CAGATA		A	G-AG		9172	
A2.CY.94.94CY017.41	GT	T-A	G			T-T	G	A	C	G-AG		9060	
B.AR.04.04AR143170	-G-		G			C	G			CG		8777	
B.AU.04.PS1038.Day174	-A-		G					A		G		8603	
B.BO.99.B0L0122			G									8829	
B.BR.05.BREPML081			GC	TCA-AGGC	GTGC	G-CTG						8988	
B.CA.97.CANB3FULL	-C-						A-C		C	G-T		9657	
B.CA.95.05CNHB.hp3	-A-		G			C			A	G		9641	
B.CO.01.PCM001			G			C						8787	
B.CU.99.Cu19	-A-											9055	
B.CY.06.CY165			G									8232	
B.DE.86.D31												9074	
B.DK.04.PWVL.012												8846	
B.DO.05.05DO.160884												8336	
B.EC.89.EC003	-ACT		G									8310	
B.ES.07.X2231	-C-		G									8950	
B.FR.92.02FR.BX08	-CA.88V1					A-C		C				8735	
B.GA.88V1	-C-		G									9190	
B.GB.86.GB8.46R						A			C	G-G		9628	
B.GE.03.03GEMZ004			G			T-A				G--A		8805	
B.HT.05.05HT.129389												8398	
B.IN.x.11807												8782	
B.JM.05.05JM.KJ108			G									8360	
B.JP.05.DR6538						A				GG-A	CTTGA-T-C	9667	
B.KR.04.04KMH5	-A-		G			CA		C				9046	
B.MM.99.mSTD101	-A-	T-A	G			CA		C		G-G	CT-TAGG-T-ACCTAAATACACT	9218	
B.NL.00.671.00T36			G						A	G		9089	
B.RU.04.04RU120205			G									8394	
B.TH.00.00TH.C3198												8390	
B.TT.01.01TT.CRC50069												9613	
B.TW.94.TWCY5	-R	G-R-A	G									8865	
B.UA.01.01UAKV167	-A-		G									8953	
B.US.07.CR0027M	-A-		G									8861	
B.UY.01.01UYTRA1179			G								A	8836	
B.YE.02.02YE507	-A-		AG							G		9031	
B.ZA.03.03ZAPS045MB2	T-C	TC-A	G			GC	T-A-G			T	G	8822	
C.AR.01.ARG4006			G									9050	
C.BR.04.04BR013	-A	C-A	G				A			T-A		8895	
C.BW.00.00BW07621			G			C						8152	
C.CN.98.YNRL9840							A-G					8191	
C.CY.05.CY040	-C	C	G	G								8921	
C.ES.07.X2118.2		C-A	G									8822	
C.ET.02.02ET.288	-C	T	G				A-G		C	T-A		8835	
C.GE.03.03GEMZ033		T-A	G				A-G			T-C		8986	
C.IL.98.98IS002		T-A	G				A-G		C-A-T	T-G		9749	
C.IN.03.03A.24	-A	TC-A	G				A-G				CTG	8817	
C.KE.00.KER2010		TC-A	G				A-G		A	T		9021	
C.MM.99.mIDU101.3		C	G				A-G		T	C		8771	
C.MW.93.93MW.965		C	G				A-G					8720	
C.SN.90.90SE.364	-A	TC-A	G				A-G		C			8822	
C.SO.89.89SM.145			G				A-G					8637	
C.TZ.02.C0178			G				A-G					8337	
C.US.98.98US.MSC3018	-C-T	C-A	G			GC				C-T		8828	
C.UY.01.TRA3011	-C	T	G				A-GA-G					8854	
C.YE.02.02YES	-A-T	T-A	G				A-GA-G			A-C	T-T	9020	
C.ZA.05.05ZAPSK240B1	-G-	C	G				A-G-G		C	T-CT		9696	
C.ZM.02.02ZM108		T-A	G							G		9176	
D.CD.83.ELI			G									8421	
D.CM.01.01CM.0009BBY												8143	
D.CY.06.CY163	GT	T-A	G				T		TGAGC-TG	GT-CA	G-A	9087	
D.KE.97.ML415.2		A	G									9490	
D.KR.04.04K08	GT	T-A	G				T	A		G		9633	
D.SN.96.SE365		T-A	G									8829	
D.TD.99.MN011		C-A	G			C						8775	
D.TZ.01.A280	G	C-A	G				A-C		T			8782	
D.UG.99.99UGK09958		T-A	G				T		TC			8797	
D.UG.99.99UGK09958		T-A	G				T					8916	
D.YE.02.02YES16	-TC	C-A	G				C-T		A			8146	
D.ZA.90.R1	-T	T-A	G				G-T					8338	
F1.A0.06.A0.06.ANG125												8903	
F1.AR.02.ARE933												9356	
F1.BE.93.VI850		TC-A	G			C	C	A	T	G		8877	
F1.BR.07.07BR844		TT-A	G								A	8925	
F1.ES.x.P1146	-A-A	T-A	G							G	A	8614	
F1.FT.93.FT09363		TC-A	G									9634	
F1.FR.96.96FR.MP411			G									9747	
F1.JP.04.DR6082			G				A					9049	
F1.RO.96.BCI.R07	-A-A	T-A	G				C-T					8782	
F1.RU.08.D88.845		T	G								CC	8707	
F2.CM.97.CM53657	-C	T-A	G			C						9049	
G.BE.96.DRCBL	G	T-A	AG			C	C-C			G-AG	GAG-CTC-AT-AGC-TG-C-TGAGTGC-TC-A	9624	
G.CM.04.04C178.15		T-A	AG				C-C					9096	
G.CU.99.Cu74												9098	
G.ES.05.P962	-GCT	T-A	AG	G								9041	
G.GH.03.03GH175G	G	T-A	AG				C-C-T			GTAGA		9725	
G.KE.93.HH8793.12.1	-A	T-A	AG				C-C	G		G-AG-A	AG-CTC-AT-AGC-TG-C-TGAG-GCG-T	9041	
G.NG.01.01NGPL0669	GACT	A	AG				T-C	G		GTAG		8637	
G.PT.x.PT2695	G	C-A	AG				C-C			A-G-AG		9655	
G.SE.93.SE6165	GT	T-A	AG				C-C			G-AG	AG-CTC-AT-AGC-TG-CAAGCC	9074	

	Sp1-II	Sp1-I	TATA box	TAR element start	3' LTR U3 end	3' LTR repeat start	TAR element end	Poly-A signal	3' LTR R repeat end	3' LTR U5 start	
B. FR. 83. HXB2	ACT. GGGGAGTGGCGA. GCCCTCAGA.	TCC.	TGCATATAAGCAGCTGCTTTTGGCTG. TACTGG. GTCCTCTCTGGTT. AGACCAGATCTGAGCTGGGAGCTCTCTGG. CTAAC TAGGGAACCACTGCTTAAGCTCAATAAAGCTTGCTTGAGTGCTTCAAG	9638							
H. BE. 93. VI991	GA.	T. A.	G.	C. T.	A.	G.	G.	G.	G.	G.	9056
H. BE. 93. VI997	GA.	T. A.	G.	C. T.	G.	T.	G.	G.	G.	G.	9055
H. CF. 90. 056	GA.	C. A.	G.	C. T.	G.	T.	G.	G.	G.	G.	8953
H. GB. 00. 00GBAC4001	GT.	T. A.	G.	C. T.	G.	T.	G.	G.	G.	G.	9081
J. CD. 97. J. 97DC KTB147	GT.	T. A.	G. A.	G.	A.	C.	C. T.	G.	G.	G.	8739
J. SE. 93. SE9289 7897	GT.	T. A.	G.	C. T.	G.	T.	G.	G.	G.	G.	8937
J. SE. 94. SE9173 7092	GT.	T. A.	G.	C. T.	G.	T.	G.	G.	G.	G.	8947
K. CD. 97. 97ZR E0TB11											8600
K. CM. 96. 96CM MP535											8604
01 AE. CF. 90. 90CF11697	GT.	T. A.	G.	A.	C.	C. T.	T. A.	G.	C.	G. A.	9604
01 AE. CN. 07. 07J5WX045	GT.	T. A.	G.	A.	C.	C. T.	T. A.	G.	C.	G. A.	8377
01 AE. HK. 04. HK001	GT.	T. A.	G.	A.	C.	C. T.	T. A.	G.	C.	G. A.	9019
01 AE. JP. x. DR0492	GT.	T. A.	G.	A.	C.	C. T.	T. A.	G.	C.	G. A.	9670
01 AE. TH. 04. BKM	GT.	T. A.	G.	A.	C.	C. T.	T. A.	G.	C.	G. A.	9639
01 AE. US. 00. 00US MSC1164	GT.	T. A.	G.	A.	C.	C. T.	T. A.	G.	C.	G. A.	8395
01 AE. VN. 98. 98VNN015											8875
02 AG. CM. 02. 02CM 0013BBY											8419
02 AG. CY. 05. CY048											8146
02 AG. ES. 06. P1261	GTC.	T. A.	AG.	CTG.							8972
02 AG. FR. 91. DJ263	GT.	T. A.	AG.	C.	C.	C.	T.	A.	G.	G. AGA.	9002
02 AG. GH. 03. 03GH121AG	GT.	T. A.	AG.	C.	C.	C.	T.	A.	G.	G. AGA.	8724
02 AG. LR. x. P044951	GT.	T. A.	G.	C.	C.	C.	T.	A.	G.	G. AGA.	9633
02 AG. NG. 01. PL0710	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AGA.	8787
02 AG. SE. 94. SE7812	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AGA.	9063
02 AG. SN. 98. 98SE MP1211	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AGA.	8851
02 AG. US. 00. 00US MSC3083	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AGA.	8401
02 AG. UZ. 02. 02UZ0683	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AGA.	8815
03 AB. RU. 97. KAL153_2	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AGA.	8808
04 cpx. CY. 94. 94CY032_3	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AGA.	9050
05 DF. BE. x. VI1310											9083
06 cpx. AU. 96. BFP90	G.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9695
07 BC. CN. 98. 98CN009											8978
08 BC. CN. 97. 97CN03_6F											8892
09 cpx. GH. 96. 96GH1211	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	8810
10 CD. TZ. 96. 96TZ BF061											8976
11 cpx. CM. 95. 95CM 1816	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9017
12 BF. AR. 99. ARMA159											9623
13 cpx. CM. 96. 96CM 1849											8916
14 BG. ES. 00. X605	G.	T. A.	AG.	C.	C.	C.	T.	A.	G.	G. AG.	8989
15 01B. TH. 99. 99TH MU2079	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	8999
16 A2D. KR. 97. 97KR004	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9064
17 BF. AR. 99. ARMA038	-A.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	8808
18 cpx. CU. 99. CU76	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	8945
19 cpx. CU. 99. CU7											8512
20 BG. CU. 99. CU103	G. G.	A.									8935
21 A2D. KE. 99. KER2003	-A.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	8816
22 01A1. CM. 01. 01CM 0001BBY											8372
23 BG. CU. 03. CB118	G.	GAG.	T. A.	AG.	G.						8964
24 BG. CU. 03. CB378											9025
25 cpx. CM. 02. 1918LE											8425
26 AU. CD. 02. 02CD MBTB047	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9650
27 cpx. FR. 04. 04CD FR. K25	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9664
28 BF. BR. 99. BREPM12609											8886
29 BF. BR. 01. BREPM16704											8979
31 BC. BR. 04. 04BR142	-C.	A.	C.	A.	A.	T.	TGT. ACAA.				9057
32 06A1. EE. 01. EE0369	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9229
33 01B. MY. 05. 05MYK1007_1	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9028
34 01B. TH. 99. 01B2478P	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	8650
35 AD. AF. 05. 05AF095	GT.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	8703
36 cpx. CM. 00. 00CMNYU830											8410
37 cpx. CM. 00. 00CMNYU926											8396
38 BF1. UY. 03. UY03 3389											8935
39 BF. BR. 04. 04BRRJ179	-A.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9057
40 BF. BR. 05. 05BRRJ055	-A.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9042
42 BF. LU. 03. 1uBF 05_03	-A.	T. A.	G.	A.	C.	C.	T.	A.	G.	G. AG.	9063
43 02G. SA. 03. J11223											9085
N. CM. 95. YBF30	GT. G.	TT.	G.	ATA. A. GC.	C.	C.	T.	A.	G.	G. AG.	9182
N. CM. 97. YBF106	GTCG.	TT.	G.	ATA. A. GC.	C.	C.	T.	A.	G.	G. AG.	9045
N. CM. 02. DJ00131											8938
N. CM. 04. 04CM 1015_04											8926
0. BE. 87. ANT70	TTC.	T. A.	AG.	C.	C.	C.	T.	A.	G.	G. AG.	9753
0. CM. x. BCF06	TTC.	T. A.	G.	C.	C.	C.	T.	A.	G.	G. AG.	9811
0. CM. 91. MVP5180	TTC.	T. A.	G.	C.	C.	C.	T.	A.	G.	G. AG.	9754
0. CM. 96. 96CMA102	TTC.	T. A.	AG.	C.	C.	C.	T.	A.	G.	G. AG.	9226
0. CM. 97. 97CMA06447	T. C.	T. A.	G.	C.	C.	C.	T.	A.	G.	G. AG.	9161
0. CM. 98. 98CMA104	T. C.	T. A.	G.	C.	C.	C.	T.	A.	G.	G. AG.	9243
0. CM. 99. 99CMU4122	TTC.	T. A.	G.	C.	C.	C.	T.	A.	G.	G. AG.	9186
0. FR. 92. VAU	TTC.	T. A.	AG.	C.	C.	C.	T.	A.	G.	G. AG.	9330
DO. FR. 08. RBF208											8561
0. SN. 99. 99SE MP1299	TTC.	T. A.	G.	C.	ACC. T.	C.	G. G. TAGA. GA.	G.	C.	C.	9820
0. US. x. I 2478B	TTC.	T. A.	AG.	C.	C.	C.	G. G. TAGA. GA.	G.	C.	C.	9881
0. US. 97. 97US08692A	TTC.	T. A.	AG.	C.	C.	C.	G. G. TAGA. GA.	G.	C.	C.	9147
0. US. 99. 99USTWLA	T. C.	T. A.	AG.	C.	C.	C.	G. G. TAGA. GA.	G.	C.	C.	9186
P. FR. 09. RBF168	G. A.	TTTCA.	G.	CAC. T.	G.	AC.	TA.	CTTAAGCA.	GGAAGCTC. AT.	AGC. TG. C. TGAGTGAGT.	9788
CPZ. CD. 90. ANT		TTTC.	G. CT.	G.	GC. T.	TAA.	CTCTCTGCC. AGGAG.	A.	TA. TT. TT.	C. GGAGACC.	9068
CPZ. CM. 05. STVcpzMT145	CPZ. GA. 88. GT.	AG.	TTT.	AAACA.	AG.	GC. C. C. T.	CA.	T. G.	A.	C. GT. A.	9730
CPZ. TZ. 08. TAN1	GT.	T. A.	G.	C.	C.	C.	T.	A.	G.	G. AG.	9068
CPZ. US. 85. US_Marilyn	-A.	TTTT.	G. T.	G.	GC.	TCT. GTAAA. GC.	TG. CTAA.	CTG.	AA.	C.	9324
	-A. A.	C.	TTTTA.	A.	GA.	C.	C.	C.	AA.	C.	9702

Extensive secondary structure in this region?

3' LTR U5 end

B.FR.83.HXB2		9719
A.CD.02.02CD_KTB035		9740
A.SN.01.DDJ369		8861
A1.AU.03.PS1044_Day0		8667
A1.CY.06.CY171		8210
A1.GE.99.99GEMZ011		8792
A1.IT.02.68080		9781
A1.KE.02.WL1990		8943
A1.RU.08.Poka1Ru		9168
A1.RW.93.93RW037A		9644
A1.SE.95.SE8538		8816
A1.TZ.01.A341		8758
A1.UA.01.01UADN139		8852
A1.UG.99.99UGA07072		8824
A1.ZA.04.04ZASK162B1		9109
A2.CD.97.97CDKT848		8972
A2.CY.94.94CY017_41		9060
B.AR.04.04AR143170		8777
B.AU.04.PS1030_Day174		8603
B.B0.99.B0L0122		8829
B.BR.05.BREP1081		8988
B.CA.97.CANB3FULL		8687
B.CN.05.05CNHB_hp3		9641
B.CO.01.PCM001		8787
B.CU.99.Cu19		9055
B.CY.06.CY165		8232
B.DE.86.D31		9074
B.DK.04.PMVL_012		8846
B.DO.05.05D0_160884		8336
B.EC.89.EC003		8310
B.ES.07.X2231		8940
B.FR.92.92FR_BX08		8735
B.GA.88.OYI		9190
B.GB.86.GB8_46R		9679
B.GE.03.03GEMZ004		8805
B.HT.05.05HT_129389		8398
B.IN.x.11807		8782
B.JM.05.05JM_KJ108		8360
B.JP.05.DR6538		9667
B.KR.04.04KPMH5		468
B.MM.99.MSTD181		9098
B.NL.00.671_00736		9359
B.RU.04.04RU128005		9089
B.TH.00.00TH_C3198		8394
B.TT.01.01TT_CRC50069		8390
B.TW.94.TWCY5		9044
B.UA.01.01UAKV167		8865
B.US.07.CR0027M		8953
B.UY.01.01UYTRA1179		8861
B.YE.02.02YE507		8836
B.ZA.03.03ZAPS045MB2		9031
C.AR.01.ARG4006		8822
C.BR.04.04BR013		9050
C.BW.00.00BW07621		9047
C.CN.98.YNRL9840		8152
C.CY.05.CY040		8191
C.ES.07.X2118_2		8921
C.ET.02.02ET_288		8802
C.GE.03.03GEW2033		8835
C.IL.98.98IS002		8986
C.IN.03.D24		9830
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Extensive secondary structure in this region?

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 CPZ.US.85.US_Marilyn

III

HIV-2/SIV Complete Genomes

Contents

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III-1 Introduction

The HIV-2/SIVsmm alignment contains a non-redundant set of all HIV-2, SIVsmm, and related species (SIVmne, SIVstm and SIVmac). Compared to HIV-1, only a small number of HIV-2 complete genomes have been determined, so this alignment contains all but a few duplicate sequences available in the database. The web alignment has a few additional sequences.

The HIV-2/SIVsmm family is presented together in spite of their different hosts, because their genomic structure is the same—the complete SIV alignment (presented in the next chapter along with a few HIV-1 sequences) is much more stretched out because of the presence of a vpx and absence of vpr genes in some of these viruses.

As with HIV-1/SIVcpz, this alignment was generated by an iterative process between automated alignment using HMMER and manual editing using BioEdit and Se-Al. As in previous years, the alignment presented is not suggested to be an “optimal alignment” with the absolute minimum number of gaps and mismatches. It is a compromise between optimal alignment, readability, and an attempt to keep insertions and deletions from altering the protein reading frame presentation. Most gaps have been introduced in multiples of 3 bases to maintain open reading frames when translated directly from the alignment.

As before, the MAC239 sequence is the master sequence in this set.

III-2 Annotated features

Features of HIV-2 annotated in the alignment that follows.

Feature	Location	Page
5' LTR U3 start	1	158
TCF-1 alpha	309-324	159
NF- κ -B-II	415-424	160
NF- κ -B-I	441-449	161
TATA Box	488-493	161
TAR element start	518	161
5' LTR U3 end	520	161
+1 mRNA start site	521	161
5' LTR R repeat begin	521	161
TAR element end	642	162
Poly-A signal	671-676	162
5' LTR R repeat end	694	162
5' LTR U5 start	695	162
5' LTR U5 end	818	163
Lys tRNA primer binding site	821-839	163
Gag and Gag-Pol start	1053	165
Gag p17 Matrix end	1457	167
Gag p24 Capsid start	1458	167
Gag p24 Capsid end	2144	171
Gag p2 Spacer start	2145	171
Gag p2 Spacer end	2195	171
Gag p8 Nucleocapsid start	2196	171
Gag p8 Nucleocapsid end	2351	172
Gag p1 Spacer start	2352	172
Gag-Pol -1 ribosomal slip site	2354	172
Pol start	2354	172
Gag p1 spacer end	2393	173
Gag p6 start	2394	173
Pol Protease start	2555	174
Gag p6 end	2585	174
Gag end	2585	174
Pol Protease end	2851	176
Pol p66 and p51 RT start	2852	176
Pol RT end	4168	183
Pol p15 RNase H start	4169	183
Pol RNase H end	4528	186
Pol p31 Integrase start	4529	186
Vif start	5340	190
Pol, Gag-Pol, and p31 Integrase end	5410	191
Vpx start	5812	193
Vif end	5984	194
Vpx end	6150	195
Vpr start	6151	195
Tat exon 1 start	6302	196
Vpr end	6456	197
Rev exon 1 start	6528	197
Tat Rev exon 1 end	6597	198
Tat Rev intron start	6598	198

Feature	Location	Page
Env signal peptide start	6604	198
Env signal peptide end	6669	198
Env gp120 start	6670	198
V1 loop start	6733	199
V1 loop end	6774	199
V2 loop start	6904	200
V2 loop end	7074	201
V3 loop start	7183	201
V3 loop end	7392	203
V4 loop start	7534	204
V4 loop end	7635	204
V5 loop start	7786	205
V5 loop end	7980	206
Rev Responsive Element (RRE) start	8123	207
Env gp120 end	8178	208
Env gp41 start	8179	208
RRE end	8479	209
Tat Rev intron end	8805	211
Tat Rev exon 2 start	8806	211
Tat end	8902	212
Rev end	9059	213
Nef start	9077	213
Env gp41, gp160 end	9243	214
Premature stop in SMM239	9355	215
3' LTR U3 start	9462	215
TCF-1 alpha binding	9770-9785	217
Nef end	9868	218
NF- κ -B-II	9876-9884	218
NF- κ -B-I	9891-9900	218
TATA box	9949-9955	219
TAR element start	9980	219
3' LTR U3 end	9978	219
3' LTR repeat start	9979	219
TAR element end	10103	220
Poly-A signal	10132-10137	220
3' LTR R repeat end	10155	220
3' LTR U5 start	10156	220
3' LTR U5 end	10279	221

III-3 Sequences

Sequences included in the HIV-2/SIV complete genome alignment.

Name	Accession	Country	Author	Reference
MAC.US.x.239	M33262	United States	Kestler, H.	<i>Science</i> 248 (4959):1109-1112 (1990)
A.CI.88.UC2	U38293	Cote D'Ivoire	Barnett, S.W.	<i>Virology</i> 222 (1); 257-61 (1996)
A.DE.x.BEN	M30502	Germany	Kirchhoff, F.	<i>Virology</i> 177 (1):305-311 (1990)
A.DE.x.PEI2	U22047	Germany	Kraus, G.	<i>ARHR</i> 14 (1); 65-77 (1998)
A.GH.x.GH1	M30895	Ghana	Hasegawa, A.	<i>ARHR</i> 5 (6):593-604 (1989)
A.GM.87.D194	J04542	Gambia	Kuehnelt, H.	<i>Proc Natl Acad Sci USA</i> 86 (7):2383-2387 (1989)
A.GM.x.ISY	J04498	Gambia	Franchini, G.	<i>Proc Natl Acad Sci USA</i> 86 (7):2433-2437 (1989)
A.GM.x.MCN13	AY509259	Gambia	Schmitz, C.	<i>J Virol</i> 78 (4):2006-2016 (2004)
A.GM.x.MCR35	AY509260	Gambia	Schmitz, C.	<i>J Virol</i> 78 (4):2006-2016 (2004)
A.GW.86.FG	J03654	Guinea- Bissau	Zagury, J.F.	<i>Proc Natl Acad Sci USA</i> 85 (16):5941-5945 (1988)
A.GW.87.CAM2CG	D00835	Guinea- Bissau	Tristem, M.	<i>J Gen Virol</i> 72 (PT 3):721-724 (1991)
A.GW.x.ALI	AF082339	Guinea- Bissau	Azevedo-Pereira, J.M.	Unpublished
A.GW.x.MDS	Z48731	Guinea- Bissau	Becker, M.	Unpublished
A.IN.95.CRIK_147	DQ307022	India	Santhosh, C.V.	<i>ARHR</i> 24 (10):1315-1317 (2008)
A.IN.x.NNVA	EU980602	India	Desai, A.	Unpublished
A.SN.85.ROD	M15390	Senegal	Clavel, F.	<i>Nature</i> 324 (6098):691-695 (1986)
B.CI.88.UC1	L07625	Cote D'Ivoire	Barnett, S.W.	<i>J Virol</i> 67 (2):1006-1014 (1993)
B.CI.09.pPRD320-20HIV2_56	AB485670	Cote D'Ivoire	Takekawa, N.	Unpublished
B.CI.x.EHO	U27200	Cote D'Ivoire	Rey-Cuille, M.A.	<i>Virology</i> 202 (1):471-476 (1994)
B.GH.86.D205	X61240	Ghana	Dietrich, U.	<i>Nature</i> 342 (6252):948-950 (1989)
B.JP.01.KR020	AB100245	Japan	Kusagawa, S.	<i>ARHR</i> 19 (11):1045-1049 (2003)
G.CI.92.ABT96	AF208027	Cote D'Ivoire	Brennan, C.A.	<i>ARHR</i> 13 (5):401-404 (1997)
AB.CI.90.7312A	L36874	Cote D'Ivoire	Gao, F.	Unpublished
AB.CM.03.03CM_510_03	EU028345	Cameroon	Yamaguchi, J.	<i>ARHR</i> 24 (1):86-91 (2008)
U.FR.96.12034	AY530889	France	Damond, F.	<i>ARHR</i> 20 (6):666-672 (2004)
MAC.US.x.17EC1	AY033233	United States	Anderson, M.G.	<i>Virology</i> 195 (2):616-626 (1993)
MAC.US.x.17EFR	AY033146	United States	Flaherty, M.T.	<i>J Virol</i> 71 (8):5790-5798 (1997)
MAC.US.x.1937	AY611495	United States	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.2065	AY611493	United States	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.251_1A11	M76764	United States	Marthas, M.L.	<i>J Med Primatol</i> 18 (3-4):311-9 (1989)

Name	Accession	Country	Author	Reference
MAC.US.x.251_32H_PJ5	D01065	United States	Rud, E.W.	(in) Brown, F, Chanock, RM and Ginsberg, HS (Eds); <i>VACCINES 92: MODERN APPROACHES TO NEW VACCINES INCLUDING PREVENTION OF AIDS</i> : 229-235; Cold Spring Harbor Laboratory Press, New York (1992)
MAC.US.x.251_BK28	M19499	United States	Hirsch, V.	<i>Cell</i> 49 (3):307-319 (1987)
MAC.US.x.80035	AY611486	United States	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.97074	AY599198	United States	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.MAC239_87082	AY600249	United States	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.MM142	Y00277	United States	Chakrabarti, L.	<i>Nature</i> 328 (6130):543-547 (1987)
MAC.US.x.SMM142B	BD131285	United States	Alizon, M.	Patent: JP 2002030099-A 2 29-JAN-2002; INSTITUT PASTEUR
MAC.US.x.r80025	AY576480	United States	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.r90131	AY576481	United States	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MNE.US.82.MNE_8	M32741	United States	Kimata, J.T.	<i>J Virol</i> 72 (1):245-256 (1998)
MNE.US.x.MNE027	U79412	United States	Kimata, J.T.	<i>J Virol</i> 72 (1):245-256 (1998)
SMM.SL.92.SL92B	AF334679	Sierra Leone	Chen, Z.	<i>J Virol</i> 70 (6):3617-3627 (1996)
SMM.US.x.F236_H4	X14307	United States	Hirsch, V.M.	<i>Nature</i> 339 (6223): 389-92 (1989)
SMM.US.x.H9	M80194	United States	Courgnaud, V.	<i>J Virol</i> 66 (1):414-419 (1992)
SMM.US.x.PBJ14_15	L03295	United States	Dewhurst, S.	<i>Nature</i> 345 (6276):636-640 (1990)
SMM.US.x.PBJA	M31325	United States	Dewhurst, S.	<i>Nature</i> 345 (6276):636-640 (1990)
SMM.US.x.PBJ_143	M80193	United States	Courgnaud, V.	<i>J Virol</i> 66 (1):414-419 (1992)
SMM.US.x.PBJ_6P6	L09212	United States	Novembre, F.J.	<i>J Virol</i> 67 (5):2466-2474 (1993)
SMM.US.x.PGM53	AF077017	United States	Novembre, F.J.	<i>J Virol</i> 72 (11):8841-8851 (1998)
SMM.US.x.SME543	U72748	United States	Hirsch, V.	<i>J Virol</i> 71 (2):1608-1620 (1997)
STM.US.x.STM	M83293	United States	Novembre, F.J.	<i>Virology</i> 186 (2):783-787 (1992)

	5' LTR U3 start	
MAC.US.x.239	TGGAAGGGATTATTACAGTCAAGA.AGACATAGAATCTTAGACATATACTTAGAAAAGGAAGAGGCATCATACAGATTGGCAGGATTACACCTCAGGACCAGGAATTAGATACCCAAAGACATTGGCTGGCTATGGAAATTAGTCCTGTAAATGTATCAGATGA	169
A.CI.88.UC2	G-T.....AGGGAT.....C-T-G-C.....G-G-A-G.....A-T-TCAT-G.....G-G-G.....T-TGC-C-G.....G-C-A-A.....CA-G-C-A-	169
A.DE.x.BEN	C-T.....AGG-G.....C-T-G-C.....A-G.....G-A-T.....A-T-TCAT-G.....G-A-G.....T-TAC-C-G.....GC-AT-A-G-AC-C-C-A-	169
A.DE.x.PE12	T-G.....AG-G.....A-G.....G-A-T.....A-C-T-TCAT-G.....G-A-G.....TTC-G.....GC-A-A-G-C-CC-C-A-G	170
A.GH.x.GH1		0
A.GM.87.D194		0
A.GM.x.ISY		0
A.GM.x.MCN13		0
A.GM.x.MCR35		0
A.GW.86.FG		0
A.GW.87.CAM2CG	C-G-T.....A.....C-G-T.....A.....G-A-TG.....A-C-T-TAGT-G.....G-A.....T-TTC.....G.....GC-A-A-G-ACC-C-A-	169
A.GW.x.ALI	G-T.....AG.....A-C-T-TCAT-G.....A-A-G.....G-T-TTC.....G.....G.....GC-A-A-G-CC-C-A-	169
A.GW.x.MDS		0
A.IN.95.CR1K.147	G-T.....A.....T.....GAGA.....A-TT.....G-G-A-T.....C.....A-C-T-AGT-G.....A.....T.....T-TTCCA-G.....GC-A-A.....GTC	27
A.IN.x.NNVA	G.....AG.....	0
A.SW.85.ROD		0
B.CI.88.UC1	C-T-AG.....AC.....C-TC.....G-T-G.....TG-T-T-GA.....AA-C-T-A-AT-G.....G-A-G-T.....G-C-G.....GC-G-A-G-A-C-G-	169
B.CI.89.pPRD320-20HIV2_56	C-T-AG.....AC.....T-C-TC.....G-T-G.....G-TG-T-T-GA.....AA-C-T-ACAT-G.....G-A-G-T.....C-C-G.....GC-G-A-A-C-C-G-	168
B.CI.x.EH0	TC-T-AG.....G-A-AC.....C-TC.....T.....TG-GT-T-GA.....A-C-ACAT-G.....G-A-T-C-TTC.....GC-G-AA-A-GAT-CA-	169
B.GH.86.D205	G-T.....AG.....C-A.....C-T-T-G-T.....TG-GT-T-GC.....AA-C-T-TCAT-G.....G-A-GC-T-C-ATAC.....T.....G.....GC-G-A-A-G-G-GC-CA-C	169
B.JP.01.KR020		0
G.CI.92.ABT96		0
AB.CI.90.7312A	T-T-A.....G-A.....T-C-T-T-G-T-GAG.....T-AG-TGGT-GA.....A-C.....A-AT-G.....G-A.....ACAC.....G.....C.....G-A-GG-A-GG-CA-T	169
AB.CM.03.03CM_510_03		0
U.FR.96.12034		0
MAC.US.x.17EC1		169
MAC.US.x.17EFR		169
MAC.US.x.1937		0
MAC.US.x.2065		0
MAC.US.x.251.1A11	T.....	169
MAC.US.x.251.32H.PJ5		169
MAC.US.x.251.BK28	G.....	169
MAC.US.x.80035		0
MAC.US.x.97074		0
MAC.US.x.MAC239_87082		0
MAC.US.x.MM142		0
MAC.US.x.SMM142B		0
MAC.US.x.r80025		0
MAC.US.x.r90131		0
MNE.US.x.82.MNE.8		0
MNE.US.x.MNE027		0
SMM.SL.92.SL92B		0
SMM.US.x.F236_H4	A-AG.....A-T-G-G.....A-A.....AA.....A-G.....T-T-CAC-A-G-C.....A-G-C.....	169
SMM.US.x.H9		0
SMM.US.x.PB114_15		0
SMM.US.x.PBJA		0
SMM.US.x.PB1_143		0
SMM.US.x.PBJ_6P6		0
SMM.US.x.PGM53	AA.....A-G.....C.....T-T-TTC.....A.....C.....G-G-C.....	95
SMM.US.x.SME543	AA.....A-G.....C.....T-T-TTC.....G.....G.....G-A-G-C.....	95
STM.US.x.STM	A-AG-A.....A-T-G-A-G.....A-A.....AA.....A-T-G.....C.....T-T-TAC.....G.....C.....A-G-C.....	169
	AG.....	201

TCF-1 alpha

MAC.US.x.239	GGCA...CAGGAGGATGAGGAG.....CATTATTTAATGCATCCAGCTCAAACCTCCAGTGGGATGACCTTGGGGAGAGGTTCTAGCATGGAAGTTTGATCCAACTCTGGCTACACTTATGAGGCATATGTTAGATACCCAGAAGAGTTTGGAAAGCAAGT	324
A.CI.88.UC2	G---T-----ACC.....A-C-GC-----C-----A-----AAG-AGA-AT-----ATACAT--G--ACA---TG--CG---A-CT-C-TG-----TGAG--CA---C-TCAC-CT-----A-----GCA-----	324
A.DE.x.BEN	G---A-----CC.....A-C-GC-----G-A-C-----A-----AAG-AGACAT--TGAGCAT--G--ACAT--TG--C-----CT-C-TG-----T-AC--CA---C-TCAC-CTG-----GCA-----	324
A.DE.x.PET2	T.....G---A-----C-----C-GC-----C-A-C-----A-----AAG-GG--CT-----CAT--G--AACAT--ATG--G-----C-T-GG-----TGAG--AC---T-T-AA-C-----A-----GTAT-----	316
A.GH.x.GH1		0
A.GM.87.D194		0
A.GM.x.IS1		0
A.GM.x.MCN13		0
A.GM.x.MCR35		0
A.GW.86.FG		0
A.GW.87.CAM2CG	..-G---G---CAC---ACTGACACTGAGACT--C-GC--T-A-C-----A-----AAG-AG-CAT-----ATGCAT--G--ACA--G-TC-----CT-C-TG-----CTT-AG-----C-T-AC-C-----A-----GCA-----	336
A.GW.x.ALI	A-GG...G---CAC---ACT.....C-GCC-GC-A-C-----TA-----AAG-AG-CAT-----A-GCAT--G--ACAT--TT--GA---C-T-AG-----TC-TGA--CA-A--C-T-A--CT-C-----G--A-----GTA-----	324
A.GW.x.MD5		0
A.IN.95.CR1K 147		0
A.IN.x.NNVA	CCAC...A-AG--GA-ACA...CTGAAACTCAC-GC--A-TGCACC-AGCACA--CAAGTA---TT--AGACAT--G--ACA---T--GA-----C-AT-A---TGA---TA--C-T-AGGCT-C-----G-A-----GCA-----	324
A.SN.85.R0D		0
B.CI.88.UC1	--A---AG--GA-CG--AACC.....AG--G-C-GG--C---A--G-TC--TTCA-----ATCCAC--G--ACC--T--C--CG---C--CCTC---AC-TGAC---TA--C-TCAAC--G-----GTATC-----	324
B.CI.09.pPRD320-20HIV2_56	A-A---G-AGA-CA-AA-C-----AG--G-C-GG--C---A--G-C--TCA-----CCAC--G--AACC--T-TC--C---C--CCTC---AC-TGAC---ATA--C-TCAAC--G-T-----GTATC-----	323
B.CI.x.EH0	AC---G---C--G--AACC.....G-C-GG-----A--G-C--GCA-----CCAC-A--ACC--T-TC--C---CT-CCTC--A--TGAC---T--C-TGAGC--G-T-----G-----GTATC-----	324
B.GH.86.D205	-A-CCGAG---G--AACC.....GCC-----C--G--A--G-TC--TCA-----ATCCAT--G--AC--TATC--C---T-CCTC---A--TGA---T--T-TCAA--G-TT-----C--GTA-C-----	327
B.JP.01.KR020		0
G.CI.92.ABT96		0
AB.CI.90.7312A	AA-CCGGG---A-G---ACC.....--G-C--G---C---A--G--CG--GCA-----T-CAT--GAGA.C---T-TC---C-----T-CCTC---A--TT-AG-----C-TCAAC--G-T-----GTATC-----	326
AB.CM.03.03CM_510_03		0
U.FR.96.12034		0
MAC.US.x.17EC1		324
MAC.US.x.17EFR		324
MAC.US.x.1937		0
MAC.US.x.2065		0
MAC.US.x.251_1A11	C-----C-----A-----	324
MAC.US.x.251_32H_PJ5	AG-----G-----A-----	324
MAC.US.x.251_BK28	AG-----G-----A-----C-----	323
MAC.US.x.80035		0
MAC.US.x.97074		0
MAC.US.x.MAC239_87082		0
MAC.US.x.MM142		0
MAC.US.x.SMM142B		0
MAC.US.x.r80025		0
MAC.US.x.r90131		0
MNE.US.82.MNE_8		0
MNE.US.x.MNE027		0
SMM.SL.92.SL92B		0
SMM.US.x.F236_H4	A-T-----A-C--ACA.....GCC-GG-----G-A-G--AT-----C-----A--G-----GAAT-A-T-T-GC--A---T-A--AG-----T--T-----	324
SMM.US.x.H9	AGT-A-T-T-AC--A---T---GAGCG-----T--TC-----	79
SMM.US.x.PBJ14_15	G-----AGT-A-T-T-AC--A---T---GAGC-----T--TC-----	79
SMM.US.x.PBJA		0
SMM.US.x.PBJ_143	A-T-----A-C--ACA.....C-G-----A-----T-----C-----A--G-----AGT-A-T-T-AC--A---T---GAGC-----T--TC-----	250
SMM.US.x.PBJ_6P6	A-T-----A-A-C--ACA.....C-G-----A--G-TA-----T-C-----A--G-----T-CAAT-A---GA-----T-T-A---C-----T--T-----	250
SMM.US.x.PGH53	A-C-----A-C--ACA.....GCC-GG-----A--G--CAT-----C-----A--G-----GAAT--T-T-GC--A---T-A--AG-----T--T-----	324
SMM.US.x.SME543		27
STM.US.x.STM		

										NF-K-B-11																			
MAC.US.x.239	CAGGCGTGT CAGAGGAAGAGGTTAGAGAAGGCTAACCGCAAGAGGCCTTCTTAACATGGCTGACAAG										AA	GGAAACTCGCTGAAACAGCAGGGACTTTCCACAAG	429																
A.CI.88.UC2	AT	C	A	TGG	AGGC	AA	G	AA	GA	A	CAT	T	GT	AA	T	A	CAGGAACAACCATACTTGGTCAAAGCAGGAAGTAGCTACT	A	G	A	A	G	T	G	464				
A.DE.x.BEN	AT	C	A	ATGG	AGGC	AA	G	AA	GA	A	CAT	T	GT	AA	T	A	CAGGAACAACCATACTTGGTCAAAGCAGGAAGTAGCTACT	A	G	ACA	GG	T	G	464					
A.DE.x.PE12	C	A	TGG	AGGC	AA	G	AA	GA	A	CATTT	GTTAA	GA	CAGGAACAGCTATATTTGGTCAGAACAGGAAGT	GAT	A	T	G	445											
A.GH.x.GH1																									0				
A.GM.87.D194																									0				
A.GM.x.ISY																									0				
A.GM.x.MCN13																									0				
A.GM.x.MCR35																									0				
A.GW.86.FG																									0				
A.GW.87.CAM2CG	AC	A	T	TGG	AGGC	AA	G	AA	GA	A	CATTT	GTTAA	GG	CAGGAACAACCATACTATGGCCAGGGCAGGAAGTAGCTACT	ACA	G	T	G	475										
A.GW.x.ALI	C	A	T	TGG	AGGC	AA	G	AA	GA	A	CATTT	GTAAGA	G	AACAGCTGATTTGGTCAGGGCAGGAAGTAAGTACT	ACA	G	T	G	461										
A.GW.x.MD5																									0				
A.IN.95.CR1K 147	T	AC	TGG	AGGC	A	G	AA	G	AA	A	CCTTT	GCTAA	G	GA	CAGGAACAACATACTTGGTCAGAACAGGAAGTAGCTACT	ACA	T	G	T	G	210								
A.IN.x.NNVA	AC	TGG	AGGC	AT	AG	G	A	A	CATTT	ATTAAAGG	GA	CAGGAACAACATACTTGGTCAGGGCAGGAAGTAGCTATT	ACA	G	T	G	466												
A.SN.85.R0D																									0				
B.CI.88.UC1	AT	AC	A	G	TGA	AGGCT	A	AA	GA	A	C	CAGACTAG	CA	GA	GACAGCAGCATAAACAGGAAGTAGCTGACACTGCACAAG	G	A	C	C	A	468								
B.CI.09.pPRD320-20HIV2_56	G	AC	A	TGG	AGGCT	A	AA	AA	A	C	CAGACTAG	CAGGA	AACAGCAGCTTAAAGAGGAAGTAGCTGACAGTGCATAAAC	A	C	T	AT	466											
B.CI.x.EH0	AA	C	A	TGG	AGGCT	AA	G	GA	AA	A	C	CAGA	TAGACAGGA	AATAACAGCACAAAGAGGAAGTAGCTAACACTGCATAGAG	A	A	T	T	G	468									
B.GH.86.D205	G	AC	G	TGG	AGGCT	A	AA	GA	A	C	CAGATTAG	CA	GA	GACAGCAGCATAAACAGGAAGTAGCTGACACTGCACAAG	A	A	C	T	A	471									
B.JP.01.KR020																									0				
G.CI.92.ABT96																									0				
AB.CI.90.7312A	AT	AC	A	G	ATGG	AGGCT	A	AA	A	A	C	CAGA	TAGACAGGAAGCAGCAGCATAAAGAGGAAGTAGCTGACGCTGCATAAGA	G	C	T	G	472											
AB.CM.03.03CM_510_03																									0				
U.FR.96.12034																									0				
MAC.US.x.17EC1																									429				
MAC.US.x.17EFR																									429				
MAC.US.x.1937																									0				
MAC.US.x.2065																									0				
MAC.US.x.251_1A11																									429				
MAC.US.x.251_32H_PJ5	C																									429			
MAC.US.x.251_BK28																									428				
MAC.US.x.80035																									0				
MAC.US.x.97074																									0				
MAC.US.x.MAC239_87082																									0				
MAC.US.x.MM142																									0				
MAC.US.x.SMM142B																									0				
MAC.US.x.r80025																									0				
MAC.US.x.r90131																									0				
MNE.US.82.MNE_8																									0				
MNE.US.x.MNE027																									0				
SMM.SL.92.SL92B																									0				
SMM.US.x.F236_H4	T																									428			
SMM.US.x.H9	T	A	GCAG																									186	
SMM.US.x.PBJ14_15	T	A	GCAG																									186	
SMM.US.x.PBJA																									0				
SMM.US.x.PBJ_143	T	A	GCAG																									378	
SMM.US.x.PBJ_6P6	T	G	A	AG																									355
SMM.US.x.PGM53	T																									435			
SMM.US.x.SME543	T																									102			
STM.US.x.STM																									102				

HIV-2/SIV Com-
plete Genomes

	TAR element end	Poly-A signal	5' LTR R repeat end	5' LTR U5 start						
MAC.US.x.239	GCAGGTAGAGCCTGGGTGTTCCCTGCTAGACTCTCACC.AGCACTGGCGGGTCTGGGAGAGTGACTCACGCTTGCTTCTGCTAAAGC..CCTCTTCAATAAAGC.TGCCATTTTAGAAGTAAGCTA..GTGTGTGTTCCCATCTCTCTAGCCGCGCTGGTCAAC				738					
A.CI.88.UC2	-C-----C-----	TG-C-CA	C-G-A	A-A	C-T-A	T-T	773			
A.DE.x.BEN	-G-----	T-A	C-G	A	C-T-A	T-T	774			
A.DE.x.PE12	-G-----	T-A	C-G	A	C-T-A	T-T	753			
A.GH.x.CA1	-G-----	TG-C-CA	C-G-A	A-A	C-T-A	T-T	218			
A.GM.87.D194	-G-----	TG-CA	C-G	A	C-T-A	T-T	218			
A.GM.x.ISY	-G-----	TG-C	C-G	AGA-A	C-T-A	T-T	219			
A.GM.x.MCN13	-G-----	G-TG-CA	C-G	AGA-A	C-T-A	T-T	219			
A.GM.x.MCN35	-G-----	G-TG-CA	C-G	AGA-A	C-T-A	T-T	219			
A.GW.96.FG	-G-----	TG-C-CA	C-G-A	CA-A	C-T-A	T-T	217			
A.GW.87.CAM2CG	-G-----	TG-CA	C-G	A-A	C-T-A	T-T	784			
A.GW.x.ALI	-G-----	TG-CA	C-G	A-A	A	C-G-T-A-AG	T-T	769		
A.GW.x.MD5	-G-----	TG-CA	C-G	T	A	C-T-A	T-T	218		
A.IN.95.CRIK.147	-G-----	TG-CA	C-G	A	A	C-T-A	T-T	519		
A.IN.x.NNVA	-G-----	TG-C	C-G	A	A	C-T-A	T-T	218		
A.SW.95.RD	-G-----	TG-C	C-G	AA	A	C-T-A	T-T	775		
B.CI.88.UC1	-G-----	TG-C	C-G	A	A	C-T-GA	T-T	768		
B.CI.09.pPRD320-20HIV2_56	-G-----	TG-C	C-G	A	A	C-T-GA	T-T	773		
B.CI.x.EH0	-G-----	TG-C	C-G	A	A	TA	C-AC-A	T-T	776	
B.GH.86.D205	-G-----	TG-C	C-G	A	A	A	C-TA	T-T	776	
B.JP.01.KR020	-G-----	TG-C	C-G	A	A	A	C-TA	T-T	0	
G.CI.92.ABT96	-G-----	TG-C	C-G	Y-G	C-AAGA	AA	A-GT	T-T	C-145	
AB.CI.90.7312A	-G-----	TG-C	C-G	A	A	A	C-TC-A	T-T	C-780	
AB.CM.03.03CM.510.03	-G-----	TG-C	C-G	A	A	A	C-TC-A	T-T	0	
U.FR.96.12034	-G-----	TG-C	C-G	A	A	C	G	C-A	T-T	270
MAC.US.x.17EC1	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	738
MAC.US.x.17EFR	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	738
MAC.US.x.1937	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	0
MAC.US.x.2065	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	0
MAC.US.x.251.1A11	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	737
MAC.US.x.251.32H.PJ5	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	738
MAC.US.x.251.BK28	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	726
MAC.US.x.80035	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	0
MAC.US.x.97074	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	0
MAC.US.x.MAC239.87082	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	0
MAC.US.x.MM142	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	219
MAC.US.x.SMM142B	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	219
MAC.US.x.r80025	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	0
MAC.US.x.r90131	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	0
MNE.US.x.82.MNE.8	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	219
MNE.US.x.MNE027	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	215
SMM.SL.92.SL92B	AGTA-GT-----T-A-A-A-A-C-ACA--AT--T	TG-C-G	A	A	A	A	A	C-T-A	T-T	219
SMM.US.x.F236.H4	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	734
SMM.US.x.H9	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	221
SMM.US.x.PBJ14.15	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	514
SMM.US.x.PBJA	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	514
SMM.US.x.PBJ.143	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	221
SMM.US.x.PBJ.6P6	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	706
SMM.US.x.PGM53	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	663
SMM.US.x.SME543	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	750
STM.US.x.STM	-G-----	TG-C	C-G	A	A	A	A	C-T-A	T-T	411

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[illegible]

MAC.US.x.239	GCAGTAAGGGCGGCAGGAACCAACCACGACGGAGTGCTCCTATAAAGCGCGGGTC...GGTACCAGA...CGGCGTGAGGAGCGG...GAGAGGAAGAGGCCTCCG...GTTGCA...GGTAAGTGCAACACA.AAAAAG...AAATAGCTGTCT.TTTAT	1022
A.CI.88.UC2	-----A-----G--A--C-AAG-TAC-A-A-GG--T-----T-A-----G-A-----CTACAC-C--ACTGTAGCCAG--AG--TGT--A-CC--	1073
A.DE.x.BEN	-----A-----G--A--C-GAG-TAC-A-AGG--T-----T-A-----G-A-----A-CTACAC-C--ACTGTAGCCAG--AG--TGT--A-CC--	1073
A.DE.x.PET2	-----A-----G--A--C-GAG-TAC-A-AGG--T-----T-A-----G-A-----A-CTACAC-C--ACTGTAGCCAG--AG--TGT--A-CC--	1041
A.GH.x.GH1	-----A-----G--A--C-GAG-TAC-A-AGG--T-----T-A-----G-A-----CTACAC-CG--ACCGTAGCCAG--AG--AGT--A-CC--	513
A.GM.87.D194	-----A-----G--A--C-GAG-TAC-G-AG--T-----T-A-----G-A-----A-CTACAC-CG--ACTGTAGCCAG--AG--TGT--A-CC--	517
A.GM.x.ISY	-----A-----G--A--C-AAG-TAC-A-AGG--T-----TC-----G-A-----A-CTACAC-C--ACTGTAGCCG--AG--TGT--A-CC--	517
A.GM.x.MCN13	-----A-----G--A--C-AAG-TAC-A-AGG--T-----TA-----G-A-----A-CTACAC-C--AATTGTAGCCAG--GG--TGT--A-CC--	518
A.GM.x.MCR35	-----A-----G--A--C-AAG-TAC-A-AGG--T-----TA-----G-A-----A-CTACAC-C--AATTGTAGCCAG--GG--TGT--A-CC--	518
A.GW.86.FG	-----A-----GC--G--C-GAG-TAC-A-AG--T-----CG-AGTC--G--G-A--G--A-CTACAC-C--ACTGTAGCCAA--G-GG--TGT--A-CC--	517
A.GW.87.CAM2CG	-----A-----AG--A--C-GAG-TAC-A-AGG--T-----TC-----G-A-----A-CTACAC-C--ACTGTAGCCCTG--GG--TGT--A-CC--	1082
A.GW.x.ALI	-----A-----G--A--C-AAG-TAC-A-AGGC--T-----T-----G-A-----A-CTACAC-C--TTGTAGCCG--GG--TGT--A-CC--	1066
A.GW.x.MDS	-----A-----G--A--C-AAG-TAC-A-AGG--T-----T-----G-A-----A-CTACAC-CG--ACTGTAGCCAA--GG--TGT--A-CC--	517
A.IN.95.CR1K 147	-----A-----G--A--C-GAG-TAC-A-G--T-----TC-----G-A-----A-CTACAC-C--ACTGTAGCCAG--GG--TG--A-CC--	817
A.IN.x.NNVA	-----A-----G--A--C-AAG-TAC-A-AGG--T-----T-A-----GGT-AA-GT...AAGT-CCT-C-A--CTGTAGC--CAG--AG--TGT--A-CC--	1066
A.SN.85.R0D	-----A-----G--C-GAG-TAC-A-AGG--A-T-----GA-----G-A-----A-CTACAC-C--ACTGTAGCCG--GG--TG--A-CC--	516
B.CI.88.UC1	-----T-----A--G--A-C-----G--A-----GAA-----GA-G-AA--G-A-TC-A-TTCTGAA...TGTC--GCTC	1055
B.CI.09.pPRD320-20HIV2 56	-----T-----A--G--G-----G--A-----GAA-----GA-G-AA--G-A-TC-A-TTTTGAA...TGTC--GCTC	1053
B.CI.x.EH0	-----T-----G--AA-A-C-----G--A-----GA-----G-AGTA-AA--A-TC-A-TTT-C...AA-TCG-C-ACTC	1052
B.GH.86.D205	-----T-----A--G--A--A-C-----G--A-----GA-----GA-T-A--A-TC-A-TTTT-C...A-TGT-C-ACTC	1050
B.JP.01.KR020	-----T-----A--G--A--A-C-----G--A-----GA-----GA-T-A--G-A-TC-A-TTTTA...AA-TGT-C-ACTC	196
G.CI.92.ABT96	-----T-----T-----G-----A-----A-----T-----G--GCA-----C-A--TTT...TAGCC...A--AG-GCTGTGAA-CC--	435
AB.CI.90.7312A	-----T-----A--G--A-C-----G--A-----GA-----GA-T-A--AACTGT...CACTGT...C-AC--	1056
AB.CM.03.03CM_510_03	-----T-----A--G--A-CT...G--A-----GAA-----GA-T-A--G-A-TC-A-TTTT...CA-TGT...C-GC--	189
U.FR.96.12034	-----A-----G-----A-CT...AG--A-----T-A...T-----A--T-AAC...C--AG-G-TGCTGCCTC	552
MAC.US.x.17EC1	-----GGT-----	1022
MAC.US.x.17EFR	-----GGT-----	1022
MAC.US.x.1937	-----A-----	128
MAC.US.x.2065	-----A-----	128
MAC.US.x.251 1A11	-----	1021
MAC.US.x.251 32H PJ5	-----	1023
MAC.US.x.251 BK28	-----G-----AG-----TG-----	1010
MAC.US.x.80035	-----	128
MAC.US.x.97074	-----	0
MAC.US.x.MAC239 87082	-----G-----GAGA-----TG-----G-----	99
MAC.US.x.MM142	-----G-----GAGA-----TG-----G-----	520
MAC.US.x.SMM142B	-----G-----GAGA-----TG-----G-----	520
MAC.US.x.r80025	-----	0
MAC.US.x.r90131	-----G-----G-----	128
MNE.US.82.MNE 8	-----G-----G-----	502
MNE.US.x.MNE027	-----G-----G-----	502
SMM.SL.92.SL92B	-----T-----G-----TTGA-CCGGTGCCA-T--CTGAGC-GGAGTAC--A-TAA--AG-CT--T-G-AC-TAAGG--A...AAA...GT-AAT-T-CT--CCT-C--	468
SMM.US.x.F236 H4	-----A-----A--G-----C-----G-----TC-G-----G--GTC-----T-GGA--AG--CCC--	1018
SMM.US.x.H9	-----C-----A-----C-----G-----TC-G-----A--G-GTC-----T-GGA--AG--CCC--	504
SMM.US.x.PBJ14 15	-----C-----A-----C-----G-----TC-G-----A--G-GTC-----T-GGA--AG--CCC--	798
SMM.US.x.PBJA	-----C-----A-----C-----G-----TC-G-----A--G-GTC-----T-GGA--AG--CCC--	797
SMM.US.x.PBJ 143	-----C-----A-----C-----G-----TC-G-----A--G-GTC-----T-GGA--AG--CCC--	504
SMM.US.x.PBJ 6P6	-----C-----A-----C-----G-----TC-G-----A--G-GTC-----T-GGA--AG--CCC--	990
SMM.US.x.PGM53	-----A-----A--G-----C-----G-----TC-G-----G--G-GTC-----T-GGA--AG--CCC--	948
SMM.US.x.SME543	-----A-----A--G-----C-----G-----TC-G-----A--GTC-----T-GGA--AG--CCC--	1034
STM.US.x.STM	-----A-----G-----CG...AG...GC--A...A-G...AG-T-GCC...G-GG--AT--G--C--	678

MAC.US.x.239
Gag

A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PET2
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS5
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CR1K 147
A.IN.x.NNVA
A.SN.85.ROD
B.CI.88.UC1
B.CI.89.pPRD320-20HIV2_56
B.CI.x.EH0
B.GH.86.D205
B.JP.81.KR020
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.03.03CM_510_03
U.FR.96.12034

MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239_87082
MAC.US.x.MN142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.82.MNE.8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PBJ14_15
SMM.US.x.PBJA
SMM.US.x.PBJ_143
SMM.US.x.PBJ_6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

Gag and Gag-Pol start

CCAGGAAGGGGTAAATAAGAT. AGAGTGGGAGATGGGCTGAGAACTCCGTCTTGTGAGGGAAGAACAGATGAATTAGAAAAATTAGGCTACGACCCACGGGAAAGAAAAAGTACATGTTGAAGCATGTAGTATGGGAGCAAAATGAATTAGATAGATTTGGATTAG 1191
M G V R N S V L S G K K A D E L E K I R L R P N G K K K Y M L K H V V W A A N E L D R F G L

A-TTTT--ACAGG--GA-G--TT-----C--AG--A--G--C-----T--G--GG-----G--A--A--A--T--G-----G--C--G--C--CA-----1241
A-CTTT--ACAGG--GA-G--TT-----C-----AG--A--C-----G--T--G--GG-----G--A--A--A--T--G-----G--C--A--C--G-----1241
A-CTTT--ACAGG--GA-G--TT-----C--G-----AG--A--T-----T--G--GG--G-----A--T--GAC--A--A--T--G-----G--GC--A--C--G-----1209
ATCTTTTA-ACAGG--GA-G--TT-----C-----AG--A--C-----G--T--G--G-----G--C--A--A--A--T--G-----G--C--A--C--G-----682
A-CTTT--ACAGG--GA-G--TT-----C-----AG--A--C-----G--T--G--G-----G--A--G--A--A--A--T--G-----G--C--C--A--G-----685
A-CTTT--ACAGG--GA-G--TT-----C--A-----AG--A--G-----G--T--G--GG--G-----A--GA--A--A--A--T--G-----G--C--C--A--G-----685
A-CTTT--ACAGG--GA-G--TT-----C-----AA--A--C-----C--T--G--GG-----A--G--C--A--A--T--G-----G--C--C--A--G-----686
A-CTTT--ACAGG--GA-G--TT-----C-----AA--A--C-----C--T--G--GG-----A--G--C--A--A--T--G-----G--C--C--A--G-----686
A-CTTT--ACAGG--GA-G--TT-----C-----AG--A--C-----T--G--GG-----A--A--A--A--A--T--G-----G--C--C--A--G-----685
A-CTTT--ACAGG--GA-G--TT-----C-----AG--A--C-----G--T--G--GG-----A--TCA--C--A--A--T--G-----G--C--C--A--G-----1250
A-CTTT--ACAGG--GA-G--TT-----C-----AG--A--C-----G--T--G--GG-----A--GA--A--A--A--T--G-----G--C--C--A--G-----1234
A-CTTT--ACAGG--GA-G--TT-----C--G-----AG--A--C-----G--T--G--GG-----A--G--A--A--A--T--G-----G--C--C--A--G-----685
A-CTTT--ACAGG--GA-GA-TT-----C--AG-G--C--AG--A--T-----G--T--G--GG-----A--GAC--A--A--T--G-----G--C--G--C--A--G-----A 986
A-CTTT--ACAGG--GA-GA-TT-----C--AG--C--AG--A--T-----G--T--G--GG-----A--GAG--A--A--T--G-----G--C--G--C--A--G-----A 1235
A-CTTT--ACAGG--GA-G--TT-----C-----AG--A--C-----G--C--T--G--GG-----G--C--A--A--A--T--G-----G--A--G--C--C-----684
TA--A--A--AGTAGG--CA.TA-----C--G-----A-----G--T--G--GG-----G--TTGTC--A--A--A--A-----TG--C--G--C-----1222
TA--A--A--AGTAGGACA.TA-----C--GG-----A-----G--T--G--GG-----G--TTGTC--A-----TG--C--G-----A-----1220
TAG-AC--A--GGTAGG--A.TA-----C--GG-----GA-----G--T--G--GG-----GA-----C--A--A--A-----TG--C--G-----G-----1218
TA--A--A--AGTAGG--CA.TA-----C--GG-----A-----G--T--G--GG-----A--T--C--A--A-----TG--C--G-----C-----1217
TA--A--A--AGTAGG--CA.TA-----C--GG-----A-----G--T--G--GG-----A--TTGTC--A--A-----TG--C--G-----C--A-----363
A-CTTG-ATA--C--GGTAGA--T-----C--G-----C--A--T-----G--T--G--GG-----A-----A--A--T--G-----G--C--G--C-----C-----604
-T--AGGA--AGTAGG--CA.TA-----C--GG-----C--A--GA-----G--T--G--GG-----A-----A--A--A-----TG--C--G-----C-----G-----1223
-T--AAG--AGTAGG--CA.TA-----C--G-----C--A-----G--T--G--GG-----G--T-----A--A-----TG--C--G-----C-----356
TG--A--A--AGG--GT--TT-----C-----T-----G--T--G-----A-----A--A--T--G-----G--C--G--C-----720

-----1191
-----1191
-----R 297
-----297
-----1190
-----1192
-----1179
-----297
-----166
-----268
-----689
-----689
-----154
-----297
-----671
-----671
-----631
A-TTTTGA-AA-GAGTAGG-----C-----G-----A-----G-----T--G--GG--G-----G-----C--T-----A--TA-----C--GA-----C-----CG-----1187
A-TTTTGA-AAA-GAGTAGG-----C-----G-----G-----T--G--GG-----T-----C-----A-----G-----C-----673
A-TTTTGA-AAA-GAGTAGG-----C-----C-----T--G--GG-----G-----A--C-----A-----G-----C-----967
A-TTTTGA-AAA-GAGTAGG-----C-----T--G--GG-----G-----CA--C-----A-----G-----C-----966
A-TTTTGA-AAA-GAGTAGG-----T-----T--G--GG-----T-----A--C-----A-----G-----C-----673
A-TTTTGA-AAA-GAGTAGG-----C-----T--G--GG-----G-----A--C-----A-----G-----C-----1159
A-TTTTGA-AA-GAGTAGG-----C-----T--G-----T-----T-----G-----C-----G-----1117
A-TTTTGA-AA-GAGTAGG-----C-----T--G-----T-----T-----G-----C-----G-----1203
A-TCTTGA--A-GAGGT-G--AG-----C-----G-----A-----G-----T--G--GG--G-----A-----G-----C-----G--C-----G-----847

MAC.US.x.239	CAGAAAGCCTGTTGGAGAACAAAGAAGGATGTCAAAAAATACTTTCGGTCTTAGCTCCATTAGTGCCAAACAGGCTCAGAAAAATTTAAAAAGCCTTTATAATACTGTCTGCGTCATCTGGTGCATTACGCAGAGAAGAAAGTGAACACACTGAGGAAGCAAAACAGATA	1361
Gag	A E S L L E N K E G C Q K I L S V L A P L V P T G S E N L K S L Y N T V C V I W C I H A E E K V K H T E E A K Q I	
A.CI.88.UC2	-----A-----TCA-----T-C-----G-T-CA-A-T-A-----A-----G-----T-----C-----T-----T-G-----G-T-----A-G-----A-AC-----	1411
A.DE.x.BEN	-----G-----TCA-----T-C-----G-T-CAGA-T-A-----A-----G-----T-----C-----T-----T-G-----G-T-----GA-AC-----	1411
A.DE.x.PEI2	-----T-----TCA-----T-C-----T-CA-A-T-A-----A-----A-----T-----T-----T-----T-G-----G-T-----A-G-----A-----	1379
A.GH.x.GH1	-----G-----TCA-----T-C-----G-T-CA-A-T-A-----A-----A-----G-----T-----C-A-----T-----T-G-----G-T-----A-AC-----	852
A.GM.87.D194	-----G-----ATCA-----T-C-----G-T-AAA-T-AA-----A-----G-----T-----C-----T-----T-G-----G-T-----A-----GA-AC-----	855
A.GM.x.TS.V	-----G-----TCA-----T-C-----T-A-----A-T-AA-----A-----G-----T-----AC-----T-----T-G-----G-T-----A-----AGA-----	855
A.GM.x.MCN13	-----G-----TCA-----T-C-----G-T-A-A-T-G-----A-----A-G-T-----T-----T-----A-----G-T-----A-G-----A-----	856
A.GM.x.MCR35	-----G-----TCA-----T-C-----G-T-A-A-T-A-----A-----A-G-T-----T-----T-----A-----G-T-----A-G-----A-----	856
A.GW.86.FG	-----G-----TCA-----T-C-----T-A-A-T-A-----A-----A-G-T-----T-----T-----A-----G-T-----A-G-----A-----	855
A.GW.87.CAM2CG	-----G-----ATCA-----T-C-----G-T-AAA-T-AA-----A-----A-G-T-----T-----T-----A-----G-T-----A-G-----AGA-----	1420
A.GW.x.ALI	-----G-----TCA-----T-C-----G-T-AAA-T-AA-----A-----A-----T-----T-----AG-T-----G-G-----G-T-----A-----A-----	1404
A.GW.x.MDS	-----G-----ATCA-----G-T-C-----G-T-AAA-T-AA-----A-----A-G-T-----T-----T-----A-----G-----G-T-----A-T-C-----	855
A.IN.95.CR1K 147	-----T-----TCA-----G-T-C-----T-A-A-T-A-----A-----G-T-----T-----T-----A-----G-T-----A-----A-----	1156
A.IN.x.NNVA	-----G-----ATCA-----G-T-C-----T-A-A-T-A-----A-----G-T-----T-----T-----A-----G-T-----A-----A-T-----	1405
A.SN.85.R0D	-----G-----TCA-----G-T-----T-A-A-T-A-----A-A-G-A-G-T-----T-----T-----A-----G-T-----A-G-----A-----	854
B.CI.88.UC1	-----G-----ATCA-----C-----T-A-----A-----A-----A-----T-----T-----T-AC-T-G-----G-T-----A-----	1392
B.CI.89.pPRD320-20HIV2_56	-----G-C-----TCA-----C-----T-A-----A-----A-G-A-----A-----T-----T-----T-AC-T-G-----G-T-----A-----	1390
B.CI.x.EH0	-----G-----GATCA-----C-GG-----T-GGAAA-----GA-----A-----T-----T-----C-----T-----T-AC-T-G-----G-T-----A-----	1388
B.GH.86.D205	-----G-----ATCA-----C-----T-AAA-----A-----A-----G-----T-----TC-----T-TC-----C-G-----G-T-----A-----	1387
B.JP.81.KR020	-----G-----TCA-----C-----T-A-----AA-----A-----A-----T-----T-----T-AC-TC-G-----T-----G-T-----T-----	533
G.CI.92.ABT96	-----G-----ATCA-----T-C-----T-----A-A-----A-----A-----T-----G-----T-----TT-G-----C-----C-----A-----T-----A-----AG-----	774
AB.CI.90.7312A	-----A-----ATCA-----G-----T-A-----A-----A-----G-----T-----T-----T-A-----A-----G-T-C-----A-----C-----	1393
AB.CM.03.03CM_510_03	-----G-C-----ATCA-----C-----T-AAA-----A-----A-----T-----T-TC-----C-G-----G-T-----A-----G-----A-----	526
U.FR.96.12034	-----G-C-----GC-----TT-A-----G-----T-----T-----G-----T-----TT-G-----T-----G-----	890
MAC.US.x.17EC1	-----	1361
MAC.US.x.17EFR	-----	1361
MAC.US.x.1937	-----R-----G-----A-----M-----R-----	467
MAC.US.x.2065	-----	467
MAC.US.x.251.1A11	-----	1360
MAC.US.x.251.32H.PJ5	-----	1362
MAC.US.x.251.BK28	-----	1349
MAC.US.x.80035	-----	467
MAC.US.x.97074	-----	336
MAC.US.x.MAC239_87082	-----T-----	438
MAC.US.x.MN142	-----	859
MAC.US.x.SMM142B	-----	859
MAC.US.x.r80025	-----D-----	324
MAC.US.x.r90131	-----	467
MNE.US.82.MNE.8	-----C-----C-----G-----G-----	841
MNE.US.x.MNE027	-----C-----C-----G-----G-----	841
SMM.SL.92.SL92B	-----A-G-----G-----T-AG-A-AC-----A-----G-----T-G-T-G-----AG-T-----TC-G-----AT-----G-----A-----T-GA-A-C-----	801
SMM.US.x.F236.H4	-----T-----T-----T-A-T-----T-G-----T-----C-----G-----T-G-T-G-----T-----T-----A-----A-----	1357
SMM.US.x.H9	-----T-----T-----T-A-T-----T-G-----T-----G-----C-----C-----C-----T-----T-----A-----A-----	843
SMM.US.x.PBJ14_15	-----T-----T-----T-A-T-----T-G-----T-----G-----C-----C-----C-----T-----T-----A-----A-----	1137
SMM.US.x.PBJA	-----T-----T-----T-A-T-----T-G-----T-----G-----C-----C-----C-----T-----T-----A-----A-----	1136
SMM.US.x.PBJ 143	-----T-----T-----T-A-T-----T-G-----T-----G-----C-----C-----C-----T-----T-----A-----A-----	843
SMM.US.x.PBJ 6P6	-----T-----T-----T-A-T-----T-G-----T-----G-----C-----C-----C-----T-----T-----A-----A-----	1329
SMM.US.x.PGM53	-----C-----T-----TA-----A-T-----T-GG-----T-----G-----T-----T-----T-----T-----A-----	1287
SMM.US.x.SME543	-----T-----T-----T-----T-----T-G-----T-----G-----T-----T-----T-----T-----T-----A-----	1373
STM.US.x.STM	-----TCA-----G-----TA-AA-----AA-----T-----G-T-----T-----T-----T-----C-----T-----G-AG-G-----	1017

Gag p17 Matrix end_Gag p24 Capsid start

MAC.US.x.239 Gag	GTGCAGAGACACCTAGTGGTGGAAACAGGAACAACAGAAACTATGCCAAAAACAAGTAGACCAACAGCACCATCTACGGCGCAGAGGAGGAATTACCCAGTACAACAA...ATAGGTGGTAACTATGTCACCTGCCATTAAAGCCCGAGAACATTAAATGCCTGGGTAAA	1528
A.CI.88.UC2	-A-----T-----CA-----TG--G-AA-----T-----C-----T--G-A-A-----C-T-C-----G--GC-----C-----TG--C-G-----CC--TC-----T-----	1578
A.DE.x.BEN	-CA-----T-----CA-----T-----TG--G-AA-----T-----C-----T--G-A-A-----C-----GCG-----C-----TG--C-G-----CC--TC-----A-----	1578
A.DE.x.PET2	-A-----T-----CA-----TG--C-AA-----GC-----G-----C-----G-----G-----C-----TC--TG--G-G-----CC--CC-----T-----	1546
A.GH.x.GH1	-A-----T-----G--CA-----TG--AA-----GT-----C-----G-----A-----C-T-T-----GACAGGC-----C-----A-----G-----C-G-----CC--TC-----T-----	1022
A.GM.87.D194	-CA-----T-----CA-----TG--G-AA-----T-----C-----T--G-A-A-----G-----C-----G-----G-----C-----T-----TG--G-G-----CC--TC-----T-----	1022
A.GM.x.TS9	-AGG-----T-----CA-----A-----TG--G-AA-----T-----C-----G-----G-----C-----T-----G-----G-----C-----T-----TG--G-G-----CC--TC-----T-----	1022
A.GM.x.MCN13	-A-----T-----C--CA-----TG--G-AA-----T-----C-----G--AG-----C-T-C-----G--C-C-T-----AC--TG--GC-G-T-----TC--CC-----T-----	1023
A.GM.x.MCR35	-A-----T-----C--CA-----TG--G-AA-----T-----C-----G--A-----C-T-C-----G--C-C-T-----AC--TG--GC-G-T-----TC--CC-----T-----	1023
A.GW.86.FG	-A-----T-----CA-----TG--G-AA-----T-----C-----G--A-----C-T-C-----G--G-----G--C-C-----AC--TA-A-----C-G-T-----CG--TC-----T-----	1016
A.GW.87.CAM2CG	-CA-T-----T-----C--CA-----TG--G-AA-----G-T-----C-----T--G--AG-----C-----G-----AGC-----C-----ACT--TG--GC--T-----CC--TC-----T-----	1587
A.GW.x.ALI	A-A-----T-----C--CA-----T--A-----G--G-AA-----GC-----C-----T--ACAG--G-----C-T-C-----G--C-C-----CAC--TG--GC-G-----C--G-----T-----	1571
A.GW.x.MDS	-CA-G-----T-----CA-----TG--G-AA-----T-----C-----G-----C-----C-----G--GA-T-----C-----C-----AC--TG--G-G-T-----CC--TC-----T-----	1022
A.IN.95.CR1K 147	-A-----T-----CA-----T-----TG--G-AA-----T-----C-----GG-----C-T-C-----C-----C-----T-----AC--TG--GC-G-T-----C-----TC-----T-----	1323
A.IN.x.NNVA	-A-----T-----CA-----TG--G-AA-----T-----CC-----AGG--G-----C-TT-C-----GC-----C-----CAC--TG--GC-G-----C-----TC-----TT-----	1572
A.SN.85.ROD	-G-----T-----CA-----TG--G-AA-----GC-----C-----AG-AG-----G-----G-----T-----G-----C-----CAC--TA-A-----GC-G-T-----CC--CC-----T-----	1021
B.CI.88.UC1	-CA-----T-----C--C-----C-----G-AA-----GCT-----C-----C-----C-----G--G-G-----C-----C-----A-----GC-----TC-----C-----	1544
B.CI.89.pPRD320-20HIV2_56	-CA-----C-----T-----C-----C--AG-----AA-----GCT-----C-----C-----C-----G--G-G-----CC-----T-----G-----GC-----CC-----CC-----C-----	1542
B.CI.x.EH0	-CA--C-----T-----CA-C-----C-----AA-----GCT-TG-----A-----GTAA--A-----C-----CT-----C-----GC-----T-----G-----G-----CC-----TC-----	1540
B.GH.86.D205	-CA-----T-----C--C-----C-----AA-----GCT--A--A-----C-----C-----C-----T-----G--G-----C--G-C-----C-----C-----GC-----CC-----C-----T-----	1539
B.JP.81.KR020	-CA-----C-----T-----C--C-A-C--G-----AAGC-----GCT-----A-----C-----T-----T-----G--G-G-----G--G-CC-----T-----CAC-----GC-----CC-----C-----	685
G.CI.92.ABT96	-----T-----A-----T-----T-----AAG--TGCC-----C-----T-----C-----T-----C-----G--G-----G--C-C-----T-----T-----T-----TC-----T-----A-----	941
AB.CI.90.7312A	-CA-----C-----T-----A--C--T-----AA-CA--T-CTG--GAC--A--G--GA-----T-----T-----C-----G--C-C-T-----G-----G-----GC-----CC-----CC-----T-----	1545
AB.CM.03.03CM_510_03	-CA-----C-----C-----CG-----AA--A--GCT--A--A-----C-----C-----C-----T-----G--G-----C-----C-----G-----GC-----CC-----C-----T-----	675
U.FR.96.12034	-A-----T-----C-----T--A--TG-----AA-----GCC-----YT--C-----T--G-CA-----G--G-G-G-----C-----T-----C-----A--TC-----T-----C--C-----	1057
MAC.US.x.17EC1	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1528
MAC.US.x.17EFR	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1528
MAC.US.x.1937	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	634
MAC.US.x.2065	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	634
MAC.US.x.251.1A11	-A-----T-----G-----T-----C-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1527
MAC.US.x.251.32H.PJ5	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1529
MAC.US.x.251.BK28	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1516
MAC.US.x.80035	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	634
MAC.US.x.97074	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	303
MAC.US.x.MAC239_87082	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	605
MAC.US.x.MN142	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1026
MAC.US.x.SMM142B	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1026
MAC.US.x.r80025	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	491
MAC.US.x.r90131	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	634
MNE.US.82.MNE.8	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1008
MNE.US.x.MNE027	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1008
SMM.SL.92.SL92B	-A-----C-----T-----A-----GT-----TG-----AAT-----GCTCA--C-----T-----C-----T-----C-----T-----G--G-----G--G-----AAA--T-----G-----ACT--C--GTC--AC-G--C-C-----G-----C-----	962
SMM.US.x.F236.H4	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1524
SMM.US.x.H9	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1010
SMM.US.x.PBJ14_15	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1304
SMM.US.x.PBJA	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1303
SMM.US.x.PBJ_143	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1010
SMM.US.x.PBJ_6P6	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1496
SMM.US.x.PGM53	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1454
SMM.US.x.SME543	-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----T-----	1540
STM.US.x.STM	-AA-----T--T-----A--G--T-----TG--A-C-AA-----TGCC-----C-----T-----G-----G-----G-----C--C--T-----A-----A-----C--G-----A-----	1184

MAC.US.x.239	ATTGATAGAGGAAAAAGAAATTTGGAGCAGAAGTAGTCCAGGATTTTCAGGCACTGTCAGAAGGTTGCACCCCCTATGACATTAAATCAGATGTTAAATTGTGTGGGAGACCATCAAGCGGCTATGCAGATTATCAGAGATATTATAACAGGAGGGCTGCAGATTGGGACT	1698
Gag	L I E E K K F G A E V V P G F Q A L S E G C T P Y D I N Q M L N C V G D H Q A A M Q I I R D I I N E E A A D W D	
A.CI.88.UC2	--AG-----G-C-G-----C-----C-G--T-C-A-C-T-----C-T-A-A-C-----A-C-T-A-A-A-G-----TG	1748
A.DE.x.BEN	--AG-G-----G-C-G-----C-----C-G--T-C-A-C-T-----C-T-C-A-A-----A-A-----C-----TG	1748
A.DE.x.PE12	G--AG-G-A-----G-C-G-----G-----C-----C-G--T-C-A-C-T-----C-T-A-A-----A-A-----G-----TG	1716
A.GH.x.GH1	--AG-----C-G-C-G-----A-----C-----C-G--T-C-C-A-C-T-----C-T-C-A-A-----A-A-----G-----TG	1192
A.GM.87.D194	--AG-----G-A-G-C-G-----G-----C-----C-G--T-C-A-C-T-----C-T-C-A-A-----A-A-----C-----TG	1192
A.GM.x.TSY	G--AG-----G-A-G-C-G-----G-----C-----C-G--T-C-C-A-C-T-----C-----A-G-A-A-----A-A-----C-----TG	1192
A.GM.x.MCN13	--AG-----G-C-G-G-G-----C-----C-G--T-C-C-A-C-T-----C-----A-A-A-G-G-CG-T-A-A-A-----TG	1193
A.GM.x.MCR35	--AG-----G-C-G-G-G-----C-----C-G--T-C-C-A-C-T-----C-----A-A-A-G-G-C-T-A-A-A-----TG	1193
A.GW.86.FG	--AG-G-----C-G-G-----C-----C-G--T-----C-T-----C-----A-A-A-G-A-T-T-A-A-A-----TG	1186
A.GW.87.CAM2CG	--AG-----G-C-G-----C-----C-G--T-----A-C-T-----C-----A-A-A-G-G-T-T-A-A-A-----C-----TG	1757
A.GW.x.ALI	--AG-A-----G-C-G-----C-----C-G--T-----A-C-T-----C-----A-A-A-G-G-T-T-A-A-A-----C-----TG	1741
A.GW.x.MDS	--AG-A-----G-C-G-----C-----C-G--T-----A-C-T-C-----C-T-----A-A-A-G-A-C-T-T-A-A-A-----TG	1192
A.IN.95.CRIK 147	--AG-----G-C-G-----A-----C-----C-G--T-C-A-C-T-----C-----A-C-A-A-G-G-T-T-A-A-A-----TG	1493
A.IN.x.NNVA	--AG-A-G-----G-C-G-----G-----C-----C-G--T-----A-C-T-----C-----A-A-A-G-A-T-T-A-A-A-----TG	1742
A.SN.85.R0D	--AG-----A-G-C-G-----C-----C-G--T-C-C-A-C-T-----C-----A-C-A-A-G-G-C-T-T-A-A-A-----TG	1191
B.CI.88.UC1	G--AG-----A-G-C-G-----A-----C-----A-A-A-T-T-----A-----C-----A-A-T-G-A-A-C-T-----G-----C	1714
B.CI.89.pPRD320-20HIV2_56	--AG-G-----C-G-C-G-----G-----C-A-----A-G-----G-----T-C-----C-----A-T-C-G-A-C-----A-----G-----C	1712
B.CI.x.EH0	--AG-A-G-----G-C-G-----A-----A-----A-----G-----T-----A-----A-A-G-A-C-----A-----T-G-G-A-T-T-A-A-----C	1710
B.GH.86.D205	G--AG-A-----G-C-G-----A-----A-----A-----T-----A-----C-----A-A-A-G-A-C-----A-----T-G-A-A-C-T-A-A-----C	1709
B.JP.81.KR020	--AG-----C-G-----A-----C-----A-----A-----T-----A-----C-----A-A-A-G-A-C-----A-----T-G-A-A-T-T-T-A-A-----C	855
G.CI.92.ABT96	---G---A-----G-C-G-----G-----G-----C-CTA-A-----T-C-A-C-----A-A-A-A-C-----A-A-T-T-T-----A-----K-----TC	1111
AB.CI.90.7312A	--AG-G-----A-G-----A-----A-----G-A-T-----T-----T-----C-----A-A-A-G-A-C-----AG-C-T-G-A-A-C-T-----G-----C	1715
AB.CM.03.03CM_510_03	--AG-----A-G-C-G-----A-----C-A-----A-----A-----T-----T-----A-----C-----A-G-----G-A-C-----A-----T-----A-A-T-T-T-A-A-----C	845
U.FR.96.12034	-C-G-----G-A-----C-----G-C-----G-----T-----A-----C-----A-----T-----A-----G-A-A-T-T-T-A-A-----A	1227
MAC.US.x.17EC1	-----	1698
MAC.US.x.17EFR	-----	1698
MAC.US.x.1937	-----TG-----	804
MAC.US.x.2065	-----	804
MAC.US.x.251_1A11	-----	1697
MAC.US.x.251_32H_PJ5	-----A-----C-----	1699
MAC.US.x.251_BK28	-----C-----	1686
MAC.US.x.80035	-----	804
MAC.US.x.97074	-----	673
MAC.US.x.MAC239_87082	-----	775
MAC.US.x.MN142	--A-----G-----T-----C-CT-----C-----T-----	1196
MAC.US.x.SMM142B	--A-----G-----T-----C-CT-----C-----T-----	1196
MAC.US.x.r80025	-----	661
MAC.US.x.r90131	-----	804
MNE.US.82.MNE_8	-----G-----C-----A-----A-----A-----	1178
MNE.US.x.MNE027	-----G-----C-T-----A-----A-----A-----	1178
SMM.SL.92.SL92B	-C-G--A-----A-----A-----C-T-A-----C-T-----A-T-A-G-A-C-----A-----A-A-T-T-A-A-----C-----C	1132
SMM.US.x.F236_H4	--AG--A-G-A-----G-----A-G-A-----C-T-----T-----A-C-----A-A-G-A-C-----A-----T-G-----T-A-A-----C-----T	1694
SMM.US.x.H9	---G---A-G-A-----G-----A-G-A-----C-T-----Y-T-----C-----A-A-----A-A-G-A-C-----A-----T-A-----T-----T-----T	1180
SMM.US.x.PBJ14_15	-----A-G-A-----G-----A-G-A-----C-T-----C-----A-C-----A-G-G-A-C-----A-----T-A-----T-A-----T-----T	1474
SMM.US.x.PBJA	-----A-G-A-----G-----A-G-A-----C-T-----C-----A-C-----A-G-G-A-C-----A-----T-A-----T-A-A-----T-----T	1473
SMM.US.x.PBJ_143	---G---A-G-A-----G-----A-G-A-----C-T-----Y-----C-----A-C-----A-G-G-A-C-----A-----T-A-----T-A-A-----T-----T	1180
SMM.US.x.PBJ_6P6	-----A-G-A-----G-----A-G-A-----C-T-----C-----A-C-----A-G-G-A-C-----A-----T-A-----T-A-A-----T-----T	1666
SMM.US.x.POM53	---G---A-G-A-----G-----A-G-A-----C-T-----C-----A-C-----A-A-----A-G-A-C-----A-----T-A-----T-A-A-----T-----T	1624
SMM.US.x.SME543	---G---A-G-A-----G-----A-G-A-----C-T-----C-----A-C-----A-A-----A-G-A-C-----A-----T-A-----T-A-A-----C-----T	1710
STM.US.x.STM	G--AG-G-----T-----G-----A-----C-T-----C-----AC-----G-G-----A-C-----A-A--G-C-----T-----A-----T-----A	1354

MAC.US.x.239
Gag
A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CRIK 147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.89.pPRD320-20HIV2_56
B.CI.x.EH0
B.GH.86.D205
B.JP.81.KR020
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.03.03CM_510_03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.80035
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239_87082
MAC.US.x.MN142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.82.MNE.8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PBJ14_15
SMM.US.x.PBJA
SMM.US.x.PBJ_143
SMM.US.x.PBJ_6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

TGCAGCACCACAAACGAGTCCA.....CAACAAGGACAACCTTAGGGAGCGCTCAGGATCAGATATTGCAGGAACAACCTAGTTTCAGTAGATGAACAAATCCAGTGGATGTACAGACAACAGAACCCCATACAGTAGGCAACATTTACAGGAGATGGATCCAACCTG 1859
L Q H P Q P A P Q Q G Q L R E P S G S D I A G T T S S V D E Q I Q W M Y R Q Q N P I P V G N I Y R R W I Q L
C-----AT---GC---CTTACCA...GC---G---G---A---C---AAGG---G---T---C---A-----A---CA-----G---G-----T---G---G---A---T---G---G---G---G---C---A-----GA-A 1912
C-----AT---GC---CTTACCA...GC---G---G---C---A---C---AAG---G---T---C---A-----A---CA-----G---G-----T---G---C---A---T---G---G---G---G---C---A-----A-A 1912
C-----A---AT---GC---CTTGCCA...GCG---G---G---A---A---AAG---G---T---A---G-----A---CA-----A---G-----TT---GC---A---T---T-----G---G---C---T---A-----GA-A 1880
CA-----AT---GC---CTTACCA...GC---G---G---A---C---AAGG---G---T---C---A-----A---CA-----A---G-----T---G---C---A---T---G---G---G---G---C---A-----GA-A 1356
C-----A---T---AT---GC---CTTACCA...GC---G---G---C---A---T---ACG---T---C---A-----A---CA-----G-----G---G---A-----T---G---C---A---T---G---G---G---G---C---T-----GA-A 1356
-----A---T---AT---GC---CTTACCA...GCG---G---G---A---A---AAG---G---T---C---A-----G---A---CA-----G-----G---G---A-----TT---G---C---A---T---G---G---A---C---T-----GA-A 1357
-----A---T---AT---GC---CTTACCA...GCG---G---G---A---A---AAG---G---T---C---A-----G---A---CA-----G-----G---G---A-----TT---G---C---A---T---G---G---A---C---T-----GA-A 1357
-TGCA-T-CAT---GC---CTTACCA...GCG---G---G---A---A---AAG---G---T---C---A-----G---A---CA-----A---G---G-----TT---C---A---T---TG-----G---C---T-----T---GA-A 1350
CCA-T-T-AT---GC---CTTACCA...GCG---G---G---C---A---C---AAG---G---T---C---A-----A---CA-----A---G---G---A-----TT---GGC---A---T---G-----G---C---T-----GA-A 1921
TGCA-T-CAT---GC---CTTACCA...GC---G---G---A---A---AAG---G---T---C---A-----A---CA-----A---G-----T---G---C---G---T---TG-----G---C---T-----GA-A 1905
C-----T---AT---GC---CTTACCA...GCG---G---G---A---A---AAG---G---T---C---A-----G---A---CA-----A---G-----T---GGC---T---TG-----G---A---C---T-----GA-A 1356
C-----A---T---AT---GC---CTTACCA...GC---G---G---A---A---AAG---T---C---A-----G---A---CA-----G---G-----TT---GC---A---T---TG-----G---A---C---T-----GA-A 1657
-----A---T---AT---GC---CTTACCA...GC---G---G---C---A---A---AAG---G---T---C---A-----A---CA-----A---G---G-----TT---GC---A---T---TG-----G---A---C---T-----GA-A 1906
-----A---T---AT---GC---CTTACCA...GCG---G---G---A---A---AAGG---T---C---A-----G---A---CA-----A---G-----TT---G---C---A---T---TG-----A---C---T-----GA-A 1355
A-----GAT---G---CTGCCA...GC-----C---CAG---G-----A-----C---C---CA-----G-----A-----GGC---A---T---TG---T---G-----G-----A-----T---A 1878
A-----GAT---G---CTGCCA...GC-----C---CAG---G-----A-----C---C---CA-----G-----A-----GGC---A---T---TG---T---G-----G-----A-----T---A 1876
AA-----T---TCG---GC---ATGCCA...GC---G---C---A---AAG---G---C---A---G-----C---C---CA-----A---G---A-----CC---A---T---TG---C-----G---A---C---T---A---G-----T---GT-A 1874
A-----A---GTC---GC---ATGCCG...GC-----C---AAG---G-----C---A---G-----C---C---CA-----G---G---G---A-----GGCC---A---T---TG---C-----G---A---C---T---A-----T---A 1873
A-----A---GTC---G---GC---ATGCCA...GC-----G---C---AAG---G-----C---A---G-----C---C---CA-----G---G---G---A-----G---CC---A---T---C-----A---A---T---A-----T---GT-A 1019
-T-A--T---A---GG---GCCGCCA...GC-----M-C---A---A-----A---G---C---A---A---A-----T---CAC---G---G---A---T-----A---T---Y---T---A-----RT-A 1275
A-----GGTG---G---CTGCCA...GC-----C---CAG---G-----A---G---C---C---CA-----G---G---A-----GGGT---A---GT---T---C-----G-----T---A-----T---G---A 1879
AA-----A---GTC---GC---CTGCCG...GC-----G---A---C---AAGG---A---G-----C---C---CA-----G---G---A-----GGGC---A---T---T---C-----G---A---T---A-----T---A 1009
CA-----A-C-A-GC---CCACCA...GC---G-----A---AAG---T---T-----A---G---A---G---G---A-----G---CG---A---T---A-----G---G---T---C---TC-----T---1391
-----1859
-----A-----R-----1859
-----G-----965
-----G-----1858
-----G-----1860
-----G-----1847
-----965
-----834
-----936
-----A-----G-----A-----A-----1357
-----A-----G-----A-----A-----1357
-----822
-----965
-----A-----G-----C-----A-----T-----1339
-----A-----G-----C-----A-----T-----1339
-A-A---AG-GG-CAA-AGCCGGCGCAA-CGGCT-GGG-A--A-A---C-A---G---CA-CCC-AG---G-AG-A---T---GGC---A---AG-C---G-AG---C-T-A-G---G---1302
-A-A---G---G---CTACCA...GC---G---A---AAG---C---T---A---G---A---G---A---Y---G---A---T---T---A---G---C---R-G---T---A 1858
-A-A---R-G---G---ATACCA...GC-----A---AAG---C---C---T---CA-S---C---T---A---T---G---G---A---T---T---C---R-G---T---A 1344
-A-A---G-G-G---G---GATACCA...C-----A---AAG---C---C---T---CA-S---C---T---A---T---G---G---A---T---T---C---R-G---T---A 1638
-A-A---R-G-G---G---ATACCA...C-----A---AAG---C---C---T---CA-S---C---T---A---T---G---G---A---T---T---C---R-G---T---A 1637
-A-A---R-G-G---G---ATACCA...C-----A---AAG---C---C---T---CA-S---C---T---A---T---G---G---A---T---T---C---R-G---T---A 1344
-A-A---G-G-G---G---GATACCA...C-----A---AAG---C---C---T---CA-S---C---T---A---T---G---G---A---T---T---C---A---G---T---A 1830
-----A---G---G---G---ATACCA...GC-----C---A---T---AAG---T---A---G---A---G---T---T---G---G---A-----G---A-----T---1788
-A-A---G-G-G---G---CTACCA...GC---G-----A---AAG---C---T---A---G---G---A-----A-----G---A-----T---T---G-----T---A 1874
-----T-----C-GGGTCCGCTGCCA...GC---G-----A---A---AAGC---G-----A-----G---T---C---CC---G-----T---A-----C-G---G---A---T---T---G-----A-----C-----T-----A 1521

[illegible]

MAC.US.x.239
Gag
A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PET2
A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CR1K 147
A.IN.x.NNVA
A.SN.85.ROD
B.CI.88.UC1
B.CI.89.pPRD320-20HIV2_56
B.CI.x.EHO
B.GH.86.D205
B.JP.81.KR020
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.03.03CM_510_03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251_1A11
MAC.US.x.251_32H_PJ5
MAC.US.x.251_BK28
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239_87082
MAC.US.x.MN142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.82.MNE_8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236_H4
SMM.US.x.H9
SMM.US.x.PBJ14_15
SMM.US.x.PBJA
SMM.US.x.PBJ_143
SMM.US.x.PBJ_6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

Gag p24 Capsid end_Gag p2 Spacer start
Gag p2 Spacer end_Gag p8 Nucleocapsid start
TGCTAACCCAGATTGCAAGCTAGTGCTGAAGGGGCTGGGTGTGAATCCACCCCTAGAAGAAATGCTGACGGCTTGTCAAGGAGTAGGGGGCCGGGACAGAAGGCTAGATTAAATGGCAGAAGCCCTGAAGAGGGCCCTCGCACCAAGTGCCTCCCTTTTGGAGCAGCCC 2199
A N P D C K L V L K G L G V N P T L E E M L T A C Q G V G G P G Q K A R L M A E A L K E A L A P V P I P F A A A
-----C--T--T--A-A-A--AA-----G--C--C--G--G--C--A--C--A--C--C--T--A--TT-AA--CCC--T--A--2252
-----C--C--T--A-A-A--GA-----G--A--C--C--G--G--C--A--C--A--C--GC--T--A--TA-G-G--AGC--T--A--2252
-----C--T--AT--A-A-A--GA-----T--T--G--G--C--G--A--A--A--C--A--C--T--A--G--CC--T--A--2220
-----C--C--T--A-A-A--GA-----G--G--T--C--G--G--T--A--C--A--C--A--C--C--C--G--TT-GA--CCC--T--A--1696
-----C--T--T--AT--A-A-A--GA-----G--G--T--C--G--G--C--A--AA--C--A--C--C--T--A--G--TT-GA-G--CC--T--A--1696
T.G-----C--T--T--A-A--A--GA-----G--G--A--C--C--G--GA--T--A--C--C--C--C--T--A--G--A-GG--CC--T--A--1693
-----C--C--T--AT--A-A-A--GA-----T--T--G--A--C--C--C--G--T--A--C--A--C--C--T--A--T--GA--CC--T--A--1697
-----C--C--T--AT--A-A-A--GA-----T--T--G--A--C--C--C--G--T--A--C--A--C--C--T--A--T--GA--CC--T--A--1697
-----C--C--T--AT--A-A-A--AT-A-AA-----T--T--CA--C--G--G--T--A--C--A--C--C--T--A--G--T-A-G--CC--C--A--1690
-----C--C--T--AT--A-A--AT-A-GA-----T--T--G--A--T--C--G--T--A--C--A--C--C--T--A--G--A-G-G--CCC--T--A--C--2261
-----C--C--AT--A-A--A--GA-----T--T--G--A--T--C--G--T--A--C--A--C--C--T--A--G--A-G-G--CT--T--A--2245
-----C--C--T--AT--A-A-A--GA-----T--T--G--A--C--C--G--T--A--C--A--C--C--T--A--G--A-GA--CC--T--A--C--1696
-----C--C--T--AT--A-A-A--GA-----T--T--G--A--C--C--G--T--A--C--A--C--C--T--A--G--A-GA--CC--T--A--C--1696
-----C--T--AT--A-A-A--A-A-AA-----T--T--G--A--C--C--G--T--A--C--A--C--T--A--G--G--CCA--T--A--C--1997
-----C--T--AA--A-A-A--A-A-GA-----A--T--G--A--C--C--G--T--A--T--A--G--T--A--G--ACC--T--A--C--T--2246
-----C--C--T--AT--A-A-A--GA-----C--T--T--G--A--C--C--G--G--T--A--C--A--G--G--T-A-A-G--T-CC--T--A--C--1695
-----T--A--T--CT-A-AA-----T--G--C--C--GA--A--C--A--G--A--GC--T--G--T--A--T-AA--T-CA--C--A--G--T--C--T--2218
-----T--A--C--CT--AA--A--C-----G--A--C--C--C--GA--A--C--A--A--A--C--T--G--T--A--A--T-CA--C--A--G--T--C--T--2216
-----AT--T--CT--AA--C--AT-----A--A--C--C--G--GA--A--C--A--G--A--GC--T--G--TT-A--A--T--GA--TTCA--C--AT--G--C--C--T--2214
-----T--T--CT--AA-----T--G--A--A--C--C--GA--A--C--A--G--A--GC--C--T--A--A--AA--T-CA--C--A--G--T--C--TT--2213
-----C--AT--A--T--C--AA--C--A-----A--A--C--C--GA--A--C--A--G--A--GC--C--G--TT-A--G--A--T--GA--TTCA--TT--A--A--T--TT--1359
-----T--AT--A--A--T--AA-----T--TT--G--T--A--C--GR--A--A--A--G--A--A--C--GC--T--T--AT--A--A--T-AAAC--TACAG--CC--A--A--T--T--1615
-----A--C--TT--GCCAC--C-----G--C--C--A--A--C--A--A--A--G--C--C--G--TT-A--A--T--AA--G--C--CA--C--A--A--C--T--T--T--2219
-----T--A--T--CT--AA-----T--G--C--C--A--A--C--A--G--A--AGC--C--G--T--A--TT-AA--G--CA--C--A--G--T--CTTT--1349
-----C--A--C--T-A--A--TT--A-----T--T--G--A--A--C--A--A--A--A--A--A--GC--G--T--A--T--ACA--TA--T--A--C-----T--1731
-----2199
-----A-----R-----1305
-----1305
-----T--A-----A-----A--A-----2200
-----A--A-----2187
-----A--A-----1305
-----1174
-----AC-----C-----A-----C-----1697
-----AC-----C-----A-----C-----1697
-----1162
-----1305
-----G-----A-----A--A--A--A--A-----T--G--C-----1679
-----G-----A--A--A--A--A-----G--C-----1679
C--C--T--A--AT-A--T--CA-----G--A--A--C-----G--A--C--A-----CC-CC-C-----G--A-----C-----A--GGGTCTTT-G-GG-AGCACAGTTTAGGG 1642
-----T--A--C--T--CA-----TT-----T--A--C--G-----A--A-----G-----AT-----A--GAGG--AT-A--C--A-----T--2198
-----G--C--T--AT-G--C--T--YA-A-----TT-----T--A--C--G-----R--A--A--AS-----C-----G--AT-----T--A--GA-G-A--G-----R-----T--1684
-----G--C--T--AT-G--C--T--A-A-----TT-----T--A--C--G-----A--A--A--A-----C-----G--AT--A--T--A--GA-G-A--G-----C-----T--1978
-----G--C--T--AT-G--C--T--A-A-----TT-----T--A--C--G-----A--A--A--A-----C-----G--AT--A--T--A--GA-G-A--G-----C-----T--1977
-----G--C--T--AT-G--C--T--YA-A-----TT-----T--A--C--G-----R--A--A--AS-----C-----G--AT--A--T--A--GA-G-A--G-----C-----R-----T--1684
-----G--C--T--AT-G--C--T--A-A-----TT-----T--A--C--G-----A--A--A--A-----C-----G--AT--A--T--A--GA-G-A--G-----C-----A-----T--2170
-----T--AT-G--C--T--CA-----TT-----T--A--C--G-----A--A--A--A-----G-----G--AT-----A--GA-G--G--A--C-----T--2128
-----T--AT-G--C--T--A-----TT-----T--A--C--G-----A--A--A--A-----A-----AT-----A--GAG--AC-A--C-----T--2214
-----T-----AT-G--AT--A--T-----CA-----G--T--A--A--A-----G--T-----A--A-----A-----C--G-----T--T--CA-----AC--C--G--C-----C-----1861

		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			
		Gag-Pol -1 ribosomal slip site																				Pol start		Gag p8 Nucleocapsid end		Gag p1 Spacer start		F			

MAC.US.x.239
 Pol
 Gag
 A.CI.88.UC2
 A.DE.x.BEN
 A.DE.x.PE12
 A.GH.x.GH1
 A.GM.87.0194
 A.GM.x.ISY
 A.GM.x.MCN13
 A.GM.x.MCR35
 A.GW.86.FG
 A.GW.87.CAM2CG
 A.GW.x.ALI
 A.GW.x.MDS
 A.IN.95.CRIK 147
 A.IN.x.NNVA
 A.SN.85.R0D
 B.CI.88.UC1
 B.CI.09.pPRD320-20HIV2_56
 B.CI.x.EH0
 B.GH.86.D205
 B.JP.01.KR020
 G.CI.92.ABT96
 AB.CI.90.7312A
 AB.CM.03.03CM_510_03
 U.FR.96.12034
 MAC.US.x.17EC1
 MAC.US.x.17EFR
 MAC.US.x.1937
 MAC.US.x.2065
 MAC.US.x.251_1A11
 MAC.US.x.251_32H_PJ5
 MAC.US.x.251_BK28
 MAC.US.x.80035
 MAC.US.x.97074
 MAC.US.x.MAC239_87082
 MAC.US.x.MM142
 MAC.US.x.SMM142B
 MAC.US.x.r80025
 MAC.US.x.r90131
 MNE.US.02.MNE.8
 MNE.US.x.MNE027
 SMM.SL.92.SL92B
 SMM.US.x.F236_H4
 SMM.US.x.H9
 SMM.US.x.PBJ14_15
 SMM.US.x.PBJA
 SMM.US.x.PBJ_143
 SMM.US.x.PBJ_6P6
 SMM.US.x.PGM53
 SMM.US.x.SME543
 STM.US.x.STM

Gag p1 spacer end, Gag p6 start
 CTTGGTCCATGGGAAAGAGCCCGCAATTTCCCATGGCTCAAGGTGATCAGGGGTGATGCCAACTGCTCCCGAGAGACCAGCTGTGGATCTGCTAAAGAACTACATGCAGTTGGGAAGCAGCAGAGAGAAAAGCAGAGAGA..... 2509
 R P W S M G K E A P Q F P H G S S A S G A D A N C S P R G P S C G S A K E L H A V G Q A A E R K A E
 L G P W G K K P R N F P M A Q V H Q G L M P T A P P E D P A V D L L K N Y M Q L G K Q Q R E K Q R E
 A-G-CT-C-----C-----G-C-CT-C-----A-A-A-CA-T-G-A-C-C-T-G--A-TT--CA--G-GAA--G-GC--AG-GAGAGACCATACAAGGAGGTGACGGA 2574
 T-G-C-C-----T-----G-A-C-CC-C-----A-A-A-T-G-CA-T-A-C-A-T-T-GG-GA-T--CAA-G-GAA--G-GC--AG-GAGAGACCATACAAGGAGGTGACGGA 2574
 A--C-----T-----G-A-C-G-C-CG-----CA-A-A-CA--A-CA-C--G-G--T--CAA-G-G-A--A-GC--A-A-TGAGACCATACAAGGAGGTGACGGA 2542
 A-G-----C-----G-C-CT-C-----A-A-A-CA-T-A-C-C-T-GG-A-GA-T--CA--G-GAG--G-GC--AG-GAGAGACCATACAAGGAGGTGACGGA 2018
 A-G-C-C-----C-----G-C-TC-C-AGTTCCG--A-CA-A-A-AT-T-A-C-A-GG-G--CAA-G-GAA-A--GC--AGACA-AGACCATACAAGGAGGTGACGGA 2015
 A-G-C-CC-----C-----G-C-C-CG--A-CA-A-A-TA-T-A-C-A-GG-T-T--CAA-A-AAGA-A--C--AGAGAGAGACCATACAAGGAGGTGACGGA 2019
 A-G-C-CC-----C-----G-C-C-CG--A-CA-A-A-TA-T-A-C-A-GG-A-T--CAA-A-AAGA-A--C--AGAGAGAGACCATACAAGGAGGTGACGGA 2019
 A--C-AC-----G-----G-C-C-CG--A-CA-A-A-TT-T-A-C-A-GG-A-T--CAA-G-AAG--G-GC--AGACAGAGACCATACAAGGAGGTGACGGA 2583
 A--C-C-----T-----G-AA-C-G-T-CG--AT-A-CA-A-A-CA-G-A-C-C--GG-C-G-T--CA--G-GAA--A--GC--AGAGAGAGGCATACAAGGAGGTGACGGA 2567
 A--C-C-----C-----G-C-G-T-CG--A-CA-A-A-CA-T-A-C-A-GG-A-T--CAA-G-GAA--G-GC--AGAGAGAGACCATACAAGGAGGTGACGGA 2018
 A-AA-C-CC-----T-----G-C-C-CG--A-CA-A-A-T-AT-T-A-C-A-GG-A-T--CAA-G-GAA--G-GC--AGAGAGAGACCATACAAGGAGGTGACGGA 2319
 A-G-C-CC-----C-----G-C-A-C-CG--A-CA-A-A-AT-T-A-C-A-GG-A-T--CAA-G-GAA--G-GC--AGAGAGAGACCATACAAGGAGGTGACGGA 2568
 -G-C-T-----C-----G-C-C-CG--A-CA-A-A-T-T-T-A-C-A-GG-A-T--CAA-G-AAGA--G-GC--AGAGAGAGACCATACAAGGAGGTGACGGA 2017
 T-A-A-C-----T-----C-----A-C-----AG-CA-T-A--GAT-----A-A-GCA-AC-CCTCGGGGGG-ACACCATCTGC--CC-CTGC--TCCAGCAGTG--GATGCTGAAAAGCTACATGCA 2552
 T-C-A-C-----T-----C-----A-G-CA-T-A--GAT-----A-ACA-CA-AC-CCTC-GGGTGC-ACCTCATCTGCA--CC-CTGC--TCCAGCAGTG--GATGCTGAAAAGCTACATGCA 2547
 T-C-C-----T-----G-C-C--G-CA-CC-----A-AG-T-G--GAT-A--AT-C-GCA-AC-CCTC-GGGTGC-ATTCATCTGCA--CC-CTGC--TCCAGCAGTG--GATGCTGAAAAGCTACATGCA 2542
 T-A-A-C-----T-----A-C-----AG-CA-T-A--GAT-A--A-A-GCA-AC-CCTCGGGGGG-ACACCATCTGC--CC-CTGC--TCCAGCAGTG--GATGCTGAAAAGCTACATGCA 2547
 T-C-C-----T-----TG-A-C-CA-CC-----A-AC-T-A--A-AT-A--A-A-A-CA-AC-CCTC-GGGTGAAT-CCATCTGC--CC-CTGC--TCCAGCAGTG--GATGCTGAAAAGCTACATGCA 1693
 T--A-T-----T-----A-C-C-C-----CT-T-A-A-A-GAT-----A-A-C-A-G-----T-----RC--G-G-A--A-AG-----1919
 --A-C-----T-----C-----A-A-AG-----T-G--GAT-A-A--A-A-GCAA-AC-C-TC-GGGAGC-ATACCATCTGC--CC-CTGC--TCC-GCAGTG--GATGCTGAAAAGCTACATGCA 2553
 T-A-A-C-----T-----A-C-G-----AG-CA-T-A--GAT-A--A-A-RGCA-AC-CCTC-GGGGG-ACACCATCTGC--CC-CTGC--TCCAGCAGTG--GATGCTGAAAAGCTACATGCA 1683
 --C-T--A--A--T-----C-----C-CG--A--CC--A-C-T--CA-A-A--G-CCCCGACAGCC-CTCCA-CG-C-CAGCAGTG--TCT--TA-AGAGTACATGCAACAGGGCAAGAA 2065
 -----2509
 M--Y-----R-----2509
 -----1615
 -----C-----A-----2508
 -----C-----2510
 -----C-----2485
 -----1615
 -----1484
 Y-----1586
 --C-T-----A-A-----C-----1995
 --C-T-----A-A-----C-----1995
 -----1472
 -----1615
 T--C-----C-A-----C-----A-----A-----1977
 T--C-A-----CA-----1977
 -----T-----C-----G-GACAAATC...AT--CA--GT-A-A-----TC-A-CA-CC-G-A--GTC--GG-GTAT-TAGA-AAAGCA--AG-GA-A-G-C-----1940
 -----C-----G-A-C-----CA-----Y-----T-----A-G-----T-----A-A-----GAA-----G-----2496
 -----C-----G-A-C-----CA-----Y-----T-----A-G-----T-----A-A-----GAAG-----G-----1982
 -----C-----G-A-C-----CA-----Y-----T-----A-G-----T-----A-A-----GAAG-----G-----2276
 -----C-----G-A-C-----CA-----Y-----T-----A-G-----T-----A-A-----GAAG-----G-----2275
 -----C-----G-A-C-----CA-----Y-----T-----A-G-----T-----A-A-----GAAG-----G-----1982
 -----C-----G-A-C-----CA-----Y-----T-----A-G-----T-----A-A-----GAAG-----G-----2468
 -----C-----G-A-C-----CA-----Y-----T-----A-G-----T-----A-A-----GAAG-----G-----2426
 T--C-----C-A-C-----CA-----T-----A-G-----T-----A-A-----GAA-----G-----2512
 T--C-----A--C-----C-----C-T--A-----C-----G-GA-GT-----C-----A-----2156

[illegible]

AGGAATAGAGTTAGGTCACATTATACCCCAAAATAGTAGGAGGAATAGGAGGTTTTATTAACTAAAGAATACAAAAATGAGAAATAGAAAGTTTTAGGCAAAAGGATTAAAGGGACAATCATGACAGGGGACACCCCGATTAAACATTTTGGTAGAAAATTTGCTAA 2825
 T G I E L G P H Y T P K I V G G I G G F I N T K E Y K N V E I E V L G K R I K G T I M T G D T P I N I F G R N L
 -----GGACA--C-T--G--G-G--G-A-C-A-C-C--T-G--A-AC-AAT-AG-A-G-CC-C-A--A-T--A-C-C--C--A-TT-G-2908
 -----A--GGACA--C-T--G--G-A--A-C-C--G--G-A--A-C-C--A--A-T--A-C-C--C--A-T--G-2908
 -----G--GGACA--GT--G--G--G-A-C-A-C-C-G--T--A-AC-AAT-AG-A-G-CC-C-A--A-T--A-C-C--C--CA-T-G-2876
 -----C--GGACA--CGTT--G--G--G-A-C-A-C--GATT--A--A-AC-AAT-AG-A-G-CC-C-A--A-T--A-C-C--C--A-C-G-2352
 -----GGACA--C-T--G--G--G-A-C-A-C--T--A-G-AC-AAT-AG-A-G-CC-C-A--A-T--A-C-C--C--A-T-G-2352
 -----GAGCA--GT--G--G--G-A-C-A-C--T--G--A-G-AC-AAT-AG-A-G-CC-C-A--A-T--A-C-C--C--A-C-G-2352
 -----G--GGACA--GT-G--G--G-A-C-A-C-C-G-T--A--A-AC-AAT-AG-A-GG-CC-C-A--A-T--A-C-C--C--A-T-G-2353
 -----G--GGACA--GT-G--T--G-A-C-A-C-C-G-T--A--A-AC-AAT-AG-A-GG-CC-C-A--A-T--A-C-C--C--A-T-G-2353
 -----A--GGACA--GT--G--G--G-A-C-A-C-C-G-T--G--A-AC-AAT-AG-A-GG-CC-C-A--A-T--A-C-C--C--G-T-G-2346
 -----A--GGACA--G--G--G--G-A-C-A-C--T--G--A-AC-AAT-AG-A-GG-CC-C-A--A-T--A-C-C--C--A-T-G-2917
 -----A--GAGCA-C--G--G--G-A-C-A-C--TG-G--A-AC-AAT-AG-A-GG-CC-C-A--A-T--A-C-T--C--CA-TT-G-2901
 -----A--AAGCA--GT--G--G-A-C-A-C-C-G-T--CC-T--G-A-GG-CC-C-A--A-T--A-C-C--C--A-TT-G-2352
 -----A--AAGTA--GT--G--G-A-C-A-C--T-C--CC-T--A-G-A-GG-CC-C-A--A-T--A-C-C--C--CA-TT-G-2653
 -----A--AAGTG--AT--G--G-A-C-A-C--T--CC-T--A-G-A-GG-CC-C-A--A-T--A-C-C--C--CA-TT-G-2902
 -----A--GAACA--G--G--G-A-C-A-C-G--T--C-AAT-AG-A-GG-CC-C-A--A-T--A-C-C--C--A-T-G-2354
 -----A--AGCA--C--G--G--G-A-C-A-C--G--G--AG-G-A--AG-A-GG-CA-T-A--A--A-A--C--A-TT--2889
 -----A--AGTA--C--G--G--G-A-C-A-C--G--G--A--G--G-A-G-CA-T-A--A--A-A--C--A-CT--2884
 -----G--A--CAGCA--C--T--G--A--A--C-T--AG--A--AG-A-G-CA-G-A--A--A-A--C--A-TT--2879
 -----G--A--AGCA--C--G--G--G-A-C-A-C--G--G--AG-G-A--AG-A-GG-CA-T-A--A-T--A-A--C--A-T--2884
 -----G--A--AGTG--C--G--G--A-C-A-C--G--G--AG--A--A--A-G-CA-T-A--A-T--A-A--C--A-T--2030
 -----A--AAGTA--GT--A--C--C--TA--GG--A--A-AC-G-CT-TG-T--T--T--A-T-C--A-G-CA-TT-G-2235
 -----A--AAGCA--C--G--G--G-A-C-A-C--G--CA--AG--A--A-G-A-GGTA-T-A--A--A-A-T--C--A-CT--2890
 -----AY--AGCA--C--G--R--G--A-C--G--G--AG-G-A--CAG-A-GG-CA-T-A--A--A-A--C--A-TT--2020
 -----G-TA-A--AA--T--T--CT--G-A--A--G-C--A--A--TTC-C--A-C-A--A-G--CA--G--T-C-A--A--A-C-T--G-C-TT-G-2390
 -----2825
 -----2825
 -----Y-----A-G-----A-----2824
 -----T-----A-----T-----G-----A-----2801
 -----2801
 -----1931
 -----1800
 -----1902
 -----A-----2311
 -----A-----2311
 -----1788
 -----1931
 -----A-----2293
 -----2293
 -----G-----GGG--C-A--G--T--G--G-T--A--C-A-A--T-G-CA-A--A--A--GGTA-A-G-AA-C-A--A-T--A-T--C--A-T-G-2256
 -----G--A-G--A--T--C--C-C--T-G-A--A--A--C--GGTA--G-A-T--G-A-T--A-T--C--C--2812
 -----G--A-G--A--T--C--C-C--T-G-A--A--A--A--GTA--G-A-T--A-T--A-T--C--C--2298
 -----G-T-A-G--A--T--C--C-C--T-G-A--A--A--A--GTA--G-A-T--A-T--A-T--C--C--2592
 -----G-T-A-G--A--T--C--C-C--T-G-A--A--A--A--GTA--G-A-T--A-T--A-T--C--C--2591
 -----G-T-A-G--A--T--C--C-C--T-G-A--A--A--A--GTA--G-A-T--A-T--A-T--C--C--2298
 -----G-T-A-G--A--T--C--C-C--T-G-A--A--A--A--GTA--G-A-T--A-T--A-T--C--C--2784
 -----G--AC--A--T--C--C-C--G-T-G-A--A--C--GGTA--G-A-T--A-T--A-T--C--C-T--2742
 -----G--A-G--A--T--C--C-C--T-G-GA--A--C--GGTA--G-A-T--G-A-T--A-T--C--C--2828
 -----G--G-----C--G-T--A--C-----GG-----T-----A--A-----G--TT-G-----A-C-----G-A-----G-AA-A-----A-T--T-----T-A-----C-----C--G--CC-AT-G-2472

MAC.US.x.239
 POL
 A.CI.88.UC2
 A.DE.x.BEN
 A.DE.x.PE12
 A.GH.x.GH1
 A.GM.87.D194
 A.GM.x.ISY
 A.GM.x.MCN13
 A.GM.x.MCR35
 A.GW.86.FG
 A.GW.87.CAM2CG
 A.GW.x.ALI
 A.GW.x.MDS
 A.IN.95.CR1K 147
 A.IN.x.NNVA
 A.SN.85.ROD
 B.CI.88.UC1
 B.CI.89.pPRD320-20HIV2_56
 B.CI.x.EH0
 B.GH.86.D205
 B.JP.81.KR020
 G.CI.92.ABT96
 AB.CI.90.7312A
 AB.CM.03.03CM_510_03
 U.FR.96.12034
 MAC.US.x.17EC1
 MAC.US.x.17EFR
 MAC.US.x.1937
 MAC.US.x.2065
 MAC.US.x.251_1A11
 MAC.US.x.251_32H_PJ5
 MAC.US.x.251_BK28
 MAC.US.x.80035
 MAC.US.x.97074
 MAC.US.x.MAC239_87082
 MAC.US.x.MN142
 MAC.US.x.SMM142B
 MAC.US.x.r80025
 MAC.US.x.r90131
 MNE.US.82.MNE_8
 MNE.US.x.MNE027
 SMM.SL.92.SL92B
 SMM.US.x.F236_H4
 SMM.US.x.H9
 SMM.US.x.PBJ14_15
 SMM.US.x.PBJA
 SMM.US.x.PBJ_143
 SMM.US.x.PBJ_6P6
 SMM.US.x.PGM53
 SMM.US.x.SME543
 STM.US.x.STM

[illegible]

MAC.US.x.239
Pol

A.CI.88.UC2
 A.DE.x.BEN
 A.DE.x.PEI2
 A.GH.x.GH1
 A.GM.87.D194
 A.GM.x.ISY
 A.GM.x.MC113
 A.GM.x.MCR35
 A.GW.86.FG
 A.GW.87.CAM2CG
 A.GW.x.ALI
 A.GW.x.MDS
 A.IM.x.CRIK_147
 A.IN.x.NNVA
 A.SN.85.R0D
 B.CI.88.UC1
 B.CI.69.pPDR320-20HIV2_56
 B.CI.x.EH0
 B.GH.86.D205
 B.JP.01.KR020
 C.CI.92.ABT96
 AB.CI.90.7312A
 AB.CM.03.03CM_510_03
 U.FR.96.12034
 MAC.US.x.17EC1
 MAC.US.x.17EF1
 MAC.US.x.1937
 MAC.US.x.2065
 MAC.US.x.251_1A11
 MAC.US.x.251_32H_PJ5
 MAC.US.x.251_BK28
 MAC.US.x.80095
 MAC.US.x.97074
 MAC.US.x.MAC239_87082
 MAC.US.x.MM142
 MAC.US.x.SMM142B
 MAC.US.x.R80925
 MAC.US.x.r90131
 MNE.US.82.NNE
 MNE.US.x.MNE027
 SMM.SL.92.SL92B
 SMM.US.x.F236_H4
 SMM.US.x.H9
 SMM.US.x.PBJ14_15
 SMM.US.x.PBJA
 SMM.US.x.PBJ_143
 SMM.US.x.PBJ_196
 SMM.US.x.PGMS3
 SMM.US.x.SMES43
 STM.US.x.STM

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MAC.US.x.239	GAATTACAGTACTGGATATAGGTGATGCATATTCTCTCATACCTCTAGATGAAGAATTAGGCAGTACACTGCCCTTTACTTTACCATCAGTAAATATGCAGAGCCAGGAAAACGATACATTTATAAGGTTCTGCCTCAGGGATGGAAGGGGTACCAGCCATCTTCCAA	3334
Pol	K R I T V L D I G D A Y F S I P L D E E F R Q Y T A F T L P S V N N A E P G K R Y I Y K V L P Q G W K G S P A I F	
A.CI.88.UC2	-G -T -A -G -G -C -C -T -A -T -T -C -T -A -CC -C -T -A -A -CT -A -A -G -A -A -A -T -	3417
A.DE.x.BEN	-G -CT -TA -T -A -G -G -C -C -T -A -C -T -A -CC -G -C -ATG -A -A -T -A -A -CT -A -A -A -A -A -T -	3417
A.DE.x.PE12	-T -A -G -G -C -C -T -A -C -G -C -A -A -T -A -C -A -G -C -A -GA -T -A -A -C -A -A -A -G -A -T -	3385
A.GH.x.GH1	-G -C -T -A -G -G -C -C -T -G -C -T -A -T -A -CC -C -A -A -TG -A -A -CT -A -A -A -A -A -A -T -	2861
A.GM.87.D194	-G -T -A -G -G -C -C -T -A -C -T -A -T -A -CC -C -A -A -TG -A -A -CT -A -A -A -A -A -A -T -	2861
A.GM.x.ISY	-T -GT -A -G -A -C -C -T -C -T -G -T -A -T -A -C -G -A -T -A -C -A -CT -A -A -A -A -A -T -	2868
A.GM.x.MCN13	-T -A -G -G -T -C -T -A -C -G -C -A -T -A -A -C -A -C -A -T -A -C -A -CT -A -A -A -A -A -T -	2862
A.GM.x.MCR35	-T -A -G -G -T -C -T -A -C -C -C -A -T -A -C -A -C -A -A -T -A -C -A -CT -A -A -A -A -A -T -	2862
A.GW.86.FG	-T -A -G -G -T -C -T -A -C -G -C -A -T -A -C -C -A -C -A -A -T -A -C -A -CT -A -A -G -A -A -T -	2855
A.GW.87.CAM2CG	-T -A -G -G -T -T -T -AT -C -C -A -T -A -C -C -G -C -A -A -A -T -A -A -CT -A -G -G -A -A -A -T -	3426
A.GW.x.ALI	-C -T -G -G -G -T -C -T -A -GC -GAGC -A -T -A -C -C -A -A -A -T -A -A -CT -A -G -A -A -A -T -	3410
A.GW.x.MDS	-C -T -A -G -G -T -C -T -A -GC -C -A -A -CC -G -C -A -A -T -A -A -CT -A -A -A -A -A -T -	2861
A.IN.95.CRIK 147	-C -T -A -G -G -T -C -T -A -GC -C -A -T -A -G -G -C -A -A -T -A -A -CT -A -A -A -A -A -T -	3162
A.IN.x.NNVA	-C -T -A -G -G -T -C -T -A -GC -G -C -A -C -G -G -C -A -A -T -A -C -A -CT -A -A -A -A -A -T -	3411
A.SN.85.R0D	-T -A -G -G -T -C -T -A -C -G -C -A -CA -T -A -C -G -C -A -A -T -A -A -CT -A -A -A -A -A -T -	2863
B.CI.88.UC1	-A -A -G -G -A -C -C -AGT -C -A -CC -A -C -A -T -A -A -C -G -A -C -A -GA -A -A -A -A -C -A -T -	3398
B.CI.89.pPRD320-20HIV2_56	-A -T -A -G -G -A -C -C -AGTG -C -A -CCC -T -C -A -A -C -G -C -G -T -GA -A -A -A -A -T -C -A -T -	3393
B.CI.x.EH0	-A -A -G -A -C -C -AGTG -C -A -CC -C -A -A -T -A -A -G -G -GA -TC -C -A -C -A -A -A -C -A -T -	3388
B.GH.86.D205	-A -A -G -A -C -C -AGT -C -A -CC -A -C -A -T -A -A -C -G -C -GA -C -A -A -A -A -G -A -C -AGT -A -T -GT -	3390
B.JP.81.KR020	-A -A -A -C -C -AGT -C -A -CC -T -C -A -A -A -A -C -G -G -A -A -C -C -C -A -A -A -G -A -C -A -T -	2540
G.CI.92.ABT96	-A -G -C -C -AG -T -T -T -C -A -T -C -C -C -A -A -C -C -C -A -G -A -A -C -A -G -A -C -T -	2744
AB.CI.90.7312A	-A -GA -A -G -A -C -C -AGTG -C -A -CCC -C -C -A -T -A -A -C -G -A -A -G -A -C -A -A -A -C -A -T -	3399
AB.CM.03.03CM_510_03	-A -A -G -G -A -C -C -AGT -C -A -CC -R -Y -C -A -T -A -A -C -CY -G -AC -C -YA -GA -A -A -R -R -C -A -T -	2529
U.FR.96.12034	-G -A -T -A -G -G -C -C -AG -C -G -GTG -C -C -A -T -T -CA -T -A -C -C -GT -A -C -A -A -A -A -T -T -	2899
MAC.US.x.17EC1		3334
MAC.US.x.17EFR		3334
MAC.US.x.1937		2440
MAC.US.x.2065		2440
MAC.US.x.251.1A11	-G -C -	3333
MAC.US.x.251.32H.PJ5		3335
MAC.US.x.251.BK28	-G -	3310
MAC.US.x.80035		2440
MAC.US.x.97074		2309
MAC.US.x.MAC239_87082		2411
MAC.US.x.MN142	-G -C -T -	2820
MAC.US.x.SMM142B	-G -C -T -	2820
MAC.US.x.r80025		2297
MAC.US.x.r90131		2440
MNE.US.82.MNE.8	-G -C -G -C -T -A -G -G -	2802
MNE.US.x.MNE027	-G -C -G -C -T -A -G -G -	2802
SMM.SL.92.SL92B	-G -A -G -A -G -C -T -AG -C -CCCG -A -A -A -A -C -A -G -C -CCA -A -GA -G -T -C -C -A -A -A -A -T -T -	2765
SMM.US.x.F236.H4	-G -C -T -G -G -C -T -G -C -A -C -A -C -A -G -C -CCA -A -A -C -AT -A -A -G -A -A -T -T -	3321
SMM.US.x.H9	-G -C -GT -G -T -C -A -C -G -C -A -A -C -AT -A -A -G -A -A -T -T -	2807
SMM.US.x.PBJ14_15	-G -C -GT -G -T -C -A -C -G -C -A -A -C -AT -A -A -G -A -A -T -T -	3101
SMM.US.x.PBJA	-G -C -GT -G -T -C -A -C -G -C -A -A -C -AT -A -A -G -A -A -T -T -	3100
SMM.US.x.PBJ_143	-G -C -GT -G -T -C -A -C -G -C -A -A -C -AT -A -A -G -A -A -T -T -	2807
SMM.US.x.PBJ_6P6	-G -C -GT -G -T -C -A -C -G -C -A -A -C -AT -A -A -G -A -A -T -T -	3293
SMM.US.x.PQW53	-G -T -G -T -C -A -T -C -G -C -A -A -C -AT -A -A -G -A -A -T -T -	3251
SMM.US.x.SME543	-G -C -T -G -T -T -C -A -T -C -G -C -A -A -C -AT -A -A -G -A -A -T -T -	3337
STM.US.x.STM	-C -T -G -G -T -C -G -GC -T -T -C -C -C -A -A -C -C -A -A -A -A -A -T -T -	2981

