

**A NEW HYPOTHESIS OF SQUAMATE EVOLUTIONARY RELATIONSHIPS
FROM NUCLEAR AND MITOCHONDRIAL DNA SEQUENCE DATA**

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ABSTRACT

Squamate reptiles serve as model systems for evolutionary studies of a variety of morphological and behavioral traits, and phylogeny is crucial to many generalizations derived from such studies. Specifically, the traditional dichotomy between Iguania and Scleroglossa has been correlated with major evolutionary shifts within Squamata. We present a molecular phylogenetic study of squamates using DNA sequence data from the nuclear genes *RAG-1* and *c-mos* and the mitochondrial *ND2* region, sampling all major clades and most major subclades. Monophyly of Iguania, Anguimorpha, and almost all currently recognized squamate families is strongly supported. However, monophyly is rejected for Scleroglossa, Varanoidea, and several other higher taxa, and Iguania is highly nested within Squamata. Limblessness evolved independently in snakes, dibamids, and amphisbaenians, suggesting widespread morphological convergence or parallelism in limbless, burrowing forms. Amphisbaenians are the sister group of lacertids, and snakes are grouped with iguanians and anguimorphs. Dibamids diverged early in squamate evolutionary history. Xantusiidae is the sister taxon of Cordylidae. Studies of functional tongue morphology and feeding mode have found significant differences between Scleroglossa and Iguania, and our finding of a nonmonophyletic Scleroglossa and a highly nested Iguania suggest that similar states evolved separately in *Sphenodon* and Iguania, and that jaw prehension is the ancestral feeding mode in squamates.

INTRODUCTION

Evolutionary biologists often seek generalities about evolutionary processes from detailed studies of particular model systems, and squamate reptiles have provided a large number of such systems (e.g., Huey et al. 1983; Vitt and Pianka 1994). An accurate squamate phylogeny is crucial to researchers studying morphological, behavioral, and life-history variation across squamate taxa, because phylogeny is a key part of comparative methodology (Miles and Dunham 1993). For example, herpetological studies of foraging mode and prey chemical discrimination (Cooper 1995; Perry 1999), demographic tactics (Clobert et al. 1998), and home-range variation (Perry and Garland 2002) have all explicitly incorporated phylogeny into their testing framework to insure appropriate, independent comparisons. Schwenk (1993) and Cooper (Cooper 1996) both discussed evolution of squamate tongue morphology and chemoreception in a phylogenetic context, and Schwenk and Wagner (2001) used this same system to illustrate the concept of evolutionarily stable configurations (ESCs). They found major shifts in squamate feeding morphology and behavior to coincide with the dichotomous split between Iguania and Scleroglossa at the base of the squamate tree. Recently, Vitt et al. (In press) discussed the global ecology of squamates from a phylogenetic perspective. These authors strongly emphasized this same dichotomy and the retention of plesiomorphic character states by iguanians.

Lepidosauria is composed of two clades: Order Rhynchocephalia, a previously widespread group currently represented by only two species in one genus of Family Sphenodontidae, and Order Squamata, a diverse assemblage including all "lizards" plus snakes, amphisbaenians, and dibamids. Camp's (1923) morphological study of squamate

relationships was the first thorough, systematic treatment of the subject, and subsequent studies (e.g., Estes et al. 1988; Lee 1998; Lee and Caldwell 2000; Reynoso 1998) have revised and expanded the morphological character set of this early work. These recent morphological studies agree on some groupings of families into higher taxa (e.g., Anguimorpha, Iguania, Scleroglossa), but the phylogenetic affinities of many higher squamate taxa remain uncertain. Several limbless clades are particularly difficult to place based on morphology. The limbless condition eliminates many valuable characters from consideration, although utilizing fossil taxa can sometimes help (e.g., Lee and Caldwell 1998; Zaher and Rieppel 1999). Furthermore, because limblessness is often associated with a fossorial lifestyle, cranial morphology in these animals is also often radically altered from that of nonburrowing squamates (Lee 1998).

Snakes (Rieppel 1983; Rieppel 1985), amphisbaenians (Gans 1978), and dibamids (Greer 1985) all exhibit characters that might place them phylogenetically outside all other squamates, although most authors now agree that all three are most likely nested somewhere within lizards. Estes et al. (1988) designated these three groups as "Scleroglossa incertae sedis," and many studies have had as their main goal a more definitive placement of these taxa. Wu et al. (1996) identified a dibamid-amphisbaenian-snake clade as the sister group to Gekkota, whereas Hallerman (1998) found support for this same limbless clade at the base of Scleroglossa. Rieppel (1984) found evidence for dibamids as the sister group of acontine skinks, and Greer (1985) suggested the possibility that dibamids were phylogenetically closest to feyliniine skinks. Reynoso (1998) placed dibamids and amphisbaenians with gekkos, and found snakes to be the sister group of anguimorphs. After including several fossil taxa and eliminating

characters thought to be convergent in head-first burrowers, Lee (1998) and Lee and Caldwell (2000) found the same dibamid-amphisbaenian-gekkotan clade, but placed snakes within Anguimorpha as the closest extant relatives of varanids.

Relationships within Amphisbaenia are also unclear. Primitive skull characters suggest that rhineurids may be the sister taxon of a clade containing all other amphisbaenians (Berman 1973). However, others (e.g., Bellairs and Gans 1983; Gans 1968) have concluded that these shovel-nosed forms are derived from amphisbaenians with rounded snouts similar to members of the Amphisbaenidae. Furthermore, retention of forelimbs by members of Bipedidae has been considered evidence that they lie outside a clade containing all other amphisbaenians (e.g., Bogert 1964; Kearney 2001).

The phylogenetic position of several other higher taxa is at least as uncertain as that of the limbless groups. For example, Xantusiidae has been variously placed as the sister taxon of Cordylidae (Estes 1983), the sister taxon of a clade containing Families Teiidae, Gymnophthalmidae, and Lacertidae (Estes et al. 1988), the sister taxon of gekkos (Macey et al. 1997a), and the sister taxon of a clade containing amphisbaenians, dibamids, and gekkos (Lee and Caldwell 2000). Scincomorpha, a large clade dating back (in slightly modified form) to Camp (1923), was given its modern definition (including Scincidae, Cordylidae, Xantusiidae, Lacertidae, Teiidae, and Gymnophthalmidae) by Estes et al. (1988) and corroborated by subsequent authors (Hallermann 1998; Reynoso 1998; Wu et al. 1996). However, Lee (1998) and Lee and Caldwell (2000) both found this group paraphyletic with respect to Anguimorpha. Skinks and cordylids were likewise recognized as a clade (Scincoidea) by Estes et al. (1988), but several subsequent

authors have either refuted (Wu et al. 1996) or at least left unresolved (Hallermann 1998; Lee 1998; Lee and Caldwell 2000) the sister-group status of skinks and cordylids.

Surprisingly few molecular studies have addressed higher-level relationships within Squamata on a broad scale. Most studies concerned with supra-familial relationships have had limited outgroup taxon sampling (e.g., Ast 2001; Donnellan et al. 1999; Macey et al. 1997*b*; Macey et al. 2000; Macey et al. 1999*a*; Odierna et al. 2002; Saint et al. 1998) and were thus not designed to examine external affinities of their respective focal groups. Donnellan et al. (1999) provided the first molecular confirmation of Kluge's (1987) conclusion that another contentious limbless group, Pygopodidae, was actually nested within gekkos as the sister group to diplodactylines. However, this study likewise used only a single outgroup (skinks). Ast's (2001) study of relationships within Varanidae (including *Lanthanotus*) purportedly supports monophyly of Varanoidea (Varanidae/Lanthanotidae + Helodermatidae). However, her outgroups consisted only of two anguids and an anneliid. This limited sampling ignores all recent morphological and molecular analyses (e.g., Estes et al. 1988; Lee and Caldwell 2000; Macey et al. 1999*a*), which suggest that *Xenosaurus* and *Shinisaurus* are at least as phylogenetically close (Estes et al. 1988; Reynoso 1998) if not closer (Lee and Caldwell 2000; Macey et al. 1999*a*) to varanids and helodermatids than are anguids. Thus, Ast (2001) did not adequately test monophyly of Varanoidea.

Harris et al. (2001; 1999) present sequence data from the nuclear proto-oncogene *c-mos* in the most well-sampled molecular phylogenetic study of higher squamate relationships. Many of the higher-level relationships recovered in these studies conflict

with those of morphological studies. However, these studies were based on only 375 base pairs (bp) of sequence, and most basal relationships are weakly supported.

Here we present results from a phylogenetic study of Squamata using three independent molecular data sets, one from the mitochondrial ND2 region and one each from the single-copy, protein-coding nuclear genes *RAG-1* and *c-mos*. Phylogenetic studies based on *RAG-1* sequence have resolved relationships across a wide array of taxa and at a broad range of hierarchical levels. Basal relationships within birds (Groth and Barrowclough 1999) eutherian mammals (as part of a larger data set, Murphy et al. 2001), turtles (Krenz 2001), and tetrapods (Townsend and Larson, unpublished data), as well as relationships within several lower-level groups such as passerines (Ericson et al. 2002) and chameleons of the genus *Rhampholeon* (Townsend, unpublished data) have been recovered using this gene. The mitochondrial ND2 region has been used to study relationships between and among numerous squamate groups (e.g., Jackman et al. 1999; Macey et al. 1997*b*; Macey et al. 2000; Macey et al. 1999*a*; Schulte et al. 1998; Townsend and Larson 2002), as well as birds (e.g., Donne-Gousse et al. 2002), mammals (e.g., Osborne and Christidis 2002) and fish (e.g., Klett and Meyer 2002).

MATERIALS AND METHODS

Taxon sampling

Rhynchocephalia is traditionally considered the closest outgroup to Squamata, although some molecular evidence (Hedges and Poling 1999) suggests the arrangement

(Rhynchocephalia+(Testudines+Archosauria)). We have therefore included representatives from all three of these taxa as outgroups. Within the ingroup, all recognized major squamate clades (i.e. lizard families) are represented, as well as many major subclades. In diverse families, we attempted to sample species from both sides of the most basal divergence. For families with uncertain intrafamilial relationships (e.g., Iguanidae), we tried to sample all major subclades to assure that the deepest divergence was spanned. A total of 69 ingroup species were sampled for *RAG-1* and the mitochondrial fragment, and 44 ingroup species (still sampling all major clades) were sampled for *c-mos*. See Appendix I for museum numbers and GenBank accession numbers (to be added upon acceptance of the manuscript) for all specimens.

Laboratory Protocols

Genomic DNA was extracted from muscle, liver, or skin tissue (stored either frozen or in 70-95% ethanol) using DNEasy Tissue Extraction Kits (Qiagen, Inc.) and stored in AE buffer. Mitochondrial PCR products were amplified from genomic DNA using an initial denaturation at 95° C for 2 min, then a denaturation at 95° C for 35 s, annealing at 50° C for 35 s, and extension at 70° for 150 s with 4 s added to each successive extension cycle, for 30 cycles. Nuclear genomic DNA was originally amplified using the touchdown protocol of Groth and Barrowclough (1999). All PCR products were purified on 1.3% low-melt agarose gels and reamplified under the same conditions used to amplify the mitochondrial genomic DNA, except that the annealing temperature was reduced to 45° C. Promega *Taq* polymerase (Promega, Inc., Madison,

Wisconsin) was used for all amplifications. Re-amplified products were purified on 0.8% high-melt agarose gels, and template extracted using Viogene Gel Extraction Kits (Viogene, Inc., Taipei, Taiwan) and sequenced completely in both directions using ABI Prism[®] Dye Terminator Cycle Sequencing Ready Reaction Kits with AmpliTaq DNA Polymerase (Perkin Elmer, Norwalk, Connecticut) following the manufacturer's instructions. Sequencing products were analyzed with ABI 373 (at Washington University) or 377 (at the Henry Doorly Zoo's Center for Conservation and Research) Automated Sequencers (Applied Biosystems, Foster City, California) or an MJ Research BaseStation (MJ Research, San Francisco, California).

Primers used in this study are listed in Appendix II. Mitochondrial sequences include approximately 70 base pairs (bp) of the ND1 (subunit 1 of NADH dehydrogenase) gene, the 3 tRNA genes for glutamine, isoleucine, and methionine (tRNA^{Gln}, tRNA^{Ile}, and tRNA^{Met}, respectively), the entire ND2 (subunit 2 of NADH dehydrogenase) gene, the 5 tRNA genes for tryptophan, alanine, asparagine, cysteine, and tyrosine (tRNA^{Trp}, tRNA^{Ala}, tRNA^{Asn}, tRNA^{Cys}, and tRNA^{Tyr}, respectively), the stem-and-loop structure representing a degenerate origin for light-strand replication (O_L), and 30 bp of the COI (subunit I of cytochrome *c* oxidase) gene. The *RAG-I* and *c-mos* sequences cover an approximately 2800 bp and 374 bp region of coding sequence, respectively. Many mitochondrial and *c-mos* sequences were obtained from GenBank (see Appendix I), and the remainder were newly generated for this study.

Alignments and Phylogenetic Analyses

Sequences were edited and assembled using SeqMan II (DNASTAR, Inc., Madison, Wisconsin). Alignments of protein-coding regions were performed on amino-acid translations using Clustal X (Thompson et al. 1997) at a variety of gap-opening and gap-extension penalties. For pairwise alignments, gap-opening penalties were set to 10, 20 and 35 with respective gap-extension penalties of 0.1, 0.45, and 0.75. Corresponding multiple-alignment penalties were 10, 15, and 20 (gap-opening) and 0.1, 0.2 and 0.3 (gap-extension). Regions for which alignments differed between the three suites of settings were excluded from all analyses. Genes coding for tRNAs were aligned manually following the structural models of Kumazawa and Nishida (1993). Length-variable loops that could not be confidently aligned were excluded from all analyses. All gaps were treated as missing data.

Incongruence length difference tests (Farris et al. 1994) were performed in PAUP* (in which they are called "partition homogeneity tests") with invariable sites removed (Cunningham 1997) to assess compatibility between different data sets.

To explore the possibility of heterogeneous selective pressures on the protein-coding nuclear genes (see Results), we used DnaSP (Rozas and Rozas 1999) to calculate ratios of synonymous substitutions per synonymous site (K_s) to nonsynonymous substitutions per nonsynonymous site (K_a) for all possible pairwise taxon comparisons. Average K_a/K_s ratios were then calculated within each major clade as well as among clades. Average K_a/K_s ratios significantly greater than one (as determined by t-tests) indicate directional selection in at least some of the species/clades compared, whereas ratios significantly less than one indicate stabilizing or purifying selection (see Messier and Stewart 1997 for a more detailed discussion).

The model of evolution and all maximum-likelihood (ML) parameters were estimated for each data set individually using hierarchical likelihood-ratio tests as implemented in Modeltest (Posada and Crandall 1998). Maximum-likelihood analyses were conducted using the heuristic search option of PAUP* (Swofford 1998) and a neighbor-joining tree as a starting tree for branch swapping.

Bayesian analyses were performed using MrBayes (Huelsenbeck and Ronquist 2001) under the same model used for the corresponding likelihood analyses. Four incrementally heated Markov chains were started from random trees and run for 1,000,000 generations each. The effect of heating the chains is to flatten the landscape somewhat, thus allowing the chains more easily to cross deep valleys and explore treespace more effectively. Chains were sampled every 1000 generations to ensure that the samples were independent. Through inspection of the likelihood scores and model parameters in the output file, we determined the number of generations required for stabilization, and discarded all trees obtained prior to stabilization as burn-in. Two independent analyses were always conducted to prevent drawing the posterior distribution from a suboptimal area of tree space. Trees from the posterior distribution were imported into PAUP* (Swofford 1998) and, after excluding the burn-in, a majority-rule consensus tree was constructed showing relative occurrences (i.e. the posterior probabilities) of all nodes in the tree.

Maximum-parsimony (MP) analyses were performed using PAUP* (Swofford 1998) under the heuristic search option with 100 random-addition replicates. Bootstrap resampling was applied to assess heuristic support for individual nodes (Felsenstein 1985a) using 1000 bootstrap replicates with 25 random additions of sequences per

replicate. Support (decay) indices (Bremer 1994) were calculated as heuristic support measures for all resolved internal branches of the tree using the "Decay Index PAUP File" feature of MacClade (Maddison and Maddison 2000). As an indicator of relative homoplasy among data sets, retention indices (Farris 1989) were also calculated.

Statistical support for individual nodes in the shortest unconstrained MP trees was assessed using the non-parametric Wilcoxon signed-ranks test (Felsenstein 1985*b*; Templeton 1983). In testing particular nodes, constraint trees that contained only a single resolved node were constructed using MacClade (Maddison and Maddison 2000). Next, the shortest trees *not* containing this node were found using PAUP* (Swofford 1998), and these trees were then compared to the shortest unconstrained tree using the "Tree Scores" option of PAUP* (Swofford 1998).

Results from the mitochondrial analysis suggest that long-branch attraction (Felsenstein 1978) might occur between certain family-level taxa. We followed Wiens and Hollingsworth's (2000) implementation of the parametric bootstrapping method of Huelsenbeck (1997) to test this hypothesis. We first used the program Seq-Gen (Rambaut and Grassly 1997) to simulate 100 data sets under the same likelihood model and estimated parameters (including branch lengths) obtained for the original mitochondrial analysis. However, the topology used for these simulations was modified from the original mitochondrial topology such that the suspicious long branches were separated. Sequence length for each simulation was equal to that of the original mitochondrial data set. Next, both parsimony and likelihood analyses were performed on each of these replicate data sets, and a tally was kept for each optimality criterion of the number of correct and incorrect reconstructions, as well as the number of times an

incorrect reconstruction joined the two long branches. If parsimony analyses tend incorrectly to join the long branches while likelihood analyses do not, this suggests that LBA is a problem, especially if independent evidence indicates that the long-branch taxa are not close relatives. Because a large number of maximum-likelihood analyses were needed for this test, it was not computationally feasible to run unconstrained searches. Instead, relationships within families were constrained to match those obtained from the original mitochondrial parsimony analysis for all parsimony and likelihood searches, but relationships among families were free to vary. Acrodonta was treated as a family for these analyses due to uncertain monophyly of Agamidae (see Results).

Lee and Caldwell's (2000) morphological results differ from our own on several points (see Fig. 8 and Results). To identify specific morphological characters that need to be reevaluated if our favored (nuclear; see Results) phylogenetic hypothesis is accepted, we used the following procedure. First, parsimony bootstrap analysis was performed on Lee and Caldwell's (2000) data for extant taxa only, all characters unordered, and excluding 27 characters identified by Lee (1998) as potentially correlated to a fossorial existence. Nodes on the morphological tree that conflict with strongly supported nodes from our molecular analysis were identified. Next, we ran a series of parsimony analyses on our nuclear data set, each constrained to contain a different conflicting node from the Lee and Caldwell (2000) topology. Then, each of these constrained topologies was pruned to contain only taxa represented in Lee and Caldwell's (2000) data set. Next, our original, unconstrained nuclear MP topology was pruned to contain these same taxa. Finally, each constrained topology was compared to our unconstrained, pruned topology using Lee and Caldwell's (2000) character data (conditions as above). For each

comparison, morphological characters that require greater numbers of changes on our unconstrained tree were identified using the “Tree Scores” option of PAUP* (Swofford, 2000). This procedure is necessarily somewhat crude, and we are not suggesting that all or even most characters identified in this manner are problematic, only that any truly problematic characters are very likely to be contained in the resulting lists.

RESULTS

Saturation and selection tests

Saturation plots for these data showed marked substitutional saturation in mitochondrial third-position transitions (Townsend 2002). In addition, parsimony analyses performed with this class of character change excluded showed substantially higher bootstrap values at several nodes, especially among gekkonids and anguimorphs, than did analyses with the full data (Townsend 2002). Therefore, mitochondrial third-position transitions were excluded from all analyses. Other partitions in both the mitochondrial and nuclear data showed only moderate (mitochondrial third-position tranversions) to minimal (all other data partitions) saturation, and their exclusion generally weakened (or left unchanged) support throughout the trees (Townsend 2002). Therefore, no other data partitions were excluded from subsequent analyses.

K_a/K_s values are remarkably uniform within and across clades for both the *RAG-1* and *c-mos* genes. The clades used for each gene include Iguanidae, Acrodonta, Gekkonidae (we treat eublepharines and pygopodines as subfamilies of Gekkonidae)

(Pough et al. 2001), Serpentes, Anguimorpha, Lacertiformes (including Amphisbaenia), and Scincoidea (including Xantusiidae). Within-clade *RAG-1* K_a/K_s values average 0.13 (0.12-0.15), and all are significantly different from 1 at the 0.05 level. The p-value for snakes is 0.01, but all others are much smaller, and highly significant even after correction for multiple tests. Between-lineage *RAG-1* K_a/K_s values average 0.11 (0.10-0.12), and all are highly significantly different from 1 (even after correction). Within-lineage *c-mos* K_a/K_s values average 0.30, and all are significantly different from 1. The p-value for snakes is 0.03, but all others are highly significant even after correction. Between-lineage *c-mos* K_a/K_s values average 0.24 (0.16-0.33), and all are highly significant. These results indicate that both genes are under strong stabilizing selection, and the degree of selection appears uniform throughout the respective data sets. Thus, no evidence exists for differential selection that might mislead results of the nuclear analyses by causing convergence in protein structure between non-sister taxa.

Phylogenetic hypotheses and statistical tests

The *RAG-1* data set corresponds to positions 84 to 3126 on the published chicken *RAG-1* gene (Carlson et al., 1991; GenBank accession no. M58530). All complete, aligned data files (with excluded positions marked as such) are found in Appendix III. The *RAG-1* MP and ML topologies and the Bayesian consensus topology are all very similar to one another, and all nodes receiving high heuristic support from the parsimony analysis (bootstrap >90%) also have posterior probabilities of >95% in the Bayesian analysis (Fig. 1). Although significant heterogeneity is observed among species for base

composition at third positions of *RAG-I* codons ($p < .001$), phylogenetic results conducted with these positions removed are congruent with analyses of the complete *RAG-I* data.

C-mos sequences correspond to positions 513 to 888 on the human *c-mos* gene (Watson et al. 1982). The Bayesian consensus topology and ML topology are once again very similar to one another, and both analyses recover all moderately- to highly-supported nodes (bootstrap $>80\%$) from the parsimony analysis (Fig. 2). Although the *c-mos* data set contains fewer species, all major clades from the *RAG-I* analysis are still represented. The topology of the *c-mos* MP strict consensus is largely compatible with the *RAG-I* topology, although many deeper relationships are not resolved (Fig. 2). Base frequencies at third positions of *c-mos* codons are not significantly heterogeneous among species sampled here ($p = .166$) and therefore avoid the possible phylogenetic biases identified by Harris (2003).

Because separate *RAG-I* and *c-mos* analyses produced congruent topologies (results of the ILD test also found no significant incongruence, $p = .71$), these two data sets were combined (Fig. 3). For clarity, results of this combined analysis will be detailed here, with references to individual analyses (Figs. 1 and 2; see also Appendix IV for individual MP and ML/Bayesian topologies) as necessary. Parsimony, Bayesian, and likelihood topologies from the combined *RAG-I* and *c-mos* data are largely congruent with each other as well as with corresponding trees from each data set analyzed singly. Parsimony and Bayesian support values are at least as high as those from the *RAG-I* data alone, and often substantially higher (Figs. 1 and 3).

The MP strict consensus is largely well resolved, and monophyly of all recognized families is recovered (when more than one subclade is represented), most

with very strong bootstrap and decay support (Fig. 3). Traditional suprafamilial groups recovered with strong support include Acrodonta, Iguania, Anguimorpha (also characterized by a one-codon insertion at positions 128-130 in the aligned *RAG-I* data set; see Appendix III), and Teiioidea. Interestingly, several nontraditional relationships are also recovered with strong support.

Most striking is the absence of a monophyletic Scleroglossa as the sister taxon of Iguania (Fig. 3). Instead, the deepest divergence is between dibamids and gekkos, and Iguania occupies a highly nested position in the tree, a very unorthodox but statistically supported arrangement (Table 2). *Dibamus* sits at the end of a moderately long terminal branch (Fig. 3) and, while its position as the sister taxon of all other squamates is stable in all combined analyses as well parsimony analysis of the *RAG-I* data alone (Appendix IV), likelihood analysis of the *RAG-I* data alone produces a topology in which the positions of gekkos and dibamids are switched (but all other relationships are unchanged; Fig. 1). This might indicate a long-branch problem with *Dibamus*. However, because the rest of the tree is stable across all analyses, this discrepancy actually argues against LBA as an explanation for the recovery of a nonmonophyletic Scleroglossa. Furthermore, when analyses are performed without *Dibamus*, relationships among the remaining ingroup taxa are unchanged, and support remains high.

Choice of outgroup also may affect placement of the root (Wheeler 1990). Graham et al. (2002) showed that if outgroups are extremely divergent from the ingroup taxa, trees will tend to root incorrectly, and furthermore, these distant outgroups will preferentially root on long terminal ingroup branches. However, average *RAG-I* sequence divergence between *Sphenodon* and the ingroup taxa is only .196/.308

(uncorrected "p" distance/ML distance; see Appendix V), which is smaller than several within-ingroup comparisons. Average ML distances between ingroup taxa and turtles and crocodylids, respectively, are generally less than five percent higher than *Sphenodon*-ingroup distances (birds are somewhat more divergent). Analyses repeated with all possible outgroup combinations always give the same ingroup topology, with support values very similar to those obtained in the original analysis. Finally, it is important to note that simply rerooting our tree to make Scleroglossa monophyletic will not yield a topology congruent with current morphological hypotheses (see Figure 9A).

Another surprising finding is that snakes, dibamids, and amphisbaenians occur in separate parts of the tree, and alternative hypotheses placing any two of snakes, amphisbaenians, and dibamids as sister taxa are statistically rejected (Table 2). Analyses based on the two different optimality criteria disagree on the exact placement of snakes. Parsimony places them as the sister taxon of a modified Lacertiformes with weak support (bootstrap/decay of 52/2; Appendix IV). However, likelihood finds a clade containing snakes, anguimorphs, and iguanians, and this arrangement is strongly supported by Bayesian results (Fig. 3). A sister-taxon relationship between snakes and Varanidae/Lanthanotidae is statistically rejected (Table 2).

Inclusion of amphisbaenians within the traditional Lacertiformes (Lacertidae + Teiioidea) is statistically supported (Table 2), and heuristic support is strong for a sister-taxon relationship between lacertids and amphisbaenians (Fig. 3). This latter relationship may be supported by a structural character as well. *Gallotia* (a lacertid) has a seven-codon deletion at *c-mos* positions 220-240, and all sampled amphisbaenians share an overlapping eight-codon deletion at positions 217-240, suggesting that the original

deletion was simply extended by one codon in an ancestral amphisbaenian. Harris et al. (1999) reported a seven-codon deletion in this general region for two gekkonines. While the alignment in this area is not completely unambiguous (Appendix III), alignments made with Clustal X (Thompson et al. 1997) at a variety of gap penalties (see Methods) suggest that the lacertid and gekkonine deletions are not identical. Furthermore, forcing the gekkonine and lacertid deletions to coincide requires two separate, smaller amphisbaenian deletions instead of the one shown in Appendix III.

Relationships within Amphisbaenia are strongly supported. The amphisbaenian family Rhineuridae is not represented in the combined *RAG-I* and *c-mos* data set due to problems with amplification of the *c-mos* fragment. However, a Templeton test performed on the *RAG-I* data alone provides strong evidence ($p < .0001$) for monophyly of the other three amphisbaenian families to the exclusion of rhineurids (Townsend 2002). Furthermore, in the combined analysis, Trogonophidae and Amphisbaenidae form a well supported clade exclusive of Bipedidae (Fig. 3).

In parsimony, Bayesian, and likelihood analyses, dibamids are the sister taxon of all other squamates, and gekkos are the second group to diverge from the ancestral squamate lineage (Fig. 3). Support is not strong for the exact placement of dibamids and gekkos relative to each other, but both parsimony and Bayesian measures strongly support the basal position of these two taxa relative to the remaining squamates (Fig. 3).

Other unconventional but well-supported findings include placement of Xantusiidae within Scincoidea (traditionally comprising Scincidae and Cordylidae), specifically as the sister taxon of Cordylidae, and placement of Helodermatidae within a Xenosauridae-Anguidae clade to the exclusion of Varanidae/Lanthanotidae, the

traditional sister group of helodermatids (Fig. 3). *Shinisaurus* and Varanidae/Lanthanotidae form a monophyletic group, and a sister-taxon relationship between *Xenosaurus* and *Shinisaurus* (the traditional Xenosauridae) is statistically rejected (Table 2).

Within Scincidae, phylogenetic positions of the two limbless subfamilies are well supported. Acontinae is the sister group of all other skinks, and Feylininae is closely related to African scincines (actually nested within this group; see Fig. 1). Monophyly of African and North American scincines is not supported (Fig. 3).

Relationships within Gekkonidae are well supported. Pygopodinae is the sister taxon of Diplodactylinae (Fig. 3, Table 2), and this relationship is further supported by a shared one-codon deletion in the *RAG-1* data set at positions 125-127 (see Appendix III). *Teratoscincus* and Sphaerodactylinae form the sister group of Gekkoninae with high bootstrap/decay and Bayesian support (Fig. 3). Parsimony recovers Eublepharinae as the sister taxon of (*Teratoscincus* + Sphaerodactylinae + Gekkoninae), but support values are low (bootstrap/decay of 65/4; Appendix IV). However, the likelihood and Bayesian analyses recover this same relationship, and Bayesian support is high (Fig. 3). Furthermore, strong independent support for this arrangement comes from a shared four-codon deletion at positions 95-106 in the *RAG-1* data set (Appendix III). No other sampled gekkonids have any deleted bases in this region, and the surrounding amino acid sequence is conserved across gekkos, making alignment unambiguous (see Appendix III).

Mitochondrial sequences correspond to positions 4419 to 5933 on the human mitochondrial genome (Anderson et al. 1981). Parsimony and likelihood/Bayesian topologies differ at several points, and therefore analyses based on the two optimality

criteria are presented separately. Parsimony analysis of the mitochondrial data yields 4 equally most parsimonious trees, and the MP strict consensus recovers many, but not all, recognized squamate families as well as some recognized suprafamilial taxa (Fig. 4). Most branches relating taxa at the family level or higher are poorly supported, however. Maximum-likelihood analysis yields a single tree (Fig. 5). The Bayesian consensus topology is similar to the ML topology (see Fig. 5), and both analyses recover all moderately- to highly-supported nodes (bootstrap >80%) from the parsimony analysis. Average ML-corrected distances between ingroup taxa are more than four times as great for the mitochondrial data as they are for the *RAG-I* data (Table 1). Likewise, although the mitochondrial data set is only roughly half the size of the *RAG-I* data set (same number of taxa), the mitochondrial MP tree is approximately 45% longer than the corresponding *RAG-I* tree (Table 1). Thus, even with third-position transitions excluded, the mitochondrial data set is more likely to show saturation at more basal nodes, perhaps explaining the low support values for most deeper relationships.

Chamaeleonidae, Acrodonta, Serpentes, Iguanidae, Scincidae, Amphisbaenia and Teiioidea all receive high bootstrap and decay-index support, while Agamidae and Anguimorpha receive more moderate support (Fig. 4). All these clades except Agamidae receive high Bayesian support (Fig. 5). Acrodonts also have a mitochondrial gene rearrangement that has been reported as a synapomorphy of the group (Macey, et al., 1997b), and our new data confirm that this rearrangement is limited to acrodonts. Not all relationships within Amphisbaenia could be evaluated because sequence could not be obtained from *Rhineura*. For this species, multiple copies of ND2 and the tRNA genes preceding it were recovered from fragments amplified with different PCR primers, and it

was not apparent from secondary structure, nucleotide bias, or stop-codon searches which (if any) of the copies were nonfunctional. *Bipes biporus* has an abnormal origin of light-strand replication (O_L), and this condition is statistically associated with novel vertebrate mitochondrial gene orders, possibly by a mechanism involving tandem duplications (Macey et al. 1997a; Macey et al. 1997c; see also Townsend and Larson 2002 for examples of both novel gene orders and tandem duplications associated with an abnormal OL in chameleons). Our results show that another amphisbaenian, *Trogonophis weigmannii*, also has an atypical O_L (see aligned data set, Appendix III). Quite possibly, *Rhineura* shares this condition, and thus may be prone to mitochondrial gene-duplication events. Because we could not amplify junctions between any of the different sequenced fragments, and homology was uncertain, *Rhineura* was excluded from the mitochondrial and combined analyses. However, relationships among the remaining amphisbaenian families are strongly supported, and mirror exactly the results of the nuclear analysis (Fig. 3). Furthermore, the lacertid-amphisbaenian clade identified in *RAG-1* and *c-mos* analyses is once again recovered with moderate parsimony (Fig. 4) and high Bayesian (Fig. 5) support.

Within Gekkonidae, the mitochondrial likelihood and Bayesian analyses find exactly the topology from the nuclear analyses. However, mitochondrial parsimony analysis fails to recover a monophyletic Gekkonidae and also shows moderate support for a sister-taxon relationship between gekkonines and sphaerodactylines, although this is not supported by a Templeton test (see Table 2). Interestingly, the branches leading to gekkonines and sphaerodactylines are roughly twice as long as the branch leading to *Teratoscincus* (Fig. 5), suggesting that LBA may account for the mitochondrial

parsimony gekkonine/sphaerodactyline clade, which is at odds with all other analyses from this study. Mitochondrial data agree with the nuclear data on the nesting of feyliniine skinks within African scincines, and a sister-taxon relationship between xantusiids and cordylids.

A *Xenosaurus*-anguid clade exclusive of helodermatids is recovered with moderate (parsimony) to strong (Bayesian) support (Figs. 4 and 5), and similar support is found for a snake-acrodont clade. Both of these results disagree with the nuclear analysis (Fig. 3), and neither is supported by the nonparametric statistical tests (Table 2).

For the snake-acrodont association, the branches subtending each of these clades are much longer than most other branches of similar depth in the tree (Fig. 5). This fact, combined with strong support for a monophyletic Iguania from the nuclear data (Fig. 3, Table 2), suggests that LBA might be responsible for this very unorthodox arrangement. Results from our parametric bootstrapping simulations support the LBA hypothesis (Fig. 6). When snakes and anguimorphs were constrained to be sister taxa (a more traditional scenario) in 100 simulated data sets, equal-weights parsimony correctly recovered this clade in only 25% of replicates, whereas in 62% of replicates parsimony incorrectly recovered a snake-acrodont clade, as in the original mitochondrial analysis. In contrast, likelihood analysis under a GTR+I+G model, with all parameter values taken from the original mitochondrial data set, recovered the correct snake-anguimorph clade 78% of the time, and incorrectly recovered a snake-acrodont clade only 14% of the time.

In a second, more extreme deviation from the original mitochondrial topology, 100 data sets were simulated in which acrodonts and iguanids formed a monophyletic Iguania as the sister taxon of a clade containing snakes and anguimorphs, a topology

compatible with all well-supported nodes from the nuclear analysis (Fig. 3). Results from this analysis further support a role for LBA in the mitochondrial results. Equal-weights parsimony recovers the correct topology only 12% of the time, and 46% of the analyses incorrectly place snakes as the sister taxon of acrodonts. Meanwhile, likelihood recovers the correct topology 56% of the time, and incorrectly recovers a snake-acrodont clade in only 5% of the simulation replicates. As a control, 100 additional data sets were simulated using the original mitochondrial topology (snakes + acrodonts), and in these analyses both parsimony and likelihood recover the correct topology 98% of the time (Fig. 6).

Wiens and Hollingsworth (2000) suggested that one criterion for demonstrating LBA in an empirical study is strong external evidence that the inferred relationship is wrong, which we have in statistical support for Iguania in the nuclear analyses. Huelsenbeck (1997) had previously proposed two other criteria, which were that the branches should be shown to be long enough to attract each other (shown in our simulations), and also, that another method less sensitive to LBA (maximum likelihood) should *not* place the two long-branch taxa together. This second criterion is not technically satisfied here, because likelihood analysis of the mitochondrial data alone also recovers a snake-acrodont clade. However, maximum likelihood is not immune to LBA (e.g., Huelsenbeck and Hillis 1993), and the fact that Huelsenbeck's criterion *is* satisfied in the combined nuclear and mitochondrial analysis (see below) suggests a strong potential for LBA in the mitochondrial analysis.

The *RAG-1* data are significantly incongruent with the mitochondrial data ($p = .01$), but the *c-mos* data are not ($p = .91$), as measured by the ILD test. This result seems

counterintuitive in the case of the *c-mos* data, but probably reflects the fact that support for many conflicting deeper nodes is low in both *c-mos* and mitochondrial analyses. Incongruence between some data partitions may indicate that conflicts exist only for one or a few nodes, not that the data partitions are wholly incongruent. Because separate analyses of the three data sets yield trees with many clades in common, we combined all data sets for a final analysis. Topologies with support values from the combined mitochondrial and nuclear analyses can be found in Appendix IV, and major findings are summarized here. A monophyletic Agamidae has moderate parsimony (bootstrap/decay of 87/18) and strong Bayesian (posterior probability >95%) support, but is not supported by a Templeton test (Table 2). Support for lacertid-amphisbaenian, trogonophid-amphisbaenid, and xantusiid-cordylid clades is statistically significant (Table 2). Parsimony analysis still places snakes as the sister taxon of acrodonts, but with low support (bootstrap/decay of 65/7), as in the mitochondrial analyses. Interestingly, the likelihood analysis, which should be more resistant to LBA, places snakes as the sister group of (Anguimorpha + Iguania), and monophyly of Iguania is supported by a posterior probability >95% in the Bayesian analysis.

Figure 7 summarizes molecular support for phylogenetic relationships within Squamata.

Comparison with morphological evidence

Comparing Lee and Caldwell's (2000) morphology-based phylogeny to ours is difficult for two reasons. First, we use individual extant species as our terminal taxa,

whereas Lee and Caldwell used composite character states to reconstruct the most recent common ancestors to individual (usually family-level) clades, and then used these hypothetical ancestors as terminal taxa (Michael Lee, pers. comm.). Also, as these authors note, their favored topology, which places snakes inside Varanoidea, and Amphisbaenia and Dibamidae as sister taxa elsewhere in the tree (see their Fig. 9), is recovered only if several fossil taxa presumably related to varanids are included. However, when fossil taxa are removed, the collective monophyly of snakes, dibamids, and amphisbaenians is strongly supported, even after excluding several characters identified by Lee (1998) as potentially convergent in head-first burrowers (Fig. 8). This result suggests that other, as yet unidentified problematic characters remain. In Appendix VI we have compiled from Lee and Caldwell (2000) lists of morphological characters that favor several relationships found with relatively strong support in their study but refuted with statistical support in ours. If our phylogeny is correct, then these characters are candidates for reevaluation due to potential problems of homoplasy or incorrectly inferred ancestral states.

DISCUSSION

Nonmonophyly of Scleroglossa

Our phylogenetic results, especially those from the nuclear data, correspond well to traditional, morphology-based views in many respects. Whenever more than one subclade is sampled, currently accepted squamate families are recovered as clades with very strong support. Furthermore, many traditional suprafamilial groupings, such as Acrodonta, Iguania, Anguimorpha, Lacertiformes (modified to include amphisbaenians), and Scincoidea (modified to contain xantusiids) are also strongly supported. However, we also find strong support for other groupings that conflict with some conclusions based on morphological evidence, the most sweeping and unconventional of which is the strong statistical rejection of a monophyletic Scleroglossa in our analyses. This grouping (though not the taxon name) dates back to Camp's (1923) study, and it is supported by numerous osteological and soft-tissue characters (Estes et al. 1988; Schwenk 1988 and subsequent authors), as well as behavioral characters related to prey prehension (Schwenk and Throckmorton 1989).

Our results suggest reinterpretation of studies that have used comparative methodology to study traits or behaviors across higher squamate taxa, especially those that contrast Scleroglossa and Iguania. For example, Schwenk (1993) found a fundamental difference in tongue morphology and prey-prehension technique between iguanian (lingual prehension) and scleroglossan (jaw prehension) lizards. Schwenk (1986) reported that the tongue of *Sphenodon* (a lingual feeder) shares many features with iguanid lizards, including muscle-fiber architecture and hyobranchial-foretongue coupling. Based on these similarities, along with independent evidence for a basal dichotomy within squamates between Iguania and Scleroglossa (Estes et al. 1988), Schwenk (1986) concluded that *Sphenodon* and iguanians exhibit the ancestral squamate

(and lepidosaurian) condition, and that the common ancestor to Scleroglossa evolved a fundamentally different feeding system and associated tongue morphology. Studies on foraging mode and prey chemical-discrimination (e.g., Cooper 1995) generally have found that non-herbivorous iguanians are ambush predators with little ability to detect chemical cues from prey items, whereas scleroglossans are often actively-foraging lizards that tongue-flick to collect chemical cues from prey items (although several exceptions exist, and this dichotomy may be oversimplified; see Perry 1999). Release of the tongue from its prey-prehension duties is thought to have allowed this new role to develop, while the functional constraints imposed by lingual prey-prehension presumably have prevented most iguanians and *Sphenodon* from developing olfactory capabilities to the same extent (Schwenk 1993).

As mentioned by Schwenk (1986), several authors (e.g., Gans 1983; see also Wu 1994) have noted that *Sphenodon* is not a basal but rather a nested taxon within Rhynchocephalia, a widely distributed group that once included a diversity of body plans and lifestyles, including long-legged terrestrial forms, long-bodied obligate aquatic forms, and specialized herbivores (Evans et al. 2001; Reynoso 2000). While *Sphenodon* is almost undoubtedly the closest living relative to squamates (but see Hedges and Poling 1999), inferring its character states to be ancestral for Squamata, especially when the characters involve largely soft tissue anatomy and behavior, is problematic.

Schwenk and Wagner (2001) use suites of characters associated with both lingual-prehension and jaw-prehension modes of feeding to illustrate their evolutionarily stable configuration (ESC) concept, arguing that the phylogenetic stability of the lingual-prehension feeding mode across a variety of habitats and lifestyles is evidence of a

complex, integrated system. Internal selection for maintenance of the entire functional system is thought to overcome possibly opposing external selection on any one component, resulting in only rare transitions from one system to another. In the example discussed here, the lingual-prehension feeding mode (and its associated olfactory and behavioral traits) is thought to be a highly integrated system with strong interdependence among its components. This interdependence has led to the persistence of the lingual feeding mode in virtually all iguanians, regardless of habitat, diet, or other ecological variation. Only when the components of this system were somehow decoupled (presumably a very rare event) in the common ancestor to scleroglossans could jaw prehension and its associated olfactory and behavioral traits evolve.

Under our phylogenetic hypothesis, iguanians and *Sphenodon* (or some possibly distant ancestor to *Sphenodon*) are inferred to have acquired lingual prey-prehension techniques independently, and jaw prehension is the ancestral feeding mode for squamates (Fig. 9). Because food prehension techniques, tongue musculature, and chemosensory ability are unknown for rhynchocephalians other than *Sphenodon*, this scenario is only slightly less parsimonious than the traditional view. Although similarities in muscle fiber and connective-tissue architecture between *Sphenodon* and iguanians may be explained most parsimoniously by symplesiomorphy (Schwenk, 1986), if lepidosaurian feeding systems truly are highly integrated and constrained, tongue morphology could evolve to be markedly similar in unrelated groups adopting the same feeding mode.

Limbless taxa

Also in direct conflict with previous morphological hypotheses, separate origins for all major limbless groups are statistically supported by the nuclear data. Furthermore, large, almost identical deletions in the *c-mos* gene of amphisbaenians and *Gallotia* (a lacertid) provide further evidence that amphisbaenians are not closely related to either snakes or dibamids. Convergence or parallelism has likely misled morphological studies that find close relationships between two or more of these limbless groups.

In fact, some morphological data support our findings with respect to each of the major limbless groups. For example, a dibamid-gekkonid relationship has been proposed several times (e.g., Underwood 1957; Wu et al. 1996), most recently by Underwood and Lee (2000), who reported that these two taxa are unique among squamates in their possession of paired egg teeth (they also cite other potential gekkonid/dibamid synapomorphies). Our results are equivocal on the exact relationship of dibamids to gekkonids, except to indicate early divergence from the ancestral squamate lineage (see Figs. 1 and 3). Because of this phylogenetic position, paired egg teeth, along with most of the other similarities (Underwood and Lee 2000), are compatible with our results whether they are viewed as synapomorphies of a dibamid-gekkonid clade or as plesiomorphies of Squamata.

The exact position of snakes is not resolved by our data, although support for a nested position within squamates is strong. Many workers (e.g., Lee 1998; Lee and Caldwell 2000; McDowell and Bogert 1954; Reynoso 1998) have suggested that snakes are closely related to anguimorph lizards. This general relationship is compatible with our data, although only Reynoso (1998) found snakes to be the sister taxon of

anguimorphs. The rest have argued for a more specific relationship *within* Anguimorpha as the sister taxon of Varanidae and/or Lanthanotidae, a phylogenetic position clearly rejected by our data.

Finally, placement of amphisbaenians near lacertids is not without precedent. Several authors have suggested a close relationship with various scincomorph taxa (e.g., Bogert 1964; Böhme 1981) or with scincomorphs as a whole (Schwenk, 1988). More recently, Wu et al. (1996) found some support for amphisbaenians as the sister group to lacertoids. Kearney (In press) disputes Wu et al.'s (1996) claim that *Sineoamphisbaena* is an amphisbaenian and instead groups it with the extinct family Macrocephalosauridae. However, Macrocephalosauridae is itself possibly contained within the scincomorphan family Teiidae (Estes 1983), which is closely related to Lacertidae.

Our findings regarding relationships among amphisbaenian families indicate that evolution of limblessness in this group has occurred multiple times. The first lineage to diverge from the ancestral amphisbaenian was that leading to Rhineuridae, a limbless taxon. The next lineage to diverge was that leading to Bipedidae, which have forelimbs, leaving the lineage that eventually split to form Trogonophidae and Amphisbaenidae, both of which completely lack external limbs. This topology suggests that either the most recent common ancestor to amphisbaenians retained forelimbs, and they were independently lost by both the Rhineuridae and Trogonophidae/Amphisbaenidae lineages, or that they were lost once in the common ancestor and then regained in the Bipedidae lineage. Because limb loss is known to have occurred independently in many squamate lineages, and no cases of reversal are known for this trait (Greer, 1991), we favor the former hypothesis.

Placement of other higher taxa

The phylogenetic position of snakes aside, relationships within Anguimorpha differ somewhat from morphology-based arrangements. Although the mitochondrial MP results recover a monophyletic Varanoidea, support is very low, and likelihood analysis of the same data fails to recover this clade. Furthermore, the two nuclear data sets find an (identical) alternative arrangement, and the combined nuclear analysis statistically rejects monophyly of Varanoidea. This taxon has been found in virtually every morphological study since McDowell and Bogert (1954), and the list of morphological synapomorphies supporting it is long (see Estes et al. 1988). However, no previous molecular studies have had the taxon sampling needed to test its monophyly, and our results are also compelling. Ours is the second molecular study (see Macey et al. 1999a) to find statistical support for the nonmonophyly of (*Xenosaurus* + *Shinisaurus*), which strongly suggests that morphology of these two taxa needs to be critically reevaluated.

