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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. Donellan 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 anniellid. 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$^{\mathrm{Gln}}$, tRNA$^{\mathrm{Ile}}$, and tRNA$^{\mathrm{Met}}$, respectively), the entire ND2 (subunit 2 of NADH dehydrogenase) gene, the 5 tRNA genes for tryptophan, alanine, asparagine, cysteine, and tyrosine (tRNA$^{\mathrm{Trp}}$, tRNA$^{\mathrm{Ala}}$, tRNA$^{\mathrm{Asn}}$, tRNA$^{\mathrm{Cys}}$, and tRNA$^{\mathrm{Tyr}}$, 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-1* 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 aligments, 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 1985*a*) 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-1* codons (*p* <.001), phylogenetic results conducted with these positions removed are congruent with analyses of the complete *RAG-1* 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-1* analysis are still represented. The topology of the *c-mos* MP strict consensus is largely compatible with the *RAG-1* 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-1* 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-1* 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-1* 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-1* 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-1* data alone (Appendix IV), likelihood analysis of the *RAG-1* 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-1* 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-1* and *c-mos* data set due to problems with amplification of the *c-mos* fragment. However, a Templeton test performed on the *RAG-1* 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-1* data (Table 1). Likewise, although the mitochondrial data set is only roughly half the size of the *RAG-1* data set (same number of taxa), the mitochondrial MP tree is approximately 45% longer than the corresponding *RAG-1* 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., 1997*b*), 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. 1997*a*; Macey et al. 1997*c*; see also Townsend and Larson 2002 for examples of both novel gene orders and tandem dupilications 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 pleisiomorphies 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-1* 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-1* 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-1* 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-1* analyses. At least in the *RAG-1* results, this is not due to lack of informative characters. Levels of *RAG-1* 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-1* 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 *Uromastyx* 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, Sidney; 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 Paolo, 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., 1997*b*); *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., 1997*b*); *Leiolepis belliana*, Phuket Province, Thailand (MVZ 215497, U82689; Macey et al., 1997*b*); *Uromastyx acanthinurus*, Ouarzazate Province, Morocco (MVZ 162567, U71325; Macey et al., 1997*a,c*); **Iguanidae:** *Anolis paternus*, Cuba (USNM 498070, U82679; Macey et al., 1997*b)*; *Phrynosoma mcallii*, San Diego Co., California (TP24443, unpublished sequence provided by Jim Schulte); *Sauromalus obesus*, California (MVZ 144194, U82687; Macey et al., 1997*b*); *Hoplocercus spinosus*, Mato Grosso, Brazil (MZUSP 907931, U82683; Macey et al., 1997*b*); *Enyaloides laticeps*, Porto Walker, Acre. Brazil (LSUMZ H13573, unpublished sequence provided by Jim Schulte); *Phymaturus somencurensus* 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., 1997*b*); *Gambelia wislizenii*, Nevada (MVZ 227883, U82682; Macey et al., 1997*b*); *Oplurus cuvieri*, Madagascar (CAS-RM10468B, U82686; Macey et al., 1997*b*); **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 (Cincinatti 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., 1997*c*); **Ampisbaenia:** *Bipes biporus*, Baja California Sur, Mexico (MVZ 137543; U71335; Macey et al., 1997*c*); *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., 1997*c*); *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., 1997*a*,*c*); *Gekko gekko*, Phuket Island, Phuket Province, (Macey et al. 1999*b*); *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., 1997*c*); **Scincidae:** *Mabuya aurata*, Turkmenistan (CAS 179697, U71330; Macey et al., 1997*c*); *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 gariepensis* Farm Avondsehijn, 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., 1997*c*); **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, Shwesettaw 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: *Diplometophon 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
F83b: TCNGAATGGAARTTYAARCTNTT R103
F94: TGGAARTTCAARCTGTTCAAAGT R75
F104: CAAAGTGAGATCNCTTGAAAA R51
F108: GTGAGATCACTTAACAAACCA R50
F117: ACTTGGAAAGCCACTTCCYGAA R46
F129: TTTCTGATGACAGCCATCTG R47
F146: ATCTRGCTAACAGTGAYAAAGG R102
F159: TGATAAAGAGAAAGTGGCAGCC R48
R357: GGTGGCTYCTCTTATAAGGATCA R41
R387: GTNTCATCATCTACTGGTCCA R39
F620: TGGARTGGCANCCCCATNC R29
R652: TCTTTCTCTTGAYYCCAYG R30
F889: ATCTGTGAGCATATCCTGGC R134
F962: AAATGYCTTAAAGTAATGGG R148
F1004a: CTAYCCTTGYTTTCCTACNGA R27
F1004b: CTATCCTTGCTTTCCGMCTGA R130
R1096: AGATGRTGGCTGTATTTTCC R61
R1107: TTATGGCTGGAAAGATGGTGA R62
R1165[b]: GATGCTGCCTCGGTCGGCCACCTTT R18
R1168: GGTGTTGTCTTGGTCGGCCACC R63
F1457a: TGTAGCCARTACCATAAAATGTA R90
F1457b: TGYAGTCARTAYCACAAAATGTA R145
R1639: GTGTCYACTGGGTARTCATC R89
F1709: TTTGGTGGCTGCCCTTATGGA R154
R1968: TTCATCAGCCAGCATAAGGCAC R85
F1989: TGCCTTATGCTGGCTGATGAA R65
R2023: TCTCTTTCTGCTACAAGAGG R101
F2568a: GGATGAATGGRAATTTTGCCAGA R38
F2568b: GGATGAATGGAAAYTTTGCTMGA R149
R2643: AGATAAAGCTCCATGAGYTCT R59
R2847: AGCACCAATGGAGCCRTCTCTT R55
R2857: TCACTTGCCCAAGCTCCAATAGA R66
R2876: TTTGTTCCCAGATTCATTTCC R70
R2918: GACTGCCTSGCATTCATTTTYC R28
R3001: RTGNGCRTTCATRAAYTTYTG 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*. (1997*a*) unless otherwise noted.

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

[a] Kumazawa and Nishida (1993)

[b] This study

[c] Macey et al. (1997*b*)

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. *Uromastyx acanthinurus*
17. *Anolis paternus*
18. *Phrynosoma mcallii*
19. *Sauromalus obesus*
20. *Hoplocercus sp.*
21. *Enyaloides laticeps*
22. *Phymaturus somencurensus*
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 gariepensis*
69. *Typhlosaurus lomii*
70. *Xantusia vigilis*
71. *Cordylus polyzonus*
72. *Zonosaurus sp.*
73. *Dibamus sp.*

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Index2            000000000111111111122222222223333333333444444444455555555556666666666777777777788888888889
Index3            123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.      TAAAGTAAGATCATTTGAAAAGACACCTCCTGGGGATAGCCACGTGGTAAATAAAGATAAAGCAGAAGAGGCAGCCTCTTTGGACAAAGG
G.gallus          TAAAGTGAGGCCATTTCAAAAAGAACCTTCTGATAAAAGCCAATGCATAAACAAGGATCAAGAACAAGAGGTAGCTTCTACAGACAAAAA
C.mydas           ??????????????????????????????????????????????GAAAATAAAGAGAAAGCAGAGAAGGAGGCTTCTTTGGACAATGG
S.punctatus       CAAAGTGAGATCATTTGAAAAGGCACCTCCTGAAGACAGCTGCCCAAAAATCAATGAGAAAGCAGAAGAGGTGGTCTCTTTGGGCAAAGC
B.thieli          TAAAGTGAGACCACTTGGAAAAATACTCCCTGAAGACAATAATCTGGCCAACAGCAATAAAGGAGAACCAGCAGCCTCTCTGGACAAAGT
C.rudis           TAAAGTAAGACCACTTGGAAAACTACTTCCTGAAGACAATCATCTGGCCAACAGCAATAAAGAAGAACCAGCAGTCTCTCTGGACAAAGT
C.brevicornis     TAAAGTAAGACCACTTGGAAAACTACTTCCTGAAGACAATCATCTGGCCAACAGCAATAAAGGAGAACCAGTAGCCTCTCTGGACAAAGT
C.salinarum       CAAAGTGAGACCACTTGGAAAGCCACTTCCTGAAGACAGTCATCTGGCTAATAGCAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
P.lesueurii       TAAAGTGAGACCACTTGGAAAGCCACTTCCTGAAGACAGTCATCTGGCTAATAGCAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
P.cocincinus      CAAAGTGAGACCACTTGGAAAGCCACTTCCTGAAGACAGTCATCTGGCTAATAACAATAAAGGAGAAGTGGCAGCCTCTCTGGACAAAGT
Hydrosaurus.sp.   CAAAGTGAGACCACTTGGAAAGCCACTTCCTGAAGACAGTCATCTGGCTAACAGCAATAAAGGAGAAGTGGCAACCTCCCTGGACAAAGT
C.calotes         CAAAGTGAGACGACTTGGAAAGCCACTTCCTGAAGACAGTCATCTGGCTAACAGCGATAAAGGACAAGTGGCAGCCCCCCTGGACAGAGC
J.tricarinata     CAAAGTGAGACGACTTGGAAAGCCACTTCGTGAAGACAGTCATCTGGCTAACAGCGATCAAGGACAAGTGGCAGCCTCCCTGGACAAAGT
P.raddei          CAAAGTGCGACCACTTGGAAAGCCACTTCCCGAAGACAGTCAAGTGGCTAACAGCGATAAAGGGCAAGTGGCAGCCTCCCTGGACAAAGT
L.belliana        CAAAGTGAGGCCACTTGGAAAGCCATTTCCTGAAGACAGTCATCTGGCTAACAGCAATAAAGGAGAAGTGGCAGACTCCCTGGACAAAGT
U.acanthinurus    CAAAGTGAGACCACTTGGAAAGCCATTTCCTGAAGACAGTCATCTGGCTAATAGCAATAAAGGAGAAGTGGCAGCCTTCCCCGACAAAGT
A.paternus        CAAAGTGAGATCAATTGAGAAGCCACTTCCTGATGACAGCCATCTGGCTAACAACAATAAAGGGAAAGCGGCAGCTTCTCTGGACCAAGT
P.mcallii         CAGAGTAAGATCACTTGAGAAGCTGCTTCCTGATGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTG------------GACAAAGT
S.obesus          ??????????????????????????????????????????????GCTAACAACAATAAAGGAAAAGTGGCTTCTTCTCTGGACAAAGT
Hoplocercus.sp.   CAAAGTGAGATCACTTGAGAAGCCACTTCCTGATGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCAGTTTCTCTGGAGAAAGT
E.laticeps        ??????????????????????????????????????????????GCTAACAACAATAAAGGAAAAGTGGCAGTTTCTCTGGACAAAGT
P.somencurensus   CAAAGTAAGATCACTTGAGAAGCCACTTTCTGCTGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCAGCTTCTCTGGACAAAGT
L.pictus          CAAAGTGAGATCACTTGAGAAGCCACTTCCTGCTGACAGTTACCTCGCTAACAACAATAAAGGAAAAGTGGCAACATCTCTGGACAAAAC
U.flaviceps       CAAAGTGCGATCACTTGAGAAGCCACTTCCTGATGACAGCCATCTGGCTAACAACCACAAAGGAAAAGTGGCAGCTTCAGTGGATAAAGT
S.crasicaudatus   CAAAGTGAGATCACCTGAGAAGCCACTTCCTGATGACAGCTGTGTGGCTAACAACCATAAAGGAAAAGTGGCAGCTTCTCTGGATAAAGT
L.carinatus       CAAAGTGAGATCACTTGAGAAGCCACTTTCTGATGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCACCTTCTCAGGACAAAGT
B.plumifrons      CAAAGTGAGATCACTTGAGAAGCCACTTTCTGATGACAGCCATCTGGCTACCAACAATAAAGGAAAAGTGGCAGCTTCTCTGGACAAAGT
G.wislizenii      CAAAGTGAGATCACTTGAGAAGCCACTTTCTGAAGACAGCCATCTGGCTAACAACAACAAAGGAAAAGTGTCAGCTTCTCTGGACAAAGT
O.cuvieri         ??????????????????????????????????????????????GTTAACAACAATAAAGGAAAAGTGGCAGCTTCTCTGGACACAGT
O.attenuatus      CAAAGTGAGATCACTTGAAAAGCCACTTCCTGAAAGCAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
E.panamintina     CAAAGTGAGATCACTTGAAAAGCCACTTCCTGAAGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
C.enneagrammus    CAAAGTGAGATCACTTGAAAAGCCACTTCCTGAAGACAGCCATCTGGCTAACAACAATAAAGGGAAAGTGGCAGCCTCTCTGGACAAAGT
A.pulchra         CAAAGTGAAATCACTTGAAAAGCCACTTCCTGAAGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
H.suspectum       CAAAGTGAGATCGCTTGAAAAGCCACTTCCTGAAGACAGCCATCTGGCTAGCAACAATAAAGGAAAAGGGGCAGCCTCTCTGGACAAAGT
X.grandis         CAAAGTGAGATCCCTTGAAAAGCCACTTGCTGAAGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCAGCCACTCTGGACAAAGT
V.griseus         CAAAGTGAGGCCGCTAGGAAAGCCACTTCCTGAAGATATCCATCTGACTAGCAGCGATAAAGAA---GTGGCAGCTTCTCTGGTCAGAGT
L.borneensis      CAAAGTGAGGCCTCTTGGAAAGCCACTTCCTGAAGACAGCCATATGGCTAACAGCAATAAAGGAGAAGTGGCAGCCTCTCTGGACAGAGT
S.crocodiluris    CAAAGTGAGATCACTTGAAAAGCCACTTCCTGAAGACAGCCATCTGGCTAACAACAATAAAGGAAAAGTGGCAGCCTCTCTGGACAAAGT
Dinodon.sp.       CAAAGTGAGATCACTTGAAAAACCTCTTCCTGAAGACAGCCACCAGGCTAACTCTGCTAAAGAAAATGTGACAGGGTCTCTGGAC---AT
R.braminus        CAAAGTGAGATCCCTTGAAAAGCCTCTTCCTGAAGGCAGCCACCAAGCT---------AAAGGAAAA---GCAGGTTCCCTGGACAGAGT
C.ruffus          CAAAGTGAGATCACTTGAAAAGCCTCTTCCTGAAGACAGCCACCAAGCTAACTGTGCTAAAGATAAAGTGACAAGTTCCCTGGAC---AT
Agkistrodon.sp.   CAAAGTGAGATCACTTGAAAAGCCTCTTCCTGAAGAAAGCCACCAGGCTAACTCTGCTAAAGAAAATGTGACAGGTTCTGTGGAC---AT
Eremias.sp.       CAAAGTGAGATCATTTAGCAAACCGCTTCTTGAAGACAGTCACCTGGCTCACAGTGATAAAGGAAAAGAGGCAGCCTCTCTGGGCAATGT
B.biporus         CAAAGTGAGATCACTTAACAAACCACTTCCTGAAGACAGTCATCTAGCTAACAGTGATAAAGGAAAAGAGACAGCCATTCTGGACAGGGG
T.weigmanni       CAAAGTGAGATCACTTAACAAACCACTTCCTGAAGACAGTCATCTGCCTAACAGTGATAAAGGAAAAGAGACAGCCATTCTGGACAGAGG
R.floridana       CAAAGTGAGATCACCTAATAAGCTACTTCCTGATGACAGTCATCTGGCTAACAATGACAAAGGCAAAGAGGCAGCTTCTCTGGACAATGT
A.xera            ???????????????????????????????????????????????????????????????AAAAGAGAGATCCACTCTGGACAGGGG
C.tigris          CAAAATCAGATCTCTGAAAAAGTCACTTTCGGAAGAGAGTCATGTGGCTGACAGTGACAAAGAGAAAGTGGCAACCTCTGTGGACAAAGG
L.parietale       CAAAATCAGATCACTGCAAAATTCACTTTCAGAAGAGGATCGTGTGGATGACGGTGTTAAAGGGAAGGTGGCAAATTATCTGGACAAAGA
E.turkmenicus     ?????????????????????GTCACTTCCTGAAGAGAGCCATCTGGCTGACAATGATAAAGGGAAAATGGCTGCCTCTCTGGACAAAGT
S.shrevei         CAAAGTGCGATCTCTTGAAAAGTCACTTTATGAAGACAGCCATCTGGCTAAAGATGATAAAGGGAAAGTGGCAGCCTCTTCGGACAAAGT
T.przewalskii     CAAAGTGAGATCTCTTGAAAAATCACTTTCTGAAGAGAGCCATCTGGCTAACAATGATAAAGAGAAAGTGGCAGCCTCTTTGGGCATAGT
G.gekko           CAAAGTGAGATCTCTTGAAAAGTCACTTCCTGAAGAGAGCCATCTGGCTAACCATGATAACGGGAAAATGCCAGCTTTTTCGGACAAAGT
P.lindneri        CAAAGTGAGATCTGTTGAAAAGGCAGTTCGTGAAGAGAGCCATCTCGMTAGCAATGATAAAGAGAAAGAGGCAGCCTCACTCGACAAAGT
Cr.ocellatus      CAAAGTGAGATCTCTTGAAAAGGCCGTTCCTGAAGAGAGCCATCCTGCTAAGACTGATAAAGAGAAAGTGGCAGCCTCACTAGACAAAGT
L.jicari          ????????????????????????????????????????????????????????????????????????????TTCCTAGACAAAGT
M.aurata          CAAAGTGAGATCACTTGAAAAACCACTTCCTGAGTGCAGCCATGTGGCTAAGCATGATAAGGGGAAAGTGGCAGATTTTCTGGACAAAGC
C.robustus        CAAAGTGAGGTCGCTTGAAAAACCACTTCCTGAATGCAGCCATATGGCTCACAACAATAAAGGGAAAGTTGCAGATCTTCTAGACAAAGC
S.sikkimensis     CAAAGTGAGATCGCTTGAAAAGCCACTTCCTGAACTCAGCCATATGGCTAACAACGATAAAGAGAAAGTGGCACAACCTCTGGACACAGC
E.inexpectatus    CAAAGTGAGATCGCTTGAAAAACCACTTCCTGAACGCAGCCATGTGGCTAACAATGATAAAGGGAAAGTGGCGGACTCTCTAGACAAAGT
E.skiltonianus    ?????????????????????ACCACTTCCTGAATGCAGCCATGTGGCTAACAATGATAAAGGGAAAGTGGCGGACTCTTGTGACAAAGT
E.anthracinus     ?????????????????????ACCACTTCCTGAACGCAGCCATGTGGCTAACAATGATAAAGGGAAAGTGGCGGACTCTCTAGACAAAGT
S.anguineus       ?????????????????????ACCACTTCCTGAACGCAACCATGTGGCTAATAATGATAAAGGGAAAGTGGCAGACTCTCTGGACAGAGC
P.eggeli          CAAAGTGAGACCGCTTGAAAAACCACTTCCTGAACGCAGCCATGTGGCTAACAATGATAAAGGGAAAGTGGCAGACTCTCTGGATAGAGC
F.polylepis       CAAAGTGAGGCCGCTTGACAAATCAGTTCCGGAGCACAGCAATGTGGCTAACAACAATCAAGAGAAGGTGGCAAAGATGCTGGACAAAGG
Ch.ocellatus      CAAAGTGAGACCGCTTGAAAAACCACATCCAGAACACAGCCATGTGGCTAACAATGATAAAGGTAAAGTGGCAGACACTTTGGACAAAGC
A.meleagris       ?????????????????????ACCACTTCCTGAACTCAGCCATATGGCTAACAATGATATAGGGAAGGTGGCGGACTCTCTGGACAAAGC
T.gariepensis     CAAAGTGAGATCGCTTGAAAAACCACTTCCTGAACTCAGCCATATGGCTAACAATGATATAGGGAAGGTGGCAGACTCTCTGGACAAAGC
T.lomii           CAAAGTGAGATCACTTGAAAAACCACTTCCTGAACTCAGCCATATGGCTAACAATGATATAGGGAAGGTGGCAGACTCTCTGGACAAAGC
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X.vigilis         CAAAGTGAGATCTCTTGAAAAGCCACTTCCTGAACACAGTCATCTGGCTAACAACGATAATGTGAAAATAGCAGCCTCTGTGGACAAAGT
C.polyzonus       ??????????????????????????????????CACAACCATCTGGCTAACAATGATAAAGGGAAAGTGGCAGCTATTCTGGACAATAT
Zonosaurus.sp.    CAAAGTGAGATCACTTGAAAAACCACTTCCTGAACACAACCATCTAGCTAACAATGATAAAGGGAAAGTGGCAGATAATCTGGACAAAGT
Dibamus.sp.       CAAAGTGAGATCACTTGAAAAGTCACTTCCTGAAGATGAC-------------------AAAGAGGAAAAGGCAGCCTCTCTGGAAAAGT

Index1            000000000111111111111111111111111111111111111111111111111111111111111111111111111111111111
Index2            999999999000000000011111111112222222222333333333344444444445555555555666666666677777777778
Index3            123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.      CAATGTGGTACATATGGATGCAGTAATCCCAGTGATG---GATAAACAGGTTGTGCTACAAGCAGAATTAAAGGTCACTAAGCAG---AC
G.gallus          CATCACGCTGCATAAAGATGAAGAAGTTCCAAGAGGA---GAAAAGTTAATTCTGACACAGAAGGACTTCATGGGCAATACGCAA---GC
C.mydas           CACTCTGGTGCAGATGGATGTGGCAGTTCCAGTGGCA---GAAAAGCCACTTCTGGCAGATACAGACTTAAATCACAATAAGCAG---GC
S.punctatus       CATTGTGATGCAAGAAGATACAGCAATTTCAACATCC---AAAAAGCCATGTCTGATGCACAGAGAATTAAGGAGTGATATGCAG---AC
B.thieli          CACAGAGAAGCAAGTG------------------TCA---CAAGTAACTTCTGAAACAGACACTGAATTGAACAAAAGCATACAG---AC
C.rudis           CAGAGAGAAACAAGTG------------------TCA---CAAGCACCTTCTGAAACAGACACTGAATTGAACAAAAGCATACAG---AA
C.brevicornis     CAGAGAGAAGCAAGTA------------------TCA---CAAGTACCTTCTGAAACAGACACTGAATTGAACAAAAGTATACAG---AC
C.salinarum       CACTGAAAATCAAGCTGAAGTGTCAACTCTACCTTCA---GAAGTATGTTCTGAAACAGATACTGAATTGAACAAAAGCATACAG---AC
P.lesueurii       CACTGAAAATCAGGCTGAAGTGTCAACTCTACCTTCA---GAAGTATGTTCTGAAACAGATACTGAATTGAACAAAAGCATACAG---AC
P.cocincinus      CACCAAAAATCAGGCTGAAGTGTCAACTCTACCTTCA---GAAGTACGTCCTGAAACAGATACTGAATTGAACAAAAGCATACAG---AC
Hydrosaurus.sp.   CACCGAAAATCAAGCTGAAGTGTCTGCTCTACCTTCA---CAAGTACCTTCTGAAACAGACACTGAATTGAACAAAAGCATACAG---AC
C.calotes         CACCGAAAATCAGGCTGAAGTGGCAGCTCTACCTTCA---CAAGTGCCTTCTGAAACAGACGCTGGATTGAGCAAAAGCATCCCG---AC
J.tricarinata     CGCCGAAACTCAGGCTGAAGTGGCAGCTCGACCTTCA---CAAGTGCCTTCTGAAAGAGACACTGAATTGAACAAAAGCATCCAG---AC
P.raddei          CAGCGGAAATCAGGTGGAAGTGTCAGCTCTACCTTCA---CAAGTGCCTTCTGAAAGAGACGCTGGATTGAACAAAAGCATCCAG---AC
L.belliana        CACTGAGAAGCAGGCAGAAGTGCCTGCTCTACCGTCA---CAAGTGCCTTCTGAAATAGACACTGAATTGAACAGAAGCATACAG---AC
U.acanthinurus    CACTGAGAAGCTGACTGAAGTGTTAGCTCCACCATCA---CAAGTGCCTCCTGAAACAGACGCTGAATTGAACAAAAGTATACAG---AT
A.paternus        CATTGAGGAAAAGACTGATATGGTAACTCTGATGCCA---CATTCACCCTTTGAAATAGACATTGAGTTGAACAAAAGCATGCAG---AC
P.mcallii         CATTGAGAAAGAGATTGAGACAGTGTCTCTAAAGTCA---AACACACCCTTTGAAACAGACACTGAGTTGAACAAAGGTATGCAG---AC
S.obesus          CATTGAAGAAAAGACTGGGGTGGTGGCTCTAATGTCA---CACCCACCCTTTGAAACTGACACAGAGTTGAACAAAGGTGTTCAG---AC
Hoplocercus.sp.   CATTGAGGAAAAGACTGAGATGGTGACTGTAATGTCA---CACTCACCCTTTGAAACAGACACTGAGTTGAACAAAGGTATCCAG---AC
E.laticeps        CATTGAGGAAAAGACTGAGAYGGTGACTGTAATGTCA---CACTCACCCTTTGAAACAGAAACTGAGTTGAACAAAGGTATTCAG---AC
P.somencurensus   CATTGAGGAAAAGACTGAGACGGTAGCTCTAATGCCA---CACTTACCCATTGAAACTGACACTGAATTGAACAAAGGTATTCAG---GC
L.pictus          CGTTGAGGAAAAGACTGAGAAGGTGGCTCTGATGTCA---CACTCACCCTTTGAAACTGACACTGAATTGAACAAT--------------
U.flaviceps       CTTTGAGGAAAAGACTGAGACAGTGGCTCTAATGTCA---CACTCACCCTTTGAAACAGAGACTGAGTTGAACAAAGGTATTCAG---AC
S.crasicaudatus   CATTGAGGAAAAGACTGAAACTGTGGGTCTAATGTCA---TACTCAACCTTTGAAACTGACACCGAGCTGAACAAAGATATTCAG---AC
L.carinatus       CGTTGAGAAAAAGACTGAGACGGTGGCTCTAATATCA---CAGTCGCCCTTTGAAACAGACACTGAGTTGAACAAAGGTATCCAG---AC
B.plumifrons      CAGTGAGGAAAAGACTGAGACTGTGGCTGTAAAGTCA---CACCCACCCTTTGAAACAGACATCCAGTTGAACAAATGTATTCAG---AA
G.wislizenii      CATTGAGGAAAAGCCTGAGACTGCGGTTCTAATGTCA---CACTCATCCTTTGAAACAGACACAGAGTTGAACAAAGGTATTCAG---AC
O.cuvieri         CAGTGAGGAAAAAACTGAGGCAGGGGCAATAATGTCA---CACTCATCCTTTGAAACAGACACTGAGTTGAACAATGGCATTCAG---AC
O.attenuatus      CGCCAAGCAACAGGATGGCGCGGTGGCTTTAATGTCTCAACAAGCACCCTTTGAAACAGGCTCTGACTTGAACAAAAGTATGCAG---GA
E.panamintina     CGCCGAGCAACAGCCTGATGCGGTGGCTTTCATGTCACAACAAGCACCCTTTGAAACAGGCTTTGACTTGAACAAAAGTATGCAG---GA
C.enneagrammus    CGCCGAGCAACAGGCTGATGCGGTGGCTTTAATGTCACACCAAGCGCCCTTTGAAACAGGCTCTGACTTGAACCAAAGTGTGCAG---CA
A.pulchra         CGCCGAGCAACAGGCTGATGCGGTTGCTTTAATGTCACAACAAGCACCCTTTGAAGCTGGCTCTGACTTGAACAAAAGTACACAG---GA
H.suspectum       CAACGAGCAACAGGCTGATGTGGCGGCTTTAATGTCACCTCAGGCACCCTTTGAAACAGACACCGAATTGAACACAAATACACAG---GC
X.grandis         CGCTGAGGAACAGGCTGATGCGGCGGCTTTAATGTCACAACAAGTGCCCTTCGGAACAGACACCAAAATGAACAAAAGTATGCAG---GC
V.griseus         CACCGAGCAACAGGTTGATTCAGCAGCTTTCATGTTACAACATGTGCCCTTTGAAGCAGGCACAGAACTGAACAAAAGTTTGCCG---GC
L.borneensis      CGGTGAGGAACAGGTTGATGCAGCAGCTTTCATTTCACAACAAGTACCCTTTGAAGCAGACACAGAACTGAACAAAAGTATTTTGCCGGC
S.crocodiluris    CACCGAGGAATGGGCTGATGCAGCCGCTTTAAAGTCACAACAAGTGTCCTTTGAAACAGACACTGAATTGAACAAAAGTATGCAG---GC
Dinodon.sp.       CACTGACGAACAACCTAAGGYAGCAGCTGTAATGTCA---CAAGTGCCCTTTGAAACAGACCCTGAGTTGAATAAAAATAGCTTG---GC
R.braminus        CAGCAATGAACAGCCTGATGTTGCTACTGTAATGTCA---CAAGTGCCCTTTGATACCAGTACTGAAATGAATACAAAGAGGCCT---AC
C.ruffus          CACTGATGAACAGCCTAATGCAGCAGCTGTAATGTCA---CAAGTGCCATTTGAAACAGATACTGAATTTAATAAAGATAGCTTA---GC
Agkistrodon.sp.   CACTGATGAACAACCTAAGGCAGCAGCTATAATGTCA---CAAGTGCTCTTTGAAGCAGACACCGAGCTGAATAAAAATAGCTTG---GC
Eremias.sp.       CACTGAGGAGCAGGCTGATGTGATCACTTCAGTGTCA---CAAGAACCTTCTGAAACAGTCACGGAAGTCAACAGCAGTGTGCAG---GC
B.biporus         TACCAGGGAACAGGCTGATGCAATGGCTTTCGTGTCA---GAAGAGCCCTTTGAAATAGACACTGGATTCAACAACAGTAAGCAG---AA
T.weigmanni       TACTGGGGAACAGGCTGATGAAATGGCTTTTGTGCCA---GAAGTAGCCTTTGAAACAGACACTGGATTCAACAATAGTAAGCAG---AC
R.floridana       CACAGAAGAACAGGCTGATGTGACAACTTTATTGTCA---CAAGAGTCCTTAGGAACAGACACTGAATTCAACAATAGCATGCAG---AC
A.xera            TACTGGGCAACGGGCTCATGCAATGACTTTTGTGTCA---GAAGTGCCCTTTGAAACCGACACTGGAATCAACAATAGTAAACAG---GC
C.tigris          CATTGCAGAGAAGGTTGATGCTCACCCTTCAATGTTA---CAGGATCCCTTGAGAAAAGACACTGAATCCAACATCAGGGTGCAG---GC
L.parietale       TGTTGGAGAGAAGGTGAATGTGGGCCCTTCAACATTA---CAGGAGCCCTTTAGAAAAGACACTGAATTCAGCAACAGGGTCCAG---GC
E.turkmenicus     CAAT------------GATGTAATTGCTTTAATGCCG---CAAGAGCCCTTTCAGACTGAAAAAAAATTGAACACTGGCATGCAG---AC
S.shrevei         CAAT------------GATGCAATGACTTTAATGCCA---CAAGAGTCCTTTCATACAGGAAAAAATCTAAACAATGGAATGCAG---AC
T.przewalskii     CAAT------------GATGCAATGACTTTAATGCCG---CAAGAGCCCATTCATACAGGAAAAAATTTGAACAATGGCGCACAG---AG
G.gekko           CAAT------------GATGCAATGACTTTAATGCCG---CAAGAGCCATTTCATAGAGGACAAAATCTGAACAACAGCATGCAG---AC
P.lindneri        CAGTGAGAAACAGGCTGATGCGACGGCTTTGATG------CAAGAACCCTTTCAGACAGGGAAAAAACTGAACAATGGAATACAG---AC
Cr.ocellatus      CAGTGAGAAGCAGGCAGATGCAACGGCTTTGATG------CAAGAACCCTTTCAGACAGGAAACAAATGGAACAATGGAACACAG---AC
L.jicari          CAATGAGAACCATGCTGATGCAATGGCTTTGATG------CAAGAACCCTTTCAGACAGGAAAAAAATTGAACAATGGCACACAG---AC
M.aurata          CACTGAGGAACAGGGAGATGTAGTGGGCTTAATGTCA---CAAGACCCCTTACGGATTGACACAGAAGGGGACAATAGTATGGCA---GC
C.robustus        CTCCAAGGAACAGGGGGATGTGGTGAGCTTAAGGTCA---CAGGACCCCTTTCGAATAGATAGAGATCAGAACCATAGTGTGAAG---AC
S.sikkimensis     CTCCAAGCAACAGGGAGATGTGGTGAGCTTAAGGTCA---CAGGGCCCCTTTCGAATAGAGAGAGATCAGAACCATAGTGTGGAG---AC
E.inexpectatus    CTCTGAGAAAGAGGAAGAGGCAGTGGGCTTAAGGTCA---CAAGACCCCTTTCAGTTAGACACAGAACTGAACAATCGTGTGGAG---AC
E.skiltonianus    CTCTGAGAAAGAGGAAGAGGCAGTGGGTTTAAGGTCA---CAAGACCCCTTTCATTTAGACACAGAACTGAACAATCGTGTGGAG---AC
E.anthracinus     CTCTGAGAAAGAGGAAGAGGCAGTGGGCTTAAGGTCA---CAAGACCCCTTTCAGTTAGACACCGAACTGAACAATCGTGTGGAG---AC
S.anguineus       CTCTGAAGAA---GAAGATGCAGTGGGCTTAAGGTCT---CAGGATCCCCTTCAGATGGACGTGGCACTGAACAAGAGCATGGAG---AG
P.eggeli          CTCTGAG------GAAGATGCAGTGGGCTTAAAGTCT---CAGGACCCCCTTCAGATGGATGCAGCACTGGACAATCGCATGGCG---AG
F.polylepis       CTCAGAA------GAAGACACAGTGGCCTTAAGGTCA---CAAGACCCCCTTCAGACGGACACAGCAGTGAACAATAGCATGGAG---AG
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Ch.ocellatus      CTCTGAGGAACAGGAAGAAGCAGTGGGCTTAAGGTCA---CAAGACCCCTTTCAGATGGACACAGCACTGAACAATAGCATGGAG---AG
A.meleagris       AGCTGAGGCACAGGAAGATGCAGTGGGCTTAATGCCA---CGAGACCCTTTTCAGACAGATACAGAACTAAACAATAGTGCAGAG---AC
T.gariepensis     AGCTGAGGCACAGGAAGATGCAGTGGGCTTAATGCCA---CGAGACTCTTTTCAGACAGATACAGAACTAAACAATAGTGCAGAG---AC
T.lomii           AGCTGAGGCACAGGAAGATGCAGTGGGCTTAATGCCA---CGAGACCCTTTTCAGACAGATACAGAACTAAACAATAGTGCAGAG---AC
X.vigilis         CACTGAGGAGCGGAGAGATGCTGTGGATTTAATGTCA---CAAGATCCCCTTCAAACAGATCCAGAATTGCAGAATACTATGAGG---AC
C.polyzonus       CACTGAGGAAGAAACAGATGCTGTGGGGTTAATGTCA---CAAGATTTCTTGCAGACAGACACAGGATTGAACAACAGTATGGAG---AC
Zonosaurus.sp.    CACTGAGGAACAGACAGATGCTGTGGGGTTAATGTCA---CAAGATCCCTTGCAGACAGATCCAGGACTGAACAACAGTATGGAC---AC
Dibamus.sp.       CACTGTGGACCAGACCGATCCAGTGGCTTTAATGTCA---CAAGAGCCCTTTCAGGCAGACATAGAATTGAACAGTGGTATGCAG---AT

Index1            111111111111111111122222222222222222222222222222222222222222222222222222222222222222222222
Index2            888888888999999999900000000001111111111222222222233333333334444444444555555555566666666667
Index3            123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.      ACTTGAAAAAGATGCCAACAATCTGAAGATGCACGATAATGCAACTCATCAAGCAAATCTGGAGGAACTTTGCCGCATCTGTGGAGTTTC
G.gallus          ACTTGAGAAAGATGTCAATGACATGAAAATACAAGACAACACAGCTCACCAGAACAACCTGAAGCAACTTTGCCGCATCTGTGGAGTTTC
C.mydas           TCTTGAAAAAGATGCTGACAACCTGAAAATACAAGAGAATGCAGCTCATCAAGCAAACCTGCAGCAGCTCTGCCGCATCTGTGGAGTTTC
S.punctatus       AGTTGGAAAAGATGCCAACAATCTGAAATCAAAGGAGAATGCAGCTCATCAAGCAAAACTGCAGCAGCTTTGCCGTATTTGTGGGGTTTC
B.thieli          AGGAAATAAAGATGTTTTTCATCTGAGCCAAAGAGAAATTGAAAACCACCAGGCAAACCTTCAGTACCTCTGCCGCATCTGTGGGGGTTC
C.rudis           AGTAAATAAAGATGTTTTTCATCTGAGCCAAAGAGAGATTGAAAACCATCAGGCAAACCTTCAGCACCTCTGCCGCATCTGTGGGGGTTC
C.brevicornis     AGTAAATAAAGATGTTTTTCATCTGAGCCAAAGAGAGATTGAAAACCATCAGGCAAACCTTCAGCACCTTTGCCGCATCTGTGGGGGTTC
C.salinarum       AATAAATAAAGACACTTTTCATCCAAGCCAAAGGGAGACTGAAAATCATCAGACAAACCTTCAGAAACTCTGTCGCATTTGTGGAGCTTC
P.lesueurii       AATAAATAAAGATGCYTTTCATCTGAGCCAAAGAGAGACTGAAAATCATCAGACAAACCTTCAGAAACTCTGTCGCATTTGTGGAGGTTC
P.cocincinus      AATAAATAAAGATGCTTTTCATCTGAGCCAAAGAGAAACTGAAAATCATCAGACAAACCTTCAGAAACTCTGTCGCATTTGTGGAGGTTC
Hydrosaurus.sp.   AATAAGTAAAGATGCTTTTCATCTGAGCCAAAGAGAGACTGAAAATCATCAGGCAAACCTTCAGAACCTCTGTCGCATATGTGGAGGTTC
C.calotes         AATAAGTAAAGATGCTTTTCGTCTGAGCCAAAGGGAGACTGAACATCATCAGGCGAACCTTCAGAACCTCTGTCGCATCTGTGGAGGTTC
J.tricarinata     AATAAGTAAGGATGCCTTTCGTCTGAGYCAAAGAGAGACTGAAAATCATCAGGCAAACCTTCAGAACCTCTGTCGCATCTGTGGAGGTTC
P.raddei          AATAAGTAAAGATGCTTTTTGTCTGAGCCAAAGAGAGACTGAAAATCATCAGGCAAACCTTCAGAACCTCTGCCGCATCTGTGGAGGTTC
L.belliana        GATAAGTAAAGATGCTTTTATTCTGAGCCAAAGGGAGATTGAAAATCATCAGGCAAACCTTCAGAACCTCTGTCGCATCTGTGGAGGTGC
U.acanthinurus    AATAAGTAAATGTGCTTTTCATCTGAACCAAACAGAGACTGAAAGTCATCAGGCAAACCTGCAGAACCTCTGTCGCATCTGTGGAGGTTC
A.paternus        AATAGATAAAGGTGCCTTTCATGTGAGCCAACGAGAGACTGAAACACACCAGGAAAACCTGCAGCATCTCTGCCGCATTTGTGGAGGCTC
P.mcallii         AATAGATAAAAGTGCCTTATATATGAGACAAAGAGAGGTTGAAACACACCAGGCAAACCTGCAGCATCTCTGCCGCCTCTGTGGAGGCTC
S.obesus          AATAGATAAGAGTGCCTTTCATATGAGCCAAAGAGAGGCTGAAACACACCAGGCAAACCTGCAGCATCTCTGCCGCATCTGTGGAGGCTC
Hoplocercus.sp.   AATAGATAAAGGTTCTTTTCATATGAACCAAAGAGAGGCTGAAACACACCAGGTAAACCTTCAGCATCTCTGCCGCATCTGTGGAGGCTC
E.laticeps        AATAGATAACGGTTCTTTTCATATGAACCAAAGAGAGGCTGAAACACACCAGATAAACCTTCAGCATCTCTGCCGCATCTGTGGAGGCTC
P.somencurensus   AGTAGATAAAGGTGCCTTTCATATGAGCCAAAGAGAAACTGAAACACACCAGGCAAACTTGCAAAATCTCTGCCGCATCTGTGGAGGCTC
L.pictus          ----------------------ATGAGCCAAAGAGAAATTGAAACTCACCAGTCATTTCTGCAAAATCTCTGCCGCATCTGTGGAAGCTC
U.flaviceps       AATAGATAAAGGTGCCTTTTTTCTGAGCCAAAAAGAGGCTGAAACACACCAGGCCAACCTTCAGCATCTCTGCCGCATCTGTGGAGGCTC
S.crasicaudatus   CATAGATAAAGGTGCCTTTTATGTGAGGCAAAGAGAGGCTGAAACACATCAGGCAAACCTTCAGCATCTCTGCCGCATCTGTGGAAGCTC
L.carinatus       AATAGATAAAAGTTCTTTTCATGTGAGCCACAGAGAGGCTGAAACACACCAGGCAAACTTGCAGAATCTCTGCCGCATCTGTGGAGGCTC
B.plumifrons      AATAGATAAGGGTGCCTTTCATATGAGCCAAACAGAGGCTGAAACACACCAGGTAAACCTGCAGCAACTCTGCCGCATCTGTGGAGGCTC
G.wislizenii      AATAGATAAAAGTGCCTTTCATATGTGCCAAARAGAGGCTGAAACACATCAGGCAAACCTGCAGCATCTTTGCCGCATCTGTGGAGGCTC
O.cuvieri         ATTAAATAAAGATTATTCTCATATGAGTCAAAAAGAGACTGAAACACACCAGGCAAACTTGCAGCATCTCTGTCGCATCTGTGGAGGCTT
O.attenuatus      AACAAACAAGGATGCCTTTCGTACAAACTACAGAGAGGCTGAAACCCATCAAGCCAACCTGCAGCACCTCTGCCGCATTTGCGGTGGCTC
E.panamintina     AATAAATAAGGATGCCTTTCATACAAACTACAGAGAGGCTGAAACCCATCAAGCCAACCTACAGCACCTCTGCCGCATTTGCGGTGGCTC
C.enneagrammus    AATAAATAAGGATGCCTTTCTTACCAACTACAGAGAGGCTGAAGCTCATCAAGCCAACCTACAGCACCTCTGCCGCATTTGCGGAGGCTC
A.pulchra         AATAAATAAGGATGCCTTTCATACAAATTACAGAGAGGCTGAAGCTCATCAAGCCAACCTACAGCACCTCTGCCGCATTTGCGGTGGCTC
H.suspectum       AATAAATAAGGGTGTCTTTCATATGAACTATAGAGAGACTGAAGCTCATCAAGCAAACTTACAGCATCTTTGCCGCATCTGCGGTGGCTC
X.grandis         AATCAATAAGGACGTCTTTCATACGAACTATAGAGAGACTAAAGCTCATCAAGCAAACCTACAGCACCTTTGCCGCATCTGCGGTGGCTC
V.griseus         AATAAATAAAGACGTCTTTCACAGCAGCTATAAAGAGATGGAAACTCATCAAGCAAACCTGCAGCACCTCTGCCGCATTTGCGGTGGTTC
L.borneensis      AATAAATAAAGACATCTTTCACAGGAGCTATAAAGAGACGGAAGCTCATCAAGCAAACCTGCAGCACCTCTGCCGCATCTGTGGTGGTTC
S.crocodiluris    AATAAATAAAAATGTCTTTCACATGAATTACAGAGAGACTGAAGCTCATCAGGCAAACCTACAGCACCTCTGCCGCATCTGCGGTGGCTC
Dinodon.sp.       AAGAGAGAAAGATGTCTTTCACATGAGCCAAAGGGAGATGGAAGCTCACCAAGCAAACCTGCAGCACCTCTGTCGCATCTGTGGAGGCTC
R.braminus        AATGGATGAAGATGCCTTTCGCATAAACCAAAGAGAGACTGAAGTTCATCAAGCACACTTGCAGCACCTCTGCCGCATCTGTGGAGGCTT
C.ruffus          AATAGATAAAGATGGTTTTCACGTGAGCCAAAGAGAGATGGAAACTCACCAAGCAAACCTGCAGCACCTCTGTCGCATCTGTGGAGGCTC
Agkistrodon.sp.   AGGAGAGAAAGAGGTGTTTCACATGAGCCAAAGGGAGACAGAAGCTCACCAAGCAAAGCTGCAGCACCTCTGTCGCATCTGTGGAGCCTC
Eremias.sp.       AAGAGATAAAAATGCCTTTCCTGTGAACCAAAGGGAGATTGAAACTCACCAAAGCAAGCTGCAGCACCTTTGTCGCATCTGTGGAGGCTC
B.biporus         AAGAGAAAAAAATGCCTTTCTTGTGACCCAAAGTGAAATTGAAGCTCACCAAGCAAAACTTCAGCACCTCTGCCGTATCTGTGGAGGGTC
T.weigmanni       AAGAGAAAAAAATGCCTTTCATATGACCCAAAGCGACATTGCAGCTCACCAAGCAAAACTTCAGCACCTCTGCCGTATCTGTGGAGGCTC
R.floridana       AAGAGATAAAAATGTCTTTTGTGTGAACCAAAGAGAGACTGAAGCTCACCAAGCAAAACTGCAGCACCTCTGTCGTGTCTGTGGAGGCTC
A.xera            AAGAGAAAAAAATGTTTTTCATGTGACCCAAAGTGAAATTGAAGCTCACCAAGCAAAACTTCAGCACCTCTGCCGTGTCTGTGGAGGCTC
C.tigris          AAGAAGCAAACATGACTTTCAGGAGACCCAAAGAGAGATAGAGTCTCATCGAGCAAAACTGCAGCATTTCTGCCGCATTTGTGGGGAATC
L.parietale       AAGAAACAGATATAACATTCAGGAATCTCAAAGAGAGATAGATGCTCACCAAGCAAAATTGCAACATCTCTGCCGAATTTGTGGGGAATC
E.turkmenicus     TATAGATAAAGATGCATTTTATGTAAACCAAAGAGAAATTGAAGCACACCAAGCAAACTTGCAGCACCTTTGTCGCATATGTGGTGGTTC
S.shrevei         TGCAGATAAAGATGCCTTTTATGTAAATCAAATCGAAGTTGAAGCACACCGAGTAAACTTGCAGCACCTCTGCCGCATATGTGGTAGTTC
T.przewalskii     TACAGATAAAGATGCCTTTTATGTAAACCGAACAGAAATTGAAGCACACCGAGTAAACTTGCAGCACCTCTGTCGCATATGTGGTGGTTC
G.gekko           GATAGCTAAAGATGCCTTTTCTGAAAACCAAAGAGAAATTGAAGCACACCGAGTAAACTTGCAGCACCTCTGTCGCATATGTGGTGGTTC
P.lindneri        TATAGATAAAGATGCTTTCTGTGTAAATCAAAGAGAAATTGAAGCACATCAAGTAAAGTTGCAGCAGCTCTGCCGCATATGTGGAGGTTC
Cr.ocellatus      TACAGATAAAGATGCTTTTTGTGTAAATCAAAGAGAAATTGAAGCACATCAAGTAAACTTGCAGCATCTGTGTCGCATATGTGGAGGTTC
L.jicari          TATAGATAAAGATGCTTTTTGTGCAAATCAAAGAGAAATTGAAGCACACCAAGTAAACCTGCAGCAGCTCTGTCGCATATGCGGAGGATC
M.aurata          AACAGATAAAGATACCTTTTGTATGAACCAAAGAGAGACTGAAGCTCACCAAGCAAGGCTGCAGCACCTCTGCCGAATCTGCGGAGCATC
C.robustus        AGTAGCTAAAGATGCCTTTCATGTGAACCTAAGAGAGAAGGAAGCTCACCAGGCAAGGCTACAGCTCCTCTGCCGAATCTGTGGTGGGAC
S.sikkimensis     AGTAGACAAA---GCCTTTCGTGTGAACCCAAGAGAGAATGAAGCTCACCAAGCAAGGCTACAGCTCCTCTGCCGAATCTGTGGAGGCTC
E.inexpectatus    GATAGATAAAGATGCCTTTCGTGTGACCCAAAGAGAGAATGAAGCTCACCAAGCAAGGCTGCAGCACCTCTGCCGAATCTGTGGAGGTTC
E.skiltonianus    GATAGATAAAGATGCCTTTCGTGTGACCCAAAGAGAGAATGAAGCTCACCAAGCAAGGCTGCAGCACCTCTGCCGAATCTGTGGAGCTTC
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E.anthracinus     GATAGATAAAGATGCCTTTCGTGTGACCCAAAGAGAGAATGAAGCTCACCAAGCAAGGCTGCAGCACCTCTGCCGAATCTGTGGAGGCTC
S.anguineus       AATAGATAAAGATGCCTTTCATATGAACCAACGAGAGAATGAAGCTCACCAAGCAAGGCTGCAGCACCTCTGCCGAATCTGTGGAAGTCC
P.eggeli          AACAGATAAAGATGCCTTTCATATGAACCAAAGAGAGAATGAAGCTCACCAAGCAAGGCTGCAGCACTCCTGCCGAATCTGTGGAAGTTC
F.polylepis       AATAGATATCGATGGCTTTCATATGAACCAAAGAGAGAGAGAGGCTCACCAAGCACGGCTGCTGCTCCTCTGCCGAATCTGTGGAAGTTC
Ch.ocellatus      AATAGATAAAGATACCTTTCATATGAACCAAAGAGAGAATGAAGCTCACCAAGCAAGGCTGCAGCACCTCTGTCGAATCTGTGGAAGTTC
A.meleagris       AACAGAAAAAGATGCCATCTGTGTGAATCAAAGAGGGAATGCAGCTCACCAAGCAAACCTGCAGCATCTCTGCCGAATCTGTGGAGGTTC
T.gariepensis     AACAGAAAAAGATGCCATCCGTGTGAATCAAAGAGAGAATGCAGCTCACCAAGCAAACCTGCAGCATCTCTGCCGAATCTGTGGAGGTTC
T.lomii           AACAGAAAAAGATGCCATCTGTGTGAATCAAAGAGAGAATGCAGCTCACCAAGCAAACCTGCAGCATCTCTGCCGAATCTGTGGAGGTTC
X.vigilis         AATAGACAAAGGTGCCTTTCATGTGAACCAAAGAGAGACTGAAGTTCACCAAGCAAATCTTCAGCACCTCTGTCGCATCTGTGGAGGATC
C.polyzonus       AATGGATAAAGATGTCTTTCATGTGAACTATAGAGAGAATACAACTCACCAAGCAAACCTTCAGCACCTCTGCCGTATCTGTGGAGGTTC
Zonosaurus.sp.    AATGGATAAAGGTGTCTTTAATGTGAACTCTAGAGAGAATGCAGTTCACCAAGCAAACCTTCAGCACCTCTGTCGTATCTGTGGAGGTTC
Dibamus.sp.       AAGAGATCAAGATGCTTTTCATGTGAACCAGAAAGAGAGTGGGGCTCACCAAGCAAATCTGCAGCACCTCTGCCGTATCTGTGGAGGCTC