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HIV-2/SIV Complete Genomes

	Pol RT end Pol p15 RNase H start																																																																											
MAC.US.x.239	TCCACTTACCAGTTGAGAAGGATGTATGGGAACAGTGGTGACAGACTATTGGCAGGTAACCTGGATACCGGAATGGGATTTTATCTCAACACCCACCGCTAGTAAGATTAGTCTTCAATCTAGTGAAGGACCCATATAGAGGGGAGAAGAAACCTATTATACAGATGGATCA 4183																																																																											
Pol	K	F	H	L	P	V	E	K	D	V	W	E	Q	W	T	Y	W	Q	V	T	W	I	P	E	W	D	F	I	S	T	P	L	V	R	L	V	F	N	L	V	K	D	P	I	E	G	E	E	T	Y	T	D	G																							
A.CI.88.UC2	-	T	-	C	-	G	-	G	-	GA	-	GACC	-	G	-	-	GATA	-	C	-	G	-	A	-	C	-	A	-	C	-	CG	-	A	-	T	-	C	-	A	-	G	-	C	-	G	-	GACA	-	T	-	C	-	-	AGGA	-	T	-	C	-	CCA	-	CAC	-	G	-	TC	-	C	-	4266						
A.DE.x.BEN	-	T	-	C	-	G	-	G	-	GA	-	GACC	-	G	-	-	GATA	-	C	-	A	-	G	-	A	-	C	-	A	-	G	-	C	-	GA	-	T	-	C	-	A	-	G	-	C	-	G	-	ACA	-	T	-	C	-	CCA	-	C	-	G	-	TC	-	C	-	4266											
A.DE.x.PE12	-	T	-	C	-	-	-	A	-	GA	-	AACC	-	G	-	-	GATA	-	C	-	A	-	G	-	A	-	C	-	A	-	C	-	CG	-	A	-	T	-	C	-	A	-	G	-	C	-	G	-	ACA	-	T	-	C	-	CCA	-	T	-	C	-	G	-	TC	-	C	-	4234									
A.GH.x.GH1	-	T	-	C	-	G	-	A	-	GA	-	GACC	-	G	-	-	GATA	-	C	-	A	-	G	-	A	-	C	-	A	-	C	-	CG	-	A	-	T	-	C	-	A	-	G	-	C	-	G	-	ACA	-	T	-	C	-	CCA	-	T	-	C	-	G	-	TC	-	C	-	4234									
A.GM.87.D194	-	T	-	C	-	G	-	A	-	GA	-	CACC	-	G	-	A	-	GATA	-	C	-	A	-	G	-	A	-	C	-	A	-	G	-	C	-	CG	-	A	-	T	-	C	-	A	-	G	-	C	-	G	-	GACA	-	T	-	CT	-	G	-	AGGA	-	T	-	C	-	CCA	-	CAC	-	G	-	TC	-	C	-	3710
A.GM.x.ISY	-	T	-	C	-	A	-	A	-	GA	-	GACC	-	G	-	-	GATA	-	C	-	A	-	G	-	A	-	C	-	A	-	C	-	CG	-	A	-	C	-	C	-	T	-	G	-	C	-	G	-	CA	-	T	-	C	-	G	-	A	-	A	-	T	-	CCA	-	C	-	G	-	TC	-	C	-	G	-	370	
A.GM.x.MCN13	-	T	-	C	-	A	-	A	-	GA	-	GAC	-	G	-	-	GAT	-	C	-	G	-	A	-	C	-	C	-	C	-	CG	-	A	-	T	-	C	-	G	-	-	G	-	C	-	C	-	CA	-	T	-	C	-	G	-	A	-	A	-	T	-	CCAA	-	AC	-	G	-	T	-	TC	-	C	-	371		
A.GM.x.MCR35	-	T	-	C	-	A	-	A	-	GA	-	GACC	-	G	-	-	GAT	-	C	-	G	-	A	-	C	-	C	-	C	-	CG	-	A	-	T	-	C	-	G	-	-	G	-	C	-	C	-	CA	-	T	-	C	-	G	-	A	-	A	-	T	-	CCAA	-	AC	-	G	-	T	-	TC	-	C	-	3711		
A.GW.86.FG	-	T	-	C	-	A	-	GA	-	ACC	-	G	-	-	GATA	-	C	-	A	-	G	-	A	-	C	-	C	-	C	-	CG	-	A	-	T	-	C	-	A	-	G	-	C	-	GC	-	CA	-	T	-	C	-	G	-	AGGA	-	G	-	G	-	CCA	-	C	-	C	-	G	-	TC	-	C	-	3704			
A.GW.87.C42C2G	-	T	-	C	-	G	-	A	-	GA	-	G	-	C	-	-	GATA	-	C	-	A	-	G	-	A	-	C	-	C	-</																																														

MAC.US.x.239	Pol	TGTAATAAACAGTCAAAAGAAAGGAAGCAGGATATATCACAGATAGGGGCAAGACAAAGTAAAGAGTTTGAAGACAGACTACTAATCAACAAGCAGAATTGGAAGCATTTCATCGGCATTGCAGACTCAGGGCCAAAGGCCAAATATTTAGTAGAGTTACAAATATGT	4353
A.CI.88.UC2	-	C-G	4436
A.DE.x.BEN	-	C-G	4436
A.DE.x.PE12	-	GG-A	4404
A.GH.x.GH1	-	C-G	3880
A.GM.87.D194	-	C-G	3880
A.GM.x.ISY	-	GG-A	3877
A.GM.x.MCR13	-	GG-A	3880
A.GM.x.MCR35	-	GG-A	3880
A.GW.86.FG	-	GG-A	3874
A.GW.87.CAM2CG	-	GG-A	4445
A.GW.x.ALI	-	GG-A	4429
A.GW.x.MDS	-	GG-A	3880
A.IN.95.CRIK 147	-	C-G	4181
A.IN.x.NNVA	-	C-G	4430
A.SN.85.R0D	-	GG-A	3882
B.CI.88.UC1	-	C-G-GCC	4417
B.CI.09.pPRD320-20HIV2 56	-	C-G-GCC	4412
B.CI.x.EH0	-	C-GCC	4407
B.GH.86.D205	-	C-G-ACC	4409
B.P.61.KR020	-	C-GGACC	4359
C.I.92.ABT96	-	-ACC	3763
AB.CI.90.7312A	-	C-G-ACC	4418
AB.CM.03.03M 510 03	-	-GCT	4418
U.FR.96.12034	-	C-GGGCT	3915
MAC.US.x.17EC1			4353
MAC.US.x.17EFR			4353
MAC.US.x.1937			3459
MAC.US.x.2065			3459
MAC.US.x.251.1A11			4352
MAC.US.x.251.32H PJ5			4354
MAC.US.x.251.BK28			4359
MAC.US.x.80035			3459
MAC.US.x.97074			3328
MAC.US.x.MAC239 87082			3430
MAC.US.x.MM142			3839
MAC.US.x.SMM142B			3839
MAC.US.x.r80025			3316
MAC.US.x.r98131			3459
MNE.US.82.MNE 8			3821
MNE.US.x.MNE027			3821
SMM.SL.92.SL92B	-	C-G-A-CAGT	3784
SMM.US.x.F236_H4	-	GG-G	4340
SMM.US.x.H9	-	GG-G	3826
SMM.US.x.PBJ14 15	-	GG-G	4120
SMM.US.x.PBJ14 13	-	GG-G	4119
SMM.US.x.PBJ 143	-	GG-G	3826
SMM.US.x.PBJ 6P6	-	GG-G	4312
SMM.US.x.PGMS3	-	GG-A	4270
SMM.US.x.SME543	-	GG-A	4356
STM.US.x.STM	-	C-GG-A-T	4000

HIV-2/SIV Complete Genomes

Pol RNase H end_Pol p31 Integrase start		
MAC.US.x.239	TTCTCTTTG.GAAAGATAGGCCAGCACAGAAGAACATGATAAATACCATAGTAATGTAAGAAATTTGGTATTCAAATTTGGATTACCCAGAAATAGTGGCCAGACAGATAGTAGACACCTGTGATAAATGTCATCAGAAAGGAGAGGCTATACATGGGCAGGCAAA	4692
Pol	Q V L F # L E K I E P A Q E E H D K Y H S N V K E L V F K F G L P R I V A R Q I V D T C D K C H Q K G E A I H G Q A	
A.CI.88.UC2	-A-T--C--G-A--T-C--G--A--T--C-A--GC--A-CCAT--A--CA-C--A-A--A--A--CCC--C-A--C--A--T--4775	
A.DE.x.BEN	-AT-A--C--C--C-T--G--A--T--C-T-A--C-AACCCAT--A--CTTC--A-A--A--A--T-A--CCC--C-A--C--A--C--4775	
A.DE.x.PET2	-AT-A--C-A--A--C-T--G--G--T--C-A--ATCCCAT--C-G--A-C--A-A--A--A--A--A--CCC--A--G-A--A--T-G--4743	
A.GH.x.GH1	-AT-G--C-A--G--C-C--C--A--T--C-A-G--C-AACCCAT--A--CA-C--A-A--A--A--A--A--CCC--C-A--C--A--T--4219	
A.GM.87.D194	-AT-A--C--C--C-T--C--A--T--C-A--C-AACCCAT--A--CA-C--A--A--A--A--A--A--CCC--C-A--C--A--C--4219	
A.GM.x.ISY	-AT-A--C-A--G-GA--C-T--G--G--T--C--G-A-CCCAT--G--ACC-G--A--A--A--A--A--A--CCC-G-C-A--G-A--4216	
A.GM.x.MCN13	-GT-G--C-A--A--C-T--G--G--C--C--C-ATCCCAT--G--A-T--A-A--A--A--A--A--CCC--A--G--A--A-T-G--4220	
A.GM.x.MCR35	-GT-G--C-A--A--C-T--G--G--C--C--C-ATCCCAT--G--A-T--A-A--A--A--A--A--CCC--A--G--A--A-T-G--4220	
A.GW.86.FG	-AT-A--C-A--G-A--A-C-G-G--A--T--C-A--C-ATCCCAT--A--AGC--A--A--A--A--A--A--CCC-TGTG--A--G--4213	
A.GW.87.CAM2CG	-A-G--C-A--T--T--G--A--T--CC--G-ATCCCAT--ATA--ATC-G--A--A--A--A--A--A--CCC--A--G--A--A-T--4784	
A.GW.x.ALI	-AT-G--TC-A--A--T--G--A--G-T--C--G-C-ATCCCAT--A--ATC-G--A--A--A--A--A--A--CCC--G--G--A--A-TG--4768	
A.GW.x.MDS	-AT-G--C-A--A--C-T--T--A--T--C--G-C-ATCCCAT--A--CA-C--A--A--A--A--A--A--CCC--A--G--A--A-T--4219	
A.IN.95.CR1K 147	-AT-G--C-A--A--C-T--G--G--A--T--C--C-ATCCCAT--A--A-C--A--A--A--A--A--A--CCC--A--A--A--A-T--4520	
A.IN.x.NNVA	-AT-G--C-A--A--C-T--T--A--T--AC--G-C-ATCCCA--A--A-C--A--A--A--A--A--A--CCC--A--G--A--A-T--4769	
A.SN.85.ROD	-GT-G--C--A--C-T--G--A--T--C--C--C-TCTCAT--A--ATT--A-G-A--A--A--T-A--CCC--A--G-A--A--T--4221	
B.CI.88.UC1	---A--C-A--A--A--A--G--G-C--A--TCAT--C-C-ACAGT--A-A-A--A--A--T--C--A--A--G-A--G-T--A--T--4756	
B.CI.09.pPRD320-20HIV2_56	---A--C-A--A--A--A--G--G-C--C-A--TCAT--A-C-ACAGT--A-A-A--A--A--T--C--A--A--G-A--T--A--T--4751	
B.CI.x.EHO	-C-A--TC-A--A--A--T--A--T--A--C-A--CCAT--GA-T-ACA-T--A--A--A--A--T--C--A--A--G-A--T--A--T--4746	
B.GH.86.D205	-CT-G--C-A--A--A--C--G--G--A--T--G-C--C--CCAT--C-A-T-ACA-T--A--A--A--A--T--C--A--A--G-A--T--A--T--4748	
B.JP.81.KR020	-C-G--TC-A--T--A--C--G--G--A--T--G--A--TCAT--A-T-ACA-T--A--A--A--A--T--C--A--A--G-A--C--A--TG--3898	
G.CI.92.ABT96	-A-A--R--A--A--T--T--A--R-TT--G-AACTCAT--G--CA-T-TCA-T--A--A--A--A--T--A-TT-A-ACC-C-GT--C-A--A--C-T--A--T--4102	
AB.CI.90.7312A	---A--C-A--A--A--C--G--G--A--T--G-C--GC--TCAT--A-T-ACA-C--A--A--A--A--T--A--A--A--G-T--A--T--4757	
AB.CM.03.03CM_510_03	-CT-G--C-A--A--A--T--G--G--R--T--G-C--MC--CCAT--Y-M-C-ACA-T--R-A--A--A--T--Y--C--C-A--R--R-A--T--A--T--3887	
U.FR.96.12034	-A-G--TC-A--A--A--T--G--G--C--T--GC-ACAGCAT--TA--ACA-T--A--A--A--A--T--A-T-T--C-GTT-C-G--A--C-G--A--T--4254	
MAC.US.x.17EC1	-----	4692
MAC.US.x.17EFR	-----	4692
MAC.US.x.1937	-----R-----R-----	T--3798
MAC.US.x.2065	-----	T--3798
MAC.US.x.251.1A11	-----G-----	T--3798
MAC.US.x.251.32H.PJ5	-----G-----G-----	T--4691
MAC.US.x.251.BK28	-----	T--4693
MAC.US.x.80035	-----	T--4668
MAC.US.x.97074	-----	T--3798
MAC.US.x.MAC239_87082	-----	R--3667
MAC.US.x.MN142	-----AG-----CA-----	RY--3769
MAC.US.x.SMM142B	-----AG-----CA-----	T--4178
MAC.US.x.r80025	-----	T--4178
MAC.US.x.r90131	-----	T--3655
MNE.US.82.MNE.8	-----C-----A-----A-----	T--3798
MNE.US.x.MNE027	-C-----C-----A-----A-----	T--4160
SMM.SL.92.SL92B	-C-G--C-A--GT-----C--C--T--C--G-G-A-CTCAG--A-AACA-C-ACA-T--A-T-A--A-TG-T--A-C--C-A--G--A-G--T--A--4123	
SMM.US.x.F236.H4	-C-A--AAA--A--A--G--G--G--A--G--C--A--T--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4680	
SMM.US.x.H9	-C-A--A--A--A--G--G--G--A--G--C--A--T--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4165	
SMM.US.x.PBJ14_15	-C-A--A--A--A--G--G--G--A--G--C--A--T--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4459	
SMM.US.x.PBJA	-C-A--A--A--A--G--G--G--A--G--C--A--T--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4458	
SMM.US.x.PBJ 143	-C-A--A--A--A--G--G--G--A--G--C--A--T--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4165	
SMM.US.x.PBJ 6P6	-C-A--A--A--A--G--G--G--A--G--C--A--T--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4651	
SMM.US.x.PGM53	-C-A--A--A--A--G--A--G--C--A--T--TA--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4609	
SMM.US.x.SME543	-C-A--A--A--A--G--A--G--C--A--T--TA--T--GC--A-A-A--A--A--A--A--C--C--A--C--A--T--4695	
STM.US.x.STM	-C-A--C-A--A--A--T-----G--A--T-----C--G--GC-A--C--G--CA--A-GC--A-A-AG--A--G--T--A--C--G--C--C--A--A--T--4339	

TTCAGATCTAGGGACTTGGCAATGGATTGTACCCATCTAGAGGGAAAAATATCATAGTTGCAGTACATGTAGCTAGTGGATTTCATAGAAGCAGAGGTAATCCACAAGAGACAGGAAGACAGACAGCACTATTCTGTGTTAAATTGGCAGGCAGATGGCCTATTACAC	4862
N S D L G T W Q M D C T H L E G K I I I V A V H V A S G F I E A E V I P Q E T G R Q T A L F L L K L A G R W P I	
-G--AA--CGT-----C-C-A-CT--A--C-T--A--T-----C-C--G-AT-----G-----C-C-A--C--CA-T-G--A-A--4945	
-G--AA--CGT-----C-AC-A-CT--A--C-T--A--T-----A-C-C--G-AT-----G-----C-C-A--C--CA-T-G--A-A-G-4945	
-G--A--G-C-----C-C-A-CT--A--C-T--A--T-----A-C-G-T-----A-T-C--G-A-G--G-A--C-C-A--C--CA-T-G--A-A--4913	
-G--AA--TGTC-----C-C-A-CT--A--G-C-T--A--T-----A-T-C--G-AT-----G-----C-C-A--C--CA-T-G--A-A--4389	
-G--AA--CGT-----C-C-A-CT--A--C-T--A--G-----T-A-----A-C-C--G-AT-----G-----C-C-A--C--CA-T-G--A-A--4389	
-G--A--C-C-----C-C-A-CT--A--C-T--A--T-----T-A-----A-C-C--G-AT-----G-A--C-C-A--C--CA-T-G--A-A--4386	
-G--AT--C-----C-C-A-CT--A--G-C-T--A--T-----T-A-----A-C-C--G-AT-----G-----C-C-A--C--CA-T-G--A-A--4390	
-G--AT--C-----C-C-A-CT--A--G-C-T--A--T-----T-A-----A-C-C--G-AT-----G-----C-C-A--C--CA-T-G--A-A--4390	
-G--A--C-----C-C-A-T--A--G-C-T--A--T-----T-A-----T-G--A--T-C--G-AT-----G-A--G-CT-AC-G--C--CA-T-G--A-A--4383	
-G--AG-G--C--C-----C-C-A-----C-----T-A-----T-----A-C-C--G-AT-----G-A--C-C-A--C--TA--G--A-A--4954	
-G--A--C-----C-C-A-CT--A--G-C-T--A--G-----T-A-----T-C--G-AT-----G-A--C-C-A--C--TA-T--A-A--4938	
-G--CT--C-----C-C-T--A--G-C-T--A--T-----T-A-----T-G--A--C-C--G-AT-----G-A--C-C-A--C--TA-T-G--A-A--4389	
-G--A--T-----C-C-A-T--A--G-C-T--A--G-----T-A-----T-G--A--C-C--G-A--G-A--C-C--C-A--TA-T--A-A--4690	
-G--AT--C-G-----C-C-A-T--A--G-C-T--A-----G-----T-A-----T-G--A--C-C--AT-----G-A--C-C-A--GC-A--TA-T--A-A--4939	
-G--A--C-----C-C-A-T--A--G-C-T--A-----T-A-----T-----A-C-C--G-AT-----A--C-C-A--G--C--A-T-G--A-A--4391	
-G--A--A--A--G-----C--A-CT--A--GG-C-A--G--C-----T-----G-----A-C--A--A--A--T-C--C-----CA-----C--4926	
-G--A--A--A--G-----C--A-CT--A--GG-C-A--G--C-----C-----G-----A-C--A--A--A--T-C--C-----CA-----C--4921	
-G--A--A--A-----C--A-T-----GG-T--A--G--T-----C-----G-----A-C--A--A--T-C--C-----GC--CA-----C--4916	
-G--C--A--A--G-----C--A-T--A--T--A--G--C-----C--G-T-----A-C--A--A--T-C--C--AC--G--CA-----C--4918	
-G--A--A--A-----A-CT-----T-A--G--C-----C-----T-----A-C--A--A--T-C--C-----C--CA-----C--4068	
-G--AT-G--T-----C--C-----T--A--G-----A--T--G--C--C--TG-----A-C--A--A--G--A--T--C-----A--G-----C--4272	
-G--A--A--A-----C--A-T--A--G--G-C--A--A--C-----C--G-T-----A-C--A--A--A--T-C--C-----GC--A--C-----C--4927	
-G--A--A--A--G-----C--C-A-T--A--G--T--A--A--C-----C--G-Y-----AR--A--C--AT-----T-C--C-----G--CA--R-----C--4057	
-A--AG-----A-----C-----CT-----G-TG--C--G-----G--C--C--T-----A--G--C--G--G--A--T--T--G--A--C--G--C--AC--GC-A--A--G-----C--T--4424	
MAC_US.x.17EC1	4862
MAC_US.x.17EFR	4862
MAC_US.x.1937	3968
MAC_US.x.2065	3968
MAC_US.x.251_1A11	4861
MAC_US.x.251_32H_PJ5	4863
MAC_US.x.251_BK28	4838
MAC_US.x.80035	3968
MAC_US.x.97074	3837
MAC_US.x.MAC239_87082	3939
MAC_US.x.MN142	4348
MAC_US.x.SMM142B	4348
MAC_US.x.r80025	3825
MAC_US.x.r90131	3968
MNE_US.82.MNE_8	4330
MNE_US.x.MNE027	4330
SMM_SL.92_SL92B	4293
SMM_US.x.F236_H4	4850
SMM_US.x.H9	4335
SMM_US.x.PBJ14_15	4629
SMM_US.x.PBJA	4628
SMM_US.x.PBJ_143	4335
SMM_US.x.PBJ_6P6	4821
SMM_US.x.PGM53	4779
SMM_US.x.SME543	4865
STM_US.x.STM	4509

MAC.US.x.239	ATCTACACACAGATAATGGTCTAACTTTGCTTCGCAAGAAGTAAAGATGGTTGCATGGTGGGCAGGGATAGAGCACACCTTTGGGGTACCATACAATCCACAGAGTCAGGGAGTAGTGGAGCAATGAATCACACCTGAAAAATCAATAGATAGAATCAGGGAACAA	5032
Pol	T H L H T D N G A N F A S Q E V K M V A W W A G I E H T F G V P Y N P Q S Q G V V E A M N H H L K N Q I D R I R E	
A.CI.88.UC2	-CT-G-----C-----CC-C-----CA--A-G-----A-----G-----T-----T-----AT-----A-----T-----C-----A--C-----A-----A--G-----G--AG-----T--A-----G	5115
A.DE.x.BEN	-CT-G-----C-----CC-C-----CA--A-G-----G-----G-----T-----T-----A--AT-----A-----T-----C-----A--C-----A-----A--G-----G--AG-----T--A-----G	5115
A.DE.x.PET2	-C-G-----C-----C-----CA-C--A-G-----G-----A--G-----A-----T-----A--AT-----A-----T-----C-----A--C--A-----A-----T--A-----C--G--AGC-----T--A--G--G	5083
A.GH.x.GH1	-CT-G-----C-----CT-C-----CA--A-G-----G-----G-----AT-----T-----A--AT-----A-----T-----C-----A--C-----A-----A--G-----G--AG-----T--A-----G	4559
A.GM.87.D194	-CT-G-----C-----CC-C-----CA--A-G-----G-----G-----AT-----T-----A--AT-----A-----T-----C-----A--C-----A-----A--G-----G--AG-----T--A-----G	4559
A.GM.x.TSY	-CT-G-----C-----C-----CA--A-G-----G-----A-----T-----C-----A--AT-----A-----T-----C-----A--C-----A-----A--G-----G--AG-----T--A-----G	4559
A.GM.x.MCN13	-CT-G-----C-----C-----CA--A-G-----G-----A-----T-----T-----A--AT-----T--C--A--T-----A--C--A-----A-----A--G-----G--AG-----T--A-----G	4560
A.GM.x.MCR35	-CT-G-----C-----C-----CA--A-G-----G-----A-----T-----T-----A--AT-----T--C--A--T-----A--C--A-----A-----A--G-----G--AG-----T--A-----G	4560
A.GW.86.FG	-C-G-----C-----C-----CA--A-G-----G-----A-----T-----T-----A--A-----A--G-----T-----C-----A--C--A-----A-----T--T--A-----G--AG-----T--A--G--G	4553
A.GW.87.CAM2CG	-CT-----G-----C-----CA--A-G-----G-----A-----T-----C-----A--A-----A-----T-----C-----A--C--A-----A-----A--G-----G--AG-----T--A-----G	5124
A.GW.x.ALI	-CT-G-----G-----C-----CA-C--A-G-----G-----A-----TT-----T-----A--AT-----A-----T-----C-----A--C--A-----A-----A--G-----G--AGC-----T--A--G--G	5108
A.GW.x.MDS	-CT-G-----G-----C-----CA--A-G-----G-----A-----AT-----T-----A--AT-----A-----T-----C-----A--C--A-----A-----C-----A--G-----G--AG-----T--A-----G	4559
A.IN.95.CRIK 147	-C-G-----C-----C-----CA--A-G-----G-----G-----AT-----T-----A--AT-----A-----T-----C-----A--C-----A-----A--G-----G--AG-----T--A-----G	4860
A.IN.x.NNVA	-C-G-----A-----C-----CA--A-G-----G-----A-----T-----T-----A--AT-----A-----T-----C-----A--C--G-----A-----T-----A--C-----C-----A--G--G	5109
A.SN.85.R0D	-CT-G--T-----C-----C-----CA--A-G--G--G-----A-----AT-----T-----A--AT-----A-----T-----C-----A--C-----A-----A--G-----G--AG-----T--A-----C-----A--G--G	4561
B.CI.88.UC1	-C-G-----C--C--C-----CA-C--A-----C--G-----CG--C-----AT-----A--A-----C-----C--T--C-----A-----A-----C--T-----A-----C-----C--G--G	5096
B.CI.89.pPRD320-20HIV2_56	-C-G-----C--C--C-----CA-C--A-----T--G-----G--C-----T-----A--AT-----C-----C--T--C-----A-----A-----C--T-----A-----C-----C--T-----A-----C-----G--G	5091
B.CI.x.EH0	-C-G-----C--C--C-----CA--A-----T--G--A-----CA--C-----AT-----A--A-----A--C--A--G-----C--T--C-----G--A-----A-----A-----C--T-----A-----G-----C-----T--A-----G	5086
B.GH.86.D205	-C-----C--C--C-----CA-C--A--C--AGT-----A--C-----T-----A--A-----A--T--C--A--C-----C--T--C-----A-----A-----C-----C--T-----A-----C-----C-----A--C--G	5088
B.JP.81.KR020	-C-----C--C--C-----CA--A-----C--G--A-----CA--C-----AT-----AG--A--G-----C--A--C-----T--T-----C-----A-----A-----C-----C--T-----A-----C-----C-----A--C--G	4238
G.CI.92.ABT96	-C-----T-----C-----C-----CA-C-----G--G-----A--C-----T-----C--C-----AG--A--A-----C-----C--C-----A--G-----A-----T-----T--T--A--G--A-----A-----T--A--T--G	4442
AB.CI.90.7312A	-CT-G-----C-----C-----A--A-----T-----G--T-----T-----A--A-----A-----C-----C-----A-----A-----A-----T-----T-----A-----G-----G-----A--T--G	5097
AB.CM.03.03CM_510_03	-C-G-----C--C--C-----CA-C--A-----T--G-----A--C-----T-----A--A-----A--G-----A-----C--T--C-----A-----A-----A-----C--T-----A-----G-----AGC-----C-----A--Y--G	4227
U.FR.96.12034	-T-G-----C-----C-----CA--A--A--G-----A-----T-----T-----T-----A-----C--T--C--G--A--C--A-----G--A-----C-----T-----A--G--C-----G-----A-----G	4594
MAC.US.x.17EC1	-----	5032
MAC.US.x.17EFR	-----	5032
MAC.US.x.1937	-----	4138
MAC.US.x.2065	-----	4138
MAC.US.x.251_1A11	-----	5031
MAC.US.x.251_32H_PJ5	-----C-----	5033
MAC.US.x.251_BK28	-----C-----	5008
MAC.US.x.80035	-----	4138
MAC.US.x.97074	-----	4007
MAC.US.x.MAC239_87082	-----	4109
MAC.US.x.MN142	-----G-----	4518
MAC.US.x.SMM142B	-----G-----	4518
MAC.US.x.r80025	-----	3995
MAC.US.x.r90131	-----	4138
MNE.US.82.MNE_8	-----C-----	4500
MNE.US.x.MNE027	-----C-----A-----	4500
SMM.SL.92.SL92B	-----G--T-----C--C-----C--T--CA-C--C--G--G--G-----A-----TT--AG--G--A--GT-----A-----G-----C-----A-----A-----C-----G--CTTA--T--T--G--AA--C-----A--A-----	4463
SMM.US.x.F236_H4	-----G--T--T-----C--T--CA-A--A-----G--A-----C-----T-----R--T--A--G-----R-----T--T-----C--A-----G-----G-----C--T--T--A--CC--G-----T--A-----	5020
SMM.US.x.H9	-----G--T--T-----C--T--CA-A--A-----G--A-----T-----T-----R--T--A--G-----R-----T--T-----C--A--G-----G-----C--T--T--A--CC-----T--A-----G	4505
SMM.US.x.PBJ14_15	-----G--T--T-----C--T--CA-A--A-----G--A-----T-----T-----R--T--A--G-----R-----T--T-----C--A--G-----G-----C--T--T--A--CC-----T--A-----G	4799
SMM.US.x.PBJA	-----G--T--T-----C--T--CA-A--A-----G--A-----T-----T-----R--T--A--G-----R-----T--T-----C--A--G-----G-----C--T--T--A--CC-----T--A-----G	4798
SMM.US.x.PBJ_143	-----G--T--T-----C--T--CA-A--A-----G--A-----T-----T-----R--T--A--G-----R-----T--T-----C--A--G-----G-----C--T--T--A--CC-----T--A-----G	4505
SMM.US.x.PBJ_6P6	-----G--T--T-----C--T--CA-A--A-----G--A-----T-----T-----R--T--A--G-----R-----T--T-----C--A--G-----G-----C--T--T--A--CC-----T--A-----G	4991
SMM.US.x.POM53	-----G--T--T-----C--T--CA-A--A-----G--A-----C-----A-----T-----G-----C-----T-----T-----C--A-----C-----C--T--T--A--CC--G-----T--A-----G	4949
SMM.US.x.SME543	-----G--T--T-----C--T--CA-A--A-----G--A-----C-----A-----T-----G-----C-----T-----T-----C--A-----C-----C--T--T--A--CC--G-----T--A-----G	5035
STM.US.x.STM	-C--G-----G-----C-----CA-C-----G--G-----A--C-----G--A-----A--A-----A-----T-----C--A-----C-----C-----T--TT--A--G--CC--G-----C-----T--A--T--G	4679

A.CI. 88.UC2
A.DE. x.BEN
A.DE. x.PEI2
A.GH. x.GH1
A.GM. 87.D194
A.GM. x.ISY
A.GM. x.MCN13
A.GM. x.MCR35
A.GW. 86.FG
A.GW. 87.CAM2CG
A.GW. x.ALI
A.GW. x.MDS
A.IN. 95.CR1K_147
A.IN. x.NNVA
A.SN. 85.ROD
B.CI. 88.UC1
B.CI. 09.PPRD320-20HIV2_56
B.CI. x.EHO
B.GH. 86.D205
B.PJ. 01.KR020
C.GH. 92.ABT96
AB.CI. 90.7312A
AB.CM. 01.03CM_510_03
U.FR. 96.12034
MAC.US. x.17EC1
MAC.US. x.17EF8
MAC.US. x.1937
MAC.US. x.2065
MAC.US. x.251_1A11
MAC.US. x.251_32H_PJ5
MAC.US. x.251_RK28
MAC.US. x.80035
MAC.US. x.97074
MAC.US. x.MAC239_87082
MAC.US. x.MM142
MAC.US. x.SMM142B
MAC.US. x.r90025
MAC.US. x.r90131
MNE.US. 82.MNE_8
MNE.US. x.MNE027
SMM.SL. 92.SL928
SMM.US. x.F236_H4
SMM.US. x.H9
SMM.US. x.PBJ14_15
SMM.US. x.PBJA
SMM.US. x.PBJ_143
SMM.US. x.PBJ_6P6
SMM.US. x.PGM53
SMM.US. x.SME543
STM.US. x.STM

[illegible]

MAC	US	x	239	CTATTACAGAGAAGGCAGAGATCAACTGTGAAGGGACCCGGTGAGCTATTGTGAAAGGGGAAGGAGCAGTCATCTTAAAGGTAGGGACAGACATTAAGGTAGTACCCAGAAAGAGGCTAAAAATTATCAAGAGTTTGGAGGAGGAAAGAGGTGGATAGCAGTGTCCC	5372
Pol				V Y Y R E G R D Q L W K G E G A V I L K V V G T D I K K V V P R R K K A K M I T I K D Y Y G G G K R E V D S S	
Vif				M E E E K R W I A V P	
A. CI. 88. UC2				---	5455
A. G. x. BEN				---	5453
A. DE. x. PEI2				---	5423
A. GH. x. GH1				---	4899
A. GM. 87. D194				---	4899
A. GM. x. JSY				---	4896
A. GM. x. MCN13				---	4900
A. GM. x. MCN15				---	4893
A. GW. 86. FG				---	5464
A. GW. 87. CAM2CG				---	5448
A. GW. x. ALI				---	4899
A. GW. x. MDS				---	5420
A. IN. 95. CR1K 147				---	5449
A. IN. x. NNVA				---	4901
A. SN. 85. ROD				---	
B. CI. 88. UC1				---	5436
B. CI. 09. pPRD320-20HIV2_56				---	5431
B. CI. x. EHO				---	5426
B. GH. 86. D205				---	5428
B. JP. 01. KR020				---	5478
G. CI. 92. ABT96				---	4782
AB. C1. 90. 7312A				---	5437
AB. CM. 03. 03CM 510 03				---	5467
U. FR. 96. 12034				---	4934
MAC. US. x. 17EC1				---	5372
MAC. US. x. 17EF8				---	5372
MAC. US. x. 1937				---	4478
MAC. US. x. 2065				---	4478
MAC. US. x. 251 1A11				---	5371
MAC. US. x. 251 32H PJ5				---	5373
MAC. US. x. 251 BK28				---	5348
MAC. US. x. 80035				---	4478
MAC. US. x. 97074				---	4347
MAC. US. x. MAC239_87082				---	4449
MAC. US. x. MM142				---	4858
MAC. US. x. SM1142B				---	4858
MAC. US. x. r80025				---	4335
MAC. US. x. r90131				---	4478
MNE. US. 82. MNE 8				---	4840
MNE. US. x. MNE027				---	4840
SMM. SL. 92. SL92B				---	4803
SMM. US. x. F236 H4				---	5360
SMM. US. x. H9				---	4845
SMM. US. x. PB31A 15				---	5139
SMM. US. x. PB3A				---	5138
SMM. US. x. PB3 143				---	4845
SMM. US. x. PB3 6P6				---	5331
SMM. US. x. PGM53				---	5289
SMM. US. x. SME543				---	5375
STM. US. x. STM				---	5017

MAC.US.x.239
Pol
Vif

A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CRIK 147
A.IN.x.NNVA
A.SN.85.ROD
B.CI.88.UC1
B.CI.09.pPRD320-20HIV2_56
B.CI.x.EHO
B.GH.86.D205
B.JP.01.KR020
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.03.03CM_510_03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239_87082
MAC.US.x.MM142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.02.MNE.8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236_H4
SMM.US.x.H9
SMM.US.x.PBJ14_15
SMM.US.x.PBJA
SMM.US.x.PBJ_143
SMM.US.x.PBJ_6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

Pol, Gag-Pol, and p31 Integrase end

ACATGGAGGATACCGAGAGGCTAGA...GAGGTGGCATGCTCATAAAATCTGAAATATAAACTAAAGATCTACAAAGGTTTGCTATGTGCCCATTTTAAAGTCGGATGGGCATGGTGGACCTGCAGCAGAGTAATCTCCCACTACAGGAAGGAACCATTT 5539

S H M E D T G E A R E V A
T W R I P E R L E R W H S L I K Y L K Y K T K D L Q K V C Y V P H F K V G W A W W T C S R V I F P L Q E G S H L

MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239_87082
MAC.US.x.MM142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.02.MNE.8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236_H4
SMM.US.x.H9
SMM.US.x.PBJ14_15
SMM.US.x.PBJA
SMM.US.x.PBJ_143
SMM.US.x.PBJ_6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

GT-----CAGTAGA-AA--TGGA-C-C-----TG--T--TC-AT-G--A-G--G--G-G-A-CC-----A-CAC-A-A-----AC-AGC-TCT-G-G-T--CT-GG--G--T--C--4973
-T-----G-----A-----C-C-C-----C-----G-T-C-T-----CA-A-A-T-----T-----T-AG--T-AG-CT-----5527
-T-----G-----A-----C-C-C-----C-----G-C-T-----A-----CA-A-T-----T-----T-AG--T-AG-CT-----5012
-T-----G-----A-----C-C-C-----C-----G-C-T-----A-----CA-A-T-----T-----T-AG--T-AG-CT-----5306
-T-----G-----A-----C-C-C-----C-----G-C-T-----A-----CA-A-T-----T-----T-AG--T-AG-CT-----5305
-T-----G-----A-----C-C-C-----C-----G-C-T-----A-----CA-A-T-----T-----T-AG--T-AG-CT-----5012
-T-----G-----A-----C-C-C-----C-----G-C-T-----A-----CA-A-T-----T-----T-AG--T-AG-CT-----5498
-T-----A-----G-----A-----C-----CT-----T-G-----G-C-----G-C-T-----A-----CA-A-T-----T-----T-AG--T-AG-CT-----5456
-T-----G-----A-----A-----C-----C-----G-----G-T-----C-----CA-A-T-----T-----T-AG--T-AG-CT-----5542
-C-----A-G-----G-----C-----T-A-G-----C-----G-----AGC-----CA-----CCA-----T-G-----T-----T-----G-T-----T-CT-G-A-G-A-GCA--CC-5186

MAC.US.x.239	AGAAGTACAAGGGTATTGGCATTTGACACCAGAAAAAGGGTGGCTCAGTACTTATGCAGTGAGGATAACCTGGTACTCAAGAAGCTTTGGACAGATGTAACACCAACTATGACAGACATTTTACTGCATAGCACTTATTCCCTTGCTTACAGCGGGAGAAGTGAGAA	5709
Vif	E V Q G Y W H L T P E K G W L S T Y A V R I T W Y S K N F W T D V T P N Y A D I L L H S T Y F P C F T A G E V R	
A.CI.88.UC2	--GA--G-CA--A-CC-A-G-----A-----TCCT-C-T--A-AC-----TA-G-A-G--C-----T-C-G-G-----CC-A-A-----C-----TG-----G-G-A-T-----A-----	5792
A.DE.x.BEN	--A--G-CA--A-CC-A-----A-----TCCT-C-----A-AT-----TA-G-A-G--C-----T-C-G-G-----CC-A-A-----G-A-T-----A-----	5792
A.DE.x.PE12	--GA--G-CA--A-CC-A-----A-----TCCT-C-----A-A-----TA-G-GG-C-----T-C-G-G-----TCCC-A-A-----T-----G-A-T-----A-----	5760
A.GH.x.GH1	--GA--G-CA--A-CC-A-G-----A-----TCCT-C-T--A-----TA-G-A-GG-C-----T-C-G-G-----CC-A-A-----T-----G-A-T-----A-----	5236
A.GM.87.D194	--GA--G-CA--A-CC-A-----A-----TCCT-C-T--A-T-----TA-G-A-G--C-----T-C-G-G-----TCCC-A-A-C-----T-----G-A-T-----A-----	5236
A.GM.x.ISY	--GA--G-CA--A-CC-A-----A-----TCCT-----A-A-G-T-----G-AGGG-C-----T-C-G-G-----CCC-A-A-C-----T-----G-A-T-----A-----	5233
A.GM.x.MCN13	--A--G-CA--A-CC-A-G-----A-----TCCT-----A-A-G-T-----TA-GG-A-GG-C-----T-C-G-G-----TCCC-A-A-----T-----A-T-----A-----	5237
A.GM.x.MCR35	--A--G-CA--A-CC-A-G-----A-----TCCT-C-T--A-A-G-T-----TA-GG-A-GG-C-----T-C-G-G-----TCCC-A-A-----T-----A-T-----A-----	5237
A.GW.86.FG	G--GA--CA--A-C-A-----A-----TCCT-C-CT--A-A-T-----TA-G-A-G--C-----T-C-G-G-----T-CCC-A-A-----T-----G-A-T-----A-----	5230
A.GW.87.CAM2CG	--GA--G-CA--A-C-A-----A-----TCCT-----A-A-G-T-----A-G-A-G--C-----C-C-G-G-----CCC-A-A-----T-----T-----A-G-A-----	5801
A.GW.x.ALI	--GA--G-CA--A-CC-A-----A-----TCCT-----A-A-T-----TA-G-A-G--C-----T-C-G-G-----TCCC-A-A-G-----T-----G-A-T-----A-----	5785
A.GW.x.MDS	--GA--G-CA--A-CC-A-----A-----TTCCT-A-----A-C-G-T-----A-G-A-A-C-----T-C-G-G-----TCCC-A-A-----A-----A-----T-----CA-----	5236
A.IN.95.CR1K 147	--GA--G-CA--A-C-A-----G--A-----TTCCT-----A-----A-G--T-----A-G--T-----T-C-G-G-A-----TCCC-A-A-----G-----A-T-----A-----	5537
A.IN.x.NNVA	--GA--G-CA--A-C-A-----A-----TTCCT-----A-----T-----TA-G-A-A-C-----T-C-G-----TCCC-A-A-G-----G-----A-T-----A-----	5786
A.SN.85.R0D	--GA--G-CA--A-C-A-----A-----TCCT-----T--A-A-T-----A-G-A-G--C-----T-C-G-G-----TG-CC-A-A-----A-----A-T-----A-----	5238
B.CI.88.UC1	--G-C-----A-C-----C-G-----GG-A-TCT-G-CT-C-----T-A-AC-A-----TAA-G-G--G-AT-----G-----TG-TGTG-----CAGC-----G-GT-----T-----CAAT-----A-G-----	5773
B.CI.89.pPRD320-20HIV2_56	--GA-C--G-----A-C-----C-G-----GG-ACCTCT-A-T-C-----T-----A-A-----AG-G--G--AC-----TG-TGTG-----CAGC-T-----G-GT-----T-----CAAT-----A-G-----	5768
B.CI.x.EH0	-----C--A--C-----A-CC-C-----GG-A-TCT-G-T-C-----T-A-AC-A-----TGAG-G-G--AT-----T-----TG-TGTA-----CGA-----G-GT-----T-CG-----TAAT-----A-G-----	5763
B.GH.86.D205	-----C--A--C-----A-CC-A-C-----GG-A-TCT-G-CT-C-----T-A-AC-A-----TGAG-G--G--AT-----T-----TG-TGTG-----CAGC-----G-GT-----T-----CAAT-----A-G-----	5765
B.JP.81.KR020	--GA-C-----A-----A-CC-C-G-----GG-A-TC-G-G-C-----T-A-AC-A-----TAAG-A-GT-C-AT-----G-----TG-TGTA-----CACC-T-----G-GT-----TT-----TAAT-----A-G-----	4915
G.CI.92.ABT96	G--A-----A-C-----C-T-----G-A-T-A-CCAG-----A-AT-----A--GA-A--AT-----G-----G-GACA-----TCAA--T-----G-AT-----TGA-----T-T-----A-----	5119
AB.CI.90.7312A	--G-C-----A-C-----C-G-----GG-A-TCT-G-T-C-----T-----AT-A-----TGA-G--G--AC-----TG-TGTG-----CAGC-T-----G-G-----T-----CAAT-----A-G-----	5774
AB.CM.03.03CM_510_03	--R-C-----A-----A-CC-A-C-G-----GG-ACCTCT-G-C-C-----T-A-AC-A-----YGAG-G-----AT-----G-----TG-TGTG-----CAGC-----G-GT-----T-----CAAT-----A-G-----	4904
U.FR.96.12034	G--G-G-----CC-----A-----G-G-A-----ATCCT-----A-T-----A--GAGGT-----AT-----G-----TG-T-GC-----CAA-----G-G-G-----T-----T-----G-----	5270
MAC.US.x.17EC1	-----	5709
MAC.US.x.17EFR	-----	5709
MAC.US.x.1937	-----A-----G-----R-----	4815
MAC.US.x.2065	-----A-----G-----R-----	4815
MAC.US.x.251_1A11	-----G-----T-----G-----	5710
MAC.US.x.251_32H_PJ5	-----G-----G-----	5710
MAC.US.x.251_BK28	-----G-----Y-----	5685
MAC.US.x.80035	-----G-----	5708
MAC.US.x.97074	-----G-----	4684
MAC.US.x.MAC239_87082	-----A-----G-----G-----	4786
MAC.US.x.MN142	-----A-----G-----G-----	5195
MAC.US.x.SMM142B	-----A-----G-----G-----	5195
MAC.US.x.r80025	-----A-----M-----Y-----	4672
MAC.US.x.r90131	-----A-----G-----G-----	4815
MNE.US.82.MNE_8	-----A-----A-----G-----C-----A-----G-----G-----G-----	5177
MNE.US.x.MNE027	-----A-----A-----G-----C-----A-----G-----G-----G-----	5177
SMM.SL.92.SL92B	G-G-----T--C--A-C-C-----A--T-ATCA-GC-----T--T-T-----G-A-A-----C-G-TGTA-----TCAG--GCA--T-----G--CAC-CG-----C	5143
SMM.US.x.F236_H4	G-----A-----A-----G-----A-----A-----C-GA-T-C-----G-T-----C-----G-----T-----A-----AC-G	5697
SMM.US.x.H9	G-----A-----A-----GR-----A-----A-----C-GA-T-C-----G-----G-----T-----A-----AC	5182
SMM.US.x.PBJ14_15	G-----G-A-A-----G-----A-----A-----C-GA-T-C-----G-----G-----T-----T-A-----AC	5476
SMM.US.x.PBJA	G-----G-A-A-----G-----A-----A-----C-GA-T-C-----G-----G-----T-----T-A-----AC	5475
SMM.US.x.PBJ_143	G-----G-A-A-----GR-----A-----A-----C-GA-T-C-----G-----G-----T-----T-A-----AC	5182
SMM.US.x.PBJ_6P6	G-----G-A-A-----G-----A-----A-----C-GA-T-C-----G-----G-----T-----T-A-----AC	5668
SMM.US.x.PGM53	G-----A-----A-----G-----A-----A-----C-GA-T-C-----G-----G-----T-----T-A-----AC	5626
SMM.US.x.SME543	G-----A-----A-----A-----C-----A-A-----C-GA-T-C-----G-----G-----T-----T-A-----ACA	5712
STM.US.x.STM	-----T-----A-----A-----A-----GAA-----T-----T-----TA-C-GA-T-C--T-----G--G-----TCAGC-----G-----	5356

HIV-2/SIV Complete Genomes

[illegible]

HIV-2/SIV Complete Genomes

[illegible]

MAC.US.x.239
Vpr

Tat exon 1 start

GGGATGAATGGGTAGTGGAGGTTCTGGAAGAACTGAAAGAAAGAACTTTAAACATTTTGTATCCCTCGCTTGCTAACTGCACCTTGGTAATCATATCTATAATAGACATGGAGACACCTTGAGGGAGCAGGAGAACTCATAGAACTCTCAACGAGCGCTCTTCATGCAT 6366

W D E W V V E V L E L K E A A K H F D P R L G N H T R R H G E D T T E G A G E L T R I L L Q R A L F S M H

MAC.US.x.17EC1
MAC.US.x.17EFER
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.88035
MAC.US.x.97074
MAC.US.x.MAC239.87082
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.x.82.MNE.8
MNE.US.x.MNE827
SMLN.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PB314.15
SMM.US.x.PBJA
SMM.US.x.PBJ.143
SMM.US.x.PBJ.6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

MAC.US.x.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.HDS
A.IN.x.CRK.147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.69.pPRD320-20HIV2.56
B.CI.x.EH0
B.GH.86.D205
B.JP.01.K9820
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.83.CN.510.03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFER
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.88035
MAC.US.x.97074
MAC.US.x.MAC239.87082
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.x.82.MNE.8
MNE.US.x.MNE827
SMLN.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PB314.15
SMM.US.x.PBJA
SMM.US.x.PBJ.143
SMM.US.x.PBJ.6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

MAC.US.x.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.HDS
A.IN.x.CRK.147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.69.pPRD320-20HIV2.56
B.CI.x.EH0
B.GH.86.D205
B.JP.01.K9820
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.83.CN.510.03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFER
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.88035
MAC.US.x.97074
MAC.US.x.MAC239.87082
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.x.82.MNE.8
MNE.US.x.MNE827
SMLN.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PB314.15
SMM.US.x.PBJA
SMM.US.x.PBJ.143
SMM.US.x.PBJ.6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

MAC.US.x.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.HDS
A.IN.x.CRK.147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.69.pPRD320-20HIV2.56
B.CI.x.EH0
B.GH.86.D205
B.JP.01.K9820
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.83.CN.510.03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFER
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.88035
MAC.US.x.97074
MAC.US.x.MAC239.87082
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.x.82.MNE.8
MNE.US.x.MNE827
SMLN.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PB314.15
SMM.US.x.PBJA
SMM.US.x.PBJ.143
SMM.US.x.PBJ.6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

MAC.US.x.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.HDS
A.IN.x.CRK.147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.69.pPRD320-20HIV2.56
B.CI.x.EH0
B.GH.86.D205
B.JP.01.K9820
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.83.CN.510.03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFER
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.88035
MAC.US.x.97074
MAC.US.x.MAC239.87082
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.x.82.MNE.8
MNE.US.x.MNE827
SMLN.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PB314.15
SMM.US.x.PBJA
SMM.US.x.PBJ.143
SMM.US.x.PBJ.6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

MAC.US.x.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.HDS
A.IN.x.CRK.147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.69.pPRD320-20HIV2.56
B.CI.x.EH0
B.GH.86.D205
B.JP.01.K9820
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.83.CN.510.03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFER
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.88035
MAC.US.x.97074
MAC.US.x.MAC239.87082
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.x.82.MNE.8
MNE.US.x.MNE827
SMLN.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PB314.15
SMM.US.x.PBJA
SMM.US.x.PBJ.143
SMM.US.x.PBJ.6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

MAC.US.x.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.HDS
A.IN.x.CRK.147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.69.pPRD320-20HIV2.56
B.CI.x.EH0
B.GH.86.D205
B.JP.01.K9820
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.83.CN.510.03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFER
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.88035
MAC.US.x.97074
MAC.US.x.MAC239.87082
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.x.82.MNE.8
MNE.US.x.MNE827
SMLN.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.H9
SMM.US.x.PB314.15
SMM.US.x.PBJA
SMM.US.x.PBJ.143
SMM.US.x.PBJ.6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

MAC.US.x.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.IS
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.HDS
A.IN.x.CRK.147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.69.pPRD320-20HIV2.56
B.CI.x.EH0
B.GH.86.D205
B.JP.01.K9820
G.CI.92.ABT96
AB.CI.90.7312A

HIV-2/SIV Complete Genomes

[illegible]

Env signal peptide start
Tat Rev exon 1 end_Tat Rev intron start

Env signal peptide end_Env gp120 start

MAC.US.x.239
Env
Tat exon 1
Rev exon 1
A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PE12
A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.F6
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CRIK 147
A.IN.x.NNVA
A.SN.85.ROD
B.CI.88.UC1
B.CI.89.pPRD320-20HIV2_56
B.CI.x.EHO
B.GH.86.D205
B.JP.01.KR020
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.03.03CM 510_03
U.FR.96.12034
MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251 1A11
MAC.US.x.251 32H PJ5
MAC.US.x.251 BK28
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239 87082
MAC.US.x.MM142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.02.MNE 8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236_H4
SMM.US.x.H9
SMM.US.x.PBJ14_15
SMM.US.x.PBJA
SMM.US.x.PBJ 143
SMM.US.x.PBJ 6P6
SMM.US.x.PGMS3
SMM.US.x.SME543
STM.US.x.STM

CACGAAAGAGAAGAAGAACTCCGAAAAAGGCTAAGGCTAATACATCTTCTGCATCAAAACAAGTAAGTATGGGATGCTTGGGAATCAGCTGCTTATGCCATCTTGGCTTTTAAAGTGCTATGGGATCTATTGTACT.....CTATATGTCACAGCTCTTTATGGGTAC 6700

S R K R R R T P K K A K A N T S S A S N K
H E R E E E L R K R L R L T H L L H Q T

A-G-CGGAC-----A-G-GAA--A-C-C-GC--A-C-G-----G-----AGCC-GG-A-----GCT-T--T-AT-AAC--CT-GCTTA-A--C-AA.....A-----G-T-T--C-----C-----6739
AGG-C-GAC-----G-A-GG-AA--A-CC-T-GC--C-G-----G-----AGCC-GG-A-----T-G-T-T-T-A-AAC--CT-GCTTA-A--GC.....AG-----G-T-T--C-----CA-----6800
AGG-C-GAC-----G-A-G--A-A--C-T-G-----G-----G-----AATGGA-AG-A-A--AA-G-T-T-T-A-AAC--CT-GCTTA-A--CG-C.....A-----G-T-T--C-----CA-----6762
A-A-C-GAC-G-----A-G--A--A-C-T-G-----G-----G-----A-ATG--GG-AA-G-TA-ATG-G-T--G-----AGCT--CT-GCTTA-A--C-C.....A-----G-T-T--C-----C-G-----6241
AGG-C-GAC-----G-A-G-AA--A-C-C-GC-C-----G-T-----G-----AGCC-GG-A-----G-T-T-T-AT-AAC--CT-GCTTA-A--C-AA.....A-----G-T-T--C-----CA-----6241
AGG-C-GAC-----G-G-----G-AA--C-T-G-C-----G-G-----G-----CAATGA--GG-AAA-T-----G-T-T-T-C-AAC--CT-GCTTA-A--C-C.....AA-----G-T-T--C-----CA-----6238
AGG-C-GAC-----G-A-G-AA--C-T-T-----G-G-----G-----ATGG--GG-A-A-----G-T-T-T-AAC--CT-GCTTA-A--C-C.....AAT-----G-T-T--C-----CA-----6242
AGG-C-GAC-----G-A-G-AA--C-T-----G-G-----G-----ATGG--GG-A-A-----G-T-T-T-AGCT--ACT-GCTT-A--C-C.....AAT-----G-T-T--C-----CA-----6242
AGG-C-GAC-----G-A-G-AA--C-T-G-----G-G-----G-----AAGG--AG-AA-----G-T-T-TG-A-AGCT--CT-GCTTA-A--C-AG.....A-T-----G-T-T--C-----CA-----6235
AGG-C-GAC-----G-A-G-AA--C-T-G-----G-G-----G-----AGC-GGCA-A-----T-T-T-T-A-AGCT--CT-GCTTA-A--C-GA...CAA-A-----G-T-T--C-----C-----6809
AGG-C-G-C-----T-A-G-AA--C-T-G-----G-G-----G-----ATG-C-AG-A-A-----G-TA-T--A-AGCT--CT-GCTTA-A--AA.....A-----G-T-T--C-----C-G-----6790
AGG-C-GAC-----G-A-G-AA--A-C-C-G-----G-G-----G-----ACGC-CAAAAT-C-----T-T-T-A-AAC--CT-GCTTA-A--C-AACCACAA-A-----A-T-T--C-----CA-----6247
AGG-C-GAC-----G-A-G-AA--A-C-GA-CT-A-----G-G-----G-----CGCA-GAA--C-----A-T-T-T-AT-AAC--CT-GCTTA-A--C-AA.....A-----A-T-T--C-----CA-----6542
AGG-C-G-C-----G-C-GA-G-AA--C-C-G-----A-C-G-----G-----AC-C-GAA--GCC-----G-T-T-T-AAC--CT-GCTTA-A--C-AACAA...A-----A-T-T--C-----CA-----6795
AGG-C-GAC-----G-A-G-AA--A-C-C-G-C-A-C-G-----G-----G-----AT--T-T-AT-AGCT--CT-GCTTA-A--C-C.....A-----A-T-T--C-----C-----6234
-GA--A-----T-T-A-G-----T-C-G-----G-G-G-----C-CACAC-A-C-----C-T---TTTGC-C-A-A-----T-TCTGG--CA-AAGAAAAAC-----T-----C-----CA-----6781
-GA--A-----T-T-A-G-----T-C-G-----C-G-G-----C-CACAC-AAC-G-----TT-AC-C-A-----TGTATG--AA-----A-----T-----C-----CA-----6770
-GA--A-----T-T-A-G-----A-C-----C-G-G-----C-CA-G-AA--T-T-C-A--G-TA-AC-C-----A-A-----TATATGG-C-AG.....AAC-T-----T-----C-----A-----6765
-GA-G-----T-G-A-GA--A-C-G-C-----C-G-G-----C-A-T-A-C-GC-GC--C-T-GC-C-----A-G-A-AG--T-TGTA--AA.....A-----T-----C-----CA-----6767
-GA--A-----T-T-A-G-----T-C-G-GC-A-----G-G-----C-CA-A-CAAT-GT-C-T-GCT-AC-C-----A-A-----CT-TATGG-CGAG.....GAT-TC-----T-----C-----CA-----5917
-TA--GA-----A-----T-T-----G-----C-A-----C-----A-C-R-C-----ACT-----T-----AA-----T-T-----C-----CA-----6113
-GA--A-----T-T-A-G-AA--A-GC-----G-G-----G-A-ATG--GG-AA--TA-AT-G-T-----G-AGCT--CT-CTTA-A--C-C.....AA-----G-T-T--C-----C-G-----6776
-GA--A-----GA--A-C-G-----C-G-G-----G-----C-A-TC-A-C-GCTGC-----A-GC-C-----C-----A-G--T-TACA-Y-AA.....A-Y-----T-----C-----CA-----5900
-CA--GA-G-----G-A-G-----T-----T-T-----G-C-----C-----C-A-TC-C-----TC-A-TG-----A-CA-GC-T-A-C-----AG-----T-----C-----CA-----6254
-----6700
-----RRR-----G-----R-----Y-----Y-----6700
-----6806
-----C-----A-----6699
-----R-----A-----6701
-----6676
-----6806
-----5675
-AC-G-----G-----G-----T-----A-----C-----T-----T-----A-----6777
-AC-G-----G-----G-----T-----A-----GCTC-AAGT-C-A-GG...TAT--T-----A-----6186
-----6183
-----3806
-C-GA-----G-----T-----C-----C-----C-T-----A-----6168
-C-GA-----G-----T-----C-----C-----C-T-----A-----6168
-CA--GA-----GT-AA--G-----C-T-GA-A-----C-----CG---C-ACT-C-----A-A-----T-----G-TA--C-GG--G-A-----AG--A-A-----A-T-----6127
AC--GA-----G-A-----C-T-C-----G-----GC-----AG-----T-TA-A--T-G-----GT-----A-----A-A-C-----A-C-----6647
A--GA-----G-A-----T-----G-----GC-C-A-Y-----CT-CA--T-----GT-----A-----A-A-C-----A-C-----6168
A--G-GA-----G-A-----G-----G-----GC-----A-----CT-CA--T-----GT-----A-----A-A-C-----A-C-----6462
A--GA-----G-A-----G-----G-----GC-----A-----CT-CA--T-----GT-----A-----A-A-C-----A-C-----6461
A--GA-----G-A-----G-----G-----GC-----A-Y-----CT-CA--T-----GT-----A-----A-A-C-----A-C-----6168
A--GA-----G-A-----T-----G-----GC-----A-----CT-CA--T-----GT-----A-----A-A-C-----A-C-----6654
AG-C-G-----G-----T-----C-----G-----C-----CT-----A-----T-----A-----T-----A-----A-----A-----6619
-ACCGA-----A-----A-----C-CT-C-----GC-----AG-----T-TA-A--T-G-----GT-----A-----A-A-C-----6698
-A--GA-----GT-AA-----A-T-C-AT-----CC-C-C-----A-----A-----T-----A-----CT-GCTT-C-----C-----AG-----G-A-----6342

[illegible]

[illegible]

[illegible]

MAC.US.x.239	AAACAGGGAATAAC...ACTGGTAATGAAAGTAGATGTTACATGAACCACTGTAACACTTCTGTTATCCAGAGTCTTGTGACAAACATTATTGGGATGCTATTAGATTAGGATTATTGTGCACCTCCAGGTTATGCTTTGCTTAGATGTAATGACACAAATTATTCAGGC	7353
Env	E Q G N N . . . T G N E S R C Y M N H C N T S V I Q E S C D K H Y W D A I R F R Y C A P P G Y A L L R C N D T N Y S G	
A.CI.88.UC2	-CAGCAAC-C-G...-A-C-CAA-C-CG-C...-GA-T...-A-A-C-A-G-A-A...-T...-G-AG--A-C-CA--A-G--C-A-A--C--T-C-C-C-G--	7383
A.DE.x.BEN	-CA-CACA-CA...-CTG-C-C...-GA-T-C--A-AA-C-A--A--T-G-C--G-G-A-C--A-G-C-T--CC-AT-A--T-C-C--	7435
A.DE.x.PE12	-CAC-ACT--GGG...-CCAGCC-C-A--T-C--A-A-C-AC--A--T-G-C--G-G-A-C--A-G--TATGC--A-C--T-C--	7376
A.GH.x.GH1	-TC-AAT--C...-AA-A-GGA--AC--T-C--A-A-C-AC--A--T-G-C--A-AG-A-C--A-G--T--CC-A-A--C--T-C--	6852
A.GM.87.D194	-CA-GACA--CGGA...-AC-G-C-C...-GA-T-C--A-A-C-A--A--G-C--G-AG-A-C--A-G--T--CC-A-A--C--T-C--	6843
A.GM.x.ISY	-TC-AT--G-G...-ACAG-CCG-AA--T-C--A-A-C-AC--A--G-C--G-G-A-C--A-G--T--CC-A-A--C--T-C--	6849
A.GM.x.MCN13	-GG-AATGGC-C...-AC-GA-C-C--T-C--A-A-G-C-AC--A--G-C--G-G-A-C--A-G--T--CC-A-A--C--T-C--	6865
A.GM.x.MCR35	-GG-AATGGC-C...-AC-C-C-C--T-C--A-A-G-C-TAC--A--G-C--G-G-A-C--A-G--T--CC-A-A--C--T-C--	6865
A.GW.86.FG	-CA-TAAC...-CTCA-G-C-G-C-AG--T-C--A-A-C-AC--A--T-G-C--G-G-A-C--A-G--T--CC-A-A--C--T-C--	6840
A.GW.87.CAM2CG	-TA-TA-C-CAG-TCAG--CACA--G-C-CG--T-C--A-A-C-AC--A--T-G-C--G-G-A-C--A-G--T--CC-A-A--C--T-C--	7438
A.GW.x.ALI	-C-TTT--C-C...-CACA-CC-G-CC-G--T-C--A-A-C-AC--A--T-G-C--A-G-A-C--A-T--C-CC-A-A--C-G--T-T--	7416
A.GW.x.MDS	G-G-AT--G...-CACA-CC-C-G-C--G-T-C--A-A-C-A--A--T-G-C--A-G-G-A-C--A-G--T-C-C-A--C--C--	G 6909
A.IN.95.CRIK 147	--C-AT-GC-C...-ACA-CTCG-A-AG--T-C--A-A-C-AC--A--T-G-C--A-A-G-A--A-G--C--A-C--T-C-C--	7177
A.IN.x.NNVA	--C-AT-GC-C-ACT-GCAC-CGCA-C-A--CC-CAGGCC-G--ATGCG--G-GGTAC-GAG-T-A--T-G--A-G-G-A--C--A-G--C--A--T-C-C--	7430
A.SN.85.ROD	-GAC--T...-GCACA-C-G-CCCAG--T-C--A-A-C-AC--A-A--G-C--A-G--A-C--A-G--CC-AT-A--T-C--	6878
B.CI.88.UC1	-CGGCAAC-GC...-CCAGC-CC-T...-GAAC-T-C-A-G--A--T--C--CAGCT-A--C--T-C--A--C--A--	7407
B.CI.89.pPRD320-20HIV2_56	-GGGTACC-GA...-GAAC-T-A-A-G--A--T--C--CAGCT-A--C--T-C--A--A--A--G--T-C--	7381
B.CI.x.EH0	-A-G--CA...-GGA--C-A--T-A-AAAC--T-A-AA--A--A--AG-T-A--T-C--A-T--A--C--T-T-A--	7397
B.GH.86.D205	-TA-TACC-GG...-AAGT-ACC-C--C-T-A-GAAC-C--AA-AA--A--CAGCT-A-G--T-C-G-G-T-TT-C-A-A--T-T-C--	7402
B.JP.81.KR020	...-GG-C--CC-T-A-AAAC--A-AA--A--CCAAT-A--C--C--C-T--TA-G--C--TT-T-C--	6525
G.CI.92.ABT96	-GTCC--G...-G-AG--G--T-A-A-C-T-G-A-A--T--G--A--A--T-G--G-T--A--T-T-C--	A 6766
AB.CI.90.7312A	-GTC-AAT--CGC...-G-A-GGGAG-GAC--C--T-T-C--A-A-C-AC--A-A-C--G-C-C--A-G--A-C--A-G--T--C--A--	7417
AB.CM.03.03CM_510_03	-CA-AAAC--TCAAGCGAAACATTAA-C-AA-C--GA-T--A-A-C-A--A-A--T-G-C--A--G--A-C-A--A-G--C-A-A--C--T-C--	6514
U.FR.96.12034	---GAAT-C...-G-AA-G--A--C--C--C--A--G--C--C--T-A--T-T--C--A--	A 6895
MAC.US.x.17EC1	-----A-----	7353
MAC.US.x.17EFR	-----A-----	7353
MAC.US.x.1937	-----W-----	6459
MAC.US.x.2065	-----	6459
MAC.US.x.251.1A11	---G---T---	7349
MAC.US.x.251.32H.PJ5	---G---A---C---T---A---G---A---	7351
MAC.US.x.251.BK28	---G---A---C---C---T---A---G---A---	7335
MAC.US.x.80035	-----	6459
MAC.US.x.97074	-----	6328
MAC.US.x.MAC239_87082	-----	6430
MAC.US.x.MN142	---G---T---T---G---G---G-A---	6848
MAC.US.x.SMM142B	---G---T---T---G---G---G-A---	6845
MAC.US.x.r80025	-----	6316
MAC.US.x.r90131	-----	6459
MNE.US.82.MNE.8	---T-G---AA---T---T-A---	6821
MNE.US.x.MNE027	---T-G---AAG---T---T-A---G-----	6824
SMM.SL.92.SL92B	-G---AGGA--T...-G-AAGC--T-T-C-T-AAG-A--A--G-C--C-C-A--C--A--C--T--	6789
SMM.US.x.F236.H4	-G-GTCAGCG--T...-AA-G-G--A--C-T--T-CAG-T-A-C-G--Y-A-C--G--T-T--T--	7303
SMM.US.x.H9	---AAT-GC--TGGA-A--AA-C-C-A-C-T--T-CAG-T-A-C-G--Y-A-C--G--T-T--C--	6830
SMM.US.x.PBJ14_15	---AAT-GC--T...-AA-C-C-A-C-T--T-CAG-T-A-C--G--A--G--G--T-T--	7133
SMM.US.x.PBJA	---AAT-GC--T...-AA-C-C-A-C-T--T-CAG-T-A-C--G--A--G--G--T-T--	7132
SMM.US.x.PBJ_143	---AAT-GC--TGAA-A--AA-C-C-A-C-T--T-CAG-T-A-C-G--Y-A--G--G--T-T--C--	6845
SMM.US.x.PBJ_6P6	---AAT-GC--T...-AA-C-C-A-C-T--T-CAG-T-A-C--G--A--G--G--T-T--	7325
SMM.US.x.PGM53	---A-T-C-CT...-G-A-A--A--T--T-CAG-T-A-C-G--A-C--G--T--	7287
SMM.US.x.SME543	-G-GCCAGCA-T...-A-G-G--A--C-G-T--CAG-T-T-G-A-C--G--A-C--G--G--T-T--	7360
STM.US.x.STM	---AATGTC-CT...-CG-A-G-C--C---GA-T-T-C-T-CAG--A-T---A-C-----CT-A-G-----A-T-----C---C---T-----A-----	6992

V3 loop end.

MAC.US.x.239	TTTATGCCTAAATGTTCTAAGGTGGTGGTCTTCTGATGCAAGGATGATGGAGACACAGACTTCTACTTGGTTTGGCTTTAATGGAAGTACAGCAGAAAATAGAACTTATATTTACTGGCATGGTAGGGATAATAGGACTATAATTAGTTTAAATAAGTATTATAATCT	7523
Env.	F M P K C S K V V V S S C T R M M E T Q T S T W F G F N G T R A E N R T Y I Y W H G R D N R T I I S L N K Y Y N L	
A.CI.88.UC2	---GCA---T---CC---A---A---A---CTG-----T-----A---G---A---A---C---T-----A---C---T-----C---C---C---AC-----	7553
A.DE.x.BEN	---GAA---G---CA---A---A---A---CTG-----T-----A---G---A---A---C---T-----C---A---C---C---C---C---AC-----	7605
A.DE.x.PET2	---GA---C---G---C---A---A---A---CTG---A-----A-----A---G---A---A---C---T-----A---C---T-----T---C---C---CAC-----	7546
A.GH.x.GH1	---CGA---A---G---C---A---A---A---CT---A-----A-----A---G---A---C---C---C---G---G---A---C---T-----C---A---C---C---C---C-----	7022
A.GM.87.D194	---GAA---G---C---A---A---A---A---CTG-----A-----A---G---A---A---C---T-----A---C---T-----A---C---C---C---C---C-----	7013
A.GM.x.IS5	---GA---C---T---C---A---A---A---CT---A-----T-----A-----A---G---AC-----C-----C---C---T-----C---C---C---C---A-----	7019
A.GM.x.MCN13	---GC---C---T---C---A---A---A---CTG---A-----C---A-----A---G---A---A---A-----C---G-----A---T---C---T-----C---A---C---C---C---A-----	7035
A.GM.x.MCR35	---GC---C---T---C---A---A---A---CTG---A-----C---A-----A---G---A---A---A-----C---C-----A---T---C---T-----C---A---C---C---C---C-----	7035
A.GW.86.FG	---GCA---C---C---A---A---A---A---CTG---A-----C---A-----A---G---A---A---A-----C---C-----A---C---C---T-----C---C---C---C---T-----	7010
A.GW.87.CAM2CG	---GCA---C---C---A---A---A---A---CTG---A-----C---A-----A---G---A-----G-----C---C-----G---A---C---T-----AA---C---A---C---C---C---C-----	7608
A.GW.x.ALI	---GCA---C---T---C---A---A---A---A---CT---A-----G-----A-----C---G-----A---C---T-----A---C---T-----A---C---C---C---C---C-----	7586
A.GW.x.MDS	---CA---C---T-----A---A---A---CT---A-----T---C-----A-----A---A-----G-----C-----A---C---T-----AA---C---A---C---C---C---GCAAG-----	7079
A.IN.95.CR1K 147	---GCA---C---T-----A---A---A---CT---CA---T---C-----A---G---A-----A-----C---C-----A---CC---T-----A---AAAG---G---C---A---C---C---C---A-----	7347
A.IN.x.NNVA	---GA---C---T---A-----A---A---A---CTG-----C-----A---G---A-----C---G-----C-----A---C---T-----A---A---C---A---C---C---C---C---AC-----	7600
A.SN.85.ROD	---GCA---C---C-----A---A---A---CT---A-----C-----A---G---A-----C---A-----C-----G-----A---C---T-----C---A---C---A---C---C---C---A-----	7048
B.CI.88.UC1	---A---A---AG---A---A---A---G---C---T-----A-----C---A-----C---T---G---GA-----G---A---G---T-----A---AA-----C---C---A---C---G-----	7577
B.CI.89.pPRD320-20HIV2_56	---C---AC---C---AG---A---A---A---G---C---T-----A-----C---A-----C---T---A-----C---G---A---G---T-----A---A-----C---A---C---G-----	7551
B.CI.x.EH0	---C---C---C---AG---A---A---A-----CTGTAC---A-----A-----C---A-----C---T---A---G-----C---G---A---C---T-----A---C-----C---A---C---TCA-----	7564
B.GH.86.D205	---C---C---C---CAG---A---A---CG---C---C---C-----A-----A-----T---C---A-----C---T---A---G---G---C---G---A---A---T-----AA---AA---C-----C---C---A---C-----CA---C-----	7572
B.JP.81.KR020	---C---C---C---AGC---A---A---A---C---C---T-----A-----A-----C---C---G-----C---T---A---G-----G---A---A-----AAAGC-----CG---C---A---C-----AA---A-----	6695
G.CI.92.ABT96	---GCA---T---C---A---A---A-----A-----T-----A-----A-----A---C---A---C---G-----A---G-----A---C---T-----G---A---C-----A-----	6936
AB.CI.90.7312A	---C---C---AG---A---A---G---C---T-----A-----A-----A---C---A-----C---T---A---G-----G---A---G---T-----A---AA-----T---A---C---G-----	7587
AB.CM.03.03CM_510_03	---CAA---T---C---A---A---A---CTG-----A-----A---A---G---A---A-----A-----C---C-----A---C---T-----A-----C---C---C-----C-----	6684
U.FR.96.12034	---T---C---A---A---A-----A-----A-----G---GA-----A---C-----A-----C-----T-----A-----A-----A---C---A---A-----C-----	7065
MAC.US.x.17EC1	-----	7523
MAC.US.x.17EFR	-----	7523
MAC.US.x.1937	-----	6629
MAC.US.x.2065	-----	6629
MAC.US.x.251_1A11	-----	7519
MAC.US.x.251_32H_PJ5	-----	7521
MAC.US.x.251_BK28	-----	7505
MAC.US.x.80035	-----	6629
MAC.US.x.97074	-----	6498
MAC.US.x.MAC239_87082	-----	6600
MAC.US.x.MM142	---C-----A-----	7018
MAC.US.x.SMM142B	---C-----A-----	7015
MAC.US.x.r80025	---C-----A-----	6486
MAC.US.x.r90131	-----	6629
MNE.US.82.MNE_8	---C-----A-----	6991
MNE.US.x.MNE027	---C-----A-----	6994
SMM.SL.92.SL92B	---GCA---T---AG---A---A---A---A-----T-----A-----A-----A-----T-----G-----G-----A---A---T-----CG---AAG---A---A---C-----T-----	6959
SMM.US.x.F236_H4	---GCT---C---A---A---A---T-----A-----A-----G---A---C-----T-----G-----A---C---T-----C---AAG---A---C---C---G-----	7473
SMM.US.x.H9	---GCT---C---A---A---A---T-----A-----A-----A---C-----T-----C---T-----A---C---T-----R---C---AAGC---A---C---C-----R-----	7000
SMM.US.x.PBJ14_15	---GCT---C---A---A---A---T-----A-----A-----A---C-----T-----T-----A---C---T-----C---AAGC---A---C---C-----R-----	7303
SMM.US.x.PBJA	---GCT---C---A---A---A---T-----A-----A-----A---C-----T-----T-----A---C---T-----C---AAGC---A---C---C-----R-----	7302
SMM.US.x.PBJ_143	---GCT---C---A---A---A---T-----A-----A-----A---C-----T-----T-----A---C---T-----R---C---AAGC---A---C---C-----R-----	7015
SMM.US.x.PBJ_6P6	---GCT---C---A---A---A---T-----A-----A-----A---C-----T-----T-----A---C---T-----A---AAGC---A---C---C-----	7495
SMM.US.x.PGM53	---GCT---C-----A---T-----A-----G---A---C-----T-----G-----A---C---T-----A---AAG---A---C-----	7457
SMM.US.x.SME543	---GCT---C-----A---T-----A-----G---A---C-----T-----G-----A---C---T-----C---ATAG---A---C-----	7530
STM.US.x.STM	---GCA---T---C-----A---A-----C---G---T---T---A-----A-----A-----C---T-----C---C-----T-----C---G---C-----C---T-----	7162

	V4 loop start	V4 loop end	
MAC.US.x.239	AACAATGAAATGTAGAAGACAGGAAATAAGACAGTITTTACCACTGACCATATTATGTCTGGATTGGTTTCCACTCA.....CAACCA...ATCAATGATAGGCCAAGCAGGCATGGTTGGTTGGAGGAAATGGAAGGATGCAATAAAGAGGTGAAGCAGACCA	7684	
Env	T M K C R R P G N K T V L P V T I M S G L V F H S Q P I N D R P K Q A W C W F G G K W K D A I K E V K Q T		
A.CI.88.UC2	T---C-T-C-AG-----G--A-A-AC-----A--CATAGG-T-T-T-----GG-GTC---CA-A-AA-T-GA-----C---AA-C-C---A-GA-C--GC-G-----A--C	7717	
A.DE.x.BEN	C---CGT---AG-----G--A-A-AC-----A--A-G-T-T-T-----G--GATC---A-A-C-----C---C-G---G-A-C--GC-G-----A--C	7766	
A.DE.x.PE12	C---C-T-AG-G-----T--G--A-A-AC-G--A-GAGA-G-T-C-----G--GATC---A-A-C-----C---TG-T--A-A-C--GC-G-----A--A-C	7710	
A.GH.x.GH1	TT-T-AC-T-AG-----C--G--A-A-AC-C--A-G-A-G-T-C-----G--GATC---ACA-A-T-G-A-----C---CAA-C-G---G-A-C--GC-G-----A--A-C	7183	
A.GM.87.D194	C---C-T-AG-----G--A-A-AC-----A--GGAAGG-T-T-T-----GG-GTCTA-CA-A-AA-TGG-----C---CA-C---TA-A-C--GC-G-----A--C	7177	
A.GM.x.ISY	C-C-AC-TT--G--A--A-----G--A-A-AC-C--A-CGCAAG-T-C-----GAAGATC---A-A-AA-C-G-A-----CC---CAA-CG-G---G-A-C--GC-G-----A--A-C	7183	
A.GM.x.MCN13	C-T-AC-T-AG-G-----GG--A-A-AC-----A-G-AAGG-T-C-----G--GGTC---A-A-A-C-GA-A-----CAA-TG-----GA-C--GC-G-----G-A-C	7199	
A.GM.x.MCR35	C-T-AC-T-AG-G-----GG--A-A-AC-----A-G-AAGG-T-C-----G--GGTC---A-A-A-C-GA-A-----CAA-TG-----GA-C--GC-G-----G-A-C	7199	
A.GW.86.FG	C-T-C-T-AG-G-G-----G--A-A-AT-----A-G-TAAG-T-C-----G--GTC---A-A-AA-C-G-A-----C-A-C---A-C--GC-G-----G--C	7174	
A.GW.87.CAM2CG	CT-T-T-T-AG-G-----GG-G-A-A-AC-----A-GCAAAGA-T-C-----GG-ATC-T--A-A--C-G-A-----C---CAA-C-C---CA-A-C--GC-G-----A--C	7772	
A.GW.x.ALI	T-T-C-T-AG-G-----G--A-A-AC-----A-G-AA-A-T-C-----G--GATC---A-A-A-C-GA-A-----C---CAA-CG---G-A-C--GC-G-----G-A-C	7747	
A.GW.x.MDS	CT-CT-C-T-AG-G-----A--GG--A-A-AC-----A--A-G-T-T-C-----G--G---AGA-A-T-G-A-----C---CAAG-C-C---G-AGA-C--GC-G-----A--G-A--	7240	
A.IN.95.CR1K_147	CT-C-AC-T-AG-G-----A--AAC--A-A-AC-----A--ATAAG-T-T-C-----GG-GTA---ACA-A-T-G-A-----C---CAA-CCGG-----C-C-GC-G-----A-A-A--	7511	
A.IN.x.NNVA	CT-T-AT-T-AG-----A--AG--TA-A-ACA--C-A-C-A-G-T-T-C-----G--ACC-A-T-GA-A-----C---CAA-C-G-----A-C--GC-G-----A--C	7761	
A.SN.85.ROD	C-GTT-C-T-AG-G-----G--T--GAA-A-A-A-TGC-----A--CAT-G-T-----CCACTAC-G-G-----A-A-A-C-GA-A-----C---CAA-C---A-C-C--GC-G-----G-A-C	7215	
B.CI.88.UC1	---C-T-C---G--G-C---CA--A-A-A-C-----A--C-AA--T-G-----G--T-C---ACC-A-C-GA--T---C---AAG-C---TA-A-C--GC-G-----A--G--	7738	
B.CI.89.pPRD320-20HIV2_56	---C-T-C---G--G-C---CC--A-A-A-C-----A--GCGAAGA-T-G-----GG-TGTT---G-A-A-C-GA--T---C---AG-C---CA-G-C--GC-G-----G--G	7715	
B.CI.x.EH0	---C-C-A-G-----C-A-TG---G-G--A-A-GA-CCG--A-TA-TC-C-T-----G--T---A-A-A-T-A-A-T---C---AA-C---CA-A-C--C-G-----AG--	7725	
B.GH.86.D205	GT-AC-C-AG-G-----C--G--G--A-A-GA-CCG--A-C-AC--T-----G--T---A-G-A-C-GA-A-T---C---AAG-C---CA-A-C--G-----AAG--	7733	
B.JP.81.KR020	G-AC-C-----G--C-A--CG-G--A-A--A-TC-AA-C-T-----G--T---T-C-A-A-A-C-G-A-C---C---CAC-G-T---G-----G--G	6856	
G.CI.92.ABT96	---A-R-----G--G--A--A--A-T-T-----A-GC-A-C-----T-----A-A-A-C-GA--T---C---C---A-C-C--GC-G-----A--G-A--	7097	
AB.CI.90.7312A	---AC-T-AG-G-----C--G--A-A-AC-C--A-G-A-G-T-C-----G--T---A-A-A-T-G-A--T---C---CAA-CG-G---G-A-C--GC-G-----A-A-C	7748	
AB.CM.03.03CM_510_03	C-T-C-C-AG-----G--A-A-AC--C-A-C-A-G-T-T-----G--CCGC---T-GA--T---C---A-C-C---CA-A-C--G-G-----A--C	6845	
U.FR.96.12034	---T-C-----G--G-----C--A--A--C-A-G-T-T-----G--T---A-C-AT--A-A-T-----T---T---A-GG-CC-G-----G--G	7226	
MAC.US.x.17EC1	---A-----G-----G-----G-----	7684	
MAC.US.x.17EFR	---A-----G-----G-----G-----	7684	
MAC.US.x.1937	---R-----W-----G-----C---M---G-----	6790	
MAC.US.x.2065	---A-----CA-----G-----A-----T-----A-----	6790	
MAC.US.x.251_1A11	---A-----CA-----G-----A-----T-----A-----	7680	
MAC.US.x.251_32H_PJ5	---A-----CA-----G-----A-----T-----A-----	7682	
MAC.US.x.251_BK28	---A-----CA-----G-----A-----T-----A-----	7666	
MAC.US.x.80035	---A-----CA-----G-----A-----T-----A-----	6790	
MAC.US.x.97074	---A-----CA-----G-----A-----T-----A-----	6659	
MAC.US.x.MAC239_87082	---A-----CA-----G-----A-----T-----A-----	6761	
MAC.US.x.MN142	---C-----G-----G-----A-----T-----G-----	7179	
MAC.US.x.SMM142B	---C-----G-----G-----A-----T-----G-----	7176	
MAC.US.x.r80025	---C-----G-----G-----A-----T-----G-----	6647	
MAC.US.x.r90131	---C-----G-----G-----A-----T-----G-----	6790	
MNE.US.82.MNE_8	---C-----G-----G-----A-----T-----G-----	7152	
MNE.US.x.MNE027	---C-----G-----G-----A-----T-----G-----	7155	
SMM.SL.92.SL92B	G---A-G-C-----CC-----A-T---C-T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7120	
SMM.US.x.F236_H4	---G-----A-----C-----A-G-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7634	
SMM.US.x.H9	---G-----A-----C-----A-G-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7161	
SMM.US.x.PBJ14_15	---G-----A-----C-----A-G-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7464	
SMM.US.x.PBJA	---G-----A-----C-----A-G-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7463	
SMM.US.x.PBJ_143	---G-----A-----C-----A-G-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7176	
SMM.US.x.PBJ_6P6	---G-----A-----C-----A-G-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7656	
SMM.US.x.PGM53	---A-G-----G-----C-----A-G-A-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7618	
SMM.US.x.SME543	---A-G-----G-----C-----A-G-A-C---T-T-G-----G-C---A-G---GA-A--C---A-----GA-A-T--GC-G---T---A-A--	7691	
STM.US.x.STM	---GC-----G-C-A---C-----A-C---C---T-G-----G-A---A-A-T---C-----G-----GA-GA-----T---G-A--	7323	