Our placement of Eublepharinae as the sister taxon of a clade containing Sphaerodactylinae, Gekkoninae, and *Teratoscincus* is unconventional, requiring, among other things, two separate losses of eyelids in non-eublepharine gekkos. Eublepharines are generally considered the sister group of all other gekkonids (Kluge 1967; Kluge 1987). If this traditional arrangement is correct, the pattern of deletions found in the *RAG-I* data has two possible explanations. The first possibility is that separate identical, four-codon deletions occurred in the two lineages leading to Eublepharinae and Sphaerodactylinae/Gekkoninae (including *Teratoscincus*), respectively. This possibility

seems unlikely, and several studies (e.g., van Dijk et al. 1999 and references therein) have suggested that indels are generally reliable phylogenetic characters less prone to homoplasy than base substitutions (but see Cunningham et al. 1997). Furthermore, Simmons et al. (2001) gave quantitative evidence that multi-codon deletions were even less prone to homoplasy than single-codon deletions. The second possibility is that all *RAG-I* deletions found within Gekkonidae are homologous, but that their distribution among extant taxa is the result of lineage sorting. In other words, polymorphism for presence/absence of the deletion existed in the common ancestor to all gekkos, and this polymorphism persisted through the divergence of eublepharines from all other gekkos and also through the split between gekkonines/sphaerodactylines and diplodactylines/pygopodines. Finally, the deletion became fixed in all but the latter. Polymorphism persisting through two separate higher-level divergences seems likely to be exceptionally rare, and to our knowledge no case of lineage sorting of a molecular polymorphism has been documented at a similar taxonomic level. The simplest explanation, especially in light of independent evidence from all three data sets for eublepharine/gekkonine/sphaerodactyline monophyly, is that a single deletion occurred in the common ancestor to eublepharines, gekkonines (including *Teratoscincus*), and sphaerodactylines.

Intrafamilial relationships of skinks are partially congruent with Greer's (1970) hypothesis. Scincinae is definitely paraphyletic with respect to Feyliniinae (which is nested within a clade of African scincines), but the southern African Acontinae is found to be the sister taxon to all other skinks (as a second molecular study with much greater taxon sampling of scincids has confirmed; Aaron Bauer, pers. comm.). As in the case of

amphisbaenians, evolution of limblessness has not occurred parsimoniously in skinks. The ancestral skink was almost certainly fully limbed, with independent evolution of limblessness and fossorial habits in acontines, feyliniines, and probably several separate lineages of lygosomines and scincines (Greer 1991).

Our placement of Xantusiidae as the sister taxon to Cordylidae agrees with Estes' (1983) conclusions. More recent assessments have disputed this placement, placing Xantusiidae as the sister taxon to Lacertiformes (e.g., Estes et al. 1988; Hallermann 1998) or even close to gekkos (Lee and Caldwell 2000). However, support values for these placements have either not been reported or are very low, and therefore the statistically supported arrangement reported here should be considered the best current hypothesis.

Relationships within Iguania are largely concordant with previous molecular findings. Recent molecular studies (Macey et al. 1997*b*; Schulte et al. 1998) found strong evidence for monophyly of the traditional Iguanidae, and both our *RAG-I* and mitochondrial results (with taxon sampling from all major iguanid sublineages) confirm this finding. However, there is an almost complete lack of resolution *within* Iguanidae in both the mitochondrial and *RAG-I* analyses. At least in the *RAG-I* results, this is not due to lack of informative characters. Levels of *RAG-I* sequence divergence within iguanids are very similar to those within agamids and gekkonids (see Appendix V), two groups whose internal relationships are generally well supported in the *RAG-I* analysis. Given the generally well-supported branching structure at similar divergence levels in the remainder of the tree, this lack of resolution suggests relatively rapid diversification within Iguanidae.

Agamidae is monophyletic in all but the *RAG-1* and *RAG-1/c-mos* likelihood analyses, and bootstrap/decay support is fairly high in the *RAG-1/c-mos*/mtDNA combined MP and Bayesian analyses, but support for Agamidae is still not statistically significant using the Templeton test. Joger (1991) found Agamidae monophyletic using albumin immunological distances, and Honda et al. (2000) reported strong heuristic support for its monophyly (MP bootstrap of 100%, but no statistical testing was performed) using 12S and 16S mitochondrial data. Macey et al. (2000) also recovered a monophyletic Agamidae, although support was not strong. Thus, although morphological conflicts remain (Frost and Etheridge 1989), the molecular consensus leans heavily in favor of a monophyletic Agamidae. Relationships among agamids are congruent with those recovered by Honda et al. (2000) and Macey et al. (2000), although support values are generally much higher in the present study. The exact relationship between the basal taxa *Leiolepis* and *Uromastix* is still uncertain, but relationships among the remaining sublineages seem fairly well established.

Paleontological implications

The morphology-based hypothesis of a basal dichotomy between Iguania and Scleroglossa predicts that a diversity of fossils bearing iguanian synapomorphies should be found relatively early in the fossil record. However, iguanians are absent from all early major assemblages, and instead their first certain appearance is in the Early Cretaceous of Asia (Gao and Nessov, 1998). If these are indeed the earliest iguanians yet discovered, then our hypothesis of a nested Iguania is strengthened. However, one

possible reason for this discrepancy is the general paucity of Gondwanan squamate fossil sites (i.e. an artifact of sampling) (Evans, 1995). Evans et al. (2002) described the species *Bharatagama rebbanensis* from the Early Jurassic Kota Formation of India, and referred it to Iguania (specifically Acrodonta). If this classification is correct, it would extend the fossil record of iguanians back by approximately 80 million years (Ma) (Evans et al., 2002) and would make these fossil squamates among the earliest yet discovered. The Kota fossils, however, consist entirely of dentary-bone fragments (some with teeth), and some character states are suggestive of sphenodontian affinities (Evans et al., 2002). Furthermore, because the initial divergence between squamates and sphenodontians occurred at least as far back as the mid-Triassic (Fraser and Benton 1989), even if the Kota fossils are iguanians there still exists a period of about 40 Ma whose squamate diversity remains unknown. Macey et al.'s (2000) analysis of acrodont biogeography is based on the assumption that the acrodont lineage was present in Gondwana prior to Gondwanan fragmentation, and in fact it is a perfectly plausible hypothesis that all of the major squamate lineages may have diversified prior to the Kota depositions (Evans 1993). To assess the congruence of the fossil record with competing squamate phylogenetic hypotheses, data from more Early Jurassic and Triassic sites (and more Gondwanan sites in general) are needed.

Our results not only refute monophyly of Scleroglossa, but also several of its constituent higher taxa, and these discrepancies also affect interpretation of the fossil record. Fossil squamate specimens are often fragmentary and poorly preserved, and consequently are often referred to more inclusive, suprafamilial taxa such as Scleroglossa, Autarchoglossa, Scincomorpha, etc., based on supposed synapomorphies of

these higher taxa. If our phylogeny is correct, however, many of these suprafamilial taxa do not represent natural groups, and therefore reference of a particular fossil to one of these taxa could lead to incorrect assumptions about the geographic and temporal appearance of the other putative members of the higher taxon.

For example, the taxon Scincomorpha (Estes et al., 1988) is traditionally composed of Scincidae, Cordylidae, Xantusiidae, Lacertidae, Teiidae, and Gymnophthalmidae. This clade has been recovered in most recent morphological phylogenetic analyses (but see Lee, 1998 and Lee and Caldwell, 2000), and the taxon name is widely used in the paleontological literature (e.g. Gao and Norell 2000; Reynoso and Callison 2000; Wu et al. 1996). However, our results indicate that Scincomorpha is not monophyletic, and instead consists of a more basal Scincoidea (modified to contain xantusiids) and a nested Lacertiformes (modified to contain amphisbaenians), the latter being more closely related to snakes, anguimorphs, and iguanians than to scincoids. The earliest "scincomorphs" are known from the Middle Jurassic, and these early species are all (with varying degrees of confidence) allied with the Paramocellodidae, an extinct lizard family thought to be the sister taxon to Scincoidea (Evans and Chure 1998). The oldest known members of Lacertiformes are referable to Teiidae, and this family does not appear until much later, at the Early-Late Cretaceous boundary (Nydam and Cifelli 2002). Thus, while the first appearances of members of the two branches of the "scincomorphs" are widely separated temporally, current taxonomy misleadingly suggests that both ancestral scincoids and lacertiforms must have been present at the time of the first occurrence of paramocellodids.

Our phylogeny suggests a broad reinterpretation of the evolutionary history of Squamata. Further phylogenetic testing of our major findings, especially nonmonophyly of Scleroglossa, is therefore critical. The coding region of *c-mos*, for example, is over 1,000 bases long, making it an obvious candidate for further studies. Identification of multiple, independent nuclear loci evolving at rates similar to (or possibly slower than) those of *c-mos* and *RAG-1* should also be a research priority.

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Appendix I. Specimen Information

Museum numbers and localities of voucher specimens from which DNA was extracted and GenBank accession numbers are given below. Acronyms are AMNH, American Museum of Natural History, New York; AMS, Australian Museum, Sydney; CAS, California Academy of Sciences, San Francisco; CM, Craig Moritz Collection, University of Queensland, Australia; EBU, Evolutionary Biology Unit, South Australian Museum; JW, John Wombey field number; LJV, Laurie J. Vitt field number; LSUMZ, Louisiana Museum of Natural History; MQAZ, Museo de Zoología de la Pontificia Universidad Católica del Ecuador; MRT, Miguel Trefaut Rodrigues field number; MVZ, Museum of Vertebrate Zoology, University of California at Berkeley; MZUSP, Museo de Zoologia, University of São Paulo, Brazil; TP, Ted Papenfuss field number; RM, J. Robert Macey field number; SBH, S. Blair Hedges field number; TMT, senior author's private collection; SAMA, South Australian Museum, Adelaide, Australia; SD, Savel Daniels field number; TNHC, Texas Memorial Museum, Austin; USNM, United States National Museum, Washington, D.C.; WHT, Wildlife Heritage Trust, Colombo, Sri Lanka; ZISP, Zoological Institute, St. Petersburg, Russia

MITOCHONDRIAL DATA:

Outgroups: *Alligator mississippiensis* (Janke and Arnason 1997); *Gallus gallus* (Desjardins and Morais 1990); *Chelonia mydas* (Kumazawa and Nishida 1995); *Sphenodon punctatus*, New Zealand (St. Louis Zoo, ISIS No. 373002); **Acrodonta:** *Brookesia thieli*, Ambohitantely Special Preserve, Madagascar (FM 13949, AF448780; Townsend and Larson, 2002); *Chamaeleo rudis*, Kabale District, Uganda (CAS 201711, AF448761; Townsend and Larson, 2002); *Calumma brevicornis*, Ambohitantely Special Preserve, Madagascar (FM 13715, AF448734; Townsend and Larson, 2002); *Ctenophorus salinarum*, north of Serpentine Lakes, South Australia (Melville et al. 2001); *Physignathus lesueurii*, New South Wales, Australia (SAMA R33417, AF128463;

Macey *et al.*, 2000); *Physignathus cocincinus*, Gia-Lai Province, Vietnam (MVZ 222159, U82690; Macey *et al.*, 1997b); *Hydrosaurus sp.*, Samar Island, West Samar Province, Philippines (TNHC 54902, AF128476; Macey *et al.*, 2000); *Calotes calotes*, Sri Lanka (WHT 1679, AF128482; Macey *et al.*, 2000); *Japalura tricarinata*, Xizang (Tibet) Autonomous Region, China (CAS 177397, AF128478; Macey *et al.*, 2000); *Phrynocephalus raddei*, Ashkabad (Ashkabad) Region, Turkmenistan (CAS 179770, U82691; Macey *et al.*, 1997b); *Leiolepis belliana*, Phuket Province, Thailand (MVZ 215497, U82689; Macey *et al.*, 1997b); *Uromastyx acanthinurus*, Ouarzazate Province, Morocco (MVZ 162567, U71325; Macey *et al.*, 1997a,c); **Iguanidae:** *Anolis paternus*, Cuba (USNM 498070, U82679; Macey *et al.*, 1997b); *Phrynosoma mcallii*, San Diego Co., California (TP24443, unpublished sequence provided by Jim Schulte); *Sauromalus obesus*, California (MVZ 144194, U82687; Macey *et al.*, 1997b); *Hoplocercus spinosus*, Mato Grosso, Brazil (MZUSP 907931, U82683; Macey *et al.*, 1997b); *Enyaloides laticeps*, Porto Walker, Acre, Brazil (LSUMZ H13573, unpublished sequence provided by Jim Schulte); *Phymaturus somuncurensus* Meseta Somuncurá, Dept. Río Negro, Argentina (SDSU 1648, AF049865; Schulte *et al.*, 1998); *Liolaemus pictus* Bariloche, 44 km west at Río Castaño Overo, Dept. Río Negro, Argentina (MVZ 162076, U82684; Schulte *et al.*, 1998); *Uracentron flaviceps*, Reserva Faunistica Cuyabeno, Prov. Sucumbios, Ecuador (QCAZ-2536, unpublished sequence provided by Jim Schulte); *Stenocercus crasicaudatus* Machu Pichu Ruins, Depto. Cuzco, Peru (MVZ 199531, AF049866; Schulte *et al.*, 1998); *Leiocephalus carinatus*, Marsh Harbor, Abaco, Bahamas (no voucher, AF049864); *Basiliscus plumifrons*, Costa Rica (MVZ 204068, U82680; Macey *et al.*, 1997b); *Gambelia wislizenii*, Nevada (MVZ 227883, U82682; Macey *et al.*, 1997b); *Oplurus cuvieri*, Madagascar (CAS-RM10468B, U82686; Macey *et al.*, 1997b); **Anguimorpha:** *Ophisaurus attenuatus*, 2.4 miles south of Weldon Springs at I-40 on Hwy 94, St. Charles Co., Missouri (MVZ-RM10468A, AF085625; Macey *et al.*, 1999); *Elgaria panamintina*, California (MVZ227761, U82692; Macey *et al.*, 1999); *Celestes enneagrammus*, La Joya, Veracruz, Mexico (MVZ 191045, AF085607; Macey *et al.*, 1999); *Anniella pulchra*, 0.2 miles SE Jct of Hwy 4 and

Big Break Road, Oakly, Contra Costa Co., California (MVZ-TP24475, AF085606; Macey et al., 1999); *Heloderma suspectum*, probably Arizona (no voucher, AF085603; Macey et al., 1999); *Xenosaurus grandis*, slopes behind Casa de Miguel Ceron, Cuatlapan, Veracruz, Mexico (MVZ 137789, U71333; Macey et al., 1999); *Varanus griseus*, east side of Nephtezavodsk, 30 km WNW of Deynau (ZISP 19576, U71334; Macey et al., 1999); *Lanthanotus borneensis*, Borneo (Cincinnati Zoo, I.D. No. unknown); *Shinisaurus crocodilurus*, China (MVZ 204291, AF085604; Macey et al., 1999); **Serpentes:** *Dinodon semicarinatus*, Japan (no voucher, AB008539; Kumazawa et al., 1998); *Rhamphotyphlops braminus*, Sagaing Division, Alaungdaw Kathapa National Park, Paya Chaung, Myanmar (CAS 210151); *Cylindrophis ruffus*, Sagaing Division, Kabaing Village, Myanmar (CAS 210518); *Agkistrodon* sp. (RM 7879); **Lacertidae:** *Eremias grammica*, Turkmenistan (CAS 179206, U71331; Macey et al., 1997c); **Ampisbaenia:** *Bipes biporus*, Baja California Sur, Mexico (MVZ 137543; U71335; Macey et al., 1997c); *Trogonophis weigmanni*, Casablanca-Anfa Province, Morocco (MVZ 162541); *Amphisbaena xera*, <.5 km inland from Playa Tamarindo, 7 km SE by road from Guanica, Puerto Rico (CAS 200734); **Teiioidea:** *Cnemidophorus tigris*, California (MVZ 179799, U71332; Macey et al., 1997c); *Leposoma parietale*, Reserva Faunistica Cuyabeno, Sucumbios Province, Ecuador (LJV 4756); **Gekkonidae:** *Eublepharis turkmenicus*, (Macey et al. 1999b); *Sphaerodactylus shrevei*, Haiti (SBH 194572); *Teratoscincus przewalskii*, Xinjiang, China (CAS 171010, U71326; Macey et al., 1997a,c); *Gekko gekko*, Phuket Island, Phuket Province, (Macey et al. 1999b); *Pseudothecadactylus lindneri*, Liverpool River, Northern Territory, Australia (AMS R90195; unpublished sequence provided by Jane Melville); *Crenadactylus ocellatus*, 10 km south of Barrow Creek, Northern Territory, Australia (SAMA R22245; unpublished sequence provided by Jane Melville); *Lialis jicari*, Manam Island, Madong, New Guinea (AMNH 105099, U71327; Macey et al., 1997c); **Scincidae:** *Mabuya aurata*, Turkmenistan (CAS 179697, U71330; Macey et al., 1997c); *Ctenotus robustus*, (JW-R6061); *Scincella sikkimensis*, (RM10280); *Eumeces inexpectatus*, (MVZ-FC10701); *Eumeces skiltonianus*, Mendocino National Forest, Snow

Mountain Wilderness, Berry Creek (CAS 220815); *Eumeces anthracinus* Washington University Tyson Research Center, St. Louis, MO (RM10668); *Scelotes anguineus*, Grahamstown, Eastern Cape, South Africa (SD294); *Proscelotes eggeli*, Tanga region, Lushoto District, Tanzania (CAS 168961); *Feylinia polylepis*, Agua Chipique at Sundi, Principe Island (CAS 219338); *Chalcides ocellatus*, pet trade (TMT47); *Acontias meleagris*, Jacobsbaai, Western Cape, South Africa (CAS 206704); *Typhlosaurus gariensis* Farm Avondsehn, Kalahari Guest Farm, Northern Cape, South Africa (CAS 214519); *Typhlosaurus lomii*, ca 47 km S of Kleinsee, DeBeers mining farm area, Farm Noup, Northern Cape, South Africa (CAS 206872); **Xantusiidae**: *Xantusia vigilis*, California (MVZ-RM2299, U71328; Macey et al., 1997c); **Cordylidae**: *Cordylus polyzonus* (RM-JV2101); *Zonosaurus* sp. pet trade animal (TNHC 55947); **Dibamidae**: *Dibamus* sp., Vinh Yen District, Tam Dao, Vinh Phu Province, Vietnam (MVZ 224112)

RAG-1 DATA:

Outgroups: *Alligator mississippiensis* (AMNH OTC73, AF143724; Groth and Barrowclough, 1999); *Gallus gallus* (Carlson et al. 1991); *Chelonia mydas* (no voucher, tissue from SBH collection; Jim Krenz, unpublished data)

All ingroup and *Sphenodon* data were newly collected for this study, and specimen information is as above except for the following:

Leiolepis belliana (MVZ 215497) is replaced by: *Leiolepis belliana*, Magwe Div., Minbu Township, Shwesehtaw Wildlife Sanctuary, Myanmar (CAS 210725)

Heloderma suspectum (no voucher) is replaced by: *Heloderma suspectum*, captive-hatched at St. Louis Zoo (ISIS 100503)

Dinodon semicarinatus (no voucher) is replaced by *Dinodon* sp., Asia (RM8730)

Eremias grammica (CAS 179206) is replaced by *Eremias* sp., Asia (RM6585)

C-mos DATA:

Note: Some *c-mos* sequences were newly generated for this study (see mtDNA and *RAG-1* specimen lists for localities) while others were downloaded from GenBank, and these are referenced to their original study.

Outgroups: *Crocodylus porosus* (SAMA R34528, AF039484; Saint et al., 1998); *Gallus gallus* no voucher, (Schmidt et al. 1988); *Pelomedusa subrufa* AF109208; (Georges et al. 1999) *Sphenodon punctatus*, New Zealand (CM43; Saint et al., 1998);

Acrodonta: *Chamaeleo jacksonii*, Nairobi Province, Kenya (CAS 199070); *Uromastyx aegyptia* (AF137531; Hutchinson et al., direct GenBank submission); *Leiolepis guentherpetersi* (AF137529; Hutchinson et al., direct GenBank submission); *Physignathus lesueurii* (AF137524; Hutchinson et al., direct GenBank submission); *Ctenophorus decresii* (SAMA R42978, AF039475; Saint et al., 1998); *Physignathus cocincinus* (EBU 0188218, AF039476; Saint et al., 1998); *Phrynocephalus mystaceus* (AF137527; Hutchinson et al., direct GenBank submission); *Calotes versicolor* (AF137525; Hutchinson et al., direct GenBank submission); **Iguanidae:**

Sauromalus obesus (AF315400; Harris et al., 2001); *Oplurus sebae* (AF315391; Harris et al., 2001); *Leiocephalus sp.* (AF315388; Harris et al., 2001); *Corytophanes cristatus* (AF315390; Harris et al., 2001); *Sceloporus grammicus* (CM331, AF039478; Saint et al., 1998);

Anguimorpha: *Elgaria multicarinata* (CM199, AF039479; Saint et al., 1998); *Varanus salvator* (AF435017; Jing et al., direct GenBank submission); *Lanthanotus borneensis* (Cincinatti Zoo, I.D. No. unknown); *Shinisaurus crocodiluris* (MVZ 204291); *Heloderma suspectum* (ISIS 100503); *Xenosaurus grandis* (MVZ 137789); **Serpentes:** *Agkistrodon piscivorus* (AF471096;

Lawson and Slowinski, direct GenBank submission); *Dinodon rufozonatum* (AF471163; Lawson and Slowinski, direct GenBank submission); *Cylindrophis ruffus* (AF471133; Lawson and Slowinski, direct GenBank submission); *Ramphotyphlops australis* (SAMA R36502, AF039474; Saint et al., 1998); **Lacertidae:** *Gallotia galloti* (AF315394; Harris et al., 2001);

Amphisbaenia: *Diplometopon zarudnyi* (AF148709; Harris et al., 2001); *Bipes biporus* (CM22, AF039482; Saint et al., 1998); *Amphisbaena xera* (CAS 200734); **Teiioidea:** *Tupinambus*

quadrilineatus (Pellegrino et al. 2001); *Bachia dorbignyi* Juruena, Matto Grosso, Brazil (MRT 977273, AF420861; Pellegrino et al., 2001); **Gekkonidae:** *Coleonyx variegatus* (AF315386; Harris et al., 2001); *Pseudothecadactylus lindneri* (AMS R90194, AF090846; Donnellan et al., 1999); *Lialis burtonis* (SAMA R29312, AF090850; Donnellan et al., 1999); *Teratoscincus przewalskii* (CAS 171010); *Tarentola boettgeri* (AF315387; Harris et al., 2001); *Sphaerodactylus shrevei* (SBH 194572); **Scincidae:** *Mabuya delalandii* (Brehm et al. 2001); *Eumeces skiltonianus* (AF315396; Harris et al., 2001); *Feylinia polylepis* (CAS 219338); *Acontias meleagris* (CAS 206704); *Proscelotes eggeli* (CAS 168961); **Xantusiidae:** *Xantusia vigilis* (AF148703; Harris et al., 2001); **Cordylidae:** *Cordylus cordylus* (AF148711; Harris et al., 2001); **Dibamidae:** *Dibamus sp.* (MVZ 224112)

Appendix II. PCR primers used in this study

A. *RAG-1* primers. All primers are written 5' to 3' and designated as forward (F) or reverse (R).

Numbers designate the position of the 3' end with respect to the *RAG-1* gene of *Gallus gallus* (see text). All primers were designed for this study unless otherwise noted.

F83a ^a : TCTGAATGGAAATTCAAGCTGTT	R1107: TTATGGCTGGAAAGATGGTGA R62
F83b: TCNGAATGGAARTTYAARCTNTT R103	R1165 ^b : GATGCTGCCTCGGTCCGCCACCTTT R18
F94: TGGAARTTCAARCTGTTCAAAGT R75	R1168: GGTGTTGTCTTGGTCGGCCACC R63
F104: CAAAGTGAGATCNCTTGAAAA R51	F1457a: TGTAGCCARTACCATAAAATGTA R90
F108: GTGAGATCACTTAACAAACCA R50	F1457b: TGYAGTCARTAYCACAAAATGTA R145
F117: ACTTGGAAGCCACTTCCYGAA R46	R1639: GTGTCYACTGGGTARTCATC R89
F129: TTTCTGATGACAGCCATCTG R47	F1709: TTTGGTGGCTGCCCTTATGGA R154
F146: ATCTRGCTAACAGTGAYAAAGG R102	R1968: TTCATCAGCCAGCATAAGGCAC R85
F159: TGATAAAGAGAAAGTGGCAGCC R48	F1989: TGCCTTATGCTGGCTGATGAA R65
R357: GGTGGCTYCTCTTATAAGGATCA R41	R2023: TCTCTTTCTGCTACAAGAGG R101
R387: GTNTCATCATCTACTGGTCCA R39	F2568a: GGATGAATGGRAATTTTGCCAGA R38
F620: TGGARTGGCANCCCCATNC R29	F2568b: GGATGAATGGAAAYTTTGCTMGA R149
R652: TCTTTCTCTTGAYYCCAYG R30	R2643: AGATAAAGCTCCATGAGYTCT R59
F889: ATCTGTGAGCATATCCTGGC R134	R2847: AGCACCAATGGAGCCRTCTCTT R55
F962: AAATGYCTTAAAGTAATGGG R148	R2857: TCACTTGCCCAAGCTCCAATAGA R66
F1004a: CTAYCCTTGYYTTTCCTACNGA R27	R2876: TTTGTTCCCAGATTCATTTC R70
F1004b: CTATCCTTGCTTTCCGMCTGA R130	R2918: GACTGCCTSGCATTCATTTTYC R28
R1096: AGATGRTGGCTGTATTTTCC R61	R3001: RTGNGCRITTCATRAAYTTYTG R106

^a R13 of Groth and Barrowclough (1999)

^b R18 of Groth and Barrowclough (1999)

B. *C-mos* primers. The following primers from Saint *et al.* (1998) were used to amplify and sequence all individuals in this study. Primers are written 3' to 5', and numbers in brackets after the primer sequence refer to the position of the primer with respect to the human *c-mos* sequence (see text).

G73 GCGGTAAAGCAGGTGAAGAAA [513]

G74 TGAGCATCCAAAGTCTCCAATC [888]

C. Mitochondrial primers. All primers are written 5' to 3' and designated as light-strand (L) or heavy-strand (H). Numbers designate the position of the 3' end with respect to the human mitochondrial genome (see text). All primers are from Macey *et al.* (1997a) unless otherwise noted.

L3002	16S	TACGACCTCGATGTTGGATCAGG
L3881	ND1	TTTGACCTAACAGAAGGAGA
L3887	ND1	GACCTAACAGAAGGAGAATCAGA
L4160 ^a	ND1	CGATTCCGATATGACCARCT
L4178	ND1	CAACTAATACACCTACTATGAAA
L4221	tRNA ^{Ile}	AAGGATTACTTTGATAGAGT
H4419a	tRNA ^{Met}	GGTATGAGCCCAATTGCTT
H4419b ^b	tRNA ^{Met}	GGTATGGGCCCAAAAGCTT
H4419c	tRNA ^{Met}	GGTATGAGCCCGATAGCTT
L4437a	tRNA ^{Met}	AAGCTTTCGGGCCCCATACC
L4437b ^c	tRNA ^{Met}	AAGCAGTTGGGCCCATRCC
H4629 ^b	ND2	AAGTATTTTGTGCGGCTTC
L4882a ^b	ND2	TGACAAAAAATTGCNCC
L4882b	ND2	TGACAAAAACTAGCCCC
H4980a	ND2	ATTTTTCGTAGTTGGGTTTGRTT
H4980b ^b	ND2	ATTTTTCGTATTTGKGTTTGTT
L5549 ^b	tRNA ^{Trp}	AACCARAGGCCTTCAAAG
H5617a	tRNA ^{Ala}	AAAATRTCTGRGTTGCATTCAG
H5617b	tRNA ^{Ala}	AAAGTGTCTGAGTTGCATTCAG
L5638a	tRNA ^{Ala}	CTGAATGCAACYCAGAYATTTT
L5638b	tRNA ^{Ala}	CTGAATGCAACTCAGACACTTT
H5692	tRNA ^{Asn}	TTGGGTGTTTAGCTGTAA
H5934	COI	AGRGTGCCAATGTCTTTGTGRTT

^a Kumazawa and Nishida (1993)

^b This study

^c Macey *et al.* (1997b)

Appendix III. Aligned Data sets

A. RAG-1 (excluded nucleotide positions underlined)

List of Taxa:

1. *Alligator mississippiensis*
2. *Gallus gallus*
3. *Chelonia mydas*
4. *Sphenodon punctatus*
5. *Brookesia thieli*
6. *Chamaeleo rudis*
7. *Calumma brevicornis*
8. *Ctenophorus salinarum*
9. *Physignathus lesueurii*
10. *Physignathus cocincinus*
11. *Hydrosaurus sp.*
12. *Calotes calotes*
13. *Japalura tricarinata*
14. *Phrynocephalus raddei*
15. *Leiolepis belliana*
16. *Uromastix acanthinurus*
17. *Anolis paternus*
18. *Phrynosoma mcallii*
19. *Sauromalus obesus*
20. *Hoplocercus sp.*
21. *Enyaloides laticeps*
22. *Phymaturus somuncurensis*
23. *Liolaemus pictus*
24. *Uracentron flaviceps*
25. *Stenocercus crasicaudatus*
26. *Leiocephalus carinatus*
27. *Basiliscus plumifrons*
28. *Gambelia wislizenii*
29. *Oplurus cuvieri*
30. *Ophisaurus attenuatus*
31. *Elgaria panamintina*
32. *Celestes enneagrammus*
33. *Anniella pulchra*
34. *Heloderma suspectum*
35. *Xenosaurus grandis*
36. *Varanus griseus*
37. *Lanthanotus borneensis*
38. *Shinisaurus crocodiluris*
39. *Dinodon sp*
40. *Ramphotyphlops braminus*
41. *Cylindrophis ruffus*
42. *Agkistrodon sp.*
43. *Eremias sp.*
44. *Bipes biporus*
45. *Trogonophis weigmanni*
46. *Rhineura floridana*
47. *Amphisbaena xera*
48. *Cnemidophorus tigris*
49. *Leposoma parietale*
50. *Eublepharus turkmenicus*
51. *Sphaerodactylus shrevei*
52. *Teratoscincus przewalskii*
53. *Gekko gekko*
54. *Pseudothecadactylus lindneri*
55. *Crenadactylus ocellatus*
56. *Lialis jicari*
57. *Mabuya aurata*
58. *Ctenotus robustus*
59. *Scincella sikkimensis*
60. *Eumeces inexpectatus*
61. *Eumeces skiltonianus*
62. *Eumeces anthracinus*
63. *Scelotes anguineus*
64. *Proscelotes eggeli*
65. *Feylinia polylepis*
66. *Chalcides ocellatus*
67. *Acontias meleagris*
68. *Typhlosaurus garipeensis*
69. *Typhlosaurus lomii*
70. *Xantusia vigilis*
71. *Cordylus polyzonus*
72. *Zonosaurus sp.*
73. *Dibamus sp.*

Index2 0000000001111111112222222223333333334444444445555555556666666667777777778888888889
Index3 12345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip. TAAAGTAAAGATCATTTGAAAAGACACCTTCTGGGGATAGCCACGTGGTAAATAAAGATAAAGCAGAAGAGGCAGCCTCTTTGGACAAAGG
G.gallus TAAAGTGAGGCCATTTCAAAAAGAACCTTCTGTAAAAAGCCATGCATAAACAAAGGATCAAGAAACAAGAGGTAGCTTCTACAGACAAAAA
C.mydas ???GAAAAATAAGAGAAAAGCAGAGAAGGAGCCTCTTTGGACAATGG
S.punctatus CAAAGTGAGATCATTTGAAAAGGCACCTTCTGAAGACAGCTGCCCAAAAATCAATGAGAAAAGCAGAAGAGGTGGTCTCTTTGGGCAAAAGC
B.thieli TAAAGTGAGACCATTGGAAAACTACTTCTCTGAAGACAATCATCTGGCCAACAGCAATAAAGGAGAACCAGCAGCCTCTCTGGACAAAGT
C.rudis TAAAGTAAGACCATTGGAAAACTACTTCTCTGAAGACAATCATCTGGCCAACAGCAATAAAGAGAACCAGCAGTCTCTCTGGACAAAGT
C.brevicornis TAAAGTAAGACCATTGGAAAACTACTTCTCTGAAGACAATCATCTGGCCAACAGCAATAAAGGAGAACCAGTAGCCTCTCTGGACAAAGT
C.salinarum CAAAGTGAGACCATTGGAAAGCCACTTCTCTGAAGACAGTCTCTGGCTAATAGCAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
P.lesueurii TAAAGTGAGACCATTGGAAAGCCACTTCTCTGAAGACAGTCTCTGGCTAATAGCAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
P.cocincinus CAAAGTGAGACCATTGGAAAGCCACTTCTCTGAAGACAGTCTCTGGCTAATAACAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
Hydrosaurus.sp. CAAAGTGAGACCATTGGAAAGCCACTTCTCTGAAGACAGTCTCTGGCTAACAACAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
C.calotes CAAAGTGAGACGACTTGGAAAGCCACTTCTCTGAAGACAGTCTCTGGCTAACAGCGATAAAGGACAAGTGGCAGCCCCCTGGACAGAGC
J.tricarinata CAAAGTGAGACGACTTGGAAAGCCACTTCTCTGAAGACAGTCTCTGGCTAACAGCGATCAAGGACAAGTGGCAGCCTCTCTGGACAAAGT
P.raddei CAAAGTGCGACACTTGGAAAGCCACTTCCCGAAGACAGTCAAGTGGCTAACAGCGATAAAGGGCAAGTGGCAGCCTCTCTGGACAAAGT
L.belliana CAAAGTGAGGCCATTGGAAAGCCATTTCTCTGAAGACAGTCTCTGGCTAACAGCAATAAAGGAGAAGTGGCAGACTCTCTGGACAAAGT
U.acanthinurus CAAAGTGAGACCATTGGAAAGCCATTTCTCTGAAGACAGTCTCTGGCTAATAGCAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
A.paternus CAAAGTGAGATCAATTGAGAAGCCACTTCTCTGATGACAGCCATCTGGCTAACACAATAAAGGGAAGCGGACGCTTCTCTGGACAAAGT
P.mcallii CAGAGTAAGATCACTTGAGAAGCTGCTTCTCTGATGACAGCCATCTGGCTAACACAATAAAGGAAAAGTG-----GACAAAGT
S.obesus ???GCTAACACAATAAAGGAAAAGTGGCTTCTCTGGACAAAGT
Hoplocercus.sp. CAAAGTGAGATCACTTGAGAAGCCACTTCTCTGATGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGTTTCTCTGGAGAAAGT
E.laticeps ???GCTAACACAATAAAGGAAAAGTGGCAGTTTCTCTGGACAAAGT
P.somencurensus CAAAGTAAGATCACTTGAGAAGCCACTTCTCTGATGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCTTCTCTGGACAAAGT
L.pictus CAAAGTGAGATCACTTGAGAAGCCACTTCTCTGATGACAGTTTACCTCGTAAACAACAATAAAGGAAAAGTGGCAACATCTCTGGACAAAAC
U.flaviceps CAAAGTGCGATCACTTGAGAAGCCACTTCTCTGATGACAGCCATCTGGCTAACAAACCATAAAGGAAAAGTGGCAGCTTCTCTGGATAAAGT
S.scrasicaudatus CAAAGTGAGATCACTTGAGAAGCCACTTCTCTGATGACAGTGTGTGGCTAACAAACCATAAAGGAAAAGTGGCAGCTTCTCTGGATAAAGT
L.carinatus CAAAGTGAGATCACTTGAGAAGCCACTTCTCTGATGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCTTCTCTGGACAAAGT
B.plumifrons CAAAGTGAGATCACTTGAGAAGCCACTTCTCTGATGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCTTCTCTGGACAAAGT
G.wislizenii CAAAGTGAGATCACTTGAGAAGCCACTTCTCTGAAGACAGCCATCTGGCTAACACAACAAGGAAAAGTGTGAGCTTCTCTGGACAAAGT
O.cuvieri ???GTTAACACAATAAAGGAAAAGTGGCAGCTTCTCTGGACACAGT
O.attenuatus CAAAGTGAGATCACTTGAAAAGCCACTTCTCTGAAGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
E.panamintina CAAAGTGAGATCACTTGAAAAGCCACTTCTCTGAAGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
C.enneagrammus CAAAGTGAGATCACTTGAAAAGCCACTTCTCTGAAGACAGCCATCTGGCTAACACAATAAAGGGAAGTGGCAGCCTCTCTGGACAAAGT
A.pulchra CAAAGTGAATCACTTGAAAAGCCACTTCTCTGAAGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
H.suspectum CAAAGTGAGATCGTTGAAAAGCCACTTCTCTGAAGACAGCCATCTGGCTAGACAACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
X.grandis CAAAGTGAGATCCCTTGAAAAGCCACTTCTCTGAAGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCCACTCTGGACAAAGT
V.griseus CAAAGTGAGGCCGCTAGGAAAAGCCACTTCTCTGAAGATATCCATCTGACTAGCAGCGATAAAGAA---GTGGCAGCTTCTCTGGTCAGAGT
L.borneensis CAAAGTGAGCCCTTGGAAGCCACTTCTCTGAAGACAGCCATATGGCTAACAGCAATAAAGGAGAAGTGGCAGCCTCTCTGGACAGAGT
S.crocodiluris CAAAGTGAGATCACTTGAAAAGCCACTTCTCTGAAGACAGCCATCTGGCTAACACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
Dinodon.sp. CAAAGTGAGATCACTTGAAAACCTCTTCTCTGAAGACAGCCACCAGGCTAACTCTGCTAAAGAAAATGTGACAGGCTCTCTGGAC---AT
R.braminus CAAAGTGAGATCCCTTGAAAAGCCTCTTCTCTGAAGGACGCCACCAAGCT-----AAAGGAAA---GCAGGTTCCCTGGACAGAGT
C.rufus CAAAGTGAGATCACTTGAAAAGCCTCTTCTCTGAAGACAGCCACCAAGCTAACTGTGCTAAAGATAAAGTGACAAAGTTCCCTGGAC---AT
Agkistrodon.sp. CAAAGTGAGATCACTTGAAAAGCCTCTTCTCTGAAGAAAGCCACCAGGCTAACTCTGCTAAAGAAAATGTGACAGGTTCTGTGGAC---AT
Eremias.sp. CAAAGTGAGATCATTTAGCAAACCGCTTCTTGAAGACAGTCACTTGGCTCACAGTGATAAAGGAAAAGAGGCAGCCTCTCTGGGCAATGT
B.biporus CAAAGTGAGATCACTTAACAAACCCTTCTCTGAAGACAGTCTAGCTAACAGTGATAAAGGAAAAGAGACAGCCATTCTGGACAGGGG
T.weigmanni CAAAGTGAGATCACTTAACAAACCCTTCTCTGAAGACAGTCACTTGGCTAACAGTGATAAAGGAAAAGAGACAGCATTCTGGACAGAGG
R.floridana CAAAGTGAGATCACCTAATAAGTACTTCTCTGATGACAGTCTCTGGCTAACAAATGACAAAGGCAAGAGGCAGCTTCTCTGGACAATGT
A.xera ???AAAAAGAGAGATCCACTCTGGACAGGGG
C.tigris CAAAATCAGATCTCTGAAAAGTCACTTTCGGAAGAGAGTCACTGTGGCTGACAGTGACAAAGAGAAAAGTGGCAACCTCTGTGGACAAAGG
L.parietale CAAAATCAGATCACTGCAAAATTCACCTTTCAGAAAGAGGATCGTGTGGATGACGGTGTTAAAGGGAAGGTGGCAAAATATCTGGACAAAGA
E.turkmenicus ?????????????????????????GTCATTCTCTGAAGAGAGCCATCTGGCTGACAATGATAAAGGAAAATGGCTGCCTCTCTGGACAAAGT
S.shrevei CAAAGTGCGATCTCTTGAAAAGTCACTTTATGAAGACAGCCATCTGGCTAAAGATGATAAAGGGAAGTGGCAGCCTCTCTCGGACAAAGT
T.przewalskii CAAAGTGAGATCTCTTGAAAATTCACCTTTCAGAAAGAGGATCGTGTGGATGACGGTGAACAATGATAAAGAGAAAAGTGGCAGCCTCTTTGGGCAATAGT
G.gekko CAAAGTGAGATCTCTTGAAAAGTCACTTCTCTGAAGAGAGCCATCTGGCTAACCATGATAACGGGAAAATGCCAGCTTTTTCTGGACAAAGT
P.lindneri CAAAGTGAGATCTGTTGAAAAGGCAGTTCTGTGAAGAGAGCCATCTCGMTAGCAATGATAAAGAGAAAAGAGGCAGCCTCACTCGACAAAGT
Cr.ocellatus CAAAGTGAGATCTCTTGAAAAGGCCGTTCTCTGAAGAGAGCCATCTGCTAAGACTGATAAAGAGAAAAGTGGCAGCCTCACTAGACAAAGT
L.jicari ???TTCCTAGACAAAGT
M.aurata CAAAGTGAGATCACTTGAAAACCACTTCTCTGAGTGCAGCCATGTGGCTAAGCATGATAAAGGGGAAAAGTGGCAGATTTTCTGGACAAAGC
C.robustus CAAAGTGAGGTGCGTTGAAAACCACTTCTCTGAATGCAGCCATATGGCTCACACAATAAAGGGAAGTGTGAGATCTTCTAGACAAAGC
S.sikkimensis CAAAGTGAGATCGCTTGAAAAGCCACTTCTCTGAACAGCAGCCATGTGGCTAACAAATGATAAAGGGAAGTGGCGGACTCTCTAGACAAAGT
E.inexpectatus CAAAGTGAGATCGCTTGAAAACCACTTCTCTGAACAGCAGCCATGTGGCTAACAAATGATAAAGGGAAGTGGCGGACTCTCTAGACAAAGT
E.skiltonianus ?????????????????????????ACCATTCTCTGAATGCAGCCATGTGGCTAACAAATGATAAAGGGAAGTGGCGGACTCTTGTGACAAAGT
E.anthracinus ?????????????????????????ACCATTCTCTGAACGCAGCCATGTGGCTAACAAATGATAAAGGGAAGTGGCGGACTCTCTAGACAAAGT
S.anguineus ?????????????????????????ACCATTCTCTGAACGCACCACTGTGGCTAATAATGATAAAGGGAAGTGGCAGACTCTCTGGACAGAGC
P.eggeli CAAAGTGAGACCGCTTGAAAACCACTTCTCTGAACGCAGCCATGTGGCTAACAAATGATAAAGGGAAGTGGCAGACTCTCTGGATGAGAGC
F.polylepis CAAAGTGAGGCCGCTTGACAAATCAGTTCCGGAGCACAGCAATGTGGCTAACACAATAAAGAGAAGTGGCAAGATGCTGGACAAAGG
Ch.ocellatus CAAAGTGAGACCGCTTGAAAACCACTTCCAGAACACAGCCATGTGGCTAACAAATGATAAAGGTAAAGTGGCAGACACTTTGGACAAAGC
A.meleagris ?????????????????????????ACCATTCTCTGAACCTCAGCCATATGGCTAACAAATGATATAGGGAAGGTGGCGGACTCTCTGGACAAAGC
T.gariepensis CAAAGTGAGATCGTTGAAAACCACTTCTCTGAACCTCAGCCATATGGCTAACAAATGATATAGGGAAGGTGGCAGACTCTCTGGACAAAGC
T.lomii CAAAGTGAGATCACTTGAAAACCACTTCTCTGAACCTCAGCCATATGGCTAACAAATGATATAGGGAAGGTGGCAGACTCTCTGGACAAAGC

<i>R. floridana</i>	TTCATCAAGCTGTGAGGTTTGTGGCACTTCTTTCCATGGGGTCAAAAGAAAGAAGCAAGCCTGAATCCACAGCTGAGCAAAAAGATCAA
<i>A. xera</i>	TGGATTGAATTGTGAGGTTTGTGGCACTTCTTTCCGTTGGGATCAAAAGAAAGAAGCAAGCTTCTGAATCCACAGCTGAGCAAAAAGGCTCAA
<i>C. tigris</i>	TTCATCAAGCTGTGAGTATTTGTACCCCTTCTTCCATGGGGTCAAGAGAAAGAAGCAAGCTCTGAATGCACAGTTGAACAAAAAGGCCAA
<i>L. parietale</i>	TTCATCCGTCTGCAATGTTTGTATTCCTTCTTCTATGGGGTCAAGAGAAAGAAGCAAGCCTAAATACACCTTGAACAAAAAGGATCAA
<i>E. turkmenicus</i>	TTCATGAGCTGTGATGTTTGTGGAACGTCCTCCTGTGGAATAAAGAGGAAGAAGAAAGCCTGAATCCACAAGTGAGTAAAAAGCTCAG
<i>S. shrevei</i>	TTCATGAAGCTGTGATGTTTGTGGCACTTCTCCCATGGGATAAAGAGAAAAAGCAAGGCCCAATCCACAGGTGAACAAAAAGCTCAG
<i>T. przewalskii</i>	TTCATGAGCTGTGACATTTGTGGCACTTCTCCCATGGAGTAAAGAGAAAGAAGCAAGCCCAACCCACAGGTGAGCAAAAAGCTCAG
<i>G. gekko</i>	TTCACAGAGATGTGATGTTTGTGGCACTTCTCCCGTGGAAATAAGAGAAAGAAGCAAGCCCAAGTCCACAGGGGGGAAAAAGCTCAG
<i>P. lindneri</i>	TTCAGGAGCTGTGATGTTTGTGGCACTTCTCCCATGGAGTGAAGAGAAAGAACAAGCCTCAATCCTCAGGTGAGCAAAAAGCTCAG
<i>Cr. ocellatus</i>	CTCAATGAGCTGTGACGTGTGTGGCACTTCTCTCGTGGAAATGAAGAGAAAGAACAAGCCTCAATCCTCAGGTGAGCAAAAAGCTCAG
<i>L. jicari</i>	TTCAGCGAGTTGTGATGTTTGTGGTACTTCTCTCGTGGAAATGAAGAGAAAGAACAAGCCCTCAATCCCCCGTGAGCAAAAAGCTCAG
<i>M. aurata</i>	TTCATCAAGTTGTGAGGTTTGTGGCACTTGTGTCCATGGGGTCAAGAGAAAGCGCAAGCTTGAATCCGCAAGTGAGCAAAAAACTCAG
<i>C. robustus</i>	TTCATCATGCTGTGATGTTTGTGGCACTTCATCCCGGGGGTCAAGAGAAAGCGCAAGCCTGAATGCGCAAGTGACCACAAAACCTCG
<i>S. sikkimensis</i>	TTCATCAAGCTGTGAGGTTTGCAGCACTTCGTCCCGGGGGTCAAGAGAAAGCGCAAGCCTGAATGCGCAAGTGAGCATAAATCCG
<i>E. inexpectatus</i>	TTCATCAAACTGTGATGTTTGGCGCACTTCATCCTGTGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAGTGAGCAAAAACCTCAG
<i>E. skiltonianus</i>	TTCATCAAGCTGTGATGTTTGGCGCACTTCGTCCCGTGGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAGTGAGCAAAAACTCCG
<i>E. anthracinus</i>	TTCATCAAGCTGTGATGTTTGGCGCACTTCGTCCCGTGGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAGTGAGCAAAAACCTCCG
<i>S. anguineus</i>	TTCATCAAGCTGTGATGTTTGCAGCACTTCTCCCGTGGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAAGTGAGCAAAAACGCGAG
<i>P. eggeli</i>	TTCATCAAGCTGTGATGTTTGGCGCACTTCTCCCGTGGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAAGTGAGCAAAAAGACTCAG
<i>F. polylepis</i>	TTCACCAAACTGTGATGTTTGTGGCACTTCTCCCGTGGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAAGTGAGCAAAAACCTCAG
<i>Ch. ocellatus</i>	TTCATCAAGCTGTGATGTTTGTGGCACTTCTCCCATGGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAAGTGAGCAAAAACCTCAG
<i>A. meleagris</i>	TTCATCAAGCTGTGATGTTTGTGGCACTTCATCCCGTGGGGTCAAGAGAAAGAAGCAAGCTTGAATCCACAAGTAAGCAAAAACCTCAG
<i>T. gariepensis</i>	TTCATCAAGCTGTGATGTTTGTGGCACTTCATCCCGTGGGGTCAAGAGAAAGAAGCAAGCTTGAATCCACAAGTAAGCAAAAACCTCAG
<i>T. lomii</i>	TTCATCAAGCTGTGATGTTTGTGGCACTTCATCCCGTGGGGTCAAGAGAAAGAAGCAAGCTTGAATCCACAAGTAAGCAAAAACCTCAG
<i>X. vigilis</i>	TTCATCAAGCTGTGATGTTTGTGTAATTCGCCCGTGGGGTCAAGAGAAAGAAGCAAGCCTGAATCCACAAGGTGAGCAAAAAGCTCAG
<i>C. polyzonus</i>	TTCATCAAGTTGTGATGTTTGTGGCACTTCTCCCGTGGGGTCAAGAGAAAGAACAAGCCTTGAATCCACAAACAAGCAAAAAGCTGAG
<i>Zonosaurus. sp.</i>	TTCATCAAGTTGTGATGTTTGTGGCACTTCTCTCGTGGAGTCAAGAGAAAGTCAAGCCTGAATCCACAGCAAGCAAAAAGCTCAG
<i>Dibamus. sp.</i>	TTCATCAATGTGTGATGTTTGTGGCACTTCCGCACGTGGCATCAAGAGAAAGACGCAAGCTTGAACCCACAGGTGAGCAAAAACCTCAA