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G.gallus          GTTTAAAACTGATTGCTACAAGAGAACTCATCCAGTACATGGACCAGTAGATGATGAAACTCTGTGGCTACTGAGAAAGAAAGAGAAAAA
C.mydas           ATTTAAAACTGATCGCTACAAGAGAAGTCATCCAGTGCATGGACCAGTGGACTGTGAAACTCAGGGACTTCTGAGAAAGAAAGAGAAAAG
S.punctatus       ATTTAAAACTGACCGATACAAGAGAAGTCATCCAGTGCATGGGCCAGTGGACAATGAAACCCAGGCACTTCTAAGAAAGAAAGAGAAAAG
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C.rudis           ATTTAAGAGTGACGCTCATAAGAGAAGCTATCCAGTTCATGGGCCAGTCGATGATGATACCCAGGCCCTTCTCAGAAAGAAGGAGAAAAA
C.brevicornis     ATTTAAGAGTGACGCTCATAAGGGAAGCTATCCAGTTCATGGACCAGTAGATGATGATACACAGGCCCTTCTCAGAAAGAAGGAGAAAAA
C.salinarum       ATTTAAAAGTGACCCTTATAAGAGAAGTTACCCAGTTCATGGGCCAGTAGATGATGATACACAAGCCCTTCTCAGAAAGAAGGAGAAAAG
P.lesueurii       ATTTAAAAGTGACCCTTATAAGAGAAGTTACCCAGTTCATGGACCAGTAGATGATGATACACAAGCTCTTCTCAGAAAGAAGGAGAAAAG
P.cocincinus      ATTTAAAAGTGACCCTTATAAGAGAAGTTACCCAGTTCATGGACCAGTAGATGATGATACACAAGCCCTTCTCAGAAAGAAGGAGAAAAG
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C.calotes         ATTGAAAAGTGGCCCTTATAAGAGAAGTTACCCAGTTCATGGACCAGTAGATGATGATACACAGGCCCTTCTCAGAAAGAAGGAGAAAAC
J.tricarinata     ATTTAAAAGTGACCCTTATAAGAGACGTTACCCAGTTCATGGACCAGTAGATGATGATACACAGGCCCTTCTCAGAAAGAAGGAGAAAAG
P.raddei          ATTTAAAAGTGATCCTTTTAAGAGAAGTTACCCAGTTCATGGACCCGTAGATGATGATACACAAGCTCTTCTCAGGAAGAAGGAGAAAAG
L.belliana        ATTTAAGAGTGATCCTTATAAGAGAAGTTACCCAGTTCATGGGCCAGTAGATGATGATACACAGGCGCTTCTTAGAAAGAAGGAGAAAAG
U.acanthinurus    ATTTAAGAGTGACCCTTATAAGAGAAGTTACCCAGTTCACGGGCCAGTAGATGATGAGACACAGGCCCTTCTCAGAAAGAAGGAGAAAAG
A.paternus        ATTTAAAACTGATCCTTATAAGAGAAGCCACCCAGTTCATGGACCAATCGATGATGAGATGCAGTCCCTTCTCAGAAAGAAAGAGAAAAA
P.mcallii         ATTTAAAACTGACCCTTATAAGAGAAGCCACCCAGTTCATGGACCAGTAGATGATGAGACTCAGGCCCTTCTCAGAAAGAAAGAGAAAAA
S.obesus          ATTTAAAACTGAACCTTGTAAGAGAAGCCATCCAGTTCATGGACCAGTAGATGATGAGACTCAGGCCCTTCTCAGAAAGAAAGAGAAAAA
Hoplocercus.sp.   ATTTAAAACTGATCCTTATAAGAGAAGCCACCCAGTTCATGGACCAGTAGATAATGAGACTCAGGCTCTTCTCAGAAAGAAAGAGAAAAA
E.laticeps        ATTTAAAACTGATCCTTATAAGAGAACCCACCCAGTTCATGGACCAGTAGATGATGAGACTCAGGCCCTTCTCAGAAAGAAAGAGAAAAA
P.somencurensus   ATTTAAAACTGACCCTTGTAACAGRAGCCACCCAGTTCATGGACCAGTAGATGATGAGACTCAGGATCTTCTCAGAAAGAAAGAAAAAAA
L.pictus          ATTTAAAATTGACCCTAATAAGAGATGGCACCCAGTTCATGGACCAGTAGATGATGAAACTCAGGCCCTTCTCAGAAAGAAAGAGAAAAG
U.flaviceps       ATTTAAAACTGACCCCTATATGAGAAGCCACCCAGTTCATGGACCAGTAGATGATGAAACTCAGGCTGTTCTCAGAAAGAAAGAAAAAAA
S.crasicaudatus   ATTTAAAATTGACCCTTATAAGAGAAGCCATCCAGTTCATGGACCAGTAGATAATGAGACTCAGGCCATTCTCAGAAAGAAAGAGAAAAA
L.carinatus       ATTTAAAACTGACCTTTATAAGAGAAACTACCCAGTTCATGGACCAGTAGATGATGAGACTCAGGCCCTTCTCAGAAAGAAAGAGAAAAG
B.plumifrons      ATTTCAAACTGACCCTTATAAGAGAAACCACCCAGTTCATGGACCAGTTGATGATGAGACTCAGGCCCTTCTCAGAAAGAAAGAGAAAAA
G.wislizenii      ATTTAAAAATGACCCTTATAAGAGAAGCCACCCAGTTCATGGACCAGTAGATGATGAGACTCAGGCTCTTCTCCGAAAGAAAGAGAAAAA
O.cuvieri         GTTTAAAACTGACCCTTATAAGAGAAGCCACCCAGTTCATGGACCAGTAGATAATGAGACTCAGGCCCTTCTCAGAAAGAAAGAGAAAAG
O.attenuatus      ATTTAAAACTGACCCTTACAAGAGAAGCCACCCTGTTCATGGGCCGGTGGATGATGAGACACAAGCTCTTCTGAGAAAGAAAGAGAAACG
E.panamintina     GTTTAAAACTGACCCTTACAAGAGAAGCCACCCTGTTCATGGGCCAGTGGATGATGAGACCCAAGCTCTTCTGAGAAAGAAAGAGAAACG
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H.suspectum       ATTTAAAACTGACCCTTACAAGAGAAGCCACCCTGTTCATGGGCCTGTGGATGATGAGACACAGGCTCTTCTGAGAAAGAAAGAGAGGAG
X.grandis         ATTTAAAACCGACCCTTACAAGAGAAGCCACCCTGTTCATGGGCCAGTGGATGATGAGACACAGGCCCTTCTGAGAAAGAAGGAGAAAAG
V.griseus         ATTTAAAACTGACCCTTGCAAGAGAAGCCACCCTGTTCATGGGCCGGTGGATGAGGAGATGCAGGCGCTTCTGAGAAAGAGAGAGAGAAA
L.borneensis      GTTTAAAACTGACCCTTGCAAAAGAAGCCACCCTGTTCATGGGCCGGTGGATGATGAGATGCAGGCCCTTCTGAGAAAGAGAGAGAGGAG
S.crocodiluris    ATTTAAAACTGACCCTTACAAGAGAAGCCACCCTGTTCATGGGCCAGTGGATGATAAGACACAGGCTCTTCTGAGAAAGAAAGAGAGAAG
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R.braminus        GTTAAACCTGGACCCTTACAAAAGGGTCCATCCAGTACATGGACCAGTAGATGAGAAGATCCAGGCTCTTTTAAGAAAGAAAGAGAAAAG
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B.biporus         ATTTAAGACTGAACTAAACAAGATAAGCCATCCAGTTCATGGGCCAGTGGATGATGTGACACAAGACCTCCTAAGAAAGAAAGAGAAAAG
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R.floridana       ATTTAAGACTGACCCTTACAAGAGAAGCCACCCAGTTCATGGGCCAGTGGATGATGAGACACAAGCCCTTCTAAGAAAGAAAGAGAAAAG
A.xera            ATTTAAGACTGAACCATACAAGAAGAGCTATCCAGTTCATGGGCCAGTGGATGATGAGACACAAGCCCTCCTTAGAAAGAGAGAGAAAAG
C.tigris          GTTTAAAACTGATCCTGGTAAGAGAAGCTACCCAGTTCATGGTCCTGTAGATGATGAGATGCAGGCCCTTCTGAAAAAGAAGGAGAAGAG
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E.turkmenicus     ATTTAAAAATGATCCTTATAAGAGAAGCCACCCAGTACATGGGCCAGTGGATGATGAAACACAGGCCCTTCTGAGAAAAAAAGAAAGAAG
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P.lindneri        ATTTAAAAATGATCTGTATAAGAGAAGCCACCCAGTACATGGACCAGTGGATAATGAAACACAGGCACTTCTGAAGAAAAAAGAAAGAAG
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M.aurata          ATTTAAAGCTGACCCTTATAAGAGAAGCCACCCAGTGCATGGACCAGTAGATAATGTGATGCAGGCCGTACTGAGAAAGAAAGAGAAAAG
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E.inexpectatus    GTTTAAAACTGACCCTTATAAGAGAAGCCACCCAGTGCACGGACCAGTGGATAATGTGGTGCAGGCCCTACTGAGGAAGAAAGAGAAAAG
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E.anthracinus     GTTTAAAACTGACCCTTATAAGAGAAGCCACCCAGTGCACGGACCAGTGGATAATGTGATGCAGGCCCTACTGAGAAAGAAAGAGAAAAG
S.anguineus       ATTTAAAACCGATGCTTATAAGAGAAGCCACCCAGTGCATGGACCAGTGGATAATGTGATGCAGGCCCTACTGAGAAAGAAAGAGAAAAG
P.eggeli          ATTTAAAACTGACCCTTATAAGAGAAGCCACCCAGTGCATGGACCAGTGGATAATGTGATGCAGGCCCTACTGAGAAAGAAAGAGAAAAG
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X.vigilis         CCTTAAAACGGACTCTTATAAGAGGAGCCATCCAGTGCATGGGCCAGTAGATGATGAGACACTAGCCCTTTTGAGAAAGAAAGAGAAAAG
C.polyzonus       ATTTAAAACTGACCCTTATAAGAGAAGCTACCCAGTGCATGGGCCTGTGGATGATGAGACACAGGCCCTTTTAAGAAAGAAAGAGAAAAG
Zonosaurus.sp.    ATTTAAAACCGACCCTTATAAAAGAAGCCACCCAGTGCATGGGCCAGTGGATGATGAGACACAGGCCCTATTAAGAAAGAAAGAGAAAAG
Dibamus.sp.       CTTTAAGACTGATCCTTCTAAAAGAAGTCACCCAGTGCATGGGCCAGTAGATGACGAAACACAAGCCATTCTGAGAAAGAAAGAGAAGAG

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G.gallus          AGCAACCTCTTGGCCAGATCTTATTGCAAAAGTTTTCAAGATTGATGTGAGAGGGGATGTTGACACTATCCATCCCACTCGATTTTGTCA
C.mydas           AGCAACATCTTGGCCGGATCTTATTGCCAAGGTTTTTAAGATTGACGTGCGAGGAGATATCGACACAATCCACCCCACTCGGTTTTGTCA
S.punctatus       AGTGACATCTTGGCCAGAACTTATTGCCAAGGTTTTTAAGACTGACGTGAGAGGAGATATTGACACAATTCATCCTACCCATTTTTGCCA
B.thieli          AGCTACATCTTGGCCAGATCTCCTTTCCAAAGTGTTCAAGATTGATGTCAGAGGAGACATTGACACAATCTATCCTACTAATTTTTGTCA
C.rudis           AGCTACATCTTGGCCAGATCTCCTTTCCAAAGTGTTCAAGATTGATGTCAGAGGAGACATTGACACAATCTACCCTACTAATTTTTGTCA
C.brevicornis     AGCTACATCTTGGCCAGATCTCCTTTCCAAAGTGTTCAAGATTGATGTCAGAGGAGACATTGACACAATCTATCCTACTAATTTTTGTCA
C.salinarum       AGCTACATCCTGGCCAGATCTCCTTGCCAAAGTGTTCAAAATTGATGTTAGAGGAGACATTGACACCATCCACCCTACTAATTTTTGTCA
P.lesueurii       GGCTACATCCTGGCCAGATCTCCTTGCCAAAGTGTTCAAAATTGATGTTAGAGGAGAYATTGACACCATCCACCCTACTAATTTTTGTCA
P.cocincinus      GGCTACATCCTGGCCAGATCTCCTTGCCAAAGTGTTCAAAATTGATGTCAGAGGAGACATTGACACCATCCACCCTACTAATTTTTGTCA
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J.tricarinata     AGCTACATCATGGCCATATCTCCTTGCCAAAGTGTTCAAGACTGATGTCAGAGGAGACATTGCCCAATTCCACCCTACTAATTTTTGTCA
P.raddei          AGCTACATCTTGGCCCGATCTCCTTGCCAAAGTGTTCAAGATTGATGTCAGAGGGGACATTGACACAATCCACCCCACCAATTTTTGCCA
L.belliana        GGCCACATCTTGGCCAGATCTCCTTGCCAAAGTGTTCAAGATTGATGTCCGAGGAGACCTTGACACAATCCATCCTACTAATTTTTGTCA
U.acanthinurus    GGCCACGTCTTGGCCAGATCTCCTTGTCAAAGTCTTCAAGACTGATGTCAGAGGCGACATTGACACAATCCATCCTACTAATTTTTGTCA
A.paternus        GGCAACATCTTGGCCTGATCTCCTTGCTAAAGTTTTAAAGATTGATGTGAAAGGAGATATTGACACAATCCATCCTACAAAGTTTTGTCA
P.mcallii         GGCAACATCTTGGCCAGATCTCCTTGCCAAAGTTTTTAAGACTGATGTGAAGGGAGACATTGACCCTATCCATCCTACAAAGTTTTGTCA
S.obesus          AGCAACATCTTGGCCAGATCTCCTTGCCAGAGTTTTTAAGATTGATGTGAAAGCAGACCTTGACACAATCCACCCTACAAAATTCTGTCA
Hoplocercus.sp.   GGCAACGTCTTGGCCAGATCTCCTTGCCAAAGTTTTTAAGATTGATGTGAAAATAGACATTGACACAATCCATCCTACAAAGTTTTGTCA
E.laticeps        GGCAACGTCTTGGCCAGATCTCCTTGCCAAAGTTTTTAAGATTGATGTGAAAATAGACATTGACACAATCCATCCTACAAAGTTTTGTCA
P.somencurensus   GGCTACATCTTGGCCAGACCTGCTTGCCAGAGTTTTTAGGATTGATGTGAAAGGAGACATTGATACAATCCATCCTACAAAGTTTTGTCA
L.pictus          GGCAACATCTTGGCCAGATCTCCTTGCCAGAGTTTTTAGGATTGATGTGAAAGGAGACATGGACACAATCCATCCTACAAAGTTTTGTCA
U.flaviceps       GGCAACATCTTGGCCAGATCTCCTTGCCAAAGTTTTTAAGATAGATGTGAAGGGAGATATTGACACAATCCACCCTACAAAGTTTTGTCA
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L.carinatus       GGCAACCTCTTGGCCAGATCTCCTTGGCAGAGTTTTTAAGATGGATGTGAGAGGAGACATTGACACAATCCATCCTACGAAGTTTTGTCA
B.plumifrons      GGCAACATCTTGGCCAGATCTCCTTGGCAAAGTTTTTAAGACTGATGTGAAAGGGGACTTTGACACAATCCATCCAACAAAGTTTTGTCA
G.wislizenii      GGCAACATCTTGGCCAGATCTCATTGCCAAAGTTTTTAAGACTGATGTGAAAGGAGACATTGACACAATCCACCCGACAAAGTTTTGTCA
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O.attenuatus      GGCCACGTCCTGGCCAGATCTCCTTGCCAAAGTGTTTAAGATCGATGTGAAAGGGGACATTGACACAATCCATCCTACTCATTTTTGCCA
E.panamintina     GGCCACGTCATGGCCAGATCTTCTTGCCAAAGTGTTTAAGATCGACGTGAGAGGAGACATTGACACAATCCATCCTACTCATTTTTGCCA
C.enneagrammus    GGCTACGTCCTGGCCAGATCTCCTTGCCAAAGTGTTTAAGGTGGACGTGCGAGGAGACATCGACACGATCCACCCTACTCAGTTTTGCCA
A.pulchra         GGCTACATCCTGGCCAGATCTTCTTGCCAAAGTGTTTAAGATTGACGTGAGAGGAGACATTGACACCATCCACCCTACTCATTTTTGCCA
H.suspectum       GGCCACGTCCTGGCCAGATCTTCTTGCCAAAGTGTTTAAGATTGATGTGAGAGGAGACATGGACACAATCCATCCTACTCATTTTTGCCA
X.grandis         AGCCACGTCCTGGCCAGATCTTCTCGGCAAAGTTTTTAAGATTGATGTGAGAGGAGACATTGATACAATCCACCCTACTCATTTTTGCCA
V.griseus         GGCCACGTCGTGGCCAGAACTTCTCACCAAGGTGTTTAAGATTGATGTGAGAGGAGACATCGACACGATCCACCCCACTCACTTTTGCCA
L.borneensis      GGCCACGTCGTGGCCAGAACTTCTCGCCAAAGTGTTTAAGATTGACGTGAGAGGAGACATCGACACAATCCACCCCACTCACTTTTGCCA
S.crocodiluris    GGCCACATCCTGGCCAGATCTTCTTGCCAAGGTTTTTAAGATTGATGTGAGAGGAGACATTGACACAATCCACCCTACTCACTTTTGCCA
Dinodon.sp.       AGCCACTTCCTGGCCAGATCTTCTTGTCAAAGTTTTTAAGATCGATGTAAGGGGAGATATTGACACCATCCACCCTACTCACTTTTGYCA
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B.biporus         AGCCACATCCTGGCCTGAACTTCTTGCTAAGGTTTTTAAGATTGATGTGAGAGGAGATATTGACACAATTCATCCGACTAATTTTTGCCA
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C.tigris          AGCTACATCCTGGCCAGGACTTCTTGCTAAGGTTTTTAAGATTGATGTGAGAGAAGACATAGACACAATCCATCCTACCAATTTTTGTCA
L.parietale       GGCTACATCCTGGCCAGGGCTTCTTGCCAAGGTGTTTAAGATTGAAGTGAGAGAAGACAAAGATACAATCCACCCTACCAATTTTTGCGA
E.turkmenicus     GGCCACTTCCTGGCCAGATCTGCTTAGCAAGGTTTTTAAGATTGATGTTAGAGGAGACATGGACATAATCCATCCTACTAATTTTTGTCA
S.shrevei         GGCCACTTCTTGGCCAGATCTACTTAACAAGGTTTTTAAGATTGATGTAAGAGGAGACATGGACACAATCCATCCAACTAATTTTTGTCA
T.przewalskii     GGCCACTTCTTGGCCAGACCTACTTAACAAGGTTTTTAAGATTGATGTGAGAGGAGACATGGACACAATCCATCCTACTAATTTTTGTCA
G.gekko           GGCCACTTCTTGGCCAGATCTACTTAACAAGGTTTTTAAGATTGATGTGAGAGGAGACATGGACACAATCCATCCTACTAATTTTTGTCA
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Cr.ocellatus	AGCCACTTCCTGGCCAGACCTACTTGCCAAGGTTTTTAAGATTGATGTGAGAGGAGACATTGACACAATCCATCCTACTAATTTTTGTCA
L.jicari	AGCCACTTCCTGGCCAGACCTACTTGTCAAGGTTTTTAAAATTGATGTGAGAGGAGACATTGACACAATCCATCCTACTAATTTTTGTCA
M.aurata	GGCTACATCTTGGCCAGAACTTCTTGCCAAGGTTTTTAAGATTGACGTGAGAGAGGACATTGACACAATCCATCCGACTAACTTTTGTCA
C.robustus	GGCTACATCTTGGCCAGAACTTCTTACCAAGGTTTTTAAGATTGATGTGAGAGGAGACATTGATACAATCCATCCTACTCACTTTTGCCA
S.sikkimensis	GGCAACATCTTGGCCAGAACTCCTCGCCAAGGTTGTTAAGATTGATGTGAGAGGAGACATTGATACCATCTATCCGACTCACTTTTGCCA
E.inexpectatus	GGCTACCTCTTGGCCAGAACTTCTCTCCAAGGTTTTTAAGATTGATGTGAGAGGAGACATTGATACAGTCCATCCTACTAACTTTTGTCA
E.skiltonianus	GGCTACCTCTTGGCCAGAACTTCTTGCCAAGGTTTTTAAGATTGATGTGAGAGGAGACATTGATACAGTCCATCCTACTAACTTTTGTCA
E.anthracinus	GGCTACCTCTTGGCCAGAACTTCTCGCCAAGGTTTTTAAGATTGATGTGAGAGGAGACATTGATACAGTCCATCCTACTAACTTTTGTCA
S.anguineus	GGCTACGTCTTGGCCAGAACTTCTTGCCAAGGTTTTTAAGATTGACGTGAGAGGAGACATTGATACCATTCACCCTACTAACTTTTGTCA
P.eggeli	GGCTACATCTTGGCCAGAACTTCTTGCCAAGGTTTTTAAGATTGACGTGAGAGGAGACATTGATACCATTCATCCTACTAACTTTTGTCA
F.polylepis	GGCTACATCTTGGCCAGAACTTCTTGCCAAAGTTTTTAAGATTGACGTGAGAGGAGACGTTGATACAATGCATCCTACTAACTTTTGTCA
Ch.ocellatus	GGCTACATCTTGGCCAGATCTTCTTGCCAAGGTTTTTAAGATTGATGTGAGAGGAGATATTGATACAATCCATCCTACTAACTTTTGTCA
A.meleagris	GGCTACATCCTGGCCAGATCTCCTTGCCAAGGTTTTTAAGATTGATGTAAGAGGAGACATTGATATAATCCATCCTACTAATTTTTGTCA
T.gariepensis	GGCTACATCCTGGCCAGATCTCCTTGCCAAGGTTTTTAAGATTGATGTAAGAGGAGACATTGATATAATCCATCCTACTAACTTTTGTCA
T.lomii	GGCTACATCCTGGCCAGATCTCCTTGCCAAGGTTTTTAAGATTGATGTAAGAGGAGACATTGATATAATCCATCCTACTAACTTTTGTCA
X.vigilis	GGCTACATCCTGGCCAGATCTTCTTGCCAAGGTTTTTAAGACTGACGTGAGAGGAGACATTGACACAGTCCATCCTACCAATTTTTGTCA
C.polyzonus	GGCTACATCCTGGCCAGATCTTCTTGCCAAGATTTTTAAGATTGATGTGAGAGGAGACATTGACACAATCCATCCTACTCAATTTTGTCA
Zonosaurus.sp.	GGCTACATCCTGGCCAGATCTTCTTGCCAAGGTTTTTAAAACAGATGTGAGAGGAGACATTGACACAATCCATCCTACTCATTTTTGTCA
Dibamus.sp.	GGCTACTTCTTGGCCAGATCTTCTTGCCAAGGTCTTTAAGATTGATGTGCGAGGAGACATTGACACAATCCATCCCACTAATTTTTGTCA

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Index3	123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.	CAATTGCTGGAGTATCATTCAGAGAAAGTTCAGCAGTTCCCCATATGAAGTGTATTTCCCGAGGAACAGTGCCATGGAATGGCAACCTCA
G.gallus	CAACTGCTGGAGTATTATCCACAGGAAATTCAGTAATACTCCATGTGAAGTTTATTTCCTAGGAACAGCACGATGGAGTGGCAGCCCCA
C.mydas	CAACTGCTGGAGCATCATCCACAGAAAGTTCAGCAACGCCCCATGTGAAGTGTATTTCCCGAGGAACAGCACCATGGAGTGGAAGTCCCA
S.punctatus	TAACTGCTGGAGCATCATCCACAGAAAGTTCAGTAATGCCCCATGTGAAGTGTATTTCCCAAGGAACAGCACCATGAAGTGGCAGCCTCA
B.thieli	CAATTGCAGGAATGTGATTCAAAGGAAATCCAGCAATTCCCAAAGTGAAGTGTACTTTCCAAGAAAAAGCACCATGGAGTGGCTTCCCCA
C.rudis	CAATTGCAGGAATGTGATTCAAAGGAAATTCAGCAATTCCCCAAGTGAAGTGTATTTTCCAAGGAAAAGCACCAAGGAGTGGCTTCCCCA
C.brevicornis	CAATTGCAGGAATGTGATTCAAAGGAAATTCAGCAATTCCCCAAGCGAAGTGTATGTTCCAATGAAAAACACCATGGAATGGCTTCCCCA
C.salinarum	CAATTGCTGGAATGTGATTCAAAGGAAATTCAGCAATACCCCAAGTAAGGTATATTTTCCAAGGAAAGGCACCATGGAGTGGCATCCCCA
P.lesueurii	CAATTGCTGGAATGTGATTCAAAGGAAATTCAGCAATTCCCCAAGTGAGGTATATTTTCCAAGGAAAGGCACCATGGAGTGGCATCCCCA
P.cocincinus	CAATTGCTGGAATGTGATTCAAAGGAAATTCAGCAATTCCCCAAGTGAAGTATATTTTCCAAGGAAAGGCACCATGGAGTGGCATCCCCA
Hydrosaurus.sp.	CAATTGCTGGAATGTGATTCAAAGGAAATTCAGCAATTCCTTGAGTGAAGTGTATTTTCCAAGGAAAGGCACCATGGAGTGGCATCCCCA
C.calotes	CACTTGCAGGAATGTGGTTCAAAGGAAATTCAGCAATGCTCCGAGTGAAGTGTATTTTCCAAGGAAAGACACCACGACGTGGCAGCCCCA
J.tricarinata	CAATTGCAGGAATGTGGTCCAAAGGAAATTCAGCAACGCTCCGAGTGAAGTGTATTTTCCAAGAAAAGACACCATGAAGTGGCAACCCCA
P.raddei	CAATTGCCGGAATGTGATTCAAAGAAAGTTCAGCAATTCCCCGAGTGAAGTGTATTTTCCAAGGAAAGAGGCCATGGAGTGGCAACCACA
L.belliana	CAATTGCTGGAATGTGATTCAAAGGAAATTCAGCAATTCCCCAAGTGAAGTGTATTTTCCAAGGAAAGGCACCATGGAGTGGCATCCCCA
U.acanthinurus	TAATTGCTGGAATGTGATTCAAAGGAAATTCAGCAATTCCTCAAGTGAAGAGTATTTTCCAAGGAAAGGCACCAAGGAGTGGCATCCCCA
A.paternus	CCAATGTTGGACTGTGGTTGAAAAGAAATTAAGCAATTCCCCATATGAAATATTTTTTCCAAGGAAAAGCCCAATGGAGTGGCAGCTCCA
P.mcallii	CCAGTGTTGGACTGTGGTTCAAAAGAAATTAAGCAATTCCCCATGTGAAATGTTTTTTCCAAGGAAAAGTCTAGTAGAGTGGCATCCCCA
S.obesus	CCACTGTTGGACTGTAGTTCAAAAGAAATTAAGCAATTCCCCATGTGAAGCATTTTTTCCAAGGAGAGCCCCAGTGGAATGGCATCCCCA
Hoplocercus.sp.	CCAATGTTGGACTGTGGTTCAAAAGAAATTAAGCAATTCCCCATGTGAAATATTTTTTTCAAGGAAATGCCCAGTGGAGTGGCATCCCCA
E.laticeps	CCAATGTTGGACTGTGGTTCAAAAGAAATTAAGCAATTCCCCATGTGAAATATTTTTTTCAAGGAAATGCCCAGTGGAGTGGCATCCCCA
P.somencurensus	CCAATGTCGGGCTGTGGTTCAAAAGAAATTAAGCAATTCCCCATGTGAAATATTTTTTCCAAGGCAAGGCCCAGTAGAGTGGCATCCCCA
L.pictus	CCAATGTTGGACTGTGGTTCAAAAGAAATTAAGCAATTCCCCATGTGAAATGTTTTCTCCAAGGCAAGGCCCAGCAGAGTGGCATCCCCA
U.flaviceps	TCAGTGTTGGACTGTGGTTCAAAAGAAATTGAACAATTCTCCATGTGAAATGTTTTTTCCGATGAAAGGCCCAGTGGAGTGGCATCCCCA
S.crasicaudatus	CCAATGTTGGACTGCGATTCAAAAGAAATTAAGCAATTCTCCATGTGAATTTTTTCCCCCAAGGAAAGGGCTAGTGGAGTGGAATCCCCA
L.carinatus	CCATTGTTGGATTGTGCTTCAAAAGAAATTAAGCAATTCCCCATGTGAAATATTCTTTCCAAGGAAAGGCTCAGTGGAGTGGCATCCCCA
B.plumifrons	CCAGTGTTGGACTGTGGTTCAAAAAAAATTAAGCAATTCCCCATGTGAACTATTTTTTCCAAGGAAAGGCCCAGTGGAATGGCATCCCCA
G.wislizenii	TCAATGTTGGGCTGTGATTCAAAAGAAATTAAGCAATTCCCCATGTGAAATATTTTTTTCAAGGAATGGCCCAGTGGAGTGGCATCCTCA
O.cuvieri	TGCATGTTGGGCTGTGGTTCAAAAGAAATTAAGTAATTCTCCTTGTGAAATATTTTTTCCAAGAAAAGACCCAGTGGAGTGGCAGCCCCA
O.attenuatus	CAATTGCTGGACCATGGTTCAAAGGAAATTCAGCAATTCTCCTTGTGAAGTATATTTTCCAAGGAATGGCATGATGGAGTGGCATCCCCA
E.panamintina	CAATTGCTGGACTGTGGTTCAAAGGAAATTCAGCAATTCCCCTTGTGAAGTATATTTTCCAAGGAATGGCACGATGGAGTGGCGTCCCCA
C.enneagrammus	CAATTGCTGGACTGTGGTTCAAAGGAAAGTCAGCAATTCCCCTTGCGAAGTGTATTTTCCAAGGAACGGTGCGATGGAGTGGCATCCCCA
A.pulchra	CAATTGCTGGAGTGTGGTTCAAAGGAAATTCAGCAATTCCCCGTGTGAAGTGTATTTTCCAAGGAATGGCACGATGGAGTGGCGTCCCCA
H.suspectum	CAATTGTTGGAATGTGGTTCAAAGGAAATTCAGCAGTTCCCCATATGGAGTGTCTTTCCCAAGGAACAGCACGATGGAGTGGCGTCCCCA
X.grandis	CAATTGTTGGAATGTGGTTCAAAGGAAATCCAGCCACTCCCCGTGTGAAGTGTATTTCCCAAGGAATGGCACAATGGAGTGGCATCCCCA
V.griseus	CAATTGTTGGAATGTGGTTCAAAGGAAGTTCAGCAATTCCCTGTGTGAAGTGTATTTTCCGAGGAATGATACAATGGAGTGGCATCCACA
L.borneensis	CAATTGCTGGAATGTGGTTCAAAGGAAATTCAGCAATTCCCCATGTGAAGTGTATTTTCCAAGGAATGGCACAATGGAGTGGCATCCACA
S.crocodiluris	CAATTGTTGGAATGTGGTTCAAAGGAAGTTCAGCAATTCCCCATGTGAAGTGTATCTTCCAAGGAATGGCACAATGGAGTGGCATCCCCA
Dinodon.sp.	CAATTGTTGGAAAGTCATTCAAAGGAAAGTCAGCAATGCCCCCCATGAAGCACATCTTCTAGAGAAAGACCCAGTGGAATGGCAGCCCCA
R.braminus	CCCCTGTTGGAATGTGATTCAACGTAAAATTAGCAATGCCCCACACAAAGTGCCCCTTCCAGGAAGAGACGCCGTAGAGTGGCATCCCCA
C.ruffus	CAATTGTTGGAATGTGATTCAAAGAAAAGTCAGCAATGCCCCACATGAAGCACTTCTTCAAGGGAAAGACACAGTGGAATGGCATCCCCA
Agkistrodon.sp.	CAATTGTTGGAAAGTGATTCAGAGAAAAGTCAGCAATGCCCCCCATGAAGCACATCTTCTAGAGAAAGACCCAGTGGAGTGGCATCCCCA
Eremias.sp.	CAACTGCTGGAATGTTGTTCAAAGGAAATTCAGCAATTCTCCATGTGAAGAGTATTTTCCAAGGAATGGCACCATGGAATGGCATCCCCA
B.biporus	CAACTGCTGGGATGTTATCCAAAGGAAATTCAGCCATTCCCCTTGCGAAGTGTCTTTTCCAAGGAATGGCGCTGTGGAGTGGCATCCCCA
T.weigmanni	CAACTGCTGGAATGTTATCCAAAGGAAATTCAGCAATTCCCCTTGCGAAGTGTATTTTCCAAGGAATGGCACTGTGGAGTGGCATCCCCA
R.floridana	CAACTGCTGGAATGTTATTCAAAGAAAATTCAGCAATGCTCCATATGATGTGTATTTTCCAAGGAATGGCACCATGGAGTGGCATCCCCA
A.xera	CAACTGCTGGAATGTTATGCAAAGGAAATTCAGCAATTCCCCTTGCGAAGTGTATTTTCCAAGGAATGATGCTGTGGAGTGGCATCCCCA
C.tigris	CAACTGTTGGAATGCTATCCAAAAGAAATTCAGCAATGGCCCGTATGAATCATGTTTTCCAAAGAAAGGTACCATGGAGTGGTGTCCCCA
L.parietale	AAACTGTTGGAATGTCATCCAAAAGAAATTCAGCAATGCCCCATGTGAATCATATTTTCTAAAGAAAGGTGCCATGGAGTGGCATCCCCA

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E.turkmenicus     CAACTGCTGGAGTGTTATCCAGAGGAAGTTCAGCAATGCCCCGTGTGAAGTGTATTTTCCAAGGAAAGGCACTGTGGAGTGGCATCCCCA
S.shrevei         CAACTGCTGGAGTGTTATCCAGAGGAAGTTCAACAATGCCCCATGTGAAGTGTATTTTCCAAGGAAAGGTACTATGGAAGGGCACCCACA
T.przewalskii     CAACTGCTGGAGTGTTATCCAGAGGAAGTTCAGCAATGCCCCATGTGAAGTGTATTTCCCAAGGAAAGGCACTATGGAGTGGCATCCCCA
G.gekko           CAACTGCTGGAGTGTTATCCAGAGGAAGTTCAGCAGTGTCCCATGTGAAGTGTATTTTCCAAGGAAAGGCACTATGGAGTGGCATCCCCA
P.lindneri        CAACTGCTGGAAAGTTATCCAGAGGAAGTTCAGCAGTGCCCCCTGTGAAGTGTATTTTCCAAGGAAAGGCACGATGGAGTGGCACCCCCA
Cr.ocellatus      CAACTGCTGGAAAGTTATCCAGAGGAAGTTCAGCAGTGGCCCTTGTGAAGTGTATTTTCCAAGGAAAGGCACGATGGAGTGGCACCCCCA
L.jicari          CAACTGTCGGAAAGTTATTCAGAGGAAGTTCAGCAGTGTCCCTTGTGAAGTGTATTTTCCAAGAAAGGGCACTATGGAGTGGCACCCACA
M.aurata          CAACTGCTGGAACTTTGTTCAGAAGAAATTCAGCAATGTCCCCTGCGAAGTGTATTTTCCAAGGAAAGGCCCTGTGGAGTGGCATCCCCA
C.robustus        CAACTGCTGGACCGTGATTCAGAGGAAATTCAGCAACGTCCCCTGTGAAGTGTATTTCCCAAGGAAAGGCCCTGTGGAGTGGCACCCCCA
S.sikkimensis     CAACTGCTGGAACGTGATTCAGAGGAAATTCAGCAGTGCCCCCTGTGAAGTGTATCTTCCAAGGAAAGGCCGTGTGGAGTGGCATCCCCA
E.inexpectatus    CAACTGCTGGAACGTTATTCAGAGGAAATTCAGCAATGTCCCCTGTGAAGTATATTTTCCAAGGAAAGGCCCCAGGGAGTGGCATCCCCA
E.skiltonianus    CAACTGCTGGAACGTTATTCAGAGGAAATTCAGCAATGTCCCCTGTGAAGTGTATTTTCCAAGGAAAGACCCCATGGAGTGGCATCCCCA
E.anthracinus     CAGCTGCTGGAATGTTATTCAGAGGAAATTCAGCAATGTCCCTTGTGAAGTGTATTTTCCAAGGAAAGGCCCCATGGAGTGGCATCCCCA
S.anguineus       CAATTGCTGGAACGTTATTCAGAGGAAATTCAGCCACGTCCCATGCGAAGTGTATTTTCCAAGGAAAGACCCCATGGAGTGGCACCCCCA
P.eggeli          CAACTGCTGGAATGTTATTCAGAGGAAATTCAGCTATGTCCCACGTGAAGTGTATTTTCCGAGGAAAGACCCCATGGAGTGGCACCCCCA
F.polylepis       CAACTGCTGGAACGTTATTCAGAGGAAATTCAGCAGTGTCCCATGTGAAATGTATTTTCCAAGGAAAGACCCCGTTGAGTGGCAGCCCCA
Ch.ocellatus      CAACTGCTGGAACGTTATTCAGAGAAAATTCAGCAATGTCCCATGTGACGTGTATTTTCCAAGGAAAGACCCTGTGGAGTGGCACCCCCA
A.meleagris       CAACTGCTGGAACGTTATTCAGAGGAAATTCAGCAATGACCCATGTGAAGTGTATTTTCCAAGGAAAGGCACCGTCGAGTGGCATCCCCA
T.gariepensis     CAACTGCTGGAACGTTATTCAGAGGAAATTCAGCAATGACCCATGTGAAGTGTATTTTCCAAGGAAAGGCACCGTCGAGTGGCATCCCCA
T.lomii           CAACTGCTGGAACGTTATTCAGAGGAAATTCAGCAATGACCCATGTGAAGTGTATTTTCCAAGGAAAGGCACCGTCGAGTGGCATCCCCA
X.vigilis         CAACTGCTGGGATTTTATTCAAAGGAAATCAAGCAATGCCCCATGTGAAGTGTATTTTTCAAGGAAAAGCACCATGGAGTGGCATCCCCA
C.polyzonus       CAACTGCTGGAGAGTTGTTCAGAGGAAATTCAGTAATGCCCCATCTGAAGTGTATTTTCCAAGGAAAGGCACCATGGAATGGCATCCCCA
Zonosaurus.sp.    CAATTGCTGGAAAGTGGTTCAGAGGAAATTCAGTAATGCCCCATGTGAAGTGTATTTTCCAAGGAAAGGCACCATGGAGTGGCATCCCCA
Dibamus.sp.       TAATTGTTGGCATGTGATCCAGAGGAAATTCAGCAATGCCCCCTGTGAAGTGTATTTTCCACGGCAAGGCACCATGGAGTGGCATCCCCA

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A.mississip.      CTCCCCAAATTGTGATGTTTGTCACACTAGCTGTCGGGGGATCAAGAGAAAGAAGCAGCCGCCCAACTTACAGCTTGCAAAACGACTGAA
G.gallus          CTCTGCAAACTGTGAAGTGTGCCACACGCCCAGCCGGGGAGTCAAGAGAAAGAGCCAACCACCCAACGTACAACATGGCAAACGTGTGAA
C.mydas           CTCCCCAAACTGCACTGTTTGTTGTACTGCTCGTTGTGGGGTCAAGAGAAAGAACCAGTCATCCAATTTACAGCTGGGCAAAAGGCTCAA
S.punctatus       CTCATTGAACTGTGAGGTTTGTGGCACTGCTCATCGTGGGGTCAAGAGAAAGAAGCAACCACTGAACCTGCCATTGGGCAAGAGACTCAA
B.thieli          TTCACCGAGCTGTGATGTTTGCAGCACTTCCTTCCGTGGAGTAAAGAGAAAGAAGCAGTTCCTGAATCCACTGTTGAGCAAAAAGCCGAG
C.rudis           TTCACCAAGCTGTGATGTCTGTGCCACTTCCTTCCATGGAGTAAAGAGAAAGAAGCGGTTCCTGAATCCACAGTTGAGCAAAAAGCCGAA
C.brevicornis     TTCACCAAGCTGTGATATTTGTGCCACTTCCTTCTGTGGAGTAAAGAGAAAGAAGCGGTTCCTGAATCCACAGTTGAGCAAAAAGCCAAG
C.salinarum       TTCATCGAGCTGTGATGTCTGTGGCACTTCTTTCCGTGGGATAAAGAGAAAGAAGCGATCTCTGAATCCACAGTTGAGTAAAAAGCCAAG
P.lesueurii       TTCATCAAGCTGTGATGTCTGTGGCACTTCTTTCCATGGGATAAAGAGAAAGAAGCGATCTCTGAATCCACAGTTGAGCAAAAAGCCAAG
P.cocincinus      TTCATCGAGCTGTGATGTCTGTGGCACTTCTTTCCGTGGGGTAAAGAGAAAGAAGCGATCCCTGAATCCACAGTTGAGCAAAAAGCCAAA
Hydrosaurus.sp.   TTCATCGAGCTGTGATGTCTGTGGCACTTCCTTCCGTGGGGTAAAGAGAAAGAAGCGGTCCCTGAATCCACAGTTGAGCAAAAAGCCAAG
C.calotes         TTCCTCAAGCTGTGACGTCTGTAGCACTTCCTTCCGTGGGATCAAGAGAAAGAAGCGGTCCCTCAACCCACAGTTGAGTAAAAAGCCCAG
J.tricarinata     TTCATCGAGCTGTGATGTCTGTGGCACTTCCTTCCGTGGGATCAAGAGAAAGAAGCGGTCCCTGAACCCACCGTTGAGTAAAAAGCCCAG
P.raddei          TTCATCGAGCTGTGATGTCTGTGGCACTTCCTTCCGTGGGGTAAAGAGAAAGAAGCGGCCTTTAAATCCACAGTTGAGCAAAAAGCCCAG
L.belliana        TTCATTGAGTTGTGATGTTTGTGGCACTTCCTTCCGTGGGGTAAAGAGAAAGAAGCGGTCTCTGAATCCACCATTGAACAAAAAGCCAAG
U.acanthinurus    TTCATCAAGCTGTGATGTTTGTGGCACTTCCTTCCGTGGGGTAAAGAGAAAAAAGCAGTCGGTGAATCCACAGCTGAGCAAAAAGCCAAG
A.paternus        TTCTTCGAGCTGTGAAGTTTGTGGCACTTCACCCCGTGGAGTGAAGAGGAGGAAGCAAGTCCTTAATCCACAGTTGAACAAAAAAATTGAG
P.mcallii         TTCCCCAAGCTGTGATGTTTGTGGTGCTTCCTTCCATGGAGTGAAGAGAAAGAAGAAAGTTCTTAATCCACAGCTGAACAAAAAAATTGAG
S.obesus          TGCCTCGAGCTGCGATGTTTGTGGTACTTCTTCCCGTGGAATGAAGAGAAAGAAGCAAGTCCTTAATCCACAGTTAAGCAAAAAAACTGAG
Hoplocercus.sp.   TTCCTCGAGCTGTGATGTTTGTGGCACTTCTTCCCGTGGAGTGAAGAGAAAGAAGCAAGTGCTTAATCCACAGTTGAGCAAAAAAATTGAG
E.laticeps        TTCCTTGAGCTGTGATGTTTGTGGCACTTCTTCCCGTGGAGTGAAGAGAAAGAAGCAAGTGCTTAATCCACAGTTGAGCAAAAAAATTGAG
P.somencurensus   TTCCTTGAGTTGTGATGTTTGTGGCACTTCCTCCCATGGAGTTAAGAGAACGAAGCAAGTCCTTAATCCACAGATGAACAAAAAAACTGAG
L.pictus          TTCCTCGAGTTGTGATGTTTGTGGCACTTCCTCCCGTGGAGTTAAGAGAAAGAAGCAAGTCCTTAATCTACAGGTGAACAAAAAAATTGAG
U.flaviceps       TGCCTTGAGCTGTGTCGTTTGTGGCACTTCCTCCCATGGAGTGAAGAGAAAGAAGCAAATATGTAATCCACAGTTGAGCAAAAAAATTGAG
S.crasicaudatus   TTCATTGAGCTGTGATGTTTGTGGCACTTCCTCCCACGGAGTGAAGAGAAAGAAGCAAATCCTAATTCCACAGCTGAGCAAAAGGTTGAG
L.carinatus       TTCCTCAAGCTGTGATGTTTGTGGCACTTCGTCCCAGGGAGTGAAGAGAAAAAAGCAAGTCCTTAATTCACAGTTGAGCAAAAAAAATGAG
B.plumifrons      TTCCTCAAGCTGTGATGTTTGTGGCACTTCCCTCCATGGAGTGAAGAGAAAGAAGCAAGTCCTTAATCCACAGCTGAGCAAAAAGTTGAG
G.wislizenii      TTCCTCAAGCTGTGATGTTTGTGGCACCTCCTCCCATGGAGTGAAGAGAAAGAAGAAAGGCTTGAATCCACAGTTGAGCAAAAAAATTGAG
O.cuvieri         TTCCTTGAGGTGTGATGTTTGTGGCACTTCCTCTCATGGAGTGAAGAGAAAGAGGCAAGTCCTTAATCCACAGTTGACCAAAAAAATTGAA
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E.panamintina     TTCGTCAAGCTGTGATGTTTGCAACACTTCCTTCCGTGGGGTCAAGAGAAAGAAGCAAGCCCCGAATCCACAGTTGAACAAAAAGCTCAG
C.enneagrammus    TTCATCGAGCTGTGACGTTTGCAGCACTTCCTTCCGTGGGGTCAAGAGAAAGAAACGAACCCTGCATCCGCAGTTGAGCAAAAAGCTCAG
A.pulchra         TTCATTGAGCTGTGATGTTTGTGGCACTTCCTTCCGTGGAGTTAAGAGAAAGAAGCAAGCCCTGAATCCACAGTTGAGCAAAAAGCTCAG
H.suspectum       TTCGTCAAGCTGTGACATCTGCGGCAGTTCCTTCCGTGGGGTCAAGAGGAAGAAGCAATCCCTGGATCCACAGCTGAGCAAAAAGCTCCG
X.grandis         TTCATCGAATTGTGACGTTTGCGGCACTTCCTTCCGTGGGGTCAAGAGAAAGAAGCAAGCCCTGAATCCACAATTGAGCAAAAAGCTCCG
V.griseus         TTCAGCCAACTGTGATGTTTGTAGCACTTCTTTCCATGGGGTCAAGAGAAAAAAGCAAGGCCTGAATCCACAGTTGAGCAAAAAGCTCAA
L.borneensis      TTCATCGAGCTGTGATGTCTGCAGCACTTCCTTTCATGGGGTCAAGAGAAAAAAGCCAGCCCTGAATCCACAGTTGAGCAAAAAGCTCAA
S.crocodiluris    TTCATCCAGCTGTGATGTTTGTGGCACTTCCTTCCGTGGGGTCAAGAGAAAGAAGCAAGCCCTGAATCCACAGTTGAGCAAAAAGCTGAG
Dinodon.sp.       TTCAACAAGCTGTGACATTTGTGTCACTTCCTTTCGTGGAGTCAAGAGGAAAAAACCAATGCTGAATTCACAGCTGAGCAAAAAACTCAG
R.braminus        TTCGTCAATCTGTGATGTTTGTGGCACTTCTTCTCATGGGGTCAAGAGAAAGAAGCTAACCCTGAATACACAGCTGAGCAAAAAGCTCAG
C.ruffus          TTCATCAAGCTGTGATGTTTGTGGCATTTCCTTTTGTGGCATCAAGAGAAAGAAGCCAACCCTGAATTCACAGCTGAGCAAAAAGCTCAG
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Eremias.sp.       TTCATCAAGCTGCGAGGTGTGTGGCACTTCCTTCCGTGGGGTCAAAAGAAAGAAGCAAGCCCTGAATCCACAGATGAGCAAAAAGCTCAG
B.biporus         TACACTGAATTGTGAGGTTTGTGGCACTTCCTTCCATGGGGTCAAACGAAAAAAGCAAGCCCTGAACCCACCGCTGAGCAAAAGGCTCAG
T.weigmanni       TGCACTGAACTGTGAGGTTTGTGGCACTTCTTTCCGTGGGGTCAAACGAAAAAAGCAAGCCCTGAATCCACAGCTGAGCAAAAGGCTCAA
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A.xera              TGGATTGAATTGTGAGGTTTGTGGCACTTCTTTCCGTGGGATCAAACGAAAGAAGCAAGCTCTGAATCCACAGCTGAGCAAAAGGCTCAA
C.tigris            TTCATCAAGCTGCAGTATTTGTACCCCTTCCTTCCATGGGGTCAAGAGAAAGAAGCAAGCTCTGAATGCACAGTTGAACAAAAGGGCCAA
L.parietale         TTCATCCGTCTGCAATGTTTGTATCCCTTCCTTCTATGGGGTCAAGAGAAAGAAGCAAGGCCTAAATACACCCTTGAACAAAAGGATCAA
E.turkmenicus       TTCAATGAGCTGTGATGTTTGTGGAACGTCCTCCTGTGGAATAAAGAGGAAGAAGAAAGCCCTGAATCCACAAGTGAGTAAAAAGCTCAG
S.shrevei           TTCAATGAACTGTGATGTTTGTGGCACTTCCTCCCATGGGATAAAGAGAAAAAGCCAAGCCCCCAATCCACAGGTGAACAAAAAGCTCAG
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G.gekko             TTCAACCAGATGTGATGTTTGTGGCACTTCCTCCCGTGGAATAAAGAGAAAGAAGCAAGCCCCAAGTCCACAGGGGGGGAAAAAGCTCAG
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Cr.ocellatus        CTCAATGAGCTGTGACGTGTGTGGCACTTCCTCTCGTGGAATGAAGAGAAAGAAACAAGCCCTCAATCCTCAGGTGAGCAAAAAGCTCAG
L.jicari            TTCAGCGAGTTGTGATGTTTGTGGTACTTCCTCTCGTGGAATGAAGAGAAAGAAACAAGCCCTCAATCCCCCGGTGAGCAAAAAGCTCAG
M.aurata            TTCATCAAGTTGTGAGGTTTGTGGCACTTTGTCCCATGGGGTCAAGAGAAAGCGGCAAGCTCTGAATCCGCAAGTGAGCAAAAAAACTCAG
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S.sikkimensis       TTCATCAAGCTGTGAGGTTTGCAGCACTTCGTCCCGGGGGGTCAAGAGAAAGCGGCAAGCCCTGAATGCGCAAGTGAGCACTAAACTCCG
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P.eggeli            TTCATCAAGCTGTGATGTTTGCGGCACCTCTTCCCGTGGGGTCAAGAGAAAGAAGCAAGCCCTGAATCCACAAGTGTGCAAAAGACTCAG
F.polylepis         TTCACCAAACTGTGATGTTTGTGGCACGTCTTCCCGTGGGGTCAAGAGAAAGAAGCAAGCCCTGAATCCACAAGTGTGCAAAAAAACTCAG
Ch.ocellatus        TTCATCAAGCTGTGATGTTTGTGGCACCTCTTCCCATGGGGTCAAGAGAAAGAAGCAAGCCCTGAATCCACAAGTGTGCAAAAAAACTCAG
A.meleagris         TTCATCAAGCTGTGATGTTTGTGGCACTTCATCCCGTGGGGTCAAGAGAAAGAAGCAAGCTCTGAATCCACAAGTAAGCAAAAAAACTCAG
T.gariepensis       TTCATCAAGCTGTGATGTTTGTGGCACTTCATCCCGTGGGGTCAAGAGAAAGAAGCAAGCTCTGAATCCACAAGTAAGCAAAAAAACTCAG
T.lomii             TTCATCAAGCTGTGATGTTTGTGGCACTTCATCCCGTGGGGTCAAGAGAAAGAAGCAAGCTCTGAATCCACAAGTAAGCAAAAAAACTCAG
X.vigilis           TTCATCAAGCTGTGATGTTTGTGGTACTTCGCCCCGTGGGGTCAAGAGAAAGAAGCAAGCCCTGAATCCACAGGTGAGCAAAAAGCTCAG
C.polyzonus         TTCATCAAGTTGTGATGTTTGTGGCACTTCCTCCCGTGGGGTCAAGAGAAAGAAACAAGCCTTGAATCCACAAACAAGCAAAAAGCTGAG
Zonosaurus.sp.      TTCATCAAGTTGTGATGTTTGTGGCACTCCCTCTCGTGGAGTCAAGAGAAAGATGCAAGCCCTGAATCCACAGACAAGCAAAAAGCTCAG
Dibamus.sp.         TTCATCAATGTGTGATGTCTGTGGCACTTCCGCACGTGGCATCAAGAGAAAGACGCAAGCTCTGAACCCACCAGTGAGCAAAAAAACTCAA