V5 loop start

```
MAC.US.x.239      TTGTCAAAACATCCCAGGTATACTGGA...ACTAACAATACTGATAAAATCAATTGACG...GCTCTGGGA...GGAGGAGATCCGGAAGTTACTTTCATGTGGACAAATTCGAGAGGAGATTCTCTACTGTGTAATAATGAATTGGTTTCTAAATTGGGTAGAAGATAG 7845
Env.             I V K H P R Y T G T N N T D K I N L T A P G G G D P E V T F M W T N C R G E F L Y C K M N W F L N W V E D R
A.CI.88.UC2      ---CAGG---C-AA---C-TG---GAG---G-T-C-TGT---AAA-A--GTG-CTC---C-A-G-G-A-A---T-C---C---C---C---G-GA-C---7881
A.DE.x.BEN       ---AC---A-C-AA---TC-TG---A-GG---T-C-T---AAA-G--GCA-CTC---C---GG-A-T---T-C---A-T---C---C---C---C---A-C-A---7930
A.DE.x.PE12      ---G---GA---C-G-C-AC-G---T-C-T-A---CAA-A--AAA-TTC---G-A---GGTA-A---T-C---A-T-A---C-C---C---C---A-A-C---7874
A.GH.x.GH1       ---A-A---AA---C-G-C-AA-G-T-T-C-T-A---AAA-A--AGA-CTC---C-A---GG-A-A---T-C---A-T---C---C---C---C---A-C-A---7347
A.GM.87.D194     ---CA---CGGA---A-TG---A-GA---T-C-T---AAG-A--ATA-TTC---C-A---G-A-A---T-C---A-T---C---C---C---C---A-A---7341
A.GM.x.IS        ---A---AA---C-TG-C-AA---T-C-T-A---A-A-AAA-ACCTC---C-A---AG-A-AT---T-C---A---T---C---C---C---C---A-C-A---7347
A.GM.x.MCN13     ---CA---AA---C-TG-A-AA-G-T-T-C-T-A---A-A--AAG-CTC---C-A-G--GG-A-A---T-C---A-T---C---C---C---C---A-A-A---7363
A.GM.x.MCR35     ---CA---AA---C-TG-A-AA-G-T-T-C-T-A---A-A--AAG-CTC---C-A-G--GG-A-A---T-C---A-T---C---C---C---C---A-A-A---7363
A.GW.86.FG       ---CG---A-AA-GAAC-GG-G-CGC-A-G-T-T-A-T-AA---A-A--GAGA-CTC---C-A---A-A-A---T-C---A-CT---C---C---C---C---GA-C---7341
A.GW.87.CAM2CG   ---CGG-G---AA---C-A--C-TAACGG-T-T-CC---C-AA---A-A-A-AGA-TTC---C-A---G-A-A---T-C---A-TT---C---C---C---C---A-A-AA-7936
A.GW.x.ALI       ---A---AA---C-TG-C-AA-CC---T-C-T-A---AAA-A--AGA-CTC---G-A---GGTA-AT---T-C---A-T---C---C---C---C---A-C-AA-7911
A.GW.x.MDS       ---A-A---C---AG---C-GT---C-TAACA-T-T-CC---C---A-A--AAA-CTC---C-A---AG-A-A---T-C---A-T---C---C---C---C---A-C-A---7404
A.IN.95.CR1K 147 ---CAG---GCGGTG---C-GG-C-AA-G-C-T-CC-TG-A---A-G--AAA-CTC---C---AGAA-A---T-C---G-A-T---CG-C---C---C---GA-C-A-7672
A.IN.x.NNVA      ---CAG---C---GG---C-T-T--A-A-T-A-T-A---A-G--AAA-TTC---C---GG-A-A---T-C---G-A-T---C-T---C---C---C---GA-C-A-7925
A.SN.85.ROD     ---CA---GA---C-TG-C-AAGG-T-T-GC-TG-A---G-A--AAA-CTC---C-A---AG-A-A---T-C---A-T---C---C---C---C---A-GA-A-7379
B.CI.88.UC1      ---CA-A---AA---A-T-C-C-G-GG-A-GA---GTA---GG-CTCGGCA-TTC---C-A-G-G-GACAT---T-C-T-G---A-T-T---T---CC---T---C---G-GA-C-A-7902
B.CI.89.pPRD320-20HIV2_56 ---CA-G---A---A-TA-G-C-TACG---A---GTA---GG-CTCGGCA-TTC---C-A-G-CA-GA-AT---T-C-T-G---A-T-T---C---CA---T---C---GC-AA-7879
B.CI.x.EH0       ---AAA-T---A-T-A---A-CA---TCTCAC-G-A-GG-AG-A---AG-AC-CGAGAA-CTC---A---A-GA-AT---T-C-T-G---T---C---TT---C---A---A-7889
B.GH.86.D205     ---CA-A---AA---GGTG-A-A---TCACA-GCG-A-G-AGTATCA-AA-A---AAA-TTC---A-A-ACA-A-AT---C-T---A-T-A---T---CC---CT---C---GA-C-AA-7903
B.JP.81.KR020    ---CA-G---A-A---A-G---C-CA---A-G-AG-A---AG-ACTCGCAA-CTC---A-A-GA-AT---T-C-T---TT-G---T---C---C---C---A---A-7020
G.CI.92.ABT96    ---G---G-C---C-AA---A-TG-C-AA-G-M-A-CC-T-A---A-A-A-GAA-TTC---A-A-AG---T---A-T-G-T---C---A---G-C-A-7261
AB.CI.90.7312A   ---A-A---AA---C-TG-C-AAGG-T-T-CC-T-A---AAA-A--ACA-CTC---C-A---GG-A-A---T-C---A-T---C---C---C---A-C-A-7912
AB.CM.03.03CM_510_03 ---A-G---A-C-AG---C-TG---GACA-T-C-T---AAA-A--GAA-CTC---C-A---GG-A-A---T-C---A-T---C---C---C---GA---7009
U.FR.96.12034    ---C-C---CA---T---C-G---T-AG-C-G-A-C-G-A---AA-A-C---T-T-A-G-A-AA-T---T-C---A---G---CA---C-C---A-C---7387
MAC.US.x.17EC1   .....A.....7845
MAC.US.x.17EFR   .....A.....7845
MAC.US.x.1937    .....R.....AR.....6951
MAC.US.x.2065    .....R.....AR.....6951
MAC.US.x.251_1A11 .....T.....T.....7841
MAC.US.x.251_32H_PJ5 .....A.....A.....7843
MAC.US.x.251_BK28 .....A.....A.....7827
MAC.US.x.80035    .....A.....A.....6951
MAC.US.x.97074    .....A.....A.....6820
MAC.US.x.MAC239_87082 .....A.....A.....6922
MAC.US.x.MN142    .....A.....A.....7340
MAC.US.x.SMM142B  .....A.....A.....7337
MAC.US.x.r80025   .....R-A.....A.....6808
MAC.US.x.r90131   .....R-A.....A.....6951
MNE.US.82.MNE.8   .....C.....T.....A-7313
MNE.US.x.MNE027   .....C.....T.....A-7316
SMM.SL.92.SL92B  ---A---C---C---TG---AGG---T---C-A---C-G---G---C-A---T---A-T---C---C---G---7281
SMM.US.x.F236_H4 ---G---G---TG---AGG---T---C-A---A-C---C---T---A---C-T---T---C---A-T-A-T---T---G-C-A-7795
SMM.US.x.H9       ---G---AG---TR-K-Y-R-AC---T-GC-A-A---A---C---T---T---TC---A-T-A-T---T---Y-TA-7322
SMM.US.x.PBJ14_15 ---G---G---T-G---AC---T-GC-A-A---A---A---T---T---TC---A-T-A-T---T---TA-7625
SMM.US.x.PBJA     ---G---G---T-G---AC---T-GC-A-A---A---A---T---T---TC---A-T-A-T---T---A-TA-7624
SMM.US.x.PBJ_143 ---G---AG---TR-K-Y-R-AC---T-GC-A-A---A---A---T---T---TC---A-T-A-T---T---Y-TA-7337
SMM.US.x.PBJ_6P6 ---G---G---T-G---AC---T-GC-A-A---A---A---T---T---TC---A-T-A-T---T---TA-7817
SMM.US.x.PGM53    ---G---A---G---TG-G-A-G---T-C---A---A---C---T-T---T---T---A-T---C---C---T---A-7779
SMM.US.x.SME543   ---G---G---TG---AGG---T---C-A-A---A-C---A---C-T-T---T---TC---A-T-A---C---C---G-C-A-7852
STM.US.x.STM      ---G---A---C-TG-C-G-CA---A-GGA-AGT---G---A-G-C---C-T---A-T-T-T-C---CT---A-C-A-7484
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MAC.US.x.239		AATACGCTAAC.....CAGAAGCCAAAGGAACAGCATAAAAGGAATTACGTGCCATGTCATATTAGACAATAATCAACACTTGGCATAAAGTAGGCCAAAATGTTTATTTCCTTCAAGAGAGGGAGACCTCACGTGTAACCTCCACAGTGACAGTCT										8000																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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A.CI.88.UC2		-CG-GCCAA-A																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		

		Rev Responsive Element (RRE) start	
MAC.US.x.239	CATAGCAACATAGATTGG.....ATTGATGGAACCAAACTAATATCACCATGAGTGACAGAGGTGGCAGAACTGTATCGATTGGAATTGGGAGATTATAAATAGTAGAGATCACTCCAATTGGCTTGGCCCCACAGATGTGAAGAGGTACACTACTGGTGGCA 8161		
Env	I A N I D W.....I D G N Q T N I T M S A E V A E L Y R L E L G D Y K L V E I T P I G L A P T D V K R Y T T G G		
A.CI.88.UC2	A-T-T-T-T-C-----CA-----T-G-C-C-T-T-T-----C-A-----C-AG-A-A-A-A-----C-A-T-AG-AA-A-A-TT-CT-G-CC...C 8170		
A.DE.x.BEN	A-T-T-T-T-CATA.....GAT-AAA-C-G-CT-T-C-C-T-T-T-----A-----C-C-A-C-----C-C-A-A-A-A-----C-A-T-CA-GA-----T-CT-AAC...C 8216		
A.DE.x.PET2	A-T-T-T-T-CAT-----TT-AT-----G-A-GC-T-T-T-----A-C-----C-A-A-A-----C-A-T-TCA-AA-A-A-TT-CT--C...C 8160		
A.GH.x.GH1	A-T-T-T-T-CGTA.....A-A-A-T-----G-A-C-T-T-T-----A-C-----A-A-----A-AG-A-A-----C-A-T-GAGA-A-A-A-TT-CT-G-C...C 7636		
A.GM.87.D194	A-T-T-T-T-C-CA-----G-A-AT-----G-C-C-T-T-T-----A-----C-C-A-----G-C-C-----GA-AG-A-A-----CCG-C-A-T-A-A-A-A-A-TT-CT-G-C...C 7630		
A.GM.x.TS9	-T-T-T-T-T-GTT-----GA-----G-----A-C-----C-A-----C-A-----AG-A-A-----C-A-T-CA-AA-A-A-T-CT--C...C 7636		
A.GM.x.MCN13	A-T-T-T-T-T-GCA-----A-----TA-T-A-----T-T-T-----A-C-----A-G-----G-A-A-A-----C-A-T-CA-AA-A-A-T-CT-AC...C 7643		
A.GM.x.MCR35	A-T-T-T-T-T-GCA-----A-A-TA-T-AG-T-T-T-----A-C-----A-G-----G-A-A-A-----C-A-T-CA-AA-A-A-T-CT-AC...C 7643		
A.GW.86.FG	A-T-C-T-T-T-GC-----G-T-----A-T-T-T-----C-A-----C-G-----G-C-----G-A-A-----C-A-T-TCA-AA-A-A-T-CT--C...C 7627		
A.GW.87.CAM2CG	A-T-T-T-T-T-CGA-----GG-AATC-GAC-A-T-T-T-----T-----C-----C-----G-----G-A-A-----C-A-T-TCACAA-A-A-T-CC--C...C 8228		
A.GW.x.ALI	A-T-T-T-T-T-CAC-----C-----G-A-T-T-T-----A-C-----C-----G-----G-A-A-----C-A-T-TCA-AA-G-A-T-CT-AC...C 8200		
A.GW.x.MDS	A-T-T-T-T-T-CGAC-----A-G-AT-T-G-A-T-T-T-----T-----A-C-----A-----G-A-A-----C-A-T-CCA-AA-AC-A-T-CT--C...C 7693		
A.IN.95.CR1K 147	A-T-T-T-T-T-GTA-----AACGAAATA-AT-A-GG-A-T-T-T-----C-----A-C-G-A-----G-----G-AG-A-A-----C-A-T-TCA-AA-AC--T-CT--C...C 7971		
A.IN.x.NNVA	A-T-T-T-T-T-AGA-----T-----A-G-T-T-T-----G-----C-A-C-A-----G-----G-A-A-----C-A-T-CCA-AA-AC-A-T-CTT-CC...T 8208		
A.SN.85.ROD	A-T-T-T-T-T-C-----CAAA-CAAT-T-G-A-C-T-T-T-----A-C-----A-CA-----G-----G-A-A-----C-A-T-A-AA-A-A-A-T-CT--C...C 7662		
B.CI.88.UC1	T-----C-----T-CGT-TATTATGATGGCA--AT-C-A-G-C-T-----A-----G-----CA-----C-G-C-----A-A-A-A-G-----T-A-T-AG-A-A-A-TT-CT-AACG...C 8203		
B.CI.89.pPRD320-20HIV2_56	T-----C-----T-A-----A-C-G-G-C-T-----A-----G-----A-----C-G-C-----A-A-A-A-G-----T-A-T-AG-A-A-A-TT-CT-A-CA...C 8168		
B.CI.x.EH0	-----C-----T-----A-AAG-TT-----TG-----A-T-----A-----C-G-C-----A-A-A-----T-A-T-AG-A-A-A-TT-CT-A-TG...C 8178		
B.GH.86.D205	-----C-----CA-C-CA-----CAAC-GTACC-C-TT-TG-----A-T-----A-----C-G-C-----A-A-A-----C-A-T-AG-A-A-A-TT-CT-A-TA...C 8192		
B.JP.81.KR020	-----C-T-T-----CAA-AAT-TAGG-----T-----A-T-----A-----C-G-C-C-C-----A-A-A-----T-A-T-AG-A-A-A-TT-CT-A-TG...C 7309		
B.CI.92.KBT96	A-----G-T-----AGA-----AAT-GGTC-AAC-----T-A-----TTT-C-----A-----G-----A-A-----T-A-----A-A-A-TT-CT--TG...C 7577		
AB.CI.90.7312A	G-T-T-T-----T-CGTA-----GACG-A-G-AAT-----GG-A-T-T-T-----C-A-----A-----AG-G-A-----T-C-A-T-TCA-AA-A-A-T-CT-AC...C 8207		
AB.CM.03.03CM_510_03	A-T-T-T-----T-CACA-----A-A-----T-G-C-C-T-T-C-----C-A-----A-G-----C-C-----GA-A-A-A-----C-A-T-AC-AAGG-----TT-CT-AAC...C 7295		
U.FR.96.12034	G-T-----T-T-C-----A-CAA-T-T-A-----T-----C-A-----A-A-G-----G-----G-A-A-GA-----T-T-----CCA-A-A-A-TT-CT-A-TG...C 7700		
MAC.US.x.17EC1	-----		
MAC.US.x.17EFR	-----		
MAC.US.x.1937	-----		
MAC.US.x.2065	-----C-A-----		
MAC.US.x.251_1A11	-----C-----		
MAC.US.x.251_32H_PJ5	-----C-----		
MAC.US.x.251_BK28	-----C-----		
MAC.US.x.80035	-----		
MAC.US.x.97074	-----		
MAC.US.x.MAC239_87082	-----		
MAC.US.x.MN142	-----A-----C-----		
MAC.US.x.SMM142B	-----A-----C-----		
MAC.US.x.r80025	-----		
MAC.US.x.r90131	-----		
MNE.US.82.MNE_8	-----		
MNE.US.x.MNE027	-----		
SMM.SL.92.SL92B	A-----T-T-----CAAC-TG-G-C-T-----A-----T-----G-----G-----A-----T-----C-----A-----C-AA-----TG 7609		
SMM.US.x.F236_H4	-----G-G-----CA-A-C-TG-G-C-----G-----C-----A-----T-----C-----AG-A-GA-----C-AAC-----TG 8126		
SMM.US.x.H9	-----G-A-----CA-C-TA-G-C-----G-----C-----G-----C-----AG-A-A-----C-AAC-----TG 7650		
SMM.US.x.PBJ14_15	-----G-A-----CA-C-TG-G-C-----G-----C-----C-----C-----AG-A-A-----C-AAC-----TG 7953		
SMM.US.x.PBJA	-----G-A-----CA-C-TG-G-C-----G-----C-----C-----C-----AG-A-A-----C-AAC-----TG 7952		
SMM.US.x.PBJ_143	-----G-A-----CA-C-TA-G-C-----G-----C-----C-----C-----AG-A-A-----C-AAC-----TG 7665		
SMM.US.x.PBJ_6P6	-----G-A-----CA-C-TG-G-C-----G-----C-----C-----C-----AG-A-A-----C-AAC-----TG 8145		
SMM.US.x.PGM53	-----G-T-----C-----G-----C-----CA-----G-----C-----T-----C-----AG-A-G-----A-----TG 8107		
SMM.US.x.SME543	-----G-G-----CA-AAC-TG-G-C-----G-----C-----T-----A-GA-----C-AAC-----TG 8183		
STM.US.x.STM	A-----T-C-----C-A-CAAT-TG-G-----C-----TGCA-----C-----A-A-----A-GA-----A-----A-A-----TG 7812		

Env gp120 end_Env gp41 start		
MAC.US.x.239	CCTCAAGAAATAAAAGAGGGTCTTTGTGCTAGGGTTCTTGCGTCAACGGCAGGTTCTGCAATGGCGCGGCTCGTTGACGCTGACCGCTCAGTCCGAACTTTATTGGCTGGGATAGTGCAGCAACAGCAACAGCTGTTGGACGTGGTCAAGAGACAACAA	8331
Env	T S R N K R G V F V L G F L G F L A T A G S A M G A A S L T L T A Q S R T L L A G I V Q Q Q Q L L D V V K R Q Q	
A.CI.88.UC2	-AG-G--G-C-----T-G-C-----C-----G--A-----CC-----T-A-----G-----C-----C-----A-A-----	8340
A.DE.x.BEN	-AGTG--G-C-----T-G-C-----G--A-----CG--CC-----T-A-C-----G-----C-----C-----A-----	8386
A.DE.x.PET2	-ACAG--G-----T-G-----AG-----G--A-----C-----T-G-----TC-G-CT-AC-G-----C-----A-----	8330
A.GH.x.GH1	-AGTG--G-C-----T-G-----G--A-----G--A-----CC-----T-G-----G-----C-----C-----A-----	7806
A.GM.87.D194	-AGTG--G-C-----T-G-C-----G--A-----G--A-----GC-----C-----T-G-----G-----C-----C-----	7800
A.GM.x.IS	-AGGG--C---G-----T-GC-----C-A-----A-G--A-----G-----G-----T-G-----T-G-----CCG-----G-----	7806
A.GM.x.MCN13	-AATG--G-C--G-----T-G-C-----A-----A-----C-----G--A-----T-G-----T-G-----C-----C-----G	7813
A.GM.x.MCR35	-AATG--G-C--G-----T-G-C-----A-----A-----C-----G--A-----T-G-----T-G-----C-----C-----G	7813
A.GW.86.FG	A-CAG--C-C--C-----T-G-----C-A-----A-----A-----C-----C-----T-A-----T-G-----C-----C-----A	7797
A.GW.87.CAM2CG	A-GGG--CC-----T-CG-----A-----A-----AGT-----A-----C-----T-A-----C-----T-G-----C-----A	8398
A.GW.x.ALI	-AAGG--G-----T-G-C-----A-----G--A-----A-----AG-T-A-----T-----T-G-----C-----C-----G	8370
A.GW.x.MDS	A-GGG--C-----T-G-----A-----A-----G-----A-----C-----T-----T-G-----C-----C-----G	7863
A.IN.95.CR1K_147	--GGG--C-C--C-----T-GC-C-----AA-----A-----A-----C-----T-----C-----G-----C-----C-----G	8141
A.IN.x.NNVA	-AGG--C-A-C-----T-G-C-----C-----A-----A-----C-----C-----C-----G-----C-----C-----G	8378
A.SN.85.R0D	A-GGG--C-C--C-----T-G-C-----A-----A-----C-----CC-CG-T-G-----G-----C-----C-----C-----	7832
B.CI.88.UC1	-AC-G--G-----T-AA-G-----AC-----T-----T-----AA-----C-----T-A-----G-----C-----C-----G	8373
B.CI.89.pPRD320-20HIV2_56	-AC-G--G-----T-AA-G-----C-----A-----G-----A-----C-----T-A-----G-----G-----C-----C-----A	8338
B.CI.x.EH0	-AC-G--G-----T-AC-----T-----A-----C-----T-G-----C-----T-G-----G-----C-----G-----A	8348
B.GH.86.D205	AAC-G--G-----T-AA-G-----A-----A-----C-----T-----T-----AA-----T-----T-A-----G-----C-----C-----CTG	8362
B.JP.81.KR020	-AC-G--G-----T-ACCG-----T-----A-----T-----C-----C-----T-T-G-C-----G-----G-----C-----A	7479
G.CI.92.ABT96	-AC-G-A-----T-A-----T-----A-----T-----T-----A-A-----T-G-----G-----G-----T-----G	7747
AB.CI.90.7312A	-GGGG--C-----T-A-C-----A-G-A-----AG-----A-----C-----T-G-----T-G-----C-----C-----A	8377
AB.CM.03.03CM_510_03	-AGGG--G-----T-A-----A-----A-----C-----T-G-----A-----C-----T-A-----G-----G-----C-----C-----A	7465
U.FR.96.12034	-AC-G--G-----G-A-A-----T-----C-----T-----T-A-----G-----G-----C-----C-----A-----A-----	7870
MAC.US.x.17EC1	-----	8331
MAC.US.x.17EFR	-----	8331
MAC.US.x.1937	-----R-----	7439
MAC.US.x.2065	-----	7437
MAC.US.x.251_1A11	-----	8327
MAC.US.x.251_32H_PJ5	-----A-----G-----	8329
MAC.US.x.251_BK28	-----	8313
MAC.US.x.80035	-----	7437
MAC.US.x.97074	-----	7300
MAC.US.x.MAC239_87082	-----	7408
MAC.US.x.MN142	-----CG-----G-----	7826
MAC.US.x.SMM142B	-----CG-----G-----	7823
MAC.US.x.r80025	-----	7294
MAC.US.x.r90131	-----	7437
MNE.US.82.MNE_8	-----A-----G-----	7805
MNE.US.x.MNE027	-C-----A-----G-----	7808
SMM.SL.92.SL92B	-----AG-----A-----G-----A-----C-A-----T-----G-----A-----A-----T-----	7779
SMM.US.x.F236_H4	-----G-----G-----G-----A-----CG-----T-G-----G-----G-----T-----	8296
SMM.US.x.H9	-----G-----G-----G-----A-----CG-----T-G-----G-----G-----T-----	7820
SMM.US.x.PBJ14_15	-----G-----G-----G-----A-----CG-----T-G-----G-----G-----T-----	8123
SMM.US.x.PBJA	-----G-----A-----A-----CG-----T-G-----G-----G-----T-----	8122
SMM.US.x.PBJ_143	-----G-----A-----G-----A-----CG-----T-G-----G-----G-----T-----	7835
SMM.US.x.PBJ_6P6	-----G-----A-----G-----A-----CG-----T-G-----G-----G-----T-----	8315
SMM.US.x.PGM53	-----G-----G-----G-----A-----CG-----T-G-----G-----G-----T-----A-----	8277
SMM.US.x.SME543	-----G-----G-----G-----A-----C-----T-G-----G-----G-----T-----T-----	8353
STM.US.x.STM	-----C-----G-----C-----G-----A-----C-----G-----G-----A-----	7982

HIV-2/SIV Complete Genomes

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A.CI.88.UC2
A.DE.x.BEN
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A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALT
A.GW.x.MDS
A.IN.95.CR1K_147
A.IN.x.NNVA
A.SN.85.ROD
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B.CI.x.EH0
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B.CI.92.ABT96
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U.FR.96.12034
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CTTGGATAAAGTATATACAAATGAGGATTTATATAGTTGTAGGAGTAATACCTGTTAAGAAATAGTGATCTATATAGTACAAATGCTAGCTAAGTTAAGGCAGGGGTATAGGCCAGTGTTCTCTTCCCACCTCTTATTTCCAGCAGACCCATATCCCAACAGGCCGGCA		S W I T K Y I Q Y G V Y I V G V I L L R I V I Y I V Q M L A K L R Q G Y R P V F S S P S Y F Q Q T H I Q Q D P A																				N P I S P T N R T Q Q D P A										8829																																	
-	C	-	C	-	A	-	T	-	G	-	-	-	A	-	A	-	GCT	-	CA	-	A	-	G	-	G	-	T	-	T	-	AG	-	GA	-	T	-	AA	-	C	-	T	-	T	-	C	-	C	-	GG	-	C	-	A	-	T	-	TACA	-	G	-	G	-	8838		
-	C	-	G	-	C	-	T	-	G	-	GC	-	A	-	G	-	A	-	GCT	-	CA	-	A	-	G	-	G	-	T	-	T	-	AG	-	GA	-	T	-	AA	-	C	-	T	-	T	-	C	-	C	-	GG	-	C	-	A	-	T	-	CA	-	G	-	G	-	8884
-	C	-	C	-	T	-	G	-	-	-	G	-	A	-	AA	-	A	-	GCT	-	CA	-	A	-	G	-	T	-	A	-	AG	-	GAC	-	T	-	AA	-	C	-	T	-	T	-	T	-	C	-	C	-	GG	-	A	-	A	-	T	-	CA	-	TG	-	A	-	8828
-	C	-	C	-	A	-	T	-	-	-	-	-	A	-	A	-	G	-	GT	-	CC	-	A	-	G	-	T	-	T	-	AG	-	GAC	-	T	-	AA	-	C	-	T	-	T	-	T	-	C	-	C	-	GG	-	C	-	A	-	T	-	CAC	-	G	-	G	-	830
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-	C	-	C	-	C	-	T	-	-	-	-	-	A	-	AA	-	A	-	G	-	TC	-	T	-	-	-	-	-	-	-	T	-	AG	-	GAC	-	T	-	AA	-	C	-	T	-	T	-	C	-	C	-	GG	-	CC	-	A	-	T	-	CA	-	TG	-	A	-	8311
-	C	-	C	-	G	-	C	-	C	-	-	-	A	-	AA	-	A	-	G	-	TC	-	T	-	-	-	-	-	-	-	T	-	AG	-	GAC	-	T	-	AA	-	C	-	T	-	T	-	C	-	GG	-	CC	-	A	-	T	-	CA	-	TG	-	A	-	8311		
-	C	-	G	-	C	-	G	-	T	-	-	-	A	-	A	-	A	-	G	-	GCT	-	T	-	-	-	-	-	-	-	T	-	AG	-	GAC	-	T	-	AA	-	C	-	T	-	T	-	C	-	C	-	GG	-	CA	-	A	-	T	-	CA	-	A	-	A	-	8295
-	C	-	G	-	C	-	GC	-	T	-	-	-	A	-	A	-	A	-	G	-	GCTC	-	T	-	-	-	-	-	-	-	T	-	AG	-	G	-	C	-	T	-	AA	-	C	-	T	-	T	-	C	-	T	-	C	-	T	-	CA	-	A	-	A	-	8296		
-	C	-	C	-	C	-	T	-	-	-	-	-	A	-	A	-	A	-	G	-	-	-	-	-	-	-	-	-	-	-	T	-	AG	-	GAC	-	T	-	AA	-	C	-	T	-	T	-	C	-	T	-	C	-	T	-	CA	-	G	-	A	-	8361				
-	C	-	C	-	C	-	T	-	G	-	-	-	A	-	A	-	A	-	G	-	T	-	-	-	-	-	-	-	-	-	T	-	AG	-	GAC	-	T	-	AA	-	C	-	T	-	T	-	C	-	C	-	GG	-	A	-	A	-	T	-	CA	-	T	-	A	-	8639
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MAC.US.x.239	CTGCCAACAGAGAAGGCAAGAAAGAGACGGTGGAGAGCGGTGGCAACAGCTCTGGCCTTGGCAGATAGAATATATTCTTCTGATCCGCCAAGTACGCCTCTTGACTTGGCTATTGACAACTGCAGAACCTTGCTATCAGAGATATACCATCTCTCA	8999
Env	L P T R E G K E R D G G E G G G N S S W P W Q I E Y I H F L I R Q L I R L L T W L F S N C R T L L S R V Y Q I L Q	
Tat exon 2	C Q P T R E G K A K K E T V E K A R V A T A P G L G R *	
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A.CI.88.UC2	-A-GG-AC-AA-C-G-CC-C-A-T-T-GA-T-C-A-C-C-A-GC-A-TG-CT-T-G-A-A-T-T-GGA-A-CGCGAAC-C-C-C-G-G	9008
A.DE.x.BEN	-A-G-AC-AA-C-GA-TC-GC-A-A-TT-GA-TG-CA-A-C-G-G-G-A-T-CT-TCG-A-A-T-GA-A-C-AGAAC-C-C-G-G	9054
A.DE.x.PE12	-A-GA-AA-C-GA-CC-A-CA-AT-AG-G-G-CA-C-A-A-T-G-CT-CG-A-A-GT-AGGA-A-C-GAGC-T-C-C-G	8998
A.GH.x.GH1	-A-G-AC-AA-C-GA-ACA-C-A-TT-GA-TG-A-C-A-C-A-A-T-CT-CG-A-A-A-T-GA-A-C-GAAC-C-C-A-G	8474
A.GM.87.D194	-A-G-AC-AA-C-GA-CC-C-A-A-TT-GA-TG-CAC-A-C-C-A-A-A-T-CT-CG-A-A-A-G-GGG-A-C-AGAAC-C-C-G-G	8468
A.GM.x.ISY	-A-GA-AA-C-GA-T-GA-C-A-T-A-G-A-C-TG-C-CA-A-A-A-G-GGA-A-C-C-C-T-T	8474
A.GM.x.MCN13	-A-G-AA-C-GA-T-A-CAA-T-AG-G-C-AG-A-A-A-G-T-G-CG-A-A-A-T-G-A-A-C-GA-C-C-T-C	8481
A.GM.x.MCR35	-A-G-AA-C-GA-T-A-CAA-T-AG-TG-A-C-AG-A-A-A-G-T-CG-A-A-A-T-G-A-A-C-GA-C-C-T-C	8481
A.GW.86.F6	-A-G-AA-C-GA-T-AGCAA-AG-A-T-C-C-CA-A-A-T-GA-A-C-GA-C-C	8465
A.GW.87.CAM2CG	-A-G-C-AA-C-GA-T-GCAA-AG-A-A-G-C-CA-A-A-T-GA-A-C-GA-C-T-C	9066
A.GW.x.ALI	-A-G-AA-C-GA-T-CAA-T-GG-A-TG-C-C-C-C-T-A-A-T-AGCT-TCG-G-A-T-GGA-A-C-GA-C-C-C	9038
A.GW.x.MDS	-A-GA-AA-C-GA-T-GCAA-AG-A-T-C-C-C-A-A-TG-T-CA-A-G-A-G-GGA-A-C-GA-C-T-T-C	8531
A.IN.95.CRIK 147	-A-G-AA-T-GA-T-CAA-TT-A-T-A-C-C-C-A-A-TG-A-T-G-CA-A-A-A-G-AGGA-A-C-GAGC-T-T-C	8809
A.IN.x.NNVA	-A-GA-AA-C-GA-T-CAA-AT-A-T-C-C-C-A-A-TG-T-G-CA-A-A-A-G-AGGA-A-C-GAGC-T-T-C	9046
A.SN.85.ROD	-A-G-AC-AA-C-GA-T-AGCAA-AG-A-A-C-C-C-CA-A-A-T-GGA-A-A-C-GAGC-T-T-C	8500
B.CI.88.UC1	-A-G-AC-AA-C-GAC-A-A-A-C-AA-G-CTT-A-T-C-CGCG-C-T-T-T-GGAA-T-G-A-A-GG-G-A-A-G-T-AGACC-C-A	9041
B.CI.89.pPRD320-20HIV2_56	-A-G-AC-AA-C-GAC-A-A-A-G-AA-G-ATT-A-T-C-CGCG-C-T-T-T-GGAA-T-G-A-A-GG-G-A-A-T-GACC-C-A	9006
B.CI.x.EH0	-A-G-AC-AA-C-GA-GA-A-CAA-AG-T-A-T-C-C-C-C-C-T-T-GGAA-T-A-A-GG-G-A-A-T-AGACC-T-A-C	9016
B.GH.86.D205	-A-G-AC-AA-C-GA-GA-A-C-A-A-G-A-T-A-T-C-C-C-T-AC-G-G-GGAA-A-T-A-A-GG-G-A-G-T-AGACC-T-A-C	9030
B.JP.01.KR020	-G-G-C-AA-C-GA-GA-C-A-A-G-A-T-A-CAG-C-C-C-T-T-GGAA-A-T-A-A-G-G-A-G-T-AGA-C-T-ACC	8147
G.CI.92.ABT96	-W-A-AA-T-G-AA-A-CAAA-T-A-T-M-G-AGGAA-A-A-G-A-CY-T-CT	8427
AB.CI.90.7312A	-A-G-AC-AA-C-GA-GA-A-C-A-A-G-T-A-T-C-C-C-C-A-T-G-GGAA-T-A-GA-GG-A-G-T-AGACC-T-A-C	9045
AB.CM.03.03CM_510_03	-A-C-AA-C-GA-GA-A-C-A-A-G-A-T-A-T-C-CG-T-C-G-GGAA-A-T-A-A-GG-A-G-T-AGACC-C-A	8133
U.FR.96.12034	-A-G-AA-T-GA-G-C-CA-T-A-T-AG-A-A-A-T-G-A-G-GGA-A-C-GA-T-G	8538
MAC.US.x.17EC1	-G-A	8999
MAC.US.x.17EFR	-G-A	8999
MAC.US.x.1937	-G-M	8107
MAC.US.x.2065	-G	8105
MAC.US.x.251.1A11	-G	8995
MAC.US.x.251.32H.PJ5	-G	8997
MAC.US.x.251.BK28	-G	8981
MAC.US.x.80035	-G	8105
MAC.US.x.97074	-G	7968
MAC.US.x.MAC239_87082	-G	8076
MAC.US.x.MM142	-A-A-G-GCA	8494
MAC.US.x.SMM142B	-A-A-G-GCA	8491
MAC.US.x.r80025	-G	7962
MAC.US.x.r90131	-G	8105
MNE.US.82.MNE.8	-A-A-C-G-GCA	8473
MNE.US.x.MNE827	-A-A-C-G-CA-T-G	8476
SMM.SL.92.SL92B	-G-A-A-C-G-A-A-C-A-AT-A-TG-G-GA-A-A-A-T-TG-CTCG-AGC-C-CC-A	8447
SMM.US.x.F236.H4	-C-A-AG-G-CA-A-G-A-T-GT-GA-A-G-GGAT-G-T-GAGC	8964
SMM.US.x.H9	-A-AG-G-RCA-A-A-T-R-G-GAT-G-T-GANC-G-A	8488
SMM.US.x.PBJ14_15	-A-AG-G-GCA-A-A-T-GT-GT-GAT-G-T-GAAC-G-A-C	8791
SMM.US.x.PBJA	-A-AG-G-GCA-A-A-T-GT-GT-GAT-G-T-GAAC-G-A-C	8790
SMM.US.x.PBJ_143	-A-AG-G-RCA-A-A-T-R-G-GAT-G-T-GANC-G-A	8503
SMM.US.x.PBJ_6P6	-A-AG-G-GCA-A-A-T-GT-GT-GAT-G-T-GAAC-G-A-C	8983
SMM.US.x.PGM53	-A-A-AG-G-CA-A-A-T-G-T-G-A-G-AT-C-T-A	8945
SMM.US.x.SME543	-C-A-AG-G-CA-A-G-A-T-A-A-G-GGAT-G-T-GA-C	9021
STM.US.x.STM	-A-A-A-C-GA-GA-CA-A-A-T-A-A-C-G-AG-G-A-A-T-GG-T-GT-C-GA-C	8650

		Env gp41, gp160 end	
MAC.US.x.239	CTTAGGAGAGGTGGAAGATGGATACTCGCAATCCCAGGAGGATTAGACAAGGGCTTGAAGTCACTCTCTTGT...GAGGGACAGAAA.....TACAATCAGGGACAGTATATGAATACCTCATGGAGAAAC...CCAGCTGAAGAGAGAGAAAAATTAGCATACAGAA	9326	
Env	L R R G G G R W I L A I P R R I R Q G L E L T L L L *		
Nef	L G E V E D G Y S Q S P G G L D K G L S L S C - E G Q K . . . Y N Q G Q Y M N T P W R N . . P A E E R E K L A Y R		
A.CI.88.UC2	G-GCA-C-CATC-G-GG-A-C--G--A--C-G-G-AGCA-AA-G-C-C--C-G--TCGG--G-T-C--C-C--C--AATG-AG-C-G--GAGT--AGC	9323	
A.DE.x.BEN	GGCG-AC-CATC-G-GG-A--G-T-A-A-A-C-G-G-AGCA-A--G-C--C--C-G--TC-G--G--C--C-GC--AAC-A--C-G--GATTG--T-GC	9369	
A.DE.x.PE12	A-GG-AC-GATC-C-GG-A--T-G-T-A-A--C-G-G--GCA-A-TG-C-C--G--CGG--TC-A--G-C-T--C-C--CT--A-C--GA-G-GGG-AC-TTG--AGC	9325	
A.GH.x.GH1	G-GCAAC-C-TC-G-GG-A--G--A--C-G--G--GCA-AA-G-C-C--C--C-G--TCGG--G-T-TC--C-C--C--G--AAT-AG-C-G--AAGTT--AGC	8789	
A.GW.87.D194	GGCGAAC-CATC-G-GG-A-C--G--A--C-G-G-AGCA-AA-G-C-C--C--C-G--TC-G--G--TC--C-C--C--A-C-ATAG-GC-G--AATT--T-AGC	8783	
A.GM.x.ISY	--GG-AC--ATC--GG--G--T-AC-A--C-G-G-AGCA-AA-TG-C-C--G--G--TC-G-A-G-C-T--C--C--AAC-A-AG--GA-T-G--GC	8768	
A.GM.x.MCN13	--GCA-C-GATC-G-GG-A--T-G--A-A-A-C-G-G-AGCA-A-G-C-C-A--C-GG--TC-G--G-C-T--C--C--AAC-AG-G-G--GA-TTG--AGC	8808	
A.GM.x.MCR35	--GCA-C-GATC-G-GG-A--T-G--A-A-A-C-G-G-AGCA-A-G-C-C-A--A-CGG--TC-G--G-C-T--C--A--AAC-AG-G-G--GA-TTG--AGC	8808	
A.GW.86.FG	--GCAAC--ATC-G-GG--T-G--AC-A--C-G-G-AGCA-A--G-C-C--C--C-G--TC-G--G-T-T-G-A--C--C--A-C-A-G-G--GA-TTG--A-C	8792	
A.GW.87.CAM2CG	T-ACAAAC-CAT--GG-A-C-T-GG--A-A-C--G--AGCA-A--G--C--C--C-G--TC-G--GG-C-T--C--C--AAT--G--GA-G--GC	9372	
A.GW.x.ALI	G-GCA-T-G-TC-G-GA--G--A--C-G-G--GCA-AA-TG-C-C--A--CGG--TC-G--G-T-T--C--C--AAC-A--G--GA-TTG--AGC	9365	
A.GW.x.MDS	T-GG-AC--AT--G-GG-A--GG--A-A--C--GCA-A-G-C-C--C-G--TC-A-A-GG-C-TC--C--AAC-AG-G-G--GATT--T--C	8837	
A.IN.95.CRIK_147	G-GGAA--AT--G-GG-A--G--A--C--GCA--G-G-C-C--C--C--TC-A-A-GG-C-TC--C--AAC-A-A-GG--GACTT--GC	9115	
A.IN.x.NNVA	T-GC-AC-CAT--G-GG-A--GG-T-A-A-A-C-G-G--GCA--G-C-C--G-C-GAATCACC-GGGAG-TACGC-G-CCGCCCATGGAGGAATC-CCATCAA-G-AGAG-CC-AC-TTGG-AT-GGG-GCAG-	9359	
A.SN.85.ROD	T-GGAAC--ATC-G-GG-A--GG-T-A-A--C--G--AGCA-AA-G-C-C--C-G-G--TC-G--G-C-T--AGG--A-C--A-G-G--AATTG--GC	8806	
B.CI.88.UC1	--C-A--GACA-CGGA-GCA-CA-G--C--A--C--A--G-C--GC--ATGC--AGA-C--AG-G-G-GGG--C	9287	
B.CI.09.pPRD320-20HIV2_56	--C-A--ACG-CGG-GGCA-CA-GG--C--A--A--G-C-A--GC--AGGAC-A-AG-G-GG-GGG--C	9252	
B.CI.x.EHO	--C--CG-CG-GA-CA-T--A--C--GC--A--G-C--T--A--AG-CT--TTG-GA-C--AG-G-G-GG--C	9262	
B.GH.86.D205	--C--CG-CG--GCA-CA--G--A--C--A--C--A--ATGC--GG-GG-C--AG-G-G-GGG--C	9285	
B.JP.01.KR020	--C-A--ACA-CG--GGCA-CG-G--C--A-C-A--G-C--GC--TGCT--GA-C-AG-G-G-GGG--C	8393	
G.CI.92.ABT96	--GG-A-G-T--G--A-G-A-A-C-G--A-G-AC--CG--T-A-T--C--AAC-A--C--G--GY	8754	
AB.CI.90.7312A	--C--GACG-CG--GG-A-CA--G--A-A-C--G--A--A-G-C--C--A--CCGC--GA-C--AG-G-G-GGG--C	9291	
AB.CM.03.03CM_510_03	--C--G-G-CG-CG--GC--C--G--A-A-C--A--A--G-C--ATGC--TG-GG-C--AG-G-G-GGG--C	8376	
U.FR.96.12034	--GG-C-G-T--C-T-GA-T-A-A--C-G--AT--G-G-T--A-CT--GGCCAAGGC-T-G-G-A--G-TC--A-T--C--AAC-G-A--T--CA--T-AGC	8850	
MAC.US.x.17EC1		9326	
MAC.US.x.17EFR		9326	
MAC.US.x.1937	G	8434	
MAC.US.x.2065	R	8432	
MAC.US.x.251_1A11	C	9322	
MAC.US.x.251_32H_PJ5	T	9324	
MAC.US.x.251_BK28	C	9308	
MAC.US.x.80035		8432	
MAC.US.x.97074		8295	
MAC.US.x.MAC239_87082		8403	
MAC.US.x.MM142	CAA-G	8821	
MAC.US.x.SMM142B	CAA-G	8818	
MAC.US.x.r80025		8289	
MAC.US.x.r90131		8432	
MNE.US.82.MNE_8	GG-A-T	8800	
MNE.US.x.MNE027	GG-A-G-T	8803	
SMM.SL.92.SL92B	GG-AC-G-T	8777	
SMM.US.x.F236_H4	GG-A-G-T	9291	
SMM.US.x.H9	GG-A-G-T	8815	
SMM.US.x.PBJ14_15	GG-A-G-T	9118	
SMM.US.x.PBJA	GG-A-G-T	9117	
SMM.US.x.PBJ_143	GG-A-G-T	8830	
SMM.US.x.PBJ_6P6	GG-A-G-T	9310	
SMM.US.x.PGM53	GG-A-G-T	9263	
SMM.US.x.SME543	GG-A-G-T	9348	
STM.US.x.STM	G-A-G-T	8777	

[illegible]

[illegible]

MAC.US.x.239
NeF

A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PET2
A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CR1K 147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.89.pPRD320-20HIV2_56
B.CI.x.EH0
B.GH.86.D205
B.JP.81.KR020
B.CI.92.ABT96
AB.CI.90.7312A
AB.CM.03.03CM_510_03
U.FR.96.12034

MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.1937
MAC.US.x.2065
MAC.US.x.251_1A11
MAC.US.x.251_32H_PJ5
MAC.US.x.251_BK28
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239_87082
MAC.US.x.MN142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.82.MNE_8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236_H4
SMM.US.x.H9
SMM.US.x.PBJ14_15
SMM.US.x.PBJA
SMM.US.x.PBJ_143
SMM.US.x.PBJ_6P6
SMM.US.x.PGM53
SMM.US.x.SME543
STM.US.x.STM

TCF-1 alpha binding

GCATTATTTAATGCATCCAGCTCAAACCTCCAGTGGGAGACCTTGGGGAGAGGTTCTAGCATGGAAGTTTGATCCAACCTGGCCCTACACTTATGAGGCATATGTTAGATACCCAGAAGAGTTTGAAGCAAGTCAGGCCCTGCAGAGGAAGAGGTTAGAAGAAGGC 9818

H Y L M H P A Q T S Q W D D P W G E V L A W K F D P T L A Y T Y E A Y V R Y P E E F G S K S G L S E E E V R R R

CA-C-GC--C--A--AAG-AGA-AT--ATACAT--G--ACA--TG--CG--A-CT-C-TG--TGAG--CA--C-TCAC-CT--A--GCA--AT--C--A--TGG-AGGC--AA-9815
CA-C-GC--G-A-C--A--AAG-AGACAT--TGAGCAT--G--ACAT--TG--C--CT-C-TG--T-AC-CA--C-TCAC-CTG--A--GCA--AT--C--A--ATGG-AGGC--AA-9861
C-C-GC--C-A-C--A--AAG-GG-CT--CAT--G-AACAT--ATG--G--C-T-GG--TGAG--AC--T-T-AA-C--A--GTAT--C--A--TGG-AGGC--AA-9808
CA-C-C--CA-C--A--AAG-AGACAT--GAGCAT--AACA--CTT--CG--C--C-G--TGA--CA--T-TCA--CTGC-T--A--GCA--AT--C--A--TGG-AGGC--AA-9278
CA-C-GC--G-A-C--A--AAG-AGA-AT--GAGCAT--G--ACA--TT--CG--C--TG--T-G--CA--C-TCA--CTGC--A--GCA--AT--C--A--TGG-AGGC--AA-9375
T-TC-GC--CT--A--GTAA-AGA-TT--GCAT--G--ACA--TC--C--C-TG--TC-TGAG--CAC-A-C-T-A-CT--G-A--GCA--AA-GA--T--CTGG-AGGC--AA-9760
T-C-G--C-A-C--A--AAG-AG--TT--GCAT--G--AACA--GAT--C--C-G--TC-TGA--CA--T-T-A-CCTGC--G-A--GCAT--C--A--CTGG-AGGC--AA-9300
T-C-G--C-A-C--A--AAG-AG--TT--GCAT--G--AACA--GAT--C--C-G--TC-TGAG--CA--T-T-A-CCTG--G-A--GCAT--C--A--CTGG-AGGC--AA-9175
T-C-GC--T-A-C--A--AAG-AG-CAT--ATGCAT--G--ACA--G-TG--CT-C-TG--CTT-AG--C-T-AC-C--A--GCA--AT--C--A--TGG-AGGC--AA-9056
T-C-GC--GC-A-C--TA--AAG-AG-CAT--A-GCAT--G--ACAT--TT--GA--C-T-G--TC-TGA--CA-A-C-T-A-CT-C--G-A--GTA--C--A-T--TGG-AGGC--AA-9860
T-C-GC--GG--A--TAAG-A--TT--AGCAT--G--AACAT--TT--G--CT-CCTG--GAG--ACA--C-T-AACTG--G-A--GCA-C--AC--A-G--ATGG-AGGC--AA-9326
T-C-GC--C--A--AAGTA--TT--AGACAT--G--ACA--T--GA--C--AT-A--TGA--TA--C-TAGGCT-C--G-A--GCA--AC--A--TGG-AGGC--AA-9353
T-C-GC--G-A--AAG-A--TT--GCAT--G--ACA--TC--G--CTTG--T-T-G--C--T-T-A-C-G--G-A--GCA--C--TGG-AGGC--AA-9298
CAG-G-C-GG--C--A--G-TC--TTCA--ATCCAC--G--ACC--T--C--CG--C--CCTC--AC-TGAC--ATA--C-TCAAC--G--GTATC--AT-AC--A-G--TGA-AGGCT--AA-9773
CAG-G-C-GG--C--A--G-C--TTCA--CCAC--G--AACC--T-TG--C--CCTC--AC-TGAC--ATA--C-TCAAC-AG-T--GTATC--G-AC--A--TGG-AGGCT--AA-9738
C--G-C-GG--A--G-C--GCA--CCAC-A--ACC--T-TG--C--CTCCTC--A--TGAC--T--C-TCAAG--G-T--G--GTATC--AA-C--A--TGG-AGGCT--AA-9748
C--GCC--C--G--A--G-TC--TCA--ATCCAT--G--AC--TATC--C--CTCCTC--A--TGA--T--T-TCAA--G-TT--C--GTA-C--G-AC--G--TGG-AGGCT--AA-9777
CAG-G-C-G--C--A--GG-C--T-CA--GTCCAC--G--ACC--TATC--C--CTCCTC--A--TGAC--ATA--C-TCAA--G--TATC--TA-C--G-AC--A--TGG-AGGCT--AA-8879
T--GC--GG-A--A--AG--CA--GGA-ACC--A--GT-G--G--C--T--AT-A--TGAC--CAG--T-T-A-ATTGC-T-T-G--CA-GT-G--G-AC--A-C--TATGG-A-GAG-AA-9246
C--G-C-G--C--A--G-CG-GCA--T--CCAT--G--AC--T-TG--C--T-CCTC--A--TT-AG--C-TCAAC--G-T--GTATC--AT-AC--A-G--ATGG-AGGCT--AA-9780
C-C-GCC--C--A--G-C--TCA--TACCAT--G--AC--T-TG--C--CCTC--GC-TGA--T--C-TCAA--G-T--GTA-C-A--G--C--A--TGG-AGGCT--AA-8865
--TG--C-GG--G-T--A--G--CAG-TGCGA--G--AC--CCT--T--T-CT--A-T-GC--C--T-A--AG-G--G-T--T--AG--G--9342

9818
9818
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924
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9472

	Nef end	NF-κ-B-II	NF-κ-B-I	
MAC.US.x.239	TAACCGCAAGAGGCCTTCTTAACATGGCTGACAAGAAGGAACTCGCTGAACAGC.....	AGGGACTTTCCACAAGGG.GATGTTACG..GGGAGGTACTGGGAGGAGCGGTGCG 9927		
Nef	L T A R G L L N M A D K K E T R *			
A.CI.88.UC2	-G-AA-----GA-A-CAT-T-GT-AA..-T-AC-----CAA-CA-ACTTGGT-AAAGCAGGAAGTAGCTACTAAGAAAT.....A.....	GCTGAGACTGC-----G-----C---A-CAA-----G-AT-----T---G-9961		
A.DE.x.BEN	-G-AA-----GA-A-CAT-T-GT-AA..-T-AC-----CAA-CA-ACTTGGT-AAAGCAGGAAGTAGCTACTAAGAAAT.....A.....	GCTGAGACTGC-----G-----C---A-CAA-----G-AT-----T---G-10007		
A.DE.x.PE12	-G-AA-----GA-A-CATTT-GTTAA..-GAC-----CAG-TA-ATTTGGT-AGAACAGGAAGTAGAT.....	GATGAACTGC-----G-----C---A-CAG-----G-GT-----A---G-9943		
A.GH.x.GH1	-G-AA-----GA-A-CAT-T-GTTAA..-C-AC-----CAG-CA-ACTTGGT-AAAGCAGGAAGTAGCTACTGAGAACAGCTGAG.....	GCTGCAGCTGC-----G-----C---A-CAA-----G-AT-----T---G-9429		
A.GM.87.D194	-G-AA-----GA-A-CAT-T-GT-AA..-T-AC-----CAA-CA-ACTTGGT-AGGGCAGGAAGTAGCTACTAAGAAAC.....	GCTGAGACTGC-----G-----C---A-CAA-----G-AT-----T---G-9420		
A.GM.x.ISY	-G-AA-----GA-A-CATTT-GTTAA..-AC-----CAA-CA-ACTTGGT-AGGACAGGAAGTAGCTACTGAAAAA.....	GCTGAGACTGC-----G-----C---A-CAG-----G-AT-----T---G-9405		
A.GM.x.MCN13	-G-AA-----GA-A-CATTT-GTTAG..-GAC-----CAG-TA-ATTTGGC-AGGGCAGGAATAACTACTGAAAAAC.....	GCTGAGACTGC-----G-----C---A-CAG-----G-AT-----T---G-9444		
A.GM.x.MCR35	-G-AA-----GA-A-CATTT-GTTAG..-GAC-----CAG-TA-ATTTGGC-AGGGCAGGAATAACTACTGAAAAAC.....	GCTGAGACTGC-----G-----C---A-CAG-----G-AT-----T---G-9319		
A.GW.86.FG	-G-AA-----G-AA-A-CATTT-GTTAA..-AC-----CAG-TA-ACTTGGT-AGGGCAGGAAGTAGCTACTGAGAAAC.....	GCTGAGACTGC-----G-----C---A-CAG-A---G-AT-----T---G-9201		
A.GW.87.CAM2CG	-G-AA-----GA-A-CATTT-GTTAA..-GG-C-----CAA-CA-AC-TGGC-AGGGCAGGAAGTAGCTACTGAAAAAC.....	GCTGAGACTGC-----G-----C---AC-AG-----G-TAT-----T---G-10020		
A.GW.x.ALI	-G-AA-----GA-A-CATTT-GT-AA..-G-AC-----CAG-TGA-TTTGGT-AGGGCAGGAAGTAGCTACTGAAAAAC.....	GCTGAGACTGC-----G-----C---A-CAG-A---G-AT-----T---G-10003		
A.GW.x.MDS	-G-AA-----G-AA-A-CCITT-CTTAA..-G-GAC-----CAG-TA-ACTTGGT-AGGGCAGGAAGTAGCTACTGAAAAAC.....	GCTGAGACTGC-----G-----C---A-CAA-----G-AT-----T---G-9472		
A.IN.95.CR1K 147	-G-AA-----G-AA-A-CCITT-GCTAA..-G-GAC-----CAA-TA-ACTTGGT-AGAACAGGAAGTAGCTACTGAAAAAC.....	GTTGAGACTGC-----G-T-----C---A-CAG-----G-AT-----T---G-9499		
A.IN.x.NNVA	-AG-----G-A-A-CATTT-ATTAAAGG-GAC-----CAA-TA-ACTTGGT-AGGGCAGGAAGTAGCTATTGAAAAAC.....	GCTGAGACTGC-----G-----C---A-CAG-----G-AT-----T---G-9992		
A.SN.85.ROD	-G-AA-----AA-A-CATTT-GTTAA..-GAC-----CAG-TA-ACTTGGT-AGGGCAGGAAGTAGCTAACAGAAAC.....	GCTGAGACTGC-----G-----C---A-CAA-----G-AT-----T---G-9443		
B.CI.88.UC1	---AA-----GA-A-C-CAGACTAG.....C-A-G-----AGCATAAACAGGAACCTA.....GCTGACACTGCACAAGAGGGGAAA..CTAGCTGACACCGC.....	---A-A-A-C---A-A-T-----G-AT-----TT---T-9922		
B.CI.89.pPRD320-20HIV2 56	-G-AA-----AA-A-CC-CAGATTAG.....C-----AGCTTAAAGAGGAACCTA.....GCTGACAGTGCATAAACAGGAA..CTAGCTGACACTGC.....	---CA-A-A-A-A---A-AT-----T---G-9886		
B.CI.x.EH0	-G-GA-----AA-A-C-CAGA-TAG.....AC-----T-A-AGCACAAAGAGGAACCTA.....GCTAACACTGCATAGAGAGGAAGAACTAGCTGATACTGC.....	---G-----C-A-AGT-----G-AT-----A---GA-9897		
B.GH.86.D205	---AA-----GA-A-C-CAGATTAG.....C-A-G-----AGCATAAACAGGAACCTA.....GCTGACACTGCACAAGAGGGGAAA..CTAGCAGACACTGC.....	---A-A-C---A-A-T-----AG-AA-----G-TT---T-9926		
B.JP.81.KR020	---AA-----GA-A-C-CAGATTAG.....C-----T-A-AGCTTGAAGAGGAACCTA.....GCTGACAGTGCATAAGAAAGAA..CTAGCTGACACTGC.....	---GAG---CA-A-AA---A-AT-----T---G-9027		
G.CI.92.ABT96	---AACAG---A-G-C-TAGAATAA.....C-----A-AGAGGACAA.....GCTGACACAGC-----GT-T---C---A-AGG---AG-TACTAT-----GA-T---T-9356			
AB.CI.90.7312A	---AA-----A-A-C-CAGA-TAG.....AC-----G-----AGCATAAAGAGGAACCTA.....GCTGACGCTGCATAAGAAAGGAACTGGCTGACACTGC.....	---G-----C---A-AGT-----G-AT-----TT---G-9932		
AB.CM.03.03CM_510_03	---AA-----GA-A-C-CAGATTAG.....AC-A-G-----GA-AGCATAAACAGGAACCTA.....GCTGACACTGCACAAGAGGGGAAA..CTAGCTGACACTGC.....	---AG-A-C---A-A-T-----G-AT---A---G-TT---T-9014		
U.FR.96.12034	-----C-CAGTA-A-AA.....T-GCTGAC-GA-AGGAAACAA.....GCTGAGACAGC-----C-A-G-G-A-CA---AG-AA-----A-G-9456			
MAC.US.x.17EC1	-----R-----			9927
MAC.US.x.17EFR	-----R-----			9927
MAC.US.x.1937	-----R-----			9035
MAC.US.x.2065	-----R-----			9035
MAC.US.x.251 1A11	-----A-A-G-----			9033
MAC.US.x.251 32H PJ5	-----G-----G-----			9922
MAC.US.x.251 BK28	-----G-----G-T-----			9925
MAC.US.x.80035	-----G-----G-T-----			9897
MAC.US.x.97074	-----G-----G-----			9033
MAC.US.x.MAC239 87082	-----G-----G-----			8859
MAC.US.x.MN142	-----G-----G-----			9004
MAC.US.x.SMM142B	-----G-----G-----			9419
MAC.US.x.r80025	-----G-----G-----			9416
MAC.US.x.r90131	-----G-----G-----			8890
MNE.US.82.MNE 8	-----CT-A-A-----G-----A-G-----			9033
MNE.US.x.MNE027	-----CT-A-A-----G-----A-G-----			9401
SMM.SL.92.SL92B	-----GCT--C-A-----AAAACCGC--A-G-TGGCGGAT--G-AGGAAACAA.....GCTGAGACAGC-----GAG-----AAG--AG-AGT-----CG--G-GAA.CG-9385			9890
SMM.US.x.F236 H4	-----T-A-A-----A-AA-G-----			9411
SMM.US.x.H9	-----T-A-A-----A-AA-AGG-----			9736
SMM.US.x.PBJ14 15	-----T-A-A-----A-AA-A-G-----AGGGACTTTCCACAAGAGACAGC-----A-G-----T-----T-CT-9735			9448
SMM.US.x.PBJA	-----T-A-A-----A-AA-A-G-----AGGGACTTTCCACAAGAGACAGC-----G-----C-----T-CT-9428			9928
SMM.US.x.PBJ 143	-----T-A-A-----A-AA-A-G-----AGGGACTTTCCACAAGAGACAGC-----A-GA-----T-CT-9865			9963
SMM.US.x.PBJ 6P6	-----T-A-A-----A-AA-A-G-----AGGGACTTTCCACAAGAGACAGC-----A-G-----T-CT-9963			9581
SMM.US.x.PGM53	-----A-TA-A-----G-----AA-G-----AGGGACTTTCCACA.....C---C-T-----A---A-T---G-9581			
SMM.US.x.SME543	-----A-TA-A-----G-----AA-G-----AGGGACTTTCCACA.....C---C-T-----A---A-T---G-9581			
STM.US.x.STM	-----A-G-----AA-G-----AGGGACTTTCCACA.....C---C-T-----A---A-T---G-9581			

	TATA box	3' LTR U3 end	TAR element start	3' LTR repeat start	
MAC.US.x.239	GGAACGCCCA	CTTTCTTGATGTATAAATATCACTGCA	TTTCGCTCTGTA	TTCAAGTCGCTCTGCGGAGAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAG	CAGGTAGAGCCTGGGTGTTCCCTGCTAGACTCTCAC
A.CI.88.UC2	-----T-A-A-AC	-----G-AC-C-T-CC-A-----	-----T-C-----	-----C-----	-----C-----
A.DE.x.BEN	-----T-A-A-AC	-----G-AC-C-T-C-T-AT-----	-----C-----	-----A-----	-----G-----
A.DE.x.PET2	-----T-A-A-C	-----G-AC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----T-----
A.GH.x.GH1	-----T-A-A-AC	-----G-ACCT-T-C-TA-AT-----	-----C-----	-----A-----	-----T-----
A.GM.87.D194	-----T-A-AT-CTC	-----G-AC-C-T-C-T-AT-----	-----C-----	-----A-----	-----T-----
A.GM.x.IS7	-----T-A-A-TC	-----G-AC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----G-----
A.GM.x.MCR13	-----T-A-A-TC	-----G-AC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----G-----
A.GM.x.MCR35	-----T-A-A-TC	-----G-AC-C-T-GC-T-AT-A-C-----	-----C-----	-----A-----	-----G-TG-----
A.GW.86.FG	-----TT-A-A-TC	-----G-AC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----TG-----
A.GW.87.CAM2CG	-----T-A-A-C-TC	-----TCAC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----TG-----
A.GW.x.ALI	-----T-A-A-C-C	-----G-AC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----TG-----
A.GW.x.MDS	-----T-A-A-C-TC	-----G-AC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----TG-----
A.IN.95.CR1K 147	-----T-A-ATC-TC	-----G-AC-C-T-GCA-TGTAC-----	-----C-----	-----A-----	-----G-----
A.IN.x.NNVA	-----T-A-ATC-TC	-----G-AC-C-T-GC-T-AT-----	-----C-----	-----A-----	-----G-----
A.SN.85.R0D	-----T-A-AT-CTC	-----AC-C-TAGC-T-AT-C-G-----	-----C-----	-----A-----	-----TA-----
B.CI.88.UC1	-----T-AAA-CTC	-----G-AC-C-T-C-T-AT-----	-----C-----	-----A-----	-----TG-----
B.CI.09.pPRD320-20HIV2 56	-----T-AAAACTC	-----G-AC-C-T-CT-AT-----	-----AC-----	-----C-----	-----TG-----
B.CI.x.EH0	-----TCAAGACTC	-----G-AC-C-T-GT-AT-----	-----C-----	-----A-----	-----TG-----
B.GH.86.D205	-----T-AAA-CTC	-----G-AC-C-T-C-AT-----	-----C-----	-----A-----	-----TG-----
B.JP.01.KR020	-----T-AAACCTC	-----G-AC-C-T-CTA-AT-----	-----AC-----	-----C-----	-----TG-----
G.CI.92.ABT96	-----C-AAAA-CTC	-----AG-----	-----C-----	-----A-----	-----TG-----
AB.CI.90.7312A	-----T-AAGCTC	-----G-AC-C-T-C-T-AT-----	-----C-----	-----A-----	-----TG-----
AB.CM.03.03CM_510_03	-----T-AAA-CTC	-----G-AC-C-T-C-T-AT-----	-----AC-----	-----C-----	-----TG-----
U.FR.96.12034	-----T-AAATGATC	-----G-AC-C-T-C-T-AT-----	-----C-----	-----A-----	-----TA-----
MAC.US.x.17EC1	-----	-----	-----	-----	-----
MAC.US.x.17EFR	-----	-----	-----	-----	-----
MAC.US.x.1937	-----	-----	-----	-----	-----
MAC.US.x.2065	-----	-----	-----	-----	-----
MAC.US.x.251_1A11	-----A-----	-----T-A-G-----	-----	-----	-----
MAC.US.x.251_32H PJ5	-----A-----	-----	-----	-----	-----
MAC.US.x.251_BK28	-----A-----	-----	-----	-----	-----
MAC.US.x.80035	-----	-----	-----	-----	-----
MAC.US.x.97074	-----	-----	-----	-----	-----
MAC.US.x.MAC239 87082	-----A-----	-----	-----	-----	-----
MAC.US.x.MM142	-----A-----	-----	-----	-----	-----
MAC.US.x.SMM142B	-----A-----	-----	-----	-----	-----
MAC.US.x.r80025	-----	-----	-----	-----	-----
MAC.US.x.r90131	-----A-----	-----	-----	-----	-----
MNE.US.82.MNE 8	-----A-----	-----	-----	-----	-----
MNE.US.x.MNE027	-----A-----	-----	-----	-----	-----
SMM.SL.92.SL92B	-----A-CGC-----	-----T-AAACTC-TA-----	-----AC-C-TT-GC-----	-----A-----	-----C-----
SMM.US.x.F236_H4	-----	-----AT-CTC-----	-----CA-----	-----A-----	-----C-A-----
SMM.US.x.H9	-----	-----AT-CTC-----	-----CA-----	-----A-----	-----G-----
SMM.US.x.PBJ14 15	-----	-----G-AT-CTC-----	-----CA-----	-----A-----	-----G-----
SMM.US.x.PBJA	-----	-----G-AT-CTC-----	-----CA-----	-----A-----	-----G-----
SMM.US.x.PBJ 143	-----	-----AT-CTC-----	-----CA-----	-----A-----	-----G-----
SMM.US.x.PBJ 6P6	-----	-----G-AT-CTC-----	-----CA-----	-----A-----	-----G-----
SMM.US.x.PGH53	-----	-----AT-TC-----	-----CA-----	-----G-----	-----G-----
SMM.US.x.SME543	-----	-----AT-CTC-----	-----CA-----	-----G-----	-----G-----
STM.US.x.STM	-----T-T-A-TC-----	-----CA-C-T-A-A-----	-----A-----	-----A-----	-----A-----

TAR element end	Poly-A signal	3' LTR R repeat end	3' LTR U5 start	
GCAGAGTGACTCCACGCTTGCTTGCTTAAAG . CCCTCTTCAATAAAG . CTGCCATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTGGTCAACTCGGTACTCAATAA . TAAGAAGACCCTGGTCTGTAGGACCCTTTCTGCTTTGGGAAAC10257				
MAC.US.x.239				
A.CI.88.UC2				
A.DE.x.BEN				
A.DE.x.PE12				
A.GH.x.GH1				
A.GM.87.D194				
A.GM.x.ISY				
A.GM.x.MCN13				
A.GM.x.MCR35				
A.GW.86.FG				
A.GW.87.CAM2CG				
A.GW.x.ALI				
A.GW.x.MD5				
A.IN.95.CR1K 147				
A.IN.x.NNVA				
A.SN.85.R0D				
B.CI.88.UC1				
B.CI.09.pPRD320-20HIV2_56				
B.CI.x.EH0				
B.GH.86.D205				
B.JP.01.KR020				
G.CI.92.ABT96				
AB.CI.90.7312A				
AB.CM.03.03CM_510_03				
U.FR.96.12034				
MAC.US.x.17EC1				
MAC.US.x.17EFR				
MAC.US.x.1937				
MAC.US.x.2065				
MAC.US.x.251_1A11				
MAC.US.x.251_32H_PJ5				
MAC.US.x.251_BK28				
MAC.US.x.80035				
MAC.US.x.97074				
MAC.US.x.MAC239_87082				
MAC.US.x.MM142				
MAC.US.x.SMM142B				
MAC.US.x.r80025				
MAC.US.x.r90131				
MNE.US.82.MNE_8				
MNE.US.x.MNE027				
SMM.SL.92.SL92B				
SMM.US.x.F236_H4				
SMM.US.x.H9				
SMM.US.x.PBJ114_15				
SMM.US.x.PBJA				
SMM.US.x.PBJ_143				
SMM.US.x.PBJ_6P6				
SMM.US.x.PGM53				
SMM.US.x.SME543				
STM.US.x.STM				

MAC.US.x.239	C.GAAGCAGGAAATCCCTAGCA	10279
A.CI.88.UC2	-A- - -G- - - - -	10312
A.DE.x.BEN	-A-G- - - - -	10359
A.DE.x.PE12		10172
A.GH.x.GH1		9480
A.GM.87.D194		9472
A.GM.x.ISY		9636
A.GM.x.MCN13		9713
A.GM.x.MCR35		9588
A.GW.86.FG	-A-G- - - - -	9431
A.GW.87.CAM2CG	G. - -G- - - - -	10372
A.GW.x.ALI		10353
A.GW.x.MDS	-C- -G- - - - -T- -	9525
A.IN.95.CRIK_147	-A-G- -T- - - - -	9851
A.IN.x.NNVA		10336
A.SN.85.ROD		9671
B.CI.88.UC1	-A-G- - - - -	10271
B.CI.09.pPRD320-20HIV2_56	T. - -G- - - - -	10235
B.CI.x.EHO	-A-G- - - - -	10242
B.GH.86.D205	- - - -G- - - - -	10269
B.JP.01.KR020		9339
G.CI.92.ABT96		9599
AB.CI.90.7312A	-T- - - - -	10282
AB.CM.03.03CM_510_03		9089
U.FR.96.12034		9607
MAC.US.x.17EC1	- - - - -	10279
MAC.US.x.17EFR	- - - - -	10279
MAC.US.x.1937		9055
MAC.US.x.2065		9054
MAC.US.x.251_1A11		10274
MAC.US.x.251_32H_PJ5	- - - - -	10277
MAC.US.x.251_BK28	- - - - -	10249
MAC.US.x.80035		9054
MAC.US.x.97974		8859
MAC.US.x.MAC239_87082		9028
MAC.US.x.MM142		9646
MAC.US.x.SMM142B		9600
MAC.US.x.r80025		8910
MAC.US.x.r90131		9053
MNE.US.02.MNE_8		9628
MNE.US.x.MNE027		9664
SMM.SL_92.SL92B		9613
SMM.US.x.F236_H4	- - -G- - - - -	10241
SMM.US.x.H9		9638
SMM.US.x.PBJ14_15		9996
SMM.US.x.PBJ14		9996
SMM.US.x.PBJ_143		9675
SMM.US.x.PBJ_6P6		10246
SMM.US.x.PGM53		10184
SMM.US.x.SME543	- - -G- - - - -	10315
STM.US.x.STM		9899

IV

PLV Complete Genomes

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IV-1 Introduction

Complete genomes of HIV-1, HIV-2, and SIV sequences are represented in the alignment. For the selection, one of each of the major subtypes and a few CRFs of the HIV-1 M group were chosen, plus one N group, 2 O group, and one P group sequence. Most of the SIV-CPZs were included, and this year 3 SIV-gorilla sequences have been added. Three HIV-2 A group and 2 HIV-2 B group sequences were included along with the single genomes sequenced to date for HIV-2 G and HIV-2 U. For the rest of the SIVs, all complete genomes were included. The principle in deciding which sequences to include in this alignment was to provide a representative sampling of all primate lentiviruses which have had complete or nearly complete genomes sequenced. Many HIV-1, HIV-2, SIVsmm and SIV-mac genomes were not included, but they can be found in the HIV-1/SIVcpz and HIV-2/SIVsmm alignments. Also, many shorter sequences from PLVs are included in the PLV protein sequence alignments later in this compendium. This year we include two phylogenetic trees, built using PhyML on the *pol* and *env* gene regions. As discussed in the 2003¹ and 2005² Compendia, there is some evidence of recombination events and/or differential rates of evolution in the history of the primate lentiviruses such that phylogenies of different regions of the genomes are not completely congruent.

The alignment was based on the previous version published last year, produced by a hidden Markov model using HMMER and manual editing using the programs BioEdit and Se-Al. It is codon-aligned, meaning that the correct translation reading frame has been maintained as much as possible; in the case of overlapping frames, obviously one will not translate correctly. We have tried to “reset” the alignment so that each new gene starts in the first frame; this means some empty columns have been inserted. The HIV-2/SIVsmm *vpx* gene is postulated to be a duplication of the *vpr* gene and thus there may be two alter-

native alignments of this region of the genome, as there are for the duplicated stem-loops of the TAR element.

The annotation is based on known protein coding regions in HIV-1 and on annotations found in SIV sequence database entries. The protein cleavage sites that create Gag p17, Gag p24 and other mature peptides from the Gag and Gag-Pol precursor polyproteins have been experimentally determined for HIV-1 and at least one strain of HIV-2, but the study of analogous cleavages in SIV polyproteins have not been published. Two representative genomes have been translated: HIV-1 subtype B strain HXB2, and MAC239. The translations are provided as a visual aid for finding landmarks in the genomes.

¹<http://www.hiv.lanl.gov/content/sequence/HIV/COMPENDIUM/2003/7.pdf>

²<http://www.hiv.lanl.gov/content/sequence/HIV/COMPENDIUM/2005/7.pdf>

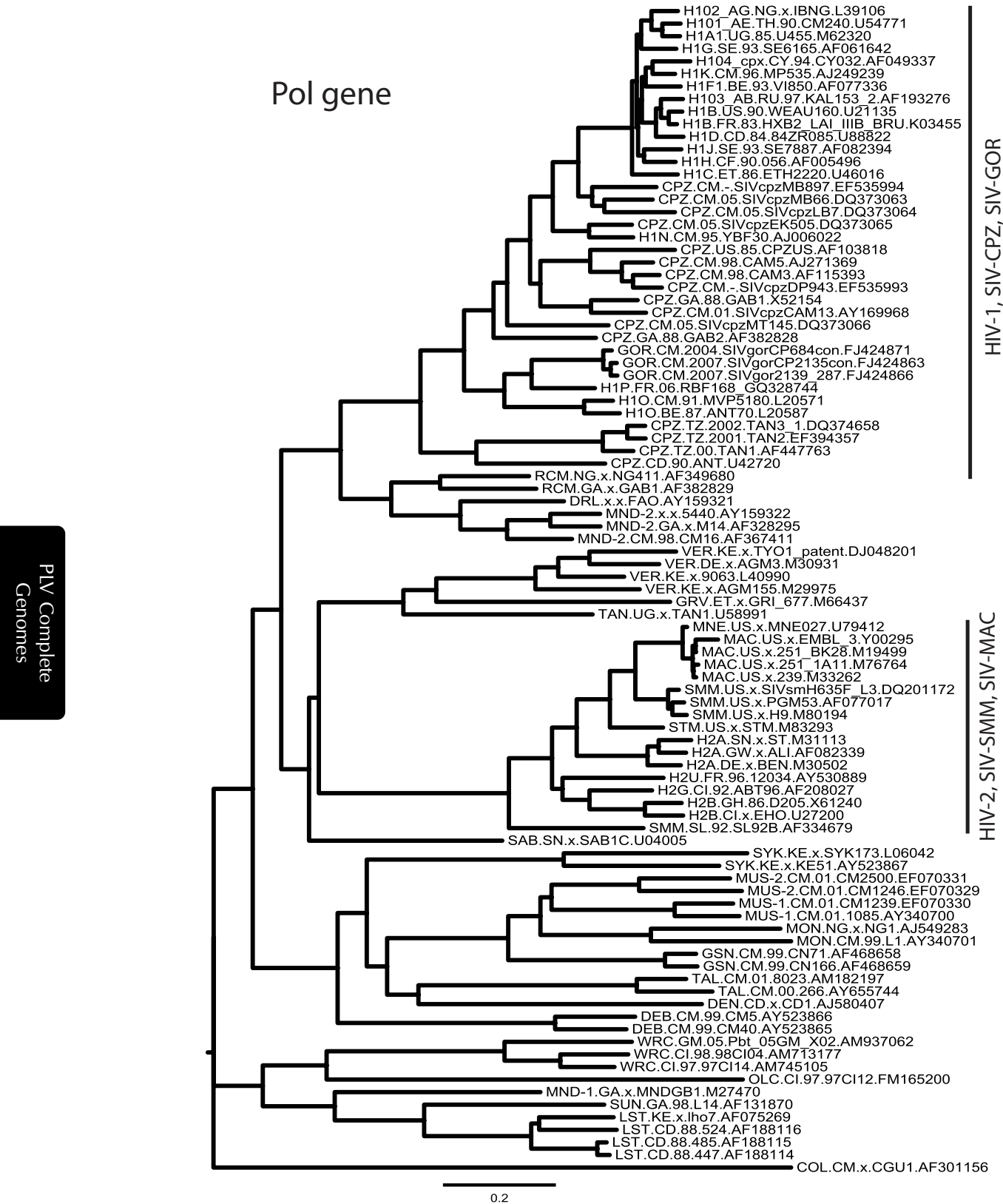


Figure IV.1: Genetic relationships among primate lentiviruses (PLVs), based on the *pol* gene. This tree shows the inferred phylogenetic relationships in the following PLV complete genome alignment, based on the *pol* gene, and using PhyML to calculate the tree.

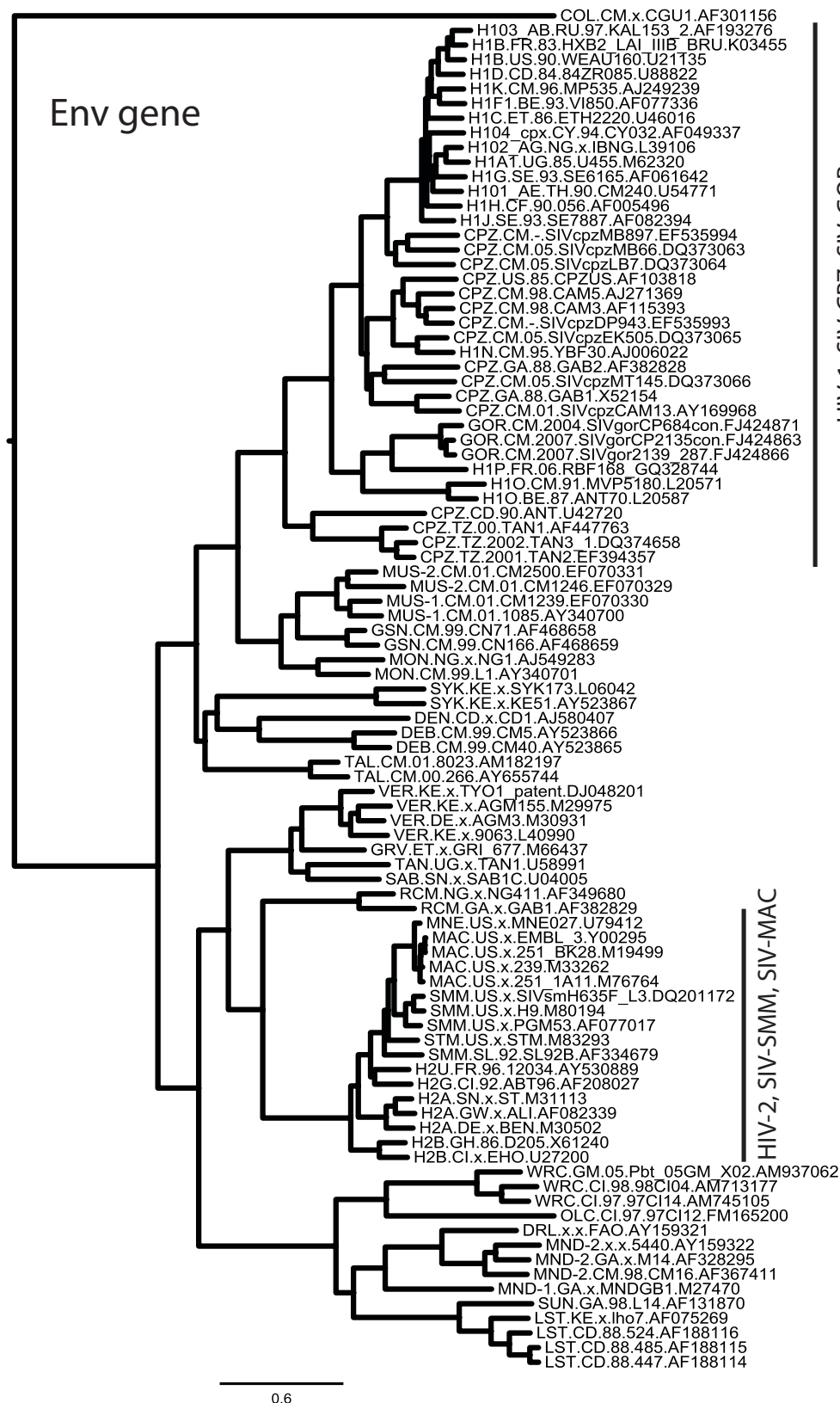


Figure IV.2: Genetic relationships among primate lentiviruses (PLVs), based on the *env* gene. This tree shows the inferred phylogenetic relationships in the following PLV complete genome alignment, based on the *env* gene, and using PhyML to calculate the tree. Note that the scale bar is different for *env* than for *pol*, reflecting the greater distances between *env* gene sequences than *pol* gene sequences.

IV-2 Sequences

Primate lentivirus (PLV) Sequences in the complete genome alignments.

Name	Accession	Country	Author	Reference
H1B.FR.83.HXB2	K03455	France	van Beveren, C.P.	(in) Weiss,RL, Teich,N, Varmus,H and Coffin,J(Eds); RNA TUMOR VIRUSES, SECOND EDITION, 2, Vol 2: 1102-1123; Cold Spring Harbor Laboratory, Cold Spring Harbor (1985)
H1A1.UG.85.U455	M62320	Uganda	Oram, J.D.	ARHR 6(9):1073-1078 (1990)
H1B.US.90.WEAU160	U21135	United States	Wei, X.	Nature 422(6929):307-312 (2003)
H1C.ET.86.ETH2220	U46016	Ethiopia	Salminen, M.O.	ARHR 12(14):1329-1339 (1996)
H1D.CD.84.84ZR085	U88822	D.R.C.	Gao, F.	J Virol 72(7):5680-5698 (1998)
H1F1.BE.93.VI850	AF077336	Belgium	Laukkanen, T.	Virology 269(1):95-104 (2000)
H1G.SE.93.SE6165	AF061642	Sweden	Carr, J.K.	Virology 247(1):22-31 (1998)
H1H.CF.90.056	AF005496	C.A.R.	Gao, F.	J Virol 72(7):5680-5698 (1998)
H1J.SE.93.SE7887	AF082394	Sweden	Laukkanen, T.	ARHR 15(3):293-297 (1999)
H1K.CM.96.MP535	AJ249239	Cameroon	Triques, K.	ARHR 16(2):139-151 (2000)
H101_AE.TH.90.CM240	U54771	Thailand	Carr, J.K.	J Virol 70(9):5935-5943 (1996)
H102_AG.NG.x.IBNG	L39106	Nigeria	Howard, T.M.	ARHR 10(12):1755-1757 (1994)
H103_AB.RU.97.KAL153_2	AF193276	Russia	Liitsola, K.	ARHR 16(11):1047-1053 (2000)
H104_cpx.CY.94.CY032	AF049337	Cyprus	Gao, F.	J Virol 72(12):10234-10241 (1998)
H1N.CM.95.YBF30	AJ006022	Cameroon	Simon, F.	Nat Med 4(9):1032-1037 (1998)
H1O.BE.87.ANT70	L20587	Belgium	Vanden Haesevelde, M.	J Virol 68(3):1586-1596 (1994)
H1O.CM.91.MVP5180	L20571	Cameroon	Gurtler, L.G.	J Virol 68(3):1581-1585 (1994)
H1P.FR.06.RBF168	GQ328744	France	Plantier, J.-C.	Nat Med 15(8): 871-2 (2009)
CPZ.CM.01.SIVcpzCAM13	AY169968	Cameroon	Nerrienet, E.	J Virol 79(2):1312-9 (2005)
CPZ.CM.05.SIVcpzEK505	DQ373065	Cameroon	Keele, B.F.	Science 313(5786):523-526 (2006)
CPZ.CM.05.SIVcpzLB7	DQ373064	Cameroon	Keele, B.F.	Science 313(5786):523-526 (2006)
CPZ.CM.05.SIVcpzMB66	DQ373063	Cameroon	Keele, B.F.	Science 313(5786):523-526 (2006)
CPZ.CM.05.SIVcpzMT145	DQ373066	Cameroon	Keele, B.F.	Science 313(5786):523-526 (2006)
CPZ.CM.-.SIVcpzMB897	EF535994	Cameroon	Heuverswyn, F.V.	Virology 368(1):155-171 (2007)
CPZ.CM.-.SIVcpzDP943	EF535993	Cameroon	Heuverswyn, F.V.	Virology 368(1):155-171 (2007)
CPZ.CM.98.CAM3	AF115393	Cameroon	Corbet, S.	J Virol 74(1):529-534 (2000)
CPZ.CM.98.CAM5	AJ271369	Cameroon	Muller-Trutwin, M.C.	J Med Primatol 29(3-4); 166-72 (2000)
CPZ.GA.88.GAB1	X52154	Gabon	Huet, T.	Nature 345(6273):356-359 (1990)
CPZ.GA.88.GAB2	AF382828	Gabon	Bibollet-Ruche, F.	ARHR 20(12):1377-1381 (2004)
CPZ.US.85.CPZUS	AF103818	United States	Gao, F.	Nature 397(6718):436-441 (1999)
CPZ.CD.90.ANT	U42720	D.R.C.	Vanden Haesevelde, M.M.	Virology 221(2):346-350 (1996)
CPZ.TZ.00.TAN1	AF447763	Tanzania	Santiago, M.L.	J Virol 77(3):2233-2242 (2003)
CPZ.TZ.2001.TAN2	EF394357	Tanzania	Takehisa, J.	J Virol 81(14):7463-7475 (2007)
CPZ.TZ.2002.TAN3_1	DQ374658	Tanzania	Takehisa, J.	J Virol 81(14):7463-7475 (2007)
GOR.CM.2007.SIVgor2139_287	FJ424866	Cameroon	Takehisa, J.	J Virol 83(4):1635-1648 (2009)
GOR.CM.2007.SIVgorCP2135con	FJ424863	Cameroon	Takehisa, J.	J Virol 83(4):1635-1648 (2009)
GOR.CM.2004.SIVgorCP684con	FJ424871	Cameroon	Takehisa, J.	J Virol 83(4):1635-1648 (2009)
H2A.DE.x.BEN	M30502	Germany	Kirchhoff, F.	Virology 177(1):305-311 (1990)
H2A.GW.x.ALI	AF082339	Guinea-Bissau	Azevedo-Pereira, J.M.	Unpublished
H2A.SN.x.ST	M31113	Senegal	Kumar, P.	J Virol 64(2):890-901 (1990)

Name	Accession	Country	Author	Reference
H2B.CI.x.EHO	U27200	Cote D'Ivoire	Rey-Cuille, M.A.	<i>Virology</i> 202 (1):471-476 (1994)
H2B.GH.86.D205	X61240	Ghana	Dietrich, U.	<i>Nature</i> 342 (6252):948-950 (1989)
H2G.CI.92.ABT96	AF208027	Cote D'Ivoire	Brennan, C.A.	<i>ARHR</i> 13 (5):401-404 (1997)
H2U.FR.96.12034	AY530889	France	Damond, F.	<i>ARHR</i> 20 (6):666-672 (2004)
SMM.SL.92.SL92B	AF334679	Sierra Leone	Chen, Z.	<i>J Virol</i> 70 (6):3617-3627 (1996)
SMM.US.x.H9	M80194	United States	Courgnaud, V.	<i>J Virol</i> 66 (1):414-419 (1992)
SMM.US.x.PGM53	AF077017	United States	Novembre, F.J.	<i>J Virol</i> 72 (11):8841-8851 (1998)
SMM.US.x.SIVsmH635F_L3	DQ201172	United States	Kuwata, T.	<i>J Virol</i> 80 (3):1463-75 (2006)
MAC.US.x.239	M33262	United States	Kestler, H.	<i>Science</i> 248 (4959):1109-1112 (1990)
MAC.US.x.251_1A11	M76764	United States	Marthas, M.L.	<i>J Med Primatol</i> 18 (3-4):311-9 (1989)
MAC.US.x.251_BK28	M19499	United States	Hirsch, V.	<i>Cell</i> 49 (3):307-319 (1987)
MAC.US.x.EMBL_3	Y00295	United States	Franchini, G.	<i>Nature</i> 328 (6130):539-543 (1987)
STM.US.x.STM	M83293	United States	Novembre, F.J.	<i>Virology</i> 186 (2):783-787 (1992)
MNE.US.x.MNE027	U79412	United States	Kimata, J.T.	<i>J Virol</i> 72 (1):245-256 (1998)
DEB.CM.99.CM40	AY523865	Cameroon	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)
DEB.CM.99.CM5	AY523866	Cameroon	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)
DEN.CD.x.CD1	AJ580407	D.R.C.	Dazza, M.C.	<i>J Virol</i> 79 (13):8560-8571 (2005)
LST.CD.88.447	AF188114	D.R.C.	Beer, B.E.	<i>J Virol</i> 74 (8):3892-3898 (2000)
LST.CD.88.485	AF188115	D.R.C.	Beer, B.E.	<i>J Virol</i> 74 (8):3892-3898 (2000)
LST.CD.88.524	AF188116	D.R.C.	Beer, B.E.	<i>J Virol</i> 74 (8):3892-3898 (2000)
LST.KE.x.lho7	AF075269	Kenya	Hirsch, V.M.	<i>J Virol</i> 73 (2):1036-1045 (1999)
SUN.GA.98.L14	AF131870	Gabon	Beer, B.E.	<i>J Virol</i> 73 (9):7734-7744 (1999)
MND-1.GA.x.MNDGB1	M27470	Gabon	Tsujimoto, H.	<i>Nature</i> 341 (6242):539-541 (1989)
OLC.CI.97.97CI12	FM165200	Cote D'Ivoire	Liegeois, F.	<i>J Virol</i> 83 (1):428-439 (2009)
WRC.CI.97.97CI14	AM745105	Cote D'Ivoire	Liegeois, F.	<i>J Virol</i> 83 (1):428-439 (2009)
WRC.CI.98.98CI04	AM713177	Cote D'Ivoire	Liegeois, F.	<i>J Virol</i> 83 (1):428-439 (2009)
WRC.GM.05.Pbt_05GM_X02	AM937062	Gambia	Locatelli, S.	<i>Virology</i> 376 (1):90-100 (2008)
MND-2.CM.98.CM16	AF367411	Cameroon	Takehisa, J.	<i>ARHR</i> 17 (12):1143-1154 (2001)
MND-2.GA.x.M14	AF328295	Gabon	Souquiere, S.	<i>J Virol</i> 75 (15):7086-7096 (2001)
MND-2.x.x.5440	AY159322		Hu, J.	<i>J Virol</i> 77 (8):4867-4880 (2003)
DRL.x.x.FAO	AY159321		Hu, J.	<i>J Virol</i> 77 (8):4867-4880 (2003)
MON.CM.99.L1	AY340701	Cameroon	Courgnaud, V.	<i>J Virol</i> 77 (23):12523-12534 (2003)
MON.NG.x.NG1	AJ549283	Nigeria	Barlow, K.L.	<i>J Virol</i> 77 (12):6879-6888 (2003)
GSN.CM.99.CN166	AF468659	Cameroon	Courgnaud, V.	<i>J Virol</i> 76 (16):8298-8309 (2002)
GSN.CM.99.CN71	AF468658	Cameroon	Courgnaud, V.	<i>J Virol</i> 76 (16):8298-8309 (2002)
TAL.CM.00.266	AY655744	Cameroon	Liegeois, F.	<i>Virology</i> 349 (1):55-65 (2006)
TAL.CM.01.8023	AM182197	Cameroon	Liegeois, F.	<i>Virology</i> 349 (1):55-65 (2006)
MUS-1.CM.01.1085	AY340700	Cameroon	Courgnaud, V.	<i>J Virol</i> 77 (23):12523-12534 (2003)
MUS-1.CM.01.CM1239	EF070330	Cameroon	Aghokeng, A.F.	<i>Virology</i> 360 (2):407-418 (2007)
MUS-2.CM.01.CM1246	EF070329	Cameroon	Aghokeng, A.F.	<i>Virology</i> 360 (2):407-418 (2007)
MUS-2.CM.01.CM2500	EF070331	Cameroon	Aghokeng, A.F.	<i>Virology</i> 360 (2):407-418 (2007)
SYK.KE.x.KE51	AY523867	Kenya	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)
SYK.KE.x.SYK173	L06042	Kenya	Hirsch, V.M.	<i>J Virol</i> 67 (3):1517-1528 (1993)
RCM.GA.x.GAB1	AF382829	Gabon	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)
RCM.NG.x.NG411	AF349680	Nigeria	Beer, B.E.	<i>J Virol</i> 75 (24):12014-12027 (2001)
GRV.ET.x.GRI_677	M66437	Ethiopia	Fomsgaard, A.	<i>Virology</i> 182 (1):397-402 (1991)

Name	Accession	Country	Author	Reference
SAB.SN.x.SAB1C	U04005	Senegal	Jin, M.J.	<i>EMBO J</i> 13 (12):2935-2947 (1994)
TAN.UG.x.TAN1	U58991	Uganda	Soares, M.A.	<i>Virology</i> 228 (2):394-399 (1997)
VER.DE.x.AGM3	M30931	Germany	Baier, M.	<i>Virology</i> 176 (1):216-221 (1990)
VER.KE.x.9063	L40990	Kenya	Hirsch, V.M.	<i>J Virol</i> 69 (2):955-967 (1995)
VER.KE.x.AGM155	M29975	Kenya	Johnson, P.R.	<i>J Virol</i> 64 (3):1086-1092 (1990)
VER.KE.x.TYO1_patent	DJ048201	Kenya	Omori, T.	Patent: WO 2007049749-A 13 03-MAY-2007; Dनावेक CORPORATION
COL.CM.x.CGU1	AF301156	Cameroon	Courgraud, V.	<i>J Virol</i> 75 (2):857-866 (2001)

H1B.FR.83.HXB2	5' LTR U3 start	163
H1A1.UG.85.U455	TGGAAGGGCTAATTCTACTCCCAACGAAGACATATCTTCTGATCTGGATCTACACACACAAAGCTACTTCCCTGATTAGCAGAACTACACACCA...GGGCCAGGG...ATCAGATATCCACTGACCTTTGGATGGTCTACAAGCTAGTACCACTTGAGCCAGA	0
H1B.US.90.WEAU160	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	163
H1C.ET.86.ETH2220	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1D.CD.84.84Z8085	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1F1.BE.93.VT89	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1G.SE.93.SE6165	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1H.CF.90.056	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1J.SE.93.SE7887	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1K.CM.96.MP535	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H101.AE.TH.90.CM240	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H102.AG.NG.x.IE6	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H103.AB.RU.97.KAL153_2	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H104.cpx.CY.94.CY032	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1N.CM.95.YBF30	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H10.BE.87.ANT76	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H10.CM.91.MP5180	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H1P.FR.06.RBF168	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.01.SIVcpzCAM13	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.05.SIVcpzEK505	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.05.SIVcpzLB7	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.05.SIVcpzMB66	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.05.SIVcpzMT145	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.-.SIVcpzMB897	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.-.SIVcpzDP943	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.98.CAM3	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CM.98.CAM5	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.GA.88.GAB1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.GA.88.GAB2	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.US.85.CPZUS	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.CD.90.ANT	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.TZ.00.TAN1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.TZ.2001.TAN2	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
CPZ.TZ.2002.TAN3_1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
GOR.CM.2007.SIVgor2139_287	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
GOR.CM.2007.SIVgorCP2135con	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
GOR.CM.2004.SIVgorCP684con	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H2A.DE.x.BEN	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H2A.GW.x.ALI	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H2A.SN.x.ST	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H2B.CI.x.EH0	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H2B.GH.86.D205	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H2G.CI.92.ABT96	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
H2U.FR.96.L2034	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
SMM.SL.92.SL92B	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
SMM.US.x.H9	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
SMM.US.x.PGM53	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
SMM.US.x.SIVsmH635F_L3	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MAC.US.x.239	5' LTR U3 start	158
MAC.US.x.251_1A11	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
MAC.US.x.251_BK28	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
MAC.US.x.EMBL_3	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
STM.US.x.STM	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	22
MNE.US.x.MNE027	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
DEB.CM.99.CM40	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
DEB.CM.99.CM5	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
DEN.CD.x.CD1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
LST.CD.88.447	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
LST.CD.88.485	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
LST.CD.88.524	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
LST.KE.x.lho7	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
SUN.GA.98.L14	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MND-1.GA.x.MNDGB1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	160
OLC.CI.97.97C112	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
WRC.CI.97.97C114	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	94
WRC.CI.98.98C104	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
WRC.GM.05.Pbt_05GM_X02	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
MND-2.CM.98.CM16	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MND-2.GA.x.M14	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MND-2.x.x.5440	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
DRL.x.x.FA0	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MON.CM.99.L1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MON.NG.x.NG1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
GSN.CM.99.CM166	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
GSN.CM.99.CN71	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
TAL.CM.00.266	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
TAL.CM.01.8023	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MUS-1.CM.01.1085	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MUS-1.CM.01.CM129	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MUS-2.CM.01.CM1246	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
MUS-2.CM.01.CM2500	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
SYK.KE.x.KE51	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
SYK.KE.x.SYK173	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
RCM.GA.x.GAB1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	55
RCM.NG.x.NG411	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
GRV.ET.x.GRI_677	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
SAB.SN.x.SAB1C	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
TAN.UG.x.TAN1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
VER.DE.x.AGM3	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0
VER.KE.x.9063	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
VER.KE.x.AGM155	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
VER.KE.x.TY01 patent	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	158
COL.CM.x.CG1	T.....AA.....G.....T.....G.....CT.....TG.....G.....A.....	0

FR.83.HXB2	GAAGTTAGAAGAA...	GCCACAAGAGGAGAGAACACAGCTGTTACACCTGTGAGC...	CTCAGTGAATGGATGACCCGGAGAGAGAAGTGTAGAGTGGAGTTTGACGCCCTAGCATTTTCATCACATGGCCCGAGAGCTGCATC	309
H1A1.UG.85.U455				0
H1B.US.90.WEAU160	---G---	---T-TG---	---A---	309
H1C.ET.86.ETH2220			---G---	0
H1D.CD.84.84ZRB85			---AT---	0
H1F1.DE.93.VT850			---A---	0
H1G.SE.93.SE6165			---AT---	0
H1H.CF.90.056			---A---	0
H1J.SE.93.SE7887			---AAA---	0
H1K.CM.96.MP535			---G-A---	0
H1O1.AE.TH.90.CM240				0
H1O2.AG.NG.x.IBNG				0
H1O3.AB.RU.97.KAL153_2				0
H1O4.cpx.CY.94.CY032				0
H1N.CM.95.YBF38	AG-GC-AG-	CTA-GAG-T-C-T-T- GGG-T-ATC-CC-G-T-A-CAT-T-	GCC- T-T-A-TA-AC-T-A- A-AC-GAT- A- T-ATCT- GCAACACC- TG-T-TATGATAACT-C-	310
H1O.BE.87.ANT170	AG-GC-GAG-	CTG-GT-T-C-AAT- AG-TG-T-TC-TC- T-A-CTT-T-	AAT- --GCT-G-TG-AC-CG-G-GA-AC-A-A-CA- T-ATCAT- GC-AAACA-T-A- TGC-AAA-C-	310
H1O.CM.91.MVP5180				0
H1P.FR.86.RBF168				0
CPZ.CM.01.SIVcpzCAM13				0
CPZ.CM.05.SIVcpzEK505				0
CPZ.CM.05.SIVcpzLB7				0
CPZ.CM.05.SIVcpzMB66				0
CPZ.CM.05.SIVcpzMT145				0
CPZ.CM.-SIVcpzMB897				0
CPZ.CM.-SIVcpzDP943				0
CPZ.CM.98.CAM3				0
CPZ.CM.98.CAM5				0
CPZ.GA.88.GAB1	-C-G- -C-	-TG- -T- -A-T-C- -G-T- CA-AT-TCAGCATGGGATGGAAG- AGGAC-	-A-G-C-G-T-C- C-C- -A-G-G-C-AAGA-T-T-A- -A-AA-	309
CPZ.GA.88.GAB2				0
CPZ.US.85.CPZUS	-G-AG- -GC GG-	-T- -C-A-TAC-C-G- -CA-T- CAGCATGGAATGGAAG- A-CAT-	G-C- -C-ATC- CA- CTGAA-G- TCGGAGA- GA-TAA-	309
CPZ.TZ.88.TAN1				0
CPZ.TZ.2001.TAN2				0
CPZ.TZ.2002.TAN3_1				0
GOR.CM.2007.SIVgor2139_287				0
GOR.CM.2007.SIVgorCP2135con				0
GOR.CM.2004.SIVgorCP684con	CTC-C-C- -G-	AG-GG-AT- GC-A-T- AG- A-CACAAACAAGCAGACATGATG- AGCAT-	G-G-GACA- T- CA- TC-ATG- G-C-A-A-CT- A- TTCACT- T-C-	303
H2A.DE.x.BEN	GTCCC-C-	GGG-GG-CACT- CTCAT-T-C-C- A-ACAACAAGCAGGATGATG- CACGCAT-	G-G-GACA- TT- A- CCTAAG- G-TCA-G-T- AA- TTTATT- A-C-	303
H2A.GW.x.ALI				0
H2A.SN.x.ST				0
H2B.ZI.91.EH0	-T-A- -C-	-AG-GG-C-AG- A-C-CATT-TC- -G-G-T- A-CACAGACTCTCCGATGGGATG- CCCCCAC-	GA- GACCC-T-TC- CA- TC-T- -G- A-G-CT-TG- TTCACGAC-TTC-	303
H2B.GH.86.D285	-CCAGC- -CGACC-	CGAG-GG-C-AG- A-C-CATT- C-AA-G- G-CACAGATCTCCTCATGGGATG- CATCCAT-	G-G-GACTC-TATC- CA- TTC-T- -G- A-G-T-TG- TTTCATAG-TT-	306
H2G.CI.92.ABT96				0
H2U.FR.96.12034				0
SMM.SL.92.SL92B				0
SMM.US.x.H0				0
SMM.US.x.PGM53	GTG-C-T-	TC-AG-AC- CACATTAT- AG-G-T- A-CTCAGATATCCCACTGGGATG- CCCTG-	G- G-TC-G-CA- A- TTCA-AAT- C-ACAGAT-TGA- TTTTATTAGA-C-	229
SMM.US.x.SIVsmH635F_L3	GTG-C- -T-	-C-GG- -AC- -CACCATT- C-G-G-T- A-CACAGACTCATCAGTGGGATG- CCCTG-	G- G-AC-G-CA- -A- TCCAGAT- G-T-A-AGCT-T-A- -ATTTATTAA-T-C-	303
MAC.US.x.239				0
MAC.US.x.251.1A11	GTGA-C- -T-G-	-AC-GG-G-AT- G-CGATTAT- AA-G-T- A-CTCAAACTTCCCACTGGGATG- CCCTTG-	G- G-TC-CA- -A- TCCAAC- G-C-ACAC-T-TGA- -ATAT-TTATAG-C-	303
MAC.US.x.251.1K28				0
MAC.US.x.251.1K28	GTGA-C- -T-G-	-AC-GG-G-AT- G-CGATTAT- AA-G-T- A-CTCAAACTTCCCACTGGGATG- CCCTTG-	G- G-TCC-CA- -A- TCCAAC- G-C-ACAC-T-TGA- -ATAT-CTAGAT-C-	303
MAC.US.x.EMBL_3				0
STM.US.x.STM				0
MNE.US.x.MNE827				22
DEB.CM.99.CM40				0
DEB.CM.99.CM5				0
DEN.CD.x.CD1				0
LST.CD.88.447				0
LST.CD.88.485				0
LST.CD.88.524				0
LST.KE.x.Uh07	TG-TGAGT-TA-	-ATCC-TC-AT- CACAAT- C-T-G-TT- AAGCAGCTGGGGGCTCTGGAAG- CCCCTG-	G- GAG-C-TATC- CAC-CA-TCCAATGT-G- T-GACTT-A	288
SUN.GA.98.L14	TG-TGA- -CAGG-	-ATCCT-TCATCCTTGTCAAGC-C-AC-G-TT- CAGCAGCAAGGGGTAAATGAAG- CCCTTG-	G- GAGAC-TATC- -CA- -TCC-ACT- G-C- T-TGATTT-A	288
MND.1.GA.x.MNDGB1				0
OLC.CI.97.97C112	CCA-GCCT-G-	A-CTTG-AT- GGGATGC- -G-T- A-TCAGACCCCTCAACCA-CTG-G-AGT-A-GG-	-C-GG-T- GTC-CA-TCCA-ATAG- A-TAC-E-	218
WRC.CI.98.98C184	TTTGT- -TGAGT-TCAGATAATACA-A-CAT-CTAT- -G-A-AGC- -T-A-CAT-TGCTGAG- CAGA-G-CCCTG-	G- CAGC-G-TC- -A- CCAAGTGGCC- TG-G-ATGAC-CTCTG- -A-GACCC-G-T- A- CCA-TA- -T-GACT- G-	TTGATTTTGT- -CAGGAAGA- TGTGACTTTTGTG-CAAGTAGA-	306
WRC.GM.05.PbT_05GM_X02				
MND-2.CM.98.CM16				0
MND-2.GA.x.M14				0
MND-2.x.x.5440				0
DRL.x.x.FA0				0
MON.CM.99.L1				0
MON.NG.x.NG1				0
GSN.CM.99.CN166				0
GSN.CM.99.CN71				0
TAL.CM.98.266				0
TAL.CM.01.8023				0
MUS-1.CM.01.1085				0
MUS-1.CM.01.CM1239				0
MUS-1.CM.01.CM1246				0
MUS-2.CM.01.CM2508				0
SYK.KE.x.KE51				0
SYK.KE.x.SYK173	-TAGAG-G-TGC-	TTGG-GT-T-AG- -T-ACT-C-CC-C-T-A-CCTCT- GGGACAGGGGA-TTC-A-CAT-	G-G-GAACCC-CAT- -AC-CA-CC-A- -G-C- T-TACA-CAG	179
RCM.GA.x.GAB1				0
RCM.NG.x.NG411	CT-CAT- G-G-	ACG- CT-T- GACA-T-TC- A-G-T- A-CACAGATGGGG- GAAG- CCTGAT-GAATAGATC-TG- -C-G-TC- A- CCGAAGT-G-G- T-GA-T-C-		29
SRV.ET.x.GRI_677	CT- -C-G-G-	T-G- -TA-T- -CA-T-C-C-G-T- -CTCAAGTGGCC- TATG-G-ATGAC-CTCTG- -A-GACCC-G-T- A- CCA-TA- -T-GACT- G-		285
SAB.SN.x.SAB1C	GTG-CCC-G-	T-G-GG-T-AG- GACA-T-T-C- -C- CCAAGATTGAA- TG-G-AA-CGACC-TGG- -A-GACCA-G-T- AA- A-TCCA-T- -TT-A-T-C-A		282
TAN.UG.x.TAN1				0
VER.DE.x.AGM3	-T-CAT- -G-	AG-G-CCT-T- GACATTAT- -GCG-T- A-CACAAATAAAA- GA-G-CCCCGAT-GCAT-AGTC-TG- GACC- G-TC- A- CCTATGT- -T-A-T-T-G		291
VER.KE.x.9863	CT-CAT- -G-	AG-G-GAT- A-GCATTAT- -A-CACACTGCAT- GAG- CCGCAT-G-ATAATC-TG- A-A-A-A- TCCAATG-G-T- -TT-A-T-C-G		291
VER.KE.x.AGM155	TTACAT- -G-	AC-A-C-T-T- A-GACATT- C-AG-C-T- A-C-CAGATGGGA- GAAG- CC-GAT-G-AT-AGCC-TG- -GA-C-G-T- -A- TCCTATGT-G- -ATA-A-T-CG		291
VER.KE.x.TY01 patent				0
COL.CM.x.CGU1				0

	TCF-1 alpha	
H1B.FR.83.HXB2	CGGAGTACTTCAAGAAC	TGCTGACA
H1A1.UG.85.U455		
H1B.US.90.WEAI160	T-AG	
H1C.ET.86.ETH2220		
H1D.CD.84.84ZR085		
H1F1.BE.93.VI850		
H1G.SE.93.SEB165		
H1H.F.90.056		
H1J.SE.93.SE7887		
H1K.CM.96.MP535		
H101.AE.TH.90.CM240		
H102.AG.NG.x.IBNG		
H103.AB.RU.97.KAL153_2		
H104.cpx.CY.94.CY032		
H1N.CM.95.YBF30		
H10.BE.87.ANT70	-A-CT-C-G	GA-A-A-ACTGCTG
H10.CM.91.MVP5180	-A-CT-CCC-G	A-TGACACTGC
H1P.FR.06.RBF168		
CPZ.CM.01.SIVcpzCAM13		
CPZ.CM.05.SIVcpzEK505		
CPZ.CM.05.SIVcpzLB7		
CPZ.CM.05.SIVcpzMB66		
CPZ.CM.05.SIVcpzMT1145		
CPZ.CM.SIVcpzMB897		
CPZ.CM.SIVcpzDP943		
CPZ.CM.98.CAM3		
CPZ.CM.98.CAM5	A-AG	T
CPZ.GA.88.GAB1		
CPZ.GA.88.GAB2		
CPZ.US.85.CP2US	-A-CG	TG
CPZ.CD.90.ANT		
CPZ.TZ.00.TAN1		
CPZ.TZ.2001.TAN2		
CPZ.TZ.2002.TAN3_1		
GOR.CM.2007.SIVgor2139_287		
GOR.CM.2007.SIVgorCP2135con		
GOR.CM.2004.SIVgorCP684con		
H2A.DE.x.BEN	-A-AG-G-TGG-C-AAG	TCAGGATGTCAGAGAAAGAA
H2A.GW.x.ALT	-A-G-A-TGG-T-AAG	TCAGGCTGCCAGAGATGAG
H2A.SN.x.ST		
H2B.CI.x.EH0	-A-G-G-TGG-T-CAG	TCAGGAATGCCAGAGAAAGAG
H2B.GH.86.D205	-A-AG-G-TGG-T-CAG	TCAGGCTACCCAGAGGAGAG
H2C.CI.92.ABT16		
H2U.FR.96.12034		
SMM.SL.92.SL92B		
SMM.US.x.H9	-A-AG-G-TGGT-GTAA	TCAGGCTTGTGAGGGAAGAG
SMM.US.x.PGM53	-A-AG-G-TGGT-GTAA	TCAGGCTTGTGAGGGAAGAG
SMM.US.x.SIVsmH635F_L3		
	TCF-1 alpha	
MAC.US.x.239	-A-AG-G-TGA-G-AAG	TCAGGCTGTGAGAGGAAGAG
MAC.US.x.251_1A11	-A-AG-G-TGA-G-AAG	TCAGGCTGTGAGAGGAAGAG
MAC.US.x.251_BK28	-A-AG-G-TGA-G-AAG	TCAGGCTGTGAGAGGAAGAG
MAC.US.x.EMBL_3		
STM.US.x.STM		
MNE.US.x.MNE027		
DEB.CM.99.CM40		
DEB.CM.99.CM5		
DEN.CD.x.CD1		
LST.CD.88.447		
LST.CD.88.485		
LST.CD.88.524		
LST.KE.x.L107	TA-CCCT-AAA	C-GCTGCGAAGATACAAATACT
SUN.GA.98.L14	G-CATACAG	C-CCTGAAGATTCAGCATGTT
MND-1.GA.x.MNDGB1		
OLC.CI.97.CI12	TTA	-AAGG-CATGTTGACATGTCATGATG
WRC.CI.97.CI14	TCCTTGGACATGCA	T-GCCACTGGGAAAGAGGCTATTGAG
WRC.CI.98.CI104	TCCTTGGACAT-TA	TAGCCCAAGGAGAAGATGTCTATTGAGACCCCTCCATAAGAGAAGCTGAAGCGGCACAAG
RCM.CM.99.Pbl.05GM_X02		
MND-2.CM.98.CM16		
MND-2.GA.x.M14		
MND-2.x.x.5440		
DRL.x.x.FAD		
MON.CM.99.L1		
MON.NG.x.NG1		
GSN.CM.99.CN166		
GSN.CM.99.CN71		
TAL.CM.00.266		
TAL.CM.01.8023		
MUS-1.CM.01.1085		
MUS-1.CM.01.CM1239		
MUS-2.CM.01.CM1246		
MUS-2.CM.01.CM2500		
SYK.KE.x.KE51	GCTG-G-GA-GGCGCG	TTGAGTGTAGAGAGACAAACA
SYK.KE.x.SYK173		
RCM.GA.x.GAB1		
RCM.NG.x.NG411		
GRV.ET.x.GRI77	GCCC	G-C-TGTTTAAGGACATGCACGAACAT
SAB.CM.SAB1C	TT-CT-GGAGGCT	C-CAGAGCAGGTGCCCTCAGCA
TAN.UG.x.TAN1	ACCC	G-C-G-TTTAAGGACATGCATGGTCTT
VER.DE.x.AGM3		
VER.KE.x.9063	ACCCAA	-AGAC-T-TTTTGAAGACATGCATGCAATA
VER.KE.x.AGM155	ACCCCA	-TCGGG-T-TTTTACATGCATGGGCTG
VER.KE.x.TY01 patent		
COL.CM.x.CGU1		

		NF-κ-B-II		NF-κ-B-I		Sp1-III		Sp1-II		Sp1-I		TATA Box	
	TCGAGCTTGTCT	ACA	AGGGACTTTCCG		CTGGGGACT	TTCCAG		GG.AGGCGTGG	CCTGGCGGGACTGGGGAGTGGCGA		GCCCT	CAGATCCTGCATAT	429
	T-T		A			G		A-T		A		G	429
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[illegible]

Extensive secondary structure		5' LTR U5 end		Lys tRNA primer binding site		
H1B.FR.83.HXB2	GACTCT..GGTAACTAGAGATCCCTCAGACCTTTT	AGTCA..GTGTGG..	AAAA..TCTCTAGCAG..	TGGCGCCCCGAACAGG..	ACCTGA..	657
H1A1.UG.85.U455	..AC..A..A..T..A..				..TC..	126
H1B.US.98.WAU160	..A..				..C..	657
H1C.ET.86.ETH220	..AGC..	..C..G..			..G..	171
H1D.CD.84.84Z8085					..T..	8
H1F1.BE.93.VI850					..T..	40
H1G.SE.93.SEB165				GGCTT..	..T..	4
H1H.CF.98.856					..T..	204
H1I.SE.93.SE7887					..A..TC..	185
H1K.CM.96.MP535	..AC..C..A..T..A..A..				..A..T..	0
H101.AE.TH.90.CM240	..AC..C..A..T..A..A..				..A..T..	204
H102.AG.NG.x.IBNG					..A..T..	185
H103.AB.RU.97.KAL153_2					..A..T..	0
H104.cpx.CY.94.CV032					..A..T..	21
H1N.CM.95.YBF30	A..C..GT..	A..C..AGAC..T..A..A..			..T..	687
H10.BE.87.ANT70	A..C..GT..	T..AC..AGAC..T..AAGCAG			..T..	659
H10.CM.91.MVP5180	A..C..GT..	T..AC..AGAC..T..AAGCAG			..GCG..	114
H1P.FR.06.RBF168	A..GT..	G..AC..CTAG..C..A..			..T..	198
CPZ.CM.01.SIVcpzCAM13	A..T..T..	T..AAAA..TAGCT..CAG..			..T..	198
CPZ.CM.05.SIVcpzEK505	A..T..T..	T..AAA..CTA..TGAATA..			..T..	202
CPZ.CM.05.SIVcpzLB7	A..T..T..	A..A..GT..GCTCGCG..G..			..T..	204
CPZ.CM.05.SIVcpzMB66	A..T..T..	TA..AC..GTAGCTCTGTG..GCC			..T..	201
CPZ.CM.05.SIVcpzMT145	A..T..T..	A..A..C..TATTGA..AGA..			..T..	201
CPZ.CM..SIVcpzMB897	A..T..T..	TAT..AAGT..TGTGG..			..T..	199
CPZ.CM..SIVcpzDP943	A..T..T..	A..AAA..TAAGTA..GT..			..T..	26
CPZ.CM.98.CAM3	A..T..T..	A..CA..T..AT..AA..A..			..GTG..	331
CPZ.GA.88.GAB1	C..T..T..	T..A..A..T..TA..CA..			..AGG..	676
CPZ.GA.88.GAB2					..T..	4
CPZ.US.85.CP205	A..T..T..	A..C..CT..A..AA..A..			..GGTG..	680
CPZ.CD.90.ANT					..T..	9
CPZ.TZ.00.TAN1	..C..CTGGGG..	T..TTTG..AGT..G..TAAGTA..	TTGTA..GTGGCTAAGTA..		..C..	206
CPZ.TZ.2001.TAN2	..TT..GCCCTGGGG..	TTTG..AGT..G..TAAGTA..			..C..	205
CPZ.TZ.2002.TAN3_1	T..GCCCTGGGG..	TTTG..AGT..G..TAAGTA..			..C..	205
GOR.CM.2007.SIVgorP2139_287	A..GT..	GTAATA..CTGA..CACA..			..T..	199
GOR.CM.2007.SIVgorCP2135conA	A..GT..	GTAAGA..CTGA..CAG..			..T..	198
GOR.CM.2004.SIVgorCP684conA	A..GT..	GTAAGA..CTGA..AGA..			..T..	118
H2A.DE.x.BEN	GTCAA..CTGGGTGTTTCATCTGAGT..AC..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..ATCCAAGGCAGG..	C..G..T..		..T..	880
H2A.GW.x.ALI	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	875
H2A.GW.x.ALI	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	326
H2A.GW.x.ALI	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	326
H2B.GH.86.D205	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	877
H2C.GI.92.ABT96	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	248
H2U.FR.96.L2034	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	373
SHM.SL.92.L92B	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	326
SHM.US.x.H9	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	326
SHM.US.x.PGM53	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	769
SHM.US.x.SIVsmH635F_L3	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	857
MAC.US.x.239	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	843
MAC.US.x.251.1A11	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	842
MAC.US.x.251.BK28	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	830
MAC.US.x.EMBL_3	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	326
STM.US.x.STM	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	507
MND2.US.CTMD227	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	263
DEB.CM.99.CM40	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	263
DEB.CM.99.CM5	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	248
DEN.CD.x.CD1	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	0
LST.CD.88.447	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	0
LST.CD.88.493	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	0
LST.CD.88.524	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	0
LST.KE.x.lho7	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	813
SUN.GA.98.L14	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	792
MND-1.GA.x.MNDGB1	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	295
OLC.CI.97.97CI11	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	584
WRC.CI.97.97CI14	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	822
WRC.CI.98.98CI04	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	825
WRC.GM.05.Pbt.05GM.X02	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	0
MND-2.CM.98.CM16	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	471
MND-2.GA.x.M14	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	393
MND-2.x.x.6440	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	22
DRL.x.x.FA0	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	243
MON.CM.99.L1	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	0
MON.NG.x.NG1	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	219
GSN.CM.99.CN166	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	230
GSN.CM.99.CN71	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	314
MON.CM.00.266	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	0
TAL.CM.01.8023	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	229
MUS-1.CM.01.1085	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	248
MUS-1.CM.01.CM1239	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	248
MUS-2.CM.01.CM1246	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	228
MUS-2.CM.01.CM2500	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	265
SYK.KE.x.KE51	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	624
SYK.KE.x.SYK173	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	22
RCM.GA.x.GAB1	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	710
RCM.NG.x.NG411	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	790
GRV.ET.x.GRI.677	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	728
SAB.SN.x.SAB1C	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	241
TAN.UG.x.TAN1	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	746
VER.DE.x.AGM3	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	745
VER.KE.x.9863	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	745
VER.KE.x.AGM155	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	745
VER.KE.x.TV01 patent	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	745
COL.CM.x.CGU1	GTCAA..CTGGGTGTTTCACCTG..AGTA..AAGACCTCTGGT..C..	TAGGACCTTTCTGCTTTGGGA..AACCAGGCAGG..	C..G..T..		..T..	285

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.....GTGA..GAGTGT	758
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H1C.ET.86.ETH2220
H1D.CD.84.84ZR085
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H1H.CF.90.056
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CPZ.CM.05.SIVcpzMT145
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CPZ.CM.-.SIVcpzDP943
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CPZ.CM.98.CAM5
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GOR.CM.2007.SIVgorCP2135con
GOR.CM.2004.SIVgorCP684con
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H2G.CI.92.ABT96
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SMM.SL.92.SL92B
SMM.US.x.H9
SMM.US.x.PGM53
SMM.US.x.SIVsmH635F_L3
MAC.US.x.239
MAC.US.x.251_1A11
MAC.US.x.251_BK28
MAC.US.x.EMBL_3
STM.US.x.STM
MNE.US.x.MNE027
DEB.CM.99.CM40
DEB.CM.99.CM5
DEN.CD.x.CD1
LST.CD.88.447
LST.CD.88.485
LST.CD.88.524
LST.KE.x.lho7
SUN.GA.98.L14
MND-1.GA.x.MNDGB1
OLC.CI.97.97CI12
WRC.CI.97.97CI14
WRC.CI.98.98CI04
WRC.GM.05.Pbt_05GM_X02
MND-2.CM.98.CM16
MND-2.GA.x.M14
MND-2.x.x.5440
DRL.x.x.FA0
MON.CM.99.L1
MON.NG.x.NG1
GSN.CM.99.CM166
GSN.CM.99.CM71
TAL.CM.00.266
TAL.CM.01.8023
MUS-1.CM.01.1085
MUS-1.CM.01.CM1239
MUS-2.CM.01.CM1246
MUS-2.CM.01.CM2500
SYK.KE.x.KE51
SYK.KE.x.SYK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GR1_677
SAB.SN.x.SAB1C
TAN.UG.x.TAN1
VER.DE.x.AGM3
VER.KE.x.9863
VER.KE.x.AGM155
VER.KE.x.TY01_patent
COL.CM.x.CGU1

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H1G.ET.84.R4Z0085
H1FL.BE.93.V1B50
H1G.SE.93.SE6165
H1H.CF.90.056
H1J.CF.93.SE7887
H1K.CM.96.MP35
H1L1.AE.93.TH.90.CM240
H102.AG.NG.x.IBNG
H103.AB.RU.97.KAL153 2
H104.CPX.CY.94.CY032
H1N1.CM.95.YBF30
H1N1.CM.87.AN170
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CPZ.CM.05.S1Vcpz2EK505
CPZ.CM.05.S1Vcpz2L87
CPZ.CM.05.S1Vcpz2MB66
CPZ.CM.05.S1Vcpz2MT145
CPZ.CM.-.S1Vcpz2MB987
CPZ.CM.-.S1Vcpz2P943
CPZ.CM.98.CAM5
CPZ.CM.98.CAM5
CPZ.GA.88.GAB1
CPZ.GA.88.GAB2
CPZ.US.85.CP2US
CPZ.CD.90.ANT
CPZ.TZ.00.TAN1
CPZ.TZ.2001.TAN2
CPZ.TZ.2002.TAN3 1
GOR.CM.2007.S1Vgor2139 287
GOR.CM.2007.S1VgorCP2135con
GOR.CM.2004.S1VgorCP684con
H2A.DE.x.BEN
H2A.GW.x.ALI
H2A.SN.x.ST
H2B.CI.x.EHO
H2B.GH.86.0205
H2G.CI.86.AB296
H2U.FL.96.12034
SHM.SL.92.S192B
SHM.US.x.H9
SHM.US.x.PGM53
SHM.US.x.S1VsmH635F_L3
MAC.US.x.239
Gao
MAC.US.x.251.1A11
MAC.US.x.251.BK28
MAC.US.x.EMBL 3
STM.US.x.STM
MNE.US.x.MNE027
DEB.CM.99.CM40
DEB.CM.99.CM52
DEN.CO.x.CD1
LST.CO.88.447
LST.CO.88.485
LST.CO.88.524
LST.KE.x.lh07
SUN.GA.98.L14
MND-1.GA.x.MNDG81
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VER.KE.x.TY01 patent
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[illegible]

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H1B. FR. 83. HXB2	CAAGGACCAAGGACCCCTTTAGAGACTATGTAGACCGGTTCTATAAACTCTAAGAGCGAGCAAGCTTCACAGGAGGTAAAAAATGGATGACAGAAACCTTGTGGTCGAAATGCGAACCAGATTGTAAAGACTATTTTAAAGCATTGGGACGACGGCTACTACT	1817
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CPZ.TZ.2002.TAN3.1	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1354
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GOR.CM.2004.SIVgorCP684con	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2126
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H2U.FR.96.12034	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1526
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SMM.US.x.H9	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2012
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MAC.US.x.251.IA11	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2082
MAC.US.x.251.BK28	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2071
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DEB.CM.99.CM5	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1587
DEN.CO.x.CD1	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1590
LST.CO.88.447	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	989
LST.CO.88.485	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	983
LST.CO.88.524	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	983
LST.KE.x.Lho7	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2073
SUN.GA.98.L14	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2060
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WRC.CI.97.97C114	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2018
WRC.CI.98.98C104	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2036
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MND.2.CM.98.CM16	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1773
MND.2.GA.x.M14	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1697
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DRL.x.x.FA0	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1327
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GSN.CM.99.CM166	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1494
GSN.CM.99.CN71	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1500
TAL.CM.00.266	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1705
MUS.1.CM.01.8023	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1203
MUS.1.CM.01.1085	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1465
MUS.1.CM.01.CM1239	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1467
MUS.2.CM.01.CM1246	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1548
MUS.2.CM.01.CM2500	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1510
SVK.KE.x.KE51	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1525
SVK.KE.x.SVK173	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1516
RCM.GA.x.GAB1	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1245
RCM.NG.x.NG411	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1245
GRV.ET.x.GRI.677	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1933
SAB.SN.x.SAB1C	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	2086
TAN.UG.x.TAN1	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1966
VER.DE.x.AG93	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1497
VER.KE.x.9063	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1996
VER.KE.x.AGM155	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1985
VER.KE.x.TY01_patent	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1993
COL.CM.x.CG01	---G---A---T---CT---T---A---A---A---T---C---T---G---A---G---G---T---	1604

[illegible]

[illegible]

H1B. FR. 83. HXB2	AGAGCAGACC.....AGAGCCAAACAGCCCAACAGAGAGCTTCAGGTCTGGGGTAGAGACAAC.....	2198
Gag	Q S R P E P T A P P E E S F R S G V E T T	
Pol	E Q T R A N S P T R R E L Q V W G R D N	
H1A1.UG.85.U455	T.....A.....TCA-A.....	1644
H1B.US.90.WEAU160	T.....A.....GAGTCT-AGACCAGAGCCAA-CCC-C-ACCAGA.....	2197
H1C.ET.86.ETH2120	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1575
H1D.CO.84.84Z6885	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1768
H1F1.BE.93.VI850	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1535
H1G.SE.93.SE6165	T.....A.....T-C-A-C-G-T-C-A-AG-T-G.....	1604
H1H.CF.90.056	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1548
H1J.SE.93.SE7887	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1515
H1K.CM.96.MP535	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1394
H101.AE.TH.90.CM240	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1757
H102.AG.NG.x.IBN6	T.....A.....T-G-ATG-A-T.....	1720
H103.AB.RU.97.KAL153.2	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1421
H104.cpx.CY.94.CY032	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1567
H1N.CM.95.YBF30	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1771
H10.BE.87.ANT70	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2232
H10.CM.91.MVP5180	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2207
H1P.FR.06.RBF168	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1641
CPZ.CM.01.SIVcpzCAM13	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1775
CPZ.CM.05.SIVcpzEK505	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1746
CPZ.CM.05.SIVcpzLB7	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1771
CPZ.CM.05.SIVcpzMB66	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1729
CPZ.CM.05.SIVcpzMT145	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1731
CPZ.CM.05.SIVcpzMB897	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1740
CPZ.CM.05.SIVcpzD943	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1760
CPZ.CM.98.CAM5	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1694
CPZ.CM.98.CAM5	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1906
CPZ.GA.88.GAB1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2262
CPZ.GA.88.GAB2	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1582
CPZ.US.85.CPZUS	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2264
CPZ.CO.90.ANT	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1657
CPZ.TZ.80.TAN1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1815
CPZ.TZ.2001.TAN2	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1877
CPZ.TZ.2002.TAN3.1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1877
GOR.CM.2007.SIVgor2139.287	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1729
GOR.CM.2007.SIVgorCP2135.con	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1738
GOR.CM.2004.SIVgorCP684.con	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1927
H2A.DE.x.BEN	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2548
H2A.GW.x.ALI	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2541