[illegible]

A. pulchra CCTGTCTGACCCAGTGGAAACGATGTGCAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGCTCTCAAAGTTATGGGGAGCTATTGCC
H. suspectum CCTGTCTGACCCGTCGAAACGACATGCAAGCACTTGTCTGCAGAGTCTGCATCCTTAAATGCTCTCAAAGTTATGGGGAGCTATTGCC
X. grandis CCTGTCTGACCCGTTAGAAACGACGTGCAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGCTCTCAAAGTTATGGGGAGCTATTGCC
V. griseus CCTGTCTGACCCAGTAGAAGCAGCATGCAAAACCTTATTCTGCAGGGTCTGCATTTTAAATGCTCTCAAAGTTATGGGGAGCTACTGCC
L. borneensis CCTGTCTGACCCAGTAGAAGCAGCATGCAAAACCTTATTCTGCAGGGTCTGCATTTCTTAAATGCTCTCAAAGTTATGGGGAGCTACTGCC
S. crocodilurus CCTGTCTGACCCAGTAGAAGCAGCTGCAAAACCTTATTCTGCAGGATCTGCATCCTTAAATGCTCTCAAAGTTATGGGGAGCTACTGCC
Dinodon. sp. CTGGCTGATCCAGTAGAAGCAACATGCAAAACCTTATTCTGCAGAGTCTGCATCCTTAAATGCTCTCAAAGTTATGGGAAGCTATTGCC
R. braminus TTTGACGGACCCAGTAGAAGCAACATGCAAAACCTTATTCTGCAGAGTCTGCATCCTTAAATGCTCTCAAAGTTATGGGCAGTTACTGTCC
C. ruffus TCTGGCTGATCCAGTAGAAGCAACGTGTAAACCTTATTCTGTAGAGTCTGCATCCTTAAATGCTCTCAAAGTTATGGGCAGCTATTGCC
Agkistrodon. sp. CCTGGCTGATCCAGTAGAAGCAACATGTAAACCTTATTCTGTAGAGTCTGCATCCTTAAATGCTCTCAAAGTTATGGGMAGCTATTGCC
Eremias. sp. CTGGCTGATCCAGTAGAAGCAGCTGTCCGCACTTATTCTGCAGGGTCTGCATCCTGAAATGCCCTCAAAGTGTCTGGGAAGTTATTGCC
B. biporus TCTGGCTGATCCGTTAGAAACGACATGTACACACTTATTTTGCAGAGTGTGCATCCTTAAATGCTCTCAAAGTCATGGGAAGTTACTGCC
T. weigmanni CCTGGCTGATCCAGTAGAAGCAACCTGTAAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGCTCTCAAATCATGGGAAGTTACTGTCC
R. floridana CCTGGCTGATCCAGTAGAAGCAACTTGTAAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGCCCTCAAATATATGGGAAGTTATTGCC
A. xera CTGGCTGATCCAGTAGAAGCAACCTGTAAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGCTCTCAAATCATGGGAAGTTACTGCC
C. tigris CCTAGCTGACCCAGTCGAGACTACATGCAAGCACTCTTTTGCAGGGTTTGATCCTTAAATGCTCTCAAAGTTATGGGAAGTTATTGCC
L. parietale TCTAGCTGACCCGTTAGAGACGACATGCAAAACCTTATTCTGCAGGATTTGTATCTGAAATGCTCTCAAAGTTATGGGAAGCTATTGCC
E. turkmenicus TCTGGCTGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGACTTGTGCATCCTTAAATGCCCTCAAAGTTATAGGAAGCTATTGCC
S. shrevei TCTGGATGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGACTCTGCATCCTTAAATGCTCTCAAAGTTATAGGAAGTTATTGTCC
T. przewalskii TCTGGCTGACCCAGTAGAAGCAACATGCAAGCACTTATTTTGCAGACTTTTGATCCTTAAATGCCCTCAAAGTTATAGGAAGTTATTGCC
G. gekko TCTGGCTGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGACATTCGATCCTTAAATGCTCTCAAAGTTATAGGAAGCTATTGCC
P. lindneri CTGGCTGACCCAGTGAAGCAACATGCAAGCACTTATTCTGTAGACTCTGCATCCTTAAATGCCCTCAAAGTTATAGGTAGCTATTGCC
Cr. ocellatus CCTGGCTGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGTAGACTCTGCATTGTTAAATGCCCTCAAAGTTATAGGCAGCTATTGTCC
L. jicari CCTGGCAGATCCAGTAGAAGCAACATGCAAGCACTTATTCTGTAGACTCTGCATCCTTAAATGCCCTCAAAGTAGTAGGCAGCTATTGTCC
M. aurata CCTGGCAGACCCAGTAGAGACCAATGCAAGCACTTATTTTGGCCAGTTTGATCCTTGAATGCCCTCAAAGTTATGGGAAGCTATTGTCC
C. robustus CTGGCAGATCCAGTGGAAACGACCTGCAAGCACTTGTCTGCCGAGTTTGATCCTTGAATGCCCTCAAAGTCATGGGAAGCTACTGCC
S. sikkimensis CCTGGCGGACGCGGTGGAACCAACCTGCAAGCACTTGTCTGCCGATTTGCCCTCTGAAATGCCCTCAAAGTCATGGGAAGCTATTGCC
E. inexpectatus CCTGGCAGACCCAGTAGAAGCAACATGCAAGCAGTGTCTGCAGAAATTTGCATCCTTAAATGCCCTCAAAGTCATGGGAAGCTATTGCC
S. skiltonianus CCTGGCAGACCCAGTAGAAGCAACATGCAAGCAGTGTCTGCAGAAATTTGCATCCTTAAATGCCCTCAAAGTCATGGGAAGCTATTGCC
E. anthracinus CTGGCAGACCCAGTAGAAGCAACATGCAAGCACTGTTCTGCAGAAATTTGCATCCTTAAATGCCCTCAAAGTCATGGGAAGCTATTGCC
S. anguineus CCTGGCAGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGAGTTTGATCCTTAAATGCCCTCAAAGTTATGGGAAGCTATTGCC
P. eggeli CTGGCAGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCCGAGTTTGATCCTTAAATGCCCTCAAAGTTATGGGAAGCTATTGCC
F. polylepis CCTGGCAGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGAGTTTGATCCTTAAATGCCCTCAAAGTTATGGGAAGCTACTGCC
Ch. ocellatus CCTGGCAGATCCAGTAAAAACCAACATGCAAGCACTTATTCTGCAGAGTTTGATCCTTAAATGCTCTCAAAGTTATGGGAAGCTATTGCC
A. meleagris CCTGGCGGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGAGTTTGATCCTTAAATGCCCTCAAAGTTATGGGAAGCTATTGCC
T. gariepensis CTGGCTGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGAGTTTGATCCTTAAATGCCCTCAAAGTTATGGGAAGCTATTGCC
T. lomii TCTGGCGGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGCAGAGTTTGATCCTTAAATGCCCTCAAAGTTATGGGAAGCTATTGCC
X. vigilis ACTGGCAGACCCAGTAGAAGCAACATGTAAAGCACTTATTCTGCAGAGTCTGCATCCTGAAATGCCCTCAGGGTAATGGGAAGCTATTGCC
C. polyzonus ACTGGCGGACCCAGTAGAAGCAACATGCAAGCACTTATTCTGTAGAGTCTGCATCCTTAAATGCCCTTAAGTAGCTCATGGGAAGCTATTGCC
Zonosaurus. sp. ACTGGCGGATCCAGTAGAAGCAGCATGCAAAACCTTATTCTGCAGAGTCTGCATCCTTAAATGCTCTTAAGTAGCTCATGGGAAGCTATTGCC
Dibamus. sp. CTGGCTGACCCAGTAGAAGCAACATGCAAGCACTTATTTTGGCAGTGTGCATCCTTAAATGCCCTCAAAGTTATGGGAAGCTATTGCC

[illegible]

U.flaviceps	AGTGACAGATTGTCAGGAGGAGGTCCTCTTTGGGAAAATACTGTCCACCCTTTCCAGACACAAGGAAGTAGATGCACAAAGAGGGCTATGT
S.crasicaudatus	AGTGACAGATTGCCAGGAGGAGGTCCTGTTTGGGAAAATACTGTCAACACTCTTTCCAGACACAAGGAGGTAGAAGACAAAGAGGGCTATGT
L.carinatus	AGTGATAGATTGTCAGGAGGAGTCTCTGTTTGGGAAAATACTCCACCACCTTTCCAGACACAAGGAGGTAGAAGACCAAAGAGGCTATGT
B.plumifrons	AGTGACAGATTGTCCTGGAGAGGTCCTGTTTGGGAAAATACTGTTACACTCTTTCCAGACACAAGAGGTTAGAAGACCAAAGAGGGCTATGT
G.wislizenii	AGTGAAGATTGTCAGGAGGAGGTCCTGTTTGGCAAATACTGTCCACCCTTTCCAGACACAAGAGGTAGAAGACCAAAGAGGGCTACGT
O.cuvieri	AGTAAAGATTGTCAGGAAGAGGTCCTGTTTGGGAAAATACTGTCCACCCTTTCCAGACACAAGGAGGTAGAAGACCAAAGAGGGCTATGT
O.attenuatus	AGTGCCAGACTGTCATGAGGAGGTCCTCTGCGGAAAATACTGCCACCCTTTCCAGGCACAAAGAGGTCAAAGACAAAGAGGGCTATGT
E.panamintina	AGTGCAAGACTGTCATGAGGAGGTCCTCTGCGGAAAATACTGCCACCCTTTCCAGGCACAAAGAGGTCAAAGACAAAGAGGGCTATGT
C.enneagrammus	AGTGCAAGACTGTCAGAGGAGGTCCTCTTTGGGAAAATACTGCCACCCTTTCCAGGCACAAAGAGGTCAAAGACAAAGAGGCTACGT
A.pulchra	CGTGCAAGACTGTCATGAAGAGGTCACCTCGGGAAAATACTGCCACCCTTTCCAGGCACAAAGAGGTTGAAGACAAAGAGGGCTATGT
H.suspectum	TGCACAGACTGTCATCAGAGGTCCTCTTTGGGAAAATACTGCCGCCTCTTTCCAGGCACAAAGTGCTGAAGACAAAGAGGGCTATGT
X.grandis	AGTGAAAGATTGTCCTTGAAGAGGTCCTCTGCGGAAAATACTGCCACCCTTTCCAGGCACAAAGAGGTAGAAGACAAAGAGGGCTACGT
V.griseus	AGTGAAGATTGTCCTTGAAGAGGTCCTACTGGGGAAGTACTGCCACCCTTTCCAGTCCACAAAGAGGTAGAGGACCAAGATGGCTATGT
L.borneensis	AGTGAAGAAATGTCATGAGGAGGTCCTCTGCGGGAAGTACTGCCACCCTTTCTTACGCCACAAAGCGGTAGAAGACAAAGAGGGCTATGT
S.crocodiluris	AGTGAAGATTGTCATGAGGAGGTCCTCTGCGGAAAATACTGCCACCCTTTCCAGGCACAAAGAGGTAGAAGACAAAGAGGGCTATGT
Dinodon.sp.	AGTAAAGGCTGTCATGAGGAGGTCCTTTTGGGAAAATACTGCCAACATCGTTCTAATCATAAAGGGGCGAGAAAGTACAGACAGCTATGT
R.braminus	AGTCATGGAATTGCCACGAGGAGATCTTTTTGGGAAAATACTGCCAACATCGTTCCAGCCATAAGAGAGGCGGAAGACAGAGACAGTTACGT
C.ruffus	AATGAAGAGGCTGTCATGAGGAGGTCCTTTTGGGAAAATACTGCCAACATGTTCTAATCATAAAGAGGCGAGAAAGCCAGACAGCTATGT
Agkistrodon.sp.	AATAAAGGCTGTCATGAGGAGGTCCTTTTGGGAAAATACTGCCAACATCGTTCTAATCATCAAAAGGGCGAGAAAGTACAGACAGCTATGT
Eremias.sp.	AGTGAAGAGGTGTCACGAGGAGGTCCTCCTGGGAAAATACTGCCACCCTTTCCATCCACAAAGAGGTAGAAGACAAAGAGGGCTATGT
B.biporus	AGTGAAGATTGTCAGGAGGAGATCCTTCTGGGAAAATACTGTGCGCATCTTTCCATCCACAAAGAGGTAAAGGACAAAGAGGGCTATGT
T.weigmanni	AGTGAAGATTGTCAGGAAGAGGTCCTTTTGGGAAAATACTGTCACCCTTTCCATCCACAAAGAGGTAGAGGACAAAGAGGGATATGT
R.floridana	TGTAAAGATTGTCATGAGGAGGTCCTCTGCGGAAAATACTGCCACCCTTTCCATCCACAAAGAGGTCGAAGCCAAAGAGGGCTACGT
A.xera	AGTGAAGATTGTCAGGAGGAGGTCCTTCTTGCAAGTATGGTCGCCATCTTTCCATCCACAAAGAGGTTGAGGACAAAGAGGGCTATGT
C.tigris	AGTGAAGATTGTCAGAGGAAGTCTCTCTGGGCAATACTGTCCACCCTTTCCAGGCACAAAGATGTAAAGAACAAAGAGGGTTATGT
L.parietale	AATGAAGAGTTGCCACCAGGAAGTCTCTGTTGGCAATACTCAACTCACCCTTTCCAGCCATAAAGATGCAAAAGGCCGAGAGGGCTTTGT
E.turkemicus	AGTAAAGACTGTTTATGAGAGGTGAGTCTTGGAAAATACTCAACCCTATCTTTCTACCCACAGAAAGACAAAGAGGACTTATGG
S.shrevei	AGTGAAGACTGTCATGAAGAAGCCACTCTTGGAAAATACTAGCCATCATCTTTCAAGTCACAAAGAGAAAAATGGCAAAGGGACTTATGT
T.przewalskii	AGTGAAGACTGTTTATGAGAAGTCACTCTTGGAAAATACTAGCCACATCTTTCTAGTCACAAAGGAGAAAAAGACAAAGGGACTTATGT
G.gekko	AGTGAAGACTGTCAGGAAGAGGTCACCTCTTGGAAAATACTAGCCATCACTTTCTCGCCACAAGAGGAGAAAAAGGACAAAGACTTTTGT
P.lindneri	AGTGAAGACTGTCACGAGAGCGTTGCCCTGGGAAAATACTAGCGGCATCTTTCTAGCCACAAGGATCACAAAGGACAAAGGCTTTTATGT
Cr.ocellatus	AGGGAAGACTGTCATGAGGATGTTGCTCTAGGAAAATACTAGCCATCATCTTTCTAGCCACAAGGATAACGAAGACAAAGGAATGTATGT
L.jicari	AGTGAAGACTGTCATGAGGAGCTGTCCTGCGGAAAATACTAGCCATCATCTTTCTAGCCACAAGGATACAAAGAGAAAGGGGACTACGT
M.aurata	TGTGAAGGAGTGTGATGAGGAAATCTCTCTGGGAAAATACTGCCATCATCTTTCCAGCCACAAGATGCAAAAGGACAAAGAGGTTATGT
C.robustus	CGTGAAGAGGTGTGACGAGGAAATCTCTCTGGA AAAATACTGGCCATCATCTTTCTAGCCACAAGATGCAAAAGGACAAAGAGGTTACGT
S.sikkimensis	CGTGAAGAGGTGTGACGAGGACATCTGTCTGGA AAAAGTACGGCCATCATCTTTCTAGCCACAAGTTGCAAGAGACAAAGAGGTTACGT
E.inexpectatus	TGTGAAGAGTGTGATGAGGAAATCTCTCTGGA AAAATACTGCCATCATCTTTCCAGCCACAAGAGCGCAAAAGACAAAGAGGGCTATGT
E.skiltonianus	TGTGAAGACTGTGATGAGGAAATCTCTCTGGA AAAATACTGCCATCATCTTTCCAGCCACAAGAGCGCAAAAGACAAAGAGGGCTATGT
E.anthracinus	TGTGAAGACTGTGATGAGGAAATCTCTCTGGA AAAATACTGCCATCATCTTTCCAGCCACAAGAGCGCAAAAGACAAAGAGGGCTATGT
S.anguineus	TGTGAAGATTGCGATGAGGAAATCTCTCTGGA AAAATACTGCCATCATCTTTCCAGCCACAAGAGCGCAAAAGACAAAGAGGGTTACGT
P.eggeli	TGTGAAGACTGTGATGAGGAAATCTCTCTGGA AAAATACTAGCCATCATCTTTCTAGCCACAAGAGCGCAAAAGACAAAGAGGGTTACGT
F.polylepis	TGTGAAGACTGCAATGAGGAAATCCCTCTGGGAAAATACTGTGTCATCGTTCCAGCCACAAGAGCTGAAGAGGCAAAAGAGGGTTATGT
Ch.ocellatus	TGTGAAGATTGTGATGAGGAAATCCCTCTGGGAAAATACTGCCATCATCTTTCCAGCCATAAAGAGCGCAAAAGACAAAGAGGGTTATGT
A.meleagris	TGTAAAGACTGCCATGAGGAAATCTCTCTGGGAAAATACTGCCATCATCTTTCCAGCCACAAGAGTGAAGAGACAAAGAGGGTTATGT
T.gariensis	TGTAAAGACTGCCATGAGGAAATCTCTCTGGGAAAATACTGCCATCATCTTTCCAGCCACAAGATGCAAAAGACAAAGAGGGTTATGT
T.lomii	TGTAAAGACTGCCATGAGGAAATCTCTCTGGGAAAATACTGCCATCATCTTTCCAGCCACAAGATGCAAAAGACAAAGAGGGTTATGT
X.vigilis	AGTGAAGATTGTCATGAGGAAGTCTGTCTGGGAAAATACTAGCGGCCATCTTTCCAGTCCACAAAGAGGCAAAAGACAAAGAGGTTATGT
C.polyzonus	AGTGAAGACTGTCATGAGGAAGTCTCTCTGGGAAAATACTAGCCATCATCTTTCCAGCCACAAGAGGAAAAAGACAAAGAGGGTTATGT
Zonosaurus.sp.	AGTGAAGAGTGTCATGAGGAAGTCTTTCTGGGAAAATACTAGCCATCATCTTTCCAGCCACAAGAGGAAAAAGACAAAGAGGGTTATGT
Dibamus.sp.	AGTGAAGACTGTAATGAGGACATCTCTCTGGGAAAATACTGCCATCATCTTTCCAGCCACAAGAGGCAAGACAAAGAGGCTATGT

[illegible]

P. raddei	AGTGAAGAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAATCGGTGTGCCTAACTTTGTTCCTGTTGGCTCTGAGATCTAGAAATGA
L. belliana	GGTAAAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAATCTGTGTGCCTAACTTTGTTCCTATTAGCCTTGAGAGCTAGAAATGA
U. acanthinurus	GGTAAAAAGCTTTTGTCTGAGAAAGAAGAAGGTGGAGATGTGAATCTGTGTGCCTAACTTTGTTCCTTTTGGCTCTGAGAGCTAGAAATGA
A. paternus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTTTGTGCTTTGAGAGCCAGAAATGA
P. mcallii	AGTTAAAGCTTTTGTCTGAAAAGGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTCGCTCTGAGAGCCAGAAATGA
S. obesus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGCTCTGAGAGCCAGAAATGA
Hoplocercus sp.	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAATGA
E. laticeps	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGCTCTGAGAGCCAGAAATGA
P. somencurensis	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTTTGAGAGCCAGAAATGA
L. pictus	AGTCAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTATTCCTACTGGCTTTGAGAGCCAGAAATGA
U. flaviceps	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAATCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAATGA
S. crasicaudatus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATATCAATCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAACGA
L. carinatus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAATCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAATGA
B. plumifrons	AGTGAAGAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAATGA
G. wislizenii	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAATGA
O. cuvieri	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTATTGGCTCTCAGAGCCAGAAATGA
O. attenuatus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCTGTGTGCTGACATTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
E. panamintina	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCCGTGTGCTGACATTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
C. enneagrammus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCTGTGTGCTGACATTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
A. pulchra	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCTGTGTGCTGACATTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
H. suspectum	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTGACATTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
X. grandis	AGTGAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAAGTCTGTGTGCTGACATTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
V. griseus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGATCTAGAAATGA
L. borneensis	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCCGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAATGA
S. crocodiluris	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATATAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
Dinodon sp.	AGTGAAGATTTTGTCTGAGAAAGAAGAAGGGAGGAGATGTGAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGATCTAGAAATGA
R. braminus	AGTGAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAAGTCAAGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGCAATGA
C. ruffus	AGTGAAGCTTTTGTCTGAGAAAGAAGAAGGGAGGAGACATGAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGATCTAGAAATGA
Agkistrodon sp.	AGTGAAGATTTTGTCTGAGAAAGAAGAAGGGAGGGACCTGAATCTGTGTGCTAACTTTGTTCTTACTAGCTTTGAGGCTAGAAATGA
Eremias sp.	AGTGAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCCAGAAATGA
B. biporus	AGTTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGTGATATAAGTCTGTGTGCTGACATTGTTCTTACTGGCTCTGCGAGCTAGAAATGA
T. weigmanni	AGTTAAAGCTTTTGTCTGAGAAAGAAGAAGGGAGGAGATGTAAATCTGTGTGCTAACTTTGTTCTTACTGGCTCTGCGAGCTAGAAATGA
R. floridana	AGTCAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAATCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
A. xera	AGTTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAATCTGTGTGCTAACTTTGTTCTTACTGGCTCTGCGAGCTAGAAATGA
C. tigris	AGTGAAGCTTTTGTCTGAGAAAGAAGAAGGGGGGATGTGAAGTCCGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
L. parietale	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAAGTCTGTGTGCTAACTTTATTCCTTACTGGCTCTAAGAGCAAGAAATGA
E. turkmenicus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTAACTTTATTCCTTACTGGCTCTGAGAGCTAGAAATGA
S. shrevei	AGTGAAGCTTTTGTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTAACTTTATTCCTTACTGGCTCTGAGAGCTAGAAATGA
T. przewalskii	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTAACTTTATTCCTTACTGGCTCTGAGATCTAGAAATGA
G. gekko	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTAACTTTATTCCTTACTGGCTCTGAGAGCTAGAAATGA
P. lindneri	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCTAACTTTATTCCTTACTGGCTCTGAGAGCTAGAAATGA
Cr. ocellatus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTATGTCTAACTTTATTCCTTACTGGCTCTTAGAGCTAGAAATGA
L. jicari	AGTAAAGCTTTTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTATGTCTAACTTTATTCCTTACTGGCTCTGAGAGCTAGAAATGA
M. aurata	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTCGAAATGA
C. robustus	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTCGAAATGA
S. sikkimensis	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTCGAAATGA
E. inexpectatus	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
E. skiltonianus	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATTCAAGTCTGTATGTCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
E. anthracinus	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
S. anguineus	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCAAGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
P. eggeli	AGTGAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAAGTCCGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
F. polylepis	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
Ch. ocellatus	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
A. meleagris	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
T. gariepensis	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
T. lomii	AGTGAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA
X. vigilis	GGTCAAGGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTGAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTTTGAGAGCTAGAAATGA
C. polyzonus	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGACGTGAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTTTGAGAGCTAGAAATGA
Zonosaurus sp.	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGACGTGAAGTCTGTGTGCTAACTTTGTTCTTACTGGCTTTGAGAGCTAGAAATGA
Dibamus sp.	AGTAAAGCTTTTGTCTGAGAAAGAAGAAGGGGGAGATGTAAATCTGTGTGCTAACTTTGTTCTTACTGGCTCTGAGAGCTAGAAATGA

P. lesueurii	GCACCGGCAAGCTGACGAGCTGGAAGCTATCATGCAAGGGAAGGGATCAGGCCTCCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
P. coicincinus	GCACCGGCAAGCTGATGAGCTGGAAGCTATCATGCAAGGGAAGGGACAGGCCTCCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
Hydrosaurus.sp.	GCATCGGCAAGCTGACGAGTTGGAAGCTATCATGGAAGGGAAGGGCTCAGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
C. calotes	GCACCGGCAAGCTGACGAGCTGGAAGCGTATGCAAGGGAAGGGCTCAGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
J. tricarinata	ACATCGGCAAGCTGATGAGCTGGAAGCGATCATGCAAGGGAAGGGCTCAGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
P. raddei	GCACCGGCAAGCTGATGAGCTAGAAGCTATCATGCAAGGGAAGGGCTCAGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
L. belliana	GCACAGACAAGCTGACGAGTGAAGCTATCATGCAAGGGAAGGGCTCGGGCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
U. acanthinurus	GCACAGGCAAGCTGATGAGCTGGAAGCTATTATGCAAGGGAAGGGCTCAGACCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
A. paternus	ACACAGGCAAGCTGATGAGTTGGAAGCTATAATGCAAGGAAAGGGATCAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
P. mcallii	ACATAGACAAGCTGATGAGCTGGAAGCTATAATGCAAGGGAAGGGGTGAGGCCTCCATCCAGCTGTTTGCTTGGCGATCAGAGTAAATAC
S. obesus	ACACAGACAGGCCGATGAGTTGGAAGCTATAATGCAAGGGAAGGGGTGAGGCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
Hoplocercus.sp.	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGATCAGTCTTCATGCAGCTGTTTGCTTGGCAATCAGAGTCAACAC
E. laticeps	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGGTGAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAACAC
P. somocurensus	ACACAGACAAGCAGATGAGCTGGAAGCTATAATGCAAGGGAAGGGGTGAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
L. pictus	ACACAGACAAGCAGATGAGTTGGAAGCTATAATGCAAGGGAAGGGGACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
U. flaviceps	ACACAGACAAGCTGATGAGCTGGAAGCGTAAATGCAAGGAAAGGGGTGAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
S. crasicaudatus	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGGACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
L. carinatus	ACACAGGCAAGCCAAATGAGTTAGAAGCTATAATGCAAGGGAAGGGTTCAGGCCTACAGCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
B. plumifrons	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGGTGAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
G. wislizenii	ACACAGACAAGCCAAATGAGTTAGAAGCTATAATGCAAGGGAAGGGGTGAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
O. cuvieri	ACACAGACAAGCTGATGAGTTAGAAGCTATAATGCAAGGGAAGGGGACAGGCCTTCACCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
O. attenuatus	ACACAGACAAGCTGATGAGTTAGAAGCTATAATGCAAGGGAAGGGAAAGACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAATAC
E. panamintina	ACACAGGCAAGCTGATGAGTTAGAAGCTATAATGCAAGGGAAGGGATCAGGCCTTCATCCGCTGTTTGCTTGGCAATCCGAGTCAACAC
C. enneagrammus	ACACAGACAAGCAGATGAGTTGGAAGCTATAATGCAAGGGAAGGATCAGGCCTTCATCCGCTGTTTGCTTGGCAATCCGAGTCAACAC
A. pulchra	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGATCAGGCCTTCATCCGCTGTTTGCTTGGCAATCCGAGTCAACAC
H. suspectum	ACACAGGCAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGATCAGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
X. grandis	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGATCAGGACTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
V. griseus	ACACAGGCAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGATCTGGCCTCCCTCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
L. borneensis	ACACAGGCAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGATCTGGCCTTCATCCGCTGTTTGCTTGGCAATCCGAGTCAACAC
S. crocodiluris	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAGGGATCAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
Dinodon.sp.	GCACAGACAAGCAGATGAATTGGAAGCTATAATGCAAGGGAAGGGATCGGACCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
R. braminus	ACACAGACAAGCAGATGAATTGGAAGCTATATGCAAGGGAAGGGATCGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
C. rufus	GCACAGACAAGCAGATGAATTGGAAGCGTAAATGCAAGGGAAGGGATCGGACCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
Agkistrodon.sp.	GCACAGACAAGCAGATGAATGGAAGCTATAATGCAAGGGAAGGGATCAGACTTCATCCAGCTGTTTGCTTGGCAATCAGAGTCAACAC
Eremias.sp.	GCATAGACAAGCCGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCAGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGGGTCAACAC
B. biporus	GCACAGACAAGCTGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCCGGCTTCATCCAGCTGTTTGCTTAGCAATTCCGAGTCAATAC
T. weigmanni	GCACAGACAAGCTGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCCGGCTTCATCCAGCTGTTTGCTTAGCGATTCCGAGTCAATAC
R. floridana	ACACAGGCAAGCTGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCAGGCCTTCATCCGCTGTTTGCTTGGCAATCCGAGTCAACAC
A. xera	GCACAGACAAGCTGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCTGGCCTTCAGTCCAGCTGTTTGCTTAGCGATTCCGAGTCAATAC
C. tigris	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGTAAGGGTTCAGGACTTCCTCCAGTGTGTTGCTTGGCAATCCGAGTCAACAC
L. parietale	ACACAGAGTAGGCTGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCAGGACTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
E. turkmenicus	ACACAGACAAGCTGATGAATTGGAAGCTATGATGCAAGGGAAGGGAAAGAACAGGACTTCCTCCAGTGTGCTTGGCAATCCGAGTAAACAC
S. shrevei	ACACAGACAAGCTGATGAGTTGGAAGCTATAATGCAAGGTAAGGGATCAGGACTTCCTCCAGTGTGTTGCTTGGCAATCCGAGTCAACAC
T. przewalskii	ACACAGACAAGCTGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCAGGACTTCATCCAGCTGTTTGCTTGGCAATCCGAGTAAACAC
G. gekko	ACATAGACAAGCCGATGAGCTGGAAGCTATGATGCAAGGGAAGGGATCAGGACTGAGTCCAGCTGTTCTGCTTGGCAATCCGAGTAAACAC
P. lindneri	ACATAGGCAAGCTGATGAGTTGGAAGCTATGATGCAAGGGAAGGGATCAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTAAACAC
Cr. ocellatus	ACATAGACAAGCTGATGAATTGGAAGCTATGATGCAAGGGAAGGGATCAGGACTGAGTCCAGCTGTTTGCTTGGCAATCCGAGTAAACAC
L. jicari	ACATAGACAAGCTGATGAATTGGAAGCTATGATGCAAGGGAAGGGTTCAGGACTGAGTCCAGCTGTTTGCTTGGCAATCCGAGTAAACAC
M. aurata	ACACAGACAAGCCGATGAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCCGCTGCTTGGCAATCCGAGTCAACAC
S. robustus	GCATAGACAAGCCGATGAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
S. sikkimensis	ACACAGACAAGCCGAGTAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
E. inexpectatus	ACACAGACAAGCCGATGAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
E. skiltonianus	ACACAGACAAGCCGATGAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
E. anthracinus	ACACAGACAAGCCGATGAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
S. anguineus	ACACAGACAAGCTGATGAATGGAAGCTATGATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
P. eggeli	ACACAGACAAGCTGATGAATGGAAGCTATGATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
F. polylepis	ACACAGACAAGCCGATGAATGGAAGCTATGATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
Ch. ocellatus	ACACAAACAAGCCGATGAATGGAAGCTATGATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
A. meleagris	GCACAGACAAGCTGATGAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
T. gariepensis	ACACAGACAAGCTGATGAATGGAAGCTATAATGCAAGGGAAGGGAAACAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC

Index2	4444444445555555555666666666677777777778888888888999999999900000000011111111122222222223
Index3	123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.	CACGTGCTGAGAAAGCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAAGCCCTTCTTTGAAAAATGTGTCTCGTAATAACAGAAAGTGGGAAT
G.gallus	CACCGCCGAGAAAGCCCTTCTTACCAGGTTATCATCCATTTTGAATGGAACCTCCCTTGAAAAATGTATCCACTAACACAGAAGTGGGAAT
C.mydas	CACGTGCTGAGAAGGCACCTTCTGCCAGGTTATCATCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCACTAATACAGAGGTGGGAAT
S.punctatus	AACGTGCTGAGAAAGCCCTTCTGCCAGGATACCATTCCATTTGAGTGGAACCTTCTTGAAAAATGTATCCACTAATACAGAAGTAGGCAT
B.thieli	AACAGCTGAAAAATCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTGGGCAT
C.rudis	AACAGCTGAAAAAGTCCCTTCTGCCAGGTTACCATTCCGTTTGAATGGAACCCGCCCTTGAAAAATGTGTCCAGTAACACAGATGTGGGCAT
C.brevicornis	AACAGCTGAGAAGTCCCTTCTGCCAGGTTACCATTCCGTTTGAATGGAACCCGCCCTTGAAAAATGTGTCCAGTAGCACAGATGTAGGCAT
C.salinarum	AACGTGCTGAAAAGGCCCTTCTGCCAGGTTACCATTCCCTTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
P.lesueurii	AACGTGCTGAAAAGGCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAGCACAGATGTAGGCAT
P.cocincinus	AACGTGCTGAAAAGGCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
Hydrosaurus.sp.	AACGTGCTGAAAAATCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
C.calotes	GACTGCTGAAAAATCCCTTCTGCCAGGATACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
J.tricarinata	GACTGCTGAAAAATCCCTTCTGCCAGGTTACTATCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
P.raddei	AGCGGCTGAAAAAGCTCTTCTACCGGTTACCATTCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
L.belliana	AACGTGCTGAGAAGTCTTCTTCTGCCAGGTTACTATCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAAACGTGGGCAT
U.acanthinurus	AACGTGCTGAAAAGTCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
A.paternus	AACGTGCTGAAAAGGCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
P.mcallii	AACGTGCTGAAAAGTCCCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
S.obesus	AACGTGCTGAAAAGTCCCTTTTGGCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
Hoplocercus.sp.	AACGTGCTGAAAAGTCCCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
E.laticeps	AACGTGCTGAAAAGTCCCTTCTTCTGCCAGGTTACCATTCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
P.somencurensus	AACGTGCTGAAAAGTCTCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCTAGTAACACAGAAGTAGGAAT
L.pictus	AACGTGCTGAAAAGTCTCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAGCACAGAAGTAGGAAT
U.flaviceps	AACAGCTGAAAAAGTCCCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
S.crasicaudatus	AAGTGCTGAAAAGTCCCTTCTTCTGCCAGGTTACCATTGCATTTGAGTGGAATCCACCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
L.carinatus	AACGTGCTGAAAAATCTCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCGCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTCCGCAT
B.plumifrons	AACGTGCTGAAAAGTCCCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
G.wislizenii	AACGTGCTGAAAAGGCCCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
O.cuvieri	AACGTGCTGAAAAGTCCCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAAGTAGGCAT
O.attenuatus	AACATCTGAAAAGTCCCTCTTCTACCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
E.panamintina	AACATCTGAAAAGTCCCTCTTCTACCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
C.enneagrammus	AACATCTGAAAAGTCCCTCTTCTACCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
A.pulchra	AACATCTGAAAAGTCCCTCTTCTACCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
H.suspectum	AACATCTGAAAAGTCCCTCTTCTACCAGGTTACCATTCCATTTGAGTGGAAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACAGGGGTGGGCAT
X.grandis	AACATCTGAAAAGTCCCTCTTCTACCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
V.griseus	AACAGCTGAAAAGTCCCTCTTCTGCCAGGTTATCATCTCTTCTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAATACAGATGTAGGCAT
L.borneensis	AACATCTGAAAAGTCCCTTCTTCTGCCAGGTTATCATCTCTTCTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAATACAGATGTAGGCAT
S.crocodiluris	AACATCTGAAAAGTCCCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
Dinodon.sp.	AACAGCTGAAAAGTCCCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
R.braminus	TACAGCTGAGAAAGCCCTTCTTCTGCCAGGTTACCATTCCATTTGAATGGGCGCTTCTTGAAAAATGTGTCTAGTGATACCAATGTAGGCAT
C.ruffus	AACAGCTGAGAAGTCCCTTCTTCTGCCAGGTTATCATCCCTTTGAATGGGCACTTCTTGAAAAATGTGTCTAGTAATACTGATGTAGGCAT
Agkistrodon.sp.	AACAGCTGAGAAGGCCCTTCTTCTGCCAGGTTATCATCCCTTTGAATGGGAACCTTCTTGAAAAATGTGTCTAGTAACACAGAGGTAGGCAT
Eremias.sp.	AACGTGCTGAAAAGTCCCTCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
B.biporus	TACAGCTGAAAAGTCCCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
T.weigmanni	TACAGCTGAAAAGTCCCTTTTCTGCCAGGTTACCATTCCATTTGAGTGGAAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
R.floridana	AACAGCTGAAAAGTCCCTCTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
A.xera	TACAGCTGAAAAGTCCCTTTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
C.tigris	AACGTGCTGAAAAGTCCCTCTTCTGCCAGGTTTCCATCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
L.parietale	AACGTGCTGAAAAGTCCCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
E.turkmenicus	GACTGCTGAAAAGTCCCTTTTCTGCCAGGTTATCATCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
S.shrevei	GACTGCTGAAAAGTCCCTTCTTCTGCCAGGTTATCATCAATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCTAGTAACACAGAGGTAGGCAT
T.przewalskii	AACGTGCTGAAAAGTCCCTTTTCTGCCAGGTTATCATCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCTAGTAACACAGAGGTAGGCAT
G.gekko	AACGTGCTGAAAAGTCCCTTCTTCTGCCAGGTTATCATCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCTTCTATCACAGAAGTAGGCAT
P.lindneri	AACGTGCTGAAAAGTCCCTTTTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
Cr.ocellatus	AACGTGCTGAAAAATCCCTTTTCTTCTGCCAGGTTATCATCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
L.jicari	AACGTGCTGAAAAGTCCCTTTTCTTCTGCCAGGTTATCATCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
M.aurata	AACGTGCTGAAAAAGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCGCCCTTCTTGAAAAATGTGTCCAGTAACATGAAGTAGGCAT
C.robustus	GACAGCTGAAAAAGCCCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
S.sikkimensis	GACGGCTGAGAAAGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACAGAGGTAGGCAT
E.inexpectatus	AACGTGCTGAAAAAGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
E.skiltonianus	AACGTGCTGAAAAAGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
E.anthracinus	AACGTGCTGAAAAAGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
S.anguineus	AACGTGCTGAAAAGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
P.eggeli	AACGTGCTGAAAAGGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
F.polylepis	AACGTGCTGAAAAGGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGCAGCCACCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
Ch.ocellatus	AACGTGCTGAAAAGGCCCTCTTCTGCCAGGTTATCATCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
A.meleagris	AACGTGCTGAAAAGGCCCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
T.gariepensis	AACGTGCTGAAAAGGCCCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
T.lomii	AACGTGCTGAAAAGGCCCTCTTCTGCCAGGTTACCATTCCATTTGAGTGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGCAT
X.vigilis	AACGTGCTGAAAAGGCCCTCTTCTGCCAGGTTACCATTCCATTTGAATGGAACCCCTTCTTGAAAAATGTGTCCAGTAACACGGAAGTAGGTAT
C.polyzonus	GAGTGCTGAAAAGGCCCTTTTCTGCCAGGTTACCATTCCATTTGAATGGACACCACCCTTCTTGAAAAATGTGTCCAGTAACACTGAAGTAGGTAT

[illegible][illegible]

G.gallus	TAAATACAGATATGAGGGCAAGATTACCAATTATTTCCACAAAACCCCTTGCTCATGTACCTGAAATCATTTGAAAGAGATGGGTCCATTGG
C.mydas	CAAGTACAGATATGAAGGCAAGATTACAAATTTATTTTCACAAAACCTTGTGCTCATGTTCCCTGAAATTTATT????????????????
S.punctatus	CAAGTACAGATATGAGGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTGCCCTGAAATCATTTGAAAGAGATGGCTCCATTGG
B.thieli	TCATTACAGATATGAAGGAAAGATTACCAATTACTTTTCACAAGACCCTTGCTCATGTTCCGGAAATATAGAAAGAGATGGGTCCATTGG
C.rudis	TCATTACAGATATGAAGGAAAGATTACCAATTACTTTTCACAAGACCCTTGCTCATGTTCCGGAAATATATCGAAAGAGATGGGTCCATTGG
C.brevicornis	TCATTACAGATATGAAGGAAAGATTACCAATTACTTTTCACAAGACACTTGCTCATGTTCCGGAAATATATCGAAAGAGATGGGTCCATTGG
C.salinarum	TCGTTATAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
P.lesueurii	TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
P.cocincinus	TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
Hydrosaurus.sp.	TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
C.calotes	TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
J.tricarinata	TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATATCGAACGAGATGGCTCCATTGG
P.raddei	TCATTACAGGTACGAGAGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCCGGAGATTATAGAAAGGATGGTTCCATTGG
U.belliana	TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCCATTGG
L.acanthinurus	CTGTTACAGATATGAGGGGAAGATCACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
A.paternus	CTGTTACAGATATGAGGGGAAGATCACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
P.mcallii	CCATTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
S.obesus	CCGTTATAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
Hoplocercus.sp.	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGGTCTATTGG
E.laticeps	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAGACCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGGTCTATTGG
P.somencurensus	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAGACCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
L.pictus	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGCTCCATTGG
U.flaviceps	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
S.crasicaudatus	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
L.carinatus	CCATTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
B.plumifrons	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
G.wislizenii	CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
O.cuvieri	CCATTACAGATATGAGGGCAAGATTACCAATTACTTTTCACAAAACCCCTTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
O.attenuatus	CAGGTACAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
E.panamintina	CAGGTACAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
C.enneagrammus	CAGGTATAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
A.pulchra	CAGGTACAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
H.suspectum	CAGGTACAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
X.grandis	CAGGTACAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
V.griseus	CAGGTATAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
L.borneensis	CAGGTACAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
S.crocodiluris	CAGGTACAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
Dinodon.sp.	CAGTTATAGATATGATGGCAAGATTACCAATTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
R.braminus	CAGTTACAGGTACAGGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
C.ruffus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
Agkistrodon.sp.	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
Eremias.sp.	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
B.biporus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
T.weigmanni	CCGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
R.floridana	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
A.xera	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
C.tigris	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
L.parietale	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
E.turkmenicus	CAAGTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
S.shrevei	CAAGTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
T.przewalskii	TAAGTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
G.gekko	CAAGTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
P.lindneri	CAAGTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
Cr.ocellatus	CAAGTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
L.jicari	CAAGTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
M.aurata	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
C.robustus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
S.sikkimensis	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
E.inexpectatus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
E.skiltonianus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
E.anthracinus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
S.anguineus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
P.eggeli	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
F.polylepis	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
Ch.ocellatus	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
A.meleagris	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
T.gariepensis	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
T.lomii	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
X.vigilis	CAGTTACAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
C.polyzonus	CAGTTATAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
Zonosaurus.sp.	CAGTTATAGATATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG
Dibamus.sp.	CAGTTATGCTATGATGGCAAGATTACCAAACTACTTTTCACAAAACCTTGTGCTCATGTTCCAGAAATATAGAAAGAGATGGATCTATTGG

X.vigilis	TGCTTGGGCAAGTGAGGGAAATGAGTCTGGAAACAAATGTTTCAGGCGCTTTC
C.polyzonus	GGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATGTTTCAGACGCTTTC
Zonosaurus.sp.	GGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATGTTTCAGGCGCTTTC
Dibamus.sp.	TGCTTGGGCCAGTGAAGGGAATGAGTCTGGGAACAACTGTTTCAGGCGCTTTC

B. *c-mos* (excluded nucleotide positions underlined)

List of Taxa:

- | | |
|--------------------------------------|---|
| 1. <i>Crocodylus porosus</i> | 25. <i>Diplometophon zarudnyi</i> |
| 2. <i>Gallus gallus</i> | 26. <i>Bipes biporus</i> |
| 3. <i>Pelomedusa subrufa</i> | 27. <i>Amphisbaena xera</i> |
| 4. <i>Sphenodon punctatus</i> | 28. <i>Coleonyx variegatus</i> |
| 5. <i>Elgaria multicarinata</i> | 29. <i>Pseudothecadactylus lindneri</i> |
| 6. <i>Varanus salvator</i> | 30. <i>Lialis burtonis</i> |
| 7. <i>Lanthanotus borneensis</i> | 31. <i>Teratoscincus przewalskii</i> |
| 8. <i>Shinisaurus crocodiluris</i> | 32. <i>Tarentola boettgeri</i> |
| 9. <i>Heloderma suspectum</i> | 33. <i>Sphaerodactylus shrevei</i> |
| 10. <i>Xenosaurus grandis</i> | 34. <i>Agkistrodon piscivorus</i> |
| 11. <i>Uromastix aegypticus</i> | 35. <i>Dinodon rufozonatum</i> |
| 12. <i>Leiolepis guentherpetersi</i> | 36. <i>Cylindrophis ruffus</i> |
| 13. <i>Chamaeleo jacksonii</i> | 37. <i>Ramphotyphlops australis</i> |
| 14. <i>Physignathus lesueurii</i> | 38. <i>Mabuya delalandii</i> |
| 15. <i>Ctenophorus decresii</i> | 39. <i>Eumeces skiltonianus</i> |
| 16. <i>Physignathus cocincinus</i> | 40. <i>Feylinia polylepis</i> |
| 17. <i>Phrynocephalus mystaceus</i> | 41. <i>Acontias meleagris</i> |
| 18. <i>Calotes versicolor</i> | 42. <i>Proscelotes eggeli</i> |
| 19. <i>Sauromalus obesus</i> | 43. <i>Xantusia vigilis</i> |
| 20. <i>Oplurus sebae</i> | 44. <i>Cordylus cordylus</i> |
| 21. <i>Leiiocephalus sp.</i> | 45. <i>Tupinambus quadrilineatus</i> |
| 22. <i>Corytophanes cristatus</i> | 46. <i>Bachia dorbignyi</i> |
| 23. <i>Sceloporus grammicus</i> | 47. <i>Dibamus sp.</i> |
| 24. <i>Gallotia galloti</i> | |