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Index2              333333333444444444455555555556666666666777777777788888888889999999999000000000011111111112
Index3              123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
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G.gallus            GATCATTGCAGAACGTGCTCGAGTTAACAGAGGCATAAAGAACCAAGTG---ATAAAGAACAAAAATGTAATGAAAGAGATTACAAACTG
C.mydas             GATCGTTGCAGAACGTGCCCGAAAAACTAAAGGTGTAAAAAAACAAGTACAGGTGAACAACAAAAACCTTATGAAAAAGATTGCCAACTG
S.punctatus         GGTCACTGCA---------CAAAAAATCAAGGGCATGAAGAACCGAGCACTGATGAAGAATAAAAACCTCATGAAAAGGATTGCTAACTG
B.thieli            GATTGTAACTAGATGTGCTAGAAAAGTAAAGCAAGTGAGGAATGTAAAGCAGGTGAACAAAAAGAGCGTAATGAAAAAGACTGCCGACTG
C.rudis             GATTGTAACTAGTTGTGCTAGAAATGTAAGACACATGAGGAATGTAAATCAAGTGAACAACAAGAGTCTAATGAGAAAGATTGCCAACTG
C.brevicornis       GATTGTAACTAGATGTGCTAGGAAAATAATGCAAGTGAGGAATGTAAAACAAGTGAACAAAAAGAGTGTAATGAGAAAGATTGCCAACTG
C.salinarum         GATTGTAGCTGGAAGTGCTAGAAAAGTAAGGCCCGTGAGGAATGTAACACAAGTGAGCAACAAAGCTGTAATGAAAAGGATTGCCAATTG
P.lesueurii         GATTGTAGCTGGAAGTGCTAGAAAAGTAAGGCCTGTGAGGAATGTAAAACAAGTGAGCAACAAAGCTGTAATGAAAAGGATTGCCAATTG
P.cocincinus        GATTGTAGCTGGATGTGCTAGAAAAGTAAGGCCTGTGAGGAATGTAAAACAAATGAGCAACAAGGCTGTAATGAAAAGGATTGTCAATTG
Hydrosaurus.sp.     GATTGTAGCAGGATGTGCTAGAAAAGCAAGGAATGTGAGGAATATGAAGCAAGTGAGCAGCAAGGCTGTAATGAAAATGATTGCCAATTG
C.calotes           GATGGTAGCTGGATGTGCTAGAAAAGTCAGGAACGTGAGGAATCTAAAACTAGTGAACAACAAGGCTCTAATGAAAAAAATTGCCAATTG
J.tricarinata       GATTGTAGCCGGATGTGCTAGAAAAGTAAGGAATGTGAGGAATCTAAAACTAGTGAACAACAAGGCTCTAATGAAAAAAATTGCCAATTG
P.raddei            GGTTGTAGCTGGAGGTGCTAGAAAACCAAGCTATGTGAGGAATGTAAAACAAGTGAACAACAAGGCTCTAATGAAAAAGATTGCCAATTG
L.belliana          GATTGTGGCTGGATGTGCTAGAAAAATAAGGCATGTGAGGAATGTAAAACAAGTGAGCAACAAGAGTGTGATGAAAAAGATTGCTAATTG
U.acanthinurus      GATTGTAGCTAGACGTGCTAGAAAAGTAAGGCATGTGAGGAATGTGAAACAAGTGAACAGCAAGAGTGTAATGAAAAAGATTGCCAACTG
A.paternus          GATGGTGGCTGGACATGCGAAAAAAATAAGACAGATAAGAAATCCGAAGCAAGTCAACCAAAAGAGTTTGATGAAAAAAATTGCCAACTG
P.mcallii           GATGGTGACTAGAAGTGCTAGAAAAAAAAGAGAAGCAAGGAATCCAAAACAAGTCAACCAAAAGAGTTTAGTGAAAATGATTGCCAGCTG
S.obesus            GCTGGTGGCTGGACGTGCTAGAAAAATAAGGCAGGTAAAGATTCCAAAACAAGTCAACCAAAAGAGTTTAATGAAAAAAATTGCCAACTG
Hoplocercus.sp.     GATGGTGGCTGGACGTGCCAGAAAAATGAGGCAGATAAGGAATCCAAAGCAAGTCAGCCAAAAGAGTTTGATGAAAAAGATTGCCAGCTG
E.laticeps          GATGGTGGCTGGACGTTCCAGAAAAATGAAGCAGATAAGGATTCCAAAGCAAGTCAGCCAAAAGAGTTTGATGAAAAAGATTGCCAGCTG
P.somencurensus     GATGGTGGCTGGACGTGCTAGAAAAATAAGGCAGATAAAGAATCCAAAACAAGTCAACCAAAAGAGTTTAATGAAAAAGATTGCCAACTG
L.pictus            GTTGGTGGCTGGACATGCTAGAAGAATGAGGCAGATAAAGAATCCAAAAAAAGTCACCCAAAAGAGTTTAATGAAAAAGATTGCCAGCTG
U.flaviceps         GTTGGTGGCTGGACGTGCTAGAAGAATAAGGCAGATAAAGAATCCAAAACAAGTCAGCCAAAAGGGTTTAATGAAAAAGATTGCCAACTG
S.crasicaudatus     GATGGTAGCTGGATGTACTAGAAGAATAAGGGAGATAAAGAATCCAAAACAAGTCAGCCAAAAGAGCTTAATGAAAAAGATTGTCAACTG
L.carinatus         GATCGTGGCTGGACATGCTAGAAAAATAAGGCAGATAAGGAATCCAAAGCAAGTCAATCAGAAGAGTTTAATGAAAAAGATTGCCAACTG
B.plumifrons        GATGGTGGCTGGATGTGCTAGAAAAATAAGACAGATAAGGAATCCAAAACAAGTCAACCAAAAGAGTTTGATGAAAAAAATTGCCAGCTG
G.wislizenii        GTTGGTGGCTGGGCATGCTAGAAAAATAAGGCAGATAAGGAATCCAAAACAAGTCAACCAAAAGAGTTTAATGAAAAAGATTGCCAGCTG
O.cuvieri           GATGGTGGGTGGATGTGCTAGAAAAATAAGACAGATAAGGAATCTAAAACAAGTGAACCAAAAGAGTTTAATGAAAAAGATTGCCAACTG
O.attenuatus        GATCGTTGTGGGGCGTGCCAGAAAAATAAGGCGCGTGAGGAATATGAGACAAGTGAACCACAAGGGTTTAATGAAAAAGATTGCGAACTG
E.panamintina       GATCGTTGTGGGACGTGCTAGAAAAATAAGGCGTGTGAGGAATATGAGGCAAGTGAACCACAAGGGTTTAATGAAAAAGATTGCCAACTG
C.enneagrammus      GATTGTTGCGGGACCTGCTAGGAAAATGAAGCGTGTGAGGAATATGCGACAAGTGAACCACAAGGGGTTAATGAAGAAGATTGCCAACTG
A.pulchra           GGTTGTTGCGGGACGTGCTAGAAAAATAAGGCGTGTGAGGAATATGAGACAAGTGAATCACAAGGGTTTAATGAAAAAGATTGCCAACTG
H.suspectum         AGTCATTGCGGGGCGTGCCAGAAAAATAAGGCATGTGAGAAATATGAGACAAGTGAACCACAAGAGTTTAATGAAAAAGATTGCCAACTG
X.grandis           GATCGGTGCGGGACGTGCTAGAAAAATAAGGCATGTGAGGAACATGAGACAAGTGAACCAGAAGAGTTTGATGAAAAAGATTGCCAACTG
V.griseus           GAACACGACAGGGCATGCTAGAAAAATAAGGCACATGAGAACTATGAAACCAGTGAACAACAAGAGCTTAATGAAGAAGATTGCCAACTG
L.borneensis        GAACCTTGCAGGGCATGCTAGAAAAATAAGGCGTGTGAAAAATATAAAACCAGTGAACCAC---CCTTTAATGAAGAAGATTGCCAACTG
S.crocodiluris      GATCGTTGCGGGACATGCTAGAAAAATAAGGTGTGTGAGGAATATGAAACAAGTGAACAACAAGACTTTAATGAAAAAGATTGCCAGCTG
Dinodon.sp.         GATTATTGCTGGGCATACGAGAAAAATAAGATGCATCAGAAAGGTAAAGCAACTGAATAACAAAAGTTTGATGAAAAAGATTTCAAACTG
R.braminus          GATTGTTCCTGGATCTAGTAGGACAGTAAGATGTGTAAGAAAGTTAAAGCAAGTAAGCCACAGACGCTTGATGAAAAAGATTTCAAACTG
C.ruffus            AATTGTTCCTGGATGTACTAGAAAAATAAGATGTGTAAGGAARGTAAAGCAAATGAATAACAAAAGTTTAATGAAAAAGATTTCAAACTG
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B.biporus         GTTTGTTGCAGGACATGCTAGAAAAATAGGGTTTGTAAGGAGTACAAAACAAGTGAGC---AAGAGTTTAATGAAAAAGATTGCCGACTG
T.weigmanni       GTTTGTTTCAGGACATGCTAGACAAATAGGGCGTGTAAGAAATACAAAACAAATGAACAACAAGAGTTTAATGAAAAAGATTGCCAACTG
R.floridana       GATCGTTGCTGGACATACTAGAAAAATAAGGCATGTAAGGAATACAAAACAAGTG---CACAAGAGTTTAATGAAAAAGATTGCCAACTG
A.xera            GTTTGTTGCAGGACATGCTAGACAAATAGGGCGTGTAAGGAGTACAAAACAAATGAACAACAAGAGTTTAATGAAAAAGATTGCCGACTG
C.tigris          GATTGGTACTGGGTGTGCTAGAAAAGTGAGTCGTGTGAGCAATCCGAAACAAATGAAGAACAAGAGCTTAATGAAAAAGATTGCAAACTG
L.parietale       GATTGGTGCTGGATGTGCTAAAAAAATCAAGCCACGTGACTAACCCAAAACAAATGAGGAACAAGAGCTTAATGAAAAGAATTACAAACTG
E.turkmenicus     GATCATTGCTGAACGTGCTAGAAAGATAATGTGTGCAAGGAGCCAAAAGCAAGTGAATAGCAAAAGCATCATGAAAAAGATTACCAACTG
S.shrevei         GATCATGGCTGAATGTGCTAGAAAGATAATATATGCAAAAAGCCAAAAACATGTGAACATCAAAAACATCCTGAAAAAGATTACCAACTG
T.przewalskii     GATCATTGCTGAACGTGCGAGAAAGATAATGTATGCAAGAAGCCGAAAGCAAGTGAACAGCAAAAGCATCATGAAAAAGATTACCAACTG
G.gekko           GATCATTGCTGAACGTGCTAGAAAGATAATGTATGCAAGAAGCCAAAAGCAAGTGAACGGCAAAAGCATCATGAAAAAGATTACCAACTG
P.lindneri        GATCATCGCAGAACGTGCTAGAAAGATAATGTACACAAGAAACCAAAAGCCAGCAAGCAGCAAAAGCCTCATGAAAAAGATCACCAACTG
Cr.ocellatus      GATCACTGCTGAACGTGCTAGAAAGGTCATGTACACAAGAAGCCCAAAGCCAGTGAACAGCAAAAGCCTCATGAAAAAGATTACCAATTG
L.jicari          GGTCATTGCAGAACATGCTAGGAAGATAATGTACACAAGAAGCCAGAAGCCAGTGAACAGCAAAAGCCTCATGAAAAAGATTACCAACTG
M.aurata          GATTATGGCGAGGTGTGCTAGACAAATAAGACCAGTAATGAGCCCCAAACAAGTGAACAGCAAAAGCCTCATGAAAAAGATTGTCAACTG
C.robustus        GATCCTGGCCAGACATGCTAGACAAATAAGACGGGTCAAGAACCCTAAACAAGTAAACAAAAGAAGTCTCATGAAAAAGATTGCAAACTG
S.sikkimensis     GATCATGGCCAGACACGCTACGCAAATCATACAGGTCAAGAACACCAAACAAGTAAACAGGAAAAGTCTCATGATAAAGATGGCGAACTG
E.inexpectatus    GATCATTGCGAGACATGCGAGACAAATAAGACAAGTCAGAAACCCCAAACAAATGAACAGTAGAAGTCTTATGAAAAAGATTGTCAACTG
E.skiltonianus    GATCATTGCGAGACATGCGAGACAAATAAGACATGTCAGGAACCCCAAACAAGAGAACAGCAGAAGTCTTATGAAAAAGATTGTCAACTG
E.anthracinus     GATCATTGCGAGACACRCGAGACAAATAAGACAAGTCAGGAACCCCAAACAAGTGAACAGCAGAAGTCTTATGAAAAAGATTGTCAACTG
S.anguineus       GAACGCTTCAAGATATGCTAGGCAAATAAGACAAGTAAGGAAATCCAAACAAGTGAGCAGCAAAAGTCTCATGAAAAAGGTTGTCAACTG
P.eggeli          GATCACTGCAAGATATGCTAGACAAATAAGACAAGTAAGGAAACCCAAACAAGTGAGCAGCAAAAGTCTCATGAAAAAGATTGTCAACTG
F.polylepis       GTTCAGTGCAAGATGTGCTAGACAAATGAGACAAGCTAGGAATCCCAAACAAGTA---------AGTCTCATGAAAAAGATGGTCAACTG
Ch.ocellatus      GATCACTGCAAGACGTGCTAGACAAATAAGACAAGTCAGGAACCCCAAACGAGTGAACAGCAAAAGTCTCATGAAAAAGATTGTCAACTG
A.meleagris       GATCATTACAAGACATGCCAGACAAATAAGACAAGTAAGGAACACCAAACAAGTGAACAGCAAAAGTCTCATGAAAAAGATTGTCAACTG
T.gariepensis     GATCATTACAAGACATGCCAGACAAATAAGACAAGTAAGGAACACCAAACAAGTGAACAGCAAAAGTCTCATGAAAAAGATTGTCAACTG
T.lomii           GATCATTACAAGACATGCCAGACAAATAAGACAAGTAAGGAACACCAAACAAGTGAACAGCAAAAGTCTCATGAAAAAGATTATCAACTG
X.vigilis         GATTGTTGCTGGACGTGTTCGACAAATAAAGCATGTAAGGACCACCAAACAATTGAGCAACAAGAGTCTCATGAAAAAGATTGCCAACTG
C.polyzonus       GATCATTGCTGGACATGCTCAGCAAATAAGGCATTTAAGGAACCCCAAACAAGTG---AACAAAAGTCTCATGAAAAAAATTGTTAACTG
Zonosaurus.sp.    GATCATTGCTGGACGGGCTCAGCAAATAAGGCATTTAAAGAACTCCCAACAAGTGAACAACAAAAGTCTCATGAAAAAAATAGTTAACTG
Dibamus.sp.       GATCATTGCAGGTCATGCAAGAAAACGAATGCGAGCAAGGAGCCCTAAACGAGTGGCCAGCAAAGGCCTCATGAAAAAGATTGCCAATTG

Index1            7777777777777777777777777777777777777777777777777777777777777777777777777777777888888888888
Index2            222222222333333333344444444445555555555666666666677777777778888888888999999999900000000001
Index3            123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.      CAAGAAGATACATCTTAGCACAAAGCTTCTTGCAGTTGACTATCCAGTAGATTTTGTTAAGGCTATCTCTTGTCAGATCTGTGAGCATAT
G.gallus          CAAGAACAGACATCTCAGCACCAAACTGCTTGCAGTTGATTATCCAGCAGATTTCATTAAATCCATCTCTTGCCAGATCTGTGAGCATAT
C.mydas           CAAGAAGATACATCTTAGCACCAAACTTCTAGCAGTTGACTACCCTGCAGATTTCGTTAAGTCCATCTCTTGCCAGGTCTGTGACCATAT
S.punctatus       CAAGAATATACACCTCAGTACCAAGATTCTTGCAGTAGACTATCCTGCAAATTTTGTGAAGTCCATCTCTTGCCAGGTTTGTGAGCATAT
B.thieli          CAATAAAATCCACCTCAGTACCAAGATCCTTGCAATAGATTATCCTGTGGAATTTGTAAAGTCGATCTCTTGCCAGGTCTGTGACCATAT
C.rudis           CAATAAAATCCACCTCAGTACCAAGATCCTTGCAGTAGATTATCCTGTGGACTTTGTAAAGTCGATCTCTTGCCAGGTCTGTGACCATAT
C.brevicornis     CAATAAAATCCACCTTAGTACCAAGATCCTTGCAGTAGATTATCCTGTGGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGACCATAT
C.salinarum       CAATAAAATCCACCTCAGTACCAAGATTCTTGCGGTAGACTATCCTGTGGACTTTGTAAAGTCAGTCTCTTGCCAGGCCTGTGAGCACAT
P.lesueurii       CAATAAAATCCACCTCAGTACCAAGATTCTTGCGGTAGACTATCCTGTGGACTTTGTAAAATCAGTCTCTTGCCAGGTCTGTGAGCACAT
P.cocincinus      CAATAAAATCCACCTCAGTACCAAGATTCTTGCAGTAGACTATCCTGTGGACTTTGTAAAGTCAGTCTCTTGCCAGGTTTGTGAGCACAT
Hydrosaurus.sp.   CAAGAAAATCCATCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGTGGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
C.calotes         CAACAAAATCCACCTGAGTACCAAGATCCTTGCCGTAGACTATCCTGTGGACTTTGTCAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
J.tricarinata     CAACAAAATCCACCTCAGTACCAAGATCCTTGCCGTAGACTATCCTGTGGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
P.raddei          CAAGAAAATCCACCTTAGTACCAAGATCCTTGCAGTAGACTATCCTGCGGATTTTGTAAAGTCAGTCTCTTGCCAGGTCTGTGAGCATAT
L.belliana        CAAGAAAATCCACCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGTGGACTTTGTAAAGGCAATCTCTTGCCAAGTCTGTGAACACAT
U.acanthinurus    CAGGAAAATCCATCTCAGTACCAAGATCCTTGCAGTGGACTATCCTGTGGACTTTGTGAAGTCAGTCTCTTGCCAGATCTGTGAGCATAT
A.paternus        CAAGAAGATTCACCTCAGCACCAAGATCCTTGCAGTAGACTACCCTTCGGACTTTGTAAAGTCAATCTCTTGCCAAATCTGTGAGCACAT
P.mcallii         CAAGAAGATTCACCTCACTACCAAAATCCTTGCAGTAGACTATCCTGCAGACTTTGTAAAGTCAATTTCTTGCCAGATTTGTGAACACAT
S.obesus          CAAGAAGATTCACCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGCGGACTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAGCATAT
Hoplocercus.sp.   CAAGAAGATTCACCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGTGGACTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAACACAT
E.laticeps        CAAGAAGATTCACCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGTGGACTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAACACAT
P.somencurensus   CAGTAAGATTCACCTCAGTACCAAGATTCTTGCAGTTGACTATCCTGCAGGTTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAGCACAT
L.pictus          CAATAAGATTCATCTCAGTACTAAGATTCTTGCAGTAGACTATCCTGCATGCTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAGCACAT
U.flaviceps       CAAGAAGATTCACTTCAGCACCAAGATCCTGGCAGTAGACTATCCTGCAGACTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAACACAT
S.crasicaudatus   CAAGAAGGTTCACTTCAGTACCAAGATCCTTTCAGTAGACTATCCTGTAGACTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAGCACAT
L.carinatus       CAAGAAAATTCACCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGTGGACTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAGCACAT
B.plumifrons      CAAGAAGATTCACCTTAGTACCAAGATCCTTGCAGTAGACTATCCCGCCGACTTTGTAAAGTCAATCTCCTGCCAGATCTGTGAGCACAT
G.wislizenii      CAAGAAGATTCACCTCAGCACCAAAATCCTTGCAGTAGACTATCCAGCAGACTTTGTAAAGTCAATCTCTTGCCAGATCTGTGACCACAT
O.cuvieri         CAAGAAGATTCACCTCAATACCAAGATCCTTGCAGTAGACTATCCTGTGGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
O.attenuatus      CAAGAAGATCCATCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGCGGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
E.panamintina     CAAGAAGATCCATCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGCGGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
C.enneagrammus    CAAGAAGATCCATCTCAGCACCAAGATCCTTGCAGTAGACTATCCTGTGGACTTCGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
A.pulchra         CAAGAAGATCCACCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGCGGACTTTGTAAAGTCGATCTCTTGCCAGGTCTGTGAGCACAT
H.suspectum       CAAGAAGATCCATCTCAGTACCAAGATGCTTGCAGTAGACTATCCTGCAGACTTTGTAAAGTCCATCTCTTGCCAGGTCTGTGAGCACAT
X.grandis         CAAGAAGATCCATCTCAGTACCAAGATCCTTGCAGTAGACTACCCTGCAGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
V.griseus         CAGCAAGATCCACCTCAGTACCAGTAGACTTGCAGTAGACTATCCCAAAGACTTTGTAAAGTCAATCTCTTGCCAAGTCTGTGAGCATAT
L.borneensis      CAGCAGGATCCACCTCAGTACCAAGAACCTTGCAGTAGACTATCCTACAGACTTTGTAAAGTCAATCTCTTGCCACGTCTGTGAGCATAT
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S.crocodiluris      CAAGAAGATCCATCTCAGTACCAAGATCCTTGCAATAGACTATCCTGCAGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCACAT
Dinodon.sp.         TAAACAAATCCATCTCAGCACAAAAATCCTTGCGATAGACTACCCTGTGGACTTTGTAAAGTCAATATCTTGCCAGATCTGTGAACACAT
R.braminus          CCAGCAGATCCACATCAGTACAAAGATCCTTGCAACCGACTACCCCGTCGACTTTGTAAAGTCAATCTCTTGCCAGGTCTGTGAGCATAT
C.ruffus            TAAGCAGATCCATCTCAGTACAAAGGTCCTTGCAATAGACTATCCTGTGGACTTTGTAAAGTCAATATCTTGCCAGATCTGTGAGCACAT
Agkistrodon.sp.     TAAGCAGATCCACCTCAGTACAAAAATCCTTGCAATAGACTACCCTGTGGACTTTGTAAAGTCAATATCTTGCCAGATCTGTGAGCACAT
Eremias.sp.         CAACAAGATACACCTCAGTACCAAGAGCCTTGCTGTAGATTATCCCATTGACTTTGTAAAATCGATCTCTTGCCAGGTCTGTGAGCATAT
B.biporus           CAACAAAATACACCTCAGTACCAAGATACTTGCCGTAGACTATCCTCTGGAATTTGTAAAGTCAATTTCTTGCCAGGTCTGTGAGCATAT
T.weigmanni         CAACAAAATACACCTCAGTACTAAGATCCTTGCAGTCGACTATCCTGTGGATTTTGTAAAGTCAATTTCTTGCCAGGTCTGTGAGCACAT
R.floridana         CAACAAGATACATCTCAGTACCAAGGTCCTTGCAGTAGACTATCCTGTGGATTTTGTAAAGTCATTCTCTTGCCAAGTCTGTGATCATAT
A.xera              CAACAAAATACACCTCAGTACCAAGATCCTTGCAGTAGACTATCCTGTGGATTTTGTAAAGTCAATTTCTTGCCAGGTCTGTGAGCACAT
C.tigris            CAAGAAGATACATCTCGACACCAGTGTCCTTGCAGTAGATTATCCTGTGGACTTTGTGAAGTCAATCTCGTGCCAAATCTGTGAACATAT
L.parietale         TAAAAAGATACATCTTGATACCAACATCCTTGCAGTAGACTATCCTGTGGATTTTGTGAAGTCAATCTCTTGCCAGATTTGTGAACATAT
E.turkmenicus       CAAAAAGATCCATCTCAGTACAAAGATGCTCACAGTGGACTATCCTGCAGATTTTGTAAAGTCAATCTCTTGCCAGATCTGTGAGCATAT
S.shrevei           CAAAAAGATCCATCTCAGTACAAAGATGCTCACAGTAGACTACCCTGCAGATTTTGTAAAGTCAATCTCCTGCCAGATTTGTGAGCATAT
T.przewalskii       CCAAAAGATCCATCTCAGTACGAAGATGCTCATAGTAGACTATCCTGCAGATTTTGTAAAGTCAATCTCTTGCCAGATTTGTGAGCATAT
G.gekko             CAAAAAGATCCATCTCAGTACAAAGATGCTCACAGTAGACTATCCTGTGGATTTTGTAAAGTCCATATCTTGCCAGATCTGTGAGCATAT
P.lindneri          CAAAAAGATTCACCTCAGTACAAATATGCTCACAGTAGACTATCCTGCAGATTTTGTGAAGTCCATCTCTTGCCAGATCTGTGAGCATAT
Cr.ocellatus        CAAAAAGATTCATCTCAGTACAAATATGCTCACAGTAGACTATCCTAAAGATTTTATAAAGTCAATCTCCTGCCAGATCTGTGAGCATAT
L.jicari            CAAAAAGATTCACCTCAGTACGGATATGCTCACAGTAGACTATCCTGCAGATTTTGTAAAATCAATCTCTTGCCAGATCTGTGAGCATAT
M.aurata            CAACAAGATACATCTCAGCTCGAAGAGCTTTGCGGTGGACTATCCTGCAGACTTTGTGAAAGCAGTCTCTTGCCAGATCTGTGAGCACAT
C.robustus          CAGCAAGATACATCTCAGTTCCAAGAGCTTAGCAGTGGACTATCCTGCGGACTTTGTGAAATCCATCTCTTGCCAGATCTGTGAGCACAT
S.sikkimensis       CAGCAAGATTCATGTCAGCACTAATAGCTTAACAGTGGACTATCCTGCGGACTTTGTGAAATCCATCTTTTGCCGGATCTGTGAGCACAT
E.inexpectatus      CAAGAAGATACATCTCAGTACAAAGAGCCTTGCGGTGGACTATCCTGCAAACTTTGTGAAATCGGTTTCTTGCCAGATCTGTGAGCACAT
E.skiltonianus      CAAGAAGATACATCTCAGTACAAAGAGCCTTGCGGTGGACTATCCTGCAGACTTTGTGAAATCGGTTTCTTGCCAGATCTGTGAGCATAT
E.anthracinus       CAAGAAGATACATCTCAGTACAAAGAGCCTTGCGGTGGACTATCCTGCAGACTTTGTGAAATCGGTTTCTTGCCAGATCTGTGAGCACAT
S.anguineus         CAAGAAGACACATCTCAGTACAAAGAGCTTTGCAGTGGACTATCCTGCAGACTTTGTGAAATCGGTTTCTTGCCGGATCTGTGAGCATAT
P.eggeli            CAAGAAGATACATCTCAGTACAAAGAGCTTTGCAGTGGACTATCCTGCAGACTTTGTGAAATCAGTCTCTTGCCAGATCTGTGAGCATAT
F.polylepis         CAAGAAAATACATCTCAGTACAAAGAGCTTTGCAGTGGACTATCCTGCAGACTTTGTGAAATCAGTGTCTTGCCGGATCTGTGAGCATAT
Ch.ocellatus        CAAGAAGATACATCTCAGTACAAAGAGCTTTGCAGTGGACTATCCTGCAGACTTTGTGAAATCAGTCTCTTGCCAGATCTGTGAGCATAT
A.meleagris         CAAGAAGATACATCTCAGCACGAAGAGTTTAGCAGTAGACTATCCTGCAGACTTTGTGAAATCAGTCTCTTGCCAGATCTGTGAGCACAT
T.gariepensis       CAAGAAGATACATCTCAGCACGAAGAGTTTAGCAGTAGACTATCCTGCAGACTTTGTGAAATCAGTCTCTTGCCAGATCTGTGAGCACAT
T.lomii             CAAGAAGATACATCTCAGCATGAAGAGTTTAGCAGTAGACTATCCTGCAGACTTTGTGAAATCAGTCTCTTGCCAGATCTGTGAGCACAT
X.vigilis           CAAGAAGATACATCTCAGTACGAAGATCCTTGCAGTAGACTATCCTGCAGACTTCGTAAAATCAATCTCTTGCCAGGTTTGTGAGCACAT
C.polyzonus         CAAGAAGATTCATCTCAGTACAAATGTCCTTGCAGTAGACTATCCTGCAGACTTTGTAAAATCAATCTCTTGTCAGGTCTGTGAGCACAT
Zonosaurus.sp.      CAAGAAGATTCATCTCAGTACAAATGTCCTTGCAGTAGACTATCCTTCAGACTTTGTAAAATCAATCTCTTGTCAAGTCTGTGAGCACAT
Dibamus.sp.         CAAGAATATACATCTCAGTGCCAAGATCCTTGCAGTAGACTATCCTGCAGACTTTGTCAAGTCAATCTCTTGCCAGGCCTGTGAACACAT


Index1              888888888888888888888888888888888888888888888888888888888888888888888888888888888888888889
Index2              111111111222222222233333333334444444444555555555566666666667777777777888888888899999999990
Index3              123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.        TCTGTCAGATCCAGTGGAAACAACGTGTAGGCACTTATTCTGTAGAACCTGCATCCTTAAATGTCTCAAAGTTATGGGCAGTTATTGCCC
G.gallus            TTTGGCAGACCCAGTGGAAACAACGTGTAGACACTTGTTTTGCAGAACTTGCATTCTCAGTTGCATCAGAGTTATGGGATGCTATTGCCC
C.mydas             TCTGGCAGACCCAGTGGAAACGACATGTAGCCACTTATTCTGTAGAACCTGCATCCTTAAGTGCCTCAAAGTTATGGGCAGCTATTGTCC
S.punctatus         TCTGGCTGACCCAGTGGAAACAACATGCAAGCATTTATTCTGCAGAACCTGTATTCTTAAATGCCTCAAAGTTATGGGCAGCTATTGCCC
B.thieli            CCTGGCTGATCCTGTAGAAACAACATGCAAGCACCTGTTCTGCAGAGCCTGCATCCTTAAATGCATCAAAGTGATGGGAAGCTATTGCCC
C.rudis             CCTGGCTGATCCTGTAGAAACAGCATGCAAGCACTTGTTCTGCAGAGCCTGCATACTTAAATGCATCAAAGTGAAGGGAAGCTATTGCCC
C.brevicornis       CCTGGCTGATCCTGTAGAAACAACATGCAAGCACTTGTTCTGCAGAGCTTGCATCCTTAAATGCATCAAAGTGATGGGAAGCTATTGCCC
C.salinarum         CCTAGCTGATCCTGTAGAAACAACATGCAAGCACTTATTCTGCAGGGCCTGCGTCCTTAAATGCATCAAAGCAATGGGAAGCTACTGCCC
P.lesueurii         CCTAGCTGATCCTGTAGAAACAACATGCAAGCACTTATTCTGCAGGGCCTGCATCCTTAAATGCATCAAAGTAATGGGAAGCTACTGCCC
P.cocincinus        CCTAGCTGATCCTGTAGAAACAACATGCAAGCACTTATTCTGCAGGGCTTGCATCCTTAAATGCATCAAAGTAATGGGAAGCTACTGCCC
Hydrosaurus.sp.     ACTGGCTGATCCTGTAGAAACAACATGCAAGCACTTATTCTGCAGGGCCTGTATCCTGAAATGCATCAAAGTAATGGGAAGCTATTGCCC
C.calotes           CCTGGCTGATCCCGTAGAAACAACTTGCAAGCACCTATACTGCAGGGCCTGCATCCTTAAATGCATCAAAGTTATGGGAAGCTATTGCCC
J.tricarinata       CCTGGCTGATCCTGTAGAAACAACTTGCAAGCACTTATACTGCAGGGCCTGCATCCTTAAATGCATCAAAGCAATGGGGAGCTATTGCCC
P.raddei            CCTGGCTGATCCTGTAGAAACCACATGCAAGCACTTATTTTGCAGGGCCTGCCTCCTTAAATGCCTCAAAGTCATGGGAAGCTTTTGCCC
L.belliana          CCTGGCTGATCCTGTAGAAACAACATGCAAGCACTTATTCTGCAGAGCCTGCATCCTTAAATGCATCAAAGTAATGGGAAGCTATTGCCC
U.acanthinurus      CTTGGCTGATCCTGTAGAAACAACATGCAGACACTTATTCTGCAGAGCCTGCATCCTTAAATGCATCAAAGTAATGGGAAGCTATTGCCC
A.paternus          CCTGGCTGACCCAGTAGAAACAACGTGCAAGCACCTATTCTGCAGAGCCTGCATCCTCAAATGCCTCAAAATAATGGGAAGCTATTGTCC
P.mcallii           CCTGGCTGATCCAGTAGAAACGACATGCAAACACTTATTCTGCAGAGTCTGCATTCTTAAATCCCTCAAAATAATGGGAAGCTATTGCCC
S.obesus            CCTGGCTGATCCAGTAGAAACAACATGCAAGCACCTATTTTGCAGAGCCTGCATCCTTAAATGTCTCAAAGTAATGGGAAGCTATTGCCC
Hoplocercus.sp.     CCTGGCTGACCCAGTAGAAACAACGTGCAAGCACCTATTCTGCAGAGCCTGCATCCTGAAATGCCTCAAAGTAATGGGAAGCTATTGCCC
E.laticeps          CCTGGCTGACCCAGTAGAAACAACGTGCAAGCACCTATTCTGCAGAGCCTGCATCCTGAAATGCCTCAAGGTAATGGGAAGTTATTGCCC
P.somencurensus     CTTGGCTGATCCAGTAGAAACGACATGCAGTCACTTATTCTGCAGAGCCTGCATCCTTAAATGCCTCAAAGTAATGGGAAGTTATTGTCC
L.pictus            ATTGGCTGATCCAGTAGAAACGACATGCAGACACTTATTCTGCAGAGCCTGCATCCTTAAATGCCTCAAAGCAATGGGAAGTTATTGCCC
U.flaviceps         CCTGGCTGACCCAGTAGAAACAACATGTAAGCACTTATTCTGCAGAGCCTGCATCCTGAAATGCCTCAAAGTAATGGGAAGCTATTGCCC
S.crasicaudatus     CCTGGCTGACCCAGTAGAAACGACATGCAAGCACTTATTCTGCAGAACCTGCATCCTGAAATGCCTCAAAGTAATGGGAAGCTATTGCCC
L.carinatus         TCTGGCTGACCCAGTAGAAACAACGTGCAAGCACTTGTTCTGCAGAACCTGCATCCTCAAATGCCTCAAAGTAATGGGAAGCTATTGCCC
B.plumifrons        CCTCGCTGACCCAGTAGAAACGACATGCAAACACTTATTTTGCAGAACCTGCATCCTTAAATGCCTCAAAGTAATGGGAAGCTATTGCCC
G.wislizenii        CCTGGCTGACCCAGTAGAAACAACGTGCAAGCACTTATTCTGCAGAACCTGCATCCTTAAAAGCCTCAAAGTAATGGGAAGCTATTGCCC
O.cuvieri           CCTGGCTGACCCAGTAGAAACAACATGCAAGCACTTATTCTGCAGAGCCTGCATACTTAAATGCCTTAAAGTAATGGGAAGTTATTGCCC
O.attenuatus        CCTGTCTGACCCAGTTGAAACAACATGCAAGCACCTATTCTGCAGAGTCTGCATCCTTAAATGCCTCAAAGTCATGGGGAGCTATTGCCC
E.panamintina       CCTGTCTGACCCAGTTGAAACAACATGCAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGCCTCAAAGTCATGGGGAGCTATTGCCC
C.enneagrammus      CCTGTCTGATCCAGTCGAAACCACGTGCAAGCACTTGTTCTGCCGAGTGTGCATCCTTAAGTGCCTCAAAGTCATGGGGAGCTACTGCCC
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A.pulchra         CCTGTCTGACCCAGTGGAAACGATGTGCAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGTCTCAAAGTTATGGGGAGCTATTGCCC
H.suspectum       CCTGTCTGACCCCGTCGAAACGACATGCAAGCACTTGTTCTGCAGAGTCTGCATCCTTAAATGCCTCAAGGTCATGGGGAGCTATTGCCC
X.grandis         CCTGTCTGACCCGGTAGAAACGACGTGCAAGCACTTATTCTGCAGAGTTTGCATCCTTAAATGCCTCAAAGTAATGGGGAGCTATTGCCC
V.griseus         CCTGTCTGACCCAGTAGAAGCAGCATGCAAACACTTATTCTGCAGGGTCTGCATTTTTAAATGTCTCAAAGTAATGGGGAGCTACTGCCC
L.borneensis      CCTGTCTGACCCAGTAGAAACGACATGCAAACACTTATTCTGCAGGGTCTGCATTCTTAAATGTCTCAAAGTAATGGGGAGCTACTGCCC
S.crocodiluris    CCTGTCTGACCCAGTAGAAACGACGTGCAAACACTTATTCTGCAGGATCTGCATCCTTAAATGTCTCAAAGTAATGGGGAGCTACTGCCC
Dinodon.sp.       CCTGGCTGATCCAGTAGAAACAACATGCAAACACTTATTTTGCAGAGTCTGCATTCTTAAATGCCTTAAAGTAATGGGAAGCTATTGCCC
R.braminus        TTTGACGGACCCAGTAGAAGCAACATGCAAACACTTATTCTGCAGAGTCTGCATCCTTAAATGTCTCAAAGTAATGGGCAGTTACTGTCC
C.ruffus          TCTGGCTGATCCAGTAGAAACAACGTGTAAACACTTATTCTGTAGAGTCTGCATTCTTAAATGTCTTAAAGTAATGGGCAGCTATTGCCC
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B.biporus         TCTGGCTGATCCGGTAGAAACGACATGTACACACTTATTTTGCAGAGTGTGCATCCTTAAATGTCTCAAAGTCATGGGAAGTTACTGCCC
T.weigmanni       CCTGGCTGATCCAGTAGAAACAACCTGTAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGTCTCAAAATCATGGGAAGTTACTGTCC
R.floridana       CCTGGCTGATCCAGTAGAAACAACTTGTAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGCCTCAAAATAATGGGAAGTTATTGCCC
A.xera            CCTGGCTGATCCAGTAGAACCAACCTGTAAGCACTTATTCTGCAGAGTCTGCATCCTTAAATGTCTCAAAATCATGGGAAGTTACTGCCC
C.tigris          CCTAGCTGACCCAGTCGAGACTACATGCAAGCACCTCTTTTGCAGGGTTTGCATCCTTAAATGTCTCAAAGTAATGGGAAGTTATTGCCC
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E.turkmenicus     TCTGGCTGACCCAGTAGAAACAACATGCAAGCACTTATTCTGCAGACTTTGCATCCTTAAATGCCTCAAAGTAATAGGAAGCTATTGCCC
S.shrevei         TCTGGATGACCCAGTAGAAACAACATGCAAGCACTTATTCTGCAGACTCTGCATCCTTAAATGCCTCAAAGTAATAGGAAGTTATTGTCC
T.przewalskii     TCTGGCTGACCCAGTAGAAACAACATGCAAACACTTATTTTGCAGACTTTGCATCCTTAAATGCCTCAAAGTAATAGGAAGTTATTGCCC
G.gekko           TCTGGCTGACCCAGTAGAAACAACATGCAAGCACTTATTCTGCAGACATTGCATCCTTAAATGTCTCAAAGTAATAGGAAGCTATTGCCC
P.lindneri        CCTGGCTGACCCAGTCGAAACAACATGCAAGCACTTATTCTGTAGACTCTGCATCCTTAAATGCCTCAAAGTATTAGGTAGCTATTGCCC
Cr.ocellatus      CCTGGCTGACCCAGTAGAAACAACATGCAAGCACTTATTCTGTAGACTCTGCATTGTTAAATGCCTCAAAGTAATAGGCAGCTATTGTCC
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M.aurata          CCTGGCAGACCCAGTAGAGACCACATGCAAGCACTTATTTTGCCGAGTTTGCATCCTGAAATGCCTCAAAGTAATGGGAAGCTATTGTCC
C.robustus        CCTGGCAGATCCAGTGGAAACGACCTGCAAGCACTTGTTCTGCCGAGTTTGCATCCTGAAATGCCTCAAAGTCATGGGAAGCTACTGCCC
S.sikkimensis     CCTGGCGGACGCGGTGGAAACAACCTGCAAGCACTTGTTCTGCCCGATTTGCCTCCTGAAATGCCTCAAAGTCATGGGAAGCTATTGCCC
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E.skiltonianus    CCTGGCAGACCCAGTAGAAACAACATGCAAGCACGTGTTCTGCAGAATTTGCATCCTTAAATGCCTTAAAGTCATGGGAAGCTATTGCCC
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F.polylepis       CCTGGCAGACCCAGTAGAAACAACATGCAAGCACTTATTCTGCAGAGTTTGCATCCTTAAATGCCTTAAAGTAATGGGAAGCTACTGCCC
Ch.ocellatus      CCTGGCAGATCCAGTAAAAACAACATGCAAGCACTTATTCTGCAGAGTTTGCATCCTTAAATGTCTTAAAGTAATGGGAAGCTATTGCCC
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T.gariepensis     CCTGGCTGACCCAGTAGAAACAACATGCAAGCACTTATTCTGCAGAGTTTGCATCCTTAAATGCCTTAAAGTAATGGGAAGCTATTGCCC
T.lomii           TCTGGCGGACCCAGTAGAAACAACATGCAAGCACTTATTCTGCAGAGTTTGCATCCTTAAATGCCCTAAAGTAATGGGAAGCTATTGCCC
X.vigilis         ACTGGCAGACCCAGTAGAAACAACATGTAAGCACTTATTCTGCAGAGTCTGCATCCTGAAGTGCCTCAGGGTAATGGGAAGCTATTGCCC
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Zonosaurus.sp.    ACTGGCGGATCCAGTAGAAGCAGCATGCAAACACTTATTCTGCAGAGTCTGCATTCTTAAATGCTTTAGAGTCATGGGAAGCTATTGCCC
Dibamus.sp.       CTTGGCTGACCCAGTAGAAACGACATGCAAGCACTTATTTTGCCGAGTGTGCATTCTTAAATGCCTCAAAGTTATGGGAAGTTATTGCCC

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A.mississip.      CTCCTGCCTATACCCTTGCTTCCCTACTGACTTAGTGACCCCAGTGAAATCCTTCCTAAACATTCTTGACTCTCTGACTTTGAGATGCCC
G.gallus          TTCCTGCTGGTATCCTTGCTTCCCTACTGATCTGGTAACCCCAGTGAAATCCTTCCTGAACATCCTTGATAGCCTGAGCATAAGATGCCC
C.mydas           CACCTGCCGATACCCTTGCTTCCCTACCGACCTGGTGAGTCCAGTGAAATCCTTCCTGAACATTCTCAATTCCCTGGCTGTGCGATGCCC
S.punctatus       CTCCTGTCGATATCCTTGCTTCCCTACTGATCTGGAGAGCCCAGTAAAGTCCTTCCTGAACATCCTTAATTCTCTGGCTGTGAGATGCCC
B.thieli          AGCCTGTTACTATCCTTGTTTTCCTACCGATCTGGTGAGCCCTGTAAAATCCTTCCTGAACATTCTCAATAGCCTGGCTCTGAGATGTCC
C.rudis           AGCCTGTTACTATCCTTGCTTTCCTACCGATCTGGTGAGCCCTGTGAAATCCTTCCTGAACATCCTCAATAGCCTCGTTCTGAGATGTCC
C.brevicornis     AGCCTGTTACTATCCTTGTTTTCCTACTGATCTAGTGAGCCCTGTGAAATCCTTCCTGAACATCCTCAATAGCCTCACTTTGAGATGTCC
C.salinarum       AGCCTGTCGCTATCCTTGTTTTCCTACAGATCTGGTGAGCCCCGTGAAATCCTTCCTGAATATCCTCAACAATCTGATCCTGAGATGTCC
P.lesueurii       AGCCTGTCGCTATCCTTGTTTTCCTACAGATCTGGTGAGCCCCGTGAAATCTTTCCTGAACATCCTCAACAATCTGATCCTGAGATGTCC
P.cocincinus      AGCCTGTCGCTATCCTTGTTTTCCTACAGATCTGGTGAGCCCTGTGAAATCCTTCCTGAACATCCTCAACAATCTGATCCTGAGATGTCC
Hydrosaurus.sp.   AGCTTGTCGCTATCCGTGTTTTCCTACAGATCTGGTGAGCCCTGTGAAATCCTTCCTGAACATCCTCAACAACCTGGTTCTGAGATGTCC
C.calotes         AGCTTGTCGCTACCCTTGTTTTCCTACGGATCTGGTGAGCCCTGTGAAATCTTTCCTGAGTATCCTCAACAACCTGGTACTGCGGTGTCC
J.tricarinata     AGCTTGTCGCTATCCTTGTTTTCCCACGGATCTGGAGAGCCCTGTGAAATCTTTCCTGAATATCCTCAACAACCTGGTACTGAGATGTCC
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P.mcallii         AGCTTGTCGCTATCCTTGCTTTCCTACTGACCTGGTAGGCCCTGTGAAATCCTTCCTGAACATCTTGAACAGTTTACCTGTGAGATGTCC
S.obesus          AGCTTGTCGCTATCCTTGCTTTCCTACTGATTTGGTGAGCCCTGTGAAATCCTTCCTGAACATCCTGAACAGTCTGCCTGTGATATGTCC
Hoplocercus.sp.   AGCTTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTGAAATCCTTCCTGAGCATCTTGAACAGCCTACCTGTGAGATGTCC
E.laticeps        GGCTTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTGAAATCCTTCCTGAGCATCTTGAACAGCCTACCTGTGAGATGTCC
P.somencurensus   AGCTTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTGAAATCCTTCCTGAGCATCCTGAATGGTCTACCTGTCAGATGTCC
L.pictus          AACTTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTAAAATCCTTCCTGAACATCCTCAATGGTCTACCTGTGAGATGTCC
U.flaviceps       AGCTTGTCGCTACCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTGAAGTCCTTCCTGAGCATCCTGAACAGTCTACCTATGAGATGTCC
S.crasicaudatus   AGCTTGTCGCTACCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTGAAATCCTTCCTGAGCATCTTGAACAGTCTACCTGTGAGATGTCC
L.carinatus       AGCTTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTCAAATCTTTCCTGAGCATTCTGAATGGTCTACCTGTGAGATGTCC
B.plumifrons      AGCTTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTGAAATCCTTCCTGAGCATCCTGAACAGTCTACCTATGAGATGTCC
G.wislizenii      AGCTTGCTGCTATCCTTGCTTTCCTACTGATCTGGAGAGCCCTGTGAAATCCTTCCTGAGCATCCTGAACAGTCTACCTGTGAGATGTCC
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O.cuvieri          AACTTGTCACTATCCTTGCTTTCCTACGGATCTGGTGTGCCCTGTGAAATCCTTCTTGACCATCCTGAATAGTCTACCTGTGATATGTCC
O.attenuatus       ATCCTGTCGCTATCCTTGCTTTCCTACTGATCTGGAGAGCCCTGTGAAATCATTCCTGAGCATCCTCAACAATTTGGCTGTGAGATGTTC
E.panamintina      ATCCTGTCGCTATCCTTGCTTTCCTACTGATCTGGAGAGCCCTGTGAAATCATTCCTGAGCATCCTCAACAATTTGGCTGTGAGATGTCC
C.enneagrammus     ATCCTGTCGCTACCCGTGCTTTCCTACTGATCTGGAGAGCCCAGTGAAGTCCTTCCTGATCATCCTCAACAGTCTGGTTGTGAGATGTCC
A.pulchra          ATCCTGTCGCTATCCTTGCTTTCCTACTGATCTGGAGAGCCCTGTGAAATCCTTCATGAGCATCCTCAACAGTCTGGCTGTGAGATGTCC
H.suspectum        ATCCTGTCGTTATCCTTGCTTTCCTACTGATCTGGAGAGCCCTGTGAAATCCTTCCTGAGCATCTTCAACAATTTGGCTGTGCGATGTCC
X.grandis          ATCCTGTCGCTACCCCTGCTTTCCAACTGATCTGGAGAGCCCTGTGAAATCCTTCCTGAGCATCCTCAACAGTTTGGCGGTGCGATGTCC
V.griseus          ATCCTGTCGCTATCCTTGCTTTCCAACTGATTTGGAGAGCCCTGTGAAATCCTTTCTGAATATCCTCAATGGTTTGGCTGTGAGATGCCC
L.borneensis       ATCCTGTCGCTATCCTTGCTTTCCGACTGATCTGGAGAGCCCTGTGAAATCCTTTCTGAATATCCTCAATGGTTTGGCTGTGAGATGCCC
S.crocodiluris     ATCCTGTCGCTATCCTTGCTTTCCTACTGATCTGGAGAGCCCTGTGAAATCCTTCCTGAGTATCCTCAATGGTTTAGCTGTGAGATGTCC
Dinodon.sp.        ATCCTGCCGATATCCTTGTTTTCCTACTGATCTGGTGAGCCCTGTAAAATCCTTCTTAAGCATCCTCAACAATTTGGTTTTGAGATGCCC
R.braminus         ATCCTGCCAATATCCTTGCTTTCCTACTGATCTGGTGAGTCCTGTGAAATCCTTCCTGAGCATCCTCAACAATTTGGTTGTGAGGTGTCC
C.ruffus           ATCCTGCCGATATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTAAAATCCTTCCTAAGCATTCTCAACAATTTGGTTGTGAGATGTCC
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B.biporus          CTCCTGTCGCTATCCGTGCTTTCCTACTGACCTGGTGAGCCCTGTGAAATCCTTCCTGAGCATCCTCAACAGTTTGGCTGTGAGATGTCC
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C.tigris           ATCCTGTCGTTATCCTTGCTTTCCTACTGATCTAGTGAGCCCAGTGAAGTCCTTCCTCAGCATCCTCAACAGTTTGGCTGTGACATGTCC
L.parietale        CTCCTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGTCCAGTGAAATCCTTTCTGAGTATCCTCAGCAATTTGGCTGTGACCTGTCC
E.turkmenicus      AGCCTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAACCCTGTGAGATCCTTCCTGAGCATACTCAGCACTTTGGCTGTGAGGTGTCC
S.shrevei          ATCTTGTCGCTATCCTTGTTTTCCTACTGATCTAGTGAACCCTGTGAGATCCTTCCTGAGTGTACTCAACTCTTTGACTGTGAGATGTCC
T.przewalskii      ATCCTGTCGCTATCCTTGTTTTCCTACTGATCTGGTGAACCCTGTGAAGTCCTTCTTGAGCATACTCAACACTTTGGCTGTGAGGTGTCC
G.gekko            ATCCTGTCGCTATCCTTGTTTTCCTACTGATCTGGTGAGCCCTGTGAGATCCTTCCTGAGCATACTCAACACTTTGGCTGTGATGTGTCC
P.lindneri         ATCCTGCCGCTATCCTTGCTTTCCTACTGATCTGGTGAACCCAGTGAGATCCTTCCTCAACGTGATCAACACTTTGGTCGTGAGGTGCCC
Cr.ocellatus       AGCCTGTCGCTATCCTTGCTTTCCGACTGATCTGATGAACCCAGTGAGATCCTTCCTCAACATGATCAACACTTTGGTTGTGAGGTGCCC
L.jicari           ATCCTGTCGCTATCCTTGCTTTCCTACTGATCTGATGAATCCAGTGAGATCCTTCCTCAATGTGATCAACACTTTGGCTGTGAGGTGCCC
M.aurata           TTCTTGTCGCTATCCTTGCTTTCCTACTGATCTTGTGAGTCCTGTCAAATCCTTCCTGAGCATCCTCAACAATTTGCCACTGAGATGTCC
C.robustus         CAGTTGCCGCTATCCTTGCTTTCCGACTGATCTTGGGAGTCCCGTCAAATCCTTCCTGAGCATCCTCAATAATCTGGCCGTGACGTGCCC
S.sikkimensis      CAGTTGCCGCTACCCTTGCTTTCCGACTGATCTGGGGAGCCCTGTCAAATCCTTCCTGAACATCCTCAACAATTTGACCATGAGATGCCC
E.inexpectatus     CAGTTGTCGCTATCCTTGCTTTCCTACTGATCTTGAGAGCCCCGTAAAATCTTTCCTGAGCATCCTCAACAATTTGGTTGTGAGATGTCC
E.skiltonianus     CAGTTGTCACTATCCTTGCTTTCCTACTGATCTTGTGAGCCCCGTAAAAATTCCTCTGACCATCCTCAACAATTTGGCTGTGAGGTGTCC
E.anthracinus      CAGTTGTCGCTATCCTTGCTTTCCTACTGATCTTGTGAGCCCCGTAAAATCCTTCCTGAGCATCCTCAACAATTTGGCTGTGAGATGTCC
S.anguineus        CTGTTGTCGCTATCCTTGCTTTCCTACTGATCTTGTGAGCCCTGTAAAATCCTTCCTGAGCATCCTCAACAATTTGGCTGTGAGATGTCC
P.eggeli           CTGTTGTCGCTATCCTTGCTTTCCTACTGATCTTGTGAGCCCTGTAAAATCCTTCCTGAGCATCCTCAACAATTTGGCTGTGAGATGTCC
F.polylepis        CTGTTGTCGCTATCCTTGCTTTCCTACCGATCTTGTGAGCCCTGTGAAATCCTTCCTGAGCATCCTCAACAATTTGGTTGTGAGATGTCC
Ch.ocellatus       CTGTTGTCGCTATCCTTGCTTTCCTACTGATCTTGTGAGCCCTGTAAAATCCTTCCTGAGCATCCTCAACAATTTGGCTGTGAGATGTCC
A.meleagris        CTGTTGTCGCTATCCTTGCTTTCCGACTGATCTTGTGAGCCCTGTAAAATCCTTCCTGAGCATCCTCAACAATTTGGCTGTGAAATGTCC
T.gariepensis      CTGTTGTCGCTATCCTTGCTTTCCGACTGATCTTGTGAGCCCTGTGAAATCCTTCCTGAGCATCCTCAACAATTTGGCTGTGAAATGTCC
T.lomii            CTGTTGTCGCTATCCTTGCTTTCCGACTGATCTTGTGAGCCCTGTGAAATCCTTCCTGAGCATCCTCAACAATTTGGCTGTGAAATGTCC
X.vigilis          ATCCTGTCGCTATCCTTGCTTTCCAACCGATCTGAAGAAGCCTGTGAAATCCTTCCTGAGCATCCTCAATAGCTTGGTTGTGAGATGTCC
C.polyzonus        AGCCTGTCGCTATCCTTGCTTTCCTACTGATCTCATGAGCCCCGTGAAATCCTTCCTGAGCATCCTCAACAGTTTGGCTATAAGATGTCC
Zonosaurus.sp.     AGCTTGTCGCTATCCTTGCTTTCTTACTGATCTCATGAGCCCTGTGAAATCTTTCCTGAACATCCTCAACAATTTGGCTATAGTGTGTCC
Dibamus.sp.        ATCCTGTCGCTATCCTTGCTTTCCTACTGATCTGGTGAGCCCTGTGAAATCTTTCCTGAGCATCCTCAACAGTTTGGCTGTAAGATGTCC

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C.mydas            TGTGAAAGAATGTGATGAGGAGGTTTTGCTGGGCAAATACTGCCATCATTTGTCCAGTCACAAAGAGGTGAAAAGGAAAGAGATTTACAC
S.punctatus        AATGAAAGAATGTGATGAAGAGGTTCCATTGGGTAAATATGGCCGTCACATCTCCAGTCACAAGGAGGCGAAAGAGAAAGAGGCTTATGC
B.thieli           TATTAAAGATTGCCAGGAGGAGGTCATTTTGGGAAAATATGGCCACCATTTTTCTAGCCACAAAAAGGCAGAAGACAAAGAGAGCCATGT
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C.brevicornis      TATTAAAGATTGCCAGGAGGAGGTCATTTTGGGAAAATACAGCCACCATTTTTCTAGCCACAAAGAGGCAAAAGACAAAGAGAGCTATGT
C.salinarum        TGTTAAAGATTGCCAGGAGGAGGTTGTTTTGGGAAAATATGCCCACCATTTTTCTAGTCACAAAGAGGCAGAAGAAAAAGAGGGCTATGC
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P.cocincinus       TGTTAAAGATTGCCAGGAGGAGGTTGTTTTGGGAAAATATGCACACCATTTTTCTAGTCACAAAGAGGCAGAAGAAAAAGAGGGCTATGC
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L.belliana         ACTCAAAGATTGCCAGGAGGAGGTTATTTTGGGGAAATACTGCCACCATTTTAATAACCACAAAGAGGCAGAAGACAAAGAGGGCTATGT
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L.carinatus        AGTGATAGATTGTCAGGAGGAGTTCTGTTTGGGAAAATACCACCACCATCTTTCCAGACACAAGGAGGTAGAAGACCAAGAAGGCTATGT
B.plumifrons       AGTGACAGATTGTCTGGAGGAGGTCTGTTTGGGAAAATACTGTTACCATCTTTCGAGACACAAAGAGGTAGAAGACAAAGAGGGCTATGT
G.wislizenii       AGTGAAAGATTGTCAGGAGGAGGTCTGTTTGGCAAAATACTGTCACCATCTTTCCAGACACAAAGAGGTAGAAGACAAAGAGGGCTACGT
O.cuvieri          AGTAAAAGATTGTCAGGAAGAGGTCTGTTTGGGAAAATACTGTCACCATCTTTCCAGACACAAGGAGGTAGAAGACAAAGAGGGCTATGT
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C.enneagrammus     AGTGCAAGACTGTCAAGAGGAGGTCTCTTTGGGAAAATATTGCCACCATCTTTCCAGGCACAAAGAGGTCAAAGACAAAGAAGGCTACGT
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H.suspectum        TGCACAAGACTGTCATCAGGAGGTCTCTTTGGGAAAATACTGCCGCCATCTTTCCAGCCACAAAGTGGTCGAAGACAAAGAGGGCTATGT
X.grandis          AGTGAAAGATTGTCTTGAAGAGGTCTCTCTGGGAAAATACTGCCACCATCTTTCCAGCCACAAAGAGGTAGAAGACAAAGAGGGCTACGT
V.griseus          AGTGAAAGATTGTCTTGAGGAGGTCTCACTGGGGAAGTACTGCCACCATCTTTCCAGTCACAAAGAGGTAGAGGACCAAGATGGCTATGT
L.borneensis       AGTGAAAGAATGTCATGAGGAGGTCTCTCTGGGGAAGTACTGCCACCATCTTTCTAGCCACAAAGCGGTAGAAGACAAAGAGGGCTATGT
S.crocodiluris     AGTGAAAGATTGTCATGAGGAGGTCTCTCTGGGAAAATACTGCCGCCATCTTTCCAGCCACAAAGAGGTAGAAGACAAAGAGGGCTATGT
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R.braminus         AGTCATGGATTGCCACGAGGAGATCTTTTTGGGGAAATACTGCCAACATCGTTCCAGCCATAAAGAGGCGGAAGACAGAGACAGTTACGT
C.ruffus           AATGAAAGGCTGTCATGAGGAGGTCTTTTTGGAAAAATACTGCCAACATTGTTCTAATCATAAAGAGGCAGAAGGCAAAGACAGCTATGT
Agkistrodon.sp.    AATAAAAGGCTGTCATGAGGAGGTCTTTTTGGAAAAATACTGCCAACATCGTTCTAATCACAAAGGGGCAGAAAGTACAGACAGCTATGT
Eremias.sp.        AGTGAAAGGGTGTCACGAGGAGGTCCTCCTGGGAAAATACTGCCACCATCTTTCCATCCACAAAGAGGTAGAAGACAAAGAGGGCTATGT
B.biporus          AGTGAAAGATTGTCAGGAGGAGATCCTTCTGGGGAAATACTGTCGCCATCTTTCCATCCACAAAGAGGTAAAGGACAAAGAGGGCTATGT
T.weigmanni        AGTGAAAGATTGTCAGGAAGAGGTCCTTTTGGGGAAATACAGTCACCATCTTTCCATCCACAAAGAGGTAGAGGACAAAGAGGGATATGT
R.floridana        TGTAAAAGATTGTCATGAGGAGGTCCTTCTGGGAAAATACTGCCACCATCTTTCCATCCACAAAGAGGCCAAAGCCAAAGAGGGCTACGT
A.xera             AGTGAAAGATTGTCAGGAGGAGGTCCTTCTTGGCAAGTATGGTCGCCATCTTTCCATCCACAAAGAGGTTGAGGACAAAGAGGGCTATGT
C.tigris           AGTGAAAGATTGTCAAGAGGAAGTCTCTCTGGGCAAATACTGTCACCATCTTTCCAGCCACAAAGATGTAAAAGAACAAGAGGGTTATGT
L.parietale        AATGAAAGATTGCCACCAGGAAGTCTCGTTGGGCAAATACAATCACCATCTTTCCAGCCATAAAGATGCAAAAAGCCGAGAGGGCTTTGT
E.turkmenicus      AGTAAAAGACTGTTATGAAGAGGTCAGTCTTGGAAAATACAACCATCATCTTTCTACCCACAAGCAGAAAAAAGACAAAGGGACTTATGG
S.shrevei          AGTGAAAGACTGTCATGAAGAAGCCACTCTTGGAAAATATAGCCATCATCTTTCAAGTCACAAAGAGAAAAATGGCAAAGGGACTTATGT
T.przewalskii      AGTGAAAGACTGTTATGAGGAAGTCACTCTTGGAAAATACAGCCACCATCTTTCTAGTCACAAGGAGAAAAAAGACAAAGGGACTTATGT
G.gekko            AGTGAAAGACTGTCAGGAAGAGGTCACTCTTGGAAAATACAGCCATCACCTTTCTCGCCACAAGGAGAAAAAGGACAAAGGAACTTTTGT
P.lindneri         AGTGAAAGACTGTCACGAGGACGTTGCCCTGGGAAAATACAGCCGCCATCTTTCTAGCCACAAGGATCACAAGGACAAAGGCTTTTATGT
Cr.ocellatus       AGGGAAAGACTGTCATGAGGATGTTGCTCTAGGAAAATACAGCCATCATCTTTCTAGCCACAAGGATAACGAAGACAAAGGAATGTATGT
L.jicari           AGTGAAAGACTGTCATGAGGACGTTGCTCTGGGAAAATACAGCCATCATCTTTCTAGCCACAAGGATAACAAAGAGAAAGGGACCTACGT
M.aurata           TGTGAAGGAGTGTGATGAGGAAATCTCCCTGGAAAAATACTGCCATCATCTTTCCAGCCACAAAGATGCAAAGGACAAAGAGGGTTATGT
C.robustus         CGTGAAAGAGTGTGACGAGGAAATCTCTCTGGAAAAATATGGCCATCATCTTTCTAGCCACAAAGATGCAAAGGACAAAGAAGGTTACGT
S.sikkimensis      CGTGAAAGAGTGTGACGAGGACATCTGTCTGGAAAAGTACGGCCATCATCTTTCTAGCCACAAAGTTGCAAAGGACAAAGAAGGTTACGT
E.inexpectatus     TGTGAAAGACTGTGATGAGGAAATCTCTCTGGAAAAATACTGCCATCATCTTTCCAGCCACAAAGACGCAAAAGACAAAGAGGGCTATGT
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S.anguineus        TGTGAAAGATTGCGATGAGGAAATCTCTCTGGAAAAATACTGCCATCATCTTTCCACCCACAAAGACGCAAAAGACAAAGAGGGTTACGT
P.eggeli           TGTGAAAGACTGTGATGAGGAAATCTCTCTGGAAAAATACAGCCATCATCTTTCTAGCCACAAAGACGCAAAAGACAAAGAGGGTTACGT
F.polylepis        TGTGAAAGACTGCAATGAGGAAATCCCTCTGGAGAAATACTGTCGTCATCGTTCCAGCCACAAAGACGTAAAAGGCAAAGAGGGTTATGT
Ch.ocellatus       TGTGAAAGATTGTGATGAGGAAATCCCTCTGGAAAAATACTGCCATCATCTTTCCAGCCATAAAGACGCAAAAGACAAAGAGGGTTATGT
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T.gariepensis      TGTAAAAGACTGCCATGAGGAAATCTCTCTGGAAAAATACTGCCATCATCTTTCCAGCCACAAAGATGCAAAAGACAAAGAGGGTTATGT
T.lomii            TGTAAAAGACTGCCATGAGGAAATCTCTCTGGAAAAATACTGCCATCATCTTTCCAGCCACAAAGATGCAAAAGACAAAGAGGGTTATGT
X.vigilis          AGTGAAAGATTGTCATGAGGAAGTCTGTCTGGGAAAATACAGCCGCCATCTTTCCAGTCACAAAGAGGCAAAAGACAAAGAAGGTTATGT
C.polyzonus        AGTGAAAGACTGTCATGAGGAAGTCTTCCTGGGAAAATACAGCCATCATCTTTCCAGCCACAAAGAGGAAAAAGACAAAGAGGGTTATGT
Zonosaurus.sp.     AGTGAAAGAGTGTCATGAGGAAGTCTTTCTGGGAAAATACAGCCATCATCTTTCCAGCCACAAAGAGGAAAAAGACAAAGAGGGTTATGT
Dibamus.sp.        AGTGAAAGACTGTAATGAGGACATCCTTCTGGGAAAATACTGCCCTCATCTTTCCAGCCACAAAGAGGCACAAGACAAAAAGGCATATGT