H2A.SN.x.ST	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1993
H2B.CI.x.HO	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2519
H2B.GH.86.D205	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2524
H2G.CI.92.ABT96	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1875
H2U.FR.96.12034	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2030
SMM.SL.92.SL92B	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1899
SMM.US.x.H9	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1938
SMM.US.x.PGM53	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2382
SMM.US.x.SIVsmH635F.L3	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2468
MAC.US.x.239	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2453
Pol	S S A S G L N D A N P P	
Gag	M A Q V L H P S	
MAC.US.x.251.1A11	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2452
MAC.US.x.251.BK28	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2441
MAC.US.x.EMBL.3	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1939
STM.US.x.STM	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2112
MNE.US.x.MNE027	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1933
DEB.CM.99.CM40	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1977
DEB.CM.99.CM5	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1971
DEN.CO.x.CD1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2032
LST.CO.88.447	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1422
LST.CO.88.485	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1422
LST.CO.98.524	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1419
LST.KE.x.lho7	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2503
SUN.GA.98.L14	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2508
MND-1.GA.x.MND61	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1841
OLC.CI.97.97C112	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2048
WRC.CI.97.97C114	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2481
TAL.CI.98.98C104	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1395
WRC.GM.05.Pbt.05GM.X02	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2167
MND-2.CM.98.CM16	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2091
MND-2.GA.x.M14	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1724
MND-2.x.x.5440	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1727
DL.x.x.FA0	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1853
MON.CM.99.L1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	459
MON.NG.x.NG1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1878
GSN.CM.99.CN166	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1878
GSN.CM.99.CN71	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1878
TAL.CM.00.20	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1624
TAL.CM.01.8023	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1891
MUS-1.CM.01.1085	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1881
MUS-1.CM.01.CM1239	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1983
MUS-2.CM.01.CM1246	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1994
MUS-2.CM.01.CM2500	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2336
SVK.KE.x.KE51	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1642
SVK.KE.x.SYK173	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2319
RCM.GA.x.GAB1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2347
RCM.NG.x.NG411	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1876
GRV.ET.x.GRI.677	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2381
SAB.SN.x.SAB1C	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	2378
TAN.UG.x.TAN1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	1964
VER.DE.x.AGM3	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	
VER.KE.x.9863	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	
VER.KE.x.AGM155	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	
VER.KE.x.TY01.patent	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	
COL.CM.x.CGU1	T.....A.....C-AGCT-CGG-T-TG-AGGAGATA-C.....	

HIB. FR. 83. HBX2
 Gag
 P01
 H1A1.UG.85.U455
 HIB.UG.90.WEAL160
 H1C.ET.86.ETH2220
 H1D.CD.84.84ZR085
 H1F1.BE.93.VI850
 H1F2.SE.93.SEG615
 H1F3.F.90.056
 H1F3.SE.93.SE7887
 H1K.CM.96.MP535
 H101.AE.TH.90.CM240
 H102.AG.NG.90.IBNG
 H103.AG.NG.97.RAL153.2
 H104.cpx.CY.94.CY032
 H1N.CM.95.YBF30
 H1O.BE.87.ANT70
 H1P.CM.91.MP5180
 H1S.FM.96.RBF168
 CPZ.CM.61.SIVcpzCAM13
 CPZ.CM.05.SIVcpzEK505
 CPZ.CM.95.SIVcpzL87
 CPZ.CM.95.SIVcpzE865
 CPZ.CM.95.SIVcpzMT145
 CPZ.CM.--.SIVcpzMB897
 CPZ.CM.--.SIVcpzDP943
 CPZ.CM.98.CAM3
 CPZ.CM.98.CAM5
 CPZ.GA.88.GAB1
 CPZ.GA.88.GAB2
 CPZ.US.85.CPZUS
 CPZ.CD.90.ANT
 CPZ.CD.97.T01.TAN1
 CPZ.TZ.2001.TAN2
 CPZ.TZ.2002.TAN3.1
 GOR.CM.2007.SIVgor2139.287
 GOR.CM.2007.SIVgorCP2135con
 GOR.CM.2007.SIVgorCP684con
 H2A.DE.X.BE1
 H2A.GN.X.ALI
 H2A.SN.X.ST
 H2B.CT.X.EH0
 H2B.HK.X.D285
 H2G.CT.X.A87B96
 H2U.FR.96.12034
 SHM.SL.92.SL2838
 SHM.US.X.H9
 SHM.US.X.PGM53
 SHM.US.X.SIVshH635F.L3

MAC.US.x.239
Pol
Gag
MAC.US.x.251.1A11
MAC.US.x.251.BK28
MAC.US.x.EMBL_3
STM.US.x.STM
MNE.US.x.MNE027
DEB.CM.99.CM40
CM.CM.99.CM5
DEN.CM.99.CM1
LST.CD.88.447
LST.CD.88.485
LST.CD.88.524
LST.KE.x.lho7
SND.GA.98.L4
MND.GA.x.MNDGB1
OLC.CI.97.97C112
WRC.CI.97.98C114
WRC.CI.98.98C104
WRC.GM.98.98GM_X02
MND.2.CM.98.CM16
MND.2.GA.x.M14
MND.2.x.x.5440
LRL.x.x.FAO
MON.CM.99.L1
MON.NG.x.NG1
GSN.CM.99.CM166
GSN.CM.99.CN71
TAL.CM.98.266
TAL.CM.81.803
MUS.1.CM.01.1085
MUS.1.CM.01.CM1239
MUS.2.CM.01.CM1246
MUS.2.CM.01.CM2500
SYK.KE.x.KE1
SYK.KE.x.SYK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GRI 677
TAN.UG.x.SABIC
TAN.UG.x.TANI
VER.DE.x.AGM3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.KE.TY patent
COL.M.x.CU1

[illegible][illegible]

H1B. FR.83. HXB2	TTAGATACAGGAGCAGATGATACAGTATTAGAAAGAAATGAGTTTG.....	CCAGGAAGATGGAAACCAAAAAATGATAGGGGGAATTGGAGGTTTATCAAAGTAAGACAGTATGATCAGATACCTATAGAAATCTGTGGACATAAAGCTATA.....	2468
Pol	L D T G A D D T V L E E M S L	P G R W K P K M I G G I G G F I K V R Q Y D Q I L I E I C G H K A I	
H1A1.UG.85.U455	C - A - A -	G - A -	1914
H1B.US.90.WEAU160	C - A -	A -	2467
H1C.ET.86.ETH2220	C - A - A -	A - T -	1860
H1D.CO.84.84Z8085	C - A - A -	A -	1990
H1F1.BE.93.VT859	C - A - A -	A -	1805
H1G.SE.93.SE6165	C - A - A - A -	A - A - AG - CT -	1865
H1H.CF.90.056	G - A - A -	G - AG - GC -	1815
H1J.SE.93.SE7887	C - AGAC -	A - CG - G - CG -	1782
H1K.CM.96.MP35	T - A - A -	A - AG - T -	1664
H101.AE.TH.90.CM240	T - A - A -	G - AG - A -	2042
H102.AG.NG.x.IBNG	C - A - A - A -	A -	1993
H103.AB.RU.97.KAL153.2	C - A - A -	A -	1694
H104.cpx.CY.94.CY032	C - A - A -	A - G -	1834
H1N.CM.95.YBF30	T - C - A - GC - ACA - A -	GAG - A - G -	2062
H1O.BE.87.ANT70	C - C - A - CA - C - ACA - A -	GA - A -	2523
H1O.CM.91.MVP5180	C - G - G - A - TA - C - ACA - A -	GA - C -	2498
H1P.FR.06.RBF168	T - C - G - TA - T - ACC - A -	GA - R -	1929
CPZ.CM.01.SIVcpzCAM13	C - G - T - C - A - C - C - TCAA - A -	AG - TT -	2048
CPZ.CM.05.SIVcpzEK505	T - A - ACAG -	GA - A -	2040
CPZ.CM.05.SIVcpzLB7	G - G - TT - AGAA -	GGG - G -	2023
CPZ.CM.05.SIVcpzMB66	G - G -	GG - T -	2014
CPZ.CM.05.SIVcpzMT145	C - C - G - T - C - A - T - CT - A - A -	GT -	2010
CPZ.CM. - SIVcpzMB897	C - G - C - G - AGAA - A -	GAG - A - GG -	2034
CPZ.CM. - SIVcpzDP943	C - C - T - GA - TA - TG - ACA - A -	A - A -	2054
CPZ.CM.98.CAM3	C - G - T - A - TA - TG - ACAAC - A -	A - A - G -	1879
CPZ.CM.98.CM5	C - G - T - C - A - TA - TG - ACA - A -	A - AG - G -	2170
CPZ.GA.88.GAB1	C - G - T - A - GAG - ACA - A -	A - CT -	2529
CPZ.GA.88.GAB2	C - G - T - TA - T - ACAAC - A -	GA - G - A - G -	1861
CPZ.US.85.CPZUS	C - T - C - CA - C - ACAAA - T -	GA - G - C - G -	2528
CPZ.CO.90.ANT	T - T - C - G - G - TCA -	A - AC - G -	1907
CPZ.TZ.00.TAN1	T - G - C - GT - T - TTGTA - C -	AAG - CAG -	2112
CPZ.TZ.2001.TAN1	T - G - C - GT - T - TTGTA - C -	AAG - CAG -	2117
CPZ.TZ.2002.TAN3.1	T - G - C - GT - T - TTGTA - C -	AAG - CAG -	2117
GOR.CM.2007.SIVgor2139.287	C - G - T - C - CT - ATC - A -	GA - T - G -	2005
GOR.CM.2007.SIVgorCP2135con	C - G - T - C - CT - ATC - A -	GA - T - G -	2004
GOR.CM.2004.SIVgorCP684con	C - G - T - C - CT - ATC - A -	GA - T - G -	1924
H2A.DE.x.BE1	C - C - G - T - CT - A - G - C - G - AGAG - A -	GGGA - C - AC - AT - CC -	2563
H2A.GW.x.ALI	C - C - G - T - CT - A - G - C - G - AGAG - A -	GGGA - C - AC - AT - CC -	2846
H2A.SN.x.ST	C - C - G - T - CT - A - G - C - G - AGAG - A -	GGGA - C - AC - AT - CC -	2298
H2B.CI.x.EH0	C - C - G - T - CT - A - G - C - G - AGAG - A -	GGGA - C - AC - AT - CC -	2824
H2B.GH.86.D205	C - C - G - T - CT - A - G - C - G - AGAG - A -	GGGA - C - AC - AT - CC -	2829
H2G.CI.92.ABT96	C - C - G - T - CT - A - G - C - G - AGAG - A -	GGGA - C - AC - AT - CC -	2180
H2U.FR.96.12034	C - GA - C - G - T - T - A - G - C - G - AGAG - A -	GGTC - G - AC - C -	2335
SMM.SL.92.SL928	C - G - C - G - C - CT - CA - G - C - G - AGAG - A -	GGTC - G - AC - C -	2201
SMM.US.x.H9	G - T - T - A - TG - C - G - AGAG -	GGTC - AT - AT - CC -	2243
SMM.US.x.PGM53	G - T - T - A - TG - G - C - G - AGAG -	GGTC - AT - AT - CC -	2687
SMM.US.x.SIVsmH635F.L3	G - T - T - A - TG - AC - G - AGAG -	GGTC - AT - AT - CC -	2773
MAC.US.x.239	C - G - G - T - T - TA - TG - AC - G - AGAG - A -	GGTC - CAT - AT - CC -	2770
Pol	L D T G A D D S I V T G I E	L G C P H Y T P K I V G G I G G F I N T K E Y K N V E I I E V L G K R I	
MAC.US.x.251.IA11	C - G - G - T - T - TA - TG - AC - G - AGAG - A -	GGTC - CAT - AT - CC -	2769
MAC.US.x.251.BK28	C - G - G - T - T - TA - TG - AC - G - AGAG - A -	GGTC - CAT - AT - CC -	2766
MAC.US.x.EMBL.3	C - G - G - T - T - TA - TG - AC - G - AGAG - A -	GGTC - CAT - AT - CC -	2244
STM.US.x.STM	C - G - G - T - T - TA - TG - AC - G - AGAG - A -	GGTC - CAT - AT - CC -	2417
MNE.US.x.MNE027	C - G - G - T - T - TA - TG - AC - G - AGAG - A -	GGTC - CAT - AT - CC -	2238
DEB.CM.99.CM40	A - C - T - G - TA - C - TTC -	GAATTAAG - C - CCT -	2283
DEB.CM.99.CM5	A - C - T - G - TA - C - TTC -	GAATTAAG - C - CCT -	2277
DEN.CO.x.CD1	A - C - T - G - TA - C - TTC -	GAATTAAG - C - CCT -	2349
LST.CO.88.447	C - T - C - T - G - TA - C - TTC -	GAATTAAG - C - CCT -	1730
LST.CO.88.485	C - T - C - T - G - TA - C - TTC -	GAATTAAG - C - CCT -	1730
LST.CO.88.524	C - T - C - T - G - TA - C - TTC -	GAATTAAG - C - CCT -	1727
LST.KE.x.lh07	C - T - C - T - G - TA - C - TTC -	GAATTAAG - C - CCT -	2814
SUN.GA.98.L14	C - G - C - G - T - C - A - G - GTCT -	GAATTAAG - C - CCT -	2819
MND.1.GA.x.MNDGB1	C - C - G - T - C - A - C - TA - T - GA - A - A -	AAATTAAG - AT - C - G -	2149
OLC.CI.97.97C112	C - G - C - T - C - A - TA - G - GG - A - GA - C -	TACATGGA - T - ATG - T -	2336
WRC.CI.97.97C114	C - G - C - T - C - A - TA - G - GG - A - GA - C -	TACATGGA - T - ATG - T -	2762
WRC.CI.98.98C104	C - G - C - T - C - A - TA - G - GG - A - GA - C -	TACATGGA - T - ATG - T -	2777
WRC.CM.05.Pb1.05GM.X02	C - G - C - T - C - A - TA - G - GG - A - GA - C -	TACATGGA - T - ATG - T -	1691
MND.2.CM.98.CM16	C - G - C - T - C - A - TA - G - GG - A - GA - C -	TACATGGA - T - ATG - T -	2469
MND.2.GA.x.M14	C - G - C - T - C - A - TA - G - GG - A - GA - C -	TACATGGA - T - ATG - T -	2396
MND.2.x.x.5440	C - G - C - T - C - A - TA - G - GG - A - GA - C -	TACATGGA - T - ATG - T -	2029
DRL.x.x.FA0	C - C - T - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2035
MON.CM.99.I1	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	761
MON.NG.x.NG1	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2178
GSN.CM.99.CN166	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2178
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TAL.CM.00.266	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	1937
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MUS.2.CM.01.CM1246	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2250
MUS.2.CM.01.CM2500	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2215
SVK.KE.x.KE51	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2319
SVK.KE.x.SVK173	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2664
RCM.GA.x.GAB1	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	1947
RCM.NG.x.NG411	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	1962
GRV.ET.x.GRI.677	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2635
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TAN.UG.x.TAN1	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2664
VER.DE.x.AG95	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2187
VER.KE.x.9063	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2692
VER.KE.x.AGM155	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2684
VER.KE.x.TY01.patent	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2689
COL.CM.x.CG01	C - G - C - G - R - G - C - C - A - TC - G - T - GAA - A -	A - AT - G - C - G - T -	2243

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164	SMH.US.x.x.PGM53	 T - A - GATGAATCTATTGGA - GTACA -	5314
165	SMH.US.x.x.SIVsmH635F_L3	 T - A - GATAA - ACTCATTTGGA - GTACA -	5600
166	MAC.US.x.239	 P L C A GA - GGAAGCCATT - GA - GTACAA -	5597
167	MAC.US.x.251.1A11	 C - CA - GA - GGAAGCCATT - GA - GTACAA -	5596
168	MAC.US.x.251.BK28	 C - CA - GA - GGAAGCCATT - GA - GTACAA -	5573
169	MAC.US.x.EMBL.3	 C - CA - GA - GGAAGCCATT - GA - GTACAA -	5065
170	STM.US.x.STM	 CT - GCAA - G - GAA - C - CACT - GA - GT - CAA -	5244
171	DEB.CM.99.CM027	 C - GAA - GA - GGAAGCCATT - GA - GTACAA -	5066
172	DEB.CM.99.CM45	 C - CACA - A - GAA - GGGG - GT - GTGAAATTA -	5104
173	DEB.CM.99.CM5	 CG - CACA - GA - GAA - G - A - GT - GTGAAATTA -	5098
174	LEN.CD.x.CD1	 GA - A - GC - CTTC - TGGA - GTAAA -	5206
175	DST.CD.88.447	 TT - A - ACA - G - CTTT - GT - GTGA - AT -	4563
176	DST.CD.88.485	 TT - A - A - A - C - CACT - GA - GT - CAA -	4563
177	LST.CD.88.524	 T - AT - ACA - G - CTTT - GT - GTGA - AAT -	4560
178	LST.KE.x.lho7	 T - A - CA - G - CTTT - GT - GTCA - AATATGCAATTTG -	5647
179	SUN.GA.98.L14	 G - ACT - AT - GG - C - GT - GTAA -	5697
180	MND-1.GA.x.MNDGB1	 AGGGAC - A - G - TT - T - GT - A - AA -	4997
181	OLC.CI.97.97CI12	 G - CCA - G - GTGAG - T - GA - AT -	5151
182	WRC.CI.97.97CI12	 G - CCA - G - CACTGAG - TGCA - AT - A -	5189
183	WRC.CI.98.98CI04	 CT - CAA - G - CACTTGGGA - TT - CA - ATCA -	5604
184	WRC.GM.05.Pbt.05GM.X02	 T - TCAA - G - CACTTGGGA - TGCAGATAA -	4521
185	MND-2.CM.98.CM16	 C - - AA - GA - GAT - A - CAG - TC - T - ATCCATC -	5296
186	MND-2.GA.x.M14	 CT - CAAA - GAAAGTC - AG - TT - TTAT - CC -	5223
187	DRL.x.x.5448	 CT - CAA - ATGTTG - TC - AA - TT - TTATC -	4859
188	MON.CM.99.L1	 CT - CAAA - GACAAAGT - A - T - GT - GTAACA -	4805
189	MON.NG.x.NG1	 CT - ACCTAGGAATCA - CAA - GAA - G -	5087
190	GSN.CM.99.CN166	 G - A - G - ATG - G - ATC - CAA -	3680
191	TAL.CM.99.266	 G - A - G - ATG - G - ATC - CAA -	5098
192	TAL.CM.01.8023	 C - AAGAAAAA - GAA - G - A -	5276
193	MUS-1.CM.01.1885	 T - GACACAA - A - A - C -	4774
194	MUS-1.CM.01.CM1239	 G - T - GACACAA - A - C - TT -	5047
195	MUS-2.CM.01.CM1246	 G - T - GACACAA - A - C - TT -	5047
196	MUS-2.CM.01.CM12508	 CT - GACAA - A - GAA - G - A -	5108
197	SYK.KE.x.KE51	 CT - GACAA - A - GAA - G - A -	5141
198	SYK.KE.x.KE5173	 CT - GACAA - A - GAA - G - A -	5489
199	RCM.GA.x.GAB1	 CT - GACAA - A - GAA - G - A -	4783
200	RCM.NG.x.NG411	 CT - GACAA - A - GAA - G - A -	4795
201	RCM.NG.x.GR1.677	 CT - GACAA - A - GAA - G - A -	5468
202	SAB.SN.x.SAB1C	 CT - GACAA - A - GAA - G - A -	5693
203	TAN.UG.x.TAN1	 CT - GACAA - A - GAA - G - A -	5494
204	VER.DE.x.AGM3	 CT - GACAA - A - GAA - G - A -	5017
205	VER.KE.x.9063	 CT - GACAA - A - GAA - G - A -	5514
206	VER.KE.x.AGM155	 CT - GACAA - A - GAA - G - A -	5514
207	VER.KE.x.TY01.patent	 CT - GACAA - A - GAA - G - A -	5519
208	COL.CM.x.CGU1	 TT - GGGTCA - GCTA - T - AGTT -	5032

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SMM.US.x.PGM53	AT-TCAGAT	5877
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H Q N.....S Q T H Q A S L S K Q
T R T.....V R L I K L L Y Q S
C A.....GGC A GA.....A CT A C S
C A.....AAC.....A.....
C A.....AGC A GA.....AA CT A
C A.....AGC.....A C A C
C A.....AGC AGTG.....AA C C
C A.....AGC A AGGC.....A C G C
C GCA.....AGTTTG AGA.....AA A C
C CT.....GGC A.....A CT A C
C T C.....AGC G AC.....A C CG
C.....AGC A GA.....AA C A C
C.....AGCC GA.....AA C G C
C A.....GAC A G.....T C
T A.....GGC CA GGC.....AA CT A C
C.....AGC A G.....A CT A C G
.....AGC CA CAGA.....A C G C G
GCAAGC.....TA CAGA A A.....A C G C G
G A C.....AAC A.....A C G C T
TT GCA G.....A A A A.....A C G CG
C G.....A A G.....A C C
TC A G.....C CA T.....A C A C
TC G G.....A.....A C G C
TCGAGC T.....CAGG T A.....A G A C CG
G GAGC GT.....AGG TCA.....AG TA ATA C AAGC
C GCT CA.....AGT AC CA A.....A C T CG C
TC GCTGCA.....AGC AC CA A.....A A CG C
T GCTTCA.....AGC AC CA A.....A A CG C
GC CTGAGGC.....A A A A.....A A C
T A GG.....A A GCA.....A C CG C
AC GCT GAGC.....GC GA A.....A C CGC
ACAACCTGTAAG.....AGC G A A.....A C G C T
C GT.....AC A A.....A C G CG C
A CA T G.....A A TCAAG CT TACGA AGCA
G CA T G.....A A TCAAG CT TACGA AGCA
GC G C A.....GA A A.....G C G
GC G A.....GA A A.....G C G
GC G C A.....GA A A.....G C G
A.....C A.....C TGC GC C G CA
A A.....T A G.....TCGT GC G CA
A A.....C A G.....TCGT GC G CA
A G.....AC AC T GC C CG
A G.....AC GC A GC G CA
AC A.....G A TC TT GC CG
A G.....G T TC T G C CA
A G.....G A C TT GA AC C
A G.....G A AC TT GC G CA
A G.....GC A G.....A C C C CA
A G.....A G.....A C C C CA

MAC.US.x.239
Tat exon 1
Rev exon 1
MAC.US.x.251.1A11
MAC.US.x.251.BK28
MAC.US.x.EMBL.3
STM.US.x.STM
MNE.US.x.MNE027
DEB.CM.99.CM40
DEB.CM.99.CM5
DEN.CD.x.CD1
LST.CD.88.447
LST.CD.88.485
LST.CD.88.524
LST.KE.x.lho7
SUN.GA.98.L14
MND-1.GA.x.MNDGB1
OLC.CI.97.97C112
WRC.CI.97.97C114
WRC.CI.98.98C104
WRC.GM.05.Pbt.05GM.X02
MND-2.CM.98.CM16
MND-2.GA.x.M14
MND-2.x.x.1440
DRL.x.x.FA0
MON.CM.99.L1
MON.NG.x.NG1
GSN.CM.99.CM166
GSN.CM.99.CM71
TAL.CM.01.8023
TAL.CM.01.8023
MUS-1.CM.01.1085
MUS-1.CM.01.CM1239
MUS-2.CM.01.CM1246
MUS-2.CM.01.CM2500
SYK.KE.x.KE51
SYK.KE.x.SYK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GRI.677
SAB.SN.x.SAB1C
TAN.UG.x.TAN1
VER.DE.x.AGM3
VER.KE.x.9863
VER.KE.x.AGM155
VER.KE.x.TY01.patent
COL.CM.x.CGU1

Tat Rev exon 1 end
Tat Rev intron start
A G.....GC A G A AC T GC CA
K.....A K N T S A S N K
R.....L R L I H L L H Q
A G.....GC A G A AC T GC CA
A G.....GC A G A AC T GC CA
A G.....GC A G A AC T GC CA
A G.....GT A G A AC T GC CA
G AT C CGCCAGCTGCTGAAAGT A C G G A T G C G
AGCTTTGCT.....GCGAATGA A G A G T A C G
CAAAGCG AC C G AAG G
GTATTT.....GAAG A GCAAGA CTGTGG CGG
GTATTT.....GAAG A GCAAGA CTGTGG CGG
ATA TT.....GAAG G GAGGA CTGTGG CAG
ATA TT.....GAGAC GCAGGA CTGTGG CAG
TC.....AGG A GCAAGAGGCTGT CGAAG
A GA.....TA CTGG AG GGT AAGAAGCTAT CGAAG
GC GTT T ATTGTACGTTTGTCTT TGC GAAGGGCTTGGTATCTCTT TT TACA AGTCACCTAGGAAGAGGAGAAAGAGGTGGTA
ACAACA.....GCTG TTCAAG
GCAA A.....GCTA CAAG
TCAG C.....GCT CAAG
T T.....GAAAAA TATCAGAAG AGT AG G CTGTGGGAAG
T T.....GAAAAA TATCACAAG AGT AAG AGCTGTGGGAAG
GTGGTT.....TCAAGATATCTGAGAC GGT ACA G CTGTGGCAAG
TC CTGT CCT.....GGCCT AGC GCAG A GAA C GC AG
CT CG.....ATTGGCGA G GCT G A AA CGGG GTCA
GC ACAG ACCT.....GATCCTAGCGTGT C A AC GC AGGTC
GC TCAG ACCT.....GCTCCTAGCGTG C A A CA TC
AGATCC CTCCT.....AGCAGC A AGG A G A C G
AGATCC CTCCT.....AGCAGC A AGG A G A C G
TCGAGC.....CTG C GC TC A C G CA TCA
GA C.....GTG A CGAA C G C TCA
TCG TT.....CTG C T AG GAA C G CG TTC
G AGGC.....CTG CA ACA A C CA CTC
AC GCT.....GAGG CTT GC GCACA AGCTC A CT G
G AA T G.....G G G T A AGCGC C T CAGG
A A G.....T A C TT G C C T T
A A G.....T A C TT GA AC TG
A.....AGA A CGG
ATT G A TCAAGT TCTCT C CA C G
TCA A.....GAA CT G C
CG.....CT G GCCT C GA CA A G
G.....C A GCCTA A CAGG C
TCG.....G GCAT G CG
TCG.....CT G TTG C T CAG C CA

Vpu start (ACG in HXB2)		
H1B. FR. 83. HXB2	ACGCAACCT.....ATACCAATAGTAGCAATAGTAGCATTAGTAGTAGCAATAATAATAGCAATAGTTGTGTGGTCCATAGTAATCATAGATAT.....AGGAAATATTTAAGCAAAAGAAAAATAGACAGGT	6185
Vpu	T Q P.....I P I V A I V A L V V A I I I A I V V W S I V I I E Y.....R K I L R Q R K I D R.....	
H1A1.UG.85.U455	T AC.....T GGA.....CTGG.....AC.....GGC GA.....C.....CT.....A.....T.....GGT.....AAA.....	5636
H1B.US.90.WEAU160	T AC.....T G.....T.....C.....GG.....C.....T.....A.....C.....TAT.....	5637
H1C.ET.86.ETH2220	T AC.....T G.....T.....C.....CA.....C.....A.....C.....TAT.....	5597
H1D.CO.84.81R085	T AC.....T G.....T.....C.....CA.....C.....A.....C.....TAT.....	5704
H1F1.BE.93.VI859	T TC TA.....T GTT GC A.....GG.....C.....T.....GC.....C.....A.....T.....TAT.....	5534
H1G.SE.93.S66165	T GT A.....T GT.....T.....G.....A.....T.....C.....GC.....C.....A.....A.....T.....TAT.....	5591
H1H.CF.90.056	T T TATA.....T GG T.....G AT GG.....CGCT G.....AC TTT.....C.....GCC.....G.....A.....A.....TAT.....	5528
H1J.SE.93.SE7887	T AT.....T G A.....T.....TA.....TT.....CC T.....T.....GC.....T.....G.....A.....A.....TAT.....	5507
H1K.CM.96.MP535	T GTGT C.....T G.....TTC AT G.....C TT G.....C CT.....T.....GC.....T.....G.....A.....A.....TAT.....	5387
H101.AE.TH.90.CM240	T AC.....T GGA.....TAGT.....G C.....GC.....CT.....T.....T.....GT.....GT.....	5756
H102.AG.NG.x.IBN9	T AC.....T A.....ACT.....G C.....G C.....T.....C.....GC.....C.....A.....AG.....TAT.....	5718
H103.AB.RU.97.KAL153_2	T T.....TGCAA.....TCCT.....G.....C.....T.....GG.....T.....G.....T.....T.....	5410
H104.cpx.CY.94.CY032	T TT TTC.....TGGGA.....CTGG.....G C G.....G C.....G.....T.....T.....A.....T.....T.....T.....	5558
H1N.CM.95.YBF30	T TG.....TC T.....G G T CA.....G.....G.....C.....G.....T.....G.....A.....A.....C.....G AT.....C TAT.....G.....	5558
H10.BE.87.ANT70	T T A.....GGGACC.....CT.....A.....ATTA TAGT.....CTTTG C.....T.....AATG.....A.....T.....AATG.....G.....G.....CTTGA.....A.....	6245
H10.CM.91.MVP5180	T T AA.....GAGAACC.....GC.....CT.....A.....T.....AGT.....CTTTGTGTC.....T.....AATG.....C.....A.....A.....TGT TAAC.....CTTAGAATTAT.....TTAGTCAAAGA.....AAC.....GATAG.....GG GCAGG.....CTTGAAA.....	5232
H1P.FR.06.RBF168	T T.....G GATGAG.....C.....T.....A.....AT GCT GG.....TT.....C.....TTGCATT.....A.....T.....GGG AG.....CC.....GC.....TTTGTCTA.....AGATTATGTAAA.....	5661
CPZ.CM.01.SIVcpzCAM13	T AT TTA.....CTTT GGTGCTT.....GCCA T.....CCTT.....TT.....C.....TAAC.....TT.....A.....AGG ATT.....TGG.....	5766
CPZ.CM.05.SIVcpzEK505	T TTGTGT.....C TAT.....AGT.....G T CA.....G.....C.....A.....AG CTC.....T.....A.....T.....G.....A.....T.....T.....TAGAATATAC.....AGA.....	5755
CPZ.CM.05.SIVcpzLB7	T G C TA.....AT GA T.....G T A.....GC.....TA.....A.....C.....C.....T.....A.....A.....TA A.....C.....T TC GCTTAT.....	5750
CPZ.CM.05.SIVcpzMB66	T G TATA.....GTGCAG A.....G.....GCTT.....T.....TTC A TA.....A T.....G T.....TC.....AA GA TA.....A.....T.....T.....AAACTCTGTAAA.....	5758
CPZ.CM.05.SIVcpzMT145	T G TA.....GA.....T.....GCT.....A.....TT.....CA.....CTTT.....GC TG.....T.....T.....CT.....ATAGC.....CT.....T.....	5721
CPZ.CM.05.SIVcpzMB897	T ATGGAA TATTCATA.....CTT GG C.....AT GG A.....TTA.....A T.....T.....GC.....T.....G.....TGGT AAAAG TTAT A TGT.....T.....	5756
CPZ.CM.05.SIVcpzDPA93	T ATGCA T.....T A.....TGGGA CA A.....GCT GA T.....T.....G A.....A.....GGC.....T.....T.....CT.....A.....C.....GGG.....CTT.....T.....ACG GG.....	5784
CPZ.CM.98.CAM3	T T A.....TGG.....GA CA A.....GCT A T GTA.....G A.....A.....T.....T.....T.....A.....C.....GGG.....CT.....TTTA AGAGTGG.....	5613
CPZ.CM.98.AM5	T T AT.....TGG.....GAGCA A.....GTT A.....T.....G A.....A.....C.....T.....T.....T.....A.....T.....GGA.....CT.....T TA AAGTGG.....	5728
CPZ.GA.88.GAB1	T ACT TG.....TTAGT.....GGCT.....TTC CA.....TT G.....GCT.....TGC TGGAAC.....TTG A.....A.....GGATACA T.....ATT A ATGGGGATAT.....AGAAGGTATAAAGACAT.....GGC TGAG C G.....	6252
CPZ.GA.88.GAB2	T TTT C.....ATGTGGGT GCTA.....G C A T G A.....GTACTCTTT.....G T.....AAT.....G.....GGT.....T.....G.....ATCTCTGTCTAT.....AAAAGGTGAAAAAGACAC.....GA GAGCA AG.....TC.....	5599
CPZ.US.85.CPZUS	T TTA A.....TGGT TGA.....GTITT.....C TT GG A.....A GGT TT.....T G GA AA C.....GGAC.....T.....CTAGATTGGT.....AGACAAATAAAA TA.....GA AAT CT.....CA G G.....TC A ATC 6274	5599
CPZ.CO.90.ANT	T ACTAA ATATTTGAGTATG TT CT.....CT TACTAT G C.....TGGATT.....CTGT.....CT.....A.....ACTC AT AGC.....T.....T TA AATATAT.....AAGCAGCAAAATAGAT.....T AGAG.....AT.....TC.....AGT.....	5638
CPZ.TZ.00.TAN1	T AT AAA.....ATAG.....GTGGG AGT.....TGTC AGTAATG CA.....GCATTC.....TTGT.....TT.....C.....GA.....T AATAGGGG.....T.....GC TGCTAATAGT.....ATAGGTATAAGAGAGA TT GA AGGGA AGCCA C TCA AGGTA.....	5722
CPZ.TZ.00.TAN2	T ATGGTA AA T GTA.....G GGG GT.....GCTT CTAAT TTA.....GTA CTTTGT.....T.....TT.....TC AA AG AGGAGGCC GC A.....ATTACATTATAAAGAGAGAGATTAGAGAGAGAAAGACAC TCA AG.....T T GA G C ATA AA 5852	5852
CPZ.TZ.2002.TAN3_1	T ATGGTA AAAT GTA.....G GGG GT.....GCTT CTAAT TTA.....GTA CTTTGT.....T.....TT.....TC AA AG AGGAGGCC GC A.....ATTACATTATAAAGAGAGAGATTAGAGAGAGAAAGACAC TCA AG.....T T GA G C ATA AA 5852	5852
GOR.CM.2007.SIVgor2139_287	T T A.....G GAT.....A AT G TA ATTA.....G A.....A T GC.....GCT T.....CT.....GA AATT GGC.....AA.....T T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AGGCT CT.....GCA T AG 5761	5761
GOR.CM.2007.SIVgorCP2135con	T T A.....G GAT.....A AT G TA ATTA.....G A.....A T GC.....GCT T.....CT.....GA AATT GGC.....AA.....T T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AGGCT CT.....GCACT AAG 5760	5760
GOR.CM.2004.SIVgorCP684con	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5760
H2A.DE.x.BE1	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5760
H2A.GW.x.ALI	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6703
H2A.SN.x.ST	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6693
H2B.CI.x.EH0	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6145
H2B.GH.86.D205	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6668
H2G.CI.92.ABT96	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6670
H2U.FR.96.12034	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6016
SMM.SL.92.SL928	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6157
SMM.US.x.H9	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6030
SMM.US.x.PGM53	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6071
SMM.US.x.SIVsmH635F_L3	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6522
MAC.US.x.239	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6603
MAC.US.x.251_1A11	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6602
MAC.US.x.251_BK28	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6579
MAC.US.x.EMBL_3	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5728
STM.US.x.STM	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6245
MNE.US.x.MNE027	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6071
DEB.CM.99.CM40	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5946
DEB.CM.99.CM5	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5927
DEN.CO.x.C01	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6221
LST.CO.88.447	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5287
LST.CO.88.485	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5287
LST.CO.88.524	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5284
LST.KE.x.lh07	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6368
SUN.GA.98.L14	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6416
MND-1.GA.x.MNDGB1	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5736
OLC.CI.97.97CI12	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5791
WRC.CI.97.97CI14	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6289
WRC.CI.98.98CI04	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6304
WRC.GM.05.Pbt_05GM_X02	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5224
MND-2.CM.98.CM16	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6293
MND-2.GA.x.M14	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6220
MND-2.x.x.5440	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5858
DRL.x.x.FA0	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5918
MON.CM.99.L1	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5112
MON.NG.x.NG1	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6112
GSN.CM.99.CN166	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6095
GSN.CM.99.CN71	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6080
TAL.CM.00.266	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6019
TAL.CM.01.8023	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5514
MUS-1.CM.01.1085	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6038
MUS-1.CM.01.CM1239	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6023
MUS-2.CM.01.CM1246	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6148
MUS-2.CM.01.CM2500	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6104
SYK.KE.x.KE51	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5894
SYK.KE.x.SYK173	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6218
RCM.GA.x.GAB1	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5892
RCM.NG.x.NG411	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5954
GRV.ET.x.GRI_677	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6201
SAB.SN.x.SAB1C	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6477
TAN.UG.x.TAN1	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6266
VER.DE.x.AGM3	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5777
VER.KE.x.9863	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6279
VER.KE.x.AGM155	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6274
VER.KE.x.TY01_patent	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	6277
COL.CM.x.CGUI	T T A.....G GAT.....A CT G TA ATCA.....G A.....A T GC.....GCT T.....CT.....GA AA T GGC.....AA GC C T C.....TATACTTAAGAGATAGAAGGGGAGAGACGCTTTTTCGCG.....GA AG CT.....T GCA T AAG 5760	5637

Vpu end
Env signal peptide end Env gp120 start

1B1.FR.83.HXB2
 Vpu
 Env
 H1A1.UG.85.U455
 H1B.US.98.WEAU160
 H1C.CT.86.ETH220
 H1D.CD.84.84Z8R85
 H1F1.BE.93.V1850
 H1G.SE.93.SE6165
 H1H.CF.98.056
 H1I.EF.98.7887
 H1K.CM.96.MP535
 H1O1.AE.TH.90.CM240
 H1O2.AG.NG.x.IBNG
 H1O3.AB.RU.97.KAL153.2
 H1O4.CPX.CY.94.CV032
 H1N.CM.x.YB30
 H1O.BE.87.AN70
 H1O.CM.91.MVP5180
 H1P.FR.96.RBP168
 CPZ.FR.01.SIVcpzCM13
 CPZ.FR.01.SIVcpzEK505
 CPZ.CM.05.SIVcpzLB17
 CPZ.CM.05.SIVcpzMB66
 CPZ.CM.05.SIVcpzMT145
 CPZ.CM.x.SIVcpzMB897
 CPZ.CM.SIVcpzDP943
 CPZ.CM.98.CAM5
 CPZ.CM.98.CAM5
 CPZ.GA.88.GAB1
 CPZ.GA.88.GAB2
 CPZ.US.85.CPZU5
 CPZ.D.98.98.98
 CPZ.TZ.09.TAN1
 CPZ.TZ.2001.TAN2
 CPZ.TZ.2002.TAN3.1
 GOR.CM.2007.SIVgor2139.287
 GOR.CM.2007.SIVgorCP2135con
 GOR.CM.2004.SIVgorCP684con
 H2A.DE.x.BEN
 H2A.GW.x.ALI
 H2A.SN.x.ST
 H2B.LI.x.HO
 H2B.GB.D205
 H2C.CI.92.AB796
 H2U.FR.96.12034
 SMM.SL.92.SL92B
 SMM.US.x.H5
 SMM.US.x.H5
 SMM.US.x.SIVsmH635F_L3
 Env signal peptide Env gp120 start
 Y1 loop start
 MAC.US.x.239
 Env
 MAC.US.x.251.1A11
 MAC.US.x.251.BK28
 MAC.US.x.EMBL.3
 STM.US.x.STM
 MND.US.x.MND927
 DEB.CM.99.CM40
 DEB.CM.99.CM5
 DEN.CD.x.CD1
 LST.CD.88.447
 LST.CD.88.483
 LST.CD.88.494
 LST.KE.x.HO
 SUN.GA.98.L14
 MND.1.GA.x.MNDGB1
 OLC.CI.97.97C112
 WRC.CI.98.98C104
 WRC.CI.98.98C104
 WRC.GM.05.Pbt.05MG.X02
 MND.2.CM.98.CM16
 MND.2.GA.x.M14
 MND.2.GA.x.M14
 DRL.x.x.FAD
 MON.CM.99.L1
 MON.NG.x.NG1
 GSN.CM.99.CM166
 GSN.CM.99.CM1246
 GSN.CM.99.CM1246
 MUS.1.CM.01.CM1239
 MUS.1.CM.01.CM1239
 MUS.2.CM.01.CM2500
 SYK.KE.x.KE51
 SYK.KE.x.SYK173
 RCM.GA.x.GAB1
 RCM.NG.x.NG411
 RCM.NG.x.NG411
 SAB.SN.x.SABIC
 TAN.UG.x.TAN1
 VER.DE.x.AGM3
 VER.KE.x.9863
 VER.KE.x.AGM155
 VER.KE.x.AGM155
 COL.CM.x.CG1.patent

H1B. FR. 83. HXB2
Env.
H1A1.UG. 85. U455
H1E. US. 90. WEAU160
H1C. ET. BE. ETH2220
H1D. BA. 94. 84Z0085
H1F1. BE. 93. V1R50
H1G. SE. 93. SE6165
H1H. CF. 90. 056
H1J. SE. 93. SE7887
H1K. CM. 96. MP5K
H1L. AE. TH. 90. CM240
H1O2. AG. NG. X. IBNG
H1O3. AB. RU. 97. KAL153 2
H1N4. cpx. CY. 94. CY032
H1N5. cpx. 95. YB30
H1O. BE. 97. AN790
H1O. CM. 91. MPV5180
H1P. FR. 06. RBF16E
CPZ. CM. 61. SV1cpv2cAM13
CPZ. CM. 65. SV1cpv2EK505
CPZ. CM. 65. SV1cpv2L187
CPZ. CM. 65. SV1cpv2MB66
CPZ. CM. 65. SV1cpv2MT145
CPZ. CM. - . SV1cpv2MB897
CPZ. CM. - . SV1cpv2P943
CPZ. CM. 98. 98M
CPZ. CM. 98. 98M5
CPZ. GA. 88. GAB1
CPZ. GA. 88. GAB2
CPZ. US. 85. CPZUS
CPZ. CD. 90. ANT
CPZ. T2. 80. TAN1
CPZ. T2. 2001. TAN2
CPZ. T2. 2002. TAN3 1
GOR. CM. 2007. SV1gor3T139 287
GOR. CM. 2009. SV1gor3T135con
GOR. CM. 2004. SV1gorCP684con
H2A. DE. X. BEN
H2A. GW. X. ALI
H2A. SN. X. ST
H2B. CT. X. ENO
H2B. GH. 86. D205
H2G. CI. 92. ABT96
H2M. FR. 92. 12034
SHM. SL. 92. L292A
SHM. CT. X. H9
SHM. US. X. PGW53
SHM. US. X. SV1SHH635F L3

[illegible]

[illegible]

		V1 loop end										V2 loop start																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					

V2 loop end

H1B. FR. 83. HXB2		ACACGCTAATGGTGAACAGTGTAAACCTCAGTCATTACACAGCCGCTGCTCKAAAGGATCTCTTGAGCCCAATTCCCATACATTTGTGCGCCGGCTGGTTTGGCAATTTAAATGTAATAAGACGTTTCAATGGAAACAGGC	6396
Env		S Y K T S C N T S V I T Q A C P K V S E C P A G F A I L K C N N K N T G F N G T G	
H1B.1.UG.85.U455			
H1B.US.98.WEAU160			
H1C.ET.86.ETH2220			
H1D.CO.84.84Z8085			
H1F.BE.93.V1650			
H1G.SB.93.S65			
H1H.CF.98.856			
H1J.SE.93.SE7887			
H1K.CM.96.MP535			
H1L1.TH.98.CM240			
H1O2.AG.NG.X.18N6			
H1O3.AB.RU.97.KAL153.2			
H1O4.cpx.CY.94.CY032			
H1N.CM.95.YBF30			
H1O1.TH.98.CM240			
H1O.CM.91.MVP5180			
H1P.FR.96.RBF168			
CPZ.CM.01.SIVcpzCM13			
CPZ.CM.05.SIVcpzKE505			
CPZ.CM.05.SIVcpzLB7			
CPZ.CM.05.SIVcpzMB66			
CPZ.CM.05.SIVcpzMT145			
CPZ.CM.1.SIVcpzMB897			
CPZ.CM.1.SIVcpzDP943			
CPZ.CM.98.CAM5			
CPZ.CM.98.CAM5			
CPZ.GA.88.GAB1			
CPZ.GA.88.GAB2			
CPZ.US.85.CPZUS			
CPZ.TZ.08.TAN1			
CPZ.TZ.2001.TAN2			
CPZ.TZ.2002.TAN3			
GOR.CM.2007.SIVgor2139.287			
GOR.CM.2007.SIVgorCP2135con			
GOR.CM.2004.SIVgorCP684con			
H2A.DE.x.BEN			
H2A.GW.x.ALI			
H2A.SN.x.ST			
H2B.GH.86.D205			
H2C.CI.92.ABT96			
H2U.FR.96.12034			
MMH.UJ.92.L928			
SMH.US.H9			
SMH.US.x.PGM53			
SMH.US.x.SIVsmH635F.L3			
MAC.US.x.239			
Env			
MAC.US.x.251.IA11			
MAC.US.x.251.BK28			
MAC.US.x.EHBL.3			
MNE.US.x.MNE827			
DEB.CM.99.CM40			
DEB.CM.99.CM5			
LST.CD.88.447			
LST.CD.88.485			
LST.CD.88.524			
LST.KE.x.lh07			
LST.GA.98.L1			
MND.1.GA.98.MNDB1			
OLRC.CI.97.97C12			
WRC.CI.97.97C14			
WRC.CI.98.98C184			
MND.2.CM.98.CM16			
MND.2.GA.x.M14			
MND.2.x.x.5440			
DRL.x.x.FAO			
MMH.US.x.L1			
MMH.US.x.NG1			
GSN.CM.99.CN166			
GSN.CM.99.CN71			
TAL.CM.98.266			
TAL.CM.98.8023			
MUS.1.CM.01.1085			
MUS.1.CM.01.CM1239			
MUS.1.CM.01.CM1246			
MUS.1.CM.01.CM2500			
SYK.KE.x.SYK173			
RCM.GA.x.GAB1			
RCM.NG.x.NG411			
TAN.ET.x.GRI1.677			
SAB.US.SAB1C			
SAB.US.x.TAN1			
VER.DE.x.AGM3			
VER.KE.x.96B3			
VER.KE.x.AGM155			
VER.KE.x.TY01.patent			
COL.CM.x.CU1			

H1B, FR. 83, HBX2
Env.
H1A1,UG. 85, U455
H1E, US. 90, WEAU160
H1C, ET. 86, ETH22220
H1D, 84, R4Z0R05
H1F1, BE. 93, V1R50
H1G, SE. 93, SE6165
H1H, CF. 90, 056
H1J, SE. 93, SE7887
H1K, CM. 96, MP530
H101, AE, TH. 90, CM240
H102, AG, NG. X, IBNG
H103, AB, RU, 97, KAL153 2
H104, CP, CX. 94, CY032
H105, 95, YBF30
H10, BE. 97, AN70
H10, CM. 91, MPV5180
H1P, FR. 06, RBF16E
CPZ, CM. 61, SV1cpzCM13
CPZ, CM. 65, SV1cpzEK505
CPZ, CM. 65, SV1cpzL457
CPZ, CM. 65, SV1cpzMB66
CPZ, CM. 65, SV1cpzMT145
CPZ, CM. -. SV1cpzMB897
CPZ, CM. -. SV1cpzDP943
CPZ, CM. 88, CAM3
CPZ, CM. 88, CAM5
CPZ, GA. 88, GAB1
CPZ, GA. 88, GAB2
CPZ, US. 85, CPZUS
CPZ, CD. 90, ANT
CPZ, TZ. 80, TAN1
CPZ, TZ. 2001, TAN2
CPZ, TZ. 2002, TAN3 1
GOR, CM. 2007, SV2gorF2139 287
GOR, CM. 2007, SV2gorF21335con
GOR, CM. 2004, SV1gorCP684con
H2A, DE. X, BEN
H2A, GW. X, ALI
H2A, SN. X, ST
H2B, CT. X, ENO
H2B, GH. 86, D205
H2G, CI. 92, ABT96
SZ, FL. 92, 1293A
SHM, SL. 92, SL92B
SHM, SL. X, H9
SHM, US. X, PGW53
SHM, US. X, SV5hmH635F L3

MAC.US.x.239
Env
MAC.US.x.251 1A11
MAC.US.x.251 BK28
MAC.US.x.EMBL 3
STM.US.x.1
MNE.US.x.MNE027
DEB.CM.99.CM40
DEB.CM.99.CM5
DEN.CO.x.CD1
LST.CO.88.447
LST.CO.88.485
LST.CO.88.524
LST.KE.x.Lho7
SUN.GA.98.L14
MIND-1.GA.x.MINDGB1
OLC.G.97.97C11.2
WRC.CI.97.97C11A
WRC.CI.98.98C01A
WRC.GM.95.Pbt 05GM_X02
MND-2.CM.98.CM16
MND-2.GA.x.M14
MND-2.x.x.5440
DRL.x.x.FA0
MON.CM.99.L1
MON.NG.x.NG1
G5N.CM.99.CM166
G5N.CM.99.CM71
TAL.CO.00.266
TAL.CO.01.8023
MUS-1.CM.01.1085
MUS-1.CM.01.CM1239
MUS-1.CM.01.CM1246
MUS-1.CM.01.CM2500
SYK.KE.x.KES1
SYK.KE.x.SYK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.FI.x.GR1 677
SAB.SN.x.SAB1C
TAN.UG.x.TAN1
VER.DE.x.AGM3
VER.DE.x.AGM3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.TY01 patent
COL.CM.x.CG1

[illegible]

H1B. FR.83. HXB2
Env
H1A1.UG.85.U455
H1B.US.96.WEAU160
H1C.ET.86.ETH2220
H1D.CO.84.84Z8085
H1F1.BE.93.VI859
H1G.SE.93.S6165
H1H.CF.90.056
H1J.SE.93.SE7887
H1K.CM.96.MP535
H101.AE.TH.90.CM240
H102.AG.NG.x.IBNG
H103.AB.RU.97.KAL153_2
H104.cpx.Y9.94.CY032
H1N.CM.95.YBF38
H1O.BE.87.ANT170
H10.CM.91.MVP5180
H1P.FR.86.RBF168
CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzLB7
CPZ.CM.05.SIVcpzMB66
CPZ.CM.05.SIVcpzMT145
CPZ.CM.05.SIVcpzMB897
CPZ.CM.05.SIVcpzDPP43
CPZ.CM.98.CAM3
CPZ.CM.98.CM98
CPZ.GA.88.GAB1
CPZ.GA.88.GAB2
CPZ.US.85.CPZUS
CPZ.CD.90.ANT
CPZ.TZ.90.TAN1
CPZ.TZ.2001.TAN2
CPZ.TZ.2002.TAN3_1
GOR.CM.2007.SIVgor2139_287
GOR.CM.2007.SIVgorCP2135con
GOR.CM.2004.SIVgorCP684con
H2A.DE.x.BEN
H2A.GW.x.ALI
H2A.SN.x.ST
H2B.CI.x.EH0
H2B.HG.86.D205
H2G.CI.92.AB196
H2D.FR.96.12034
SMM.SL.92.SL928
SMM.US.x.H9
SMM.US.x.PGM53
SMM.US.x.SIVsmh635F_L3

MAC.US.x.239
Env
MAC.US.x.251.1A11
MAC.US.x.251.BK28
MAC.US.x.EMBL_3
STM.US.x.STM
MNE.US.x.MNE027
DEB.CM.98.CM40
DEB.CM.99.CM5
DEN.CO.x.CD1
LST.CO.88.447
LST.CO.88.485
LST.CO.88.524
LST.KE.x.LH07
SUN.GA.98.L14
MND.1.GA.x.MNDGB1
OLC.CI.97.97C112
WRC.CI.97.97C114
WRC.CI.98.98C104
WRC.GM.05.Pdt_05GM_X02
MND.2.CM.98.CM16
MND.2.GA.x.M14
MND.2.x.x.5440
DRL.x.x.FA0
MON.CM.99.L11
MON.NG.x.NG1
GSN.CM.99.CN166
GSN.CM.99.CN71
TAL.CM.00.266
TAL.CM.01.8023
MUS.1.CM.01.CM1085
MUS.1.CM.01.CM1239
MUS.2.CM.01.CM1246
MUS.2.CM.01.CM2500
SVK.KE.x.KE51
SVK.KE.x.SVK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GRI_677
SAB.SN.x.SABIC
TAN.UG.x.TAN1
VER.DE.x.AGM3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.TY01_patent
COL.CM.x.CG01

V3 loop start

ATAGTACAGCTGGAACACATCTGTAGAAATTAATTGTACAAAGCCCAACAAACAT...ACAAGAAAGAAATCCGTATCCAGAGAGACCAGGAGAGCATTTGTT...ACAATAGAAAA...ATAGGAAATATGAGCAAGCAACATTGTAACATTAGTAG 7228

V3 loop end

V4 loop start

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7643

V4 loop end

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7639

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7625

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7674

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7282

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7114

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6980

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6919

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7285

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6351

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6348

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6354

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7420

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7479

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6754

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6816

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7323

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7371

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6265

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7330

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7247

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6957

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6991

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7197

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-5786

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7162

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7153

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7010

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7216

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7098

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7233

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7162

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6912

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7216

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6930

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6974

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7208

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7508

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7297

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6835

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7337

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7317

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-7316

-GTT-A-TAA-T-TTATAA-C-AC-G-A-G-AGGA-T-G-...GTTT-CC-G-ACC-T-...ATGT-T-ATTG-TT-C-...CAGT-CA-CC-ATC-AT-AT-GGCCA-AG-G-...TGG-...GGT-...G-6638

[illegible]

[illegible]

Alignments

PLV Complete Genomes

[illegible]

	V5 loop start	V5 loop end	Rev Responsive Element (RRE) region
H1B.FR.83.HXB2	TAAT	AGCAACAATGAGTCCGAGATCTTCAGACCTGGAGGAGGATATGAGGGCAAAATGGAGAAGTGAATTATATAAATAT	AAAGTAGTAAAAATTGAACATTAGGAGTAGCACCCACCAAGGCAAGAGAGAG
Env	N	S N E S E I F R P G G G D M R D N W R S E L Y K Y	K V V K I E P L G V A P T K A K R R
H1A1.UG.85.U455	-C-AAC	-T-CAA-AAAT	-G-
H1B.US.90.WEAU160	-G-AGT	GAAG-G-CC-A	-A-
H1C.ET.86.ETH2220	-C-A	GAGCCAC-T-GCACA	-A-
H1D.CO.84.847085	-GC	-AT-T-C-C-AAT	-C-T
H1F1.BE.93.VI859	-G-	G-G-G-A-CATT	-C-
H1G.SE.93.S6E165	-G-AAAT	AACAATACA-AT-CA-G-AGT	-G-
H1H.CF.90.056	-C	GCGTCTGCA-AAAT-T-C	-G-
H1J.SE.93.SE7887	A-CAGG	GGGAATGGC-TG-G-GCA-T	-A-C
H1K.CM.96.MP535	-GT-AAT	-AT-T-C-C-TAAT	-C-G
H101.AE.TH.90.CM240	-G	-T-G-ACAAAT-A-C	-G-
H102.AG.NG.x.IBNG	-C	CAG-G-TTA-T-T-A	-T
H103.AB.RU.97.KAL153_2	-C	-A-TA-T	-G-
H104.cpx.CY.94.CY032	GCC	G-CCA-GAACA-AG-ATAT-CTC	-A-C
H1N.CM.95.YBF30	ATGGAAACAGC	G-CA-CAAT-TA-CA-T-AAT	-G-
H1O.BE.87.ANT170	ATGG	-ATTG-CA-GTGA-A-T-CAC-T	-G-
H1O.CM.91.MVP5180	-T-AAAT	GCC-A-G-GCAGCAA-ACC-T-A-C	-G-
H1P.FR.86.RBF168	-GT	-T-ACATA-T-CA-T-AAT	-G-
CPZ.CM.01.SIVcpzCAM13		-T-CTAATA-T-CA-T-AAT	-G-
CPZ.CM.05.SIVcpzEK505		TATACAAAGTCTGGA-C-AAGT-C-C-A-ATAT-CAC	-G-
CPZ.CM.05.SIVcpzLB7		AAACAC-CA-CAATATC-C	-G-
CPZ.CM.05.SIVcpzMB66		CAGCAA-AAACAGAC-G-TG-CA-A-CC-G-C-TT	-G-
CPZ.CM.05.SIVcpzMT145		CCGAGAAGATCAGGAGAGAATCAGG-TG-CA-TAA-ACATA-G-TT-T-TAAC	-G-
CPZ.CM.05.SIVcpzMB897		A-GAG	-G-
CPZ.CM.05.SIVcpzD943		ACTCCCGAGAAATGGGACT-AT-C-A-CAAGTTA-CAC-ATAC	-G-
CPZ.CM.98.CAM3		C-TC	-G-
CPZ.CM.98.CAM5		ATGGAA	-G-
CPZ.GA.88.GAB1		GTGACT	-G-
CPZ.GA.88.GAB2		G-CGGGGA-CAA-ACAGAAG-TTAC-TGTC	-G-
CPZ.US.85.CPZUS		CGGAGTC	-G-
CPZ.CD.90.ANT		AT	-G-
CPZ.TZ.90.TAN1		C-CAAT	-G-
CPZ.TZ.2001.TAN2			-G-
CPZ.TZ.2002.TAN3_1			-G-
GOR.CM.2007.SIVgor2139_287			-G-
GOR.CM.2007.SIVgorCP2135con			-G-
GOR.CM.2004.SIVgorCP684con			-G-
H2A.DE.x.BEN			-G-
H2A.GW.x.ALI			-G-
H2A.SN.x.ST			-G-
H2B.CI.x.EH0			-G-
H2B.GH.86.D205			-G-
H2C.CI.92.ABT96			-G-
H2U.FR.96.12034			-G-
SMM.SL.92.SL92B			-G-
SMM.US.x.H9			-G-
SMM.US.x.PGM53			-G-
SMM.US.x.SIVsmh635F_L3			-G-
MAC.US.x.239			-G-
Env	D	N O T N I T M S A E V G A E L Y R L E L G D Y	K L V E I T P G T G A C P T D V G K R Y
MAC.US.x.251.1A11	-G-GGA	-AA-C-A-CTAAT-TCA-CATGA-T-C	-GG-GCA-CTG-ATC-TTG
MAC.US.x.251.BK28	-G-GGA	-AA-C-A-CTAAT-TCA-CATGA-T-C	-GG-GCA-CTG-ATC-TTG
MAC.US.x.EMBL_3	-G-GGA	-AA-C-A-CTAAT-TCA-CATGA-T-C	-GG-GCA-CTG-ATC-TTG
STM.US.x.STM	-CAAT	-CAAT	-CAAT
MNE.US.x.MNE027	-G-GGA	-AA-C-A-CTAAT-TCA-CATGA-T-C	-GG-GCA-CTG-ATC-TTG
DEB.CM.99.CM40	-G-GGA	-AA-C-A-CTAAT-TCA-CATGA-T-C	-GG-GCA-CTG-ATC-TTG
DEB.CM.99.CM5	-G-GGA	-AA-C-A-CTAAT-TCA-CATGA-T-C	-GG-GCA-CTG-ATC-TTG
DEN.CO.x.CD1	-G-GGA	-AA-C-A-CTAAT-TCA-CATGA-T-C	-GG-GCA-CTG-ATC-TTG
LST.CO.88.447	-G-ACCAGAA	GAAACCTGGGGAGAA-T-TGTCCTG	AGATTCTTGCTCCCTCTGGGAA-CAA-TC
LST.CO.88.485	GG-GCCAGAG	GAAACCTGGGGAGAA-T-TGTCCTG	AGATTCTTGCTCCCTCTGGGAA-CAA-TC
LST.CO.88.524	GG-ACCACAT	GAAAGACTTAGGAGGAA-TCTGTCT	TAAGTTTCTGCTCCCTCTGGGAA-CAA-TC
LST.KE.x.LH07	GG-ACCACAT	GAAAGACTTAGGAGGAA-TCTGTCT	TAAGTTTCTGCTCCCTCTGGGAA-CAA-TC
SUN.GA.98.L14	GG-AGACTG	AAGGTAAATG-ATCA-CAT-TTG	AGC-TTC-AGCC-CTACCA-C-CTTACA-TC
MND-1.GA.x.MNDG81	AG-AGTAATGAA	CAA-ATGCA-A-TAAATTTCTGCTCCCA-T-A	CTTCA-TC
OLC.CI.97.97C112	A-TACAAAAGTAGAGAAC	GAA-GC-AG-G-CATTG-T-CC-CC-T	-C-ACGT-A-TC
WRC.CI.97.97C114	CTGGGAA	AGAAATC-AG-GATTC-AA-CTCTTCCA-C	ACA-TC
WRC.CI.98.98C104	TGGGAA	A-TAAGC-AG-GAATTC-AA-CTCTTCCA-C	ACA-TC
WRC.GM.05.Pd1_05GM_X02	TGGGAA	A-CGGG-G-GGATTC-AA-CTCTTCCA-C	ACA-TC
MND-2.CM.98.CM16	AG-AGAGGGA	A-ATC-AAATTTGTGCC-CA-AT	GG-ACAA-TGA-TT-GCG-T-GG-GCAC
MND-2.GA.x.M14	-G-AGGA	AAGA-A-CTA-AAAGTTT-TGCC-CA-AT	GG-ACAA-TGA-TT-GCG-T-GG-GCAC
MND-2.x.x.5440	-G-GATGAC	GA-ATATC-AAATTTTATACC-CA-ATTGG	CTCAA-TC
DRL.x.x.FA0	GG-GCAGAG	GAAACAG-AG-TTCCA-C-AT	TAAATTTATACGCA-AT
MON.CM.99.L11	-G-GGAC	CAAGC-AGCTTGTGAT-CC-TTC	C-GAG-TCT
GSN.CM.99.CN166	-G-AGGC	TCT-AA-TGA-CCGTCG-CC-G	GCT-TGCC-ACCTA
GSN.CM.99.CN71	GGACAT	TCC-AAT-TGA-CCC-TGCC-CC-G	AGCC-TGCA
TAL.CM.90.266	CCGCGCTCT	AGT-C-AAACGT-GAGCCTCTGTC	G-AC-T
MUS-1.CM.01.8023	-GGGGAAT	GA-ATT-AGGTGTGGAACCTCTG	C-A-TGC
MUS-1.CM.01.1085	-GAGAT	-GAGAT	-GAGAT
MUS-1.CM.01.CM1239	-AGAC	ACAG-AA-TGA-CC-TCC-GA-G	-T-GCC
MUS-2.CM.01.CM1246	CGGCAAT	ACA-AA-TGA-CCCCCT-CCA-G-C	-CGC
MUS-2.CM.01.CM2500	-GGCGAC	A-T-T-ATCGATTGA-CCC-TCC	-CCA-G
SVK.KE.x.KE51	-CCAAAT	-AC-T-GAATTTTG-ACCTACT	CTA-G
SVK.KE.x.SVK173	CCCGAG	-TAC-T-GAA-TTTA-CC-AC-G	-A-G
RCM.GA.x.GAB1		TT	CAGT
RCM.NG.x.NG411	AG-AAAT	ATGACA-CAATGTCA-CTTGCT	CT-AG
GRV.ET.x.GRI_677	C-CAAGTCT	GG-CCA-AAATGTGA-CTT-AT	CTCTT
SAB.SN.x.SAB1C	C-G-AAA	AA-AG-C-AATGTGA-GTT-TC	CTCTT
TAN.UG.x.TAN1	C-GAAA	GAAAG-CTAATGTGA-ATTGAC	CTA-T
VER.DE.x.AGM3	-G-AAG	AA-AG-CTAATGT-AATT-AT	TCCTT
VER.KE.x.9063	-C-AAC	-ATAGA-C-AATGTGA-AAT-T	TCCTT
VER.KE.x.AGM155	-CCAG	-AA-AG-CAATGT-AATTG	TCCTT
VER.KE.x.TY01_patent	-G-AAA	-AA-AGA-C-AA-GTGA-ACT-A	TCCTT
COL.CM.x.CG01	AG-AGGA	GAC-ATG-TGG-A-TGGGTGTCT	ATCC-G

		Env gp120 end Env gp41 start																										
H1B_FR.83.HXB2	Env	TGTTGTCAG	AGAGAAAAAGAGCAGTGG	GGAAATAGGAGCTTTGTTCTTGGGTTGCTTGGGAGCAGGAGGACATATGGGCGAGCTCAATGACGCTGACGGTACAGCCAGACAAATTATTGTCTGGTATAGTGACGAGCAGACAAAT	7886																							
H1A1.UG.85.U455	Env	V V Q	R E K R A V	G I G A L F L G F L G A A G S T M G A A S M T L T V Q A R Q L L S G I V Q Q Q N N	7316																							
H1B.US.90.WEAU160	Env	G	CA	ATGC	A	G	A	T	G	A	A	G	7317															
H1C.ET.86.ETH2220	Env	G	A	A	A	A	A	A	A	A	A	A	7318															
H1D.CO.84.842085	Env	G	A	A	A	A	A	A	A	A	A	A	7319															
H1F1.BE.93.VI859	Env	G	A	A	A	A	A	A	A	A	A	A	7320															
H1G.SE.93.SE6165	Env	G	A	A	A	A	A	A	A	A	A	A	7321															
H1H.CF.90.056	Env	G	A	A	A	A	A	A	A	A	A	A	7322															
H1J.SE.93.SE7887	Env	G	A	A	A	A	A	A	A	A	A	A	7323															
H1K.CM.96.MP535	Env	G	A	A	A	A	A	A	A	A	A	A	7324															
H101.AE.TH.90.CM240	Env	G	A	A	A	A	A	A	A	A	A	A	7325															
H102.AG.NG.x.IBNG	Env	G	A	A	A	A	A	A	A	A	A	A	7326															
H103.AB.RU.97.KAL153_2	Env	G	A	A	A	A	A	A	A	A	A	A	7327															
H104.cpx.CY.94.CY032	Env	G	A	A	A	A	A	A	A	A	A	A	7328															
H1N.CM.95.YBF38	Env	G	A	A	A	A	A	A	A	A	A	A	7329															
H1O.BE.87.ANT70	Env	G	A	A	A	A	A	A	A	A	A	A	7330															
H1O.CM.91.MVP5180	Env	G	A	A	A	A	A	A	A	A	A	A	7331															
H1P.FR.86.RBF168	Env	G	A	A	A	A	A	A	A	A	A	A	7332															
CPZ.CM.01.SIVcpzCAM13	Env	G	A	A	A	A	A	A	A	A	A	A	7333															
CPZ.CM.05.SIVcpzEK505	Env	G	A	A	A	A	A	A	A	A	A	A	7334															
CPZ.CM.05.SIVcpzLB7	Env	G	A	A	A	A	A	A	A	A	A	A	7335															
CPZ.CM.05.SIVcpzMB66	Env	G	A	A	A	A	A	A	A	A	A	A	7336															
CPZ.CM.05.SIVcpzMT145	Env	G	A	A	A	A	A	A	A	A	A	A	7337															
CPZ.CM.05.SIVcpzMB897	Env	G	A	A	A	A	A	A	A	A	A	A	7338															
CPZ.CM.05.SIVcpzDP943	Env	G	A	A	A	A	A	A	A	A	A	A	7339															
CPZ.CM.98.CAM3	Env	G	A	A	A	A	A	A	A	A	A	A	7340															
CPZ.CM.98.CAM5	Env	G	A	A	A	A	A	A	A	A	A	A	7341															
CPZ.CM.98.GAB1	Env	G	A	A	A	A	A	A	A	A	A	A	7342															
CPZ.CM.98.GAB2	Env	G	A	A	A	A	A	A	A	A	A	A	7343															
CPZ.US.85.CPZUS	Env	G	A	A	A	A	A	A	A	A	A	A	7344															
CPZ.CM.98.ANT	Env	G	A	A	A	A	A	A	A	A	A	A	7345															
CPZ.CM.98.TAN1	Env	G	A	A	A	A	A	A	A	A	A	A	7346															
CPZ.CM.98.TAN2	Env	G	A	A	A	A	A	A	A	A	A	A	7347															
CPZ.CM.98.TAN3	Env	G	A	A	A	A	A	A	A	A	A	A	7348															
GOR.CM.2007.SIVgor2139_287	Env	G	A	A	A	A	A	A	A	A	A	A	7349															
GOR.CM.2007.SIVgorCP2135con	Env	G	A	A	A	A	A	A	A	A	A	A	7350															
GOR.CM.2004.SIVgorCP684con	Env	G	A	A	A	A	A	A	A	A	A	A	7351															
H2A.DE.x.BEN	Env	G	A	A	A	A	A	A	A	A	A	A	7352															
H2A.GW.x.ALI	Env	G	A	A	A	A	A	A	A	A	A	A	7353															
H2A.SN.x.ST	Env	G	A	A	A	A	A	A	A	A	A	A	7354															
H2B.CI.x.EH0	Env	G	A	A	A	A	A	A	A	A	A	A	7355															
H2B.GH.86.D205	Env	G	A	A	A	A	A	A	A	A	A	A	7356															
H2C.CI.92.ANT96	Env	G	A	A	A	A	A	A	A	A	A	A	7357															
H2D.FR.96.12034	Env	G	A	A	A	A	A	A	A	A	A	A	7358															
SMM.SL.92.SL92B	Env	G	A	A	A	A	A	A	A	A	A	A	7359															
SMM.US.x.H9	Env	G	A	A	A	A	A	A	A	A	A	A	7360															
SMM.US.x.PGM53	Env	G	A	A	A	A	A	A	A	A	A	A	7361															
SMM.US.x.SIVsmh635F_L3	Env	G	A	A	A	A	A	A	A	A	A	A	7362															
		Env gp120 end Env gp41 start																										
MAC.US.x.239	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8304
MAC.US.x.251_1A11	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8305
MAC.US.x.251_BK28	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8306
MAC.US.x.EMBL_3	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8307
STM.US.x.STM	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8308
MNE.US.x.MNE027	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8309
DEB.CM.99.CM40	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8310
DEB.CM.99.CM5	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8311
DEB.CM.99.CM6	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8312
DEB.CM.99.CM7	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8313
DEB.CM.99.CM8	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8314
DEB.CM.99.CM9	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8315
DEB.CM.99.CM10	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8316
DEB.CM.99.CM11	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8317
DEB.CM.99.CM12	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8318
DEB.CM.99.CM13	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8319
DEB.CM.99.CM14	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8320
DEB.CM.99.CM15	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8321
DEB.CM.99.CM16	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8322
DEB.CM.99.CM17	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8323
DEB.CM.99.CM18	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8324
DEB.CM.99.CM19	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8325
DEB.CM.99.CM20	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8326
DEB.CM.99.CM21	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8327
DEB.CM.99.CM22	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8328
DEB.CM.99.CM23	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8329
DEB.CM.99.CM24	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8330
DEB.CM.99.CM25	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8331
DEB.CM.99.CM26	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8332
DEB.CM.99.CM27	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8333
DEB.CM.99.CM28	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8334
DEB.CM.99.CM29	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8335
DEB.CM.99.CM30	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8336
DEB.CM.99.CM31	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8337
DEB.CM.99.CM32	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8338
DEB.CM.99.CM33	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8339
DEB.CM.99.CM34	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8340
DEB.CM.99.CM35	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8341
DEB.CM.99.CM36	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G	TTCTG	A	G-G	GT	C-CT	T	C	ACT	G	G	A	C	AC	G	8342
DEB.CM.99.CM37	Env	CTACTGGTGGC	ACCTCA	A-T	GG-C	TTT	TGC	G	T-G	T	TC	C-A	G															

H1B. FR.83. HXB2	TTGCTG...AGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCAGACTCTGGGGCATCAAGCAGCTCAGGCAAGAACTCTGGCTGTGGAAGATACCTAAGGATCAACAGCTCCTGGGATTTGGGGTTGCTCTGGAAGAACTCATTTGCACCACTGCTGCTCTTG	8053
Env	L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	
H1A1.UG.85.U455	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7483
H1B.US.90.WEAU160	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8060
H1C.ET.86.ETH2220	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7429
H1D.CO.84.84Z8085	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7574
H1F1.BE.93.VT859	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7530
H1G.SE.93.SE6165	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7471
H1H.CF.90.056	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7372
H1J.SE.93.SE7887	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7360
H1K.CM.96.MP35	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7213
H101.AE.TH.90.CM240	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7606
H102.AG.NG.x.IBNG	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7559
H103.AB.RU.97.KAL153.2	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7230
H104.cpx.CY.94.CY032	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7621
H1N.CM.95.YBF30	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7403
H10.BE.87.ANT70	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8107
H10.CM.91.MVP5180	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8124
H1P.FR.06.RBF168	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7574
CPZ.CM.01.SIVcpzCAM13	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7637
CPZ.CM.05.SIVcpzEK505	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7536
CPZ.CM.05.SIVcpzL87	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7564
CPZ.CM.05.SIVcpzMB66	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7577
CPZ.CM.05.SIVcpzMT145	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7562
CPZ.CM.05.SIVcpzMB897	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7561
CPZ.CM.05.SIVcpzDP943	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7616
CPZ.CM.98.CAM3	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7466
CPZ.CM.98.CM95	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7772
CPZ.GA.88.GAB1	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8090
CPZ.GA.88.GAB2	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7437
CPZ.US.85.CPZUS	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8058
CPZ.CD.90.ANT	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7485
CPZ.TZ.00.TAN1	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7659
CPZ.TZ.2001.TAN2	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7699
CPZ.TZ.2002.TAN3.1	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7753
GOR.CM.2007.SIVgor2139.287	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7611
GOR.CM.2007.SIVgorCP2135con	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7595
GOR.CM.2004.SIVgorCP684con	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7542
H2A.DE.x.BE1	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8526
H2A.GW.x.ALI	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8510
H2A.SN.x.ST	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7956
H2B.CI.x.EH0	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8488
H2B.GH.86.D205	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8502
H2G.CI.92.AB196	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7388
H2U.FR.96.12034	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8010
SMM.SL.92.SL928	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7919
SMM.US.x.H9	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7960
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SMM.US.x.SIVsmH635F.L3	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8493
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MAC.US.x.251.BK28	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8453
MAC.US.x.EMBL.3	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7602
STM.US.x.STM	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8122
MNE.US.x.MNE027	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7948
DBE.CM.99.CM40	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7793
DEB.CM.99.CM5	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7714
DEN.CO.x.CD1	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8110
LST.CD.88.447	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7233
LST.CD.88.485	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7230
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DR.L.x.x.FA0	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	7894
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VER.KE.x.TY01_patent	C L L R A I E A Q Q H L L Q L T V W G I K Q L Q A R I L A V E R Y L K D Q Q L L G I W G C S G K L I C T T A V P W	8177
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SMM.US.x.S1Vsmh635F L3

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 VER.KE.x.TV01 patent
 COL.CM.x.CG1

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Env gp41, gp160 end		Nef start																								GCTGAGCCAGCAGCATAG 8882																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
H1B_FR.83.HXB2		ATTTTGTATAAG												ATGGGTGGCAAGTGGTCAAAAAGTAGTGTGATTGGATGGCTACTGTAAAGGAAGAATGAGACGA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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COL.CM.x.CG1

[illegible][illegible]

	3' LTR U3 start	Nef premature end in HXB2	
H1B. FR. 83. HXB2	CTGTAGATCTTAGCCACTTTTAAAAAGAAAGGGGGGACTGGAGGGCTAATTCACCTCCAAAGAAAGACAGATATCTTGATCTGTGGATCTACACACACAAGGCTACTCCCTGATTAGCAGAACTACACACACAGGCCAGGG	GTC 9195	
Nef	A V D L S H F L K E K G G L E G L I H S Q R R Q D I L D L W I Y H T Q G Y F P D * Q N Y T P G P G	V	
H1A1.UG.85.U455	-T-T-C-TT	-A-G-A-A	-A-G-T-T
H1B.US.90.WEAU160	-GCAT	-T-T	-G-T-T
H1C.ET.86.ETH2220	-AT-C	-C-T	-G-A-A
H1D.CO.84.847085	-C-T	-G-A	-G-A
H1F1.BE.93.VI859	-T-T	-T-T	-G-T
H1G.SE.93.SE6165	-T-T-C-TT	-T-T	-G-A-T
H1H.CF.90.056	-T-T	-T-T	-G-T
H1J.SE.93.SE7887	-T-T	-T-T	-G-T
H1K.CM.96.MP535	-T-T	-T-T	-G-T
H101.AE.TH.90.CM240	-T-T	-T-T	-G-T
H102.AG.NG.x.IBNG	-C-C	-T-T	-G-T
H103.AB.RU.97.KAL153_2	-T-C	-T-T	-G-T
H104.cpx.CY.94.CY032	-T-T	-T-T	-G-T
H1N.CM.95.YBF30	-T-T	-T-T	-G-T
H10.BE.87.ANT170	-AT-T	-C-C	-G-T
H10.CM.91.MVP5180	-CT-T	-C-C	-G-T
H1P.FR.06.RBF168	-AT-T	-C-C	-G-T
CPZ.CM.01.SIVcpzCAM13	-CT-T	-C-C	-G-T
CPZ.CM.05.SIVcpzEK505	-T-T	-T-T	-G-T
CPZ.CM.05.SIVcpzLB7	-T-T	-T-T	-G-T
CPZ.CM.05.SIVcpzMB66	-T-T	-T-T	-G-T
CPZ.CM.05.SIVcpzMT145	-CT-T	-CTCT	-G-T
CPZ.CM.05.SIVcpzMB897	-CT-T	-CTCT	-G-T
CPZ.CM.05.SIVcpzDP943	-T-T	-T-T	-G-T
CPZ.CM.98.CAM3	-T-T	-T-T	-G-T
CPZ.CM.98.CM5	-T-T	-T-T	-G-T
CPZ.GA.88.GAB1	-T-T	-T-T	-G-T
CPZ.GA.88.GAB2	-CT-T	-C-C	-G-T
CPZ.US.85.CPZUS	-AT-C	-T-T	-G-T
CPZ.CD.90.ANT	-A-C	-T-T	-G-T
CPZ.TZ.00.TAN1	-A-C	-T-T	-G-T
CPZ.TZ.2001.TAN2	-A-C	-T-T	-G-T
CPZ.TZ.2002.TAN3_1	-A-C	-T-T	-G-T
GOR.CM.2007.SIVgor2139_287	-AT-T	-C-C	-G-T
GOR.CM.2007.SIVgorCP2135con	-AT-T	-C-C	-G-T
GOR.CM.2004.SIVgorCP684con	-AT-T	-C-C	-G-T
H2A.DE.x.BEN	-A-C	-T-T	-G-T
H2A.GW.x.ALI	-A-C	-T-T	-G-T
H2A.SN.x.ST	-A-C	-T-T	-G-T
H2B.CI.x.EH0	-A-C	-T-T	-G-T
H2B.GH.86.D205	-A-C	-T-T	-G-T
H2C.CI.92.ABT96	-A-C	-T-T	-G-T
H2D.FR.96.12034	-A-C	-T-T	-G-T
SMM.SL.92.SL92B	-A-C	-T-T	-G-T
SMM.US.x.H9	-A-C	-T-T	-G-T
SMM.US.x.PGM53	-A-C	-T-T	-G-T
SMM.US.x.SIVsmH635F_L3	-A-C	-T-T	-G-T
MAC.US.x.239	-AA-CA-GTCT-T-A	-A-TTA-T-AGTGC	-TAGA-T-A-CA-ACT-AG-AA-GGA-G
Nef	A I D M S H F L K E K G G L E G I Y I Y A R R H R I L D I Y L E K E G I I P D W Q D Y T S G P G		
MAC.US.x.251.1A11	-AA-CA-GTCT-T-A	-A-TTA-T-AGTGC	-TAGA-T-A-CA-ACT-AG-AA-GGA-G
MAC.US.x.251.BK28	-AA-CA-GTCT-T-A	-A-TTA-T-AGTGC	-TAGA-T-A-CA-ACT-AG-AA-GGA-G
MAC.US.x.EMBL_3	-AA-CA-GTCT-T-A	-A-TTA-T-AGTGC	-TAGA-T-A-CA-ACT-AG-AA-GGA-G
STM.US.x.STM	-AA-C-GTCA-T-A	-A-TTA-T-AGTGC	-TAGA-T-A-CA-ACT-AG-AA-GGA-G
MNE.US.x.MNE027	-AA-CA-GTCT-T-A	-A-TTA-T-AGTGC	-TAGA-T-A-CA-ACT-AG-AA-GGA-G
DEB.CM.99.CM40	-TGA-CTACTCT-T-A	-G-ATG-TT-T-GGCC	-G-T-T-A-G-TCATGC-C-GA-TGA-TGG
DEB.CM.99.CM5	-TGA-CTACTCT-T-A	-G-ATG-TT-T-GGCC	-G-T-T-A-G-TCATGC-C-GA-TGA-TGG
DEN.CO.x.CD1	-TGA-C-GTCA-T-A	-A-C-G-ATA-TT-T-AGT-C	-G-T-C-TT-A-C-C-ATGC-C-GA-TGA-T
LST.CD.88.447	-TGA-C-CTCA-T-A	-T-TAGG-G	-G-C-T-T-ATG-T-CTGTG-GA-TGA-TGG
LST.CD.88.485	-TGA-C-CTCA-T-A	-T-TAGG-G	-G-C-T-T-ATG-T-CTGTG-GA-TGA-TGG
LST.CD.88.524	-TGA-C-CTCA-T-A	-T-TAGG-G	-G-C-T-T-ATG-T-CTGTG-GA-TGA-TGG
LST.KE.x.Lh07	-TGA-C-CTCA-T-A	-T-TAGG-G	-G-C-T-T-ATG-T-CTGTG-GA-TGA-TGG
SUN.GA.98.L14	-TGA-CTCTCT-T-A	-G-ATA-TT-T-GCC	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MND-1.GA.x.MNDGB1	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
OLC.CI.97.97C112	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
WRC.CI.97.97C114	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
WRC.CI.98.98C104	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
WRC.GM.05.Pdt_05GM_X02	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MND-2.CM.98.CM16	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MND-2.GA.x.M14	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MND-2.x.x.5440	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
DR.L.x.x.FA0	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MON.CM.99.L1	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MON.NG.x.NG1	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
GSN.CM.99.CM166	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
GSN.CM.99.CM71	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
TAL.CM.00.266	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
TAN.UG.x.TAN1	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MUS-1.CM.01.1085	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MUS-1.CM.01.CM1239	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MUS-2.CM.01.CM1246	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
MUS-2.CM.01.CM2500	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
SVK.KE.x.KE51	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
SVK.KE.x.SVK173	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
RCM.GA.x.GAB1	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
RCM.NG.x.NG411	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
GRV.ET.x.GRI_677	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
SAB.SN.x.SAB1C	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
TAN.UG.x.TAN1	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
VER.DE.x.AGM3	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
VER.KE.x.9063	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
VER.KE.x.AGM155	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
VER.KE.x.TY01_patent	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG
COL.CM.x.CG01	-TGA-CT-CTCT-T-A	-G-ATA-TT-TAG-AGG	-G-A-T-T-T-ATG-C-CAATGC-C-TGA-TGG

BIL. FR. 83. HBX2
 Nef
 H1A1.UG.95.0455
 H1B1.UG.90.WEAL0260
 H1C1.96.EHT02228
 H1D1.CA.84.RA8Z0R05
 H1F1.BE.93.VI850
 H1G.SF.93.SE6165
 H1H.CF.90.056
 H1I.SF.93.SF7887
 H1K.CM.96.MP535
 H1O1.AE.TH.90.CM240
 H1O2.AG.NG.x.IBNG
 H1O3.AB.RG.97.KAL153
 H1O4.CY.94.CY032
 H1N.CM.95.YBF30
 H1O.BE.87.ANT70
 H1O.CM.91.MP5180
 CPZ.CM.96.RGF168
 CPZ.CM.95.SIVcpzCAM13
 CPZ.CM.95.SIVcpzEK505
 CPZ.CM.95.SIVcpzLB7
 CPZ.CM.95.SIVcpzMB66
 CPZ.CM.95.SIVcpzMT145
 CPZ.CM.95.SIVcpzMB897
 CPZ.CM.95.SIVcpzPD943
 CPZ.CM.98.CAM3
 CPZ.CM.98.CAM5
 CPZ.GA.88.GAB1
 CPZ.GA.88.GAB2
 CPZ.US.85.CPZU5
 CPZ.CD.90.ANT
 C1Z.TZ.00.TAN1
 C1Z.TZ.2081.TAN2
 C1Z.TZ.2082.TAN3
 GOR.CM.2087.SIVgorC2139 287
 GOR.CM.2087.SIVgorC2135 380
 GOR.CM.2087.SIVgorC684 320
 H2A.DE.BE1
 H2A.GW.x.ALI
 H2A.SN.x.ST
 H2B.CT.x.EHO
 H2B.GM.96.D205
 H2G.CT.92.ABT96
 H2U.FR.96.12034
 SMM.SL.92.S192B
 SMM.SL.x.H9
 SMM.SL.x.PGM53
 SMM.US.x.SIVsmH635F_L3
 MAC.US.x.239
 Nef
 MAC.US.x.251 I A11
 MAC.US.x.251 BK28
 STM.US.x.STM
 MNE.US.x.MNE027
 DEB.CM.99.CM40
 DEB.CM.99.CM5
 DEN.CT.x.CD1
 LST.DC.98.447
 LST.DC.88.485
 LST.DC.88.524
 LST.KE.x.lh07
 SUNJ.GA.98.L14
 SUNJ.GA.98.L14
 SUNJ.GA.98.L14
 OLC.CT.97.97C112
 WRC.CT.97.97C114
 WRC.CT.98.98C074
 WRC.GM.05.BT05GM_X02
 MND.CM.98.CM16
 MND.2.GA.x.M14
 MND.2.x.x.5440
 DRL.x.x.FAO
 MND.CM.99.L1
 MND.NG.x.NG1
 GSN.CM.99.CM166
 GSN.CM.99.CN71
 TAL.CM.00.266
 TAL.CM.01.8023
 MUS.1.CM.01.1885
 MUS.1.CM.01.CM1239
 MUS.2.CM.01.CM1246
 MUS.2.CM.01.CM2500
 SYK.KE.x.KE51
 SYK.KE.x.SYK173
 RCM.GA.x.GAB1
 RCM.NG.x.NG411
 GRV.ET.x.GRI 677
 SAB.NG.x.SAB1C
 TAN.UG.x.TAN1
 VER.DE.x.AGM3
 VER.KE.x.9063
 VER.KE.x.AGM155
 VER.KE.x.TY01 patent
 COL.CM.x.CG11

[illegible]

[illegible]

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	TATA box	3' LTR U3 end	3' LTR repeat start							
MAC.US.x.239	--A-TTTC TTG.ATG	--AT-TCA---	A-CGCTC	ATTCA-TC-G-	GC-GGA-AGGCTGG	---TGAGC	---GT---	CCAGCACTA	GCAGGTAGAGCCTGGGTGTTCC	10059
MAC.US.x.251.1A11	A-GTTC TTG.ATG	---AT-TCA---	A-CGCTC	ATGTC-T-C-	GC-GGA-AGGCTGG	---TGAGC	---GT---	CCAGCACTA	GCAGGTAGAGCCTGGGTGTTCC	10534
MAC.US.x.251.BK28	A-TTTC TTG.ATG	---AT-TCA---	A-CGCTC	ATTCA-TC-G-	GC-GGA-AGGCTGG	---TGAGC	---GT---	CCAGCACTA	GCAGGTAGAGCCTGGGTGTTCC	10029
MAC.US.x.EMBL_3	--ATTTC TTG.ATG	---AT-TCA---	A-CGCTC	ATTCA-TC-G-	GG-C-AAGGCTGG	---TGAGC	---GT---	CCAGCACTA	GCAGGTAGAGCCTGGGTGTTCC	9168
STM.US.x.STM	---TTTAC TT. CTG	---AT-CAA-C	T-A-AGCTC	ATTCA-TC-A	GC-GGA-AGGCTGG	---TGAGC	---GT---	CCAGCACTA	GCAGGTAGAGCCTGGGTGTTCC	9713
MNE.US.x.MNE027	A-TTTC TTG.ATG	---AT-TCA---	A-CGCTC	ATTCA-TC-G-	GC-GGA-AGGCTGG	---TGAGC	---GT---	CCAGCACTA	GCAGGTAGAGCCTGGGTGTTCC	9536
DEB.CM.99.CM40	G-CGCTG-A	A-A-C-A	C-T	GCTATCCA						9227
DEB.CM.99.CM5	C-GTGT-A			GCTATCCA						9138
DEN.CD.x.CD1	A-CGCTTC-A	A-T-A	T-A	A-TCGG-T			C-	CCAGCGGCTGG		9620
LST.CD.88.447	A-TT-G									8588
LST.CD.88.485	A-TT-G	A-								8589
LST.CD.88.524	A-TT-G									8594
LST.KC.x.Lho7	A-TT-G									9766
SUN.GA.98.L14	A-TT-A		C-C-C	T-G-AG-	GC-CAGAG-AT-	GC-GAC-C	A--G--ACCT	AG-GCTGGCTTGTCGCTCCTGAGTGAGCACTGCTAAG		9809
MND-1.GA.x.MNDGB1	CA-TG-TG-CT		A-CGCT	T-G-AGTCTCTA-TACA-AGGCT-A				TTGTATCTCTGA-GC		9080
OLC.CI.97.97CI12										8678
WRC.CI.97.97CI14										9484
WRC.CI.98.98CI04										9461
WRC.GM.05.Pbt_05GM_X02	AGACTT-TGGTT-TGCCCT	A-T-ATGCT-TGATG-A-CTGG-TGCACTTCTTGC	GAGGCTA	GCCTAGAGT-G-GG-CCCA-T	CCTAG	CTTGGTGCCTGAGTGGTGGTCCACTTGGCCAAGAGACT-AG-TAGGAG			8602	
MND-2.CM.98.CM16										9518
MND-2.GA.x.M14	AA-T-TTGACT-T	C-C-T	T-GCCGT	ATT-A-TC	C-T					9529
MND-2.GA.x.S440	CA-C-TGGG-T	CT	T-GCCGT	A-AC-A	C-T	GA-AGGCTG	TGAGC	TTGT	CT-GG-TGAGTCTCTG-AAGGAG-TGCCTGCTTGATG-CT-GGCGGT	9355
BL.CM.x.A40	CT-G-A-A	A-T	T-AC-GATG	A-AC-A	TG-AGGCTA			TTG	AGTCTGTGAAGGAGGCTACCTGCTCGAGCG-CG-GTGGTTCGCAAGGCCCTTGGC	9451
MON.CM.99.L1	TCGT-T-A	CA-A	AC-C	AG-ATCCT	GGAGTC					9448
MON.NG.x.NG1	T-ACCTCTAGATCTCT	A-AC	C	AGM-ATCCGC	GGAGTC			GTCT	CCAC-GGGCT	8109
GSN.CM.99.CN166	C-GCTAT	A-A	A-AC	C	AG-GACTCT	GGAGTC				9414
GSN.CM.99.CN71	A-CGCTAT	A-A	A-AC	C	AG-GACTCT	GGAGTC				9410
TAL.CM.00.266	A-T	A-C		A-ATCCT-T	G-T-C					9338
TAL.CM.01.8023										8845
MUS-1.CM.01.1085	T-ACCTCTAGATTCC	A-AC	C	AG-ATCCC	GGAGTC					9420
MUS-1.CM.01.CM1239	T-GCCTCAGATTTC	A-CA-GC	C	AG-ATCCC	GGAGTCAGTTC	CT-C-CA-GC-GC	C-CTCGGAA	G-GTAA-AGCGGCTTGAGAGCCTTGCCTAGGAGAACTG		9465
MUS-2.CM.01.CM1246	ATC-A	A-AC	C	AG-ATCCA	GAAGTC					9484
MUS-2.CM.01.CM2500	A-T		C	G-ATCCAGACGGAGTC						9430
SYK.KC.x.KE51										9068
SYK.KC.x.SYK173		A-C-A	C	AGCTATCCGCGGAG-TGCAACTA		G-		CCAGCGGCTT	GGG-AGCCTCTGAGAGACTGGTAGAGCGGCC-GGGA	9438
RCM.NG.x.GAB1	TCCT-G		C-GC-T	AA-AC	CCTG-AGGCTA-G		T-T	T	A-GTCTTAGAGACTCCAGCTTGAGCCTGGGTGTTTCGCT	9217
RCM.NG.x.GAB1	TCCT-G		C-GC-T	A-CA	CCTG-AGGCTA		TTGT	T	A-GTCTTAGAGACTACGCTTGAGCCTGGGTGTTTCGCT	9308
SAB.SUN.x.SABIC	AG-G-TG	A-A	CGC-GCT	ACTCAG	T-A-GAGCTA	CG-A	T-G	T	GCCTA-ACCGCTTGGA-A	9451
TAN.UG.x.TAN1	CGT-CT-G	CA-A	CGC-GCT	AA-ACA	GC-T-AGGCTG		T-T	T	A-GTCTG-AACAGCTTGAG-CTTGGGTGTTTCGCT	9828
VER.DE.x.AGM3	A-G	A-A	CGC-GCT	ACTCAG	T-AC-A-GAGA-C		T-T	T	G-GCCTA-ACCTGGCTGGCCATCCAGGGG-A	9646
VER.DE.x.AGM3	A-G	A-A	CGC-GCT	ACTCAG	T-AC-A-GAGA-C		T-T	T	GCCTA-ACCTGGCTGGCCATCCAGGGG-A	9171
VER.DE.x.9863	A-G	A-A	CGC-GCT	ACTCAG	T-AC-A-GAGA-C		T-T	T	GCCTA-ACCTGGT-TGGCCA-CCAGGGG-A	9671
VER.DE.x.GM155	A-G	A-A	CGC-GCT	ACTCAG	T-AC-A-GAGA-C		T-T	T	GCCTA-ACCTGGT-TGGCCA-CCAGGGG-A	9652
VER.KC.x.TV01 patent	A-G	A-A	CGC-GCT	ACTCAG	T-AC-A-GAGA-C		T-T	T	GCCTA-ACCTGGT-TGGCCA-CCAGGGG-A	9635
COL.CM.x.CGU1	--GCTA-A--GCCT-T-A	TCAG-AGC	CGAGAGCT	CGAGG						8735

[illegible]

	Extensive secondary structure in this region?									
	Poly-A signal	3' LTR R repeat end				3' LTR U5 start				
H1B.FR.83.HXB2	AATAAAG...CTTGCC	TTGAG	..TG..CTTCAA..GTAGTG	..TGTGCCCGTC..TG..TT	..GTG..TGACTCT	..GGT	..AA..CTAGAGA	..TCCCT	..CAGA	CCCTTTTAGTCAGTGTGGAA
H1A1.UG.85.U455			GTG--G-		A-T					-AC-A--A-T.GTGA
H1B.US.90.WEAU160										-A-
H1C.ET.86.ETH2220										
H1D.CD.84.84ZRO85										
H1F1.BE.93.VT89										
H1G.SE.93.SE6165		AA-CC								
H1H.CF.90.056			T							
H1J.SE.93.SE7887			G..CGCATGC..AAGCC							
H1K.CM.96.MP535										
H101.AE.TH.90.CM240			A							
H102.AG.NG.x.IE6										
H103.AB.RU.97.KAL153_2										
H104.cpx.CY.94.CY032										
H1N.CM.95.YBF30										
H10.BE.87.ANT76			AG							
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CPZ.CM.05.SIVcpzEK505			CT-AA							
CPZ.CM.05.SIVcpzLB7			CTGCA							
CPZ.CM.05.SIVcpzMB66			A-A							
CPZ.CM.05.SIVcpzMT145			CTGCA							
CPZ.CM.-.SIVcpzMB897			AA--G							
CPZ.CM.-.SIVcpzDP943			A-G							
CPZ.CM.98.CAM3			A-G..A-C	TA-CA	C..A..A				TCC	CTCAGAA..TA..A..A..GTA-GT
CPZ.CM.98.CAM5										
CPZ.GA.88.GAB1			TGTAT..G..A-C	TA-CA	C..A..AC				TCC	CTCAGAT..TAAA..ATA..GTCAA
CPZ.GA.88.GAB2			CTC-A..A	T-A-TG	C..A..A			GT	TCC	CTCAGAC..TAAA..CATAA..G-A
CPZ.US.85.CPZUS			CT-A..A	TA-C	C..A..A				TCC	CTCAGAA..T--AA..A..GTA-GT
CPZ.CD.90.ANT										
CPZ.TZ.90.TAN1	C		A..TG-T							
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CPZ.TZ.2002.TAN3_1	C	TGA								
GOR.CM.2007.SIVgor2139_287		A	AA							
GOR.CM.2007.SIVgorCP2135con		A	AA							
GOR.CM.2004.SIVgorCP684con										
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H2A.GW.x.ALI	AA	AGA..A..CAGGTT	AAG	TGT..CCCAT..TCT..CCTAGTC	CC..GCCTGG	CA..TCGG	GTTC..TCTGA	ATAACAAGA	CCTGGTCTGTTAGGACCCCTTCTGCTT	TGGGAATCCA..GCA
H2A.SN.x.ST	AG	AGA..A..CA								
H2B.CI.x.EH0	A	TA	AGA..A..CAAGAC	AGT	TGT..CCCAT..TCT..CCTAGTC	CC..GCCTGG	CA..TCGG	GCTCCAC	TA..GAAA	CCTGGTCTGTTAGGACCCCTTCTGCTT
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SMM.SL.92.SL92B	G	AAC	AGA..A..CAAGTC							
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MAC.US.x.251_BK28		AT..T	AGA..A..TAAG-T	GT	TGT..CCCAT..TCT..CCTAGTC	CC..GCCTGG	CAAC..TCGG	CTCGGTA	ATAAAGAAGA	CCTGGTCTGTTAGGACCCCTTCTGCTT
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DEB.CM.99.CM5										
DEN.CD.x.CD1										
LST.CD.88.447										
LST.CD.88.485										
LST.CD.88.524										
LST.KE.x.lho7		AA	TTGCTCATTG-T	AAA	TACAAGTAGT	CTCA	AGTAGTC	T-TC	CTTTC	CCC
SUN.GA.98.L14										
MND-1.GA.x.MNDCB1		AG	TTTACTGCAAGCAA	TGT	CCCGTGT	TCTC	TCTCC			
OLC.CI.97.97C112	TGTCCTC	T	AAC	TAGAA	TTAGA	CA				
WRC.CI.97.97C114										
WRC.CI.98.98C104										
WRC.GM.05.Pbt_05GM_X02		AG	CTTTTGCTTAGCA	AAGCGTG	GGTTAGTT	TTGT		AAGAAGTAGAACCCCT	G-AG	CT
MND-2.CM.98.CM16										
MND-2.GA.x.M14										
MND-2.x.x.5440										
DRL.x.x.FA0										
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MON.NG.x.NG1										
GSN.CM.99.CN166										
GSN.CM.99.CN71										
TAL.CM.00.266										
TAL.CM.01.8023										
MUS-1.CM.01.1085										
MUS-1.CM.01.CM1239										
MUS-2.CM.01.CM1246										
MUS-2.CM.01.CM2500										
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SYK.KE.x.SYK173		T	GTGGTAAACGCAAG-A	ACGTC	GCT	C-CA	CTGT-C	TG-GT	CACC	CCCCA-A-GTG
RCM.GA.x.GAB1		C	ATGCCAG	AGTTTAC	TG-A	GC-A		TGTGCTGTTT-A	CCTCTCAGCAGT	AACGACTCTGGGGTGA-GA
RCM.NG.x.NG411		C	ATGCTTCTAGCTT	AACGAGATC	AGT	TG	CCATTT-A	TCTCTCA	TGAACGACTCTGGGGT-G-GA	
GRV.ET.x.GRI_677		C	TCGC	AGT	C-CTA	ATTG-G	CAAG	CT-ATTG	TGCGCGCA	CCT.CTAGAGG
SAB.SN.x.SAB1C		T		AGTTTACAAG-A	GCA		TGTGCCATTATTCTCAG			
TAN.UG.x.TAN1		G	TG	C-A		A-T	ATCTGAG	CAAGTGCC	CATT	CGCGCCC-TCC-AG
VER.DE.x.AGM3		T	CG-TG	CA	AG	CA	AGACTT	GAGAGA	CATT	C-TG-TG
VER.KE.x.9863	AC	T	TG	CA	AGA	G	CT	ATCTGAGTCAAGTGCCCT	ATTGAGC	CC-CAC
VER.KE.x.AGM155			TG	CA	AGA	G	CT	ATCTGAGTCAAGTGCCCT	ATTGAGC	CC-CAC
VER.KE.x.TY01_patent										
COL.CM.x.CGU1										

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H1B.FR.83.HXB2	AATCTCTAGCA..	9719
H1A1.UG.85.U455	-----	9178
H1B.US.98.WEAU160	-----	9719
H1C.ET.86.ETH2220	-----	9031
H1D.CD.84.84ZR085	-----	8975
H1F1.BE.93.VI850	-----	8903
H1G.SE.93.SE6165	-----	9074
H1H.CF.98.056	-----	8953
H1J.SE.93.SE7887	-----	8943
H1K.CM.96.MP535	-----	8604
H101.AE.TH.90.CM240	-----	9203
H102.AG.NG.x.IBNG	-----	9201
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H1N.CM.95.YBF30	-----	9182
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H10.CM.91.MVP5180	-----	9793
H1P.FR.06.RBF168	-----	8654
CPZ.CM.01.SIVcpzCAM13	-----	9284
CPZ.CM.05.SIVcpzEK505	-----	9132
CPZ.CM.05.SIVcpzLB7	-----	9170
CPZ.CM.05.SIVcpzMB66	-----	9281
CPZ.CM.05.SIVcpzMT145	-----	9208
CPZ.CM.-.SIVcpzMB897	-----	9167
CPZ.CM.-.SIVcpzDP943	-----	9247
CPZ.CM.98.CAM3	-----	9170
CPZ.CM.98.CAM5	-----	9261
CPZ.GA.88.GAB1	-----	9811
CPZ.GA.88.GAB2	-----	9146
CPZ.US.85.CPZUS	-----	9781
CPZ.CD.90.ANT	-----	9068
CPZ.TZ.08.TAN1	-----	9326
CPZ.TZ.2001.TAN2	-----	9346
CPZ.TZ.2002.TAN3_1	-----	9400
GOR.CM.2007.SIVgor2139_287	-----	9252
GOR.CM.2007.SIVgorCP2135con	-----	9246
GOR.CM.2004.SIVgorCP684con	-----	9143
H2A.DE.x.BEN	---C-----	10359
H2A.GW.x.ALI	-----	10353
H2A.SN.x.ST	-----	9672
H2B.CI.x.EH0	---C-----	10242
H2B.GH.86.D205	-----	10269
H2C.CI.92.ABT96	-----	9599
H2U.FR.96.L2034	-----	9607
SMM.SL.92.SL92B	-----	9613
SMM.US.x.H9	-----	9638
SMM.US.x.PGM53	-----	10184
SMM.US.x.SIVsmH635F_L3	---C-----	10315
	3' LTR U5 end	
MAC.US.x.239	---C-----	10279
MAC.US.x.251_1A11	---C-----	10274
MAC.US.x.251_BK28	---C-----	10249
MAC.US.x.EMBL_3	-----	9264
STM.US.x.STM	-----	9892
MNE.US.x.MNE027	-----	9664
DEB.CM.99.CM40	-----	9227
DEB.CM.99.CM5	-----	9158
DEN.CD.x.CD1	-----	9679
LST.CD.88.447	-----	8588
LST.CD.88.485	-----	8589
LST.CD.88.524	-----	8594
LST.KE.x.lno7	-----	9957
SUN.GA.98.L14	6-CGG-----	10006
MND-1.GA.x.MNDGB1	-----	9215
OLC.CI.97.97CI12	-----	8678
WRC.CI.97.97CI14	-----	9484
WRC.CI.98.98CI04	-----	9461
WRC.GM.05.Pbt_05GM_X02	-----	8709
MND-2.CM.98.CM16	-----	9518
MND-2.GA.x.M14	-----	9529
MND-2.x.x.5440	---C-----	9647
DRL.x.x.FA0	---C-----	9731
MON.CM.99.L1	-----	9448
MON.NG.x.NG1	-----	8260
GSN.CM.99.CN166	-----	9414
GSN.CM.99.CN71	-----	9410
TAL.CM.08.266	-----	9338
TAL.CM.01.8023	-----	8845
MUS-1.CM.01.1085	-----	9420
MUS-1.CM.01.CM1239	-----	9508
MUS-2.CM.01.CM1246	-----	9484
MUS-2.CM.01.CM2500	-----	9430
SYK.KE.x.KE51	-----	9068
SYK.KE.x.SYK173	-----	9597
RCM.GA.x.GAB1	.T.-C---C-.GT	9465
RCM.NG.x.NG411	---C-A-C-.G	9557
GRV.ET.x.GRI_677	---A---C-----	9623
SAB.SN.x.SAB1C	---CT-----	10036
TAN.UG.x.TAN1	-----C-----	9784
VER.DE.x.AGM3	CCATGT-----	9325
VER.KE.x.9863	---A---C-----	9815
VER.KE.x.AGM155	---A---C-----	9794
VER.KE.x.TY01_patent	---A---C-----	9778
COL.CM.x.CGU1	-----	8728

V

HIV-1/SIVcpz Proteins

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V-1 Introduction

The HIV-1/SIVcpz protein alignments are based the complete genome nucleotide alignment, but in some cases a few sequences were removed because they were too short to be informative (especially in Nef), had many stop codons or a strange segment of amino acids. As with the other alignments in this compendium, they are intended to display the usual genetic variation of the world-wide HIV epidemic in a compact form. They are annotated in more detail than the complete genome nucleotide alignment.

V-2 Annotated features

Features of HIV-1 annotated in the alignment that follows.

Feature	Protein	Location	Page
Gag start, p17 start	Gag	1	318
membrane binding	Gag	1-30	318
nuclear localization	Gag	11-35	318
nuclear localization	Gag	106-116	318
phosphorylation site	Gag	112	318
p17 end	Gag	132	318
p24 start	Gag	133	318
CyPA binding	Gag	205-241	320
major homology region	Gag	285-304	320
p24 end	Gag	364	322
p2 start	Gag	365	322
p2 end	Gag	377	322
p7 start	Gag	378	322
Zn motif	Gag	392-404	322
Zn motif	Gag	413-425	322
p7 end	Gag	432	322
p1 start	Gag	433	322
p1 end	Gag	448	322
p6 start	Gag	449	322
Vpr binding	Gag	455-460	324
Vpr binding	Gag	489-494	324
p6 end, Gag end	Gag	501	324
Gag-Pol TF start	Pol	1	326
Gag-Pol TF end	Pol	56	326
protease start	Pol	57	326
protease end	Pol	155	328
p66, p51 RT start	Pol	156	328
M41L	Pol	196	328
D67N	Pol	222	328
K70R	Pol	225	328
D110 catalytic site	Pol	265	328
polymerase motif	Pol	337-342	330
T215Y	Pol	370	330
K219Q	Pol	374	330
p51 RT end	Pol	595	332
p15 RNase H start	Pol	596	332
p66 RT, p15 RNase H end	Pol	715	334
p31 Integrase start	Pol	716	334
p31 Integrase end	Pol	1003	338
Pol end	Pol	1003	338
Vif start	Vif	1	340
Vif end	Vif	192	342
Vpr start	Vpr	1	344
oligomerization	Vpr	2-43	344
amphipathic α -helix	Vpr	16-34	344
H(S/N)RIG motifs	Vpr	73-84	344
frameshift in HXB2	Vpr	72	344
Vpr end in HXB2	Vpr	79	344

Feature	Protein	Location	Page
Vpr end	Vpr	97	344
Tat start	Tat	1	346
disulfide bonding	Tat	22-37	346
NLS	Tat	49-57	346
exon 1 end	Tat	72	346
exon 2 start	Tat	73	346
Tat end	Tat	101	346
Rev start	Rev	1	348
exon 1 end	Rev	25	348
exon 2 start	Rev	26	348
NLS	Rev	34-49	348
Leu-rich effector domain	Rev	75-83	348
Rev end	Rev	116	348
Vpu start	Vpu	1	350
transmembrane domain	Vpu	1-27	350
cytoplasmic domain	Vpu	28-82	350
α -helix	Vpu	31-49	350
phos	Vpu	53	350
phos	Vpu	57	350
α -helix	Vpu	59-72	350
Vpu end	Vpu	83	350
Env start	Env	1	352
signal peptide	Env	30	352
gp120 start	Env	31	352
glycosylation NVT	Env	88-90	352
V1	Env	131-156	352
glycosylation NDT	Env	136-138	352
glycosylation NSS	Env	141-143	354
glycosylation NCS	Env	156-158	354
V2	Env	156-196	354
glycosylation NIS	Env	160-162	354
glycosylation NDT	Env	186-188	354
glycosylation NTS	Env	197-199	354
glycosylation NKT	Env	230-232	354
glycosylation NGT	Env	234-236	354
glycosylation NVS	Env	241-243	354
glycosylation NGS	Env	262-264	354
glycosylation NFT	Env	276-278	354
glycosylation NTS	Env	289-291	356
glycosylation NCT	Env	295-297	356
V3	Env	296-331	356
glycosylation NNT	Env	301-303	356
V3 tip	Env	312-315	356
glycosylation NNT	Env	339-341	356
glycosylation NKT	Env	356-358	356
CD4	Env	368	356
CD4	Env	370	356
V4	Env	385-418	356
glycosylation NST	Env	386-388	356
glycosylation NST	Env	392-394	356
glycosylation NST	Env	397-399	356
glycosylation NNT	Env	406-408	356
CD4	Env	427	358

Feature	Protein	Location	Page
CD4	Env	429	358
CD4	Env	438	358
glycosylation NIT	Env	448-450	358
V5	Env	460-471	358
glycosylation NES	Env	463-465	358
fusion peptide	Env	510-527	358
gp120 end	Env	511	358
gp41 start	Env	512	358
immunodominant region	Env	588-607	360
glycosylation NAS	Env	611-613	360
glycosylation NKS	Env	616-618	360
glycosylation NHT	Env	624-626	360
glycosylation NYT	Env	637-639	360
glycosylation NGS	Env	750-752	362
glycosylation NAT	Env	816-818	362
gp41 end	Env	857	362
Env end	Env	857	362
Nef start	Nef	1	364
myristoylation	Nef	2-7	364
acidic cluster	Nef	62-65	364
poly-P helix	Nef	69-78	364
phos	Nef	77	364
phos	Nef	81	364
HXB2 premature Nef end	Nef	124	364
normal Nef end	Nef	207	366

V-3 Sequences

Sequences included in the HIV-1 protein alignments.

Name	Accession	Proteins	Author	Reference
B.FR.83.HXB2	K03455	All	van Beveren, C.P.	(in) Weiss,RL, Teich,N, Varmus,H and Coffin,J(Eds); <i>RNA TUMOR VIRUSES, SECOND EDITION, 2</i> , Vol 2: 1102-1123; Cold Spring Harbor Laboratory, Cold Spring Harbor (1985)
A.CD.02.02CD_KTB035	AM000055	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Nef	Vidal, N.	<i>ARHR</i> 22 (2):182-187 (2006)
A.SN.01.DDJ369	AY521631	All	Meloni, S.T.	<i>J Virol</i> 78 (22):12438-12445 (2004)
A1.AU.03.PS1044_Day0	DQ676872	All	Li, B.	<i>J Virol</i> 81 (1):193-201 (2007)
A1.CY.06.CY171	FJ388950	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Kousiappa, I.	<i>ARHR</i> 25 (8); 727-40 (2009)
A1.GE.99.99GEMZ011	DQ207944	All	Zarandia, M.	<i>ARHR</i> 22 (5):470-476 (2006)
A1.IT.02.60000	EU861977	All	Riva, C.	<i>ARHR</i> 24 (10); 1319-25 (2008)
A1.KE.02.ML1990	EU110092	All	Land, A.M.	<i>ARHR</i> 24 (6):865-872 (2008)
A1.RU.08.PokA1Ru	FJ864679	All	Bychenko	Unpublished

Name	Accession	Proteins	Author	Reference
A1.RW.93.93RW037A	AB287379	All	Sakamoto	Unpublished
A1.SE.95.SE8538	AF069669	All	Carr, J.K.	<i>AIDS</i> 13 (14):1819-1826 (1999)
A1.TZ.01.A341	AY253314	All	Arroyo, M.A.	<i>ARHR</i> 20 (8):895-901 (2004)
A1.UA.01.01UADN139	DQ823357	All	Saad, M.D.	<i>ARHR</i> 22 (8):709-714 (2006)
A1.UG.99.99UGA07072	AF484478	All	Harris, M.E.	<i>ARHR</i> 18 (17):1281-1290 (2002)
A1.ZA.04.04ZASK162B1	DQ396400	All	Rousseau, C.M.	<i>J Virol Methods</i> 136 (1-2):118-125 (2006)
A2.CD.97.97CDKTB48	AF286238	All	Gao, F.	<i>ARHR</i> 17 (8):675-688 (2001)
A2.CY.94.94CY017_41	AF286237	All	Gao, F.	<i>ARHR</i> 17 (8):675-688 (2001)
B.AR.04.04AR143170	DQ383750	All	Pando, M.A.	<i>Retrovirology</i> 3 , 59 (2006)
B.AU.04.PS1038_Day174	DQ676871	All	Li, B.	<i>J Virol</i> 81 (1):193-201 (2007)
B.BO.99.BOL0122	AY037270	All	Carr, J.K.	<i>AIDS</i> 15 (15):F41-F47 (2001)
B.BR.05.BREPM1081	FJ195091	All	Diaz, R.S.	<i>Virology</i> 381 (2):184-193 (2008)
B.CA.97.CANB3FULL	AY779553	All	Cali, L.	<i>ARHR</i> 21 (8):728-733 (2005)
B.CN.05.05CNHB_hp3	DQ990880	All	Tan, J.-x.	<i>Chin Med J(Engl)</i> 120 (9); 831-3 (2007)
B.CO.01.PCM001	AY561236	All	Sanchez, G.I.	<i>Am J Trop Med Hyg</i> 74 (4); 674-7 (2006)
B.CU.99.Cu19	AY586542	All	Sierra, M.	<i>JAIDS</i> 45 (2):151-160 (2007)
B.CY.06.CY165	FJ388947	Gag, Pol, Vif, Vpr, Tat, Vpu, Env	Kousiappa, I.	<i>ARHR</i> 25 (8); 727-40 (2009)
B.DE.86.D31	U43096	All	Kreutz, R.	<i>ARHR</i> 8 (9):1619-1629 (1992)
B.DK.04.PMVL_012	EF514699	All	Andresen, B.S.	<i>ARHR</i> 23 (11):1442-8 (2007)
B.DO.05.05DO_160884	EU839597	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Nadai, Y.	<i>PLoS ONE</i> 2009 ;4(3):e4814 Epub 2009 Mar 12
B.EC.89.EC003	AY173959	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Hierholzer, J.	<i>ARHR</i> 18 (18):1339-1350 (2002)
B.ES.07.X2231	EU786680	All	Fernandez-Garcia, A.	<i>ARHR</i> 25 (1); 93-102 (2009)
B.FR.92.92FR_BX08	AY713411	All	Brown, B.K.	<i>J Virol</i> 79 (10):6089-6101 (2005)
B.GA.88.OYI	M26727	All	Huet, T.	<i>AIDS</i> 3 (11):707-715 (1989)
B.GB.86.GB8_46R	AJ271445	All	Farrar, G.H.	<i>J Med Virol</i> 34 (2):104-113 (1991)
B.GE.03.03GEMZ004	DQ207940	All	Zarandia, M.	<i>ARHR</i> 22 (5):470-476 (2006)
B.HT.05.05HT_129389	EU839602	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Nadai, Y.	<i>PLoS ONE</i> 2009 ;4(3):e4814 Epub 2009 Mar 12
B.IN.x.11807	EF694037	All	Lakhashe, S.	<i>ARHR</i> 24 (1):92-99 (2008)
B.JM.05.05JM_KJ108	EU839605	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Nadai, Y.	<i>PLoS ONE</i> 2009 ;4(3):e4814 Epub 2009 Mar 12
B.JP.05.DR6538	AB287363	All	Sakamoto	Unpublished
B.KR.04.04KMH5	DQ295193	All	Cho	Unpublished
B.MM.99.mSTD101	AB097870	All	Takebe, Y.	<i>AIDS</i> 17 (14):2077-87 (2003)
B.NL.00.671_00T36	AY423387	All	Geels, M.J.	<i>J Virol</i> 77 (23):12430-12440 (2003)