L.borneensis	AGAACAAAATGTTTGCAA
S.crocodiluris	AGAACAAAATGTTTGCAA
H.suspectum	AGAACAAAATGTTTGCAA
X.grandis	AGAACAAAATGTTTGCAA
U.aegypticus	AGAACAAAATGTCTGCAA
L.guentherpetersi	AGAACATAATGTTTGCAA
C.jacksonii	AGAACAGAAATGTTTGTA
P.lesueurii	AGAACAAAATGTTTGTA
C.decrepii	AGAACAAAATGTTTGTA
P.cocincinus	AGAACAAAATGTTTGTA
P.mystaceus	AGAACAAAATGTTTGCAA
C.versicolor	GGAACACAATGTTTGCAA
S.obesus	AGAACAAAATGTTTGCAA
O.sebae	ANAACAAAATGTTTGCAA
Leiocephalus.sp.	AGAACAAAAGTTTGCAA
C.cristatus	AGAACAAAATGTTTGCAA
S.grammicus	AGAACAAAATGTTTGCAA
G.galloti	TGAACAAAATGTTTGCAA
D.zarudnyi	TGAACAAAACGTTTGCAA
B.biporus	TGAACAAAATGTTTGCAA
A.xera	TGACCAAAATGTTTGCAA
C.variegatus	TGAACAAAATATTTGCAA
P.lindneri	TGAACAAAATATTTGCAA
L.burtonis	CGAACAAAATATTTGC--
T.przewalskii	TGAACAAAATATTTGCAA
T.boettgeri	TGAACAAAATATTTGCAA
S.shrevei	GGAACAAAATATTTGCAA
A.piscivorus	AGAACATAATGTTTGCAA
D.rufozonatum	AGAACATAATGTTTGCAA
C.ruffus	AGAACATAATGTTTGCAA
R.australis	AGAATATAATGTTTGCAA
M.delalandii	TGAACAAAATGTTTGCAA
E.skiltonianus	TGAACAAAATGTTTGCAA
F.polylepis	TGAACAAAATGTTTGCAA
A.meleagris	TGAACAAAATGTTTGCAA
P.eggeli	TGAACAAAATGTTTGCAA
X.vigilis	TGAACAAAATGTTTGCAA
C.cordylus	TAAACAAAATGTATGCAA
T.quadrilineatus	TGAACAAAATGTCTGCAA
B.dorbignyi	TGAACAAAATGTTTGCAA
Dibamus.sp.	TGAACAAAATGTTTGCAA

C. Mitochondrial DNA (excluded nucleotide positions underlined)

Note: Taxa followed by an asterisk (members of Acrodonta) have had genes for tRNA^{Glu} and tRNA^{Ile} rearranged to align them with the rest of the data set

List of Taxa:

1. *Alligator mississippiensis*
2. *Gallus gallus*
3. *Chelonia mydas*
4. *Sphenodon punctatus*
5. *Brookesia thieli**
6. *Chamaeleo rudis**
7. *Calumma brevicornis**
8. *Ctenophorus salinarum**
9. *Physignathus lesueurii**
10. *Physignathus cocincinus**
11. *Hydrosaurus sp.* *
12. *Calotes calotes**
13. *Japalura tricarinata**
14. *Phrynocephalus raddei**
15. *Leiolepis belliana**
16. *Uromastyx acanthinurus**
17. *Anolis paternus*
18. *Phrynosoma mcallii*
19. *Sauromalus obesus*
20. *Hoplocercus sp.*
21. *Enyaloides laticeps*
22. *Phymaturus somuncurensis*
23. *Liolaemus pictus*
24. *Urocentron flaviceps*
25. *Stenocercus crassicaudatus*
26. *Leiocephalus carinatus*
27. *Basiliscus plumifrons*
28. *Gambelia wislizenii*
29. *Oplurus cuvieri*
30. *Ophisaurus attenuatus*
31. *Elgaria panamintina*
32. *Celestes enneagrammus*
33. *Anniella pulchra*
34. *Heloderma suspectum*
35. *Xenosaurus grandis*
36. *Varanus griseus*
37. *Lanthanotus borneensis*
38. *Shinisaurus crocodilurus*
39. *Dinodon sp*
40. *Ramphotyphlops braminus*
41. *Cylindrophis ruffus*
42. *Agkistrodon sp.*
43. *Eremias grammica*
44. *Bipes biporus*
45. *Trogonophis weigmanni*
46. *Amphisbaena xera*
47. *Cnemidophorus tigris*
48. *Leposoma parietale*
49. *Eublepharis turkmenicus*
50. *Sphaerodactylus shrevei*
51. *Teratoscincus przewalskii*
52. *Gekko gekko*
53. *Pseudothecadactylus lindneri*
54. *Crenadactylus ocellatus*
55. *Lialis jicari*
56. *Mabuya aurata*
57. *Ctenotus robustus*
58. *Scincella sikkimensis*
59. *Eumeces inexpectatus*
60. *Eumeces skiltonianus*
61. *Eumeces anthracinus*
62. *Scelotes anguineus*
63. *Proscelotes eggeli*
64. *Feylinia polylepis*
65. *Chalcides ocellatus*
66. *Acontias meleagris*
67. *Typhlosaurus garipeensis*
68. *Typhlosaurus lomii*
69. *Xantusia vigilis*
70. *Cordylus polyzonus*
71. *Zonosaurus sp.*
72. *Dibamus sp.*

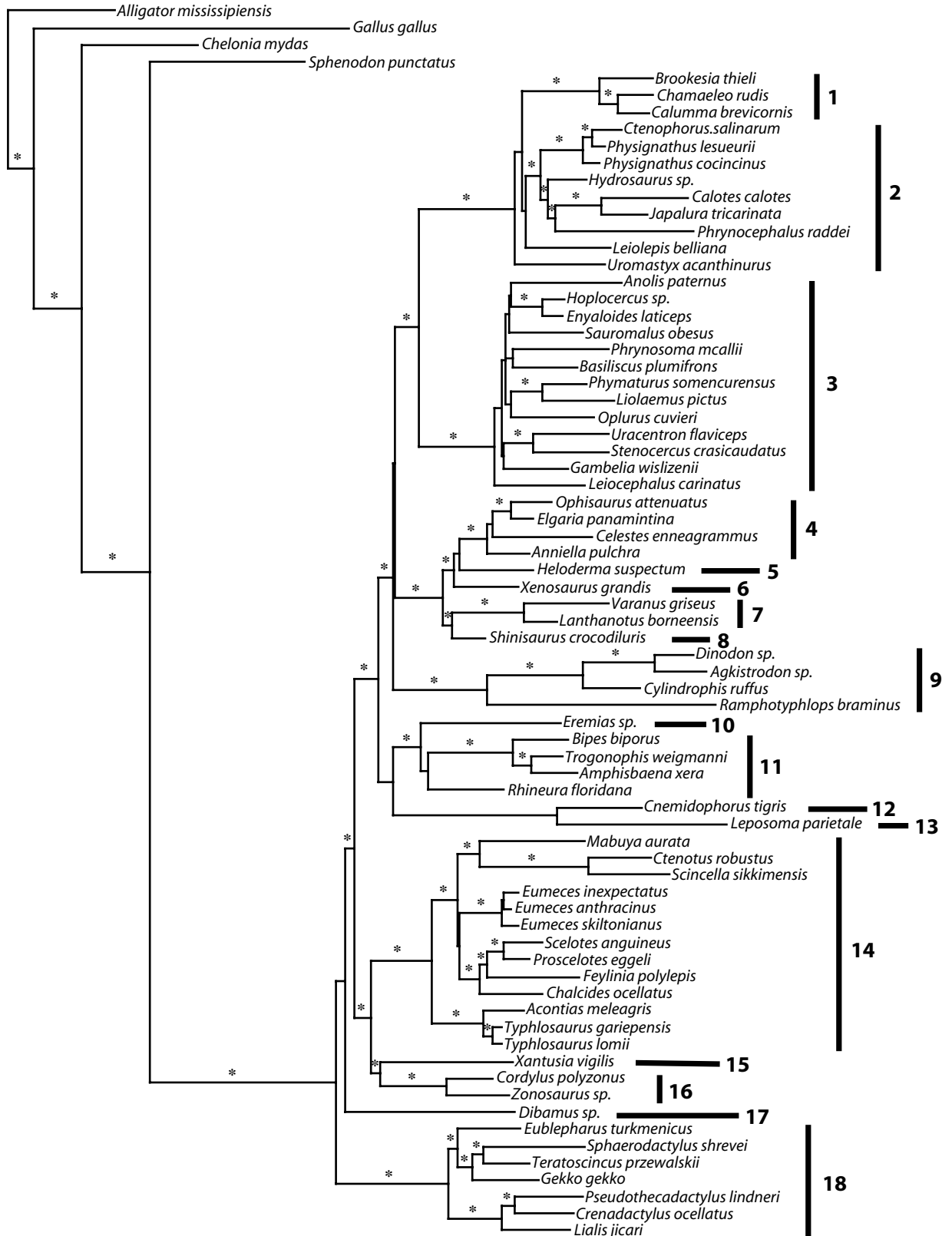
[illegible]

C. salinarum	CACCTCTCCAACAGCCGCTATCATTTCTTTCACTCATTTTTCTTTCCATAGCAGGCTTACCCCCACTAACAGGATTTACACCAAACTACT
P. leusterii	CACCTACCAGCCGCTGCCACCCCTCCTAATGTTACTACTTCTCTCTATAGCGGGTCTCCCTCCACTAACAGGGTTACACCAAAATTACT
P. cocincinus	ATCTCACCAACGCCCGCTTCTCAATGACACTTATACTACTACTACCTAGCAGGCTTCCACCCCTTGCCGGATTTACACCAAACTAGC
Hydrosaurus.sp.	ACAACCTCAGCAGCAACATAACGACAACTACTCTCTATCACTAGGAGGCTCCCTCCATTAACAGGGTTTCATCCAAAATTACT
C. calotes	ACCTCCCCACTAGCAACCAACAATAGTCTTACTCTGTCTATCAACAGCCGGGTTACCCCCACTACCGGCTTTTTACCAAAATTAAT
J. tricarinata	ACATCTCCAATGCAACCAACAACAATACTTATTTGTGCTCTCAACAGCCGGACTTCCACCACCTACCGGGTTTTTACCAAACTACT
P. raddei	ACCTCTACACAACAATTTCTCGATTTCTTCAATCTATAACAGCGGCTTACCGCATTCACAGGATTCATACCAAGAATGACT
L. belliana	ACAACCCCA---ATAATCATCTCCTAATACCAATTATAATATCACTAGGAGGACTACCCCCACTAACAGGATTCACACCAAACTCTT
U. acanthinurus	ACAACACCAACAATCAGACACTACTAGCCCTACTACTACTATCGACAGGCGGACTCCCACCATTACCGGATTCCTACCAAACTACT
A. paternus	TTTTACCCCATCACTAACGATTATAATAATCTTTCACTTCTTTCACTAGGGGACTACCAACCACTAACTGGATTTGTACCAAAGTGGCT
P. mcallii	ACCTCCCCACAACACTACACCCCTTGCCATATTAATCTACTATCCTTAGGGGACTTCCCCCCTTACCGGCTTTCACCAAAATGACT
Sauromalus.obesus	TCTTCCCCCACACTAACCATCATAATAACTTGACACTACTATCGCTAGGAGGCTTCCCCCCTTAACCTGGGTTTATACCAAAATGACT
Hoplocercus.sp.	ACCTCCCCCACTTAGTTTATACCCACAATATTACCTACTATCCTTAGGGGGCTCCCCCCTATCAGGGTTCTCTCCCAAAATGAAT
E. laticeps	ACGTCCCAACATTAATTATTATAATACTACCTCCCTCCTCTAGGTGGACTTCCCCCCTAGTCAGGCTTCTTACCAAAATGACT
P. somuncurensis	ACATCCCCAACAATAAACCATCATTTATTTTCCATAACACTACTCTCACTCGGCGGACTTCCCCCCTTACCGGCTTTTTTACCAAAATGACT
L. pictus	TCATCCCCAATTACTACCGTTCFAACAGCTATAACCTCCTATCCTTAGGAGGCTCCCTCCACTAACAGGATTTATACCAAAATGACT
U. flaviceps	ACCTCCCCCGCTTTAAACAATCAGATGGCCCTCACACTTATTTCTAGGAGGACTCCCCCCCATATCAGGCTTTTATCCAAAGTGGCT
S. crassicaudatus	CTATCACTTGCCTTACGACAACAATTTGCCCTACTAACACTACTCTCACTAGGAGGCTTACCCCCACTTCAGGATTTATACCAAAATGACT
L. carinatus	TTATCTCCTACACTAATAATTATAACGATACTAGCCCTCCTATCACTAGGAGGACTCCCACCATTGACAGGATTTATTTCCAAAGTACT
B. plumifrons	ACATCACCACCAACAACCTCTATAATAATACTCACACTACTCTCTCTTGGGGGCTCCCTCCACTAACAGGCTTCATCCCAAAATGACT
G. wislizenii	TCTTCCCCAAGTCTACAAATTACTATAATACTTACACTACTATCTTCTAGGCGGCTGCCACCATTATCCGGATTTATACCAAAATGACT
O. cuvieri	TATTTCCCAATACATGACCAACAATAATACTAACCGCTCTTTCTTCTAGGTGGCTTCCCCCCTAACAGGATTTCTGCCAAATGGCT
O. attenuatus	ACCTCCCCAATACTAACCCCACTACCATAATAACCTCCTATCACTAGGAGGCTTCCCCCCTATCAGGATTTATGCTTAAATGACT
E. panamintina	ACATACCCCATACTCTCTTCACTAACAAATAAFAACACTTCTATCTTTAGGAGGACTTCCCCCCTACAGGCTTCTTGCCCAAAATGACT
C. enneagrammus	ACTTCCCCCTATATTAAGTGGCTGACAAATAAACCTACTATCTTGGGGGACTTCCCCCCTTAACCTGGCTTACTTCCAAATGACT
A. pulchra	ACATCACCACCTCTTAACACCACTTACCATAAACACCTCCTGTCACTAGGAGGCTTACCCCCACTAACCGGATTTCTACCAAAATGACT
H. suspectum	ACAACACCTTATACTAGCTACAATACTAATAAATTTGTCTCTTATCAATAGGAGGCTTCCACCACATATCTGGGTTCTTGCCAAATGGCT
X. grandis	ACCTCCCCAACCCATAATCTATTAACAATAATACTCCTATTTATCCTTAGGAGGACTCCCCCCCCTAACCGGGTTCTTACCAAAATGGCT
V. griseus	CACCTACCCCTCATAGCGAGCCTTCTCCTACTATCCCTTCTCACTAGGAGGACTTCCCCCCTATCAGGATTTCTCCCTAAATGACT
L. borneensis	ACACTCCCCCCCCCTCAACACCTTTTCGCGAGCCTCACTACTCTCACTAGGAGGCTTACCTCCACTAACAGGATTTTTTGCCAAATGACT
S. crocodilurus	ACATCCCCCATACTTATGCCACTACTACTATCACTTACTATCCTTAGGAGGCTTCTCTCCACTGACAGGCTTTTTACCAAAAGTACT
D. semicarinatus	AACCTCCCCATACACCATAACTATCTCTATAAACCTCTTATCTATAGGAGGACTACGCCCCCTATCAGGATTCATACCAAAATGGTT
R. braminus	TCCTCAACCCACACCTCCTCTATATATACTTCTAATCTTATATCAATCGCAGGGTTACCAACCAATACCGGCTTGTGCCCAAAATGACT
C. rufus	ACATCCCCACAACCTGACATCAGGCATTACACTTACAATCCTATCACTAAGCGGCTTACCACCACCTAACAGGATTCATGCCAAATGACT
Agkistrodon.sp.	GCCTCCCCCTATTAACCTTAATTATACTAACAACAATCCTATCCTTAAGTGGCTTCTTCCCCCTCACAGGGTTTATACCAAAATGACT
E. grammica	ACCTCCCCAATATACATCAATTTTCCCTAAATACCTTATCTCACTAGGAGGCTTACCCCGCTCATTGGATTTCTTACCAAAATGACT
B. biporus	ACAACCCACATGCAATGATAATATTACTAATAACACTTCTCTCACTTGGCGGACTACCGCCACTATCAGGCTTCATACCAAGCTACT
T. weigmanni	AGCATCCCATACAACAATAGTCTTACTACTACTCACACTTATCTCACTAGGAGGCTTACCCCCCTCTCCGGCTTCATACATAAATGGCT
A. xera	ACCGCCCCCTCAATAATACTAACAGCCCTCTTAACACTCATCTCCTTGGCGGACTACCCCCAACCCAGGGCTTCTTAATAAATGGTT
C. tigris	CTGTACCCCCCATACAACATCTTACAATACTCACTGACATCTCTTAGGAGGCTTCCCCAATTAACAGGATTTATGCCCAAAATGACT
L. parietale	TTGTCCCCAGCAATAATAACAATATTACTTCTAATTTCTCATCTCATTAGGAGGCTTCCACCAATAACCGGATTTTTTACCAAAATGATT
E. turkmenicus	ACTTCCCCAACATCCATCACTTCTTACTAATACTATCTTCTCTCACTAGGAGGACTTCCACCACCTATCAGGATTTATACCAAACTACT
S. shrevei	CGCAACCCACAGCTACTATFCCAATAACCTACTCACCGCCATGTCCCTCGGAGGACTTCCCCCAATTAACCGGCTTCACACCAAGTGACT
T. przewalskii	AACAGCCCCACACTCCTCACCATTTCATAATCATCCTAATATCACTAGGAGGCTTACCCCCACTAACAGGATTTATACCAAAATGACT
G. gecko	CAATCCCTTCACTCAATAACAATAGTAATAAATTTCCATTATATCACTAGGAGGCTTACCCCATTAACAGGCTTCTTGCCAAATGACT
P. lindneri	AAAACCCCGCCCTTAATAATAAACCACTACTCACCTTTATATCTTAGGAGGACTACCTCCACTAACTGGCTTTATCTCTAAATGATT
Cr. ocellatus	CAATCCCCACCCCTCTCATATTTTCCATATTAATCTATCCTTAGGAGGATTAACCCCTTACAGGATTCGTACCAAAATGACT
L. jicari	ATCTCTCCCCCTTACTCGCAATCACAATATTAACCTTATTATCACTAGGCGGACTACCCCCACTAACCGGCTTCTCTCCTAAATGATT
M. aurata	ATCTCCCCACCCATAACCGGCCACAATAATAGTCTGTCTAATATCACTAGGTGGCTTCCACCCCTAACAGGATTTATGCTTAAATGACT
C. robustus	ATTTCCCCAACTACAGAGCCCTTATATTAACCTTATATGTCTCACTAGGAGGCTTCCCCCCTAACCTAGGCTTTTATACCAAAATGGTT
S. sikkimensis	CTTTCCCCCTACTAACCGGCTCAATACATAAATTTTACTAATATCAATAGGGGGCTTCCCCCTCTTTCAGGCTTTATACCAAAATGATT
E. inexpectatus	ATCTCACTTACAATATCAGCCCTAGCCCTAACACTACTTATATCACTAGCGGCTTCCCCCCTTACTGGCTTCATGCCAAATGACT
E. skiltonianus	ATTTTCGCCCACTACAACAGCCCTTATGTCTATATTTGTCTCATATCTTACTAGCTGGCCCTACCCCATTTACCGGCTTCACGCCAAATGGCT
E. anthracinus	GTCTCACCCACAATACAGCCCTCATAGCTATACTACTCATATCACTAGGCGGCTTACCCCATTTACCGGATTCATGCCAAATGACT
S. anguineus	TCTTCCCCAACACAACAGCCCTTACTACTTATCTACTTATATCCTTAGGTGGACTGCCACCTCTCACAGGATTTATACCAAAATGATT
P. eggeli	ACCGCCCCAACACAACACCTTCACTACTTATCCTACTAATATCCTTGGCGGCTTACCCCATTTACAGGCTTTATACCAAAATGACT
P. polylepis	ATCTCACCAACAATAAACACCTTCTCACTACTTACTAATAATCCTCGGAGGACTTCCACCCCTAACCGGATTCATACCAAAATGATT
Ch. ocellatus	ATTTCCACCAACAACAGTACTACTACTTATAGTCTTAATATCACTAGGCGGCTTCCCCCTTACAGGATTCATACCAAAATGACT
A. meleagris	ATTACTCCAGTAACAACAACCTTATTACTAATATTTAATAATCACTGGGAGGCTTACCCCACTAACAGGATTTATGCCAAATGGTT
T. lomii	ATCACACCAATAACAACAACAACACTACTAACGCTACTAATATCACTAGGAGGCTTACCCACCTAACAGGATTCATACCAAAATGACT
X. gariensis	ATCACACCAACAACAGACAATAACACTAACACTATTAATATCACTTGGAGGCTTACCCCACTAACAGGATTCATGCCAAATGATT
T. vigilis	CTTTCCCCACCCCTCACTACCTTTTATACCTTTAACATTTATTTGTCTCTAGGAGGCTTACCACCTAACAGGATTTCTACCAAAATGATT
C. polyzonus	ACCACCTCAATACCCCTGCTTAACTCACTAACACTATTATTAATCCTTAGGCGGACTTACCCCATTCACAGGATTTTACCAAAATGATT
Zonosaurus.sp.	ACCTCCCCAACACTCTCCACCTTACTATAATAACCTTGTCTATCACTAAGCGGACTTCCCCCTTAACAGGATTTTTTACCAAAATGGTT
Dibamus	ACATCCATAACCTCCACAACATTAATAATGCTCGCTATCATGTCTTAGGGGGCTTACCCCTTGGCTTGGCTTCATGCCCAAAATGGCT

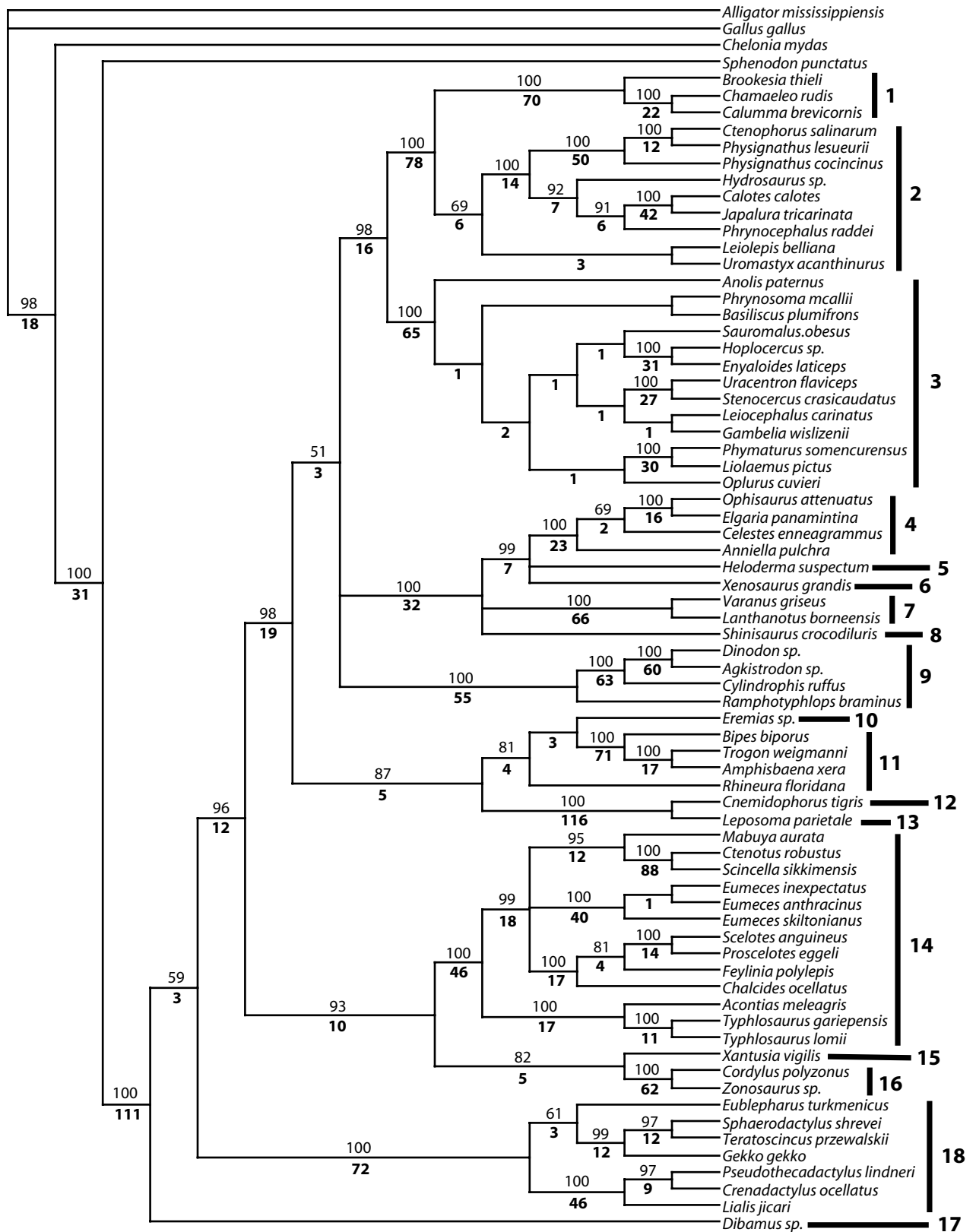
B.plumifrons	-ATCAACCGTTGACTCTTCTCAACT
G.wislizenii	-ATCACCCGTTGATTCTTCTCAACA
O.cuvieri	-ATTAATCGTTGATTTTCTCAACA
O.attenuatus	-CTAACTCGCTGACTATTTCTACT
E.panamintina	-ACAACCTCGCTGATTATCTCAACC
C.enneagrammus	-ATAACACGATGACTATTCTCTACA
A.pulchra	-ATCACCCGCTGATTATCTCAACC
H.suspectum	-ATTACTCGCTGACTCTTTTCAACT
X.grandis	-CTAACTCGATGGTTCTTTCAACC
V.griseus	-ATCACCCGCTGACTATTCTCCACC
L.borneensis	-ATAACCCGTTGACTCTTCTCCACA
S.crocodilurus	-ATCACTCGCTGATTCTTCTCGACC
D.semicarinatus	-ATCACTCGTTGACTATCTCGACA
R.braminus	-ATAAACCGTTGACTATTCTCAACT
C.ruffus	-ATCACTCGTTGATTATCTCAACA
Agkistrodon.sp.	-ATCACCCGTTGACTATTTTCAACA
E.grammica	-CTAATTCGTTGATTTTTTCAACT
B.biporus	-CTCACCCGTTCAATCTTCTCAACA
T.weigmanni	-CTTACACGTTGATTTTCTCCACA
A.xera	-CTCACCCGTTGATTTTCTCTACA
C.tigris	-ATTACTCGTTGATTTTTTCTACA
L.parietale	-ATTACACGATGATTCTTTCTACC
E.turkmenicus	-CTTTCCCGTTGACTATTTTCAACA
S.shrevei	-ATCAACCGTTGATTTTCTCAACA
T.przewalskii	-ATCCCTCGTTGATTCTTCTCAACC
G.gecko	-CTAACACGCTGGTTTTTTTCGACT
P.lindneri	-CTCTCTCGATGATTATCTCAACA
Cr.ocellatus	-ATTTCTCGTTGACTGTTCTCAACT
L.jicari	-ATTTCTCGTTGATTCTTCTCAACA
M.aurata	-ATTAATCGTTGATTCTTCTCAACC
C.robustus	-ATCAATCGTTGATTCTTCTCAACT
S.sikkimensis	-ATTAATCGTTGATTCTTCTCAACC
E.inexpectatus	-ATCAATCGTTGATTTTCTCAACC
E.skiltonianus	-ATTAATCGTTGACTTTTCTCAACC
E.anthracinus	-ATTAATCGTTGACTCTTCTCAACC
S.anguineus	-ATTAACCGTTGACTTTTCTCAACC
P.eggeli	-ATCAATCGTTGATTCTTCTCAACC
F.polylepis	-ATCAATCGTTGATTCTTCTCAACC
Ch.ocellatus	-ATCAATCGTTGACTATCTCAACC
A.meleagris	-ATCAATCGTTGATTCTTCTCAACA
T.lomii	-ATTAACCGTTGATTCTTCTCAACA
T.gariepensis	-ATTAACCGTTGATTTTCTCGACA
X.vigilis	-ATCACTCGTTGACTTTTCTCAACC
C.polyzonus	-ATCTCCCGCTGATTTTTTCAACA
Zonosaurus.sp.	-ATCTCCCGCTGATTTTTTCAACA
Dibamus	-ATCAATCGTTGATTCTTCTCAACC

Appendix IV. Separate MP and ML topologies for all analyzed data partitions. All MP topologies have bootstrap and decay values above and below the branches, respectively. All ML topologies have asterisks marking branches supported by posterior probabilities >95% in the Bayesian analyses.

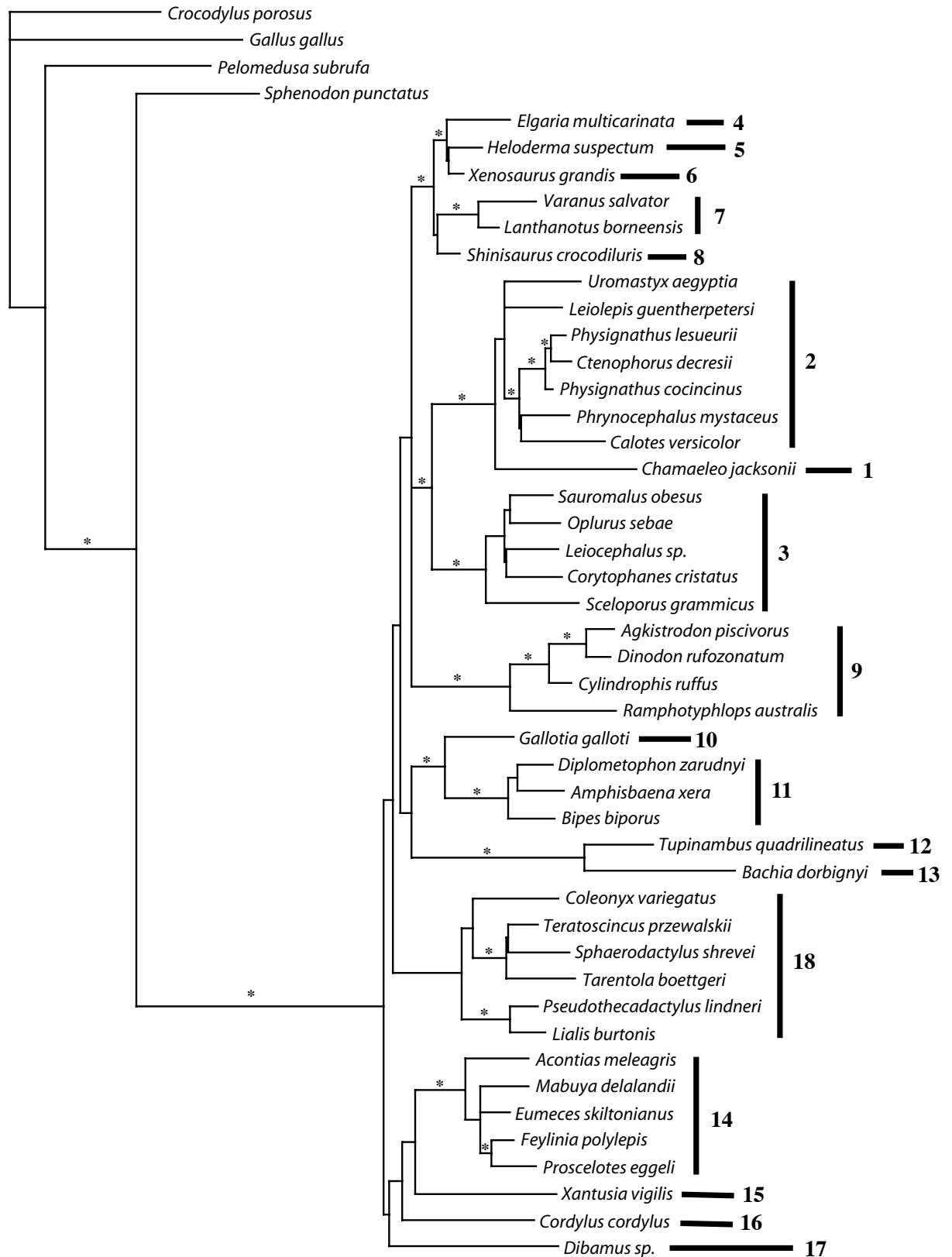
RAG ML



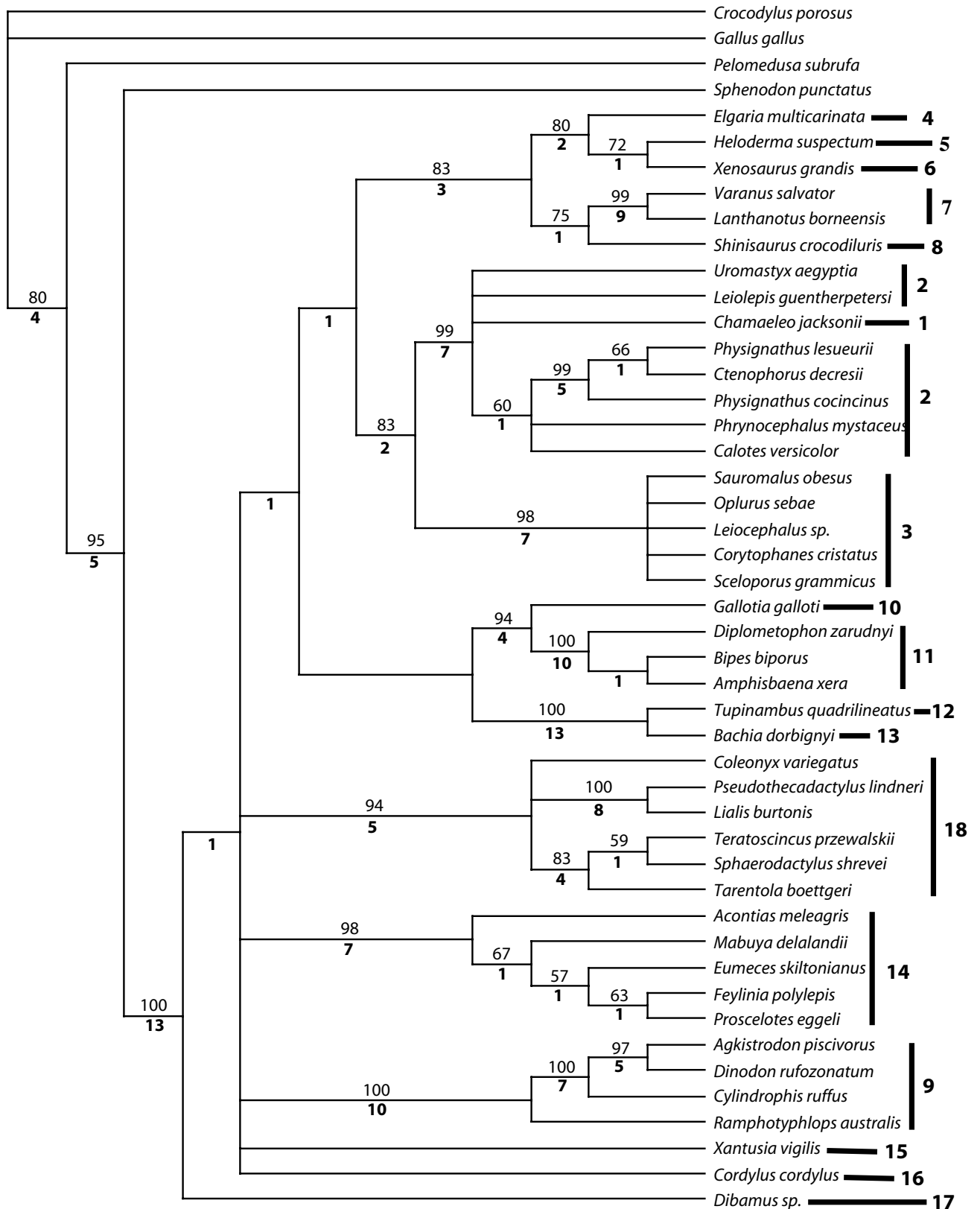
— 0.01 substitutions/site



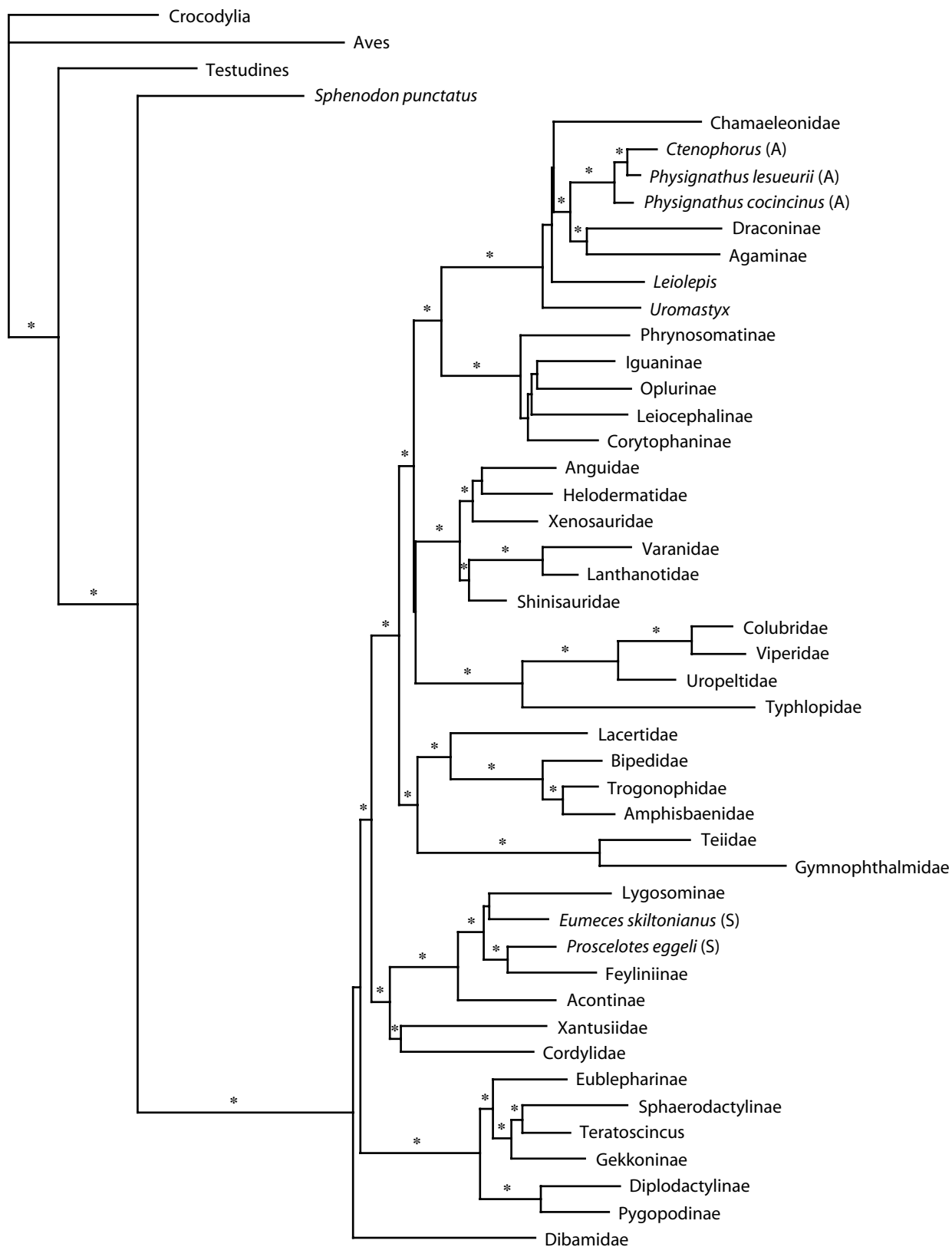
c-mos ML



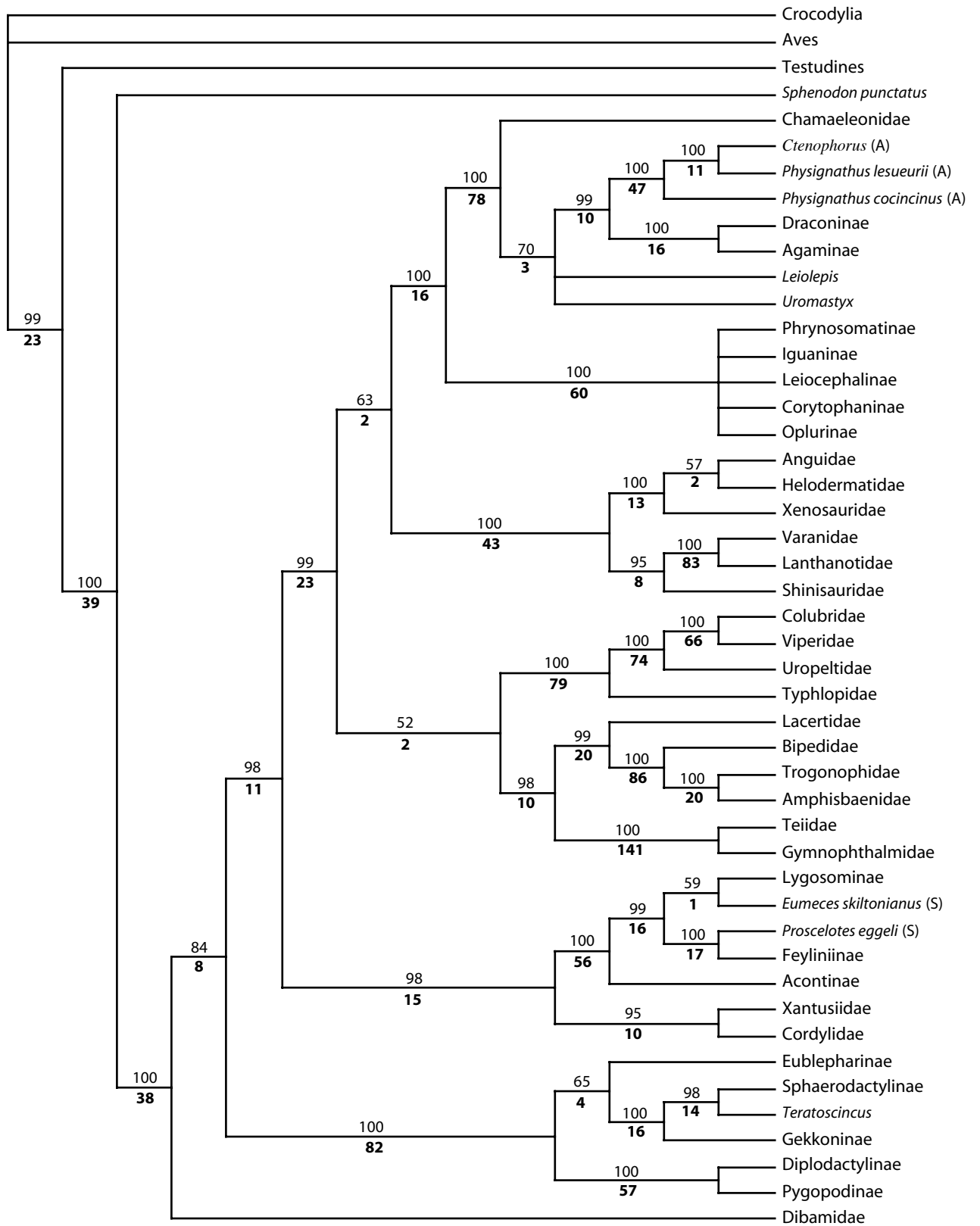
c-mos MP



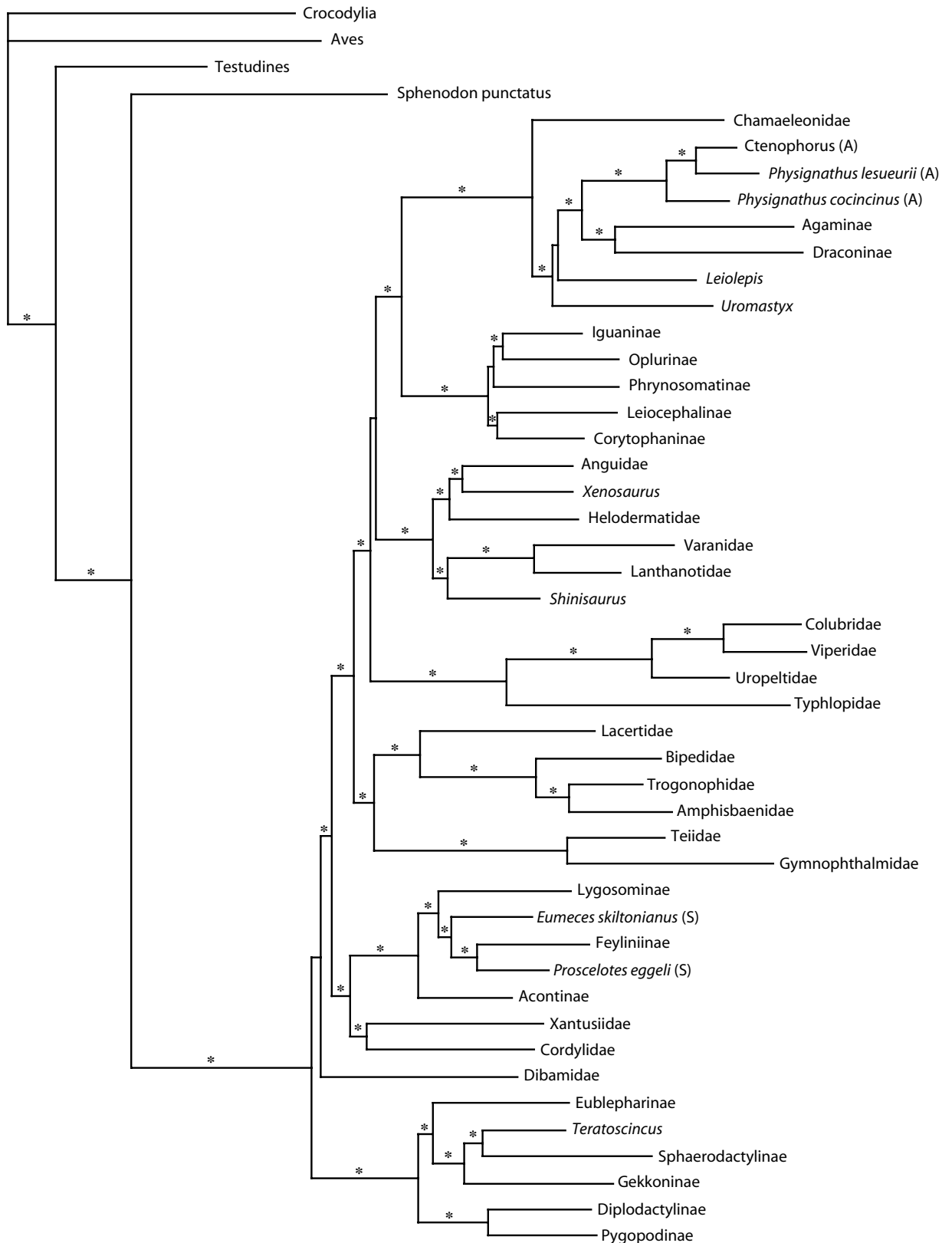
RAG/c-mos ML



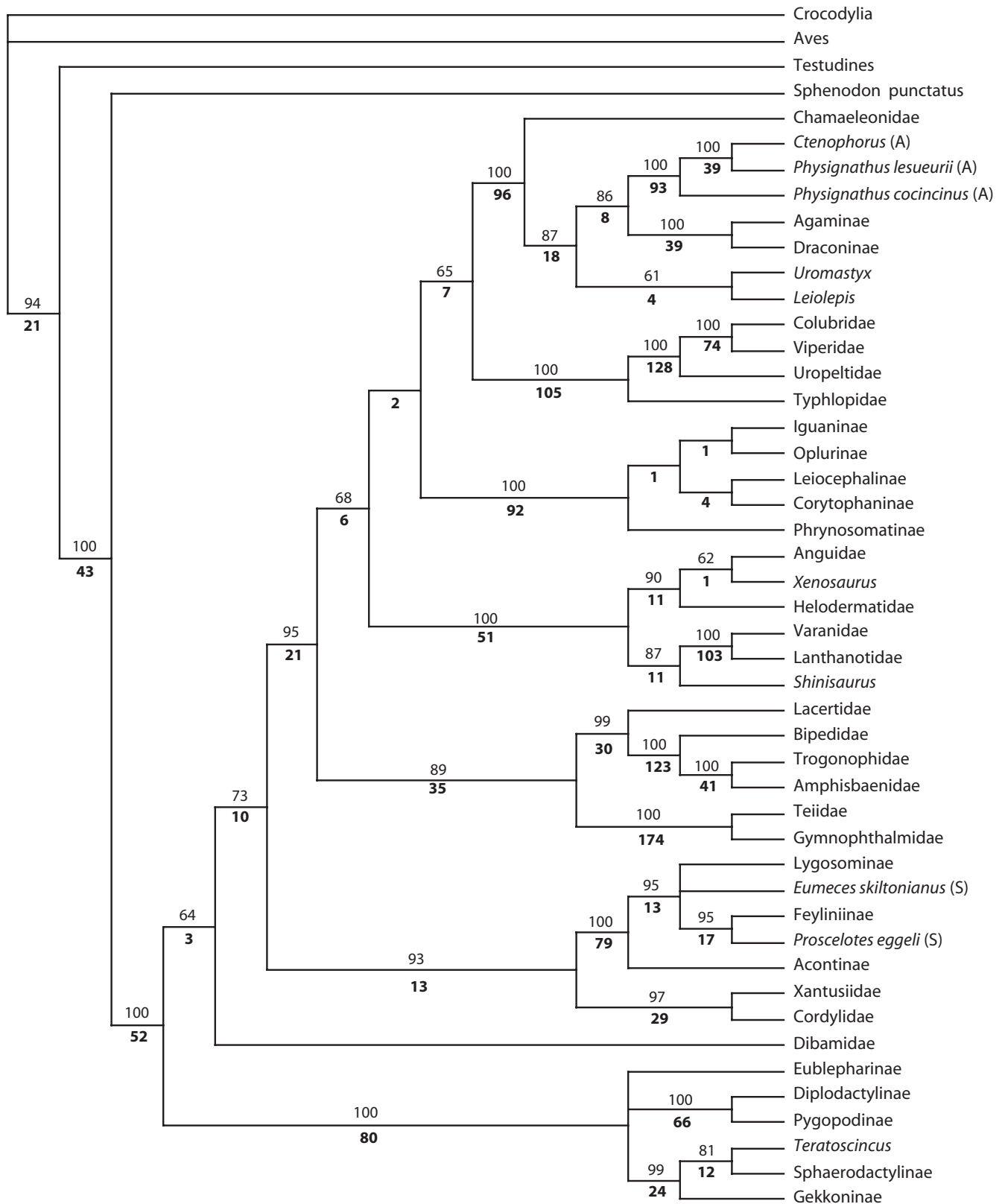
RAG/c-mos MP



RAG/c-mos/mtDNA ML



0.1 substitutions/site



Appendix V. Alternative phylogenetic hypotheses used in Wilcoxon signed-ranks (Templeton) tests. Lengths of trees are given in parentheses. Numbers refer to taxa listed on the cover sheet to the corresponding aligned data set (Appendix III). For considerations of space, if there were more than eight most parsimonious alternative topologies, only the first eight are given here.