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G.gallus           CCCCATAAATAAAGGTGGCCGACCAAGGCAGCATCTTCTGTCTTTGACCAGGAGAGCTCAGAAACATCGTCTGAGAGAACTGAAACGTCA
C.mydas            GCACGTAAATAAAGGTGGCCGACCGAGGCAACACTTACTCTCATTGACCAGGAGAGCGCAAAAGCATCGTCTGAGAGAACTTAAGCTTCA
S.punctatus        ACACATAAATAAAGGTGGCCGACCAAGACAACACCTACTGTCGTTGACCAGGAGAGCTCAAAAGCACCGCCTGAGAGAGCTTAAGCTTCA
B.thieli           GTATGTAAACAAAGGGGGTCGACCAAGACAACACTTACTTTCACTGACCAGGAGAGCTCAAAAACACCGCCTAAGAGAACTCAAACTCCA
C.rudis            GTATATAAACAAAGGGGGTCGACCGAGACAGCATCTGCTTTCACTGACCCGAAGAGCTCAAAAACACCGCCTAAGAGAACTCAAATTCCA
C.brevicornis      GTATATAAATAAAGGGGGTCGACCAAGACAGCACCTGCTTTCACTGACCCGAAGAGCTCAAAAACACCGCCTAAGAGAACTCAAATTCCA
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P.raddei           GTATATAAACAAAGGTGGACGGCCGAGACAGCATCTGCTTTCCCTGACCCGGAGAGCTCAAAAACACCGTCTAAGAGATCTCAAACTTCA
L.belliana         ATTCATAAATAAAGGTGGTCGACCAAGACAACACCTGCTTTCACTGACCCGGAGAGCACAAAAACACCGCCTAAGAGAACTCAAACTCCA
U.acanthinurus     GCATATAAACAAAGGTGGTCGCCCAAGACAACATCTGCTTTCACTGACCCGGAGAGCTCAAAAACACCGCCTGAGAGAACTCAAACTCCA
A.paternus         ATGCATAAACAAAGGTGGTCGACCAAGACAACACTTACTTTCCTTGACACGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCAACA
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Hoplocercus.sp.   GTTCATAAACAAAGGTGGCCGACCAAGACAACACTTACTTTCACTGACACGGAGAGCTCAAAAGCACCGTCTAAGAGAACTCAAGCTACA
E.laticeps        GTGCATAAACAAAGGTGGCCGACCAAGACAACACTTACTTTCATTGACACGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTACA
P.somencurensus   GTACATAAACAAAGGTGGTCGCCCAAGACAACACTTGCTTTCCTTGACACGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTGCA
L.pictus          GTACGTAAACAAAGGTGGTCGTCCAAGACAACACTTGCTTTCATTGACGCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTGCA
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C.enneagrammus    GTACGTCAACAAAGGCGGCCGGCCAAGACAACACTTACTCTCACTGACCCGGAGAGCTCAAAAGCACCGGCTAAGAGAACTCAAGCATCA
A.pulchra         GTACATCAACAAAGGTGGCAGACCAAGACAACACTTACTCTCACTGACCCGGAGAGCTCAAAAGCACCGGCTAAGAGAACTCAAGCATCA
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X.grandis         GCACATCAACAAAGGTGGCCGGCCAAGACAACACTTACTCTCACTGACCCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCATCA
V.griseus         GTATGTTAACAAGGGTGGCCGTCCAAGACAGCACTTACTCTCACTGACCCGGAGAGCGCAAAAGCATCGCCTACGAGAGCTCAAACTTCA
L.borneensis      GTATGTCAACAAAGGTGGCCGACCAAGACAACACTTACTCTCACTGACCCGGAGAGCTCAAAAGCATCGCCTAAGAGAACTCAAACTTCA
S.crocodiluris    GCATGTCAACAAAGGTGGCCGACCAAGACAACACTTACTCTCACTGACCCGAAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
Dinodon.sp.       CTATATCAACAAAGGTGGCCGACCGAGACAACATTTGCTTTCACTGACCCGGAGAGCTCAAAAGCACCGCTTGAGAGAACTCAAGCTTCA
R.braminus        CTTCATAAACAAGGGTGGCCGACCGAGGCAGCACTTGCTTTCACTGACCCGGAGAGCTCAAAAGCACCGTCTGAGAGAACTCAAGCTTCA
C.ruffus          CTATATCAACAAAGGTGGCCGACCGAGACAACATTTGCTTTCACTCACCCGGAGAGCTCAAAAGCACCGTCTGAGAGAACTCAAGCTTCA
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Eremias.sp.       GTATGTAAACAAAGGTGGCCGGCCAAGACAACATTTACTTTCATTGACCCGGAGAGCACAAAAGCACCGCCTAAGAGAACTCAAACTTCA
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A.xera            GTATGTAAACAAAGGTGGCAGGCCAAGACAACACTTACTTTCATTGACCCGGAGAGCACAAAAACATCGTCTAAGAGAACTCAAGCTTCA
C.tigris          GTACGTAAACAAAGGGGGGCGACCAAGACAGCACTTACTTTCACTGACTAGACGGGCCCAGAAGCACCGCCTAAGAGACCTGAAGCTTCA
L.parietale       CTATACAAACAAAGGGGGTCGGCCAAGACTGCACTTGCTGTCGCTGACCAGACGTGCCCAAAAGCACCGTCTAAGAGATCTCAAGCTTCA
E.turkmenicus     GCATGTAAACAAAGGTGGCAGACCAAGGCAACACTTACTTTCACTGACCCGGAGAGCTCAAAAGCATCGCCTAAGAGAACTCAAGCTTCA
S.shrevei         CCATGTTAATAAAGGTGGCCGACCAAGGCAACACTTACTTTCACTGACCCGGAGAGCCCAAAAACATCGCCTAAGAGAACTCAAGCTTCA
T.przewalskii     GCATGTAAATAAAGGGGGCCGACCAAGGCAACACTTACTTTCATTGACCCGGAGAGCCCAAAAGCATCGCCTGAGAGAACTCAAGCTTCA
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P.lindneri        GCATGTCAACAAAGGTGGCCGACCAAGGCAACACTTACTTTCACTGACCCGAAGAGCTCAAAAGCATCGGCTGAGAGAACTCAAGCTTCA
Cr.ocellatus      GCATGTAAACAAAGGTGGCCGACCAAGGCAACACTTACTTTCACTGACCCGAAGAGCTCAAAAGCATCGGCTGAGAGAACTCAAGCTTCA
L.jicari          GCATGTAAACAAAGGTGGCCGACCAAGGCAACACTTACTTTCCCTGACCCGAAGAGCTCAAAAGCATCGGCTGAGAGAACTCAAGCTTCA
M.aurata          GCACATAAACAAAGGCGGTCGACCAAGACAACACTTGCTTTCGCTGACCCGGAGAGCTCAGAAGCACCGCCTGAGAGAACTCAAGCTTCA
C.robustus        GCACATCAACAAAGGTGGCCGACCACGACAACACTTGCTGTCGTTGACCCGGAGAGCTCAAAAGCACCGCCTGAGAGAGCTCAAGCTTCA
S.sikkimensis     GCACATCAACAAAGGTGGCCGACCACGACAACACTTGCTGTCGTTGACCCGGAGAGCTCAAAAGCACCGCCTAAGAGAGCTCAAGCTTCA
E.inexpectatus    GCACATAAACAAAGGTGGCCGACCAAGACAACACTTACTTTCGTTGACCCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
E.skiltonianus    GCACATAAACAAAGGTGGCCGACCAAGACAACACTTACTTTCGTTGACCCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTGCA
E.anthracinus     GCACATAAACAAAGGTGGCCGACCAAGACAACACTTACTTTCGTTGACCCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
S.anguineus       GCACATAAACAAAGGTGGCCGACCAAGACAACACTTACTTTCATTGACTCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCT
P.eggeli          GCACATAAACAAAGGTGGCCGACCAAGGCAACACTTACTTTCATTGACTCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
F.polylepis       GCACATAAACAAAGGTGGCCGGCCAAGACAACACTTACTTTCATTGACTCGAAGAGCTCAGAAGCACCGCCTGAGAGAACTGAAGCTTCA
Ch.ocellatus      GCACATAAACAAAGGTGGTCGGCCAAGACTACACTTATTGTCATTGACTCGGAGAGCCCAAAAGCACCGCCTAAGAGAACTGAAGCTTCA
A.meleagris       GCACATAAATAAAGGTGGCCGACCGAGACAACACTTACTTTCGTTGACTCGGAGGGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
T.gariepensis     GCACATAAATAAAGGTGGCCGACCGAGACAACACTTACTTTCGTTGACTCGGAGGGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
T.lomii           GCACATAAATAAAGGTGGCCGACCGAGACAACACTTACTTTCGTTGACTCGGAGGGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
X.vigilis         GCATGTAAACAAAGGTGGCCGGCCAAGACAACACTTACTTTCATTGACCCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
C.polyzonus       GCACATAAACAAAGGTGGCCGACCAAGACAACATTTACTTTCATTGACTCGGAGAGCTCAAAAGCACCGCCTAAGAGAACTCAAGCTTCA
Zonosaurus.sp.    GCACATAAACAAAGGTGGCCGACCAAGACAGCATTTACTTTCATTGACTCGGAGAGCTCAGAAGCACCGCCTAAGAGAACTCAAGCTTCA
Dibamus.sp.       GCATATAAACAAAGGTGGCCGACCAAGACAACACTTGCTTTCATTGACCCGGAGAGCTCAGAAGCACCGCCTCAGAGAACTCAAGCTTCA

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G.gallus          AGTCAAGGCTTTTGCTGAGAAAGAAGAGGGTGGTGATATAAAGGCTGTATGCATGACTTTGTTCCTGCTAGCTTTAAGAGCAAAAAACGA
C.mydas           AGTCAAAGCTTTTGCTGAGAAAGAAGAAGGAGGTGATATAAAGGCTGTGTGCCTAACTTTGTTCCTGCTGGCTCTGAGAGCAAGAAATGA
S.punctatus       AGTCAAAGCTTTTGCCGAGAAAGAAGAAGGAGGAGATGTAAAGTCTGTGTGCCTGACTTTGTTTTTGCTGGCTTTAAGAGCCAGAAATGA
B.thieli          AGTAAAAGCTTTTGCTGAAAAAGAAGAAGGGGGAGATGTGAAATCTGTGTGCCTAACTTTGTTCTTATTGGCCCTGAGAGCTAGAAATGA
C.rudis           AGTGAAAGCCTTTGCTGAAAAAGAAGAAGGAGGGGATGTGAAATCTGTGTGCCTAACCTTGTTCTTATTGGCTCTGAGAGCTGGGAATGA
C.brevicornis     AGTTAAAGCCTTTGCTGAAAAAGAAGAAGGAGGAGATGTGAAATCTGTGTGCCTAACCTTGTTCTTACTGGCTCTGAGAGCTGGAAACGA
C.salinarum       AGTAAAAGCTTTTGCTGAGAAAGAAGAAGAAGGAGATGTGAAATCAGTGTGCTTAACTTTGTTCCTATTGGCTCTGAGAGCTAGAAATGA
P.lesueurii       AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGAGGAGATGTGAAATCAGTGTGCTTAACTTTGTTCCTATTGGCTCTGAGAGCTAGAAATGA
P.cocincinus      AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGAGGAGATGTGAAATCAGTGTGCTTAACTTTGTTTCTATTGGCTCTGAGAGCTAGAAATGA
Hydrosaurus.sp.   AGTCAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTGAAATCAGTGTGCCTAACTTTGTTCCTATTGGCTCTGAGAGCTAGAAATGA
C.calotes         AGTGAAAGCGTTTGCCGAGAAAGAAGAAGGAGGGGATGTGAAATCGGTGTGCCTAACTTTGTTCCTCTTGGCTCTGAGAGCTAGAAACGA
J.tricarinata     AGTGAAAACTTTTGCTGAGAAAGAAGAAGGGGGAGACGTGAAATCAGTGTGCCTAACTTTGTTCCTCTTGGCTCTGAGAGCTAGAAACGA
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P.raddei          AGTGAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTGAAATCGGTGTGCCTAACTTTGTTCCTGTTGGCTCTGAGATCTAGAAATGA
L.belliana        GGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTGAAATCTGTGTGCCTAACATTGTTCCTATTAGCCTTGAGAGCTAGAAATGA
U.acanthinurus    GGTAAAAGCTTTTGCTGAGAAAGAAGAAGGTGGAGATGTGAAATCTGTGTGCCTAACTTTGTTCCTTTTGGCTCTGAGAGCTAGAAATGA
A.paternus        AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTTTTGCTGGCTTTGAGAGCCAGAAATGA
P.mcallii         AGTTAAAGCTTTTGCTGAAAAGGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTCTTACTCGCTCTGAGAGCCAGAAATGA
S.obesus          AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTTCTACTGGCCTTGAGAGCCAGAAATGA
Hoplocercus.sp.   AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTCCTACTGGCTCTGAGAGCCAGAAATGA
E.laticeps        AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTCCTGCTGGCTCTGAGAGCCAGAAATGA
P.somencurensus   AGTAAAAGCTTTTGCTGAGAAAGAAGAGGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTCCTACTGGCTTTGAGAGCCAGAAATGA
L.pictus          AGTCAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAATCTGTGTGTCTAACTTTATTCCTACTGGCTTTGAGAGCCAGAAATGA
U.flaviceps       AGTAAAAGCTTTTGCAGAGAAAGAAGAAGGGGGAGATGTCAAATCTGTGTGTCTAACTTTGTTCCTTCTGGCCCTGAGAGCCAGAAATGA
S.crasicaudatus   AGTAAAAGCTTTTGCAGAGAAAGAAGAAGGGGGAGATATCAAATCTGTGTGTCTAACTTTGTTCCTACTGGCCCTGAGAGCCAGAAACGA
L.carinatus       AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAATCTGTGTGTCTCACTTTGTTCCTACTGGCTCTGAGAGCGAGAAATGA
B.plumifrons      AGTGAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTCCTACTGGCTCTGAGAGCCAGAAATGA
G.wislizenii      AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTCCTACTGGCTCTGAGAGCCAGAAATGA
O.cuvieri         AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTAACTTTGTTCCTATTGGCTCTCAGAGCCAGAAATGA
O.attenuatus      AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCTGTGTGTCTGACATTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
E.panamintina     AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCCGTGTGTCTGACATTGTTTCTACTGGCTCTGAGAGCTAGAAATGA
C.enneagrammus    AGTAAAAGCTTTTGCTGAGAAAGAAGAAGAAGGGGATGTGAAGTCTGTGTGCCTGACTTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
A.pulchra         AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGCGGAGATGTAAAGTCTGTGTGTCTGACTTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
H.suspectum       AGTAAAAGCATTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTGACTTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
X.grandis         AGTGAAAGCTTTTGCTGAGAAAGAAGAAGAAGGAGATGTGAAGTCTGTGTGTCTGACCTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
V.griseus         AGTAAAAGCTTTTGCAGAGAAAGAAGAGGGGGGAGATGTAAAGTCTGTGTGTCTAACTTTGTTCCTACTGGCTCTGAGATCTAGAAATGA
L.borneensis      AGTAAAAGCTTTTGCTGAGAAAGAAGAGGGGGGAGATGTAAAGTCCGTGTGTCTAACTTTGTTCCTACTGGCTCTGAGAGCGAGAAATGA
S.crocodiluris    AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATATAAAGTCTGTGTGTCTAACTTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
Dinodon.sp.       AGTGAAAGATTTTGCAGAAAAAGAAGAAGGAGGAGATGTGAAGTCTGTGTGCCTAACTTTGTTCCTGCTGGCTTTGAGATCTAGAAATGA
R.braminus        AGTGAAAGCTTTTGCTGAAAAAGAAGAAGGGGGAGATGTGAAGTCAGTGTGTCTCACTTTGTTCCTGTTGGCTCTGAGAGCTAGCAATGA
C.ruffus          AGTGAAAGCTTTTTCAGAAAAAGAAGAAGGAGGAGACATGAGGTCTGTGTGCCTAACTTTGTTCCTGCTGGCTTTGAGATCTAGAAATGA
Agkistrodon.sp.   AGTGAAAGATTTTGCAGAAAAAGAAGAAGGAGGGGACCTGAAATCTGTGTGCCTAACTTTGTTCCTGCTAGCTTTGAGGTCTAGAAATGA
Eremias.sp.       AGTGAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTAAAGTCTGTGTGTCTAACTTTGTTCCTACTGGCTCTGAGAGCGAGAAATGA
B.biporus         AGTTAAAGCTTTTGCTGAGAAAGAAGAAGGGGGTGATATAAAGTCTGTGTGTCTGACTTTGCTCCTGCTGGCTCTGCGAGCTAGAAATGA
T.weigmanni       AGTTAAAGCTTTTGCTGAGAAAGAAGAAGGAGGAGATGTAAAATCTGTGTGTCTAACTTTGTTCCTGCTGGCTCTGCGAGCTAGAAATGA
R.floridana       AGTCAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTAAAATCTGTGTGTCTAACATTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
A.xera            AGTTAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTAAAATCTGTGTGCCTAACTTTGTTCCTGCTGGCTCTGCGAGCTAGAAATGA
C.tigris          AGTGAAAGCTTTTGCTGAAAAAGAAGAAGGGGGGGATGTGAAGTCCGTGTGCCTAACTTTGTTCCTGTTGGCTCTGAGAGCTAGAAATGA
L.parietale       AGTAAAGACTTTTGCTGAGAAAGAAGAAGAGGGAGATGTGAAGTCTGTGTGCTTAACTTTATTCCTGCTGGCTCTAAGAGCAAGAAATGA
E.turkmenicus     AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGCCTAACTTTATTTCTGCTGGCTCTGAGAGCTAGAAATGA
S.shrevei         AGTGAAAACTTTTGCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGTCTAACCTTATTTCTGTTGGCTCTGAGAGCTCGAAATGA
T.przewalskii     AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTGTGTCTAACTTTATTTCTGCTGGCTTTGAGATCTAGAAATGA
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Cr.ocellatus      AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTATGTCTAACTTTATTTCTGCTTGCTCTTAGAGCTAGAAATGA
L.jicari          AGTAAAAGCTTTTTCTGAGAAAGAAGAAGGTGGAGATGTGAAGTCTGTATGTCTAACCTTATTTCTGCTTGCCCTGAGAGCTAGAAATGA
M.aurata          AGTGAAGGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTCACTTTGTTCCTTCTGGCTCTGAGAGCTCGAAATGA
C.robustus        AGTGAAGGCGTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCCTGACTTTGTTCCTCCTGGCTCTGAGAGCTCGAAATGA
S.sikkimensis     AGTGAAGGCGTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGCCTGACTTTGTTCCTCCTGGCTCTGAGAGCTCGAAATGA
E.inexpectatus    AGTGAAGGCTTTTGCTGAGAAAGAAGAAGGGGGAGATTTCAAGTCTGTGTGTCTAACTTTGTTCCTCCTGGCTCTGAGAGCTAGAAATGA
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E.anthracinus     AGTGAAGGCTTTTGCTGAGAAAGAAGAAGGGGGAGATTTCAAGTCTGTGTGTCTAATTTTGTTCCTCCTGGCTCTGAGAGCTAGAAATGA
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A.meleagris       AGTGAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTGACTTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
T.gariepensis     AGTGAAGGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTGACTTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
T.lomii           AGTGAAGGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTCAAGTCTGTGTGTCTGACTTTGTTCCTACTGGCTCTGAGAGCTAGAAATGA
X.vigilis         GGTCAAGGCCTTTGCTGAGAAAGAGGAAGGGGGAGATGTAAAGTCTGTGTGTCTGACTTTGTTCTTACTGGCTTTGAGAGCTAGAAATGA
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Dibamus.sp.       AGTAAAAGCTTTTGCTGAGAAAGAAGAAGGGGGAGATGTAAAATCTGTGTGTCTTACTTTGTTCCTTCTGGCTCTGAGAGCTAGAAATGA

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C.mydas           ACACAGACAGGCAGATGAGTTGGAAGCTATAATGCAAGGAAAGGGATCAGGGCTTCACCCAGCTGTTTGCCTGGCAATCCGAGTCAACAC
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B.thieli          GCATAGGCAGGCTGATGAACTGGAAGCTATCATGCAAGGAAAGGGCTCAGGTCTTCCCCCAGCTGTTTGCCTAGCAATCCGAGTCAACAC
C.rudis           GCACAGGCAGGCTGATGAGCTGGAAGCTATCATGCAAGGGAAAGGCACAGGCCTTCCCCCAGCTGTTTGCCTAGCAATCCGAGTCAACAC
C.brevicornis     GCACAGGCAGGCTGATGAGCTGGAAGCTATCATGCAAGGGAAAGGCTCAGGCCTTCCCCCAGCTGTTTGCCTAGCAATCCGAGTCAACAC
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J.tricarinata     ACATCGGCAAGCTGATGAGCTGGAGGCGATCATGCAAGGCAAGGGCTCAGGCCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
P.raddei          GCACCGGCAAGCTGATGAGCTAGAAGCTATCATGCAAGGCAAGGGCTCAGGCCTTCCCCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
L.belliana        GCACAGACAAGCTGACGAGCTGGAAGCTATCATGCAAGGGAAGGGCTCGGGCCTTCACCCAGCAGTTTGCTTGGCAATCCGAGTCAACAC
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V.griseus         ACACAGGCAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAAGGATCTGGCCTCCCTCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
L.borneensis      ACACAGGCAAGCTGATGAGTTGGAAGCTATAATGCAAGGGAAAGGATCTGGCCTTCATCCCGCTGTTTGCTTGGCAATCCGAGTCAACAC
S.crocodiluris    ACACAGACAAGCTGATGAGTTGGAAGCCATAATGCAAGGGAAAGGATCAGGCCTTCATCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
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S.shrevei         ACACAGACAAGCTGATGAATTGGAAGCTATGATGCAAGGGAAAGGAACAGGACTTTCTCCAGCAGTTTGCTTGGCAATTCGAGTAAACAC
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C.robustus        GCATAGACAAGCCGATGAACTGGAAGCCATAATGCAAGGGAAGGGAACAGGTCTTCACCCAGCTGTTTGCTTGGCAATCCGAGTCAACAC
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G.gallus          TTTTCTCAGCTGTAGCCAGTATCACAAAATGTACCGAACTGTAAAAGCTGTCACTGGGAGGCAGATTTTCCAGCCACTGCATGCTCTTCG
C.mydas           CTTTCTCAGCTGTAGCCAGTACCATAAAATGTACAGAACGGTAAAAGCTATAACTGGGAGGCAGATCTTCCAACCATTGCATGCTCTCCG
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C.rudis           ATTCCTTAGCTGTAGCCAATACCATAAAATGTACAGGACAGTGAAAGCAATAACAGGAAGACAGATATTTCAGCCCTTGCATGCCCTCCG
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L.pictus          TTTTCTCAGCTGTAGCCAGTACCATAAAATGTATAGGACTGTAAAAGCTGTAACTGGGAGACAAATATTCCAGCCACTCCATGCACTTCG
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M.aurata          CTTTCTCAGCTGTAGTCAGTACCACAAAATGTACAGGACTGTAAAAGCAATAACAGGAAGGCAAATTTTCCAGCCTTTGCATGCTCTCCG
C.robustus        CTTTCTCAGTTGCAGCCAATACCATAAAATGTATCGGACTGTAAAAGCAATAACAGGAAGGCAAATTTTCCAGCCTTTGCATGCTCTCCG
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E.inexpectatus    CTTTCTCAGCTGTAGTCAGTACCACAAAATGTACAGAACGGTAAAAGCAATAACAGGAAGGCAAATTTTCCAGCCTTTGCATGCTCTCCG
E.skiltonianus    CTTTCTCAGCTGTAGTCAGTACCACAAAATGTACAGAACGGTAAAAGCAATAACAGGAAGGCAAATTTTCCAGCCTTTGCATGCTCTCCG
E.anthracinus     CTTTCTCAGCTGTAGTCAGTACCACAAAATGTACAGAACTGTAAAAGCAATAACAGGAAGGCAAATTTTCCAGCCTTTGCATGCTCTCCG
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T.gariepensis     CTTTCTCAGCTGCAGTCAGTATCACAAAATGTACAGAACCGTAAAAGCAATAACAGGAAGGCAAATTTTCCAGCCTTTGCATGCTCTCCG
T.lomii           CTTTCTCAGCTGCAGTCAGTATCACAAAATGTACAGAACCGTAAAAGCAATAACAGGAAGGCAAATTTTCCAGCCTTTGCATGCTCTCCG
X.vigilis         TTTTCTCAGTTGCAGCCAGTACCATAAAATGTACAGGACTGTAAAAGCAATAACAGGACGGCAGATTTTCCAGCCATTGCATGCTCTCCG
C.polyzonus       CTTTCTCAGCTGCAGCCAGTACCATAAAATGTACAGAACAGTAAAAGCAATAACAGGAAGGCAGATTTTCCAGCCATTGCATGCTCTCCG
Zonosaurus.sp.    CTTTCTCAGCTGCAGCCAGTACCATAAAATGTACAGAACTGTGAAAGCAATAACAGGGAGGCAGATTTTCCAGCCATTGCATGCTCTCCG
Dibamus.sp.       CTTTCTCAGCTGTAGCCAGTACCATAAAATGTACAGAACTGTAAAAGCGATAACAGGAAGGCAGATTTTCCAGCCATTGCATGCACTCCG

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G.gallus          CACCGCCGAGAAAGCCCTCTTACCAGGTTATCATCCTTTTGAATGGAAACCTCCCTTGAAAAATGTATCCACTAACACAGAAGTGGGAAT
C.mydas           CACTGCTGAGAAGGCACTCTTGCCAGGTTATCATCCATTTGAGTGGAAACCCCCTTTGAAAAATGTGTCCACTAATACAGAGGTGGGAAT
S.punctatus       AACTGCTGAGAAAGCCCTTCTGCCAGGATACCATCCATTTGAGTGGACACCTCCTCTGAAAAATGTATCCACTAATACAGAAGTAGGCAT
B.thieli          AACAGCTGAAAAATCCCTTCTGCCAGGTTACCATCCATTTGAGTGGAAACCACCCTTGAAAAACGTGTCCAGTAACACAGATGTGGGCAT
C.rudis           AACAGCTGAAAAGTCCCTTCTGCCAGGTTACCATCCGTTTGAGTGGAACCCGCCCTTGAAAAATGTGTCCAGTAACACAGATGTGGGCAT
C.brevicornis     AACAGCTGAGAAGTCCCTTCTGCCAGGTTACCATCCGTTTGAGTGGAAACCGCCCTTGAAAAATGTGTCCAGTAGCACAGATGTAGGCAT
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P.lesueurii       AACTGCTGAAAAGGCCCTTCTGCCAGGTTACCATCTATTTGAGTGGAAACCACCCTTGAAAAATGTGTCCAGTAGCACAGATGTAGGCAT
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Hydrosaurus.sp.   AACTGCTGAAAAATCCCTTCTGCCAGGTTACCATCCATTTGAGTGGAAACCACCCTTGAAAAATGTGTCCAGTAACACAGATGTAGGCAT
C.calotes         GACTGCTGAAAAATCCCTTCTGCCAGGATACCATCCATTCGAGTGGGAACCACCCTTGAAAAATGTGTCCAGTAACACGGATGTAGGCAT
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S.obesus          AACTGCTGAAAAGTCCCTTTTGCCAGGTTACCATTCATTTGAGTGGAAACCACCCTTGAAAAATGTTTCCAGTAACACAGAAGTAGGTAT
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E.laticeps        AACTGCTGAAAAGTCCCTCTTGCCAGGTTACCATCCATTTGAATGGAAACCACCCTTGAAAAATGTCTCCAGTAACACAGAAGTAGGTAT
P.somencurensus   AACTGCTGAAAAGTCTCTCTTGCCAGGTTACCATCCATTTGAGTGGAAACCACCCTTGAAAAATGTTTCTAGTAACACAGAAGTAGGAAT
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C.ruffus          AACAGCTGAGAAGTCCCTTCTGCCTGGTTATCATCCCTTTGAATGGGCACCTCCCTTGAAAAATGTGTCTAGTAATACTGATGTAGGCAT
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E.turkmenicus     GACTGCTGAAAAGTCCCTTTTGCCAGGTTATCATCCATTTGAATGGAAACCACCCTTGAAAAATGTGTCTAGTAACACAGAAGTAGGCAT
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F.polylepis       AACTGCTGAAAAGGCCCTCCTGCCAGGTTACCATCCATTTGAATGGCAACCACCTTTGAGAAATGTGTCCAGTAACACTGAAGTAGGCAT
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X.vigilis         AACTGCTGAAAAAGCCCTTCTGCCAGGCTACCATCCATTTGAATGGAAACCACCCTTGAAAAACGTGTCCAGTAACACGGAAGTAGGTAT
C.polyzonus       GAGTGCTGAAAAGGCCCTTTTGCCAGGCTACCATCTATTTGAATGGACACCACCCTTGAAAAACGTGTCCAGTAACACTGAAGTAGGTAT
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Dibamus.sp.       AACTGCTGAGAAGTCTCTCCTGCCAGGTTATCATCCATTTGAGTGGAAACCACCCTTGAAAAATGTGTCCAGTACTACAGAAGTAGGCAT

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G.gallus          TATAGATGGACTATCAGGACTACCCCTCTCGATTGATGACTACCCAATAGACACAATTGCAAAGAGATTTCGATATGATACAGCCTTGGT
C.mydas           TATAGATGGGCTGTCAGGCCTGCCACACTCAGTTGATGACTACCCAGTAGACACGATTGCCAAGAGGTTTCGATATGATGCAGCCTTGGT
S.punctatus       TATGGATGGGCTCTCAGGGCTACCACTCTCAGTTGATGACTACCCAGTAACCACAATTGCAAAGAGATTTCGTTATGATTCAGCCTTGGT
B.thieli          TATTGATGGGCTTTCAGGCATACAACATTTGGTTGATGACTACCCTGTAGACACAATTGCAAAGAGATTTCGCTATGATGTAGCTTTGGT
C.rudis           TAATGACGGGCTTTCAGGCATACAACATTTGGTTGATGACTACCCCGTAGACACAATTGCAAAGAGATTTCGCTATGATGTAGCTTTGGT
C.brevicornis     TGTTGATGGGCTTTCAGGCATACAGCATTTGGTTGATGACTACCCTGTAGACACAATTGCAAAGAGATTTCGATATGATGTAGCTTTGGT
C.salinarum       TATCGACGGGCTTTCAGGCATACAGCATTCGGTTGATGACTATCCTGTAGATACAATTGCAAAGAGATTTCGGTATGATGTAGCTTTGGT
P.lesueurii       TATCGACGGGCTTTCGGGCATACAACATTTGGTTGATGACTATCCTGTAGATACAATTGCAAAGAGATTTCGGTATGATGTAGCTTTGGT
P.cocincinus      TATTGACGGGCTTTCGGGCATACAACATTTGGTTGATGACTATCCTGTAGATACAATTGCAAAGAGATTTCGGTATGATGTAGCTTTAGT
Hydrosaurus.sp.   TATCGATGGGCTTTCAGGCATACAACATTTGGTTGATGACTATCCTGTAGATACAATTGCGAAGAGATTTCGGTATGATGCAGCTTTGGT
C.calotes         CATTGATGGGCTTTCAGGCATACAGCAGCTGGTCGACGACTATCCCGTAGATACAATTGCAAAGAGATTTCGGTATGATGCCGCTTTGGT
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P.raddei          TATTGATGGGCTTTCGGGCATGCGACCTTTGGTTGATGACTATCCCGTAGATACAATCGCAAAAAGATTTCGGTACGATGCAGCTTTGGT
L.belliana        TATTGATGGGCTTTCAGGCATACAACATTTGGTTGACGACTACCCTGTAGACACAATTGCAAAGAGATTTCGATATGACGCAGCTTTAGT
U.acanthinurus    TATTGATGGACTTTCAGGCATACAACATTCCGTTGATGACTACCCGGTAGATACAATTGCCAAGAGATTTAGGTATGATGCAGCTTTGGT
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S.obesus          TATTGATGGGCTTTCAGGCATACAATATTCGGTTGATGATTACCCAGTGGACACAATTGCAAAGAGATTTCGATATGATGCAGCTTTGGT
Hoplocercus.sp.   TATTGATGGGCTTTCAGGTATACAACATTTGGTTGATGATTACCCAGTGGACACAATCGCAAAGAGATTTCGATATGATGCAGCTTTGGT
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P.somencurensus   TATTGATGGGCTTTCAGGCATACAACATCTGGTTGATGATTACCCAGTAGACACAATCGCAAAGAGATTTCGATATGATGCAGCTTTGGT
L.pictus          TATTGATGGGCTTTCAGGCATACAACATTTGGTTGATGATTACCCAGTAGACACAATTGCAAAAAGATTTCGATATGATGCAGCTTTGGT
U.flaviceps       TATTGATGGACTTTCAGGCATTCAACATTGGGTGGATGACTACCCAGTAGACACAATTGCTAAGCGATTTCGATATGATGCAGCTTTGGT
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L.carinatus       TATTGATGGACTTTCAGGCATACAACATTTGGTTGATGACTACCCAGTAGACACAATCTCAAAGAGATTTCGATATGATGCAGCTTTGGT
B.plumifrons      TATTGATGGGCTTTCAGGCATACAACATTTGGTTGATGATTACCCAGTTGACACAATCGCAAAGAGATTTCGATATGATGCCGCTTTGGT
G.wislizenii      CATTGATGGGCTTTCAGGCATACAACATTTGGTTGATGACTACCCAGTAGACACAATTGCGAAGAGATTTCGATATGATGCAGCTTTGGT
O.cuvieri         TATTGATGGGCTTTCAGGCATACAACATTTAGTTGATGACTATCCAGTAGACACAATTGCAAAGAGATTTCGATATGATGCAGCTTTGGT
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C.enneagrammus    TATCGATGGGCTCTCGGGGATACAACATTTGGCTGATGACTACCCAGTAGACACGATTGCGAAGAGATTTCGATATGATGCAGCTTTGGT
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H.suspectum       TATCGACGGGCTGTCAGGGATACAACATCTGGCTGATGACTACCCAGTAGACACGATTGCGAAGAGATTTCGATATGATGCAGCTTTGGT
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V.griseus         TATTGATGGGCTTTCAGGGATGCAGCATTTGGCTGATGACTACCCAATAGATACGATAGCAAAGAGATTTCGATACGACACAGCTTTGGT
L.borneensis      TATTGATGGGCTTTCAGGGATGCAGCATTTGGCTGATGACTACCCAATAGATACGATAGCAAAGAGATTTCGATATGATGCAGCTTTGGT
S.crocodiluris    TATTAATGGGCTCTCAGGGATACAACATTTGGCTGATGACTACCCAGTAGATACGATTGCGAAGAGATTTCGATATGATGCAGCTTTGGT
Dinodon.sp.       TATTGATGGGCTGTCAGGAATACAACAGTCTGTGGATGACTACCCAGTGGATACAATTGCAAAGCGATTTCGATATGATGTAGCTTTGGT
R.braminus        TATTGATGGACTTTCAGGCATACAATACTCTGTTGATGACTATCCAGTAGACACAACTGCAAAAAGGTTTCGATATGATGTTGCTTTAGT
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C.tigris          CATAGATGGGCTTTCAGGCATACAACATTTGGTTGATGACTACCCAGTAGATACGATAGCCAAGAGATTCCGATATGATGCCGCCTTGGT
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C.robustus        TATAGATGGACTCTCAGGCCTGCAACATTTGGTAGATGACTACCCAGTAGACACCATTGCGAAGAGATTTCGGTATGATGCAGCTTTGGT
S.sikkimensis     TATAGATGGACTCTCAGGCCTGCAACATTTGGTAGATGACTACCCAGTAGACACGATTTCAAAGAGGTTTCGGTATGATGCAGCTTTGGC
E.inexpectatus    TATAGATGGACTCTCAGGCCTACAACATTTGGTAGATGACTATCCAGTAGACACGATTGCAAAGAGGTTTCGGTATGATGCAGCTTTGGT
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F.polylepis       TATAGATGGACTCTCAGGCCTACAACATTTGGTAGATGACTATCCAGTAGACACAATTGCAAAGAGGTTTCGGTATGATGCAGCTTTGGT
Ch.ocellatus      TATAGATGGGCTCTCAGGCCTACAACGTTTGGTCGATGAGTATCCAGTAGACACAATTGCAAAGAGGTTTCGGTATGATGCAGCTTTGGC
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T.gariepensis     TATCGATGGACTTTCAGGCCTACAGCATTTGGTGGATGACTACCCAGTAGACACGATTGCAAAGAGGTTTCGATATGATGCAGCTTTGGC
T.lomii           TATCGATGGACTTTCAGGCCTACAGCATTTGGTGGATGACTACCCAGTAGACACGATTGCAAAGAGGTTTCGATATGATGCAGCTTTGGC
X.vigilis         CATAGATGGACTATCAGGCCTACAACATTTGGTTGATGACTACCCAGTAGATACCATTGCCAAGAGGTTTCGATATGATGCAGCATTGGC
C.polyzonus       TATAGATGGACTATCAGGCATACAACACTTGGTTGATGACTACCCAGTAGACACAATTGCAAAGAGGTTTCGATATGACGCAGCTTTGGT
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G.gallus          TTCTGCTTTAAAGGACATGGAGGAAGAAATCTTGGAGGGCATGAAGGCTAAAAACCTGGATGACTATCTGAATGGTCCCTTCACTGTGGT
C.mydas           TTCTGCCTTAATGGACTTGGAGGAAGACATTTTGGAAGGCATGAAAGCACAAGATCTGGATGACTACTTGAATGGCCCATTCACTGTTGT
S.punctatus       TTCAGCACTAATGGATATGGAAGAAGACATCCTGGAAGGAATGAAATCTCAAGACCTGGATGACTACCTGAATGGCCCCTTCACTGTGGT
B.thieli          TTGTACCCTGATGGACATGGAAGAAGACATACTAGAAGGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCTTTCACGGTGGT
C.rudis           TTCTACCTTGATGGACATGGAAGAAGACATACTAGAAGGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCTTTCACTGTGGT
C.brevicornis     TTCTACCTTGATGGACATGGAAGAAGACATACTAGAAGGGCTGAAAACTCAGGATTTGGATGACTATTTGAAAGGCCCTTTCACTGTGGT
C.salinarum       TTCTGCCCTGATGGACATGGAAGAAGACATTATAGAAGGGCTGAAATCTCAGGACTTTGATGACTATTTGAAAGGCCCTTTCACTGTGGT
P.lesueurii       TTCTGCCCTGATGGACATGGAAGAAGACATTATAGAAGGGCTGAAATCTCAGGACTTCGATGACTATTTGAAAGGCCCTTTCACTGTGGT
P.cocincinus      TTCTGCCCTGATGGACATGGAAGAAGACATTATAGAAGGGCTGAAATCTCAGGACTTGGATGACTATTTGAAAGGTCCCTTCACTGTGGT
Hydrosaurus.sp.   TTCTGCCCTGATGGACATGGAAGAAGACATTCTAAGAAGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCTTTCACTGTGGT
C.calotes         TTCTGCTCTGATGGACATGGAGGAGGACATTCTGGAAGGGCTGAAAACTCAGGATTTGGATGACTATTTGAAAGGCCCCTTCACGGTGGT
J.tricarinata     TTCTGCCCTGATGGACATGGAGGAAGACATTCTAGAAGGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCTTTCACGGTGGT
P.raddei          TTCTGCCCTGATGGACATGGAAGAAGACATTCTGGATGGCCTGAAAACTCAGGACTTGGACGACTATTTGAAAGGCCCATTCACTGTAGT
L.belliana        TTCTGCCCTGATGGACATGGAAGAAGATATTCTAGAAGGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCTTTCACTGTGGT
U.acanthinurus    TTCTGCCCTGATGGATATGGAAGAAGACATTCTAGAAGGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCTTTCACTGTGGT
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P.mcallii         TTCTGCCTTGATGGATATGGAAGAAGACATCCTAGAAGGCCTGAAAAGCCAGAACTTGGATGATTATTTCAAAGGCCCTTTCACTGTGGT
S.obesus          TTCTGCCTTGATGGATATGGAAGAAGACATCCTAGAAGGCCTGAAAAGTCAGGATCTGGATGACTACTTCAAAGGTCCATTCACTGTGGT
Hoplocercus.sp.   TTCTGCCTTGATGGATATGGAAGAAGATATCCTAGAAGGCCTGAAAAGTCAAGACTTGGATGACTACTTCAAAGGCCCTTTCACTGTGGT
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P.somencurensus   TTCGGCCTTGATGGATATGGAAGAAGACATCCTAGAAGGCCTGAAAAGCCAGGACTTGGATGACTAYTTCAAAGGCCCTTTCACTGTGGT
L.pictus          TTCTGCCTTGATGGATATGGAAGAAGACATCCTAGAAGGCCTAAAAAGTCAAGACTTGGATGACTACTTCAAAGGCCTTTTCACTGTGGT
U.flaviceps       TTCAGCTTTAATGGATATGGAAGAAGACATCCTAGAAGGCCTGAAAAGTCAGGACTTAGATGACTACTTTAAAGGCCCTTTCACTGTAGT
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B.plumifrons      TTCTGCCTTGATGGATATGGAAGAAGACATCCTAGAAGGCCTGAAAAGTCAGGACGTGGATGACTATCTCAAGGGCCCTTTCACTGTGGT
G.wislizenii      TTCTGCCTTGATGGATATGGAAGAAGACATCCTAGAAGGCCTGAAAAGTCAGGACTTGGATGACTACTTCAAAGGCCCTTTCACGGTGGT
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C.enneagrammus    TTCTGCTCTAATGGATATGGAAGAAGACATCCTGGAGGGGCTGAAAACCCAGGACTTGGATGACTATTTGAAAGGACCCTTCACCGTGGT
A.pulchra         TTCTGCCCTAATGGATATGGAAGAAGATATCCTAGAGGGGTTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCCTTCACTGTGGT
H.suspectum       TTCTGCCCTAAAGGATATGGAAGAAGACATCCTAGAAGGGCTGAAAACTCAGGACTTAGATGACTATTTGAAAGGCCCCTTCACTGTGGT
X.grandis         TTCTTCCCTAATGGATATGGAAGAAGACATCCTAGAAGGGCTGAAAACTCAGAACTTGGACGACTATTTGAAAGGCCCCTTCACTGTGGT
V.griseus         TTCTGCCCTAATGGATATGGAAGAAGACATCCTAGAAGGGCTGAAAATTCAGGACTTGGATGACTATTTGAAAGGCCCTTTCACTGTGGT
L.borneensis      TTCTGCCCTAATGGATATGGAAGAAGACATCCTAGAAGGGCTGAAAATCCAGGACTTGGATGACTATTTAAAAGGGCCTTTCACTGTGGT
S.crocodiluris    TTCTGCCCTGATGGATATGGAAGAAGACATCCTAGAAGGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGCCCCTTCACTGTGGT
Dinodon.sp.       GGCTGCCCTTATGGATCTAGAAGAAGAAATTTTAGAGGGACTGAAAACTCATGACTTGGATGACTATTTGAAAGGACCCTTCACTGTAGT
R.braminus        GGCTGCCCTTATGGATATAGAAGAAGATGTCCTGGAAGGTCTGAAAACTCAGGAACTGGACGACTATTTGAAAAGACCCTTCACTGTGGT
C.ruffus          GGCTGCCCTTATGGATATGGAAGAAGAAATCTTAGAAGGACTAAAAACTCATGACTTGGATGACTATTTGAAAGGACCCTTCACTGTAGT
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T.weigmanni       TTCTGCCCTAATGGATATGGAAGAAGACATTCTTGAAGGGCTGAAAACTCAGGACTTGGATGACTATTTGAAAGGGCCTTTCACTGTGGT
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C.tigris          TTCTGCCCTAATGGATATGGAGGAAGACATCCTGGAAGGGCTGAAAACTCATGATTTGGATGACTATTTGAAAGGTCCCTTCACAGTGGT
L.parietale       TTCTGCCCTAATGGATATGGAGGAAGACATCCTGGAAGGGCTGAAATCTCATGATTTGGATGATTATTTGAAAGGCCCCTTCACAGTGGT
E.turkmenicus     GTCTGCCTTGAAGGATATGGAAGATGACATCCTCGAAGGACTGAAAGCTCATGACCTAGATGACTATTTGAAAGGACCTTTCACTGTGGT
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T.przewalskii     GTCTGCCTTGATGGATATGGAAGAAGACATCCTTGAAGGACTGAAATCTCATGATCTGGATGATTATTTGAAAGGACTCTTCACTGTGGT
G.gekko           GTCTGCCTTGATGGATATGGAAGAAGACATCCTTGAAGGACTGAAATCTCATGATCTGAATGATTATTTGAAAGGACCTTTCACTGTGGT
P.lindneri        GTCTGCCTTGATGGATATGGAAGAAGACATTCTTGAAGGACTGAAATCACATGATCTAGATGATTATTTGAAAGGGCCCTTCACTGTGGT
Cr.ocellatus      GTCCACCTTGATGGATATGGAAGAAGACATCCTTGAAGGACTGAAATCACATGACCTAGATGATTATTTGAAAGGGCCTTTCACGGTGGT
L.jicari          GTCTGCCTTGATGGATATGGAAGAAGACATCCTTGAAGGACTTAAATCACATGATCTAGATGATTATTTGAAAGGACCATTCACTGTGGT
M.aurata          TTCAGCCCTCATGGATATGGAAGAAGATATCTTTGAAGGGCTAAAATCTAAAGATGTGAATGACTATGTGAAAGGCCCATTCACAGTGGT
C.robustus        TTCTGCCGTCATGGATATGGAAGAAGATATCTTTGAAGGGCTGAAATCCCAAGACTTGGATGATTACGAGAAAGGCCCTTTCACGGTAGT
S.sikkimensis     TTCTGCTCTCATGGATATGGAAGAAGATATCTTTGAAGGGCTGAAATCCCAAGACTTGGATGATTATGAGAAAGGTCCCTTCACGGTGGT
E.inexpectatus    TTCTGCCCTCATGGATATGGAAGAAGATATCTTTGAAGGGCTGAAATCTCAAGACTTGGATGACTATGTGAAAGGCCCCTTCACAGTGGT
E.skiltonianus    TTCTGCCCTCATGGATATGGAAGAAGATATCTTTGAAGGGCTGAAATCTCAAGACTTGGATGACTATGTGAAAGGCCCCTTCACAGTGGT
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S.anguineus        TTCTGCCCTCATGGATATGGAAGAAGATATCTTTGAAGGGCTGAAATCGCAAGACTTGGATGACTATGTGAAAGGCCCCTTCACAGTGGT
P.eggeli           TTCTGCCCTCATGGATATGGAAGAAGATATCTTTGAAGGGCTGAAATTGCAAGACTTGGATGACTATGTGAAAGGCCCCTTCACAGTGGT
F.polylepis        TTCTGCCCTCATGGATATGGAAGAAGATATCTTCGAAGGGCTGAAATCTCAAGACTTGGGTGATTATGTGAAAGGTCCCTTCACAGTGGT
Ch.ocellatus       TTCTGCCCTCATGGATATGGAAGAAGATATCTTTGAAGGGCTGAAAGCTCAAGACTTGGATGACTATGAGAAAGGCCCCTTCACAGTGGT
A.meleagris        TTCTGCTCTCATGGATATGGAAGAAGACATCTTTGAAGGGCTGAAATCTCAAGATTTGGATGACTACTTGAAAGGCCCCTTCATGGTAGT
T.gariepensis      TTCTGCTCTCATGGATATGGAAGAAGACATCTTTGAAGGGCTGAAATCTCAAGATTTGGATGACTACTTGAAAGGCCCCTTCATGGTAGT
T.lomii            TTCTGCTCTCATGGATATGGAAGAAGACATCTTTGAAGGGCTGAAATCTCAAGATTTGGATGACTACTTGAAAGGCCCCTTCATGGTAGT
X.vigilis          TTCTGCCCTGATGGATATGGAGGAAGACATAATTGAAGGGCTGAAATCTCAGGGCTTGGATGACTATGTGAAAGGTCCCTTCACTGTGGT
C.polyzonus        TTCTGCCCTAATGGATATGGAAGAAGATATCTTGGAAGGGCTCAAATCTCATGATCTGGATGACTACATGAAAGGCCCCTTCACTGTGGT
Zonosaurus.sp.     TTCTGCCCTAATAGATATGGAAGAAGACATCTTTGAAGGGCTTAAATCTCATGACTTGGATGACTACGTGAAAGGCCCTTTCACTGTGGT
Dibamus.sp.        TTCAGCCCTTATGGATATGGAAGAAGACATAATTGAAGGGCTGAAATCTCAGAACCTGGATGATTATCTGAAAGGCCCTTTCATCGTGGT