B.RU.04.04RU128005	AY682547	All	Galkin, A.N.	<i>ARHR</i> 22 (11):1192-1197 (2006)

Name	Accession	Proteins	Author	Reference
B.TH.00.00TH_C3198	AY945710	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Watanaveeradej, V.	<i>ARHR</i> 22 (8):801-7 (2006)
B.TT.01.01TT_CRC50069	EU839608	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Nadai, Y.	<i>PLoS ONE</i> 2009 ;4(3):e4814 Epub 2009 Mar 12
B.TW.94.TWCYS	AF086817	All	Huang	Unpublished
B.UA.01.01UAKV167	DQ823362	All	Saad, M.D.	<i>ARHR</i> 22 (8):709-714 (2006)
B.US.07.CR0027M	FJ469689	All	Wang, Y.E.	<i>J Virol</i> 83 (4):1845-1855 (2009)
B.UY.01.01UYTRA1179	AY781127	All	Vinolses, J.	<i>Am J Trop Med Hyg</i> 72 (4):495-500 (2005)
B.YE.02.02YE507	AY795904	All	Saad, M.D.	<i>ARHR</i> 21 (7):644-648 (2005)
B.ZA.03.03ZAPS045MB2	DQ396398	All	Rousseau, C.M.	<i>J Virol Methods</i> 136 (1-2):118-125 (2006)
C.AR.01.ARG4006	AY563170	All	Carrion, G.	<i>ARHR</i> 20 (9):1022-1025 (2004)
C.BR.04.04BR013	AY727522	All	Sanabani, S.	<i>ARHR</i> 22 (2):171-176 (2006)
C.BW.00.00BW07621	AF443088	All	Novitsky, V.	<i>J Virol</i> 76 (11):5435-5451 (2002)
C.CN.98.YNRL9840	AY967806	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Qiu, Z.	<i>ARHR</i> 21 (12):1051-1056 (2005)
C.CY.05.CY040	FJ388901	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Kousiappa, I.	<i>ARHR</i> 25 (8); 727-40 (2009)
C.ES.07.X2118_2	EU884500	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Fernandez-Garcia, A.	<i>ARHR</i> 25 (1); 93-102 (2009)
C.ET.02.02ET_288	AY713417	All	Brown, B.K.	<i>J Virol</i> 79 (10):6089-6101 (2005)
C.GE.03.03GEMZ033	DQ207941	All	Zarandia, M.	<i>ARHR</i> 22 (5):470-476 (2006)
C.IL.98.98IS002	AF286233	All	Rodenburg, C.M.	<i>ARHR</i> 17 (2):161-168 (2001)
C.IN.03.D24	EF469243	All	Dash, P.K.	<i>Retrovirology</i> 5 (1):25 (2008)
C.KE.00.KER2010	AF457054	All	Dowling, W.E.	<i>AIDS</i> 16 (13):1809-1820 (2002)
C.MM.99.mIDU101_3	AB097871	All	Takebe, Y.	<i>AIDS</i> 17 (14):2077-87 (2003)
C.MW.93.93MW_965	AY713413	All	Brown, B.K.	<i>J Virol</i> 79 (10):6089-6101 (2005)
C.SN.90.90SE_364	AY713416	All	Brown, B.K.	<i>J Virol</i> 79 (10):6089-6101 (2005)
C.SO.89.89SM_145	AY713415	All	Brown, B.K.	<i>J Virol</i> 79 (10):6089-6101 (2005)
C.TZ.02.CO178	AY734556	All	Arroyo, M.A.	<i>AIDS</i> 19 (14):1517-1524 (2005)
C.US.98.98US_MSC3018	AY444800	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Tovanabutra, S.	<i>ARHR</i> 21 (5):424-429 (2005)
C.UY.01.TRA3011	AY563169	All	Carrion, G.	<i>ARHR</i> 20 (9):1022-1025 (2004)
C.YE.02.02YE511	AY795906	All	Saad, M.D.	<i>ARHR</i> 21 (7):644-648 (2005)
C.ZA.05.05ZAPSK240B1	DQ369991	All	Rousseau, C.M.	<i>J Virol Methods</i> 136 (1-2):118-125 (2006)
C.ZM.02.02ZM108	AB254141	All	Tatsumi	Unpublished
D.CD.83.ELI	K03454	All	Alizon, M.	<i>Cell</i> 46 (1):63-74 (1986)

Name	Accession	Proteins	Author	Reference
D.CM.01.01CM_0009BBY	AY371155	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Kijak, G.H.	<i>ARHR</i> 20 (5):521-530 (2004)
D.CY.06.CY163	FJ388945	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Kousiappa, I.	<i>ARHR</i> 25 (8); 727-40 (2009)
D.KE.97.ML415_2	AY322189	All	Fang, G.	<i>J Infect Dis</i> 190 (4):697-701 (2004)
D.KR.04.04KBH8	DQ054367	All	Cho	Unpublished
D.SN.x.SE365	AB485648	All	Takekawa	Unpublished
D.TD.99.MN011	AJ488926	All	Vidal, N.	<i>JAIDS</i> 33 (2):239-246 (2003)
D.TZ.01.A280	AY253311	All	Arroyo, M.A.	<i>ARHR</i> 20 (8):895-901 (2004)
D.UG.99.99UGK09958	AF484499	All	Harris, M.E.	<i>ARHR</i> 18 (17):1281-1290 (2002)
D.YE.02.02YE516	AY795907	All	Saad, M.D.	<i>ARHR</i> 21 (7):644-648 (2005)
D.ZA.90.R1	EF633445	All	Jacobs, G.B.	<i>ARHR</i> 23 (12):1575-8 (2007)
F1.AO.06.AO_06_ANG125	FJ900269	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Guimaraes, M.L.	<i>Retrovirology</i> 6 , 39 (2009)
F1.AR.02.ARE933	DQ189088	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Aulicino, P.C.	<i>ARHR</i> 21 (2):158-164 (2005)
F1.BE.93.VI850	AF077336	All	Laukkanen, T.	<i>Virology</i> 269 (1):95-104 (2000)
F1.BR.07.07BR844	FJ771010	All	Sanabani, S.S.	<i>Virol J</i> 2009 Jun 16;6:78
F1.ES.x.P1146	DQ979023	All	Sierra	Unpublished
F1.FI.93.FIN9363	AF075703	All	Laukkanen, T.	<i>Virology</i> 269 (1):95-104 (2000)
F1.FR.96.96FR_MP411	AJ249238	All	Triques, K.	<i>ARHR</i> 16 (2):139-151 (2000)
F1.JP.04.DR6082	AB480298	All	Sakamoto	Unpublished
F1.RO.96.BCI_R07	AB485658	All	Takekawa	Unpublished
F1.RU.08.D88_845	GQ290462	All	Fernandez-Garcia, A.	<i>ARHR</i> 25 (11):1187-1191 (2009)
F2.CM.97.CM53657	AF377956	All	Carr, J.K.	<i>Virology</i> 286 (1):168-181 (2001)
G.BE.96.DRCBL	AF084936	All	Oelrichs, R.B.	<i>ARHR</i> 15 (6):585-589 (1999)
G.CM.04.178_15	FJ389363	All	Yamaguchi, J.	<i>ARHR</i> 25 (4):469-473 (2009)
G.CU.99.Cu74	AY586547	All	Sierra, M.	<i>JAIDS</i> 45 (2):151-160 (2007)
G.ES.05.P962	EU786670	All	Fernandez-Garcia, A.	<i>ARHR</i> 25 (1); 93-102 (2009)
G.GH.03.03GH175G	AB287004	All	Takekawa	Unpublished
G.KE.93.HH8793_12_1	AF061641	All	Salminen, M.	<i>ARHR</i> 8 (9):1733-1742 (1992)
G.NG.01.01NGPL0669	DQ168576	All	Carr	Unpublished
G.PT.x.PT2695	AY612637	All	Esteves	Unpublished
G.SE.93.SE6165	AF061642	All	Carr, J.K.	<i>Virology</i> 247 (1):22-31 (1998)
H.BE.93.VI991	AF190127	All	Janssens, W.	<i>AIDS</i> 14 (11):1533-1543 (2000)
H.BE.93.VI997	AF190128	All	Janssens, W.	<i>AIDS</i> 14 (11):1533-1543 (2000)
H.CF.90.056	AF005496	All	Gao, F.	<i>J Virol</i> 72 (7):5680-5698 (1998)
H.GB.00.00GBAC4001	FJ711703	All	Holzmayr, V.	<i>ARHR</i> 25 (7):721-726 (2009)
J.CD.97.J_97DC_KTB147	EF614151	All	Abecasis, A.B.	<i>J Virol</i> 81 (16):8543-8551 (2007)
J.SE.93.SE9280_7887	AF082394	All	Laukkanen, T.	<i>ARHR</i> 15 (3):293-297 (1999)
J.SE.94.SE9173_7022	AF082395	All	Laukkanen, T.	<i>ARHR</i> 15 (3):293-297 (1999)
K.CD.97.97ZR_EQTB11	AJ249235	All	Triques, K.	<i>ARHR</i> 16 (2):139-151 (2000)
K.CM.96.96CM_MP535	AJ249239	All	Triques, K.	<i>ARHR</i> 16 (2):139-151 (2000)

Name	Accession	Proteins	Author	Reference
01_AE.CF.90.90CF11697	AF197340	All	Anderson, J.P.	<i>J Virol</i> 74 (22):10752-10765 (2000)
01_AE.CN.07.07JSWX045	FJ441290	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Guo	Unpublished
01_AE.HK.04.HK001	DQ234790	All	Tsui	Unpublished
01_AE.JP.x.DR0492	AB253423	All	Sakamoto	Unpublished
01_AE.TH.04.BKM	DQ314732	All	Thitithanyanont	Unpublished
01_AE.US.00.00US_MSC1164	AY444804	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Tovanabutra, S.	<i>ARHR</i> 21 (5):424-429 (2005)
01_AE.VN.98.98VNND15	FJ185235	All	Liao, H.	<i>Virology</i> 391 (1):51-56 (2009)
02_AG.CM.02.02CM_0013BBY	AY371125	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Kijak, G.H.	<i>ARHR</i> 20 (5):521-530 (2004)
02_AG.CY.05.CY048	FJ388902	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Kousiappa, I.	<i>ARHR</i> 25 (8); 727-40 (2009)
02_AG.ES.06.P1261	EU786671	All	Fernandez-Garcia, A.	<i>ARHR</i> 25 (1); 93-102 (2009)
02_AG.FR.91.DJ263	AF063223	All	Carr, J.K.	<i>Virology</i> 247 (1):22-31 (1998)
02_AG.GH.03.03GH181AG	AB286855	All	Sakamoto	Unpublished
02_AG.LR.x.POC44951	AB485636	All	Takekawa	Unpublished
02_AG.NG.01.PL0710	DQ168577	All	Carr	Unpublished
02_AG.SE.94.SE7812	AF107770	All	Laukkanen	Unpublished
02_AG.SN.98.98SE_MP1211	AJ251056	All	Toure-Kane, C.	<i>ARHR</i> 16 (6):603-609 (2000)
02_AG.US.00.00US_MSC3083	AY444811	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Tovanabutra, S.	<i>ARHR</i> 21 (5):424-429 (2005)
02_AG.UZ.02.02UZ0683	AY829214	All	Carr, J.K.	<i>JAIDS</i> 39 (5):570-575 (2005)
03_AB.RU.97.KAL153_2	AF193276	All	Liitsola, K.	<i>ARHR</i> 16 (11):1047-1053 (2000)
04_cpx.CY.94.94CY032_3	AF049337	All	Gao, F.	<i>J Virol</i> 72 (12):10234-10241 (1998)
05_DF.BE.x.VI1310	AF193253	All	Laukkanen, T.	<i>Virology</i> 269 (1):95-104 (2000)
06_cpx.AU.96.BFP90	AF064699	All	Oelrichs, R.B.	<i>ARHR</i> 14 (16):1495-1500 (1998)
07_BC.CN.98.98CN009	AF286230	All	Rodenburg, C.M.	<i>ARHR</i> 17 (2):161-168 (2001)
08_BC.CN.97.97CNGX_6F	AY008715	All	Piyasirisilp, S.	<i>J Virol</i> 74 (23):11286-11295 (2000)
09_cpx.GH.96.96GH2911	AY093605	All	McCutchan, F.E.	<i>ARHR</i> 20 (8):819-826 (2004)
10_CD.TZ.96.96TZ_BF061	AF289548	All	Koulinska, I.N.	<i>ARHR</i> 17 (5):423-431 (2001)
11_cpx.CM.95.95CM_1816	AF492624	All	Wilbe, K.	<i>ARHR</i> 18 (12):849-56 (2002)
12_BF.AR.99.ARMA159	AF385936	All	Carr, J.K.	<i>AIDS</i> 15 (15):F41-F47 (2001)
13_cpx.CM.96.96CM_1849	AF460972	All	Wilbe, K.	<i>ARHR</i> 18 (12):849-56 (2002)
14_BG.ES.00.X605	AF450096	All	Delgado, E.	<i>JAIDS</i> 29 (5):536-543 (2002)
15_01B.TH.99.99TH_MU2079	AF516184	All	Viputtijul, K.	<i>ARHR</i> 18 (16):1235-1237 (2002)
16_A2D.KR.97.97KR004	AF286239	All	Gao, F.	<i>ARHR</i> 17 (8):675-688 (2001)
17_BF.AR.99.ARMA038	AY037281	All	Carr, J.K.	<i>AIDS</i> 15 (15):F41-F47 (2001)
18_cpx.CU.99.CU76	AY586540	All	Thomson, M.M.	<i>AIDS</i> 19 (11):1155-63 (2005)
19_cpx.CU.99.CU7	AY894994	All	Casado, G.	<i>JAIDS</i> 40 (5):532-537 (2005)
20_BG.CU.99.Cu103	AY586545	All	Sierra, M.	<i>JAIDS</i> 45 (2):151-160 (2007)
21_A2D.KE.99.KER2003	AF457051	All	Dowling, W.E.	<i>AIDS</i> 16 (13):1809-1820 (2002)

Name	Accession	Proteins	Author	Reference
22_01A1.CM.01.01CM_0001BBY	AY371159	All	Kijak, G.H.	<i>ARHR</i> 20 (5):521-530 (2004)
23_BG.CU.03.CB118	AY900571	All	Sierra, M.	<i>JAIDS</i> 45 (2):151-160 (2007)
24_BG.CU.03.CB378	AY900574	All	Sierra, M.	<i>JAIDS</i> 45 (2):151-160 (2007)
25_cpx.CM.02.1918LE	AY371169	All	Kijak, G.H.	<i>ARHR</i> 20 (5):521-530 (2004)
26_AU.CD.02.02CD_MBTB047	FM877782	All	Vidal, N.	<i>ARHR</i> 25 (8):823-832 (2009)
27_cpx.FR.04.04CD_FR_KZS	AM851091	All	Vidal, N.	<i>ARHR</i> 24 (2):315-321 (2008)
28_BF.BR.99.BREPM12609	DQ085873	All	Sa Filho, D.J.	<i>ARHR</i> 22 (1):1-13 (2006)
29_BF.BR.01.BREPM16704	DQ085876	All	Sa Filho, D.J.	<i>ARHR</i> 22 (1):1-13 (2006)
31_BC.BR.04.04BR142	AY727527	All	Sanabani, S.	<i>ARHR</i> 22 (2):171-176 (2006)
32_06A1.EE.01.EE0369	AY535660	All	Adojaan, M.	<i>JAIDS</i> 39 (5):598-605 (2005)
33_01B.MY.05.05MYKL007_1	DQ366659	All	Tee, K.K.	<i>JAIDS</i> 43 (5):523-529 (2006)
34_01B.TH.99.OUR2478P	EF165541	All	Tovanabuttra, S.	<i>ARHR</i> 23 (6):829-833 (2007)
35_AD.AF.05.05AF095	EF158041	All	Sanders-Buell, E.	<i>ARHR</i> 23 (6):834-839 (2007)
36_cpx.CM.00.00CMNYU830	EF087994	All	Powell, R.L.	<i>ARHR</i> 23 (8):1008-1019 (2007)
37_cpx.CM.00.00CMNYU926	EF116594	All	Powell, R.L.	<i>ARHR</i> 23 (7):923-933 (2007)
38_BF1.UY.03.UY03_3389	FJ213783	All	Ruchansky	Unpublished
39_BF.BR.04.04BRRJ179	EU735535	All	Guimaraes, M.L.	<i>AIDS</i> 22 (3):433-435 (2008)
40_BF.BR.05.05BRRJ055	EU735537	All	Guimaraes, M.L.	<i>AIDS</i> 22 (3):433-435 (2008)
42_BF.LU.03.luBF_05_03	EU170155	All	Struck	Unpublished
43_02G.SA.03.J11223	EU697904	All	Badreddine, S.	<i>ARHR</i> 23 (5):667-674 (2007)
N.CM.95.YBF30	AJ006022	All	Simon, F.	<i>Nat Med</i> 4 (9):1032-1037 (1998)
N.CM.97.YBF106	AJ271370	All	Roques, P.	<i>AIDS</i> 18 (10):1371-1381 (2004)
N.CM.02.DJO0131	AY532635	All	Bodelle, P.	<i>ARHR</i> 20 (8):902-908 (2004)
N.CM.04.04CM_1015_04	DQ017382	All	Yamaguchi, J.	<i>ARHR</i> 22 (1):83-92 (2006)
O.BE.87.ANT70	L20587	All	Vanden Haesevelde, M.	<i>J Virol</i> 68 (3):1586-1596 (1994)
O.CM.x.BCF06	AB485666	All	Takekawa	Unpublished
O.CM.91.MVP5180	L20571	All	Gurtler, L.G.	<i>J Virol</i> 68 (3):1581-1585 (1994)
O.CM.96.96CMA102	AY169803	All	Yamaguchi, J.	<i>ARHR</i> 19 (11):979-988 (2003)
O.CM.97.97CMABB447	AY169813	All	Yamaguchi, J.	<i>ARHR</i> 19 (11):979-988 (2003)
O.CM.98.98CMA104	AY169802	All	Yamaguchi, J.	<i>ARHR</i> 19 (11):979-988 (2003)
O.CM.99.99CMU4122	AY169815	All	Yamaguchi, J.	<i>ARHR</i> 19 (11):979-988 (2003)
O.FR.92.VAU	AF407418	All	Vartanian, J.P.	<i>J Gen Virol</i> 83 (Pt 4):801-805 (2002)
DO.FR.08.RBF208	GQ351296	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Vessiere, A.	<i>AIDS</i> 24 (7): 1079-82 (2010)
O.SN.99.99SE_MP1299	AJ302646	All	Toure-Kane, C.	<i>ARHR</i> 17 (12):1211-1216 (2001)
O.US.x.I_2478B	AB485668	All	Takekawa	Unpublished
O.US.97.97US08692A	AY169805	All	Yamaguchi, J.	<i>ARHR</i> 19 (11):979-988 (2003)
O.US.99.99USTWLA	AY169814	All	Yamaguchi, J.	<i>ARHR</i> 19 (11):979-988 (2003)
P.FR.09.RBF168	GU111555	All	Plantier, J.-C.	<i>Nat Med</i> 15 (8): 871-2 (2009)
CPZ.CD.90.ANT	U42720	All	Vanden Haesevelde, M.M.	<i>Virology</i> 221 (2):346-350 (1996)
CPZ.CM.05.SIVcpzMT145	DQ373066	All	Keele, B.F.	<i>Science</i> 313 (5786):523-526 (2006)
CPZ.GA.88.GAB1	X52154	All	Huet, T.	<i>Nature</i> 345 (6273):356-359 (1990)
CPZ.TZ.00.TAN1	AF447763	All	Santiago, M.L.	<i>J Virol</i> 77 (3):2233-2242 (2003)
CPZ.US.85.US_Marilyn	AF103818	All	Gao, F.	<i>Nature</i> 397 (6718):436-441 (1999)

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	membrane binding										phosphorylation site										p17 end p24 start																																																										
	Gag start, p17 start/nuclear localization										nuclear localization																																																																				
B. FR. 83. HXB2	MGARASVLGGELDRWEIKRLRPGGKKYKLIKHIWVASRELRFVAVNPLGLETSEGRQILGQLQPSLQTSSEELRSLVNTYATLYCVHQRIEIKDTKEALDKIEEENKSKKKAQQA...										DTGHSNQ...										VSNQYPYIVONIQGMVH										144																																																
H. BE. 93. V1991	K	A	-	R	-	L	-	L	-	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	146										
H. BE. 93. V1997	K	A	-	R	-	L	-	L	-	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144										
H. CF. 90. 056	K	A	-	R	-	L	-	L	-	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144										
H. GB. 00. 00GBAC4001	K	A	-	R	-	L	-	L	-	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	143										
J. CD. 97. J. 97DC KTB147	x	-	E	S	I	-	S	E	A	-----	W	-	R	R	-	E	-----	R	R	-	L	-----	D	Y	L	-----	**	A	-	G	E	-	V	I	-	D	-	A	-	I	K	-	F	-	E	-----	*	D	R	-	L	-	S	-	E	-	K	K	E	-----	V	K	Y	N	S	-----	H	-	L	-	M	-	E	L	-----	132			
J. SE. 93. SE9280 7887	I	-	K	-	D	-----	Q	R	I	-	L	-----	D	L	-----	S	A	K	-	O	-	V	-	A	-	T	-	I	-	K	-	F	-	L	-	V	-	A	-	T	-	I	-	K	-	F	-	E	-----	*	D	R	-	L	-	S	-	E	-	K	K	E	-----	V	K	Y	N	S	-----	H	-	L	-	M	-	E	L	-----	144
J. SE. 94. SE9173 7022	I	-	K	-	D	-----	Q	R	I	-	L	-----	D	L	-----	S	A	K	-	O	-	V	-	A	-	T	-	I	-	K	-	F	-	L	-	V	-	A	-	T	-	I	-	K	-	F	-	E	-----	*	D	R	-	L	-	S	-	E	-	K	K	E	-----	V	K	Y	N	S	-----	H	-	L	-	M	-	E	L	-----	144
K. CD. 97. 97ZR E0TB11	K	-	K	-	Q	-----	R	-	L	-----	L	N	-	V	-----	I	R	-	L	-----	D	L	-----	S	A	K	-	O	-	V	-	A	-	T	-	I	-	K	-	F	-	E	-----	*	D	R	-	L	-	S	-	E	-	K	K	E	-----	V	K	Y	N	S	-----	H	-	L	-	M	-	E	L	-----	140						
K. CM. 96. 96CM MP535	K	-	K	-	Q	-----	R	-	L	-----	L	N	-	V	-----	I	R	-	L	-----	D	L	-----	S	A	K	-	O	-	V	-	A	-	T	-	I	-	K	-	F	-	E	-----	*	D	R	-	L	-	S	-	E	-	K	K	E	-----	V	K	Y	N	S	-----	H	-	L	-	M	-	E	L	-----	140						
01 AE. CF. 90. 90CF11697	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144								
01 AE. CN. 07. 0735WX045	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144								
01 AE. HK. 04. HK001	I	-	T	-	E	K	-	A	-----	R	-	L	-----	L	D	-	A	D	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144							
01 AE. JP. x. DR0492	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144								
01 AE. TH. 04. BKM	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144								
01 AE. US. 00. 00U5 MSC1164	T	-	K	-	A	-----	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	142								
01 AE. VN. 98. 98VND15	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144								
02 AG. CM. 02. 02CM 0013BBY	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144								
02 AG. CY. 05. CY048	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	144								
02 AG. ES. 06. P1261	I	-	K	-	S	-----	V	-----	R	-	L	-----	L	D	-	A	D	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	141								
02 AG. FR. 91. DJ263	K	-	S	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	141								
02 AG. GH. 03. 03GH181AG	I	-	Q	-	A	-----	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	141								
02 AG. LR. x. P044951	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	141								
02 AG. NG. 01. PL0710	K	-	S	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	137								
02 AG. SE. 94. SE7812	K	-	A	-----	R	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	141								
02 AG. SN. 98. 98SE MP1211	x	-	K	-	A	-----	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V	-----	G	-	I	-	N	O	R	T	-	P	-	A	A	-----	D	T	G	H	S	N	O	-----	V	S	O	N	Y	P	I	V	O	N	I	Q	G	M	V	H	-----	140								
02 AG. US. 00. 00U5 MSC3083	K	-	S	-----	S	-	R	-	L	-----	L	D	-	A	D	-	Q	-	A	K	-	T	D	-	I	-	V	-----	D	V																																																	

Proteins

HIV Sequence Compendium 2010

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	CyPA binding										major homology region									
B.FR.83.HXB2																				
H.BE.93.VI991																				
H.BE.93.VI997																				
H.CF.90.056																				
H.GB.00.00GBAC4001																				
J.CD.97.J.97DC.KTB147																				
J.SE.93.SE9289.7897																				
J.SE.94.SE9173.7022																				
K.CD.97.972R.EQT811																				
K.CM.96.96CM.MP535																				
01 AE.CF.90.90CF11697																				
01 AE.CN.07.073SWX045																				
01 AE.HK.04.HK001																				
01 AE.JP.x.DR0492																				
01 AE.TH.04.BKM																				
01 AE.US.00.00US.MSC1164																				
01 AE.VN.98.98VND15																				
02 AG.CM.02.02CM.0013BBY																				
02 AG.CY.05.CY048																				
02 AG.ES.06.PI261																				
02 AG.FR.91.DJ263																				
02 AG.GH.03.03GH121AG																				
02 AG.LR.x.P044951																				
02 AG.NG.01.PL0710																				
02 AG.SE.94.SE7812																				
02 AG.SN.98.98SE.MP1211																				
02 AG.US.00.00US.MSC3083																				
02 AG.UZ.02.02UZ0683																				
03 AB.RU.97.KAL153_2																				
04 cpx.CY.94.94CY032_3																				
05 DF.BE.x.VI1310																				
06 cpx.AU.96.BFP90																				
07 BC.CN.98.98CN009																				
08 BC.CN.97.97CN06_6F																				
09 cpx.GH.96.96GH2911																				
10 CD.TZ.96.96TZ.BF061																				
11 cpx.CM.95.95CM.1816																				
12 BF.AR.99.ARMA159																				
13 cpx.CM.96.96CM.1849																				
14 BG.ES.00.X605																				
15 01B.TH.99.99TH.MU2079																				
16 A2D.KR.97.97KR004																				
17 BF.AR.99.ARMA038																				
18 cpx.CU.99.CU76																				
19 cpx.CU.99.CU7																				
20 BG.CU.99.CU103																				
21 A2D.KE.99.KER2003																				
22 01A1.CM.01.01CM.0001BBY																				
23 BG.CU.03.CB118																				
24 BG.CU.03.CB378																				
25 cpx.CM.02.1918LE																				
26 AU.CD.02.02CD.MBT047																				
27 cpx.FR.04.04CD.FR.KZ5																				
28 BF.BR.99.BREPM12609																				
29 BF.BR.01.BREPM16704																				
31 BC.BR.04.04BR142																				
32 06A1.EE.01.EE0369																				
33 01B.MY.05.05MYKL007_1																				
34 01B.TH.99.01B2478P																				
35 AD.AF.05.05AF095																				
36 cpx.CM.00.00CMNYU830																				
37 cpx.CM.00.00CMNYU926																				
38 BF1.UY.03.UY03_3389																				
39 BF.BR.04.04BRRJ179																				
40 BF.BR.05.05BRRJ055																				
42 BF.LU.03.03BF.05_03																				
43 02G.SA.03.03J11223																				
N.CM.95.YBF30																				
N.CM.97.YBF106																				
N.CM.02.02J00131																				
N.CM.04.04CM.1015_04																				
O.BE.87.ANT70																				
O.CM.x.BCF06																				
O.CM.91.MVP5180																				
O.CM.96.96CMA102																				
O.CM.97.97CMA86447																				
O.CM.98.98CMA104																				
O.CM.99.99CMU4122																				
O.FR.92.VAU																				
DO.FR.08.RBF208																				
O.SN.99.99SE.MP1299																				
O.US.x.I.2478B																				
O.US.97.97US08692A																				
O.US.99.99USTWLA																				
P.FR.09.RBF168																				
CPZ.CD.90.ANT																				
CPZ.CM.05.SIVcpzMT145																				
CPZ.GA.08.GAS																				
CPZ.TZ.00.TAN1																				
CPZ.US.85.US_Marilyn																				

[illegible]

F.HR. 93.H.XHB2
 H.BE. 93.VI991
 H.BE. 93.VI997
 H.CF. 90.056
 H.GB. 00.00GBAC4001
 J.C. 97.J. 97DC KTB147
 J.SE. 93.SE9288 7887
 J.SE. 93.0913 7022
 K.C. 97.97ZR E0T11
 K.CM. 96.96CM MP535
 01 AE. CF. 90.90CF I1697
 01 AE. CN. 07.07JSWX045
 01 AE. HK. 04.HK001
 01 AE. JP. x.DR04M
 01 AE. TH. 04.BK92
 01 AE. VN. 93.09US MSC1164
 01 AE. VN. 98.98VNDV15
 02 AG. CM. 02.02ZCM 0013BBY
 02 AG. CY. 05.CY048
 02 AG. ES. 06.P1261
 02 AG. FR. 01.DJ263
 02 AG. GR. 01.01GUS MSC181AG
 02 AG. LR. x.P0C44951
 02 AG. NG. 01.PL0710
 02 AG. SE. 94.SE57812
 02 AG. SN. 98.98SE MP1211
 02 AG. SN. 98.98SN MSC3083
 02 AG. UZ. 02.02UZ0683
 03 AB. RU. 97.KA153 2
 04 cpv. CY. 94.CY032_3
 05 DF. BE. x.VI1310
 06 cpv. AU. 96.BF90
 07 BC. CN. 97.CNXC009
 08 BC. CN. 97.97CNCX 6F
 09 cpv. GH. 96.96GH2911
 10 CD. TZ. 96.96TZ BF061
 11 cpv. CM. 95.95CM 1816
 12 BF. AR. 99.ARMA159
 13 cpv. CM. 96.96CM 1849
 14 BG. ES. 00.X605
 15 01B. TH. 99.99TH MU2079
 16 A2D. KR. 97.97KR004
 17 BF. AR. 99.ARMA038
 18 cpv. CU. 99.CU76
 19 cpv. CU. 99.CU3
 20 BG. CU. 99.CU103
 21 01D. KE. 99.KE92003
 22 01B. CN. 98.01CM 0001BF
 23 BG. CU. 03.CB118
 24 BG. CU. 03.CB378
 25 cpv. CN. 02.1918LE
 26 AU. CD. 02.02ZCD MBT0047
 27 cpv. FR. 04.04CD FR KZ5
 28 BF. BR. 09.BREP112609
 29 BF. BR. 01.BREP116704
 31 BC. BE. 04.04BR142
 32 06A1. ER. 01.EE0369
 33 01B. MY. 05.05MYKL007_1
 34 01B. TH. 99.09UR0478P
 35 AD. AF. 05.05AF095
 36 cpv. CM. 00.00CMNYU830
 37 cpv. CM. 00.00CMNYU926
 38 BF1.UY. 03.UY03 3389
 39 BF. BR. 04.04BRR1075
 40 BF. BR. 05.BSRR1355
 42 BF. LU. 03.LU0F 05_03
 43 02G. SA. 03.11223
 N.CM. 95.YBF30
 N.CM. 97.YBF106
 N.CM. 02.DJ00131
 N.CM. 04.04CM 1015_04
 0.B. 87.ANT70
 0.CM. x.BCF06
 0.CM. 91.MV95180
 0.CM. 96.96CMA102
 0.CM. 97.97CMBAB447
 0.CM. 98.98CMA104
 0.CM. 99.99CMA1422
 0.F. 92.VAU
 DO. FR. 08.RBF208
 O.SN. 99.99SE MP1299
 O.US. x.I 2478B
 O.US. 97.97US08692A
 O.US. 99.99USTWLA
 P.FR. 09.RBF168
 CPZ. CD. 90.ANT
 CPZ. CM. 95.SIVcpzMT145
 CPZ. CN. 98.CAB1
 CPZ. TZ. 00.TAN1
 CPZ. US. 85.US Marilyn

[illegible]

Vpr binding				Vpr binding p6 end, Gag end				
..EPTA	..PPEESFRSGV	..ETTTPPQKQ	..EPIDKEL	..YPLTSLRSLFGNDPSSQ*				500
	-A-LGM-E	-I-F-Q	-MG-R-QS	-S-V-K	-LL-			500
	-A-LLGR-E	-I-PS-P	-QK-R-Q	-P-I-K	-L-			497
S	-A-LGM-E	-I-S-P	-QK-QV	-P-V-K				498
S	-A-NM-E	-I-PS	-QK-R-Q	-HP-SI-K				499
S	-A-HGM-E	-I-PSL	-QK-R-Q	-HP-SI-K				491
	-A-DLWM-E	-INPS-L	-QK-R-Q	-HP-AI-K				499
	-A-LLGM-E	-IAS-P	-DOEGRCOT	-P-SI-K				499
S	-A-DGMRE	-I-PS	-LYPSLKOLKQ	-QK-R-P	-SV-K			501
	-A-LGM-E	-I-PS	-QK-R-PT	-P-AI-K				499
	-A-LGM-E	-VI-S-P	-QK-QV	-P-V-K				497
S	-T-IWGM-G	-IVS-P	-QK-R-QA	-S-SV-K				498
	-A-NGM-E	-I-PS-L	-QK-R-QQ	-P-SI-K				497
	-A-LGM-E	-M-S-P	-QK-R-Q	-VP-V-K	-L-P			497
	-AG-YGME	-I-SSL-K	-QT-R-OP	-A-				504
	-ME	-I-SSL	-N-R-P	-ST-AI-K	-LL-			499
	-A-NL-M-E	-I-SSL	-LETR-P	-YN-AI-K	-LL-			497
	-F-E	-A-S	-T-M	-A-S				497
	-A-SF-E	-K	-M	-A-K				496
	-F-E	-F	-QK-RG	-YP-D-K	-*-K			503
P	-F-E	-SR-QD	-MA-K	-H*-*				504
S	-F-E	-SP-S	-QT-Q	-A-K				504
	-F-E	-V-L	-T	-K				502
SRLEP	-F-E	-M-S	-V	-A-K	-*-K			499
P	-F-E	-A-S	-V	-A-K	-L-			502
S	-F-E	-A-S	-K-Q	-C-SA				501
S	-A-F-E	-A-S	-Q-NQD	-YP-A				499
RLEP	-F-E	-S-S	-T-E	-SV-K				471
	-A-F-E	-A-S	-VG-DM	-WD				501
	-F-E	-A-S	-G	-A-K				502
I-PPE	-F-G	-S	-N-P	-A				500
S	-A-GF-E	-S-E	-T	-A-K				508
	-F-E	-P-S	-SR	-A-K	-*			496
	-F-G	-P-S	-V	-A-K				496
	-KF-E	-I-PS	-V	-A-K				500
	-F-E	-I-S	-T-M	-A				501
	-F-E	-A-S	-T	-A			-K	501
PSQSR	-F-E	-A-S-R	-T	-A-K				504
	-F-E	-K	-VE	-A-K	-S-*			511
	-F-E	-A-S	-D	-L	-A-K			493
	-KF-E	-AP	-G-TGE	-A-K	-LL-			502
	-F-E	-Q-S	-D	-A-E				504
G	-F-E	-A	-A-K					501
PRT	-F-E	-A	-Q	-A-K	-LL-			506
P	-A-GF-E	-A-S	-R	-C				510
	-A-KF-E	-A-S	-R-E-M	-A	-L-			499
	-A-F-E	-I-S-P	-TV-D	-A-K	-S-			503
	-A-FE	-PS-P	-K-R-P	-K-S	-L-			501
PPL	-A-FA	-PS-P	-K-R-P	-K-S	-L-			492
	-A-KFE	-MPT	-K-R-P	-K-S	-L-			502
	-A-PA	-PA-P	-SK-R-P	-K-S	-L-			493
PLE	-A-FE	-IPN-S	-SK-R-P	-K-S	-L-			492
	-A-FE	-PA-P	-K-P	-K-S	-L-			499
A-PLÉ	-A-FE	-A-P-P	-LK-R-A	-K	-L-			491
	-A-YE	-PA-P	-K-R-P	-I-K	-S-			498
	-A-APS	-PA-P	-QK-P	-YKE-SA	-L-P			491
PLPT	-A-FE	-PT-L	-K-R-P	-K-S	-L-			497
	-A-KF-E	-AL-A	-LKER-P	-K-S	-L-			506
	-A-FE	-PA-P	-K-R-P	-K	-L-			491
	-A-GF	-PA-P	-KEDREP	-K	-L-			491
	-A-FE	-PA-P	-QK-R-P	-K-S	-L-			493
PPAESFRVRPEPTA	-A-FE	-PT-P	-LKEH	-K-S	-L-			486
	-A-FE	-Dx-PA-P	-KGG-P	-I-K	-S-			504
	-A-FE	-AL	-SK-P	-K-S	-L-P			491
	-A-FE	-A-PS-PR	-QK-R-P	-K-S	-L-			489
	-L-FE	-PA-P	-AK	-K-S	-LLP			488
	-L-FE	-PT	-LK-G-S	-H	-K-S			489
	-L-FE	-PA-P	-K-R-P	-I-K	-S-			49
	-A-GF-E	-I-PS	-QK	-A-K	-L-			491
	-I-GF-E	-V-PS	-QK-DK	-EL	-A-K			501
	-A-GF-E	-I-PS	-OR		-L-			497
	-A-GF-E	-M-P-R	-OR	-C	-A-K			500
	-A-I-PS	-QK-N	-D	-K	-L-K			501
	-T-GF-E	-M-PS	-EQAQKQ	-A				500
	-A-GF-E	-I-PS	-QK-DK	-EL	-A-K			507
	-A-I-GF-E	-IKPS	-QK-DK	-EL-SA	-K			503
	-A-GF-E	-I-PS	-QK-Q	-D-V	-K-S			497
	-A-GF-E	-I-PS	-QK-DK	-DL	-K-S			497
	-A-GF	-I-PS	-QK	-K	-S			501
	-A-GFRE	-M-PS-P	-QK-EGQ	-GLYP	-A-K	-Q+*		501
	-A-GFRE	-I-PS-P	-QK-EG	-YP	-A-K	-+L		464
	-A-GFRE	-I-PS-P	-QK-G	-YP	-A-K	-*		495
PPA	-A-GF-E	-IAPS-P	-QK-EG	-YP	-A-K	-E		494
	-A-GF	-EVT-LH	-QK-EGQ	-YP	-A-K	-*		505
	-A-LGTR	-V-PS-PR	-QK-EGQ	-YP	-A-K	-*		493
	-A-GFKE	-I-PS	-QK-EGQ	-GLYP	-A-K	-S-+P		496
	-A-E	-IAPS-L	-QKEEG	-YP	-A-K	-S-*		497
S	-A-GFRE	-PS-P	-QK-EGM	-YP	-A-K	-*		492
	-A-GF-E	-I-PS-PR	-QK-DQ	-CP	-K	-Q+*		495
	-A-GF-E	-I-PS-P	-QK-M	-YP	-K	-*		501
	-A-N-GF-E	-IAPS	-QKE	-S	-K	-Q+K		493
	-A-GF-E	-IAPS	-RE	-S	-T	-K-S		493
S	-A-GF-Q	-IAPS	-QKE-D	-I	-K-S	-*		497
	-A-C-GFRE	-IAPS-AR	-RE-S	-P	-A-K	-*		500
S	-A-GF-R	-APS-P	-RE-E	-L	-K	-*		499
	-A-GF-E	-IAPS-P	-KE-I	-H	-A-K	-S-*		498
	-A-GF	-IAPS	-RE	-P	-A-K	-Q+		498
	-A-GF-E	-IAPS	-K	-K	-S	-*		497
	-A-LGF-E	-IAPS	-MKE	-YP	-K	-S-*		499

	Vpr binding		Vpr binding p6 end, Gag end	
B. FR. 83. HXB2	...EPTA...	...PPEESFRSGV...	...ETTTTPQKQ...	...EPIDKEL...YPLTSLRSLFGNDPSSQ*
H. BE. 93. VI991	...A--GF-E	...I-PS-PR	...LKEQ-P	...Q*
H. BE. 93. VI997	...A--GF-E	...M-SS-P	...LK--P	...FA-K
H. CF. 90. 056	...A--GF-E	...M-PS-P	...QLKDKE	...P-A
H. GB. 00. 00GBAC4001	...A-C-GF-E	...M-P-P	...MKE-P	...S-LL
J. CD. 97. J. 97DC KTB147	...A--GF-E	...KI-PS	...RKELY	...SA-K
J. SE. 93. SE9280 7897	...A--LGL	...ETPS-P	...K	...K
J. SE. 94. SE9173 7022	...A--LGF	...ETPS-P	...K	...K
K. CD. 97. 97ZR E0TB11	...A--GF-E	...KI-PS-LR	...MK-O-Q	...GP--K--S-L
K. CM. 96. 96CM MP535	...A--GF-E	...I-PS-PR	...TK--Q	...SP--K--S-L
01 AE. CF. 90. 90CF11697	...A--LGM-E	...I-SF-P	...OK--H	...PS-V-K
01 AE. CN. 07. 07J5WX045	...A--DWGMEG	...I-SL-P	...OK-R-H	...SV-K
01 AE. HK. 04. HK001	...A--NW-R	...I-SL-L	...OK--H	...PS-SI-K
01 AE. JP. x. DR0492	...A--WEMRE	...I-SL-L	...OK--H	...PP-A-K
01 AE. TH. 04. BKM	...A--NW-M-E	...K-SL-M	...QE-DP	...P-V-K
01 AE. US. 00. 00US MSC1164	...A--NWGM-E	...I-SL-L	...OK--H	...PP-SV
01 AE. VN. 98. 98VNN015	...A--NWGM-E	...I-SL-L	...OK--H	...PP-SI-K
02 AG. CM. 02. 02CM 0013BBY	...A--GM-E	...PSS-P	...K	...YP-A-K
02 AG. CY. 05. CY048	...A--GM-E	...I-S-P	...G-GI	...YP--K
02 AG. ES. 06. P1261	...A--GT-E	...I-SS-P	...G-GI	...YP-A-K
02 AG. FR. 91. DJ263	...A--LGM-E	...I-S-P	...AR-OG	...YP-A-K
02 AG. GH. 03. 03GH181AG	...A--LGM-E	...I-SS-P	...R-G	...YP--K
02 AG. LR. x. P0C44951	...A--GM-E	...I-S-P	...R-G	...YP--K
02 AG. NG. 01. PL0710	...A--LGM-E	...I-SS-PQ	...R-G	...YP--K
02 AG. SE. 94. SE7812	...A--LGI-E	...I-SS-P	...G-G	...YP-A-K
02 AG. SN. 98. 98SE MP1211	...A--GM-E	...I-SS-P	...G-G	...YP--K
02 AG. US. 00. 00US MSC3083	...A--LGM-E	...I-S-P	...G-G	...YP-A-K
02 AG. UZ. 02. 02UZ0683	...A--NWGM-E	...I-SS-PQ	...R-G	...YP-A-K
03 AB. RU. 97. KAL153 2	...S	...A-N-GM-E	...I-PS-L	...QK-R-Q
04 cpx. CY. 94. 94CY032 3	...A--CLERKE	...SS-L	...R	...K--S-L
05 DF. BE. x. VI1310	...S	...A--F-E	...IASS-P	...QK-EG
06 cpx. AU. 96. BFP90	...I--GF-E	...IAPS-P	...SKE-E	...KGL-A-K
07 BC. CN. 98. 98CN009	...A--F-E	...S	...T	...K
08 BC. CN. 97. 97CNGX 6F	...A--FE	...PA	...K-R-P	...S-L
09 cpx. GH. 96. 96GH2911	...S	...A--GM-E	...S6-P	...XKDGEOP
10 CD. TZ. 96. 96TZ BF061	...A--GF-E	...I-PS	...QK--P	...H-A-K
11 cpx. CM. 95. 95CM 1816	...A--GF-E	...VAPS	...KEELY	...A-K
12 BF. AR. 99. ARMA159	...A--GF-E	...I-SS-P-R	...QK-EGQ	...YP-A-K
13 cpx. CM. 96. 96CM 1849	G--PPESR	...PEPTA	...A--GF-E	...IAPS-P
14 BG. ES. 00. X605	...A--GF-E	...IAPS-P	...KE-V	...A-K
15 01B. TH. 99. 99TH MU2079	...S	...A--NWGM-E	...SL-L	...QK-R-H
16 A2D. KR. 97. 97KR004	...A--D-GM-E	...PL	...LKNR-Q	...HT-AI-K
17 BF. AR. 99. ARMA038	...L--GF-E	...TI-PQ-P	...K-EG	...YP-A-K
18 cpx. CU. 99. CU76	...A--LGF-E	...IAPS-P	...SKEEK	...FS-K
19 cpx. CU. 99. CU7	...GF-E	...I-PS	...DQK	...A-K
20 BG. CU. 99. CU103	...A--GF-E	...IAPS-P	...GQKE-D	...I-K
21 A2D. KE. 99. KER2003	...A--M-GF-E	...I-PS	...QK	...SV-K
22 01A1. CM. 01. 01CM 0001BBY	...A--VGM-E	...I-SS	...QRE-Q	...PP-V-K
23 BG. CU. 03. CB118	...A--GF-E	...IAPS-P	...G-KEQD	...I-K
24 BG. CU. 03. CB378	...A-E	...IAPS-P	...QKE-D	...I-K
25 cpx. CM. 02. 1918LE	...A--LGF-E	...I-PS-P	...QK	...L-MA-K
26 AU. CD. 02. 02CD MBT047	V--	...A--NLGMEE	G--PS-P	...KEG-Q
27 cpx. FR. 04. 04CD FR KZ5	...A--LGIME	M-SY-P	...LK--P	...V-K
28 BF. BR. 99. BREPM12609	...A--F-E	...PS-P	...QKEEG	...YP-A-K
29 BF. BR. 01. BREPM16704	S--	...A--LGF-E	R-PS-P	...QK-EGK
31 BC. BR. 04. 04BR142	...PPASR	...LEPTA	A--FE	...PS-P
32 06A1. EE. 01. EE0369	...A--FEE	...AA-SS	...KK	...SA
33 01B. MY. 05. 05MYKL007 1	...F-E	...V	...V	...K
34 01B. TH. 99. OUR2478P	...F-E	G--S	...S	...SA-K
35 AD. AF. 05. 05AF095	...A--GF-E	I-PS	...QK-G-Y	...A-K
36 cpx. CM. 00. 00CMNYU830	...A-N-GI-E	MSSS	...SR-G	...YP--K
37 cpx. CM. 00. 00CMNYU926	...A--EVKE	VASS-L	...G	...YP-A-K
38 BF1. UY. 03. UY03 3389	S--	...A--GF-EETPPP	KQE	...QK-EGM
39 BF. BR. 04. 04BRJ179	P--	...TA	A--LMF-E	A-S
40 BF. BR. 05. 05BRJ055	...A--GF-E	I-P-P	...QKNEG	YP--K
42 BF. LU. 03. LU0F 05 03	RPEP	...TA	A--GF-E	I-PS-L
43 02G. SA. 03. J11223	...A--GF-E	IAPS	...RE-S	P-A-K
N. CM. 95. YBF30	K--	...L--YGFQE	KS-QGKEMQE	NOERT-N
N. CM. 97. YBF106	N. CM. 97. YBF106	...L--YGFQE	KS-QGKEMQE	NOERT-T
N. CM. 02. DJ00131	RK	...L--YGFQE	KS-QGKEMQE	NOERT-T
N. CM. 04. 04CM 1015 04	K--	...L--YGFQE	KS-QGKEMQE	NOERT-NSL
O. BE. 87. ANT70	H-S	...M-EVVK-Q	NOEQ.KGG	PN.EL
O. CM. x. BCF06	S-S	...M-EVKEL	K--S	GGEKE
O. CM. 91. MVP5180	S-S	...M-EAVKEQ	NOEQ.KGD	QE
O. CM. 96. 96CMA102	P-S	...M-EVMO-Q	KNONO.EOR	D.PN
O. CM. 97. 97CMA0447	P-S	...M-EVVK-Q	NOEQ.KGD	GD.ON
O. CM. 98. 98CMA104	A-S	...M-EVVK-Q	NOEQ.KGD	SN
O. CM. 99. 99CMU4122	S-S	...M-EE-K-P	SOEQ.KGD	PN
O. FR. 92. VAU	S-S	...M-EMMK-Q	EDON--G	QN
DO. FR. 08. RBF208	P-S	...M-EVMO-Q	N--E	KGEON
O. SN. 99. 99SE MP1299	S-S	...M-TEEMK-Q	NOEQ.KED	QN
O. US. x. I 2478B	P-S	...M-EVMK-Q	N--G	KGDP
O. US. 97. 97US08692A	P-S	...M-EVMK-Q	NOEQ.KGD	PT
O. US. 99. 99USTWLA	PPA-S	...M-EVVK-Q	NOEQ.KED	SN
P. FR. 09. RBF168	Q	...M-MEED	M-RDK-RE	xEE-E-E
CPZ. CD. 90. ANT	V--	...A--I-YQEEH	KR-QKGLK	G.EE
CPZ. CM. 05. STVcpzMT145	...M--YGFQE	...M--YGFQE	...M--YGFQE	...M--YGFQE
CPZ. GA. 98. GAB1	...T--YGYQE	...T--YGYQE	...T--YGYQE	...T--YGYQE
CPZ. TZ. 00. TAN1	...EKGKAEQ	...AQT-VVP	...TAPPL-MTM	...KGGF-K-I-S-Q
CPZ. US. 85. US_Marilyn	...T-D-GYQE	...V-QEQKQKE	...KEPFO	...K--S-Q--E

Gag-Pol TF start										Gag-Pol TF end, protease start										
B. FR. 83. HXB2	FFREDLAFQ	GKAREFSSEQT	RANS	PTRELOVWG	RDNNPSEA	GADRGQT	VSFNFPQVTLWQRP	ITIKIGGQ	KEALLDTGADT	VLVEE	MSLPGRWKPKMIGG	IGGK	IKVRQYDQILIE	121						
A. CD. 02. 02CD KT8035	S	R	L P K	G	AS PRDG	LP	EG	E	L ISL	I	VRV	D	ID	K	120					
A. SN. 01. 00J369	N	Q			S APWEG	PL	EG	E	L ISL	I	V V	D	IN	K	121					
A1. AU. 03. P51044 Day0	N	Q	E K P		S GA WDG	LP	EG	G	PTLS	I	I VR E	R	D	ID	K R	121				
A1. CY. 06. CY171	N	Q	RE K	I	S RDG	PL P T	TE		R				D	ID	K	121				
A1. GE. 99. 99GEMZ011	N	Q	RE K	I	S T WDG	PL	TE	AS	I		VR		D	ID	K	121				
A1. IT. 02. 60000	N	Q			S GPLDG	KPL T	TE	AS C	I		V		D	IN	K	121				
A1. KE. 02. ML1990	T	Q	RE K	D	S A GDG	SPL	TE	D	PT	I	I VR	R	D	ID	K	121				
A1. RU. 08. POKAIRU	N	Q	RE K		S RFWDE	G PL	TE	D	PTC	I			D	ID	K	126				
A1. RU. 03. 93RW037A	N	Q	RE K		S S WDG	G PL	TE	D	PTC	I			D	ID	K	124				
A1. SE. 95. SE8538	N	Q	RE K		S D WDG	S LP	TE	G	PTLS	I	V V		D	IN	K R	121				
A1. TZ. 01. A341	N	Q	E K		G ND GDG	NSLP	TE	AG	L T S	I	V V		D	IN	K	121				
A1. UA. 01. 01UADN139	N	Q	RE K		S WDG	PL P T	TE	A	A	I	VR		D	ID	K	121				
A1. UG. 99. 99UGA07072	N	Q	E K		S A WDG	DLPL	TE	A	GPTLS	I	VR		D	IN	K R	121				
A1. ZA. 04. 04ZAK16281	N	Q			S WDG	LP T E	TE	AA	G	S	I	V	D	IN	K	121				
A2. CD. 97. 97CDKT848	N	Q	RE	D	S NG	LLA	TE	E	AA	VHPC	I	V E	R	D	IN	WK	114			
A2. CY. 94. 94CY017 41	N	Q	RE K	N	S ENG	LL P	TGD		IQ C	I	V E		D	IN	K	121				
B. AR. 04. 04AR143170	T	P	R	A				D	LS	I			D	N S		121				
B. AU. 04. PS1038 Day174	N	P			x	S L	XE		C	I	S		D	N x K		118				
B. BO. 99. B0L0122	N	P	RE			G	TE	PL	VS	G	I	K V		D	N	K	122			
B. BR. 05. BREPM1081	N	P	E	P			VEGS	P	I	YG	I	K V		D	N	K	122			
B. CA. 97. CANB3FUL	N	P												D	N	K	122			
B. CN. 05. 05CNH8 hp3	N	P	E											D	N	K	122			
B. CO. 01. PCMO01	N	P	E											D	N	K	121			
B. CU. 99. Cu19	N	P												D	N	K	121			
B. CY. 06. CY165	S	P	G P	RSNSGEFSDQT	KOTRA	NS	GND	S	A		I	K V	I	D	C K	K	124			
B. DE. 86. D31	N	P		A										D	IN	K	136			
B. DK. 04. PWWL 012	N	P	R E	LP		GK	S	L				R E		x	D	D	119			
B. DO. 05. 05DO 160884	N	P					EGP	P	VS	S	I						123			
B. EC. 89. EC003	N	P	R	F			N	E	I	I	S	I		D	N	K	123			
B. ES. 07. X2231	N	P					G	H		LG	I	V		D	N		125			
B. FR. 92. 92FR BX08	N	P					S	L						D	N		120			
B. GA. 98. 09YT	N	P												D	N		121			
B. GE. 96. G88 46R	N	P												D	N		121			
B. GE. 03. 03GEMZ004	N	P	E K	PP										D	N		121			
B. HT. 05. 05HT 129389	N	P	LP	D			VEG							D	N	K	120			
B. IN. x. 11807	N	P												D	N		121			
B. JM. 05. 05JM KJ108	T	PT												D	N		121			
B. JP. 05. 05JP DR6538	N	P	R	P										D	N	K	120			
B. KR. 04. 04KMH5	N	P												D	N		121			
B. MM. 99. mSTD101	N	P												D	N		121			
B. NL. 00. 671 00T36	N	P	E		PFSEQ	TRANS								D	N		131			
B. RU. 04. 04RU128005	N	P												D	N		120			
B. TH. 00. 00TH C3198	N	P	E	P										D	N	K	120			
B. TT. 01. 01TT CRC50069	N	P												D	N	K	120			
B. TW. 94. TWCYS	N	P	K	P										D	N	K	121			
B. UA. 01. 01UAKV167	N	P			PTN	RANS								D	N		124			
B. US. 07. CR0027M	N	P			IS	SG	R							D	N		128			
B. UY. 01. 01UYTRA1179	N	P												D	N		124			
B. YE. 02. 02YES07	N	P												D	N		121			
B. ZA. 03. 03ZAP5045MB2	N	P												D	N	K	121			
C. AR. 01. ARG4006	N	Q	K	XP										D	N		116			
C. BR. 04. 04BR013	N	Q			PTT	RANS								D	N		125			
C. BW. 00. 00BW07621	N	P												D	N		117			
C. CN. 98. YNRL9840	N	P												D	N		117			
C. CY. 05. CY048	N	Q				TNSS								D	N		122			
C. ES. 07. X2118 2	N	Q												D	N		123			
C. GE. 02. 02GET 288	N	Q												D	N		123			
C. GE. 03. 03GEMZ033	N	P												D	N		117			
C. IL. 98. 98IS002	N	P												D	N		117			
C. IN. 03. D24	N	P												D	N		121			
C. KE. 00. KER2010	N	P												D	N		125			
C. MM. 99. mIU10103	N	P												D	N		117			
C. MW. 93. 93MW 965	N	P												D	N		118			
C. SN. 90. 90SE 364	N	Q												D	N		113			
C. SO. 89. 89SM 145	N	P												D	N		128			
C. TZ. 02. C0178	N	P												D	N		117			
C. US. 98. 98US MSC3018	N	P												D	N		115			
C. UY. 01. UYTRA3011	N	P												D	N		117			
C. YE. 02. 02YES11	N	P												D	N		115			
C. ZA. 05. 05ZAPSK240B1	N	P												D	N		117			
C. ZM. 02. 02ZM108	N	P												D	N		112			
D. CD. 83. ELI	N	P												D	N		120			
D. CM. 01. 01CM 0009BBY	N	P												D	N		122			
D. CY. 06. CY163	N	P												D	N		120			
D. KE. 97. ML415 2	N	Q												D	N		120			
D. KR. 04. 04KHB8	N	Q												D	N		120			
D. SN. x. SE365	N	Q												D	N		126			
D. TD. 99. MN011	N	Q												D	N		126			
D. TZ. 01. A280	N	Q												D	N		122			
D. UG. 99. 99UGK09958	N	Q												D	N		122			
D. YE. 02. 02YES16	N	Q												D	N		122			
D. ZA. 90. R1	N	P												D	N		120			
F1. A0. 06. A0 06 ANG125	N	Q	RE	GK	K									D	N		123			
F1. AR. 02. ARE933	N	Q	E K P											D	N		121			
F1. BE. 93. V1850	N	Q												D	N		121			
F1. BR. 07. 07BR844	N	P	K	P	KV									D	N		127			
F1. ES. x. P1146	N	PE	GK	P										D	N		119			
F1. FR. 93. FTN9363	N	Q												D	N		120			
F1. FR. 96. 96FR MP411	N	Q												D	N		123			
F1. JP. 04. DR6082	N	Q												D	N		116			
F1. RO. 96. BCI R07	N	P												D	N		121			
F1. RU. 08. D88 845	N	Q	RE	x										D	N		120			
F2. CM. 97. CM53657	N	Q	E	WK										D	N		121			
G. BE. 96. DRCLB	N	Q												D	N		201			
G. CM. 04. 04 178 15	N	Q												D	N		201			
G. CU. 99. Cu74	T	Q	RE	G	K A									D	N		117			
G. ES. 05. P962	N	Q												D	N		120			
G. GH. 03. 03GH175G	N	Q												D	N		119			
G. KE. 93. HH8793 12 1	x	N												D	N		121			
G. NG. 01. 01NGRL0669	N	Q												D	N		120			
G. PT. x. PT269	N	Q												D	N		120			
G. SE. 93. SE6165	N	Q												D	N		120			

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B. FR. 83. HXB2	FFREDLAFIQ...GKAREFSSEQT...RANS...PTRREQLVQWG...RDNNSPSEA...GADROGT...VSFNFPQVTLWQRPLVTIKIGGQKKEALLDTGADDTVLEE. MSLPGRWPKPMKIGGIGFVKVRQYDOILIE	121	
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H. CF. 90. 056	---N--Q---RE-K-P-A	---S--R-RR---G-DPL---AEGQG---T-LS-I---I-V-E-R---IN-K---E-VA	120
H. GB. 00. 00GBAC4001	---N--Q---RE-K-P-A	---S--M-R-R---G-DTP---DEGK---L-I---I-V-E-R---IN-K---E-VA	119
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J. SE. 93. SE9289 7897	---Q---RE-L-P	---S--PRAR---GDL-P-T---EG---S-I---R-R---D-ID-RK---NEVP	119
J. SE. 94. SE9173 7032	---Q---RE-L-P	---S--PR-R---GDP-P-T---EG---S-I---R-R---D-ID-RK---NEVP	119
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01 AE. CF. 90. 90CF11697	---N--SO---E	---S--GDG---LL-P---E---PF-S-I-F---I-V-E---D-IN-K	121
01 AE. CN. 07. 073SWX045	---N--P---G-L	---S--R-GDG---LL-T---E---SL-I---I-V-E-R---D-IN-K	119
01 AE. HK. 04. HK001	---N--SO---E	---SGK-E---G-LL-T---E-G---PF-L-I---I-V-E---D-IN-K	118
01 AE. JP. x. DR0492	---N--Q---R	---S--K-GDE---G-LL-T---E---S-S-I---I-V-E-I---D-IN-Q-K-V-S-V---VP	121
01 AE. TH. 04. BKM	---N--Q---R	---S--K-EDG---GE-LL-N---G-P---S-S-I---I-V-E-I---D-IN-K	120
01 AE. US. 00. 00US MSC1164	---N--P---GK-N	---S--GDG---LL-T---E---SS-LS-I---I-V-E---D-IN-K	121
01 AE. VN. 98. 98VND15	---N--P---GK-N	---S--K-GDG---LL-T---E---SS-LS-I---I-V-E---D-IN-K	120
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02 AG. GH. 03. 03GH121AG	---N--Q---E-K-P	---S--RGG---LP---TEG---IS-I---I-V-E-I---D-IN-K	121
02 AG. LR. x. P044951	---N--Q---RE-KL	---S--RGG---LP---TEG---IS-I---I-V-E-I---D-IN-K	121
02 AG. NG. 01. PL0710	---N--Q---E-K	---S--KPGDG---LL-T---TEG-A---IS-I---AVR-E-I---D-IN-K	121
02 AG. SE. 94. SE7812	---N--Q---E-K	---AS-PWDR---LL---TGG---IS-LS-I---I-V-E-I---D-IN-K	121
02 AG. SN. 98. 98SE MP1211	---N--Q---E-KL	---S--WDG---LL-P---TGG---IP-S-I---F-VR-E-IK-N---K-IN-K	121
02 AG. US. 00. 00US MSC3083	---N--Q---E-K	---S--RGG---LP---TGG---IS-S-I---I-V-E-I---D-IN-K	121
02 AG. UZ. 02. 02UZ0683	---N--Q---E-K	---S--RGG---LL-A---TGG-E-A---IS-S-I---I-V-E-I---D-ID-K	121
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09 cpx. GH. 96. 96GH1211	---N--Q---R-LP	---S-S-R---G-TL-T---E-A---A-LS-I---IN-K	120
10 CD. TZ. 96. 96TZ BF061	---N--Q---E-P-A	---S--R-RR---G-SPL-P-T---EGGAI---S-I---I-V-A-R---IN-K	119
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14 BG. ES. 00. X605	---T-Q---I	---S--GDG---LL-T---E---YS-S-I---P-P-D-INF-K-N	120
15 01B. TH. 99. 99TH MU2079	---N--P---RE-N	---S--G-WNG---G-PL-A---EK---TH-C-I---V-E-R---D-IN-K	121
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19 cpx. CU. 99. CU7	---T-P---P-A	---C-R-RR---G-SSL-P---R-EGE---L-L-I---VR-I---D-IN-K	117
20 BG. CU. 99. Cu103	---N--Q---E-G-L-V	---S-DVR-R---PL-T---E---LS-I---N-K	120
21 A2D. KE. 99. KER2003	---N--Q---E-L-G	---S-RGDG---LL-P---E-E---AS-S-I---D-ID-K	121
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43 02G. SA. 03. J11223	---E-VS---RET-KLPDNNK	---E-H---AT-W-S---GEEHTGEGDAG---EPGEDRE---LSVPTL-I---VI-V---KEVR---I---LO-E-K	128
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0. US. x. I 2478B	---QI--SGG---HE-OLYA-TS	---API---DGGGDEGT---E---GT---KG-P-NRTL-C-IP-D-I-ARV-H-C-V---NN-IO-E-K	117
0. US. 97. 97US08692A	---QI--SGG---HE-OLYA-TS	---API---DGGGDEGT---ESGT-KGG---PNR---L-XCP-IP-D-I-ARV-H-C-V---NN-IO-E-K	114
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H.CF.90.056	-K-----I-----	T-----R-----S-----I-----	N-----Y-----		288
H.GB.00.00GBAC4001	-K-----I-----T-----	T-----R-----I-----	N-----Y-----		288
J.CD.97.J.97DC.KTB147	-E-K-----M-L-----I-----R-E-----	TQ-E-----F-----RV-----x-----	Y-----		287
J.SE.93.SE9280.7887	-E-K-----I-----M-L-----I-----	TQ-A-L-E-----R-----	Y-----		288
J.SE.94.SE9173.7022	-E-K-----I-----M-L-----I-----	TQ-A-L-E-----R-----	Y-----		288
K.CD.97.97ZR.EQT811	-Q-----M-----	T-----I-----P-----	K-----		290
K.CM.96.96CM.MP535	-Q-----M-----	T-----I-----P-----	K-----		290
01 AE.CF.90.90CF11697	-KR-----M-----D-T-----*-----*	T-K-E-----E-----V-----	Y-G-----		288
01 AE.CN.07.073SWX045	-KR-----M-L-----D-T-----	T-K-E-----A-----A-----H-S-----	G-----		288
01 AE.HK.04.HK001	-K-----M-----D-----	T-K-E-----I-----	K-X-----		286
01 AE.JP.x.DR0492	-K-----F-----MM-----D-T-----	T-K-E-----N-DR-----	N-----L-----		290
01 AE.TH.04.BKM	-K-----M-L-----D-T-----	T-K-E-----A-----	S-----		289
01 AE.US.00.00US.MSC1164	-K-----I-----M-----D-T-R-----	T-K-E-----S-----	N-----		290
01 AE.VN.98.98VNN015	-K-----M-----D-T-----	T-K-E-----G-----	S-----		289
02 AG.CM.02.02CM.0013BBY	-K-----M-----	T-----R-----	E-----		290
02 AG.CY.05.CY048	-KR-----M-----	T-M-----	H-E-----		290
02 AG.ES.06.P1261	-K-----M-----S-----	TD-----	KE-----RV-----		290
02 AG.FR.91.DJ263	-K-----M-----	T-L-----	K-----T-----		290
02 AG.GH.03.03GH181AG	-KR-----S-----M-----L-K-----	TD-A-----I-G-R-G-----S-----	K-----V-----		290
02 AG.LR.x.P0C44951	-K-----M-----	TD-A-----E-----	K-----		290
02 AG.NG.01.PL0710	-K-----M-----I-----	TD-M-----	K-----V-----		290
02 AG.SE.94.SE7812	-K-----M-----	TD-A-----R-----I-N-R-----I-----	K-----		290
02 AG.SN.98.98SE.MP1211	-K-M-S-----K-I-----L-----A-L-H-----	TD-A-----R-----I-N-R-----I-----	K-----		290
02 AG.US.00.00US.MSC3083	-K-V-----M-----	TD-----	H-----		290
02 AG.UZ.02.02UZ0683	-K-----M-----K-----	TD-----	Y-----		290
03 AB.RU.97.KAL153_2	-K-----M-L-----T-----	TD-K-----G-----	O-----		290
04 cpx.CY.94.94CY032_3	-K-----M-L-----	T-D-----I-----	PE-----		289
05 DF.BE.x.VI1310	-Q-----M-----	T-D-----R-----I-----R-----	I-----KE-----		290
06 cpx.AU.96.BFP90	-K-----I-----M-----	T-K-----	I-----K-----		292
07 BC.CN.98.98CN009	-K-----M-L-----	TA-D-----T-----I-----	R-----Y-----		290
08 BC.CN.97.97CN06.F6	-Q-----M-L-----	TA-D-----T-----D-----I-R-S-----	K-----V-----		286
09 cpx.GH.96.96GH2911	-Y-----M-----VD-----	T-K-----R-----I-----	Y-----		289
10 CD.TZ.96.96TZ.BF061	-E-K-----M-----	T-----	S-----		288
11 cpx.CM.95.95CM.1816	-K-----I-----M-L-----	T-----	A-----CV-----		290
12 BF.AR.99.ARMA159	-E-K-----I-----M-----	T-K-----	K-----V-----		297
13 cpx.CM.96.96CM.1849	-K-----I-----M-----L-----	T-----R-----I-----	S-----S-----		289
14 BG.ES.00.X605	-K-----M-L-----	T-K-E-----I-----	V-----S-----		289
15 01B.TH.99.99TH.MU2079	-EKR-----M-V-L-----	T-K-----	M-----R-----H-----		290
16 A2D.KR.97.97KR004	-K-----M-L-----	T-----	KE-----		290
17 BF.AR.99.ARMA038	-KR-----M-----	T-----I-----	PE-----		288
18 cpx.CU.99.CU76	-Q-----M-----	T-D-----I-----	S-----		289
19 cpx.CU.99.CU7	-K-----I-----M-----D-----	T-----D-----I-----	S-----		289
20 BG.CU.99.CU103	-K-----M-----Q-----	T-MD-----R-----I-----	x-----S-----		288
21 A2D.KE.99.KER2003	-K-----M-----A-----I-----	T-K-----I-----	Y-G-----T-----		290
22 01A1.CM.01.01CM.0001BBY	-K-----T-----M-----	T-----L-----I-----N-----	E-----		286
23 BG.CU.03.CB118	-KR-----I-----M-----	T-----	KE-----V-----		281
24 BG.CU.03.CB378	-S-K-----I-----I-----	T-ND-----R-----I-----	S-----KE-----		289
25 cpx.CM.02.1918LE	-K-----M-----V-----	IT-N-----V-----I-----	KE-----		288
26 AU.CD.02.02CD.MBT047	-K-----M-----	T-----R-----I-----R-----	I-----K-----		288
27 cpx.FR.04.04CD.FR.KZ5	-T-----M-----	T-----	KE-----		290
28 BF.BR.99.BREPM12609	-K-----M-----M-----	T-----K-----	KE-----V-----		290
29 BF.BR.01.BREPM16704	-K-----M-L-----R-----R-----	T-N-R-----I-----	N-----S-----		296
31 BC.BR.04.04BR142	-K-----M-----L-----	T-----R-----I-----	K-----R-----		290
32 06A1.EE.01.EE0369	-KR-----M-----	T-----I-----G-----	K-----		290
33 01B.MY.05.05MYKL007_1	-K-----I-----M-L-----N-R-----	A-A-----I-----	R-----K-----		290
34 01B.TH.99.09R2478P	-K-----M-L-----N-R-----	T-----I-----	R-----T-----		289
35 AD.AF.05.05AF095	-K-----I-V-M-----A-----	T-A-----R-----	R-----K-----		290
36 cpx.CM.00.00CMNYU830	-K-----M-----N-S-----S-----	T-N-----RV-----I-----	R-----S-----		288
37 cpx.CM.00.00CMNYU926	-D-VT-----I-----L-----	M-AD-----M-L-----K-----	R-----I-H-E-----		294
38 BF1.UY.03.UY03.3389	-A-----D-----L-----	L-A-L-EA-----N-R-----M-L-----K-----	N-----I-H-E-----		293
39 BF.BR.04.04BRJ179	-T-----M-----	T-----	KE-----		290
40 BF.BR.05.05BRJ055	-K-----I-----M-L-----	K-----	K-----		294
42 BF.LU.03.luBF.05.03	-E-K-----I-----M-----	T-L-----I-----	S-----		289
43 02G.SA.03.J11223	-E-K-----I-----M-----	T-L-----I-----	S-----		289
N.CM.95.YBF30	-Q-R-V-----	T-E-R-----R-----	I-----E-----Q-----C-K-----		297
N.CM.97.YBF106	-Q-R-V-----	T-E-R-----R-----	I-----E-----Q-----C-K-----		297
N.CM.02.DJ00131	-Q-R-V-----	T-E-R-----R-----	I-----E-----Q-----C-K-----		295
N.CM.04.04CM.1015_04	-Q-R-V-----	T-E-R-----R-----	I-----R-----Q-----C-K-----		297
0.BE.87.ANT70	-E-REVO-----I-GL-----AP-----SK-E-----TA-Q-Q-R-----I-----G-----E-----G-Q-Q-----C-P-----V-----	286			
0.CM.x.BCF06	VO-KEVO-----L-I-GL-----AP-----SK-E-----TA-Q-Q-R-----I-----G-----E-----G-Q-Q-----C-P-----V-----	286			
0.CM.91.MVP5180	VO-KEVO-----L-I-GL-----AP-----SR-E-----TA-Q-Q-R-----I-----G-----E-----G-Q-Q-----C-P-----V-----	286			
0.CM.96.96CMA102	-E-KEVO-----I-GL-----AP-----SK-E-----TA-Q-Q-R-----I-----G-----E-----G-Q-Q-----C-P-----V-----	287			
0.CM.97.97CMA86447	-E-K-VO-----I-GL-----AP-----SR-E-----TA-Q-Q-R-----I-----G-----E-----G-Q-Q-----C-P-----V-----	288			
0.CM.98.98CMA104	-E-REVO-----I-GL-----AP-----SR-E-----TA-Q-Q-R-----I-----G-----E-----G-Q-Q-----C-P-----V-----	286			
0.CM.99.99CMU4122	-E-REVO-----I-GL-----AP-----SR-E-----TA-Q-Q-R-----I-----G-----E-----G-Q-Q-----C-P-----V-----	285			
0.FR.92.VAU	LE-REVR-----L-I-GL-----TP-----SR-E-----T-K-L-Q-R-----I-----G-----E-----G-Q-Q-----C-PE-----V-----	287			
DO.FR.08.RBF208	LE-R-VK-----I-GL-----AP-----I-SK-E-----TA-Q-Q-R-----I-----N-----G-Q-Q-I-----C-P-----V-----	286			
0.SN.99.99SE.MP1299	-E-REVL-----I-GL-----AP-----I-SK-E-----TA-Q-Q-R-----I-----G-Q-Q-----C-P-----V-----	286			
0.US.x.I.2478B	-E-REVO-----I-GL-----AP-----I-SK-E-----TA-Q-Q-R-----I-----G-Q-Q-----C-P-----V-----	286			
0.US.97.97US08692A	-E-REVO-----I-GL-----AP-----I-SK-E-----TA-Q-Q-R-----I-----G-Q-Q-----C-P-----V-----	283			
0.US.99.99USTWLA	-E-R-MOR-----L-I-GL-----TP-----SR-E-----TA-Q-Q-R-----I-----x-----I-----*-----x-----Ex-QRQ-----C-P-----V-----	280			
P.FR.09.RBF168	-E-REVV-----I-L-----S-----S-----I-----A-K-----SK-E-----RA-Q-Q-Q-----T-----I-----S-----x-----x-----G-Q-R-----C-P-----V-----	282			
CPZ.CD.90.ANT	-GORTVLA-----L-N-----V-CLL-----KV-----E-----R-----SK-E-----K-DKL-A-N-R-----D-----I-----TS-----I-----Q-----I-----O-----F-----	290			
CPZ.CM.05.SIVcpzMT145	-E-K-ITS-----V-V-----V-KL-----D-K-F-----SA-----SK-E-----T-K-----E-----I-----	289			
CPZ.GA.88.GAB1	-E-R-VV-----L-V-----L-V-----S-K-----K-----E-----I-----	288			
CPZ.TZ.00.TAN1	-GNKEVRA-----E-I-----I-K-L-----S-V-K-Q-E-----SK-E-----T-KL-----AV-----I-----TS-----L-----R-RNM-----I-----P-----L-----	286			
CPZ.US.85.US.Marilyn	-E-R-Q-S-----S-K-----K-----R-----R-----A-----T-Q-----TRV-----I-----	292			

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12 BF.AR.99.ARMA159
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-----V-----KKGS-----AV-----VA-----R-----A-----M-----I-----D-----P-----E-----
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-----D-----A-----V-----D-----K-S-----A-----V-----VVL-----R-----MD-----D-----D-----S-----V-----D-----S-----DE-----
-----N-----A-----D-----KK-S-----V-----VV-----M-----C-----D-----D-----L-----D-----D-----K-----P-----E-----
-----D-----S-----D-----KRKST-----A-----I-----R-----A-----W-----D-----D-----L-----D-----D-----P-----E-----
T-----D-----D-----KR-ST-----I-----M-----I-----R-----A-----D-----D-----I-----D-----I-----P-----E-----
-----V-----V-----H-----K-----T-----A-----A-----I-----R-----D-----I-----D-----D-----A-----P-----
-----L-----E-----F-D-----AK-----I-----R-----D-----D-----E-----V-----D-----D-----S-----E-----
-----V-----R-----KQ-----A-----M-----D-----D-----S-----P-----
T-----L-----L-----S-----QY-----T-----A-----A-----A-----A-----E-----D-----S-----K-----R-----N-----
-----V-----L-----S-----KS-----S-----I-----R-----D-----MD-----D-----D-----N-----R-----D-----K-----S-----
-----D-----S-----T-----I-----R-----D-----A-----D-----D-----T-----D-----DK-----IIS-----
R-----S-----E-----D-----S-----A-----A-----D-----D-----IE-----S-----R-----D-----A-----S-----
-----V-----N-----K-----A-----R-----D-----D-----S-----R-----D-----K-----R-----S-----
-----V-----L-----K-----Q-----A-----M-----D-----D-----R-----A-----D-----D-----S-----
-----V-----L-----K-----Q-----A-----M-----D-----D-----I-----D-----D-----P-----
-----V-----N-----K-----A-----G-----I-----R-----DI-----D-----D-----S-----A-----
-----V-----L-----SI-----C-----A-----M-----S-----I-----DK-----S-----
A-----V-----L-----K-----A-----A-----M-----H-----A-----
-----E-----V-----L-----Y-----K-----V-----A-----A-----V-----E-----V-----R-----D-----K-----P-----
-----x-----L-----Y-----K-----T-----A-----A-----A-----A-----E-----E-----K-----S-----
-----Q-----A-----V-----S-----T-----S-----R-----AG-----I-----R-----A-----D-----V-----I-----DK-----S-----
-----V-----E-----ENS-----S-----T-----K-----R-----V-----A-----I-----R-----M-----T-----DK-----S-----
-----E-----E-----S-----T-----R-----V-----A-----I-----R-----A-----I-----I-----SK-----S-----
I-----E-----L-----LN-----TK-----A-----G-----I-----R-----D-----P-----Y-----R-----K-----P-----
-----E-----ED-----K-----T-----R-----AQ-----I-----R-----S-----D-----D-----I-----A-----
-----D-----ND-----K-----T-----SR-----R-----D-----D-----L-----V-----D-----D-----DK-----R-----I-----
-----S-----D-----S-----K-----T-----AM-----R-----D-----D-----D-----A-----V-----D-----D-----K-----I-----S-----
A-----A-----V-----L-----K-----T-----V-----A-----I-----R-----L-----SD-----D-----P-----E-----
-----A-----H-----K-----T-----L-----AM-----C-----I-----R-----L-----D-----D-----I-----D-----I-----NE-----
C.ET.02.02ET 288-----DD-----KR-----T-----L-----AL-----I-----R-----D-----D-----A-----V-----S-----I-----D-----I-----S-----
C.GE.03.03GEM2033-----V-----HD-----K-----T-----R-----AM-----R-----D-----A-----D-----R-----T-----A-----V-----S-----I-----D-----I-----I-----
C.IN.03.D24-----S-----A-----E-----D-----K-----T-----R-----AM-----R-----D-----A-----D-----R-----D-----A-----V-----S-----I-----D-----K-----S-----
C.KE.00.KER2010-----A-----A-----HD-----K-----T-----A-----R-----D-----D-----D-----D-----V-----V-----D-----K-----S-----
C.MM.99.mDU101 3-----A-----E-----HD-----K-----T-----AM-----R-----D-----D-----D-----D-----D-----D-----D-----K-----S-----
C.MW.93.93MW 965-----E-----HD-----K-----T-----AM-----R-----D-----D-----D-----D-----D-----D-----D-----DK-----S-----
C.SN.90.90SE 364-----HD-----K-----T-----A-----R-----D-----D-----D-----D-----D-----D-----D-----D-----I-----S-----
C.SO.89.89SM 145-----R-----Y-----HD-----K-----T-----AM-----R-----D-----A-----D-----Y-----D-----A-----M-----I-----D-----I-----S-----
C.TZ.02.C0178-----A-----D-----HD-----K-----T-----AM-----R-----D-----A-----D-----Y-----D-----A-----M-----I-----D-----DK-----IIS-----
C.US.98.98US MSC3018-----A-----Y-----HD-----K-----T-----R-----AM-----I-----R-----A-----D-----D-----D-----A-----M-----I-----D-----I-----S-----
C.UY.01.TRA3011-----A-----D-----HD-----K-----T-----R-----AM-----I-----R-----A-----D-----D-----D-----M-----V-----TKD-----I-----D-----IIS-----
C.YE.02.02YE511-----A-----HD-----K-----T-----AL-----V-----R-----D-----D-----S-----I-----D-----D-----SI-----
D.CD.83.ELI-----R-----V-----ES-----SW-----K-----KS-----A-----R-----S-----I-----R-----R-----A-----P-----
D.CM.01.01CM 0009BBY-----K-----K-----S-----W-----K-----KS-----A-----R-----S-----I-----I-----R-----A-----M-----P-----
D.CY.06.CY163-----K-----D-----W-----QY-----K-----K-----R-----AI-----I-----R-----A-----M-----S-----I-----D-----DK-----PF-----
D.KE.97.ML415 2-----L-----D-----QY-----K-----K-----R-----AQ-----C-----R-----R-----A-----I-----R-----R-----D-----DK-----SI-----
D.KR.04.04KBH8-----L-----D-----K-----R-----S-----K-----Q-----R-----R-----A-----I-----R-----R-----D-----D-----AIP-----
D.SN.x.SE365-----R-----T-----A-----V-----E-----W-----QY-----K-----T-----AL-----G-----I-----R-----A-----D-----M-----I-----D-----DK-----S-----
D.TD.99.MN011-----R-----T-----A-----V-----E-----W-----QY-----K-----T-----AL-----G-----I-----R-----A-----D-----M-----I-----D-----DK-----S-----
D.TZ.01.A280-----R-----V-----D-----W-----QY-----K-----T-----AL-----G-----I-----R-----A-----D-----M-----I-----D-----DK-----S-----
D.UG.99.99UGK09958-----R-----V-----D-----W-----QY-----K-----T-----AL-----G-----I-----R-----A-----D-----M-----I-----D-----DK-----S-----
D.YE.02.02YE516-----R-----V-----D-----W-----QY-----K-----T-----AL-----G-----I-----R-----A-----D-----M-----I-----D-----DK-----S-----
D.ZA.90.R1-----K-----V-----KE-----K-----S-----SQ-----C-----R-----A-----M-----T-----A-----SS-----K-----D-----RA-----S-----
F1.AO.06.AO 06 ANG125-----K-----R-----D-----N-----KV-----S-----AQ-----L-----D-----D-----SI-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.AR.02.ARE933-----A-----V-----PKL-----R-----T-----K-----S-----AQ-----C-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.BE.93.VI850-----A-----V-----PKL-----R-----T-----K-----S-----AQ-----C-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.BR.07.07BR844-----A-----V-----PKL-----R-----T-----K-----S-----AQ-----C-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.ES.x.P1146-----A-----V-----PKL-----R-----T-----K-----S-----AQ-----C-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.FI.93.FIN9363-----A-----V-----PKL-----R-----T-----K-----S-----AQ-----C-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.FR.96.96FR MP411-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.JP.04.DR6082-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.R0.96.BCI R07-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F1.RU.08.D08 845-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
F2.CM.97.CM53657-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.BE.96.DRCBL-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.CM.04.178 15-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.CU.99.Cu74-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.ES.05.P962-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.GH.03.03GH175G-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.KE.93.HH0712 12-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.NG.01.01NGPL0669-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.PT.x.PT2695-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----
G.SE.93.SE6165-----A-----A-----E-----V-----T-----K-----S-----I-----E-----D-----VAR-----C-----S-----R-----L-----D-----D-----D-----T-----A-----D-----S-----K-----D-----A-----P-----

p51 RT end p15 RNase H start

H. 3R. HBX2
H.BE. 93.VI991
H.BE. 93.VI997
H.CF. 90.056
H.GB. 00.00GBAC4001
I.D. 97.J. 97DC KT8147
J.S.E. 93.SE9280 7887
J.S.E. 94.SE9173 7022
K.C.D. 97.97ZR E0TB11
K.M. 96.96CM MP535
01 AE. CF. 90.90CF11637
02 AE. ES. 96.07158
01 AE. HK. 04.HK001
01 AE. JP. x.DR0492
01 AE. TH. 04.BK84
01 AE. US. 00.00US MSC1164
01 AE. VN. 98.98VNDN1
02 AG. CM. 02.02CM 0013BBY
02 AG. ES. 96.07158
02 AG. ES. 96.12161
02 AG. FR. 91.DJ263
02 AG. GH. 03.03GH181AG
02 AG. LR. x.POC44951
02 AG. NG. 01.LP710
02 AG. SE. 97.97SE7812
02 AG. SN. 98.98SE MP1211
02 AG. US. 00.00US MSC3083
02 AG. UZ. 02.02UZ0683
03 AB.RU. 97.KAL152
04 cpx. CY. 94.94CY032_3
05 DF.BE. x.VI1310
06 cpx. AU. 96.BF90
07 BC. CN. 98.98CN009
08 BC. CN. 97.97CNQG 6F
09 cpx. GH. 96.96GH2911
10 CD.TZ. 96.96TZ BF061
11 cpx. CM. 95.95CM 1816
12 BF. AR. 99.ARMA159
13 cpx. CM. 96.96CM 1849
14 BG. ES. 00.X605
15 01B. TH. 99.99TH MU2079
16 AZD. KR. 97.97KR004
17 BF. AR. 99.ARMA036
18 cpx. CU. 99.CU76
19 BG. CU. 99.CU7
20 BG. CU. 99.CU103
21 AZD. KE. 99.KEK2003
22 01A1. CM. 01.01CM 0001B
23 BG. CU. 03.CB118
24 BG. CU. 03.CB378
25 cpx. CM. 02.1918LE
26 AU. CD. 02.02CD MBT0047
27 cpx. FR. 04.04CD FR KZ5
28 BF. BR. 99.BREPM12609
29 BF. BR. 01.BREPM16704
31 BC. BR. 04.04BR14
32 06A1.EE. 01.EE0369
33 01B. MY. 05.05MYKL007 1
34 01B. TH. 99.09UR2478P
35 AD. AF. 05.05AF095
36 cpx. CM. 00.00CMNYU836
37 cpx. CM. 00.00CMYU926
38 BF1. UY. 03.UY03 3389
39 BF. BR. 04.04BRBB1179
40 BF. BR. 05.05BRBF055
42 BF. LU. 03.LBFF 05_03
43 02G.SA. 03.J11223
N.CM. 95.VBF30
N.CM. 95.VBF36
N.CM. 02.D100131
N.CM. 04.04CM 1015_04
O.BE. 87.ANT70
O.CM. x.BCF06
O.CM. 91.MVP5180
O.CM. 96.96CMA102
O.CM. 97.97CMA0447
O.CM. 98.98CMA104
O.CM. 99.99CMA4122
O.FR. 92.VAU
DO. FR. 08.RBF208
O.SN. 99.99SE MP1299
O.US. x.I 24788
O.US. 97.97US08692A
O.US. 99.99USTWLA
P.FR. 09.RBF168
CPZ. CD. 98.ANT
CPZ. CD. 98.VB16
CPZ. GA. 88.SAB1
CPZ. TZ. 00.TAN1
CPZ. US. 85.US Marilyn

p51 RT end p15 RNase H start

ENREILKEPVHGVVYDPSKDLIAEIQKQGQGWYQIYQEPF. KNLKTKGYARMRGATNDVKQLTEAVQKITTESIIVGK. TPKFKLPIQKETWETWTEYQWATWPEWFEVNTPLVLWYQLKEKPIVGAETFYVDGAANRETKLGKAGYVTVNRGRQKVLTLD	625
R A E PD K S V A I R H H T E Y M D K I S E	627
R I R E K N S V A I R H H T A A Y I I DK K A E	628
R SA E V LD KR T R V SC I R D II M I DK N	624
K SA E V LD KR S A V AL A R R D M S T DK	625
K ARE V LD KR S SQV AL A R R D M S V DK I	625
ND Y H I S V A G R G T T H Q KR D SI E	627
N E V V D K S R A V VA R R A A D A L S E	625
V T T G V V D K S R DV AM R R M S S D	625
T V V V D T K S R A V A A R L M D S	627
T E V V D T K S R V A G R G M M S	626
N V V D K S R V A G R R M M D S	627
T V V D K S R V A I I R A L D S NE	627
P V D KRGS QV VAV R R A M D I D	627
A V D KR S A V V R R A M D	627
T V D KR S L VS R R A M D	627
T V D KR S V V V R R DA M V DK	627
T V D KR S V VA R R A M S	627
T V D KR S V VA R R A M D I R D N S	627
T V D KR S V RVA V R R A M D	627
T V D KR S V VA R R DA D	627
A V D L T S R A C R D TD A Q D S SE	626
V L A V A A R I L L DK A S E	627
V Y H IKS AL R T Q D E	629
I A E D K T AM R I D	627
A V D K T AM I R D	623
V D H K S R V V AQ C I D D	626
S S V LD KR T R VI C I R R D	625
V F Y KRGS V VA L R V D T AE S K DK S E	627
E E V LD KRGS V A R V D DK K II E	634
A A V D K S R V A R M D S S E	626
D V PD KR ST VM A R L D T AE S K DK A S E	627
V YD KR S V V VA I R A S I E	625
V D K KS SL I R A R M D S	626
D D KS AQ A Q M M D K S	623
L D KR ST AM A R M M D I S E	625
L K S V VA G R A M S E	627
L KST V AQ R A M S D K S	623
N E V D Y KS AQ A M 618 D K P	
D E V D KRGS AA A G I R D I R D S E	626
R V D KRKS A V V M R R D D M DK E	625
I V D KR C I A VM A R R D Q DK E	625
I A N T T VA I T I S K D A S E	627
A V ND H K T R L AM V R R D D T V M D C S E	633
T V V D R S R V A R R R M D I S DK S E	627
L V V D KR S V V L I R A MD D S E	626
IL V L V E E xL D F S x KR S R A V A I R R A RD G Q DK I SF E	624
R E V V C S T V SV R R A M T AE S T D A S E	631
H S KLK T V V VSL A R LR D T A I D P	627
T E D KRGS E QV VA R R V V A DH R D V S Q D S E	630
L G E V LH K S I V V R VA R V V A A T S F D SIA	634
R L G E V Y Y A V V VA G I V V A DH T S Y K F D SIEN	632
R L E E S X K KS I V V A N I T S Y K F D SEN	633
R Q Q D WVN GE EH T OKAS IR A VI VSO I L VTR AD S I R S M Y N EQ K IIK DE	623
K Q D WVN H E V DEH OKAS EIR MA V VSO A L VTR A S I T Y N EQ K IK EE	623
K Q D WVS H E V DEH OKAS IR A V VSO A L R VTR A S I T Y N EQ K NIIK EE	623
K Q D WVS E V DEH T OKAS IR A VL VSO I L VTR AD S I R S M Y N EQ K IIK DE	623
R Q D WVN E V DEH T OKAS EIR IA V VAO L VTR A A T S I R S M D Y D EQ K IIN DE	625
K Q D WVN E V DEH T OKAS IR A VL VSO A L VTR AD S I R S M Y N EQ K IIN DE	623
R Q D WVN E V DEH T O AS IR A VI VSO A L VTR AD S I R S M Y N EQ K IK EE	622
K Q D WVN E V DEH OKAS IR ANVI VSO A I L VTR V AD S I K N I D I EQ K IIK DE	624
R Q D WVN DE DEH S OKAS IR AAV VSO L VTR D AD S I R SD R Y D Ex K IIK EE	622
K Q D WVN W DEH T OKAS IR A VL RVSO A I L TR AD S I S M Y D Ek IIK EE	623
K Q D WVN E DEH Q AS IR A VL VSO A L TR A AD S I S I Y N EQ K IIK EE	623
K Q D WVN E DEH Q AS EIR A VL VSO A L TR A AD S I R I Y N EQ K IIK EE	620
R Q D WVN E S V DEH T OKAS IR A V ASO A * L VTR AD S I T Y D EQ K IIQ EE	613
K Q E E VD E EH QKAT IR A VI TSO L R VNRSM SD S I D P I D IIK EG	619
KQ QOKIE Y Q GLP K T S NEG L A PT T E R AGV GL E V Q TR DA SD IR N LAD PE Y NSQ D SR KH OK	627
Q VST A E D F H GKO IR A T A R V M A AD I S T E Y T TTID Y R DK K IIS EN	625
KQ K Q A KLP Q A EG KSP T EIR AGLI GN I I V L V S SO D V V I IR N LSD PE YSKO EN	623
E E V V RS F RH Q S IR V V A V LV V S D I K T A E Q K D II EN	628

[illegible]

p66 RT, p15 Rnase H end p31 Integrase start

B.FR.83.HXB2
H.BE.93.VI991
H.BE.93.VI997
H.CF.90.056
H.GB.00.00GBAC4001
J.CD.97.J.97DC.KTB147
J.SE.93.SE9289.7897
J.SE.94.SE9173.7022
K.CD.97.97ZR.EQT811
K.CM.96.96CM.MP535
01 AE.CF.90.90CF11697
01 AE.CN.07.073SW045
01 AE.HK.04.HK001
01 AE.JP.x.DR0492
01 AE.TH.04.BKM
01 AE.US.00.00US.MSC1164
01 AE.VN.98.98VND15
02 AG.CM.02.02CM.0013BBY
02 AG.CY.05.CY048
02 AG.ES.06.PI261
02 AG.FR.91.DJ263
02 AG.GH.03.03GH121AG
02 AG.LR.x.P044951
02 AG.NG.01.PL0710
02 AG.SE.94.SE7812
02 AG.SN.98.98SE.MP1211
02 AG.US.00.00US.MSC3083
02 AG.UZ.02.02UZ0683
03 AB.RU.97.KAL153_2
04 cpx.CY.94.94CY032_3
05 DF.BE.x.VI1310
06 cpx.AU.96.BFP90
07 BC.CN.98.98CN009
08 BC.CN.97.97CN06.FF
09 cpx.GH.96.96GH2911
10 CD.TZ.96.96TZ.BF061
11 cpx.CM.95.95CM.1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM.1849
14 BG.ES.00.X605
15 01B.TH.99.99TH.MU2079
16 A2D.KR.97.97KR004
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 A2D.KE.99.KE2003
22 01A1.CM.01.01CM.0001BBY
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02CD.MBT047
27 cpx.FR.04.04CD.FR.KZ5
28 BF.BR.99.BREPM12609
29 BF.BR.01.BREPM16704
31 BC.BR.04.04BR142
32 06A1.EE.01.EE0369
33 01B.MY.05.05MYKL007_1
34 01B.TH.99.09R2478P
35 AD.AF.05.05AF095
36 cpx.CM.00.00CMNYU830
37 cpx.CM.00.00CMNYU926
38 BF1.UY.03.UY03.3389
39 BF.BR.04.04BRRJ179
40 BF.BR.05.05BRRJ055
42 BF.LU.03.1uBF.05.03
43 02G.SA.03.J11223
N.CM.95.YBF30
N.CM.97.YBF106
N.CM.02.DJ00131
N.CM.04.04CM.1015_04
O.BE.87.ANT70
O.CM.x.BCF06
O.CM.91.MVP5180
O.CM.96.96CM102
O.CM.97.97CMA8447
O.CM.98.98CM104
O.CM.99.99CMU4122
O.FR.92.VAU
DO.FR.08.RBF208
O.SN.99.99SE.MP1299
O.US.x.I.2478B
O.US.97.97US08692A
O.US.99.99USTWLA
P.FR.09.RBF168
CPZ.CD.90.ANT
CPZ.CM.05.SIVcpzMT145
CPZ.GA.08.08GA0131
CPZ.TZ.00.TAN1
CPZ.US.85.US_Marilyn

p66 RT, p15 Rnase H end, p31 Integrase start
TNQKTELQAIYLAQDSGLEVINVTDSQYALGIIQAQPDQSESELVNOIIIEQLIKKEKVYLAWPAAHKGIGGNEQVDKLVSAQIRKVLFDGIDKAQ.DEHEKYHSNWRAMASDFNLPPVVAKEIVASCDK.CQLKGEAMHGQVDCSPGIWQLDCTHLEGKVLVAVHVA 795
-----E-P-----K-----F-S-----S-----VQ-----I-----I-----793
-----E-R-N-E-I-----EA-R-N-E-I-----792
-----E-R-N-V-I-----E-R-N-K-N-I-----I-----O-----794
-----E-R-N-K-N-I-----I-----I-----M-----I-----I-----793
-----H-R-Q-----K-----R-S-----S-----R-----E-----I-----792
-----H-R-I-----K-----S-----E-----ED-----I-----793
-----H-S-----K-----DR-S-----S-----Ex-N-----I-----I-----795
-----A-C-S-----K-D-----RI-S-----E-N-----I-----I-----795
-----H-H-SD-----H-----R-I-----K-E-R-S-----E-R-T-----I-----N-----793
-----H-H-S-----R-V-----T-----E-R-----I-----I-----793
-----H-S-----R-I-S-----S-----NK-S-----N-----E-R-T-----I-----N-----791
-----H-H-P-----R-V-----S-----S-----E-R-T-V-----I-----N-----795
-----H-H-EP-----R-V-----S-----E-R-T-----I-----N-----794
-----H-H-S-----R-V-----S-----E-R-T-----I-----N-----795
-----H-H-S-----R-V-----S-----E-R-T-----I-----N-----794
-----H-H-S-----R-----E-D-S-----K-RI-----E-R-----I-----M-----795
-----H-H-S-----R-----K-E-D-S-----N-----E-R-----C-----I-----I-----795
-----A-S-----R-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-S-----R-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----Y-H-S-----R-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-H-SQ-----R-I-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-H-S-----R-T-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-L-E-S-----R-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-H-S-----R-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-H-S-----R-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-S-----K-D-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----H-S-----K-D-----K-K-G-D-I-----S-----E-R-----C-----Q-----Q-----G-----I-----795
-----A-H-S-----I-----R-D-----R-D-S-----N-----E-----G-----I-----I-----795
-----A-H-S-----I-----R-D-----R-D-S-----N-----E-----G-----I-----I-----794
-----A-H-S-----I-----R-D-----R-D-S-----N-----E-----G-----I-----I-----795
-----N-P-----K-----I-S-----N-----ED-R-----N-----I-----I-----I-----797
-----H-CI-S-----K-----R-S-----S-----E-R-----I-----Q-----I-----I-----795
-----H-T-S-----K-----R-S-----S-----E-R-----I-----Q-----I-----I-----795
-----H-H-S-----K-----K-E-R-S-----S-----E-R-----I-----Q-----I-----I-----795
-----N-S-----K-----P-----R-----E-N-----I-----I-----L-----I-----794
-----E-H-S-----K-----S-----S-----H-R-----E-R-----I-----I-----I-----793
-----A-H-S-----K-----S-----S-----V-I-----E-N-----I-----I-----T-----795
-----A-Q-S-----R-----S-----S-----N-----ED-R-----T-----I-----T-----I-----802
-----A-QI-S-----R-V-----S-----S-----E-----I-----I-----I-----794
-----Q-R-S-----R-V-----S-----S-----E-R-----T-----I-----I-----I-----794
-----H-K-S-----R-I-L-K-E-R-S-----E-S-----E-R-----H-----C-----V-----I-----I-----795
-----A-H-K-S-----K-I-----S-----I-----E-N-----H-----C-----V-----I-----I-----795
-----E-H-Q-----K-I-----E-S-----S-R-----E-----D-N-----I-----I-----R-----I-----793
-----N-S-----K-----S-----R-----S-----E-----I-----I-----I-----I-----794
-----H-S-----K-----S-----S-----S-----E-R-----N-----I-----I-----I-----791
-----R-H-S-----R-----G-KR-S-----S-----E-R-----H-----I-----I-----I-----793
-----H-H-S-----R-----L-K-E-S-----S-----I-----ED-R-----T-V-----I-----N-----I-----795
-----H-S-----K-----S-----S-----E-----K-----I-----I-----I-----I-----791
-----H-H-S-----K-----I-----S-----N-----E-R-----I-----I-----L-----I-----786
-----H-H-S-----K-----I-----S-----N-----E-R-----I-----I-----L-----I-----794
-----H-S-----R-I-----K-E-S-----I-S-----ED-----N-----I-----I-----I-----V-----793
-----Q-S-----R-K-----S-----S-----S-----E-R-----I-----I-----I-----I-----793
-----H-S-----K-----S-----S-----I-----E-----S-D-----I-----I-----I-----795
-----A-Q-S-----K-----N-----S-----I-----E-N-----V-----I-----I-----I-----795
-----Q-S-----K-----L-N-R-S-----S-----N-----E-----E-----I-----T-----I-----I-----801
-----N-S-----K-----S-----S-----E-R-----N-----I-----I-----I-----I-----795
-----H-H-S-----R-V-----E-S-----K-S-----E-R-----T-----I-----A-N-----RV-----795
-----H-H-S-----K-V-----E-S-----S-----E-R-----T-----I-----N-----I-----I-----795
-----H-H-S-----K-----K-E-D-S-----T-----E-----E-R-----I-----Q-----N-----M-----I-----794
-----H-H-SK-----R-----K-E-D-S-----K-I-----ED-R-----I-----I-----I-----I-----795
-----H-H-ES-----R-D-I-----KI-E-R-S-----I-S-----GV-----ED-KR-----N-----I-----I-----792
-----A-H-S-----K-K-S-----E-I-T-----I-----E-N-----I-----I-----I-----I-----799
-----H-S-----K-----S-----I-----I-----E-N-----I-----I-----I-----I-----798
-----A-Q-S-----K-----I-----S-----T-----I-----ED-----K-----I-----I-----C-----x-----795
-----H-S-----R-----K-E-D-S-----I-S-----E-R-----K-----D-----I-----C-----Q-----M-----797
-----A-LM-E-RD-----M-HS-K-S-----R-S-----S-----I-----ED-DR-----K-----I-----I-----N-----V-----I-----802
-----A-L-E-Q-A-----M-HS-K-D-G-----S-----S-----ED-R-----K-----I-----I-----I-----I-----800
-----L-SH-K-P-----V-HS-K-S-----S-----S-----ED-R-----K-----I-----I-----I-----I-----800
-----LM-x-Q-----M-HS-K-S-----S-----S-----ED-R-----K-----I-----I-----I-----I-----800
-----A-M-L-KET-----V-SS-T-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----K-L-E-G-----I-----P-----HI-----I-----EV-----I-----M-----I-----791
-----A-M-VLI-KEA-----V-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----P-----HI-----I-----Y-----E-----M-----I-----791
-----A-M-VLI-KEQ-----V-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----P-----HI-----I-----Y-----E-----M-----I-----791
-----A-M-VL-KEK-----V-SS-T-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-E-G-----I-----I-----N-----P-----HI-----I-----Y-----E-----M-----A-----I-----791
-----A-M-VL-KEK-----V-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----N-----P-----HI-----I-----Y-----E-----M-----T-----I-----793
-----A-M-VL-KB-----V-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----N-----P-----HI-----I-----Y-----E-----M-----T-----I-----789
-----A-M-L-K-KET-----F-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----x-L-G-----I-----I-----N-----P-----HI-----I-----Y-----E-----M-----T-----I-----790
-----A-M-VL-KEK-----V-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----N-----P-----HI-----I-----Y-----E-----M-----T-----I-----792
-----A-M-VL-KEK-----V-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----K-L-G-----I-----N-----P-----HI-----I-----Y-----E-----M-----T-----I-----790
-----RA-M-VL-KEK-----Q-V-SS-T-S-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----N-----P-----HI-----I-----Y-----E-----M-----T-----I-----791
-----A-M-VL-KEK-----T-SS-T-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----P-----HI-----I-----Y-----E-----M-----T-----I-----791
-----A-M-VL-KEK-----T-SS-T-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----P-----HI-----I-----Y-----E-----M-----T-----I-----791
-----A-M-VL-KEK-----T-SS-T-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----P-----HI-----I-----Y-----E-----M-----T-----I-----788
-----A-M-xL-KER-----V-SS-T-D-PI-Q-----T-Q-T-----KI-KD-R-E-Q-----ED-----L-G-----I-----I-----P-----HI-----I-----Y-----E-----M-----T-----I-----776
-----A-E-VL-KE-KQA-----V-S-T-D-P-QK-E-M-T-----DI-KD-R-E-Q-----ED-----K-L-G-----I-----INN-P-----HV-----R-----V-----I-----I-----787
-----QA-LM-E-TGP-----VL-GT-----P-EE-QK-R-OI-S-----Q-Q-E-----ED-D-----SL-DEY-----I-----I-----Q-----HV-----R-----V-----I-----I-----S-----795
-----A-VLM-Q-V-----V-L-SH-H-DI-----I-S-----R-----E-----K-----Q-----I-----Q-----I-----I-----I-----I-----794
-----QA-K-L-L-DQO-----V-S-----V-H-----V-----H-----V-----I-----H-----V-----I-----I-----I-----I-----794
-----QA-W-V-D-K-AQ-----VM-VL-GL-----D-PI-E-QK-TQ-TAI-----E-KN-----I-----NE-----ED-D-----K-L-DEY-----I-----I-----Q-----P-----HI-----I-----Y-----E-----I-----I-----791
-----A-T-V-K-ENT-----V-V-G-----V-HS-----E-----I-----S-----IS-----ED-D-----T-----S-----S-----I-----I-----I-----I-----797

A. FR. 83. HBX2	SGYIEAEVIPAETGQETAYFLKLK.	GRWPVKTIHTDNGSMFTGATVRAACW	WAGIKOEFGIPYNPQSQGVVSM	MNKLKKIIGQVRDQAEHLKTAVQMAV	IHNFKRKG. IGGYSAGERIVDIIATD	IQTKELQKQITKIQNFVRYRDSRNL	WKGPAKLLWKGEGA	963
A. CD. 02. 02CD KT8035	-M	-A	-I	-V	-STA-KT	-VO	-VL	963
A. SN. 01. 00J369					S-A-K	N-Q	I	962
A1. AU. 03. PS1044 Day0				-VV	S-A-K	N-Q	I	961
A1. CY. 06. CY171				-VV	P-SSA-K	N-Q	I	963
A1. GE. 99. 99GEMZ011				-VV	P-SSA-K	D-Q	I	963
A1. IT. 02. 60080				-VV	SSA-K	N-Q	x	963
A1. KE. 02. ML1990				-VV	S-A-K	N-Q	V	957
A1. RU. 08. POKA1RU				-VV	P-SMA-K	N-Q	I	963
A1. RW. 93. 93RW037A				-VV	S-A-K	N-Q	I	963
A1. SE. 95. SE8538		G	I	-VV	S-AFK	NVO-Y	HK	963
A1. TZ. 01. A341				-VV	S-A-K	N-Q	I	963
A1. UA. 01. 01UADN139	-M		I	A	-V	P-SSA-K	N-Q	963
A1. UG. 99. 99UGA07072				-VV	P-S-AFK	N-Q	I	963
A1. ZA. 04. 04ZASK162B1			A	RV	P-S-A-K	NVO	I	962
A2. CD. 97. 97CDKT848				-V	P-S-A-K	DV	I	956
A2. CY. 94. 94CY017 41		T	D	I	-V	P-IS-K	Q	963
B. AR. 04. 04AR143170					G-IST-K		I	963
B. AU. 04. PS1038 Day174		x		I	-STX-K	-V	I	955
B. BO. 99. BOL0122					SMA-K		N	964
B. BR. 05. BREPM1081				V	SMA-K		T	963
B. CA. 97. CANB3FULL					S-K		L	966
B. CN. 05. 05CNHB hp3		I	T	I	R-STS-K		N	963
B. CO. 01. PCM001			P	I	P-STA-K	-V	N	963
B. CU. 99. Cu19				V	P-ISPA-K		S	966
B. CY. 06. CY165				I	S-K		L	978
B. DE. 06. 031				I	ST-K	V		963
B. DK. 04. PMVL 012				T	P-Sx-K			957
B. DO. 05. 05DO 160884					SN-K		R	964
B. EC. 89. EC003				I	S-A-K	D	I	967
B. FR. 07. X2231					S-K		M-S-L	963
B. FR. 92. 92FR BX08					ST-K		N	961
B. GA. 88. 0YT				I	ST-K		N	963
B. GB. 86. GB8 46R			D	I	R-ST-K			969
B. GE. 03. 03GEMZ004				I	S-V-K		T	962
B. HT. 05. 05HT 129389				I	S-V-K			958
B. IN. x. 11807	-M			V	S-A-K		E	963
B. JM. 05. 05JM KJ108				V	S-K		I	962
B. JP. 05. DR6538					ST-K			963
B. KR. 04. 04KMH5					SN-K			963
B. MM. 99. mSTD101		T	I		P-SMS-K		VE	964
B. NL. 00. 671 00T36					P-ISTA-K		E	971
B. RU. 04. 04RU128005					SM-K			962
B. TH. 00. 00TH C3198		T			R-SMS-K		Y	963
B. TT. 01. 01TT CRC50069		I	I		-VV-S-G	SNV-K	Q-E	962
B. TW. 94. TWCY5					S-A-K		K	963
BA. 01. 01UAKV167				IV	SMA-K		I	970
B. US. 07. CR0627W			I		ST-K		R	966
B. UY. 01. 01UYTRA1179			I		ST-K		I	963
B. YE. 02. 02YES07					S-K			964
B. ZA. 03. 03ZAPS045MB2			R		S-K		L	963
C. AR. 01. ARG4006			I		SMA-K		Q	958
C. BR. 04. 04BR013			I		SM-K		Q	967
C. BW. 00. 00BW7621	-M		Y	I	S-A-K		R	959
C. CN. 98. YNRL9840					S-A-K		Q	959
C. CY. 05. CY040					S-A-K		Q	964
C. ES. 07. X2118 2			Y	x	S-A-K		Q	956
C. ET. 02. 02ET 288			Y		SSA-K		Q	965
C. GE. 03. 03GEMZ033			Y		SSA-K		Q	958
C. IL. 98. 98I5002					V-P	SMA-K		963
C. IN. 03. D24			Y		SQA-K			967
C. KE. 00. KER2010			Y		S-A-K		R	959
C. MM. 99. mIDU101 3	-M				S-AAK	H	R	959
C. MW. 93. 93MW 965			Y		S-A-K		Q	960
C. SN. 90. 90S 364					S-K		E	955
C. SO. 89. 89SM 145			Y		SMA-K	H		970
C. TZ. 02. C0178			Y		STA-K		E	959
C. US. 98. 98US MSC3018	-M		K	Y	-V	STA-K		957
C. UY. 01. TRA3011				QV	P-SM-K		Q	958
C. YE. 02. 02YES11				Y	S-A-K		E	957
C. ZA. 05. 05ZAPSK240B1	-M		Y		VL	S-K	I	959
C. ZM. 02. 02ZM108	-M				VL	T-S-K	Q	954
D. CD. 83. ELT					-VV	S-A-K		962
D. CM. 01. 01CM 0009BBY			Y		-VV	S-A-K		964
D. CY. 06. CY163					-VV	S-A-K		962
D. KE. 97. ML415 2	-M	K		I	IV	S-A-K	V	962
D. KR. 04. 04KHB					-V	S-V-K		962
D. SN. x. SE365					-VV	S-K		968
D. TD. 99. MN011					-V	R-S-K		964
D. TZ. 01. A280				I	-VV	S-A-K		964
D. UG. 99. 99UGK09958					-VV	S-A-K		962
D. YE. 02. 02YES16					-VV	SGA-K		964
D. ZA. 90. RL					-VV	S-A-K	L	962
F1. A0. 06. A0 06 ANG125	-L	A		I	-I	S-A-K	Q	965
F1. AR. 02. ARE933					I	P-S-A-K-S	Q	962
F1. BE. 93. V1850	-E				I	S-A-K-S	Q	964
F1. BR. 07. 07BR844					I	T-S-K		969
F1. ES. x. P1146					I	SSA-K	D-Q	961
F1. ET. 93. ETN0363		D			I	S-A-K	Q	963
F1. FR. 96. 96FR MP411					I	SSA-K	Q	965
F1. JP. 04. DR6082	-L				I	A-S-A-K		958
F1. RO. 96. BCI R07					I	R-SGA-K	Q	963
F1. RU. 08. D88 845					I	ST-K	Q	962
F2. CM. 97. CM53657					I	STV-K		963
G. BE. 96. DRCLT					I	S-A-K		959
G. CM. 04. 178 15					I	G-SM-K	S-T	961
G. CU. 99. Cu74					I	S-A-K	N-T	959
G. ES. 05. P962		F	I		I	M-G-SMA-K	N-T	962
G. GH. 03. 03GH175G					I	VL	S-A-K	963
G. KE. 93. HH8793 12 1					I	S-A-K	R-D-T	960
G. NG. 01. 01NGML0669					I	S-K	S-T	962
G. PT. x. PT2695					I	RI	S-A-K	962
G. SE. 93. SE6165					I	TV	S-A-K	960

B.FR.83.HXB2
H.BE.93.VI901
H.BE.93.VI902
H.CF.90.856
H.GB.00.00GBAC4001
J.D.97.J.97DC.KT8147
J.SE.93.5E9280.7887
J.SE.94.5E9173.7022
K.CD.97.97ZR.ET0811
K.CM.96.96CMM535
01 AE.CF.00.90CF16097
01 AE.CM.97.07.5WK045
01 AE.CM.97.04.HK801
01 AE.JP.X.8R8492
01 AE.TH.TX.DK0M
01 AE.US.00.00US.MSC1164
01 AE.VN.98.98VNDN15
02 AG.CM.02.02CM.0013BBY
02 AG.CY.05.CY948
02 AG.CY.05.0261
02 AG.FR.91.DJ263
02 AG.GH.03.03GH.H181AG
02 AG.LR.LX.POC44951
02 AG.NG.01.PL0710
02 AG.NG.02.027812
02 AG.SN.98.98SE.MP1211
02 AG.US.00.00US.MSC3083
02 AG.UZ.02.02UZ.020683
03 AB.RU.97.KAL153.2
04 cpx.CY.94.94CY032_3
05 DF.BE.X.VI1310
06 cpx.AU.96.BF9P0
07 BC.CN.98.98CNO09
08 BC.CN.97.97CNC9F
09 cpx.GH.96.96GH2911
10 CD.TZ.96.96TZ.BF061
11 cpx.CM.95.95CM.1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM.1849
14 BG.ES.00.X605
15 01B.TH.99.99TH.MU2079
16 AZD.US.97.97KR004
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7C
20 BG.CU.99.CU103
21 AZD.KE.99.KER2003
22 01A1.CM.01.01CM.0001B
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02CD.MBTB047
27 cpx.FR.04.04CD.FR.KZ5
28 BF.BR.99.BREPM12609
29 BF.BR.01.BREPM16704
31 BC.BR.04.04BR14
32 06A1.EE.01.EE0369
33 01B.MY.05.05MYKL007.1
34 01B.TH.99.09UR2478P
35 AD.AF.05.05AF095
36 cpx.CM.00.00CMNYU836
37 cpx.CM.00.00CMNYU926
38 BF1.UY.03.UY03.3389
39 BF.BR.04.04BRN1179
40 BF.BR.05.05BRR0J55
42 BF.LU.03.LuBF.05.03
43 02G.SA.03.J11223
N.CM.95.YBF30
N.CM.97.YBF106
N.CM.02.DJ08131
N.CM.04.04CM.1015_04
O.BE.87.ANT70
O.CM.X.BCF06
O.CM.91.MVP5180
O.CM.96.96CMA182
O.CM.97.97CMA447
O.CM.98.98CMA104
O.CM.99.99CMAJ4122
O.FR.92.VAU
DO.FR.08.RBF208
O.SN.99.99SE.MP1299
O.US.X.I.24788
O.US.97.97US08692A
O.US.99.99USTWLA
P.FR.09.RBF168
CPZ.CD.90.ANT
CPZ.CM.95.SIVcpzMT145
CPZ.CA.88.CAB1
CPZ.TZ.00.TAN1
CPZ.US.85.US.Marilyn

[illegible]

p31 Integrase end			Pol end			
B.FR.83.HXB2	VVIQNSDIKVVPRRKA	IIIRDY	GKQ	MAGDDC	VASRQDE	1003
A.CD.02.02CD_KTB035	-----E-----	-----G-----	-----G-----			1004
A.SW.01.00J369	-----S-----	-----G-----	-----G-----			1003
A1.AU.03.P51044_Day0	-----T-----	-----G-----	-----G-----			1002
A1.CY.06.CY171	-----N-----	-----G-----	-----G-----			1004
A1.GE.99.99GEMZ011	-----N-----	-----G-----	-----G-----			1004
A1.IT.02.60000	-----x-----	-----G-----	-----G-----			997
A1.KE.02.ML1990	-----K-----	-----GG-----	-----G-----			1004
A1.RU.08.PoKAIrU	-----N-----	-----G-----	-----N-----			1009
A1.RW.93.93RW037A	-----S-----	-----G-----	-----G-----			1004
A1.SE.95.SE8538	-----S-----	-----G-----	-----G-----			1004
A1.TZ.01.A341	-----LK-----	-----G-----	-----N-----			1004
A1.UA.01.01UADN139	-----N-----	-----G-----	-----G-----			1004
A1.UG.99.99UGA07072	-----G-----	-----G-----	-----G-----			1004
A1.ZA.04.04ZASK162B1	-----E-----	-----G-----	-----G-----			1003
A2.CD.97.97CDKT848	-----G-----	-----G-----	-----G-----			997
A2.CY.94.94CY017_41	-----G-----	-----G-----	-----G-----			1004
B.AR.04.04AR143170	-----E-----	-----x-----	-----G-----			1004
B.AU.04.PS1038_Day174	-----E-----	-----x-----	-----G-----			995
B.B0.99.B0L0122	-----S-----	-----G-----	-----G-----			1005
B.BR.05.BREPW1001	-----S-----	-----G-----	-----G-----			1004
B.CA.97.CANB3FULL	-----S-----	-----G-----	-----G-----			1007
B.CN.05.05CNHB_hp3	-----S-----	-----G-----	-----G-----			1004
B.CO.01.PCM001	-----S-----	-----G-----	-----G-----			1004
B.CU.99.Cu19	-----S-----	-----G-----	-----G-----			1007
B.CY.06.CY165	-----S-----	-----G-----	-----G-----			1019
B.DE.06.031	-----E-----	-----V-----	-----G-----			1004
B.DK.04.PMVL_012	-----E-----	-----G-----	-----G-----			998
B.DO.05.05D0_160884	-----E-----	-----E-----	-----G-----			1005
B.EC.89.EC003	-----I-----	-----G-----	-----G-----			1008
B.ES.07.X2231	-----E-----	-----G-----	-----G-----			1004
B.FR.92.92FR_BX08	-----x-----	-----G-----	-----G-----			1001
B.GA.88.0YT	-----S-----	-----G-----	-----G-----			1004
B.GB.86.GB8_46R	-----S-----	-----G-----	-----G-----			1010
B.GE.03.03GEMZ004	-----S-----	-----G-----	-----G-----			1003
B.HT.05.05HT_129389	-----S-----	-----G-----	-----G-----			999
B.IN.x.11007	-----S-----	-----G-----	-----G-----			1004
B.JM.05.05JM_KJ108	-----V-----	-----G-----	-----G-----			1003
B.JP.05.DR6538	-----V-----	-----G-----	-----G-----			1004
B.KR.04.04KMH5	-----V-----	-----G-----	-----G-----			1004
B.MM.99.mSTD101	-----S-----	-----G-----	-----G-----			1005
B.NL.00.671_00T36	-----S-----	-----G-----	-----G-----			1012
B.RU.04.04RU128005	-----TE-----	-----G-----	-----G-----			1003
B.TH.00.00TH_C3198	-----S-----	-----G-----	-----G-----			1004
B.TT.01.01TT_CRC50069	-----E-----	-----G-----	-----G-----			1003
B.TW.94.TWCY5	-----S-----	-----G-----	-----G-----			1004
B.UA.01.01UAKV167	-----S-----	-----G-----	-----G-----			1011
B.US.07.CR0027M	-----S-----	-----G-----	-----G-----			1007
B.UY.01.01UYTRA1179	-----V-----	-----G-----	-----G-----			1004
B.YE.02.02YE507	-----S-----	-----G-----	-----G-----			1005
B.ZA.03.03ZAPS045MB2	-----S-----	-----G-----	-----G-----			1004
C.AR.01.ARG4006	-----L-----	-----V-----	-----K-----	-----A-----	-----N-----	999
C.BR.04.04BR013	-----L-----	-----V-----	-----K-----	-----A-----	-----N-----	1008
C.BW.00.00BW07621	-----I-----	-----V-----	-----K-----	-----A-----	-----G-----	1000
C.CW.98.YNRL9840	-----V-----	-----K-----	-----K-----	-----A-----	-----E-----	1000
C.CY.05.CY040	-----V-----	-----K-----	-----K-----	-----A-----	-----M-----	1005
C.ES.07.X2118_2	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	997
C.ET.02.02ET_288	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	1006
C.GE.03.03GEMZ033	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	999
C.IL.98.98IL5002	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	1004
C.IN.03.D24	-----S-----	-----G-----	-----G-----	-----A-----	-----G-----	1008
C.KE.00.KER2010	-----S-----	-----G-----	-----G-----	-----A-----	-----G-----	1000
C.MM.99.mIDU101_3	-----S-----	-----G-----	-----G-----	-----A-----	-----G-----	1000
C.MW.93.93MW_965	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	1001
C.SN.90.90SE_364	-----S-----	-----G-----	-----G-----	-----A-----	-----G-----	996
C.SO.89.89SM_145	-----S-----	-----G-----	-----G-----	-----A-----	-----G-----	1011
C.TZ.02.C0178	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	1000
C.US.98.98US_MSC3018	-----K-----	-----PK-----	-----A-----	-----G-----	-----G-----	998
C.UY.01.TRA3011	-----L-----	-----V-----	-----K-----	-----A-----	-----M-----	999
C.YE.02.02YES11	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	998
C.ZA.05.05ZAPSK240B1	-----V-----	-----K-----	-----K-----	-----A-----	-----G-----	1000
C.ZM.02.02ZM108	-----LR-----	-----V-----	-----A-----	-----G-----	-----Q-----	995
D.CD.83.ELI	-----K-----	-----V-----	-----G-----	-----G-----	-----G-----	1003
D.CM.01.01CM_0009BBY	-----S-----	-----G-----	-----G-----	-----G-----	-----G-----	1005
D.CY.06.CY163	-----L-----	-----E-----	-----V-----	-----G-----	-----G-----	1003
D.KE.97.ML415_2	-----S-----	-----E-----	-----G-----	-----G-----	-----G-----	1003
D.KR.04.04KRBH	-----S-----	-----E-----	-----G-----	-----G-----	-----G-----	1003
D.SN.x.SE365	-----E-----	-----V-----	-----G-----	-----G-----	-----G-----	1009
D.TD.99.MN011	-----H-----	-----V-----	-----V-----	-----G-----	-----G-----	1005
D.TZ.01.A280	-----E-----	-----V-----	-----G-----	-----G-----	-----G-----	1005
D.UG.99.99UGK09958	-----E-----	-----V-----	-----G-----	-----G-----	-----G-----	1003
D.YE.02.02YES16	-----E-----	-----V-----	-----G-----	-----G-----	-----G-----	1005
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F1.A0.06.A0_06_ANG125	-----E-----	-----V-----	-----G-----	-----N-----	-----G-----	1006
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G.CU.99.Cu74	-----NE-----	-----A-----	-----G-----	-----G-----	-----G-----	1000
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 ---V---K-K-N---K-K-Y---TK-KT---V-Q-K-V---T-OP-HX---OGK-K---M-K-C-N-TA-Q-V-RP-L---P-KO---T---WGA---R--- 159
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 ---V---I-N---H-K-K-Y---R-KT---V-Q-T-V---T-OP-HX---LRK-K---M-K-C-N-TA-Q-V-RP-L---P-KO---T---WGA---R--- 162
 ---L---QVKA-N---Y-K-R-R-TEN-V---RN-V-S-Y-V-V---HV-V---MP-E-H---Q-Y-K-K-I-T-RM-H-T-TA-V-I-QR-LTK---PT-SQ-T-L-R-VVKAR---SR--- 162