A. *RAG-1 + c-mos*

The 11 most parsimonious trees from the unconstrained analysis (length 8807 steps):

- 1.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),(11,12))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 2.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),(11,12))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 3.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),12),11))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 4.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),11),12))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 5.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),(11,12))),((13,(((14,16),(15,17))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 6.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),12),11))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 7.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),11),12))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 8.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),12),11))),((13,(((14,16),(15,17))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 9.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),11),12))),((13,(((14,16),(15,17))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 10.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 11.(1,(2,(3,(4,((((((5,((((6,7),8),(9,10)),11),12))),((13,16),(14,15)),17))),((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));

The two most parsimonious trees obtained by constraining Scleroglossa to form a monophyletic group (length 8850 steps):

- 1.(1,(2,(3,(4,((((5,((((6,7),8),(9,10)),(11,12))),((13,(((14,16),(15,17))),((((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((34,((35,36),37)),(38,39))),47),((((40,41),(42,43)),44),(45,46))))))));
- 2.(1,(2,(3,(4,((((5,((((6,7),8),(9,10)),(11,12))),((13,(((14,17),(15,16))),((((18,19),20),(21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),((((34,((35,36),37)),(38,39))),47),((((40,41),(42,43)),44),(45,46))))))));

The two most parsimonious trees obtained by constraining Iguania not to form a monophyletic group (length 8823 steps):

- 1.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,27),26),25),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 2.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,27),26),25),((13,(((14,17),(15,16))),((18,19),20),(21,22),23))),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));

The three most parsimonious trees obtained by constraining (Serpentes + Dibamidae) to form a monophyletic group (length 8848 steps):

- 1.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((((24,27),26),25),47),((34,((35,36),37)),(38,39))))));
- 2.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),11),12))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((((24,27),26),25),47),((34,((35,36),37)),(38,39))))));
- 3.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),12),11))),((13,(((14,17),15),16))),((18,19),20),(21,22),23))),((28,(29,(30,31))),((32,33))))),((((40,41),(42,43)),44),(45,46))),((((24,27),26),25),47),((34,((35,36),37)),(38,39))))));

The five most parsimonious trees obtained by constraining (Serpentes + Amphisbaenia) to form a monophyletic group (length 8837 steps):

- 1.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,17)),15)),((18,19),20),(21,22),23))),((((24,27),26),25),(29,(30,31))),((28,(32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 2.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),15),16))),((18,19),20),(21,22),23))),((((24,27),26),25),(29,(30,31))),((28,(32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 3.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,(15,17))),((18,19),20),(21,22),23))),((((24,27),26),25),(29,(30,31))),((28,(32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 4.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),(15,16))),((18,19),20),(21,22),23))),((((24,27),26),25),(29,(30,31))),((28,(32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 5.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,16),(15,17))),((18,19),20),(21,22),23))),((((24,27),26),25),(29,(30,31))),((28,(32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));

The three most parsimonious trees obtained by constraining (Dibamidae + Amphisbaenia) to form a monophyletic group (length 8882 steps):

- 1.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33))),((29,(30,31)),47))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))));
- 2.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33))),((((40,41),(42,43)),44),(45,46))),((29,(30,31)),47)),((34,((35,36),37)),(38,39))));
- 3.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33))),((29,(30,31)),47))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))));

The eight most parsimonious trees obtained by constraining (Serpentes + *Varanus/Lanthanotus*) to form a monophyletic group (length 8852 steps):

- 1.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),15),16))),((((18,19),20),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 2.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),15),16))),((((18,(19,20)),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 3.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,17)),15))),((((18,19),20),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 4.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),(15,16))),((((18,19),20),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 5.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,16),(15,17))),((((18,19),20),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 6.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,17)),15))),((((18,(19,20)),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 7.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),(15,16))),((((18,(19,20)),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 8.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,16),(15,17))),((((18,(19,20)),23),((21,22),((24,27),26),25))),((28,(29,(30,31))),((32,33))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));

Eight of the nine most parsimonious trees obtained by constraining (Lacertidae + Teiioidea) to form a monophyletic group (length 8826 steps):

- 1.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),11),12))),(13,((14,17),15),16))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33)),(29,(30,31))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 2.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),11),12))),(13,((14,17),(15,16))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33)),(29,(30,31))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 3.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),15),16))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33)),(29,(30,31))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 4.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),12),11))),(13,((14,17),15),16))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33)),(29,(30,31))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 5.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),11),12))),(13,((14,16),(15,17))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33)),(29,(30,31))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 6.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),(13,((14,17),(15,16))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33)),(29,(30,31))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));
- 7.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),12),11))),(13,((14,17),(15,16))),((24,27),26),25))),((18,19),20),(21,22),23))),((28,(32,33)),(29,(30,31))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47))));

8.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,((14,16),(15,17)))),((24,27),26),25))),((18,19),20),((21,22),23))),((28,(32,33)),(29,(30,31))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));

The three most parsimonious trees obtained by constraining (Lacertidae + Amphisbaenia) not to form a monophyletic group (length 8826 steps):

- 1.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((24,27),26),25))),((18,19),20),((21,22),23))),((28,(32,33)),(29,(30,31))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 2.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((24,27),26),25))),((18,19),20),((21,22),23))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 3.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),11),12))),((13,16),(14,15)),17))),((24,27),26),25))),((18,19),20),((21,22),23))),((28,(32,33)),(29,(30,31))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));

The most parsimonious tree obtained by constraining Varanoidea (*Heloderma* + *Varanus/Lanthanotus*) to form a monophyletic group (length 8834 steps):

- 1.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((18,20),(19,(21,22))),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));

Eight of the 27 most parsimonious trees obtained by constraining (*Xenosaurus* + *Shinisaurus*) to form a monophyletic group (length 8827 steps):

- 1.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),11),12))),((13,16),(14,15)),17))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 2.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 3.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),11),12))),((13,((14,17),15),16))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 4.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),11),12))),((13,((14,17),(15,16))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 5.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),12),11))),((13,((14,17),15),16))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 6.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,((14,17),15),16))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 7.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),11),12))),((13,((14,16),(15,17))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));
- 8.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,((14,17),(15,16))),((18,19),(20,23),(21,22))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),(45,46))),((34,((35,36),37)),(38,39))),47)))));

Eight of the 22 most parsimonious trees obtained by constraining (Scincidae + Cordylidae) to form a monophyletic group exclusive of Xantusiidae (length 8817 steps):

- 1.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,((14,17),15),16))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));
- 2.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,((14,17),(15,16))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));
- 3.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,((14,16),(15,17))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));
- 4.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),12),11))),((13,((14,17),15),16))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));
- 5.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),11),12))),((13,((14,17),15),16))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));
- 6.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),(11,12))),((13,((14,17),15),16))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));
- 7.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),12),11))),((13,((14,17),(15,16))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));
- 8.(1,(2,(3,(4,(((((((5,((((6,7),8),(9,10)),11),12))),((13,((14,17),(15,16))),((18,19),20),((21,22),23))),((24,27),26),25))),((28,(29,(30,31)),(32,33))))),((((40,41),(42,43)),44),46),45))),((34,((35,36),37)),(38,39))),47)))));

The two most parsimonious trees obtained by constraining Acontinae not to form a the sister taxon to the remaining Scincidae (length 8822 steps):

- 1.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17)),((18,19),20),((21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),(((40,44),(41,(42,43))),((45,46))),((34,((35,36),37)),(38,39)),47)))));
- 2.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),11),12))),((13,16),(14,15)),17)),((18,19),20),((21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),(((40,44),(41,(42,43))),((45,46))),((34,((35,36),37)),(38,39)),47)))));

The two most parsimonious trees obtained by constraining (Diplodactylinae + Pygopodinae) not to form a monophyletic group (length 8863 steps):

- 1.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17)),((18,19),20),((21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),(((40,41),(42,43)),44),((45,46))),((34,((35,36),37)),39,38)),47)))));
- 2.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),11),12))),((13,16),(14,15)),17)),((18,19),20),((21,22),23))),((((24,27),26),25),((28,(29,(30,31))),((32,33))))),(((40,41),(42,43)),44),((45,46))),((34,((35,36),37)),39,38)),47)))));

The two equally most parsimonious trees obtained by constraining Scincomorpha (including Amphisbaenia) to form a monophyletic group (length 8830 steps):

- 1.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17)),((24,27),26),25),((18,19),20),((21,22),23))),((28,(29,(30,31))),((32,33))),((40,(41,(42,43))),44),((45,46))),((34,((35,36),37)),(38,39)),47)))));
- 2.(1,(2,(3,(4,((((((5,(((6,7),8),(9,10)),(11,12))),((13,16),(14,15)),17)),((24,27),26),25),((18,19),20),((21,22),23))),((28,(29,(30,31))),((32,33))),((40,41),(42,43)),44),((45,46))),((34,((35,36),37)),(38,39)),47)))));

B. Mitochondrial DNA

The four most parsimonious trees from the unconstrained analysis (length 14328 steps):

- 1.(1,(2,((3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((39,42),40),41)),((((30,31),33),32),35),((34,(36,37)),38))),((69,(70,71))),((17,((((18,19),((23,26)),((21,22),28)),(24,29)),((20,25),27))),72),((56,((((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52)))),(47,48))),4)))));
- 2.(1,(2,((3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((39,42),40),41)),((((30,31),33),32),35),((34,(36,37)),38))),((69,(70,71))),((17,((((18,19),((21,22),28)),(24,29)),(23,26))),((20,25),27))),72),((56,((((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52)))),(47,48))),4)))));
- 3.(1,(2,((3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((39,42),40),41)),((((30,31),33),32),35),((34,(36,37)),38))),((69,(70,71))),((17,((((18,19),((23,26)),((21,22),28)),(24,29)),((20,25),27))),72),((56,((((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52)))),(47,48))),4)))));
- 4.(1,(2,((3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((39,42),40),41)),((((30,31),33),32),35),((34,(36,37)),38))),((69,(70,71))),((17,((((18,19),((21,22),28)),(24,29)),(23,26))),((20,25),27))),72),((56,((((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52)))),(47,48))),4)))));

The two most parsimonious trees obtained by constraining Scleroglossa to form a monophyletic group (length 14345 steps):

- 1.(1,((2,(3,((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((((17,27),(20,25)),((18,19),((21,22),28)),(24,29))),((23,26)),((((30,31),33),32),35),((34,(36,37)),38))),((((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52)))),(47,48))),((69,(70,71))),((56,((((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72))),((39,42),40),41))))),4)))));
- 2.(1,((2,(3,((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((((17,27),(20,25)),((18,19),((21,22),28)),(24,29))),((23,26)),((((30,31),33),32),35),((34,(36,37)),38))),((((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52)))),(47,48))),((69,(70,71))),((56,((((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72))),((39,42),40),41))))),4)))));

The seven most parsimonious trees obtained by constraining (Serpentes + Acrodonta) not to form a monophyletic group (length 14343 steps):

- 1.(1,((2,((3,(47,48)),((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((39,42),40),41),((44,(45,46))))),((((((((17,27),(20,25)),((18,19),((21,22),28)),(24,29))),((23,26)),((((30,31),33),32),35),((34,(36,37)),38))),((56,(62,(63,64))),((57,58),((59,61),60)),((65,(67,68)),66))),72)),((69,(70,71))),((43,49),((50,(51,52)),((53,55),54))))),4)))));
- 2.(1,((2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((30,31),33),32),35),((34,38),(36,37))),((39,42),40),41))),((((((17,27),(20,25)),((23,26)),(24,29)),(18,19)),(21,22),28)),((56,((((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),((69,(70,71))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52))))),4)))));

3.(1,((2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((30,31),33),32),35),((34,38),(36,37))),((39,42),40),41))),((((17,27),(20,25)),(23,26)),(24,29)),(18,19)),(21,22)),28)),((56,(((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),(69,(70,71))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52))))),4));

4.(1,(2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((30,31),33),32),35),((34,38),(36,37))),((39,42),40),41))),((((17,27),(20,25)),(23,26)),(24,29)),(18,19)),(21,22)),28)),((56,(((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),(69,(70,71))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52))))),4));

5.(1,((2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((30,31),32,33),35),((34,38),(36,37))),((39,42),40),41))),((((17,27),(20,25)),(23,26)),(24,29)),(18,19)),(21,22)),28)),((56,(((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),(69,(70,71))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52))))),4));

6.(1,((2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((30,31),32,33),35),((34,38),(36,37))),((39,42),40),41))),((((17,27),(20,25)),(23,26)),(24,29)),(18,19)),(21,22)),28)),((56,(((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),(69,(70,71))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52))))),4));

7.(1,(2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((((30,31),32,33),35),((34,38),(36,37))),((39,42),40),41))),((((17,27),(20,25)),(23,26)),(24,29)),(18,19)),(21,22)),28)),((56,(((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),(69,(70,71))),((43,(44,(45,46))),((53,55),54)),(49,(50,(51,52))))),4));

The six most parsimonious trees obtained by constraining (*Serpentes* + *Varanus* + *Lanthanotus*) to form a monophyletic group (length 14349 steps):

1.(1,((2,(3,(47,48)),((((((5,(6,7)),((((8,9),10),11),((12,13),14),15,16))),((36,37),((39,42),40),41))),((((30,31),33),32),35),((34,38))),((((17,27),(20,25)),(18,19),((21,22),28),24,29))),23,26)),((56,(((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),(69,(70,71))),((43,(44,(45,46))),49),((50,(51,52)),((53,55),54))))),4));

2.(1,((2,(3,(47,48)),((((((5,(6,7)),((((8,9),10),11),((12,13),14),15,16))),((36,37),((39,42),40),41))),((((30,31),33),32),35),((34,38))),((((17,27),(20,25)),(18,19),((21,22),28),24,29))),23,26)),((56,(62,(63,64))),((57,58),((59,61),60)),((65,(67,68)),66))),72)),(69,(70,71))),((43,(44,(45,46))),49),((50,(51,52)),((53,55),54))))),4));

3.(1,((2,(3,(47,48)),((((((5,(6,7)),((((8,9),10),11),((12,13),14),15,16))),((36,37),((39,42),40),41))),((((30,31),32,33),35),((34,38))),((((17,27),(20,25)),(18,19),((21,22),28),24,29))),23,26)),((56,(((57,58),((59,61),60)),((65,(67,68)),66)),(62,(63,64))),72)),(69,(70,71))),((43,(44,(45,46))),49),((50,(51,52)),((53,55),54))))),4));

4.(1,((2,(3,(47,48)),((((((5,(6,7)),((((8,9),10),11),((12,13),14),15,16))),((36,37),((39,42),40),41))),((((30,31),33),32),35),((34,38))),((((17,27),(20,25)),(18,19),((21,22),28),24,29))),23,26)),((56,(62,(63,64))),((57,58),((59,61),60)),((65,(67,68)),66))),72)),(69,(70,71))),((43,(44,(45,46))),49),((50,(51,52)),((53,55),54))))),4));

5.(1,((2,(3,(47,48)),((((((5,(6,7)),((((8,9),10),11),((12,13),14),15,16))),((36,37),((39,42),40),41))),((((30,31),32,33),35),((34,38))),((((17,27),(20,25)),(18,19),((21,22),28),24,29))),23,26)),((56,(62,(63,64))),((57,58),((59,61),60)),((65,(67,68)),66))),72)),(69,(70,71))),((43,(44,(45,46))),49),((50,(51,52)),((53,55),54))))),4));

6.(1,((2,(3,(47,48)),((((((5,(6,7)),((((8,9),10),11),((12,13),14),15,16))),((36,37),((39,42),40),41))),((((30,31),32,33),35),((34,38))),((((17,27),(20,25)),(18,19),((21,22),28),24,29))),23,26)),((56,(62,(63,64))),((57,58),((59,61),60)),((65,(67,68)),66))),72)),(69,(70,71))),((43,(44,(45,46))),49),((50,(51,52)),((53,55),54))))),4));

The two most parsimonious trees obtained by constraining (*Sphaerodactylus* + *Gekko*) not to form a monophyletic group (length 14339 steps):

1.(1,((2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((39,42),40),41)),(47,48)),((((30,31),33),32),35),((34,(36,37)),38))),69,(70,71))),((17,((((18,19),23,26)),21,22),28),24,29)),20,25,27))),72),56,(((57,58),((59,61),60)),((65,(67,68)),66))),62,(63,64))))),((43,(44,(45,46))),49,((50,52),51),((53,54),55))))),4));

2.(1,((2,(3,((((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((39,42),40),41)),(47,48)),((((30,31),33),32),35),((34,(36,37)),38))),69,(70,71))),((17,((((18,19),23,26)),21,22),28),24,29)),20,25,27))),72),56,(((57,58),((59,61),60)),((65,(67,68)),66))),62,(63,64))))),((43,(44,(45,46))),49,((50,52),51),((53,54),55))))),4));

The most parsimonious tree obtained by constraining (*Xenosaurus* + *Heloderma* + Anguidae) to form a monophyletic group (length 14339 steps):

1.(1,((2,(3,(47,48)),((((5,(6,7)),((((8,9),10),11),((12,13),14)),(15,16))),((39,42),40),41)),((((((((17,27),(20,25)),(18,19),((21,22),28),24,29))),23,26)),((43,(44,(45,46))),49),((50,(51,52)),((53,55),54))),((((((((30,31),33),32),35),34),36,37))),38),72)),69,(70,71))),56,(((57,58),((59,61),60)),((65,(67,68)),66)),62,(63,64))))),4));

D. *RAG-1*, *c-mos*, and mtDNA

The 3 most parsimonious trees from the unconstrained analysis (length 19393 steps):

- 1.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));
- 2.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));
- 3.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((40,41),((42,44),43))));

The two most parsimonious trees obtained by constraining (Lacertidae + Amphisbaenia) not to form a monophyletic group (length 19423 steps):

- 1.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,(21,23)),((19,20),22))),((28,(32,33)),(29,(30,31))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));
- 2.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,(21,23)),((19,20),22))),((28,(32,33)),(29,(30,31))),((34,(35,(36,37))),38),(45,46))),47),(39,((40,41),((42,44),43))));

The five most parsimonious trees obtained by constraining Agamidae not to form a monophyletic group (length 19411 steps):

- 1.(1,(2,(3,(4,((((((((5,12),((6,7),8),(9,10))),11),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));
- 2.(1,(2,(3,(4,((((((((5,12),((6,7),8),(9,10))),11),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((40,41),((42,44),43))));
- 3.(1,(2,(3,(4,((((((((5,12),((6,7),8),(9,10))),11),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));
- 4.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10))),12),11),((24,25),26),27))),((13,17),(15,16)),14))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));
- 5.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10))),12),11),((24,25),26),27))),((13,17),(15,16)),14))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));

The three most parsimonious trees obtained by constraining (Xantusiidae + Cordylidae) not to form a monophyletic group (length 19422 steps):

- 1.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),46,45))),47),(39,((42,44),43)),(40,41))));
- 2.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((34,(35,(36,37))),38),46,45))),47),(39,((42,44),43)),(40,41))));
- 3.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(30,31))),((32,33))),((39,((40,41),((42,44),43))),47),((34,35),(36,37)),38),45,46))));

The most parsimonious tree obtained by constraining (Trogonophidae + Amphisbaenidae) not to form a monophyletic group (length 19434 steps):

- 1.(1,(2,(3,(4,((((((((5,((((6,7),8),(9,10)),(11,12))),((24,25),26),27))),((13,14),(15,16)),17))),((18,23),21),((19,20),22))),((28,(29,(31),30)),((32,33))),((34,(35,(36,37))),38),(45,46))),47),(39,((42,44),43)),(40,41))));

Appendix VI. Pairwise genetic distance matrices. Species numbers correspond to those listed in the appropriate sections of Appendix III. Upper triangle contains uncorrected “p” distances, lower triangle contains maximum-likelihood distances.

RAG-1 genetic distances

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1		0.172	0.126	0.155	0.227	0.223	0.22	0.219	0.212	0.212	0.214	0.231	0.227	0.223	0.219	0.21	0.21	0.211	0.201	0.207
2	0.256		0.173	0.196	0.252	0.25	0.248	0.248	0.245	0.245	0.246	0.264	0.258	0.26	0.253	0.246	0.237	0.241	0.236	0.235
3	0.166	0.256		0.145	0.216	0.212	0.211	0.213	0.208	0.207	0.204	0.225	0.216	0.216	0.213	0.207	0.203	0.206	0.196	0.197
4	0.216	0.309	0.193		0.213	0.213	0.212	0.201	0.196	0.194	0.2	0.222	0.213	0.209	0.204	0.205	0.199	0.2	0.191	0.191
5	0.398	0.496	0.367	0.348		0.054	0.051	0.098	0.094	0.093	0.092	0.127	0.109	0.126	0.097	0.102	0.156	0.155	0.143	0.144
6	0.389	0.492	0.357	0.348	0.06		0.035	0.095	0.092	0.091	0.091	0.124	0.109	0.126	0.099	0.102	0.16	0.148	0.148	0.144
7	0.382	0.483	0.355	0.348	0.056	0.037		0.093	0.089	0.088	0.09	0.124	0.11	0.124	0.096	0.102	0.157	0.144	0.142	0.14
8	0.374	0.469	0.353	0.317	0.12	0.116	0.112		0.021	0.029	0.059	0.1	0.082	0.104	0.084	0.089	0.153	0.15	0.141	0.136
9	0.357	0.464	0.343	0.308	0.114	0.111	0.107	0.022		0.021	0.052	0.095	0.077	0.099	0.078	0.082	0.148	0.142	0.139	0.132
10	0.355	0.461	0.34	0.303	0.112	0.109	0.105	0.03	0.022		0.052	0.095	0.076	0.098	0.076	0.081	0.147	0.143	0.134	0.129
11	0.361	0.467	0.333	0.314	0.111	0.11	0.108	0.067	0.058	0.057		0.086	0.067	0.085	0.067	0.073	0.145	0.14	0.136	0.129
12	0.403	0.528	0.383	0.37	0.166	0.161	0.16	0.123	0.115	0.115	0.103		0.066	0.114	0.11	0.113	0.172	0.169	0.163	0.156
13	0.397	0.507	0.363	0.344	0.137	0.137	0.138	0.097	0.09	0.089	0.077	0.074		0.103	0.093	0.098	0.16	0.155	0.152	0.15
14	0.385	0.516	0.365	0.339	0.164	0.163	0.16	0.128	0.12	0.119	0.101	0.144	0.127		0.112	0.114	0.168	0.167	0.158	0.152
15	0.372	0.493	0.355	0.326	0.12	0.122	0.118	0.1	0.092	0.089	0.078	0.14	0.114	0.142		0.083	0.15	0.145	0.138	0.134
16	0.353	0.47	0.338	0.328	0.128	0.127	0.126	0.107	0.097	0.097	0.085	0.144	0.121	0.147	0.099		0.152	0.144	0.142	0.136
17	0.356	0.441	0.337	0.322	0.221	0.227	0.221	0.214	0.204	0.202	0.199	0.251	0.228	0.243	0.209	0.213		0.096	0.087	0.075
18	0.356	0.45	0.338	0.318	0.216	0.203	0.197	0.205	0.192	0.193	0.187	0.243	0.218	0.239	0.198	0.196	0.116		0.084	0.078
19	0.335	0.441	0.317	0.3	0.195	0.204	0.194	0.191	0.187	0.18	0.182	0.234	0.213	0.223	0.187	0.193	0.104	0.099		0.062
20	0.347	0.436	0.318	0.299	0.196	0.196	0.188	0.182	0.174	0.169	0.169	0.219	0.207	0.21	0.178	0.181	0.087	0.09	0.07	
21	0.346	0.434	0.325	0.304	0.193	0.198	0.191	0.186	0.178	0.174	0.173	0.226	0.211	0.217	0.18	0.184	0.087	0.088	0.068	0.024
22	0.344	0.449	0.331	0.318	0.213	0.21	0.202	0.197	0.187	0.183	0.187	0.241	0.225	0.227	0.192	0.191	0.105	0.095	0.081	0.077
23	0.352	0.448	0.325	0.312	0.218	0.218	0.211	0.201	0.194	0.189	0.184	0.249	0.231	0.235	0.196	0.198	0.124	0.108	0.097	0.09
24	0.366	0.461	0.34	0.32	0.232	0.232	0.223	0.211	0.2	0.199	0.194	0.239	0.229	0.237	0.203	0.209	0.117	0.114	0.101	0.089
25	0.37	0.475	0.352	0.329	0.229	0.225	0.218	0.213	0.201	0.196	0.189	0.246	0.227	0.242	0.205	0.209	0.121	0.116	0.099	0.091
26	0.354	0.447	0.344	0.327	0.211	0.205	0.199	0.194	0.184	0.183	0.177	0.233	0.22	0.223	0.194	0.192	0.111	0.11	0.092	0.08
27	0.366	0.459	0.333	0.319	0.208	0.201	0.199	0.191	0.183	0.18	0.171	0.23	0.209	0.218	0.189	0.184	0.102	0.087	0.078	0.068
28	0.342	0.447	0.309	0.291	0.209	0.202	0.196	0.191	0.178	0.178	0.176	0.232	0.211	0.22	0.188	0.188	0.097	0.093	0.079	0.066
29	0.347	0.435	0.343	0.305	0.2	0.195	0.195	0.192	0.182	0.175	0.172	0.233	0.207	0.221	0.185	0.193	0.108	0.106	0.09	0.081
30	0.355	0.437	0.315	0.29	0.216	0.211	0.211	0.197	0.183	0.18	0.173	0.229	0.207	0.225	0.185	0.193	0.195	0.186	0.179	0.163
31	0.333	0.434	0.301	0.281	0.207	0.204	0.2	0.185	0.172	0.172	0.164	0.226	0.2	0.216	0.184	0.184	0.19	0.18	0.174	0.16
32	0.365	0.468	0.331	0.307	0.242	0.242	0.237	0.217	0.207	0.206	0.197	0.248	0.234	0.243	0.224	0.225	0.228	0.214	0.214	0.194
33	0.342	0.435	0.305	0.272	0.199	0.201	0.201	0.183	0.173	0.171	0.163	0.221	0.198	0.208	0.18	0.185	0.195	0.181	0.172	0.158
34	0.33	0.437	0.308	0.281	0.206	0.205	0.203	0.198	0.181	0.183	0.174	0.228	0.212	0.225	0.193	0.184	0.191	0.187	0.184	0.168
35	0.338	0.443	0.301	0.281	0.206	0.205	0.199	0.194	0.185	0.181	0.17	0.22	0.2	0.214	0.188	0.187	0.19	0.183	0.175	0.161
36	0.369	0.479	0.343	0.316	0.244	0.239	0.241	0.225	0.221	0.218	0.211	0.266	0.253	0.258	0.234	0.233	0.241	0.221	0.215	0.214
37	0.334	0.438	0.303	0.292	0.209	0.21	0.207	0.191	0.185	0.184	0.173	0.231	0.211	0.228	0.195	0.192	0.21	0.194	0.184	0.186

RAG-1 genetic distances

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
38	0.305	0.416	0.277	0.252	0.179	0.181	0.177	0.168	0.154	0.154	0.141	0.206	0.183	0.198	0.166	0.161	0.17	0.155	0.155	0.139
39	0.414	0.509	0.377	0.359	0.289	0.285	0.28	0.269	0.265	0.262	0.267	0.3	0.295	0.307	0.27	0.264	0.267	0.268	0.266	0.254
40	0.406	0.515	0.387	0.362	0.326	0.32	0.315	0.304	0.293	0.292	0.285	0.329	0.31	0.305	0.29	0.301	0.308	0.302	0.291	0.274
41	0.378	0.501	0.356	0.337	0.271	0.268	0.261	0.25	0.243	0.239	0.234	0.283	0.271	0.284	0.244	0.25	0.256	0.248	0.237	0.228
42	0.414	0.514	0.374	0.364	0.289	0.286	0.28	0.269	0.267	0.266	0.272	0.312	0.299	0.309	0.275	0.268	0.278	0.268	0.27	0.26
43	0.356	0.451	0.321	0.306	0.218	0.22	0.217	0.209	0.197	0.198	0.187	0.225	0.22	0.235	0.191	0.198	0.214	0.212	0.198	0.197
44	0.351	0.477	0.33	0.302	0.227	0.237	0.224	0.229	0.217	0.215	0.205	0.261	0.24	0.245	0.197	0.215	0.231	0.214	0.203	0.212
45	0.347	0.466	0.318	0.292	0.219	0.228	0.218	0.212	0.202	0.198	0.193	0.247	0.234	0.237	0.196	0.21	0.224	0.212	0.2	0.202
46	0.324	0.414	0.288	0.274	0.201	0.202	0.198	0.19	0.18	0.18	0.166	0.219	0.201	0.218	0.178	0.186	0.182	0.176	0.182	0.168
47	0.358	0.475	0.339	0.309	0.225	0.246	0.231	0.23	0.218	0.214	0.208	0.267	0.248	0.252	0.209	0.228	0.235	0.219	0.208	0.213
48	0.402	0.52	0.366	0.356	0.263	0.261	0.259	0.262	0.254	0.247	0.248	0.288	0.274	0.288	0.254	0.264	0.263	0.255	0.243	0.25
49	0.445	0.551	0.403	0.378	0.305	0.312	0.304	0.293	0.298	0.29	0.287	0.338	0.322	0.328	0.3	0.314	0.317	0.308	0.283	0.298
50	0.337	0.415	0.305	0.299	0.26	0.27	0.253	0.24	0.237	0.233	0.227	0.282	0.265	0.274	0.239	0.235	0.233	0.234	0.216	0.21
51	0.368	0.455	0.339	0.328	0.291	0.297	0.285	0.277	0.271	0.262	0.254	0.325	0.299	0.298	0.27	0.276	0.257	0.258	0.247	0.246
52	0.334	0.408	0.303	0.277	0.267	0.274	0.26	0.25	0.243	0.231	0.232	0.295	0.277	0.278	0.249	0.244	0.23	0.234	0.218	0.216
53	0.343	0.427	0.316	0.304	0.272	0.283	0.268	0.259	0.255	0.247	0.242	0.303	0.285	0.289	0.25	0.249	0.236	0.241	0.229	0.225
54	0.349	0.433	0.308	0.295	0.307	0.305	0.306	0.28	0.271	0.265	0.263	0.316	0.296	0.302	0.282	0.268	0.276	0.264	0.252	0.248
55	0.353	0.452	0.321	0.301	0.29	0.295	0.297	0.269	0.263	0.26	0.254	0.31	0.29	0.295	0.277	0.267	0.258	0.258	0.25	0.241
56	0.355	0.443	0.313	0.305	0.281	0.29	0.284	0.265	0.265	0.263	0.255	0.314	0.287	0.289	0.272	0.269	0.26	0.259	0.235	0.242
57	0.37	0.477	0.348	0.316	0.292	0.291	0.284	0.263	0.247	0.246	0.244	0.296	0.268	0.288	0.268	0.255	0.25	0.245	0.236	0.223
58	0.402	0.489	0.362	0.328	0.323	0.318	0.318	0.314	0.296	0.297	0.286	0.321	0.305	0.33	0.305	0.301	0.295	0.291	0.289	0.27
59	0.41	0.494	0.379	0.337	0.336	0.338	0.333	0.332	0.315	0.313	0.303	0.332	0.322	0.345	0.324	0.325	0.307	0.304	0.304	0.283
60	0.349	0.442	0.307	0.276	0.245	0.253	0.246	0.237	0.219	0.222	0.217	0.268	0.232	0.261	0.237	0.225	0.223	0.222	0.215	0.202
61	0.347	0.441	0.309	0.279	0.249	0.256	0.248	0.241	0.221	0.225	0.219	0.269	0.235	0.263	0.237	0.225	0.226	0.222	0.214	0.206
62	0.342	0.431	0.306	0.272	0.241	0.25	0.242	0.235	0.217	0.218	0.213	0.261	0.23	0.255	0.233	0.222	0.217	0.213	0.207	0.195
63	0.362	0.474	0.306	0.304	0.256	0.26	0.253	0.248	0.228	0.225	0.222	0.272	0.247	0.271	0.243	0.244	0.238	0.233	0.232	0.217
64	0.341	0.446	0.305	0.28	0.252	0.256	0.25	0.238	0.222	0.216	0.217	0.264	0.236	0.263	0.241	0.233	0.233	0.228	0.224	0.213
65	0.377	0.467	0.341	0.312	0.275	0.272	0.271	0.267	0.251	0.243	0.243	0.296	0.271	0.296	0.255	0.25	0.261	0.239	0.237	0.231
66	0.34	0.445	0.313	0.285	0.255	0.257	0.252	0.24	0.221	0.221	0.215	0.265	0.235	0.269	0.236	0.234	0.233	0.225	0.223	0.216
67	0.329	0.429	0.283	0.271	0.249	0.249	0.24	0.24	0.222	0.221	0.218	0.264	0.246	0.257	0.239	0.235	0.225	0.22	0.217	0.209
68	0.32	0.415	0.273	0.257	0.237	0.24	0.231	0.219	0.204	0.205	0.204	0.256	0.231	0.25	0.226	0.222	0.207	0.205	0.199	0.19
69	0.309	0.41	0.266	0.252	0.237	0.239	0.23	0.219	0.204	0.203	0.205	0.252	0.229	0.248	0.224	0.22	0.205	0.202	0.199	0.19
70	0.342	0.431	0.291	0.277	0.227	0.237	0.229	0.215	0.203	0.198	0.186	0.248	0.227	0.246	0.218	0.211	0.211	0.207	0.2	0.186
71	0.306	0.395	0.283	0.267	0.238	0.24	0.227	0.223	0.208	0.21	0.213	0.265	0.239	0.255	0.222	0.222	0.203	0.207	0.191	0.18
72	0.331	0.436	0.308	0.28	0.248	0.243	0.235	0.223	0.214	0.212	0.211	0.261	0.24	0.258	0.221	0.223	0.216	0.215	0.202	0.192
73	0.331	0.432	0.304	0.267	0.26	0.264	0.257	0.245	0.232	0.235	0.223	0.276	0.256	0.275	0.237	0.231	0.234	0.231	0.229	0.215

RAG-1 genetic distances

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
1	0.208	0.206	0.209	0.211	0.212	0.209	0.213	0.204	0.207	0.212	0.203	0.217	0.206	0.203	0.207	0.216	0.204	0.193	0.232	0.229
2	0.235	0.239	0.239	0.24	0.244	0.238	0.24	0.236	0.233	0.239	0.238	0.249	0.237	0.239	0.241	0.249	0.236	0.232	0.26	0.265
3	0.201	0.203	0.201	0.205	0.21	0.206	0.203	0.193	0.208	0.197	0.191	0.204	0.192	0.196	0.193	0.207	0.191	0.182	0.221	0.226
4	0.194	0.198	0.196	0.197	0.202	0.202	0.199	0.187	0.193	0.189	0.185	0.197	0.181	0.186	0.186	0.199	0.19	0.173	0.215	0.218
5	0.143	0.153	0.155	0.161	0.16	0.151	0.15	0.15	0.145	0.155	0.15	0.168	0.146	0.151	0.151	0.169	0.152	0.136	0.188	0.205
6	0.146	0.152	0.155	0.162	0.159	0.148	0.147	0.147	0.142	0.154	0.149	0.169	0.147	0.15	0.151	0.167	0.152	0.137	0.187	0.204
7	0.142	0.147	0.151	0.157	0.155	0.145	0.145	0.144	0.142	0.152	0.147	0.166	0.147	0.149	0.147	0.168	0.151	0.134	0.185	0.201
8	0.139	0.145	0.146	0.151	0.152	0.142	0.141	0.14	0.141	0.145	0.138	0.155	0.137	0.146	0.144	0.159	0.142	0.129	0.178	0.196
9	0.134	0.139	0.142	0.145	0.146	0.137	0.136	0.133	0.135	0.137	0.13	0.15	0.131	0.137	0.139	0.157	0.138	0.121	0.176	0.191
10	0.132	0.137	0.139	0.144	0.143	0.136	0.134	0.133	0.131	0.136	0.131	0.15	0.13	0.138	0.137	0.156	0.138	0.121	0.176	0.191
11	0.131	0.138	0.136	0.142	0.139	0.133	0.129	0.132	0.13	0.131	0.126	0.146	0.125	0.133	0.13	0.152	0.131	0.113	0.178	0.188
12	0.159	0.167	0.17	0.165	0.168	0.161	0.16	0.161	0.162	0.162	0.16	0.17	0.158	0.162	0.158	0.18	0.163	0.15	0.193	0.206
13	0.152	0.159	0.162	0.159	0.159	0.155	0.149	0.15	0.149	0.15	0.147	0.164	0.145	0.154	0.147	0.174	0.152	0.138	0.192	0.198
14	0.156	0.16	0.163	0.164	0.167	0.157	0.154	0.156	0.157	0.16	0.155	0.168	0.15	0.161	0.155	0.176	0.161	0.146	0.195	0.196
15	0.135	0.141	0.143	0.146	0.147	0.142	0.139	0.138	0.137	0.138	0.138	0.16	0.135	0.143	0.141	0.165	0.144	0.128	0.179	0.19
16	0.138	0.141	0.144	0.15	0.149	0.141	0.136	0.138	0.142	0.142	0.137	0.159	0.137	0.138	0.139	0.163	0.142	0.125	0.175	0.194
17	0.075	0.087	0.1	0.095	0.098	0.092	0.085	0.082	0.09	0.141	0.139	0.16	0.142	0.14	0.139	0.164	0.149	0.128	0.176	0.195
18	0.077	0.081	0.09	0.093	0.096	0.091	0.075	0.079	0.089	0.138	0.135	0.154	0.135	0.139	0.137	0.155	0.142	0.12	0.179	0.195
19	0.061	0.07	0.082	0.084	0.084	0.078	0.068	0.069	0.077	0.133	0.13	0.153	0.128	0.137	0.132	0.152	0.136	0.12	0.176	0.189
20	0.023	0.068	0.077	0.076	0.078	0.069	0.06	0.059	0.071	0.123	0.122	0.142	0.12	0.127	0.123	0.152	0.137	0.11	0.17	0.181
21		0.066	0.074	0.077	0.077	0.069	0.059	0.06	0.068	0.125	0.123	0.142	0.123	0.128	0.125	0.151	0.136	0.112	0.173	0.183
22	0.074		0.056	0.087	0.088	0.08	0.07	0.071	0.073	0.135	0.131	0.152	0.128	0.13	0.132	0.151	0.135	0.116	0.176	0.187
23	0.085	0.063		0.095	0.09	0.086	0.082	0.081	0.083	0.14	0.137	0.156	0.137	0.14	0.138	0.16	0.144	0.12	0.183	0.191
24	0.09	0.105	0.117		0.073	0.09	0.083	0.076	0.09	0.135	0.135	0.152	0.133	0.141	0.139	0.162	0.148	0.124	0.181	0.197
25	0.09	0.106	0.109	0.085		0.09	0.081	0.076	0.088	0.139	0.14	0.158	0.136	0.14	0.14	0.167	0.147	0.123	0.181	0.193
26	0.08	0.094	0.103	0.11	0.11		0.076	0.073	0.084	0.133	0.128	0.15	0.13	0.134	0.135	0.152	0.138	0.112	0.18	0.193
27	0.066	0.081	0.097	0.1	0.096	0.089		0.063	0.076	0.127	0.123	0.148	0.123	0.13	0.126	0.15	0.134	0.11	0.175	0.186
28	0.067	0.082	0.097	0.09	0.09	0.086	0.072		0.074	0.127	0.123	0.143	0.122	0.127	0.127	0.15	0.134	0.106	0.175	0.184
29	0.078	0.085	0.097	0.109	0.106	0.1	0.089	0.086		0.135	0.134	0.156	0.132	0.138	0.137	0.159	0.138	0.121	0.18	0.186
30	0.165	0.183	0.191	0.184	0.191	0.179	0.169	0.169	0.182		0.032	0.073	0.054	0.075	0.077	0.114	0.096	0.07	0.169	0.18
31	0.161	0.174	0.186	0.184	0.191	0.171	0.163	0.162	0.181	0.034		0.068	0.044	0.067	0.068	0.11	0.088	0.063	0.165	0.173
32	0.194	0.212	0.22	0.215	0.226	0.208	0.207	0.196	0.219	0.084	0.077		0.07	0.095	0.087	0.132	0.113	0.087	0.179	0.186
33	0.161	0.171	0.186	0.181	0.186	0.175	0.164	0.162	0.178	0.06	0.048	0.079		0.068	0.065	0.11	0.089	0.057	0.167	0.174
34	0.169	0.174	0.19	0.195	0.193	0.18	0.174	0.168	0.188	0.087	0.076	0.114	0.078		0.065	0.111	0.091	0.065	0.163	0.171
35	0.162	0.176	0.187	0.191	0.192	0.181	0.166	0.167	0.184	0.089	0.077	0.103	0.074	0.074		0.108	0.087	0.059	0.166	0.172
36	0.212	0.213	0.23	0.237	0.246	0.216	0.211	0.211	0.229	0.144	0.137	0.173	0.138	0.138	0.134		0.057	0.089	0.177	0.197
37	0.183	0.184	0.199	0.209	0.205	0.189	0.182	0.182	0.188	0.116	0.105	0.142	0.106	0.108	0.102	0.064		0.068	0.164	0.181

RAG-1 genetic distances

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
38	0.142	0.149	0.156	0.164	0.162	0.144	0.141	0.135	0.158	0.08	0.07	0.103	0.064	0.073	0.065	0.106	0.078		0.152	0.165
39	0.258	0.267	0.282	0.28	0.279	0.277	0.265	0.265	0.275	0.244	0.236	0.265	0.243	0.234	0.237	0.262	0.234	0.211		0.168
40	0.276	0.286	0.295	0.314	0.302	0.302	0.284	0.281	0.286	0.267	0.253	0.279	0.257	0.25	0.249	0.308	0.269	0.234	0.241	
41	0.233	0.24	0.251	0.251	0.251	0.244	0.239	0.246	0.25	0.218	0.209	0.243	0.213	0.212	0.215	0.243	0.216	0.182	0.092	0.207
42	0.259	0.26	0.276	0.278	0.274	0.282	0.268	0.262	0.273	0.254	0.245	0.284	0.248	0.241	0.24	0.273	0.241	0.217	0.05	0.244
43	0.191	0.201	0.206	0.223	0.226	0.204	0.193	0.196	0.213	0.175	0.171	0.198	0.17	0.177	0.167	0.206	0.174	0.148	0.263	0.277
44	0.208	0.212	0.22	0.225	0.23	0.217	0.209	0.209	0.224	0.185	0.182	0.208	0.176	0.183	0.174	0.213	0.178	0.155	0.264	0.273
45	0.2	0.21	0.219	0.219	0.228	0.21	0.211	0.204	0.216	0.19	0.183	0.209	0.174	0.181	0.176	0.207	0.176	0.156	0.249	0.267
46	0.17	0.184	0.185	0.186	0.189	0.175	0.174	0.165	0.179	0.15	0.146	0.185	0.146	0.149	0.141	0.185	0.157	0.122	0.232	0.243
47	0.206	0.221	0.227	0.236	0.236	0.224	0.225	0.222	0.226	0.196	0.191	0.215	0.183	0.192	0.183	0.213	0.184	0.165	0.258	0.279
48	0.241	0.262	0.265	0.281	0.283	0.255	0.255	0.254	0.249	0.234	0.225	0.256	0.23	0.227	0.222	0.244	0.221	0.202	0.312	0.33
49	0.292	0.293	0.314	0.342	0.341	0.301	0.306	0.314	0.294	0.29	0.288	0.319	0.286	0.296	0.278	0.295	0.274	0.253	0.342	0.384
50	0.21	0.22	0.229	0.233	0.24	0.221	0.22	0.213	0.235	0.215	0.198	0.249	0.196	0.2	0.193	0.247	0.213	0.174	0.291	0.303
51	0.245	0.247	0.256	0.259	0.267	0.254	0.24	0.248	0.25	0.234	0.219	0.282	0.232	0.24	0.223	0.257	0.231	0.203	0.319	0.328
52	0.215	0.217	0.225	0.23	0.242	0.23	0.215	0.219	0.228	0.21	0.2	0.255	0.206	0.209	0.201	0.239	0.211	0.184	0.281	0.293
53	0.226	0.239	0.243	0.239	0.254	0.238	0.234	0.233	0.244	0.213	0.204	0.253	0.21	0.212	0.208	0.24	0.22	0.186	0.294	0.311
54	0.25	0.264	0.272	0.262	0.278	0.266	0.262	0.256	0.267	0.235	0.228	0.27	0.23	0.231	0.231	0.269	0.247	0.21	0.313	0.324
55	0.237	0.255	0.265	0.257	0.275	0.259	0.257	0.248	0.255	0.229	0.225	0.27	0.226	0.227	0.229	0.264	0.235	0.207	0.311	0.322
56	0.242	0.251	0.258	0.258	0.272	0.254	0.248	0.245	0.259	0.235	0.232	0.274	0.233	0.236	0.229	0.261	0.237	0.206	0.306	0.318
57	0.229	0.23	0.236	0.239	0.252	0.246	0.226	0.231	0.245	0.215	0.218	0.256	0.214	0.219	0.208	0.276	0.238	0.197	0.305	0.265
58	0.271	0.274	0.284	0.295	0.305	0.286	0.286	0.269	0.286	0.244	0.239	0.253	0.236	0.238	0.23	0.296	0.248	0.221	0.333	0.213
59	0.284	0.301	0.302	0.303	0.322	0.299	0.294	0.279	0.306	0.254	0.252	0.263	0.252	0.254	0.246	0.301	0.267	0.234	0.346	0.266
60	0.201	0.216	0.221	0.225	0.23	0.212	0.211	0.201	0.214	0.177	0.177	0.223	0.178	0.178	0.174	0.233	0.196	0.158	0.266	0.237
61	0.204	0.218	0.224	0.225	0.233	0.215	0.216	0.206	0.213	0.181	0.18	0.227	0.181	0.18	0.178	0.235	0.196	0.161	0.273	0.236
62	0.194	0.209	0.215	0.216	0.221	0.208	0.205	0.198	0.206	0.175	0.173	0.218	0.174	0.172	0.168	0.23	0.192	0.155	0.264	0.23
63	0.219	0.234	0.241	0.243	0.244	0.239	0.224	0.214	0.235	0.197	0.19	0.237	0.189	0.202	0.188	0.243	0.207	0.172	0.279	0.243
64	0.213	0.222	0.233	0.23	0.236	0.229	0.219	0.21	0.222	0.188	0.182	0.225	0.18	0.193	0.182	0.236	0.199	0.167	0.275	0.242
65	0.23	0.243	0.242	0.255	0.259	0.246	0.237	0.233	0.235	0.22	0.212	0.257	0.209	0.214	0.208	0.258	0.22	0.192	0.298	0.262
66	0.219	0.223	0.23	0.234	0.242	0.236	0.222	0.214	0.222	0.197	0.193	0.236	0.189	0.195	0.185	0.234	0.206	0.171	0.267	0.244
67	0.207	0.219	0.216	0.223	0.229	0.23	0.217	0.204	0.22	0.187	0.185	0.217	0.192	0.191	0.183	0.239	0.206	0.171	0.267	0.197
68	0.191	0.203	0.201	0.203	0.21	0.206	0.198	0.188	0.198	0.172	0.168	0.211	0.174	0.173	0.169	0.219	0.187	0.149	0.252	0.24
69	0.191	0.202	0.198	0.201	0.208	0.205	0.2	0.187	0.201	0.171	0.167	0.21	0.173	0.172	0.168	0.22	0.189	0.15	0.251	0.237
70	0.179	0.203	0.211	0.222	0.227	0.206	0.194	0.19	0.209	0.182	0.171	0.198	0.169	0.174	0.166	0.227	0.192	0.144	0.268	0.27
71	0.184	0.195	0.207	0.211	0.212	0.195	0.192	0.182	0.197	0.183	0.172	0.217	0.173	0.176	0.167	0.217	0.19	0.148	0.264	0.266
72	0.198	0.201	0.209	0.221	0.221	0.209	0.203	0.199	0.21	0.189	0.18	0.227	0.182	0.186	0.175	0.222	0.19	0.161	0.269	0.266
73	0.208	0.221	0.227	0.238	0.251	0.221	0.223	0.217	0.222	0.207	0.196	0.232	0.192	0.197	0.195	0.234	0.196	0.173	0.278	0.301