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G.gallus           AGTAAAAGAGTGCTGTGACGGAATGGGAGATGTCAGCGAGAAGCATGGAAGTGGTCCTGCTGTCCCAGAGAAGGCTGTACGCTTTTCATT
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B.thieli           GATTAAGGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGTCCTGCAGTCCCTGAGAAAGCAGTTCGATTCTCTTT
C.rudis            GATCAAGGAGTCCTGTGATGGAATGGGAGATGTCAGTGAGAAACATGGTTGTGGTCCGGCGGTCCCTGAGAAAGCAGTTCGATTCTCTTT
C.brevicornis      GATTAAGGAGTCCTGTGATGGAATGGGAGATGTCAGTGAGAAACATGGTTGTGGTCCTGCGGTCCCTGAGAAAGCAGTTCGATTCTCTTT
C.salinarum        GATTAAGGAGTCCTGTGATGGAATGGGAGATGTCAGTGAGAAGCATGGTTGTGGTCCTGCGGTCCCTGAGAAGGCAGTTAGATTCTCTTT
P.lesueurii        GATTAAGGAGTCCTGTGATGGAATGGGAGATGTCAGTGAGAAGCATGGTTGTGGTCCTGCAGTCCCTGAGAAGGCAGTTAGATTCTCTTT
P.cocincinus       GATTAAGGAGTCCTGTGATGGAATGGGAGATGTTAGTGAGAAGCATGGTTGTGGTCCTGCAGTCCCTGAGAAGGCAGTTAGATTCTCTTT
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C.calotes          GATTAAGGAGTCCTGCGATGGAATGGGAGACGTCAGTGAGAAGCATGGTTGTGGCCCTGCAGTCCCTGAGAAAGCCGTTCGATTCTCTTT
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Hoplocercus.sp.    GATTAAAGAGTCCTGTGATGGAATGGGAGATGTTAGTGAGAAACATGGCTGTGGCCCAGCTGTCCCTGAGAAAGCAGTTCGATTCTCTTT
E.laticeps         GATTAAAGAATCCTGTGATGGAATGGGAGATGTTAGTGAGAAACATGGCTGTGGCCCAGCTGTCCCTGAGAAAGCAGTTCGATTCTCTTT
P.somencurensus    GATTAAAGAGTCCTGTGATGGAATGGGAGATGTTAGTGAGAAACATGGCTGTGGCCCAGCTGTTCCTGAGAAAGCAGTTCGATTCTCTTT
L.pictus           GATTAAAGAGTCCTGTGATGGAATGGGAGATGTTAGTGAGAAACATGGTTGTGGACCAGCTGTCCCTGAAAAAGCAGTCCGATTCTCTTT
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B.plumifrons       GATTAAAGAGTCCTGTGATGGAATGGGAGATGTTAGTGAGAAACATGGCTGTGGCCCAGCTGTCCCTGAGAAAGCAGTTCGATTCTCTTT
G.wislizenii       GATTAAAGAGTCCTGTGATGGAATGGGAGATGTGAGTGAGAAACATGGCTGTGGCCCAGCTGTCCCTGAGAAAGCAGTTCGATTCTCTTT
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X.grandis          GATTAAAGAGTCCTGTGATGGAATGGGGGATGTTAGTGAAAAGCATGGCTGCGGCCCGGCTGTCCCCGAGAAAGCAGTTCGATTCTCTTT
V.griseus          GATTAAAGAGTCCTGTGATGGAATGGGGGATGTTAGTGAAAAGCACGGCTGTGGCCCAATGGTCCCTGAGAAGGCAGTTCGATTCTCTTT
L.borneensis       GATTAAAGAATCCTGTGATGGAATGGGGGATGTTAGTGAAAAGCATGGCTGTGGCCCAGCGGTCCCTGAGAAAGCAGTTCGGTTCTCTTT
S.crocodiluris     GATTAAAGAGTCCTGTGATGGAATGGGGGATGTTAGTGAAAAGCATGGCTGTGGGCCAGCTGTCCCTGAGAAAGCAGTTCGATTCTCTTT
Dinodon.sp.        GATTAAAGAATCCTGCGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCAGCTGTTCCTGAAAAGGCAGTTCGATTCTCCTT
R.braminus         GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCAGCTGTCCCAGAAAAGGCAGTGCGATTTTCCTT
C.ruffus           GATTAAAGAATCCTGTGATGGAATGGGTGATGTCAGTGAAAAGCATGGCTGTGGCCCAGCTGTGCCTGAAAAGGCAGTTCGATTCTCCTT
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Eremias.sp.        GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCATCAGTCCCTGAGAAAGCAGTTCGATTCTCTTT
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C.tigris           GATCAAAGAGTCTTGTGATGGGATGGGAGACGTCAGTGAAAAGCATGGCTGTGGCCCAGCTGTTCCTGAAAAAGCAGTCCGCTTCTCTTT
L.parietale        GATCAAGGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGTCCAGCTGTACCTGAGAAAGCAGTCCGCTTCTCTTT
E.turkmenicus      TATCAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGTCCAGCTGTCCCTGAAAAAGCAGTTCGATTCTCCTT
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T.przewalskii      GATCAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCAGCTGTCCCTGAAAAAGCAGTTAGATTCTCTTT
G.gekko            GATCAAAGAATCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCGGCTGTCCCTGAAAAAGCAGTTCGGTTTTCTTT
P.lindneri         GATCAAAGAGTCCTGTGATGGAATGGGAGACGTCAGTGAAAAGCATGGCTGTGGCCCACCAGTCCCTGAAAAAGCGGTTCGATTCTCTTT
Cr.ocellatus       CATCAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCAGCAGTCCCTGAAAAAGCAGTTCGATTCTCTTT
L.jicari           GATCAAAGAGTCCTGTGATGGAATGGGAGATGTGAGTGAAAAGCATGGCTGTGGCCCAGCGGTCCCTGAAAAAGCAGTTCGATTCTCTTT
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M.aurata          GGTTAAAGAGTCCTGTGATGGCATGGGAGATGTCAGCGAGAAGCATGGCTGTGGACCAGCTGTCCCAGAGAAAGCAGTGAGATTCTCTTT
C.robustus        GATCAAAGAGTCTTGTGATGGCATGGGAGATGTGAGCGAGAAGCATGGCTGTGGCCCAGCTGTCCCTGAGAAAGCAGTGCGCTTCTCTTT
S.sikkimensis     GATCAAAGAGTCCTGTGATGGCATGGGAGATGTGAGCGAGAAGCATGGCTGTGGCCCAGCTGTCCCTGAGAAAGCAGTGCGCTTCTCTTT
E.inexpectatus    GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGCGAAAAGCATGGCTGTGGTCCAGCTGTCCCGGAGAAAGCAGTGCGATTCTCTTT
E.skiltonianus    GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGCGAAAAGCATGGCTGTGGCCCAGCTGTCCCGGAGAAAGCAGTGCGATTCTCTTT
E.anthracinus     GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGCGAAAAGCATGGCTGTGGCCCAGCTGTCCCGGAGAAAGCAGTGCGATTCTCTTT
S.anguineus       GATTAAAGAGTCCTGCGATGGAATGGGCGATGTCAGCGAAAAGCATGGCTGTGGTCCAGTTGTCCCTGAGAAAGCCGTGCGATTCTCTTT
P.eggeli          GATTAAAGAGTCCTGTGATGGAATGGGTGATGTCAGCGAAAAGCATGGCTGTGGTCCAGTTGTCCCTGAGAAAGCTGTGCGATACTCTTT
F.polylepis       GATCAAAGAGTCCTGTGATGGAATGGGCGATGTCAGCGAAAAGCATGGCTGTGGTCCAGTTGTCCCCGAGAAAGCAGTGCGCTTCTCTTT
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T.gariepensis     GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAACATGGCTGTGGCCCAGCTGTCCCTGAGAAAGCAGTGCGATTCTCTTT
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X.vigilis         GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGGCCCCCTGTCCCTGAGAAAGCAGTTCGATTCTCTTT
C.polyzonus       GATTAAAGAATCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCAGCTGTACCCGAGAAAGCAGTTAGATTCTCATT
Zonosaurus.sp.    GATTAAAGAGTCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGCTGTGGCCCAGCTGTACCTGAGAAAGCAGTCAGATTCTCATT
Dibamus.sp.       GGTTAAAGAATCCTGTGATGGAATGGGAGATGTCAGTGAAAAGCATGGATGTGGCCCACCTGTCCCTGAGAAAGCAGTTCGCTTCTCTTT

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A.mississip.      CACTGTCATGACCATCGCTATAACTCATGGCAATACAAATGTAAGGATCTTTGAAGAAGTCAAGCCCAATTCAGAGCTATGTTGCAAGCC
G.gallus          TACAGTCATGAACATTGCTATAGACCACGAGAACGAAAGGATAAGGATCTTTGAAGAAGTAAAGCCCAATTCAGAGTTGTGTTGCAAACC
C.mydas           CACACTCATGAACATCACTATAGCTCATGGTAAAGAAAACATAAGGCTCTTTGAAGAAGTCAAGCCCAATTCAGAGCTGTGTTGCAAGCC
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B.thieli          CACACTTATGAGCATCTCTGTTGCTCAAAGCAATGCAAATGTAAAGATTTTTGAAGAAACTAAACCCAATTCTGAACTGTGTTGCAAACC
C.rudis           CACACTTATGAGCATCTCTGTTGCTCAAAGTAATGCAAATGTAAAGATTTTTGAAGAAGCTAAGCCCAATTCTGAGCTGTGTTGCAAACC
C.brevicornis     CACACTTATGAGCATCTCTGTTGCTCAAAGTAATACAAATGTAAAGATTTTTGAAGAAACTAAGCCCAATTCTGAACTGTGTTGCAAACC
C.salinarum       CACACTTATGAGTATCTCTGTAGCTCAGGGTGATGCAAATGTAAAGATTTTTGAAGAAAATAAGCCCAACTCTGAACTGTGTTGTAAACC
P.lesueurii       CACACTTATGAGTATCTCTGTAGCTCATGGTGATGCAAATGTAAAGATTTTTGAAGAAAGTAAGCCCAACTCTGAACTGTGTTGCAAACC
P.cocincinus      CACATTTATGAGTATCTCTGTAGCTCATGGTGATGCAAATGTAAAGATTTTTGAAGAAAATAAGCCCAACTCTGAACTGTGTTGCAAACC
Hydrosaurus.sp.   CACACTTATGAATATCTCTGTAGCTCATGGTGATGTAAATGTAAAGATTTTTGAAGAAAATAAGCCCAATTCTGAACTGTGTTGCAAACC
C.calotes         CACCCTTATGAGCATCTCTGTAACTCATGGCGATGCAAACGTAAAGATTTTTGAAGAAAGTAAGCCCAATTCTGAACTGTGTTGCAAACC
J.tricarinata     CACATTTATGAGCATCTCTGTAGCTCATGGTGATGCAAATGTAAAGGTTTTTGAAGAAAGTAAACCCAATTCTGAACTGTGTTGCAAACC
P.raddei          CACGCTTATGAGCATCTCTGTACCTCATGGGGATTCGAATGTAAAGATTTTTGAGGAAAATAAGCCCAATTCTGAGCTGTGCTGCAAACC
L.belliana        CACGTTAATGAGAATATCTGTTGCTCATAATGATGGCAATGTAAAGATTTTTGAAGAAAATAAGCCCAATTCTGAACTGTGTTGCAAACC
U.acanthinurus    CACACTTATGAGCATCTGTGTTGCTCATGGTAATGCCAATGTCAAGATTTTTGAAGAAACTAAGCCGAATTCTGAGCTGTGTTGCAAACC
A.paternus        CACAGTCATGACCATCTCTGTCACTCATGGCAATGCAAGCGTAAGGGTTTTTGAAGAATGCAAGCCCAATTCAGAGCTGTGTTGTAAGCC
P.mcallii         CACACTCATGAGCATCTCTGTCACTCATGAAAATTCAAGCATAAGGATTTTTGAAGAAAACAAGCCCAATTCAGAGCTATGTTGCAAACC
S.obesus          CACACTCATGAGCATCTCTGTCACTCATGACAATGCAAGCATAAGGATTTTTGAGGAAAACAAGCCCAATTCAGAACTGTGTTGTAAACC
Hoplocercus.sp.   CACACTCATGAGCATCTCTGTCACTCATGGCAATGCAAGCATAAGAGTTTTTGAAGAAAACAAGCCCAATTCAGAGCTGTGTTGTAAACC
E.laticeps        CACACTCATGAGCATCTCTGTCACTCATGACAATGCAAGCATAAGGGTTTTTGAAGAAAACAAGCCCAATTCAGAGCTGTGTTGTAAACC
P.somencurensus   CACACTCATGAGCATCTCTGTCACAAAAGACAATGCAAGCATAAGGATTTTTGAAGAAAACAAGCCCAATTCAGAGTTGTGTTGTAAACC
L.pictus          CACACTCATGAGCATTTCTGTCACTCGAGACAATGAAAGCATAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAGTTGTGTTGTAAACC
U.flaviceps       CACACTCATGAGCATCTCTGTCATTCATGACAATGGAAGCATAAGGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGTAAACC
S.crasicaudatus   CACGCTCATGAGCATCTCTTGTACTCATGACAATGCAAGCATAAGGATTTTTGAAGAAAACAAGCCCAATTCAGAGCTGTGTTGTAAGCC
L.carinatus       CACACTCATGAGCATTTCTGTTACTCATGACAATGGAAGCATAAGGATTTTTGAAGAAAACAAGCCAAATTCAGAGCTGTGTTGTAAGCC
B.plumifrons      CACACTCATGAGCATCTCTGTCACTCATGGCAATGCAAGCATAAGGATTTTTGAAGAAAATAAGCCCAATTCAGAACTGTGTTGTAAACC
G.wislizenii      CACGCTTATGACCATTTCTGTTACTCATGACAATGCAAATATAAGGATTTTTGAAGAAAACAAGCCCAATTCAGAGCTGTGTTGTAAACC
O.cuvieri         CACACTCATGAGCATCTCTGTCGCTCATAACAATGCAACTGTAAGGATTTTTGAAGAAAACAAGCCCAACTCAGAGCTGTGTTGTAAACC
O.attenuatus      CACTCTCATGAGCATCACTGTCGCTCATGATAATGGGAGCACAAAGGTTTTTGAAGAAACCAAGCCCAACTCAGAACTCTGTTGCAAACC
E.panamintina     CACCCTCATGAGCATCACTGTCGCTCATGACAATGGGAGCACAAAGGTTTTTGAAGAAACCAAGCCCAACTCGGAACTTTGTTGCAAACC
C.enneagrammus    CACCCTCATGACCATCACTGTCGCTCATGACAACAGGAACACAAAGGTCTTTGAAGAAACCAAGCCCAACTCGGAGCTTTGCTGCAAACC
A.pulchra         CACCCTCATGAGCATCACTGTTGCTCATGACAATGGGAGCACAAAGATTTTTGAAGAAAGCAAGCCCAACTCGGAGCTTTGTTGCAAACC
H.suspectum       CACCCTCATGAGCATCACTGTCACACATGACAATGGGAGTGCAAAGATTTTTGAAGAAACCAAGCCTAATTCGGAGCTTTGTTGCAAACC
X.grandis         CACCCTCATGAGCATCACTGTCACTCATGACAACGGGAGCACAAAGGTTTTTGAAGAAACCAAGCCCAATTCGGAGCTTTGTTGCAAACC
V.griseus         CACCATCATGAGCATCACTGTCTGTCATGACAGTGGGAGCACAAAGATTTTTGAAGAAACCAAGCCCAATTCAGAGCTTTGTTGCAAACC
L.borneensis      CACCCTCATGAGCATCACTATCTCTCATGACAATGGGAGCACAAAGATTTTTGAAGAAACCAAGCCCAATTCAGAACTTTGTTGCAAACC
S.crocodiluris    CACCCTCATGAGCATCACTGTTGCTCATGACAATGGGAGTGCAAAGATTTTTGAAGAAACCAAGCCCAATTCAGAGCTTTGTTGCAAACC
Dinodon.sp.       CACCCTCATGAGCATCACTGTAACTCATGACCATGGCAGTGCGAGGATTTTTGAAGAAAACAAACCCAATTCAGAGTTGTGTTGTAAGCC
R.braminus        TACGCTCATGAGTATCACGGTCACTCATGACAATAGCAGTGTGAAGATTTTTGAAGAAAATAAGCCCAATTCAGAGTTGTGTTGTAAGCC
C.ruffus          TACCCTCATGAGCATCACTGTCAGTCATGACAATGGCAACGTGAAGATTTTTGAAGAAATCAAACCCAATTCAGAACTGTGTTGTAAGCC
Agkistrodon.sp.   CACCCTTATGAGCATCACTGTAACTCATGAGCGTGGCAGTGCAAGGATTTTTGAAGAAAGCAAACCCAATTCAGAGTTGTGTTGTAAGCC
Eremias.sp.       CACACTCATGAGCATCACTGTAGCTCATGAGAAGGGAAGCTCCAATATCTTTGAAGAAAGCAAGCCCAATTCAGAACTGTGTTGCAAACC
B.biporus         CACGCTCATGAGCATCACTGTCACTCATGAGAATGGAAACTCAAAGATTTTTGAAGAGAATAAGCCCAATTCAGAGCTGTGTTGCAAACC
T.weigmanni       CACGCTCATGAGCATCACTGTAACTCATGACAATGGAAACGCAAAGATTTTTGAAGAGAACAAGCCCAATTCAGAGCTGTGCTGCAAACC
R.floridana       CACACTCATGAGCATCACTGTAGCTCATGACAATGGAAGTGCAAAGATTTTTGAAGAAAATAAGCCCAATTCAGAGTTGTGTTGCAAACC
A.xera            CACGGTCATGAGCATCACTGTAACTCATGACAATGGAAACTCAAAGATTTTTGAAGAGAACAAACCCAATTCAGAGCTCTGCTGCAAACC
C.tigris          CACATTTATGAGCATTGTTGTGGATAATAACAACAAAAGTGTTAGGATATTTGAAGAAAGCAAGCCCAATTCAGAACTGTGTTGTAAACC
L.parietale       CACGCTRATGAGCATTGCTATCGACGAAAACAACAAAAGTATTAGGATCTTTGAAGAAAGCAAGCCCAATTCAGAATTGTGCTGTAAACC
E.turkmenicus     CACCCTCATGAACATCACCATGGCTCATGGCAATGAATGTATAAGAATTTTTGAAGAAAGCAAGCCCAATTCAGAGCTGTGTTGCAAACC
S.shrevei         CACAGTCATGAACATCACTGTGGCTCATGGCAATGTAAATATAAGAATTTTTGAAGAAAACAAGCCTAATTCAGAACTGTGTTGCAAACC
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T.przewalskii       CACAGTCATGAACATCACCATAGCTCATGGCAATGAAAATATAAGAATTTTTGAAGAAAACAAGCCCAATTCAGAATTGTGTTGCAAACC
G.gekko             CACAGTCATGAACATCACTGTGGCACATGACAATGAAAGTATAAGAATTTTTGAAGAAACCAAGCCCAATTCAGAGTTGTGTTGCAAACC
P.lindneri          CACACTCATGAACATCACTTTGGCTCATGGCAATGAAAAGATAAGGATTTTCGAAGAAAACAAGCCTAATTCAGAGCTGTGTTGCAAGCC
Cr.ocellatus        CACACTCATGACCATCACTGTGGCTCATGGGAATGAAAATATAAGGATTTTTGAAGAAACCAAGCCTAATTCAGAGCTGTGTTGCAAGCC
L.jicari            CACACTCATGAACATTACTGTGGCTCATGGCAATGAAAATGTAAGGATTTTTGAAGAAAATAAACCTAATTCAGAGCTGTGTTGTAAACC
M.aurata            CACACTTATGAGCATCACTGTCACTCAGGGCAACGAAAGTATAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
C.robustus          CACACTCATGAGCATCAGTGTTGCACACGACAAAGGAAGTATAAAGATTTTTGAAGAAAGCAAGCCCAACTCTGAACTCTGTTGCAAACC
S.sikkimensis       CACACTCATGAGCATCACTGTTGCACACGACAAAGGAAATATAAAGGTTTTTGAAGAAAGCAAGCCCAACTCTGAACTCTGTTGCAAACC
E.inexpectatus      CACACTTATGAGCATCACTGTAGCTCATGACAATGGAAGTATCAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
E.skiltonianus      CACACTTATGAGCATCACTGTAGCTCATGACAATGGAAGTACCAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
E.anthracinus       CACACTTATGAGCATCACTGTAGCTCATGACAATGGAAGTATCAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
S.anguineus         CACGCTTATGAGCATCACGGTAGCTCATGGCAATGAAAATACAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
P.eggeli            CACACTTATGAGCATCACGGTAGCTCATGGCAATGAAAATACAAAGGTTTTTGAGGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
F.polylepis         CACACTTATGAGCATCACTATAGCTCACAGCAATGAAAATATAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
Ch.ocellatus        CACAGTTATGAGCATCACCGTAGCTCATGACAAAGGAAGTGTAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTATGTTGCAAACC
A.meleagris         CACACTCATGAGCATCACTGTAGCTCATAACAATGAAAATATAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
T.gariepensis       CACACTCATGAGCATCACTGTAGCTCATAACAATGAAAATATAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
T.lomii             CACACTCATGAGCATCACTGTAGCTCATAACAATGAAAATATAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAACTGTGTTGCAAACC
X.vigilis           CACACTCATGAGCATCACGATAGCCCATGGCAATGAAGAGATAAAGGTTTTTGAAGAAAACAAGCCCAATTCTGAGCTGTGTTGCAAACC
C.polyzonus         TACACTCATGAGCATCACTGTTGCTCATGGCAAAGAAAGTATAAAGATTTTTGAAGAAAACAAGCCCAATTCAGAGCTGTGTTGCAAACC
Zonosaurus.sp.      CACACTCATGAGCATCACAGTAGCTCATGGCAAAGAAAGTATAAAGATTTTTGAAGAAAACAAGCCCCATTCAGAGCTGTGTTGCAAACC
Dibamus.sp.         CACACTCATGAACATCACTGTAGCTCATGGCAATGCTCATATAAAGGTTTTTGAAGAAAGCAAGCCCAATTCAGAGCTGTGTTGCAAACC

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G.gallus            CTTGTGTCTTATGCTGGCTGATGAATCAGACCATGAAACTCTGACAGCAATCCTGAGCCCTCTCATAGCAGAGAGAGAGGCTATGAAGAA
C.mydas             CTTGTGCCTTATGCTGGCTGATGAATCGGATCATGAGACTCTGACAGCCATCCTGAGCCCTCTCATAGCAGAAAGAGAGACCATGAAAAG
S.punctatus         TTTGTGCCTTATGCTGGCGGATGAATCAGATCATGAGACTCTGACAGCCATCCTGAGTCCTCTCATAGCAGAAAGAGAAGCCATGAAAAG
B.thieli            TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGATGCTCACAGCCATCCTGAGCCCTCTCGTAGCAGAAAGAGAGGCCATGAAAAA
C.rudis             TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACGCTCACAGCTATCTTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAA
C.brevicornis       TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACGCTCACAGCCATCTTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAA
C.salinarum         TTTGTGCCTTATGCTGGCTGATGAATCCGACCATGAGACGCTCACTGCCATCCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAA
P.lesueurii         TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACGCTCACAGCCATCCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAG
P.cocincinus        TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACACTCACAGCCATCCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAG
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C.calotes           TCTGTGTCTGATGCTGGCTGACGAATCAGACCACGAGACACTCACAGCCATCCTGAGCCCTCTTGTAGCAGAAAGGGAGGCCATGAAACA
J.tricarinata       TTTGTGCCTGATGCTGGCCGATGAATCCGACCATGAGACACTCACAGCCATCCTGAGCCCTCTTGTAGCAGAAAGGGAGGCCATGAAACA
P.raddei            TTTGTGCTTGATGCTGGCAGACGAATCAGACCATGAGACACTCACGGCCATTCTAAGCCCTCTTGTAGCCGAAAGAGAAGCCATGAAAAA
L.belliana          TTTGTGCCTYATGCTTGCTGATGAGTCAGACCACGAGACACTCACAGCTATCCTGAGCCCACTTGTAGCAGAAAGAGAGGCCATGAAAAA
U.acanthinurus      TTTGTGTCTTATGCTGGCTGATGAATCAGATCATGAGACACTCACAGCCATCCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAA
A.paternus          CTTGTGCCTAATGCTGGCTGATGAATCAGACCATGAGACGCTCACAGCCATCCTGAGTCCTCTTGTGGCAGAAAGAGAGGCCATGAAAGA
P.mcallii           TTTGTGCCTTATGCTGGCTGATGAGTCAGACCATGAGACACTCACAGCCATCCTGAGTCCTCTTGTGGCAGAAAGAGAGGCCATGAAAGA
S.obesus            TTTGTGCCTTATGCTTGCTGATGAATCAGACCATGAGACACTGACAGCCATCCTGAGTCCTCTTGTGGCAGAAAGAGAGGCCATGAAAGA
Hoplocercus.sp.     TTTGTGCCTCATGCTGGCTGATGAATCAGACCACGAGACACTCACAGCCATCCTGAGTCCTCTTGTGACAGAAAGAGAAGCCATGAAAGA
E.laticeps          TTTGTGCCTTATGCTGGCTGATGAATCAGACCACGAGACACTCACAGCCATCCTGAGTCCTCTTGTGACAGAAAGAGAGGCCATGAAAGA
P.somencurensus     TTTGTGCCTTATGCTGGCTGATGAATCAGATCACGAGACACTCACAGCCATCCTGAGTCCTCTTGTGGCAGAAAGAGAGGCCATGAAAGA
L.pictus            TTTGTGCCTTATGCTGGCTGATGAATCAGACCACGAGACGCTCACAGCCATCCTGAGTCCTCTTGTGGCTGAAAGAGAGGCCATGAAAAG
U.flaviceps         TTTGTGCCTTATGTTAGCTGATGAATCAGACCATGAAACACTCACAGCCATCCTGGGCCCTCTTGTGGCAGAAAGAGAAGCCATGAAAAA
S.crasicaudatus     TTTGTGCCTTATGTTGGCTGATGAATCAGACCATGAAACACTCACAGCCATCCTGAGTCCTCTTGTGGCAGAAAGAGAGGCCATGAAGAA
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B.plumifrons        TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACACTCACAGCCATCCTGAGTCCTCTTGTGACAGAAAGAGAGGCCATGAAAGA
G.wislizenii        TTTGTGCCTTATGCTGGCTGATGAATCAGATCATGAGACCCTCACAGCCATCCTGAGTCCTCTTGTGGCAGAAAGAGAGGCCATGAAAGA
O.cuvieri           TTTGTGTCTTATGCTGGCTGATGAATCAGACCATGAGACACTCACAGCCATCCTGAGTCCTCTTGTGGTAGAAAGAGAGGCCATAAAAGA
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E.panamintina       TTTGTGCCTTATGCTGGCTGATGAATCGGACCATGAGACACTTACGGCTATCCTCAGTCCTCTTGCAGCAGAAAGAGAGGCCATGAAGAG
C.enneagrammus      TCTGTGCCTCATGTTGGCTGATGAATCGGACCATGAGACACTCACGGCTATCCTCAGTCCTCTCATAGCAGAAAGAGAGGCCATGAAGAG
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H.suspectum         TTTGTGCCTTATGCTGGCTGATGAATCAGATCATGAGACACTCACGGCCATCCTGAGTCCCCTTGTAGCAGAAAGAGAGGCCATGAAGAG
X.grandis           TTTATGCCTCATGCTAGCTGATGAATCGGACCATGAGACACTCACGACCATTCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAGAG
V.griseus           TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACACTCACGGCCATCCTGAGCCCTCTTATAGCAGAAAGAGATTCCATGAAGAG
L.borneensis        TTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACATTCACGGCCATCCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAGAA
S.crocodiluris      TCTGTGCCTTATGCTGGCTGATGAATCAGACCATGAAACACTCACGGCCATACTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAGAG
Dinodon.sp.         TTTGTGCCTTATGTTGGCTGATGAGTCAGATCATGAGACACTCACGGCCATCCTGAGTCCTCTTATAACGGAACGGGAAGCCATGAAACA
R.braminus          TTTGTGCCTTATGCTGGCGGACGAGTCAGACCATGAGATCCTCACCACCATCCTGAGTCCTCTTGTGGCGGAAAGGAAGGCCATGAAAAA
C.ruffus            TTTGTGCCTTATGCTGGCTGATGAGTCAGACCATGAGACACTCACCACCATCCTGAGTCCCCTTATGGCAGAAAGGGAAGCCATGAAAAA
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B.biporus           TTTGTGCCTCATGCTGGCAGATGAATCAGATCATGAGACACTCACAGCCATCCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAA
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C.tigris         TTTGTGCCTTATGCTGGCTGATGAATCAGACCACGAGACACTCACAGCCATCCTGAGCCCTCTTGTAGCAGAACGAGAGGCCATGAAGAA
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E.turkmenicus    CTTATGCCTTATGCTTGCTGACGAATCAGACCACGAGACATTTACTGCTATCCTGAGTCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAA
S.shrevei        CTTGTGCCTGATGCTTGCTGATGAATCAGACCATGAAACATTCACAGCTATTTTAAGTCCTCTTGTGGCAGAAAGAGAAGCCATGAAAAA
T.przewalskii    CTTATGCCTGATGCTTGCTGATGAATCAGACCATGAGACATTCACTGCTATCCTGAGTCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAG
G.gekko          CTTATGCCTTATGCTTGCTGATGAATCAGACCATGAGACATTCACTGCTATCCTGAGTCCTCTTGTAGCAGAAAGAGAGGCCATGAAGAA
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Cr.ocellatus     CTTGTGCCTTATGCTTGCTGATGAATCAGACCATGAGACTTTCACTGCTATCCTGAGTCCTCTGGTAGCAGAAAGAGAGGCCATGAAAAA
L.jicari         CTTGTGCCTTATGCTTGCTGATGAATCAGACCATGAGACCTTCACTGCTATCCTGAGTCCTCTGGTAGCAGAAAGAGAGGCCATGAAAAA
M.aurata         TTTGTGCCTGATGTTGGCTGATGAATCAGACCACGAGACCCTCACAGCTATCTTAAGCCCCCTTGTCGCAGAAAGGGAGGCCATGAAAAG
C.robustus       TTTGTGCCTGATGCTGGCTGATGAATCGGACCACGAAACCCTCACGGTTATCTTGAGCCCTCTTGTGGCGGAAAGGGAGGCCATGAAAAA
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E.inexpectatus   TTTGTGCCTGATGCTGGCTGATGAATCAGACCATGAGACCCTCACAGCTATTTTGAGCCCTCTTGTAGCTGAAAGGGAGGCCATGAAAAG
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S.anguineus      TTTGTGCCTGATGCTGGCTGATGAATCAGACCATGAGACCCTCACAACTATCTTAAGCCCTCTTGTGGCAGAAAGGGAGGCCATGAAAAG
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F.polylepis      TTTGTGCCTGATGCTGGCTGACGAGTCAGACCACGAGACCTTCACAGCTATCTTGAGCCCTCTTGTGGCAGAAAGGGAGGCCATGAAAAG
Ch.ocellatus     TTTGTGCCTGATGCTGGCTGATGAATCAGACCATGAGACCCTCACAGCTATCTTGAGCCCTGTTATAGCAGAAAGGGAGGCCATGAAAAG
A.meleagris      TTTGTGTCTGATGCTGGCTGATGAATCAGACCATGAGACTCTCACAGCCATCCTGAGCCCTCTTATAGCAGAAAGAGAGGCCATGAAAAG
T.gariepensis    TTTGTGCCTGATGCTGGCTGATGAATCAGACCATGAGACTCTCACAGCCATCCTGAGCCCTCTTATAGCAGAAAGAGAGGCCATGAAAAG
T.lomii          TTTGTGCCTGATGCTGGCTGATGAATCAGACCATGAGACTCTCACAGCCATCCTGAGCCCTCTTATAGCAGAAAGAGAGGCCATGAAAAG
X.vigilis        TTTGTGCCTCATGCTGGCTGATGAATCAGACCATGAGACACTCACGGCCATCCTGAGCCCACTTGTAGCAGAAAGAGAGGCTATGAAGGA
C.polyzonus      CTTGTGCCTTATGCTGGCTGATGAATCAGACCATGAGACACTCACAGCCATTCTGAGCCCTCTTGTAGCAGAAAGAGAGGCCATGAAAAG
Zonosaurus.sp.   CTTGTGCCTTATGCTGGCTGATGAATCAGACCACGAGACATTCTCTGCCGTTCTGAGCCCTCTTGTAGCAGAAAGGGAGGCCATGAAAAA
Dibamus.sp.      TTTGTGTCTTATGCTGGCTGATGAATCAGACCATGAGACACTCACAGTCATCCTGAGCCCTCTTGTAACAGAAAGAGAAGCCATGAAAAA

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C.rudis          TAGTTTACTGATACTCGATATGGCTGGAATCCCCAGAATGTTCAAATTCATCTTTAGAGGTACTGGATATGATGAAAAACTTGTCCGTGA
C.brevicornis    TAGTTTACTGATACTTGATATGGCTGGAATCCCCAGAATGTTCAAATTCATCTTTAGAGGTACTGGATATGATGAAAAACTTGTCCGTGA
C.salinarum      TAGTGAACTGATACTTGATATGGCTGGCATTCCAAGAATGTTCAAATTCATCTTCAGAGGTACTGGATATGATGAAAAACTTGTCCGTGA
P.lesueurii      TAGTGAACTGATACTTGATATGGCTGGAATTCCGAGAATGTTCAAATTCATCTTCAGGGGTACTGGATATGATGAAAAACTTGTCCGTGA
P.cocincinus     TAGTGAACTGATACTTGATATGGCTGGAATTCCGAGAATGTTCAAATTCATCTTCAGGGGTACTGGATATGATGAAAAACTTGTCCGTGA
Hydrosaurus.sp.  CAGTGTACTGATACTTGATATGGCTGGAATCCCCAGAATGTTCAAATTTGTCTTCAGGGGTACTGGATATGATGAAAAACTTGTCCGTGA
C.calotes        TAGCGTGCTAATGCTTGATATGGCTGGAATCCCCAGGATGTTCAAATTTGTCTTTAGGGGTACTGGGTATGATGAAAAACTTGTCCGTGA
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P.raddei         CAGTGTCCTCATACTTGATATGGCTGGAATCCCTAGAATGTTCAAATTCATCTTCAGGGGCACCGGATATGATGAAAAACTTGTCCGTGA
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U.acanthinurus   TAGTGTACTGATGCTTGATATGGCTGGAATCCCCAGAATGTTCAAATTCATCTTTAGAGGTACAGGATATGATGAAAAACTTGTCCGTGA
A.paternus       CAGTGTACTGATACTTGATATGGCTGGAATCCCAAGAACATTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAACTTGTCCGTGA
P.mcallii        CAGTGTACTGACACTTGATATGGCTGGAATCCCCAGAATATTCAAATTTATCTTTAGAGGCACTGGCTATGATGAGAAGCTAGTTCGTGA
S.obesus         CAGTGTACTGATACTTGATATGGCTGGAATCCCAAGAACATTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAGCTTGTCCGTGA
Hoplocercus.sp.  CAGTGAACTGATACTTGATATGGCTGGAATCCCAAGAACATTCAGATTCATCTTTAAGGGCACTGGATATGATGAAAAGCTTGTCCGTGA
E.laticeps       CAGTGTATTGATACTTGATATGGCTGGAATCCCAAGAATGTTCAGATTCATCTTTAGGGGCACTGGATATGATGAAAAGCTTGTCCGTGA
P.somencurensus  CAGTGTAGTGATACTTGATATGGCTGGAATTCCAAGAACATTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAGCTTGTTCGTGA
L.pictus         TAGTGTACTGACACTTGATATGGCTGGAATCCCAAGAACATTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAGCTTGTTCGTGA
U.flaviceps      CAGTGAACTGATACTTGATATGGCTGGAATCCCAAGAACATTCAAATTCATTTTTAGGGGCACTGGATACGATGAAAAGCTTGTCCGTGA
S.crasicaudatus  TAGTGCACTGATACTTGATATGGCTGGAATCCCAAGAACATTCAAATTCATTTTTAGGGGCACTGGATATGATGAAAAACTTGTCCGTGA
L.carinatus      CAGTTTACTAATACTTGATATGGCTGGAATCCCAAGAATGTTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAGCTTGTCCGTGA
B.plumifrons     CAGTGTACTGATACTTGATATGGCTGGAATCCCAAGAATGTTCAAATTCATATTTAGAGGCACTGGATATGATGAAAAGCTTGTCCGTGA
G.wislizenii     CAGTGTACTGATACTTGATATGGCTGGAATCCCAAGAACATTCAAATTCATTTTTAGGGGCACTGGGTATGATGAAAAACTAGTCCGTGA
O.cuvieri        CAGTATACTGATACTTGATATGGCTGGAATCCCAAGAACATTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAGCTTGTCCGTGA
O.attenuatus     CAGTGTGTTGATACTGGATATGGCTGGAATCCCCAGAATGTTCAAATTTGTCTTTAGGGGGACTGGATATGATGAAAAGCTTGTCCGTGA
E.panamintina    CAGTGTGTTGATACTGGATATGGCTGGAATCCCCAGAATGTTCAAATTCGTCTTTAGGGGGACTGGATATGATGAAAAGCTGGTCCGTGA
C.enneagrammus   CAGCGTGTTGATCCTGGATATGGCTGGAATCCCCAGAATGTTCAAATTCATCTTTCGGGGGACTGGATACGATGAGAAGCTCGTCCGTGA
A.pulchra        CAGTGTGTTGATACTGGATATGGCTGGAATCCCCAGAATGTTCAAATTCATTTTTAGAGGGACTGGATATGATGAAAAGCTTGTCCGTGA
H.suspectum      CAGTATATTGATATTGGATATGGCTGGAATCCCCAGAATGTTCAAATTCATTTTTAGGGGCACTGGGTATGATGAAAAGCTTGTCCGTGA
X.grandis        CAGCGTACTGATACTGGATATGGCTGGAATCCCCAGAATGTTCAAATTCATCTTCAGGGGCACTGGATATGATGAAAAGCTTGTCCGTGA
V.griseus        TAGTGTATTAATCCTGGATATGGCTGGAATCCCCAGAATGTTCAAGTTCATCTTCAGAGGCACTGGGTATGATGAAAAGCTTGTCCGTGA
L.borneensis     TAGTGTATTGATACTGGATATGGCTGGAATCCCCAGAATGTTCAAATTCATCTTCAGAGGCACTGGATATGATGAAAAGCTTGTCCGTGA
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Dinodon.sp.      TAGCGCACTGATCCTTTATATGGCTGGTATTCCTAGAATTTTCAAATTCATATTTAGGGGCACTGGATATGATGAAAAACTTGTCCGTGA
R.braminus       CAGCGAATTGGTGCTTGAGATGCGTGGGATACCCAGACTATTCAGATTCATATTTCGGGGCACGGGATATGATGAAAAGCTTGTCCGTGA
C.ruffus         TAGTGCATTAATTCTTTATATGGCTGGTATTCCCAGAACTTTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAGCTTGTCCGTGA
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B.biporus         TAGCATATTGATATTTGATATGGGTGGGATCCCCAGAATGTTCAAATTTGTTTTCCGTGGCACTGGATACGATGAAAAGCTTCTCCGTGA
T.weigmanni       TAGCACATTGATACTTGAAATGGGTGGGATTCCCAGAATGTTCACATTTGTTTTTCGTGGCACTGGATACGATGAAAAGCTTGTCCGTGA
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A.xera            TAGCACATTGATACTTGATATGGGTGGGATTCCCAGAATGTTCAAATTTGTTTTTCGTGGGACTGGATACGATGAAAAGCTTGTTCGTGA
C.tigris          TAGCGTATTAATACTTGAGATGAGTGGGATTCCCAGAATGTTCAAATTTGTCTTCAGAGGTACTGGATATGATGAGAAGCTTGTCCGTGA
L.parietale       TAGCGTATTACTACTTGAAATGGGTGGGATCCCCAGAATGTTCAAATTTGTCTTCAGAGGTACTGGATATGATGAGAAGCTTGTTCGTGA
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S.shrevei         CAGTGGATTGTTACTTGATATGGGTGGAATTCCAAGAACCTTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAACTTGTCCGTGA
T.przewalskii     CAGTGAACTGGTACTTGATATGGGTGGAATCCCAAGAACCTTCAAATTCATCTTTAGGGGCACTGGATATGATGAAAAACTTGTCCGTGA
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M.aurata          CAGTGAACTGATACTTGAGATGGGTGGAATACCCAGAGTATTCAAATTCATATTTAGGGGCACTGGATATGATGAAAAGCTTGTTCGTGA
C.robustus        CAGCGAATTGGTGCTTGAGATGCGTGGGATACCCAGACTATTCAGATTCATATTTCGGGGCACGGGATATGATGAAAAGCTTGTCCGTGA
S.sikkimensis     CAGTGAGTTGGTCCTTGAGATGGGTGGGATACCCAGATTATTCAGATTCATATTTAGGGGCACAGGGTATGATGAAAAGCTTGTCCGTGA
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Dibamus.sp.       CAGCACATTGCTACTTGATATGGGTGGAATCCCCAGAGCATTCAAATTCATCTTTAGGGGCACTGGGTATGATGAAAAGCTTGTCCGTGA

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C.calotes         AGTAGAAGGCCTCGAAGCTTCAGGCTCTACTTACATTTGTACACTTTGCGACACAACACGCCAAGAGGCCTCTCAGAACTTGATCCTTCA
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R.braminus         AGTAGAGGGCCTTGAAGCATCAGGCTCTACTTACATATGTACACTTTGTGATGCAACACGCCTGGAAGCCTCTCAGAACTTGATCTTCCA
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G.gallus           CTCCATCACCAGGAGCCACGCTGAAAATCTGGAGCGATATGAAATATGGAGGTCCAACCCATATCACGAATCTGTTGATGAGCTCCGTGA
C.mydas            CTCCATAACAAGAAGTCATGCTGAAAACCTGGAGCGGTATGAGGTATGGAGGTCCAACCCATATAATGAATCTGTTGATGAGTTACGTGA
S.punctatus        CTCCATCACCAGGAGCCACACTGAAAACCTGGAGCGGTACGAAGTGTGGCGGTCCAATCCATACCACGAGTCAGTTGAGGAGCTACGCGA
B.thieli           CTCCATAACAAGGTGTCATGCTGAAAACCTGGAACGATATGAGGTATGGAGGTCTAATCCTTACCATGAGACTGTTGATGAACTACGTGA
C.rudis            CTCCATAACAAGGAGTCACGCTGAAAACCTGGAACGATATGAGGTATGGAGGTCAAATCCTTACCAGGAGACTGTTGATGAATTACGTGA
C.brevicornis      CTCCATAACAAGGAGTCATGCTGAAAACCTGGAACGATATGAGGTATGGAGATCAAATCCTTACCAGGAGACTGTTGATGAATTACGTGA
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P.lesueurii        CTCCATAACAAGGAGTCATGCTGAAAACTTGGAACGCTATGAGGTATGGAGATCAAATCCCTACCATGAGACTGTTGATGAACTACGTGA
P.cocincinus       CTCCATAACAAGGAGTCATGCTGAAAACCTGGAACGCTATGAGGTATGGAGATCAAATCCCTACCATGAGACTGTTGATGAACTACGTGA
Hydrosaurus.sp.    CTCCATAACAAGGAATCATGTGGAAAACTTGGAACGCTATGAGGTATGGAGATCAAATCCCTACCATGAGACTGTTGATGAACTACGTGA
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Hoplocercus.sp.    CTCCATCACAAGGAGTCATGCAGAAAACCTACAACGCTATGAGGTGTGGAGGTCCAACCCCTACCACGAGACTGTTGATGAACTGCGTGA
E.laticeps         CTCCATCACAAGGAGTCATGCGGAAAACCTAGAACGGTATGAGGTGTGGAGGTCCAACCCCTACCATGAGACCGTTGATGAACTGCGTGA
P.somencurensus    TTCCATCACAAGGAGTCATGAGGAAAACCTAGAACGGTATGAGATGTGGAGGTCCAACCCCTACCATGAAACTGTTGATGAACTGCGTGA
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L.carinatus        CTCAATCACAAGGAGTCATGCAGAAAACCTAGAACGGTATGAAGTGTGGAGATCCAACCCCTACCAGGAGACTGTTGATGAACTACGTGA
B.plumifrons       TTCCATCACAAAGAATCATGTGGAAAACTTAGAAAGGTACGAGGTGTGGAGGTCCAACCCCTATCGTGAGACTGTTGATGAACTGCGTGA
G.wislizenii       TTCCATCACAAGGAGTCATGCTGAAAACCTAAAACGGTACGAGGTGTGGAGGTCCAACCCCTACCATGAGACGGTTGATGAACTACGTGA
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E.panamintina      CTCCATAACGAGGAGTCATGCTGAAAACTTGGAACGGTATGAGGTGTGGAGGTCCAACCCGTACCATGAGACTGTTGATGAACTACGTGA
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H.suspectum       CTCCATAACGAGAAGTCATGCTGAAAACCTGGAACGGTATGAGGTGTGGCGGTCCAACCCCTACCACGAGACTGTTGATGAACTACGTGA
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V.griseus         CTCCATAACAAGGAATCATGCTGAAAACCTGGAACGGTATGAGGTGTGGAGGTCCAACCCCTACCATGAAACTGTTGATGAACTACGTGA
L.borneensis      CTCCATAACAAGGAATCATACTGAAAACCTGGAACGGTATGAGGTGTGGAGGTCCAACCCCTACCATGAGACTGTTGATGAACTACGTGA
S.crocodiluris    CTCCATAACAAGGAGTCATGCTGAAAACTTGGAACGGTATGAGGTGTGGAGGTCCAACCCCTACCACGAGACTGTTGATGAACTACGTGA
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Eremias.sp.       TTCCATAACGAGAAGTCATACTGAAAACCTAGAGCGATATGAGGTGTGGAGATCAAACCCCTTCCATGAGACGGTTGAAGAACTACGTGA
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C.tigris          TTCCATAACAAGGAGTCATGCTGAAAACCTTGAGCGGTATGAAGTATGGAGATCTAATCCTTACCATGAAACTGTTGATGAACTACGGGA
L.parietale       TTCCATAACAAGGAGTCATGTGGAAAACCTTGAGAGGTATGAAGTCTGGAGGTCTAATCCTTACCATGAAACAGTTGATGAACTACGGGA
E.turkmenicus     CTCCATAACAAGAAGTCATGCTGAGAACCTGGAGCGGTATGAAGTGTGGAGGTCCAACCCCTATCATGAAACGGTGGATGAACTACGTGA
S.shrevei         CTCCATAACAAGAAGTCATGCTGAAAACCTGGAGAGGTATGAAGTGTGGAGGTCCAACCCCTATCATGAAACTGCTGATGAACTACGTGA
T.przewalskii     CTCCATAACAAGAAGTCACACTGAAAACCTGGAGCGGTATGAAGTGTGGAGGTCCAACCCCTATCATGAAACTGTTGATGAACTACGTGA
G.gekko           CTCCATAACAAGAAGTCATGCCGAAAACCTGGAGCGTTATGAAGTGTGGAGGTCCAACCCCTATCATGAAACTGTTGATGAACTACGTGA
P.lindneri        CTCCATAACAAGAAGTCATGCTGAAAACCTGGAGCGGTATGAAGTGTGGAGGTCCAATCCTTACCACGAAACTGTCGATGAACTCCGTGA
Cr.ocellatus      CTCCATAACAAGAAGTCATGCTGAAAACCTGGAGCGGTATGAGGTGTGGCGGTCCAACCCTTATCATGAAAGCGTCGAAGCACTGCGTGA
L.jicari          CTCCATAACAAGAAGTCACGCTGAAAACCAGGAGCGGTATGAAGTGTGGAGGTCCAACCCTTATCACGAAACTGTTGATGAACTACGTGA
M.aurata          CTCCATAACAAGGAATCATGCTGAAAACCTAGAGCGATACGAGATGTGGCGGTCCAATCCCTACCATGAGACTGTTGATGAGCTACGTGA
C.robustus        CTCCATAACGAGGAATCACACTGAAAACCTAGAGCGGTATGAGATGTGGCGGTCCAATCCCTACCACGAGACTGTTGACGAACTGCGCGA
S.sikkimensis     CTCCATAACCAGGAATCACGCTGAAAACCTAGAGCGGTACGAGATGTGGCGGTCCAATCCCTACCACGAGACTGTTGACGAGCTGCGCGA
E.inexpectatus    CTCCATAACGAGGAATCATGCTGAAAACTTAGAGCGGTATGAGATGTGGCGGTCCAATCCCTACCATGAGACTGTTGACGAACTACGTGA
E.skiltonianus    CTCCATAACGAGGAATCATGCTGAAAACTTAGAGCGGTATGAGATGTGGCGGTCCAATCCCTACCATGAGACTGTTGACGAACTACGTGA
E.anthracinus     CTCCATAACGAGGAATCATGCTGAAAACCTAGAGCGGTATGAGATGTGGCGGTCCAATCCCTACCATGAGACTGTTGACGAACTACGTGA
S.anguineus       CTCCATAACAAGAAATCATGCTGAAAACCTAGAGCGGTATGAGATGTGGCGGTCCAATCCTTACCATGAGACTGTTGACGAACTACGTGA
P.eggeli          CTCCATAACGAGGAATCATGCTGAAAACCTAGAGCGGTATGAGATGTGGCGGTCCAATCCTTACCATGAGACTGTTGACGAACTACGTGA
F.polylepis       CTCCATCACGAGGAATCACGCTGAAAACCTCGAGCGGTATGAGATGTGGCGGTCCAATCCTTACCATGAGAGTGTTGATGAACTACGTGA
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A.meleagris       CTCCATAACAAGGAACCATGCTGAAAACCTAGAGCGGTATGAGATGTGGAGGTCCAACCCGTACCATGAAACTGTTGATGAACTACGTGA
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X.vigilis         CTCTGTCACGAGAAATCATGTGGAAAACCTAGAGCGGTATGAGGTATGGAGGTCTAACCCCTACCATGAGACAGTTGATGAACTACGTGA
C.polyzonus       CTCCATCACAAGGAGTCATGCTGAAAACCTAGAGCGGTATGAAGTGTGGAGGTCCAACCCCTACCATGAGACTGTTGATGAACTACGTGA
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Dibamus.sp.       CTCCATAACAAGGAGTCATGCTGAAAACCTGGAGCGGTATGAAGTGTGGAGATCCAATCCCTATCATGAGACCGTAGATGAACTACGTGA

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C.brevicornis     CAGAGTGAAAGGGGTTTCTGCCAAGCCTTTTATTGAGACTGTTCCTTCGATAGATGCTTTGCATTGTGATATTGGCAATGCAGCTGAATT
C.salinarum       CAGAGTGAAGGGAGTTTCTGCCAAGCCATTTATTGAGACTGTTCCTTCAATAGACGCTTTGCATTGTGATATCGGCAATGCAGCAGAATT
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P.cocincinus      CAGAGTGAAGGGAGTTTCTGCCAAGCCATTTATTGAGACTGTTCCTTCAATAGACGCTTTGCATTGTGATATTGGCAATGCAGCAGAATT
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S.crasicaudatus   CAGAGTGAAGGGGGTTTCTGCAAAGCCTTTTATTGAGACTGTTCCTTCAATAGATGCCTTGCACTGTGACATTGGCAATGCAGCTGAATT
L.carinatus       CAGAGTGAAGGGGGTCTCTTCAAAGCCCTTTATTGAGACTGTTCCTTCAATAGATGCCTTGCACTGTGACATTGGCAATGCAGCTGAATT
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C.robustus         CAGAGTGAAGGGTGTTTCCGCCAAGCCTTTCATCGAAACAGTTCCTTCAATCGACGCGCTGCACTGTGACATCGGCAATGCTACCGAGTT
S.sikkimensis      CAGAGTGAAGGGTGTTTCGGGCAAGCCTTTCATCGAAACGGTCCCTTCGATCGACGCGCTGCACTGTGACATCGGCAACGCGACCGAGTT
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Dibamus.sp.        CAGAGTGAAGGGTGTTTCTGCCAAGCCTTTTATTGAGACTGTGCCTTCGATAGATGCATTGCACTGTGATATTGGCAATGCAGCTGAGTT

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G.gallus           TTACAGGATTTTCCAGATGGAGATTGGTGAAGTCTATAAGAATCCTGATGCGACTAAAGAGGAGAGGAAGAGGTGGCAGTTGACTCTTGA
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E.laticeps         TTACAAGATATTCCAGTTTGAGATTGGTGAAGTCTACAAAACCCTTGATGCATCGAAAGAAGAGAGAAAGAGATGGCAGTCAACTCTTGA
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S.crasicaudatus   TTACAAGATATTGCAGTTTGAGATTGGCGAAGTCTACAAAAACTCCAGTGCATCAAAAGAAGAGAGAAAGAGATGGCAGTCAACACTTGA
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S.sikkimensis     TTACAAGATCTTCCAATTCGAGGTGGGGGAAGTGTACAAAAAGCCCAATGCATCCAAAGAAGAGAGAAAGAGGTGGCAGTCAACTCTCGA
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S.anguineus       ATACAAGATCTTCCAATTTGAGATTGGTGAAGTGTACAAGACTCCCAATGCATCCAAAGAAGAGAGAAAGAGGTGGCAATCAACTCTAGA
P.eggeli          TTACAAGATCTTCCAATTCGAGATTGGTGAAGTGTACAAAACCCCCAATGCATCAAAAGAAGAGAGAAAGAGGTGGCAATCAACTCTTGA
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A.meleagris       TTACAAGATCTTCCAATTTGAGGTTGGGGAAGTGTACAAGAAGCCCGACCCGTCCAAAGAAGAGAGAAAGAGGTGGCAGTCAACTCTCGA
T.gariepensis     TTACAAGATCTTCCAGTTTGAGATTGGTGAAATGTACAAAAACTCCAATGCAACAAAAGAAGAGAGAAAGAGGTGGCAATTAACCCTTGA
T.lomii           TTACAAGATCTTCCAGTTTGAGATTGGTGAAGTGTACAAAAACTCCAATGCAACAAAAGAAGAGAGAAAGAGGTGGCAATTAACCCTTGA
X.vigilis         TTACAAGATATTCCAGTTTGAGATTGGTGAAGTGTACAAAACCCCCAATGTGTCTAAAGAAGAGAGAAAGAGGTGGCAGTCAACTCTTGA
C.polyzonus       TTACAAAATATTCCAGTTTGAGATTGGTGAAGCATATAAAAACCCTGATGCTTCAAAAGAAGAGAGAAAGAGGTGGCAATCAACTCTTGA
Zonosaurus.sp.    TTACAAAATATTCCAGTTTGAGATAGGCGAAGTATATAAAAACCCTCATGCATCAAAAGAAGAGAGAAAGAGGTGGCAATCAACTCTTGA
Dibamus.sp.       TTACAAGATATTCCAGTTGGAGATTGGTGAGGTATACAAAACCGCTGATGCACCAAAAGAAGAGAGAAAGAGGTGGCAAACTACCCTTGA