 ---L---Q-VKA-N---K-M-K-NK-Q---CRN-KV-V-Y-VAE---DIMV---MP-EE-H---Q-Y-K-K-I-T-RM-H-N-TE---R-I-QR-LT---S-SQ-T-F-K-KVK---RN--- 162
 ---L---I-QVKA-N---Y-K-M-K-AN-R---RN-KV-A-Y-VAE---DI-V---MP-EE-H---Q-Y-K-K-I-T-RM-H-T-TE---I-QR-LTK---L-SQ-T-F-K-KVK---RN--- 162
 ---L---QVKA-N---Y-K-R-R-KD-Y---RN-V-G-Y-V-L-Cx-V---MP-EE-H---Q-Y-K-K-I-T-RM-H-T-TE---I-QR-LTK---PE-SQ-T-L-R-VVKAR---RN--- 162
 ---L---QVKA-N---Y-K-R-K-OR-H---TRN---G-Y-V-T-NI-V---MP-EE-H---Q-Y-K-K-I-T-RM-H-T-TE---I-QR-LTK---PE-SQ-T-L-R-VVKD---RS--- 162
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 ---L---QVKA-N---Y-K-R-R-TKE-H-K-F-FRN-A-G-Y-V-M-CV-V---MP-E-H---Q-Y-N-T-I-T-RM-H-T-TE---II-QR-LTK---S-SQ-T-L-R-VVVK---RN--- 162
 ---L---QVKA-N---Y-K-R-R-TD-Y-K---IN-V-R-Y-V-P-CIMV---MP-EE-H---QYK-R-I-T-K-H-T-TE---R-T-QR-LQ-PE-SQ-T-L-R-VVKA---RNR--- 162
 ---AL---QVKA-N---Y-K-R-R-TKD-C-K-F-LN-V-S-V-M-WV-V---MP-K-E-H---QY-K-T-I-T-RM-H-T-TE---R-A-QK-LTK---S-SQ-T-L-R-VVKE---RN--- 162
 ---L---Q-VK-N---Y-K-R---T-D-Y---F-RN-V-G-Y-V-M-PWI-V---MP-E-H---Y-K-K-I-T-RM-I-A-TE---I-QR-LT---P-SQ-T-L-R-VVVK---RN--- 162
 ---K---L---QVKA-N---Y-K-R-R-TKD-Y---CRN---S-Y-I-P-FI-V---MP-E-M-H---QY-K-A-I-T-RM-H-T-TE---I-QR-LTK---P-SQ-T-L-R-VVRE---RH--- 162
 ---L---QVKA-N---Y-K-R-R-TKD-Y---CRN---T-S-Y-I-P-FI-V---MP-E-M-H---QY-K-A-I-T-RM-H-T-TE---I-QR-LTK---P-SQ-T-L-R-VVKE---RH--- 162
 ---L---QVKA-N---Y-K-R-K-KD-Y---TRN---G-Y-V-G-MT-V---MP-E-H---EY-N-K-I-T-RM-H-T-TE---C-QK-LT---FHK-SQ-T-L-R-VVVG---TSR--- 162
 ---TS-EKVA-N---Y-K-R-K-TKN---TV---G-Y-V-A-TI-V---MP-EE-H-A-V---QK-T-I-T-R-H-Q---V-R-I-QR-LNK---S-SQ---F-KVVGVK---R--- 162
 I-K-KIEMI---NI---IWETKVLK-K---ND-KGGE---PTLDKK-V-VF---QC-P-H---A---ERK-I---T-M-Q-Q-P---Q-V-Q-I-ERLTLY-H-KK---SQ-T---FCKILEFRGY-PKGPRL--- 167
 ---NI---Y-R-K-KN---DGTN---MA-QIY---INQ-K-IV---M---H---A---CGK---T-R-H---TAT---N-I-EKA-L-K-FPE---S---W-KO-VKT---NR--- 163
 ---K---Y-R-K-I---FR-YSK-T---A-SP-A---R---S---ACT---R-I-OL-A-Y---R---F-K-SER---RHR--- 163
 ---QV-MI---L-K-T---IFTKCKD-K---TDT-KRAG-I---TE-RSK-VLH---AC-P-H---IGL---QK---I-T---TR-T---AAG-V-Q-I-ERLTIF-HF-S-RQ---T-F-FRKVVSODKQPKGPRR--- 168
 ---L---V-K-N---Y-R-K-K-K---TN-VN---IDK---KT-I---K---QA---H---QK-K-I-M-K---Q---V-RP-I-K-K-PT---F-F-K-VGOS---RR--- 162

Vif

HIV-1/SIVcpz Proteins

Vif end

LP	SV	TK	LT	ED	RN	WK	PQ	KT	GH	RG	SR	TM	GH	*
R									R					C
R									R					C
R	A								P					N
R									R	R	N			C
R									R	R	N			C
R	RI					R			PKE					C
R									R	R	N			C
R	A								R	R	N			C
R	K								R		N		H	Y
R	RI	A							R	R	N			C
R	A					S			R	R	N			C
R	K								R					C
R	V								R					C
R									R					C
R						E					ENR			
xx								I						
LOI											K	N	H	
A											E			
A								RI			E	N	S	
A								R	I					
R													L	
A											K			
A									R					
A											E			
R								H	D				Y	
K								R			C			
V									D		Q			
R											E			Y
R														
R								R			NN			
K								E	I		E	P		
R									R		N			
A													S	
R											E			
R													H	
A	A								R		EN			
R											E		S	
K													H	
V														
R													H	
R														
R														
A									T					
R	V								RDR		N	I		
R	V								R	R	N			
K	V								R	R	N			
R	V								R	R	N		I	
R	V					N			R	R	N			
S	V								R	R	N		V	
R	V								R	R	N			
S	A	K							R	R	N			
R	V					N			R	R	N			
Q	V								R	R	N			
IR	V					N			R	R	N			
K	V								R	R	N			
R	V								R	R	N			
IR	V					N			RIR		N			
IR	V								R	R	N		S	
R	V					N								

HIV-1/SIVcpz Proteins

HIV-1/SIVcpz Proteins

Vpr start	amphipathic α -helix oligomerization				frameshift in HXB2 H(S/N)RIG motifs								Vpr end in HXB2				
MEQAPEDQGPQREPHNWTLEELKNEAVRHFPRIW.LHGLGQHIYETYGDTWAGVEAIRILQQLFIHXFRIGCRHSRIGVTR.Q													RRARNGASRS*				
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	S	R	D	TG
	Y	M	D	H	P	Y	N	E	Q	V	Q	I	R	G	G	D	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	G	R	G	SG-x
	Y	M	D	H	P	Y	N	E	V	T	V	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
S	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T	H	Y	Q	II	R	G	S	
	Y	M	D	H	P	Y	N	E	T								

Vpr start	amphipathic α -helix oligomerization		Vpr end in HXB2 frameshift in HXB2 ² H(S/N)RIG motifs		Vpr end
	MEQAPEDQGPQREPHN	EWTLLEELKNEAVRHFPRIW.LHGLGQHIYET	YGDWTAGVEAIRILQQLLFHx	FRIGCRHSRIGVTR..Q....RRARNGASRS*	
B.FR.83.HXB2		S	Y	P	
H.BE.93.VI991		S	Y	P	
H.BE.93.VI997		S	Y	P	
H.CF.90.056		S	Y	P	
H.GB.00.00GBAC4001		S	Y	P	
J.CD.97.J.97DC.KTB147		S	Y	P	
J.SE.93.SE9289.7897		S	Y	P	
J.SE.94.SE9173.7022		S	Y	P	
K.CD.97.97ZR.EQT811		S	Y	P	
K.CM.96.96CM.MP535		S	Y	P	
01 AE.CF.90.90CF11697		S	Y	P	
01 AE.CN.07.07J5WX045		S	Y	P	
01 AE.HK.04.HK001		S	Y	P	
01 AE.JP.x.DR0492		S	Y	P	
01 AE.TH.04.BKM		S	Y	P	
01 AE.US.00.00US.MSC1164		S	Y	P	
01 AE.VN.98.98VND15		S	Y	P	
02 AG.CM.02.02CM.0013BBY		S	Y	P	
02 AG.CY.05.CY048		S	Y	P	
02 AG.ES.06.PI261		S	Y	P	
02 AG.FR.91.DJ263		S	Y	P	
02 AG.GH.03.03GH181AG		S	Y	P	
02 AG.LR.x.P0C44951		S	Y	P	
02 AG.NG.01.PL0710		S	Y	P	
02 AG.SE.94.SE7812		S	Y	P	
02 AG.SN.98.98SE.MP1211		S	Y	P	
02 AG.US.00.00US.MSC3083		S	Y	P	
02 AG.UZ.02.02UZ0683		S	Y	P	
03 AB.RU.97.KAL153_2		S	Y	P	
04 cpx.CY.94.94CY032_3		S	Y	P	
05 DF.BE.x.VI1310		S	Y	P	
06 cpx.AU.96.BFP90		S	Y	P	
07 BC.CN.98.98CN009		S	Y	P	
08 BC.CN.97.97CN06.F		S	Y	P	
09 cpx.GH.96.96GH2911		S	Y	P	
10 CD.TZ.96.96TZ.BF061		S	Y	P	
11 cpx.CM.95.95CM.1816		S	Y	P	
12 BF.AR.99.ARMA159		S	Y	P	
13 cpx.CM.96.96CM.1849		S	Y	P	
14 BG.ES.00.X605		S	Y	P	
15 01B.TH.99.99TH.MU2079		S	Y	P	
16 A2D.KR.97.97KR004		S	Y	P	
17 BF.AR.99.ARMA038		S	Y	P	
18 cpx.CU.99.CU76		S	Y	P	
19 cpx.CU.99.CU7		S	Y	P	
20 BG.CU.99.CU103		S	Y	P	
21 A2D.KE.99.KE2003		S	Y	P	
22 01A1.CM.01.01CM.0001BBY		S	Y	P	
23 BG.CU.03.CB118		S	Y	P	
24 BG.CU.03.CB378		S	Y	P	
25 cpx.CM.02.1918LE		S	Y	P	
26 AU.CD.02.02CD.MBT047		S	Y	P	
27 cpx.FR.04.04CD.FR.KZ5		S	Y	P	
28 BF.BR.99.BREP12609		S	Y	P	
29 BF.BR.01.BREP16704		S	Y	P	
31 BC.BR.04.04BR142		S	Y	P	
32 06A1.EE.01.EE0369		S	Y	P	
33 01B.MY.05.05MYKL007_1		S	Y	P	
34 01B.TH.99.09R2478P		S	Y	P	
35 AD.AF.05.05AF095		S	Y	P	
36 cpx.CM.00.00CMNYU830		S	Y	P	
37 cpx.CM.00.00CMNYU926		S	Y	P	
38 BF1.UY.03.UY03.3389		S	Y	P	
39 BF.BR.04.04BRRJ179		S	Y	P	
40 BF.BR.05.05BRRJ055		S	Y	P	
42 BF.LU.03.1uBF.05.03		S	Y	P	
43 02G.SA.03.111223		S	Y	P	
N.CM.95.YBF30		S	Y	P	
N.CM.97.YBF106		S	Y	P	
N.CM.02.DJ00131		S	Y	P	
N.CM.04.04CM.1015_04		S	Y	P	
O.BE.87.ANT70		S	Y	P	
O.CM.x.BCF06		S	Y	P	
O.CM.91.MVP5180		S	Y	P	
O.CM.96.96CMA102		S	Y	P	
O.CM.97.97CMA8447		S	Y	P	
O.CM.98.98CMA104		S	Y	P	
O.CM.99.99CMU4122		S	Y	P	
O.FR.92.VAU		S	Y	P	
DO.FR.08.RBF208		S	Y	P	
O.SN.99.99SE.MP1299		S	Y	P	
O.US.x.I.2478B		S	Y	P	
O.US.97.97US08692A		S	Y	P	
O.US.99.99USTWLA		S	Y	P	
P.FR.09.RBF168		S	Y	P	
CPZ.CD.90.ANT		S	Y	P	
CPZ.CM.05.SIVcpzMT145		S	Y	P	
CPZ.GA.88.GAB1		S	Y	P	
CPZ.TZ.00.TAN1		S	Y	P	
CPZ.US.85.US_Marilyn		S	Y	P	

	Tat start	disulfide bonding	NLS	exon 1 end	exon 2 start	Tat end	
B. FR. 83. HXB2	MEPVDPRLPEWPKHGPSQPKTACTCNVCKKCCFHQ	P-S-K-G	TH	GTSHS-KD-NHIP	SLP-T	QWE-S-E-S-EM	SK-R
A. CD. 02. 02CD KTB035	-L-N-N-Q	P-S-K-G	TH	GTP-SNKO-NPVR	IP-A	Q-S-E-S-E	SK-R
A. SN. 01. DDJ369	-L-N-N-Q	P-S-K-G	TH	GTP-SNKO-NPVR	IP-A	Q-S-E-S-E	SK-R
A1. AU. 03. PS1044 Day0	-D-N-N-T	NK-Y-P	S-LN-G	GPP-GNKNY-NPVP	IP-T	QR-S-E-P	SK-R
A1. T. 06. CY171	-D-N-N-S	W-M-L-K-G	H	GTSHS-KD-NHIP	SLP-T	QWE-S-E-S-EM	SK-R
A1. GE. 99. 99GEM2011	-D-N-N-S	W-M-L-K-G	H	GTSHS-KD-NHIP	SLP-T	QWE-S-E-S-EM	SK-R
A1. IT. 02. 60800	-D-N-N-SK	W-L-LN-G	R	GTP-NKO-NPVP	IP-T	QR-S-E-P	SK-R
A1. KE. 02. ML1990	-D-N-N-T-P-N	Y-V-SH-G	K	GPPHS-KD-NPIP	IP-T	Q-V-S-E-S-M	SKA-KS-R
A1. RU. 08. PokA1Ru	-D-N-N-S	W-L-K-G	H	GTSHS-KD-NHIP	SLP-T	QWE-S-E-S-EM	SK-R
A1. RW. 93. 93RW037A	-D-N-N-T-NK	Y-P-LN-G	K	GTP-G-KD-NPVP	IP-T	Q-V-S-E-S-E	SKA-R-A
A1. 95. SE8538	-D-N-N-NI-N	Y-P-A-LN-G	K	GTP-GNKNY-NPVP	IP-T	QR-S-E-P	SKA-R
A1. T2. 01. A341	-D-N-N-I-NK	Y-P-A-LN-G	K	GTP-GNKNY-NPVP	IP-T	QR-S-E-P	SKA-R
A1. UA. 01. 01UADN139	-D-NI-N-S	R-W-I-LK-G	P	G-PHS-KD-NHIP	SLP-T	QWE-S-E-S-EM	SK-R
A1. UC. 99. 99UGA07072	-D-N-N-A-ST-H	Y-P-LN-G	P	G-PHS-KD-NHIP	SLP-T	QWE-S-E-S-EM	SK-R
A1. ZA. 04. 04ZASK162B1	-N-D-N-S-P-S	Y-W-LN-G	R	GSPPS-KD-NPIP	IP-T	Q-V-S-E-S-E	SKA-R
A2. CD. 97. 97CDKTB48	-D-N-N-S	W-L-K-G	P	GTP-GNKNY-NPVP	IP-T	QR-S-E-P	SKA-R
A2. CY. 94. 94CY017 41	-D-N-N-K-R	Y-LN-G	P	GTP-GNKNY-NPVP	IP-T	QR-S-E-P	SKA-R
B. AR. 04. 04AR143170	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. AU. 04. PS1038 Day174	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. BO. 99. B0L0122	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. BR. 05. BREPM1081	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. CA. 97. CANB3FULL	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. CN. 05. 05CNHB hp3	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. CO. 01. PCNR01	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. CU. 99. Cu19	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. CY. 06. CY165	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. DE. 86. D31	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. DK. 04. PMVL 012	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. DO. 05. 05DO 160884	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. EC. 89. EC003	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. ES. 07. X2231	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. FR. 92. 92FR BX08	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. GA. 88. 0Y1	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. GB. 86. G88 46R	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. GE. 03. 03GENZ004	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. HT. 05. 05HT 129389	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. IN. x. 11807	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. JM. 05. 05JM KJ108	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. JP. 05. DR6538	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. KR. 04. 04K045	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. MM. 99. mSTD101	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. NL. 00. 671 00T36	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. RU. 04. 04RU128005	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. TH. 00. 00TH C3198	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. TT. 01. 01TT CRCS50069	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. TW. 94. TWY5	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. UA. 01. 01UAKV167	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. US. 07. CR0027M	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. UY. 01. 01UYTRA1179	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. YE. 02. 02YE507	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
B. ZA. 03. 03ZAPS045MB2	-S-N-T	R-G	P	PRD-S	S-P	K-A	G-V
C. AR. 01. ARC4006	-K-N-N-P-K	S-SY-LN-G	P	S-PPSGED-NLI-E	L-T	QA-SE-S	SK-K
C. BR. 04. 04BR013	-K-N-N-P-K	S-SY-LN-G	P	S-PPSGED-NLI-E	L-T	QA-SE-S	SK-K
C. BW. 00. 00BW07621	-Q-N-N-N	P-NK-F-S-SY-L	Q-G	H-PPG-KD-NPIP	IP-T	QR-S-E-P	SK-R
C. CN. 98. YNRL9840	-Q-N-N-N	P-NK-F-S-SY-L	Q-G	H-PPG-KD-NPIP	IP-T	QR-S-E-P	SK-R
C. CY. 05. CY040	-I-K-N-N	NQ-Y-SY-L	Q-G	S-PPS-ED-NLI	L-T	Q-N-S-SE-S	SKA-K
C. ES. 07. X2118 2	-I-K-N-N	NQ-Y-SY-L	Q-G	S-PPS-ED-NLI	L-T	Q-N-S-SE-S	SKA-K
C. ET. 02. 02ET 288	-N-N-N-P	NQ-Y-SY-L	Q-G	S-PPS-ED-NLI	L-T	Q-N-S-SE-S	SKA-K
C. GE. 03. 03GENZ033	-N-N-N-K-F	Y-P-A-L-G	Q-G	S-PPS-ED-NPIP	IP-T	QR-S-E-P	SKA-K
C. IL. 98. 98I5002	-N-N-N-NK-F	Y-P-A-L-G	Q-G	S-PPS-ED-NPIP	IP-T	QR-S-E-P	SKA-K
C. IN. 03. D24	-N-N-N-S-NT-F	R-SY-A-L-G	P	S-PPS-ED-NIV	LPR	Q-S-SE-S	SKA-K
C. KE. 00. KER2010	-L-K-N-N	NT-SY-L	Q-G	S-PPS-ED-DLI	LP-T	Q-S-SE-S	SKA-K
C. MM. 99. mIDU101 3	-D-I-N-N	E-N-R-SY-L	Q-G	S-PPS-ED-NPI	LP-T	QR-S-E-P	SKA-K
C. MR. 93. 93MR 965	-D-I-N-N	NR-R-SY-L	Q-G	S-PPS-ED-NPI	LP-T	QR-S-E-P	SKA-K
C. SN. 90. 90SE 364	-N-N-N-NK-R	Y-SY-L	Q-G	S-PPS-ED-NPI	LP-T	QR-S-E-P	SKA-K
C. SO. 89. 89SM 145	-E-N-N-C	N-L-SY-L	Q-G	S-PPS-ED-NPI	LP-T	QR-S-E-P	SKA-K
C. TZ. 02. C0178	-N-N-N-P-NQ	H-SY-L	Q-G	S-PPS-ED-NPI	LP-T	QR-S-E-P	SKA-K
C. US. 98. 98US MSC3018	-N-N-N-N	F-SY-L	Q-G	S-PPS-ED-NLI	LP-T	Q-S-SE-S	SKA-K
C. UY. 01. TRA3011	-N-N-N-N	F-SY-L	Q-G	S-PPS-ED-NLI	LP-T	Q-S-SE-S	SKA-K
C. YE. 02. 02YE511	-I-K-N-N	R-NK-F-SY-L	Q-G	S-PPS-ED-NLI	LP-T	Q-S-SE-S	SKA-K
C. ZA. 05. 05ZAPSK240B1	-I-N-N-N	NG-SY-L	Q-G	S-PPS-ED-NPI	LP-T	Q-S-SE-S	SKA-K
C. ZM. 02. 02ZM108	-N-N-N-Q-P-K-F	Y-SY-L	Q-G	S-PPS-ED-NPI	LP-T	Q-S-SE-S	SKA-K
D. CD. 83. ELI	-D-N-N-N	R-P-NK-H	Y-P	L-N-G	G	GPP-GG-A-VPVP	S
D. CM. 01. 01CM 0009BBY	-D-N-N-N	S-NS-Q-Y	L-K-G	G	G	GPP-GG-A-VPVP	S
D. CY. 06. CY163	-D-N-N-N	S-NS-Q-Y	L-K-G	G	G	GPP-GG-A-VPVP	S
S. KE. 97. ML415 2	-D-N-N-N	S-NS-Q-Y	L-K-G	G	G	GPP-GG-A-VPVP	S
D. KR. 04. 04K8H	-D-N-N-N	R-N-L	L-K-G	G	G	GPP-GG-A-VPVP	S
D. SN. x. SE365	-D-N-N-N	P-N-Y	N-G	G	G	GPP-GG-A-VPVP	S
D. TD. 99. MN011	-D-N-N-N	S-S-S-I	L-G	G	G	GPP-GG-A-VPVP	S
D. TZ. 01. A280	-D-N-N-N	R-P-N	Y-N-G	G	G	GPP-GG-A-VPVP	S
D. UG. 99. 99UGK09958	-D-N-N-N	R-P-N	Y-N-G	G	G	GPP-GG-A-VPVP	S
D. YE. 02. 02YE516	-D-N-N-N	R-S-P-P	L-G	G	G	GPP-GG-A-VPVP	S
D. ZA. 90. R1	-D-N-N-N	R-P-NK-H	Y-L-S-G	G	G	GPP-GG-A-VPVP	S
F1. A0. 06. A0 06 ANG125	-II-N-D-N-T	P-F-V-Y	R-T-G	S-PPS-KV-N-VPE	L-A	S-E-S	SK-K
F1. AR. 02. ARE933	-L-N-D-N-T	P-F-V-Y	R-LAR-G	H-TPHGT-I-DLVP	L-A	N-S-E	SKA-K
F1. BE. 93. VI850	-S-D-N-T	P-K-R	W-T-G	H-TP-S-V-N-P	L-A	S-E-S	SKA-K
F1. BR. 07. 07BR844	-I-N-D-N-T	P-K-R	Y-W-T-G	H-TP-SN-DLVP	L-A	N-S-E	SKA-K
F1. ES. x. P1146	-I-N-D-N-T	P-K-N	Y-H-A-G	H-TP-D-KV-NPVP	L-A	N-S-E	SKA-K
F1. FI. 93. FIN9363	-L-N-D-N-T	P-P-N	Y-L-G	H-TP-S-DVP	L-A	RN-S-E	SKA-K
F1. FR. 96. 96FR MP411	-L-N-D-NQ	P-K-R	Y-C-A-G	TP-S-S-KNPIPE	L-A	S-E-S	SKA-K
F1. JP. 04. DR6082	-S-D-N-T	A-P-K-R	W-T-G	H-PP-G-I-DLVP	I-A	Q-N-Q	SKA-K
F1. RO. 96. BCI R07	-L-N-D-N-T	P-K-NR	Y-H-T-G-D	H-TP-S-PI-NPVP	L-A	N-S-E	SKA-K
F1. RU. 08. D88 845	-L-N-D-N-T	A-P-K	R-TH-G	GTx-S-I-NPVP	S	Q-E-S	SKA-K
C2. CM. 97. CHS3657	-M-K-N-N	E-NK	L-S-G	S-S-EI-NPVP	L-A	G-N-N-E	SKA-K
G. BE. 96. DRCL	-D-N-N-N	P-N-SVAAL	L-N-G	KH-GTPHS-KD-TPVP	F-TT	N-Q-S-E	SKA-K
CM. 04. 178 15	-D-N-N-N	NK-V-W	L-D-G	KH-GTPPG-EN-DTIP	LTT	N-Q-S-E	SKA-K
G. CU. 99. Cu74	-D-N-N-N	N-R-W	S-LH-G	KH-GTP-G-KD-NPVP	LPTT	N-Q-S-E	ASK-K
G. ES. 05. P962	-D-N-N-N	NK-V-W	L-N-G	KH-ATPPG-KD-NPVP	LPTT	N-Q-S-E	ASK-K
G. GH. 03. 03GH175G	-D-N-N-N	T-P-NK	V-W-LN-G	K-GTP-G-KD-NPVP	LPTT	N-Q-S-E	ASK-K
G. KE. 93. HH8793 12 1	-D-N-N-N	NK-I-W	L-N-G	KH-PP-DNK-VAVQE	S-H	N-Q-S-E	ASK-K
NG. 01. 01NGPL0669	-D-N-N-N	R-K-V-W	L-N-G	KH-TP-S-PI-NPVP	L-A	N-S-E	SKA-K
G. PT. x. PT2695	-D-N-N-N	K-F-V-W	L-N-G	KH-GTP-S-TD-NPVP	LPTT	N-D-E-S	EM-S
G. SE. 93. SE6165	-D-N-N-N	P-NK-F-V-W	L-N-G	KH-GTP-S-KG-DPVP	x-LPTT	N-S-E	ASK-K

B.FR.83.HXB2
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 J.SE.94.5E9173 7022
 K.CD.97.97ZR E0TB11
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 02 AG.SE.94.SE7812
 02 AG.SN.98.98SE MP1211
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 04 cpx.CY.94.94CY032 3
 05 DF.BE.x.VI1310
 06 cpx.AU.96.BFP90
 07 BC.CN.98.98CN009
 08 BC.CN.97.97CN06 6F
 09 cpx.GH.96.96GH2911
 10 CD.TZ.96.96TZ BF061
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 12 BF.AR.99.ARMA159
 13 cpx.CM.96.96CM 1849
 14 BG.ES.00.X605
 15 01B.TH.99.99TH MU2079
 16 A2D.KR.97.97KR004
 17 BF.AR.99.ARMA038
 18 cpx.CU.99.CU76
 19 cpx.CU.99.CU7
 20 BG.CU.99.CU103
 21 A2D.KE.99.KE2003
 22 01A1.CM.01.01CM 0001BBY
 23 BG.CU.03.CB118
 24 BG.CU.03.CB378
 25 cpx.CM.02.1918LE
 26 AU.CD.02.02CD MBT0047
 27 cpx.FR.04.04CD FR KZ5
 28 BF.BR.99.BREPM12609
 29 BF.BR.01.BREPM16704
 31 BC.BR.04.04BR142
 32 06A1.EE.01.EE0369
 33 01B.MY.05.05MYKL007 1
 34 01B.TH.99.01B2478P
 35 AD.AF.05.05AF095
 36 cpx.CM.00.00CMNYU830
 37 cpx.CM.00.00CMNYU926
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 CPZ.TZ.00.TAN1
 CPZ.US.85.US_Marilyn

Tat start disulfide bonding NLS exon 1 end_exon 2 start Tat end

MEPVDPLRPWKHPGSQPKTACTNCKKCCFHQ...VCFITKALGISYGRKKRRQ...R.RRAHQNSQTHQASLKQPTSQP...RGD.PTGPKK+KKKV.ERET...ETDPF.D*

-D--NQ--N--R--N--Y--L-LK-G--Y--GTPKSL-D-TLIP-x-L-RT--S--E--ASK--A--C--W
 -D--NQ--N--N--P--N--Q--S--L-LK-G--SR--ATPASV-D-NHIP-L-RT--S--E--ASK--A--C--
 -D--K--N--Q--N--Y--M-LK-G--S--H-TPASL-D-N-I-L-RT--H--O--E--ASK--*--
 -D--K--N--NG--N--Y--L-LK-G--GTPAGL-DN-DPIP-LPRT--ASKA--L-H--
 -D--NI--NQ--NQ--R--Y--P--L-LK-G--H--A-PSG-K--DPIPG-L-T--QRE-S--QEKs--E--SKA--P-R--
 -D--NR--N--Y--Y--L-LK-G--S--PPG-K--DPV-L-T--QRE--E--SKA--P-R--
 -D--NR--N--Y--Y--L-LK-G--S--PPG-KN-DLPE-LF-T--QRE--E--SKA--P-R--
 -D--NI--NQ--NQ--R--Y--L-LK-G--C--E--TTTPYA-KN-KDPIP-LP-A--S--E--SK--K--*--
 -D--NI--NQ--NQ--R--Y--L-LK-G--N--P--TTPY--EN--DP-R--L--E-Q-D--S--SK--K--Q--
 -S--N--T--SK--W--L-LK-G--KH--GPPPG-KD-NPIP-LPTT--N--S--E--AKKA--K--*--A--
 -N--N--R-T-N-SK--I-W--L-LK-G--H--KH--P-S-KD-NPVP-LPII--N--S--E--ASKA--QC-A--
 -N--N--K-T--K--I-SW--L-LK-G--KH--GTPRS-EG-NPVP-SL-TS--N-Q-D-E-S--AGK--*--
 -N--N--T--SK--R-W--L-LN-G--KH--TP-S-KD-HTIPE-PPIT--N-D-S--E--ASKA--C-A--
 -L--N--N--T--ST--I--W--L-LK-G--KH--GTP-SHKD-NPVP-R-LPTI--N-S-D--S--E--ASKA--A-C--
 -N--N--T--S--W--L-LK-G--KH--GTP-S-KS-NPVP-R-LPTI--N--S--E--SKA--C--
 -K--N--N--T-N-NT--W--L-LK-G--KH--GTP-S-KD-NPVP-R-LPTI--N--D--S--E--ASKA--*--
 -D-I-K--N--A-P-SK--W--P--I-LN-G--R--GPP-SR-D-NPIP-LPR-LPTNG-N--EKS--ASK--Q*-
 -L-S--N--T--SK--M-W--L-LN-G--R--TP-DC-D-NPVP-FPTT--N--ES--E--ASK--A-C--
 -L-S--N--A-SK--M-W--L-LN-G--GR--GPPPSR-D-NPVP-LPTT--N--D--S--E--ASK--G-C-A--
 -S--N--T--SK--I-W--L-LN-G--R--GTP-SR-D-NPVP-LPTT--N--D--S--E--ASK--OG--
 -L--N--N--T--NK--A-W--L-LN-G--R--GTP-SR-D-NPVP-LPTT--N--D--S--E--ASK--RG-C-A--
 -D--SI--N--T--SK--A-W--L-LN-G--KR--GSPRS-H-DR-NPVP-LPTT--N--S--E--ASK--NLC-Y
 -L-S--N--T--SK--I-W--L-LK-G--R--GTP-SH-D-NPVP-LPTT--N--A--S--E--ASK--RC-A--
 -L-S--N--T--SK--I-W--L-LN-G--KR--GTP-SR-DN-DPVP-LPTT--N-A--S--E--AGK--C--
 -L-K--N--T--SK--L-W--L-LN-G--R--GTP-SR-D-NPVP-LPTT--E-Q--S--E--ASK--G-C--
 -S--N--K-T--SK--W--L-LN-G--R--GTP-SR-D-NPVP-LPTT--N--D--Q--E--ASK--C-V--
 -DL--S--N--T--NK--M-W--L-LN-G--R--GTS-SR-D-NPVP-LPTA--N--D--Q--E--ASK--C-V--
 -P-DN-D-V-P-A--M--H--
 -D--N--T-D-NK-F--W--L-LK-G--KH--GSL-G-KG-NLIP--L-Q--PN--S--E-Q--ASK--A--A--
 -D--N--N--R--NQ--M--Y--N--G--P--PP-G-A-DPVE-P--KO--E--SK--A-Q--W
 -KI--NQ--R--K--Y--P--LN-G--Q-PPG-KN-DPV--L-T--QRE-Q--EKS--E--SKA--P-R--
 -K--S--MK-G--F--S-P-S-ED-NLI-LPRT--Q--SE--S--SK--K--
 -N--N--E--N--R-SY--L--QK-G--S-P-S-ED-NLI-SLPTT--Q--QA-SE--S--SK--KPA--
 -L--N--A--NK--R--Y--H--LN-G--A-SG-KSN-DPIP-LP-T--N--S--E--ASK--KS-Q--
 -H-N--N--NK-H-A-SY--L--Q-S--S-PPS-ED-NLI--S--A--A--W
 -NI--NQ--NQ--Y--H-LK-G--P-SHS-KN-DHIPE-L-A--TRK--V-E-S-E--SK--P-R--
 -L--N--N--K-S-P-K--R--Y--W-V-G--P-G--N--I-A--N--S--E--SKA--KS-C--
 -D--KI--NQ--P--K--I--W--LN-G--S-SH--N-DLIP-LPI--N-Q--S--E--SK--*--W
 -D--N--N--K--I--W--LN-G--KH--GPP-SDRD-NPVP-LPTT--N--D-E-S--SK--K--
 -D--LN--N--R-T-N--I--W--L-LK-G--KH--GTP-S-KD-NPAP-L-IS--K--D-KS-E-ASKA--*--
 -D--N--N--R-NK--R-Y-P--LN-G--P--PP-GGTG-NPIPE-SLPR--QRI--TE-S-TE--SKA--C--
 -I--N-D--N--T-P-R-F-E--Y--W-T-G--N--P--PP-GNPP-V-P-AP-A--N--S--E--SKA--K-Q--W
 -NI--NQ--N--R--Y--L-LK-G--TTPTYD-KH-DLPE-L-RT--SW--Q-E--ASKA--A-QC--
 -D--N--N--NT--L-TK-G--GPP-SH-D-NPVP-LPDT--E--T-S--E--SK--K--
 -D--N--N--NK--V--W--LN-G--KH--GPPPG-KD-NPVP-IPIT--N--S-EE--SK--T-C-A--
 -D--N--N--R-NK-H-R-Y-I--K-L-G--R--PP-GD-A-VPVP--S--S-A--C
 -L--S--N--T-N-F-V-W--LN-G--KH--GTP-G-KD-NPIP-LP-T--KR--S--E-S-E--SK--NR-A--
 -D--N-D--N--NK--M--W--LN-G--KH--GTP-D-KD-IPVP-LPTT--N--S--E--SK--A--
 -D--N--N--NK--V--W--L-LK-G--KH--GTPLSNKD-NPVP-LPTA--N--KS-E--SK--KA--
 -D--NI--N--G-P-N--R--K-G--S--GTPPS-KD-NPVP-IPIT--N-Q--E-S--ASK--Y-A--
 -RNID--N--P-NK--Q-Y--L--G--P--GTSRSN-D-NP-P-S-A--QRE-SP-E-S--SK--Q-R--
 -D--N--NQ--NQ--R--Y--H-LK-G--F--T-PYGNNK-DPIQE-SIP-T--QR--S--SE-S--SKA--RA-R--
 -Q--R--NK--L--MK-G--P--DN-NN-V--A-S--N--E-S--S--T--A--
 -R--NK--G--T--D--D-V--A-F--S--T--A--
 -D--K--N--N--R-SY--L--G--S-PPS-ED-NLI--VP-S--Q--SEKS--SK--C--
 -HKI--NQ--R--P--P--Y--Y--M--LN-G--Y--T-PPG-KN-DPE--V-T--QRE--E--SKA--TPNR--
 -L--N--N--K-T-S--R--W--L-LK-G--KH--GTP-S-ED-NP-P-L-IS--N--DS--S--ASKA--GLC-A--
 -N--N--N--T--SK--N--W--L-LK-G--KH--GTP-S-KD-NPIPE-LPTI--N-Q--S--E--ASKA--*--
 -DL--D-D--N--T-P-NK-F-V-SY--LN-G--TP-S-D--NP-P--P-A--Q-I-S--E-S--SKA--P-R--
 -L--NI--N--R--N-F--W--LN-G--R--G-P-SR-D--DPV--LPAI--KN--S--E--ASK--N-C--
 -D--N--N--N--TK-G--T-A-SR-DN-H-VP--LPTT--N--S--E--ASKA--C-A--
 -I--K--N--T-P-NK--R--Y--W-T-G--H--TP-SN-I--DPVP--V-A--N--S--E--SK--K-C-A--
 -D--K--K--T--G--TP--I--DPVE-I-A--HRN--S--E--SKA--K--*--
 -D--K--R--G--P--SP-GR-S-G--SRAP-Q--E--S--E--
 -I--K--E--R--R--G--P--NPPD-E--AT--x--D-H--
 -L--S--N--T--SK--W--L-LN-G--R--GTP-SR-D-NPVP-LPIT--SEN--S--E--SK--
 -N--N--R--Y--L--Y--TK-G--S--TP-S-KS-DLPE-L-Q--Q--Q--Q-KO-EAL--SK--A-C--
 -N--N--NK--Y--M--C--TK-G--S--PPKS-KD-DPIPE-L-RO--QP--Q--Q-KO-AL--GK--A-C--
 -N--N--NG--Y--Y--C--TK-G--S--P-TASHKNDKDPVE-L-Q--QP--Q--Q-KO-AL--GK--A-C--
 -N--N--NK--N--Y--Y--TK-G--S--KTPNS-KDY-DPIPE-L-Q--P--Q--Q--Q-AL--SK--A-LC--
 -D--EVP--H--QIP-N--R--Y--Y--VR-G--G--P--AASHPD-KDPVP--SPTIT--KRK-QEROE-QEEE--KKA--GPGGY-PR
 -D--EIP--H--K-Q-P-N--R--Y--F--TK-G--H--PA-AASYPDNKDVPVE-SP-HT--RK-QKROE-QE--A--GASGH-PC
 -D--EMP--H--K-Q-P-N--R--Y--Y--TK-G--H--PA-AASYPDNKDVPVE-SL-HT--GRK-QKROE-QE--K--GPSGO-PC
 -D--EVP--H--Q-H-NK--S--Y--Y--TR-G--S--AAGHSNDKDLVE-SP-IT--KRK+EROE-QE--K-A--GPGGY-HC
 -D--EVP--H--Q-P-NA--Y--Y--L-TK-G--H--PA-AASCSNNDKDLV-STST--NRK+KROE-QE--K-K--G-GD-PC
 -D--EMP--H--Q-NK--S--Y--Y--L-LK-G--P--TASHPDNDKDPVE-SP-IT--NRK+EROE-QE--K--GPG+Y-HC
 -D--EMP--H--Q-P-NK--Y--Y--TS-G--P--AAHHPDNKDLPVE-SPTIT--NRK-QEROE-QE--K--GP+Y-PC
 -D--I--EMP--H--Q-P-NA--Q-Y--Y--L-TK-G--H--PA-AASYPDNKDVPVE-SP-NN--KRK+EROE-QE--TK--GAGGL-HC
 -D--N--N--S--NS--Q--F--TK-G--G--GPP-GG--VPVP--STGT--SRE-QKHQE-QE--K-K--GP+H-PR
 -D--EMP--H--Q-P-NK--A--Y--Y--AS-G--PA-AARHPDN-DIVPE-L-YIT--NRK-QKROE-QE--N-P--CPR+Y-PG
 -D--EMP--H--P-P-K--Y--Y--TS-G--PA-AASRPDNKDLPVE-SP-IT--NRK-QKROE-QE--KKA--GP+Y-PR
 -D--EMP--H--L-P-K--Y--Y--TS-G--PA-AASRPDNKDLPVE-SP-IT--NRK-QKROE-QE--KKA--GP+Y-PR
 -D--HEMP--H--S-Q-P-NT--S--Y--I--TK-G--PTTAERHTDNKDVPVE-SPTIT--SRK+EROE-QE--KKA--GAGG+PR
 -DQ--D-P-QQ--SSP-N--A--Y--Y--TK-G--PA--DN-N-N--DPV--*LA*TG.IQOE+HQ--QT--KQA--TA-RS--C
 -D--AETP--L--PAT-A-P-N--C--Y--P--L-TK-G--R-ARRN--TTAES-ENN-DPV--*SLPKT--SRI-QSSQ-K-E--EK--GSGGG-PC
 -IE-D--N--K-R-E-NK-F--Y--J--L-TK-G--GR--KP-SS-OD-NKDP-R--L--IR--Q--SEKO--E--TS--A-QS-W
 -D--I--P--Y--A--Y--L--TK-G--T-R--T--N-KE--ST--ASK--A--Q--T--
 -x-QVA--E--AA-E-P--P--TK--R-G--K-SAVH-TNN-DPVRO-SLPKR--SRI-QNSQE-SQEE--AL--TSGG-PR
 -D--NI--Q--N--V--TK-G--GR-R--TKAKS-ADN-DP-R--F-P-Q--L-N-Q-Q-Q-Q--AL--KQ--TSQR--

[illegible]

	Rev start	exon 1 end	exon 2 start	NLS	Leu-rich effector domain	Rev end	
B. FR. 83. HXB2	MAGRSGDS	.D.EELIRTVRLIKLLYQSNPPPN	...PEG.TRQARRNRWR.RER	...QRQHS.ISERILGTYLGRSAEPVLPQLPLERLTDCN	EDCGTSGT.....QGVGSPQILVE.SPT...VLESGTKE*	116	
H.BE.93.VI991	N.....G-L-AC-I-R	..xH-Y-E	..A-..Q	..A-..G-V-A-C-GP	S.....GEK.....TSG.....A.....GT-A	116	
H.BE.93.VI997	AG.....Q-POVCKI-II	..Y-E	..A-..A	RA.....TDC-PP	K.....GEK-K-G-P	117	
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H.GB.00.00GBAC4001	H.....G-LQVCKI-I	..Y-E	..RAE	A-..H-C-AGPV	S.....E.....K.....S-P-A	117	
J.CD.97.J.97DC KITB147	D.....O-LLA-I-I	..G-Y-K	..N-S	A-..N-D-SAC-P	F-I-R-S.....D.....GT-D-SG	117	
J.SF.93.SF9289 7887	N.....DQ-LLA-I-I	..Y-K	..N-S	A-..N-D-SSC-P	I-R-S.....N.....GT-D-SG	117	
J.SE.94.SF9173 7022	R-..E.QO-LTP-I-I	..Y-K	..A-..RE	Q-V-SSC-T	S-N-D.....S.....QGTGEG-L-P	117	
K.CD.97.972ZR E0TB11	R-..P.....Q-LT-T-I	..E-Y	..L-S-T	A-..K-S-L-SAC	I-K-N-N-D.....P.....KGTG-L-S	117	
K.CM.96.96CM MP535	NT.....D-LQA-I-I	..Y-P	..K	R-..L-VACV-T	H-T-S.....Q0SGTET-G-SG	124	
01 AE.CF.90.90CF11697	NT.....LKA-I-I	..F-S	..S	A-..SA-L-NH-PT	H-N.....Q0SGTET-R-SG	124	
01 AE.CN.07.073SWX045	ST.....LGA-A-I	..S-P	..A-T-K	A-..RK-SSVV-T	S-H.....Q0SGTET-R-SG	124	
01 AE.HK.04.HK001	ST.....L-A-I-NI	..L-S	..T-K	A-..RA-L-SSC-T	H-S.....S.....Q0SGTET-S-SG	124	
01 AE.JP.x.DR0492	ST.....L-AI-T-I	..D-F-P	..S-T-K	A-..K-RA-H-C-T	H-S.....G.....Q0SGTET-K-SG	124	
01 AE.TH.04.BKM	ST.....L-A-A-RI	..E-F-S	..S	A-..RA-SAC-T	H-S.....Q0SGTET-R-SG	124	
01 AE.US.00.00US MSC1164	ST.....L-A-I-RI	..E-Y-S	..T-K	A-..RE-S-C-PT	H-S.....Q0SGTET-R-SG	124	
01 AE.VN.98.98VNN015	A-..D-L-A-I-I	..Y-DPYPT	..A-..SE	RSC	I-S-C.....G.....Q0SGTET-SSG	128	
02 AG.CM.02.02CM 0013BBY	A-..L-..I-I	..S-P	..S-K	A-..L-RA-S-C	I-R-S.....N.....Q0SGTET-S	124	
02 AG.CY.05.CY048	A-..D-L-A-I-I	..Y-P	..T-K	A-..VRA-L-Q-V-CAC	I-C-S.....G.....Q0SPGTET-E	124	
02 AG.ES.06.P1261	A-..L-V-I-I	..Y-P	..T-K	A-..RA-F-S-C	I-C-S.....G.....Q0PGTET-P-SG	124	
02 AG.FR.91.DJ263	A-..L-A-I-I	..Y-P	..T-K	A-..EVRA-L-F-S-C	I-H-S.....Q0PGTET-P-SG	124	
02 AG.GH.03.03GH181AG	NA.....G-LGI-IVRI	..S-P	..K	A-..G-I-V-C-E	I-H-S.....Q0PGTET-P-SG	124	
02 AG.IR.x.P044951	A-..L-AI-I-I	..Y-P	..G-K	A-..GA-L-S-C-P-SF	I-S-S.....Q0SGTKT-VS	124	
02 AG.NG.01.PL0710	NA.....L-A-T-I	..Y-P	..K	A-..RA-S-C-P	I-R-S.....S.....Q0SGTET-S	117	
02 AG.SN.98.98SE MP1211	A-..G-L-A-I-RI	..Y-P	..S-K	A-..VRA-S-C-P	P-I-C-S.....S.....Q0SGTET-S-TS	124	
02 AG.US.00.00US MSC3083	A-..L-I-I	..Y-P	..T-K	A-..RA-SSC	I-S-S.....A.....Q0SGTET-G-SG	117	
02 AG.UZ.02.02UZ0683	V.....L-A-I-I	..Y-P	..T-K	A-..RA-F-V-SSC-PT	I-C-S.....A.....Q0SGTAT-S	124	
03 AB.RU.97.KAL153 2	S.....LK-I-I	..F-S	..S	A-..H-Q-S-PE	L-H-S.....D.....Q0SGTAT-S	117	
04 cpx.CY.94.94CY032 3	NI.....D-FKAA-A-I	..Y-N-T	..A-..K-L	A-..L-A-P	K-N-S.....DK-VS	118	
05 DF.BE.x.VI1310	R-..D-LKA-I-I	..L-S	..A-..N-G	L-S-E	N-N-S.....S-P-A	117	
06 cpx.AU.96.BFP90	DR-LLA-I-I	..Y-K	..N-S	A-..N-D-V-S-C	I-R-S.....N.....N-SG-PDM	117	
07 BC.CN.98.98CN009	E.....A-LKA-T-I	..Y-E	..R-K	A-..SAC	I-HISGS-SG.....Q0SGTET-SGK	123	
08 BC.CN.97.97CNX 6F	08 BC.CN.97.97CNX 6F	A-LA-I-I	..Y-E	..R-K	A-..N-L-SAC-PT	I-HISGS-SG.....Q0SGTET-SGK	123
09 cpx.GH.96.96GH2911	N.....Q-LAA-V-I	..Y-K	..A-..S-N	RAC-PE	N-S.....RG.....Q0PGTET-SGK	117	
10 CD.TZ.96.96TZ BF061	N.....A-LQA-I-I	..S	..A-..GG-DA-PE	N-N.....H-GH-S	AD-SG-C-I-G	117	
11 cpx.CM.95.95CM 1816	N.....DQ-LTA-I-II	..Y-K	..Q-S-S	A-..N-D-Q-SSC-P	N-S.....S-N-Dx-PG	116	
12 BF.AR.99.ARMA159	LKA	..Y-K	..A-..S-RA-ID	PE-F-G.....Q0SGTET-G-P	G.....I-G	117	
13 cpx.CM.96.96CM 1849	V-LT-I-I	..N-Y-S	..Q-K	A-..GQ-S-C	H-S.....Q0SGTET-G-P	124	
14 BG.ES.00.X605	ST.....D-L-AIEI-I	..Y-P	..x	..A-..V-SACV-T	..S-H-N-S.....S-L.....Q0SGTET-G-S	123	
15 01B.TH.99.99TH MU2079	ST.....L-A-I-I	..H-Y-S	..A-S-T	..A-..KR-RE-SPC	S.....Q0SGTET-R-SG	124	
16 A2D.KR.97.97KR004	P.....D-L-A-A-RI	..S-D	..R-S-K	..A-..RA-SAC-PT	L-H-S.....K.....Q0PGTET-R-S	124	
17 BF.AR.99.ARMA038	D-LKAI-F	..K	..A-..NK-G-A	..P-L-H-S.....K.....Q0SGTET-GS-V	VPS-I	117	
18 cpx.CU.99.CU76	Q-LT-SI-I	..Y-E	..A-..SA	..N-C-GP	S.....F.....Q0SGTET-GS-V	124	
19 cpx.CU.99.CU7	D-L-VI-I-I	..Y-T	..QR-A-K	..A-..S-C-E-F	H-N-S.....R-G-S	116	
20 BG.CU.99.CU103	ST.....D-L-VI-I-I	..Y-P	..A-..RA-L-T	..T-C-PP	S.....Q0SGTET-R-VS	124	
21 A2D.KE.99.KE2003	R.....DD-LKAI-F	..S	..A-..A-VSYH-E	I-N-N-R.....A.....Q0SGTET-G-R	I-G-E	117	
22 01A1.CM.01.01CM 0001BBY	ST.....L-A-I-I	..Y-K	..R-K	..A-..K-D-L-SAC	H-S.....Q0SGTET-R-S	124	
23 BG.CU.03.CB118	ST.....L-I-I	..F-Y-P	..A-..Q-ADC	..PP	S.....I.....Q0SGTET-R-G	124	
24 BG.CU.03.CB378	ST.....LLAI-I-I	..Y-P	..A-..V-T	..C-P-L	S.....SS.....Q0SGTET-GS-S	124	
25 cpx.CM.02.1918LE	VN.....LQA-I-I	..S-P	..A-..T-L	..ASC-LE	H-S.....S.....Q0SGTET-R-VS	124	
26 AU.CD.02.02CD MBT047	P.....A-LGAI-I	..L-K	..R-S	..A-..NK-D-S-C	..GPP-S-S.....F-N.....Q0PGTET-R-S	124	
27 cpx.FR.04.04CD FR KZ5	NE.....Q-LTAI-I	..I-K	..Y-K	..R-K	..A-..E-D-K-V-S-C	..P-P-C-S.....F-N.....Q0PGAET-R-S	117
28 BF.BR.99.BREPM12609	D-K-I-I	..F-S	..S	..A-..L-RW-SMH-PE	..F-I-S.....A.....Q0SGTET-V	117	
29 BF.BR.01.BREPM16704	K-F	..S-S	..A-..RW-SMH-PT	..I-S.....SG.....Q0SGTET-N-V	A-I	123	
31 BC.BR.04.04BR142	N.....A-LQA-I-I	..Y	..A-..RA-S-C	..P-FL-I-NIN-S.....SG.....Q0PGTAE-N-V	G-R-KE	123	
32 06A1.EE.01.EE0369	N.....Q-LLA-I-I	..N-Y-K	..N-S	..A-..H-D-H-S-C	..P-FL-I-NIN-S.....SG.....Q0PGTAE-N-V	123	
33 01B.MY.05.05MYKL007 1	STST.....LKA-I-I	..Y-S	..A-T-K	..A-..VCA-L-D-SAC-T	..H-I-N-S.....Q.....GTET-R-SG	122	
34 01B.TH.99.01B2478P	ST.....L-A-T-I	..Y-S	..K	..A-..K-RE-D-ISC-T	N-S.....K.....Q0SGTET-R-VS	117	
35 AD.AF.05.05AF095	L-A-I-I	..H-K	..R-S-K	..A-..N-D-Q-AC-P	H-R.....Q0SGTET-R-VS	124	
36 cpx.CM.00.00CMNYU830	A.....L-V-T-I	..Y-P	..S-R-K-Q	..A-..RA-S-C-FE	H-S.....Q0PGTET-G-V	125	
37 cpx.CM.00.00CMNYU926	G.....Q-L-A-I-NI	..Y-P	..K	..A-..RA-L-S-C	H-N-S.....RD.....Q0PGTET-L-G	124	
38 BF1.UY.03.UY03 3389	L-KAI-Y-I	..F-K	..A-..RA-L-SSC-PE	HIS-S.....E.....Q0TE-N-PV	P-A-I-D	117	
39 BF.BR.04.04BRJ179	L-K-Y-I	..Y-K	..T	..A-..RE-F-SAC-RE	HIS-S.....E.....Q0GAE-TSG	117	
40 BF.BR.05.05BRJ055	D-L-A-A-V	..AD-S	..S	..A-..RK-W-ISNH-PT	..F-H-S.....V-E	117	
42 BF.LU.03.03BF 05 03	R.....T-LQ-R	..S	..A-..QT.x-GW-N	..PE-H-S.....SR-P	116		
43 02G.SA.03.03J11223	A.....L-A-I-I	..Y-S	..AR	..A-..SAC-R	H-S.....SR-P	124	
N.CM.95.YBF30	VN.....L-LA-V-I	..Y	..SK	..A-..RA-SSC-GPP	..D-P-D.....HE.....S-P	124	
N.CM.97.YBF106	VN.....D-LKA-KI-I	..Y-D	..SSO	..A-..RA-A-GPO	..D-P-G.....TK.....S-DP	123	
N.CM.02.DJ00131	VN.....D-LA-I-I	..Y-N	..MNO	..A-..RE-AA-A-VHGPDDNNLVE	..Q-SIRDP.....S-AP	123	
N.CM.04.04CM 1015 04	VN.....K-LTA-I-I	..Y	..NO	..A-..CA-S-C-GLO-GDPP	NT.....S-DP	123	
O.BE.87.ANT70	E.....Q-LQAI-I	..I-Q-S	..R-S-N-K	..A-..A-VDT-LAA-V-A-VHGPDDNNLVE	..Q-SIRDP.....GDOL	121	
O.CM.x.BCF06	DE.....Q-LQAI-I	..I-H-T	..G-S-N-K	..R-..A-VDT-LAT-T	..VHGPDDNNLVE.....Q-SIRDP	122	
O.CM.91.MVP5180	EE.....Q-LQAI-I	..I-C-T	..A-S-N-K	..R-..A-VDT-LAT-T	..VHGPDDNNLVE.....Q-SIRDP	121	
O.CM.96.96CM182	D.....D-LQAI-I	..I-H-S	..X-S-N-K	..R-..A-VDT-LAT-T	..VHGPDDNNLVE.....Q-SIRDP	121	
O.CM.97.97CMAB6447	D.....D-LQAI-I	..I-H-S	..X-S-N-K	..R-..A-VDT-LAT-T	..VHGPDDNNLVE.....Q-SIRDP	121	
O.CM.98.98CM104	D.....D-LQAI-I	..I-H-S	..X-S-N-K	..R-..A-VDT-LAT-T	..VHGPDDNNLVE.....Q-SIRDP	121	
O.CM.99.99CMU4122	D.....D-LQAI-I	..I-H-S	..X-S-N-K	..R-..A-VDT-LAT-T	..VHGPDDNNLVE.....Q-SIRDP	121	
O.FR.92.VAU	EE.....Q-LQAI-I	..I-H-T	..TS-N	..R-..A-VDT-LAA-F	..ASVVHGPDDNNLVE.....Q-SIRDP	121	
DO.FR.08.RBF208	RE.....D-LKV-F	..F-N-Q	..A-S-T	..A-..DT-LASx-T	..F-HGPDDNNLVE.....Q-SIRDP	121	
O.SN.99.99SE MP1299	DG.....Q-L-AI-I	..I-SHTS	..T-S-S	..T-..HAHVD-LAA-A	..VHGPDDNNLVE.....Q-SIRDP	122	
O.US.x.I 2478B	D.....V-QP-LQA-I-I	..H-S	..I-S-N-K	..R-..A-DT-LAA-V-T	..IVHGPDDNNLVE.....Q-SIRDP	122	
O.US.97.97US08692A	D.....V-QP-LQA-I-I	..H-S	..I-S-N-K	..R-..A-DT-LAA-V-T	..IVHGPDDNNLVE.....Q-SIRDP	122	
O.US.99.99USTWLA	E.....Q-LQAI-I	..I-Q-S	..A-S-N-K	..R-..A-VDT-LAT-T	..IVHGPDDNNLVE.....Q-SIRDP	122	
P.FR.09.RBF168	DE.....L-R-T-I	..I-W-E	..GSSRNS	..K-S.....PNNPVDTPGPTADORA	..LPARXCFACxL-D-R	122	
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	transmembrane domain		α-helix		phos cytoplasmic domain		α-helix		Vpu end	
	Vpu start									
B.FR.83.HXB2	T...QPPII.....VAIV.....ALVVAIIII.AIVVWS....									82
A.CD.02.02CD.KTB035	M...SLE.....WS-I.....I-F-V.....T-F-LRK.....									82
A.SN.01.DDJ369	M...ALE.....C-I.....G-I-V-L.....T-G-K-LRK.....									82
A1.AU.03.P51044.Day0	M...T-LE.....WS.....G-L.....T-G-K-L-K.....									82
A1.CY.06.CY171	M...T-LE.....Y.....VA.....A-L-G-RLOK.....									82
A1.GE.99.99GEMZ011	M...T-LE.....Y.....VFV.....T-G-L-K.....									82
A1.IT.02.68060	M...S-LQ.....C-I.....VG-L-L-T.....T-G-L-K.....									82
A1.KE.02.WL1990	I...STLH.....AL.....G-I-L-G-II.....T-G-L-K.....									82
A1.RU.08.Poka1Ru	M...L-LV.....C-A.....IVF.....T-LAAL-L-K.....									82
A1.RW.93.93RW037A	M...S-LE.....C-A.....G-L.....T-G-K-L-K.....									82
A1.SE.95.SE8538	I...SALE.....WS.....G-L-L-T.....T-G-CKRLQK.....									82
A1.TZ.01.A341	V...S-LH.....C.....G-I-L-L-T.....T-G-L-K.....									82
A1.UA.01.01UADN139	M...T-LE.....Y.....VSL.....F-T-A-G-LRK.....									82
A1.UG.99.99UGA07072	M...T-LE.....S-A.....G-L-L-L-T.....T-G-L-K.....									82
A1.ZA.04.04ZASK162B1	M...T-LE.....C-A.....G-L.....T-G-L-K.....									82
A2.CD.97.97CDKT848	M...S-LA.....LS.....G-S-L-T.....T-V-F-KK.....									82
A2.CY.94.94CY017.41	M...L-LV.....L.....G-T-L-L-T.....T-F-K-KK.....									82
B.AR.04.04AR143170	M...LQ.....A.....I-VA.....T-L-K.....									82
B.AU.04.P51038.Day174	M...LN.....L.....G-L.....T-A.....									82
B.BO.99.B010122	M...SLI.....M.....A-L.....T-A.....									82
B.BR.05.BREP1081	M...K-LQ.....A.....VG-L-G-T.....L-R.....									82
B.CA.97.CANB3FULL	M...HSLO.....F.....V-I-A.....T-G.....									82
B.CN.05.05CNHB.hp3	L...ALT.....F.....I-VA.....T-LL.....									82
B.CO.01.PCM081	M...HALO.....S.....TA.....T-GL-I-V.....									82
B.CU.99.Cu19	M...HSLO.....L.....I-A.....T-I-N.....									82
B.CY.06.CY165	M...H-LQ.....A.....S-VA.....T-V-L.....									82
B.DE.86.D31	M...SLOV.....A.....VA.....T-F.....									82
B.DK.04.PMVL.012	M...LV.....L.....A-A.....T-L-VK.....									82
B.DO.05.05DO.160884	M...HS.OV.....I.....A-A-I.....F.....									82
B.EC.89.EC093	M...N-LEL.....S-I.....V-L.....T-F.....									82
B.ES.07.X2231	M...L-LE.....L.....L-LE.....T-YL-VK.....									82
B.FR.92.92FR.BX08	M...SLE.....L.....V.....T-G-F.....									82
B.GA.88.OYI	I...YSLQ.....L.....VT.....T-LL.....									82
B.GB.86.GB8.46R	V...YV-Q.....LT.....G-V-I.....F-K.KK.....									82
B.GE.03.03GEM2004	M...LALN.....L.....G-I-A-L-I.....F-V.....									82
B.HT.05.05HT.129389	L...SL.....L.....S-L.....T-KR.....									82
B.IN.x.11807	M...LV.....A.....V-V.....F-L-K.....									82
B.JM.05.05JM.KJ108	M...SLE.....I.....V.....T-Y.....									82
B.JP.05.DR6538	M...LLE.....S.....VT.....I-T.....F.....									82
B.KR.04.04KPMH5	M...LV.....L.....T.....T-L-K-K.....									82
B.MM.99.MSTD101	M...SLT.....W.....A.....T-AL-L-KLVKE-E.....									82
B.NL.00.671.00T36	M...SLT.....A.....A.....T-F.....									82
B.RU.04.04RU128005	M...SLE.....A.....G-A.....T-L-K-L.....									82
B.TH.00.00TH.C3198	M...TLT.....L.....A.....T-L.....									82
B.TT.01.01TT.CRC50069	M...SL.....A-T.....I-A.....T-A.....									82
B.TW.94.TWCY5	M...L-A.....L.....A.....T-LL.....									82
B.UA.01.01UAKV167	Q...TAIV.....AL-I.....I-VA.....T-L.....									82
B.US.07.CR0027M	M...PSLY.....YS-I.....A.....T-F.....									82
B.UY.01.01UYTRA1179	M...LQ.....L.....VA.....T-FL.....									82
B.YE.02.02YE507	M...LHL.....A-I.....A.....T-GL-R.....									82
B.ZA.03.03ZAP5045MB2	M...SLV.....L.....IVA.....T-L.....									82
C.AR.01.ARG4006	M...LL.....EDYRLG-G.....I-L-I-T.....AY-LV-KR.....									82
C.BR.04.04BR013	M...LDLT.....YRVYRLG-G.....I-LVL-I-T.....AY-LV-KR.....									82
C.BW.00.00BW67621	M...ELIIA.....VDRIGVA.....II-L.....AY-L-K-K.....									82
C.CN.98.YNRL9840	M...LG.....IDYRLG-G.....I-L.....T-Y-RLV.....									82
C.CY.05.CY040	M...LSLLARV.....DYRL-G.....FI-L-I-I.....AYL-LV.....									82
C.ES.07.X2118.2	M...LELLAEV.....DYRLG-G.....S-L-T-I.....IYR-L.....									82
C.ET.02.02ET.288	M...FSFTERV.....DAR-G-G.....I-L-L-I-T.....AY-L.....									82
C.GE.03.03GEM2033	M...MCR.....VLLAKV.....DYRLG-G.....I-L-L-IA.....T-AY-L-KRL.....									82
C.IL.98.98IS002	M...MVDLL.....LLEKVDYRL-VI.....I-VA-T.....T-Y-L.....									82
C.IN.03.D24	M...LDL.....NYKLTVG.....F-I-L-L-T.....T-Y-LV.....									82
C.KE.00.KER2010	M...LDLLARV.....DYRLG-G.....I-L-I-T.....T-Y-L.....									82
C.MM.99.MIDU101.3	M...LE.....IDYRLG-G.....I-L-I-T.....T-Y-LVK.....									82
C.MW.93.93MW.965	M...LEIAK.....V.....DYRLG-G.....I-L-I-T.....T-Y-LV.....									82
C.SN.90.90SE.364	M...VDLLAKV.....DYRLG-G.....I-L-I-T.....T-Y-LV.....									82
C.SO.89.89SM.145	M...LNLLAGV.....DYRI-G.....FS-L-I.....T-Y-L.....									82
C.TZ.02.C0178	M...VDFLE.....DYRLG-G.....I-L-I-T.....T-AYL-L.....									82
C.U5.98.98US.MSC3018	M...L.....LEV.....DYRIGVA.....I-LS-T.....T-Y-L.....									82
C.UY.01.TRA3011	M...L.....LFIKIDYRL-VG.....I-S-V-I.....T-AY-LV.....									82
C.YE.02.02YE511	M...LDLLAKV.....DYRI-G.....F-L-I-T.....T-AY-LV.....									82
C.ZA.05.05ZAP5K240B1	M...LDLYAGV.....DYRIGV.....L-L-I-T.....T-Y-LV.....									82
C.ZM.02.02ZM108	M...LNLLEKVDYKITVA.....FII-L-I-T.....T-AYL-L.....									82
D.CD.83.ELI	M...LG.....I-A.....L-L-T.....T-F-R-KK-R.....									82
D.CM.01.01CM.0009BBY	M...SLE.....L-A.....L-L-T.....T-AY-VK-N.....									82
D.CY.06.CY163	M...SLE.....L-A.....L-L-T.....T-Y-K.....									82
D.KE.97.ML415.2	M...MALE.....L.....L-L-T.....T-WTRK-N.....									82
D.KR.04.04KRBH8	V...MOPPV.....I-G.....TL-I-T.....T-F-CKRLRK-N.....									82
D.SN.x.SE365	M...SLE.....L-A.....I-L-L-T.....T-F-V-R.....									82
D.TD.99.MN011	M...LV.....L-A.....A-L-I-T.....T-Y-K.....									82
D.TZ.01.A280	M...T-LE.....T-A.....I-S-L-T.....T-Y-R-KK-K.....									82
D.UG.99.99UGK09958	M...SLE.....L.....L-L-I-T.....T-LF-CRLKE-Q.....									82
D.YE.02.02YE516	M...SLLT.....I.....YI-L-I-T.....T-Y-K-L-KR-N.....									82
D.ZA.90.R1	M...LV.....L.....L-L-L-T.....T-F-R-RK.....									82
F1.A0.06.A0.06.ANG125	M...SYL.....LT-I.....V-L.....T-AY-VVK-N.....									82
F1.AR.02.ARE933	M...SYLLA.....IG-T.....I-L-T.....T-AY-K-LV-R-N.....									82
F1.BE.93.VI850	M...SYLLA.....IG-A.....I-L-T.....T-AY-K-LV-N.....									82
F1.BR.07.07BR844	M...PDLLA.....S-A.....I-F-I-T.....T-AY-VV-N.....									82
F1.ES.x.P1146	M...SHVLA.....IV.....FI-L-L-T.....T-Y-V.....									82
F1.FI.93.FIN9363	M...SLLA.....LS.....FI-L-V-T.....T-F-K-LV-N.....									82
F1.FR.96.96FR.MP411	M...SNLYV.....IT.....FII-L-T.....T-F-K-L-N.....									82
F1.JP.04.DR6082	M...SY-LA.....IS-I.....I-S-V.....T-YL-LV-N.....									82
F1.R0.96.BCI.R07	M...SHVLA.....I.....I-L-I-T.....T-AY-LV-N.....									82
F1.RU.08.D08.845	M...TE-I.....IG.....I-L-V-T.....T-F-N.....									82
F2.CM.97.CM53657	M...SSLLT.....I.....YI-L-I-T.....T-Y-K-L-KR-N.....									82
G.BE.96.DRCBL	M...LE.....S.....G-I-S-A.....T-F-RK-KR-E.....									82
G.CM.04.178.15	M...L-LQ.....A.....G-FMA.....T-L-E-RK-K-LN.....									82
G.CU.99.Cu74	M...KSLE.....S.....G-II-G-A.....T-F-Q-E-RK-K.....									82
G.ES.05.P962	L...E-LA.....AS.....G-I-F-A.....T-FL-RK-KR-K.....									82
G.GH.03.03GH175G	M...SLE.....S.....G-I-S-A-I.....T-F-RK-K-E-K.....									82
G.KE.93.HH0793.12.1	M...SLE.....S.....G-I-F-A-I.....T-LVQ-E-RK-K.....									82
G.NG.01.01NGP.L0669	M...SLE.....S.....G-I-F-A-I.....T-LVQ-E-RK-K.....									82
G.PT.x.PT2695	M...SLG.....F.....G-I-G-A-I.....T-F-Q-KE-RK-N-Q.....									82
G.SE.93.SE6165	M...SLV.....L.....G-I-F-A.....T-F-E-RK-KR-G.....									82

	transmembrane domain										phos cytoplasmic domain												
Vpu start											α-helix										Vpu end		
1. QPIPT	VAIV	ALVV	AIIV	WVS	IVII	EYR	KILR	ORKID	RLID	RLIERAE	DSGNE	SEGEI	SA	LV	EMGV	EMG	HHAP	PDV	DDL	82			
M...N-LG	IG-G	F	T	AY	L-K	E-IR	D-DT	EE	S-KL	LNLGY	A	EE	S-T	R	LTFGY	A	80						
M...Y-IG	IG-G	I-F	T	Y	LVK	K	I-G	D	EE	S-T	R	LTFGY	A	80									
M...Y-LG	LG-G	TF	VI	T	Y	K-LV	K	E-IG	D-DT	EE	S-KL	M	LNLGY	A	81								
M...Y-LG	IG-G	I-G	L-C	I	T	YL	LVQ	KR	LE-IR	D-DT	EE	S-TL	R	LNLGY	A-V	81							
M...LD	A	G-I	V	VI	T	F	V	N-IR	D-DT	DE	E-KL	P-DL	N	N	82								
M...I-LQ	A	FI	FL	GM	T	Y	K-L	K	N-IR	D-DT	EE	A-DL	R	P-DL	N	82							
M...VSQ	A	I	FFL	C	T	Y	K-L	K	N-IR	D-DT	DE	A-L	P-DL	N	N	82							
V...MVLPT	G-I	A-L	L	I	T	AYL	VV	KR-N	W-F	IR	DT	EE	A-AL	G-T	L-LIG	I-NN	82						
M...MVSIA	IS	I	I	I	T	Y	LVK	KR-N	W	IR	DA	EE	A-DI	G-L	L-LIG	I-NN	82						
M...SALO	S	G-I	L-L	T	T	F	K	E-IR	G	DT	NE	A-TL	V	DFD	VG	N	81						
M...T-LE	S	G-I	L-L	T	T	A	K	VE-IR	DT	DE	A-KL	DFD	VG	N	82								
M...T-LQ	S	G-I	L-L	T	T	GL	V	KKIR	E	DT	DE	A-KL	DFD	VG	N	82							
M...S-LE	S	G-I	L-L	T	T	A	K	K	IR	E	DT	DD	A-KL	DFN	VG	NN	82						
L...T-LE	S	G-I	L-L	T	T	A	L	RV	K	IR	E	DT	DE	A-KL	DFD	VG	NN	82					
M...T-LE	S	G-I	L-L	T	T	L	A	F	VK	IR	E	DT	DE	A-KL	DFD	VG	NN	82					
M...T-LE	C	G-I	L-L	T	T	G	F	K	DE	A-KL	DFD	VG	N	82									
M...L-LQ	A-VA	G	F	A	I	T	F	RK	Q-L	IR	D-DT	EE	S-TL	M-V	DYDFFVN	N	82						
M...SLOW	AP	G	P	F	A	T	AF	RK	K	L-IRQ	D-DT	EE	S-TL	M	DNIG	N	82						
M...LA	A	G	F	A	T	Y	RK	K	K-LN	IR	D-DT	EE	S-TL	M	DDNI	N	82						
M...SLE	T	G	F	A	A	T	F	RK	K	K-L	IR	D-DA	EE	S-TL	M	YDHIL	N	82					
M...SLA	A	G	F	A	T	L	RK	K	Q-L	IR	D-DT	EE	S-TL	M	YDHIL	N	82						
M...SLA	A	G	F	A	T	L	RK	K	Q-L	IR	D-DT	EE	S-TL	M	YDHIL	N	82						
M...SLK	A	G	F	A	V	T	L	RK	K	H	IR	D-DT	EE	S-TL	M	YDHIL	N	82					
M...SLK	A	G	F	A	A	T	Y	RK	K	IR	G-D	EE	S-TL	M	YDHIL	N	82						
M...NSLD	A	G	F	A	T	Y	RK	K	L	IR	D-DT	EE	S-TL	M	YDHIL	N	82						
M...LAV	A	G	F	L	T	F	RK	G	K-L	IR	D-DT	EE	S-TL	L	YDN	AL	I	N	83				
M...LE	AS	G	I	F	A	T	YFQ	E	RK	K	L-N	IR	D-DT	EE	S-TL	L	YDRLF	D	N	82			
M...SLE	A	G	F	A	T	AY	RK	K	K-L	IR	D-D	EE	S-TL	M	YDHIL	N	82						
M...SLA	A	VG	G	F	T	F	IR	DT	EE	S-TL	M	YDHIL	N	82									
M...LFWE	W	G	L	V	T	L	F	K-LR	R	S-YN	IR	D-DA	EE	S-TL	G	NFD	VG	N	79				
M...SDLT	I-V	I	L	T	Y	K	L-V	N	YK	IR	DA	EE	A-AL	G-V	PFI	G-I	NN	82					
M...ALE	A	G	FLA	T	F	Q	E	RK	K	E	K-L	IR	DT	DE	A-TL	M	DFD	VG	NN	82			
M...TLT	L	A	T	L	K	IR	D-DQ	EE	S-AF	M	82												
M...LDLE	L-VG	I	L	T	Y	RLVK	W	K	IR	DT	EE	S-T	D	RRL	L	N	81						
M...SLQ	AS	GII	F	A	IA	T	F	V	RK	K	IR	DT	EE	A-KL	P	DS	N	82					
M...LSLLARVYKLRV	I	L	T	I	R	Y	Q	LVE	PT	W	K	IR	R	HD	D	DT	EE	S-T	D	NLRLL	N	87	
M...ISLQ	AS-I	F	VV	T	GL	L	IR	DT	EE	A-QL	P	D	L	N	82								
M...SLVT	L	A	L	A	L	IR	DA	EE	A-AF	G-L	L	L	I	GNI	N	82							
M...NAL	IS	I	F	L	V	T	AY	LVH	K	E	K-L	IR	DT	DD	A-KL	NFD	VG	N	82				
M...LE	A	G	I	G	A	I	F	Q	KE	RK	K	Q	IL	IR	DT	EE	A-IL	DFD	VG	NN	81		
M...S-LE	S	G	I	L	T	A	I	N	K	Q	VK	IR	E	DT	DE	A-KL	DLD	VG	NN	82			
M...NSLQ	LS	G	I	F	L	V	T	F	K	KK	N	W	K	IS	DT	EE	S-TL	M	NLDFG	A	N	81	
M...ALE	L	T	L	L	L	E	IR	DA	EE	IS	AL	M	I	N	82								
M...FE	G-I	I	F	V	VC	T	Y	K	K	G	FE	IRD	Y	DT	EE	S-KL	M	N	N	GY	A	V	80
M...ALQ	A	G	I	F	A	T	Y	RK	E	E	K-L	IR	D-DT	EE	S-TL	M	L	DFD	VG	NN	82		
M...SLEV	A	G	I	G	A	I	A	F	L	KE	RK	K	Q	IL	IR	DT	DE	A-VL	D	DFD	VG	NN	82
M...ALQ	I-A	T	T	T	F	R	K	R	C	IR	DR	EE	S-KL	Y	N	82							
M...LE	CT	G	I	L	L	T	A	IK	VR	K	LE	IR	DT	DD	A-KL	NFD	VG	NN	82				
M...HSLE	A-V	G	I	G	A	I	A	F	L	KQ	RK	K	IL	IR	DT	EE	A-AL	D	DFD	VG	NN	82	
M...SLE	A	G	I	G	A	I	A	IF	Q	KE	RK	IL	IR	DT	DE	A-TL	D	DFD	VG	NN	82		
M...SLE	F	G	I	F	V	VI	T	YL	I	RK	K	Q	LE	IRT	DT	EE	S-TL	M	DFDA	VG	NN	82	
M...T-LQ	Y	G	I	L	L	T	LV	K	K	IR	D-DT	EE	S-AL	D	N	N	GY	NV	82				
M...ISLKT	IS-A	I	F	L	VV	T	Y	L	K	R	L	IR	D-DT	EE	A-RL	P	D	L	GND	N	82		
M...ALI	A	VA	T	F	IR	DA	EE	E	AL	GD	PLVL	GNI	NN	82									
M...SLO	I	VA	T	F	R	K	L	IR	DT	EE	A-IL	DNV	D	D	VG	N	79						
M...FTL	ERIDYR	G-G	LI	L	I	T	Y	LV	R	W	VK	IR	DT	EE	E	T	D	NLRLL	P	80			
M...ALE	S	G	II	SLA	T	L	Q	E	RK	E	K-L	IR	DT	DE	S-TL	M	NFD	VG	NN	82			
K...T-LE	S	G	IA	L	S	T	A	LQ	K	VK	IR	DT	DE	A-KL	DFD	VG	NNV	82					
M...S-LE	S	G	I	L	L	I	A	E	VK	IQ	DT	DE	A-KL	NFD	IG	N	82						
M...P-LH	L	G	L	L	T	G	LKRL	I	K	IS	D-DT	DE	A-KL	NYDL	GND	NN	82						
M...SLQ	A-A	G	F	A	GG	T	L	K	I	K	LE	IK	K	NT	EE	S-TL	DFD	VG	NN	82			
M...LE	YS	G	F	A	T	L	K	RK	N	IR	D-DT	EE	S-TL	M	L	DFD	VG	NN	82				
M...SNLLV	LG	I	L	T	Y	V	R	N	YE	IR	DA	EE	A-AL	G-VQ	LVI	GNI	NN	82					
M...SDLA	IG	T	I	L	T	AYL	FV	R	N	YE	IR	DA	EE	A-AL	G-V	PFIL	G	I	NN	82			
M...SLQ	A	G	VA	T	LL	L	K	E	IA	DT	EE	S-TL	M	82									
M...SLV	L	L	K	A	IS	D-DH	EE	S-AL	I	Q	82												
M...LE	A	G	I	FLA	T	F	R	K	L	IR	DT	EE	A-IL	DNV	D	D	VG	N	79				
M...LS	LGFI	G	A	VS	VI	A	LLYR	K	KL	E	K	HIRO	IR	E	D	DAEWL	GDGEW	TL	L	SSSKL	QGNW	N	84
M...LW	LGFI	G	A	VS	VI	A	LLYR	K	KL	E	K	HIRO	IR	E	D	DAEWL	GDGEW	TL	L	SSSKL	QGNW	N	84
M...LW	LGFI	G	A	VS	VI	A	LLYR	K	KL	E	K	HIRO	IR	E	D	DAEWL	GDGEW	TL	L	SSSKL	QGNW	N	84
M...LS	LGFS	G	A	VS	VI	A	LLYR	K	KL	E	K	HIRO	IR	E	D	DAEWL	GDGEW	TL	L	SSSKL	QGNW	N	84
M...HHRDL	L-I	ISALLF	NVL	I	G	FILR	KYL	QKEO	KE	E	L	ERLR	IR	IRD	DY	N	E	EQEV	DLVLSH	FDN	PMF	84	
M...HHRDL	L-I	SALCL	S-I	I	INLR	NYL	Q	OD	REO	L	ERLR	VR	IKO	DYD	N	E	EQEV	DLMHS	FDN	PMF	84		
M...HQRNL	L-II	SALCL	NVL	I	FNLR	YLVO	Q	OD	REO	L	ERLR	IK	IRD	DY	NE	E	QOEV	LIHSH	FAN	PMF	84		
M...HYRDL	STLI	ISVALL	NVL	M	FILR	YL	HKRO	RE	E	L	ERLR	IR	IKO	DY	N	E	EQEV	DLVLSH	FDN	PMF	84		
M...HYRDL	LILI	ISVALL	N	I	T	FILR	KYL	Q	OD	REO	ELL	NR	K	IR	VRD	DY	N	E	EQEV	DLVHSH	FAN	PMF	83
M...HYRDL	LILI	ISVALL	N	I	T	FILR	KYL	Q	OD	REO	ELL	NR	K	IR	VRD	DY	N	E	EQEV	DLVHSH	FAN	PMF	83
M...HKDL	LILI	ISVALL	NVL	I	FVLK	QCL	Q	OTKRE	E	I	RLR	IR	IED	DY	N	E	EQTV	DLIHS	FDN	PMF	84		
M...HHOGL	LILI	VIALL	NVL	M	FNLR	YL	Q	OD	TA	E	L	ER	R	IR	VED	DY	N	E	EQEV	DLVLSH	FDN	PMF	84
M...LE	L	A	L	T	Y	KK	N	Q	IR	E	DR	EE	S-TL	MD	D	VA	NI	82					
M...HHRDL	L-II	TSALLT	NV	L	T	FILR	QYL	KQK	QKRE	E	L	ERLR	IR	QIED	DY	D	TE	EQEV	DLVHSY	FDN	PMF	84	
M...HHRDL	LLLI	ISALL	N	IL	M	FILR	KYL	QKROD	RE	E	L	ERLR	IR	IRD	DY	NE	E	EQEV	GRHLVHSF	FDN	PMF	85	
M...HHRDL	L-II	ISALL	N	IL	M	FILR	KYL	QKROD	RE	E	L	ERLR	IR	IRD	DY	NE	E	EQEV	GRHLVHSF	FDN	PMF	85	
M...YKDL	LFLL	YSALFT	TAL	T	M	FVLK	IL	QKROGKRE	E	L	DRLR	IR	IRD	DY	N	E	EQEV	DLVH	H	FDN	PMF	84	
M...H-RDE	AVLI	IAG	LL	C	I	G	KVLL	FVLKE	ERDK	FV	QRL												

HIV-1/SIVcpz

	Env start	signal peptide gp120 start	glycosylation NVT	glycosylation NDT	
				V1	
B.FR.83.HXB2		MRVKE...KYQHLWRWGW...GTMLLGLMIMCATEK...LWVTVYGVVPWKEATTLTFCASDAKAYDEVHNVWATHACVPTDPNPQEVVLVNVYENFNMMKNDMVEQMHEIISLDWQ.SLKPCVKLT.PLCVSLKCTDLKND...			137
A.SN.01.DD3369		T-MGIORNCPTW...IIF-LII-K...D-E...ER...ID-E...E-N...T...T-N-HNVTKT...			136
A1.AU.03.PS1844_Day0		-A-GIOMNLHC-L...I-IL-A-A-O...R...D-E...-IN-x...E-N...Q...T-N-SHEVIF...NSTL			139
A1.CY.06.CY171		-KARGMORN...-G...M-FW-MIM-K-A-N...R-E...-K...MN-E...S-QT...Q...T-N-K-NST...SSNSTSSN			144
A1.GE.99.99GEM2011		-KARGMORN...-G...FFW-IIM-K-A-N...RD-E...-K...D-K-II-E...K-SN-QT...T-N-NNPIT...			136
A1.IT.02.60800		-KARGMORN...-N...IFW-IIM-K-A-N...RD-E...-K...D-IM-D...E-N...QT...T-N-DEPNVT...NSN			139
A1.KE.02.ML1996		-MGTORN...-L...II-LT-K-N...D-E...-K...IH-D...E-N...QT...T-N-NVTVND...			138
A1.RU.08.Pol18ru		-KARGMORN...-G...L-W-MIM-KVAGN...RD-K...-K...D-DI...QT-N...T-N-S-PTE...			136
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		glycosylation NDT													
		V1													
Env start	signal peptide gp120 start	glycosylation NVT													
MRVKE...KYQHLWRWGWRW...	GTMLGLMLICATEK...LWVTYYGVVPVWKEATTLFCASDAKAYDTEVHNWATHACVPTDPNPQEVVL...VNVTFENFMNMKMDMEVQMHEIISLDQ...SLKPCVKLT...PLCVSLKCTDLKND...		137												
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T - MR - N - POW - G -	LI - L - Y - AGN -	K - EP - K -	S - M - A - D - D - QT -	T - D - SNITRN -	133										
T - M - TORN - PS -	LI - L - AQN -	K - E - K -	S - M - M - E - S - E - N - T -	T - N - NVN -	136										
T - M - TORN - P - LSG -	ILI - LM - TG - N -	K - S - K -	S - M - E -	T - E - GEV - G - K -	136										
TK - M - TOMMWN - K -	L - IF -	MGA -	D - K -	S - S - K -	R - ITM - E -	I -	T - N - EATINNSTDNSM -	143							
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- TOMIWP - K -	LI - LVI -	SDN -	RD - D -	HE - I -	-	IH - E -	N - Q - V -	T - N - NANLT -	139						
- TOMNW - N - K -	LI - LVI -	SNN -	H - RD - D -	HE -	-	IYM - E -	N - Q - V -	T - N - NKVRAINVTS -	141						
- TOMNWP - K -	LI - LVI -	SD -	D - E -	R - HE -	-	TY - E -	K - A - V -	T - N - TANLT -	136						
- TOMNWP - K -	LI - LVI -	SD -	RD - E -	HVP -	-	IP - E -	N - Q - V -	T - N - SATLP -	136						
- MGIORN - PL -	V - ISLLMI -	N - DK -	RD - E -	-	A -	S - IH - K -	K - D - N - T -	T - H - PFNKT -	135						
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- MGIOKN - PLS - K -	MIIF - IMT -	K - EN -	RD - K -	-	A -	IP - K -	E -	T - Y - Y - YNYT -	135						
- MGIMORN - PL - K -	MIIFWIM -	N - EK -	RD - E -	-	A -	IH - K -	K - N -	T - D - HNVN -	135						
- MGIOKNFTPC - K -	MIIFWIM -	K - ED -	RD - E -	-	A -	MI - E -	Q - K - D - A -	T - N - FNV -	135						
- MGIOKN - PL - L	MIIFWIM -	N - NN -	M - RD - E -	N - T -	A -	IH - E -	K -	T - D - HINIS -	135						
- G - M - IQKSCPP - K -	MIIFWIM -	N - D -	-	-	A -	IH - E -	K -	T - N - RL - N -	135						
- MGIOKN - PL -	MIIFWIM -	N - GN -	RD - E -	-	A -	IH - G -	D - S -	T - H - Q - NLTS -	135						
- MGILKSCPPF -	MI - WT - I -	N - EN -	RRD - E -	-	E -	S - MH - E -	N - V -	T - E - HNYNYT -	136						
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- GIRKNC - P -	I -	N - NN - W -	-	-	-	G -	N -	-	T - H - AAFNGT -	136					
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- R - MGMSGW -	MGMSGW -	LLFYLLVSLIKV - G -	ED -	H -	-	R - E -	HS - A -	I - Q -	L - P - K -	E - K - A - Q -	E -	TML - NNSNG -	129		
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- MGMSGW -	MGMSGW -	LLFYLLVSLIKV - G -	ED -	H -	-	R - E -	HS - A -	I - Q -	L - P - K -	E - K - A - Q -	E -	TML - NNSNG -	129		
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- T - M - KKS - K - SWIL -	CIAMALITP -	LSGR -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- K - MKKNRK -	SWLS -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- K - M - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- K - M - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
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- AM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133
- KAM - KRN - K - LWLT -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	YI -	133</

HIV-1/SIV cpz Proteins

	glycosylation NIS				glycosylation NVS			
	glycosylation NDT		glycosylation NCS		glycosylation NGT		glycosylation NGS	
	V1		V2		glycosylation NKT		glycosylation NKT	
	glycosylation NSS	glycosylation NTS	glycosylation NSS	glycosylation NTS	glycosylation NSS	glycosylation NTS	glycosylation NSS	glycosylation NTS
B. FR. 83. HXB2	...TNTNSSSGRMIMEKEIKNSFNISTSI	...KVOKEYAFFYKLDI. IPIDND	...TTSYKLTSCNTSVITQACPKVSEFPIHYHCAPAGFAILKCNKTFNGTGPCTNVSTV	...QCTHGIRPVSVTQLLLNGSLAE	...VVISRVNFTDNA	281		
H. BE. 93. V1991	...NV-KS-N-TDIN-G-TQ-OR	...VT-A-D-N-VH-L-RA-VQ-EGER	...NKSNDH-R-IN	...K	...D	...G-K	...V-E-I-K-I-T	288
H. BE. 93. V1997	...DTNSSSTVATSPSANS-LT	...VT-V-D-Q-RVH-L-R-V-V-ETSN	...NNSNS-R-IN	...D	...K	...K	...GQ-T-K-I-T	287
H. CF. 90. 056	...T-N-TSSMEAG-LT	...VT-VL-D-Q-VH-L-R-V-V-N	...S-Q-R-IN	...L	...K	...K	...Q-IT-TK-IS-T	284
H. GB. 00. 00GBAC4001	...TS-N-SASLEGEQKL	...VT-A-D-RKK-VQ-L-RI-V-V-NDEYNG	...TNGTNR-L-R-IN	...T	...K	...K	...GQ-I-K-I-T	284
J. CD. 97. J. 97DC KTB147	...TT-PSPT-TNPLGM	...T-E-GD-RRK-L-Q-V-VS-S	...NS-I-IN	...K	...DNK	...K	...I-K-I-K-K-IS	288
J. SE. 93. 5E9280 7887	...S-TT-NSSVSSPDIMT	...T-E-N-RKK-L-RQ-V-V-NS	...NKN-I-IN	...K	...D-N	...S-K	...I-GD-II-E-IS	278
J. SE. 94. 5E9173 7922	...NS-D-N-SASNSPEIM	...VT-E-N-RKK-L-RQ-V-V-NS	...NKN-I-IN	...K	...D-N	...S-K	...V-GD-II-E-IS	280
K. CD. 97. 972R E0TB11	...RTNANKNDNTINATVTS	...T-ELKD-KKRVSL	...VQ-KQSEI	...NOSESEDR	...TV	...N-C	...II-EDI-K-T	289
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01 AE. CF. 90. 90CF11697	...DTY-GTAKLNDTIGD-VR	...VT-EL-D-K-EVH-L-VP-VR-GEKNKN	...SSGNSSE-I-H	...K	...D	...T-Y	...D-II-E-L-N	288
01 AE. CN. 07. 0735W045	...N-TAVNNTNIGMLTD-VR	...T-MT-EL-D-Q-VH-L-VQMGSN	...SSSE-R-IN	...K	...D	...E-N	...II-E-L-N	288
01 AE. HK. 04. HK001	...SNNT-QNIN-VTIGNMTD-VR	...MT-ELTD-Q-V-L-VE-N	...ST-R-IN	...K	...D	...T-YV-NK-S	...II-E-L-N	288
01 AE. JP. x. DR0492	...TNDGN-ITNA-NMIGNITD-VR	...KMT-VL-D-KKT-VH-L-VQ-KGNKN	...RNSNISQ-R-IN	...K	...I	...D	...II-E-L-N	294
01 AE. TH. 04. BKM	...SSIGNITD-LR	...T-EL-D-K-VH-L-R-L-V-E-N	...SNSSE-R-IN	...K	...I	...D	...II-E-L-N	284
01 AE. US. 00. 00US MSC1164	...NV-ITKD-NKIGNITD-VR	...MT-EL-D-KH-VH-L-R-L-V-E-N	...NSSE-R-IN	...K	...I	...D	...II-E-L-N	286
01 AE. VN. 98. 98VND015	...NSNA-LTNNINNTIGNITD-VT	...T-MT-ELKD-Q-VH-L-V-H-SN	...NNSSE-R-IN	...K	...I	...D	...II-E-L-N	282
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02 AG. CY. 05. CY048	...SS-GT-YRINSEIM	...VT-EL-D-K-NV-L-RH-V-VE-NDN	...NSD-R-IN	...A	...T	...Y	...GR-R-E-I-N	280
02 AG. ES. 06. P1261	...SS-NTDTAS-KDRP-T	...D-T-VL-D-KE-MA-L-S-V-VQ-MKT	...DNS-R-IN	...A	...T	...Y	...GR-R-E-I-N	280
02 AG. FR. 91. DJ263	...NNSNS-PINRITIDSDME	...MT-EL-D-K-VS-L-R-V-VQ-NES	...GNSQ-R-IN	...H	...A	...K-R-TL	...I-E-I-N	289
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20 BG. CU. 99. CU103	...STVTSSD-NI	...Y-T-E-KD-RKKQ-L-R-V-V-MKNSN	...NSNNYSR-R-IN	...V-A-K	...D	...RD-E	...K-IM-E-L	279
21 A2D. KE. 99. KER2003	...SEG-TQN-MOTVDM	...T-VV-D-RKQV-L-V-N-D	...NT-ST-R-IN	...A	...T	...RD-R	...II-E-L	280
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24 BG. CU. 03. CB378	...QTK-CTEE-NSTVINCK	...T-ELQD-KKQ-L-I-V-N-SSS	...NNYSR-R-IN	...V-A-K	...D	...Y	...DKG-IM-E-L	287
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28 BF. BR. 99. BREPM12609	...TNMNTATNTGSSVEAME-M	...VT-GD-M-L-V-V-A	...NA-T-IN	...L	...L	...K	...II-E-L	284
29 BF. BR. 01. BREPM16704	...ASTQAP-TK-NSSW-N-E-M	...VT-RKD-MK-L-HT-VSTGEG	...DN-I-IT	...I	...T	...L-D-K	...D-I-K	287
31 BC. BR. 04. 04BR142	...HNGTIV	...T-MT-EL-D-GR-VH-L-R-V-LESE	...SYED-R-IN	...A	...D	...YV	...K-N	283
32 06A1. EE. 01. EE0369	...ATINGTSEGKNTVNM-E-MT	...VT-E-ED-KKT-L-V-EGKNN	...NGNSA-I-IN	...ATN-E	...T	...RD-N	...G-S-II-E-I-T	290
33 01B. MY. 05. 05MYK1007 1	...NV-RQTNAPSILENVT-E-S	...TT-EL-D-K-V-L-VS-GMK	...SNSE-R-IN	...K	...D	...T-Y	...IM-E-L-T	285
34 01B. TH. 99. 01B2478P	...TNGPNITE-R	...MT-E-D-K-V-L-LVQ-MGS	...GGE-R-IN	...K	...I	...D	...II-E-I-N	277
35 AD. AF. 05. 05AF095	...TENMM	...T-EL-D-R-V-SL-VQ-ED	...NSS-R-IN	...A	...T	...ENK	...DG-IIL-E-IS	273
36 cpx. CM. 00. 00CMNYU830	...NVSKDMQ	...TT-VL-D-I-VHSL-R-V-ASN	...NDSSR-R-IN	...A	...T	...K-D-Q	...KN-TI-E-I-N	279
37 cpx. CM. 00. 00CMNYU926	...KSLDGG-EI	...Y-MT-EL-D-K-I-SL-V-V-GDN	...NET-R-IN	...T	...Y	...D-EY	...GK-M-E-I-N	278
38 BF1. UY. 03. UY03 3389	...KTDTSTLE-A	...T-MT-E-D-QL-VQSL-V-G-N	...SSRY-R-IN	...T-K	...WD	...Y	...II-Q-IS	287
39 BF. BR. 04. 04BRJ179	...TNGTHNSTLKEDP-A-Q	...FMT-EV-D-K-VH-L-R-V-S-SS	...NSSSGE-R-IN	...S-A	...W	...D-R	...K-II-Q-IS	283
40 BF. BR. 05. 05BRJ055	...QNSTQGGDN-TVLKE-P-A-Q	...MT-EV-D-QK-VH-L-R-T-NGE	...NDNGT-R-IN	...A	...WD	...Y	...N-I-Q-IS	287
42 BF. LU. 03. LU0F 05 03	...xxxxxxxxxx	...VTLG-KS-M-L-RS-V-V-NS	...NS-N-M-I	...L	...I	...D-K	...D-II-Q-IS	263
43 02G. SA. 03. J11223	...KTNVKCEDV-NL	...VT-EL-D-KK-I-V-V-GNS	...NNSGD-R-IN	...V-T	...D	...KE-N	...I-K-S	278
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N. CM. 97. YBF186	...SAGNSTNRNEDL-DROM	...T-E-D-RKKQV-SL-VE-V-V-KDGT	...DNNT-R-IN	...TAV	...TT	...P-M	...EGN-S-N-S	280
N. CM. 02. 02J00131	...RTTDEKPKNGTDL-ARHM	...T-E-HD-KKQ-L-VS-V-V-LNETN	...NKTREI-T-IN	...SITT	...TT	...P-M	...EGN-S-K-E-K	264
N. CM. 04. 04CM 1015 04	...ETVDN-ELDTGYKM	...VT-ERKD-KKLA-SL-AE-V-VQLNESD	...STNOT-R-I	...K-TSV	...TT	...P-M	...EGN-S-K-E-K	264
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O. CM. x. BCF06	...SASNTTDLRIAGL-EIPM	...VT-FLND-RKE-RQ-L-VS-LVK-S	...S-I-R-M	...SITT-R	...T	...Y-F	...TD-L-P-I-V-T	278
O. CM. 91. MVP5180	...KT-LINETN-MR	...VT-VLTD-KEOKO-L-VS-LSKVNSN	...AVNG-T-M	...N-SITT-K	...T	...Y-F	...DTD-L-H-I-V-T	279
O. CM. 96. 96MA102	...ANAKSETTEVHM-Q-E	...VT-VVKD-KE-KO-L-VT-L-VQ-SDNGNG	...TTGKGM-T-IN	...SITT	...T	...Y-F	...TE-T-K-ITV	279
O. CM. 97. 97CMA06447	...LSNATOGM-V-K-E	...VT-VLKD-KE-KO-L-VS-LAKVDSG	...ONGT-R-IN	...SITT	...T	...Y-F	...TE-T-K-ITV	279
O. CM. 98. 98CMA104	...NTNTTTHPSGM-Q-N	...VT-V-KD-KE-KO-L-VS-L-RFNETN	...NKTREI-T-IN	...SITT	...T	...Y-F	...IE-T-N-I-V-T	279
O. CM. 99. 99CMA1122	...TNATASAAV-K-E	...VT-VLKD-KE-QO-L-RS-LNK-E-ST	...TS-M-T-IN	...SITT-K	...T	...G-Y-F	...DTE-Q-R-ITV	278
O. FR. 92. VAU	...I-TTN-PLNSNNTK-V-Q-D	...VT-VLKD-KE-KO-L-VT-L-VK-NATS	...NE-M-R-IN	...SITT-R	...T	...Y-F	...ETG-L-K-TV	278
DO. FR. 08. RBF208	...DTSPTATSVNSSST-V	...T-VT-ELTD-TK-H-L-R-VE-GEKN	...NTNM-T-R-IN	...K	...xT-Q	...L	...D-R	285
O. SN. 99. 99SE MP1299	...NY-NS-INNDTSSPENLV-Q-E	...VT-VVKD-KE-KO-L-VS-LMK-MEAN	...DTKDM-T-IN	...SITT-K	...T	...Y-F	...STE-N-ITA	282
O. US. x. I 2478B	...ATNNSGDSFENPV-E	...VT-VLKD-KERRQ-L-VS-LARV-DSETSGSNTTSGSNTTSSGN-K-T-IN	...SITT-R	...T	...F	...STE	...T-H-ITV	291
O. US. 97. 97US08692A	...TNDSSINPI-TENPNSIENPV-E	...VT-VLKD-KE-RQ-L-VS-LARV-S	...IGN-A-T-IN	...SITT-K	...T	...F	...STE-T-H-ITV	290
O. US. 99. 99USTWLA	...TTNT-TAKTTNPE-TNPV-K-D	...VT-VVKD-KE-QO-L-VS-LK-G-ETA	...NI-T-IN	...SITT-K	...T	...Y-F	...ETG-K-I-V-T	286
P. FR. 09. RBF168	...ASCNN-SS-VNSTADNDLDFK	...TT-VLKD-K-GQO-L-RT-L-ALNETA	...NN-L-R-IN	...TT	...T	...Y-LM	...O-G-ITH	286
CPZ. CD. 90. ANT	...STTTSTVTPKTTPT-VDMGKLOE-Q	...Q-GFKD-K-MK-I-LG-MKKODNN	...E-NC-Y-WH	...TT	...S-E-ST	...Y	...R-EDED-T-V-M-K	281
CPZ. CD. 90. 02PMZ145	...OAKNLNKTSSPPL-M	...VT-D-KKQV-SL-VE-V-VN-E	...NKTREI-T-IN	...SITT	...T	...P	...D-D-S-K-K	271
CPZ. CD. 98. GAB1	...NSAT-TLTPVTNLSPPNY-VY	...QT-EF-KKQI-SL-RE-VKE-GN	...NN-Y-HN	...				

glycosylation NST

ENV

[illegible]

	CD4 ⁺	CD4	glycosylation NIT	glycosylation NES	fusion peptide	gp120 end	gp41 start	
RIKQII.NMWO.KVGKAMYPISGQIR.ČSSNITGLLLTRDGG.....NSNNESEIFRPGGDMRDNRSLEYKYKVVKIEPLGVAPTAKKR.RVV.....QREKRAVG.IGALFLGFLGAAGSTMGAASMTLTQARQLLSGVQQNNLLRAIEAQOH				V5				564
B.FR.83.HXB2	-V-K-	R-Q-	-Q-V-K-	-V-I-	L-SSF-T-	N-K	E-L-V-	I-A-S-Q
A.SN.01.DDJ369	-V-	TP-Q-	R-A-	E-I-N-	DNTSTN-T-	R-I-T-	S-V-I-	S-570
A1.AU.03.P51044_Day0	-L-I-NK-R-L-QS-	LP-V-GIE-D-TS-	A-GS-	GN-SNN-T-	T-N-KN-	E-I-R-	E-I-L-A-	S-579
A1.CY.06.CY171	R-Q-	K-N-	E-I-G-	GT-SSN-T-	I-N-	Q-I-	E-I-L-A-	S-560
A1.GE.99.99GEM2011	R-Q-I-	A-X-E-	X-G-	GNSSIN-T-		I-R-	E-I-L-A-	S-565
A1.IT.02.60000	RI-Q-	N-Q-K-	E-I-EN-	REN-DS-	E-I-K-	E-I-R-	E-I-L-V-	S-562
A1.KE.02.ML1990	R-Q-	I-K-	E-I-	DNSSN-T-	E-I-N-	E-I-R-	E-I-L-V-I-	S-564
A1.RU.08.P0418U	V-R-	RA-Q-I-	E-V-	VN-TVN-T-	N-N-	E-I-R-	E-I-L-V-I-	S-557
A1.RW.93.93RW037A	-R-	RA-I-	P-I-K-	V-I-SN-STN-T-		I-R-	E-I-V-I-	S-562
A1.SE.95.5E8538	R-Q-	E-V-	E-I-N-SAN-T-	I-I-	E-I-R-		E-I-L-A-	S-554
A1.TZ.01.A341	R-Q-	R-N-S-	V-I-T-SST-T-	T-E-I-	R-		E-I-L-A-	S-562
A1.UA.01.01UADN139	R-I-	Q-V-K-	E-I-GW-TN-T-				E-I-L-V-I-	S-563
A1.UG.99.99UGA07072	-L-	R-Q-	P-E-	E-I-LE-LN-TNN-T-	I-I-R-		E-I-L-V-	S-567
A1.ZA.04.04ZASK162B1	R-R-	A-V-K-	T-MI-K-SIN-T-		I-E-R-		E-I-L-V-	S-551
A2.CD.97.97CDKT848	R-R-	A-I-K-	T-II-N-GTN-T-		L-R-		E-I-L-V-	S-566
A2.CY.94.94CY017_41	R-E-	E-S-	S-SN-S-		I-R-		TM-M-S-	V-D-555
B.AR.04.04AR143170	R-K-	R-K-	Nx-KT-DT-T-		R-R-		T-M-	V-558
B.AU.04.PS1038_Day174	R-K-	R-K-	DN-RST-T-		N-R-		T-M-	V-558
B.BO.99.09BOL0122	K-R-	R-E-S-	R-E-K-I-		N-K-I-R-		TF-M-	L-L-544
B.BR.05.BREPM1081	G-N-		IN-STN-T-K-		QV-R-		V-V-	V-558
B.CA.97.CANB3FULL	V-R-	E-I-A-P-N-	K-INKTDT-T-		R-		A-M-	I-T-R-567
B.CN.05.05CNHB_hp3	K-	R-E-	R-V-V-N-		N-TL-M-		TM-M-	V-558
B.CO.01.PCM001	V-L-	K-S-	N-GT-NT-T-		N-MV-		A-T-	V-571
B.CU.99.Cu19	V-L-	R-V-S-	K-GMNN-GTNN-T-		QV-SL-R-		R-A-	V-567
B.CY.06.CY165	E-	L-K-	II-T-ETS-T-T-K-I-N-K-		I-Q-		L-VA-	S-K-D-558
B.DE.86.D31	E-	R-Y-N-	I-IN-TGN-T-		R-N-K-		V-V-	V-550
B.DK.04.PMVL_012	E-	R-I-	A-V-OT-GT-		A-ELK-I-R-		L-V-S-	L-S-562
B.DO.05.05DO_160884	V-	G-K-	I-SD-DNSSN-T-				M-M-	L-L-S-551
B.EC.89.EC003	V-	E-K-	K-TT-GT-		A-I-R-		ML-M-	R-L-563
B.EC.97.X2231	V-	E-T-	RE-NT-T-T-				M-M-	R-L-557
B.FR.92.92FR_BX08	V-	E-K-	II-D-ETRGN-T-		N-R-I-Q-R-		TL-M-	IA-A-L-565
B.GA.88.OYT	V-	E-T-	A-H-RE-NGDATN-T-				L-M-	V-570
B.GB.86.GB8_46R	R-V-	K-K-V-	II-DQ-		Y-R-E-		V-V-	V-562
B.GE.03.03GEM2004	R-V-	E-K-	L-L-NSDAN-T-		Q-N-K-R-I-R-R-		V-M-	V-K-562
B.HT.05.05HT_129389	R-V-L-	P-E-	K-K-NG-TDT-V-				V-M-	V-L-572
B.IN.x.11807	R-E-	K-L-	L-NT-NETG-GT-T-		Q-I-R-		V-M-	V-L-561
B.JM.05.05JM_KJ108	R-V-	Y-K-	T-K-KT-PT-A-		R-I-R-		TL-M-	I-R-568
B.JP.05.DR6538	R-E-	A-K-	G-KT-PT-A-		R-I-R-		TL-M-	I-A-568
B.KR.04.04KMH5	V-	E-R-	A-K-G-				IT-L-V-	A-555
B.MM.99.mSTD101	R-E-	K-K-	G-SNSTN-T-		A-I-M-		L-V-	V-555
B.NL.00.671_09136	V-	E-A-N-S-	I-W-NKN-GNKT-T-DT-T-				T-M-	L-R-S-R-559
B.RU.04.04RU128005	V-	E-A-N-S-	I-W-NKN-GNKT-T-DT-T-				T-M-	L-R-S-R-559
B.TH.00.00TH_C3198	A-	R-P-T-	V-I-RN-TNDS-V-V-		K-I-N-V-L-R-R-		SPT-L-	L-554
B.TW.94.TWCYS	R-E-	I-E-L-K-	M-I-V-NSSNN-T-		N-K-R-R-			L-573
B.UA.01.01UAKV167	R-E-	K-I-S-	R-I-V-NSSNN-T-		N-K-R-R-			L-583
B.US.07.CR0027W	R-E-	O-R-S-	K-M-KG-NETR-DT-T-		A-K-R-Q-		M-M-	V-580
B.UY.01.01UYTRA1179	E-	A-K-S-	I-N-ENQITP-V-		A-RV-I-R-		I-M-V-	S-V-569
B.YE.02.02YE507	F-	VE-	I-I-NT-DN-T-		*			M-558
B.ZA.03.03ZAP045MB2	K-V-R-	E-Q-VK-M-T-	R-I-T-S-		E-N-I-X-		E-IVGL-V-	I-S-561
C.AR.01.ARG4006	E-Q-	K-A-I-K-	K-V-TEN-EGE-TT-T-		A-E-K-I-E-		E-VG-V-	I-M-566
C.BR.04.04BR013	E-R-	A-K-T-K-	V-TEN-EGE-TT-T-		A-E-K-I-E-		E-VG-V-	I-M-566
C.BW.00.00BW07621	F-	Q-R-P-D-T-K-	V-EGG-NETR-DT-T-		E-K-I-G-		E-A-V-	S-M-569
C.CN.98.NYRL9840	E-R-	A-N-T-K-T-V-	OG-SN-T-x-		E-K-E-		E-L-VIF-x-	S-K-568
C.CY.05.CY040	E-R-	K-I-T-R-	M-NT-NT-T-		E-K-G-A-		E-A-L-VL-	I-V-558
C.E5.07.X2118_2	E-R-	A-Y-T-N-	G-S-CT-T-		E-K-I-G-		E-A-L-VL-	I-V-566
C.ET.02.02ET_288	E-R-	K-I-T-R-	M-NT-NT-T-		E-K-I-G-		E-A-L-VL-	I-V-566
C.GE.03.03GEM2033	E-R-	A-Y-T-N-	G-S-CT-T-		E-K-I-G-		E-A-L-VL-	I-V-566
C.IL.98.98IS002	E-R-	A-Y-T-N-	G-S-CT-T-		E-K-I-G-		E-A-L-VL-	I-V-566
C.IN.03.D24	K-E-	R-I-A-N-T-K-	V-N-TES-NT-		E-K-I-A-		E-EKRAVL-G-	I-S-576
C.KE.00.KER2010	E-R-	A-N-T-K-T-K-Q-	T-KT-T-		N-K-E-K-I-E-		E-K-I-S-	S-563
C.MM.99.mIDU101_3	E-R-	A-N-T-K-T-K-Q-	T-KT-T-		N-K-E-K-I-E-		E-K-I-S-	S-566
C.MW.93.93MW_965	E-R-	A-N-T-K-T-K-Q-	T-KT-T-		N-K-E-K-I-E-		E-K-I-S-	S-566
C.SN.90.90SE134	E-Q-	K-N-T-T-	L-NDPK-RTEEQ-NT-R-		E-K-I-G-		E-L-M-	I-A-V-561
C.S0.89.89SM_145	R-F-T-	E-N-T-K-	W-SS-KETS-TT-T-		L-R-E-K-I-A-		E-L-M-	I-A-V-570
C.TZ.02.C0178	D-	E-N-T-K-	L-LD-SST-T-		A-E-K-I-T-		E-L-M-	I-K-546
C.US.98.98US_MSC3018	V-	G-R-E-N-T-R-	DG-GTT-T-		E-K-I-T-		E-L-M-	S-K-559
C.UY.01.TRA3011	E-R-	A-N-T-T-	N-GKD-T-		E-K-I-A-		E-L-M-	S-563
C.YE.02.02YE511	E-R-	A-N-T-T-	N-GKD-T-		E-K-I-A-		E-L-M-	S-563
C.ZA.05.05ZAPSK240B1	K-	E-R-A-K-T-A-	N-VSN-KTDA-KT-T-		I-N-E-Q-L-		E-L-VI-	L-S-580
C.ZM.02.02ZM108	KMVAGR-	I-ERN-L-	IN-STN-T-		Q-R-R-		E-I-L-M-	R-V-M-561
D.CD.83.ELI	E-E-	A-K-T-T-	NNNS-GN-G-ST-		N-K-I-R-		E-I-L-M-	L-V-573
D.CM.01.01CM_0009BBY	T-I-C-G-V-T-	PA-I-Q-K-	ITG-A-DNSSON-T-		RV-I-R-		E-I-L-M-	IA-A-LV-565
D.CY.06.CY163	E-R-	A-I-K-	I-A-TN-T-		N-K-RL-		E-I-L-M-	V-A-566
D.KE.97.ML415_2	L-R-	E-V-S-	L-IH-TS-T-		R-L-T-		E-I-L-M-	V-A-558
D.KR.04.04KRBH	D.SN.x.SE365	E-A-K-	K-ASN-T-		R-R-		E-I-L-M-	V-A-553
D.TD.99.MN011	G-	A-L-T-N-	N-VN-SRE-		R-I-R-		E-I-L-M-	L-560
D.TZ.01.A280	UG.99.99UGK09958	E-L-Q-	A-TNDSQ-T-		T-R-L-T-		E-I-L-M-	L-551
D.UG.99.99UGK09958	D.YE.02.02YE516	E-L-Q-	A-TNDSQ-T-		T-R-L-T-		E-I-L-M-	L-551
D.YE.02.02YE516	D.ZA.96.R1	E-L-Q-	A-TNDSQ-T-		T-R-L-T-		E-I-L-M-	L-551
D.ZA.96.R1	F1.A0.06.A0_06_ANG125	G-O-A-N-T-N-	N-EG-KTT-		E-N-K-E-		E-K-I-T-	T-I-553
F1.A0.06.A0_06_ANG125	F1.AR.02.ARE933	E-R-NNH-HA-N-T-	G-TGNC-TDGTG-CT-T-		N-K-E-R-Q-		K-M-I-A-G-	I-552
F1.AR.02.ARE933	F1.BE.93.VI850	G-R-TS-A-N-T-N-	N-NESNI-T-E-N-K-		E-E-Q-		A-LGALFLX-T-x-	I-539
F1.BE.93.VI850	F1.BR.07.07BR844	G-GR-EE-R-TA-TD-N-T-	W-G-N-GN-SIN-T-		E-K-I-Q-		K-ILGM-V-S-	I-T-A-S-557
F1.BR.07.07BR844	F1.ES.x.P1146	G-O-TA-A-N-T-N-	N-OE-GR-DTE-		N-K-E-K-I-E-R-Q-		K-A-L-L-S-	I-H-A-S-K-569
F1.ES.x.P1146	F1.FI.93.FIN9363	E-R-A-A-N-T-N-	N-OS-SN-SL-T-		E-K-I-RP-P-		K-A-L-V-S-	L-Q-560
F1.FI.93.FIN9363	F1.FR.96.96FR_MP411	G-O-SA-A-R-N-N-T-	Q-NNA-NKTE-RT-T-		E-N-K-N-E-R-Q-		K-R-M-L-M-	NI-I-551
F1.FR.96.96FR_MP411	F1.JP.04.DR6082	G-O-A-A-S-T-N-	N-O-T-T-		E-I-R-Q-Q-		K-A-L-L-L-	I-K-571
F1.JP.04.DR6082	F1.R0.96.BCI_R07	G-R-A-A-K-V-N-S-I-	D-KN-TNNDTL-		R-Q-K-RE-		E-Q-L-VL-	S-K-565
F1.R0.96.BCI_R07	F1.RU.08.D88_845	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
F1.RU.08.D88_845	F2.CM.97.CM53657	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
F2.CM.97.CM53657	G.BE.96.DRCBL	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.BE.96.DRCBL	G.CM.04.178_15	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.CM.04.178_15	G.CU.99.CU74	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.CU.99.CU74	G.ES.05.P962	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.ES.05.P962	G.GH.03.03GH175G	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.GH.03.03GH175G	G.KE.93.HH8793_12_1	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.KE.93.HH8793_12_1	G.NG.01.01NGPL0669	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.NG.01.01NGPL0669	G.PT.x.PT2695	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.PT.x.PT2695	G.SE.93.SE6165	R-V-R-R-A-A-Q-R-	I-DN-ST-		KN-T-KS-I-R-R-		E-V-I-T-	I-V-S-555
G.SE.93.SE6165								

	CD4	CD4	glycosylation NIT	glycosylation NES	fusion peptide	gp120 end	gp41 start															
B. FR. 83. HBX2	RIKQII. NMWQ.	KVGKAMYAPPI	SGQIR. .	CSNSNITGLLLTRDGG.	NSNNESEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTKAKR. RVV.	QREKRAVG. IGALFLGFLGAAGSTMGAASMTLTQVQARQLLSGIVQ0QNLLRAIEAQOH		564														
H. BE. 93. VI991	K- - - - -	R- - - - -	R- N- T- .	I- - - - -	I- F- R-	E- R-	E- - - - -	570														
H. BE. 93. VI997	K- - - - -	R- - - - -	K- S- T- .	V- - - - -	I- Y- ED.	K- G- DNVT.	E- R-	563														
H. CF. 90. 056	K- - - - -	R- - - - -	Q- N- M- .	V- - - - -	I- I- E-	ASA- NVT.	E- - - - -	556														
H. GB. 00. 00GBAC4001	K- - - - -	R- - - - -	Q- N- T- .	V- - - - -	I- L- RY.	VD- GTNVTL.	Q- - - - -	563														
J. CD. 97. J. 97DC KTB147	K- R- - - -	R- - - - -	A- N- T- .	T- - - - -	NT.	KES- S- T- .	T- K- - - -	564														
J. SE. 93. SE9289 7897	K- - - - -	R- - - - -	A- N- T- .	T- - - - -	NRG.	NG- GT- T- .	T- N- K-	558														
J. SE. 94. SE9173 7032	K- - - - -	R- - - - -	A- N- T- .	T- - - - -	NRNG.	NG- GT- T- .	T- N- K-	560														
K. CD. 97. 972R E0TB11	-----	-----	I- - - - -	TA- N- T- .	R- - - - -	MI- ND.	NTRTE- T- .	Q- - - - -	559													
K. CM. 96. 96CM MP535	-----	-----	I- - - - -	A- S- N- .	-----	MI-	N- THN- T- .	Q- - - - -	550													
01 AE. CF. 90. 90CF11697	-----	-----	E- - - - -	EAVN.	V- - - - -	II-	ATN- T- .	N- K-	564													
01 AE. CN. 07. 0735WX045	-----	-----	G- - - - -	I- N- .	I- - - - -	I-	TTN-	N- I- K-	554													
01 AE. HK. 04. HK001	-----	-----	ET- - - -	R- S- Q- .	V- - - - -	II-	GS- T- T- .	I-	559													
01 AE. JP. x. DR0492	-----	-----	G- - - - -	R- N- .	V- - - - -	I-	AN- ATN- T- .	N- I- K-	566													
01 AE. TH. 04. BKM	-----	-----	ET- - - -	T- N- .	V- - - - -	I-	DSQSN- T- .	N- I- K-	572													
01 AE. US. 00. 00US MSC1164	KL- - - - -	EA- - - -	S- N- .	V- - - - -	I-	A-	A- K- DT- .	N- I- K-	560													
01 AE. VN. 98. 98VND15	-----	-----	R- - - - -	R- N- .	V- - - - -	I-	TNSR.	TNETNETNE- IK-	568													
02 AG. CM. 02. 02CM 0013BBY	-----	-----	R- - - - -	R- I- K- .	E- - - - -	-----	N- STN- T- .	IQ- - - - -	564													
02 AG. CY. 05. CY048	-----	-----	V- R- .	R- - - - -	Q- I- K- .	E- - - - -	N- ASN- T- .	E- - - - -	560													
02 AG. ES. 06. P1261	K- - - - -	F- - - - -	R- - - - -	P- V- .	E- - - - -	-----	ND- TN- T- .	E- K-	561													
02 AG. FR. 91. DJ263	-----	-----	V- - - - -	L- - - - -	I- - - - -	K- - - - -	SN- STN- T- .	-----	570													
02 AG. GH. 03. 03GH121AG	-----	-----	R- - - - -	I- - - - -	K- - - - -	D- - - - -	SE- GT- T- .	L- - - - -	567													
02 AG. LR. x. P044951	-----	-----	V- - - - -	Q- I- .	Q- I- .	D- - - - -	N- ST- T- .	D- I-	553													
02 AG. NG. 01. PL0710	-----	-----	V- - - - -	Q- I- .	Q- I- .	D- - - - -	IE- AON- T- .	-----	549													
02 AG. SE. 94. SE7812	-----	-----	V- R- .	Q- - - - -	P- E- .	E- - - - -	D- NT- T- .	SH-	567													
02 AG. SN. 98. 98SE MP1211	K- - - - -	R- - - - -	Q- I- .	E- V- .	D- - - - -	I-	DNT- GD- T- .	SH-	561													
02 AG. US. 00. 00US MSC3083	-----	-----	R- - - - -	R- - - - -	Q- E- .	E- - - - -	T- D- ST- T- .	I- I-	561													
02 AG. UZ. 02. 02UZ0683	-----	-----	V- - - - -	R- - - - -	Q- E- .	E- - - - -	I- STN- T- .	-----	560													
03 AB. RU. 97. KAL153 2	-----	-----	E- - - - -	R- - - - -	A- - - - -	-----	QS- VT- .	T- - - - -	548													
04 cpx. CY. 94. 94CY032 3	-----	-----	L- FV- R- .	E- - - - -	S- A- S- N- .	D- - - - -	II-	T- NT-	562													
05 DF. BE. x. VII310	K- - - - -	V- R- .	G- - - - -	A- A- N- A- .	N- T- .	I- A- NG.	ND- S- DT- .	E- Q- I- R- .	Q- - - - -	569												
06 cpx. AU. 96. BFP90	K- - - - -	V- R- .	R- - - - -	A- N- T- .	V- - - - -	II-	NE- V- T- .	K- I- W- R- .	-----	567												
07 BC. CN. 98. 98CN009	-----	-----	E- - - - -	E- N- T- .	K- - - - -	V- - - - -	TET- DT- T- .	-----	560													
08 BC. CN. 97. 97CNX 6F	-----	-----	E- - - - -	E- N- T- .	K- - - - -	V- - - - -	TEP- NT- .	N- - - - -	E- K-	565												
09 cpx. GH. 96. 96GH12911	-----	-----	V- R- .	R- - - - -	R- - - - -	I-	SDG- T- .	T- N- K-	E- - - - -	560												
10 CD. TZ. 96. 96TZ BF061	-----	-----	R- - - - -	G- - - - -	I- - - - -	A- L- N- .	V- - - - -	A-	N- SQN- T- .	-----	548											
11 cpx. CM. 95. 95CM 1816	K- - - - -	V- R- .	R- - - - -	Q- K- M- .	N- T- .	-----	KNSSKT- T- .	I- K-	E- K-	572												
12 BF. AR. 99. ARMA159	K- - - - -	V- L- .	E- - - - -	A- E- N- T- .	N- - - - -	-----	ET- QT- T- .	N- K-	E- - - - -	550												
13 cpx. CM. 96. 96CM 1849	-----	-----	FV- .	R- - - - -	Q- I- .	E- - - - -	S- V- .	GN- RTN- T- .	N- K-	568												
14 BG. ES. 00. X605	-----	-----	V- - - - -	I- - - - -	-----	-----	I-	G- TN- T- .	N- K-	563												
15 01B. TH. 99. 99TH MU2079	-----	-----	R- V- .	E- - - - -	R- - - - -	K- - - - -	KN.	E- TT- TT- .	A-	555												
16 A2D. KR. 97. 97KR004	-----	-----	V- - - - -	R- - - - -	N- T- K- .	T- - - - -	MI- NS.	GG- ATN- T- .	-----	563												
17 BF. AR. 99. ARMA038	-----	-----	V- R- .	E- - - - -	Q- A- N- V- .	N- - - - -	-----	QNGSGP- .	E- N- K-	556												
18 cpx. CU. 99. CU76	-----	-----	V- R- .	RT- Q- .	SR- N- T- .	-----	I- S- LI.	xhXt- NVT- .	-----	558												
19 cpx. CU. 99. CU7	-----	-----	VV- .	x- - - - -	P- V- Q- .	K- - - - -	-----	NN- T- .	A- G-	559												
20 BG. CU. 99. Cu103	-----	-----	V- R- .	R- - - - -	A- S- T- .	I- - - - -	I- N-	T- RT- .	A-	550												
21 A2D. KE. 99. KER2003	-----	-----	-----	E- - - - -	E- H- N- .	-----	T-	NTSNM- .	N- K-	560												
22 01A1. CM. 01. 01CM 0001BBY	-----	-----	01A1. CM. 01. 01CM 0001BBY	RA- Q- .	P- T- T- .	x- - - - -	-----	DK- SAN- T- .	-----	548												
23 BG. CU. 03. CB118	-----	-----	V- R- .	R- - - - -	A- S- T- .	V- - - - -	II-	P- STN- T- .	LA-	555												
24 BG. CU. 03. CB378	-----	-----	V- R- .	R- - - - -	E- S- .	E- - - - -	II- T-	NK- TT- .	A-	565												
25 cpx. CM. 02. 1918LE	-----	-----	R- - - - -	R- - - - -	Q- V- .	-----	I- A-	TA- NT- .	-----	558												
26 AU. CD. 02. 02CD MBT047	-----	-----	V- R- .	E- - - - -	VA- M- Q- .	I- - - - -	I-	KDK- DT- .	N- K-	559												
27 cpx. FR. 04. 04CD FR KZ5	-----	-----	V- - - - -	RT- Q- I- .	R- I- Q- .	E- - - - -	I- R-	H- HTN- T- .	N- K- - - -	564												
28 BF. BR. 99. BREPM12609	-----	-----	R- - - - -	E- - - - -	-----	-----	SN.	ET- MT- T- .	A-	576												
29 BF. BR. 01. BREPM16704	-----	-----	L- A- .	TSP- R- .	-----	T- L- S- N- .	SN.	TT- RN- T- .	-----	578												
31 BC. BR. 04. 04BR142	-----	-----	E- - - - -	R- - - - -	K- A- T- .	-----	I-	DK- DT- T- .	-----	550												
32 06A1. EE. 01. EE0369	K- R- - - -	V- R- .	-----	AR- - - -	A- N- T- .	-----	S-	KES- T- S- .	N- K-	558												
33 01B. MY. 05. 05MYKL007 1	-----	-----	GA- - - -	Q- I- N- .	V- - - - -	I- - - - -	AN.	AS- T- T- .	N- K-	562												
34 01B. TH. 99. 01B2478P	-----	-----	G- - - - -	Q- - - - -	T- N- .	I- - - - -	I-	TTDT- T- .	E- NIK-	551												
35 AD. AF. 05. 05AF095	-----	-----	RT- Q- I- .	R- E- .	V- - - - -	T- - - - -	-----	NSSLN- T- .	-----	552												
36 cpx. CM. 00. 00CMNYU830	K- - - - -	K- - - - -	R- - - - -	Q- - - - -	A- R- .	-----	E- - - - -	KN- STN- T- .	-----	557												
37 cpx. CM. 00. 00CMNYU926	-----	-----	V- - - - -	R- - - - -	P- V- .	E- - - - -	M-	INKTDN- T- .	-----	557												
38 BF1. UY. 03. UY03 3389	-----	-----	V- - - - -	V- - - - -	TA- A- D- T- .	R- - - - -	-----	QKNN.	GSCTEATCTQ- .	Q- N- K-	552											
39 BF. BR. 04. 04BRJ179	K- R- - - -	V- - - - -	E- - - - -	A- A- N- A- .	N- T- .	-----	SG.	S- GT- QN- T- .	N- K-	552												
40 BF. BR. 05. 05BRJ055	K- - - - -	V- - - - -	E- - - - -	A- A- N- T- .	N- S- .	-----	QN.	ET- NT- T- .	N- K-	559												
42 BF. LU. 03. luBF 05 03	-----	-----	E- - - - -	A- A- N- T- .	-----	-----	LA.	NOTG- QNDT- .	-----	520												
43 02G. SA. 03. J11223	-----	-----	V- R- .	R- - - - -	E- I- T- .	R- - - - -	-----	I- STNDT- .	K- - - - -	544												
N. CM. 95. YBF30	-----	-----	R- V- .	L- T- R- .	GI- - - - -	R- VLN- .	T- - - - -	V- EYS-	PDKET- VY- S- .	N- VNL- .	Q- - - - -	552										
N. CM. 97. YBF106	-----	-----	V- xL- T- R- .	GI- - - - -	R- NLS- .	N- S- .	I- EHS-	E- GNKTVY- S- .	N- VNL- .	Q- - - - -	536											
N. CM. 02. 0200131	-----	-----	R- V- .	L- T- R- .	GI- - - - -	R- NLS- .	N- S- .	I- EHS-	E- GNKTVY- S- .	N- VNL- .	Q- - - - -	536										
N. CM. 04. 04CM 1015 04	-----	-----	V- L- T- R- .	GI- - - - -	R- N- T- .	N- S- .	I- EHS-	VSGNSTVY- S- .	N- VNL- .	Q- - - - -	525											
0. BE. 97. ANT70	KLR- VV- RS- I- .	RGOSGL- .	K- NLT- .	M- - - - -	MI- OM- NTV.	-----	S- NNVT- .	I- K- I- T- FN- .	RVK- FS- .	RIA-	P- IST- RTH- .	L- M- - - -	V- S-	AT- A- THT- K- .	D- - - - -	Q- - - - -	562					
0. CM. x. BCF06	K- R- VV- RS- I- .	GELGL- .	P- DLT- .	K- - - - -	MI- QL- TPY.	-----	SCONVT- .	T- - - - -	I- - - - -	N- - - - -	IOVK- FS- .	IS-	PIIIGL- NTHH- G- .	L- M- - - -	V- S-	AT- A- RTQGV- K- .	D- - - - -	Q- - - - -	579			
0. CM. 91. MVP5180	KLR- LV- RS- M- .	GESRI- .	P- NLT- .	H- - - - -	MI- QL- OP.	-----	WNSTGENTL- .	V- K- I- TK- N- .	Q- K- FS- .	MS-	PIIINI- HTPH- .	L- M- - - -	V- S-	AT- A- RTHSV- K- .	D- - - - -	Q- - - - -	572					
0. CM. 96. 96CA182	KL- - - -	VV- RS- I- .	G- SGL- .	K- NLT- .	R- - - - -	MI- QI- OPWG.	-----	SNITNDT- .	V- - - - -	E- I- TQ- FN- .	RVK- FS- .	IA-	P- IGT- GTH- DR- .	L- M- - - -	V- S-	ATA- TON- MK- .	D- - - - -	Q- - - - -	576			
0. CM. 97. 97CMA86447	KL- - - -	VV- RS- I- .	RGESGL- .	K- NLT- .	I- - - - -	MI- EP-	G- SRHIL- .	V- K- I- T- FN- .	RVK- FS- .	IA-	P- IGT- GTH- .	L- M- - - -	V- S-	ATA- THT- IK- .	D- - - - -	Q- - - - -	560					
0. CM. 98. 98CMA104	KL- - - -	VV- RS- I- .	Q- SGL- .	K- NLT- .	M- - - - -	MI- EM- SWNGSAT.	KOINAT- .	INAT- .	I- - - - -	K- I- TQ- FN- .	RVK- FS- .	IA-	P- IGT- GTH- .	L- M- - - -	V- S-	ATA- THT- IK- .	D- - - - -	Q- - - - -	580			
0. CM. 99. 99CMU4122	K- - - - -	VV- RS- I- .	RGESGL- .	K- PLK- .	E- - - - -	MI- QK- EPWN.	KT- THAT- .	K- I- T- FN- .	RVK- FS- .	IA-	P- IGT- GTH- .	L- M- - - -	V- S-	TAT- A- THT- MK- .	D- - - - -	Q- - - - -	571					
0. FR. 92. VAU	LR- VV- RD- M- .	RG- SGL- .	P- NLV- .	R- - - - -	MI- QL- TPWN.	-----	KTHPN- TTL- .	K- I- TQ- F- .	RVK- FS- .	IA-	PTIGT- .	STH-	A- LAM- .	I- S-	ATA- RTQH- IK- .	D- - - - -	Q- - - - -	575				
DO. FR. 08. RBF208	-----	-----	G- - - - -	I- - - - -	A- - - - -	N- T- .	I- - - - -	NSN.	DSHS- KN- T- .	N- K-	-----	I-	-----	-----	-----	-----	-----	564				
0. SN. 99. 99SE MP1299	-----	-----	VV- RS- I- .	Q- G- SGL- .	RK- NLT- .	-----	L- MI- QL- MPWN.	ST- SNAT- .	T- - - - -	K- I- T- F- .	VK- FS- .	IA-	P- IGT- .	GT-	L- M- - - -	V- S-	ATA- A- TQS- MK- .	D- - - - -	Q- - - - -	575		
0. US. x. I 2478B	LR- VV- RS- M- .	RG- SGL- .	R- NLT- .	G- K- .	MI- EM- EPWKNQNSTDGNQ.	-----	TDKRS- .	T- N- K- I- T- LR- .	R- K- FS- .	IT-	P- IGF- .	GTR-	L- M- - - -	V- S-	ATA- THT- IK- .	D- - - - -	Q- - - - -	599				
0. US. 97. 97US08692A	LR- VV- RS- M- .	RG- SGL- .	R- NLT- .	G- K- .	MI- EM- EPW.	-----	ESHRES- .	T- N- K- I- T- LR- .	R- K- FS- .	IT-	P- IGF- .	GTR-	L- M- - - -	V- S-	ATA- THT- IK- .	D- - - - -	Q- - - - -	588				
0. US. 99. 99USTWLA	LR- VV- RS- M- .	RG- SGL- .	K- SLT- .	-----	I- ALIK.	-----	R- S- PNIT- .	K- I- TQ- N- .	RVKFS- .	IS-	P- IGT- .	NH-	L- M- - - -	V- S-	GI- S- RTHS- IR- .	D- - - - -	Q- - - - -	573				
P. FR. 09. RBF168	-----	-----	L- V- .	S- M- .	-----	SGLF- .	E- LQ- .	H- - - - -	I- D- .	ASP.	Y- A- SSNTLLT- .	T- E- NI- .	P-	QVKA- A- .	RVS- PTIM- .	AHDAH- K- GA- .	L- M- - - -	MS-	AV-	H- - - - -	M- - - - -	576
CPZ. CD. 90. ANT	-----	-----	V- - - - -	H- G- I- S- .	GI- LA- RR- NVS- .	T- S- .	IM- GO.	IIY- TVKVS- AA- RVA- Q- A- SR- Q- .	E- D- S- .	TG-	PEIK- .	QHS- Q- GI- .	LF- L- S- .	-----	IA- A- T- N- xH- .	A- - - - -	Q- - - - -	T- - - - -	555			
CPZ. CM. 05. SIVcpzMT145	-----	-----	R- V- .	S- M- R- .	-----	GIF- R- N- T- .	T- - - - -	M- EIKHOREDO.	GEDBODNNTYVCLT- .	N- K- I- .	-----	I- Q-	SR- YA- EK- .	QHH-	-----	-----	-----	555				
CPZ. GA. 98. 98GAF1	-----	-----	R- V- .	SS- M- R- .	-----	PGI- R- N- T- .	T-															

	glycosylation NAS			glycosylation NHT			glycosylation NYT																						
	immunodominant region			glycosylation NKS			glycosylation NYT																						
B. FR. 83. HBX2	LLQLTVWGVIKQLQARILAVERYLKQDQLLGWGSGLKLCITTAVPWNASWS																												
A. SN. 01. DDJ369	M-K	-V	-	N	-S		YSE	-DNM	-LQ	-K	-S	-D	-YN		-D	-A		-S	-RI		-I	-T	-I	-K		-S	-S		
A1. AU. 03. PS1044_Day0	M-K	-V	-L	-	N	-NT	-NKSE	-DNM	-LQ	-K	-S	-QI	-YN		-T	-I	-A	-N	-D	-SQ		-I	-I	-T	-I	-S	-T	-N	
A1. CY. 06. CY171	-K	-V	-	-	N	-S	-QSD	-DNM	-Q	-VI	-NI	-YG	-LA		-D	-A	-N	-T	-D		-I	-I	-T	-I	-I	-LP	-H	-N	
A1. GE. 99. 99GEM2011	-K	-V	-	-	N	-S	-YSE	-DNM	-Q	-K	-VI	-NI	-YG		-D	-A	-G	-D	-S	-S		-I	-I	-T	-I	-I	-LA	-H	-N
A1. IT. 02. 60080	-K	-V	-	-	N	-S	-HDD	-NL	-Q	-XK	-NI	-YN	-Q	-XS		-D	-A	-G	-D	-S		-I	-I	-T	-I	-I	-LT	-N	-N
A1. KE. 02. ML1990	-K	-V	-	-	N	-S	-FDE	-NL	-Q	-XK	-NI	-YN	-Q	-XS		-D	-A	-G	-D	-S		-I	-I	-T	-I	-I	-LT	-N	-N
A1. RU. 08. POK18Ru	-K	-V	-	-	N	-S	-YSE	-DNM	-LQ	-K	-S	-QI	-YN		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-LT	-N	-N	
A1. RW. 93. 93RW037A	-K	-V	-	-	N	-S	-QSK	-DNM	-LQ	-K	-S	-DI	-Y	-A		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-IT	-D	-N
A1. SE. 95. SE8538	-K	-V	-	-	N	-S	-QSE	-DNM	-LQ	-K	-S	-OT	-YR	-A		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-IT	-D	-N
A1. TZ. 01. A341	-K	-V	-	-	N	-S	-YDD	-DNM	-LQ	-K	-S	-DI	-Y	-A		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-IT	-D	-N
A1. UA. 01. 01UADN139	-K	-V	-	-	N	-S	-HDE	-NM	-Q	-K	-VI	-NI	-YG	-K		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-LT	-H	-N
A1. UG. 99. 99UGA07072	-K	-V	-	-	N	-S	-QSE	-DNM	-LQ	-K	-S	-QI	-YN		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-LT	-N	-N	
A1. ZA. 04. 04ZASK162B1	-K	-V	-	-	N	-S	-YDD	-DNM	-LQ	-K	-S	-DI	-Y	-A		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-LT	-N	-N
A2. CD. 97. 97CDKTB48	M-R	-V	-L	-Q	-A	-D	-R	-S	-TO	-KNM	-LQ	-K	-ST	-DI	-YM	-L	-D	-A	-N	-D	-R	-I	-I	-I	-I	-I	-I	-I	-N
A2. CY. 94. 94CY017 41	-K	-V	-	-	N	-S	-QDE	-DNM	-LQ	-K	-S	-NI	-YR	-L		-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-I	-I	-N
B. AR. 04. 04AR143170	M	-V	-	-S	-RF	-M	-T		-KG	-DNM	-Q	-E	-D	-GT	-L	-D	-A	-N	-D	-SQ		-I	-I	-T	-I	-I	-I	-I	-N
B. AU. 04. PS1038_Day174	F	-V	-	-	-	-	-	-	-XQxE	-ENM	-Q	-E	-D	-EV	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. BO. 99. B0L0122	M	-V	-	-	-	-	-	-	-SK	-DNM	-Q	-E	-D	-G	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
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B. CO. 01. PCM001	-V	-	-	-	-	-	-	-	-DM	-NM	-Q	-E	-D	-G	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. CU. 99. CU19	-V	-	-	-	-	-	-	-	-DK	-NM	-Q	-E	-D	-I	-YN	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
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B. DE. 86. D31	-V	-	-	-	-	-	-	-	-MDM	-NM	-Q	-E	-D	-I	-YN	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. DK. 04. PMVL 012	M	-V	-	-	-	-	-	-	-DNM	-Q	-E	-D	-GT	-YE	-L	-Q	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. DO. 05. 05DO 160884	-V	-	-	-	-	-	-	-	-R	-RDY	-ENM	-Q	-E	-D	-EI	-YO	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-N
B. EC. 89. EC003	-V	-	-	-	-	-	-	-	-FNE	-NM	-Q	-E	-D	-G	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. FR. 92. 92FR BX08	-V	-	-	-	-	-	-	-	-Y	-S	-DNM	-Q	-E	-D	-G	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-N
B. GA. 88. OYT	-V	-	-	-	-	-	-	-	-NE	-DNM	-Q	-E	-D	-H	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. GB. 86. GB8 46R	-R	-V	-	-	-	-	-	-	-DK	-NM	-Q	-E	-D	-NT	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. GE. 03. 03GEMZ004	-V	-	-	-	-	-	-	-	-DM	-NM	-Q	-E	-D	-Y	-LD	-I	-D	-K	-Q	-N	-D	-S	-I	-I	-T	-I	-I	-I	-N
B. HT. 05. 05HT 129389	-V	-	-	-	-	-	-	-	-DY	-NM	-Q	-E	-D	-G	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. IN. x. 11807	A	-V	-	-	-	-	-	-	-VDR	-NM	-Q	-E	-D	-G	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. JM. 05. 05JM KJ108	-V	-	-	-	-	-	-	-	-GD	-NM	-Q	-E	-D	-N	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. JP. 05. DR6538	-V	-	-	-	-	-	-	-	-T	-Y	-NM	-Q	-E	-D	-N	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-N
B. KR. 04. 04KMH5	-V	-	-	-	-	-	-	-	-DD	-NM	-Q	-E	-D	-H	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
B. MM. 99. mSTD101	-V	-	-	-	-	-	-	-	-DD	-NM	-Q	-E	-D	-H	-YT	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
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B. TW. 94. TWYCS	M	-V	-	-	-	-	-	-	-TYDE	-NM	-Q	-E	-D	-DH	-YN	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
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C. AR. 01. ARG4006	M	-V	-	-	-	-	-	-	-DN	-NM	-Q	-E	-D	-DT	-YR	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
C. BR. 04. 04BR013	M	-V	-	-	-	-	-	-	-K	-A	-NM	-Q	-E	-D	-GT	-YR	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-N
C. BW. 00. 00BW07621	M	-V	-	-	-	-	-	-	-D	-QDD	-NM	-Q	-E	-D	-GT	-YR	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-N
C. CN. 98. YNRL9840	M	-V	-	-	-	-	-	-	-QDD	-NM	-Q	-E	-D	-GT	-YR	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
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C. GE. 03. 03GEMZ033	M	-V	-	-	-	-	-	-	-QDD	-NM	-Q	-E	-D	-GT	-YR	-L	-K	-I	-D	-H	-X	-S	-I	-I	-T	-I	-I	-I	-N
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C. SO. 89. 89SM 145	M	-V	-	-	-	-	-	-	-QDD	-NM	-Q																		

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Proteins

Emv

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	myristoylation Nef start		acidic cluster	phos poly-P helix	phos	HXB2 premature Nef end	
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11 cpx. CM. 95. 95CM 1816	-----RIV. -EI- -I- -I- -I-	-----TSPTA- PG- -V- K- -V- -GE- -D- -D- -D-	-----R- -R- -F- G- F- -GF- -D- -Y- KK- -E- -V- -W- -I- -C- -F-	149				
12 BF. AR. 99. ARMA159	-----IV. -EI- -L- -I- -I-	-----P- -EG- -V- Q- -NR- -R- N- P- L- -D- -D-	-----R- -R- -F- G- F- -D- -Y- KK- -E- -V- -W- -I- -C- -F-	146				
13 cpx. CM. 96. 96CM 1849	-----R- TV. -A- -I- -I- -I-	-----TG- -V- Q- -DR- -V- -LA- KDYV- -G- -D- -D-	-----K- -R- -G- F- -GF- -D- -Y- KK- -E- -V- -W- -I- -C- -F-	139				
14 BG. ES. 00. X605	-----C- IV. -E- -KI- -I- -I-	-----TP- -VG- -V- Q- -A- -N- -PD- -SE- -D- -D-	-----R- -R- -N- S- F- -F- -D- -Y- KQ- -E- -V- -N- -F- -W- -I- -C- -F-	147				
15 01B. TH. 99. 99TH MU2079	-----S- -I- -I- -I- -I-	-----Q- -KIKQ- -I- -I- -I- -I-	-----R- -R- -F- E- F- -F- -D- -Y- KK- -E- -V- -N- -F- -W- -I- -C- -F-	140				
16 A2D. KR. 97. 97KR004	-----R- LP. -AI- -TP- -I- -I- -I-	-----PAAERTPPAA- EG- -V- Q- -ATR- -V- IN- -DS- -D-	-----R- -R- -F- E- F- -R- -D- -Y- K- -E- -V- -F- -W- -I- -C- -F-	156				
17 BF. AR. 99. ARMA038	-----A- -I- -I- -I- -I-	-----AEP- -EG- -V- -RR- -V- -S- N- PDL- -D- -D-	-----R- -R- -G- L- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	144				
18 cpx. CU. 99. CU76	-----LV. -EI- -I- -I- -I-	-----PRTPPAESQ- ER- -SG- -N- S- -PTHGR- -EE- -D- -D-	-----R- -R- -G- F- -F- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	146				
19 cpx. CU. 99. CU7	-----I- -A- -Q- -I- -I-	-----G- -V- -R- -D- -D- -D- -D-	-----R- -R- -G- L- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	147				
20 BG. CU. 99. Cu103	-----N- -A- -L- -I- -I-	-----TP- -AG- -V- Q- -A- -N- -PD- -DSE- -D- -D-	-----R- -R- -F- -F- -F- -D- -Y- KQ- -E- -V- -N- -F- -W- -I- -C- -F-	143				
21 A2D. KE. 99. KER2003	-----IV. -I- -I- -I- -I-	-----TD- -G- -P- -R- -T- -PD- -D- -D-	-----R- -R- -G- F- -F- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	147				
22 01A1. CM. 01. 01CM 0001BBY	-----IV. -Q- -I- -Q- -I-	-----TPA- EG- -V- Q- -D- -V- -M- -NH- S- V- -DN- -D-	-----R- -R- -G- F- -F- -D- -Y- KK- -E- -V- -N- -F- -W- -I- -C- -F-	130				