RAG-1 genetic distances

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
1	0.217	0.23	0.212	0.207	0.208	0.198	0.21	0.227	0.241	0.202	0.215	0.202	0.204	0.208	0.207	0.212	0.215	0.226	0.228	0.209
2	0.257	0.26	0.242	0.25	0.248	0.229	0.249	0.261	0.268	0.228	0.242	0.227	0.232	0.235	0.238	0.239	0.246	0.25	0.252	0.238
3	0.211	0.22	0.201	0.203	0.199	0.186	0.207	0.216	0.228	0.191	0.206	0.191	0.195	0.193	0.197	0.196	0.209	0.214	0.22	0.195
4	0.206	0.216	0.196	0.194	0.191	0.182	0.197	0.216	0.223	0.192	0.204	0.182	0.194	0.19	0.192	0.196	0.199	0.202	0.206	0.183
5	0.18	0.187	0.155	0.159	0.155	0.147	0.156	0.175	0.193	0.175	0.189	0.178	0.179	0.195	0.187	0.183	0.189	0.202	0.207	0.168
6	0.179	0.186	0.156	0.165	0.16	0.147	0.168	0.175	0.197	0.18	0.193	0.183	0.185	0.195	0.189	0.188	0.189	0.2	0.208	0.173
7	0.176	0.183	0.154	0.158	0.155	0.146	0.161	0.174	0.192	0.172	0.187	0.176	0.178	0.195	0.19	0.185	0.185	0.2	0.207	0.169
8	0.17	0.178	0.15	0.16	0.151	0.14	0.159	0.176	0.188	0.166	0.184	0.172	0.175	0.184	0.178	0.178	0.177	0.198	0.206	0.165
9	0.166	0.176	0.144	0.154	0.146	0.135	0.154	0.172	0.19	0.165	0.182	0.169	0.173	0.18	0.175	0.178	0.168	0.19	0.198	0.155
10	0.164	0.176	0.144	0.153	0.144	0.135	0.152	0.169	0.186	0.163	0.178	0.163	0.169	0.177	0.174	0.178	0.168	0.192	0.198	0.157
11	0.162	0.179	0.138	0.148	0.141	0.127	0.149	0.168	0.185	0.159	0.174	0.163	0.166	0.176	0.171	0.173	0.167	0.186	0.194	0.154
12	0.185	0.197	0.158	0.175	0.169	0.156	0.178	0.188	0.206	0.186	0.206	0.193	0.194	0.197	0.197	0.2	0.191	0.2	0.204	0.179
13	0.18	0.191	0.156	0.166	0.163	0.147	0.169	0.182	0.201	0.177	0.194	0.184	0.186	0.189	0.187	0.187	0.178	0.194	0.201	0.162
14	0.185	0.195	0.163	0.168	0.164	0.155	0.171	0.189	0.202	0.181	0.194	0.185	0.187	0.191	0.189	0.188	0.186	0.204	0.209	0.176
15	0.167	0.18	0.141	0.143	0.142	0.133	0.148	0.171	0.191	0.165	0.181	0.17	0.169	0.184	0.181	0.179	0.178	0.193	0.201	0.164
16	0.169	0.176	0.144	0.152	0.15	0.138	0.158	0.177	0.197	0.163	0.183	0.168	0.168	0.176	0.176	0.178	0.171	0.191	0.201	0.157
17	0.171	0.18	0.151	0.159	0.156	0.133	0.161	0.173	0.193	0.159	0.171	0.159	0.159	0.177	0.169	0.171	0.167	0.186	0.191	0.155
18	0.169	0.178	0.151	0.151	0.15	0.131	0.153	0.171	0.193	0.161	0.172	0.161	0.163	0.174	0.171	0.172	0.165	0.187	0.193	0.155
19	0.162	0.177	0.143	0.144	0.144	0.134	0.147	0.166	0.183	0.151	0.167	0.152	0.157	0.168	0.167	0.16	0.161	0.186	0.192	0.151
20	0.158	0.172	0.143	0.15	0.144	0.126	0.15	0.169	0.188	0.148	0.167	0.152	0.155	0.166	0.162	0.164	0.154	0.176	0.182	0.144
21	0.161	0.173	0.139	0.148	0.144	0.127	0.146	0.165	0.187	0.149	0.167	0.152	0.156	0.169	0.161	0.164	0.158	0.177	0.183	0.144
22	0.164	0.172	0.145	0.149	0.149	0.135	0.153	0.174	0.185	0.154	0.167	0.152	0.162	0.174	0.169	0.168	0.157	0.179	0.19	0.152
23	0.169	0.18	0.147	0.154	0.154	0.136	0.157	0.176	0.195	0.157	0.171	0.156	0.163	0.177	0.173	0.17	0.161	0.183	0.191	0.154
24	0.168	0.179	0.155	0.156	0.153	0.135	0.16	0.182	0.205	0.159	0.172	0.159	0.161	0.171	0.169	0.17	0.161	0.186	0.189	0.155
25	0.168	0.177	0.157	0.158	0.157	0.137	0.16	0.183	0.205	0.163	0.176	0.164	0.168	0.179	0.177	0.177	0.168	0.191	0.197	0.159
26	0.165	0.182	0.145	0.151	0.148	0.13	0.154	0.17	0.188	0.153	0.169	0.158	0.161	0.174	0.17	0.169	0.165	0.183	0.189	0.149
27	0.163	0.175	0.139	0.147	0.149	0.128	0.155	0.171	0.191	0.153	0.164	0.151	0.159	0.172	0.169	0.166	0.155	0.183	0.186	0.149
28	0.166	0.173	0.142	0.147	0.145	0.124	0.154	0.169	0.194	0.15	0.167	0.154	0.159	0.169	0.166	0.165	0.158	0.176	0.18	0.144
29	0.169	0.178	0.151	0.156	0.152	0.132	0.156	0.169	0.187	0.161	0.169	0.158	0.165	0.176	0.17	0.172	0.165	0.184	0.193	0.151
30	0.155	0.173	0.13	0.137	0.14	0.117	0.143	0.162	0.188	0.152	0.163	0.15	0.15	0.162	0.158	0.163	0.151	0.167	0.17	0.132
31	0.15	0.169	0.129	0.136	0.136	0.114	0.141	0.158	0.187	0.143	0.155	0.145	0.145	0.159	0.156	0.161	0.153	0.164	0.169	0.131
32	0.168	0.187	0.144	0.151	0.151	0.138	0.154	0.174	0.2	0.169	0.186	0.173	0.171	0.18	0.178	0.182	0.171	0.171	0.173	0.157
33	0.152	0.169	0.128	0.132	0.131	0.114	0.136	0.16	0.186	0.142	0.162	0.149	0.149	0.159	0.157	0.161	0.151	0.161	0.169	0.132
34	0.152	0.166	0.133	0.137	0.136	0.117	0.142	0.16	0.191	0.146	0.167	0.15	0.151	0.16	0.157	0.163	0.154	0.165	0.171	0.133
35	0.155	0.167	0.127	0.132	0.133	0.112	0.137	0.158	0.184	0.142	0.159	0.147	0.149	0.16	0.159	0.16	0.149	0.16	0.166	0.131
36	0.168	0.181	0.149	0.152	0.148	0.137	0.151	0.167	0.189	0.168	0.174	0.165	0.163	0.178	0.175	0.175	0.182	0.191	0.192	0.162
37	0.155	0.166	0.132	0.133	0.132	0.121	0.137	0.156	0.18	0.152	0.161	0.151	0.154	0.168	0.161	0.164	0.165	0.169	0.178	0.144

RAG-1 genetic distances

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
38	0.136	0.155	0.116	0.12	0.121	0.099	0.126	0.147	0.171	0.131	0.147	0.137	0.137	0.15	0.148	0.148	0.143	0.155	0.162	0.122
39	0.078	0.045	0.176	0.176	0.169	0.162	0.174	0.197	0.207	0.188	0.201	0.184	0.189	0.197	0.195	0.196	0.193	0.205	0.21	0.178
40	0.15	0.169	0.184	0.18	0.179	0.167	0.183	0.207	0.225	0.194	0.206	0.19	0.196	0.202	0.201	0.2	0.177	0.15	0.176	0.164
41		0.083	0.164	0.165	0.163	0.149	0.162	0.188	0.197	0.173	0.186	0.177	0.175	0.187	0.184	0.186	0.189	0.196	0.203	0.169
42	0.099		0.18	0.178	0.172	0.16	0.173	0.199	0.213	0.185	0.199	0.186	0.186	0.195	0.191	0.194	0.197	0.206	0.21	0.177
43	0.241	0.273		0.119	0.117	0.098	0.124	0.159	0.182	0.159	0.174	0.163	0.165	0.173	0.171	0.175	0.16	0.17	0.176	0.144
44	0.243	0.27	0.155		0.052	0.099	0.058	0.161	0.178	0.158	0.173	0.16	0.162	0.173	0.172	0.169	0.163	0.178	0.186	0.146
45	0.239	0.258	0.151	0.058		0.096	0.039	0.157	0.179	0.154	0.163	0.159	0.159	0.171	0.171	0.17	0.164	0.178	0.186	0.146
46	0.208	0.232	0.12	0.122	0.117		0.099	0.146	0.168	0.138	0.151	0.143	0.14	0.156	0.154	0.152	0.145	0.164	0.171	0.129
47	0.238	0.261	0.165	0.066	0.042	0.122		0.158	0.179	0.158	0.169	0.165	0.164	0.175	0.172	0.173	0.167	0.18	0.189	0.152
48	0.29	0.317	0.226	0.23	0.222	0.2	0.227		0.112	0.177	0.185	0.172	0.175	0.189	0.188	0.19	0.181	0.198	0.207	0.168
49	0.314	0.358	0.277	0.271	0.274	0.246	0.276	0.141		0.194	0.201	0.193	0.192	0.207	0.207	0.203	0.197	0.211	0.223	0.187
50	0.259	0.284	0.228	0.228	0.219	0.187	0.228	0.265	0.307		0.089	0.065	0.068	0.096	0.089	0.09	0.166	0.184	0.188	0.147
51	0.287	0.317	0.259	0.259	0.238	0.213	0.252	0.285	0.325	0.109		0.07	0.083	0.11	0.106	0.105	0.172	0.191	0.197	0.16
52	0.266	0.287	0.235	0.231	0.229	0.197	0.241	0.254	0.306	0.075	0.08		0.059	0.096	0.091	0.09	0.165	0.184	0.188	0.148
53	0.263	0.291	0.243	0.239	0.232	0.194	0.242	0.262	0.307	0.079	0.1	0.067		0.101	0.098	0.095	0.171	0.185	0.189	0.155
54	0.29	0.308	0.259	0.259	0.255	0.222	0.264	0.293	0.34	0.119	0.141	0.118	0.126		0.061	0.068	0.176	0.19	0.187	0.163
55	0.287	0.303	0.257	0.26	0.256	0.22	0.261	0.289	0.341	0.11	0.135	0.112	0.123	0.069		0.066	0.176	0.196	0.195	0.163
56	0.285	0.302	0.263	0.252	0.251	0.214	0.259	0.292	0.328	0.109	0.132	0.108	0.117	0.078	0.075		0.172	0.191	0.197	0.161
57	0.296	0.315	0.229	0.236	0.238	0.201	0.244	0.275	0.316	0.245	0.258	0.241	0.257	0.268	0.267	0.256		0.119	0.126	0.085
58	0.313	0.336	0.25	0.27	0.269	0.237	0.276	0.313	0.349	0.286	0.299	0.282	0.29	0.302	0.312	0.3	0.154		0.07	0.107
59	0.329	0.349	0.264	0.288	0.288	0.254	0.296	0.338	0.383	0.296	0.315	0.296	0.303	0.298	0.313	0.317	0.167	0.081		0.112
60	0.251	0.266	0.2	0.202	0.202	0.171	0.214	0.244	0.288	0.206	0.231	0.205	0.221	0.237	0.237	0.229	0.101	0.134	0.144	
61	0.257	0.269	0.198	0.202	0.204	0.167	0.214	0.244	0.29	0.208	0.233	0.203	0.219	0.237	0.24	0.229	0.102	0.135	0.146	0.017
62	0.246	0.263	0.191	0.196	0.195	0.162	0.207	0.235	0.282	0.2	0.228	0.199	0.215	0.233	0.233	0.221	0.097	0.13	0.137	0.012
63	0.258	0.288	0.21	0.214	0.209	0.175	0.223	0.262	0.306	0.22	0.241	0.222	0.24	0.247	0.257	0.245	0.117	0.158	0.162	0.074
64	0.248	0.278	0.205	0.211	0.204	0.173	0.219	0.25	0.296	0.205	0.221	0.203	0.222	0.235	0.237	0.228	0.108	0.151	0.154	0.066
65	0.279	0.305	0.234	0.23	0.228	0.203	0.233	0.26	0.311	0.234	0.257	0.23	0.255	0.261	0.264	0.251	0.127	0.17	0.178	0.097
66	0.245	0.266	0.201	0.207	0.207	0.17	0.213	0.25	0.291	0.212	0.235	0.212	0.229	0.251	0.255	0.246	0.118	0.148	0.163	0.076
67	0.251	0.266	0.189	0.21	0.202	0.17	0.218	0.244	0.285	0.213	0.227	0.208	0.229	0.239	0.237	0.231	0.129	0.122	0.146	0.097
68	0.235	0.252	0.184	0.198	0.189	0.155	0.206	0.223	0.27	0.196	0.204	0.189	0.204	0.226	0.223	0.215	0.122	0.156	0.156	0.084
69	0.233	0.253	0.184	0.196	0.188	0.155	0.205	0.222	0.265	0.193	0.204	0.186	0.2	0.222	0.22	0.213	0.122	0.158	0.159	0.086
70	0.241	0.269	0.188	0.197	0.191	0.158	0.202	0.239	0.281	0.194	0.233	0.19	0.202	0.23	0.228	0.229	0.194	0.23	0.234	0.166
71	0.234	0.265	0.192	0.204	0.188	0.157	0.204	0.228	0.282	0.187	0.209	0.189	0.199	0.222	0.212	0.208	0.182	0.227	0.238	0.144
72	0.239	0.265	0.198	0.21	0.203	0.164	0.224	0.25	0.293	0.203	0.233	0.203	0.213	0.243	0.232	0.227	0.186	0.225	0.237	0.154
73	0.251	0.281	0.207	0.209	0.203	0.175	0.214	0.261	0.301	0.196	0.237	0.206	0.215	0.24	0.231	0.231	0.211	0.259	0.268	0.18

RAG-1 genetic distances

	61	62	63	64	65	66	67	68	69	70	71	72	73
1	0.208	0.206	0.213	0.206	0.218	0.205	0.202	0.199	0.194	0.207	0.191	0.202	0.202
2	0.237	0.234	0.249	0.241	0.244	0.24	0.235	0.231	0.229	0.234	0.221	0.235	0.235
3	0.196	0.195	0.194	0.194	0.207	0.197	0.185	0.181	0.177	0.187	0.185	0.196	0.192
4	0.184	0.181	0.195	0.185	0.197	0.185	0.18	0.175	0.172	0.184	0.179	0.185	0.178
5	0.17	0.166	0.174	0.172	0.18	0.173	0.171	0.166	0.166	0.159	0.166	0.17	0.176
6	0.173	0.171	0.176	0.175	0.179	0.175	0.173	0.168	0.168	0.165	0.167	0.167	0.177
7	0.169	0.167	0.172	0.171	0.178	0.172	0.167	0.163	0.163	0.161	0.161	0.163	0.174
8	0.166	0.164	0.17	0.166	0.178	0.165	0.167	0.157	0.157	0.154	0.159	0.159	0.168
9	0.156	0.154	0.16	0.157	0.17	0.155	0.157	0.148	0.148	0.147	0.151	0.154	0.162
10	0.158	0.155	0.158	0.154	0.166	0.156	0.157	0.149	0.148	0.145	0.152	0.153	0.163
11	0.155	0.152	0.157	0.155	0.166	0.153	0.156	0.149	0.149	0.138	0.154	0.151	0.156
12	0.179	0.176	0.181	0.178	0.19	0.177	0.178	0.175	0.173	0.169	0.18	0.177	0.183
13	0.162	0.161	0.17	0.164	0.179	0.163	0.17	0.163	0.162	0.159	0.166	0.166	0.173
14	0.176	0.173	0.181	0.177	0.19	0.179	0.175	0.173	0.172	0.169	0.175	0.175	0.182
15	0.163	0.162	0.167	0.166	0.171	0.163	0.166	0.16	0.159	0.155	0.157	0.156	0.164
16	0.157	0.156	0.167	0.161	0.168	0.161	0.163	0.157	0.156	0.15	0.157	0.156	0.16
17	0.156	0.152	0.162	0.16	0.172	0.159	0.156	0.147	0.146	0.149	0.144	0.151	0.16
18	0.155	0.15	0.161	0.159	0.163	0.157	0.155	0.148	0.146	0.148	0.149	0.152	0.161
19	0.151	0.147	0.161	0.157	0.161	0.156	0.154	0.144	0.144	0.144	0.139	0.144	0.159
20	0.146	0.141	0.152	0.151	0.158	0.152	0.149	0.139	0.139	0.136	0.133	0.139	0.152
21	0.146	0.14	0.154	0.151	0.158	0.154	0.148	0.14	0.14	0.133	0.136	0.143	0.148
22	0.153	0.148	0.161	0.156	0.164	0.156	0.154	0.146	0.146	0.146	0.142	0.143	0.156
23	0.155	0.151	0.165	0.161	0.164	0.159	0.153	0.145	0.143	0.151	0.148	0.147	0.157
24	0.155	0.151	0.165	0.158	0.169	0.16	0.154	0.145	0.143	0.155	0.149	0.154	0.162
25	0.16	0.154	0.166	0.162	0.171	0.164	0.159	0.149	0.148	0.158	0.15	0.154	0.169
26	0.151	0.147	0.164	0.159	0.166	0.162	0.159	0.147	0.146	0.147	0.141	0.148	0.153
27	0.151	0.146	0.156	0.154	0.161	0.155	0.153	0.143	0.144	0.14	0.139	0.144	0.155
28	0.147	0.142	0.151	0.149	0.159	0.151	0.146	0.138	0.137	0.138	0.133	0.142	0.152
29	0.151	0.147	0.162	0.155	0.161	0.155	0.155	0.144	0.145	0.149	0.143	0.148	0.155
30	0.133	0.131	0.143	0.139	0.154	0.143	0.139	0.131	0.13	0.135	0.136	0.139	0.149
31	0.133	0.13	0.139	0.135	0.15	0.141	0.137	0.128	0.127	0.129	0.13	0.134	0.142
32	0.159	0.155	0.164	0.159	0.172	0.164	0.156	0.152	0.152	0.144	0.156	0.16	0.163
33	0.133	0.13	0.139	0.135	0.148	0.139	0.141	0.132	0.131	0.127	0.13	0.135	0.14
34	0.134	0.13	0.146	0.143	0.152	0.143	0.141	0.131	0.131	0.131	0.133	0.138	0.144
35	0.133	0.128	0.139	0.136	0.15	0.137	0.137	0.129	0.129	0.126	0.128	0.132	0.143
36	0.162	0.161	0.167	0.164	0.173	0.163	0.166	0.157	0.157	0.159	0.155	0.156	0.162
37	0.143	0.141	0.15	0.146	0.155	0.149	0.15	0.14	0.142	0.142	0.14	0.14	0.142

RAG-1 genetic distances

	61	62	63	64	65	66	67	68	69	70	71	72	73
38	0.123	0.12	0.13	0.128	0.14	0.13	0.131	0.117	0.118	0.113	0.117	0.124	0.13
39	0.181	0.177	0.184	0.182	0.192	0.177	0.179	0.172	0.172	0.179	0.177	0.178	0.183
40	0.164	0.161	0.168	0.167	0.176	0.167	0.145	0.168	0.166	0.18	0.18	0.179	0.194
41	0.172	0.167	0.174	0.169	0.182	0.167	0.171	0.163	0.163	0.165	0.162	0.164	0.169
42	0.178	0.176	0.187	0.182	0.193	0.176	0.178	0.171	0.172	0.178	0.176	0.176	0.184
43	0.143	0.139	0.15	0.147	0.161	0.144	0.14	0.137	0.137	0.139	0.14	0.143	0.148
44	0.145	0.143	0.152	0.151	0.159	0.148	0.151	0.145	0.143	0.143	0.147	0.15	0.149
45	0.147	0.143	0.15	0.147	0.159	0.148	0.147	0.14	0.139	0.14	0.139	0.146	0.146
46	0.126	0.124	0.131	0.131	0.147	0.129	0.129	0.12	0.121	0.122	0.121	0.125	0.131
47	0.152	0.149	0.156	0.155	0.161	0.151	0.155	0.149	0.148	0.146	0.147	0.157	0.151
48	0.168	0.165	0.176	0.171	0.176	0.171	0.169	0.158	0.157	0.165	0.16	0.171	0.175
49	0.188	0.185	0.194	0.191	0.196	0.188	0.186	0.18	0.177	0.184	0.185	0.189	0.192
50	0.148	0.145	0.155	0.147	0.16	0.15	0.151	0.143	0.141	0.142	0.137	0.146	0.142
51	0.162	0.159	0.165	0.155	0.171	0.162	0.159	0.147	0.147	0.162	0.15	0.162	0.164
52	0.147	0.145	0.157	0.147	0.159	0.151	0.15	0.14	0.138	0.14	0.14	0.147	0.148
53	0.153	0.152	0.164	0.156	0.17	0.158	0.159	0.147	0.144	0.146	0.144	0.151	0.152
54	0.163	0.162	0.169	0.163	0.173	0.17	0.165	0.159	0.156	0.16	0.156	0.166	0.165
55	0.165	0.162	0.172	0.163	0.175	0.172	0.164	0.157	0.155	0.158	0.151	0.16	0.159
56	0.16	0.157	0.169	0.16	0.17	0.169	0.162	0.154	0.153	0.161	0.15	0.159	0.161
57	0.086	0.082	0.095	0.09	0.101	0.096	0.103	0.099	0.099	0.142	0.135	0.137	0.15
58	0.107	0.104	0.122	0.118	0.129	0.115	0.1	0.121	0.122	0.16	0.159	0.158	0.174
59	0.113	0.107	0.123	0.119	0.132	0.124	0.114	0.12	0.121	0.161	0.164	0.163	0.177
60	0.016	0.011	0.065	0.059	0.082	0.066	0.082	0.073	0.074	0.126	0.113	0.12	0.134
61		0.013	0.065	0.059	0.084	0.066	0.083	0.075	0.076	0.128	0.114	0.12	0.136
62	0.013		0.063	0.056	0.081	0.064	0.079	0.071	0.072	0.124	0.111	0.117	0.131
63	0.074	0.071		0.034	0.07	0.063	0.088	0.082	0.082	0.131	0.123	0.125	0.146
64	0.066	0.062	0.036		0.064	0.056	0.086	0.077	0.077	0.124	0.118	0.12	0.137
65	0.099	0.095	0.082	0.074		0.075	0.101	0.095	0.096	0.139	0.129	0.134	0.149
66	0.076	0.073	0.071	0.062	0.088		0.088	0.081	0.081	0.132	0.121	0.125	0.147
67	0.098	0.092	0.104	0.102	0.124	0.105		0.03	0.029	0.128	0.117	0.119	0.139
68	0.087	0.081	0.096	0.089	0.115	0.095	0.032		0.008	0.117	0.104	0.108	0.129
69	0.088	0.082	0.096	0.09	0.117	0.096	0.031	0.008		0.118	0.105	0.108	0.128
70	0.17	0.162	0.174	0.161	0.19	0.177	0.168	0.15	0.15		0.112	0.115	0.138
71	0.146	0.14	0.161	0.151	0.171	0.157	0.15	0.129	0.131	0.142		0.054	0.133
72	0.155	0.15	0.164	0.155	0.18	0.164	0.154	0.136	0.136	0.147	0.061		0.136
73	0.183	0.174	0.2	0.183	0.209	0.203	0.188	0.169	0.169	0.186	0.178	0.184	

c-mos genetic distances

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1		0.215	0.198	0.216	0.299	0.316	0.299	0.282	0.302	0.293	0.302	0.316	0.341	0.288	0.288	0.288	0.28
2	0.317		0.226	0.232	0.309	0.326	0.307	0.281	0.301	0.295	0.34	0.334	0.348	0.309	0.306	0.298	0.318
3	0.285	0.357		0.206	0.277	0.297	0.28	0.26	0.263	0.272	0.317	0.317	0.332	0.298	0.289	0.286	0.289
4	0.32	0.369	0.314		0.251	0.274	0.254	0.232	0.249	0.246	0.265	0.279	0.304	0.248	0.248	0.245	0.251
5	0.545	0.608	0.519	0.415		0.123	0.1	0.075	0.075	0.061	0.15	0.159	0.175	0.148	0.15	0.139	0.134
6	0.62	0.681	0.595	0.481	0.151		0.058	0.084	0.097	0.095	0.173	0.167	0.189	0.164	0.167	0.162	0.15
7	0.56	0.601	0.542	0.424	0.118	0.064		0.058	0.084	0.067	0.156	0.15	0.176	0.145	0.15	0.142	0.134
8	0.494	0.523	0.465	0.361	0.084	0.097	0.065		0.056	0.042	0.134	0.125	0.159	0.125	0.128	0.117	0.111
9	0.561	0.596	0.491	0.408	0.085	0.116	0.096	0.061		0.036	0.136	0.131	0.156	0.136	0.134	0.123	0.125
10	0.535	0.575	0.508	0.398	0.067	0.112	0.075	0.045	0.039		0.139	0.134	0.159	0.128	0.131	0.12	0.117
11	0.563	0.708	0.639	0.447	0.196	0.241	0.207	0.17	0.177	0.18		0.092	0.139	0.092	0.089	0.086	0.084
12	0.604	0.683	0.66	0.482	0.215	0.235	0.202	0.16	0.171	0.174	0.109		0.123	0.081	0.089	0.078	0.089
13	0.704	0.745	0.693	0.545	0.242	0.273	0.242	0.211	0.209	0.212	0.181	0.158		0.123	0.123	0.117	0.145
14	0.517	0.607	0.583	0.402	0.191	0.223	0.187	0.156	0.174	0.161	0.107	0.094	0.152		0.025	0.022	0.067
15	0.508	0.589	0.538	0.396	0.194	0.225	0.194	0.158	0.168	0.163	0.102	0.103	0.152	0.026		0.025	0.075
16	0.504	0.561	0.536	0.387	0.176	0.215	0.18	0.142	0.151	0.146	0.098	0.089	0.143	0.023	0.026		0.061
17	0.506	0.644	0.56	0.408	0.17	0.198	0.17	0.136	0.158	0.145	0.097	0.105	0.189	0.075	0.085	0.067	
18	0.545	0.578	0.585	0.416	0.214	0.262	0.214	0.177	0.19	0.186	0.154	0.131	0.196	0.103	0.113	0.095	0.11
19	0.519	0.644	0.543	0.461	0.197	0.217	0.191	0.165	0.197	0.178	0.198	0.19	0.28	0.191	0.193	0.175	0.188
20	0.548	0.683	0.5	0.441	0.202	0.211	0.187	0.165	0.193	0.183	0.226	0.198	0.288	0.218	0.22	0.188	0.207
21	0.458	0.602	0.499	0.456	0.206	0.208	0.183	0.165	0.197	0.174	0.193	0.212	0.261	0.204	0.193	0.187	0.188
22	0.517	0.675	0.534	0.433	0.189	0.181	0.167	0.143	0.168	0.155	0.177	0.186	0.231	0.166	0.173	0.156	0.16
23	0.574	0.745	0.585	0.475	0.212	0.219	0.189	0.159	0.161	0.156	0.213	0.196	0.286	0.215	0.212	0.194	0.215
24	0.518	0.602	0.526	0.406	0.172	0.196	0.145	0.133	0.146	0.134	0.277	0.254	0.261	0.239	0.229	0.232	0.237
25	0.576	0.649	0.537	0.454	0.193	0.249	0.168	0.159	0.161	0.155	0.262	0.284	0.277	0.282	0.277	0.275	0.245
26	0.527	0.63	0.517	0.432	0.192	0.238	0.183	0.157	0.159	0.153	0.248	0.251	0.29	0.241	0.246	0.23	0.23
27	0.528	0.653	0.552	0.455	0.207	0.254	0.198	0.179	0.181	0.172	0.271	0.296	0.286	0.253	0.253	0.256	0.277
28	0.448	0.674	0.531	0.439	0.237	0.274	0.22	0.188	0.218	0.198	0.289	0.276	0.305	0.275	0.296	0.274	0.272
29	0.464	0.646	0.558	0.473	0.213	0.27	0.212	0.193	0.216	0.192	0.284	0.298	0.373	0.272	0.274	0.262	0.286
30	0.418	0.615	0.507	0.422	0.205	0.252	0.212	0.19	0.212	0.184	0.283	0.309	0.362	0.277	0.268	0.267	0.269
31	0.461	0.634	0.517	0.433	0.211	0.278	0.219	0.18	0.189	0.175	0.252	0.248	0.313	0.229	0.236	0.208	0.228
32	0.475	0.664	0.545	0.429	0.22	0.271	0.232	0.204	0.223	0.208	0.278	0.275	0.35	0.24	0.247	0.226	0.24
33	0.509	0.682	0.584	0.427	0.202	0.278	0.22	0.189	0.198	0.175	0.26	0.266	0.351	0.237	0.244	0.224	0.235
34	0.617	0.731	0.663	0.451	0.202	0.263	0.229	0.218	0.218	0.212	0.284	0.28	0.322	0.27	0.265	0.258	0.264

c-mos genetic distances

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
35	0.625	0.732	0.671	0.457	0.202	0.268	0.224	0.209	0.218	0.203	0.279	0.265	0.333	0.255	0.25	0.244	0.249
36	0.525	0.626	0.576	0.42	0.187	0.23	0.194	0.177	0.2	0.186	0.244	0.236	0.28	0.207	0.203	0.206	0.221
37	0.578	0.738	0.645	0.448	0.22	0.291	0.256	0.212	0.229	0.214	0.29	0.297	0.331	0.263	0.243	0.252	0.26
38	0.562	0.589	0.572	0.432	0.228	0.24	0.199	0.189	0.2	0.194	0.287	0.287	0.324	0.267	0.274	0.248	0.256
39	0.553	0.541	0.528	0.411	0.19	0.226	0.179	0.155	0.169	0.16	0.253	0.263	0.307	0.25	0.251	0.227	0.234
40	0.526	0.593	0.55	0.405	0.19	0.226	0.174	0.155	0.173	0.164	0.239	0.238	0.293	0.236	0.237	0.213	0.211
41	0.548	0.58	0.56	0.4	0.204	0.246	0.196	0.168	0.178	0.173	0.259	0.274	0.313	0.265	0.266	0.241	0.259
42	0.566	0.593	0.587	0.427	0.222	0.266	0.201	0.189	0.2	0.19	0.265	0.29	0.31	0.256	0.258	0.242	0.25
43	0.537	0.566	0.585	0.426	0.241	0.287	0.243	0.22	0.236	0.212	0.324	0.336	0.402	0.282	0.273	0.267	0.291
44	0.459	0.539	0.54	0.373	0.196	0.259	0.205	0.181	0.187	0.182	0.244	0.267	0.321	0.268	0.256	0.25	0.262
45	0.559	0.656	0.635	0.403	0.283	0.356	0.278	0.266	0.296	0.283	0.313	0.304	0.436	0.357	0.34	0.338	0.357
46	0.686	0.803	0.861	0.562	0.322	0.428	0.335	0.315	0.349	0.328	0.386	0.395	0.499	0.391	0.416	0.388	0.404
47	0.572	0.614	0.482	0.428	0.259	0.287	0.24	0.212	0.224	0.218	0.322	0.318	0.356	0.31	0.312	0.288	0.327

c-mos genetic distances

	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
1	0.293	0.29	0.3	0.268	0.288	0.305	0.289	0.31	0.3	0.295	0.26	0.263	0.25	0.271	0.274	0.288	0.316
2	0.301	0.32	0.33	0.309	0.329	0.34	0.302	0.323	0.317	0.323	0.313	0.309	0.305	0.309	0.315	0.326	0.345
3	0.292	0.28	0.269	0.277	0.283	0.292	0.286	0.292	0.287	0.3	0.284	0.289	0.278	0.281	0.283	0.298	0.323
4	0.254	0.274	0.262	0.268	0.259	0.276	0.249	0.276	0.266	0.274	0.257	0.271	0.252	0.26	0.251	0.257	0.265
5	0.162	0.15	0.154	0.156	0.148	0.162	0.134	0.15	0.15	0.158	0.17	0.159	0.156	0.159	0.164	0.153	0.153
6	0.187	0.162	0.159	0.156	0.142	0.164	0.145	0.178	0.173	0.182	0.187	0.187	0.179	0.192	0.187	0.192	0.187
7	0.162	0.148	0.145	0.142	0.134	0.148	0.114	0.131	0.141	0.15	0.159	0.156	0.156	0.162	0.167	0.162	0.17
8	0.139	0.131	0.131	0.131	0.117	0.128	0.108	0.128	0.127	0.141	0.142	0.145	0.144	0.139	0.153	0.145	0.162
9	0.148	0.15	0.148	0.15	0.134	0.128	0.117	0.128	0.127	0.141	0.159	0.159	0.159	0.145	0.164	0.15	0.162
10	0.145	0.139	0.142	0.136	0.125	0.125	0.108	0.125	0.124	0.135	0.148	0.145	0.142	0.136	0.156	0.136	0.159
11	0.125	0.148	0.165	0.145	0.136	0.159	0.189	0.181	0.176	0.187	0.193	0.198	0.196	0.181	0.192	0.184	0.198
12	0.109	0.142	0.148	0.156	0.142	0.148	0.175	0.191	0.176	0.199	0.187	0.198	0.204	0.178	0.189	0.187	0.195
13	0.15	0.192	0.196	0.184	0.167	0.198	0.182	0.192	0.199	0.197	0.201	0.231	0.229	0.209	0.22	0.226	0.212
14	0.089	0.145	0.162	0.153	0.131	0.162	0.172	0.198	0.176	0.182	0.19	0.189	0.193	0.17	0.173	0.173	0.192
15	0.097	0.148	0.165	0.148	0.136	0.162	0.166	0.194	0.179	0.182	0.201	0.192	0.19	0.175	0.178	0.178	0.189
16	0.084	0.136	0.145	0.145	0.125	0.15	0.169	0.195	0.17	0.185	0.19	0.187	0.19	0.159	0.167	0.167	0.187
17	0.095	0.142	0.154	0.142	0.125	0.162	0.17	0.176	0.168	0.194	0.184	0.195	0.187	0.167	0.173	0.17	0.187
18		0.173	0.188	0.187	0.173	0.195	0.185	0.205	0.186	0.2	0.198	0.206	0.209	0.184	0.187	0.184	0.209
19	0.239		0.068	0.075	0.078	0.1	0.189	0.2	0.176	0.193	0.17	0.178	0.164	0.15	0.159	0.162	0.198
20	0.266	0.078		0.08	0.085	0.105	0.193	0.212	0.192	0.21	0.188	0.182	0.168	0.179	0.182	0.188	0.211
21	0.263	0.086	0.092		0.075	0.117	0.172	0.175	0.174	0.179	0.19	0.181	0.162	0.178	0.187	0.184	0.206
22	0.235	0.089	0.098	0.085		0.117	0.178	0.197	0.185	0.202	0.173	0.187	0.173	0.162	0.17	0.162	0.187
23	0.275	0.12	0.128	0.144	0.142		0.178	0.194	0.197	0.209	0.176	0.17	0.164	0.153	0.159	0.153	0.209
24	0.264	0.275	0.281	0.24	0.245	0.25		0.112	0.12	0.117	0.173	0.167	0.166	0.175	0.163	0.187	0.171
25	0.3	0.292	0.312	0.24	0.28	0.272	0.136		0.066	0.058	0.183	0.18	0.19	0.195	0.191	0.198	0.194
26	0.264	0.246	0.273	0.235	0.256	0.278	0.148	0.074		0.065	0.177	0.18	0.18	0.179	0.176	0.185	0.185
27	0.289	0.279	0.307	0.246	0.289	0.301	0.144	0.063	0.071		0.2	0.189	0.189	0.203	0.188	0.202	0.194
28	0.296	0.236	0.265	0.273	0.239	0.245	0.246	0.258	0.245	0.293		0.109	0.116	0.106	0.123	0.115	0.207
29	0.308	0.25	0.254	0.259	0.263	0.233	0.233	0.25	0.251	0.268	0.137		0.045	0.097	0.114	0.106	0.206
30	0.31	0.223	0.226	0.221	0.236	0.223	0.229	0.265	0.247	0.264	0.146	0.049		0.105	0.125	0.099	0.198
31	0.257	0.199	0.247	0.248	0.216	0.199	0.244	0.275	0.243	0.289	0.128	0.116	0.125		0.072	0.064	0.187
32	0.269	0.218	0.258	0.269	0.235	0.21	0.224	0.269	0.238	0.263	0.155	0.141	0.156	0.081		0.097	0.192
33	0.257	0.22	0.265	0.261	0.219	0.201	0.271	0.284	0.26	0.297	0.141	0.128	0.119	0.071	0.115		0.192
34	0.301	0.289	0.309	0.304	0.263	0.31	0.239	0.283	0.262	0.279	0.323	0.31	0.29	0.27	0.284	0.284	

c-mos genetic distances

	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
35	0.286	0.289	0.291	0.304	0.264	0.304	0.251	0.291	0.264	0.281	0.308	0.31	0.285	0.28	0.284	0.284	0.041
36	0.246	0.241	0.253	0.245	0.227	0.264	0.214	0.243	0.246	0.238	0.274	0.271	0.247	0.264	0.258	0.268	0.068
37	0.292	0.278	0.301	0.288	0.267	0.278	0.218	0.288	0.271	0.278	0.29	0.282	0.258	0.269	0.273	0.28	0.15
38	0.272	0.271	0.273	0.269	0.24	0.279	0.242	0.25	0.234	0.277	0.274	0.236	0.242	0.244	0.297	0.286	0.309
39	0.254	0.243	0.235	0.232	0.237	0.256	0.202	0.177	0.2	0.211	0.225	0.181	0.192	0.219	0.248	0.236	0.289
40	0.239	0.225	0.231	0.237	0.215	0.229	0.216	0.219	0.224	0.255	0.226	0.175	0.184	0.197	0.234	0.224	0.274
41	0.279	0.246	0.255	0.242	0.22	0.252	0.228	0.223	0.218	0.244	0.229	0.22	0.216	0.215	0.268	0.254	0.259
42	0.251	0.264	0.271	0.258	0.253	0.274	0.233	0.231	0.225	0.243	0.242	0.211	0.213	0.216	0.255	0.245	0.312
43	0.309	0.255	0.281	0.246	0.254	0.264	0.278	0.298	0.27	0.292	0.294	0.296	0.273	0.244	0.286	0.266	0.332
44	0.278	0.217	0.258	0.251	0.242	0.246	0.195	0.231	0.225	0.231	0.258	0.275	0.247	0.254	0.285	0.265	0.258
45	0.375	0.353	0.336	0.382	0.346	0.325	0.275	0.307	0.315	0.34	0.31	0.327	0.311	0.302	0.293	0.339	0.396
46	0.445	0.44	0.401	0.475	0.442	0.323	0.347	0.403	0.439	0.443	0.335	0.372	0.398	0.367	0.361	0.398	0.455
47	0.328	0.292	0.312	0.324	0.295	0.308	0.259	0.273	0.283	0.29	0.308	0.303	0.288	0.259	0.278	0.288	0.353

c-mos genetic distances

	35	36	37	38	39	40	41	42	43	44	45	46	47
1	0.319	0.291	0.302	0.301	0.305	0.294	0.303	0.307	0.296	0.273	0.296	0.319	0.302
2	0.345	0.32	0.337	0.314	0.298	0.315	0.31	0.312	0.298	0.295	0.307	0.343	0.298
3	0.326	0.303	0.318	0.297	0.283	0.292	0.295	0.303	0.303	0.292	0.306	0.349	0.263
4	0.268	0.26	0.268	0.262	0.254	0.251	0.249	0.26	0.26	0.24	0.243	0.29	0.254
5	0.153	0.145	0.162	0.168	0.148	0.148	0.156	0.167	0.175	0.153	0.195	0.209	0.178
6	0.189	0.17	0.201	0.174	0.167	0.167	0.179	0.189	0.198	0.189	0.228	0.253	0.189
7	0.167	0.151	0.184	0.151	0.139	0.136	0.151	0.153	0.175	0.159	0.19	0.212	0.167
8	0.156	0.139	0.159	0.146	0.125	0.125	0.134	0.148	0.164	0.145	0.184	0.203	0.153
9	0.162	0.153	0.167	0.151	0.134	0.136	0.139	0.153	0.173	0.148	0.198	0.217	0.159
10	0.153	0.145	0.159	0.149	0.128	0.131	0.137	0.148	0.159	0.145	0.192	0.209	0.156
11	0.195	0.178	0.198	0.197	0.181	0.173	0.184	0.187	0.214	0.178	0.206	0.234	0.209
12	0.187	0.173	0.201	0.194	0.184	0.17	0.19	0.198	0.217	0.189	0.201	0.234	0.206
13	0.217	0.195	0.214	0.216	0.209	0.203	0.212	0.212	0.251	0.22	0.253	0.273	0.228
14	0.184	0.159	0.187	0.188	0.181	0.173	0.19	0.184	0.195	0.195	0.228	0.237	0.203
15	0.181	0.156	0.175	0.194	0.184	0.175	0.193	0.187	0.192	0.189	0.223	0.248	0.206
16	0.178	0.159	0.181	0.18	0.17	0.162	0.179	0.178	0.189	0.187	0.223	0.237	0.195
17	0.178	0.164	0.181	0.18	0.17	0.156	0.184	0.178	0.198	0.189	0.228	0.24	0.209
18	0.201	0.181	0.201	0.188	0.181	0.173	0.195	0.178	0.209	0.198	0.234	0.256	0.209
19	0.198	0.175	0.192	0.191	0.178	0.167	0.181	0.189	0.181	0.164	0.226	0.251	0.195
20	0.202	0.185	0.205	0.192	0.174	0.171	0.185	0.193	0.193	0.188	0.219	0.236	0.205
21	0.206	0.178	0.198	0.188	0.17	0.173	0.176	0.184	0.175	0.184	0.237	0.262	0.209
22	0.187	0.17	0.189	0.174	0.175	0.162	0.165	0.184	0.181	0.181	0.226	0.256	0.198
23	0.206	0.189	0.192	0.194	0.184	0.17	0.181	0.195	0.184	0.181	0.22	0.206	0.203
24	0.175	0.158	0.158	0.174	0.151	0.161	0.167	0.17	0.194	0.149	0.188	0.213	0.176
25	0.197	0.175	0.198	0.18	0.136	0.163	0.166	0.169	0.204	0.172	0.201	0.239	0.186
26	0.184	0.179	0.191	0.172	0.153	0.168	0.165	0.168	0.192	0.171	0.208	0.255	0.191
27	0.193	0.173	0.194	0.196	0.158	0.185	0.179	0.179	0.203	0.173	0.22	0.255	0.194
28	0.201	0.187	0.193	0.189	0.165	0.165	0.168	0.173	0.198	0.184	0.204	0.21	0.201
29	0.206	0.187	0.192	0.169	0.139	0.134	0.162	0.156	0.201	0.195	0.212	0.226	0.198
30	0.196	0.176	0.181	0.175	0.148	0.142	0.162	0.159	0.193	0.181	0.204	0.235	0.192
31	0.192	0.187	0.187	0.177	0.164	0.15	0.162	0.162	0.175	0.187	0.203	0.226	0.178
32	0.192	0.181	0.187	0.203	0.178	0.17	0.19	0.181	0.195	0.201	0.201	0.226	0.187
33	0.192	0.187	0.192	0.197	0.173	0.164	0.181	0.175	0.184	0.189	0.217	0.237	0.189
34	0.039	0.061	0.12	0.205	0.198	0.189	0.181	0.209	0.217	0.184	0.24	0.256	0.22

c-mos genetic distances

	35	36	37	38	39	40	41	42	43	44	45	46	47
35		0.058	0.131	0.202	0.195	0.187	0.176	0.206	0.217	0.187	0.234	0.245	0.223
36	0.065		0.109	0.183	0.178	0.167	0.173	0.189	0.195	0.164	0.24	0.251	0.192
37	0.167	0.131		0.205	0.187	0.181	0.195	0.209	0.201	0.175	0.245	0.267	0.214
38	0.304	0.258	0.304		0.059	0.059	0.076	0.07	0.157	0.166	0.225	0.242	0.191
39	0.284	0.245	0.264	0.065		0.045	0.075	0.056	0.145	0.159	0.203	0.226	0.167
40	0.269	0.227	0.254	0.065	0.047		0.081	0.05	0.15	0.167	0.198	0.214	0.178
41	0.249	0.237	0.28	0.087	0.085	0.092		0.092	0.153	0.151	0.198	0.215	0.176
42	0.307	0.266	0.307	0.079	0.06	0.054	0.106		0.162	0.173	0.206	0.223	0.181
43	0.332	0.279	0.291	0.207	0.184	0.192	0.199	0.211		0.167	0.251	0.253	0.178
44	0.263	0.218	0.24	0.213	0.199	0.211	0.187	0.221	0.214		0.22	0.245	0.181
45	0.384	0.38	0.407	0.35	0.301	0.29	0.295	0.308	0.422	0.335		0.139	0.215
46	0.429	0.43	0.481	0.41	0.364	0.341	0.347	0.362	0.442	0.409	0.175		0.253
47	0.359	0.281	0.335	0.28	0.231	0.248	0.247	0.254	0.255	0.251	0.338	0.45	