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G.gallus          CAAACATCTCAGGAAGAAGATGAAATTAAAACCTATGATGAGGATGAGTGGGAACTTTGCTAGAAAGCTCATGTCCAAAGAGACAGTAGA
C.mydas           CAAGCACCTTAGGAAGAAGATGAACCTGAAGCCCATAATGAGGATGAATGGAAACTTTGCTAGAAAGCTTATGACCAAAGAGACAGTGGA
S.punctatus       CAAGCATCTCAGAAAGAAAATGAACTTGAAACCAATAATGAGGATGAATGGAAACTTTGCTAGAAAGCTCATGACCAAAGAAACAGTGGA
B.thieli          CAAACACCTCCGAAAGAAGATGCACTTGAAACCTATGACAAGGATGAATGGAAATTTTGCTAGAAAGCTTATGAGTATGGAAACTGTGGA
C.rudis           CAAACACCTCCGAAAGAAGATGAACTTGAAGCCTATGACAAGGATGAATGGAAATTTTGCTAGAAAGCTTATGACTATGGAAACTGTGGA
C.brevicornis     CAAACACCTCCGAAAGAAGATGAACTTGAAGCCTATGACAAGGATGAATGGAAATTTTGCTAGAAAGCTTATGAGTATGGAAACTGTGGA
C.salinarum       CAAACATCTCAGGAAGAAGATGAACTTGAAACCTATGATAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCATGGAGACTGTGCA
P.lesueurii       CAAACATCTCAGGAAGAAGATGAACTTGAAACCTATGATAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCATGGAGACTGTGCA
P.cocincinus      TAAACATCTCAGGAAGAAGATGAACTTGAAACCTATGATAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCATGGAAACTGTGCA
Hydrosaurus.sp.   CAAACACCTCAGGAAGAAGATGAACTTGAAACCTATGATAAGAATGAATGGAAATTTTGCGAGAAAGCTCATGACCATGGAGACTGTGGA
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J.tricarinata     CAAACACCTCAGGAAGAAGATGAACCTGAAACCTATGATAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCTCGGGAACTGTGGA
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L.belliana        CAAACACCTCAGGAAGAAGATGAACTTGAAGCCTGTGCTGAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAGGAGACTGTGGA
U.acanthinurus    CAAACATCTCAGGAAGAAGATGAACTTGAAACCTGTGACAAGGATGAATGGAAATTTTGCTAGAAAACTCATGACCATGGAGACTGTGGA
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P.mcallii          CAAACACCTCAGAAAGAAGATGAACCTGAAGCCTGTGGCAAGGATGAATGGGAATTTTGCCAGAAAGCTCATGACCAAAGAGACTGTGGA
S.obesus           CAAACACCTCAGAAAGAAGATGAACTTGAAGCCTGTAACAAGGATGAATGGGAATTTTGCCAGAAAGCTCATGAGTAAGGACACTGTGGA
Hoplocercus.sp.    CAAACACCTCAGAAAGAAGATGAACTTGAAGCCTATAACAAGGATGAATGGGAATTTTGCCAGAAAGCTCATGAGCAAGGAAACTGTGGA
E.laticeps         CAAACACCTCAGAAAGAAGATGAACTTGAAGCCTATAACAAGGATGAATGGGAATTTTGCCAGAAAGCTCATGAGCAAGGAGACTGTGGA
P.somencurensus    CAAACACCTCAGAAAGAAGATGAATTTGAAGCCTGTAGGAAGGATGAATGGGAACTTTGCCAGAAAACTCATGACCAAGGAGACTGTGGA
L.pictus           CAAGCATCTCAGAAAGAAGATTAATTTGAAGCCTGTAACAAGGATGAATGGGAACTTTGCCAGAAAGCTCATGACCAAGGAGACTGTGGA
U.flaviceps        CAAACACCTGAGAAAGAAGATGAACTTGAAGCCTATAACAAGGATGAATGGGAATTTTGCCAGAAAGCTCATGACCAAGGAGACTGTGGA
S.crasicaudatus    CAAACACCTCAGAAAGAAGATTAACTTGAAGCCTGTAACAAGGATGAATGGCAATTTTGCCAGAAAACTCATGAGCAAGGAGACTGTGGA
L.carinatus        CAAACACCTCAGAAAGAAAATGAACCTGAAGCCCATAACAAGGATGAATGGGAATTTTGCCAGAAAGCTCATGACCAAGGAGACTGTGGA
B.plumifrons       CAAACACCTCAGAAAGAAGATGAACTTGAAGCCTGTCACCAGAATGAATGGGAATTTTGCCAGAAAGCTCATGACCAAGGACACTGTGGA
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H.suspectum        CAAACACCTCAGAAAGAAGATGAACCTGAAGCCTGTAACAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAGGAGACTGTGGA
X.grandis          CAAACACCTCAGAAAGAAGATGAACCTGAAGCCTGTAACAAGGATGAATGGGAATTTTGCTAGAAAGCTCATGAGCAAGGAGACTGTGGA
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L.borneensis       CAAACACCTCAGAAAGAAGATGAATCTAAAACCTGTAACAAGGATGAATGGAAATTTTGCTAGAAAGCTTATGACGAAGGAGACCGTGGA
S.crocodiluris     CAAACACCTCAGAAAGAAGATGAACCTGAAGCCTATAACAAGGATGAATGGAAATTTTGCCAGAAAGCTCATGACAAAGGAGACTGTGGA
Dinodon.sp.        CAAACACCTTAGAAAAAAGATGAATTTGAAACCTGTAACAAGGATGAATGGAAATTTTGCAAGAAAACTCATGAGTAGAGAGACCGTGGA
R.braminus         CAAACATCTTCGAAAGAAGATGAGCCTGAAGCCAATGACAAGGATGAATGGAAACTTTGCTAGAAAGCTCATGACCAAAGAGACGGTGGA
C.ruffus           CAAACACCTTAGAAAAAAAATGAATTTGAAACCTATAGCAAGGATGAATGGAAATTTTGCAAGAAAACTCATGAGTAGGGAGACTGTGGA
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B.biporus          TAAGCACCTTAGGAAGGTGATGAACTTAAAGCCTGTAGCAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAACAGACTGTGGA
T.weigmanni        TAAGCACCTTAGGAAGGTGATGAGCTTAAAGCCTGTAGTAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAAGAGACTGCAGA
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A.xera             TAAGCACCTTAGGAAAGTGATGAGCTTAAAACCTATAGCAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGAGCAAAGAGACTGTGGA
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L.parietale        TAAGCACCTCAGAAAGAAAATGAACTTGAAACCCATGGTAAGAATGAATGGAAACTTTGCTAGAAAACTCATGACCAAACAAGCTGTGGA
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P.lindneri         CAAACACCTCAGGAAGAAAATGAACTTGAAGCCTGTAATGAGGATGAACGGAAATTTTGCTAGAAGGCTCATGTCCAAAGAGACAGTAGA
Cr.ocellatus       CAAACACCTCAGGAAGAAAATGAACTTGAAGCCTGTAACAAGGATGAATGGAAATTTTGCTAGAAGGCTCATGTCAAAAGAGACAGTGGA
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M.aurata           CAAACATCTTAGGAAGAAGATGAACATGAAGCCTATGACAAGGATGAATGGAAATTTTGCTAGAAAGCTAATGACCAAAGAGACTGTGGA
C.robustus         CAAACATCTTCGAAAGAAGATGAGCCTGAAGCCAATGACAAGGATGAATGGAAACTTTGCTAGAAAGCTCATGACCAAAGAGACGGTGGA
S.sikkimensis      CAAGCATCTTCGAAAGAAGATGAGCCTGAAGCCGATGACCAGGATGAATGGAAATTTTGCGAGAAAGCTCATGACCAAAGAGACCGTGGA
E.inexpectatus     CAAACATCTTAGAAAGAAGATGAGCCTGAAGCCTATAACACGGATGAATGGAAATTTTGCTAGAAAGCTCATGAGCAAAGAGACTGTGGA
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E.anthracinus      CAAACATCTTAGAAAGAAGATGAGCCTGAAGCCTATAACACGGATGAATGGAAATTTTGCTAGAAAGCTCATGAGCAAAGAGACTGTGGA
S.anguineus        CAAACATCTTAGAAAGAAGATGAACCTGAAGCCTATAACAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAAGAGACCGTGGA
P.eggeli           CAAACATCTTAGAAAGAAGATGAACCTGAAGCCTATAGCAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAAGAGACCGTGGA
F.polylepis        CAAACATCTTAGAAAGAAGATGAACCTGAAGCCTGTCACAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAAGAGACCGTGGA
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T.gariepensis      CAAGCATCTTAGAAAGAAGATGAGCCTGAAGCCCATAACAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAAGAGACAGTGGA
T.lomii            CAAGCATCTTAGAAAGAAGATGAGCCTGAAGCCCATAACAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAAGAGACAGTGGA
X.vigilis          CAAACACCTTAGAAAGAAGATGAACCTGAAGCCTGTCACAAGGATGAATGGCAATTTTGCGAGAAAGCTCATGACCAAAGAGACAGCAGA
C.polyzonus        TAAACATCTGAGAAAGAAGATGAATCTGAAGCCTGTAACAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGTCCAAAGAGACAGTGGA
Zonosaurus.sp.     TAAACATCTGAGAAAGAAGATGAATCTGAAGCCTGTAACAAGGATGAATGGAAATTTTGCTAGAAAGCTCATGACCAAAGAGACAGTGGA
Dibamus.sp.        CAAACACCTCCGAAAGAAAATGAATCTAAAGCCCATAGGAAGGATGAATGGAAATTTTGCTAGAAAGCTTATGACCAAAGAGACAGTGGA

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G.gallus           GGCAGTATGTGAATTAATAAAGTGTGAGGAAAGGCATGAAGCCCTAAAAGAACTAATGGACCTTTATCTGAAAATGAAACCAGTATGGCG
C.mydas            AGCAGTATGTGAATTAATAAAGTGTGAGGAAAGGCATGATGCACTAAGAGAACTGATGGACCTTTACCTTAAGATGAAACCAGTGTGGAG
S.punctatus        AGCAGTATGTGAATTAATAAAAAGTGAGGAAAGACATGAAGCCCTAAGAGAACTAATGGACCTTTACCTTAAGATGAAACCAGTGTGGCG
B.thieli           AGCAGTTTGTGAATTAATAAAATGTGAAGAGAGACATGAAGCCCTTAGAGAACTCATGCACCTTTATCTTAAAATGAAACCAGTATGGCG
C.rudis            AGCAGTTTGTGAATTAATAAAATGTGAAGAGAGACATGAAGCCCTTAGAGAACTCATGGACCTTTATCTTAAAATGAAACCAGTATGGCG
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P.cocincinus       AGCAGTTTGTGAATTAATAAAATGTGAGGAGAGACATGAAGCCCTCAGAAAGCTCATGGACCTTTATCTTAAGATGAAACCAGTTTGGCG
Hydrosaurus.sp.    AGCAGTTTGTGAACTAATGAAGTGTGAGGAGAGACATGAAGCCCTCAGAGAGCTCATGGACCTTTATCTTAAGATGAAACCAGTTTGGCG
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P.raddei          AGCAGTTTGCGAATTAATAAAGTGTGAGGAGAGACATGAAGCCCTCAGAGAGCTCATGGAGCTTTATCTTAAGATGAAACCAGTTTGGCG
L.belliana        AGCGGTTTGTGAATTAATAAAGTGTGAGGAGAGACAGGAAGCCCTCAGAGAACTCATGGACCTTTATCTTAAGATGAAGCCAGTATGGCG
U.acanthinurus    AGCGGTCTGTGAATTAATAAAGTGTGAGGAGAGACATGACGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
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S.obesus          AGCAGTTTGTGAATTAATAAAGAGTGAGGAGAGACAGGAAGCTCTTAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTGTGGCG
Hoplocercus.sp.   AGCAGTCTGTGAATTAATAAAAAGTGAGGAGAGACATGAAGTCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTGTGGCG
E.laticeps        AGCAGTCTGTGAGTTAATAAAAAGTGAGGAGAGACACGAAGTCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAGCCAGTGTGGCG
P.somencurensus   AGCAGTTTGTGAATTAATAAAGAGTGAGGAGAGACATGAAGCCCTCAGAGAACTCATGGATCTTTACCTTAAGATGAAACCAGTGTGGCG
L.pictus          AGCAGTTTGTGAATTAATAAAGAGTGAGGAGAGACATGAACCCCTCAGAGAACTCATGGACCTTTACCTTAAAATGAAACCAGTGTGGCG
U.flaviceps       AGCGGTTTGTGAATTAATAAAGAATGAGGACAGACATGAAGCCCTAAGAGAACTCATGGACCTTTACCTTAAGATGAAGCCAGTGTGGCG
S.crasicaudatus   AGCAGTTTGTGAATTAATAAAGAATGAGGAGAGACATGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTGTGGCG
L.carinatus       AGCAGTTTGTGAATTAATAAAGAATGAGGAGAGACACGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAAATGAAACCCGTGTGGCG
B.plumifrons      AGCAGTTTGTGAATTAATAAAGAGTGAGGAGAGACACGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTGTGGCG
G.wislizenii      AGCAGTTTGTGAATTAATAAAGAGTGAGGAGAGACATGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTGTGGCG
O.cuvieri         AGCAGTCTGTGAATTAATAAAGAATGAGGAGAGACAGGAAGCTCTCAAAGAACTCATGGATCTTTATCTTAAGATGAAACCAGTGTGGCG
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C.enneagrammus    AGCAGTTTGTGAACTGGTTATGTGTGAGGAGAGGCACGAAGCCCTCAGAGAACTCATGGACCTTTACCTGAAGATGAAACCAGTCTGGCG
A.pulchra         AGCAGTTTGTGAACTGGTCAAGTGTGAGGAGAGGCATGAAGCCCTCAGAGAGCTCATGCACCTTTATCTTAAGATGAAACCAGTCTGGCG
H.suspectum       AGCAGTTTGTGAACTAATCAAGTGTGAGGAGAGGCATGAATCCCTCAGAGAACTCATGGACCTTTATCTTAAGATGAAACCAGTATGGCG
X.grandis         AGCAGTTTGTGAACTAATCAAGTGTGAGGAGAGGCAGGAAACCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
V.griseus         AGCAGTTTGTGAACTCATTGGGAGTGAGGAGAGGCATGAAGCCCTCAGAGAACTCATGGACCTGTACCTTAAGATGAAACCAGTATGGCG
L.borneensis      AGCAGTTTGTGAACTAATTAGGTGTGAGGAGAGGCAAGAAGCTCTCAGAGAACTCATGGGCCTTTACCTTAAGATGAAACCAGTATGGAG
S.crocodiluris    AGCAGTTTGTGAACTAATCAAGTGTGAGGAGAGGCATGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
Dinodon.sp.       TGCAGTCTGTGAATTAATAAAATGTGAGGAGAGACATGAAGCCCTCAGAGAATTAATGGACCTTTACCTGAAGATGAAACCAGTATGGAG
R.braminus        AGCGGTTTGTGAGCTAATTCCGTGTGAAGAGAGACATGAAGCCCTCAGAGAACTCATGGACCTCTATCTGAAGATGAAACCAGTGTGGCG
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B.biporus         AGCAGTTTGTGAATTAATAAAGTGTGATGAGAGACAGGAAGCTCTTAAAGAACTCATGGACCTTTACCTTAAAATGAAACCGGTATGGCG
T.weigmanni       AGCAGTCTGTGATTTAATAAAGTGTGATGAGAGACAGGAAGCTCTTAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
R.floridana       AGCAGTTTGTGAATTAATAAAGTGTGATGAGAGACAGGAAGCCCTTAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
A.xera            AGCAGTCTGTGATTTAATAAAGTGTGATGAGAGGCAGGAAGCTCTTAGAGAACTCATGGACCTTTACCTGAAGATGAAACCAGTATGGCG
C.tigris          AGCAGTCTGTGAATTAATAAGCTGTGAAGAAAGAAAACAAGCTCTTAGAGAACTCATGGAACTTTACCTTAAGATGAAACCAGTATGGCG
L.parietale       TGCAGTTTCTGAATTAATAAGTTGTGAAGAGAGAAAACAAGCTCTTAAGGAACTCATGGACCTTTATCTCAAGATGAAACCAGTATGGCG
E.turkmenicus     AGCAGTTTGTGAACTCATAAAGTGTGAGGACCGACATGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
S.shrevei         AGCAGTATGTGAACTCATGCGGTGTGAAGAGAGACATGAAGCACTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
T.przewalskii     AGCAGTATGTGAACTCATAAAGAGTGAGGACCGACATGAAGCACTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
G.gekko           AGCCGTTTGTGAACTCATAAAGAGTGAGGACCGCCATGAAGCACTTAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
P.lindneri        AGCCGTCTGTGAACTCATGAAGTGTGAGGAGAGGCATGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
Cr.ocellatus      AGCAGTCTGTGAACTCATAAACTGTGAGGAGAGGCATGAAGCCCTCAGAGAACTCATGGACCTTTACCTTAAGATGAAACCAGTATGGCG
L.jicari          AGCTGTTTGTGAACTCGTGAAATGTGAGGAGAGATGCGAAGCCCTCAGAGAACTCATGGCCCTTTACCTTAAGATGAAACCAGTATGGCG
M.aurata          AGCTGTTTGTGATCTAATTAAGTGTGAGGAAAGGCATGAAGCCCTCAGAGAACTCATGGACCTTTATCTGAAGATGAAACCCGTGTGGCG
C.robustus        AGCGGTTTGTGAGCTAATTCCGTGTGAAGAGAGACATGAAGCCCTCAGAGAACTCATGGACCTCTATCTGAAGATGAAACCAGTGTGGCG
S.sikkimensis     AGCGGTTTGTGAACTCATTCAGTGCGAAGAGAGGCATGAAGCCCTCAGAGAACTCATGCACCTCTATCTGAAGATGAAACCGGTGTGGCG
E.inexpectatus    AGCGGTTTGTGAGCTAATTAAGTGTGAAGAAAGACATGAAGCCCTCAGAGAACTCATGGACCTTTATCTTAAGATGAAACCCGTGTGGCG
E.skiltonianus    AGTGGTTTGTGAGCTAATTAAGTGTGAAGAAAGACATGAAGCCCTCAGAGAACTCATGGACCTTTATCTTAAGATGAAACCCGTGTGGCG
E.anthracinus     AGCGGTTTGTGAGCTAATTAAGTGTGAAGAAAGACATGAAGCCCTCAGAGAACTCATGGACCTTTATCTTAAGATGAAACCCGTGTGGCG
S.anguineus       AGCAGTTTGTGAACTAATTAAGTGTGAAGAGAGACATGAAGCCCTCAGAGAACTCATGGACCTTTATCTTAAGATGAAACCCGTGTGGCG
P.eggeli          AGCGGTTTGTGAACTAATTAAGTGTGAAGAGAGACATGAAGCCCTCAGAGAACTCATGCACCTTTATCTTAAGATGAAACCCGTGTGGCG
F.polylepis       AGCGGTTTGTGAACTAATTAAGTGTGAAGAGAGACATGAAGCCCTCAGAGAACTCATGGACCTTTATCTGAAGATGAAACCCGTGTGGCG
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A.meleagris       AGCGGTTTGTGAGCTAATTCCGTGTGAAGAGAGACATGAAGCCCTCAGAGAACTCATGGACCTCTATCTGAAGATGAAACCAGTGTGGCG
T.gariepensis     AGCAGTTTGTGAACTAATCAAGTGTAAAGAAAGACACGAAGCCCTGAGAGAACTCATGGACCTTTATCTTAAGATGAAACCAGTGTGGCG
T.lomii           AGCAGTTTGTGAATTAATCAAGTGTGAAGAAAGACATGAAGCCCTGAGAGAACTCATGGACCTTTATCTTAAGATGAAACCAGTGTGGCG
X.vigilis         ACCAGTCTGTGAACTAATAAAAAGCGAGGAGAGACATGAAGCCCTCAAAGAGCTCATGGACCTTTATCTTAAGATGAAACCAGTATGGCG
C.polyzonus       AGCAGTCTGTGAACTAATAAAGTGTGAGAAAAGACATGAAGCTCTCAAAGAACTCATGGACCTTTATCTTAAGATGAAACCAGTATGGCG
Zonosaurus.sp.    AGCAGTTTGTGAACTAATCAAGTGTGAGAAGAGACATGAAGCCCTCAAAGAACTCATGGATCTTTATCTTAAGATGAAACCAGTATGGCG
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Index2            111111111222222222233333333334444444444555555555566666666667777777777888888888899999999990
Index3            123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.      ATCTTCATGTCCTGCCAAGGAGTGCCCAGAACTGTTGTGCCAGTACAGTTTCAACTCACAACGTTTTGCTGAGCTCCTATCCACAAAGTT
G.gallus          ATCTTCGTGCCCTGCCAAAGAGTGTCCAGAATTGCTGTGCCAGTACAGCTATAATTCACAGCGTTTTGCGGAGCTCCTGTCTACCAAGTT
C.mydas           GTCTTCATGCCCAGCCAAAGAGTGCCCAGAATTGCTGTGTCAGTATAGCTTCAATTCACAACGTTTTGCTGAACTCCTGTCCACAAAGTT
S.punctatus       GTCTTCATGCCCAGCCAAAGAATGTCCAGAACTGCTATGCCAGTATAGTTTCAACTCACAACGTTTCGCTGAGCTGTTGTCCACAAAATT
B.thieli          GTCATCATGTCCCACTATAGAATGTCCAGAGTTAGTATGTCAATATAGTTTCAATTCTCAACGTTTTGCAGAATTGCTGTCTACAAAGTT
C.rudis           GTCATCATGTCCTACTAAAGAATGTCCAGAGCTTGTATGTCAATATAGTTTCAATTCTCAACGTTTTGCGGAACTGCTATCTACAAAGTT
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C.brevicornis     CTCATCATGTCCTACTAAAGAATGTCCACAGCTAGTATGTCAATATAGTTTCAATTCTCAACGTTTTGCAGAATTGCTGTCTACAAAGTT
C.salinarum       GTCTTCATGTCCCACGAAAGAATGTCCAGAGCTAGTATGTCAATATAGTTTCAATTCTCAACGTTTTGCAGAATTGCTGTCTACAAAATT
P.lesueurii       GTCTTCAAGTCCCACCAAAGAATGTCCAGAGCTAGTATGTCAATATAGTTTCAATTCTCAGCGTTTTGCAGAATTGCTGTCTACAAAATT
P.cocincinus      GTCTTCATGTCCCACCAAAGAATGTCCAGAGCTAGTATGTCAATATAGTTTCAATTCTCAGCGTTTTGCAGAATTGCTGTCTACAAAATT
Hydrosaurus.sp.   GTCTTCATGCCCCACCAAGGAATGTCCAGAGCTAGTTTGTCAATATAGTTTCAATTCTCAGCGTTTTGCAGAATTGCTGTCTACAAAATT
C.calotes         GTCTTCTTGCCCCACCAAAGAGTGCCCAGAGCTAGTATGTCAATACAGTTTCAATTCTCAGCGTTTTGCTGAATTGCTGTCTACAAAATT
J.tricarinata     GTCTTCTTGCCCCACCAAAGAATGCCCAGAGTTAGTATGTCAATATAGTTTCAATTCTCAGCGTTTTGCTGAATTGCTGTCTACAAAATT
P.raddei          TTCTTCATGCCCCACCAAAGAATGTCCAGAGCTAGTGTGTCAATATAGTTTCAATTCTCAGCGTTTTGCAGAATTGCTTGCTACAAAATT
L.belliana        GACTTCATGCCCCACCAAGGAATGTCCAGAGCTAGTATGTCAATATAGTTTCCATTCTCAGCGTTTTGCAGAATTGCTGTCTACAAAATT
U.acanthinurus    ATCTTCGTGTCCCACCAAAGAATGTCCAGAGCTAGTATGCCAATATAGTTTCAATTCTCAGCGTTTTGCAGAGTTACTATCTACAAAGTT
A.paternus        GTCTTCATGCCCCACCAAAGAATGCCCAGAATTAGTATGCCAGTATAGCTTCAATTCTCAACGGTTTGCAGAGCTGCTGGCTACAAAATT
P.mcallii         GTCTTCATGTCCCACCAAAGAATGCCCAGAACTAGTATGCCAGTATAGTTTCAATTCCCAGCGCTTTGCAGAGCTGCTAGCCACAAAATT
S.obesus          GTCTTCATGTCCCACAAAAGAATGCCCAGAACTTGTATGTCAGTATAGTTTCAATTCTCAACGTTTTGCAGAGCTACTGGCTACCAAATT
Hoplocercus.sp.   GTCTTCATGTCCCACCAAAGAATGCCCAGAACTAGTATGCCAGTATAGCTTCAATTCTCAACGTTTTGCAGAGCTACTGGCTACAAAATT
E.laticeps        GTCTTCATGTCCCACCAAAGAATGCCCAGAACTCGTATGCCAGTATAGCTTCAATTCTCAACGTTTTGCAGAGCTACTGGCTACAAAATT
P.somencurensus   ATCTTCATGTCCTGCCAAAGAATGCCCAGAACTAGTATGCCAATATAGTTTCAATTCTCAACGATTTGCAGAGTTGCTGGCTACAAAATT
L.pictus          GTCTTCATGTCCTACCAAAGAATGCCCAGAACTAGTGTGCCAGTATAGTTTCAATTCTCAACGCTTTGCAGAGTTGCTGGCTACAAAATT
U.flaviceps       CTCTTCTTGTCCCAGCAAAGAATGCCCAGAACTAGTATGCCAGTATAGTTTCAACTCCCAACGTTTTGCAGAGCTTTTGGCTACAAAATT
S.crasicaudatus   ATCTACTTGTCCCAGCAAAGAATGCCCAGAGCTAGTATGCCAGTATAGTTTCAATTCTCAACGTTTTGCGGAGCTGCTGGCTACAAAATT
L.carinatus       GTCTTCATGTCCCACCAAAGAATGCCCAGAACTAGTATGTCAGTATAGTTACAATTCTGAACGGTTTGCAGAGCTACTGGCTACAAAATT
B.plumifrons      GTCTTCATGTCCCACCAAGGAATGCCCAGAACTAGTATGCCAGTATAGTTTTAATTCTCAACGTTTTGCGGAGCTGCTGGCTACAAAATT
G.wislizenii      GTCTTCATGTCCAACCAAAGAATGCCCAGAACTAGTATGCCAGTATAGCTTCAATTCTCAACGTTTTGCAGAGCTGCTGGCTACAAAATT
O.cuvieri         GTCTTCATGTCCTACCAAAGAATGCCCAGAACTGGTATGCCAATATAGTTTTAATTCTCAACGTTTTGCAGAGCTGCTGGCTACAAAATT
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E.panamintina     GACTTCATGTCCCACCAAGGAATGCCCAGAACTGGTATGCCAGTACAGTTTCAACTCTCAACGTTTTGCAGAGTTGCTGTCCACAAAGTT
C.enneagrammus    GTCTTCATGTCCCACTAAGGAATGCCCAGAACTGGTATGCCAGTACAGTTTCAACTCTCAACGTTTTGCAGAGTTGCTGTCCACCAAGTT
A.pulchra         GTCTTCATGTCCCACCAAGGAATGCCCAGAACTGGTATGCCAGTACAGTTTCAACTCTCAACGTTTTGCAGAGTTGCTGTCCACAAAGTT
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L.borneensis      GTCTTCATGTCCCACCAAAGAATGCCCAGAACTGGTGTGCCAGTACAGTTTCAATTCTCAACGTTTTGCAGAGTTGCTGTCCACAAAGTT
S.crocodiluris    GTCTTCATGTCCCACCAAGGAATGCCCAGAACTAGTCTGCCAGTACAGTTTCAACTCTCAACGTTTTGCAGAGTTGCTGTCCACAAAGTT
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L.parietale       GTCCTCATGCCCCACAATAGAATGTCCAGAACTTGTATGCCAATATAGCTTCCATTCTCAGCGTTTTGCTGAATTGCTGTCCACTAAATT
E.turkmenicus     ATCTTCATGTCCCAGTAAGGAGTGCCCAGAACTACTATGCCAGTACAGCTTCAACTCCCAACGTTTTGCAGAGTTGCTGTCCACAAAATT
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G.gekko           ATCTTCATGTCCCAGCAAGGAGTGTCCAGAACTACTATGCCAGTACAGCTTCAACTCTCAACGTTTTGCAGAGTTGTTGTCCACAAAATT
P.lindneri        ATCTTCCTGTCCCAGCAAGGAGTGCCCAGAACTTCTATGCCAGTACAGCTTCAACTCCCAGCGTTTTGCAGAATTGCTATCCACAAAATT
Cr.ocellatus      ATCTTCCTGTCCCAGCAAGGAGTGCCCAGAATTGCTATGCCAGTACAGCTTCAACTCCCAACGTTTTGCAGAATTGCTATCCACAAAATT
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C.robustus        ATCCTCATGCCCCACCAAGGAGTGCCCAGAACTTGTATGCCAGTACAGCTTCAACTCTCAACGTTTTGCAGAGTTGCTGTCCACCAAGTT
S.sikkimensis     ATCCTCATGTCCCACCAAGGAGTGCCCAGAACTCGTCTGCCAGTACAGCTTCAACTCCCAACGTTTTGCAGAGTTGTTGTCCACCAAGTT
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P.eggeli          ATCTTCATGTCCCACCAAGGAATGCCCAGAACTAGTATGCCAGTACAGTTTCAACTCTCAACGGTTTGCAGAATTGCTGTCCACAAAGTT
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X.vigilis         GTCCTCATGTCCCACCAAGGAATGTCCAGAACTAGTTTGCCAGTACAGCTTCAACTCTCAACGTTTTGCAGAGTTGCTGTCCACCAAATT
C.polyzonus       TTCCTCAAGTCCTACCAAGGAATGCCCAGAATTAGTATGCCAGTATAGCTTCAACTCTCAACGGTTTGCAGAGCTGCTGTCTACAAAGTT
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Dibamus.sp.       GTCCTCATGTCCCACCAAGGAATGCCCAGAACTGTTATGCCAGTACAGCTTCAACTCTCAGAGCTTCGCAAAGTTGTTGTCCACCAAATT

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Index3            123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
A.mississip.      CAAGTATAGATATGAGGGCAAAATTACAAATTACTTTCATAAAACTCTTGCTCATGTTCCTGAAATCATAGAAAGAGATGGGTCCATTGG
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C.mydas           CAAGTACAGATATGAAGGCAAGATTACAAATTATTTTCACAAAACTCTTGCTCATGTTCCTGAAATTATT????????????????????
S.punctatus       CAAGTACAGATATGAGGGCAAGATTACAAACTACTTTCACAAAACTCTTGCTCATGTCCCTGAAATCATTGAAAGAGATGGCTCCATTGG
B.thieli          TCATTACAGATATGAAGGAAAGATTACCAATTACTTTCACAAGACCCTTGCTCATGTTCCGGAAATTATAGAAAGAGATGGGTCCATTGG
C.rudis           TCATTACAGATATGAAGGAAAGATTACCAATTACTTTCACAAGACCCTTGCTCATGTTCCGGAAATTATCGAAAGAGATGGGTCCATTGG
C.brevicornis     TCATTACAGATATGAAGGAAAGATTACCAATTACTTTCACAAGACACTTGCTCATGTTCCGGAAATTATCGAAAGAGATGGGTCCATTGG
C.salinarum       TCGTTATAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATAGAAAGAGATGGCTCCATTGG
P.lesueurii       TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATAGAAAGAGATGGCTCCATTGG
P.cocincinus      TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATAGAAAGAGATGGCTCCATTGG
Hydrosaurus.sp.   TCGTTACAGATATGAGGGCAAGATTACTAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATAGAAAGAGATGGCTCCATTGG
C.calotes         TCGCTACAGATATGACGGCAAAATTACCAATTACTTTCATAAAACCCTCGCTCATGTTCCAGAAATCATAGAACGCGATGGCTCTATTGG
J.tricarinata     TCGTTACAGATATGACGGCAAAATTACCAATTACTTCCATAAAACCCTCGCTCATGTTCCAGAAATTATCGAACGAGATGGCTCCATTGG
P.raddei          TCATTACAGGTACGAGAGCAAGATTACTAATTACTTTCATAAAACTCTTGCTCATGTCCCGGAGATTATAGAAAGGGATGGTTCCATTGG
L.belliana        TCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCATAAAACCCTTGCTCATGTTCCAGAAATTATAGAAAGAGATGGATCCATTGG
U.acanthinurus    CTGTTACAGATATGAGGGGAAGATCACCAATTACTTTCATAAAACCCTTGCTCATGTTCCAGAAATTATAGAAAGAGATGGCTCCATTGG
A.paternus        CTGTTACAGATATGCAGGAAAAATTACTAATTACTTTCATAAAACCCTTGCTCATGTTCCAGAAATTATTGAACGAGATGGATCTATTGG
P.mcallii         CCATTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTCGCTCATGTTCCAGAAATTATTGAAAGAGATGGCTCTATTGG
S.obesus          CCGTTATAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATTGAGAGAGATGGATCTATTGG
Hoplocercus.sp.   CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACTCTTGCTCATGTTCCAGAAATTATTGAAAGAGATGGGTCTATTGG
E.laticeps        CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAGACCCTTGCTCATGTTCCAGAAATTATTGAAAGAGATGGGTCTATTGG
P.somencurensus   CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAGACCCTTGCTCATGTTCCAGAAATTATTGAAAGAGATGGATCTATTGG
L.pictus          CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATTGAAAGAGATGGATCTATTGG
U.flaviceps       CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTCGCTCATGTTCCAGAAATTATTGAAAGAGATGGATCTATTGG
S.crasicaudatus   CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATTGAGAGAGATGGA????????
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B.plumifrons      CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATTGAAAGGGATGGA????????
G.wislizenii      CCGTTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACGCTTGCTCATGTTCCAGAAATTATTGAAAGAGATGGA????????
O.cuvieri         CCATTACAGATATGAGGGCAAGATTACCAATTACTTTCACAAAACCCTTGCTCATGTTCCAGAAATTATTGAAAGAGATGGATCTATTGG
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E.panamintina     CAGGTACAGATATGATGGCAAGATTACCAATTACTTTCACAAAACACTTGCCCATGTTCCAGAAATTATAGAAAGAGACGGCTCCATTGG
C.enneagrammus    CAGGTATAGATATGATGGCAAGATTACCAATTACTTTCACAAAACGCTGGCCCATGTTCCGGAAATTATCGAAAGAGATGGCTCCATTGG
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H.suspectum       CAGGTACCGATATGATGGCAAGATTACCAATTACTTTCACAAAACTCTTGCTCATGTTCCGGAAATTATAGAAAGAGATGGCTCCATTGG
X.grandis         CAGGTACAGATACGATGGCAAGATTACTAATTACTTTCACAAAACTCTTGCTCATGTTCCGGAAATTATAGAAAGAGATGGCTCCATTGG
V.griseus         CAGGTATAGATATGATGGCAAGATTACCAATTATTTCCACAAAACTCTTGCTCATGTTCCAGAAATTATAGAGAGAGATGGCTCCATTGG
L.borneensis      CAGGTACAGATATGATGGCAAGATTACCAATTATTTCCACAAAACTCTTGCTCATGTTCCAGAAATTATAGAGAGAGATGGCTCCATTGG
S.crocodiluris    CAGGTACAGATATGATGGCAAGATTACCAATTACTTTCACAAAACTCTTGCTCATGTTCCGGAAATTATAGAAAGAGATGGCTCCATTGG
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A.xera            CAGTTACAGATATGTCGGAAAGATTACAAATTACTTTCATAAAACTCTAGCTCATGTTCCAGAAATAATAGAAAGAGATGGTTCCATTGG
C.tigris          CAGTTACAGATACGAAGGCAAGATTACAAATTACTTTCATAAAACTCTTGCTCATGTTCCAGAAATTATAGAAAGAGATGGTTCCATTGG
L.parietale       CAGATATAGATATGAAGGCAAAATTACAAATTACTTTCATAAAACTCTTGCTCATGTTCCCGAAATTATAGAAAGAGATGGTTCCATTGG
E.turkmenicus     CAAATACCGATATGAAGGCAAGATAACAAATTACTTCCACAAAACTCTTGCTCATGTGCCAGAAATTATAGAAAGAGATGGTTCTATTGG
S.shrevei         CAAGTACAGATATGAGGGCAAGATAAGCAATTACTTCCATAAAACTCTTGCTCATGTGCCAGAAATTATAGAAAGAGATGGTTCTATTGG
T.przewalskii     TAAGTACAGATATGAGGGCAAGATAACCAATTACTTCCACAAAACTCTTGCTCATGTGCCAGAAATCATAGAAAGAGATGGTTCTATTGG
G.gekko           CAAGTACAGATATGCAGGCAAGATAACAAATTACTTCCACAAAACTCTTGCTCATGTGCCAGAGATTATAGAAAGAGATGGTTCTATTGG
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C.robustus        CAGTTACAGGTACAAGGGCAAGATTACAAACTACTTTCACAAAACGCTGGCTCACGTCCCCGAAATCATCGAAAGAGACGGCTCCATTGG
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S.anguineus       CAGTTACAGATATGAGGGCAAGATTACAAATTACTTTCACAAAACTCTTGCTCATGTTCCAGAAATTATAGA??????????????????
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A.meleagris       CAGTTACAGGTACAAGGGCAAGATTACAAACTACTTTCACAAAACGCTGGCTCACGTCCCCGAAATCATCGAAAGAGACGGCTCCATTGG
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X.vigilis         CAGTTACAGATATGAAGGCAAGATTACAAATTACTTTCACAAAACTCTTGCTCATGTTCCAGAAATTATAGAAAGGGATGGTTCCATTGG
C.polyzonus       CAGTTATAGATATGAGGGCAAGATTACAAATTACTTTCACAAAACTCTTGCTCATGTTCAAGAAATTATAGAAAGAGATGGTTCCATTGG
Zonosaurus.sp.    CAGTTATAGATACGAGGGCAAGATTACAAATTATTTTCACAAAACTCTTGCTCATGTTCAAGAAATTATAGAAAGAGATGGCTCCATTGG
Dibamus.sp.       CAGTTATCGCTATGAGGGCAAGATTACAAATTACTTCCACAAAACCCTTGCCCATGTTCCCGAAATTATAGAAAGAGATGGCTCCATTGG
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A.mississip.      TGCCTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATTGTTTAGACGTTTCC
G.gallus          TGCTTGGGCAAGTGAAGGAAATGAGTCCGGAAACAAACTATTTAGGAGGTTCC
C.mydas           ?????????????????????????????????????????????????????
S.punctatus       TGCCTGGGCAAGTGAAGGGAATGAGTCTGGGAACAAATTGTTTAGGCG?????
B.thieli          TGCTTGGGCAAGTGAGGGAAATGAATCTGGGAACAAACTGTTCCGGCGTTTTC
C.rudis           TGCTTGGGCAAGTGAGGGAAATGAATCTGGGAACAAACTGTTCCGGCGTTTTC
C.brevicornis     TGCTTGGGCAAGTGAGGGAAATGAATCTGGGAACAAACTGTTCCGGCGTTTTC
C.salinarum       TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTCTTCCGACGTTTTC
P.lesueurii       TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTCTTCCGACGTTTTC
P.cocincinus      TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTCTTCCGACGTTTTC
Hydrosaurus.sp.   TGCTTGGGCAAGTGAGGGAAATGAGTCTGGAAACAAACTCTTCCGGCGTTTCC
C.calotes         CGCTTGGGCAAGTGAGGGAAACGAGTCTGGAAACAAACTCTTCCGGCGTTTTC
J.tricarinata     TGCTTGGGCAAGTGAAGGAAATGAGTCTGGAAACAAACTCTTCCGGCGTTTTC
P.raddei          TGCTTGGGCAAGTGAGGGCAATGAGTCTGGAAACAAACTCTTCCGGCGTTTTC
L.belliana        TGCTTGGGCTAGTGAGGGAAATGAATCTGGGAACAAACTCTTCCGGCGTTTTC
U.acanthinurus    AGCTTGGGCAAGTGAGGGAAATGAATCTGGGAACAAACTCTTCCGGCGTTTTC
A.paternus        TGCTTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTTTTCAGACGTTTTC
P.mcallii         TGCTTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTATTCAGACGTTTTC
S.obesus          TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTTTTCAGACGTTTTC
Hoplocercus.sp.   AGCTTGGGCAAGTGAGGGAAACGAGTCTGGGAACAAACTTTTCAGACGCTTTC
E.laticeps        TGCTTGGGCAAGTGAGGGAAACGAGTCTGGGAACAAACTTTTCAGACGCTTTC
P.somencurensus   TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTTTTCAGACGCTTTC
L.pictus          TGCTTGGGCATGTGAGGGCAATGAGTCTGGGAACAAACTTTTCAGGCGCTTTC
U.flaviceps       TGCTTGGGCAAGTGAGGGAAATGAGTCAGGGAACAAACTTTTCAGACGCTTTC
S.crasicaudatus   ?????????????????????????????????????????????????????
L.carinatus       TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTTTTCAGGCGCTTTC
B.plumifrons      ?????????????????????????????????????????????????????
G.wislizenii      ?????????????????????????????????????????????????????
O.cuvieri         TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTTTTCAGACGCTTTC
O.attenuatus      TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAGCTGTTTAGGCGTTTTC
E.panamintina     TGCTTGGGCAAGTGAGGGCAATGAGTCTGGGAACAAACTGTTTAGGCGTTTTC
C.enneagrammus    TGCTTGGGCAAGTGAGGGAAACGAGTCTGGGAACAAACTGTTTAGGCGCTTTC
A.pulchra         TGCTTGGGCCAGTGAGGGAAATGAGTCTGGGAACAAACTGTTTAGGCGCTTTC
H.suspectum       TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTGTTTAGACGCTTTC
X.grandis         TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAACAAACTGTTTAGGCGCTTTC
V.griseus         TGCTTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTGTTTAGGCGCTTTC
L.borneensis      TGCTTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTGTTTAGGCGCTTTC
S.crocodiluris    TGCTTGGGCAAGTGAGGGAAATGAGTCTGGGAATAAACTGTTTAGGCGCTTTC
Dinodon.sp.       TGCCTGGGCAAGTGAGGGGAATGAGTCAGGCAACAAACTGTTCAGACGCTTTC
R.braminus        CGCGTGGGCAAGCGAAGGCAACGAATCCGGGAACAAATTGTTCAGGCGCTTCC
C.ruffus          TGCCTGGGCAAGTGAGGGAAATGAGTCAGGCAACAAACTGTTCAGACGCTTTC
Agkistrodon.sp.   TGCCTGGGCAAGTGAAGGAAATGAGTCAGGCAACAAACTGTTCAGACGCTTTC
Eremias.sp.       TGCTTGGGCAAGTGAGGGCAATGAATCTGGGAACAAGTTATTCAGGCGCTTTC
B.biporus         TGCTTGGGCTAGTGAAGGAAATGAATCTGGGAACAAACTGTTCAGGCGTTTTC
T.weigmanni       TGCTTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTGTTCAGGCGATTTC
R.floridana       TGCTTGGGCAAGTGAAGGAAATGAGTCTGGAAACAAGCTATTCAGGCGCTTTC
A.xera            TGCTTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTGTTCAGGCGATTTC
C.tigris          TGCTTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTGTTCAGGCGCTTTC
L.parietale       TGCTTGGGCAAGTGAGGGAAATGAGTCTGGCAACAAACTGTTCAGACGCTTTC
E.turkmenicus     TGCTTGGGCAAGTGAAGGAAATGAATCTGGAAACAAACTATTCAGGCGTTTTC
S.shrevei         TGCTTGGGCAAGTGAAGGAAATGAGTCTGGAAACAAACTATTTAGGCGTTTTC
T.przewalskii     TGCTTGGGCAAGTGAAGGAAATGAGTCTGGAAACAAATTATTTAGGCGTTTTC
G.gekko           TGCTTGGGCAAGTGAAGGAAATGAGTCTGGAAACAAACTGTTCAGGCGTTTTC
P.lindneri        TGCCTGGGCAAGTGAAGGAAATGAGTCTGGAAACAAACTATTCAGACGTTTTC
Cr.ocellatus      TGCCTGGGCAAGTGAAGGAAATGAGTCTGGGAACAAACTATTCAGACGTTTTC
L.jicari          TGCTTGGGCAAGTGAAGGAAATGAGTCTGGAAACAAACTATTCAGACGTTTTC
M.aurata          TGCCTGGGCAA??????????????????????????????????????????
C.robustus        CGCGTGGGCAAGCGAAGGCAACGAATCCGGGAACAAATTGTTCAGGCGCTTCC
S.sikkimensis     CGCTTGGGCAAGCGAAGGCAACGAATCCGGGAACAAATTGTTCAGGCGCTTTC
E.inexpectatus    TGCTTGGGCGAGTGAAGGAAATGAATCTGGGAACAAATTGTTCAGGCGCTTTC
E.skiltonianus    TGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATTGTTCAGGCGCTTTC
E.anthracinus     TGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATTGTTCAGGCGCTTTC
S.anguineus       ?????????????????????????????????????????????????????
P.eggeli          TGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATTGTTCAGGCGCTTTC
F.polylepis       TGCTTGGGCAAGCGAAGGAAATGAATCTGGGAACAAATTGTTCAGGCGCTTTC
Ch.ocellatus      TGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATTGTTCAGGCGCTTTC
A.meleagris       CGCGTGGGCAAGCGAAGGCAACGAATCCGGGAACAAATTGTTCAGGCGCTTCC
T.gariepensis     TGCTTGGGCAAGTGAAGGCAATGAGTCTGGGAACAAATTGTTCAGGCGCTTTC
T.lomii           TGCTTGGGCAAGTGAAGGCAATGAGTCTGGGAACAAATTGTTCAGGCGCTTTC
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X.vigilis         TGCTTGGGCAAGTGAGGGAAATGAGTCTGGAAACAAATTGTTCAGGCGCTTTC
C.polyzonus       GGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATTGTTCAGACGCTTTC
Zonosaurus.sp.    GGCTTGGGCAAGTGAAGGAAATGAATCTGGGAACAAATTGTTCAGGCGCTTTC
Dibamus.sp.       TGCTTGGGCCAGTGAAGGGAATGAGTCTGGGAACAAACTGTTCAGGCGCTTTC
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B. *c-mos* (excluded nucleotide positions underlined)

List of Taxa:

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

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Index2            000000000111111111122222222223333333333444444444455555555556666666666777777777788888888888
Index3            123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
Qualifier3        1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1.
C.porosus         TGCAGCAAGAACCGTNTGGCATCACGGCAGAGCTTCTGGGCTGAGCTGAATGTAGCCCAGTTACGTCACAAAAACGTGGTACGTGTTGT
G.gallus          AGCAGCAAAAACCGGCTGGCATCCCGACAGAGCTTCTGGGCTGAGCTGAACGTAGCCCGACTGCAGCATGATAATGTGGTGCGTGTGGT
P.subrufa         TGCAGCAAGAACCGGCTGGCATCGCGGCAAAGCTTCTGGGCTGAGCTGAACGTGGCCCGGCTACACCATAACAATGTGGTACGTGTTGT
S.punctatus       TGTAGCAAGAACCGGCTGGCATCTCNGCAAAGCTTCTGGGCAGAGCTGAATGTGGCTCGTCTATGCCATGAGAATGTGGTGCGTGTTGT
E.multicarinata   TGCAGTAAGAATCATTTGGCATCAAGGCAGAGCTTCTGGGCAGAACTAAATGTGGCATGTCTTGACCACAACAATGTGGTGCATGTAAT
V.salvator        TGCAGTAAGAATCGCTTGGCATCAAGGCAGAGCTTCTGGGCAGAACTAAATGTGATGCACCTTGACCATAACAATGTGGTGCGTATAGT
L.borneensis      TGCAGTAAGAATCGCTTGGCATCAAGGCAGAGCTTCTGGGCAGAACTAAATGTGACACGCCTTGACCATAACAATGTGGTGCGTGTAGT
S.crocodiluris    TGCAGTAAGAATCGTTTGGCATCAAGGCAGAGCTTCTGGGCAGAACTAAATGTGACACGCCTTGACCATAACAATGTGGTGCGTGTAGT
H.suspectum       TGCAGTAAGAATCGTTTGGCATCAAGGCAGAGCTTCTGGGCAGAACTAAATGTGGCACGCCTTGACCATAACAATGTGGTGCATGTAGT
X.grandis         TGCAGTAAAAATCGTTTGGCATCAAGGCAGAGCTTCTGGGCAGAACTAAATGTGGCACGCCTTGACCATAACAATGTGGTGCATGTAGT
U.aegypticus      TACAGTAAGAATCGTTTGGCATCACGACAGAGTTTCTGGGCAGAACTAAATGTCGCACACCTTCACCATAACAATGTGGTGCATGTAAT
L.guentherpetersi TGCAGTAAGAATCGTTTGGCATCACGACAGAGCTTCTGGGCAGAATTAAATGTGGCACACCTTCACCATCACAATGTGGTGCATGTAAT
C.jacksonii       TGCAACAAGAATCGTTTGGCATCAAGACAGAGCTTCTGGGCGGAACTCAATGTGGCATACCTTCACCACAGCAATGTGGTGCGTATAAT
P.lesueurii       TGCAGTAAGAATCGCTTGGCATCACGACAGAGTTTCTGGGCAGAACTCAATGTGGCACATCTTCACCATAACAACGTGGTGCATGTAAT
C.decresii        TGCAGTAAGAATCGCTTGGCATCACGACAGAGTTTCTGGGCAGAACTAAATGTGGCACATCTTCACCATAACAACGTGGTGCATGTAAT
P.cocincinus      TGCAGTAAGAATCGTTTGGCATCACGACAGAGTTTCTGGGCAGAACTAAATGTGGCACATCTTCACCATAACAATGTGGTGCATGTAAT
P.mystaceus       TCCAGTAAGAATCGTTTGGCATCACGACAGAGCTTCTGGGCAGAACTAAATGTGGCACATCTTCACCATAACAATGTGGTGCATGTAAT
C.versicolor      TGCAGTAAGAACCCTCTGGCATCAAGACAGAGCTTCTGGGCAGAACTAAATGTGGCACACCTTCGCCATAGCAATGTGGTGCATGTAAT
S.obesus          TGCAGTAAGAACAGTCTGGCATCACGGCAGAGTTTCTGGGCAGAATTAAACGTGGCACATCTTGAACATAAAAATGTGGTACGTGTAAT
O.sebae           TGTAGTAAGAACAGTTTGGCATCACGGCAGAGTTTCTGGGCAGAATTAAATGTGGCACATCTTGACCATAACAATGTGGTACGTGTAGT
Leiocephalus.sp.  TGCAGTAAGAACAGTTTGGCATCACGACAGAGTTTCTGGGCAGAATTAAATGTGGCCCATCTTGACCATAACAATGTGGTACGTGTAGT
C.cristatus       TGCAGTAAGAATAGTTTGGCATCACGGCAGAGTTTTTGGGCAGAACTGAATGTGGCACATCTCAACCATAACAATGTGGTACGTGTAGT
S.grammicus       TGCAGTAAAAACAGTTTAGCATCACGGCAGAGTTTCTGGGCAGAATTAAATGTGGCACATCTTGACCATCAAAATGTGGTGCGTGTAGT
G.galloti         TGCAGTAAGAACCGTTTGGCATCACGGCGGAGCTTCTGGGCAGAACTAAATGCGGCGCGCCTTGACCACAACCATGTGGTGCGCATAGT
D.zarudnyi        ----------------------------AGAGCTTCTGGGCAGAACTAAATGCAGCACGCCTTGACCATAGCAATGTGGTACGTGTAAT
B.biporus         TGCAGTAAGAACCGTCTGGCATCACGGCAGAGTTTCTGGGCAGAATTAAATGCAGCACGCCTTGACCATAGCAATGTGGTACATGTAAT
A.xera            TGCAGTAAGAACTCTCTGGCATCACGGCAGAGTTTCTGGGCGGAACTAAATGCAGCACGCCTTGACCATAGCAACGTGGTACATATAAT
C.variegatus      -GCAGCAAGAACAGTTTGGCATCAAGGCAGAGCTTCTGGGCAGAACTCAATGTGGCATACCTTGATCATCAAAATGTGGTGCGTGTCGT
P.lindneri        AGCGGTAAGAACAGTTTAGCATCACGGCAGAGCTTCTGGGCAGAATTAAATGTGGCACGCCTTGATCATAAAAACGTGGTGCGTGTAGT
L.burtonis        ----GTAAGAACAGTTTAGCATCACGGCAGAGCTTCTGGGCAGAATTAAATGTGGCACGGCTTGATCATAAAAACGTGGTGCGTGTAGT
T.przewalskii     TGCAGTAAGAACAGTTTAGCATCACGGCAGAGCTTCTGGGCAGAACTAAACGTGGCACGCCTTGATCATCAAAATGTGGTGCGTGTAAT
T.boettgeri       TGCAGTAAGAACAGTTTAGCATCACGGCAGAGCTTCTGGTCAGAACTAAACGTAGCGCGCCTTGATCATCAAAATGTGGTGCGTATAAT
S.shrevei         AGCAGTAAGAACAGTTTAGCATCAAGGCAGAGCTTCTGGGCAGAACTAAATGTGGCACGTCTTGATCATCAAAATGTAGTGCATGTAAT
A.piscivorus      TGCAGTAAGAACCATTTGGCATCACGGCAAAGCTTCTGGGCAGAACTAAATGTAGTACGTCTTGACCATAACAATGTGGTACGCATAGT
D.rufozonatum     TGTAGTAAAAACCATTTGGCATCACGGCAAAGCTTCTGGGCAGAACTAAATGTAGCACGTCTTGACCATAACAATGTGGTACACATAGT
C.ruffus          TGCAGTAAGAACCATTTGGCATCACGACAGAGCTTCTGGGCAGAACTAAATGTAGCACGTCTTGGCCATAACAACGTGGTACGCATAGT
R.australis       TGCAGTAAGAACCATTTGGCATCACGGCGGAGTTTCTGGGCAGAACTAAATGTAGCACGTTTGGGCCATAACAATGTGGTCCGCATAGT
M.delalandii      TGCAGTAAGANNCGTTTGGCATCACAACAAAGCTTCTGGGCAGAACTGAATGTGGCACGCCTTAGTCNTAACAATGTGGTACGTGTAAT
E.skiltonianus    AGCAGTAAGAACCGTTTGGCATCGCGACAAAGCTTCTGGGCAGAACTAAATGTGGCACGCCTTAATCATAACAATGTGGTACGTGTAAT
F.polylepis       TGCAGTAAGAATCGTTTGGCATCACGACAAAGCTTCTGGGCAGAATTAAATGTGGCACGCCTTAGTCATAACAATGTGGTACGTGTAAT
A.meleagris       TGCAGTAAGAACCATTTGGCATCACGACAAAGCTTCTGGGCAGAGCTAAATGTGGCACGCCTTARGCATAACAATGTGGTACGTGTATT
P.eggeli          TGCAGTAAGAACCGCTTGGCATCACGACAAAGCTTCTGGGCAGAACTAAATGTGGCACGCCTTAGTCATAATAATGTGGTACGTGTAAT
X.vigilis         TGCAGTAAGAACCGCCTGGCATCACGACAGAGTTTCTGGGCAGAACTAAATGTGGCTCTTCTTACCCATGACAATGTGGTGCGTGTAAT
C.cordylus        TGCAGTAAGAACCATCTGGCATCACGGCAGAGCTTCTGGGCAGAACTAAATGTGGCGCGCCTTGGCCATAACAATGTGGTGCGTGTAAT
T.quadrilineatus  TGTAGTAAGAACCGTTTGGCATCACGGCAAAGCTTTTGGGCAGAGTTAAATGTAGCATGCCTCAACCATCAGAATGTTGTGCGTGTTAT
B.dorbignyi       TGTAGTAAAAACCGTTTGGCATCAAGGCAAAGCTTCTGGGCAGAACTCAATGTTGCATCCCTTGACCACCAGAACGTTGTGCGCGTGAT
Dibamus.sp.       TGCACTAAGAACCGGCTGGCATCGCGGCAGAGCTTCTGGGGAGAACTAAACGTTGCGCGTCTTGGCCATGACAATGTGGTGCGTGTCGT