23 BG. CU. 03. CB118	-----N- -AA- -I- -I- -I-	-----APPAENP- AG- -V- Q- -AR- -DR- -V- -DSE- -D- -D-	-----R- -R- -F- -F- -F- -D- -Y- KQ- -E- -V- -N- -F- -W- -I- -C- -F-	148				
24 BG. CU. 03. CB378	-----S- -P- -SVI- -I- -I- -I-	-----TPPTRTRGASONLASHES- VG- -V- Q- -AR- -V- N- PD- -DSE- -D- -D-	-----R- -R- -F- -F- -GF- -D- -Y- KQ- -E- -V- -N- -F- -W- -I- -C- -F-	163				
25 cpx. CM. 02. 1918LE	-----N- RV. -EI- -I- -I- -I-	-----TPPAE- AA- -EG- -Q- -A- -S- -PD- -S- E- -D- -D-	-----R- -R- -G- F- -F- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	137				
26 AU. CD. 02. 02CD MBT047	-----V- -E- -I- -I- -I-	-----TP- -TG- -V- -D- -V- -SF- -PD- -GE- -D- -D-	-----R- -R- -F- -GF- -D- -Y- Q- -K- -E- -V- -N- -F- -W- -I- -C- -F-	147				
27 cpx. FR. 04. 04CD FR KZ5	-----Q- -PV. -A- -K- -I- -I-	-----P- -G- -V- Q- -A- -NN- -N- PD- -V- -DSE- -D- -D-	-----R- -R- -D- -W- KK- -E- -V- -N- -F- -W- -I- -C- -F-	147				
28 BF. BR. 99. BREPM12609	-----RGTG. -EA- -I- -I- -I-	-----TRPA- -G- -V- -R- -HN- -D- -D- -D-	-----R- -R- -G- L- -R- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	150				
29 BF. BR. 01. BREPM16704	-----C- MS. -AA- -I- -I- -I-	-----TEPGP- -EG- -Q- -A- -Y- -D- -D- -D-	-----R- -R- -I- -I- -I- -I- -I- -I-	151				
31 BC. BR. 04. 04BR142	-----N- -CIPV. -AI- -L- -AHPAA. ERIGSERVRG- EG- -P- Q- -DR- -L- -RDN- -D- -Q- -E-	-----R- -R- -F- -F- -F- -D- -Y- KQ- -E- -V- -N- -F- -W- -I- -C- -F-	162					
32 06A1. EE. 01. EE0369	-----IV. -EI- -L- -I- -I-	-----TP- -EG- -V- Q- -D- -H- PT- -D- -D- -D-	-----R- -R- -G- F- -GF- -D- -Y- KK- -E- -V- -N- -F- -W- -I- -C- -F-	146				
33 01B. MY. 05. 05MYK1007 1	-----IV. -K- -I- -Q- -I-	-----TP- -GG- -V- Q- -D- -V- -MN- DSV- -R- -NEE- -D- -D-	-----R- -R- -F- -F- -F- -D- -Y- KK- -E- -V- -N- -F- -W- -I- -C- -F-	146				
34 01B. TH. 99. 01B2478P	-----IV. -Q- -I- -I- -I-	-----TP- -EG- -V- Q- -D- -V- -MN- DSV- -R- -NEE- -D- -D-	-----R- -R- -F- -F- -F- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	146				
35 AD. AF. 05. 05AF095	-----KV. -E- -K- -Q- -I-	-----PA- -QG- -V- Q- -D- -V- -MNHPS- V- -D- -D-	-----R- -R- -S- -G- F- -F- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	144				
36 cpx. CM. 00. 00CMNYU830	-----I- -QI- -D- -Q- -I-	-----TP- -IG- -V- -DR- -TS- -DY- -D- -D-	-----R- -R- -G- F- -F- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	131				
37 cpx. CM. 00. 00CMNYU926	-----LV. -Q- -I- -Q- -I-	-----TP- -EG- -V- Q- -A- -R- -ST- -PD- -G- DPD- -D- -D-	-----R- -R- -F- -F- -F- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	132				
38 BF1. UY. 03. UY03 3389	-----RRIV. -ADI- -TP- -I- -I- -I-	-----PTAERG- AK- -EG- -Q- -DRR- -KDN- PDV- -D- -D-	-----R- -R- -G- -L- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	146				
39 BF. BR. 04. 04BRJ179	-----K- -AI- -D- -TP- -I- -I- -I-	-----PTAERG- AK- -EG- -Q- -SR- -L- -KDN- PDV- -D- -D-	-----R- -R- -L- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	155				
40 BF. BR. 05. 05BRJ055	-----R- P. -EI- -A- -I- -I-	-----EPAADG- R- -G- -Q- -A- -L- -VSN- D- -N- -D-	-----R- -R- -HR- -I- -RKE- -K- -E- -V- -N- -F- -W- -I- -C- -F-	152				
42 BF. LU. 03. luBF 05 03	-----LV. -A- -K- -I- -I-	-----TP- -VG- -P- -L- -T- -V- -D- -D-	-----R- -R- -G- L- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	146				
43 02G. SA. 03. J11223	-----R- MG. -SEI- -I- -TP- -I- -I- -I-	-----PTAAEG- GT- -EG- -Q- -AR- -PQ- -D- -D- -D-	-----R- -R- -F- -GF- -D- -Y- KK- -E- -V- -F- -W- -I- -C- -F-	154				
N. CM. 95. YBF30	-----KI- -LV. -EI- -I- -I-	-----TOEPAY- -VGA- -Q- -ANR- -IR- -RDN- EST- -D- -D-	-----R- -R- -I- -Q- -F- -D- -Y- RK- -E- -V- -N- -F- -W- -I- -C- -F-	152				
N. CM. 97. YBF106	-----KI- -LV. -EI- -I- -I-	-----TPT- -VGA- -Q- -ANR- -T- -KDN- OTV- -D- -D-	-----R- -R- -F- -F- -F- -D- -Y- RK- -E- -V- -N- -F- -W- -I- -C- -F-	146				
N. CM. 02. 0200131	-----IV. -S- -I- -I- -I-	-----RPHEDP- -VG- -x- Q- -ANR- -L- -T- Y- RTN- PTV- -V- -GE-	-----R- -R- -W- -R- -V- -D- -Y- K- -E- -V- -N- -F- -W- -I- -C- -F-	153				
N. CM. 04. 04CM 1015 04	-----KS- -V- -EI- -I- -I-	-----RQTOAA- -A- -VG- -Q- -ANR- -T- -RDN- ETV- -V- -E-	-----R- -R- -F- -F- -F- -D- -Y- RK- -E- -V- -N- -F- -W- -I- -C- -F-	152				
0. BE. 87. ANT70	-----NALR. GKFE. -AA- -T- -I- -I- -I-	-----RTFPES- C- PG- -QI- -E- AAR- G- P- -Y- H- PON- -L- F- -SHQ- -D-	-----A- -M- -I- -F- -F- -D- -Y- HK- -E- -V- -N- -F- -W- -I- -C- -F-	152				
0. CM. x. BCF06	-----NA- -RKFA. -SE- -Q- -Q- -I- -I- -I-	-----SSDPQD- C- PG- -V- -E- AAR- G- PD- -Y- PON- -L- F- -SHT- -D-	-----R- -R- -F- -F- -F- -D- -Y- HK- -E- -V- -N- -F- -W- -I- -C- -F-	150				
0. CM. 91. MYP5180	-----NA- -KFA. -SE- -D- -Q- -I- -I- -I-	-----SSDPQD- C- PG- -V- -E- ATR- G- S- -H- PON- -L- F- -DSHKD- -D-	-----R- -R- -F- -F- -F- -D- -Y- HK- -E- -V- -N- -F- -W- -I- -C- -F-	151				
0. CM. 96. 96MA182	-----NVLG. GKFA. -SA- -D- -KA- -I- -I- -I-	-----PAAPEP- C- PG- -EL- -E- AAR- G- P- -Y- PON- -L- F- -SHD- -D-	-----R- -R- -F- -F- -GF- -D- -Y- PE- -E- -V- -N- -F- -W- -I- -C- -F-	153				
0. CM. 97. 97CAB6447	-----N. CM. 97. 97CAB6447	-----KFS. -SA- -D- -Q- -I- -I- -I-	-----R- -R- -F- -F- -GF- -D- -Y- H- -E- -V- -N- -F- -W- -I- -C- -F-	151				
0. CM. 98. 98MA104	-----NVLG. KFA. -SA- -D- -Q- -I- -I- -I-	-----PAAPEP- C- PG- -x- E- AAR- G- P- -Y- PON- -L- F- -SHD- -D-	-----R- -R- -V- -F- -GF- -D- -Y- DA- -E- -V- -N- -F- -W- -I- -C- -F-	150				
0. CM. 99. 99CMU4122	-----NALR. RFP. -SAI- -K- -I- -I- -I-	-----TSPEP- C- xG- -PV- -E- AAR- G- P- -Y- PON- -L- F- -SHD- -D-	-----R- -R- -V- -F- -F- -V- -N- -D- -Y- HG- -E- -V- -N- -F- -W- -I- -C- -F-	149				
0. FR. 92. VAU	-----NVLG. KWA. -SE- -R- -QTS- -I- -I- -I-	-----PDQSSDTP- PG- -R- V- -E- ADRRG- P- -Y- PON- -L- F- -GSHOGG- -I-	-----R- -R- -G- F- -F- -D- -Y- HK- -E- -V- -N- -F- -W- -I- -C- -F-	154				
0. SN. 99. 99SE MP1299	-----NVLG. DTFK. -SA- -G- -I- -I- -I-	-----TSPPD- C- PG- -QI- -E- AAR- G- P- -Y- PON- -L- F- -SHD- -D-	-----R- -R- -G- F- -F- -D- -Y- HK- -E- -V- -N- -F- -W- -I- -C- -F-	150				
0. US. x. I. 2478B	-----NALR. KFA. -A- -I- -I- -I-	-----ASPKP- DC- PG- -EV- -E- AAR- G- P- -Y- PON- -L- F- -SHD- -D-	-----R- -R- -G- F- -F- -D- -Y- Q- -E- -V- -N- -F- -W- -I- -C- -F-	150				
0. US. 97. 97US08692A	-----NALR. KFA. -A- -I- -I- -I-	-----ASPKP- DC- PG- -EV- -E- AAR- G- P- -Y- PON- -L- F- -SHD- -D-	-----R- -R- -G- F- -F- -D- -Y- Q- -E- -V- -N- -F- -W- -I- -C- -F-	150				
0. US. 99. 99USTWLA	-----NILT. KFE. -A- -R- -Q- -I- -I- -I-	-----TSPPDQ- C- PG- -EV- -E- AGR- G- PN- Y- PON- -L- F- -YQD- -D-	-----R- -R- -Q- -F- -H- -N- -D- -Y- HK- -E- -V- -N- -F- -W- -I- -C- -F-	150				
P. FR. 09. RBF168	-----NA- -K- -LV. -A- -N- -Q- -I- -I- -I-	-----TAPETPA. -G- -EI- -KE- AQGKG- P- -KYNSKN- -L- F- -H- -D- -D-	-----R- -R- -V- -F- -F- -F- -D- -Y- PG- -E- -V- -N- -F- -W- -I- -C- -F-	148				
CPZ. CD. 98. ANT	-----SA- -IKWV. -ARQAIRKI. -H- -I- -I- -I-	-----TNPI- PCGNE- ASR- -L- -TIGTEKDVITYS- DHT- -G- -T- -D-	-----R- -R- -M- -E- -L- -D- -Y- xLK- -AA- -M- -MFN- -I- -W- -I- -C- -F-	140				
CPZ. CD. 95. SIVcpzMT145	-----NA- -LV. -EI- -I- -I- -I-	-----PT- -G- -EV- -Q- -IASR- -V- IR- -P- -E- -EMOD- -D-	-----K- -R- -F- -G- -F- -D- -Y- RK- -E- -V- -N- -F- -W- -I- -C- -F-	146				
CPZ. GA. 88. GAB1</								

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normal Nef end
PVEPKIEEA.NKGENTSLLHPVSLHGMDDPEREVLEWRFDLSRLAFHHVARELHPEYF..KNC*
--DS-AV---TER--N---INQ-R---K--M-Q---LK-L-Q-Q---FY..D-
--DQAEV--T-TG--N---CO-V--T-G--M-K---LK-I-A-KY-DWY--DR-
--D-EV-K--TEA--N---ICO---DD--T-M-K--K-LK-----FY..D-
--D-SEV---TE--N---ICO---E--M-K---LT-R-----Y..D-
--D--V---TG--N---ICO---D-K--M-K---LK-R-Q-M---FY..D-
--D-EV-K--TE--N---ICO---E--M-K---LT-I--K---FY..D-
--D-EDV---TE--N---ICO---E--M-K---LT-R-L---DFY..D-
--D-GEV-R--TE--N---ICO---DD--Q---K-M-H-Y--FY..D-
--EEV-K--E--N---ICO---E--T-M-K--K-LK-R-H-----
--D-EV-K--TE--N---ICO---D-K--Q---LK-R-Q---FY..*
--D-AEV---TE--N---ICO-V--E--M-K---LT-I--K---FY..D-
--D-EV-K--TE--N---ICO---E--T-M-K---LT-R-L---FY..D-
--DQAEV-QD-TQ--N---ICO-I--Q-K--M-K---LK-L--M---FY..D-
--D-SEV---TE--N---ICO-AE--K-K--LR-L--Q---FY..D-
--SEV---TQ--N---ICO-V--R-E-RS-RR-R---Y..D-
--QE-----T--I--M-Q-I--K--Q-K-----I--Y..D-
--DQEV-K--E--NC--M-Q---K--M-K---M--K---D-
--LD-QV-R--E--N--M-Q---K--V-K-----M--FY..D-
--D--V---E--NC--I--Q---K--V-K-----M--Y..D-
--E-----E--NV--M--E--G--V-K-----M--K--Y..D-
--D-EQV---E--NC--M-Q-T--M-K-----M--K--FY..D-
--EEV-K--E--N--M--K--Q-K-----M--F--D-
--S-EQV---E--N--M--E--K--M-K-----M--K--Y..D-
--D-EV-K--E--NC--M-Q-I--G--M-K-----M--Y..D-
--D-E--K--SE--NC--NQ--K--V-K-----M--Y..D-
--QE-V---A--NC--M-Q---K--M-K--K--K--I--Y..*
--QERV-E--NR--N--M-Q---Q-K-----M--K--Y..D-
--MD-QV---E--N--I---K--V-K-----R-M--V--Y..D-
--D-EV-K--E--NC--M-Q-IE--K--V-K-N---M--FY..D-
--K-EDV-K--E--NC--M-Q-E-T-G--M-K-----I--D-
--EE-K--E--N--M-Q---Q-K-----M--K-----D-
--M-EQV---E--NC--M--E--V-K--S-L-R-Q---FY..D-
--ERV---TE--NC--IN--G--M-K-----Y-M--K--D-
--D-EQV-A--TA--N---INQ-A--K--M-K-----Y-M--K--Y..*
--D-QV-K--E--NC--M-Q-I--G--M-K-----I--K-----*
--DQE-V---E--N--M--K--M-K-----I--K-----*
--EQV-K--E--KC--M-Q---K--V--T--R--Y..D-
--D-QV-K--E--NC--M-Q---K--M-K-----M--I--Y..D-
--V--V-TA--NC--MNQ--V--S--M--Y..D-
--D-EV-K--E--NC--M-Q---K--V--S--M--Y..EDR-
--EE-K--T--NC--M-Q---G-T-Q-K-----Y..D-
--D-E---E--RNN--M-Q---K--Q-K--H--R-I--I-----D-
--D-REV---T--N--M--E-SDG--Q-K--L-RR-M-----Y..D-
--D-KEV---E-D-N--M--E-EHG--Q-K--L-RR-M-----Y..D-
--D-KEV---E--NC--M-Q-RI--DH--M-K--S-RR-----Y..D-
--D-SEV---E--NC--I--EDK--M-K--IS-HR-L-----Y..D-
--D-GEV-D--NC--M-Q-V--DK--M-K--RR-L-----FY..D-
--D-REV-D--NC--I--E--Q-K--L-RR-M-----Y..D-
--D-GEV---T--NC--CO--E-EHG--K-K--S-RR-L--T--FY..D-
--D-REV---E--NC--M-Q-IE--R-Q--L-HR-L--Q---Y..D-
--D-RDV---T--DNC--CO--E-EHG--Q-K--Q-LR-R--Q---FY..D-
--D-REV-K--E--NC--M-Q-IE--R-Q--L-HR-L--Q---FY..D-
--D-REV-E--NC--M--E--G--K-K--S-RR-L--I--Y..D-
--D-REV-D--N--M-Q--E-ED--M-K--H-RR-----Y..D-
--D-SEV---E--NC--M--E-ED--K-K--L-RR-M-----Y..D-
--D-REV---E--N--M-M--E-HK--Q-K--L-HR-M-----Y..D-
--D-REV---E--N--I--E-GDG--M-K--HR-----FY..D-
--D-REV-K--E--NC--M-Q-IE--R-Q--L-HR-L--I--Y..D-
--D-GGV---SE--DNC--ANQ--EH--K-K--L-RR-M-----Y..D-
--D-QEV-D-TE--TN---ICO-E---Q-K--N---E-K--M--FY..*
--KEV---TE--NC--MCO-E---M--N-K--YE-K-KM---FY..D-
--SEEV---E--NC--M-Q-IE--Q-K--N-K--E-K--M--FY..D-
--D-EEV---TE--DNC--LCO-IE-E-Q-V--N-K--E-K--K--FY..D-
--D-KV-V-E-TE--NC--MNQ-G--K--V--N--E-K-K-K--FY..D-
--D-KEV-T-TE--SC--I--Q---E-T-K--V--N--E-K-K-K--FY..D-
--D-KE---D-A--SC--NO--E--M--N--E-K--IK-----D-
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02 AG.SN.98.98SE.MP1211
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08 BC.CN.97.97CN03_6F
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10 CD.TZ.96.96TZ.BF061
11 cpx.CM.95.95CM.1816
12 BF.AR.99.ARMA159
13 cpx.CM.96.96CM.1849
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15 01B.TH.99.99TH.MU2079
16 A2D.KR.97.97KR004
17 BF.AR.99.ARMA038
18 cpx.CU.99.CU76
19 cpx.CU.99.CU7
20 BG.CU.99.CU103
21 A2D.KE.99.KE92003
22 01A1.CM.01.01CM.0001BBY
23 BG.CU.03.CB118
24 BG.CU.03.CB378
25 cpx.CM.02.1918LE
26 AU.CD.02.02CD.MBTB047
27 cpx.FR.04.04CD.FR.KZS
28 BF.BR.99.BREPM12609
29 BF.BR.01.BREPM16704
31 BC.BR.04.04BR142
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36 cpx.CM.00.00CMNYU830
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--D-QEV-R-.E--NC--Y-ICQ--E-E-G--M-K-----T-T--K-----FY..D-
--N-QEV-Q-.E--N--M--E-DG--M-K-----LT-L-VK-----Y..D-
--D-QEV-K-.E--N--MCQ--E-E-K--V-----H--R-R--Q-----FY..D-
--D-GEV-R-.E--DNR--ICQ--E-ED--M-K--TS--RR-M-----FY..D-
--D-SEV--E--NC--ICQ--E-E-K--S--RR-I-----FY..D-
--D-REV--TE--NC--NQ--E-EH--K-K--S--RK-----M--Y..D-
--D-AEV--T-TE--DNC--INO--E-EH--I-M-K--S--RR-----D-Y..D-
--D-KEV--D--D-SNC--M-Q-V-E--M-K--S--RR-I-----R--Y..D-
--D-REV--D--NC--A-Q-I-E--M-K--A-RK-L-----FY..D-
--D-REV--N--SC--M-Q-IE-ED--M-K--S--RR-I--K--FY..D-
--D-REV--D--S--I-Q-IE-E-M-K--A--RR-I--M--FY..D-
--D-REV--D-T--NC--Q-LE-G-M-K--A-RK-I-----D-Y..D-
MD-AEV--T--N--ICQ--E-EDK--V-Y-RN--TR-I-----FY..D-
ID-AE--E--N--ICQ--E-ED--V--S--RT-R-----Y..D-
ID-ATV--TE--S--I-Q-IE-ED--V--Y--R-L--K--FY..D-
MD-AEV--N--N--ICQ--IE-TD-Q-V--S--K-R-Q-----FY..D-
MD-AEV--TE--N--ICQ--E-DH-Q-V-K--Q--R--H--Y..D-
MD-AD-KD-TE--N--ICQ--E-ED--V--T--K--M--FY..D-
MD-AEV--Q--N--R-T--E-EDK--K--K--T-----Y..D-
MD-AE--K--TE--NA--ICQ--IE-AD-D-V--K--K--T-----FY..D-
--D-AEV--TE--N--ICQ--E-K--M-K-----LT-R-----FY..D-
--D-QEV--TE--C--I-Q--E-E--K-K-----YK-----FY..D-
--N-EEV-K-.E--DNC--M--E-DD--Q-K--S--LR-I--R--FY..D*
--D-EEV--L-T--NC--ICQ--AE-E--K-K--S--RR-I--K--FY..D-
--D-REV--E--NC--CQ--E-EH--K-K--Q--HR-R-----FY..D-
--D-REV--C--DNC--CQ--E-EH--K-K--Q--HR-R-----FY..D-
--D-KEV--TG--N--MCQ--V-S-GG--M--T-LK-I--K--FY..D-
--D-REV--NC--M--E-KHG--V-K--T--HK-I-----Y..D-
--D-REV--A--NC--L-Q-T--E--M-K--S--RR-I-----DFY..D*
--D-VEV-K-.E--NC--M-Q--E-ED--I-K--LR-L--K--WY..D*
ID-KEV--E--NC--M-Q-IE-A--M-K--S--RK-I-----FY..D-
--D-AE--T--N--ICQ--E-ADN--R-K--S--RR-I-----NFY..D-
--D-SDV--N--NC--M-Q--E-E--K-Q--A--RK-I-----Y..D-
--S-AEV--TE--TN--ICQ--IE--K-V--H--LV-K-----FY..D-
--EE-K-.E--NC--M-Q-E-ED--K-K--S--R--R--FY..Q*
--DSNEV--E--N--ICQ--E--K-K--A--RR-I--Q--FY..D-
--D-KEA-KD-TE--NC--ACQ--K--V--N--E-K-IK--FY..D-
MD-AEV--N--N--ICQ--E-N--I--S--RR-L-----FY..D-
--D-SEV--D-T--N--MCQ-Q-I-----R-K--PH--LK-R-Q-K--FY..D-
--D-ADV--SN--N--ICQ--E-DDK--M--S--RR-I--R--DFY..D-
MD-AEV--R--N--I-Q--E-D-G--V--S--RR-I-----FY..D-
--D-AEV--N--AM--E-S-G--M-K--Q--RK-T-----Y..D-
--D-KEV--E--N--M--E--M-K--LR--K--FY..D-
--D-EQV-A-.E--N--M-Q--K--M-K-----M--Y..D*
--D-QV--E--N--M-Q--M-K-----M--F--D-
--D-REV--A--N--M--E-THG--M-K--L--RR-M-----FY..D-
--D-REV--T--NC--IC--AE-E-G--M--S--RR-I--K--FY..D-
--D-KEV--E--NC--M-Q-I--ED--M-K--A--RK-----Y..D-
--D-GEVK--SC--M-Q-IE-E--M-K--A--RK-I-----FY..D-
--D-VEV-K-.E--N--MCQ--E-G--M-K-----LK-R-Q--FY..D-
--D-EV-K-.E--NC--M-Q-A--EDK--V-----LR-I--R--FY..D*
--S-EEV-R-.E--DNC--M-Q--ED--V-K--K-----Y..D-
--D-EEV-K-.E--NC--M--E-E-K--Q--AT-----FH..D-
--x-QV-K-.TE--M--E-T--V-K--K--H-M--Y..D-
MD-ADV--E--N--ICQ--E-ED--V--S--RR-----Y..D-
LSAEAV--E-D-NA--ICQ--A--DHK--V--S--RR-----FY..D-
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--SEEEA-RLG-TC-RAN--ACA--FE-THK-I-M-K--RS-GNT--MIT--L--QKD-
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--SAEEA-RLG-TN-DA--ACN--AE-AHG-I-K-Q--RS-GLT--LQK--L--PK*
--SEAEA--LG--SDRAK--ACN--FG-RHG-I-K-Q--RS--IT--KVTN--L--LKD-
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--SEAEA--LG--H-RAK--LCA--FG-AHG-I-K-Q--RS-GLT--KIT--L--PKD-
--SEAEA--LG--CVTAK--ACN--SE--HG-I-K-Q--RS-GNI--KVT--L--LKD-
--SEAEA-ALG-C-RA--ACN--YE-QHK-I-K-Q--RS--NT--LIT--L--SKD-
--SEAEA--LG--C-RA--ACN--FE-NHGQ1-K-Q--RS-GST--MVTN--L--NKD-
--TE-EAKRLG-VC-RAH--ACN--FE--HG-I-K-Q--RS-GNT--KIT--L--PKD-
--TE-EAKRLG-VC-RAH--ACN--FE--HG-I-K-Q--RS-GNT--KIT--L--PKD-
--TEQEA-QLG-D-GAM--ACN--SE-HHG-M-K-Q--S-GIT--MVT--L--IKN-
--SEVEV--MGDEQ-KAK--ACTY-DS-HH--I-M-K--RS-GER--LQK--L--TKD-
--SP-PDD--RNI--ACT--DG--HK-I-R-E--AS-MRR-I--R--RD*
LP-EEV-K-.E--NC--MCQ--E-E--V-T--K--LR-L--K--Y..RD*
LTREQV-Q-.E-D-NC--ICQ--E-EDK--V-----LR-I--Q--Y..D*
--D-PEDD-K--NI--ACS--TT--DG-T-I--S--RR-I--RY--*G-
LTREEV-Q--TNI--MCQ--E-EHG--I-Q--TE--RR-R-K-----R*

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VI

HIV-2/SIV Proteins

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VI-1 Introduction

The number of HIV-2 and SIV sequences is growing much more slowly than for HIV-1, particularly for sequences of complete or near-complete genomes. In selecting the set of sequences to present here, we eliminated some sequences derived from the same sample, patient, or isolate. We further omitted a few that were very closely related. Within each of the protein alignments, we have included a slightly different set of sequences, drawing on both genome-length and subgenomic fragments in order to best represent viral diversity. Thus for HIV-2, we selected A and B genomes and subgenomic fragments that best represent the diversity of the virus in that region. We also included a single AB recombinant and both genomes available from other HIV-2 groups (G and U).

In these alignments, as in the database, we label sequences according to their native host. Thus, transfers of SIVsmm into humans have produced HIV-2 groups A through G. Unintentional transfers of SIVsmm into captive macaques are named according to the receptive host (Rhesus macaques = mac, Stump-tailed macaques = stm, and Pig-tailed macaques = mne). However, intentional, experimental cross-species transfers of virus remain labeled as being from the original host (e.g., HIV-1 injected into a chimpanzee is labeled HIV-1, not SIVcpz; and SIVsmm injected into a Rhesus macaque is labeled SIVsmm, not SIVmac).

VI-2 Annotated features

Features of HIV-2 annotated in the alignment that follows.

Feature	Protein	Location	Page
Gag p15 start	Gag	1	374
p15	Gag	135	374
p27	Gag	136	374
p27	Gag	364	376
p2	Gag	365	376
p2	Gag	381	376
p8	Gag	382	376
p8	Gag	433	376
p1	Gag	434	376
p1	Gag	447	376
p6	Gag	448	376
PTAP motif	Gag	458-461	376
PSAP in HIV-2 B, U	Gag	476-479	376
p6 end	Gag	510	377
Gag end	Gag	510	377
Pol p15 start (-1 from Gag)	Pol	1	378
p15	Pol	67	378
protease	Pol	68	378
protease	Pol	166	379
p51 RT start	Pol	167	379
D catalytic site	Pol	276	379
DD catalytic site	Pol	351	380
p51 RT end	Pol	605	381
p15 RNase H start	Pol	606	381
p15 RNase H end	Pol	725	382
p31 Integrase start	Pol	726	382
p31 Integrase end	Pol	1018	384
Pol end	Pol	1018	384
Vif start	Vif	1	385
Vif end	Vif	214	386
Vpx start	Vpx	1	387
Vpx end	Vpx	112	387
Vpr start	Vpr	1	388
Vpr end	Vpr	101	388
Tat start	Tat	1	389
exon 1 end	Tat	99	389
exon 2 start	Tat	100	389
Tat end	Tat	130	389
Rev start	Rev	1	390
exon 1 end	Rev	24	390
exon 2 start	Rev	25	390
Rev end	Rev	107	390
Env start	Env	1	392
signal peptide end	Env	22	392
gp120 start	Env	23	392
V3	Env	311-344	393
gp120 end	Env	525	395
gp41 start	Env	526	395

Feature	Protein	Location	Page
Env end	Env	879	397
Nef start	Nef	1	398
R17Y mutation	Nef	17	398
max HIV-1 similarity	Nef	153-182	398
premature stop in Mac239	Nef	93	398
normal Nef end	Nef	262	399

VI-3 Sequences

Sequences included in the HIV-2/SIV protein alignments.

Name	Accession	Proteins	Author	Reference
MAC.US.x.239	M33262	All	Kestler, H.	<i>Science</i> 248 (4959):1109-1112 (1990)
A.CI.88.UC2	U38293	All	Barnett, S.W.	<i>Virology</i> 222 (1): 257-61 (1996)
A.DE.x.BEN	M30502	All	Kirchhoff, F.	<i>Virology</i> 177 (1):305-311 (1990)
A.DE.x.PEI2	U22047	All	Kraus, G.	<i>ARHR</i> 14 (1): 65-77 (1998)
A.GH.x.GH1	M30895	All	Hasegawa, A.	<i>ARHR</i> 5 (6):593-604 (1989)
A.GM.87.D194	J04542	All	Kuehnel, H.	<i>Proc Natl Acad Sci USA</i> 86 (7):2383-2387 (1989)
A.GM.x.ISY	J04498	All	Franchini, G.	<i>Proc Natl Acad Sci USA</i> 86 (7):2433-2437 (1989)
A.GM.x.MCN13	AY509259	All	Schmitz, C.	<i>J Virol</i> 78 (4):2006-2016 (2004)
A.GM.x.MCR35	AY509260	All	Schmitz, C.	<i>J Virol</i> 78 (4):2006-2016 (2004)
A.GW.86.FG	J03654	Gag, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Zagury, J.F.	<i>Proc Natl Acad Sci USA</i> 85 (16):5941-5945 (1988)
A.GW.x.ALI	AF082339	Gag, Pol, Vif, Vpx, Tat, Rev, Env, Nef	Azevedo-Pereira	Unpublished
A.GW.x.MDS	Z48731	All	Becker	Unpublished
A.IN.95.CRIK_147	DQ307022	All	Santhosh, C.V.	<i>ARHR</i> 24 (10):1315-1317 (2008)
A.IN.x.NNVA	EU980602	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env	Desai	Unpublished
A.SN.85.ROD	M15390	All	Clavel, F.	<i>Nature</i> 324 (6098):691-695 (1986)
B.CI.88.UC1	L07625	All	Barnett, S.W.	<i>J Virol</i> 67 (2):1006-1014 (1993)
B.CI.09.pPRD320-20HIV2_56	AB485670	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env	Takekawa	Unpublished
B.CI.x.EHO	U27200	All	Rey-Cuille, M.A.	<i>Virology</i> 202 (1):471-476 (1994)
B.GH.86.D205	X61240	All	Dietrich, U.	<i>Nature</i> 342 (6252):948-950 (1989)
B.JP.01.KR020	AB100245	All	Kusagawa, S.	<i>ARHR</i> 19 (11):1045-1049 (2003)
G.CI.92.ABT96	AF208027	All	Brennan, C.A.	<i>ARHR</i> 13 (5):401-404 (1997)
AB.CI.90.7312A	L36874	All	Gao	Unpublished

Name	Accession	Proteins	Author	Reference
AB.CM.03.03CM_510_03	EU028345	Gag, Vif, Vpx, Tat, Rev, Env, Nef	Yamaguchi, J.	<i>ARHR</i> 24 (1):86-91 (2008)
U.FR.96.12034	AY530889	All	Damond, F.	<i>ARHR</i> 20 (6):666-672 (2004)
MAC.US.x.251_1A11	M76764	All	Marthas, M.L.	<i>J Med Primatol</i> 18 (3-4):311-9 (1989)
MAC.US.x.251_32H_PJ5	D01065	All	Rud, E.W.	(in) Brown, F, Chanock, RM and Ginsberg, HS(Eds); <i>VACCINES 92: MODERN APPROACHES TO NEW VACCINES INCLUDING PREVENTION OF AIDS: 229-235</i> ; Cold Spring Harbor Laboratory Press, New York (1992)
MAC.US.x.251_BK28	M19499	Gag, Pol, Vif, Vpx, Vpr, Rev, Env, Nef	Hirsch, V.	<i>Cell</i> 49 (3):307-319 (1987)
MAC.US.x.MM142	Y00277	All	Chakrabarti, L.	<i>Nature</i> 328 (6130):543-547 (1987)
MAC.US.x.17EC1	AY033233	All	Anderson, M.G.	<i>Virology</i> 195 (2):616-626 (1993)
MAC.US.x.17EFR	AY033146	All	Flaherty, M.T.	<i>J Virol</i> 71 (8):5790-5798 (1997)
MAC.US.x.SMM142B	BD131285	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev	Alizon, M.	Patent: JP 2002030099-A 2 29-JAN-2002; INSTITUT PASTEUR
MAC.US.x.r80025	AY576480	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Nef	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.r90131	AY576481	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Nef	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MNE.US.82.MNE_8	M32741	All	Kimata, J.T.	<i>J Virol</i> 72 (1):245-256 (1998)
MNE.US.x.MNE027	U79412	All	Kimata, J.T.	<i>J Virol</i> 72 (1):245-256 (1998)
SMM.SL.92.SL92B	AF334679	All	Chen, Z.	<i>J Virol</i> 70 (6):3617-3627 (1996)
SMM.US.x.F236_H4	X14307	All	Hirsch, V.M.	<i>Nature</i> 339 (6223): 389-92 (1989)
SMM.US.x.PBJ14_15	L03295	All	Dewhurst, S.	<i>Nature</i> 345 (6276):636-640 (1990)
SMM.US.x.PBJA	M31325	All	Dewhurst, S.	<i>Nature</i> 345 (6276):636-640 (1990)
SMM.US.x.PBJ_6P6	L09212	All	Novembre, F.J.	<i>J Virol</i> 67 (5):2466-2474 (1993)
SMM.US.x.PGM53	AF077017	All	Novembre, F.J.	<i>J Virol</i> 72 (11):8841-8851 (1998)
SMM.US.x.SME543	U72748	All	Hirsch, V.	<i>J Virol</i> 71 (2):1608-1620 (1997)
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MAC.US.x.97074	AY599198	Pol, Vpr, Rev	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.MAC239_87082	AY600249	Pol, Vpr, Rev	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
SMM.US.x.H9	M80194	Pol	Courgnaud, V.	<i>J Virol</i> 66 (1):414-419 (1992)
SMM.US.x.PBJ_143	M80193	Pol	Courgnaud, V.	<i>J Virol</i> 66 (1):414-419 (1992)
A.GW.87.CAM2CG	D00835	Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Tristem, M.	<i>J Gen Virol</i> 72 (PT 3):721-724 (1991)

Name	Accession	Proteins	Author	Reference
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MAC.US.x.2065	AY611493	Pol, Vpx, Vpr, Rev, Nef	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)
MAC.US.x.80035	AY611486	Pol, Vpr, Rev	O'Connor, D.H.	<i>J Virol</i> 78 (24):14012-14022 (2004)

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MAC.US.x.239      MGVRNSVLGGKKADELEKIRLRPNKGKKKYLKHVVAAANELDRFGLAESLLENKEGCQKILSVLAPLVPTGSENLSKLYNTVCVIVCIHAEKVKHTEEAQIVQRHLVVETGTTETMPKTSRPTAPSSGRGGMYPVQQ.IGGNYVHLPLSPRTLNAWVKLIEKKFGAE 169
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 A.GM.x.ISY
 A.GM.x.MCN13
 A.GM.x.MCR35
 A.GW.86.FG
 A.GW.x.ALI
 A.GW.x.MDS
 A.IN.95.CR1K_147
 A.IN.x.NNVA
 A.SN.85.R0D
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 B.CI.09.pPRD320-20HIV2_56
 B.CI.x.EH0
 B.GH.86.D205
 B.JP.01.KR020
 G.CI.92.ABT96
 AB.CI.90.7312A
 AB.CM.03.03CM_510_03
 U.FR.96.12034
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 MAC.US.x.251.32H.PJ5
 MAC.US.x.251.BK28
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 MAC.US.x.17EFR
 MAC.US.x.SMM142B
 MAC.US.x.r80025
 MAC.US.x.r90131
 MNE.US.82.MNE.8
 MNE.US.x.MNE027
 SMM.SL.92.SL92B
 SMM.US.x.F236.H4
 SMM.US.x.PBJ14_15
 SMM.US.x.PBJA
 SMM.US.x.PBJ_6P6
 SMM.US.x.PGM53
 SMM.US.x.SME543
 STM.US.x.STM

VVPGFQALSEGCTPYDINQMLNCVGDHQAAMQIIRDIINEEAADWDLQHPQAP..00GQLREPSGSDIAGTTSSVDEIQWMYRQNPVPGNIYRRWIQLGLQKCVRMYPNTILDVKQGPKEPFQSYVDIFYKSLRAEQTDAAVKNNMTQTLLIQNANPCKLVL 335
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A.DE.x.BEN	-----M-----	-----MG-S-----	-----A-RY-----	-----K-----	PG-I-N-E-----	R-----	VT-AP-I-----	A-AE-----	ER-Q-RK-----	QRERPYKEVTE.DLLHLEQ	497								
A.DE.x.PE12	-----M-----	-----I-----	-----A-----	-----R-T-----	D-----	SG-N-E-----	I-----	VTR-P-T-----	A-A-----	EK-L-Q-RK-K-QKMRPYKEVTE.DLLHLEQ	498								
A.GH.x.GH1	-----M-----	-----T-P-----	-----V-R-----	-----A-----	-----K-----	TG-----	E-----	M-V-APP-I-----	A-----	ER-Q-RE-----	QRERPYKEVTE.DLLHLEQ	499							
A.GM.87.D194	-----M-----	-----S-----	-----T-A-----	-----R-A-R-----	-----K-----	SG-I-N-E-----	M-R-Q-----	A-AP-I-----	I-----	EK-Q-RK-----	QRERPYKEVTE.DLLHLEQ	498							
A.GM.x.ISY	-----M-----	-----I-----	-----MR-A-----	-----KR-A-----	-----	SG-I-N-----	-----	VVPSS-T-----	M-----	EK-Q-RK-----	QRERPYKEVTE.DLLHLEQ	497							
A.GM.x.MCN13	-----M-----	-----T-A-----	-----KR-T-----	-----	-----	PG-I-N-----	V-M-R-----	V-P-T-----	V-----	E-Q-R-----	QRERPYKEVTE.DLLHLEQ	498							
A.GM.x.MCR35	-----M-----	-----T-A-----	-----KR.T-----	-----	-----	PG-I-N-----	V-M-R-----	V-P-T-----	V-----	E-Q-R-----	QRERPYKEVTE.DLLHLEQ	498							
A.GW.86.FG	-----M-----	-----T-----	-----VM-A-----	-----TF-----	-----WS-----	SG-N-----	I-H-A-----	A-P-T-----	L-----	EK-Q-R-----	QRERPYKEVTE.DLLRFEQ	496							
A.GW.x.ALI	-----M-----	-----MT-A-----	-----R.T-----	-----	-----K-----	PG-L-N-E-----	TG-I-----	-----	VTR-P-T-----	AE-A-----	EQ-Q-RK-----	QRERPYKEVTE.DLLHLEQ	498						
A.GW.x.MDS	-----M-----	-----MT-A-----	-----R.T-----	-----	-----	TG-I-----	-----	V-P-T-----	A-----	EK-Q-RK-----	QRERPYKEVTE.DLLHLEQ	498							
A.IN.95.CRIK_147	-----M-----	-----P-----	-----T-R-----	-----	-----	TG-N-E-----	IS-R-----	V-P-T-----	M-----	EK-Q-RK-----	QRERPYKEVTE.DLLHLEQ	498							
A.IN.x.NNVA	-----M-----	-----G-----	-----MG-T-----	V-----	-----T-R-----	K-----	PG-I-N-----	M-R-----	V-IP-T-----	M-----	EK-Q-RK-----	QRERPYKEVTE.DLLHLEQ	498						
A.SN.85.R0D	-----M-----	-----VIG-A-----	-----AF-----	-----	-----	PG-I-TN-----	-----	V-P-T-----	V-----	EK-Q-R-----	QRERPYKEVTE.DLLHLEQ	498							
B.CI.88.UC1	-----M-----	-----I-----	-----T-A-----	K-----	AGKRGIVT-----	V-----	T-K-----	QG-I-S-----	E-----	T-P-VT-S-----	M-----	EGMTPRGATPSAPPADPAV-MLKSYMKGROORE-	498						
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B.CI.x.EH0	-----M-----	-----I-----	-----T-STN-----	P-----	AGKR.TVT-----	A-----	T-K-----	QQG-I-S-----	E-----	F-----	V-AP-IV-S-----	MN-FGMTPOGATPSAPPADPAE-MLKNYMOLGKKQKEN	496						
B.GH.86.D205	-----M-----	-----I-----	-----T-A-----	V-----	K-----	AGKRGIVT-----	Q-----	T-----	-----	T-P-VT-S-----	MN-EGMTPRGATPSAPPADPAV-MLKSYMOMGROORE-	498							
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AB.CI.90.7312A	-----PH-----	-----I-----	K-----	T-A-----	K-----	AG-RGTVT-----	G-----	T-K-----	PG-N-N-----	E-----	V-----	P-EIV-S-----	MNT-EGKTHOGATPSAPPADPAV-MLKSYMOLGKQOREK	498					
AB.CM.03.03CM_510_03	-----M-----	-----I-----	K-----	T-A-----	F-----	TGKRGIVT-----	G-----	T-----	K-----	QG-I-S-----	E-----	V-----	T-P-VT-S-----	MN-EXMTPQGVTPSAPPADPAV-MLKSYMOMGKQORE-	497				
U.FR.96.12034	-----M-----	-----I-----	-----Q-M-----	V-----	G-----	R-VR-----	T-----	K-----	E-PG-N-S-----	ETKV-----	E-----	P-----	T-----	AE-----	TPTAPPADPAVDLLKSYMQOGKK...QKEN	498			
MAC.US.x.251_1A11	-----M-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	487		
MAC.US.x.251_32H_PJ5	-----M-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	487		
MAC.US.x.251_BK28	-----M-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	483		
MAC.US.x.MM142	-----T-----	-----A-----	K-----	-----	-----	-----	-----	N-----	-----	-----	-----	-----	-----	-----	-----	-----	483		
MAC.US.x.17EC1	-----M-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	487		
MAC.US.x.17EFR	-----M-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	487		
MAC.US.x.SMM142B	-----T-----	-----A-----	K-----	-----	-----	-----	-----	N-----	-----	-----	-----	-----	-----	-----	-----	-----	483		
MAC.US.x.r00025	-----M-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	487		
MAC.US.x.r90131	-----M-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	487		
MNE.US.82.MNE_8	-----M-----	-----	-----	G-L-----	K-----	-----	-----	T-----	Q-G-----	-----	F-----	M-----	T-----	-----	-----	-----	483		
MNE.US.x.MNE027	-----M-----	-----K-----	-----	G-L-----	K-----	-----	-----	-----	Q-G-----	-----	F-----	M-----	T-----	-----	-----	-----	483		
SMM.SL.92.SL92B	-----M-----	-----M-D-----	TGSLVA-QFRGAAGQGN-PI-R-F-----	T-----	-----	K-----	EEGRIQ-N-NQK-----	-----	-----	TTS-T-S-----	D-----	ARIV-E-LEKAQREKT.....R	484						
SMM.US.x.F236_H4	-----M-----	-----R-DOL-----	V-K-----	Q-----	T-----	K-----	TG-----	E-----	MP-I-----	-----	-----	KM-RK-----	N	484					
SMM.US.x.PBJ14_15	-----I-----	-----D-TQG-L-----	V-K-----	Q-----	I-----	-----	AG-----	E-----	MP-T-----	-----	-----	KM-RR-----	N	484					
SMM.US.x.PBJA	-----I-----	-----D-TQG-L-----	V-K-----	Q-----	I-----	-----	AG-----	E-----	MP-T-----	-----	-----	KM-RR-----	N	484					
SMM.US.x.PBJ_6P6	-----I-----	-----D-TQG-L-----	V-K-----	Q-----	I-----	-----	AG-----	E-----	MP-T-----	-----	-----	KM-RR-----	N	484					
SMM.US.x.PGMS3	-----M-----	-----	-----	R-DOL-----	V-K-----	-----	-----	-----	TG-----	E-----	F-----	MP-T-----	-----	R-----	KM-RK-----	N	484		
SMM.US.x.SME543	-----M-----	-----I-----	-----	R-DOL-----	V-K-----	Q-R.T-----	-----	G-----	TG-----	E-----	F-----	MP-T-----	-----	KM-RK-----	N	484			
STM.US.x.STM	-----M-----	-----	VFQ-D-L-----	-----	QG-R-TV-----	A-----	T-K-----	KG-----	QQG-Q-----	E-----	V-----	F-----	H-----	IP-----	T-----	A-----	RS-----	K-----	484

	p6 end
	Gag end
MAC.US.x.239	REKPYK.EVTEDLLHLSLFGGDQ*
A.CI.88.UC2	G-T-RR--A-----K---
A.DE.x.BEN	-T-HR--E-----K---
A.DE.x.PE12	G-T-H--A-----K---
A.GH.x.GH1	GKA-HR--A-----K---
A.GM.87.D194	G-T-HR-GA-----K---
A.GM.x.ISY	G-T-HR--T-----N---
A.GM.x.MCR13	G-A-CR--T-----*K---
A.GM.x.MCR35	G-A--R--T-----*K---
A.GW.86.FG	A-T-CR--T-----K---
A.GW.x.ALI	G-T-H-- -- -- --K---
A.GW.x.MDS	GKT-C--T-----T---
A.IN.95.CR1K_147	GGA-CG--M-----K---
A.IN.x.NNVA	G-A-CG--T-----K-L-
A.SN.85.ROD	G-T--REPP-----K---
B.CI.88.UC1	--R-----E---
B.CI.89.pPRD320-20HIV2_56	--R-----E---
B.CI.x.EH0	--R-----E---
B.GH.86.D205	--R-----E---
B.JP.01.KR020	-----E---
G.CI.92.ABT96	-N-----XX---S---D---
AB.CI.90.7312A	QGR-----E---
AB.CM.03.03CM_510_03	-R-----E---
U.FR.96.12034	-R-----N---
MAC.US.x.251_1A11	-----M-----
MAC.US.x.251_32H_PJ5	-----
MAC.US.x.251_BK28	-----
MAC.US.x.MM142	-G-----
MAC.US.x.17EC1	-----
MAC.US.x.17EFR	-----
MAC.US.x.SMM142B	-G-----
MAC.US.x.r00025	-----
MAC.US.x.r90131	-----
MNE.US.82.MNE_8	KR-----E---
MNE.US.x.MNE027	KR-----A-----E---
SMM.SL.92.SL92B	-SR-----E---
SMM.US.x.F236_H4	-R-----E---
SMM.US.x.PBJ14_15	-R-----E---
SMM.US.x.PBJA	-R-----E---
SMM.US.x.PBJ_6P6	-R-----E---
SMM.US.x.PGM53	-R-----E---
SMM.US.x.SME543	-R-----E---
STM.US.x.STM	-KT-----E---

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	Pol p15 start (-1 from Gag)	p15 protease	
MAC.US.x.239	FFRPVSMGKEAPQPHGSSASGADAMCSPPRGSPGSCGSAKHLHVGGAERKAER...	KQREALQ.GDGRGFAAPQFLWRRPVVTAHIEGQPEVLLDGTADDSIVTGIELGPHPTKIVGGIGGFINTKEYKNVEIELVLRKIKGTIMTGDTPIINIFGR	155
A.CI.88.UC2	---DLGT---L-R-P-S---T-ST-SRSGS-PVR-IF-A-EK-GAEGETIQGGDG.RLTPAPRAG-DTS-R---	L-K---K---Y-D---A---DN---V---K-N-VRA	168
A.DE.x.BEN	---VGPT---S-L-RDP-P---T-STSGRS-S-TVG-IY-AREK-GAEGETIQGGDG.GLAAPRAE-DTS-R---	L-K---K---Y-D---A---DN---K-N-VRA	168
A.X.x.GH12	---S-L-RDP-PA---T-ST-SRSP-SRP-VL-IF-AREK-AEGETIQGGDG.GLTAPRAG-DTT-R---	L-K---K---Y-V---A---SN-S---K-N-VRA	168
A.GH.x.GH1	---DG---S-L-RDP-S---T-ST-SRS-S-IGKIY-A-ER-GAEGETIQGGDG.RLTPAPRAGKSTS-R---	L-K---K---Y-V---A---Q-DN-V---I-I-K-N-VRA	168
A.GM.87.D194	---DGPET---A-L-R-P-S---T-ST-NRS-S-PVG-IY-AREK-AEGETIQGGDG.GLTAPRAG-D-P-R---	L-T---K---F-D---A---DN---K-N-VRA	168
MAC.US.x.97074	---X---		155
MAC.US.x.MAC239.87082			155
MAC.US.x.MM142	---PL---	---RT---L---	151
MAC.US.x.SMM142B	---PL---	---RT---L---	151
MAC.US.x.r98025			155
MAC.US.x.r90131			155
MNE.US.82.MNE.8	---L-P---PN---K---T---K---	---A---A---K---	151
MNE.US.x.MNE027	---L-P---PN---T---K---T---K---	---G---A---A---	151
SMM.SL.92.SL92B	---P---S-L-ADNI-I-TVST---SPSPDSQGVSRSTEGKD---EEQ---	---G---R---R-L---L---A---G---R---RT-K---V-RE-L	148
SMM.US.x.F236_H4	---A-P---PD---T---S---TE---ED-K-G-G---E---T---	---A---N---Y-E---A---N---D-K-K-V	151
SMM.US.x.H9	---A-P---PD---T-X-S---TE---EG-K-G-G---E---T---	---NG---I---Y-E---I---A---N---D-K-K-V	151
SMM.US.x.PBJ14.15	---A-P---PD---T---S---TE---ED-K-G-G---E---T---	---NG---I---Y-E---I---A---N---D-K-K-V	151
SMM.x.PBJA	---A-P---PD---T---S---TE---ED-K-G-G---E---T---	---NG---I---Y-E---I---A---N---D-K-K-V	151
SMM.US.x.PBJ.143	---A-P---PD---T-X-S---TE---EG-K-G-G---E---T---	---NG---I---Y-E---I---A---N---D-K-K-V	151
SMM.US.x.PBJ.6P6	---A-P---PD---T---S---TE---ED-K-G-G---E---T---	---NG---I---Y-E---I---A---N---D-K-K-V	151
SMM.US.x.PGM53	---A-P---PD---T---S---TE---ED-K-G-G---E---T---	---G---A-Y-E---A---N---D-K-K-V	151
SMM.US.x.SME543	---V-P---PD---T---S---TE---ED-K-G-G---E---T---	---G---Y-E---A---N---D-K-K-V	151
STM.US.x.STM	---L-P---L-PNT---PS-R---EK---A-E---E-EDT---	---A---LQ---V---F-N-K---K---	151
A.GM.x.IS1	---A-T---L-R-PKFA-NT-ST-N-S---PTG-V-AREKT-AETKTIORSDR.GLAASRAR-DTT-RD---	L-K---K---Y-D---A---SN-S---D-R-N-KVRA	168
A.GM.x.N13	---DGPDP---L-R-P-PA-NT-ST-SRSP-PTG-S-Y-ARKKTK-TERETIORSDR.GLTAPRAG-GTM-RD---	L-LK---LK---YV---A---SN-S---K---KVRA	168
A.GM.x.MCR35	---DGPDP---L-R-P-PA-NT-ST-SRSP-PTG-IY-ARKKTK-TERETIORSDR.GLTAPRAG-STI-RD---	L-LK---YV---A---SN-S---K---KVRA	168
A.GW.87.CAM2CG	---D-PL---R-P-ST-NT-ST-I-S---TG-IY-AREK-GAETETIQGGDG.GLTAPRTR-GPM-DN---	L-K---Y---A---SN-S---ED-K-N-V-A	168
A.GW.x.ALI	---A-P---S-L-RNP-SA-INT-ST-SRA-S-P-GAVY-A-EK-K-AERETIQGGDG.GLTAPRAG-DTT-R---	L-K---Y---A---SN-S---ED-K-N-V-A	168
A.GW.x.MDS	---D-P---L-R-PGSA-NT-ST-SRS---PTG-IY-AREK-GAERETIQGGDG.GLAAPRAGKDTM-DN---	L-N---Y---A---SN-S---N---KVRA	168
A.GH.x.ATK.147	---DKPPS---S-L-R-P-ST-NT-ST-S---PTG-IY-AREK-GAERETIQGGDG.GLTAPRAG-GT-N---	L-K---Y---A---SN-S---N---KVRA	168
A.IN.x.NNVA	---DGPDP---L-R-PNPA-NT-ST-N-S---PTG-IY-AREK-GAERETIQGGDG.GLTAPRAG-ST-R-N---	L-LK---Y---A---SD-N---N---KVRA	168
A.SN.85.ROD	---TGPL---L-R-P-SA---T-ST-S-S---TG-IY-AREKT-AERETIQGSDR.GLTAPRAGGDTI-GATN---	L-K---Y---A---NN-S---N---KVRA	169
B.CI.88.UC1	---VRTL---S-L-DP---S-TI-T-D-R-HDTSGGDTIC-PC-SSSGDAEKLHEDGETAERE-P-T---	L---R-C---A---SN---D-V-VRA	169
B.CI.09.pPRD320-20HIV2.56	---IRTL---S-L-P-EG-TI-T-D-NT-HDTSGGDSICTPC-SSSGDAEKLHAAREAEARE-P-T---	L---K-S---A---SN---D-V-VRA	169
B.CI.x.EH0	---VRPL---S-R-PGTP-DS-I-A-DE-IRHDTSGDSDICTPC-SSSGDAEKLHATREAEAGE-T---	L---K-T-S---A---SN---D-V-VRA-V	168
B.GH.x.D285	---VRTL---S-L-TI-T-DE-R-HDTSGGDTIC-PC-SSSGDAEKLHADGETETET-T---	L---K-Y-S---V---A---SD---D-V-VRA	168
B.BP.91.KR820	---I-PL---S-CSP-TP-DT-I-TTNE-REHDTSGGNAIC-PC-SSSGDVEGLHAAREKAERG-G-T---	L---K-Y-S---A---SD---D-V-K-RA	169
G.CI.92.ABT96	---V-TL---S-L-DP-P-S-SISTTD---SRPTS---X-EE-KG---AEKQT---	XX---L---Y-S---A---SN-S---K-V---QA-V	151
AB.CI.90.7312A	---A-TL---S-L-P---DS-I-A-DEH-R-ODTSGSDTIC-PC-SSSGDAEKLHATREAEAREAG---	L---Q-Y---A---SN---I---V-KVRS	169
U.FR.96.12034	---A-PL-K-S-L---P-PA-T-P-SPSRT-S---DPDPSSSGSSGS-KELHATGQE...TKGE---TI---	G---K-I-Y---K-N---A-K-E-Y---T-E-E---KFH-N-K---T-R	165
MAC.US.x.17EC1			155
MAC.US.x.17EFER			155
MAC.US.x.1937	---X-X---	---X---E---	155
MAC.US.x.2065			155
MAC.US.x.251.1A11	---X---		155
MAC.US.x.251.32H.PJ5			155
MAC.US.x.251.32H			151
MAC.US.x.80035			151

HIV-2/SIV Proteins

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HIV-2/SIV Proteins

MAC.US.x.239
 A.CI.88.UC2
 A.DE.x.BEN
 A.DE.x.PET2
 A.GH.x.GH1
 A.GM.87.D194
 MAC.US.x.97074
 MAC.US.x.MAC239 87082
 MAC.US.x.MM142
 MAC.US.x.SMM142B
 MAC.US.x.r80025
 MAC.US.x.r90131
 MNE.US.82.MNE 8
 MNE.US.x.MNE027
 SMM.SL.92.SL92B
 SMM.US.x.F236 H4
 SMM.US.x.H9
 SMM.US.x.PBJ14 15
 SMM.US.x.PBJA
 SMM.US.x.PBJ 143
 SMM.US.x.PBJ 6P6
 SMM.US.x.PGM53
 SMM.US.x.SME543
 STM.US.x.STM
 A.GM.x.ISY
 A.GM.x.MCN13
 A.GM.x.MCR35
 A.GW.87.CAM2CG
 A.GW.x.ALI
 A.GW.x.MDS
 A.IN.95.CR1K 147
 A.IN.x.NNVA
 A.SN.85.RDD
 B.CI.88.UC1
 B.CI.09.pPRD320-20HIV2 56
 B.CI.x.EH0
 B.GH.86.D205
 B.JP.01.KR020
 G.CI.92.ABT96
 AB.CI.90.7312A
 U.FR.96.12034
 MAC.US.x.17EC1
 MAC.US.x.17EFR
 MAC.US.x.1937
 MAC.US.x.2065
 MAC.US.x.251 1A11
 MAC.US.x.251 32H PJ5
 MAC.US.x.251 BK28
 MAC.US.x.80035

p15 RNase H end_p31 Integrase start
 SQYVMGIIIGTCPTSESRLVNQIIEEMIKKSEIYVAWPAHKIGGNGQEDHLVSQGIHQVLFLEKIEPAQEEHDKYHSNVKELVKFGLPRIVARQIVDTCDKCHQKGEATHGOANSDLGTWQMDCTHLEGGKIIIVAVHVASGFIEAEVIPQETGRQTALFLKLKAGR 833
 ---VAQ---I---D---EAV---I---V---E---I---IH---I---QL---N---AQ-Q---V-AEI-V---S---S---846
 ---VA-Q---N-I---EAV---V---E---II---TH---I---LL---NS-AQ-Q---V-AEI-V---Y---S---S---846
 ---VA-Q---K---ETL---V---E---SH---KL---N---AQ-Q---VDAE---S---S---846
 ---VV-Q---I---D---EAV---V---R---E---M---TH---I---QL---N---AQ-Q---V-AEI-V---S---S---846
 ---VA-Q---N-I---D---EAV---V---E---I---TH---I---QL---N---AQ-Q---V-AEI-V---S---S---846
 ---X---I---833
 ---X---833
 ---S---I---L---K---V---833
 ---S---I---L---K---V---829
 ---V---V---833
 ---X---833
 ---L---K---V---829
 ---L---K---V---829
 ---LN---Q-S-D-DI-A---QLVQ---EAV-IG---N-V-R---S---D---AQ-YNI-QL---K---NA-N-Q---T-AEV---V---R---I-S---826
 ---A-Q---EAV---V---#K---E---K---X---L---K---L---X---V-XX---G---X---829
 ---VA-Q---K---EAV---X-E---V---E---E---K---X---L---K---L---X---V-XX---G---X---829
 ---VA-Q---EAV---V---E---E---L---K---V-AE---829
 ---VA-Q---EAV---V---E---E---L---K---V-AE---829
 ---VA-Q---EAV---X---V---E---E---X---L---K---X---V-XX---G---X---829
 ---VA-Q---EAV---V---E---E---L---K---V-AE---829
 ---A-Q---EAV---V---E---E---I---L---K---H---V-AE---829
 ---VA-Q---EAV---V---E---E---I---L---K---R---V-AE---829
 ---Q---K---EAV---V---E---E---I---L---K---V-AE---S---829
 ---V-Q-A---I-K---EAV---V-Q---R---G---AH---NL---N-AQ-Q---V-AE---S---846
 ---VA-Q---I---EAV---V-Q---E---SH---KL---N-AQ-Q---VDAE---S---846
 ---VA-Q---I---EAV---V-Q---E---SH---KL---N-AQ-Q---VDAE---S---846
 ---VA-Q---N-I---EAV---V---E---T---SH---DI-QL---N-AQYQ---V-AEV---S---845
 ---VA-Q---N-I---EAV---V---E---SH---NL---N-AQ-Q---V-AE---V-I---S---846
 ---VV-Q---N-I---EAV---V---E---SH---QL---N-AQ-Q---V-A---V---846
 ---VA-Q---NKI---EAV---V---E---SH---R---KL---N-AQ-Q---V-AE---V---846
 ---VA-Q---N---EAV---V---E---N---SH---KL---N-AQ-Q---V-AE---V---S---846
 ---SASQ---KI---EAV---V---E---SH---I---NL---NS-AQ-Q---V-AE---S---847
 ---VA-Q---T-P---EAV---G---R-L---V---E---G---H---QL---K---NS---Q---V---V-AE---V---847
 ---A-Q---TD-PI-K---EAV---L---V---E---G---H---I---QL---K---NS---Q---V-AE---V---847
 ---VAAQ---T-PI-RE---EK---G---L---V---I---E---N---H---I---QL---NS---Q---V-E---V---846
 ---AAQ---T-PI-AK---EAV---G---L---V---I---E---G---H---I---QL---K---NS---Q---V-A---V---846
 ---AAQ---T-PI-KT-V---EAV---G---L---V---HI---N---E---G---H---I---QL---K---NS---Q---V-AE---847
 ---X---AXQ---T-P-K---X---EXL-G---V-X---HI---X---EXF---TH---I-QL-K---NSYHS-Q---V-AE---V---V---829
 ---VA-Q---T-PI-K---EAV---L---V---E---G---H---I-QL-K---NS---Q---V-V-AE---V---S---847
 ---I---A-Q---T-P-SK---L-R-EAV-G---V---E---QH---I-QL-K---N-HV-Q---M---V-TEV---VV---842
 ---X---X---V-X---833
 ---V---833
 ---K---V---833
 ---V---833
 ---V---V---833
 ---V---829
 ---V---833

	p31 Integrase end	
	Pol end	
MAC.US.x.239	DSSSHMEDTGEAR.EVA*	1019
A.CI.88.UC2	---P-L-GAR-DG----	1033
A.DE.x.BEN	---P-L-GAR-DG.-M-C	1033
A.DE.x.PE12	---L-G-R-DG----	1033
A.GH.x.GH1	---HLEGARE-DG----	1033
A.GM.87.D194	---L-GAR-DG----	1033
MAC.US.x.97074	-----	1020
MAC.US.x.MAC239_87082	-----	1020
MAC.US.x.MM142	-----	1016
MAC.US.x.SMM142B	-----	1016
MAC.US.x.r80025	-----	1020
MAC.US.x.r90131	-----	1020
MNE.US.82.MNE_8	-----	1016
MNE.US.x.MNE027	-----	1016
SMM.SL_92.SL92B	G--AS---Q*KNSGAL--	1013
SMM.US.x.F236_H4	--G--L-----	1016
SMM.US.x.H9	--G--L-----	1016
SMM.US.x.PB114_15	--G--L-----	1016
SMM.US.x.PB3A	--G--L-----	1016
SMM.US.x.PB3_143	--G--L-----	1016
SMM.US.x.PB3_6P6	--G--L-----	1016
SMM.US.x.PGM53	--GP-L-----	1016
SMM.US.x.SMES43	--G--L-----	1016
STM.US.x.STM	--G--L---R-G----	1016
A.GM.x.ISY	--G--L-GAR-DG.-M--	1033
A.GM.x.MCN13	--G--L-GAR-DG.-M--	1033
A.GM.x.MCR35	--G--L-GAR-DG.-M--	1033
A.GW.87.CAM2CG	--L-GAR-NG-----	1032
A.GW.x.ALI	--GP-L-GAR-DG----	1033
A.GW.x.MDS	--GP-L-G-R-DG----	1033
A.IN.95.CR1K_147	--GP-L-G-R-DG----	1033
A.IN.x.NNVA	--GP-L-G-R-DG----	1033
A.SN.85.ROD	--G--L-GAR-DG.-M--	1034
B.CI.88.UC1	-CGTD---RQ---M-Q	1034
B.CI.09.pPRD320-20HIV2_56	-CGADV---RQ---M-Q	1034
B.CI.x.EH0	-C-ADV---MQ---Q	1033
B.GH.86.D205	-C-AD---RQ---M-Q	1033
B.JP.01.KR020	-C-AN---Q---M-Q	1034
G.CI.92.ABT96	--TN---RQTG----	1016
AB.CI.90.7312A	-C-TDV---RQ---M-Q	1034
U.FR.96.12034	---NL-GAEKV---M-L	1029
MAC.US.x.17EC1	-----	1020
MAC.US.x.17EFR	-----	1020
MAC.US.x.1937	-----	1020
MAC.US.x.2065	-----	1020
MAC.US.x.251_1A11	-----	1020
MAC.US.x.251_32H_PJ5	-----	1020
MAC.US.x.251_BK28	-----	1016
MAC.US.x.80035	-----	1020

MAC.US.x.239
 A.CI.88.UC2
 A.DE.x.BEN
 A.DE.x.PET2
 A.GH.x.GH1
 A.GM.87.D194
 A.GM.x.ISY
 A.GM.x.MCN13
 A.GM.x.MCR35
 A.GW.86.FG
 A.GW.87.CAM2CG
 A.GW.x.ALI
 A.GW.x.MDS
 A.IN.95.CR1K 147
 A.IN.x.NNVA
 A.SN.85.R0D
 B.CI.88.UC1
 B.CI.09.pPRD320-20HIV2_56
 B.CI.x.EH0
 B.GH.86.D205
 B.JP.01.KR020
 G.CI.92.ABT96
 AB.CI.90.7312A
 AB.CM.03.03CM_510_03
 U.FR.96.12034
 MAC.US.x.17EC1
 MAC.US.x.251_1A11
 MAC.US.x.251_32H_PJ5
 MAC.US.x.251_BK28
 MAC.US.x.17EPR
 MAC.US.x.MM142
 MAC.US.x.SMM142B
 MAC.US.x.r00025
 MAC.US.x.r00131
 MNE.US.82.MNE_8
 MNE.US.x.MNE027
 SMM.SL.92.SL92B
 SMM.US.x.F236_H4
 SMM.US.x.PB114_15
 SMM.US.x.PBJA
 SMM.US.x.PBJ_6P6
 SMM.US.x.PGM53
 SMM.US.x.SME543
 STM.US.x.STM

Vif start

MEEKKRWIAVPTWRIPERLE.RWHSILIKLYKYTKDLQKVCVPHFKVGWAWWTCRSVIFPLQEGSHLEVOGWHLTPEKGLSTYAVRITWYSKNFWDVTPNYADILLHSTYFPCFTAGEVRRAIRGEQLLSCCRFPRAHKYQVPSLQYLALKVVS..DVRSGENPT 167
 ---G-S-V---V-G-M---V---R---EG-R-H---KGE-I-A-N---SHS-L-TEK---DC-I---C-A---K---NY-Q-A---V-QQ-ND-P-RKG-A 168
 ---DRN-V---V-G-M-K-A-V---R---EE-R-H---GK-I-A-N---SH-L-TEK---DC-I-S---K---NY-Q-A---V-QQ-ND-P-RKGT-A 168
 ---GE-V---V-G-M-K-V---HR---EG-H---GN-I-A-N---S---TER---DC-S-I-S---K---NY-Q-RSK-L-F-V-QQ-NG-P-KNST- 168
 ---G-N-VPTWRVPGR-M---V---R-R-EE-R-H---KGE-I-A-N---SHS-TER-D-I-S---K---NY-Q-V---V-QQ-ND-P-RKGT-A 168
 ---G-N-V---V-G-M---V-H-R---EE-R-H---EGE-I-A-N---SHS-L-TEK---DC-S-I-S---K---NY-Q-A---V-QQ-NG-P-RKGAA 168
 ---DQG---V-G-M-K---R---ED-R-H---KGN-I-A-N---S-S-M-EG---DC-T-I-S---K---NY-Q-SK---F-V-QQ-NDKP-RD-T- 168
 ---G-N-V---V-G-M-K-V---R---ED-H---KGN-I-A-N---S-S-M-TER---DC-S-I-S---K---NY-Q-RA---F-V-QQ-ND-P-RNGTP 168
 ---G-N-V---V-G-M-K-V---R---ED-H---KGN-I-A-N---S-S-M-TER---DC-S-I-S---K---NY-Q-RA---F-V-QQ-ND-P-RNGTP 168
 ---G-V-I-V-G-M---V---R-E-H---K-N-I-A-N---SHS-TER-DC-T-I-S---K---KY-RS---F-V-QQ-ND---NSA- 168
 ---G-S---V-G-M-K-V---G-EQ-H---RGD-R-I-A-N---S-M-TEK---DC-T-I-S---K---KY-RS---F-V-QQ-ND-P-RDRT- 168
 ---G-S-V---V-G-M-K-V---R-E-H---GR-I-A-N---S---TEK---DC-S-I-G-S---K---NY-Q-S---F-V-QQ-NGKP-RNST- 168
 ---G-T-V---V-G-M-K-V---R-E-H---KGN-I-A-N---S-L-TEK---DC-S-I-T---A---K---NY-Q-S-T---F-V-QQ-NG-P-RDST- 168
 ---D-V---KV-G-M-K-V---E-H---KDN-I-I-A-N-E-S---TE---DCT-S-I-A---KI---NY-Q-RT-T---F-V-QQ-ND---RDGT- 168
 ---G-V---V-G-M-K-V---R-E-H---NNN-N-I-A-N-S---TEK---D-S-I-G-A---KV---NY-Q-T-T---F-V-QQ-ND---RDST- 168
 ---D-V---V-G-M-K-V---E-H---KGN-I-A-N-S-S---TEK---DC-V-I---K---NY-RA---F-V-QQ-ND-P-RDST- 168
 ---G-N-V---G-K-V---HR-E-Q-S-H---K-EAY-N-R-F-S-L-KRS-Y-DV-Q-GS-S-N---KI-Y-NY-S-EG---F-R-IOEGKDG---SA- 169
 ---N-V---G---V---HR-E-Q-S-H---K-A-Y-I-N-R-L-S---RES-Y-DV-Q-GS-S-N---KI-Y-NY-S-DR---F-R-IOEGKNG---SA- 169
 ---N---C---R---O-S-H---K-A---N-R-F-S-L-ERS-Y-DV-R-GS-SS-N---KI-H-NY-S-TG---F-R-IOEGKDG---ST- 169
 ---D-V---G---R-GE-O-S-H---I-NK-AW-N-R-F-S-L-K-S-Y-DV-Q-GS-S-N---KI-Y-NY-S-EG---F-R-IOEGKNG---SA- 169
 ---N---G-K-V---HR-E-Q-T-H---K-A-Y-I-N-R-F-A-L-K-S-Y-DV-H-GS-F-N---KI-Y-NY-S-RG---F-R-IOEGGNGP---SAA- 169
 ---G---G-K---F-F---AV-H---TKEA-I-N---Q-L-TRK-Y-ET-Q-GS-D---I---NY-T-R---F-Q-QK-GHG-K-SX- 168
 ---G-N-V---K-G-K-V---HR-GE-O-S-H---KG-AC-N-R-F-S-L-EES-Y-DV-Q-G-S-N---KI-Y-NY-S-EG---F-R-IOEGKNG---SA- 169
 ---D-V---K-G-A---GE-O-S-H-X---DKXAX-X-N-R-L-L-XER-Y-DV-Q-GS-S-N---KI-Y-NY-S-EG---F-R-IOEGKNG---K-T- 169
 ---N-V---V-R---H-#-N-E-H---KK---A-N---S-L-TRG---DC-Q-GS-S---N-S-RQ---F-RALQ..G-KR--- 166
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 -----G-----Y-----R-----R-----D-----V-----K-----R-----R-----Y----- 167
 -----R-----R-----D-----V-----K-----R-----R-----Y----- 167
 -----V-----A-----H-----N-----R-----D-----E-----R-----H-----R-----H----- 167
 -----V-----A-----H-----N-----R-----D-----E-----R-----H-----R-----H----- 167
 -----X-X----- 167
 -----H-----K-Q-N-R-H-R-DC-----T-----R-----Y-----R----- 167
 -----E-Q-N-R-H-R-DC-----T-----R-----Y-----R----- 167
 ---G-V-V-SR-IVE-C-FH-RE-E-A-H-Y-A-E-V-N-S-EK-DV-Q-A-A-HA-Q-V-Y-GYAV-HSS-Q-L-LQ-ND-PK-K- 169
 ---N-V---H-N-MA-H-RDET-N-A---R---D-T---SE-K---K-K-K-N---T---H---D--- 167
 ---N-V---G-K-H-N-A-H-KDEA-N---R---D-T-G---SE-K---K-K-K-N---T---H--- 167
 ---N-V---G-K-H-N-A-H-KDEA-N---R---D-T-G---SE-K---K-K-K-N---T---H--- 167
 ---N-V---K-G-K-H-N-A-H-RDE-N-A---R---D-T-G---SE-Q---K---K-K-N---T---H---R-D- 167
 ---N-V---H-N-MA-H-RDKT-N---H---R---DC-T---SE-Q---K---K-K-N---T---H---R-D- 167
 ---V---G---H-N-E-S-A-H---GEA-N---E---TR-S-DC-Q-G---K---TK-N---E---H---R-TA 167

214
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Vif end

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WQKWRDRNRRLRMKAQNSQRGDKQGGPKPTKAGNFPGLAKVLGLTA*
R--HW--V-R-DY-SLE-----APR-H-V-E-----
R--HW--V-REDH-SL-G-SE-SAPR-H-V-E-----
R-R-SNWF-L-RKDQ-H-SE-AS-Y-V-E-----
R--HW--V-LR-DY-SL-SE-SAPR-H-V-E-----
R--HW--V-R-DY-SL-G-SE-SAPR-H-V-E-----
R--NY--L-R-DG-SH-SE-AQ-Y-V-E-----
R--Y--QL-R-DG-SH-SES-APR-Y-V-E-----
R--Y--L-R-DD-SH-SES-APR-Y-V-E-----
R-R-G-Y--R-D-Y-SES-PR-H-V-E-----
R--Y--L-R-D-SY-SES-AP-Y-V-E-----
R--Y--V-R-D-L-ES-AP-H-V-E-----
R-R-Y-A-L-R-D-SH-ES-APR-Y-V-E-----
R-R-Y--L-R-DG-SH-ES-AQ-TH-V-E-----
R-R-Y--L-REDG-SH-SES-AQ-H-V-E-----
R-R-Y--L-R-D-SH-SES-PRTY-V-E-E-----
R-R-N--SI-L-RK-NNRAQ-GSSQ-LAPRTH-E-----
R-R-G-S--I--RK-TSRTO-GSSQSFAPRTH-E-----
R-R-NS--I-RD-I-TSQ-SSSQSLAQ-TY-E-----
R-R-NS--SI-L-RK-NNRAQ-GS-Q-FAPRTH-E-----
R-R-N--SI-L-RK-NNRAQ-GSSQSSAQ-TY-E-----
R-R-G--I--RK-XR-Q-DSSQSF-Q-Y-E-----
R-R-S--I--RK-NSRTO-GSSQ-FAPRTH-E-----
RE-R-N--SI-X-RK-NNRAQ-GSSQ-LAPRTH-E-----
R-FR-NC--FQL-RK-CERYQ-GSSATSSQ-TY-A-----

S--S--S--D--
S--S--D--
S--V--E--
S--S--S--VD--
S--S--D--
R--N--VT-Y-G-PESSNSTT--RV--E--GR--
N-K--RN-GSS-S-AE--
N--L-R--RN-GSSSEFAE-T--V--
N--L-R--RN-GSSSEFAE-T--
N--I--RN-GSSSELAE--
GN--RN-GSS-S-AE--
R--G-GSI-V-T-G-H-P-S-S-E-TD--

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	Vpx start		Vpx end
MAC.US.x.239	MSDPRERIPPGNSGEETIGEAFFELNRTVEEINREAVNHLPRELIFQVWQRSWWEYHDEQGMSPSYVKYRYLCLTIQKALFMHCKKGCRCLEGEHGAGGWR.PGPPPPPPPPGLA*		112
A.CI.88.UC2	-T-----V-----D-----I-----AL-----R-----L-----S-----T-----M-----M-----I-----L-----T-----G-----P-----V-----		113
A.DE.x.BEN	-T-----V-----E-----I-----AL-----R-----A-----T-----M-----I-----T-----F-----R-----T-----W-----DM-RE-LEDQ-----V-----		114
A.DE.x.PE12	-A-----KTV-----G-----V-----A-----E-----M-----A-----R-----DL-----Q-----T-----R-----M-----Y-----M-----I-----V-----T-----G-----P-----V-----		112
A.GH.x.GH1	-T-----V-----D-----I-----AL-----R-----D-----T-----M-----V-----I-----F-----R-----T-----G-----P-----S-----V-----		113
A.GM.87.D194	-A-----V-----D-----I-----AL-----A-----T-----T-----IM-----VYI-----F-----T-----R-----P-----V-----		113
A.GM.x.I51	-TN-----T-----E-----D-----D-----A-----R-----R-----T-----M-----V-----F-----T-----R-----P-----S-----V-----		113
A.GM.x.MCN13	-T-----TV-----E-----N-----D-----A-----R-----T-----O-----T-----M-----T-----R-----T-----G-----P-----V-----		113
A.GM.x.MCR35	-T-----TV-----E-----N-----D-----I-----A-----R-----R-----O-----T-----M-----T-----R-----T-----G-----P-----V-----		113
A.GW.86.FG	-T-----TV-----E-----A-----D-----A-----H-----R-----T-----T-----M-----MY-----A-----RDGT-----G-----M-----QK-----GD.Q-----V-----		113
A.GW.87.CAM2CG	-T-----TV-----E-----A-----D-----A-----R-----R-----O-----T-----M-----V-----I-----F-----R-----T-----G-----P-----V-----		113
A.GW.x.ALI	-AN-----TV-----D-----D-----AL-----R-----O-----T-----M-----MYT-----FM-----T-----G-----P-----S-----V-----		113
A.GW.x.MDS	-A-----TV-----EQ-----A-----D-----A-----R-----T-----T-----M-----MYI-----GR-----T-----R-----P-----V-----		113
A.IN.95.CR1K 147	-T-----TV-----A-----D-----A-----G-----G-----A-----T-----M-----I-----I-----VRR-----T-----G-----P-----S-----V-----		113
A.IN.x.NNVA	-T-----TV-----A-----E-----A-----G-----G-----A-----T-----M-----M-----I-----ARR-----T-----G-----G-----S-----L-----WV-----		113
A.SN.85.R0D	-T-----TV-----A-----A-----A-----R-----E-----T-----I-----VY-----VR-----T-----R-----P-----V-----		113
AB.CI.90.7312A	-V-----D-----V-----A-----E-----IV-----L-----A-----R-----D-----I-----T-----L-----M-----V-----FA-----T-----RG-----P-----R-----		112
AB.CM.03.03CM_510_03	-D-----D-----X-----E-----IT-----L-----V-----C-----A-----R-----S-----T-----L-----M-----M-----V-----YT-----T-----RQ-----X-----S-----		112
B.CI.88.UC1	-V-----D-----D-----E-----IT-----L-----V-----C-----A-----RE-----S-----T-----L-----M-----M-----V-----YT-----Q-----P-----S-----		112
B.CI.09.pPRD320-20HIV2_56	-V-----D-----V-----A-----E-----LA-----L-----K-----K-----A-----R-----I-----T-----L-----M-----MYI-----IA-----T-----RR-----P-----Q-----		112
B.CI.x.EH0	-V-----D-----V-----ET-----L-----HL-----V-----K-----A-----RE-----I-----T-----M-----M-----I-----FA-----G-----R-----P-----S-----		112
B.GH.86.D205	-V-----D-----V-----A-----E-----IT-----L-----V-----A-----RE-----I-----T-----L-----M-----M-----V-----YT-----Q-----P-----S-----		112
B.JP.01.KR020	-V-----D-----V-----E-----IT-----L-----V-----A-----E-----TI-----T-----M-----Y-----LAR-----A-----R-----P-----S-----		112
G.CI.92.ABT96	-X-----E-----D-----E-----XT-----I-----R-----A-----T-----L-----M-----M-----V-----T-----QK-----P-----Q-----		112
U.FR.96.12034	-G-----E-----V-----S-----E-----RD-----A-----Q-----Q-----R-----E-----T-----Q-----P-----S-----I-----		113
MAC.US.x.17EC1			113
MAC.US.x.17EFR			113
MAC.US.x.1937			113
MAC.US.x.2065			113
MAC.US.x.251_1A11			113
MAC.US.x.251_32H_PJ5	-V-----Q-----M-----		113
MAC.US.x.251_BK28	-Q-----T-----		113
MAC.US.x.MM142			113
MAC.US.x.r00025			113
MAC.US.x.r00131	-Q-----T-----		113
MAC.US.x.SM142B	-Q-----		113
MNE.US.02.MNE_8			113
MNE.US.x.MNE027			113
SMM.SL.92.SL92B	-T-----HN-----AL-----QT-----Q-----R-----C-----V-----Y-----A-----VQ-----M-----M-----Q-----FR-----T-----R-----SQ-----T-----		113
SMM.US.x.F236_H4	-K-----D-----D-----A-----R-----Y-----M-----V-----T-----M-----GE-----T-----		113
SMM.US.x.PB114_15	-D-----D-----A-----R-----M-----V-----T-----M-----GE-----T-----		113
SMM.US.x.PBJA	-D-----D-----A-----R-----M-----V-----T-----M-----GE-----T-----		113
SMM.US.x.PBJ_6P6	-D-----D-----A-----R-----M-----V-----T-----M-----GE-----T-----		113
SMM.US.x.PG053	-E-----G-----A-----R-----M-----E-----T-----V-----R-----E-----S-----		113
SMM.US.x.SME543			113
STM.US.x.STM	-A-----E-----H-----D-----R-----PG-----S-----R-----T-----		113

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MAC.US.x.239      M...EERPENEQPQREPDEWVVEELKEEKHFDPRLLTALGNHIYNRHGDTLEGAGELIRILQRALFMHFRGGCIHSRIGQPGGGNPLSAIPPSRSM*L
A.CI.88.UC2      #GRS*MIV-I**R-----I-D-Y-N-R-K-S-L-V-GSR-TRRRT-CP-T-TP-G-H-
A.DE.x.BEN       -TEAPT-F-DGT-R-DLGDSD-I-T-R-I--R-----I-YY-H-----R-KT-V-A-NR-*TRRRT-CP-A-TP-A-H-
A.DE.x.F22       -TEAPT-F-D-T-P-G-G-TGL-R-R-----I-Y-CA-----S-R-NV-V-A-NR-TR-ET-Q-TP-Q-
A.GH.x.GH1       -TEAPT-F-DGT-R-LGGD-IRL-G-I--R-----I-Y-HS---P-R-NV-V-L-A-NR-S-TRRRT-FP-A-TP-G-Y-
A.GM.87.D194     -TEAPT-F-DGT-R-LGST-I-T-K-I--C-I-Y-----R-V-V-I-A-DR-K-TRRRA-CP-A-TP-G-H-
A.GM.x.ISY       -TEAPA-F-DGT-P-G---I-I-R-I--R-----YY-T-----R-V-T-A-G-----R-R-TP-N-Q-
A.GM.x.MCN131    -TEAPT-F-DGT-P-G---II-I-RK1-K---Y-HT-----R-NV-----A-RL-T-RT-FP-TSTP-T-Q-
A.GM.x.MCF35     -TEAPT-F-DGT-P-G---II-I-RK1-K---Y-HT-----R-NV-----A-RL-T-RT-FP-TSTP-T-Q-
A.GW.86.FG       -TEAPT-L-DRT-P-G-A-I-I-R-IE-K---R-----RY-T-----R-A-G-----A-G-TP-G-H-
A.GW.87.CAM2CG   -TEAPT-L-DGT-P-G---I-I-ROI-----G-A-----R-R-V-T-A-N-TR-----TP-R-
A.GW.x.MDS       -TEAPT-L-DGT-P-G---I-I-R-IT---RS-----R-T-A-G-TR-----TP-T-Q-
A.IN.95.CR1K_147 -TEAPT-L-DGT-P-G---I-I-R-I--R-----IY-D-Y-----R-V-T-A-G-----R-T-TP-R-
A.IN.x.NNV4      -TEAPT-L-DRT-P-G---I-I-R-I--R-----RY-T-Y-P-----R-V-T-A-G-----R-TP-R-
A.SN.85.R0D      -AEAPT-L-VDGT-L-G---II-I-R-I--R-----I-KY-T-A-G-----R-KV-----R-TP-N-Q-
B.CI.88.UC1      -AEAAP-T-S---E-ED-M-I-Q-R-----F-S---A-K-K-L-A-Q-----
B.CI.89.pPRD320-20HIV2_56 -AEAAP-T-D---E-ED-I-Q-R-----F-S---A-K-K-L-Q-----
B.CI.x.EH0       -AEAAP-T-DKN-EQ-D-I-Q-----F-S-N-KL-L-Q-----
B.GH.86.D205     -AEAAP-I-N---E-IG-I-I-Q-----F-S---A-K-K-L-A-Q-S-T-P-
B.JP.01.KR020    -TEAAP-T-D---E-ED-I-Q-R-----F-G-IA-L-Q-----V-
AB.CI.90.7312A   -AEAAS-T-D---E-ED-I-Q-R-----F-S---A-K-K-L-Q-----T-EG-Q-
G.CI.92.ABT96    -AEETI---D-A-----I-----Y-D-----K-L-D-RC-GNA-TT-GVF-
U.FR.96.12034    --A-I-DGA---G---R-I---VR---Y-----K-I-L-R-SSR-TTV-----
MAC.US.x.17EC1   -----
MAC.US.x.17ECR   -----X-X-----T-----X-
MAC.US.x.1937    -----
MAC.US.x.2065     -----*---G-----G-----T-----R-----GV-
MAC.US.x.251.1A11 -----
MAC.US.x.251.32H.PJ5 -----
MAC.US.x.251.BK28 -----N-----T-----
MAC.US.x.80035    -----T-----
MAC.US.x.97074    -----T-----
MAC.US.x.MAC239.87082 -----
MAC.US.x.MM142    -----K-----I-S-S-----T-----
MAC.US.x.SMM142B -----K-----I-S-S-----T-----
MAC.US.x.r60025   -----T-----
MAC.US.x.r90131   -----
MNE.US.82.MNE.8  -----D-----Y-D-----K-----T-S-----T-R-
MNE.US.x.MNE027   -----D-----Y-D-----K-----N-S-----
SMM.SL.92.SL92B  ---H-A-D-TNP---IRD-----YV-DTY-I-I-K-K-L-H-T-R-P-GS-SA-DV-
SMM.US.x.F236.H4  ---A-D-A-----Y-D-----I-S-A-S-----GV-
SMM.US.x.PBJ14_15 -T-D-A-----I-N-----Y-D-----I-R-S-----T-GV-
SMM.US.x.PBJ3A    -T-D-A-----I-N-----Y-D-----I-R-S-----T-GV-
SMM.US.x.PBJ_6P6 -T-D-A-----K-V-N-----Y-D-----I-A-SR-T-GV-
SMM.US.x.PGM53    -A-D-A-----I-----Y-D-----I-S-A-SR-T-A-
STM.US.x.STM      -TH---D-----I-O-R-----S-Y-D-----K-----R-----AT-T-GV-

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	Tat start	exon 1 end	exon 2 start	Tat end	
MAC.US.x.239	METPLRQENSLESSNRSSCISEADASTPESANLGEELISQLYRPLEACYNTCYCKCCYHCQFCLKGLGICYEQSRKRRTPKKAKANTSSASNKPISNRTRHCOPEKAKKETVEKAVATAPGLGR*				130
A.CI.88.UC2	-----KAP-S-K-Y-P-P-T-MEVAAG-L-KQ-L-A-H-----P-T-P-----SF-L-L-----W-VKGG-----RT-THPP-TPD-S-IQ-GDSR-T-KQ--P-TP--TS-----				131
A.DE.x.BEN	-----KAP-S-KPY-P--T-R-VTAQ-L-KQ-L-A-H-----P-T-K-----R-SF-L-L-S-----S-RKGR-----R-T-TPSP-PD-S-T-GDS-T-EQ-K-S-AT-V-TC--Q-----				131
A.DE.x.PET2	-----SKAP-S-M-C-P--T-Q-VKSO-L-KQ-RL-----Q-----N-P-----L-----RKGR-----HS-----D-S-T-GNS-T-KQTK-P-T-LE-R--Q-----				131
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A.IN.95.CR1K 147	-NERAD--G-QRK--R-----Q--S--N-R--Q--L-I-T--S-T--ANS-V-QT--G-T-OEL--HP--SQ--LAET			100
A.IN.x.NNVA	-TERAG--GPERK--R-----Q--R--N-R--Q--I-I--S-T--A-S-V-QT--G-T-OEL--HP--SQ--LAEA			100
A.SN.85.R0D	-NERAD--G-QRK--R-----Q--S--N-R--KQ--R-I--S-T--A-S--QT--H--G-T-OEL--HL--SQ--LAET			100
B.CI.88.UC1	-TTR-KD..Q-G--L-----QT--S--N-R--K--GL-I--R-LS-S-EE--V-R--E-TV-DL-N--S--TA-AFTCIPPVWDQLVPRSNPSSNEGCERDS			150
B.CI.89.pPRD320-20HIV2_56	-TTR-KD..Q-G--L-----QA--S--N-R--K--GL-I--R-S-S-EE--V-R--E-T-DL-N--S--TT-AFACIPPVWDQLAPRSNPSSNEGCGRDS			150
B.CI.x.EH0	-NAR--D..Q-G--L-----Q--S--N-R--KQ--GL-I--HPL-S-EG--R--I-KDL-N--S--TA-ASTCIPPIWDQLVPRSNPSSSQGGRDS			150
B.GH.86.D205	-TAR-GD..Q-E--L-----Q--S--N-R--K--GL-I--H--STA-AEE--N--R--TV-DL-N--P-LNOSP--TT-APGCVPPVWDQLVPRSNPSSSQGGRDS			153
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MAC.US.x.80035	-S-----S-----R-----K-----			107
MAC.US.x.97074	-S-----S-----R-----K-----			107
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MAC.US.x.r80025	-RS-TG--R-----S-S--KR--Q--I--LRRIR--A--			107
MAC.US.x.r90131	-RS-TG--R-----S-S--KR--Q--I--LRRIR--A--			107
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SMM.US.x.F236_H4	-ST-E--R-----F--Q--R--R--Q--I--V--G--EL--SA--P-N-VAKSP--			100
SMM.US.x.PBJ14_15	T-SNGE--R-----S--D--R--R--Q--I--V--R--EL-N-ASA--P-K-AA-SP--			100
SMM.US.x.PBJA	-SN-E--R-----D--R--R--Q--I--V--R--EL-N-ASA--P-K-AA-SP--			100
SMM.US.x.PBJ_6P6	-SN-E--R-----D--R--R--Q--I--V--R--EL-N-ASA--P-K-AA-SP--			100
SMM.US.x.PGM53	-SSAG--R-----F--Q--R--R--Q--I--V--A-S--V--D-SL-N--SV--NP--R--			104
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107
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180
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172
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108
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101
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105
101
100

MAC.US.x.239*
A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PEI2 GSGINRETL.....
A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY DRDISKETL.....
A.GM.x.MCN13
A.GM.x.MCR35
A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CR1K_147
A.IN.x.NNVA
A.SN.85.ROD
B.CI.88.UC1
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B.CI.x.EHO
B.GH.86.D205
B.JP.01.KR020 DAVLQEHKGEGRV-
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AB.CM.03.03CM_510_03
G.CI.92.ABT96
U.FR.96.12034
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MAC.US.x.17EFR
MAC.US.x.2065
MAC.US.x.251_1A11
MAC.US.x.251_32H_PJ5
MAC.US.x.251_BK28
MAC.US.x.80035
MAC.US.x.97074
MAC.US.x.MAC239_87082
MAC.US.x.MM142
MAC.US.x.SMM142B
MAC.US.x.r80025
MAC.US.x.r90131
MNE.US.82.MNE_8
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SMM.SL.92.SL92B
SMM.US.x.F236_H4
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SMM.US.x.PBJA
SMM.US.x.PBJ_6P6
SMM.US.x.PGMS3
SMM.US.x.SME543
STM.US.x.STM

[illegible]

MAC.US.x.239
A.CI.88.UC2
A.DE.x.BEN
A.DE.x.PET2
A.GH.x.GH1
A.GM.87.D194
A.GM.x.ISY
A.GM.x.MCR13
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A.GW.86.FG
A.GW.87.CAM2CG
A.GW.x.ALI
A.GW.x.MDS
A.IN.95.CR1K 147
A.IN.x.NNVA
A.SN.85.R0D
B.CI.88.UC1
B.CI.09.pPRD320-20HIV2 56
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B.GH.86.D205
B.JP.01.KR020
G.CI.92.ABT96
AB.CI.90.7312A
AB.CM.03.03CM_510_03
U.FR.96.12034
MAC.US.x.251.1A11
MAC.US.x.251.32H.PJ5
MAC.US.x.251.BK28
MAC.US.x.17EC1
MAC.US.x.17EFR
MAC.US.x.MN142
MNE.US.02.MNE 8
MNE.US.x.MNE027
SMM.SL.92.SL92B
SMM.US.x.F236.H4
SMM.US.x.PB314.15
SMM.US.x.PB3A
SMM.US.x.PB3 6P6
SMM.US.x.PGWS3
SMM.US.x.SME543
STM.US.x.STM

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---N--K--C--D--C--N--R--H--I--A-- 332
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---P--R--S-ED--K--N--SK--N-- 330
---P-G-Q--Q-RQ--R--G--ES--Y--A-N--GS--I-- 332
---P-G--N--R--I--SA--ES-K-H--S-L-A-N--KS--R--E-- 330
---P-V--R--R--NS--ETD-K--S--A-N-T--S--R-- 335
---P-V--R--R--NS--ETD-K--S--A-N-T--S--R-- 335
---P-V--R--R--NS--ETD-K--S--A-N-T--S--R-- 335
---P-V--R--K--R-I--STT.SR--K--A-N--S--S--IR-- 334
---P-G--I--R--I--PA--S-K-Q--S--A--NS-- 332
-E-SLVG--R--S-I--NVT--E--R--L--T--A-N--S-- 328

V3

MAC.US.x.239		FHS..QP.INDRPKQAWCFGGKWKDAKEVKQITVHKPRYT.G.TNNTKINLT.APG.GGDPEVTFWNTNCRGEFLYCKMMWFLNWVEDRNTA.....QKPKQEKHKNRYVPC*HIROINTWHKVGNVYLP*PPREGD*LT*CNSTVTS*LIANDIW...IDGNOTNITMSAE																												485									
A.CI.68.IC2	AV	KK	R	K	N	F	LAG	K	D	G	FV	K	V	S	Y	F	N	T	N	TSOK	Q	A	K	OY	F	E	A	E	I	I	I	DKNRTH	F	476					
A.DI.68.BE1	T	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	477						
A.DE.x.PEI2	R	I	E	R	D	O	F	K	M	L	Q	R	D	O	F	K	M	L	Q	R	D	O	F	K	M	L	Q	R	D	O	F	K	M	L	478				
A.GH.x.GH1	T	R	R	K	R	RE	MO	LI	K	D	KN	F	K	R	S	AY	N	T	N	PNOT	QH	A	K	OY	F	E	A	E	I	I	I	V	NS	F	464				
A.GM.87.D194	R	VY	KK	G	Q	N	IE	MR	LA	G	D	G	F	K	I	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	S	FD	S	F	462			
A.GM.x.XCP1	KL	KK	R	K	R	RE	MO	LI	K	D	KN	F	K	R	S	AY	N	T	N	NKTGOQ	H	A	K	OY	F	E	A	E	I	I	V	DGD	R	F	466				
A.GM.x.MCN13	V	K	R	K	R	RE	MO	E	LA	K	N	RSR	EN	K	F	K	R	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	A	NE	N	D	F	466	
A.GM.x.MCR35	V	K	R	K	R	RE	MO	E	LA	K	N	RSR	EN	K	F	K	R	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	A	NE	N	D	F	466	
A.GW.86.FG	V	KK	R	E	Q	E	MO	E	LA	K	N	RSR	EN	K	F	K	R	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	A	NE	N	D	F	463	
A.GW.87.CAM2CG	R	I	K	R	K	R	RE	MO	LAE	K	I	TD	TFK	ER	S	Y	S	F	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	E	R	NOT	F	D	473		
A.GW.x.ALI1	K	R	K	R	K	R	RE	MO	E	LA	K	N	RSR	EN	K	F	K	R	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	A	NE	N	D	F	463
A.GW.x.MDS	K	R	K	R	K	R	RE	MO	E	LA	K	N	RSR	EN	K	F	K	R	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	A	NE	N	D	F	463
A.IN.95.CR1K 147	R	V	T	R	K	R	MO	K	VAE	AV	KOPKN	TF	K	S	AY	N	T	N	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	NEIDKR	F	D	469				
A.IN.x.NNVA	T	R	R	K	R	E	MO	AE	R	I	E	K	F	K	S	AY	N	T	N	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	NEIDKR	F	D	469			
A.SN.85.R0D	HY	K	R	K	R	MO	E	LA	R	D	R	N	SFA	K	S	AY	N	T	N	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	NEIDKR	F	D	469			
B.CI.88.UC1	L	T	R	K	R	IE	R	E	I	K	ER	R	V	G	S	AY	N	T	N	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	NEIDKR	F	D	469			
B.CI.69.PPRD320-20HIV2 56	R	V	E	R	E	N	IE	MR	E	VM	IK	IT	V	G	S	AY	N	T	N	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	NEIDKR	F	D	469			
B.CI.88.UC1	K	R	K	R	K	R	RE	MO	E	LA	K	N	RSR	EN	K	F	K	R	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	A	NE	N	D	F	463
B.GH.86.D295	K	R	K	R	K	R	RE	MO	E	LA	K	N	RSR	EN	K	F	K	R	S	Y	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	A	NE	N	D	F	463
B.JP.01.KR020	Q	R	R	K	N	TO	E	I	A	D	A	K	A	EHSQ	S	Y	N	T	N	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	NEIDKR	F	D	469			
G.CI.92.ABT96	E	R	R	E	E	MO	E	V	S	K	D	KX	TF	T	E	S	K	T	I	MTL	L	Q	ROR	F	E	A	E	I	I	I	E	E	N	RSN	H	IF	487		
AB.CI.90.7312A	K	R	R	K	R	RE	MO	LI	K	D	RN	TF	K	T	S	AY	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	DVGN	R	F	475				
AB.CM.03.03CM 510 03	R	R	R	R	R	RE	MO	LI	K	D	T	F	K	E	S	AY	N	T	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	DVGN	R	F	475				
U.FR.96.12034	A	NN	N	G	Q	E	AN	H	K	ISQ	A	E	A	S	K	AY	N	T	N	N	TKNTOT	HG	A	K	OY	F	E	A	E	I	I	V	DVGN	R	F	475			
MAC.US.x.251 1A11	R																												484										
MAC.US.x.251 32H PJ5	N																												484										
MAC.US.x.251 BK28	M																												484										
MAC.US.x.17C1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	487					
MAC.US.x.17EFR	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	487					
MAC.US.x.MM142	V	E	R	R	N	E	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	488					
MNE.US.82.MNE 8	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	493			
MNE.US.x.MNE627	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	E	R	E	N	E	493			
SMM.SL.92.SL92B	E	R	E	R	RE	MO	K	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	493				
SMM.US.x.F236 H4	E	R	E	S	K	Q	E	L	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	493					
SMM.US.x.PBJ34 15	E	R	E	S	K	Q	E	L	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	493					
SMM.US.x.PBJ34	E	R	E	S	K	Q	E	L	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	493					
SMM.US.x.PBJ 6P6	E	R	E	S	K	Q	E	L	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	493					
SMM.US.x.PGMS3	E	R	E	S	K	Q	E	L	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	493					
SMM.US.x.SME543	E	R	E	S	K	Q	E	L	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	R	D	493					
STM.US.x.STM	E	R	E	R	E	RG	E	L	D	A	RIV	D	A	RIV	D	A	RIV	D	A	RIV	D	A	RIV	D	A	RIV	D	A	RIV	D	A	RIV	D	A	493				

MAC.US.x.239	VAELYRL	EGDYKLV	ITPIGLAPT	DKRYTTGGTS	RNRKGVFLGFLG	FLATAGSAMGAAS	LT	TAQSRTLLAGIV	QOQQQLLDVVKRQ	QELLRLTVWG	TKNLQTRVTAIE	KYLKDQAQLNAWG	CAFRQVCHTTVPW	PNASLTPKMNNETWQEWERKVD	FLEENI	651
A.CI.88.UC2	I	F	SE	SSA	PA	L	S	I	A	S	T	V	D	R	M	641
A.DE.x.BEN	I	F	QR	SST	PV	R	S	M	A	D	H	S	V	D	S	636
A.DE.x.PET2	I	F	SE	SSA	PQ	V	S	HPGLYW	M	R	R	S	Y	L	E	629
A.GH.x.GH1	I	V	F	RE	SSA	PV	S	M	A	S	D	S	V	D	S	628
A.GM.87.D194	I	V	PF	KE	SSA	PV	S	M	A	S	D	S	V	D	S	627
A.GM.x.ISY	V	F	AE	SSA	PG	H	L	T	A	FR	A	R	S	V	DT	629
A.GM.x.MCN13	V	F	AE	SST	PM	S	M	A	S	D	S	S	V	DT	E	631
A.GM.x.MCR35	F	AE	SST	PM	S	M	A	S	D	S	S	S	V	DT	E	631
A.GW.86.FG	F	S	SSA	HQ	HT	S	M	A	S	D	S	S	V	DT	D	628
A.GW.87.CAM2CG	F	SQ	SPA	HG	P	A	T	V	T	A	S	I	A	E	D	638
A.GW.x.ALI	F	SER	SST	PR	S	M	A	S	D	S	R	S	V	N	K	634
A.GW.x.MDS	F	PE	SSA	HG	H	T	A	S	M	A	S	S	V	S	E	648
A.IN.95.CR1K 147	V	V	F	SE	SS	#	G	HT	L	E	T	P	V	D	D	639
A.IN.x.NNVA	D	F	PE	SFA	SR	QT	D	S	P	M	A	A	DS	E	DT	636
A.SN.85.R0D	F	KE	SSA	HG	HT	VS	P	M	A	Q	R	S	V	D	A	637
B.CI.88.UC1	G	F	EI	SST	P	M	L	M	T	S	L	S	ET	D	E	640
B.CI.09.pPRD320-20HIV2 56	G	F	NI	SSA	P	R	M	S	A	S	L	S	E	N	TDM	630
B.CI.x.EH0	S	K	F	SI	SSV	P	L	S	V	A	S	S	V	E	K	635
B.GH.86.D205	S	F	R	SSV	KP	M	T	S	PV	A	S	S	ET	N	M	639
B.JP.01.KR020	S	F	S	SSA	P	P	S	S	A	L	S	S	KNF	N	D	628
G.CI.92.ABT96	F	N	SSV	PK	M	T	S	M	R	S	R	S	DALGA	KT	E	656
AB.CI.90.7312A	I	V	F	SE	SST	PG	H	T	A	S	M	A	S	V	D	640
AB.CM.03.03CM_510_03	I	F	TEG	SST	PG	S	M	A	X	S	X	S	V	E	N	629
U.FR.96.12034	R	F	P	SSV	P	S	M	S	I	DT	N	D	M	E	NY	646
MAC.US.x.251 1A11	N	R	L	S	D	D	650									
MAC.US.x.251 32H PJ5	N	R	L	S	D	D	650									
MAC.US.x.251 BK28	N	R	L	S	D	D	653									
MAC.US.x.17EC1	N	R	L	S	D	D	651									
MAC.US.x.17EFR	N	R	L	S	D	D	651									
MAC.US.x.MN142	N	R	L	S	D	D	654									
MNE.US.82.MNE 8	N	R	L	S	D	D	653									
MNE.US.x.MNE027	N	R	L	S	D	D	654									
SMM.SL.92.SL92B	M	H	S	K	S	L	D	V	D	M	K	E	A	658		
SMM.US.x.F236 H4	I	S	R	T	A	V	S	ET	V	N	M	O	A	657		
SMM.US.x.PB314 15	AF	S	T	A	V	S	A	DT	N	M	KO	N	A	661		
SMM.US.x.PB3A	AF	S	T	A	V	S	A	DT	N	M	KO	N	A	661		
SMM.US.x.PB3 6P6	F	S	T	A	V	S	A	DT	N	M	KO	N	A	661		
SMM.US.x.PGM53	S	R	A	V	S	R	S	V	N	M	Q	D	A	660		
SMM.US.x.SME543	R	T	A	S	H	R	S	D	V	N	D	M	G	A	659	
STM.US.x.STM	N	S	T	T	S	T	S	D	V	D	M	A	654			

MAC.US.x.239	TALLEEAQIQQEKMYELQKLNWDVFGNWFDLASWIKYIQYGVYIVGVILLRIVYIVQMLAKLRQGYRVPVFSSPPSYFQQTTHIQDDPALPTREGKRDGGEGGGNSWPQIEYIHFLIRQLIRLLTWLFSNCRITLSRVYQILOPILQRLSATLQRIEVLRTLT	821
A.CI.88.UC2	SQS-----T-----I-A--A-V--L-SRF-K-----G-L-I-HT-RGQ-AN-ET-G-A-DAS-YDF--P-N-QL--HL-T--G-Y-I-D--ANSPTRRL-S-N-...TA--DW--LKAA	807
A.DE.x.BEN	SQS-----IL-----T-V-----H--I-A--A-V--L-SRF-K-----G-L-I-HK-RGQ-AN-ET-E-V-GDS-YDL--P-N-VQ--HL-T--IG-YNI-D--KNSPTRRL-S-S-...TA--DW--LKAA	802
A.DE.x.PET2	SRS-Q-----VII-I-A--V--L-SR-K-----G-I-I-HK-WEQ-D-ETDE-A-NSI-D--P-A-----G-Y-V-KD--SFPT--L-F-S-ORA-TT--DW--LTAA	799
A.GH.x.GH1	SQS-Q-----T-----V-A--L-SR-K-----G-L-I-HT-RGQ-AN-ET-E-DRDDD-YDL*-P-N-----HL-T--G-YKI-D--TNSPTRL-S-N-...TA--DW--LKAA	793
A.GM.87.D194	SQS-Q-----T-----I-G-A--L-SR-K-----G-L-I-HT-RGQ-AN-ET-E-A-DDS-FGL--PLN-Q--HL-T--G-YNS-G--KNSPTRRL-S-S-...TA--DW--LKAA	793
A.GM.x.ISY	SES-Q-----T-----M--I-VA--V--SR-K-----G-I-I-HK-WEQ-D-ET-E-V-NDV-SR--P--L-----L-L-----L-DW--LKAA	788
A.GM.x.MCN13	S00-Q-----T-----II-IVV--SR-K-----G-L-I-HK-WEQ-A-ET-E-V-NNV-D--P-R--H--AG-YNI-N--ISLT-R-VF-S-ORA-TA--DW--DAA	801
A.GM.x.MCR35	S00-Q-----S-----II-IVV--SR-K-----G-L-I-HK-WEQ-A-ET-E-V-NNV-D-L*-P-R--H--G-YNI-N--ISLT-R-AF-S-ORA-TA--DW--DAA	800
A.GW.86.FG	SQS-Q-----T-L-FT--VR--V--I-VA--SR-K-----G-I-I-HK-QEQ-A-ET-E-V-SN--DR--P-A-----L--G-YNI-D--ISP--F-S-ORA-TA--DW--LKAA	798
A.GW.87.CAM2CG	SQS--L-----N-----T--S-----I-V--V--SR-K-----S-G-I-I-HK-EQ-AS-ET-E-V-GN--DR--G-YNI-N--IF-T--N--DW--PKVA	801
A.GW.x.ALI	SEQ-R-----T-----T--L-TA-V-----I-IVA--V--SR-K-----G-I-I-HK-QEQ--GET-E-V-DNV-DRL--P-A-L-----HL-A--IG-Y-I-D--ISP--FRS-ORA-TT--DW--LKAA	804
A.GW.x.MDS	S0K-Q-----Q-----I-----T-----I-V--V--SR-K-----G-I-I-HK-REQ-D-ET-E-V-GN--DR--P-A-----L--R-YNS-D--IFLT--F-N-----DQ--LRTA	811
A.IN.95.CR1K 147	SQS-Q-----S-----T-----C-----I-V--V--SR-K-----G-I-I-HK-LEQ-A--I-E-V-DN--YR*-P-A-----HL--R-YNS-KD--SFLT--N-----DW--LKTA	801
A.IN.x.NNVA	SQS-Q-----I-----T-----I-A-V--V--L-CSF-K-----G-I-I-HK-QEQ-D--T-E-V-DN--YR--P-A-----LL--R-YNS-KD--SFLT--N-----DW--LRTA	799
A.SN.85.R0D	SKS-Q-----I-----T-V-----L-I-A-A--V--SR-K-----G-I-I-HK-RGQ-AN-ET-E--SN--DRY--P-A-----R-Y-I-D--SFLT--L-Y-N-----DW--LRTA	800
B.CI.88.UC1	-----R-----FT--MA--RL-L-V-A-L-V-----M--R-K-----T-IP-RKHRGQ-AN-ET-DE-NE-AYR-----A-----RN-I-YNG-N-LKTS--A-----QP--LS-A	799
B.CI.09.pPRD320-20HIV2_56	-Q-----H-----S-----FT--MA--RL-L-V--L-V-----VI--R-K-----T-IP-HKHRGQ-AN-ET-DE-RE-DYR-----A-----RN-I-YNG-N-L-TS--A-----QP--LS-A	789
B.CI.x.EH0	-K-----Q-I-S-----FT--MA--RL-L-I-IVV--A--I--R-K-----T-IP-RK-RGQ-AN-ET-EG--NNE-YR-----P--RD-I-Y-G--KTF-T--V-----OP--LPPA	794
B.GH.86.D205	-K-----E-----K-----Q-----S-----FT--A--I-L-VI-LVV--V--L-R-K-----V-IP-HKGQGR-AS-ET-EG-DDDYR-----R-----RN-I-YNS-S-LKIF-P-LVF-----QP--LP-A	801
B.JP.01.KR020	-R-----Q-----T-V--VYL-L-V-A--V-----V-I-GR-----X-----V-I-RK-QEX-K-EI-GES-NK--YR-----X--GN--Y--A--IX-T--LF--I-R--A--H--LA	826
G.CI.92.ABT96	SES-Q-----V-----IVA--VI--V--IGR-R-----G-----IR-HK-QEQ-AN-ET-EG--ND--YR-----RN--I-YDG-----LKTf-T--A-----QP--LLFA	799
AB.CI.90.7312A	S0I-Q-----S-----T-----R-----A-VV-X-A--XSR-K-----SG-V-I-HT-QGQ--S-ET-EG--ND-DYR-----V--L--RN-I-YNG--LKTS-----P--LPFA	788
U.FR.96.12034	-Q--A-----N-I-----T-V--VYL-L-V-A-I-I-----V-L-GS-K-----H--VE-IP-R-QEQ-KGEI-EGA-DS--YR-----R-----H-----Y-S-D--IC-S--LF-SI-----R-H-LA	809
MAC.US.x.251.1A11	-----I-V-----V-----*-----T-----G-----A-----R-V-----	819
MAC.US.x.251.32H.PJ5	-----N-----T-----I-I-----R-----T-----K--KG--GS-----A-----F--F-T-----L-----	820
MAC.US.x.251.BK28	-----N-----T-----I-I-----R-----T-----K--KG--GS-----A-----F--F-T-----L-----	821
MAC.US.x.17EC1	-----N-----T-----I-I-----R-----T-----K--KG--GS-----A-----F--F-T-----L-----	821
MAC.US.x.17EFR	-----N-----T-----I-I-----R-----T-----K--KG--GS-----A-----F--F-T-----L-----	820
MAC.US.x.MN142	-----R-----R-----R-Q--K--T-G--GS-----A-----F--F-T-----V-----	823
MNE.US.82.MNE.8	-----R-----R-----R-Q--K--T-G--GS-----A-----F--F-T-----V-----	822
MNE.US.x.MNE027	-----R-----R-----R-Q--K--T-G--GS-----A-----F--F-T-----V-----	824
SMM.SL.92.SL92B	-QM--RL-----T--VR--FL-I-IV--V--SR-----H-I--R-QE-AK--T-GE-N--YRL-----I--YN-LTR-A-A-N--QLC--EIS-P--LV-R-AG	828
SMM.US.x.F236.H4	-Q-----I-----T--R--L-L-G--V--R-----A-V-IP-HKGQEP-K-E-G--DR-SR-----S--DW-L-S--V-S--T--V--I-I-TA	827
SMM.US.x.PBJ14_15	-OS-----T-----I-----T--R--L-L-G--V--R-----A-V-VP-TGQE-K-E-G--GR-R-----S--DW-L-NC-T--V-S-R--A--I-VQIA	831
SMM.US.x.PBJA	-OS-----T-----I-----T--R--L-L-G--V--R-----A-V-IP-TGQE-K-E-G--GR-R-----S--DW-L-NC-T--V-S-R--A--I-VQIA	831
SMM.US.x.PBJ.6P6	-OS-----T-----I-----T--R--L-L-G--V--R-----A-V-IP-TGQE-K-E-G--GR-R-----S--DW-L-NC-T--V-S-R--A--I-VQIA	831
SMM.US.x.PGM53	-QA-----I-----T--R--L-L-VG--V--R-----P-A-V-IP-HKGQEP-K-E-GE-DR-SR-----N--Y-L-I--VF-----V--IS	827
SMM.US.x.SME543	-Q-----I-----T--R--L-L-VG--V--R-----P-A-V-IP-HKGQEP-K-E-GE-DR-SR-----N--Y-L-I--VF-----V--IS	829
STM.US.x.STM	-Q-----V-----T--VR--L-I-LVM--VA--M-L--R-K-----CR-IP-HKGQEQ-K-T-EG--DR--IN-----T-----V-----YN-F-AC--I-T-H-TF--I-RI-----V-LGAA	824

HIV-2/SIV Proteins

	Nef start	R17Y mutation	premature stop in Mac239	max HIV-1 similarity
MAC.US.x.239	MGGATSMRRSPSGDLRQRLLRARGETYGRLLGEVEDGYSQSGGLDKGLSSLS	SC.EGQK..YNOGQYMNTPWRNPAEEREKLAYRKONMDDIDE-DDD.LVGVSVR.PKVPLRTMSYKLAIDMSHF	IKKEGGLEGIIYSARRHRILDIYLEKEEGIIPDWQDYTS	SGPGI 164
A.CI.88.UC2	--ASG-KKL-KQ-QG-E-----GG-V-QCSASGGES--Q-SGREQK-P-----Q-R-D-----T-M-GQ-ES-KQ-----V-SD-N-Q-----T-SR--P-T-----V-----MF-RD-----L-----V-----N-H--V	165		
A.DE.x.BEN	--ASG-KKL-KH-RG-E-----DG-KQRDASGGE--FOEESGREON-P-----Q-Q-E-S-----T-Q-DL-Q-----V-SD-----I-P-T-R-R-E-T-----Q-MF-R-----N-H--V	165		
A.DE.x.PET2	--ASG-KKC-SLQG-E-----C-GQWDGSGAGE-L-FOE-SGR-QNLP-----R-Q-DF-----T-AG-GTL-KQ-----V-ADN-N-I-P-T-R-A-T-----V-I-LN--D-M-E-----M-----N-H--V	165		
A.GH.x.GH1	--ASG-KKH-KH-QR-E-----H-GG-VQOCNASGGE--QE-SG-QK-P-----Q-R-DF-----T-I-GQ-KL-KQ-----SS-----P-T-R-A-T-----V-----KR--D-MF-RD-----L-----N-H--V	164		
A.GM.87.D194	--ASG-KK-EH-QG-E-----GG-VKQRNASGGES--QE-SGREQK-P-----Q-Q-EF-----T-AIGQ-NS-KQ-----V-SD-----P-M-R-E-T-----F-RE-----LF-----N-H--V	165		
A.GM.x.ISY	--ASG-KK-----RG-QE-----GAC-G-WD-S-G--FHE-SGREOKLP-----R-Q-DF-----T-T-K-ES-Q-----V-SD-----DT-SR--A-T-RM-V--DL-D--M-E-----M-----N-H-L-V	165		
A.GM.x.MCN13	--ASG-KE-----QG-E-----C-GHCSGSGGE-L-QEESGREOR-P-Y-----R-Q-DF-----T-K-G-EL-KQ--R-V-SD-----T-R-----ELTHR--V-----M-E-----A--H--	165		
A.GM.x.MCR35	--ASG-KE-----QG-E-----C-GHCSGSGGE-L-QEESGREOR-P-Y-----R-Q-DF-----T-K-G-EL-KQ--R-V-SD-----K-T-R-----E-THR-----M-E-----K-----N-H--	164		
A.GW.86.FG	--ASG-KK-K-LQG-QE-Q-----C-GRCN-SGG--L-HE-SGREON-P-----R-Q-DFV--T-A--EL-KQ--V-LD--Q-FP-T-R--P-TF--V-----LF-Q-----L-D-----A--N--V	148		
A.GW.87.CAM2CG	--ASG-KK-----LQG-QE-----AG-C-ECYNAL-GESLR-QE-S-REON--R-Q-DF-----A-A-GK-N-Q-----SD-----PAT-R-----T-----V-----LF-E-----L-D-----A--N--V	165		
A.GW.x.ALI	--ASG-KK-G-LQG-E-----QTP--C-GQCSGSGG--Q-SGR-QKLP-----R-Q-DF-----T-T--EL-KQ--V-LD--S--Y-T-RT--A-T--V-----L-R-----MF-E-----N-H--	166		
A.GW.x.MDS	--ASG-KK-----RG-QE-----AGAC-GHMD-LGGE-R-QE-S--QR-P-----Q-Q-DF-----T-T-G-DS-Q--V-SD-----Y-T-RT--A-T--V-----MF-E-----N-H--	165		
A.IN.95.CR1K 147	--ASG-KKH-K--RG-E-----QA-CVGQWK-LGGE--QE-S--QR-P-----Q-Q-DF-----T-T-KG-DL-Q--V-SD-----T-R-----T-RM-----L-----MF-E-L-#-----N-H--	139		
A.SN.85.RDD	--ASG-KKH--PRG-QE-----AGAC-GYWN-SGGE-RFQE-S-REQK-P-----RQ-Q-DF-----KD-A--NL-Q--V-SD--Q-R-T-----P-THR--L-TR--MF-E-K-N-----A--N-H--V	165		
AB.CI.90.7312A	--S-G-KKQ-KQQRG-E-----Q-GP--S-SRRGES--EES-R-N-P-----TA-GA-GGG--Q-DIEE--DDE-N-E--Y--Q--P-T-----F-E-----T-F-N-R--VGG--N-Y--	147		
AB.CM.03.03CM_510_03	--S-G-KK-EQQRG-E-----V-ERP-K-S-GRRERS-R--EES-D-N-P-----NALGA-GGG--Q-A-ES--D-E--AY--SR--P-T-T-----L--D--E-----T-F-N--VSG--N-H--	146		
B.CI.88.UC1	--S-G-KKQ-KQQRG-E-----TQE-P-K-SEGQRKQS-R--S-D-N-P-----R-----NA-RA-GGG--Q-DT--SDE-N-E--Y--NR--S-T-M-----E-----T-N--VSG--N-Y--	147		
B.CI.x.EH0	--S-G-KKQ-KQQPG-E-----RGPR-ESS--RQERSL-Y--S--N-P--D-----KTLGA-GGG--DS-E--DDE-N-E--R--G--P-TF--V--L--E--F-E-K-T-N--VSG--N-H--V	147		
B.GH.86.D205	--S-G-KK-ERQOG-EK--VPERP--S--RREOS-R--ES-D-N-P-----NARGA-GGG--Q-DA-E--SDE-E-AICKT-I--P-T--V--Q--M-E-----T-F-N--VSG--N-H--	148		
B.JP.01.KR020	--S-G-KKQ-KQRRG-E-----QTQEGP--SE-QRGQS-R--S--DSN-P-----R-----SA-GAQGGG--Q-GIE--SDE-N-E--Y--NR--P-T-----W-----E-L-T-N--VSG--N-H--V	147		
G.CI.92.ABT96	--S-G-KK-APQQLG-K-Q--P-K-WEGL-E-----YREESG--Q--T-F-----T-A--X-N-V-SD-N--P-Y--V-----E-----M-Q--N-A--	165		
U.FR.96.12034	--S-KKH-KR-K-E-A--N--W-GL--FELYQ-SG-D--RF--A-GQG-SE-EF-----T-TGKD-Q-KQ--V-E-N--A--R-A--T--V-----D-F-Q-----N-----N--T	167		
MAC.US.x.17EC1	-----S-----G-----K-----Q-----I-----K-----	165		
MAC.US.x.17EFR	-----S-----G-----K-----Q-----EX-----T-----A-----I-----K-----	165		
MAC.US.x.1937	-----XX-----X-X-----X-----E-----E-----T-----A-----T-----	165		
MAC.US.x.2065	-----T-----ST-----E-----S-----L-E-----E-----E-----P-M-R-----A-T-----V-----M-----I-H-----	165		
MAC.US.x.251.1A11	-----R-----KSA-----K-----L-----G-----R-----E-----K-----P-----I-----IP-E-AR-----X-----	165		
MAC.US.x.251.32H.PJ5	-----K-A-----K-----N-----FKG-----S-----L-----G-----R-----E-----K-----P-----I-----IP-E-AR-----X-----	165		
MAC.US.x.251.BK28	-----KK-K-PR-----N-----FKG-----S-----L-----G-----R-----E-----K-----P-----I-----IP-E-AR-----X-----	165		
MAC.US.x.MM142	-----T-K--KSP-----WE-L-----L-S--S-L-----F--K--G-----I--E-N--P--R--II--V-----E-K-M-----M--N--P	165		
MAC.US.x.r80025	-----T-KK-KSP-----WEGL-----L-S--S-L-----F--K--G-----I--E-N--P--R--II--V-----E-K-M-----M--N--P	165		
MAC.US.x.r90131	-----IT-SKPA-KH-----KK-S--DS--WDGL-E-SQ--Q-S-RA-N-CLTRD-Y--V-EF-----T-Q-QQ-Q-C--D-E-A-V-W--A-----D-E-----N-----	166		
MNE.US.82.MNE 8	-----KKQYKRG-N-E-Q--D--WEGL-GE--QDASG-----P--CE-F-----T-A-D-Q--V-SA--CP-S-R-V-I-T-----D-K-L-----N-A--	163		
MNE.US.x.MNE027	-----VT-KKQ-RG-N-YE-Q--D--WEGL-GE--QDASG-----P--CE-F-----T-A-D-Q--V-SA--CP-S-R-V-I-T-----D-K-L-----N-A--	163		
SMM.SL.92.SL92B	-----VT-KKQ-RG-N-YE-Q--D--WEGL-GE--QDASG-----P--CE-F-----T-A-D-Q--V-SA--CP-S-R-V-I-T-----D-K-L-----N-A--	163		
SMM.US.x.F236.H4	-----A-G-KKQ--QR-G-GEK-Q--H-K-WEGL-----R-E-GRDWNH-L-F--G--SE-F-----R--K-Q--V-DD-E-I--H--A-----E-----T-----N-----	165		
SMM.US.x.PBJ14_15	-----KKQH-RG-N-E-----WEGL-E-----L-ASG-----P--SE-----TA-KA-G-Q--V-DE--H--A-----A-----NEK-----M-M-----N-L--T	165		
SMM.US.x.PBJ 6P6	-----ASG-KKQRKQH-E-E-----K--EGLGE-SGP-Q-AS--N-H--P-R--E-F--K--A-SA-E-Q--V-E-N--A-H-R--E-T-----L--S-----E-----M-----V--N-A--	165		
SMM.US.x.PGM53				
SMM.US.x.SME543				
STM.US.x.STM				

VII

PLV Proteins

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VII-1 Introduction

The selection of Primate Lentivirus Protein sequences for the following alignments was based on the sequences in the complete genome alignment as a starting alignment, and complete or nearly complete genes from other isolates were added if they increased the diversity of samples represented. For example, several diverse African green monkey virus isolates have been sequenced only in a region of the *env* gene, and recent Gorilla sequences are only available in the *pol* and *env* genes. When necessary, some of the more common sequences (such as HIV-1 M group) were removed to make room on the Compendium pages for these diverse virus sequences. More complete alignments are available from our web site <http://www.hiv.lanl.gov/content/sequence/NEWALIGN/align.html> where space limitations are not an issue.

The annotation is mainly based on knowledge from HIV-1, and should therefore be taken with a grain of salt for HIV-2 and SIV sequences.

VII-2 Sequences

Sequences included in the PLV protein alignments.

Name	Accession	Proteins	Author	Reference
H1B.FR.83.HXB2	K03455	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	van Beveren, C.P.	(in) Weiss,RL, Teich,N, Varmus,H and Coffin,J(Eds); RNA TUMOR VIRUSES, SECOND EDITION, 2, Vol 2: 1102-1123; Cold Spring Harbor Laboratory, Cold Spring Harbor (1985)
H1A1.UG.85.U455	M62320	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Oram, J.D.	ARHR 6(9):1073-1078 (1990)
H1B.US.90.WEAU160	U21135	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Wei, X.	Nature 422(6929):307-312 (2003)
H1C.ET.86.ETH2220	U46016	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Salminen, M.O.	ARHR 12(14):1329-1339 (1996)
H1D.CD.84.84ZR085	U88822	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Gao, F.	J Virol 72(7):5680-5698 (1998)
H1F1.BE.93.VI850	AF077336	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Laukkanen, T.	Virology 269(1):95-104 (2000)
H1G.SE.93.SE6165	AF061642	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Carr, J.K.	Virology 247(1):22-31 (1998)
H1H.CF.90.056	AF005496	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Gao, F.	J Virol 72(7):5680-5698 (1998)
H1J.SE.93.SE7887	AF082394	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Laukkanen, T.	ARHR 15(3):293-297 (1999)
H1K.CM.96.MP535	AJ249239	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Triques, K.	ARHR 16(2):139-151 (2000)
H101_AE.TH.90.CM240	U54771	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Carr, J.K.	J Virol 70(9):5935-5943 (1996)

Name	Accession	Proteins	Author	Reference
H102_AG.NG.x.IBNG	L39106	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Howard, T.M.	<i>ARHR</i> 10 (12):1755-1757 (1994)
H103_AB.RU.97.KAL153_2	AF193276	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Liitsola, K.	<i>ARHR</i> 16 (11):1047-1053 (2000)
H104_cpx.CY.94.CY032	AF049337	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Gao, F.	<i>J Virol</i> 72 (12):10234-10241 (1998)
H1N.CM.95.YBF30	AJ006022	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Simon, F.	<i>Nat Med</i> 4 (9):1032-1037 (1998)
H1O.BE.87.ANT70	L20587	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Vanden Haesevelde, M.	<i>J Virol</i> 68 (3):1586-1596 (1994)
H1O.CM.91.MVP5180	L20571	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Gurtler, L.G.	<i>J Virol</i> 68 (3):1581-1585 (1994)
H1P.FR.06.RBF168	GQ328744	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Plantier, J.-C.	<i>Nat Med</i> 15 (8); 871-2 (2009)
CPZ.CM.01.SIVcpzCAM13	AY169968	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Nerrienet, E.	<i>J Virol</i> 79 (2):1312-9 (2005)
CPZ.CM.05.SIVcpzEK505	DQ373065	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Keele, B.F.	<i>Science</i> 313 (5786):523-526 (2006)
CPZ.CM.05.SIVcpzLB7	DQ373064	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Keele, B.F.	<i>Science</i> 313 (5786):523-526 (2006)
CPZ.CM.05.SIVcpzMB66	DQ373063	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Keele, B.F.	<i>Science</i> 313 (5786):523-526 (2006)
CPZ.CM.05.SIVcpzMT145	DQ373066	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Keele, B.F.	<i>Science</i> 313 (5786):523-526 (2006)
CPZ.CM.-.SIVcpzMB897	EF535994	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Heuverswyn, F.V.	<i>Virology</i> 368 (1):155-171 (2007)

Name	Accession	Proteins	Author	Reference
CPZ.CM.-.SIVcpzDP943	EF535993	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Heuverswyn, F.V.	<i>Virology</i> 368 (1):155-171 (2007)
CPZ.CM.98.CAM3	AF115393	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env	Corbet, S.	<i>J Virol</i> 74 (1):529-534 (2000)
CPZ.CM.98.CAM5	AJ271369	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Muller-Trutwin, M.C.	<i>J Med Primatol</i> 29 (3-4): 166-72 (2000)
CPZ.GA.88.GAB1	X52154	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Huet, T.	<i>Nature</i> 345 (6273):356-359 (1990)
CPZ.GA.88.GAB2	AF382828	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Bibollet-Ruche, F.	<i>ARHR</i> 20 (12):1377-1381 (2004)
CPZ.US.85.CPZUS	AF103818	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Gao, F.	<i>Nature</i> 397 (6718):436-441 (1999)
CPZ.CD.90.ANT	U42720	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Vanden Haesevelde, M.M.	<i>Virology</i> 221 (2):346-350 (1996)
CPZ.TZ.00.TAN1	AF447763	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Santiago, M.L.	<i>J Virol</i> 77 (3):2233-2242 (2003)
CPZ.TZ.2001.TAN2	EF394357	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Takehisa, J.	<i>J Virol</i> 81 (14):7463-7475 (2007)
CPZ.TZ.2002.TAN3_1	DQ374658	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Takehisa, J.	<i>J Virol</i> 81 (14):7463-7475 (2007)
GOR.CM.2007.SIVgor2139_287	FJ424866	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Takehisa, J.	<i>J Virol</i> 83 (4):1635-1648 (2009)
GOR.CM.2007.SIVgorCP2135con	FJ424863	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Takehisa, J.	<i>J Virol</i> 83 (4):1635-1648 (2009)
GOR.CM.2004.SIVgorCP684con	FJ424871	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Takehisa, J.	<i>J Virol</i> 83 (4):1635-1648 (2009)

Name	Accession	Proteins	Author	Reference
H2A.DE.x.BEN	M30502	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Kirchhoff, F.	<i>Virology</i> 177 (1):305-311 (1990)
H2A.GW.x.ALI	AF082339	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Azevedo-Pereira	Unpublished
H2A.SN.x.ST	M31113	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Kumar, P.	<i>J Virol</i> 64 (2):890-901 (1990)
H2B.CI.x.EHO	U27200	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Rey-Cuille, M.A.	<i>Virology</i> 202 (1):471-476 (1994)
H2B.GH.86.D205	X61240	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Dietrich, U.	<i>Nature</i> 342 (6252):948-950 (1989)
H2G.CI.92.ABT96	AF208027	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Brennan, C.A.	<i>ARHR</i> 13 (5):401-404 (1997)
H2U.FR.96.12034	AY530889	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Damond, F.	<i>ARHR</i> 20 (6):666-672 (2004)
SMM.SL.92.SL92B	AF334679	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Chen, Z.	<i>J Virol</i> 70 (6):3617-3627 (1996)
SMM.US.x.H9	M80194	Gag, Pol, Vif, Vpx, Vpr, Tat	Courgnaud, V.	<i>J Virol</i> 66 (1):414-419 (1992)