mtDNA genetic distances

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1		0.353	0.358	0.409	0.411	0.4	0.405	0.415	0.408	0.417	0.409	0.409	0.421	0.42	0.4	0.415	0.368	0.365	0.368	0.373
2	1.136		0.24	0.332	0.387	0.355	0.368	0.368	0.374	0.378	0.364	0.361	0.377	0.38	0.355	0.374	0.326	0.318	0.309	0.323
3	1.201	0.539		0.324	0.373	0.35	0.36	0.358	0.369	0.38	0.356	0.354	0.383	0.362	0.336	0.365	0.305	0.299	0.286	0.308
4	1.74	1.047	0.979		0.39	0.375	0.392	0.418	0.411	0.401	0.389	0.388	0.393	0.373	0.382	0.406	0.337	0.346	0.335	0.358
5	1.901	1.573	1.36	1.529		0.209	0.2	0.332	0.342	0.325	0.313	0.327	0.333	0.311	0.308	0.315	0.359	0.361	0.334	0.33
6	1.806	1.257	1.198	1.439	0.375		0.149	0.317	0.326	0.306	0.295	0.314	0.321	0.311	0.297	0.316	0.35	0.324	0.321	0.336
7	1.794	1.305	1.222	1.509	0.329	0.202		0.327	0.318	0.304	0.302	0.308	0.31	0.308	0.296	0.309	0.361	0.336	0.336	0.341
8	1.888	1.416	1.247	1.902	1.024	0.948	0.955		0.159	0.22	0.285	0.314	0.328	0.3	0.302	0.329	0.364	0.356	0.353	0.35
9	1.852	1.401	1.361	1.798	1.036	0.932	0.863	0.237		0.208	0.288	0.316	0.33	0.312	0.294	0.326	0.367	0.349	0.349	0.349
10	1.92	1.413	1.414	1.667	0.905	0.807	0.792	0.425	0.351		0.291	0.329	0.321	0.303	0.305	0.307	0.367	0.36	0.354	0.357
11	1.92	1.305	1.226	1.627	0.808	0.716	0.759	0.693	0.681	0.716		0.301	0.286	0.275	0.263	0.282	0.349	0.326	0.305	0.329
12	1.933	1.34	1.216	1.617	0.964	0.894	0.843	0.865	0.903	0.971	0.784		0.233	0.287	0.314	0.317	0.357	0.352	0.34	0.351
13	2.055	1.385	1.466	1.459	0.91	0.857	0.773	0.927	0.909	0.832	0.673	0.463		0.308	0.306	0.306	0.347	0.345	0.347	0.336
14	2.05	1.563	1.313	1.424	0.824	0.85	0.796	0.821	0.86	0.811	0.658	0.708	0.775		0.302	0.321	0.347	0.349	0.336	0.352
15	1.773	1.175	1.061	1.448	0.786	0.75	0.732	0.771	0.757	0.789	0.571	0.852	0.75	0.787		0.283	0.35	0.331	0.307	0.315
16	1.887	1.335	1.316	1.727	0.752	0.804	0.774	0.939	0.886	0.809	0.645	0.829	0.773	0.872	0.624		0.344	0.336	0.32	0.33
17	1.321	0.987	0.819	1.049	1.154	1.069	1.115	1.193	1.212	1.217	1.082	1.082	0.995	1.045	1.022	1.001		0.226	0.203	0.226
18	1.299	0.911	0.801	1.106	1.209	0.92	0.994	1.15	1.087	1.185	0.916	1.121	0.997	1.124	0.928	0.987	0.47		0.162	0.209
19	1.385	0.877	0.752	1.055	1.009	0.953	1.032	1.167	1.134	1.178	0.818	1.038	1.029	1.036	0.805	0.911	0.366	0.263		0.183
20	1.386	0.93	0.827	1.219	0.992	1.017	1.052	1.13	1.121	1.134	0.96	1.116	0.966	1.125	0.808	0.929	0.412	0.391	0.299	
21	1.297	0.874	0.793	1.157	1.003	0.923	0.945	1.166	1.204	1.119	0.956	0.996	0.961	1.11	0.913	0.985	0.395	0.342	0.324	0.233
22	1.481	0.992	0.809	1.097	0.924	0.959	0.973	1.164	1.214	1.274	1.018	0.96	0.984	1.221	0.923	0.996	0.476	0.358	0.347	0.476
23	1.351	1.01	0.772	0.924	1.028	0.945	0.951	1.142	1.202	1.27	1.019	1.074	1.046	1.109	1.03	1.087	0.491	0.351	0.355	0.466
24	1.453	1.008	0.963	1.109	1.209	1.049	1.05	1.161	1.21	1.213	1.027	1.23	1.16	1.285	0.948	1.167	0.471	0.483	0.373	0.502
25	1.464	0.911	0.787	1.074	1.093	1.018	1.058	1.086	1.015	1.184	1.007	1.09	1.016	1.072	0.963	1.051	0.434	0.476	0.363	0.456
26	1.383	0.905	0.743	0.979	1.02	0.948	0.917	1.141	1.179	1.153	0.92	1.071	1.019	1.211	0.897	0.976	0.41	0.423	0.312	0.4
27	1.32	0.959	0.724	1.059	1.097	0.969	0.982	1.12	1.05	1.065	0.943	1.083	1.018	1.048	0.854	0.953	0.334	0.324	0.282	0.33
28	1.356	1.002	0.781	1.159	0.958	0.986	0.999	1.088	1.062	1.131	0.945	1.001	0.977	0.986	0.858	0.878	0.457	0.383	0.295	0.356
29	1.436	0.883	0.751	1.108	1.024	0.984	1.032	1.024	1.118	1.206	0.89	1.115	1.095	1.082	0.937	0.939	0.411	0.374	0.295	0.442
30	1.333	0.995	0.795	1.092	1.171	1.142	1.121	1.293	1.182	1.379	1.058	1.188	1.207	1.046	0.955	1.032	0.627	0.607	0.571	0.608
31	1.432	0.923	0.809	1.076	1.151	1.022	1.123	1.36	1.186	1.309	1.047	1.219	1.199	1.166	1.005	1.001	0.609	0.66	0.584	0.613
32	1.367	0.95	0.881	1.051	1.186	1.086	1.102	1.342	1.124	1.271	1.011	1.242	1.194	1.188	1.057	1.113	0.64	0.649	0.593	0.646
33	1.338	0.927	0.832	1.078	1.194	1.055	1.084	1.326	1.261	1.328	0.998	1.344	1.185	1.131	0.881	1.106	0.665	0.724	0.626	0.683
34	1.441	0.98	0.828	1.122	0.983	1.008	1.068	1.37	1.338	1.295	0.994	1.21	1.023	1.101	0.911	1.016	0.709	0.685	0.582	0.613
35	1.505	0.906	0.852	1.017	1.231	1.1	1.145	1.424	1.235	1.331	0.99	1.198	1.174	1.274	0.984	1.101	0.712	0.635	0.617	0.733
36	1.67	1.148	0.94	1.339	1.302	1.069	1.16	1.216	1.304	1.33	1.266	1.134	1.25	1.275	1.021	1.366	0.762	0.845	0.718	0.725
37	1.476	1.151	0.949	1.084	1.133	1.107	1.144	1.301	1.353	1.321	1.194	1.202	1.129	1.281	0.986	1.146	0.739	0.735	0.732	0.752

mtDNA genetic distances

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
38	1.417	1.075	0.956	1.061	1.18	1.097	1.07	1.366	1.386	1.331	1.156	1.392	1.193	1.212	1.086	1.189	0.655	0.676	0.544	0.632
39	1.868	1.631	1.423	1.578	1.446	1.203	1.245	1.439	1.461	1.553	1.471	1.38	1.521	1.402	1.276	1.456	1.31	1.219	1.122	1.201
40	1.998	1.462	1.328	1.584	1.43	1.428	1.562	1.542	1.593	1.691	1.598	1.528	1.754	1.568	1.421	1.412	1.222	0.988	1.162	1.176
41	2.173	1.859	1.603	1.774	1.511	1.315	1.399	1.443	1.535	1.498	1.434	1.481	1.518	1.467	1.475	1.562	1.3	1.291	1.253	1.433
42	2.205	1.769	1.5	1.907	1.433	1.439	1.442	1.646	1.525	1.564	1.401	1.478	1.601	1.446	1.349	1.612	1.367	1.198	1.112	1.232
43	1.547	1.097	0.83	1.269	1.356	1.2	1.195	1.351	1.367	1.327	1.175	1.183	1.114	1.319	1.168	1.266	0.713	0.641	0.679	0.719
44	1.675	1.332	1.097	1.373	1.413	1.35	1.314	1.555	1.415	1.489	1.299	1.479	1.378	1.53	1.374	1.632	1.055	1.005	1.066	1.117
45	1.641	1.2	0.96	1.124	1.389	1.295	1.197	1.525	1.637	1.534	1.336	1.213	1.242	1.289	1.222	1.392	0.879	0.914	0.846	0.961
46	2.087	1.375	1.041	1.198	1.276	1.284	1.198	1.54	1.683	1.517	1.326	1.233	1.349	1.35	1.287	1.396	0.953	0.935	0.893	0.97
47	1.507	1.036	0.75	1.127	1.362	1.294	1.271	1.286	1.365	1.412	1.194	1.183	1.19	1.238	1.078	1.341	0.745	0.746	0.66	0.654
48	1.582	1.126	0.942	1.284	1.486	1.367	1.376	1.616	1.601	1.761	1.381	1.584	1.416	1.638	1.312	1.412	0.926	0.88	0.885	0.814
49	1.467	1.011	0.909	1.175	1.28	1.241	1.244	1.417	1.363	1.436	1.324	1.494	1.378	1.238	0.989	1.202	0.781	0.711	0.695	0.645
50	1.721	1.16	1.059	1.417	1.666	1.419	1.45	1.446	1.505	1.655	1.345	1.595	1.548	1.408	1.329	1.599	0.957	0.867	0.85	0.867
51	1.467	0.978	0.867	1.125	1.38	1.296	1.348	1.405	1.429	1.515	1.089	1.407	1.263	1.472	1.064	1.216	0.866	0.698	0.691	0.712
52	1.405	1.315	1.169	1.358	1.625	1.521	1.473	1.681	1.497	1.672	1.231	1.587	1.426	1.514	1.141	1.376	0.986	0.956	0.898	1.045
53	1.348	0.932	0.858	0.951	1.194	1.093	1.16	1.201	1.278	1.362	1.079	1.322	1.138	1.291	1.01	1.094	0.653	0.696	0.614	0.644
54	1.545	1.077	0.909	1.019	1.251	1.105	1.244	1.567	1.602	1.597	1.431	1.474	1.418	1.372	1.167	1.352	0.812	0.736	0.702	0.813
55	1.343	0.92	0.776	0.986	1.356	1.216	1.312	1.482	1.382	1.536	1.256	1.274	1.31	1.391	1.103	1.227	0.654	0.657	0.696	0.772
56	1.149	0.833	0.703	0.977	1.13	0.985	1.007	1.221	1.1	1.073	1.093	1.131	1.055	1.033	1.031	1.056	0.537	0.542	0.456	0.523
57	1.227	0.956	0.709	1.023	1.238	1.186	1.235	1.156	1.127	1.312	1.09	1.262	1.166	1.174	1.06	1.141	0.609	0.565	0.512	0.538
58	1.371	0.966	0.775	0.988	1.134	1.025	0.99	1.251	1.228	1.296	0.99	1.156	1.038	1.088	1.061	1.083	0.606	0.626	0.508	0.606
59	1.31	0.897	0.648	1.013	1.065	0.998	0.973	1.103	1.102	1.149	1.042	1.147	1.061	1.042	0.984	1.057	0.565	0.496	0.477	0.586
60	1.357	0.914	0.703	1.03	1.149	1.091	1.01	1.237	1.165	1.205	1.064	1.106	1.039	1.105	1.038	1.097	0.604	0.546	0.501	0.602
61	1.328	0.868	0.662	1.073	1.06	0.987	0.971	1.242	1.109	1.192	1.037	1.107	0.998	1.109	1.051	1.097	0.478	0.521	0.447	0.574
62	1.388	0.969	0.81	0.98	1.068	1.033	1.045	1.253	1.236	1.275	1.192	1.137	1.104	1.164	1.15	1.147	0.584	0.619	0.608	0.63
63	1.435	0.955	0.732	1.05	1.114	1.089	1.079	1.242	1.288	1.299	1.095	1.098	1.102	1.049	1.102	1.049	0.629	0.573	0.54	0.566
64	1.365	0.958	0.809	1.002	1.182	1.065	1.061	1.181	1.153	1.272	1.209	1.258	1.134	1.262	1.131	1.142	0.615	0.579	0.582	0.657
65	1.406	0.908	0.758	0.968	0.996	0.926	0.911	1.111	1.132	1.166	1.015	1.091	1.091	1.059	0.97	0.985	0.645	0.582	0.526	0.589
66	1.134	0.922	0.716	0.964	0.962	0.896	0.946	1.06	1.099	1.124	0.916	1.085	1.099	0.994	0.848	0.922	0.585	0.501	0.452	0.566
67	1.196	0.971	0.677	1.078	0.969	0.967	0.989	1.089	1.112	1.174	0.962	1.097	1.196	1.023	0.93	0.928	0.595	0.532	0.476	0.608
68	1.159	0.88	0.687	1.025	0.991	0.914	0.953	1.066	1.118	1.113	0.9	1.084	1.093	0.963	0.893	0.937	0.597	0.558	0.473	0.553
69	1.492	1.026	0.771	1.054	1.232	1.135	1.104	1.425	1.321	1.287	1.271	1.421	1.36	1.298	1.139	1.042	0.659	0.688	0.6	0.735
70	1.412	0.871	0.685	0.879	1.167	1.05	1.12	1.415	1.253	1.156	1.124	1.253	1.087	1.095	1.082	1.139	0.697	0.688	0.609	0.682
71	1.367	0.962	0.72	1.027	1.134	1.073	1.064	1.236	1.388	1.366	1.084	1.119	1.071	1.221	1.022	1.036	0.687	0.675	0.616	0.625
72	1.469	0.848	0.642	1.044	1.034	1.028	0.958	1.238	1.165	1.246	1.04	1.106	1.014	1.141	1.034	1.006	0.523	0.562	0.491	0.579

mtDNA genetic distances

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
1	0.367	0.382	0.378	0.38	0.379	0.375	0.366	0.369	0.369	0.369	0.374	0.375	0.364	0.384	0.388	0.39	0.389	0.376	0.414	0.415
2	0.319	0.325	0.332	0.334	0.317	0.324	0.324	0.325	0.311	0.333	0.324	0.325	0.316	0.334	0.315	0.34	0.347	0.339	0.397	0.369
3	0.299	0.299	0.298	0.326	0.295	0.296	0.289	0.291	0.289	0.306	0.306	0.315	0.299	0.313	0.313	0.321	0.323	0.324	0.373	0.355
4	0.356	0.338	0.331	0.349	0.346	0.337	0.341	0.347	0.345	0.347	0.338	0.341	0.344	0.359	0.34	0.375	0.353	0.338	0.405	0.388
5	0.333	0.326	0.344	0.352	0.352	0.338	0.347	0.328	0.341	0.363	0.357	0.367	0.36	0.337	0.358	0.369	0.357	0.361	0.388	0.369
6	0.326	0.327	0.324	0.332	0.34	0.329	0.334	0.327	0.331	0.366	0.343	0.354	0.344	0.339	0.349	0.338	0.352	0.347	0.356	0.367
7	0.325	0.336	0.333	0.34	0.347	0.336	0.338	0.339	0.345	0.361	0.365	0.365	0.351	0.35	0.355	0.351	0.36	0.353	0.363	0.381
8	0.351	0.355	0.358	0.351	0.352	0.356	0.355	0.346	0.34	0.376	0.378	0.38	0.366	0.38	0.386	0.353	0.371	0.382	0.379	0.379
9	0.358	0.36	0.36	0.356	0.347	0.364	0.349	0.346	0.353	0.364	0.364	0.359	0.36	0.376	0.367	0.36	0.371	0.383	0.381	0.377
10	0.353	0.368	0.368	0.355	0.359	0.359	0.351	0.354	0.359	0.38	0.375	0.373	0.372	0.371	0.379	0.366	0.372	0.375	0.387	0.396
11	0.327	0.342	0.339	0.336	0.338	0.334	0.325	0.326	0.324	0.35	0.345	0.341	0.332	0.337	0.34	0.355	0.353	0.357	0.382	0.374
12	0.338	0.334	0.347	0.358	0.347	0.346	0.35	0.341	0.352	0.365	0.369	0.369	0.372	0.368	0.368	0.348	0.355	0.385	0.375	0.384
13	0.342	0.342	0.351	0.363	0.346	0.355	0.347	0.345	0.356	0.375	0.374	0.373	0.361	0.355	0.375	0.372	0.36	0.376	0.396	0.403
14	0.349	0.364	0.347	0.36	0.346	0.367	0.346	0.334	0.349	0.349	0.357	0.363	0.351	0.356	0.37	0.367	0.372	0.365	0.38	0.372
15	0.328	0.332	0.343	0.328	0.334	0.333	0.318	0.324	0.332	0.34	0.349	0.357	0.323	0.324	0.343	0.328	0.34	0.355	0.372	0.366
16	0.337	0.341	0.352	0.354	0.344	0.34	0.333	0.326	0.332	0.35	0.347	0.359	0.352	0.341	0.357	0.371	0.355	0.366	0.385	0.371
17	0.217	0.233	0.238	0.236	0.231	0.217	0.193	0.234	0.215	0.275	0.266	0.274	0.279	0.301	0.288	0.293	0.295	0.281	0.373	0.354
18	0.198	0.202	0.194	0.235	0.233	0.222	0.186	0.203	0.204	0.272	0.277	0.277	0.287	0.291	0.274	0.307	0.289	0.291	0.36	0.325
19	0.187	0.191	0.19	0.204	0.202	0.186	0.166	0.173	0.175	0.258	0.258	0.266	0.265	0.274	0.264	0.284	0.289	0.253	0.345	0.337
20	0.16	0.234	0.236	0.247	0.232	0.221	0.193	0.199	0.228	0.269	0.272	0.282	0.277	0.281	0.294	0.289	0.297	0.278	0.36	0.339
21		0.225	0.229	0.231	0.222	0.216	0.193	0.214	0.212	0.282	0.269	0.296	0.285	0.295	0.294	0.304	0.303	0.302	0.354	0.326
22	0.442		0.177	0.234	0.242	0.224	0.202	0.202	0.196	0.289	0.289	0.296	0.302	0.293	0.305	0.308	0.3	0.288	0.357	0.339
23	0.44	0.3		0.249	0.244	0.223	0.215	0.206	0.209	0.289	0.282	0.289	0.284	0.3	0.287	0.312	0.313	0.298	0.349	0.337
24	0.464	0.482	0.54		0.239	0.235	0.229	0.233	0.225	0.304	0.304	0.29	0.299	0.288	0.296	0.301	0.313	0.304	0.36	0.336
25	0.437	0.51	0.518	0.475		0.217	0.22	0.216	0.231	0.269	0.268	0.275	0.278	0.292	0.291	0.305	0.301	0.284	0.353	0.343
26	0.393	0.434	0.41	0.456	0.383		0.191	0.216	0.213	0.289	0.276	0.271	0.279	0.291	0.291	0.309	0.302	0.276	0.37	0.329
27	0.333	0.37	0.418	0.464	0.411	0.328		0.192	0.2	0.259	0.266	0.277	0.289	0.288	0.287	0.291	0.304	0.269	0.36	0.321
28	0.405	0.368	0.384	0.464	0.395	0.394	0.35		0.199	0.265	0.267	0.281	0.274	0.281	0.289	0.306	0.305	0.271	0.356	0.334
29	0.385	0.359	0.4	0.451	0.446	0.395	0.383	0.367		0.273	0.26	0.276	0.279	0.276	0.276	0.303	0.307	0.272	0.362	0.328
30	0.676	0.734	0.696	0.809	0.613	0.656	0.566	0.585	0.64		0.143	0.196	0.179	0.265	0.236	0.291	0.287	0.26	0.386	0.363
31	0.612	0.758	0.683	0.788	0.602	0.616	0.605	0.6	0.586	0.19		0.182	0.179	0.262	0.225	0.294	0.28	0.249	0.364	0.359
32	0.727	0.784	0.694	0.701	0.639	0.577	0.64	0.649	0.648	0.322	0.283		0.191	0.28	0.225	0.304	0.284	0.251	0.379	0.368
33	0.696	0.827	0.702	0.793	0.665	0.641	0.742	0.627	0.684	0.284	0.283	0.322		0.284	0.227	0.305	0.293	0.257	0.38	0.36
34	0.689	0.699	0.729	0.658	0.653	0.616	0.69	0.621	0.619	0.542	0.52	0.594	0.639		0.268	0.266	0.3	0.267	0.362	0.354
35	0.717	0.835	0.7	0.739	0.711	0.688	0.695	0.723	0.664	0.464	0.432	0.427	0.459	0.576		0.286	0.276	0.266	0.367	0.361
36	0.83	0.889	0.874	0.827	0.848	0.82	0.791	0.826	0.871	0.743	0.761	0.795	0.827	0.612	0.687		0.264	0.295	0.357	0.36
37	0.802	0.766	0.824	0.854	0.775	0.754	0.791	0.806	0.827	0.673	0.647	0.669	0.71	0.709	0.635	0.576		0.271	0.372	0.365

mtDNA genetic distances

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
38	0.764	0.709	0.721	0.775	0.663	0.597	0.595	0.613	0.628	0.566	0.512	0.526	0.568	0.554	0.589	0.763	0.601		0.361	0.359
39	1.205	1.226	1.11	1.216	1.186	1.299	1.214	1.129	1.23	1.393	1.227	1.375	1.344	1.186	1.27	1.258	1.301	1.245		0.334
40	1.05	1.068	1.066	1.143	1.191	1.021	1.01	1.071	1.078	1.265	1.252	1.359	1.284	1.208	1.291	1.337	1.302	1.311	1.101	
41	1.382	1.294	1.335	1.396	1.195	1.225	1.128	1.143	1.252	1.207	1.344	1.495	1.352	1.281	1.302	1.444	1.421	1.17	0.431	1.14
42	1.2	1.152	1.344	1.294	1.086	1.249	1.118	1.156	1.182	1.417	1.341	1.428	1.35	1.282	1.314	1.222	1.565	1.288	0.396	1.076
43	0.683	0.727	0.69	0.731	0.62	0.703	0.724	0.755	0.686	0.802	0.838	0.841	0.921	0.785	0.838	0.957	0.927	0.845	1.446	1.455
44	1.166	1.053	1.101	1.169	1.114	1.002	0.966	1.004	1.043	1.176	1.245	1.251	1.164	1.108	1.174	1.18	1.118	1.104	1.359	1.4
45	0.887	0.924	0.995	0.951	0.892	0.971	0.938	0.896	0.929	1.032	1.054	0.896	1.113	0.99	0.996	1.055	0.959	0.964	1.419	1.45
46	0.915	0.962	1.046	1.003	0.955	0.984	0.894	0.857	0.903	1.183	1.057	1.127	1.175	1.087	1.119	1.138	1.08	1.041	1.562	1.493
47	0.775	0.771	0.744	0.877	0.795	0.648	0.695	0.735	0.759	0.805	0.746	0.741	0.933	0.732	0.845	1.041	0.868	0.784	1.47	1.189
48	0.95	0.948	0.861	1.04	1.014	0.877	0.913	0.91	0.911	1.087	1.036	1.02	1.041	1.04	0.995	1.252	1.122	0.926	1.608	1.33
49	0.627	0.802	0.716	0.787	0.751	0.673	0.633	0.676	0.746	0.73	0.711	0.756	0.872	0.785	0.821	0.944	0.945	0.767	1.347	1.347
50	0.878	0.957	0.879	0.954	0.943	0.967	0.977	0.821	0.888	0.967	0.935	1.025	1.055	0.916	0.963	1.206	1.307	1.041	1.58	1.681
51	0.709	0.764	0.741	0.917	0.722	0.709	0.747	0.739	0.809	0.811	0.845	0.885	0.885	0.764	0.832	1.093	0.843	0.819	1.33	1.327
52	0.929	1.105	1.048	1.055	0.939	0.947	0.948	0.995	0.998	1.143	1.064	1.068	1.122	1.01	1.039	1.199	1.193	1.055	1.407	1.584
53	0.628	0.708	0.718	0.75	0.75	0.702	0.646	0.654	0.638	0.8	0.824	0.791	0.788	0.862	0.851	0.998	0.984	0.849	1.324	1.2
54	0.792	0.842	0.834	0.973	0.825	0.761	0.786	0.818	0.75	0.897	0.848	0.965	0.892	0.833	0.84	0.953	0.94	0.84	1.308	1.264
55	0.747	0.762	0.85	0.821	0.665	0.688	0.717	0.731	0.636	0.82	0.816	0.837	0.851	0.793	0.745	0.957	0.955	0.803	1.341	1.17
56	0.604	0.623	0.563	0.603	0.559	0.511	0.538	0.532	0.555	0.607	0.612	0.629	0.635	0.706	0.586	0.831	0.656	0.603	1.21	1.18
57	0.592	0.605	0.613	0.682	0.641	0.596	0.547	0.59	0.624	0.712	0.708	0.737	0.75	0.691	0.677	0.924	0.805	0.671	1.382	1.195
58	0.694	0.643	0.591	0.657	0.664	0.584	0.654	0.614	0.654	0.736	0.704	0.651	0.699	0.661	0.695	0.819	0.713	0.701	1.266	1.212
59	0.656	0.59	0.595	0.634	0.535	0.552	0.558	0.539	0.569	0.581	0.556	0.587	0.612	0.611	0.619	0.854	0.72	0.61	1.163	1.188
60	0.645	0.597	0.621	0.72	0.607	0.575	0.574	0.534	0.593	0.646	0.572	0.614	0.652	0.603	0.613	0.875	0.686	0.67	1.235	1.031
61	0.587	0.577	0.565	0.615	0.512	0.524	0.541	0.479	0.548	0.577	0.557	0.585	0.649	0.637	0.615	0.796	0.68	0.627	1.183	1.067
62	0.718	0.628	0.579	0.762	0.718	0.624	0.631	0.595	0.657	0.767	0.716	0.669	0.787	0.717	0.702	0.876	0.74	0.711	1.118	1.182
63	0.635	0.579	0.6	0.757	0.623	0.616	0.579	0.53	0.607	0.621	0.601	0.649	0.668	0.646	0.637	0.852	0.712	0.662	1.212	1.087
64	0.696	0.57	0.632	0.69	0.638	0.588	0.572	0.615	0.604	0.709	0.716	0.668	0.767	0.682	0.768	0.875	0.737	0.685	1.243	1.127
65	0.624	0.582	0.585	0.672	0.647	0.536	0.539	0.532	0.521	0.661	0.623	0.708	0.658	0.604	0.636	0.774	0.635	0.654	1.149	1.131
66	0.6	0.558	0.565	0.614	0.614	0.534	0.523	0.514	0.534	0.646	0.631	0.677	0.687	0.713	0.631	0.833	0.65	0.713	1.089	1.155
67	0.604	0.559	0.559	0.681	0.616	0.539	0.525	0.522	0.577	0.634	0.61	0.691	0.649	0.679	0.671	0.809	0.662	0.716	1.141	1.117
68	0.609	0.576	0.56	0.633	0.612	0.552	0.525	0.539	0.589	0.662	0.627	0.744	0.681	0.651	0.664	0.783	0.655	0.696	1.051	1.059
69	0.728	0.76	0.777	0.803	0.742	0.679	0.679	0.647	0.782	0.767	0.756	0.672	0.755	0.703	0.668	0.85	0.785	0.69	1.251	1.146
70	0.698	0.785	0.665	0.807	0.673	0.634	0.683	0.604	0.677	0.684	0.659	0.679	0.69	0.776	0.658	0.813	0.846	0.695	1.338	1.209
71	0.739	0.671	0.677	0.781	0.685	0.653	0.652	0.65	0.66	0.732	0.709	0.76	0.713	0.737	0.677	0.96	0.71	0.609	1.334	1.04
72	0.603	0.544	0.615	0.616	0.586	0.582	0.52	0.521	0.527	0.665	0.636	0.6	0.715	0.621	0.66	0.797	0.719	0.561	1.367	1.205

mtDNA genetic distances

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
1	0.42	0.418	0.389	0.395	0.398	0.419	0.378	0.387	0.388	0.402	0.39	0.381	0.373	0.39	0.369	0.358	0.361	0.375	0.377	0.378
2	0.397	0.392	0.34	0.364	0.348	0.367	0.328	0.343	0.331	0.344	0.329	0.368	0.312	0.323	0.315	0.3	0.32	0.328	0.318	0.325
3	0.367	0.367	0.301	0.336	0.312	0.328	0.288	0.319	0.316	0.335	0.311	0.352	0.3	0.309	0.291	0.279	0.288	0.302	0.277	0.289
4	0.395	0.401	0.362	0.37	0.352	0.355	0.339	0.351	0.367	0.378	0.352	0.377	0.327	0.329	0.337	0.329	0.34	0.335	0.332	0.337
5	0.377	0.377	0.375	0.379	0.377	0.366	0.362	0.378	0.366	0.381	0.376	0.394	0.353	0.354	0.368	0.353	0.362	0.349	0.347	0.361
6	0.354	0.366	0.351	0.368	0.361	0.361	0.352	0.367	0.364	0.367	0.369	0.381	0.336	0.338	0.355	0.33	0.348	0.336	0.334	0.345
7	0.366	0.37	0.362	0.371	0.364	0.364	0.357	0.376	0.364	0.374	0.375	0.387	0.35	0.36	0.369	0.341	0.362	0.338	0.342	0.345
8	0.372	0.377	0.383	0.39	0.381	0.384	0.365	0.401	0.383	0.381	0.379	0.399	0.358	0.386	0.384	0.362	0.359	0.368	0.358	0.37
9	0.378	0.367	0.381	0.375	0.397	0.393	0.37	0.399	0.378	0.384	0.376	0.39	0.367	0.389	0.375	0.354	0.354	0.37	0.358	0.362
10	0.374	0.376	0.368	0.38	0.382	0.382	0.37	0.405	0.383	0.387	0.384	0.394	0.374	0.386	0.382	0.347	0.365	0.374	0.358	0.361
11	0.368	0.37	0.351	0.358	0.359	0.355	0.354	0.378	0.366	0.37	0.344	0.354	0.339	0.374	0.36	0.347	0.347	0.33	0.343	0.342
12	0.372	0.373	0.353	0.376	0.356	0.364	0.345	0.39	0.393	0.388	0.38	0.396	0.37	0.376	0.365	0.344	0.358	0.352	0.354	0.349
13	0.388	0.396	0.352	0.381	0.367	0.375	0.357	0.38	0.384	0.393	0.369	0.387	0.354	0.378	0.37	0.349	0.36	0.345	0.352	0.347
14	0.373	0.372	0.365	0.382	0.361	0.373	0.357	0.39	0.358	0.37	0.38	0.384	0.359	0.369	0.375	0.336	0.357	0.352	0.346	0.352
15	0.372	0.363	0.357	0.37	0.36	0.362	0.343	0.369	0.338	0.367	0.341	0.344	0.336	0.354	0.345	0.34	0.344	0.349	0.339	0.342
16	0.384	0.389	0.367	0.394	0.376	0.378	0.374	0.386	0.365	0.384	0.358	0.38	0.347	0.371	0.36	0.344	0.357	0.352	0.345	0.346
17	0.365	0.365	0.289	0.329	0.309	0.321	0.289	0.312	0.304	0.33	0.314	0.339	0.27	0.295	0.275	0.249	0.271	0.269	0.26	0.271
18	0.354	0.349	0.265	0.325	0.313	0.315	0.287	0.312	0.282	0.31	0.273	0.324	0.27	0.286	0.269	0.25	0.252	0.276	0.239	0.256
19	0.341	0.333	0.275	0.321	0.299	0.308	0.275	0.311	0.276	0.304	0.275	0.317	0.254	0.275	0.273	0.229	0.239	0.248	0.232	0.241
20	0.368	0.343	0.29	0.332	0.322	0.319	0.275	0.301	0.268	0.304	0.276	0.34	0.263	0.296	0.29	0.249	0.246	0.266	0.261	0.266
21	0.358	0.34	0.283	0.344	0.312	0.317	0.294	0.325	0.27	0.307	0.283	0.321	0.261	0.294	0.289	0.264	0.267	0.289	0.28	0.28
22	0.354	0.337	0.286	0.334	0.311	0.321	0.288	0.314	0.292	0.319	0.289	0.348	0.271	0.301	0.289	0.264	0.263	0.277	0.258	0.263
23	0.361	0.359	0.282	0.333	0.324	0.334	0.29	0.307	0.286	0.315	0.29	0.344	0.28	0.302	0.308	0.257	0.269	0.272	0.265	0.272
24	0.359	0.348	0.289	0.349	0.324	0.327	0.302	0.328	0.299	0.326	0.324	0.34	0.286	0.319	0.298	0.269	0.284	0.285	0.279	0.296
25	0.346	0.336	0.267	0.334	0.306	0.317	0.298	0.331	0.283	0.309	0.277	0.315	0.282	0.299	0.27	0.253	0.271	0.282	0.25	0.271
26	0.357	0.351	0.287	0.33	0.327	0.322	0.281	0.316	0.277	0.331	0.286	0.325	0.276	0.289	0.278	0.25	0.271	0.27	0.259	0.265
27	0.337	0.331	0.282	0.318	0.315	0.307	0.288	0.318	0.265	0.325	0.284	0.323	0.262	0.291	0.28	0.251	0.249	0.28	0.259	0.258
28	0.341	0.339	0.291	0.319	0.316	0.304	0.292	0.315	0.273	0.299	0.281	0.327	0.269	0.299	0.279	0.248	0.261	0.274	0.254	0.256
29	0.347	0.342	0.278	0.329	0.317	0.309	0.289	0.314	0.29	0.316	0.298	0.335	0.266	0.284	0.267	0.254	0.266	0.28	0.256	0.266
30	0.361	0.364	0.305	0.354	0.336	0.35	0.303	0.344	0.295	0.324	0.301	0.355	0.301	0.318	0.302	0.273	0.29	0.303	0.271	0.285
31	0.359	0.36	0.313	0.358	0.333	0.331	0.293	0.331	0.292	0.317	0.307	0.342	0.295	0.306	0.298	0.267	0.282	0.293	0.263	0.268
32	0.379	0.368	0.309	0.362	0.32	0.348	0.299	0.329	0.295	0.331	0.312	0.352	0.292	0.314	0.304	0.279	0.292	0.279	0.271	0.272
33	0.367	0.361	0.318	0.348	0.338	0.346	0.32	0.337	0.312	0.328	0.31	0.352	0.291	0.312	0.305	0.27	0.29	0.285	0.278	0.281
34	0.364	0.356	0.307	0.348	0.34	0.348	0.298	0.338	0.307	0.325	0.302	0.335	0.31	0.307	0.302	0.299	0.29	0.291	0.28	0.277
35	0.357	0.356	0.316	0.35	0.327	0.34	0.31	0.334	0.311	0.322	0.303	0.34	0.308	0.301	0.292	0.271	0.283	0.292	0.277	0.276
36	0.359	0.328	0.32	0.345	0.337	0.342	0.326	0.352	0.32	0.345	0.335	0.349	0.319	0.309	0.319	0.309	0.317	0.308	0.309	0.313
37	0.371	0.382	0.319	0.346	0.32	0.335	0.31	0.34	0.328	0.359	0.31	0.362	0.33	0.322	0.329	0.279	0.3	0.289	0.292	0.288

mtDNA genetic distances

	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
38	0.349	0.355	0.311	0.343	0.32	0.326	0.301	0.318	0.298	0.333	0.302	0.341	0.306	0.303	0.304	0.271	0.286	0.287	0.273	0.286
39	0.202	0.195	0.376	0.369	0.375	0.39	0.379	0.393	0.37	0.391	0.364	0.378	0.368	0.362	0.362	0.362	0.377	0.369	0.355	0.36
40	0.347	0.334	0.368	0.37	0.374	0.381	0.35	0.361	0.363	0.389	0.37	0.382	0.346	0.354	0.346	0.348	0.352	0.362	0.357	0.337
41		0.208	0.371	0.361	0.361	0.364	0.371	0.392	0.38	0.386	0.365	0.389	0.357	0.363	0.361	0.344	0.37	0.373	0.354	0.363
42	0.418		0.363	0.371	0.391	0.374	0.361	0.388	0.355	0.385	0.365	0.376	0.354	0.358	0.355	0.356	0.376	0.382	0.354	0.364
43	1.536	1.411		0.317	0.304	0.306	0.313	0.316	0.298	0.321	0.284	0.314	0.279	0.307	0.283	0.283	0.276	0.292	0.267	0.288
44	1.413	1.508	0.922		0.273	0.282	0.339	0.37	0.341	0.357	0.33	0.348	0.327	0.33	0.328	0.308	0.328	0.339	0.312	0.324
45	1.449	1.714	0.839	0.643		0.221	0.323	0.344	0.335	0.331	0.312	0.335	0.317	0.319	0.324	0.296	0.301	0.311	0.3	0.298
46	1.487	1.539	0.889	0.723	0.422		0.334	0.353	0.339	0.341	0.324	0.36	0.313	0.34	0.325	0.322	0.322	0.331	0.31	0.313
47	1.514	1.493	0.899	1.2	0.983	1.074		0.217	0.32	0.326	0.312	0.33	0.304	0.307	0.311	0.273	0.292	0.3	0.29	0.296
48	1.76	1.708	0.93	1.389	1.092	1.181	0.427		0.345	0.344	0.327	0.362	0.316	0.326	0.326	0.315	0.312	0.319	0.308	0.315
49	1.613	1.401	0.779	1.05	1.016	1.1	0.94	1.168		0.317	0.272	0.313	0.263	0.288	0.285	0.285	0.289	0.314	0.293	0.292
50	1.684	1.745	0.965	1.29	1.045	1.053	1.054	1.161	0.934		0.266	0.296	0.291	0.304	0.307	0.309	0.311	0.321	0.3	0.313
51	1.439	1.416	0.725	1.038	0.924	1.015	0.896	0.994	0.642	0.646		0.283	0.265	0.266	0.266	0.282	0.285	0.286	0.278	0.277
52	1.718	1.534	0.864	1.147	1.015	1.259	1.038	1.288	0.904	0.764	0.675		0.279	0.306	0.308	0.327	0.324	0.339	0.329	0.341
53	1.332	1.309	0.718	0.992	0.897	0.902	0.873	0.991	0.63	0.811	0.672	0.674		0.215	0.212	0.265	0.273	0.281	0.269	0.273
54	1.477	1.356	0.894	1.024	0.94	1.108	0.932	1.092	0.725	0.885	0.671	0.86	0.413		0.24	0.279	0.3	0.302	0.285	0.288
55	1.395	1.27	0.73	1.047	0.994	1.005	0.919	1.052	0.726	0.84	0.629	0.832	0.421	0.513		0.284	0.287	0.299	0.261	0.276
56	1.145	1.295	0.741	0.877	0.795	1.003	0.711	0.932	0.745	0.919	0.721	0.917	0.63	0.741	0.721		0.19	0.209	0.177	0.19
57	1.495	1.57	0.695	0.994	0.818	1.005	0.785	0.921	0.737	0.87	0.752	0.937	0.658	0.855	0.75	0.311		0.18	0.181	0.18
58	1.392	1.46	0.721	1.087	0.852	0.973	0.781	0.93	0.874	0.89	0.708	0.989	0.676	0.844	0.758	0.37	0.285		0.191	0.191
59	1.258	1.279	0.65	0.899	0.832	0.911	0.797	0.869	0.761	0.779	0.704	0.978	0.642	0.748	0.612	0.284	0.296	0.307		0.103
60	1.409	1.367	0.739	0.961	0.818	0.894	0.816	0.936	0.75	0.867	0.708	1.031	0.661	0.744	0.667	0.314	0.292	0.32	0.114	
61	1.193	1.34	0.621	0.959	0.846	0.966	0.803	0.881	0.693	0.841	0.714	1.027	0.671	0.739	0.648	0.325	0.325	0.347	0.122	0.127
62	1.337	1.401	0.749	0.908	0.884	0.889	0.819	0.898	0.807	0.983	0.768	1.174	0.671	0.757	0.844	0.363	0.396	0.382	0.336	0.301
63	1.303	1.263	0.679	1.015	0.89	0.914	0.866	0.978	0.744	0.867	0.72	1.138	0.676	0.787	0.775	0.369	0.369	0.365	0.296	0.27
64	1.411	1.451	0.652	0.995	0.953	1.032	0.814	1.061	0.765	1.013	0.695	1.045	0.661	0.716	0.711	0.398	0.385	0.435	0.322	0.336
65	1.169	1.414	0.791	0.941	0.827	0.931	0.846	0.954	0.752	0.927	0.801	1.183	0.697	0.724	0.8	0.339	0.397	0.388	0.313	0.289
66	1.123	1.199	0.684	0.93	0.936	0.921	0.711	0.902	0.701	0.926	0.698	1.062	0.633	0.765	0.711	0.321	0.328	0.402	0.34	0.322
67	1.157	1.247	0.692	0.944	0.919	0.922	0.694	0.903	0.76	0.909	0.74	1.082	0.648	0.812	0.706	0.317	0.33	0.414	0.333	0.343
68	1.072	1.186	0.683	0.946	0.917	0.903	0.696	0.898	0.728	0.922	0.722	1.07	0.668	0.796	0.734	0.311	0.34	0.403	0.329	0.352
69	1.291	1.263	0.727	1.034	1.03	1.025	0.839	0.996	0.836	1.054	0.69	0.961	0.769	0.791	0.882	0.596	0.612	0.663	0.641	0.638
70	1.348	1.294	0.811	0.988	0.905	0.995	0.797	0.971	0.806	0.95	0.813	1.063	0.713	0.697	0.624	0.54	0.562	0.613	0.559	0.573
71	1.264	1.399	0.811	1.121	1.08	1.078	0.828	1.064	0.895	1.121	0.769	1.144	0.789	0.802	0.754	0.566	0.669	0.674	0.628	0.671
72	1.308	1.267	0.637	0.916	0.867	0.951	0.79	0.896	0.727	0.904	0.65	1.033	0.657	0.736	0.692	0.492	0.493	0.466	0.49	0.473

mtDNA genetic distances

	61	62	63	64	65	66	67	68	69	70	71	72
1	0.375	0.378	0.386	0.373	0.38	0.351	0.354	0.354	0.382	0.38	0.375	0.383
2	0.312	0.325	0.332	0.327	0.324	0.315	0.324	0.307	0.328	0.32	0.319	0.307
3	0.277	0.301	0.295	0.303	0.3	0.289	0.279	0.28	0.292	0.279	0.288	0.275
4	0.342	0.33	0.341	0.338	0.329	0.326	0.34	0.332	0.333	0.311	0.334	0.335
5	0.347	0.347	0.35	0.358	0.336	0.335	0.33	0.34	0.364	0.353	0.353	0.342
6	0.331	0.335	0.343	0.345	0.323	0.316	0.322	0.315	0.348	0.34	0.354	0.338
7	0.34	0.349	0.35	0.348	0.329	0.331	0.333	0.329	0.352	0.353	0.348	0.333
8	0.37	0.368	0.371	0.362	0.35	0.348	0.347	0.349	0.375	0.381	0.363	0.363
9	0.358	0.366	0.375	0.354	0.351	0.35	0.348	0.354	0.369	0.367	0.373	0.348
10	0.363	0.367	0.375	0.367	0.354	0.349	0.355	0.351	0.358	0.353	0.368	0.364
11	0.341	0.356	0.345	0.361	0.331	0.328	0.331	0.322	0.355	0.348	0.338	0.331
12	0.349	0.353	0.35	0.365	0.342	0.34	0.34	0.337	0.378	0.361	0.348	0.341
13	0.347	0.354	0.355	0.364	0.354	0.352	0.361	0.35	0.375	0.353	0.347	0.336
14	0.354	0.359	0.346	0.369	0.342	0.335	0.335	0.33	0.363	0.343	0.354	0.35
15	0.342	0.351	0.356	0.349	0.34	0.317	0.327	0.324	0.348	0.344	0.337	0.348
16	0.348	0.353	0.35	0.359	0.339	0.334	0.33	0.333	0.342	0.353	0.337	0.335
17	0.238	0.258	0.275	0.268	0.271	0.264	0.267	0.266	0.278	0.285	0.283	0.25
18	0.24	0.262	0.263	0.26	0.263	0.239	0.244	0.249	0.28	0.283	0.272	0.254
19	0.222	0.255	0.25	0.259	0.245	0.225	0.225	0.225	0.264	0.267	0.256	0.238
20	0.258	0.268	0.263	0.271	0.264	0.256	0.259	0.251	0.289	0.284	0.27	0.258
21	0.26	0.286	0.275	0.28	0.272	0.262	0.26	0.261	0.289	0.29	0.289	0.264
22	0.251	0.268	0.26	0.257	0.257	0.254	0.25	0.257	0.292	0.299	0.281	0.244
23	0.255	0.261	0.268	0.275	0.263	0.259	0.253	0.256	0.298	0.285	0.282	0.267
24	0.27	0.296	0.297	0.282	0.279	0.269	0.277	0.269	0.305	0.306	0.303	0.272
25	0.243	0.286	0.277	0.272	0.28	0.267	0.266	0.265	0.292	0.285	0.282	0.262
26	0.248	0.267	0.272	0.263	0.256	0.254	0.254	0.258	0.282	0.28	0.281	0.267
27	0.248	0.269	0.265	0.261	0.249	0.248	0.244	0.246	0.28	0.279	0.27	0.243
28	0.238	0.264	0.256	0.27	0.25	0.245	0.244	0.248	0.275	0.271	0.273	0.244
29	0.251	0.272	0.266	0.263	0.247	0.247	0.255	0.258	0.293	0.281	0.275	0.249
30	0.266	0.301	0.284	0.295	0.29	0.281	0.277	0.283	0.299	0.286	0.292	0.279
31	0.261	0.287	0.276	0.291	0.277	0.272	0.268	0.271	0.293	0.28	0.291	0.278
32	0.263	0.278	0.287	0.29	0.295	0.278	0.279	0.289	0.286	0.288	0.296	0.267
33	0.282	0.299	0.288	0.299	0.287	0.281	0.27	0.279	0.293	0.284	0.285	0.287
34	0.286	0.287	0.284	0.289	0.275	0.295	0.289	0.283	0.281	0.3	0.297	0.284
35	0.274	0.284	0.277	0.299	0.276	0.275	0.281	0.281	0.279	0.284	0.28	0.282
36	0.299	0.31	0.314	0.312	0.294	0.3	0.297	0.294	0.302	0.3	0.319	0.297
37	0.28	0.291	0.294	0.295	0.278	0.275	0.278	0.279	0.3	0.315	0.294	0.292

mtDNA genetic distances

	61	62	63	64	65	66	67	68	69	70	71	72
38	0.275	0.281	0.282	0.289	0.28	0.288	0.286	0.283	0.278	0.28	0.268	0.26
39	0.358	0.347	0.365	0.365	0.359	0.347	0.349	0.343	0.358	0.367	0.372	0.373
40	0.335	0.352	0.347	0.347	0.352	0.344	0.342	0.33	0.344	0.346	0.335	0.35
41	0.349	0.358	0.362	0.366	0.355	0.348	0.348	0.342	0.36	0.355	0.351	0.359
42	0.354	0.366	0.36	0.365	0.368	0.351	0.35	0.344	0.353	0.358	0.359	0.356
43	0.259	0.289	0.282	0.273	0.301	0.272	0.27	0.271	0.282	0.297	0.3	0.273
44	0.325	0.315	0.328	0.327	0.319	0.314	0.31	0.315	0.326	0.321	0.334	0.315
45	0.301	0.304	0.307	0.314	0.301	0.313	0.307	0.307	0.32	0.31	0.327	0.302
46	0.322	0.31	0.32	0.331	0.323	0.315	0.31	0.309	0.319	0.32	0.332	0.317
47	0.29	0.293	0.307	0.298	0.302	0.275	0.273	0.277	0.294	0.292	0.298	0.288
48	0.306	0.308	0.322	0.33	0.316	0.306	0.306	0.307	0.321	0.317	0.334	0.313
49	0.277	0.302	0.29	0.297	0.291	0.282	0.288	0.283	0.303	0.298	0.316	0.287
50	0.307	0.326	0.31	0.332	0.325	0.317	0.312	0.314	0.322	0.322	0.339	0.32
51	0.279	0.293	0.288	0.282	0.301	0.281	0.282	0.282	0.268	0.298	0.288	0.271
52	0.336	0.356	0.352	0.338	0.349	0.342	0.341	0.338	0.323	0.34	0.348	0.345
53	0.269	0.274	0.278	0.274	0.282	0.265	0.266	0.271	0.286	0.279	0.292	0.273
54	0.282	0.285	0.292	0.282	0.288	0.279	0.287	0.283	0.284	0.28	0.295	0.284
55	0.267	0.3	0.298	0.284	0.297	0.281	0.278	0.284	0.296	0.261	0.289	0.28
56	0.192	0.206	0.209	0.215	0.195	0.188	0.184	0.184	0.252	0.252	0.256	0.237
57	0.191	0.21	0.208	0.207	0.208	0.189	0.186	0.189	0.257	0.257	0.272	0.233
58	0.201	0.206	0.207	0.226	0.212	0.215	0.216	0.213	0.275	0.272	0.281	0.236
59	0.105	0.196	0.187	0.196	0.195	0.198	0.192	0.191	0.26	0.256	0.272	0.237
60	0.112	0.179	0.172	0.201	0.182	0.187	0.194	0.198	0.265	0.262	0.279	0.231
61		0.185	0.185	0.205	0.19	0.19	0.182	0.188	0.268	0.263	0.273	0.234
62	0.31		0.152	0.204	0.195	0.2	0.203	0.203	0.262	0.259	0.26	0.254
63	0.296	0.208		0.19	0.169	0.191	0.193	0.188	0.272	0.26	0.276	0.239
64	0.352	0.363	0.313		0.194	0.209	0.208	0.21	0.264	0.274	0.274	0.246
65	0.308	0.345	0.264	0.32		0.187	0.182	0.186	0.272	0.278	0.274	0.225
66	0.33	0.369	0.321	0.377	0.316		0.072	0.073	0.251	0.265	0.259	0.229
67	0.321	0.39	0.337	0.385	0.308	0.077		0.067	0.254	0.258	0.25	0.229
68	0.329	0.378	0.323	0.382	0.316	0.078	0.07		0.252	0.256	0.267	0.235
69	0.647	0.644	0.649	0.63	0.696	0.582	0.599	0.606		0.26	0.272	0.261
70	0.581	0.59	0.552	0.641	0.682	0.623	0.605	0.602	0.585		0.239	0.275
71	0.642	0.581	0.655	0.628	0.656	0.602	0.588	0.637	0.644	0.487		0.278
72	0.482	0.565	0.488	0.538	0.442	0.481	0.489	0.504	0.603	0.628	0.674	

Appendix VII. Lists of morphological characters from Lee and Caldwell (2000) that, if my favored phylogenetic hypothesis is correct, are candidates for reevaluation due to potential problems of homoplasy or incorrectly inferred ancestral state. Character numbers correspond to those from Lee & Caldwell (2000).