Index1            000000000111111111111111111111111111111111111111111111111111111111111111111111111111111111
Index2            999999999900000000001111111111222222222233333333334444444444555555555566666666667777777777
Index3            012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789
Qualifier3        .1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1
C.porosus         GGCTGCCAGCACGTGTGCCCCGGCTGGCCAGGACAGCTTGGGTACTATCATCATGGAATATGCAGGCAGTGTTACCCTGCACCATGTCA
G.gallus          GGCTGCTAGCACGTGTGCCCCTGCCAGCCAGAACAGCCTGGGCACCATCATCATGGAGTATGTTGGCAATGTCACCCTGCACCATGTCA
P.subrufa         AGCTGCCAGCACTAGCGCTCCTGCCAACCAAGACAGCCTGGGAACCATAATCATGGAATATGCGGGCCAGACGACCCTGCACCACGTCA
S.punctatus       AGCTGCCAGTACATGTGCCCCTTCCAGCCAGGATAGTCTGGGCACCATCATCATGGAGTATGCAGGCAATACCACCCTACATCATGTCA
E.multicarinata   AGCTGCCAGCACATGTACCCCTGCCAATCAGGATAGTTTGGGCACTATAATAATGGAATATGTAGCTAACAGCACTCTGCACCATGTTA
V.salvator        TGCTGCCAGCACATTTGCCCCTGTCAATCAGGATAGTTTGGGCACCATAATAATGGAATATGTAGGTAACAGAACTTTGCACCATGTTA
L.borneensis      AGCTGCCAGCACATGTGCCCCTGCCAATCAGGATAGTTTGGGCACCATAATAATGGAATATGTAGGTAACAGCACTCTGCACCATGTTA
S.crocodiluris    AGCTGCCAGCACATGTGCCCCTGCCAATCAGGATAGTCTGGGCACCATAATAATGGAATATGTAGGTAACATCACTCTGCACCATGTTA
H.suspectum       AGCTGCCAGCACATGTGCTCCTGCCAATCAGGATAGTTTGGGCACCATAATAATGGAATATGTAGGGAACAGCACTCTGCATCAGGTTA
X.grandis         AGCTGCCAGCACATGTGCCCCTGCCAATCAGGATTGTTTGGGCACCATAATAATGGAATATGTAGGTAACAGCACTCTGCACCATGCTA
U.aegypticus      AGCTGCTAGTACATGTGCACCTTCCAGTCAGGATACTTTGGGCACCATAATAATGGAATATGTAGGTAACAGTACTCTGCACCATGTTA
L.guentherpetersi AGCTGCTAGCACATGTGCTCCCTCCAGTCAGGATACTTTGGGCACCATAATAATGGAATATGTAGGTAACAGCACTCTGCACCACATTA
C.jacksonii       AGCTGCTAGCACACGTGCCCCCTCCACTCAGGATACTTTGGGCACCATAATAATGGAATATGTAGGTGACAGCACTCTGCACCATGTTA
P.lesueurii       AGCTGCTAGCACATGTGCCCCCTCCAGCCTGGATACTTTGGGCACCATAATAATGGAATATGTAGGTAACAGCACCCTGCACCATGTTA
C.decresii        AGCTGCTAGCACATGTGCCCCCTCCAGCCAGGATACTTTGGGCACCATAATAATGGAATATGTAGGTCATAGCACCCTGCACCATGTTA
P.cocincinus      AGCTGCTAGCACATGTGCCCCCTCCAGCCAGGATACTTTGGGCACCATAATAATGGAATATGTAGGTAACAGCACCCTGCACCATGTTA
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P.mystaceus       AGCTGCCAGCACATGTGCCCCTTCCAGCCAGGATACTTTGGGCACCATAATAATGGAATATGTAGGTAACAGAACCCTGCACCATGTGA
C.versicolor      AGCTGCTAGCACGTGTGCCCCCTCCAGCCAGGATACTCTGGGCACCATAATAATGGAATATGTCGGGAACAGCACCCTGCACCATGTTA
S.obesus          AGCTGCTAGCACATGTGCCCCTGCGAGTCAGGATAGTTTGGGCACCATTATAATGGAATATGTAGGTAACAGCACTCTGCACCACATTA
O.sebae           AGCTGCCAGCACATGTTCCCCTGCCAGTCAAGATAGCGTGGGCACCATAATCATGGAATATGTAGGTAACAGCACTCTGCACCACATTA
Leiocephalus.sp.  AGCTGCAAGTACATGTGCCCCTGCCAGTCAGGATAGTTTGGGCACTATAATAATGGAATATGTAGGTAATAGCACTCTGCACCATGTTA
C.cristatus       CGCTGCTAGCACATGTGCCCCTGACAGTCAGGATAGTTTAGGCACCATAATAATGGAATATGTAGGTAACAGCACTCTGCATCATGTTA
S.grammicus       AGCTGCTAGCACATGTGCTCCTGCTACTCAAGATAGTTTGGGCACCATAATAATGGAATATGTAGGCAGCAGCACTCTGCACCACGCTA
G.galloti         AGCTGCTAGCACCTGTGCCCCTGGCAATCAGGATAGTTTGGGCACCATAATAATGGAATATGTAGGAAATAGCACACTCTACCATGTTA
D.zarudnyi        AGCTGCAAGTACAAGCGTTCCTGCCCATCAGGATAGTTTGGGCACCATAATAATGGAATATGTAGGTAACAGCACTCTGCACCATGTTA
B.biporus         AGCTGCAAGTACAAGTGCCCCTGCCAATCAGGATAGTTTGGGCACCATAATAATGGAATATGTAAGTAACAACACTCTGCATCATGTTA
A.xera            AGCTGCAAGTACAAGTGTCCCTGCCAATCAGGATAGTTTGGGCACCATAATAATGGAATATGTAGGTAACAGCACTCTGCACCATGTTA
C.variegatus      AGCTGCTAGCACAAGCTCCCCTGCTGGGCAGGACAGTTTGGGGACCATAATAATGGAATATGTAGGTAACAGTACTCTGCATCATGTTA
P.lindneri        AGCTGCTAGCACATGGTCACCTGCTGGTCAGGACAGTTTGGGGACTATAATAATGGAATATGTAGGTAACAGCACTTTGCACCATGTTA
L.burtonis        AGCTGCTAGCACATGGTCCCCTGCTAGTCAGGACAGTTTGGGGACTATAATAATGGAATATGTCGGTAATAGCACTTTGCACCATGTTA
T.przewalskii     AGCTGCTAGCACATGTTCCCCTGCTGGTCAGGACAATTTGGGGACCATAATAATGGAATATGTAGGTAACAGCACTCTGCATCATGTTA
T.boettgeri       AGCTGCTAGCACATGTTCCCCTGCTGGCCAAGATAGTTTGGGGACAATAATAATGGAATATGTAGGTAACAGCACCCTGCATCATGTTA
S.shrevei         AGCTGCTAGCACATGCTCCCCTGCTAGTCAGGACAGTTTAGGGACCATAATAATGGAATATGTAGGTAACAGCACTCTGCATCATGCTA
A.piscivorus      AGCTGCTAGCACATGTACCCCTGCTAGTCAGGATAGTTTGGGTACCATAATTATGGAATATGCAGGTAATTGCACTCTACATCATGTTA
D.rufozonatum     AGCTGCTAGCACATGTACCCCTACTAGTCAGGATAGTTTGGGTACCATAATTATGGAATATGCAGGTAATTGCACTCTACATCATGTTA
C.ruffus          AGCTGCTAGCACATGCACCCCTGCTAGTCAGGATAGTTTGGGCACCATAATTATGGAATATGTAGGTAATTGCACTCTACACCATGTTA
R.australis       AGCTGCTAGCACATGGACCCCTGCTAGCCAGGATAGTTTGGGTACCATAATAATGGAATATGTAGGTAATTGCACTTTGTACCATGTCA
M.delalandii      AGCTGCTAGTGCATGTTCTCCTGCCAGTCAGGACAGTTTGGGTACCATCATAATGGAATATGTAAGTAGCAGCACTTTACACCATGTTA
E.skiltonianus    AGCTGCTAGTGCATGTTCTCCTGCCAATCAGGACAGTTTGGGTACCATCATAATGGAATATGTAGGTAACAGCACTTTGCACCATGTTA
F.polylepis       AGCTGCTAGTGCATGTTCTCCTGCTATTCAGGACAGTTTGGGTACCATCATAATGGAATATGTAGGTAACAGCACTTTGCACCATGTTA
A.meleagris       AGCTGCTAGTGCAAGTTCTCCTGCCAGTCAGGACAGTTTGGGTACCATCATAATGGAATATGTAGGTAACAGCACTTTGCATCATGTTA
P.eggeli          AGCTGCTAGTGCGTGTTCTCCTGCCATTCAGGACAGTTTGGGTACCATCATAATGGAATATGTAAGTAACAGCACTCTGCACCATGTTA
X.vigilis         AGCTGCTAGTACATGTGCCCCTGCTAGTCAAAACAGTTTGGGTACCATCATAATGGAGTATGTTGGTAGTGGCACTCTGCATGATGCTA
C.cordylus        AGCTGCTAGTACATGTGCCCCTGCCAGTCAGGATAGTTTAGGTACCATCATAATGGAATATGTAGGCAATGGTACTCTGCACAACGTTA
T.quadrilineatus  TGCTGCTAGCACGTGTGCTCCTCCCAGTCAGGATAGCATGGGCACAATAATCATGGAATATGCAGGTAACAGTACTCTGCACCATATTA
B.dorbignyi       TGCTGCTAGCACATGTGATCCTTCTTGTCAAGACAGCGTGGGCACAATAATCATGGAATACGTAGGCACCAGTACTCTGCACCATATTA
Dibamus.sp.       AGCTGCTAGCACGTGTGCTCCTGCCACTCAGGACAGTGTCGGTACCATTATAATGGAATATGTAGGTAACAGCACTCTGCACCATGTTA

Index1            11111111111111111111122222222222222222222222222222222222222222222222222222222222222222222
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Index3            90123456789012345678901234567890123456789012345678901234567890123456789012345678901234567
Qualifier3        ..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..
C.porosus         TCTATGGTACTGGCTGGGCACAGAGAAAGGAAGATGATGATGGGGGAGGATGCAGCCAAGAGGTCCTGAGCATGCCTGAGTCCCTACGC
G.gallus          TCTACGGCACTAGAGATGCGTGGAGGCAGGGCGAGGAGGAGGAAGGAGGATGTGGGAGGAAGGCTCTGAGCATGGCGGAGGCTGTGTGC
P.subrufa         TCTATGGCACTGGCTGCCTGCAGGGAAAGGGAGAGGATGATGGGGGGGCCTGTGGCAAGGCACCCTTAAGCATTGCTGAGTCCCTGGGT
S.punctatus       TTTATGGGACTGGCTGTGCACAGGGAATAGGAGAGGATGGTAGAGCTGGATGTGGGGGCGAGCCATTGAGCATAGTCCAGTCCCTCACC
E.multicarinata   TCTATGGGACTGGCAGTATGACAGCAAAAAGGAAGAATGATGGTTTTGGATGTGGCCATATGAGTTTGAGCATAGCTCAGGCTCTGAAT
V.salvator        TCTATGGAACTGGCAATATGACAGCAAAAAGTAAGGATGATGGGCCTGGAGATGGCCATGTGTGTTTGAGCACAACTCAGGCTCTGGGC
L.borneensis      TCTATGGGACTGCCAGTATGACAGCAAAAAGTAAAGATGATGGGCTTGGATATGGCCATGTGCATTTGAGCACAGCTCAGGCTSTGGGC
S.crocodiluris    TCTATGGGACTGGTGGTACGACAGCAAAAAGGAAGGATGATGGGCTTGGATCTGGCCATGTGTGTTTGAGCATAGCTCAGGCTCTGGGC
H.suspectum       TCTATGGAACTGGCAATATGGCAGCAAAAAGGAAGGATGATGGTTTTGGATGTGGCCATGCGTGTTTGAGCATAGCTCATGCTCTGGGC
X.grandis         TCTATGGGACTGGCAGTATGACAGCAAAAAGGAAGGAT---GGTTTTGGATGTGGCCATGTGTGTTTGAGCATAGCTCAGGCTCTGGGC
U.aegypticus      TTTATGGAACTGACTGCACAGCAACAGAAAAGAAGGATGATGGGCTTGGATGTGGCCATGCATTTTTTAATTTAGTTCAAGCTATACGC
L.guentherpetersi TCTATGGAAATGGCTGCACATCAACAGAAAGGAAGGATGATGTGCTTGGACATGGCCATGTATTTTTGAATTTAGCTCAGGCAGTACGC
C.jacksonii       TCTATGGAACTGACTGCATAGCAGCAGTAAGGAAGGACGATGAACTTTTACATGGGCCTAAGTTTTTGACTATCGCTCAAGCTGTAAGC
P.lesueurii       TCTATGGAACTGGCTGCACAACAGCAGAAAGAAAGGATGATGGACTTGGATGTGGCTATGCGTTTTTGAATCTAGCTCAGGCTGTACGC
C.decresii        TCTATGGAACTGGCTGCACAGCAACAGAAAGAAAGGATGATGGACTTGAATGTGGCTATGCATTTTTGAATCTAGCTCAGGCTATATGC
P.cocincinus      TCTATGGAACTGGCTGCACAACAGCAGAAAGAAAGGATGATGGACTTGGATGTGGCTATGTGTTTTTGAATCTAGCTCAGGCTGTATGC
P.mystaceus       TCTATGGAACTGGCTGCACAACAGCAGAAAAGAAGGATGATGGGCTTGGATGTGGCTATGTGTGTTTAAGTTTAGCTCAGGCTGTACTC
C.versicolor      TCTACGGAACTGGCTGCATAACAGCAGAAAGGAAGGATGATGGGCTTGGATGTGGCTATGTGCTTTTGGATTTAGCTCAGGCTGTACTC
S.obesus          TCTATGGGACTCACTGCAAGACAGCAACGAAGAAGGATGATGGGCTTGGATGTGGCCATGTGTCTTTGAGCATAACTGAGGCATTAGGT
O.sebae           TCTATGGGACTGACTGCAAGATATCAAAGTGGAAGGATGTTGGGCTTGGAGGTGGCCATGTGCCTTTGAGCATAACTGAGGCATTAAGC
Leiocephalus.sp.  TCTATGGGACTGACTGCAAGACAGCAAAGAGGAAGAATGATGGGCGTGTATGTGGCCATATGTCTTTGAGCATAACTGAAGCATTAGGC
C.cristatus       TCTATGGGACTGACTGCAAAACAGCAAGGAGGAAGGACGATGGGCTTGGATGTGGCCATGTGTCTTTGAGCATAACTAAGGCATTAGGC
S.grammicus       TCTATGGGACTGACTGCAGGGCAGCAAAAAGGAAGGATGATGGGCTTGGATGTGGCCATGTGTGTTTGAGCCTAACTCAGGCCCTGGGC
G.galloti         TCTATGGGACTGGCTGTATGGCAGCAAAAAGGAAAGATGAC---------------------AAGCTGAGTATAGCTCAGTGTCTGGGC
D.zarudnyi        TCTATGGGACTGGCTCTATGGCAGCAAAAGAGAGAGAG------------------------AAGCTGAGTATAGCTCAATCTCTGGGC
B.biporus         TCTATGGAACTGGCTCAATGACAGCAAAAGAGAGAGAT------------------------AAGCTAAGTATAGCTCTGTCTCTGGGC
A.xera            TCTATGGGACTGGCTCTATGGCAGCAAAAGAAAGAGAG------------------------AAGCTGAGTATAGCTCGATCTCTGGGC
C.variegatus      TCTATGGGACTGACTGGATAACAGCCCAAAAGAAGGATGATGGGCTTGGATATGGCCGAGAGTCTTTAAGCATGGGTGAGTGTCTGAGC
P.lindneri        TCTATGGGACTGCCTGTATAACAGCTAAAAGGAAGGATGATGGCCTTGGAGGTGGCCGAGAGCCCTTAAGCCTGCCTCAGTCTCTGAGC
L.burtonis        TCTATGGGACTGACTGTGTAACAGCTAAAGGGAAGGATGATGGTCTTGGAGGTGGCCGAGAGTCCTTAAGCATGCCTCAGTCTCTGAGC
T.przewalskii     TCTATGGGACTAACTGGGTAACAGTCAAAAGGAAGGATGATGGCCTTGGATGTGGCCAAGAGTCCTTAAGCCTTGCTCAGTCTCTGCAC
T.boettgeri       TCTATGGGACTAACTGGTTAACAGCAAAAAGAAAGGATGATGGCCTTGGATGTGGCCGAGAGAACTTAAGCTTAGCTCAGTCCCTGCGC
S.shrevei         TCTATGGGACTAACTGGGTAACAGTCAAAAGGAAGGAAGATAGCCTTGGATGTGGCCAAGAGTCCTTAAGCCTAGCTCAGTCTCTGCAC
A.piscivorus      TCTATGGGACTGGCTATTTAACA---GGAAATAACAATGATATCCTTAAATGTGACCATGAGTTTTTGAGTACAGCTCAGGCTGTCATT
D.rufozonatum     TCTATGGGACTGGTTATTTAACA---GGAAATAAT---GATGGCCTTAAATGTGACCATGGGTTTTTGAGTACAGCTCAGGCTGTCATT
C.ruffus          TCTATGGGACTGGCTATTTAAGA---GGAAAAGAGAATGATGGGCTTAAATGTGACCATGGGTTTTTGAGTACAGCTCAGGCTGTCAGT
R.australis       TCTATGGGACTGGCTGCTTTGCA---AGAAAGAAGGATGATGAGCTTAAATGTGGCTGTGTATTTTTGAGCATAGCTCAGTCTCTTAAG
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M.delalandii      TCTATGGAACTGGAAGTATGACAACAAAAAGGAAGGATAATGGGCTTGGTTGTGGATATGAACCTTTGAGTATAACACAGTCTCTGAGC
E.skiltonianus    TCTATGGGACTGGAAGTATGATAACAAAAAGGAAGGATGATGGGCTTGGTTGTGGCTGTGAACCTTTGAGTATAACACAATCTCTGAGC
F.polylepis       TCTATGGGACTGAAAGTATAACA---AAAAGGAAGAATAATGGGCTTGGTTGTGGCTATAAACCTTTGAGTATAACACAGTCTCTGAGC
A.meleagris       TTTATGGGACTGGTAGTATGACAACAAAAAGGAAAGATAATGGACTTGGATGTGGCCATGAGTCTTTGAGTATAATGCAGTCTCTGAGC
P.eggeli          TCTATGAGACTGAAAGTATAACA---AAAAGGAAGAATAATGGACTTGGTTGTGGTTATGAACCTTTAGGTATAACACAATCTCTGAGC
X.vigilis         TCTATGGGACCAGCAGTATGATAGCAAAAAGAAGGGATGATGGGCTTGGCTGTGGCCAAGAGTCTTTGAGCATAACTCAGTCTCTTAAG
C.cordylus        TCTATGGGACTGGCAGTGCGGTAACAAAAAAGAAAGACAATGAGTTTGGATGTGGTCATGAGTCTCTGAGCATAGCTCAGTCTTTGAGT
T.quadrilineatus  TCTATGGGACTAAATGTGTGGAAACAAAAGGGAAGAGTGATGGACTTGAATATAGCCATGCCAACTTGAACTTAGTGCAGTGTCTGAGC
B.dorbignyi       TCTATGAGACTGAATGTACAAAAACAAAAAGCAAAGGTAATGGACTTGGATGTAGCCATGACAATTTGAACTTAGTGCAGTGTCTGGAG
Dibamus.sp.       TTTATGGGAGTAGCTGCCTGAGAGCAAAAGGAAAGAAAGATGGGTTTGGATGTAGCCAACAGTCCTTGATAATAGCTCAATCTCTGAGC

Index1            22222222222222222222222222222223333333333333333333333333333333333333333333333333333333333
Index2            66777777777788888888889999999999900000000001111111111222222222222333333333344444444445555555
Index3            89012345678901234567890123456789012345678901234567890123456789012345678901234567890123456
Qualifier3        1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1.
C.porosus         TATTCCTGTGACATTGTGACTGGCTTAGCCTTTCTTCACTCACAATGCATTGTGCACCTGGACCTGAAGCCTGCCAATGTGTTCATCAC
G.gallus          TACTCGTGTGACATCGTGACTGGCTTAGCCTTCCTTCACTCGCAGGGCATCGTGCACCTCGACCTGAAGCCTGCCAATATCCTCATCAC
P.subrufa         TATTCTTCTGAGATTGTGACTGGCTTAGTCTTCCTCCACTCCCAGTGCATTGTGCACCTCGACTTGAAGCCTGCTAATGTGTTCATCAC
S.punctatus       TATTCCTGTGACATTGTGACTGGCTTAGTTTTCCTTCATTCACAATGCATTGTGCACCTGGACTTGAAGCCAGCTAACATATTCATCAC
E.multicarinata   TACTCCTGTGACATTGTGGCAGGCTTAATCTTCCTTCACTCCCAGTTGATTGTGCATCTGGATTTAAAACCTGCTAACATATTCATCAC
V.salvator        TATGCCTGTGACATCATGGCAGGATTAGTCTTCCTCCATTCACACTTGATTGTGCATCTGGATTTAAAACCTGCTAACATATTCATCAC
L.borneensis      TATGCCTGTGACATCATGGCAGGATTAGTCTTTCTCCATTCACACCTGATTGTGCATCTGGATTTAAAACCTGCCAACATATTCATCAC
S.crocodiluris    TACTCCTGTGACATTGTGGCAGGCTTAGTCTTTCTCCATTCACAGTTGATTGTGCATCTGGATTTAAAACCTGCTAACATATTCATCAC
H.suspectum       TACTCTCGTGACATTGTGGCAGGCTTAGTCTTTCTCCATTCACAGTTGATTGTGCATCTGGATTTAAAACCTGCTAACATATTCATCAC
X.grandis         TACTCCCGTGACATTGTGGCAGGCTTAGTCTTTCTCCATTCACAGTTGATTGTGCATCTGGATTTAAAACCTGCGAACATATTCATCAC
U.aegypticus      TATTCCTGTGACATTGTAGCAGGTTTACTCTTTCTTCATTCCCAGTTGATTGTGCATTTGGATTTAAAGCCTGCTAACATATTCATCAC
L.guentherpetersi TACTCCTGTGACATTGTAGCAGGTTTAGTTTTTCTCCATTCACAGTTGATTGTTCATTTGGATTTAAAGCCTGCTAACATATTCATAAC
C.jacksonii       TACTCACGGGATATTGTAGCAGGTCTAGTCTTTCTCCATTCACAGTTGATTGTGCATTTGGATTTAAAGCCTGCTAACATATTCATCAC
P.lesueurii       TACTCCTGTGACATTGTAGCAGGTTTAGTATTTCTCCATTCACAGTTGATTGTGCACTTGGATTTAAAGCCTGCTAACATATTCATCAC
C.decresii        TACTCCTGTGACATTGTAGCAGGTTTAGTCTTTCTCCATTCACAGTTGATTGTGCACTTGGATTTAAAGCCTGCTAACATATTCATCAC
P.cocincinus      TACTCTTGTGACATTGTAGCAGGTTTAGTCTTTCTCCATTCACAGTCGATTGTGCACTTGGATTTAAAGCCTGCTAACATATTCATCAC
P.mystaceus       TACTCCTGTGACATTGTAGCAGGTTTAGTCTTTCTCCATTCACAACTGATTGTGCATTTGGATTTAAAGCCTGCTAACGTATTCATCAC
C.versicolor      TACTCCTGTGACATTGTGGCAGGTTTGGTCTTTCTCCATTCACGGTTGATTGTGCACTTGGACTTAAAGCCTGCTAACATATTCATCAC
S.obesus          TATTCCTGTGACATTGCAGCAGGTCTAGTCTTCCTCCATTCACATTTGATTGTGCACTTGGATTTAAAACCTGCTAATATATTCATCAC
O.sebae           TATTCTTGTGACATTGCAGCAGGTCTAGTCTNCCTCCATTCACATTNGATTGTGNATTNGGATTTAAAACCTGCTNATATATTCATNAC
Leiocephalus.sp.  TATTCCTGTGACATTGCAACAGGTCTAGCCTTCCTCCATTCACATTTGATTGTGCATTTGGATTTAAAACCTGCCAATGTATTCATCAC
C.cristatus       TATTCCTGTGATATTGTAGCAGGTCTAGTCTTCCTCCATTCACATTTGATTGTGCATTTGGATTTAAAACCTGCTAATGTATTCATCAC
S.grammicus       TATTCTTGTGACATTGCTGCAGGTCTAGTTTTTCTGCATTCACATTTAATTGCGCATTTGGATTTAAAACCTGCTAATATATTCATCAC
G.galloti         TACTCCTGCGACATTGTGGCAGGCTTAGTATTTCTCCATTCACAGCTGATTGTGCATCTGGATTTAAAACCTGCCAACATATTCATCAC
D.zarudnyi        TACTCCTGCAACATTGTGGCAGGCTTAGTGTTTCTGCATTCACAGCTGATTGTGCATCTGGATTTAAAACCTGCCAACGTATTCATCAC
B.biporus         TACTCCTGCAACATTGTGGCAGGCTTAGTGTTTCTCCATTCACAGTTGATTGTGCATCTGGATTTAAAACCTGCCAACATACTCATCAC
A.xera            TACTCCTGCAACATTGTGGGAGGCTTAGCATTTCTCCATTCACAGTTGATTGTGCATCTGGATTTAAAACCTGCCAACATATTCATCAC
C.variegatus      TACTCCTGTGACATTGTGGCAGGCTTAGTTTTTCTCCATTCACAGTTAATTGTGCACCTGGACTTAAAACCTGCCAACATATTCATAAC
P.lindneri        TACTCCTGTGACATTGTGGCAGGCTTAGCCTTTCTCCATTCCCAGTTAATTGTGCACCTGGATTTGAAACCTGCCAACATTTTCATCAC
L.burtonis        TATTCCTGTGACATTGTGGCAGGCTTAGCCTTTCTCCATTCCCAATTAATTGTGCACCTGGATTTAAAACCTGCCAACATATTCATCAC
T.przewalskii     TACTCCCGTGACATTGTGACAGGTTTAGTCTTTCTCCATTCACAGTCAGTTGTGCACCTGGATTTAAAACCTGCTAATATATTCATCAC
T.boettgeri       TACTCCTGTGACATTGTGGCAGGTCTAGTCTTCCTCCATTCACAGTTAATTGTGCACCTGGATTTAAAACCTGCTAACATATTCATCAC
S.shrevei         TATTCCTGTGACATTGTGGCTGGTTTAGCCTTTCTCCATTCACAGTTAATTGTGCACCTGGATTTAAAACCGGCTAACATATTCATCAC
A.piscivorus      TACTCCCATGATATTGTGGCAGGGTTAATGTTTCTTCATTCTCAGTTAATTGTGCATCTGGATTTAAAACCTGCTAACATATTCATCAC
D.rufozonatum     TACTCCTGTGATATTGTGGCAGGATTAATGTTTCTCCATTCTCAGTTAATTGTGCATCTGGATTTAAAACCTGCTAACATATTCATAAC
C.ruffus          TACTCCTGTGATATTGTGGCAGGATTAATGTTTCTCCATTCACAGTTAATTGTGCATCTGGATTTAAAACCTGCTAACATATTCATCAC
R.australis       TACTCCCGTGACATTGTGGCAGGGTTAATGTTTCTCCATTCACAGTTAATAGTGCATCTGGATTTAAAACCAGCTAACATATTCATCAC
M.delalandii      TACGCATGTGATATAGTGGCAGGCTTGGTCTTTCTCCATTCACAATTAATTGTGCATCTTGATTTAAAACCTGCCAATATATTCATCAC
E.skiltonianus    TACTCGTGTAACATTGTGGCAGGCTTGGTCTTTCTCCATTCACAATTAATTGTGCATCTGGATTTAAAACCTGCCAACATATTCATCAC
F.polylepis       TACTCGTGTGACATTGTGGCAGGCTTGGTCTTTCTCCATTCACAACTAATTGTGCATCTGGATTTGAAACCTGCTAACATATTCATCAC
A.meleagris       TACTCATGTGATATTGTGGCAGGCTTGGTCTTTCTCCATTCACAATTAATTGCACATCTGGATTTAAAACCTGCCAATATATTCATCAC
P.eggeli          TACTCGTGTGACATTGTGGGAGGCTTGGTCTTTCTCCATTCACAATTAATTGTGCATCTGGATTTAAAACCTGCCAACATATTCATCAC
X.vigilis         TACTCGTGTGACATTGGGGCAGGCTTGGTCTTTCTCCATTCACAGTTGATTGTGCATCTGGATTTAAAACCTGCCAATGTATTTATCAC
C.cordylus        TATTCATGTGATGTTGTGGCAGGCTTAATTTTTCTCCATTCACAGTTAATTGTGCACTTGGATTTAAAACCTGCCAACATATTCATCAC
T.quadrilineatus  TACTCCTGTGACATTGTSTCAGGCTTAGTTTTTCTTCATTCTCACCTGATAGTTCACCTGGATTTAAAACCTGCCAACATATTCATCAC
B.dorbignyi       TACTCTTGTGACATTGCGTCAGGCTTAGTTTTTCTTCATTCTCAACTAATAGCCCATCTGGATTTAAAACCTGCCAACATTTTCATCAC
Dibamus.sp.       TACTCGTCAGATATCATGGCAGGCTTAGTCTTTCTCCATTCACAGTTGATTGTCCATCTGGATTTAAAACCTGCTAACATATTCATCAC

Index1            33333333333333333
Index2            55566666666667777
Index3            78901234567890123 4
Qualifier3        .1..1..1..1..1..1.
C.porosus         TGAGCAGGGGTTGTGCAA
G.gallus          TGAGCACGGAGCGTGCAA
P.subrufa         CGAGCAGGG?????????
S.punctatus       TGAGCAGGATGTCTGCAA
E.multicarinata   AGAACAAAATGTTTGCAA
V.salvator        AGAACAAAATGTTTGCAA
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L.borneensis      AGAACAAAATGTTTGCAA
S.crocodiluris    AGAACAAAATGTTTGCAA
H.suspectum       AGAACAAAATGTTTGCAA
X.grandis         AGAACAAAATGTTTGCAA
U.aegypticus      AGAACAAAATGTCTGCAA
L.guentherpetersi AGAACATAATGTTTGCAA
C.jacksonii       AGAACAGAATGTTTGTAA
P.lesueurii       AGAACAAAATGTTTGTAA
C.decresii        AGAACAAAATGTTTGTAA
P.cocincinus      AGAACAAAATGTTTGTAA
P.mystaceus       AGAACAAAATGTTTGCAA
C.versicolor      GGAACACAATGTTTGCAA
S.obesus          AGAACAAAATGTTTGCAA
O.sebae           ANAACAAAATGTTTGCAA
Leiocephalus.sp.  AGAACAAAAGGTTTGCAA
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
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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 somencurensus*
23. *Liolaemus pictus*
24. *Urocentron 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 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 gariepensis*
68. *Typhlosaurus lomii*
69. *Xantusia vigilis*
70. *Cordylus polyzonus*
71. *Zonosaurus sp.*
72. *Dibamus sp.*

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Index2             00000000011111111112222222222333333333344444444445555555555666666666677777777778888888888
Index3             12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789
Qualifiers1        ND1......................................................................................
Qualifiers2        1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1.
A.mississippiensis AACTTCCTACCCATAACACTAACCCTCTGCCTATGACACTCATCAGTGCCAATATCAATGTTTGGACTACCACCAATGACT--------
G.gallus           AACTTCCTCCCCCTAACCCTAGCCTTATGCCTCTGACATACCAGCATACCAATCAGCTACGCCGGCCTCCCCCCAATC-----------
C.mydas            AACTTCCTCCCAATCACTCTTGCACTATGCCTATGACATATTTCCATACCAATTACCTTCTCAGGACTCCCACCTATACCA--------
S.punctatus        AAACTACTCCCATCACACCGTACATTATGCCTTTGACACACATCCATGCCTATTACCTTATCAGGGGTTCCCCCAGCAATT--------
B.theili           CAATTTTTACCACTAACACTAGCCATATGCTTAATTTACTCAACAATACCACTTACACTAGCAGCCCTGCCA-----------------
C.rudis            CAATTTCTTCCACTAACACTAGCCATATGTTTAATTTACACAACCCTACCTCTATCACTAACAGCCCTTCCA-----------------
C.brevicornis      CAGTTTTTACCACTAACACTAGCCCTATGTTTACTCTACACAATAACACCCCTTGCACTAACAGCACTCCCA-----------------
C.salinarum        CAATTCCTCCCAATTACCCTAGCATCGTGCATCCTGTTCACTACAATTCCCATAACCATAACCTCAATACCACCAAACAGCTTCTC---
P.leusterii        CAATTTCTCCCAATCACCCTGGCCTCCTGCCTCCTATTCACCATCACACCCATAACCATAGCCTCATCCCCACCAAACAACTTCCA---
P.cocincinus       CAATTCCTTCCAATAACCCTAGCCTCCTGCCTTCTATATACAACTATACCTCTAGCCATAGCTTCACTCCCACCAAACAACCTCGC---
Hydrosaurus.sp.    CAATTCCTCCCAATCACACTATCAATGTGCGTACTCTACACTATTCTACCACTATCAGCTGCAACCCTACCACCAAACAACTACAC---
C.calotes          CAATTTCTACCACTTACACTAGCTATATGCCTCTTATTTACCATCTTACCCCTATCAACAGCCTCAGCCCCACCAATAAACTATT----
J.tricarinata      CAATTCCTCCCAATTACACTAGCTGCATGCCTGCTTTATACTATACTACTCCTTTCAACATCATCCATCCCACCAAACAACTACAC---
P.raddei           CAATTCCTACCAATAACCCTAGCATCTTGCTTATTATACACAATAATACCTACATCAATTATAGCTCTCCCCCCAACAACCCTAAA---
L.belliana         CAATTCCTACCAATGACTTTAACAATATGCCTACTGTACACTATTGCTCCTACAGCCCTAGCCTCTCTACCACCAAACAC---------
U.acanthinurus     CAATTCCTACCCCTGACCTTAGCCATATGCCTAATATACACAAACCTCCCATCAGCCCTAGCTGCTCTACCACCAGACAACCA------
A.paternus         CAATTTCTCCCAATTACTTTAGCTTTATGCCTATGACACACAACACTTTTAACGTCCATATCTTTTATTCCTCCACAA-----------
P.mcallii          CAGTTTCTTCCAATTACATTAGCACTTTGCCTATGACACACATCACTACCAATCTCAACATTTGGACTCCCACCACAACAA--------
Sauromalus.obesus  CAATTTCTGCCCCTCACACTAGCCCTATGCCTATGACACATCTCACTCCCAACCTCAACATTCGCACTACCCCCAATTAAC--------
Hoplocercus.sp.    CAATTTCTGCCCCTTACCCTAGCCCTATGCCTATGGCACATCTCCATTCCAACCATAACATTTGCCCTGCCACCACTCCCA--------
E.laticeps         CAATTCCTCCCACTAACATTAGCCTTATGCCTCTGACACACAGCAATACCTCTATCAATATTTGCCACCCCCCCCCACTAC--------
P.somuncurensis    CAATTTTTACCATTAACACTAGCAATATGCCTATTACACACCTCAATACCAACTTCAATATTTGCTCTTCCACCACAA-----------
L.pictus           CAATTTTTACCATTAACACTAGCAATGTGTCTATGACACACCTCAATACCAATTTCACTACTAGCCACCCCCCCCATAACA--------
U.flaviceps        CAATTCTTACCTATCACATTAGCCCTGCTCATTTGACACACCTCATTTCCTGTCTCAATATTCGGTCTACCCCCTCAAGAA--------
S.crassicaudatus   CAATTCCTACCAATCACACTTGCCCTGTGCTTATGACACACGTCCCTCCCAATCGCAATATTTTCCCTCCCCCCACAA-----------
L.carinatus        CAATTTTTACCAATTACATTAGCCATGTGCCTATGACACACCACACTTCCAATCGCAATATTTGCTTTTCCCCCACAA-----------
B.plumifrons       CAATTTTTACCAATCACCCTAGCCCTCTGCCTATGACACGTAGCCCTTCCAATCTCCACATTTGCCCTCCCCCCACAACTA--------
G.wislizenii       CAATTCCTACCGTTAACACTAGCCCTATGCCTGTGACACATCTCCATGCCAATTTCTATGTTCTCTTTACCACCCCAGTCG--------
O.cuvieri          CAATTTCTTCCAATCACATTAGCCCTATGCCTATGGTATACCTCACTCCCAACAATAACCTTCACCCTACCCCCACAACAA--------
O.attenuatus       CAATTCCTACCAATTACCCTAGCCCTCTGCCTGTGACACATTTCATTCCCAATCTTCCTACTAGGGGTCCCACCAGTC-----------
E.panamintina      CAATTCCTACCAATTACCCTCGCCTTATGTCTATGACACATCTCACTTCCAGTTTTCTTATCAGGAACCCCTCCAACAAAC--------
C.enneagrammus     CAATTCTTACCCATTACGCTAGCCCTATGCCTATGATATATTTCACTTCCAATTTTTTTAGCAAGCATCCCCCCAACACACTCCCAT--
A.pulchra          CAATTCCTACCAATAACACTAGCCCTCTGCCTATGACATATCTCCTTCCCCCTATTCCTATCAGCAATCCCCCCAATC-----------
H.suspectum        CAATTCTTGCCAATTACATTGGCGCTATGTCTCTGACATATCTCATTTCCAATTTCACTCTCCGGACTACCACCAATAATTACA-----
X.grandis          CAATTCCTTCCCCTCACCCTAGCCTTATGCCTCTGACACATCTCCTTCCCTACCTTTCTCGCAGGCCTCCCCCCACAA-----------
V.griseus          CAATTCCTACCCCTCACAATGGCCCTCTGCCTCCTACAAACCTCCCTCACAATTTCACTCGGAGGACTACCTCCCCTACCCAAC-----
L.borneensis       CAATTCCTACCCCTAACTCTCGCAATGTGCCTGTGACATACGACCATCCCAATTGCCTTCTCAGGCTTGCCCCCACTCACC--------
S.crocodilurus     CAATTTCTACCAATCACACTCGCTCTATGCCTATGACATATATCATTTCCAATCTCGATGTCAGGACTTCCCCCAAAC-----------
D.semicarinatus    CAATATCTTCCACTCACCCTAGCTATATACCTTCTAAACACCTCCACTAGTATAGCTTTATGCGGTACACCCCCACAA-----------
R.braminus         ?????????????????????????????????????????????????????????????????????????????????????????
C.ruffus           ?????????????????????????????????????????????????????????????????????????????????????????
Agkistrodon.sp.    ?????????????????????????????????????????????????????????????????????????????????????????
E.grammica         CAGTTTCTCCCAATTACACTAGCACTTTACCTGTGATACATTGCACTTCCCATTACATTAGCAGGTCTCCCACCTATAAAC--------
B.biporus          CAATTCCTTCCCCTATCCCTCGCCATTTGCCTATGACACACCTGCTTACCAATTGCCGTTGCTGGCCAACCACCAAGCAAC--------
T.weigmanni        CAATTTCTTCCTCTTACACTCGCCACCTGTCTCTGACACACAACAATGCCAATCACACTAAACGGTCTGCCCCCTTCATAT--------
A.xera             CAATTTCTGCCATTTACACTTACAATATGCCTATGACACGCGACTATGCCACTCACCACAACCTGCCTACCCCCCGCCTAC--------
C.tigris           CAATTTCTACCTATCACCCTAGCACTATGTCTATGACACACCTCGTTTCCTATCTCCCTATCAGGCCTCCCACCAAAC-----------
L.parietale        CATTTTTTACCCATCACATTAGCACTCTGCCTCTGACACGCCGCTCTACCCATCATATTGGCAGGCCTCCCACCAAACAAC--------
E.turkmenicus      AATTTTTTACCATTAACTCTTGCTCTTCTTCTCTGATATATTTCAATTACGGTATCAACAGCCAGCACCCCCCCTCTCCTA--------
S.shrevei          AATTTTTTACCACTCACACTGGCACTATGCCTATGACACACACTAATCCCCATCATTCTCGCCGGGGCCCCACCAATGGCC--------
T.przewalskii      AATTTCCTCCCAATCACACTTGCCTTATACCTATTCTACCTTTCAACCCCAATTGCACTATCAAGCGTACCCCCTCTATCAGACCTTGG
G.gecko            AATTTCCTACCCATTACCTTAGCCCTATGCCTGTGACATATCTCAATCCCCATTGCCCTCGCAGGCACCCCCCCAATAAATCAA-----
P.lindneri         AACTTCTTACCACTAACACTAGCCGCATGCCTATGACATATTTCCATTCCTCTATCCTCGACGGGCCTGCCACCAATACCACAA-----
Cr.ocellatus       ACCTTCCTTCCACTAACCTTAGCTCTATGCCTATGACACATTTCACTCCCCCTCTCCCTCTCAGGACTCCCCCCAAACACCCAA-----
L.jicari           AACTTTCTCCCAATTACACTCGCCCTCTGCCTCATACACTCAACCCTCCCAATTTCCCTCTCAGGACTTCCTCCAACCACACTA-----
M.aurata           AACTTCCTACCTCTAACCTTAGCCCTATTCCTGTGACACACCACATTTCCAATCACGCTATCAGGATTACCCCCACAA-----------
C.robustus         AACTTTCTACCAATTACCCTAGCCCTATTCATATGACATGTCTCATTTCCAACAATACTAGCAGGTCTTCCCCCACAA-----------
S.sikkimensis      AACTTCCTGCCTATCACCCTAGTTATATTCTTATGACACACCTCCTTCCCAATAATACTGTCAGGGCTCCCACCTCAG-----------
E.inexpectatus     AACTTCCTACCTATCACACTAGCCCTCTTTCTATGACACACCTCATTCCCAACAACGCTTTCCGGGCTTCCACCACAA-----------
E.skiltonianus     AACTTCCTCCCACTCACACTCGCCCTATTTATATGACACGCCTCATTTCCAACAATACTCTCCGGACTTCCCCCACAA-----------
E.anthracinus      AACTTTCTCCCAATCACACTCGCCCTATTTCTATGACACACCGCACTCCCAACATCCTTCTCTGGACTCCCCCCCCAA-----------
S.anguineus        GCATTCTTGCCCCTAACGCTAGCCATATTCCTATGACACACATCATTCCCAACGATGTTATCCGGCCTGCCTCCACAA-----------
P.eggeli           ACAATCTGGCCTGTAATTCTTGCCATATTCCTATGACACACCTCATTCCTACCAATATTATTTGGGCTGCCCCCGCAA-----------
F.polylepis        ACATTTTTGCCAATCACATTAGCTATGTTCTTATGACACACATCATTTCCAACAACCCTTTCTGGAATCCCCCCACAA-----------
Ch.ocellatus       ACATTCCTGCCACTAACCCTAGCCATATTCCTATGGCACACTTCCTTCCCGACTACACTATCTGGATTACCACCACAA-----------
A.meleagris        AACTTCCTACCACTAACACTTGCCCTATTCCTATGACACTCCTCATTTCCAACAACAATAGCAGGATTGCCACCACAACAA--------
T.lomii            AGTTTCCTACCACTAACACTTGCCATTTTCCTATGACAAACCTCATTCCAAACAACCACGGCAGGACTACCACCACAA-----------
T.gariepensis      AACTTCCTACCACTAACACTTGCCCTTTTCCTATGACACGCATCATTCCCAACGACCTTAGCAGGACTACCACCACAA-----------
X.vigilis          AACTTCCTACCCCTAACACTAGCTCTTTGCCTATGACATATCTCATTTCCAATTACACTAACAGGACTCCCCCCCTAC-----------
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C.polyzonus        AACTTCCTTCCCTTAACCCTGGCCCTTTGTCTTCTCCACATCTCCCTACCAATCACCCTCTCAGGACTCCCCCCTCAACAC--------
Zonosaurus.sp.     AAATTTCTACCGCTGACCCTAGCACTATGCTTACTACACGTATCCCTCCCTATCGCACTATCAGCCCTCCCACCACAATAC--------
Dibamus            AACTTCCTACCTATTACGCTAGCCATATGCATGTGACACGCCTCATTCCCAATCACCATATCAGGACTTCCCCCAACAAC--------

Index1             00000000001111111111111111111111111111111111111111111111111111111111111111111111111111111
Index2             99999999990000000000111111111122222222223333333333444444444455555555556666666666777777777
Index3             01234567890123456789012345678901234567890123456789012345678901234567890123456789012345678
Qualifiers1        ........................ILE..............................................................
Qualifiers2        .1......................AA>>>>>..D>>>.........D>>>.AC>>>..COD..AC>>>.....T>>>>.......T>>>
A.mississippiensis -TA---------------------GGATCCGTGCCTGAACCATA--AAGGGCTACTTTGATAGAGTAGATAATAGGGGTTAGAGCCCCC
G.gallus           -TAA--------------------GGAAGCGTGCCTGAACAAA---AAGGATCACTATGATAAAGTGAACAT-AGAGGTATAACCCCTC
C.mydas            -TA---------------------GGACACGTGCCTGAACA-----AAGGATCACCTTGATAGGGTGAATAATAGAGGTTAAAATCCCC
S.punctatus        -T----------------------GGACATGTGCCTGAATA-----AAGGATCACTTTGATAGAGTGAACTAAAAAGGTTTAAACCCTT
B.theili           ------------------------GGAAAGGTGCCCGAGACC----AAGGACTACTTTGATAAAGTAAAAAC-AGAGACACAA--TCTC
C.rudis            ------------------------GGAAGTGTGCCCGAGAAT----AAGGAATACTTTGATAGAGTAAACAC-AGAGACACAAC-CCTC
C.brevicornis      ------------------------GGAAGCGTGCCCGAGAACT---AGGGACTGCTTTGATAGAGCAGACAC-AGAGACACAAA-CCTC
C.salinarum        ------------------------GGAAGCGTGCCTGAAAACCT--AAGGGCTACTTTGATAAAGTATATATGGAAACAACAAC-ATTC
P.leusterii        ------------------------GGAAGCTTGCCTGAAACTAT--AAGGACTACTTTGATAAAGCAGACATGGAATTAAACCATACTC
P.cocincinus       ------------------------GGAAGCGTGCCCGAAACCAC--AAGGACTACTTTGATAAAGTAAACATGGAGCTCACAAT-ACTC
Hydrosaurus.sp.    ------------------------GGAAATGTGCCTGAGCAGA---AGGGGCTATTTTGATGTGATAGATATAGAGACCAACCACCCTC
C.calotes          ------------------------AGAAGTGTGCCCGAATAAC---AAGGACTATTTTGATAAAATAGACACAGAGACCAAAA--TCTC
J.tricarinata      ------------------------AGAAGTGTGCCCGAAGAACAC-AAGGGCCATTTTGATAAAATAGACATAGAGCCACCTAC-ACTC
P.raddei           ------------------------AGAAGTGTGCCCGAGAT-----AGGGGTTATTTTGATGAAATAAACACAGAGTAACATT--ACTC
L.belliana         ------------------------GGAGACGTGCCCGAGAATC---AGGGACTATTTTGATAAAATAGACACAGAGACCAACC--CCTC
U.acanthinurus     ------------------------GGAAGCGTGCCTGATTA-----AAGGGCTGTCTTGATAAGACAAACATAGAGGGCCAACATCCTC
A.paternus         -T----------------------GAAAATGTGCCTGAAATTT---AAGGATAACTTTGATAGAGTTAACAATAGAGGCTAGAACCCTC
P.mcallii          -TAAGAT-----------------GGAAGTGTGCCCGAATTTT---AAGGGTTACTTTGATAGAGTAAATAATAGAGGTTAAAATCCTC
Sauromalus.obesus  -TAGCTCAAAA-------------GGAAATGTGCCCGAGCATC---AAGGATTACTTTGATAGAGTAAATTACAGAGGTTTAAATCCTC
Hoplocercus.sp.    -TAAC-------------------GGAAGCGTGCCTGAACTA----AAGGACTACTTTGATAGAGTAAAACATAGCGGTTTAAGCCCGC
E.laticeps         -TAA--------------------GGAAGTGTGCCCGAACAACT--AGGGACTACTTTGATAGAGTAGACAATAGAGGTTAAAACCCAC
P.somuncurensis    -TAAAA------------------GGAAATGTGCCCGAGATCAT--AAGGACTACTTTGATAGAGTACGACACAGAGACTAAGACCCTC
L.pictus           -TA---------------------GGAAATGTGCCCGAGATACT--AAGGGATACTTTGATAGAGTATATTACAGAGACTAAAC-CCTC
U.flaviceps        -TA---------------------GGAAATGTGCCTGAGCCTT---AAGGGTTACTTTGATAGAGTGAAACACAGAGAATAAAA-CCTC
S.crassicaudatus   -TAACCAT----------------GGAAGCGTGCCTGAGCTAC---AAGGATTACTTTGATAGAGTAAACCACAGAGGTCTAAACCCTC
L.carinatus        -TAACA------------------GGAAATGTGCCCGAGAACC---AAGGACCACTTTGATAGAGTGTTACACAGGGGTGAAACTCCCC
B.plumifrons       -TAAA-------------------GGAAATGTGCCTGAACACA---TAGGGCTACTTTGATAGAGTAGAATATAGGGGTTAAAATCCAC
G.wislizenii       -TAAAA------------------GGAAACGTGCCTGAACTACT--AAGGATTACTTTGATAGAGTAAACAATAGAGGTTAAAATCCTC
O.cuvieri          -TA---------------------GGAAATGTGCCTGAGTATTT--AAGGGTTACTTTGATAGAGTAAACCACAGGGACTAAAC-CCCC
O.attenuatus       -TAACCCACCCCACCAA-------GGAAACGTGCCTGAATTACA--AAGGATTATTGTGATAGAATAAACTACAGAGGTTAAAATCCTC
E.panamintina      -TAGAC------------------GGAAGTGTGCCTGAACTA----AAGGACTACCTTGATAGAATAGACAACAGAGGTTAAAATCCTC
C.enneagrammus     -TAAC-------------------GGAAATGTGCCTGAATTA----AAGGACTACTTTGATAGAGTAAAAAATAGAGGTTAAAATCCCC
A.pulchra          -TAACACTAAA-------------GGAACTGTGCCTGAACTA----AAGGGTTACTTTGATATAATAAACAATAGAGGTTACAGTCCTC
H.suspectum        -TA---------------------GGAGATATGCCTGAACTA----AAGGGCTACTTTGATAGAGTAAAAAATAGGGACTTAGC-CCCC
X.grandis          -TAATCCTA---------------GGAAATGTGCCTGAATTA----AAGGACTACTTTGATAGAGTAACTAACAGAGGTTTAAACCCTC
V.griseus          -T----------------------GGAAATGTGCCTGAACTA----AAGGGCTATTTTGATAGAATAGACCATAGGAACAACAC-TTCC
L.borneensis       -TAAGA------------------GGAAATGTGCCCGAAATT----AAGGATTATTTTGATAGAATACACCACAGGAGTTAAAAATCTC
S.crocodilurus     -AGACCCA----------------GGAAATATGCCTGAAACT----AAGGATTACTTTGATAGAGTACAC-ATAGGGGTTAAAATCTCC
D.semicarinatus    -T----------------------GGGGGTGTGCCCGAGT------AGGGACTACCTTGATAGAGTAG-ACACGGAACCATAAAACTCC
R.braminus         ?????????????????????????????????????????????????????????????????????????????????????????
C.ruffus           ?????????????????????????????????????????????????????????????????????????????????????????
Agkistrodon.sp.    ?????????????????????????????????????????????????????????????????????????????????????????
E.grammica         -TAGCACCC---------------GGATGTGTGCCCGAGTATTT--AAGGGTTACTTTGATAGAGTAAATTACAGGGATTAATTACCCC
B.biporus          -TA---------------------GGACCCGTGCCCGAGACCAA--AAGGACTACTTTGATAGAGTATGAAC-AGGGGTTTAAATCCCC
T.weigmanni        -TA---------------------GGAAGCGTGCCCGACCTAT---AGGGGCTACTTTGATAGAGTAGACCACAGGAGTTTAAATCCCC
A.xera             -TA---------------------GGAAGCGTGCCTGAATATA---AAGGGCTACTTTGATAGAGTAGACCATAGGACTTACC--CTCC
C.tigris           -TAA--------------------GGAAATGTGCCCGAGAATTT--AAGGATTACTTTGATAGAGTAAAATACAGGGACACCATAACCC
L.parietale        -T----------------------GGAAATGTGGCCGATGAT----AAGGTTTACTTTGATAGAGTAATATATAGGGACCCAAACCCCC
E.turkmenicus      -TAAAA------------------GGAAGCGTGCCTGAATGACA--AAGGACTACTTTGATAGAGTATACTAAATGGGTTCAATTCCCC
S.shrevei          -TAACCAACGAACTT---------GGAAGCGTGCCGGAAAACAAT-AAGGACTACTTTGATAGAGTAAACCATGGAGACCACAACACTC
T.przewalskii      ATA---------------------GGAAGTGTGCCCGAACAGCAC-AAGGACTACTTTGATAGAGTACACCACGGAGGTTAAAATCCCC
G.gecko            -T----------------------GGAAATGTGCCCGAACAGCAT-AAGGACTACTTTGATAGAGTATTTTATAGGGGTTAAATCCCCC
P.lindneri         -TAAA-------------------GGAAATGTGCCCGAGCATAT--AAGGGCTACTTTGATAGAGTAGATTACAGAGACTCAACCCCTC
Cr.ocellatus       -TAACAGC----------------GGAAGTGTGCCCGAGTTT----AAGGAATACTTTGATAGAGTACATCACAGGGATTAAACCACCC
L.jicari           -TAGTTCAA---------------GGACGCGTGCCTGAACACTT--AAGGACTACTTTGATAGAGTACACTACAGGGGTTAAAATCCCC
M.aurata           -TAACA------------------GGAAGTGTGCCCGAATGGTCT-AAGGATTACTTTGATAGAGTAAAAAACAGAGGTTAAACTCCTC
C.robustus         -TAACACAAA--------------GGAAGCGTGCCCGAATTTT---AAGGGTTACTTTGATAGAGTAAACAACAGAGGTTAAAATCCTC
S.sikkimensis      -TAACC------------------GGAAATGTGCCCGAATTTT---AAGGGTTACTTTGATAGAGTAAAACACAGAGGTTAAAATCCCC
E.inexpectatus     -TAATTAA----------------GGAAATGTGCCCGAAGCTC---AAGGATTACTTTGATAGAGTAAAACACAGAGGTTAAAACCCTC
E.skiltonianus     -TAGCCAA----------------GGAAATGTGCCCGAAAC-----AAGGACTACTTTGATAGAGTAGAACACAGGGGTTAAAATCCCC
E.anthracinus      -TAATCAA----------------GGAAATGTGCCCGAAGTTT---AAGGATTACTTTGATAGAGTAAAATACAGAGGTTAAA-CCCTC
S.anguineus        -TAACAAC----------------GGAAATGTGCCCGAAATCTA--AAGGACTACTTTGATAGAGTATATTATAGGAGTTAAAATCTCC
P.eggeli           -TAAGCCCA---------------GGAAATGTGCCCGAATCCC---AAGGACTACTTTGATAGAGTATATTACAGGGGTTAAAATCCCC
F.polylepis        -TA---------------------GGAAGTGTGCCCGAATCTC---AAGGACTACTTTGATAGAGTATGACACAGGGGTTAAAATCCCC
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Ch.ocellatus       -TAACA------------------GGAAATATGCCTGAATTTT---AAGGGCTACTTTGATAGAGTATTCTACAGGGGTTAAAATCCCC
A.meleagris        -T----------------------GGAAGTGTGCCCGAATTACT--AAAGACTACTTTGATAGAGTACGACACAGGGGTTCAAATCCCC
T.lomii            -TAAT-------------------GGAAGTGTGCCCGAACTACC--AAGGACTACTTTGATAGAGTACTATACAGGGGTTTAAATCCCC
T.gariepensis      -TAGAT------------------GGAAGTGTGCCCGAATAACA--AAGGGCTACTTTGATAGAGTACGACACAGGGGTTTAAACCCCC
X.vigilis          -TAACACA----------------GGAACTGTGCCCGAATATTT--AAGGACTACTTTGATAGAGTAAGCTACAGGGGTTAAAATCCCC
C.polyzonus        -TAAATCTT---------------GGAGCTGTGCCTGAACCA----AAGGGCTACTTTGATAGAGTAGAACATAGGGGGTCAAACCCCT
Zonosaurus.sp.     -TA---------------------GGATGTGTGCCTGAATT-----AAAGGACTACTTTGATAGAGTAGAACATAGGGACTTAAATCTC
Dibamus            -TAA--------------------GGAAGCATGCCCGAGCATTAA-AAGGATTACTTTGATAGAGTACACAACAGGGGTTAAAATCCCC