SMM.US.x.PGM53	AF077017	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Novembre, F.J.	<i>J Virol</i> 72 (11):8841-8851 (1998)
SMM.US.x.SIVsmH635F_L3	DQ201172	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Kuwata, T.	<i>J Virol</i> 80 (3):1463-75 (2006)

Name	Accession	Proteins	Author	Reference
MAC.US.x.239	M33262	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Kestler, H.	<i>Science</i> 248 (4959):1109-1112 (1990)
MAC.US.x.251_1A11	M76764	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Marthas, M.L.	<i>J Med Primatol</i> 18 (3-4):311-9 (1989)
MAC.US.x.251_BK28	M19499	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Hirsch, V.	<i>Cell</i> 49 (3):307-319 (1987)
MAC.US.x.EMBL_3	Y00295	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Franchini, G.	<i>Nature</i> 328 (6130):539-543 (1987)
STM.US.x.STM	M83293	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Novembre, F.J.	<i>Virology</i> 186 (2):783-787 (1992)
MNE.US.x.MNE027	U79412	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Kimata, J.T.	<i>J Virol</i> 72 (1):245-256 (1998)
DEB.CM.99.CM40	AY523865	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)
DEB.CM.99.CM5	AY523866	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)
DEN.CD.x.CD1	AJ580407	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Dazza, M.C.	<i>J Virol</i> 79 (13):8560-8571 (2005)
LST.CD.88.447	AF188114	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Beer, B.E.	<i>J Virol</i> 74 (8):3892-3898 (2000)
LST.CD.88.485	AF188115	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Beer, B.E.	<i>J Virol</i> 74 (8):3892-3898 (2000)

Name	Accession	Proteins	Author	Reference
LST.CD.88.524	AF188116	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Beer, B.E.	<i>J Virol</i> 74 (8):3892-3898 (2000)
LST.KE.x.lho7	AF075269	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Hirsch, V.M.	<i>J Virol</i> 73 (2):1036-1045 (1999)
SUN.GA.98.L14	AF131870	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Beer, B.E.	<i>J Virol</i> 73 (9):7734-7744 (1999)
MND-1.GA.x.MNDGB1	M27470	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Tsujimoto, H.	<i>Nature</i> 341 (6242):539-541 (1989)
OLC.CI.97.97CI12	FM165200	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Liegeois, F.	<i>J Virol</i> 83 (1):428-439 (2009)
WRC.CI.97.97CI14	AM745105	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Liegeois, F.	<i>J Virol</i> 83 (1):428-439 (2009)
WRC.CI.98.98CI04	AM713177	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Liegeois, F.	<i>J Virol</i> 83 (1):428-439 (2009)
WRC.GM.05.Pbt_05GM_X02	AM937062	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Locatelli, S.	<i>Virology</i> 376 (1):90-100 (2008)
MND-2.CM.98.CM16	AF367411	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Nef	Takehisa, J.	<i>ARHR</i> 17 (12):1143-1154 (2001)
MND-2.GA.x.M14	AF328295	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Souquiere, S.	<i>J Virol</i> 75 (15):7086-7096 (2001)
MND-2.x.x.5440	AY159322	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Hu, J.	<i>J Virol</i> 77 (8):4867-4880 (2003)
DRL.x.x.FAO	AY159321	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Hu, J.	<i>J Virol</i> 77 (8):4867-4880 (2003)

Name	Accession	Proteins	Author	Reference
MON.CM.99.L1	AY340701	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Courgnaud, V.	<i>J Virol</i> 77 (23):12523-12534 (2003)
MON.NG.x.NG1	AJ549283	Gag, Pol, Vif, Vpr, Tat, Rev, Env	Barlow, K.L.	<i>J Virol</i> 77 (12):6879-6888 (2003)
GSN.CM.99.CN166	AF468659	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Courgnaud, V.	<i>J Virol</i> 76 (16):8298-8309 (2002)
GSN.CM.99.CN71	AF468658	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Courgnaud, V.	<i>J Virol</i> 76 (16):8298-8309 (2002)
TAL.CM.00.266	AY655744	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Liegeois, F.	<i>Virology</i> 349 (1):55-65 (2006)
TAL.CM.01.8023	AM182197	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Liegeois, F.	<i>Virology</i> 349 (1):55-65 (2006)
MUS-1.CM.01.1085	AY340700	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Courgnaud, V.	<i>J Virol</i> 77 (23):12523-12534 (2003)
MUS-1.CM.01.CM1239	EF070330	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Aghokeng, A.F.	<i>Virology</i> 360 (2):407-418 (2007)
MUS-2.CM.01.CM1246	EF070329	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Aghokeng, A.F.	<i>Virology</i> 360 (2):407-418 (2007)
MUS-2.CM.01.CM2500	EF070331	Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env, Nef	Aghokeng, A.F.	<i>Virology</i> 360 (2):407-418 (2007)
SYK.KE.x.KE51	AY523867	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)
SYK.KE.x.SYK173	L06042	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Hirsch, V.M.	<i>J Virol</i> 67 (3):1517-1528 (1993)
RCM.GA.x.GAB1	AF382829	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Bibollet-Ruche, F.	<i>J Virol</i> 78 (14):7748-7762 (2004)

Name	Accession	Proteins	Author	Reference
RCM.NG.x.NG411	AF349680	Gag, Pol, Vif, Vpx, Vpr, Tat, Rev, Env, Nef	Beer, B.E.	<i>J Virol</i> 75 (24):12014-12027 (2001)
GRV.ET.x.GRI_677	M66437	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Fomsgaard, A.	<i>Virology</i> 182 (1):397-402 (1991)
SAB.SN.x.SAB1C	U04005	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Jin, M.J.	<i>EMBO J</i> 13 (12):2935-2947 (1994)
TAN.UG.x.TAN1	U58991	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Soares, M.A.	<i>Virology</i> 228 (2):394-399 (1997)
VER.DE.x.AGM3	M30931	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Baier, M.	<i>Virology</i> 176 (1):216-221 (1990)
VER.KE.x.9063	L40990	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Hirsch, V.M.	<i>J Virol</i> 69 (2):955-967 (1995)
VER.KE.x.AGM155	M29975	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Johnson, P.R.	<i>J Virol</i> 64 (3):1086-1092 (1990)
VER.KE.x.TYO1_patent	DJ048201	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Omori, T.	Patent: WO 2007049749-A 13 03-MAY-2007; Dनावेक CORPORATION
COL.CM.x.CGU1	AF301156	Gag, Pol, Vif, Vpr, Tat, Rev, Env, Nef	Courgnaud, V.	<i>J Virol</i> 75 (2):857-866 (2001)

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Gag start, p17 start nuclear localization										nuclear localization										p17 end, p24 start																				
MGAASV.LSGGELDRWEIKRLRPGGKKYKLTHTVWASRELERFAVNPGLLETSEGRQILGQLQPSLSTQSEELRSYNTVATLYCVHRIEIKDTKEALDKIEEFO																														NKSKKKAQAQAADTG.HSNQVSNYPIVONIGOMG										143
KK-S-----N-----R-----L-----N-----K-----L-----D-----D-----A-----K-----IK-----A-----T-----K-----F-----V-----K-----V-----										N-ORT-----N-----E-NR-----										S-----A-----P-----										143										
I-R-EK-A-K-----H-M-L-N-K-L-D-D-A-K-IR-A-K-----I-F-----V-----K-----V-----										E-QO-T-G-ADR-GKD-----M-----										L-----										141										
I-K-A-Q-----R-M-LI-----LD-----A-----QK-IR-----Q-MR-----T-----IK-----F-----A-----V-----Y-----K-----AGVT-----										N-R-----G-----N-----S-----										L-----										141										
T-K-A-----R-S-----R-L-----P-----L-----IE-I-AIK-T-K-F-L-V-RK-DV-----M-----E-----I-----										K-QE-T-M-N-----										L-----										143										
I-K-D-----RI-L-----D-----SAK-Q-V-A-----TQ-IK-----I-I-----I-----IK-----I-F-----V-----F-----K-----V-----L-----										N-QO-K-ET-KK.DNS-----										L-----P-----										143										
K-A-----R-----R-L-----L-----SF-A-----O-IE-----ST-K-L-----K-----I-----W-----V-----										OR-T-E-A-DKG-----										L-----										139										
K-A-----E-RI-L-----L-----S-----A-----O-LME-SA-R-----K-----F-----I-----W-----D-----M-----L-----										OQ-T-G-S-SK-----										A-----A-----										140										
K-A-----R-----R-L-----L-----S-----A-----O-LME-SA-R-----K-----F-----I-----W-----D-----M-----L-----										O-T-TG-S-SK-----										A-----T-----										143										
K-A-----R-----R-L-----L-----S-----A-----O-LME-SA-R-----K-----F-----I-----W-----D-----M-----L-----										S-O-T-AA-G-SN-----										A-----										144										
S-T-K-A-Q-S-K-S-----R-M-L-----C-----MD-AD-AKL-N-E-A-K-----I-----AL-V-----S-O-QM-O-----K-K-E-----										QHKPEKPNP-GAAAAATDSNI-R-----L-----TA-----										L-----										14										
T-SK-A-Q-S-K-S-----R-M-L-----C-----MD-AD-AKL-N-E-A-K-----I-----AL-V-----S-O-QM-O-----K-K-E-----										SRKASD-KEDTSAR-AG-----S-----A-----										L-----										14										
T-SK-A-Q-S-K-S-----R-M-L-----C-----MD-AD-AKL-N-E-A-K-----I-----AL-V-----S-O-QM-O-----K-K-E-----										SRKASD-KEDTSAR-AG-----S-----A-----										L-----										14										
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T-SK-A-Q-S-K-S																																								

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		p24 end_p2 start		p2 end_p7 start		Zn motif		Zn motif		
H1B.FR.83.HXB2	QASQEVKNMWTETLLVONANPCKITLKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVNSAT	IMMORGNFRNOR				KIVKCFNCKGKEGHTARNCRAPRKK		GCWCKGKEGHOMKDC		427
H1A1.UG.85.U455	-T-D-	S-R-G-	-QOTS	-GP		RRI	L-K			421
H1A1.US.90.WEAU160	-T-	G-D	-T	M	SP	TI		Q		427
H1C.ET.86.ETH2220	-T-D-	D	R-G-S	A	N-TT	RAI	L			424
H1D.CD.84.84ZRB85			G	A	SASAA	KS	KGT			428
H1F1.BE.93.VT050	-D-G-D		G	ANUS	KS	KG				428
H1G.SE.93.SE6165	-D-G-D	R-OG-S	S	ASGA-AA	S	KGP		R		428
H1H.CF.90.056	-T-D-	R-OG-SI	S	TN-A	K	KG		R		428
H1J.SE.93.SE7887	-T-D-	D	SG	TN	DKH	R	Q-I-K			426
H1K.CM.96.MP535	-T-	D	G-S	I	PV	V-K	KGH			422
H101.AE.TH.90.CM240	-T-	S	TG	S	HAQHA	V	KG			425
H102.AG.NG.x.IEBC	-T-D-	S-R-TG	S	QAN		RTI	R-L-K-R	Q		422
H103.AB.RU.97.KAL153.2	-T-D-	R-SG-V	S	Q-AN	KS-GP	RI	L			425
H104.cpx.CY.94.CY032	-T-	S-TG	S	AS-A-AA	KSK-KG	RTI	L			428
H1N.CM.95.YBF30	-T-	QL-G	A	QOPT-S	VFA	KGI		Q	KN	431
H10.BE.87.ANT70	-T-	Q-S-G	V-T	ATA00DLKGGYTAVF	ONPTRK	GTL	L-K-RG		KN	432
H10.CM.91.MVP5180	-T-	S	T	ASA00DLKGGYTAVF	ONP-RK	GPI	L-K-R		KN	432
H1P.FR.06.RBF168	S-D-I	Q-G-N	T-KI	AAANQAND	LK-GYTVFMQSGQ	R-P	I-I-K-K-R		KS	425
CPZ.CM.01.SIVcpzCAM13	-T-D-	Q-G-S	A	TM-QSO-RT	D-FF-K-PGATP	RKI-Y	L-K-R		S	434
CPZ.CM.05.SIVcpzEK505	-T-	N-R-G-S	A	T-AQTATS	VF	KGI	L-K		RS	431
CPZ.CM.05.SIVcpzL87	-T-	S-R-G-S	A	ANAA	TV	KGP				428
CPZ.CM.05.SIVcpzMB66	-T-D-	S-R-G	GDEP-F	AQH-NDA	KROFK-PK	RVI	L-K-R	Q-R-Q	NM	428
CPZ.CM.05.SIVcpzMT145	-D-I	N-R-G	S	E-F	GONRRPN	KI	L		RN	418
CPZ.CM.-SIVcpzMB897	-T-D-	Q-R-G	S	ANTTVM	E-F	VKI-K				426
CPZ.CM.-SIVcpzDP943	-T-T-D-X	N-R-G	A	Q-TS	VFL	NGRPT		Q-I	A	425
CPZ.CM.98.CAM3	-T-	N-R-G	A	LO-PT	GVFL	NGKPT			N-PA	428
CPZ.CM.98.CAM5	-T-	S-R-G	A	Q	NVF	NGRVN			N-E-T	427
CPZ.GA.88.GAB1	-D-	Q-R-G	S	M-Q-OGRA	DVFF-K-OGAPK	RKI	L-K-R	R-Q		437
CPZ.GA.88.GAB2	-D-	Q-R-G	A	IQOTS	S-F-AGG-TPP	RR	L-K-R		QN	430
CPZ.US.85.CPZUS	-P-T	R-G-V	A	C-MK-PS	SVFL-K-AGKPG	RKI	L-R		A	429
CPZ.CD.90.ANT	-P-A	I	H-TG-S-L	ASAN-AQGT	AVFL	GNRGGK		R-Q	L-N-PA	450
CPZ.T2.00.TAN1	-P-T	H	UG-L	ASA-AGG	VN-L-G-KRPLPK	KGOLQ	V			455
CPZ.TZ.2001.TAN2	-P-	H-TG-S-L	S-KI	AAANTG	GGIN	LO-GR-PPGKK				428
CPZ.TZ.2002.TAN3.1	-P-T	H-TG-S-L	AY-KI	AAANTT	GGIN	LO-GR-PPGKK				428
GOR.CM.2007.SIVgor2139.287	-D-I	Q-G-N	T	AAAHSDLKGGYTAVF	K-GNNOGIKK	GP	V-I-K-R		RS	427
GOR.CM.2007.SIVgorCP2135con	-D-I	Q-G-N	T-X	AAAHSDXKGGYTAVF	K-GXNOGIKK	GP	V-I-K-R		RS	427
GOR.CM.2004.SIVgorCP684con	-D-I	Q-G-N	T	AAAHSDLKGGYTAVF	K-GNNOGIKK	GP	V-I-K-R		RS	427
H2A.DE.x.BEN	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
H2A.GW.x.ALI	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
H2A.SN.x.ST	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
H2B.CI.x.EHO	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
H2B.GH.86.D205	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
H2C.CI.92.ABT96	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
H2U.FR.96.12034	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
SMM.SL.92.SL92B	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
SMM.US.x.H9	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
SMM.US.x.PGM53	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
SMM.US.x.SIVsmH635F.L3	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		426
		p27_p2		p2_p8						
MAC.US.x.239	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		428
MAC.US.x.251.1A11	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		428
MAC.US.x.251.BK28	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		428
MAC.US.x.EMBL.3	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		428
STM.US.x.STM	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		428
MNE.US.x.MNE027	-TDA-	Q-I	LV-G-MNP	L	I	LM	LKEALPVP	FAAA-Q		428
DEB.CM.99.CM40	-D-A	T-MI	RI-G-MNP	LH	QO	LM	LKEALPVP	FAAA-Q		428
DEB.CM.99.CM5	-D-A	T-MI	RI-G-MNP	LH	QO	LM	LKEALPVP	FAAA-Q		428
DEN.CD.x.CD1	-D-S	L-TS	QI-E-NP	LO	Q	PT	LASAFQKGLCHGSRKGAOPVPR			428
LST.CD.88.447	GG-H	E-K-KM	RMVI	EG-S	D-K	A	GKI	ATAMQOMR	QN-V-VTPP-EQ	429
LST.CD.88.485	GG-H	E-K-KM	RMVI	EG-S	D-K	A	GKI	ATAMQOMR	QN-V-VTPP-EQ	429
LST.CD.88.524	GG-H	E-K-KM	RMVI	EG-S	D-K	A	GKI	ATAMQOMR	QN-V-VTPP-EQ	429
LST.KE.x.Lho7	GG-H	E-K-KM	RMVI	EG-S	D-K	A	GKI	ATAMQOMR	QN-V-VTPP-EQ	429
SUN.GA.98.L14	SG-E	E-K-KM	LV	ETPS	R	S	GKI	ASAFROQV	ROA-V-ONLPPRNSQ	430
MND.1.GA.x.MNDGB1	-G	M-QH	IE	E-QS	KG	LE	Q	LM	LRP-ONVQORPAP	430
OLC.CI.97.97C112	-G	T-K	I	GV	NP	L	Y	SKIM-O	LOEAL-H-SO	430
WRC.CI.97.97C114	-GAP	Q-DK-I	A	G-OOP	L	Y	SKIM-O	LOEAL-H-SO	A-V-OAQAKP	430
WRC.CI.98.98C104	-GAP	Q-DK-I	A	G-OOP	L	Y	SKIM-O	LOEAL-H-SO	A-V-OAQAKP	430
WRC.GM.05.Pbt.05GM.X02	-GVP	Q-DK-I	A	G-OOP	L	Y	SKIM-O	LOEAL-H-SO	A-V-OAQAKP	430
MND.2.CM.98.CM16	RTDPO	T-O-I	S	G-MNPS	PL	KY	QMM	QKMS	AV-NSGGPPRG	433
MND.2.GA.x.M14	RTDPO	T-O-I	S	G-MNPS	PL	KY	QMM	QKMS	AV-NSGGPPRG	433
MND.2.x.x.5440	RTDPO	T-O-I	AT	G-MNPS	LL	KY	QMM	QKMS	AV-NSGGPPRG	433
DRL.x.x.FA0	HTDAA	Q-I	V-G-MNPS	LL	M	REQAAA	QNP	GPP		433
MON.CM.99.L1	-TD-A	Q	L-M-G-S	D-LO	M-S-I	AGAIAN	MPMN-V-ARGPPQ			435
MON.NG.x.NG1	-D-A	OS	L-M-G-S	LO	A-S-L	ATAT	NMP-M	N-V-GRGG		435
GSN.CM.99.CM166	-D-A	OS	L-M-G-S	LO	A-S-L	ATAT	NMP-M	N-V-GRGG		435
GSN.CM.99.CN71	-D-A	OS	L-M-G-S	LO	A-S-L	ATAT	NMP-M	N-V-GRGG		435
TAL.CM.00.266	-TD-A	Q	A-M-Q	LO	Q-S-LM	AEALK	ONTOQVIA	V-O-GGPP		434
TAL.CM.01.8023	-TD-A	Q	A-M-Q	LO	Q-S-LM	AEALK	ONTOQVIA	V-O-GGPP		434
MUS.1.CM.01.1085	-SD-A	S	L-SM-G	LO	T-S-LM	LASAF	KQAG	TL-N-V-GAKGARG		434
MUS.1.CM.01.CM129	-SD-A	S	L-SM-G	LO	T-S-LM	LASAF	KQAG	TL-N-V-GAKGARG		434
MUS.2.CM.01.CM1246	-D-A	OS	LV-M-G-K	LO	A-S-LM	ASAL	ROMS	QL-N-V-G-ARPK		434
MUS.2.CM.01.CM2500	-D-A	OS	LV-M-G-K	LO	A-S-LM	ASAL	ROMS	QL-N-V-G-ARPK		434
SYK.KE.x.KE51	-DPA	OS	LV-M-G-K	LO	A-S-LM	ASAL	ROMS	QL-N-V-G-ARPK		434
SYK.KE.x.SYK173	-DPA	OS	LV-M-G-K	LO	A-S-LM	ASAL	ROMS	QL-N-V-G-ARPK		434
RCM.GA.x.GAB1	-DPA	OS	LV-M-G-K	LO	A-S-LM	ASAL	ROMS	QL-N-V-G-ARPK		434
RCM.NG.x.NG411	-DPA	OS	LV-M-G-K	LO	A-S-LM	ASAL	ROMS	QL-N-V-G-ARPK		434
GRV.ET.x.GRI.677	-P-D	Q	L-G-MNP	LI	AQ	LMV	M-NGO	N-V-V-PQKGP		434
SAB.SN.x.SABIC	-TDA-	OS-I	L-G-MNP	LI	AQ	LMV	M-NGO	N-V-V-PQKGP		434
TAN.UG.x.TAN1	-TP-D	Q	L-G-MNP	LI	AQ	LMV	M-NGO	N-V-V-PQKGP		434
VER.DE.x.AGM3	-G	Q-S-I	L-G-MNP	LI	AQ	LMV	M-NGO	N-V-V-PQKGP		434
VER.KE.x.9063	-G	Q-S-I	L-G-MNP	LI	AQ	LMV	M-NGO	N-V-V-PQKGP		434
VER.KE.x.AGM155	-G	Q-S-I	L-G-MNP	LI	AQ	LMV	M-NGO	N-V-V-PQKGP		434
VER.KE.x.TY01.patent	-G	Q-S-I	L-G-MNP	LI	AQ	LMV	M-NGO	N-V-V-PQKGP		434
COL.CM.x.CGU1	P-AG-I-A-ANN	-I-H	R-G-QK-PS	D-LA	D-K	Q	FOQER	TN	IEVKTAKFCNCGIGHARMCKPRIGGAGRGRGRGRGFRGAPRRP	434

	p7 end_p1 start	p1 end_p6 start	Vpr binding	Vpr binding	Vpr binding	Vpr binding	p6 end_Gag end		
H1B.FR.83.HXB2	ERQANFLGKWP	SYKGR	PGNFLOS	RPE	PTAPPEES	FRSGVE	TTTTPPOKEPTI	DKELY	PLTSLRSLFGNDPSSQ*
H1A1.UG.85.U455									
H1B.US.90.WEAU160									
H1C.ET.86.ETH2220									
H1D.CD.84.84Z8085									
H1F1.BE.93.VT850									
H1G.SE.93.SE6165									
H1H.CF.90.056									
H1J.SE.93.SE7887									
H1K.CM.96.MP535									
H101.AE.TH.90.CM240									
H102.AG.NG.x.IBNG									
H103.AB.RU.97.KAL153_2									
H104.CY.CV.94.CY032									
H1N.CM.95.YBF30									
H10.BE.87.ANT70									
H10.CM.91.MVP5180									
H1P.FR.06.RBF168									
CPZ.CM.01.SIVcpzCAM13									
CPZ.CM.05.SIVcpzEK505									
CPZ.CM.05.SIVcpzLB7									
CPZ.CM.05.SIVcpzMB66									
CPZ.CM.05.SIVcpzMT145									
CPZ.CM.05.SIVcpzMB897									
CPZ.CM.05.SIVcpzDP943									
CPZ.CM.98.CAM3									
CPZ.CM.98.CAM5									
CPZ.GA.88.GAB1									
CPZ.GA.88.GAB2									
CPZ.US.85.CPZUS									
CPZ.CD.90.ANT									
CPZ.TZ.00.TAN1									
CPZ.TZ.2001.TAN2									
CPZ.TZ.2002.TAN3_1									
GOR.CM.2007.SIVgor2139_287									
GOR.CM.2007.SIVgorCP2135con									
GOR.CM.2004.SIVgorCP684con									
H2A.DE.x.BEN									
H2A.GW.x.ALI									
H2A.SN.x.ST									
H2B.CI.x.EH0									
H2B.GH.86.D205									
H2G.CI.92.ABT96									
H2U.FR.96.12034									
SMM.SL.92.SL92B									
SMM.US.x.H9									
SMM.US.x.PGM53									
SMM.US.x.SIVsmH635F_L3									
MAC.US.x.239									
MAC.US.x.251.1A11									
MAC.US.x.251.BK28									
MAC.US.x.EMB1_3									
STM.US.x.STM									
MNE.US.x.MNE027									
DEB.CM.99.CM40									
DEB.CM.99.CM5									
DEN.CD.x.C01									
LST.CD.88.447									
LST.CD.88.485									
LST.CD.88.524									
LST.KE.x.lh07									
SUN.GA.98.L14									
MND.1.GA.x.MNDGB1									
OLC.CI.97.97C112									
WRC.CI.97.97C114									
WRC.CI.98.98C104									
WRC.GM.05.Pbt.05GM.X02									
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MND.2.GA.x.M14									
MND.2.x.x.5440									
DRL.x.x.FA0									
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MON.NG.x.NG1									
GSN.CM.99.CM166									
GSN.CM.99.CN71									
TAL.CM.00.266									
TAL.CM.01.8023									
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MUS.1.CM.01.CM1239									
MUS.2.CM.01.CM1246									
MUS.2.CM.01.CM2500									
SYK.KE.x.KE51									
SYK.KE.x.SYK173									
RCM.GA.x.GAB11									
RCM.NG.x.NG411									
GRV.ET.x.GRI.677									
SAB.SN.x.SAB1C									
TAN.UG.x.TAN1									
VER.DE.x.AGM3									
VER.KE.x.9063									
VER.KE.x.AGM155									
VER.KE.x.TY01 patent									
COL.CM.x.CG11									

FR.83.XH82	FFREDLAF	LOGKAREFSSERAN	SPTRRRE	LOWGRD	LNNSPCEAF	ADROG	TVSFMQVPTVLWQRPVLVTIKIGGOLKEALLTDGADTVLEMSL	PGRWKPMKMGIGGFIKVRQYDQITLIECGHKAI	G	129			
H1A1.UG.85.U455	N	O-E	S-N	WDG-K	DL-CT	E	D-S	I	D-N	K	I	K-T	130
H1B.US.90.WEAU160	N	V	P	T	Q	T	E	N	A	I	V	E	131
H1C.ET.86.ETH2220	N	P	G-L	P	FGFGEI	T	PLTEGTG	GO	L	LS	I	V	132
H1D.CD.84.B4Z8285	N	O-E	K-P	S	R-ORG	PL	E-R	TV	P	LS	I	V	133
H1F1.BE.93.VI850	N	O-E	K-P	D-T	PR-RRG	SPLP	DECK	ATSL	I	V	E	R	134
H1G.SE.93.SE6165	N	O-E	K-P	A-T	R-RRG	DPL	A-EG	T	LS	I	V	E	135
H1H.CF.90.056	N	O-E	L-P	S	PRARRG	PLP	T	EG	T	LS	I	V	136
H1J.SE.93.SE7887	N	O-E	G	S	R-R-GN	PL	DO	TE	P	S	I	V	137
H1K.CM.96.MP535	N	O-E	G	S	GDG	NGGRD	LLT	DO	TE	S	S	I	138
H101.AE.TH.90.CM240	N	O-E	K	GT	WDG	T	SL	T	EG	AI	S	I	139
H102.AG.NH.x.IBNG	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	140
H103.AB.RU.97.KAL152	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	141
H104.CPX.CY.CY032	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	142
H1N.CM.93.YB30	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	143
H10.BE.87.AN770	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	144
H10.CM.91.MVP5180	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	145
H1P.FR.06.RBF168	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	146
H1Q.CM.91.SIVcpzCAM13	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	147
CPZ.CM.05.SIVcpzEK505	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	148
CPZ.CM.05.SIVcpzLB7	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	149
CPZ.CM.05.SIVcpzMB66	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	150
CPZ.CM.05.SIVcpzMT145	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	151
CPZ.CM.05.SIVcpzMB897	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	152
CPZ.CM.05.SIVcpzDP943	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	153
CPZ.CM.98.CAM3	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	154
CPZ.CM.98.CAM5	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	155
CPZ.GA.88.GAB1	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	156
CPZ.GA.88.GAB2	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	157
CPZ.GA.88.GAB3	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	158
CPZ.CM.92.CP2U5	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	159
CPZ.CD.90.ANT	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	160
CPZ.TZ.00.TAN1	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	161
CPZ.TZ.2001.TAN2	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	162
CPZ.TZ.2002.TAN3	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	163
GOR.CM.2007.SIVgor2139	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	164
GOR.CM.2007.SIVgorCP2135con	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	165
GOR.CM.2004.SIVgorCP684con	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	166
H2A.DE.x.BEN	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	167
H2B.CM.91.H1	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	168
H2B.SN.x.TI	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	169
H2B.CM.x.EH0	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	170
H2B.GH.86.D205	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	171
H2M.CI.92.AB196	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	172
H2L.CM.92.AB196	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	173
SHM.SL.92.S192B	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	174
SHM.US.x.H9	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	175
SHM.US.x.PGM53	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	176
SHM.US.x.S1VsmH635F_L3	N	O-E	K	A	WDG	N	PL	P	T	EG	T	LS	177

[illegible]

[illegible]

PLV Proteins

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H1B. US. 90. WEAU100
H1C. ET. 86. ETH2220
H1C. ET. 84. B4Z7805
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H1G. SE. 86. SE6165
H1H. CF. 90. 056
H1J. SE. 93. SE7887
H1K. CM. 96. H983
H101. AE. TH. 90. CM240
H102. AG. NG. X. IBNG
H103. AB. RU. 97. KAL352 1
H104. CMpx. CY. 94. CY032
H105. US. 95. YB30
H10. BE. 87. 1700
H10. CM. 91. MVP5180
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CPZ. CM. 05. SVCPZKAM13
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CPZ. CM. 05. SVCPzDP943
CPZ. CM. 98. CAM3
CPZ. CM. 98. CAM5
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CPZ. GA. 88. GAB2
CPZ. US. 85. CPZUS
CPZ. CD. 90. ANT
CPZ. TZ. 09. TAN1
CPZ. TZ. 09. TAN2
CPZ. TZ. 2002. TAN3 1
GOR. CM. 2007. SVGor2139
GOR. CM. 2007. SVGorCP21
GOR. CM. 2008. SVGorCP68
H2A. GN. X. ALT
H2A. SN. X. ST
H2B. CI. X. EHO
H2B. GH. 86. D205
H2C. TZ. 92. TAN6
H20. FL. 92. L2934
SMH. SL. 96. 12828
SMH. US. X. H95
SMH. US. X. PGMS3
SMH. US. X. H96H635F 13

MAC.US.x.239
MAC.US.x.251.1A11
MAC.US.x.251.BK28
STM.US.x.STM
DEB.CM.x.MN027
DEB.CM.x.CM40
DEB.CM.x.CM5
DEN.CD.x.CD1
LST.CD.88.447
LST.CD.88.485
LST.CD.88.524
LST.KE.x.lho7
SUN.GA.98.L14
MND-1.GA.x.MNDGB1
WRC-1.CI.97.9C12
WRC-1.CI.97.97C14
WRC-1.GM.98.CI04
WRC.GM.05.PT.05GM.X02
MND-2.GA.x.CM16
MND-2.GA.x.M14
MND-2.x.x.5440
DRL.x.x.FA0
MOL.x.MX.99.L1
MOL.NG.x.NG1
GSM.CM.99.CM166
GSM.CM.99.CN71
TAL.CM.00.026
TAL.CM.01.0023
MUS-1.CM.01.1085
MUS-1.CM.01.CM1239
MUS-2.CM.01.CM1246
SVK.KE.x.KE51
SVK.KE.x.SV173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GRI 677
SUN.CM.x.SALIC
TAN.UG.x.TANI
VER.DE.x.AGM3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.9063.TV.patent
COL.CM.x.CU1

[illegible][illegible]

p51 RT end p15 RNase H start

[illegible]

p51 RT end p15 RNase H start

[illegible]

118.FR.83.HXB2	TTNQKTELQAIYALQDQSGLEVINVTDSQYALGIIQAQPDQSESELVNQITEQLKKEKYYLWAPVPAHKGIGNEQVDKLVSAG	IR	.KVLFLDGD	.KAQDEHEK	.YHSNWRAMASDFNLPPVVAKEIVASCDQKQLK	.GEAMHGQVDCSPGIIQWLDCTHLEGKVLIV	790											
H1A1.UG.85.U455	H-H	S					I	789										
H1D.US.90.WEAU160	H-H	S					I	797										
H1C.TI.86.CTH2220	H-H	S					I	790										
H1D.CD.84.84Z8085	H-H	S					I	790										
H1F1.BE.93.VI850	A	N	S				I	791										
H1G.SE.93.SEG165	A	Q	RS				I	787										
H1H.CF.90.056	A						I	787										
H1I.SE.93.SF787	H-H	R	S				I	788										
H1K.CM.96.MP535	A	H	C	S			I	790										
H101.AE.TH.90.CM240	H-H	S					I	795										
H102.AG.NG.x.IBNG	H-H	S					I	790										
H103.AB.RU.97.KAL153_2	H-H	S					I	795										
H104.cpx.CV.94.CV032	H-H	S					I	790										
H1N.CM.95.YBF30	A	LM	E	RD			I	789										
H10.BE.87.ANT70	A	M	L	KE			I	797										
H10.CM.91.MVP5180	A	M	VLI	KE			I	786										
H1P.FR.06.RBF168	A	XE	VL	KE			I	780										
H1Q.CM.95.SIVcpzCAM15	QA	G	L	EQ			I	790										
CPZ.CM.05.SIVcpzEK503	QA	VLM	A	Q			I	796										
CPZ.CM.05.SIVcpzLB7	A	Q	P				I	793										
CPZ.CM.05.SIVcpzMB66	A	Q	EV				I	793										
CPZ.CM.05.SIVcpzMT145	QA	VLM	Q	V			I	788										
CPZ.CM.SIVcpzMB897	RA						I	798										
CPZ.CM.SIVcpzDP943	A	T	V	AEHI			I	797										
CPZ.CM.98.CAM3	A	T	V	AEHI			I	795										
CPZ.CM.98.CAM5	A	T	V	AEHI			I	791										
CPZ.GA.88.GAB1	QA	K	LL	DQ			I	795										
CPZ.GA.88.GAB2	A	E	LR	I			I	797										
CPZ.US.85.CP2U5	A	T	V	K	ENT		I	798										
CPZ.CD.90.ANT	QA	LM	E	TGP			I	792										
CPZ.TZ.00.TAN1	QA	W	VD	K	AQ		I	790										
CPZ.TZ.2001.TAN2	QA	W	D	R	AA		I	786										
CPZ.WD.2002.TAN3_1	QA	W	D	R	AA		I	787										
GOR.CM.2007.SIVgor2139_287	A	E	VL	EE	KN		I	782										
GOR.CM.2007.SIVgorCP2135con	A	E	VL	EE	KN		I	782										
GOR.CM.2004.SIVgorCP684con	A	E	VL	EE	KN		I	782										
H2A.DE.x.BEN	QA	EVFRM	AI	PKA	IV	VM	VAG	TE	NRI	EM	A	V		I	814			
H2A.SN.x.H40	QA	FA	VT	PKA	IV	VM	VAG	TE	KL	RE	EM	AI	V		I	814		
H2B.CI.x.EH0	QA	E	FA	P	Q	IV	VM	VA	TET	PI	RE	EM	I	V		I	814	
H2B.GH.86.D205	QA	E	FA	T	EPD	IV	VM	A	TET	PI	AK	EM	A	VG		I	813	
H2G.CI.92.AB165	QA	FA	K	PK	IX	VM	X	AG	TET	P	SK	E	R	A	VG		I	797
H2H.FR.96.TL2034	QA	E	FAM	E	PK	IV	VM	AG	TET	P	SK	E	R	A	VG		I	797
SMML.SL.92.SL928	A	QA	LL	K	PSK	V	LM	AG	TE	SE	D	DI	A	IG		I	794	
SMML.US.x.H9	QA	E	F	A	PKA	IV	VM	VAG	TE	R	KM	AI	V		I	797		
SMML.US.x.PGM53	QA	E	F	A	PKA	IV	VM	VAG	TE	R	EM	AI	V		I	797		
SMML.US.x.SIVsmH635F_L3	QA	E	F	A	PKA	IV	VM	VAG	TE	R	EM	AI	V		I	797		
p15 RNase H end_p31 Integrase start																		
MAC.US.x.239	QA	E	FLM	T	PKA	IV	VM	TGC	TE	R	EM	SEI	V		I	801		
MAC.US.x.251_1A11	QA	E	FLM	T	PKA	IV	VM	TGC	TE	R	KEM	SEI	V		I	801		
MAC.US.x.BK28	QA	E	FLM	T	PKA	IV	VM	TGC	TE	R	KEM	SEI	V		I	801		
MAC.US.x.EMB1_3	QA	E	HGIE	PKR	IVEL	VCY	NNMRF	TE	R	EM	VR	V		I	801			
MAC.US.x.STM	QA	E	FAM	A	PKA	IV	VM	TGC	TE	R	EM	AI	V		I	797		
MNE.US.x.MNE027	QA	E	FLM	T	PKA	IV	VM	TGC	TE	R	EM	TEI	V		I	797		
DEB.CM.99.CM40	A	E	L	EEGPKSKM				LEH	SET	HKI	EKV	QA	OG	OT		I	795	
DEB.CM.99.CM45	A	E	L	EEGPKSKM				LEH	SET	HKI	EKV	QA	OG	OT		I	795	
LEN.CD.x.CD1	A	E	IGVLM	R	PKR			AGT	IT	HQI	E	QMG	DI	IT		I	817	
DST.CD.88.447	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
LST.CD.88.485	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
LST.CD.88.424	QA	E	VL	K	KST			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
LST.CD.88.424	QA	E	VL	K	KST			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV	K	ECK	DO	G		I	809	
SUN.GA.98.L14	QA	E	VL	K	NSK			VTIKVLOS	TET	HPV								

[illegible]

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H1A1.UG.85.U455
H1B.US.90.WEAU160
H1C.ET.86.ETH2220
H1D.CD.84.84Z8085
H1F1.BE.93.V1F50
H1G.SE.93.SE6165
H1H.CF.90.056
H1J.SE.93.SE7887
H1K.CM.96.MP535
H101.AE.TH.90.CM240
H102.AG.NG.x.IENG
H103.AB.RU.97.KAL153_2
H104.cpx.CY.94.CY032
H1N.CM.95.YBF30
H10.BE.87.ANT76
H10.CM.91.MVP5180
H1P.FR.06.RBF168
CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzLB7
CPZ.CM.05.SIVcpzMB66
CPZ.CM.05.SIVcpzMT145
CPZ.CM.05.SIVcpzMB897
CPZ.CM.05.SIVcpzDP943
CPZ.CM.98.CAM3
CPZ.CM.98.CAM5
CPZ.GA.88.GAB1
CPZ.GA.88.GAB2
CPZ.US.85.CPZUS
CPZ.CD.90.ANT
CPZ.TZ.00.TAN1
CPZ.TZ.2001.TAN2
CPZ.TZ.2002.TAN3_1
GOR.CM.2007.SIVgor2139_287
GOR.CM.2007.SIVgorCP2135con
GOR.CM.2004.SIVgorCP684con
H2A.DE.x.BEN
H2A.GW.x.ALI
H2A.SN.x.ST
H2B.CI.x.EH0
H2B.GH.86.D205
H2G.CI.92.ABT96
H2U.FR.96.12034
SMM.SL.92.SL92B
SMM.US.x.H9
SMM.US.x.PGM53
SMM.US.x.SIVsmH635F_L3

MAC.US.x.239
MAC.US.x.251_1A11
MAC.US.x.251_BK28
MAC.US.x.EMBL_3
STM.US.x.STM
MNE.US.x.MNE027
DEB.CM.99.CM40
DEB.CM.99.CM5
DEN.CD.x.CD1
LST.CD.88.447
LST.CD.88.485
LST.CD.88.524
LST.KE.x.lho7
SUN.GA.98.L14
MND-1.GA.x.MNDGB1
OLC.CI.97.97CI12
WRC.CI.97.97CI14
WRC.CI.98.98CI04
WRC.GM.05.Pbt_05GM_X02
MND-2.CM.98.CM16
MND-2.GA.x.M14
MND-2.x.x.5440
DRL.x.x.FA0
MON.CM.99.L1
MON.NG.x.NG1
RGM.CM.99.CM166
GSN.CM.99.CM71
TAL.CM.00.266
TAL.CM.01.8023
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MUS-1.CM.01.CM1239
MUS-2.CM.01.CM1246
MUS-2.CM.01.CM2500
SYK.KE.x.KE51
SYK.KE.x.SYK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GRI_677
SAB.SN.x.SAB1C
TAN.UG.x.TAN1
VER.DE.x.AGM3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.TY01_patent
COL.CM.x.CGU1

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.....A.....G.....
.....E.....I.....V.....G.....
.....N.....E.....G.....
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.....G.....G.....
.....N.....G.....
.....G.....G.....NOEME.....
.....KG.....E.....T-SM.....G-T-SESVEOPSEIP
.....KG.....T-SM.....N-T-SESMEOPGEIP
.....QG.E.....DI-R-SESLE.....
.....G.....G.....S00ME.....
.....L-OE.E.....E-AN-L.....D.....N.....
.....L-OE.E.....S.....NONME.....
.....L-KE.....VE-N-L.....D.....S.....
.....K-KE.EV.....GSM.....G-SONLE.....
.....KERE.EV-I.....SM.....GG-SOGL.....
.....KE-E.EV.....GSM.....G-N-QNLE.....
.....QG.EL.....N.....
.....G.....KH.....V.....L.....GG-NONME.....
.....KE-E.EV.....K.....A-SM.....G-S.....
.....K-OE.E.....KE-R-KIEDR-DL.....G-N.....
.....KEGE.....KE.....AGMD.....D-N-T.....
.....KEGE.....KE.....AGSD.....D-N-T.....
.....KEGE.....KE.....V-ANSMD.....D-N-TONME.....
.....KG.....DT-G-SESLEQSS.....
.....KG.....DT-G-SESLEQSS.....
.....KG.....DT-G-SESLEQSS.....
.....IVKVG.T.....GROEL-SSPHLEGAREDG-HACPCOVPEIQNK
.....D-IVKVG.T.....GROEL-SSPHLEGAREDG-VA.....
.....D-IVKVG.A.....II-K.....GROEM-SGSNLEGAREDG-VA.....
.....I-KVG.T.E.....I-N-GGKEL-CSADVEDTMOAR-VAQSN.....
.....I-KVG.T.E.....H-GGKGL-CSADMEDTMOAR-MAQSD.....
.....I-KVG.T.E.....K-GGKEV-SSTHMETGTGTG-VA.....
.....L-KVG.T.....I-K-GGKEL-SSSNLEGAEKVR-MALPD0TPEYNTK
.....L-KVG.T.E.....K-GROEMSSASMEDO.....
.....ILKVG.T.E.....K-GGKEL-SGSHLEDTGEAR-VA.....
.....ILKVG.T.E.....K-GGKEL-SGPHLEDTGEAR-VA.....
.....ILKVG.T.E.....K-GGKEL-SGSHLEDTGEAR-VA.....
p31 Integrase end
Pol end
.....ILKVG.T.....K-GGKEV-SSSHMEDTGEAR-VA.....
.....ILKVG.T.....K-GGKEM-SSSHMEDTGEAR-VA.....
.....ILKVG.T.....K-GGKEV-SSSHMEDTGEAR-VA.....
.....ILKVG.T.....K-GGKEV-SSSHMEDTGEAR-VA.....
.....ILKVG.T.....K-GGKEV-SSSHLEDTGEAR-VA.....
.....ILKVG.T.....K-GGKEV-SSSHMEDTGEAR-VA.....
.....CKTEVG.....V-KE-D-DSKVNTONSNE.....
.....CKTEVG.....V-KE-GVDKTDTONPSE.....
.....KTOAG-FP.....K-NAE-SRKGEONKGM-D-ET-I.....
.....VKEGD-T-FS.....LVK-EGPKDSGGHNN.....
.....VKEGD-T-FS.....LVK-EGPKDSGSLDNN.....
.....VKEGE-N-FSI.....LVK-EGPKDSQSSMDNQ.....
.....VKEGE-N-FS.....LVK-E-GPK-SESLDNN.....
.....KQ-GEN-L.....LVK-GESSSVEM-G.....
.....LKQYE-E-I.....C-K-E-SGKNSQ-NLESV.....
.....LLKEGD.KYFS-L.....VKP-VDSANV.....
.....L-ETPEG-IT.....L-KVWNGEGMDRSSSDKN.....
.....L-VETPEG-IT-K.....KVWNGEGMDRSSSNKD.....
.....L-V-TPEG-LLT.....KTWDGKGMDSSSTTN.....
.....KEGT-L.....TVDS-PH-EA.....
.....KEGT-L.....TVDSNPHMERQETA.....
.....KEGV-L.....K-TVDSNPHMGR.....
.....KEGT-L-I.....K-NVDSHTNMES.....
.....KTEEG-LT.....KP-TTENVGDDTNOYNLRK-GLAN.....
.....L-KTDQGEVIT.....P-SKEDVGSKPSAHQIREV-GMAD.....
.....V-TQAGE-IT.....KP-EAKTE-VGG-TIAKND.....
.....V-TQAGE-IT.....KP-EAK-E-VGS-AHTSNDRE-GRMAD.....
.....LRTDEGEVIT.....KP-QALGNKIDLESSKEQDAEMGRDN.....
.....LRTDEGEVIT.....KP-QA-GNKTDLEGSKEQDAEMGRDN.....
.....R-KTD-GEVIT.....KP-AKEDVGSKSDTGDLRKE-RLDN.....
.....VKTEQGEVIT.....KP-AKENVGSKNTGDRHKE-GLDN.....
.....L-KTKEGE-VT.....K-TRQNV-SEPDSVHVYRKE-GLAD.....
.....I-KTDQGE-IT.....K-TKENV-SDPNPVYORKE-GLAD.....
.....TPDQVIA.....SSD-ERVDSGTHLEITSK-N.....
.....V-TEEG-FA.....T-H-ER-DGSGH-ENDPKTD.....
.....EETG-L.....KE-RKQVDSKANLAGROEEN.....
.....E-QE-L.....K-RKEVDRETNMEGROES.....
.....KEGE.....K-ERKTM-SEGSMEGVREANKQMGDSLDQOE.....
.....EQG.EL-TI.....K-L-SOAPLEGNG-TAGEVD.....
.....KEGE.EL.....KE-ERKTVG-KTNMEG.....
.....K.GGVEL-EY.....K-EPRKRMG-ESNLEGAGGA-N.....
.....K.EGEEL-I.....K-EPRKRMG-GWMLGLRP-NOMAR-NSQILD0.....
.....LK.EGEEL.....K-EPRKTLG-ETHLEGAGGS-HQMAG-DS.....
.....LK.DGS-L.....K-EPKQRVNEGDEVEGTRGS-N.....
.....RNSQGLTF-K.....V-T-LQYGEDV-SENLLSNGQKEAETVKGMD.....

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H1G.SE.93.S6E165
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H1K.CM.96.MP535
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H1N.CM.95.YBF30
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H10.CM.91.MVP5180
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CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzL87
CPZ.CM.05.SIVcpzMB66
CPZ.CM.05.SIVcpzMT145
CPZ.CM.-SIVcpzMB897
CPZ.CM.-SIVcpzDP943
CPZ.CM.98.CAM3
CPZ.CM.98.CAM5
CPZ.GA.88.GAB1
CPZ.GA.88.GAB2
CPZ.US.85.CPZUS
CPZ.CO.90.ANT
CPZ.TZ.00.TAN1
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VER.KE.x.90853
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ME...NRWQVMIVQVQDMMR.LRTWKS...LVKHHMYVSGKARGWYFRHHYSEPHPR1.SSEVHIPLG...DARLVITTYWGLHTGERDWH...LGQGVSIENWRKRYSTQVDPDELADQLI 107
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H1F1.BE.93.V1050
H1G.SE.93.S6E165
H1H.CF.90.056
H1J.SE.93.SE7887
H1K.CM.96.MP535
H101.AE.TH.90.CM240
H102.AG.NG.x.IBNC
H103.AB.RU.97.KAL153.2
H104.cpx.CY.94.CY032
H1N.CM.95.YBF30
H10.BE.87.ANT76
H10.CM.91.MVP5180
H1P.FR.06.RBF168
CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzLB7
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CPZ.CM.05.SIVcpzMT145
CPZ.CM..SIVcpzMB897
CPZ.CM..SIVcpzDP943
CPZ.CM.98.CAM3
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CPZ.US.85.CPZUS
CPZ.CD.90.ANT
CPZ.TZ.90.TAN1
CPZ.TZ.2001.TAN2
CPZ.TZ.2002.TAN3.1
GOR.CM.2007.SIVgor2139.287
GOR.CM.2007.SIVgorCP2135con
GOR.CM.2004.SIVgorCP684con
H2A.DE.x.BEN
H2A.GW.x.ALI
H2A.SN.x.ST
H2B.CI.x.EH0
H2B.GH.86.D205
H2C.CI.92.ABT96
H2U.FR.96.12034
SMM.SL.92.S1928
SMM.US.x.H9
SMM.US.x.PGM53
SMM.US.x.SIVsmH635F.L3

MAC.US.x.239
MAC.US.x.251.1A11
MAC.US.x.251.BK28
MAC.US.x.EMB1.3
STM.US.x.STIV
MNE.US.x.MNE027
DEB.CM.99.CM40
DEB.CM.99.CM5
DEN.CD.x.C01
LST.CD.88.447
LST.CD.88.485
LST.CD.88.524
LST.KE.x.Lho7
SUN.GA.98.L14
MND.1.GA.x.MNDGB1
QLC.CI.97.97C112
WRC.CI.97.97C114
WRC.CI.98.98C104
WRC.GM.05.Pbt.05GM.X02
MND.2.CM.98.CM16
MND.2.GA.x.M14
MND.2.x.x.5440
DRL.x.x.FA0
MON.CM.99.L1
MON.NG.x.NG1
GSN.CM.99.CM66
GSN.CM.99.CM71
TAL.CM.00.266
TAL.CM.01.8023
MUS.1.CM.01.1085
MUS.1.CM.01.CM129
MUS.2.CM.01.CM1246
MUS.2.CM.01.CM2500
SYK.KE.x.KE51
SYK.KE.x.SYK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GRI.677
SAB.SN.x.SABIC
TAN.UG.x.TAN1
VER.DE.x.AGM3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.TY01.patent
COL.CM.x.CGUI

HLYYFDCFSDSAIRKALLGHI..VSPRCEYOAGHNK.....VGSLLQYLALALIT.....PKKIKPPLPSVTKLTEDRWNPQK.....TKGHRGSHTMNGH.....*
-H-E-R-I-Q-R-K-V-TRA-K-R-R-L-R-
-H-E-N-I-L-I-T-K-A-S-V-K-R-R-N-
-MH-AE-I-YR-D-T-A-R-K-V-RO-R-R-
-M-A-T-R-I-N-T-A-E-Q-V-E-R-T-
-H-E-I-Q-R-N-KV-V-S-RSR-E-A-R-ENP-
-MH-E-I-RV-R-N-P-Q-T-T-VA-R-V-R-V-
-MC-I-E-I-Q-D-T-R-RR-Q-V-T-E-
-I-E-V-I-R-C-T-VA-RRP-V-K-V-R-O-
-Q-G-I-QV-RR-PS-K-T-R-R-ET-R-R-
-N-E-I-R-R-S-R-N-A-T-T-R-A-KE-R-ENP-
-E-N-I-R-S-R-R-V-R-R-D-S-
-MH-E-I-R-S-T-K-V-R-R-ENOI-
-H-TA-Q-V-RP-L-P-KQ-T-T-WVG-A-R-EH-MO-NPI-
-H-TA-V-I-OR-LTK-PT-SQ-T-L-R-VVK-ARSR-O-HLR-IRDOLK-PS-
-TR-TAG-V-Q-ER-LTK-HF-T-SQ-T-F-K-VVK-V-RN-RR-
-H-Q-V-R-I-DR-LNK-S-SQ-T-F-KVVG-KV-R-QI-K-I-S-R-ROE-L-S-CYKP-
-SQ-A-R-I-E-A-RE-RO-T-F-K-VK-E-RLR-A-T-R-PEN-S-
-TA-Q-V-RP-I-K-P-KQ-T-I-WVG-VQ-RR-RH-I-D-T-L-
-N-AE-I-RV-FP-K-T-IS-LQ-RQPTR-S-A-S-I-S-
-H-TAT-N-I-EKA-L-K-FPE-S-T-W-KQ-VK-S-PRR-A-A-NS-RO-K-N-
-H-AE-I-Q-FP-T-T-IS-LK-R-PK-S-A-R-KE-PMSS-C-
-H-AA-V-TQ-V-K-P-QQ-K-WVG-VE-KR-A-A-H-IRDOOE-
-O-AA-V-KQ-Y-K-P-QQ-R-WVR-VG-K-RH-IRV-DE-
-H-AA-V-KQ-Y-K-PT-QQ-X-F-R-WVG-VQ-KT-IX-A-Y-R-OEN-X-
-S-AET-R-I-OL-A-KE-R-A-ERHR-A-W-T-ENL-R-
-C-AA-V-R-I-E-TKV-FPR-PQ-Q-FVQVK-T-K-I-A-H-R-RDOENL-S-
-TA-V-RP-I-K-PT-F-K-VG-OS-RR-C-OPEN-S-
-Q-P-Q-V-Q-I-ER-ILTY-H-KK-SQ-T-FCKILEF-RGY-GPRRQF-LSI-RR-MR-ENO-
-TR-TAG-V-Q-I-ER-ILTF-HF-S-RO-T-F-FRKVESODKO-GPRR-HRT-T-R-EN-LS-C-
-TR-TAG-V-Q-I-ER-ILTF-HF-T-SQ-T-F-FKVVEQYKK-GPRR-H-R-T-K-N-I-
-TR-TAG-V-Q-I-ER-ILTF-HF-T-RO-T-F-FKVVEQYKK-GPRR-H-R-T-K-N-C-
-Q-TE-V-IV-EK-LLYK-N-P-SQ-T-R-VG-KVRVR-F-Q-AA-T-RS-Q-MR-KEN-S-
-Q-TE-V-IV-EK-LLYK-N-P-SQ-T-R-VG-KVRVR-F-Q-AA-T-RS-Q-MR-KEN-ST-
-Q-TE-V-IV-EK-LLYK-N-P-SQ-T-R-VG-KVRVR-F-Q-AA-T-RS-Q-MR-KEN-S-
-ST-TAGEV-R-IR-EK-LLSC-N-PQA-KAO-P-FVVVO-ONGKPOWRRDNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-GT-S-TAGEV-R-IR-EK-LLSC-N-PQA-KAO-P-FVVVO-ONGKPOWRRDNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-S-TAGEV-R-IR-EK-LLSC-N-PQA-KYO-P-FVVVO-ONGKPOWRRDNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-GS-SS-TANEV-R-IR-EK-LLSH-N-PSA-TGO-P-FRVVVEGKDGSGEGSTTRKORRRNSRRGIRMRARDNIRTQQSSSSSLAQ-TYFPLGAEVLGILA-
-GS-S-TANEV-R-IR-EK-LLSY-N-PSA-EGO-P-FRVVVEGKDGSGEGSATRKORRRNSRRGIRMRARDNIRTQQSSSSSLAQ-TYFPLGAEVLGILA-
-GS-S-TAGEV-R-IR-EK-LLSC-N-PTA-KRO-P-FVVVO-ONGKPOWRRDNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-GS-S-TAGEV-R-IR-EK-LLSC-N-PTA-KRO-P-FVVVO-ONGKPOWRRDNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-S-TAGEV-R-IR-EK-LLSC-N-PTA-KRO-P-FVVVO-ONGKPOWRRDNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-S-TAGEV-R-IR-EK-LLSC-N-PTA-KRO-P-FVVVO-ONGKPOWRRDNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-GT-P-EGEV-R-IR-EK-LLSC-KFPA-KNO-P-TVSHV-XSQEGPTWKQWRNRNRGRRLAT-NXRRNKQGSSESFAF-ANFPLGAKVLGILA-
-GT-P-EGEV-R-IR-EK-LLSC-KFPA-KNO-P-TVSHV-XSQEGPTWKQWRNRNRGRRLAT-NXRRNKQGSSESFAF-ANFPLGAKVLGILA-
-ST-P-EGEV-R-IR-EK-LLSC-KFPA-KNO-P-TVSHV-XSQEGPTWKQWRNRNRGRRLAT-NXRRNKQGSSESFAF-ANFPLGAKVLGILA-
-ST-P-EGEV-R-IR-EK-LLSC-KFPA-KNO-P-TVSHV-XSQEGPTWKQWRNRNRGRRLAT-NXRRNKQGSSESFAF-ANFPLGAKVLGILA-

-ST-P-TAGEV-R-IR-EQ-LLSC-RFPA-KYO-P-KVSDV..RSOGENPTWKQWRNRNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-P-TAGEV-R-IR-EQ-LLSC-RFPA-KYO-P-KVSDV..RSOGENPTWKQWRNRNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-P-TAGEV-R-IR-EQ-LLSC-KFPA-RYO-P-KVSDV..RSOGENPTWKQWRNRNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-P-TAGEV-R-IR-EQ-LLSC-KFPA-RYO-P-KVSDV..RSOGENPTWKQWRNRNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-P-TAGEV-R-IR-EQ-LLSC-RFPA-KYO-P-KVSDV..RSOGENPTWKQWRNRNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-ST-P-TAGEV-R-IR-EQ-LLSC-RFPA-KYO-P-KVSDV..RSOGENPTWKQWRNRNRRLRMAK-NSRGDKQKRGSKPPTK-ANFPLGAKVLGILA-
-R-P-QQ-V-Q-IR-E-LLQO-QOYHRGPEG-KGPP-I-RVAVKHGKVTPTTPTTHLKNTHDKA-VAAGHARSKRGSFKTLHGR-VMGSLSLCRPSCPTRLDRRTSMGCVSH-
-R-P-QQ-V-Q-IR-E-LLQO-QOYHRGPEG-KGPP-I-RVAVKHGKVTPTTPTTHLKNTHDKA-VAAGHARSKRGSFKTLHGR-VMGSLSLCRPSCPTRLDRRTSMGCVSH-
-KOH-S-TRQ-V-Q-IR-EV-LST-ARKKA-YHP-RTGP-REPPSLQYLQAAIRYG-VTTIPT-LSFKNGRHS-AATGSSMGYHRGG-KTLQRRDHHMMGSLVTTISAPTLDRRTSHGSRHRHFKHNAERNMEAL-
-CK-N-TRD---W-EK-IMAF-AMPT-K-GC-L-F-C-R-Q-OHVQKAA-ESRKTSLRGLWTKRAMGSMVSRHHGNGKGGGOTFPFPR-FGSLGLILCOOYRVRRGSLHEIHHYSK-
-CK-N-TRD---W-EK-IMAF-AMPT-K-GC-L-F-C-R-Q-OHVQKAA-ESRKTSLRGLWTKRAMGSMVSRHHGNGKGGGOTFPFPR-FGSLGLILCOOYRVRRGSLHEIHHYSK-
-VK---WHRD-VR-IR-EK-LLHS-KMPT-K-GC-L-F-C-R-Q-OHVQKAA-ESRKTSLRGLWTKRAMGSMVSRHHGNGKGGGOTFPFPR-FGSLGLILCOOYRVRRGSLHEIHHYSK-
-FK-N-TQRD-R-ER-ITMC-Q-PL-K-GC-L-F-C-R-Q-OHVQKAA-ESRKTSLRGLWTKRAMGSMVSRHHGNGKGGGOTFPFPR-FGSLGLILCOOYRVRRGSLHEIHHYSK-
-YK---WTSRC-R-M-EK-LLHE-RN-VA-K-GC-L-F-C-R-Q-OHVQKAA-ESRKTSLRGLWTKRAMGSMVSRHHGNGKGGGOTFPFPR-FGSLGLILCOOYRVRRGSLHEIHHYSK-
-HFY-H-VH-IR-EK-LLK-RFP-KA-OG-L-F-C-R-Q-OHVQKAA-ESRKTSLRGLWTKRAMGSMVSRHHGNGKGGGOTFPFPR-FGSLGLILCOOYRVRRGSLHEIHHYSK-
-W-A-WTO---I-MP-DHRY-OLET-G-L-L-R-VNRGK-SS-GSGATGATGGLGERH-RN-CRGGKALSGVIGPSFSLCSKTYQ-
-SOH-E-WTONVV-NIRTGKIN-IDA-Q-HK-A-G-L-T-C-QV-OHEOL....ORAGAFRRTS-NS-GPSRYARALCNKGTAFPGKSPCKSISLLSTERV-
-SOHV-WTONVV-DTIRSGRLDRINA-Q-HK-A-G-L-T-C-QV-OHEOL....OGTSTYRRTS-NS-GPSRYARALCNKGTAFPGKSPCKSISLLSTERV-
-SOH-E-WTO-VKNTIROGYLHPIDS-K-HO-L-G-L-T-A-C-QV-OHEOL....R-RKA-NRRTPGMT-GSSRYARAVCHGKTAFPGKSPCKSISLLSTERV-
-WK-LP-TEQ-Q-KR-LTV-YFHW-K-GK-LSYATCNRGRGPRD-RR-RRGSKYLVG-LSGENOSGGKITLPPRVPPFSLERMHTLA-
-WE-P-TAA-V-V-Y-ER-LVA-YSPW-K-GO-T-L-R-Y-KFCRNGR-STRTGTTGRRSG-RVAG-IIGTSEGRSGITLPPRVPPFSLERMHTLA-
-GE-P-T-Q---F-ER-LVA-YFHW-K-GO-T-L-R-Y-KFCRNGR-STRTGTTGRRSG-RVAG-IIGTSEGRSGITLPPRVPPFSLERMHTLA-
-F-P-T-Q---GV-YR-IOA-YFPR-K-GO-T-L-R-Y-KFCRNGR-STRTGTTGRRSG-RVAG-IIGTSEGRSGITLPPRVPPFSLERMHTLA-
-TH-A-QOLDV-R-IR-EK-LLGO-QHL-T-Y-PK-TPLT-EKL-FLALVRYGATPT-SSA-LDLPDGH-KTG-TGRHLGAKRRSP-LTKGRAPMHLGTNGAAC-
-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-GSN.CM.99.CM66-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-GSN.CM.99.CM71-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-TAL.CM.00.266-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-TAL.CM.01.8023-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-MUS.1.CM.01.1085-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-MUS.1.CM.01.CM129-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-MUS.2.CM.01.CM1246-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-MUS.2.CM.01.CM2500-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-SYK.KE.x.KE51-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-SYK.KE.x.SYK173-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-RCM.GA.x.GAB1-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-RCM.NG.x.NG411-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-GRV.ET.x.GRI.677-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-SAB.SN.x.SABIC-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-TAN.UG.x.TAN1-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-VER.DE.x.AGM3-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-VER.KE.x.9063-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-VER.KE.x.AGM155-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-VER.KE.x.TY01.patent-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-
-COL.CM.x.CGUI-TR-S-QA-DV-R-IR-EA-XLGN-HHIO-T-Y-NK-TPPT-EKL-FLACFYKGTCTE-SSTLDLPRGSH-ARRSAGRHMGPKRGGPXALLTKGRAPMHLGTNGAAC-

Vif end

Vif end

MAC.US.x.239
H2A.DE.x.BEN
H2A.GW.x.ALI
H2A.SN.x.ST
H2B.CI.x.EH0
H2B.GH.86.D205
H2G.CI.92.ABT96
H2U.FR.96.12034
SMM.SL.92.SL92B
SMM.US.x.H9
SMM.US.x.PGMS3
SMM.US.x.S1VsmH635F_L3
MAC.US.x.251.1A11
MAC.US.x.251.BK28
MAC.US.x.EMBL_3
STM.US.x.STM
MNE.US.x.MNE027
MND-2.CM.98.CM16
MND-2.GA.x.M14
MND-2.x.x.5440
DRL.x.x.FA0
RCM.GA.x.GAB1
RCM.NG.x.NG411

^Vpx start
MSD..PRERIP..PGNSGEETIGEAFEWLNRVTYEEINREAVNHLPRELIFQVWORSWEYNHDEQGMSPSYVKYRYLCLIQKALFMHCKKGCRLGEGHGAGGW.RPGPPPPPPPPGLA*
-T---V---E-I-AL-----R-----A-T---M---I-T-F-R-T-W-DM-RE-LEDQ-----V-
-AN---TV---D---AL-----R-----O-T---M---MYT-FM-T-G---P---S-----V-
-AG---T---D---A-----R-----I-T---M---M-I-S-R-T-G---P---S-----V-
-V---V---ET-L-HL-V-----K-A-RE---I-T---M---M-I-FA-G-R---P---S-----
-V---D-V---A-ET-L-----A-RE---I-T---L-M---M-V-YT---Q---P---S-----
-X---E-D---E-XT---I-----R-----A-T---L-M---M-V---T-QK---P---Q-----
-G---E-V---S-E---RD---A-Q-----Q-R---E-T---Q---P---S-----I-
-T---HN-AL-OT-Q-----R-C---V---Y---A---VQ-M---M-Q-FR-T-R---SQ---T-----
-XX---X---XX-X-D-H-X---A---X---R-X---M---V-T-X---GE-----S-----
-----E-----G---A-----R-----M---E-T-----V---R---E-----S-----
-----M---E-T-----M---E-T-----M---E-T-----M---E-T-----M---E-T-----
-----O-----M-----O-----M-----O-----M-----O-----M-----
-----SNX-----PG-----S-R-----
-----A-E---H---D-----R-----PG-----S-R-----
-AE....GA-EI-EGA....VDLNT--E-SL-K--Q--RL-FHP-FL-RL-NACI-H---RHQR-L-A-----L-MN--M-T-MQE-P-RSG--P-----MV-
-AE....A-EA-QGA....VGLEQ--E-SL-QV---QL-FHP-FL-RL-NTCV-H---RLRRTLN-A-----L-MH--M-V-MQO-P-RSG--S-----M-
-AE....A-EA-EGA....VGLEQ--ETSL-R---RL-FHP-FL-RL-NTCV-H---RHQR-LD-A-----L-MH--MYT-MQO-P-RNG-RPR-----M-
-AERQSV--A-AE-MGA....V-LE---Q-SLLR--Q--RL-FHP-FL-RL-NTCM-HY--ALQL-FT-S---L-L--M---FQO--S--QGR-PPPLRPAGDRL---PP--
-AE....A...EVPT-AGEAEFQWLRDMLEKVNLEA.RL-FHP-F-RL-RTCV-H---VHQR-LE-AA---L-M---I-OT--SQR.....PNPR-AV-ERITIL-M-
-AE..G--V...EAPT-AGDVEF-PWLHRMLT-VNLEA.RL-FHP-F-RL-RTCV-H---RL-R-LE-AG---L-M---I--QS--SQR.....Q-QAREA-ERIQIL-M-^

112
114
113
113
112
112
112
113
113
113
113
113
113
113
66
113
113
100
100
100
114
105
109

	Vpr start	amphipathic α -helix		frameshift in HXB2	Vpr end in HXB2		Vpr end
		oligomerization	H(S/N)RIG motifs				
H1B. FR. 83. HXB2	MEQA	PEDGQRPQREPHNEWTLELLEELKNEAVRHFRPRLHGLGHQIHYETGD	TWAGVEAIIIRILQQLFIH#FRIGCRHSRIGVTR				96
H1A1.UG.85.U455		YA-A-S-H-D-Q-N	E-Q-IIP	G-G			96
H1A. US. 90. WEAU160		Y-A-S-V-S	T-I-P				97
H1C. ET. 86. ETH2220		Y-A-Q-P-N-Y	S-L-T-M	Q-IL			97
H1D. CD. 84. 84ZRB85		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H1F1. BE. 93. VTF50		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H1G. SE. 93. SE6165		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H1H. CF. 90. 056		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H1J. SE. 93. SE7887		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H1K. CM. 96. MP535		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H101. AE. TH. 90. CM240		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H102. AG. NG. X. IENG		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H103. AB. RU. 97. KAL153.2		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H104. cpx. CY. 94. CY032		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
H1N. CM. 95. YBF30		Y-A-I-S-P-S-Y	Q-I-V-P	S			96
H10. BE. 87. ANT70		Y-A-I-S-P-S-Y	Q-I-V-P	S			96
H10. CM. 91. MP5180		Y-A-I-S-P-S-Y	Q-I-V-P	S			98
H1P. FR. 06. RBF168		Y-A-I-S-P-S-Y	Q-I-V-P	S			101
CPZ. CM. 01. SIVcpzCAM13		Y-A-I-S-P-S-Y	Q-I-V-P	S			99
CPZ. CM. 05. SIVcpzEK505		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
CPZ. CM. 05. SIVcpzLB7		Y-A-I-S-P-S-Y	Q-I-V-P	S			96
CPZ. CM. 05. SIVcpzMB66		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
CPZ. CM. 05. SIVcpzMT145		Y-A-I-S-P-S-Y	Q-I-V-P	S			99
CPZ. CM. - SIVcpzMB897		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
CPZ. CM. - SIVcpzDP943		Y-A-I-S-P-S-Y	Q-I-V-P	S			96
CPZ. TZ. 2001. TAN2		Y-A-I-S-P-S-Y	Q-I-V-P	S			84
CPZ. TZ. 2002. TAN3.1		Y-A-I-S-P-S-Y	Q-I-V-P	S			84
CPZ. TZ. 00. TAN3		Y-A-I-S-P-S-Y	Q-I-V-P	S			84
CPZ. CM. 98. CAM3		Y-A-I-S-P-S-Y	Q-I-V-P	S			96
CPZ. CM. 98. CAM5		Y-A-I-S-P-S-Y	Q-I-V-P	S			96
CPZ. GA. 88. GAB1		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
CPZ. GA. 88. GAB2		Y-A-I-S-P-S-Y	Q-I-V-P	S			96
CPZ. US. 85. CPZUS		Y-A-I-S-P-S-Y	Q-I-V-P	S			101
CPZ. CD. 90. ANT		Y-A-I-S-P-S-Y	Q-I-V-P	S			89
GOR. CM. 2007. SIVgor2139.287		Y-A-I-S-P-S-Y	Q-I-V-P	S			99
GOR. CM. 2007. SIVgorCP2135con		Y-A-I-S-P-S-Y	Q-I-V-P	S			99
GOR. CM. 2004. SIVgorCP684con		Y-A-I-S-P-S-Y	Q-I-V-P	S			99
H2A. DE. x. BEN		Y-A-I-S-P-S-Y	Q-I-V-P	S			105
H2A. GW. x. ALI		Y-A-I-S-P-S-Y	Q-I-V-P	S			106
H2A. SN. x. ST		Y-A-I-S-P-S-Y	Q-I-V-P	S			105
H2B. CI. x. EHO		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
H2B. GH. 86. D205		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
H2B. CI. 92. A6T96		Y-A-I-S-P-S-Y	Q-I-V-P	S			103
H2U. FR. 96. 12034		Y-A-I-S-P-S-Y	Q-I-V-P	S			98
SMM. SL. 92. SL92B		Y-A-I-S-P-S-Y	Q-I-V-P	S			101
SMM. US. x. H9		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
SMM. US. x. PGM53		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
SMM. US. x. SIVsmH635F_L3		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
MAC. US. x. 239		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
MAC. US. x. 251. IA11		Y-A-I-S-P-S-Y	Q-I-V-P	S			101
MAC. US. x. 251. BK28		Y-A-I-S-P-S-Y	Q-I-V-P	S			98
MAC. US. x. EMBL. 3		Y-A-I-S-P-S-Y	Q-I-V-P	S			98
STM. US. x. STL		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
MNE. US. x. MNE827		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
DEN. CD. x. CD1		Y-A-I-S-P-S-Y	Q-I-V-P	S			99
LST. KE. x. Lh07		Y-A-I-S-P-S-Y	Q-I-V-P	S			115
SUN. GA. 98. L14		Y-A-I-S-P-S-Y	Q-I-V-P	S			117
MND. 1. GA. x. MNDGB1		Y-A-I-S-P-S-Y	Q-I-V-P	S			105
LST. CD. 88. 447		Y-A-I-S-P-S-Y	Q-I-V-P	S			115
LST. CD. 88. 485		Y-A-I-S-P-S-Y	Q-I-V-P	S			115
DEB. CM. 99. CM40		Y-A-I-S-P-S-Y	Q-I-V-P	S			118
DEB. CM. 99. CM5		Y-A-I-S-P-S-Y	Q-I-V-P	S			118
LST. CD. 88. 524		Y-A-I-S-P-S-Y	Q-I-V-P	S			115
OLC. CI. 97. 97C112		Y-A-I-S-P-S-Y	Q-I-V-P	S			97
WRC. CI. 97. 97C114		Y-A-I-S-P-S-Y	Q-I-V-P	S			133
WRC. CI. 98. 98C104		Y-A-I-S-P-S-Y	Q-I-V-P	S			133
WRC. GM. 05. Pbt 05GM. X02		Y-A-I-S-P-S-Y	Q-I-V-P	S			133
MND. 2. CM. 98. CM16		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
MND. 2. GA. x. M1		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
MND. 2. x. x. 5440		Y-A-I-S-P-S-Y	Q-I-V-P	S			102
DRL. x. x. FA0		Y-A-I-S-P-S-Y	Q-I-V-P	S			101
MON. CM. 99. L1		Y-A-I-S-P-S-Y	Q-I-V-P	S			121
MON. NG. x. NG1		Y-A-I-S-P-S-Y	Q-I-V-P	S			155
GSN. CM. 99. SGN166		Y-A-I-S-P-S-Y	Q-I-V-P	S			136
GSN. CM. 99. CN71		Y-A-I-S-P-S-Y	Q-I-V-P	S			116
TAL. CM. 00. 266		Y-A-I-S-P-S-Y	Q-I-V-P	S			115
TAL. CM. 01. 8023		Y-A-I-S-P-S-Y	Q-I-V-P	S			115
MUS. 1. CM. 01. 1085		Y-A-I-S-P-S-Y	Q-I-V-P	S			136
MUS. 1. CM. 01. CM1239		Y-A-I-S-P-S-Y	Q-I-V-P	S			136
MUS. 2. CM. 01. CM1246		Y-A-I-S-P-S-Y	Q-I-V-P	S			136
MUS. 2. CM. 01. CM2500		Y-A-I-S-P-S-Y	Q-I-V-P	S			136
RCM. GA. x. GAB1		Y-A-I-S-P-S-Y	Q-I-V-P	S			101
RCM. NG. x. NG411		Y-A-I-S-P-S-Y	Q-I-V-P	S			116
SVK. KE. x. KE51		Y-A-I-S-P-S-Y	Q-I-V-P	S			114
SVK. KE. x. SVK173		Y-A-I-S-P-S-Y	Q-I-V-P	S			119
GRV. ET. x. GRI. 677		Y-A-I-S-P-S-Y	Q-I-V-P	S			141
SAB. SN. x. SAB1C		Y-A-I-S-P-S-Y	Q-I-V-P	S			120
TAN. UG. x. TAN1		Y-A-I-S-P-S-Y	Q-I-V-P	S			120
VER. DE. x. AGM3		Y-A-I-S-P-S-Y	Q-I-V-P	S			120
VER. KE. x. 9063		Y-A-I-S-P-S-Y	Q-I-V-P	S			120
VER. KE. x. AGM155		Y-A-I-S-P-S-Y	Q-I-V-P	S			120
VER. KE. x. TY01. patent		Y-A-I-S-P-S-Y	Q-I-V-P	S			120
COL. CM. x. CGU1		Y-A-I-S-P-S-Y	Q-I-V-P	S			93

[illegible]

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H1D.CD.84.84ZROB5
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CPZ.TZ.2007.TAN2
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CPZ.US.85.CPZU5
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H2B.GH.86.D205
H2G.CI.92.ABT96
H2G.FR.96.L2034
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DRL.x.x.F40
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GSN.CM.99.CM166
GSN.CM.99.CM71
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LST.CD.88.485
LST.CD.88.524
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MON.CM.99.L1
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MUS-2.CM.01.CM1240
MUS-2.CM.01.CM2500
OLC.CI.97.97C112
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RCM.NG.x.NG411
SAB.SN.x.SAB1C
SUN.GA.98.L14
SVK.KE.x.KE51
SVK.KE.x.SYK173
TAL.CM.00.266
TAL.CM.01.8023
TAN.UG.x.TAN1
VER.DE.x.AGN3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.TYO1 patent
WRC.CI.97.97C1
WRC.CI.98.98C104
WRC.GM.05.Pbt.05GM.X02

GYTRPFKTTSSGSGSACKH
GSTRPVETSSGSGGPRCK
GSTRPVKTTSSGSGGQSCKR

LIEDTTSFARE

TVTRP

PLV Proteins

	Rev start	exon 1 end	exon 2 start	NLS	Leu-rich effector domain	Rev end
H1B.FR.83.HXB2	MAGRS.	GDSDEELIRTVRLTKLYQS	NPPNN.	PEGTQRAQRNRNRWRERQRQISHTSIRLTGYLGR	SAEVPYLQLPPLRLTLDCNEDCGTSGTG	GVGSPQIIL.VESPTVLESSTKE
H1A1.UG.85.U455	-R	NP-D-LKA-I-I	C-R-S-K	A-D-L-SOC	I-R-S-S	OPGGTET-G-S-SA-G-N
H1B.UG.90.HAU160	-R	D-LKA-I-I	-	-	P-D-	-
H1C.ET.86.ETH2220	-	LKA-I-I	-	A-TL-GW-N	-	-
H1D.CD.84.84ZRO85	-	D-LTA-I-I	-	A-Y-G-S	-	-
H1F1.BE.93.VI850	-	T-LKA-KC-I	-	A-RAL-D-S	-	-
H1G.SE.93.SEB165	-	L-A-KA-I	-	A-SA-TTC	-	-
H1H.CF.98.065	-	L-LOVCK-I	-	A-RE-C-C	-	-
H1I.SE.93.SE7887	-	DQ-LA-I	-	A-N-D-PSSC	-	-
H1K.CM.96.MP535	-R	P-Q-LT-I-T-E	-	A-K-S-L-SAC	-	-
H1O1.AE.TH.90.CM240	-	ST-L-A-I-I	-	A-SA-S-C	-	-
H1O2.AG.NG.x.IBNG	-	L-A-I-I	-	A-RA-S-C	-	-
H1O3.AB.RU.97.KAL153_2	-	-	-	A-H-L-Q	-	-
H1O4.CPX.CY.94.CY032	-	NI-D-FKAA-A-I	-	A-N-T-A	-	-
H1N.CM.95.YBF30	-	VN-L-A-V-I	-	A-SK	-	-
H1O.BE.87.ANT70	-	E-DQ-LQAIOI-I	-	A-R-ADTLAA-V-VVHG	-	-
H1O.CM.91.MPV5180	-	EE-QQ-LQAIOI-I	-	R-A-V-DLAT-A-VVHG	-	-
H1P.FR.06.RBF168	-	DEDL-L-A-I-I	-	Q-D-AG-ASR	-	-
CPZ.CM.91.SIVcpzCAM13	-	DEDL-L-A-I-I	-	A-V-L-V	-	-
CPZ.CM.05.SIVcpzEK505	-	VN-L-AI-V-I	-	A-RAL-SSCV-G	-	-
CPZ.CM.05.SIVcpzLB7	-	R-L-A-I-I	-	A-H-SE-AG-S-C-E	-	-
CPZ.CM.05.SIVcpzMB66	-G	N-L-A-I-I	-	A-N-L-S-C-E	-	-
CPZ.CM.05.SIVcpzMT145	-	E-G-N-L-AI-I-RI-E	-	Y-S-QS-R-K	-	-
CPZ.CM.-SIVcpzMB897	-	-	-	F-S-P-R-K	-	-
CPZ.CM.-SIVcpzDB943	-	E-A-TR-LOV-I-I-D	-	Y-D-NK-P	-	-
CPZ.TZ.2001.TAN2	-	EE-AN-LO-I-I-D	-	Y-S-AA-S-T	-	-
CPZ.TZ.2002.TAN3_1	-	EE-AN-LO-I-I-D	-	Y-S-GA-S-A	-	-
CPZ.TZ.08.TAN1	-	EE-AN-LY-I-I-D	-	Y-S-GA-S-T	-	-
CPZ.CM.98.CAN3	-	E-AC-LOA-I-I-D	-	Y-D-NK	-	-
CPZ.CM.98.CAN5	-	E-E-TR-LOA-I-I-D	-	-	-	-
CPZ.GA.88.GAB1	-	EPDQ-AR-LOA-KI-I	-	Y-S-NR-S-K	-	-
CPZ.GA.88.GAB2	-	E-R-L-A-KA-I-D	-	Y-S-NR-S	-	-
CPZ.US.85.CPZUS	-	G-A-Q-L-K-I-I-A	-	Y-F-NS-S	-	-
CPZ.CD.98.ANT	-	EELGEG-Q-LKA-KI-I	-	Y-K-A-S-A-K	-	-
GOR.CM.2007.SIVgor2139_287	-	DEDLQ-LTKI-I-R	-	W-E-GPS-NST	-	-
GOR.CM.2007.SIVgorCP2135con	-	DEDLQ-LTKI-I-R	-	C-E-GPS-NST	-	-
GOR.CM.2004.SIVgorCP684con	-	DEDLQ-LTKI-I-RI	-	W-E-GPS-NST	-	-
H2A.DE.x.BEN	SE-A	D-G-QGKL-LR-H-T	-	Y-Q-GP-ASO	-	-
H2A.GW.x.ALI	TE-A	GE-D-Q-KL-LR-H-T	-	Y-Q-GP-ASO	-	-
H2A.MF.x.ALI	SE-A	E-R-K-LR-H-T	-	Y-Q-GP-ASO	-	-
H2B.CI.x.EHO	NA	ERD-QGKL-LH-H-T	-	Y-Q-GP-ASO	-	-
H2B.GH.86.D205	TA	EGD-QGKL-LH-H-T	-	Y-Q-GP-ASO	-	-
H2C.CI.92.ABT96	SNL	EE-RKRL-HF-H-T	-	Y-Q-GP-XANO	-	-
H2Q.FR.96.12034	SNL	E-GVQ-LR-H-H-T	-	Y-Q-GP-ANO	-	-
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SMU.SS.x.SIVsmH635F_L3	SST	-E-RKRL-HF-H-T	-	Y-Q-GP-ANO	-	-
MAC.US.x.239	SWHE	RE-RKRL-H-H-T	-	Y-T-GP-ANO	-	-
MAC.US.x.251.1A11	SSHE	RE-RKRL-H-H-T	-	Y-T-GP-ANO	-	-
MAC.US.x.251.BK28	SSHE	RE-RKRL-H-H-T	-	Y-T-GP-ANO	-	-
MAC.US.x.EMBL_3	SSHE	RE-RKRL-H-H-T	-	Y-T-GP-ANO	-	-
STM.US.x.STM	SDO	E-RKRL-QF-H-T	-	Y-Q-GP-ANO	-	-
RME.US.x.MME027	SLG	EE-R-RTI-RI-H-T	-	Y-T-GPS-ANO	-	-
RGN.GA.x.GAB1	D-ROKID	D-CM-LI	-	Y-Q-NK-KK	-	-
RNC.NG.x.NG411	LLGEEEE	A-Q-RI-RI-H-IHL	-	Y-Q-SG-ANO	-	-
SAB.SN.x.SABIC	SLGO	L-R-F-I-F-TT	-	Y-P-GQ-ARO	-	-
GRV.ET.x.GRI7_677	SLGK	KQALKI-T-G	-	Y-Q-FS-ARO	-	-
TAN.UG.x.TANI	SLG	D-RI-RTI-RI-H-T	-	QY-P-G-ARO	-	-
VER.DE.x.ACM3	R-L	AF-MKN	-	Y-Q-ARO	-	-
VER.KE.x.9063	PLGP	RKFVS-AY-NRT	-	Y-P-V-ARO	-	-
VER.KE.x.AGM155	PLGP	R-L-L-AF-R	-	Y-S-V-ARO	-	-
VER.KE.x.TY01 patent	PLGP	R-L-L-W-ST	-	Y-P-SG-ARO	-	-
DEB.CM.99.CM40	HAGGR	SAE-NTROLLK-V-S-IKILVY	-	Y-K-GG-SAST	-	-
DEB.CM.99.CM5	HAGGR	A-QA-L-L-RTKISLYS	-	Y-K-GG-SAST	-	-
MON.CM.99.L1	NGR	RRLLSALAARVLAQESRILSSFFSD	-	Y-R-Q	-	-
MON.NG.x.NG1	-AERG	AAVODILRLA-GAIRITRESRLTSLPSTY	-	A-E-VX-LC	-	-
GSN.CM.99.CN166	DHARGN	QK-QNLLIACR-IKTLHRSRLTSLPAD	-	A-G-VE-NR	-	-
GSN.CM.99.CN71	DPANGR	QK-QNLLIACR-IKTLKRSRLTSLPAD	-	A-VRO-H	-	-
MUS-1.CM.01.1085	-Y-E	NVOELI-ACRATILYOSRLTSPSSY	-	A-KK-R	-	-
MUS-2.CM.01.97C1239	-A-G	NVOELI-TCRITILYOSRLTSPSSY	-	Q-D-D-R	-	-
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GOR.CM.2007.SIVgor2139.287	K-M...EKKK-LW...LSYCL-SSLII...P...GLSS-A...RDVE...V...HS-A-I-Q...	H-P...K-D-E-N-A-Q...I...	TMT-LNPDNS		131
GOR.CM.2007.SIVgorCP2135con	SL...LILL-IE...ATHYA...Q-N-V-A-NVYSO-Q-I-Q...	S-I...F-P-E-X-T-DI-N-N-D-QD...	VM-T-N-KTET-XQTNXN		125
GOR.CM.2004.SIVgorCP684con	SL...L-LT-IE...KTEHYA...R-K-V-A-SFVSK-Q-I-Q...	S-T...F-L-E-T-DI-N-N-D-QD...	VM-TMT-SNDTKGS-KSTATTISANT		132
MON.CM.99.L1	KL...A-ST-CLMILT...VNGSN-T...P...PP...PNYGSK-AG-N-LASS-L...	T-S...LY...I-E-AYO...Y-E-V-MK-FS-A...	RM-L-VEINTVS-ASTTAPSTPT		137
MON.NG.x.NG1	MR...MKTIIVLTLCLM-T-TSGSX...SGN-S-F...Y-P...PP...PYGSK-AG-N-LASS-L...	S-V-RALP...I-S-AYN...Y-E-V-MK-FS-A...	RM-R-OXINES-TVXPTTXX-ATTP		147
GSN.CM.99.CM166	KT...VESMMILAVS-ALMAL-IPG...LKECT-F...RD...PP...PDIASRDK...I-N...	S-S-A-P...I-K-I-T-K...M-DEVUD-MV-FN-A...	GMV-NLNTS-SEPTTTP-PPHST		147
CPZ.CM.98.CAM3	K-M...EKIKG-SLIEKY-FM-LIIP-LT...GSDO-A...D-P...E-S-LNK-A-I-SO...	QIP...N-T-A-N-T...	I-TM-KRVTFNSTS-RNKSTMTT		147
CPZ.CM.98.CAM5	KAM...ERKKNW...IICY-M-LIIP-LT...GHEW-A...E...E-S-LNK-A-I-SO...	V...YMP-S-S-N-A-Q-S...	I-TMO-T-IST-TN		140
TAL.CM.00.266	KYL...AVI...FC-AYLGR...IIGNOY-I...N...PP...MARDQ-S-SO...	S-QNL...PV-L-Y-DVY...K-Y-DHIA-MD-FLTATR-T...	I-RM-E-ITKNLTISANTTAPT		129
TAL.CM.01.8023	KCL...QVLCIAICVIANIGK-LT...SA-DOFL...N...PP...MARDQ-S-SO...	S-QNL...PV-L-Y-DVY...K-Y-DHIA-MD-FLTATR-T...	RM-RMA-ITKNLTGYVAPPTNSTN		139
GSN.CM.99.CN71	MR...VGRKMLVVS-T-LALLPGS...RSKVT-F...RD-K...PP...DIITSRDK...I-N...	S-S-S-P...I-E-K-VY-DEVUD-MV-FN-A-R...	RM-KLWPTS-T-TP-TTTATSPS		147
MUS.1.CM.01.1085	PRM...T-LRA-S-T-LT-LLS-SI...IIGWGO-F...D...PP...NIANR-PG-I-T-L...	A-Q...ISGKFDIYK-Y-D-TD-VR-IFN-A...	M-KM-AKVT-Y-RS		135
MUS.1.CM.01.CM1239	PRM...S-LMG-M-T-LT-LLS-SI...IIGWGO-F...D...PP...NIANR-PG-I-T-L...	A-Q...ISGKFDIYK-Y-D-TD-VR-IFN-A...	M-KM-SRINVRTPS		134
MUS.2.CM.01.CM1246	PAM...ERTRILTALST-ALSLSLIR...KHA-Q-F-R-S-N...PP...NIANR-PG-I-T-L...	A-Q...ISGKFDIYK-Y-D-TD-VR-IFN-A...	M-KM-DE-NISMS		137
MND.1.GA.x.MNDG81	KCP...GLFL...I-CLA#LV.G...IIG-OY-F...K...H-I...DNSSL-V-TN-I-SL-DYD...	ETPIDK...TGLIRE-OI-Y-AWHAMG-ML-TI...	IN-Y-KMO-QETE-VSA-TAKPITPTPT		133
WRC.CI.97.CT14	IF...VLGL-GIAI...SLAVOY...Q-EDS...DF-L...NRSL-VSTR-I...HLEHLE...	OYMEIK...TRKVAE-OI-Q-AWGTGT-MI-TL...	I-Y-KMO-PGEGETE-OPCESNTT		128
WRC.CI.98.CM104	NTF...IFIAVVG-GIGL...GLG-OYI...Q-E-K...DFML...NRSL-V-TH-L...HIEIET...	OYMEIK...TKKVEE-EV-Q-AWGTGT-MI-TL...	IN-Y-KMS-LQKAP-S-NTKDFNPEISV		131
OLC.CI.97.97C112	K...L-V-CL-WLSLGI...SIGOY-F-T-K-RDSN...D-M-V...ANKSL-V-T-L-SFDEDEI...	EQPIPV-EFVYVNSD-EV-R-AWFG-A-L-AV...	F-KMO-E-PSANFTPEITPITTAAPT		134
MUS.2.CM.01.CM2500	A-M...T-SA-VFLT-LLSCSL...IWG-O-F...D...PP...NIANR-PG-I-T-L...	A-Q...I-GEYFDIYK-Y-D-TD-VR-IFN-A...	M-RM-K-NSTRP		130
DEB.CM.99.CM40	LI...QLLL-LI-GLIVIGTGK...OKKOYL...VD-K...VD...T-NSS-SG-VT-L-HALVRE...	PMP-Q-AFD...PIE-LWQ-MT-YK-F...Y-MQ-IKSTNTPPTPT-TTTTITAT	Y-MQ-IKSTNTPPTPT-TTTTITAT		138
DEB.CM.99.CM5	LSL...LIIIAS-FLVGA...P-KOO...F...G...T-NSS-SG-VT-L-HALVRE...	PMP-Q-AFD...PIE-LWQ-MT-YK-F...Y-MQ-IKSTNTPPTPT-TTTTITAT	Y-MQ-IKSTNTPPTPT-TTTTITAT		138
DEB.CD.x.CM5	RRTLKVL...LWLT-GIIC...F-I-A-RNSA...E-YOR...T-NSS-SG-VT-L-HALVRE...	PMP-Q-AFD...PIE-LWQ-MT-YK-F...Y-MQ-IKSTNTPPTPT-TTTTITAT	Y-MQ-IKSTNTPPTPT-TTTTITAT		138
H2A.DE.x.BEN	EPG...RNOL...FVVI-LTSACL...VYCQY-F-I-A-N-S-IP...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	AMN-SRVOGN-T-PNPRSSSTISR		131
H2A.GW.x.ALI	MSS...RNOL...VTI-LASACL...VYCQY-F-I-A-N-S-IP...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	IAM-SNISTEST-T-P-PGSTL		131
H2A.SN.x.ST	KMG...RNOL...FVAS-LASACL...IYCVQY-F-I-A-N-S-IP...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	AMR-NSTTAKNT-STPTTTTIA		131
H2B.CI.x.EH0	AHV...MNYL...VTIL-LSTIG...VWG-NF-F-I-A-N-S-IP...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	TH-NKTSWASSAKSETTSASLRSS		134
H2B.GH.86.D205	AYF...SS-L-PIAL-LGISG...FVCQY-F-I-A-RN...VP-I...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	AMN-SKETNPGNA-TITTKPTT		134
H2G.CI.92.ABT96	AYL...NOL...IATXLLSTYG...FYCTKY-F-I-A-RN...VP-I...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	IAMR-NKTEITKNWGLGTITVTPVAT		134
H2U.FR.96.12034	AHL...NOL...IAL-CLNAC...IYCTQY-F-I-A-RN...VP-I...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	IAMR-SKETNMRWGLGTGATTTSPA		134
SMM.SL.92.SL92B	ACL...LHL...IDI-FLSVLG...TWCQY-F-I-A-RN...VP-I...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	IAM-NKNET-RWGLTRAATTSSPT		134
SMM.US.x.PGM53	GCL...NOL...IAI-LLSAYG...IYCTQY-F-I-A-RN...VP-I...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	ITMR-NKTEIT-RWGLTKNETIPTTTT		134
SMM.US.x.SIVsmH635F.L3	GCL...NOL...IAL-LVSLE...LCVQY-F-I-A-RN...VP-I...KNRDT-G-IQ-L-DNDYD...	IIL-A-DA-N-TVT-AV-VWH-FET-I...	IAMR-NKTEIT-RWGLTRAATTTTAK		134

		signal peptide env gp120 start																		
Env start																				
MAC.US.x.239	GCL	NOL	IAI-LLSVYG	IYCT-Y	F	A-RN	IP		KNRDT-G	TQ-L	DNDGYD	AL	S-DA-N	TVT	AI-VWQ	FET-I	S	ITMR-NKSET-RWGLTK-ITTTASTT	134	
MAC.US.x.251.1A11	GCL	NOL	IAI-LLSVYG	IYCT-Y	F	A-RN	IP		KNRDT-G	TQ-L	DNDGYD	LAL	S-DA-E	TVT	AI-VWQ	FET-I	S	ITMR-NKSET-RWGLTK-STT.TTAA	133	
MAC.US.x.251.BK28	GCL	NOL	IAI-LLSVYG	IYCTQY	F	A-RN	IP		KNRDT-G	TQ-L	DNDGYD	LAL	S-DA-E	TVT	AI-VWQ	FET-I	S	ITMR-NKSET-RWGLTK-STTITIAA	134	
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STM.US.x.STM	ACP	NOL	IAI-LLSACL	IYCTQY	F	A-RN	IP		KNRDT-G	TQ-L	DNDGYD	LAI	A-DA-D	TVT	AI-VWQ	FET-I	S	IAMR-NKNET-KWGLTKGVITVTPV	134	
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LST.CD.88.447	LCP	LIL	LILTRVQGE	K-K-OY	F	K-E-V	VP-I		SANNLS-V	TS-L	DLOSVAO	IPTH-ISL	TKETID	OIIIO-AWSAMT-MV-TIM		VN-Y	RM-EGEGIG-KTAKTKT-STTP	134		
LST.CD.88.485	DCL	KULL	FLLFLGAQGE	AK-OY	F	K-E-V	VP-I		SANNLS-V	TS-L	DLOSVAO	IPTH-ISL	TKETID	OIIIO-AWSAMT-MV-TIM		IN-Y	RM-EGEGIG-KTAKTKT-STTP	134		
LST.CD.88.524	ACP	NIL	LLCLGLTAG	EK-OY	F	K-E-V	VP-I		SANNLS-V	TS-L	DLOSVAO	IPTH-ISL	TKETID	OIIIO-AWSAMT-MV-TIM	T	IN-Y	RM-EGEGIG-KTAKTKT-STTP	134		
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SUN.GA.98.L14	CP		ELLIGFSLLLG	STAIQY	F	T-K-EP	V-VP-I		SANNLS-V	TS-L	DLOTYA	PIGLE	TEGLSN	OI-O-AWQAMT-MV-TIM		IN-Y	KM-PPKPTIPSS-VKSSCDYWT	123		
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MND.2.GA.x.5440	LRY		LRVYG	G-TVSQ	F	T-K-KP	R-H		DNNS-V	TS-L	SLLHYE	OLITP	ETPIQE	ET-R-ANGA-S-MI-AV	R	Y	Y-EGEGIG-EFOAKTTPVPTT	134		
DRL.x.x.FA0	IRH	I	IIG-CI-GFLGIS	IG-H	F	T-K-EP	S-H	I	DN-SF	V-TS	SLLHYE	TEIN	IE	TVPMTE	EVIK-AWALS	MI-AV	IN-Y	KME-S-IIVNAASTTTPPTTVATT	135	
SVK.KE.x.KE51	KLF	NIIIS	VV-LVLSLIG	RLEQY	F	N-E-D	Q-VP-M		PHTGGK	KN	SSEQIEV	R-N	ISG-Y	TA-NSSHGIR	LLQ-MSD-FL	ADR	S-M	IRTL-VE-DESSG-LTTIT	131	
SVK.KE.x.SYK173	AAF	RTYI	VCLFSL-SLGF	MEKQOY	F	I-H-ED	Y-AP-T		SHGKG	KN	SADQIEV	R-N	ITG-Y	PA-NSSHMTRO	LL-MSA-FL	ANR	S-M	IRML-LDNPSATS	124	
RCM.GA.x.GAB1	DK	LVILVVI	I-LVGO	SOKPOYI	F	RNS	VP-M		DNQOS	G-LN-I	EGGISP	ST	S-R	DA-N-SLY	AKDNVWN	Y-ST	R-S	ITMN-SAINGSDWGP-APPITTKT	135	
RCM.NG.x.GA11	ARKL	ISIGIII	LLGIII	VG-OY	F	F-NSS	VP-M		DNAOS	G-LN-I	EGGISP	ST	S-K	DA-E-SLY	AKSNVWN	Y-ST	R-M	ITMY-A-NGSDWGTATQSPMTTTRA	135	
GRV.ET.x.GRI.677	GRIL	L	LIIGI	SI-G	IGN-Y	F	I-NSS	VQA-M	PNT	M-TN	I-D	HONT	P	I-EA-D	PL-K-AESN	HL-FE-TMR	S-I	IKMS-VE-NGAT-KATTIATTIMT	135	
SAB.SN.x.SABIC	KLL	TVLL	WLSGCVSLMWLVQ	Y	F	I-NSS	VQA-M	K	PNT	L-TN	I-D	EPEGTAE	PIP	I-K	DA-NR	PL-A-AESN	HL-FEST	S-M	IKMN-YR-EGGAA-T-TPTSTARPE	136
TAN.UG.x.TAN1	GPL	RKGK	VL-VILGLSLIGL	LYGTQYI	F	I-NSS	VQA-M	K	PNT	L-TN	I-D	HDYT	Q	S-K	EA-DR	PL-A-AESN	HL-FEST	M	IKMN-K-TSTAP-S-TPTSSSTT	137
VER.DE.x.AGM3	KLT	LLIG	I-LIGI	GVVL	N-RQO	F	I-NSS	VQA-M	PTTRL	TN-I	D-HYT	P	I-P	EA-ADR	PL-A-AGSN	HL-FE-T	S	IKMS-VE-NSSEP-TTPKSTASTTN	135	
VER.KE.x.9863	KPL	LGIV	LIAIGI	S-L	LS-RO	F	I-NSS	VQA-M	PTTRL	TN-I	D-HYT	P	I-P	EA-ADR	PL-A-AGSN	HL-FE-T	S	IKMS-VE-NSSEP-TTPKSTASTTN	135	
VER.KE.x.AGM155	TKF	LGIF	IV-IGI	GIGI	S-KOO	F	I-NSS	VQA-M	PTTRL	TN-I	D-HYT	P	I-P	EA-ADR	PL-A-AGSN	HL-FE-T	S	IKMS-VE-NSSEP-TTPKSTASTTN	135	
VER.KE.x.TYV1 patent	VT	ITI	GIIIGI	GIGI	VLS-O	I-F	I-NSS	VQA-M	PTPSTL	TN-I	D-HYT	P	I-P	EA-ADR	PL-A-AASN	HL-FE-TM	S	IKMN-VE-NSTRERATITTPKSTG	135	
COL.CM.x.CGU1	LRY	LFIN	LVLGIV	LSNK	Q	A-E	DVNDQOF	F	SSPEIQOVLG	L-PPPGK	V-QMPP	A-DLF	K-SFGSEVWIIITQTLT	R-R-A	AY-APMI	KVNRTE-GT-TVAPT	130			

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11B.FR.83.HXB2	STMGASMTLTVQARQLLSGIVQOQNLL	RAIEAQHLLQLTWGIKQLQARLAVERYLKQDQLLGIWGSCKGLTCTTAVPWNASWSNKS	LEQTVNHTTLMQEDREINNTSLTSHLSEESQNOQKEQNELEDKXAS	LWNWFNITNWLWYKLF	685
H1A1.UG.85.U455					686
H1B.US.90.WEAU160					687
H1C.ET.86.ETW220					688
H1D.84.84ZRO85					689
H1F1.BE.93.VI850					690
H1G.SE.93.SE6165					691
H1H.CF.90.056					692
H1J.SE.93.SE7887					693
H1K.CV.96.NPS35					694
H1M1.AE.TH.96.CM240					695
H1O2.AG.NG.x.IBNG					696
H1O3.AB.RU.97.KAL153.2					697
H104.cpx.CY.94.CY032					698
H1N.CM.95.YBF30					699
H1O.RE.97.MVT70					700
H1O.CM.91.MWP5180					701
H1P.FR.06.RBF168					702
CPZ.CM.01.SIVcpzCAM13					703
CPZ.CM.01.SIVcpzEK505					704
CPZ.CM.05.SIVcpzL1B7					705
CPZ.CM.05.SIVcpzMB66					706
CPZ.CM.05.SIVcpzMT145					707
CPZ.CM.1.SIVcpzMB897					708
CPZ.CM.1.SIVcpzDP943					709
CPZ.CD.96.NT					710
CPZ.TZ.2001.TAN2					711
CPZ.TZ.2002.TAN3.1					712
CPZ.TZ.00.TAN1					713
CPZ.GA.88.GAB2					714
CPZ.GA.88.GAB1					715
CPZ.US.95.CP205					716
GOR.CM.2007.SIVgor2139.287					717
GOR.CM.2007.SIVgorCP2135con					718
GOR.CM.2004.SIVgorCP684con					719
MON.CM.99.L1					720
GAT.ATA.S.S.A.E					721
GAT.ATA.S.S.A.E					722
GAT.ATA.S.S.A.E					723
GAT.ATA.S.S.A.E					724
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GAT.ATA.S.S.A.E					815
GAT.ATA.S.S.A.E					816
GAT.ATA.S.S.A.E					817
GAT.ATA.S.S.A.E					818
GAT.ATA.S.S.A.E					819
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GAT.ATA.S.S.A.E					981
GAT.ATA.S.S.A.E					982
GAT.ATA.S.S.A.E					983
GAT.ATA.S.S.A.E					984
GAT.ATA.S.S.A.E					985
GAT.ATA.S.S.A.E					986
GAT.ATA.S.S.A					

PLV Proteins

FR. 83. HBX2	IMVGGVLGRIVFAVLSTNVRVGRGYSPLSFOLHPT	PRGPDPRPEEGIEEGERDGR	RSIRLVNGSLALWDDLRSLCLFYSHRLRLDLIVTRIVELGG	RRGWEALKYV	WNLLQYVMSOEKNSVAITLSDNATAIAVAEGTRDV	829
H1A1. U6. 85. U455	VI - - - - - T I - - - - -	E - LG - GR - - - - -	S - F - IA - N - - - - -	FA - A - A - - - - -	LS - GR - I - - - - -	828
H1B. US. 90. WEAU160	- - - - - T I - - - - -	- - - - - A - - - - -	G - S - F - IA - N - - - - -	I - AK - - - - -	- - - - - C - - - - -	832
H1C. ET. 86. ETH2220	- - - - - I - - - - -	- - - - - LG - - - - -	OG - - - - -	F - IF - - - - -	I - AA - - - - -	829
H1D. CD. 84. 84Z8985	- - - - - I - - - - -	- - - - - G - - - - -	OG - V - T - - - - -	F - S - A - N - - - - -	I - AA - - - - -	830
H1E. 93. V18180	- - - - - I - - - - -	- - - - - K - - - - -	L - - - - -	RH - FI - A - T - - - - -	DRGL - - - - -	835
H1G. SE. 93. SE6165	- - - - - I - - - - -	- - - - - L - - - - -	LTHH - - - - -	Q - E - - - - -	OG - V - T - - - - -	839
H1H. CF. 90. 056	- - - - - I - - - - -	- - - - - LV - N - - - - -	T - G - - - - -	V - F - PVW - - - - -	S - RL - - - - -	818
H1J. SE. 93. SE7887	- - - - - I - - - - -	- - - - - I - - - - -	TEA - G - - - - -	OG - T - - - - -	F - A - N - - - - -	821
H1K. CM. 96. MP535	- - - - - I - - - - -	- - - - - I - - - - -	A - V - - - - -	- - - - -	RQ - N - I - - - - -	815
H1L. AE. TH. 90. 0240	- - - - - I - - - - -	- - - - - I - - - - -	PSHH - - - - -	- - - - -	I - AA - T - - - - -	830
H1O2. 90. 0240	- - - - - I - - - - -	- - - - - I - - - - -	THHH - - - - -	OK - E - R - G - - - - -	OG - V - T - - - - -	835
H1O3. AB. RU. 97. KAL153_2	- - - - - I - - - - -	- - - - - I - - - - -	G - - - - -	R - A - - - - -	- - - - -	818
H1O4. cpx. CY. 94. CV032	- - - - - I - - - - -	- - - - - I - - - - -	- - - - -	L - L - T - - - - -	Q - L - G - T - - - - -	828
H1N. CM. 95. YBF30	- - - - - I - - - - -	- - - - - A - I - - - - -	IT - IT - I - A - - - - -	- - - - -	ET - GGV - - - - -	825
H1O. BE. 87. AN179	- - - - - I - - - - -	- - - - - I - - - - -	VIMI - N - KNI - - - - -	Q - L - - - - -	TPNH - - - - -	828
H1P. CM. 95. PMS180	- - - - - I - - - - -	- - - - - I - - - - -	IL - - - - -	TPV - CM - - - - -	RT - G - - - - -	830
H1P. FR. 06. RBF168	- - - - - I - - - - -	- - - - - I - - - - -	IL - - - - -	LL - XXV - R - I - - - - -	V - L - LGLN - - - - -	835
CPZ. CM. 01. SIVcpzCAM13	- - - - - L - A - I - - - - -	- - - - - I - - - - -	IMS - V - VIR - - - - -	- - - - -	Q - E - GTLGETGG - - - - -	837
CPZ. CM. 05. SIVcpzEK505	- - - - - L - A - I - - - - -	- - - - - I - - - - -	ISIM - M - A - - - - -	- - - - -	RT - DA - L - NG - V - - - - -	838
CPZ. CM. 05. SIVcpzLB87	- - - - - I - - - - -	- - - - - I - - - - -	IVC - I - - - - -	- - - - -	LAQ - G - T - - - - -	838
CPZ. CM. 05. SIVcpzMB66	- - - - - I - - - - -	- - - - - I - - - - -	I - - - - -	- - - - -	R - D - - - - -	838
CPZ. CM. 05. SIVcpzMT145	- - - - - I - - - - -	- - - - - I - - - - -	IG - LI - K - L - - - - -	- - - - -	GLGET - K - - - - -	838
CPZ. CM. 05. SIVcpzMB897	- - - - - I - - - - -	- - - - - I - - - - -	I - - - - -	- - - - -	R - D - - - - -	838
CPZ. CM. 05. SIVcpzDP943	- - - - - L - A - A - I - - - - -	- - - - - I - - - - -	GVIM - LIAK - - - - -	- - - - -	G - T - - - - -	838
CPZ. CD. 90. ANT	- - - - - I - - - - -	- - - - - AI - - - - -	LLVL - CLRK - - - - -	- - - - -	PTON - - - - -	828
CPZ. TZ. 2001. TAN2	- - - - - I - - - - -	- - - - - I - - - - -	LMFV - VNV - K - - - - -	- - - - -	PTQA - - - - -	835
CPZ. TZ. 2001. TAN3_1	- - - - - I - - - - -	- - - - - I - - - - -	LMFV - VNV - K - - - - -	- - - - -	PTQA - - - - -	835
CPZ. GA. 88. GAB2	- - - - - I - - - - -	- - - - - I - - - - -	IL - - - - -	VI - - - - -	IG - V - N - R - S - - - - -	828
CPZ. GA. 88. GAB1	- - - - - L - A - I - - - - -	- - - - - I - - - - -	IMT - F - V - R - - - - -	- - - - -	OG - EGE - LG - D - - - - -	827
CPZ. US. 85. CPZUS	- - - - - LIV - AS - I - - - - -	- - - - - I - - - - -	GVIF - L - AK - - - - -	- - - - -	OG - EGE - LG - D - - - - -	827
GOR. CM. 2007. SIVgor2139_287	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
GOR. CM. 2007. SIVgor2139_287	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
GOR. CM. 2004. SIVgorCP684con	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MON. CM. 99. L1	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MON. NG. x. NG1	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
GSM. CM. 99. CN166	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
CPZ. CM. 98. C43	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
CPZ. CM. 98. C45	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
TAL. CM. 00. 266	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
TAL. CM. 01. 8023	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
GSM. CM. 99. CN21	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MUS. 1. CM. 01. 1085	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MUS. 2. CM. 01. CM139	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MUS. 2. CM. 01. CM1226	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MND. 1. GA. x. MNDG14	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
WRC. CI. 97. 97C11	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
WRC. CI. 98. 98C104	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
WRC. GM. 05. PBT 05GM X02	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MUS. 2. CM. 01. CM2500	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
DEB. CM. 99. CM40	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
DEB. CM. 99. CM5	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
DEN. CD. x. CD1	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
H2A. DE. x. BEN	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
H2A. SN. x. ST	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
H2B. CI. x. EHO	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
H2B. GH. 86. D205	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
H2C. CI. 92. ABT96	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
H2M. CL. 92. 92B8	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
SMH. US. x. PGMS3	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
SMH. US. x. SIVsmH365F_L3	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MAC. US. x. 239	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MAC. US. x. 251 1A11	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MAC. US. x. 251 Bk28	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MAC. US. x. EMBL 3	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
STM. US. x. STM	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MNE. US. x. MNE027	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
LST. CD. 88. 485	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
LST. CD. 88. 524	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
LST. KE. x. Lho7	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
SUN. GA. 98. L14	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
MND. 2. GA. x. M14	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
DRL. x. x. FAO	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
SYK. KE. x. KE51	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
SYK. KE. x. SYK173	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
CRV. GA. x. GAB1	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
CRV. NG. x. G543	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
GRV. DE. 6. 677	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
SAB. SN. x. SAB1C	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
TAN. UG. x. TAN1	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
VER. DE. x. AGM3	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
VER. KE. x. 9063	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
VER. KE. x. 1555	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
VER. KE. x. TV01 patent	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809
COL. CM. x. CGU1	- - - - - I - - - - -	- - - - - I - - - - -	LM - IIMCH - - - - -	- - - - -	ILGRN - - - - -	809

856
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gp41 end
Env end

*
IEVV...QGACRAIRHIPRRIROGLER...ILL...*
--IG...TIG...LN...A...
--I...RT...L...A...
--LI...RIW...FCN...A...A-Q...
-DI...RR-K-VL...T...A...
--L...R-G-VLN...A...
--A...R...LN-T...A...
-VI...R-W...L...F...S...
-IA...R-F...L...A...
-IG...R-F...LL...A...
--A...W...L...T...
-IG...RVG...N...F...A...
-IG...RF...M-N...A-K...A-Q...
--A...R...CN...A...
-LA...RIG-G-L...A-I...
-AGI...RIGTG-N...S...
-LGL...RIGGFL...A...V...
-I-G...QTIG-GFLN...I...S...
-RA...IVF-I-GN...T...
--L...RIG-G-L...A...
-I...RIG-G-L...F...A...
-IA...RF-G-LN...A...
L-AI...TRLG-G-L...A...
--IA...RVG-G-L...A...
--RIG-G-L...S...
LLAL...TIV-I-EV...I-A-N...
--GI...TVIG-G-N...I-A-N...
-G...VYIA-G-N...A-N...
-G...VYIA-G-N...L-A-N...
--A...TRIG-G-L...A-E...
-AF...VTL-I-N...A...
-LT...RRLFLG-I...S...
-AIA...RIG-G-LN...S...
-AIA...RIG-G-LN...S...
-AIA...RIG-G-LN...S...
LHAG...GRLW--VA...A-I-F-N...
LRLG...GRLW-GLVAV...A-I-L-N...
LHAC...RRVW-EFLA...A-I-LFN...
L-A...TIG-G-L...S...
-F...IVG-G-L...S...
LAAA...RW-GE-AA--T--Y-CFT...
LAAA...RW-VQ-AA--T--Y-C-A...
VOT...GRVW-EFLA...A-I-L-N...
LQAG...RRVW-EFLA...V-A-I-L-N...
LOIG...RRVW-EFLA...A-I-L-N...
LOFS...KIW-KFLA...A-I-L-N...
-IAA...GTC-W-L--SA--P-N...
KTAA...SSRI-MLATRLCASFDKCR--SFSERRQ**
ETTG...SSRWKLIITRLCSSLNKSR--R-F...
ETSR...SSSI-G-TARLCTNLNPCR--GQO...
QOKK...RRGSPLOKAQEQLGREGAE...TTGV...
LQ-S...KOL-K-FLA--K--A-I-L-N...
LOGL...VR-GG-LRV-A--A-L-N...
QGL...VMGG-NLLA--A--A-L-L-N...
LAAL...TR-A-EVAL--V-N...I...
W-AA...RRIG-G-LAV--A-L-A...
WGA...WVG-R-LAV--A-I-A...
WGT...GOIG-G-LAV--A-I-A...
WG-L...RR-AGE-IA--A-L-A...
W-AL...RR-A--IA--L-T...
WKT...GRVG-G-LA--L-T...
W-TL...GRVG-WL-A--F-L-A...
W-TL...GRVG-G-AA--L-M-N...
W-TL...GRVG-WLA--L-A...
W-TL...GRVG-G-LA--V--L-T...
Env end
W-TL...RRGG-W-LA--L-T...
*-AL...RRGG-W-LA--L-T...
W-TL...RRGG-W-LA--L-T...
W-TL...RRGG-W-LA--L-T...
W-TL...GRVG-R-GA--L-T...
W-TL...GRVG-W-LA--E-L-T...
NLRL...GOKK-WRFRFRG-SGFPs-TTETA...
DIRL...GOKK-WRFRFRG-SGFPs-TTETA...
NIRL...GNR-RW-RFRF-SGLPs-TTETT...
NIQL...GKKK-WRLRFGG-SGISS-ATETA...
RSRTFSLGRKW-PKWNRT-GS-IPS-TTETT...
RGAA...AIG--GN--A-V-L-N...
RGAA...AFG-G-WN--A-A-L-N...
ARAL...RALAGEVAA--A-V-LFN...
LAYA...RRVAENVAAL--L--Y-N...
YAAT...RRVVE-VAAL--L--I-Y-N...
CA-A...RDFAGWPAMVC--L-CN...
CA-C...RDPAGWPATLC--F-F-N...
GAI...RS-Y--VINS--V--K-V-G...
RHAC...RSIV-VIAH--M-E--WFN...
WNAC...RS-Y--LEH--M-E--WFN...
WLAC...RS-Y--INS--V--G--N...
WLAC...RSTY-H-ISS--V--E--N...
WLAC...RS-Y--INS--V--E-V-N...
WLAC...RS-Y-N-VNS--V--E--N...
LRSA...ARGW-RAPEYL-GWIYDRPQ...GPA...

H1B.FR.83.HXB2
H1A1.UG.85.U455
H1B.US.90.WEAU160
H1C.ET.86.ETH2220
H1D.CD.84.84ZRB85
H1F1.BE.93.V1F1
H1G.SE.93.SE6165
H1H.CF.90.056
H1J.SE.93.SE7887
H1K.CM.96.MP535
H101.AE.TH.90.CM240
H102.AG.NG.x.IENG
H103.AB.RU.97.KAL153_2
H104.cpx.CY.94.CY032
H1N.CM.95.YBF30
H10.BE.87.ANT76
H10.CM.91.MVP5180
H1P.FR.06.RBF168
CPZ.CM.01.SIVcpzCAM13
CPZ.CM.05.SIVcpzEK505
CPZ.CM.05.SIVcpzLB7
CPZ.CM.05.SIVcpzMB66
CPZ.CM.05.SIVcpzMT145
CPZ.CM.-.SIVcpzMB897
CPZ.CM.-.SIVcpzDP943
CPZ.CD.90.ANT
CPZ.TZ.2001.TAN2
CPZ.TZ.2002.TAN3_1
CPZ.TZ.00.TAN1
CPZ.GA.88.GAB2
CPZ.GA.88.GAB1
CPZ.US.85.CP2US
GOR.CM.2007.SIVgor2139_287
GOR.CM.2007.SIVgorCP2135con
GOR.CM.2004.SIVgorCP684con
MON.CM.99.L1
MON.NG.x.NG1
GSN.CM.99.CN166
CPZ.CM.98.CAM3
CPZ.CM.98.CAM5
TAL.CM.00.266
TAL.CM.01.8023
GSN.CM.99.CN71
MUS-1.CM.01.1085
MUS-1.CM.01.CM1239
MUS-2.CM.01.CM1246
MND-1.GA.x.MNDGB1
WRC.CI.97.97CI14
WRC.CI.98.98CI04
WRC.GM.05.Pbt_05GM_X02
OLC.CI.97.97CI12
MUS-2.CM.01.CM2500
DEB.CM.99.CM40
DEB.CM.99.CM5
DEN.CD.x.CD1
H2A.DE.x.BEN
H2A.GW.x.ALI
H2A.SN.x.ST
H2B.CI.x.EH0
H2B.GH.86.D205
H2G.CI.92.ABT96
H2U.FR.96.12034
SMM.SL.92.SL92B
SMM.US.x.PGM53
SMM.US.x.SIVsmH635F_L3
MAC.US.x.239
MAC.US.x.251_1A11
MAC.US.x.251_BK28
MAC.US.x.EMBL_3
STM.US.x.STM
MNE.US.x.MNE027
LST.CD.88.447
LST.CD.88.485
LST.CD.88.524
LST.KE.x.lho7
SUN.GA.98.L14
MND-2.GA.x.M14
MND-2.x.x.5440
DRL.x.x.FA0
SYK.KE.x.KE51
SYK.KE.x.SYK173
RCM.GA.x.GAB1
RCM.NG.x.NG411
GRV.ET.x.GRI_677
SAB.SN.x.SAB1C
TAN.UG.x.TAN1
VER.DE.x.AGM3
VER.KE.x.9063
VER.KE.x.AGM155
VER.KE.x.TY01_patent
COL.CM.x.CGU1

PLV Proteins

myristoylation

Nef start

acidic cluster poly-P helix

phos

H1B.FR.83.HXB2

H1A.UG.95.1455

H1C.ET.86.ETH220

H1D.CD.84.842R085

H1F1.BE.93.V1850

H1G.UG.92.56165

H1H.CF.90.850

H1J.SE.93.5E7887

H1K.CM.96.MP535

H1E1.AE.78.RC.M240

H1B2.ET.86.ETH220

H1O3.AB.RU.97.KAL153_2

H1O4.cpx.CY.94.CY032

H1N.CM.95.YBF30

H1O.BE.87.NF170

H1O2.ET.86.ETH220

CP2.CM.01.SIVcpzCAM13

CP2.CM.05.SIVcpzEK505

CP2.CM.05.SIVcpzLB7

CP2.CM.05.SIVcpzMB66

CP2.CM.05.TAN145

CP2.CM.05.SIVcpzMB887

CP2.CM.05.SIVcpzDP943

CP2.TZ.2001.TAN2

CP2.TZ.2002.TAN3_1

CP2.CM.05.TAN3

CP2.CM.98.CAMS

CP2.CM.88.GAB1

CP2.CM.88.GAB2

CP2.US.85.CPZUS

CP2.CD.90.TAN

GOR.CM.2007.SIVgorT2139_287

GOR.CM.2007.SIVgorCP2135con

GOR.CM.2004.SIVgorCP684con

SAB.SN.s.SABIC

GOR.ET.GX.GP.677

VER.KE.s.TAN1

VER.KE.s.9063

VER.KE.s.AGM155

VER.KE.s.TY01.patent

VER.DE.s.AGM3

ASG.s.KHSGKPLQGL

H2A.GX.s.ALT

H2A.SN.s.EH

H2B.CI.s.STO

H2B.GX.86.D295

H2B.GX.86.T96

H2D.FR.96.12034

SMM.SL.92.5L928

SMM.US.s.PGM53

SMM.US.s.STV5mH635F_L3

MGKGWKS

SSVIGWPTVRMRRAEP

AAADR

VGA

ASR

DLEKH

GAITS

SSNTA

ATNA

ACAA

LEAQ

EEEE

GVFP

TPV

PLR

PMTY

KA

AVLS

HLF

KEKGG

LEGL

HSR

RROR

DILD

WTY

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-IV

-AI

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-KTD

RERRR

PEP

G

-V

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HXB2 premature Nef end	normal Nef end
H1B.FR.83.HXB2	YFPD-QNYTPGGG...VRYPLTFGWCYKLVPEVPDKIEEA.NKGENTSLHPVSLHGMD...PEREVLEWRFSRLAFHHVARELHPEYFKNC...
H1A1.UG.85.U455	F--W-----I-----D-AEV--TG--N--ICQ--V--E-K-M-K--T-LK-R-Y--FY-D
H1B.US.90.WEAU160	F--W-----T--C--F--E-V--E--N--M--H-K-M-K--K--D--
H1C.ET.86.ETH2220	F--W-----I-----D-SEV-I--E-NC-A--E-ED-K-K--H-RR-M--Y-D
H1D.CD.84.84Z8085	F--W-----I-----FE-D-EV-K--TE-DNC--ICQ--E--E-K-V--N--E-K-K-KY--
H1F1.BE.93.V1F1	F--W-----I-----D-EEV-K--E-NC--ICQ--E--ED--R-K--M--R--FYOD
H1G.SE.93.SE6165	---W-----I--F--F--MD-AEV--E--N--M--ED--V--S--RR-I--Y-D
H1H.CF.90.056	---W-----E-F--F--N-OEV-Q--E--N--M--DG--M-K--LT-L-VK--D--
H1J.SE.93.SE7887	---W-----I-----D-SEV--E-NC--ICQ--IE--E--Q-K--S-RR-I--FY-D
H1K.CM.96.MP535	F--W-----I-----D-AEV--T-TE-DNC--INO--E--EH--I-M-K--S-RR--D-Y-D
H101.AE.TH.90.CM240	F--W-----I--C--F--D-EEV--D--E-NC--ICQ--IE--E--M-K--A-RK--Q--Y-D
H102.AG.NG.x.IENG	F--W-----I--F--F--MD-AEV--E--N--M--DD--I--R--T--Y-D
H103.AB.RU.97.KAL153.2	---W-----I--F--F--D-AEV--TE--N--ICQ--E--E-K-M-K--LT-R--FY-D
H104.cpx.CY.94.CY032	F--WD-----E-F-C--F--D-OEV--TE--C--I-Q--E--E--K-K--YK--FY-D
H1N.CM.95.YBF30	IL--WH-----I--V--F--LSAEV--E-D-NA--ICQ--A--DHK--V--S-RR--FY--
H10.BE.87.ANT70	F--W-----T--F--LF--SEEEA-RLG--TC-RAN--ACA--FE--THK--I-M-K--RS-GWT--MIT--L-QKD
H10.CM.91.MVP5180	F--W-C-----P-F--LF--SAEEA-RLG--TW-DA--ACN--AE--AHG--I-K-Q--RS-GLT--L-LQK--L-PK
CPZ.CM.01.SIVcpzCAM13	F--W-----E-PC--F--LTTEQV-A--E-D-NC--ICQ--E--ESK--I--LR-I--K--Y-D
CPZ.CM.05.SIVcpzEK505	I--W-----I--F--F--LS-EEV--Q-D-NV--MCO--E--DK--V--S-RV-R--FYQ
CPZ.CM.05.SIVcpzLB7	I--W-----I--I--G-F--LT-EEV--N--NL--ICQ--E--EDK--I-KY--Q-LR-I--S-Y
CPZ.CM.05.SIVcpzMB66	F--W-----I-----F--L-EEV-R--E-D-NI--ICQ--QE--EA--V-T--K-LR--Y-D
CPZ.CM.05.SIVcpzMT145	F--W-----I-----F--LP-EEV-K--E-NC--MCO--E--E--V-T--K-LR--K--YRD
CPZ.CM--SIVcpzMB897	F--W-----I--V--F--D-EEV--D--D-NV--MCO--QE--EH--V-Q--H-LR--Y-D
CPZ.CM--SIVcpzDP943	F--W-----I--F--F--LT-EEV-K--E-DTNI--ICQ--EIE--EHG--V-Y--LR-I--Q--YQD
CPZ.TZ.2001.TAN2	I--W-----I--R-LF--D-PED--D-QNI--R-ACS--SN--G-T-I--S-RR-I--RY
CPZ.TZ.2002.TAN3.1	I--W-----I--VR-LF--D-PED--D-KNI--ACS--SN--G-T-I--S-RR-I--RF-Y
CPZ.TZ.00.TAN1	V--W-----I--CR-LF--D-PED--D-KNI--ACS--TT--DG-T-I--S-RR-I--RY
CPZ.CM.98.CTM5	F--W-----I--LT-EEV-K--E-NC--MCO--E--EH--V-Q--H-LR--Y-D
CPZ.GA.88.GAB1	F--W-----T--T-F-C--F--LTTEQV-Q--E-D-NC--ICQ--E--EDK--V--LR-I--Q--Y-D
CPZ.GA.88.GAB2	---WN-----Y--F--S-EAV--N--DNL--LCT--FE--E-K-I-K--Q-LR-L-K--YRD
CPZ.US.85.CPZUS	I--W-----I--F--F--LTTEEV-Q--TNI--MCO--E--EHG--I-Q--TE--RR-R-K--R
CPZ.CD.90.ANT	I--W-----EE--CR--F--SPPD--D-RNI--ACT--DG--HK--I-R-E--AS-MRR--I--R--RD
GOR.CM.2007.SIVgor2139.287	---W-----I--LF--SEAEA-MGTAS-RAI--ACS--R--HG-I-V--RA-GTT--LQK--L-RE
GOR.CM.2007.SIVgorCP2135con	---W-----I--LF--SEAEA-MGTAS-RAI--ACS--R--HG-I-V--RA-GTT--LQK--L-RE
GOR.CM.2004.SIVgorCP684con	---W-----Y-LF--SEAEA-MGTAS-RAI--ACS--R--HG-T-V--RA-GTT--LOK--L-ORD
SAB.SN.x.SABIC	IVDGV--D--T--KC--F--D-LSE-AK--S--HC--AQVAYE--AWK-T-V-K--PL--VDY--WR--QVPSAOG
GRV.ET.x.GRI.677	IID-W-A-S--I--RV-F-F--D-LHE-AR--C--RHC--M--AQMGEDP--GI--DHG--V-K--PK--VEY--R-DM--DMHEHAKR
TAN.UG.x.TAN1	IID-W-A-S--I--K-R-F-F--D-VSQ-AQ-D--RHC--AQIENES--WK-T-V-K--NPH--VOY--N-D--SFQDMHGLVKRK
VER.KE.x.9063	IID-WNAWSK--I--RC-F-F--MHE-AE-TC--RHY-A--AQIKEEDP--GI--SHG-T-V-K--PM--VOY--D-NROYEDMHGLVKRK
VER.KE.x.AGM155	IID-WNAWSK--I--RC-F-F--A-LHE-AE-TC--RHC-V-AQ--EDP-GI--NHG-I-A-K--PM--VOY--D-SREYFTDLYSTVTGN
VER.KE.x.TY01.patent	IID-WNAWSK--I--F-KC-F-F--D-LHE-AQ-TC--RHC-V-AQMGEDP--GI--SHG-I-V-K--PM--IQY--D-NREYFTDMHGLVKRK
VER.DE.x.AGM3	IID-WNAWSK--I--RC-F-F--D-LHE-AE-TC--RHC-V-AQMGEDP--GI--NHG--V-K--PM--VOY--D-NRKYLTDMHGLVKRK
H2A.DE.x.BEN	II--W--H--I--MY-LW--S--LSQ-AE-ED--ANC-V--AQTSRH--EHG-T-V-Q--M--YNYK--FT-Y--E-GHKSGLPEKEWKARLKARGIPYSE
H2A.GW.x.ALI	II--W--H--I--MF-LW--D--D-ANDKAD-ED--RLY-VGSAQTSCEE--HWG-A-V-K--S--YSYO--FTKC--E-GYKSLGPEDEWKARLKARGIPFSSKNRNS
H2A.SN.x.ST	IIG-W--H--I--KF-LW--D--VPO-GD-DS--THC-V--AQTSRH--HG-T-V--PT--SYE--FTRY--E-GYKSLGPEDEWKARLKARGIPES
H2B.CI.x.EHO	IVSGW--H--I--KF-LW--IN-MIA-PE-DE--THC-V--AQTSAW--HE-T-V-Q--L--YDY--FSRF--E-GYQSGMPEKEWKARLKARGIPTE
H2B.GH.86.D205	IVSGW--H--I--KY-LW--I--X--LW--D--T-VSD-AQ-ED--THC-V--AQTSW--IHG-T-I-Q--L--YDY--FNRF--E-GYQSGLPEEWEKARLKARGIPTD
H2G.CI.92.AB196	II--W--A--I--X--LW--D--T-VSD-AQ-ED--THC-V--AQTSW--T--A-K--PT--YDPR--FI--E-RWKSGLPEAVWKEKRLKARGIPTE
H2U.FR.96.12034	II--W--A--I--W-M-LW--E--D-ANDKAD-ED--RLY-VGSAQTSCEE--HWG-A-V-K--S--YSYO--FTKC--E-GYKSLGPEEWEKARLKARGIPVKNK
SMM.SL.92.S192B	II--W--S--I--KF-LW--D--VSD-AQ--D--THY-V--AQTSQHS--HWG-A-K-NPH--YTYE-FVR--E-GWKSGLTEEEVERRLANKPKPKQKMKADKKETS
SMM.US.x.PGM53	II--W--S--I--MF-LW--S--ASD-AQ-ED--THY-V--AQTSOW--WG--A-K--Q--YRYE-FIR--E-GSKSGLSEEEVKRRLTARGLL--KMAADKKETS
SMM.US.x.SIVsmH635F_L3	II--W--L--I--T-MY-LW--D--VSD-AQ-ED--THC-V--AQT-OW--WG--A-K--PE--YSYK-FIKY--E-GSKSGLSEEEVKRRLTARGLY--KMAADKKETS
max HIV-1 similarity	normal Nef end
II--W-D-S--I--K--LW--N-VSD-AQ-ED--EHY-M--AQTSOW--WG--A-K--PT--YTYE-VYRY--E-GSKSGLSEEEVRRRLTARGLL--NMADKKETR	263
II--W-D-S--I--K--LW--N-VSD-AQ-ED--EHY-M--AQTSOW--WG--PA-K--PT--YTYE-VYRY--E-GSKSGLSEEEVRRRLTARGLL--NMADKKETR	264
II--W-D-S--I--K--LW--N-VSD-AQ-ED--RHY-MQ--AQTSKW--WG--A-K--PT--YTYE-YARY--E-GSKSGLSEEEVRRRLTARGLL--NMADKKETR	263
II--W-D-S--I--K--LW--N-VSD-AQ-ED--RHY-MQ--AQTSKW--WG--T-K--PT--YTYE-VYRY--E-GSKSGLSEEEVRRRLTARGLL--NMADKKETR	260
IV--W--A--I--KQ--LW--D-MSN-AQ-EDDGTHY-V--AQT-OW--WG--V-K--PL--HTYE-FVR--E-GSKSGLPKKEEVRRLTARGLL--KMAADKKETS	265
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