1. Morphological hypothesis rejected by the molecular data: **Monophyly of Scleroglossa**

Characters for reevaluation: 11, 23, 27, 31, 34, 36, 37, 38, 40, 47, 51, 66, 67, 69, 77, 78, 81, 87, 94, 97, 99, 103, 112, 114, 126, 128, 147, 160, 166, 189, 194, 201, 217, 218, 221, 234, 240, 254, 257

2. Morphological hypothesis rejected by the molecular data: **Monophyly of (Amphisbaenia + Dibamidae)**

Characters for reevaluation: 1, 7, 11, 27, 32, 40, 42, 47, 54, 59, 61, 62, 67, 69, 71, 78, 81, 82, 83, 87, 88, 91, 94, 95, 102, 107, 114, 125, 132, 152, 157, 159, 160, 166, 171, 173, 183, 185, 186, 188, 189, 190, 193, 194, 199, 201, 207, 208, 209, 219, 223, 225, 227, 231

3. Morphological hypothesis rejected by the molecular data: **Monophyly of (Snakes + Amphisbaenia + Dibamidae)**

Characters for reevaluation: 1, 7, 11, 16, 27, 32, 38, 40, 42, 44, 47, 59, 61, 62, 67, 69, 71, 78, 81, 87, 89, 91, 92, 95, 100, 127, 132, 138, 139, 142, 147, 152, 157, 160, 166, 171, 173, 183, 185, 186, 188, 189, 190, 193, 194, 201, 206, 208, 209, 216, 219, 223, 225, 227, 231, 237, 250, 253, 254

4. Morphological hypothesis rejected by the molecular data: **Monophyly of (Xenosaurus + Shinisaurus)**

Characters for reevaluation: 19, 20, 27, 48, 113, 125, 132, 139, 147, 154, 249, 251

5. Morphological hypothesis rejected by the molecular data: **Monophyly of Varanoidea (Helodermatidae + Varanus/Lanthanotus)**

Characters for reevaluation: 27, 40, 57, 78, 81, 109, 114, 128, 129, 131, 133, 135, 147, 162, 163, 164, 166, 167, 172, 173, 174, 194, 204, 232, 254

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Table 1. Data Set Characteristics

Data set	Total	No. of Characters		MP tree length	Retention Index ^a	Average pairwise genetic distance ^b
		Variable	Parsimony-Informative			
<i>RAG-I</i>	2765	1726	1489	9900	.602	.213 (.149)
1 st pos		469	367			
2 nd pos		358	256			
3 rd pos		899	866			
<i>c-mos</i>	359	237	212	1097	.578	.238 (.169)
1 st pos		72	64			
2 nd pos		57	42			
3 rd pos		120	114			
MtDNA^c	1497	1254	1137	14328	.396	.905 (.310)
1 st pos		295	277			
2 nd pos		273	222			
3 rd pos		318	311			
tRNA loops		66	51			
tRNA stems		301	275			

^aFarris 1989.

^bAverage maximum-likelihood corrected percent sequence divergence between all ingroup taxa, calculated for each data set under its own evolutionary model and set of parameter values (found in corresponding figure legends). Average uncorrected percent sequence divergences are in parentheses.

^cThird-position transversions excluded.

Table 2.
Results of Wilcoxon Signed-Ranks (Templeton) Tests of Topology

Alternative hypotheses tested ^a	<i>P</i> ^b
<i>RAG-I</i> and <i>c-mos</i>:	
Monophyly of Scleroglossa	.0002* (.0004*)
Nonmonophyly of Iguania	.028* (.056)
Monophyly of (Serpentes + Dibamidae)	.0001* (.0003*)
Monophyly of (Serpentes + Amphisbaenia)	.007* (.035)
Monophyly of (Dibamidae + Amphisbaenia)	<.0001*
Monophyly of (Serpentes + <i>Varanus/Lanthanotus</i>)	.0001* (.0008*)
Monophyly of (Lacertidae + Teiioidea) to the exclusion of Amphisbaenia	.044* (.396)
Nonmonophyly of (Lacertidae + Amphisbaenia)	.066 (.198)
Monophyly of Varanoidea (<i>Heloderma</i> + <i>Varanus/Lanthanotus</i>)	.0088* (.0088*)
Monophyly of (<i>Xenosaurus</i> + <i>Shinisaurus</i>)	.029* (.791)
Monophyly of (Scincidae + Cordylidae) to the exclusion of Xantusiidae	.188 (1.000)
Acontinae not the sister taxon of other Scincidae	.095 (.190)
Nonmonophyly of (Diplodactylinae + Pygopodinae)	<.0001*
Monophyly of Scincomorpha (including Amphisbaenia)	.027* (.054)
mtDNA:	
Monophyly of Scleroglossa	.155 (.310)
Nonmonophyly of (Serpentes + Acrodonta)	.195 (1.000)
Monophyly of (Serpentes + <i>Varanus</i> + <i>Lanthanotus</i>)	.200 (1.000)
Nonmonophyly of (<i>Sphaerodactylus</i> + <i>Gekko</i>)	.296 (.592)
Monophyly of (<i>Xenosaurus</i> + <i>Heloderma</i> + Anguidae)	.278 (.278)
<i>RAG-I</i>, <i>c-mos</i>, and mtDNA:	
Nonmonophyly of (Lacertidae + Amphisbaenia)	.0002*(.0004*)
Nonmonophyly of Agamidae	.159 (.795)
Nonmonophyly of (Xantusiidae + Cordylidae)	.031* (.093)
Nonmonophyly of (Trogonophidae + Amphisbaenidae)	.0002*(.0002*)

^a A significant result means that the stated alternative hypothesis is rejected. See Appendix IV for phylogenetic topologies used in tests.

^b One-tailed probabilities are shown, and probabilities in parentheses have been Bonferonni-corrected to account for multiple tests. Asterisks indicate statistical significance at the 0.05 level.

Figure 1. *RAG-I* data, maximum-likelihood phylogram (GTR + I + G model, -lnL=50519.59; A=0.3007, C=0.2242, G=0.2254, T=0.2497; AC=1.3332, AG=4.7011, AT=0.9186, CG=0.8644, CT=5.7274, GT=1.0; I=0.3352, G=1.7108). Asterisks indicate branches that receive a posterior probability of 95% or greater in the Bayesian analysis. Parsimony bootstrap proportions >70% (above branches) and decay indices (below branches) are provided for all nodes congruent between analyses based on the two optimality criteria. Numbers to the right denote major taxonomic units as follows: 1. Chamaeleonidae 2. Agamidae* 3. Iguanidae 4. Anguidae 5. Helodermatidae 6. Xenosauridae 7. Varanidae 8. Shinisauridae 9. Serpentes 10. Lacertidae 11. Amphisbaenia 12. Teiidae 13. Gymnophthalmidae 14. Scincidae 15. Xantusiidae 16. Cordylidae 17. Dibamidae 18. Gekkonidae. (*) denotes uncertain monophyly of Agamidae. Outgroup branches with hatch marks have been shortened for aesthetics of figure.

Figure 2. *C-mos* data, maximum-likelihood phylogram (HKY + I + G model, -lnL=5431.51627; A=0.2712, C=0.2527, G=0.2231, T=0.2530; Ti/Tv=2.4357; I=0.3084, G=3.5785) with parsimony bootstrap proportions and decay indices are added where appropriate. Annotations and numbering as in Figure 1.

Figure 3. Combined *RAG-I* and *c-mos* data, maximum-likelihood phylogram (GTR + I + G model, -lnL=44562.45; A=0.3022, C=0.2212, G=0.2243, T=0.2523; AC=1.4034, AG=4.9417, AT=0.9147, CG=0.9256, CT=5.9064, GT=1.0; I=0.3543, G=2.0844) with

parsimony bootstrap proportions and decay indices are added where appropriate. A = Amphibolurinae, S = Scincinae. Other annotations as in Figure 1.

Figure 4. Mitochondrial data, strict consensus of 4 most parsimonious trees (L=14328, RI=0.396). Parsimony bootstrap proportions >70% are shown above branches and decay indices are in bold below branches. Numbering as in Figure 1.

Figure 5. Mitochondrial data, maximum-likelihood phylogram (GTR + I + G model, -lnL=52671.75841; A=0.4150, C=0.3394, G=0.0593, T=0.1863; AC=0.3588, AG=2.5905, AT=0.4988, CG=0.3158, CT=2.4827, GT=1.0; I=0.0951, G=0.5652). Asterisks indicate branches that receive a posterior probability of 95% or greater in the Bayesian analysis. Long internal branches leading to snakes and acrodonts are in bold (see text). Numbering as in Figure 1.

Figure 6. Results from two sets of 100 parametric simulations designed to detect potential long-branch attraction in the mitochondrial analysis. In these figures, Ac = acrodonts, An = anguimorphans, I = iguanians, and S = snakes. For all simulations, the long-branch taxa (snakes and acrodonts) were separated in the model trees by making snakes the sister taxon of anguimorphs. In the model tree for set I (top), Iguania was nonmonophyletic, and for set II (bottom), Iguania was monophyletic (see text). For clarity, only the relevant portions of the model trees are shown; the remainder of each tree was identical to the original mitochondrial ML topology of Figure 5. The tables show the number of times incorrect (A) and correct (B or C) topologies were recovered

under MP and ML, respectively. D represents various alternative topologies. As a control, 100 simulated data sets were constructed using as a model the exact ML topology of Figure 5. Parsimony and likelihood both recovered the model topology for 98% of these control data sets.

Figure 7. Summary of squamate phylogenetic relationships supported by molecular data. Solid bars denote branches supported by MP bootstrap values and Bayesian posterior probabilities of $\geq 95\%$ in analyses of both nuclear and mitochondrial DNA. Hatched bars denote branches supported by bootstraps and posterior probabilities $\geq 95\%$ in the nuclear analysis, and posterior probabilities $\geq 95\%$ in the mitochondrial analysis. Open bars denote branches supported by bootstraps and posterior probabilities $\geq 95\%$ in the nuclear analysis but are not congruent with any mitochondrial topology. This summary topology is incongruent with prevailing morphological hypotheses.

Figure 8. Maximum-parsimony consensus tree from the reanalysis of morphological data of Lee and Caldwell (2000). Only extant taxa are included, character states are unordered, and 27 characters identified by Lee (1998) as potentially convergent in head-first burrowers have been removed. Bootstrap values are above branches, decay indices below in bold. Note that snakes, amphisbaenians, and dibamids form a strongly supported clade in this analysis.

Figure 9. Evolution of feeding mode in lepidosaurs. White branches indicate lingual prehension, black branches jaw prehension, and the gray branch is equivocal. A. Under

a traditional monophyletic Scleroglossa, produced here by rerooting our nuclear topology, the lingual-feeding evolutionarily stable complex (ESC) arose once in an ancestral lepidosaurian, and was lost in an ancestor to Scleroglossa. B. Under our nuclear topology, feeding mode is more labile, with lingual feeding arising at least twice, once in the lineage leading to *Sphenodon* (or possibly an ancestral lepidosaurian), and once in an ancestor to Iguania. Jaw prehension is the ancestral feeding mode of squamates.

Figure 1. RAG ML/MP

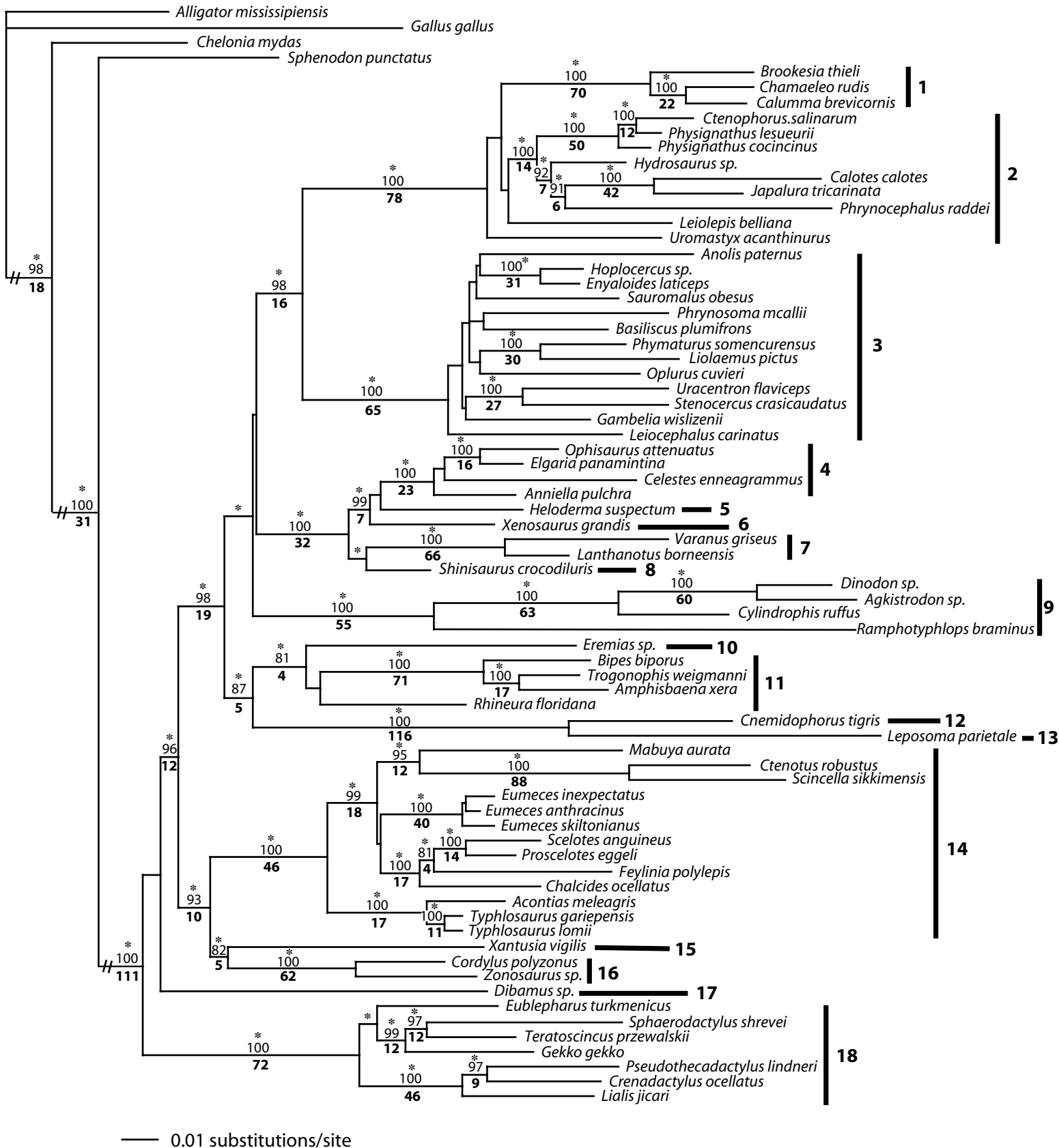
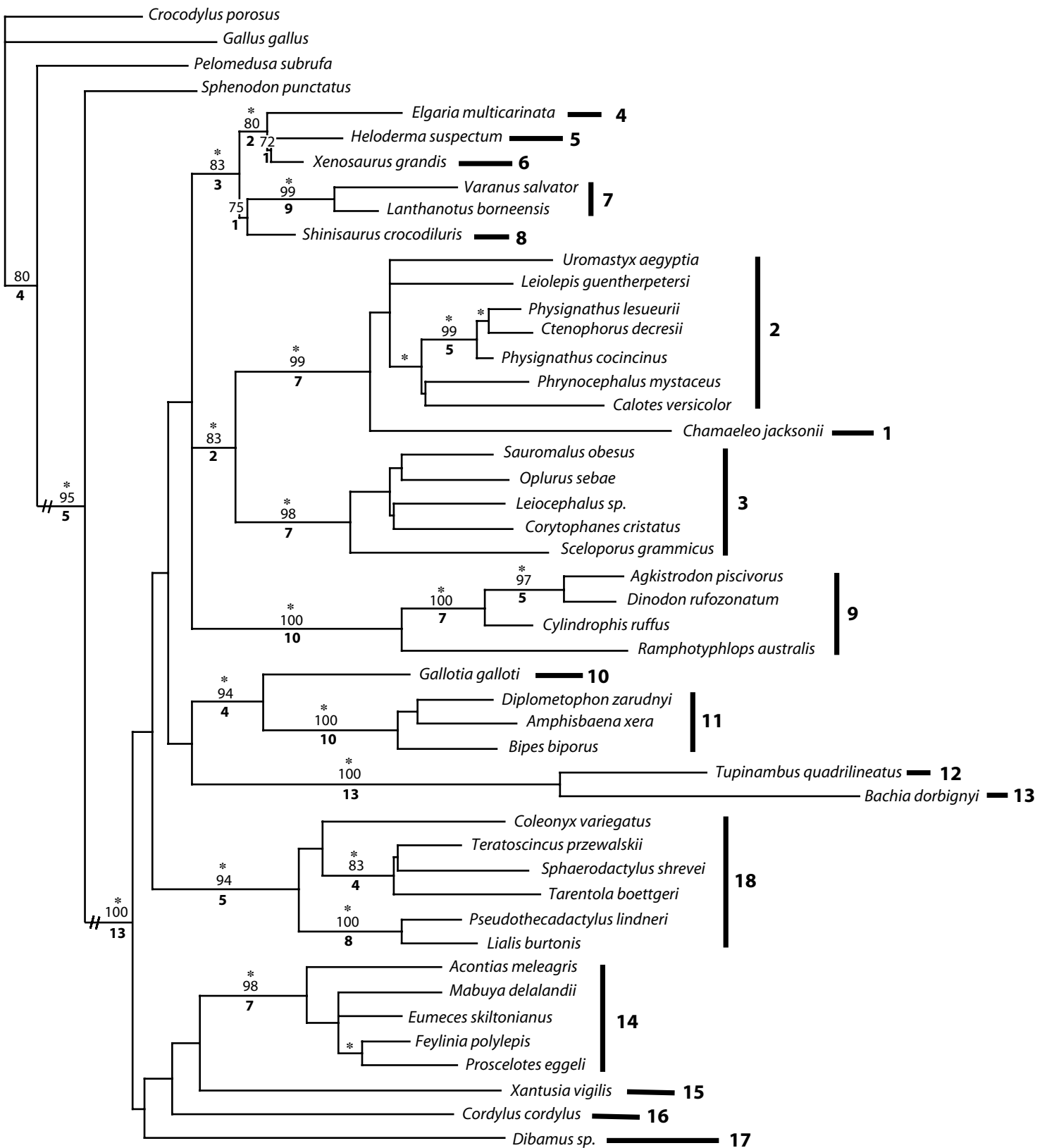
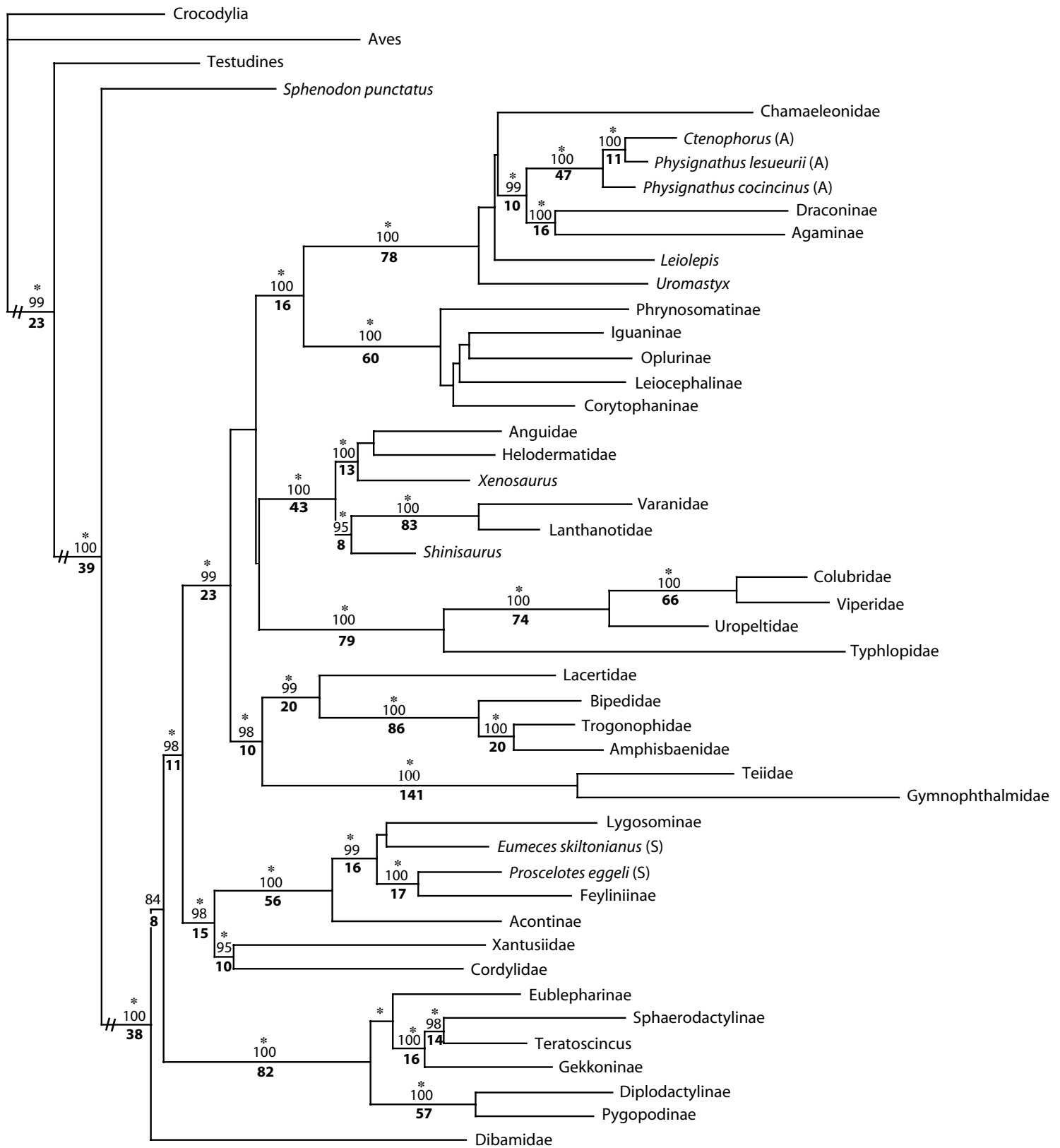


Figure 2. c-mos ML



0.05 substitutions/site

Figure 3. RAG/c-mos ML/MP



0.05 substitutions/site

Figure 5. mtDNA MP

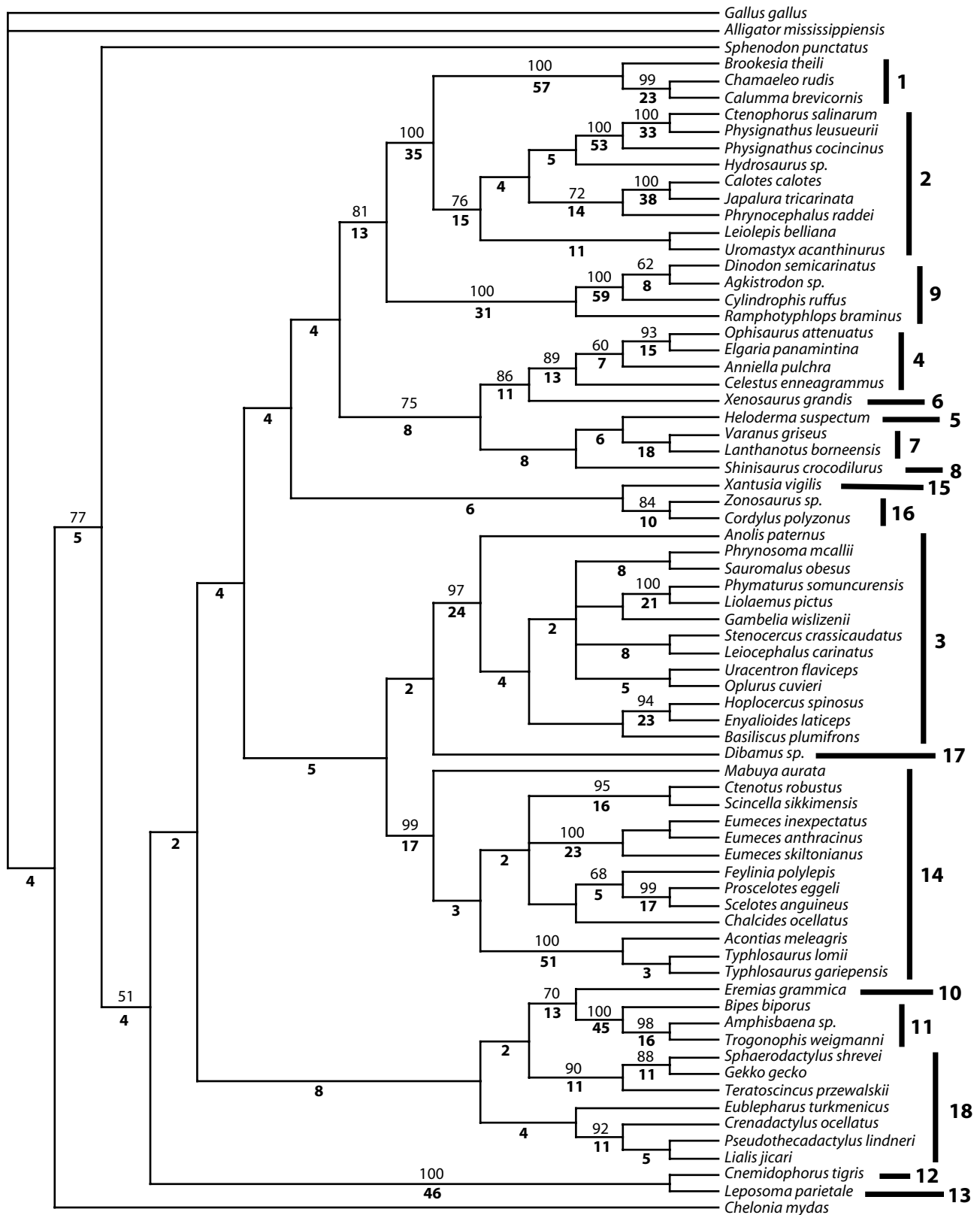


Figure 5. mtDNA ML

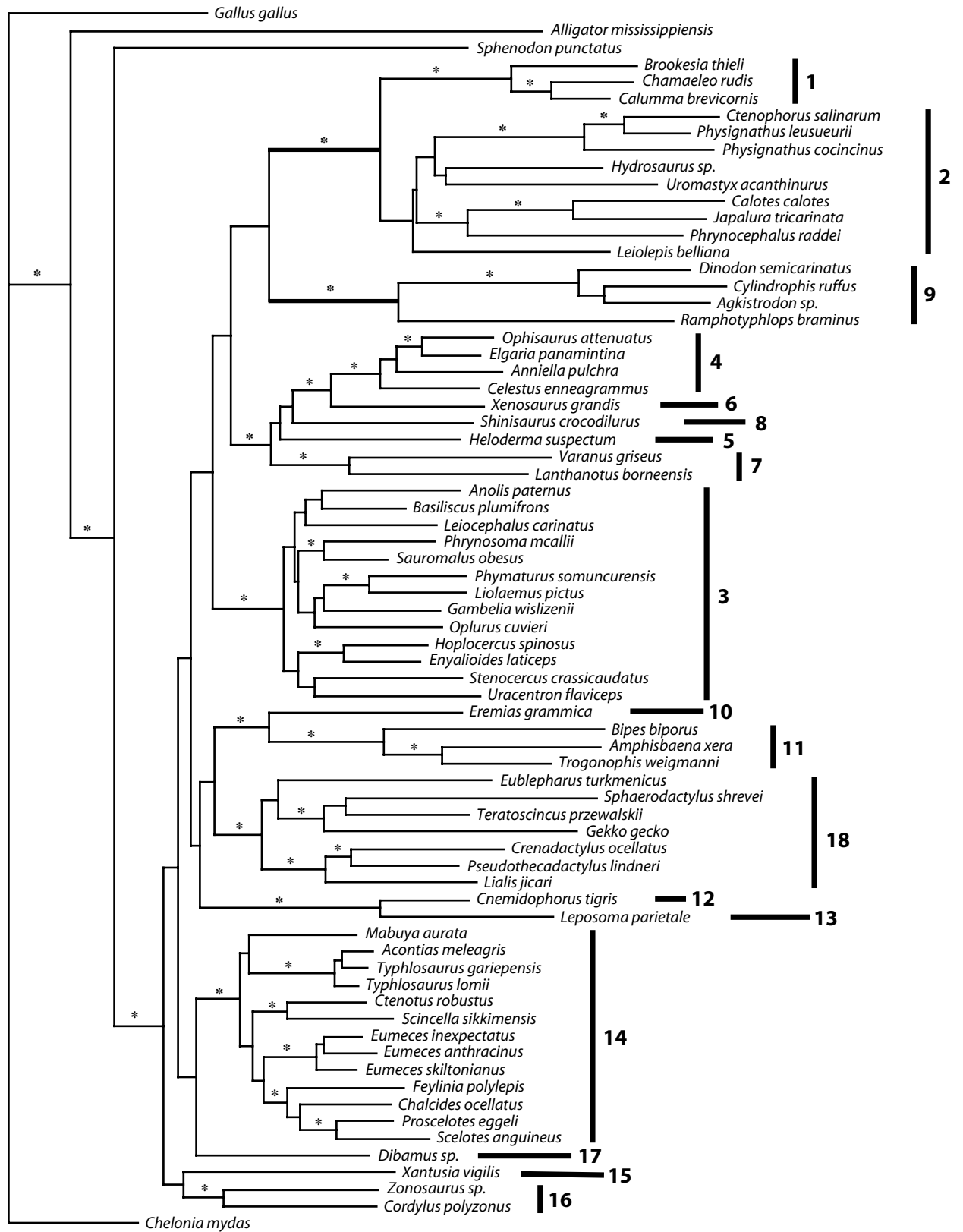
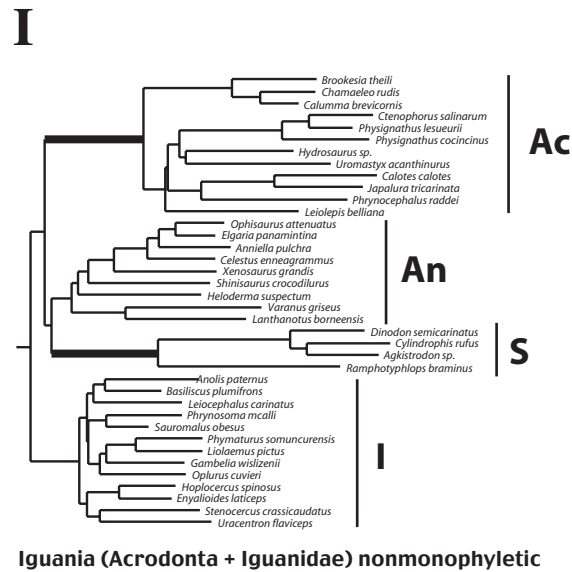


Figure 6. Long Branch Attraction

Simulated Topologies



Topologies recovered from analyses of simulation replicates

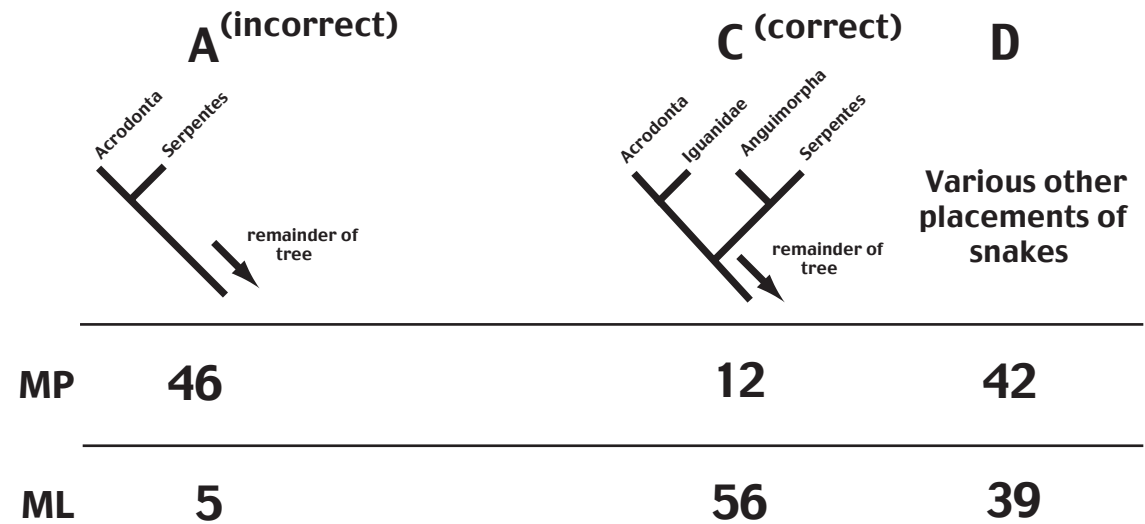
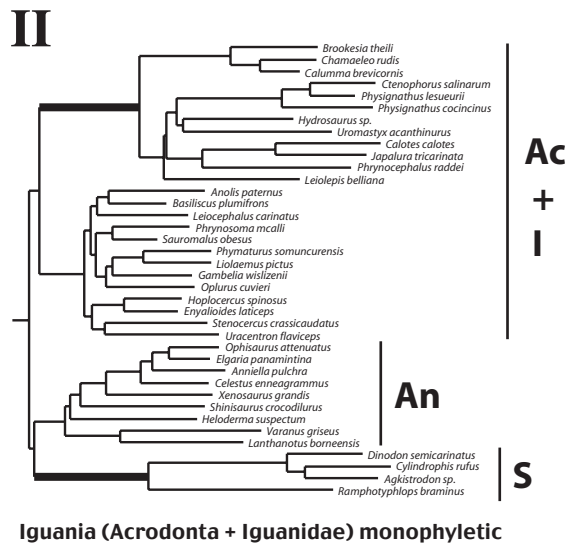
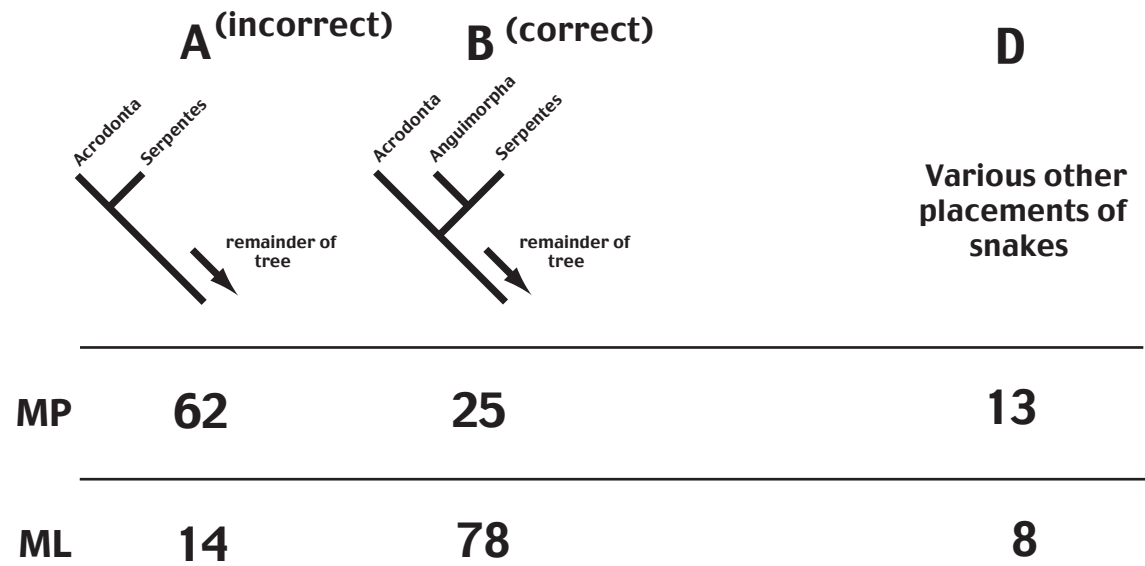


Figure 7. Summary of Squamate Relationships

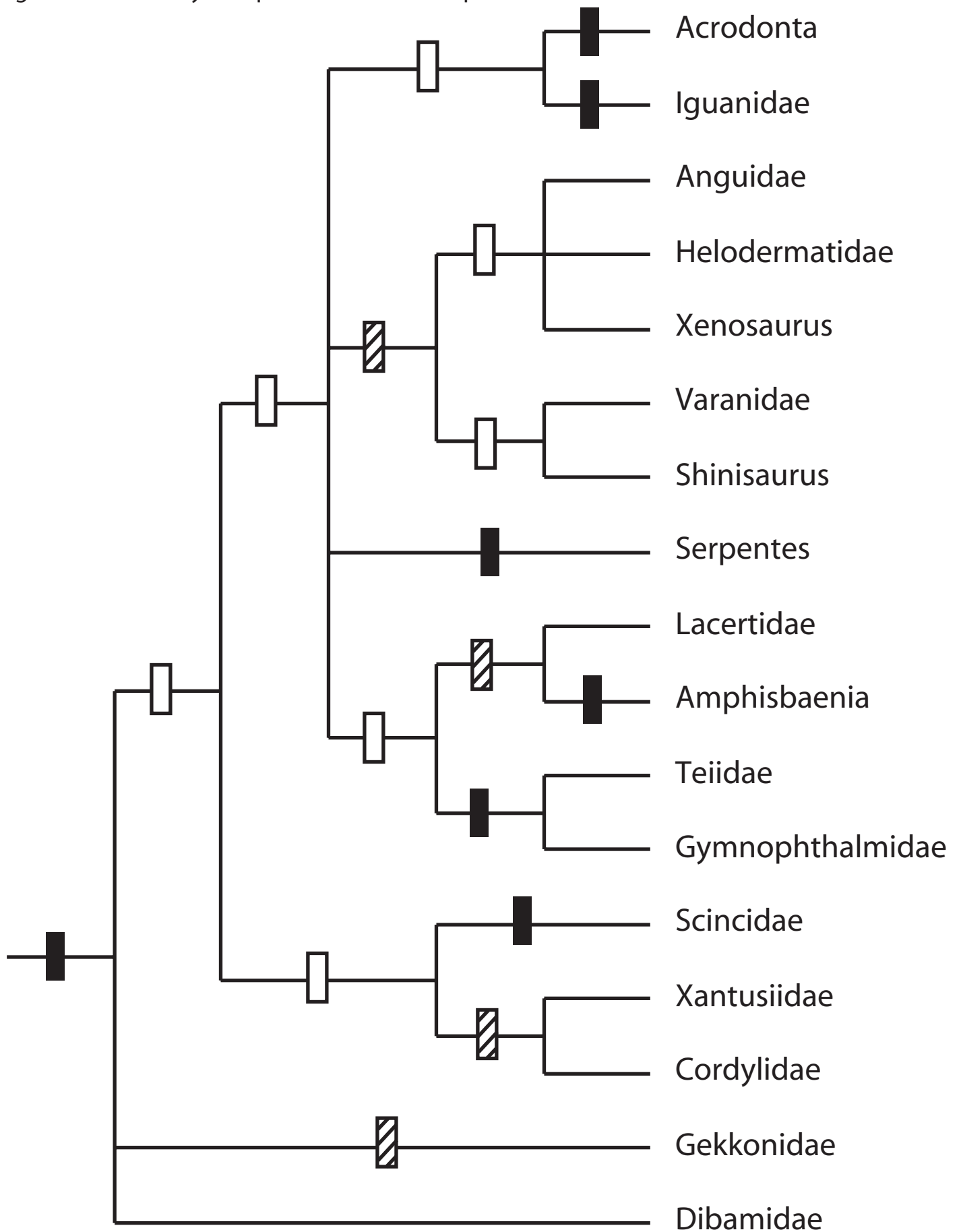


Figure 8. Lee & Caldwell Extant Taxa MP

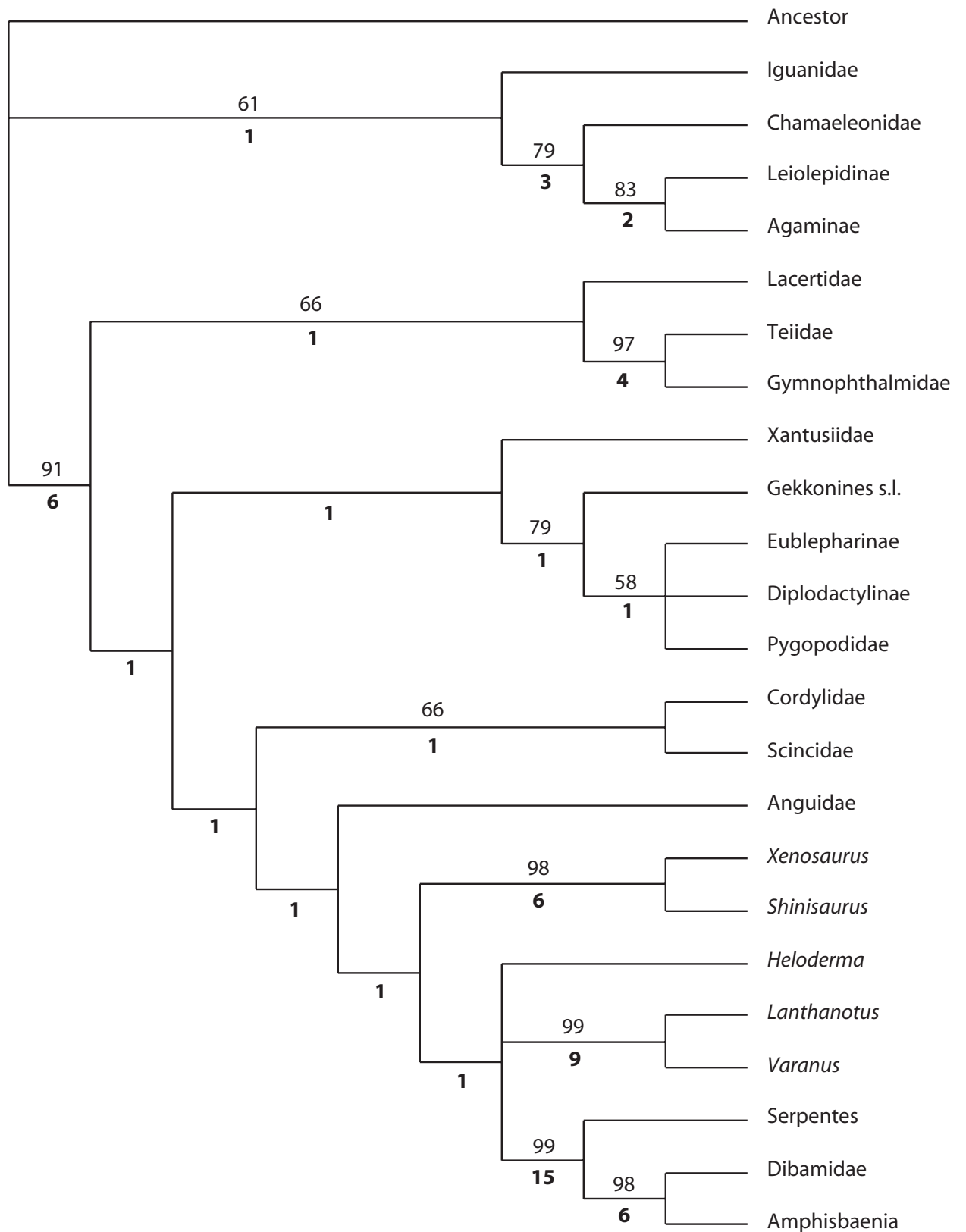


Figure 9. Evolution of Feeding Mode