Index1             11111111111111111111122222222222222222222222222222222222222222222222222222222222222222222
Index2             78888888888999999999900000000001111111111222222222233333333334444444444555555555566666666
Index3             90123456789012345678901234567890123456789012345678901234567890123456789012345678901234567
Qualifiers1        ......ILE........GLN.....................................................................
Qualifiers2        >AA>>>>>*........*<<<<<AA<<<<T.......<<<<T......<<<AC..COD..<<<AC.<<<D.........<<<D..<<<<
A.mississippiensis TCGCATCC----------TAGGGAGATAGGATTCGAACCTATTCAA--AAGGAATCAAAATCCTTCCTACTTCCCTT--ATAGTACCCC
G.gallus           TCACTTCCTTAATC---CTAGAAAAGTAGGAATCGAACCTACACAG--AAGAGATCAAAACTCTTCATACTCCCTCT--ATATTATTTT
C.mydas            TCGTCTCCT--------TTAGAAAAATAGGACTCGAACCTACACCA--GAGAGATCAAAACTCCCCATACTCCCATT--ATACTATATC
S.punctatus        TCATCTCC----------TAGAAAAATGGGAATCGAACCCAAACAT--TAGAGACCAAAACTCCATGTACCCCATC---ATACTGTTTT
B.theili           TCTTTTCCCTCTTTCCA-TAGCGAAGAAGGGGTTGAACCAACATCA--AAAAACTCAAAATCTTATGCATTTCTATT--ATGCTACCCG
C.rudis            TCACTTCCC---------TAGAGGAAAAGGAGTTGAACCAATATTA--TAAAACCCAAAATTTTACGTATTTCAATT--ATACTACCCT
C.brevicornis      TCTCTTCCC---------TAGGGAAGAAGGAGTTGAACCAACATCA--TAAAACCCAAAATTTTACGCATTTCAATT--ATACTACCCC
C.salinarum        CCACTTCCC---------TAGAGGAAGAGGACTCGAACCTCCATTT--AAAAATTCAAAATTTTCAGTATTTCCATCT-ATACCACCCT
P.leusterii        CCACTTCCCA--------TAGGGGAAGAGGAATCAAACCTCCGTTT--AAAAATTCAAAATTTTCAGTATTCTCATCTTATACTACCCC
P.cocincinus       CCACTTCCCA--------TAGAGAAGAAGGACTCGAACCAACACCT--AAAAACCCAAAATTTTTAGTACTCCCACCT-ATACTACTCT
Hydrosaurus.sp.    TCATCTCCCCCCCCA---TAGAGAAAAAGGAGTCGAACCTTTACCC--AAAAATCCAAAATCTTTAGTACTTCCAACT-ATACTACCCT
C.calotes          TCACTTCTACTTC-----TAGAGAAAGAGGACTTGAACCCCA-TCT--AAGAGACCAAAACTCTTCGTATATCCTATT-ATACTTTACC
J.tricarinata      TCACTTCTC---------TAGAAAGAGAGGACTCGAACCTCTATAG--AAGAATCCAAAACTCTTCGTACTTCCAACT-ATACTACACT
P.raddei           TCACTTCCAT--------TAGAGAAAGAGGACTCGAACCTCCATAA--AAAAATCCAAAATTTTTTGCACTACCACCT-ATGCTACTCT
L.belliana         TCGTCTCCCAT-------TAGAAGAATGGGACTCGAACCCACAATA--AAAAATCCAAAATCTTTTGTACTCCCAACT-ATACTATCTC
U.acanthinurus     TCGATTCCCCCT------TAGCAGGGAAGGAATCGAACCAACACCG--AAAAACCCAAAATATTTCATACCTCCACT--ATACTACCTG
A.paternus         TCATTTTC----------TAGAAAACCAGGACTCGAACCTGTACCT--AAAAACTCAAAATCATTTGTACTTCTTT---ATACTATTTT
P.mcallii          TTACTTCCT---------TAGAAGAACAGGATTTGAACCTGCACAA--AAAGACTCAAAATCTTCAGCACTCCATT---ATACTATCTT
Sauromalus.obesus  TCATTTCC----------TAGAAGAACAGGACTTGAACCTGCACCT--AAAGACTCAAAATCTCCAGCACTTCATT---ATACTATCTT
Hoplocercus.sp.    TCACTTCC----------TAGAAGAACAGGGCTCGAACCTGCACCA--AAAGACTCAAAATCCTTTGCACTCCATT---ATGCAACCTC
E.laticeps         TCACTTCC----------TAGAAAAACAGGACTTGAACCTGCACCT--AAAAACTCAAAATCTCTCGCACTTCCTT---ATGCAATCTC
P.somuncurensis    TCATTTCCT---------TAGAAGGACAGGACTCGAACCCGCACTT--AAGAACTCAAAACTCCTAGTACTTCATT---ATACTACCAT
L.pictus           TCATTTCCT---------TAGAAGGACAGGACTCGAACCCGCACCT--AGAAGCTCAAAACTTCCAGCACTCCATT---ATACTACCAT
U.flaviceps        TCATTTCC----------TAGAAAAATAGGACTTGCACCTACACTT--AAAAACTCAAAATTTTTAGCACTCCATT---ATGCTATTTC
S.crassicaudatus   TCACTTCCT---------TAGAAAAACGGGACTCGAACCCGCACCT--AAAGACTCAAAACCTTTAGCACTACACT---ATGCTATTTC
L.carinatus        TCATCTCCT---------TAGAAGAACAGGAATTGAACCCGCACTT--AAAGACTCAAAACCTTTTGTACTCCATT---ATACTATCTC
B.plumifrons       TCATTTCCC---------TAAAAGAACAGGACTCGAACCTGCACCA--AAAGACTCAAAATCTTTAGTACTCCACT---ATACTATCTT
G.wislizenii       TCGCTTCCT---------TAGAAGAATGGGACTTGAACCCACACCA--AGAGACTCAAAATCTCAAGCACTCCATT---ATGCTACCCT
O.cuvieri          TCATTTCCT---------TAGGAAGACAGGATTCGAACCTGCACTT--AGAAACTCAAAATTACTTGTACTCCATTA--CTACAACCTC
O.attenuatus       TCGCTTCCC---------TAGGAAAACAGGAATCGAACCTGCACCA--GAAAACTCAAAATTCTCTGTACTCCCATTTTATACTTCTTC
E.panamintina      TCACTTCC----------TAGAAAGACAGGAATTGAACCTGCACCA--AAAAACTCAAAATCTTCTGTACTCCCATT--ATACTACTTC
C.enneagrammus     TCATTTCC----------TAGAAAAACAGGAGCCGAACCTGCACTG--AAAAACTCAAAATTTTTTGTACTT-CATT--ATACTATTTT
A.pulchra          TCAGCTCCA---------TAGAAAAACAGGAAATGAACCTGTACTT--AAAAACTCAAAATTCTTCGTACTTCCATT--ATACTACCTC
H.suspectum        TTATCTCCT---------TAAAGAGACAGGATTTGAACCTGCACCA--AAAAACTCAAAATTTCATGTACTTCCTTT--ATACTACCCT
X.grandis          TCACTTCCT---------TAGAAAGACGGGAATTGAACCCGCACTA--AAAAACTCAAAATCTTCTGCACGCCCATT--ATACTACTTT
V.griseus          TCATTTCCCC--------TAGAAA-ACAGGACTCGAACCTGTACTA--TAAAACCCAAAATTTTATGTACTTCCATT--ATACCAACTT
L.borneensis       CTCATTTCC---------TAGAAAAACAGGCCTTGAACCTGCCCTC--AAAGGCTCAAAACCTTTCGTACTCCCACT--ATACTACTTT
S.crocodilurus     TTATTTCCT---------TAGAAAAACAGGATTTGAACCTGCACCT--TGGGACTCAAAACCCCTCGTACTCCCATT--TTACTACTTT
D.semicarinatus    CACCCCTCC---------TAGAAGGCCAAGACTCGAACTTGAACTA--AAAAGCCCAAAACTTTGCATACTACCAAT--ATATTACCTT
R.braminus         ?????????????????????????????????????????????????????????????????????????????????????????
C.ruffus           ?????????????????????????????????????????????????????????????????????????????????????????
Agkistrodon.sp.    ?????????????????????????????????????????????????????????????????????????????????????????
E.grammica         TCACCTCCTT--------TAGAAGAATAGGAATTGAACCTACACCT--GAGATCCCAAAACTCTCTGTACTACCTCT--ATACTACCTT
B.biporus          TCGGCTCCA---------TAGAAAAATGGGCATCGAACCCATCCTT--CGGGGTCCAAAACCCCGCGTACTACCACT--ATACTACTTA
T.weigmanni        TCACTTCCCT--------TAGAAAAACAGGCCTCGAACCTGCACCA--CAGAGCCCAAAACTCCATGTACAACCACT--ATACTATTTC
A.xera             TCACTTCCT---------TAGAAAACTAGGTCTCGAACCTACACTG--CGGGAATCAAAACCCCACGTACTACCACATTATACTATATT
C.tigris           TCATTTCCT----------AGAAAAATGGGATTCGAACCCACACCA--AAGAGACCAAAACTCTTCGTACTCCCACT--ATACTACTTC
L.parietale        TCATTTCCC---------TAGAAAAATGGGACTCGAACCCACACCA--AAGAGATCAAAACTCTCCGTACAGCCAATT-ATACTTCCTT
E.turkmenicus      TCACTTCC----------TAAAAGAATAGGACACGAACCTACACAAT-TAAGGCTCAAAACCTTATGTACTACCAAATTATACTACCTT
S.shrevei          CCACTTCCCAAACA----TAGAAAAGTGGACTACGAATCCACACCA--AGAGACTCAAACTCTCCCGTACTTCCAACT-ATACTACTTT
T.przewalskii      CCACTTCCT---------TAGAAGAACGAGCACCGAACCCGCACCA--CAAGGCCCAAAACCTTATGTACTTCCAATT-ATACTACCTC
G.gecko            TCATTTCC----------TAGAAAATCGGGTCACGAACCCAAACCT--TAAGATCCAAAACCTTATGTACTACCAACTTATACTAATCT
P.lindneri         TCATTTCCTCCATCC---TAGAAGAACAGGACACGAACCTACACAC--TAAAGCTCAAAACTTTATGTACTACCCATT-ATACTATCCT
Cr.ocellatus       TCACTTCCTACTGCCCATTAGAAAAACAGGCCACGAACCTGCACAT--CAAAGTCCAAAACTTTATGTACTACCAATT-ATACTATCTT
L.jicari           TCGCCTCCTT--------TAGAAGAATGGGTCTTGAACCCACACAA--CAAAGCTCAAAACTTTGCGTACTACCCAATTATACTATCCC
M.aurata           TCACTCCCTAC-------TAGAAAAATAGGACACGAGCCTATACCT--AAGGGCCCAAAACCCCTCGTACTACCAT--TATACTATTTC
C.robustus         TCACTTCCCACACACT--TAGAAAAACAGGACACGAACCTGCACCT--GAGGACTCAAAACCCTACGTACTTCCAT--TATACTATTTT
S.sikkimensis      TCATTTCCTGT-------TAGAAAGACAGGACACGAACCTGCACCG--AAAGGCCCAAAACCCTTCGTACTCCAC---TATACTACTCT
E.inexpectatus     TCATTTCCTCAAT-----TAGAAAAACAGGGTCCGAACCTGCACTA--AGGAGCCCAAAACCCCCTGTACTTCCAC--TATACTATTTT
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E.skiltonianus     TCATTTCCTA--------TAGAAAAACAGGACCCGAACCTGCACTA--AAGGGCCCAAAACCCTCTGTACTTCCAC--TATACTACTTT
E.anthracinus      TCCTTTCCTATAT-----TAGAAAAACAGGACCTGAACCTGCACCA--AAGAGCTCAAAACCCTCTGTACTTCCAC--TATACTATTTT
S.anguineus        TCATTTCCT---------TAGAAAAACAGGACTTGAACCTGCACCA--AAGAGCTCAAAACCCTTCGTACTCCCAA--TATACTATTTT
P.eggeli           TCATTTCTTTT-------TAGAAAAACAGGATTTGAACCTGCACCA--AAGAGCTCAAAACCCTCTGTACTCCCCC--TATACTACTTT
F.polylepis        TCACCTCCTAC-------TAGAAAGACAGGACTCGAACCTGCACAA--AAGAGCTCAAAACCCTTTGTACTCCCACT-ATACTACCTTC
Ch.ocellatus       TTATTTCCTACAC-----TAGAAAAACAGGACTTGAACCTGCACCA--AAGAGCTCAAAACCCTTTGTATTCCCAC--TATACTATTCT
A.meleagris        TCACTTCCCAT-------TAGAAAAACAGGACCTGAACCTGCACTA--AAGAGCTCAAAACCCTTCGTACTTCCAC--TATACTACTTT
T.lomii            TCACTTCTCAC-------TAGAAAAACAGGACCTGAACCTGCACCA--AAGAACTCAAAACTCTCCGTACTCCCACC-TATACTATTTT
T.gariepensis      TCACTTCCCAC-------TAGAAAAACAGGACATGAACCTGCACCA--AAGAGCTCAAAACCCCCCGTACTCCCGCT-TATACTACTTT
X.vigilis          TCTATTCCT---------TAGACAACCAGGATCCGA-CCTACACCT--AAGAGCCCAAAACTCCTCGTACTACCAAC-TATACTACTGT
C.polyzonus        CAGCTCT-----------TAAAAAAATAGGAATTGAACCTATACCT--GAGAACCCAAAATTCCCCGTACTTCCAT--TATACTTTTTC
Zonosaurus.sp.     CCTCACCTCCTA------TAGAAAAACAGGTATCGAACCTGCACCT--AAGGGCCCAAAACCCTCTGCACTCCCAAT-TATACTATTTC
Dibamus            TTACTTCCC---------TAGGAAGACAGGACCCGAACCTGCACCC--AAGAGCCCAAAACTCTTCGTACTACCACTT-ATACTACCTC

Index1             22222222222222222222222222222233333333333333333333333333333333333333333333333333333333333
Index2             66777777777788888888889999999999900000000001111111111222222222223333333333444444444455555
Index3             89012345678901234567890123456789012345678901234567890123456789012345678901234567890123456
Qualifiers1        GLN..............MET.....................................................................
Qualifiers2        <AA..............AA>>>>>..D>>>........D>>>.AC>>>..COD..AC>>>....T>>>>..........T>>>>AA>>>
A.mississippiensis CTA---------------GAAGTGTAAGCTAACCAA--AGCTATTGGGCCCATACCCCAAAAATGAAGACTAACT----CCTTCCACTC
G.gallus           CTA---------------GTAAGGTCAGCTAACTA---AGCTATCGGGCCCATACCCCGAAAATGATGGTTTAACC---CCTTCCCCTA
C.mydas            CTA--------------AGTAAAGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCGAAAATGTCGGTTAAAAT---CCCTCCTATA
S.punctatus        CTAA-------------AGTAAAGTCAGCTAATAA---AGCTTCTGGGCCCATGCCCCAAAAATGTTGGTTAAAC----CCTTCCTTTA
B.theili           CTACTCACTAC------ATTAGAATCTGCTACAT---AAGCAATTGGGCCCATACCCCAAAAACGATAATAC-------AAGTCTTCTA
C.rudis            CTATAAAC---------ACTAGAATCTGCTACAC---AAGCAATTGGGCCCATACCCCAAAAACGATAACAT-------ATATCTTCTA
C.brevicornis      CTATACAAA--------ACTAGGATCTGCTACAT---AAGCAATTGGGCCCATGCCCCAAAAACGATAACACA------ACATCTCCTA
C.salinarum        CTATCA----------CGCTAGGGTATGCTACATTA--AGCAGTTGGGCCCATGCCCCAAAAACGGTGAAT--------ACACCCCCTA
P.leusterii        CTACAAAT---------GTTAAGGTATGCTACATCA--AGCAGTTGGGCCCATGCCCCAAAAACGGTGAAT--------ACACCCCCTA
P.cocincinus       CTACAA-----------GCTAGGGTATGCTACATTTA-AGCAATTGGGCTCATGCCCCAAAAACGGTGAAA--------ACACCCCCTA
Hydrosaurus.sp.    CTAACCAA---------ATTAGGATCTGCTACATTTA-AGCAGTTGGGCCCATACCCCAAAAACGGTGACTA-------ACACCTCCTA
C.calotes          CTACAGAC---------ATTAGGGTCTGCTACATA---AGCAGTTGGGCCCATGCCCCAAAAACGGAATAT--------AAACCCCCTA
J.tricarinata      CTACAA-----------ACTAGAGTCTGCTACACA---AGCAGTTGGGCCCATACCCCAAAAACGGTAACAC-------TTACCCTCTA
P.raddei           CCACTTGAAC-------ATTAGGATCTGCTACATA---AGCAGTTGGGCCCATGCCCCAAAAACGGTGAC---------ACACCTCCTA
L.belliana         CTACCTACAAGTCTAT-ATTAGGATCTGCTACGGA---AGCAGTTGGGCCCATACCCCAAAAACGGTGATT--------TCACCTCCTA
U.acanthinurus     CTATACAA---------ATTAGGGTCTGCTACGTCTA-AGCAATTGGGTTCATGCCCCAAAAACGGTGCCA--------CCACCCCCTA
A.paternus         CT---------------AGTAAAGTCAGCTAAAAA---AGCTATTGGGCCCATACCCCAAAAATGTTGGTTTAAAC---CCTTCCTATA
P.mcallii          CT---------------AGTAAAGTCAGCTAACTA---AGCTATCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCTCTA
Sauromalus.obesus  CT---------------AGTAAAGTCAGCTAACCCA--AGCTATCGGGCCCATACCCCGAAAATGTTGGTTTAAAT---CCTTCCTCTA
Hoplocercus.sp.    CT---------------AGTAAAGTCAGCTAAAAA---AGCTATTGGGCCCATACCCCAAAAATGCTGGTGCAACT---CCTTCCTTTA
E.laticeps         CT---------------AGTATAGTCAGCTAAATA---AGCTATCGGGCCCATACCCCGAAAATGTCGGCTTAAAT---CCCCCCTTTA
P.somuncurensis    CT---------------AGTAAAGTCAGCTAATCA---AGCTATCGGGCCCATACCCCGAAAATGTTGGTTTAACC---CCTTCCTATA
L.pictus           CT---------------AGTAAAGTCAGCTAAACA---AGCTATCGGGCCCATACCCCGAAAATGTTGGTTCAACT---CCTTCCTATA
U.flaviceps        CT---------------AGTAGAGTAAGCTAAACA---AGCTATTGGGCCCATACCCCAAAAATGTTGGTAAAACA---CCTTCCCCTA
S.crassicaudatus   CT---------------AGTAAAGTCAGCTAACTA---AGCTATCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCTTTA
L.carinatus        CT---------------AGTAAAGTCAGCTAACCTA--AGCTATCGGGCCCATACCCCGAAAATGTTGGCCAAACC---CCTTCCTTTA
B.plumifrons       CT---------------AGTAAAGTCAGCTAAAAA---AGCTATCGGGCCCATACCCCGAAAATGTTGGTTTAATC---CCTTCCTATA
G.wislizenii       CT---------------AGTAAAGTCAGCTAATTA---AGCTATCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCTCTA
O.cuvieri          CT---------------AGTAAAGTCAGCTAAACA---AGCTATCGGGCCCATACCCCGAAAATGTTGGTTTAAAT---CCCTCCTCTA
O.attenuatus       CT---------------AGTAAAGTCAGCTAAATA---AGCTCTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCTTTA
E.panamintina      CT---------------AGTAAAGTCAGCTAAATA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCTTTA
C.enneagrammus     CT---------------AGTAAAGTCAGCTAATTA---AGCTTTTGGGCCCATACCCCAAAAATGTTGGTTTAAAC---CCCTCCTTTA
A.pulchra          CT---------------AGTAAAGTCAGCTAACT----AACTTTTGGGCCCATACCCCAAAAATGTTGGTTTAAAC---CCTTCCTTCA
H.suspectum        AT---------------AATAAGATCAGCTAAACA---AGCTCTCGGGCCCATACCCCGAAAATGTTGGTTCGAAA---CCCGCTCTTA
X.grandis          CT---------------AGTAAGGTCAGCTAAAAA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCCATA
V.griseus          CT---------------AGTGAGGTCAGCTAACCA---AGCTATCGGGCCCATACCCCGAAAATGTCGGTTACAAA---CCTTCCCTCA
L.borneensis       CT---------------AGTAAGGTCAGCTAACTCA--AGCTTTTGGGCCCATACCCCAAAAATGTTGGTGAAAAT---CCCTCCCCTG
S.crocodilurus     CT---------------AGTAAAGTCAGCTAATTA---AGCTTTTGGGCCCATACCCCAAAAATGTTGGTTTAACA---CCATCCTCTA
D.semicarinatus    CTA--------------AGTAAGGTCAGCTAAATA---AGCTATCGGGCCCATACCCCGAAAATGCCACA---------ACGGCCCCTA
R.braminus         ????????????????????????????????GTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGAACGC------TCAACCTTTA
C.ruffus           ????????????????????????????????????????????????CCCATACCCCGAAAATGTCCT----------ACGACCTTTA
Agkistrodon.sp.    ????????????????????????????????????????CTTCCGGGCCCATACCCCGAAAATGTCCAC---------CGGGCCTTTA
E.grammica         CC---------------AGTAAAGTCAGCTAACTA---AGCTCTTGGGCCCATACCCCAAAAATGTTGGTCAAAC----CCCTCCTTTA
B.biporus          CT---------------AGTAAAGTCAGCTAGCACA--AGCTATTGGGCCCATACCCCAAAAACGTTGGAAATAT----CCATCCTTTA
T.weigmanni        CT---------------AGTAGAGTCAGCTAAATA---AGCTTTTGGGCCCATACCCCAAAAATGTTGGTAATCC----CCCTCCTCTA
A.xera             CT---------------AGTAAAGTCAGCTAAAAA---AGCTCTTGGGCCCATACCCCAAAAATGTTGGTTTAAC----CCCTCCTTTA
C.tigris           CT---------------AGCACAGTCAGCTAATCA---AGCTCTCGGGCCCATACCCCGAAAATGTTGGATAAGA----CCAACCTCTG
L.parietale        CT---------------AGCACAGTCAGCTAACCTA--AGCTTTTGGGCCCATACCCCAAAAATGTTGGCCACAA----CCAACCTATG
E.turkmenicus      TT---------------AGTAAAGTCAGCTAATAA---AGCTTTCGGGCCCATGCCCCGAAAATGTTGGTATAAAAT--CCCTCCTATA
S.shrevei          GTA--------------AGTAGAGTCAGCTAAGCA---AGCTTTCGGGCCCATACCCCGACAACGTTGGTACCCAAA--CCCTCCTCTA
T.przewalskii      CT---------------AGTAAAGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCGACAATGTTGGTACACAAT--CCTTCCTATA
G.gecko            CT---------------AGTAGGATCAGCTAAATCA--AGCTTTCGGGCCCATACCCCGACAATGTTGGAAATATCACTCCCGCTCCTA
P.lindneri         CT---------------AGTAAAGTCAGCTAACTA---AGCTTTCGGGCCCATACCCCGACAATGTTGGTACCTAAT--CCTTCCTTTA
Cr.ocellatus       CT---------------AGTAAAGTCAGCTAATAA---AGCTTTCGGGCCCATACCCCGACAATGTTGGTATCATAAC-CCTTCCTATA
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L.jicari           CT---------------AGTAAAGTCAGCTAAATA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTTCAAT--CCCTCCTTTA
M.aurata           CT---------------AGTAAAGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAACC---CCTTCCTATA
C.robustus         CT---------------AGTACAGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCTTTA
S.sikkimensis      CT---------------AGTAAGGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCAAAAATGTTGGTTTAACC---CCTTCCCCTA
E.inexpectatus     CT---------------AGTAAAGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCGCCTTTA
E.skiltonianus     CT---------------AGTAAAGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCTTCCTCTA
E.anthracinus      CT---------------AGTAAAGTCAGCTAACTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAT---CCCTCCTCTA
S.anguineus        CT---------------AGTAAAGTCAGCTAAACA---AGCTCTCGGGCCCATACCCCGATAATGTTGGTTTAAAC---CCTTCCTATA
P.eggeli           CT---------------AGTAGAGTCAGCTAACTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCCTCCTCTA
F.polylepis        TACC-------------AGTAAAGTCAGCTAATTA---AGCTTTCGGGCCCATACCCCGAAAATGT-GGTTTAAAC---CCCTCCTCTA
Ch.ocellatus       GT---------------AGTAGAGTCAGCTAATTG---AGCTTTCGGGCCCATACCCCGAGAATGTTGGTTTAAAC---CCTTCCTCTA
A.meleagris        CT---------------AGTAAAGTCAGCTAACTA---AGCTTTCGGGCCCATACCCCGAAAATGCTGGTTCAAAC---CCTTCCTCTA
T.lomii            CT---------------AGTAAAGTCAGCTAACTA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCTTCCTCTA
T.gariepensis      CT---------------AGTAAAGTCAGCTAAATA---AGCTTTCGGGCCCATACCCCGAAAATGTTGGTTTAAAC---CCTTCCTCTA
X.vigilis          CTA--------------AGTAAAGTCAGCTAAAAA---AGCTTTCGGGCCCATACCCCGAAAATGTCGGTTTAACA---CCCTCCTTTA
C.polyzonus        CT---------------AGTAAAGTCAGCTAAATA---AGCTTTCGGGTCCATACCCCGAAAATGTTGGTTTAACC---CCCTCCTTTA
Zonosaurus.sp.     CT---------------AGTAAAGTCAGCTAATTA---AGCTCTCGGGCCCATACCCCGAAAATGTTGGTCAAAT---CCTTCCTATA
Dibamus            CTA---------------GTAAAGTCAGCTAATAA---AGCTTTTGGGCCCATACCCCAAAAATGTCGGTTAAACC---CCTTCCTTTA

Index1             33333333333333333333333333333333333333333334444444444444444444444444444444444444444444444
Index2             55566666666667777777777888888888899999999990000000000111111111122222222223333333333444444
Index3             78901234567890123456789012345678901234567890123456789012345678901234567890123456789012345
Qualifiers1        MET....ND2...............................................................................
Qualifiers2        >>*....1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1
A.mississippiensis CTACCACATG---CCCCTCTCCCAACCAATTATCCTAGCAACACTAACCATTACAACACTAATTTTTCTACTATCAACCCATCTGGTCC
G.gallus           CTA----ATGAACCCCCATGCAAAACTAATCTGCACAGTAAGCCTCATCATGGGAACCAGCATCACAATCTCCAGCAACCATTGAATCT
C.mydas            CTA----ATGAACCCCTACGCACATACAATTATCATCCTAAGCCTAATTATAGGACCACTACTCACAATCTCCAGTAACCACTGAATCC
S.punctatus        CTA----ATGCACCCCTCCATCACCTCTTTGCTCCTTATCGCCCTATCCACAAGCACTATTATTACAATATCAAGCTACCATTGAATAT
B.theili           ATA----TTGTCACCACTCACCCTACTAATCGTTACCTTTAATCTTTTTTTTGGAACAATAATTACCGCATCAAGTCACCACTGACTTC
C.rudis            GTA----TTGAACATACTAACCAAATTAATAATTATAATTAACCTCATTATAGGAACCATTATTACTGCCTCAAGCCACCACTGACTTA
C.brevicornis      GTA----TTGAACCTACTAACACAACTGATAATTACATTAAACCTAATTCTAGGAACAATTATCACCGCTTCTAGCCATCACTGGCTAA
C.salinarum        ACAC---TTGCCACCACTAGCCCTCTTTATAATCACACTAGGAATTATTACAGGAACACTAATAGTAACCTCAGCCAATCATTGATTAA
P.leusterii        ACA----TTGCCACCAACAGCCCTTTTTATAATCGCACTAGGAATTATTCTCGGCACACTAATAGTCACCTCAGCCAACCACTGACTGA
P.cocincinus       CCAA---ATTTCAGCCCTTACAACCCTAGCCCTTACAACCAGCATCACCACCAGCATACTAATCACAGCCTCAGCAAACCATTGACTTA
Hydrosaurus.sp.    ATACCTCTTGCCGCCACTAGTACTTTCATTTGTCATTGCTGGCATCACCACCGGCACTGTAATCACCATATCCAGCCACCACTGACTTA
C.calotes          ATA----ATT---------CCCACTACCATAATTTTTACAGGCATTATTTTAAGCACCATCCTAGCCACAACTAGTAGTAATTGACTGC
J.tricarinata      GTA----ATACCTTCCCTGACTACCGCTGTGTTATTCCTAGGCGTCACAACAGGCACAGCCATCGCAATATCTAGCCATCATTGACTGA
P.raddei           ATAC---ATTTCCCCCACATCTATCGTAATCATTACCATAAGTATTACCATAAGCACTATTATAGTTATATCAAGCTCCAACTGACTTA
L.belliana         ATATC--TTGCCCCCATTAATACTCCCAATTTTAATCCTCGGCGTCACCATAGGCACCATCTTCGCTGCATCCAGTCACCACTGACTAA
U.acanthinurus     ATA----TTGCCACCATCCACCACCCTAATCTTCTACACAAGCCTCGTATCAGGCACACTAATTGTCATATCAAGCCACCATTGGCTGG
A.paternus         CTA----ATGAGCCCATTTATTCTTACAATTATTTTTTCAAGCTTAGCAACAGGCACAATTATTACTATAACCAGCTACCACTGACTTA
P.mcallii          CTA----ATGAGCCCCACAACAACAACCATCTTAGTCTCAAGCCTTGCTACTGGCACAATCATCACAGCCTCAAGCCACCATTGACTAA
Sauromalus.obesus  CTA----ATGAGCCCTACCACAACATCCCTACTTCTCTCAAGCCTTGCAATAGGCACCATCATCACCGCATCCAGCCACCACTGAATGA
Hoplocercus.sp.    CTA----ATGAGCCCACTAACAACCTCAATTGTCCTCTCCAGCTTAGCCACCGGCACTATCATCACAATATCCAGCCACCACTGAATTA
E.laticeps         CTA----ATGAGCCCCCTAGCAACAACAATCATCCTCTCAAGCCTGGCCACCGGCACCATCATCACCGCCTCAAGCTACCACTGGATAA
P.somuncurensis    CTA----ATGAGCCCAATCACAATAACACTACTCATCTTCAGCCTTGCAACAGGTACAATTATTACAGCATCTAGCTTCCACTGACTAC
L.pictus           CTA----ATGAGCCCAACAACCACAACAATCTTAATCTCAACCCTAACCATAGGAACAATTATTACAGCATCAAGCCACCACTGATTAT
U.flaviceps        CTA----ATGAGCCCACTCACAACATCAATTATTTTATCCAGCCTAGCAACAGGCACGATCATTACAGCCTCAAGCTTTCACTGACTGA
S.crassicaudatus   CTA----ATGAACCCAGCCACCTCAACCATCATCCTATCTAGCCTAGCAACAGGAACAATTATCACCGCTTCTAGCTTTCACTGATTCA
L.carinatus        CTA----ATGAGCCCGCTTACAACAACAATCCTTCTATCCAGCCTAGCAACAGGCACAATCATTACTGCAACCAGCTACCACTGATTAA
B.plumifrons       CTA----ATGAGCCCCATCACAACAACAATTATTATTACAAGCTTAGCAACTGGCACAGTCATTACATCCACCAGCTACCACTGATTAA
G.wislizenii       CTA----ATGAGCCCAACCGCAACTATAATCCTAATTTCAAGCTTAGCAACAGGCACCATTATTACTACATCAAGCCACCACTGATTAT
O.cuvieri          CTA----ATGAGCCCAATAACAACTACACTACTAATCTCAAGCCTTGCTACAGGAACAATCATCACAGCATCAAGTTACCACTGATTAA
O.attenuatus       CCA----ATGAGCCCAATAATCACCTCCATCCTGTTCCTAAATCTTGCAACAGGGACTATTATCACAATATCTAGCTTCCACTGACTCC
E.panamintina      TCA----ATGAGCCCAATAATTACTTCAATCCTAATCCTCAACCTAGCAACAGGAACTATTATTACCATATCAAGCTACCATTGACTTC
C.enneagrammus     CCA----ATAAACCCAACAATTATCTCGATCCTCTTATCCAACCTAGCTATCGGCACAATCATTACCATATCAAGTTATCATTGACTCC
A.pulchra          CCA----ATGAGCCCGTTAATCACCACAATCTTAATACTTAATCTTGCAACAGGCACAATCATCACTATATCAAGCCATCACTGACTTC
H.suspectum        TTA----ATGAATCCCATAATTACAATAATCTTAATCTTCAGTATTACTACTGGAACCATTATTACCATATCCAGCCAACATTGACTTC
X.grandis          CTA----ATGAGCCCAACTACCCAATCCCTCCTCCTCTCCAACATTGCTATTGGCACCATTATTACAATATCAAGCCACCACTGACTAC
V.griseus          CTA----ATCAACCCCCTCATTAACTTCACCCTACTTTTCAGCATAATCATCGGAACCGCCCTAACAATAACCAGCCACCACTGAATAA
L.borneensis       CTA----ATGAGCCCAACCATTAATCTTATCCTACTTTCAAGCCTGGCAACCGGCACAATCCTTACACTATCCAGCTACCACTGGATAT
S.crocodilurus     CTA----ATGAACCCATACATCCTAACACTACTCATGTCCAGCACAGCAACCGGAACCATCATCACAATAACTAGCTACCACTGAATCC
D.semicarinatus    CTA----ATTAACCCAATATCCTGATTAATTATCACAACAAGCATTGCCCTAAGCACCACTATAATCACATCAACAACACACTGACTTA
R.braminus         TTA----ATTTCCCCTATTTCAGCATTAATAATGACAACAAGCATCATCCTTGGAACACTGATCACAGCTTCAAGCAAGCACTGACTAA
C.ruffus           CTA----ATCAACTTAATATCCTGAATCACAATCCCAACCAGCATTACACTAAGCACAATCTTAGTCACCACATCAACACACTGAATCA
Agkistrodon.sp.    CTA----ATGAACCCAATATCCCTAATAACTATTACAATTAGCATCATCATAAGCACCACCTTAATTACCACAACAACACACTGACTTA
E.grammica         CTA----ATGAACCCACTAATCTCATCCCTAATACTCTCCAACTTAGCCCTAGGGGTAATCATTACCGCCACCAGCTTTCACTGATTCC
B.biporus          CTA----ATTAACCCCTATACGCTCACCTTCATAGCATCCATAATAATCACCGGCACAGCCATCGTAGCCACCTCTTCACACTGACTTC
T.weigmanni        CTA----ATGAACCCACTCCTTTGCTCCATACTATTTTCCTCCATAGCCACAGGGACAATCATCGCTGCCTCAGCAAACCACTGACTAC
A.xera             CTA----ATGAACCCGTACGTTGCCTCGCTCCTAGTCTCCTCCTTTGCCACTGGCACAATCATCGCCGCTTCATCAAATCACTGACTAA
C.tigris           CTAA---ATGTCCCCCCTAATCAACACTATTTAGTTTTATCAATAATTACAGGAACCCTAATCACAATAAACAGCAGCCACTGACTGC
L.parietale        CTA----ATATCACCACTAATTTTATGTATTCTTATAACAACACTCGCTATAGGTACCCTAATTACACTAATAAGCAACCACTGATTAA
E.turkmenicus      CTA----ATTAACCCCATAATCTTATTCATTTTACTTTTTAGCCTAGCCATGGGCACCATTACCACCCTTTCTAGCTATCACTGACTTT
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S.shrevei          CTA----ATTAACCCAGTAATATTTTCACTACTAATTATAACCCTAGCCACCAGCACCATCATCACCATAACAAGCCACCACTGACTCC
T.przewalskii      CTA----ATAAACCCCTTAGTCTTATCCATTCTTATGTCAAGCCTTTCTACTGGCACAATTATTACAATATCCAGCCACCACTGACTCC
G.gecko            CTAC---ATAAGCCCCCTAATTTGATCGCTATTAATCACAGGCCTGTCAACAGGGACAGTCATCACCATGTCTAGTCATCACTGATTAC
P.lindneri         CTA----ATAAACCCCGCCATCTTCTCTATATTACTATTAACTGTAGCCTCGGGCACAATTATTACACTATCTAGCCATCACTGACTAC
Cr.ocellatus       CTA----ATTAACACCATTATAATAATACTTCTCACCTCATGCATAATTTTAGGAACTATTATCACTTTATCCAGCTCTCACTGACTAT
L.jicari           CTA----ATAAACCCAATAACATTCACCCTACTCATCTTCTCCTTAGCACTCGGAACTCTAATCACCATGTCCAGCTCCCACTGACTAC
M.aurata           CTA----ATGAACCCACTTATATATTCACTCATTCTATCAAGCATTGCAACAGGAACAATTATTACAATATCAAGTTTCCACTGACTCA
C.robustus         CTA----ATGAGCCCTCTTATATCCTCACTAATCCTTTCAAGTTTAGCCCTAGGCACCATAATCACAATATCAAGCTTCCACTGACTGA
S.sikkimensis      CTA----ATGAACCCCATTATACTCTCACTAATCATCTCAAGCCTTGCCTTAGGCACAGTTATCACCATATCCAGCTTTCATTGACTAC
E.inexpectatus     CTA----ATGAACCCAATTATATTATCAGTCATTATTTCAAGTCTGGCCCTAGGCACTATCATTACTATATCCAGCCACCACTGACTGC
E.skiltonianus     CTA----ATGAACGCCATTATATCATCAATCATAATTTCAAGCCTAGCCGTTAGCACCATCATCACCATGTCCAGCCATCATTGACTAC
E.anthracinus      CTA----ATGAGCCCCCTTATACTATCAATTATTATATCAAGCCTAGCCCTAGGCACCATCATCACCGCAGCCAGCCACCACTGGCTTA
S.anguineus        CTA----ATGAATCCCATCATAATACTAATTATCCTATCAAGCCTTGGCTTAGGCACTACTATCACAATGTCAAGTCACCACTGACTGC
P.eggeli           CTA----ATGAACCCCATCATAACATCTATTATCATCTCGAGCCTAGCCTTAGGTACCATCATCACAATATCGAGCTACCACTGACTCC
F.polylepis        CTG----ATGAACCCAATTATAATATTTATCATTATCTCAAGCCTGGCCTTAGGGACAATCATCACAATGGCCAGTCACCACTGACTTC
Ch.ocellatus       CTA----ATGAACCCAATCATAATAGCCATTATTATCTCAAGCCTAGCCTTGGGCACAGTCATTACAATATCGAGCTACCACTGAATAT
A.meleagris        CTA----ATGAATCCAGTCATAACATTTATCATTATATCAAACCTAGGACTTGGTACAATCATCACAGCATCAAGCTTTCACTGACTAA
T.lomii            CTA----ATGAACCCAATCATAACATCAATCATCATGTCTAACCTAGGCCTTGGAACAATCATCACAGCATCAAGTTTCCACTGACTAA
T.gariepensis      CTA----ATGAACCCAACCATAATATTCATTATCATATCAAACCTAGGACTTGGGACAATAATCACAGCATCAAGCTTCCACTGACTAA
X.vigilis          CTA----ATGAGCCCTATCATTCAATCCCTTATTCTATCAAGCCTAGCAACAGGCACAATCATCACAATAACAAGTCAAAGCTGAATCC
C.polyzonus        CTA----ATTAACCCCTTTATCATCTCACTTTTCATCTCAAGCCTAGCCATAGGCACCATCATTACAATGACAAGCCACCATTGACTAA
Zonosaurus.sp.     CTA----ATGAGCCCAACCATTCTCCTAATAATCCTATCAGGTCTAGGAACAGGTACAATAATTACAATATTTAGCTATCACTGACTTC
Dibamus            CTA----ATGAATCCCACTGCCCTTTCACTAATTTTATCAGGCTTAGGAGCAGGCTCAATCATTACAATAACCAGCTACCACTGACTTG

Index1             44444444444444444444444444444444444444444444444444444455555555555555555555555555555555555
Index2             44445555555555666666666677777777778888888888999999999900000000001111111111222222222233333
Index3             67890123456789012345678901234567890123456789012345678901234567890123456789012345678901234
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Qualifiers2        ..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..
A.mississippiensis TAATCTGAGTTGCACTAGAACTTAACACACTAGCGATCCTCCCCCTAATTGCTCACAAATCTCACCCACGAGCCATCGAAGCCTCCACA
G.gallus           TAGCCTGAACAGGCTTAGAGATCAACACCTTAGCCATCATCCCCCTCATCTCCAAGTCACACCACCCCCGAGCGATTGAAGCCACTATC
C.mydas            TAGCATGAACCGGCCTAGAAATCAGCACTCTAGCTATTATCCCACTAGTCGCTAAACAACACCATCCACGAGCAACTGAAGCCGCCACC
S.punctatus        TCGCTTGAGCTGGATTGGAAATTAATATACTCTCTATACTACCCCTAATCTCAAAAGAACACCACCCCCGAGCCGTAGAAGCCACCATA
B.theili           TAGCCTGAGCAGGTCTAGAACTAAATATATTATCTATTTTAGTTATTATTATACAACCGAAACACCCACGAGCTGCTGAAGCAGCAATT
C.rudis            TAGCTTGAGCAGGCCTAGAACTAAACATATTGTCAATCCTAGCAATTATTATAAAACCAAAACACCCCCGCGCTGCCGAAGCAGCTATC
C.brevicornis      TGGCCTGAGCGGGCTTAGAATTAAATATACTATCTATACTAGTCATTATTGTAAAACCCAAAAGCCCCCGTGCCGCCGAAGCGGCTATT
C.salinarum        CAGCCTGACTAGGCCTAGAATTAAACATAATCTCAATCATCCCAATAATTGCAAAACAAAGCACCTTCGATCAACGGAGTCCGCAACA
P.leusterii        CAGCCTGATTAGGTCTAGAACTAAACATAATCTCCGTTCTTCCAATAATCACAAAACAAAAACACATCCGATCAACAGAAGCCGCAACA
P.cocincinus       CCGCTTGAATCGGATTAGAACTAAACACAATTTCAATTTTGCCAATCATTATAAAACAAAAAAACCTACGATCAGCAGAAGCTGCAATA
Hydrosaurus.sp.    TAGCCTGACTAGGACTAGAACTTAACACACTAGCCATCCTACCAATCATCTCAAAGCCAAAACACCCACGATCAATCGAAGCAGCAACA
C.calotes          TAGCCTGACTAAGCCTCGAACTAAACACCCTATCAATCCTTCCAATAATCTCAAAAACAAAACACCCACGAGCAATCGAAGCTGCCACA
J.tricarinata      CCGCTTGAGTTGGATTAGAACTAAATACGCTAGCCCTACTACCAGTTATCTCAAAAACTAAACACCCCCGATCAATTGAAGCCTCAACA
P.raddei           TAGCCTGAGTCGGACTAGAACTAAACATATTAGCCATTCTTCCAATCATCTCAAAACCAAAAACCCTACGAGCATCAGAAGCCACAACT
L.belliana         TAGCATGACTAGGACTAGAATTAAACACCCTATGTCTACTTCCACTAATTTCAAAACCAAAACACCCTCGAGCAACAGAAGCCACAACA
U.acanthinurus     CAGTTTGAGTAGGACTTGAACTAAACACACTAGCCATCATCCCAATCATCTCTAGCCCAAAACACCCACGCGCAACAGAAGCTGCAACA
A.paternus         TGGCCTGAATTGGATTAGAGATAAACACACTAGCAATTATTCCCATTATCTCAACAACACATCACCCACGAGCCACAGAAGCTTCCACA
P.mcallii          TGGCTTGAATTGGCCTAGAAATAAATACACTAGCCATTGTTCCAATAATCTCAAAACAACATCACCCACGAGCCACAGAAGCTGCAACA
Sauromalus.obesus  TAGCTTGAATTGGCCTAGAAATAAATACCCTGGCCATCATTCCAATTATCTCAAAACAACACCACCCCCGAGCCACAGAAGCTGCAACC
Hoplocercus.sp.    TAGCCTGAGTTGGACTAGAAATAAACACACTAGCCATCATCCCAATTATCTCCAAACAACACCACCCACGATCCACAGAAGCCTCAACA
E.laticeps         TAGCCTGAATTGGCCTAGAAATAAACACCCTGGCTATTATTCCCATTATTTCACAAGAACACCACCCACGAGCCACAGAAGCCGCAACA
P.somuncurensis    TAGCCTGAATTGGCCTAGAAATAAACACGCTAGCCATTATCCCACTGATTTCTAAACAACACCACCCGCGATCAACTGAAGCAGCAACA
L.pictus           TTGCCTGAATCGGGTTAGAACTAAACACTCTCTCAATCATCCCACTAATTACAAAAAAACATCACCCACGAGCCACAGAAGCAGCCACA
U.flaviceps        TAGCCTGAATCGGACTAGAAATTAACACCTTGGCCATTATTCCGCTAATCTCCAAAATACACCACCCACGATCAACAGAAGCTGCAACA
S.crassicaudatus   TAGCCTGAATCGGACTAGAAATAAACACCCTGGCCATCATCCCAATTATTTCAAAACAACATCATCCACGAGCCACAGAAGCAGCAACC
L.carinatus        TAGCCTGAATTGGGCTAGAACTAAACACACTAGCCATCATTCCGATTATCTCAAAACGACACCACCCGCGAGCGACAGAGGCCGCAACT
B.plumifrons       TAGCTTGAATTGGCCTAGAAATAAATACACTATCAATCATCCCAATCATCTCAAAACGACACCACCCACGAGCCACAGAAGCCGCAACA
G.wislizenii       TAGCCTGAATTGGCCTAGAAATTAATACCCTGGCTATTATCCCAATTATCTCAAAACAACACCACCCACGATCAACAGAAGCCGCAACA
O.cuvieri          TAGCCTGAATTGGCCTAGAAATTAATACTCTATCCATCATCCCCATCATTTCAAAACAACACCACCCACGAGCTACCGAAGCAGCAACC
O.attenuatus       TAGCATGAATAGGACTGGAACTGAACACTCTGGCCATCCTACCAATCATCTCTAAATCCCATCACCCACGAGCCACAGAAGCCTCAACA
E.panamintina      TCGCATGAATAGGACTAGAACTAAACACCATAGCAATCTTACCCATTATCTCAAAATCACATCATCCACGATCCACAGAGGCCTCAACA
C.enneagrammus     TAGCATGAATGGGACTGGAACTAAACACATTAGCCATCCTCCCAATTATCTCAAAGTCTCATCACCCACGAGCCACAGAAGCCTCTACT
A.pulchra          TCGCATGAATGGGACTAGAACTAAACACTCTAGCAATTCTCCCTATCATTTCAAAATCTCACCACCCTCGCGCTACAGAAGCCTCAACA
H.suspectum        TTGCCTGGATGGGGTTAGAACTTAATACACTAGCTGTTATCCCAATCATTTCAAAAAAACACCACCCGCGAGCAACTGAAGCTGCAACT
X.grandis          TAGCGTGAATGGGATTAGAACTAAACACCCTAGCAATACTTCCCATTATTTCAGCTACCCACCACCCGCGAGCCACAGAAGCTTCTACA
V.griseus          TAGCATGATTAGGCCTAGAATTAAACACCCTGGCCATCATTCCTATCATCTCAAAAACCCACCACCCACGAGCAACTGAAGCCTCAACA
L.borneensis       TTGCATGAATCGGCCTAGAACTGAACACACTAGCTATCGTACCAATCATATCAAAAGCCCACCACCCACGGGCAACAGAAGCCGCAACA
S.crocodilurus     TGGCCTGAGTCGGCCTAGAATTAAATACACTCTCAATCACCCCAATTATTGCTAAAATACATCACCCACGAGCAACAGAAGCCGCAACA
D.semicarinatus    TAACATGAGCCTGCCTAGAAATTAACACCCTATCCATAGTCCCACTAATCTCAAAACCAAACCACCCCCGAGCAACAGAAGCAGCAACA
R.braminus         TAGCCTGAGTCGGCCTAGAAATAAACACACTCGCAATCATCCCATTAATCGCAAAACCACACCACCCACGTGCAATAGAAGCAACAACA
C.ruffus           TAGCCTGAACCTGCCTAGAAATCAACACCATATCCATAATCCCAATTATCTCAAAACCACATCACCCACGAGCCACAGAAGCAGCAACA
Agkistrodon.sp.    TAGCCTGAGTTTGCCTAGAAATCAACACCCTGTCTATAGTACCAATCATCTCAAAACCCCATCACCCGCGGGCAACGGAAGCAACAACA
E.grammica         TAGCATGAATCGGCCTAGAACTAAACACCCTAGCCATTATTCCCATCCTAGCCAAACAACATCACCCACGTGCCACTGAAGCAGCCACA
B.biporus          TTGCCTGAATCGCCCTCGAACTAAACACAATAGCAATCTTGCCACTACTAACACAAACACACACCCCCCGGACGACCGAATCAGCAACA
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T.weigmanni        TGGCCTGAATAGGCCTAGAATTAAATACACTGGCCATCCTTCCCCTCCTAGCAACAACCCACACACCACGTGCAACAGAAGCTGCCACC
A.xera             TAGCCTGAATTGGCCTAGAACTCAACACCCTCGCCGTCCTCCCCCTAATAGCAAAAACACACACACCACGTGCGACAGAGTCCGCCATC
C.tigris           TAGCCTGACTAGGACTAGAAATTAATATAATAGCCATCGTACCACTAATCTCAAAAACCCATCACCCACGAGCAACAGAAGCCGCAATT
L.parietale        TAGCCTGAGCCGGCCTAGAAATTAATATACTCTCTATTATACCCCTTATTGCAAAATCCCACCACCCCCGTGCAACAGAAGCCACAACT
E.turkmenicus      TAGCCTGACTCGGACTTGAAATCAATACAATAGCAATTATCCCTATTATTACTAAAAAACACCACCCACGAGCCACAGAAGCCGCTACA
S.shrevei          TAGCCTGACTAGGACTAGAGTTAAACACCCTGGCAATAATCCCAATCATCAACAAATCCCACCACCCACGAGCAACAGAAGCCGCAACA
T.przewalskii      TTGCCTGATTTGGCCTTGAAATAAATACACTAGCCATTATCCCACTTATTTCAAAACACCACCACCCACGAGCAACAGAAGCCGCAACA
G.gecko            TAGCTTGATTAGGCCTAGAACTGAACACCCTCAGCATCCTTCCCATTATTTCTAAATCACATCACCCACGAGCAACGGAAGCAGCAACA
P.lindneri         TAGCCTGAGCAGGACTAGAAATAAACACACTAGCCATCATTCCCATCATCTCAAAACAGCACCACCCTCGAGCAACAGAGGCAGCAACA
Cr.ocellatus       TAGCCTGAGCAGGTCTAGAAATAAATACCCTAGCAATTATCCCCATAATCTCAAAACAACATCACCCTCGAGCAACCGAAGCTGCAACA
L.jicari           TAGCATGGGCCGGACTGGAAATAAACACCTTAGCAATCATTCCTATCATTTCAAAACAACACCACCCACGAGCAACAGAAGCCGCAACC
M.aurata           TAGCATGAGTCGGACTAGAACTAAATACCCTCGCAATTATTCCAATTATCGCAAAACAACATCACCCACGAGCAACAGAAGCCACAACA
C.robustus         TGGCCTGAATTGGACTAGAACTAAACACACTAGCAATCATTCCAATAATTGCAAAACAACACCACCCACGAGCAACAGAAGCCACTACA
S.sikkimensis      TCGCTTGAGTGGGGTTAGAACTAAATACCCTTGCCATTATCCCACTTATTGCTAAACTTCACCACCCCCGCGCAACAGAAGCTACCACC
E.inexpectatus     TAGCCTGAGTCGGATTAGAGTTAAACACATTAGCAATCGTCCCAATCATTGCAAAACAACACCACCCCCGTGCAACAGAAGCCACAACC
E.skiltonianus     TAGCCTGAATTGGACTAGAACTAAACACACTAGCAATCATCCCCATCATTGCAAAACAACACCACCCCCGTGCAACGGAGGCCACAACT
E.anthracinus      TAGCCTGAATCGGACTAGAACTAAACACACTAGCAATCATCCCTATTATTGCAAAACAACACCACCCTCGCGCAACCGAGGCTACAACC
S.anguineus        TCGCATGAATTGGATTAGAAGTTAATACACTAGCAATTCTCCCAATCATTGCAATACAACACCACCCTCGTGCAACCGAAGCAGCAACA
P.eggeli           TTGCATGAGTTGGGTTAGAACTAAATACACTAGCAATTATCCCAATTATCGCAAAACACCACCACCCGCGTGCAACCGAAGCGGCAACA
F.polylepis        TAGCCTGAGTCGGGCTAGAACTAAATACACTATCAATTATCCCAATCATTGCAAAACAACACAACCCCCGCTCAACTGAAGCAGCAACA
Ch.ocellatus       TGGCCTGAATTGGCCTAGAACTAAATACCCTGGCGATCATCCCTATTATTGCAAAACAACACCACCCACGCGCAACTGAGGCCGCAACA
A.meleagris        TAGCCTGAATCGGACTAGAACTAAACACACTAGCCATCATCCCAATTATCGCAAAACAACATCACCCACGAGCAACAGAAGCTTCCACA
T.lomii            TCGCCTGAGTCGGATTAGAATTAAACACACTAGCCATCATCCCAATTATCGCAAAACAACACCACCCACGAGCAACAGAAGCCTCAACA
T.gariepensis      TAGCCTGAATTGGACTAGAGCTAAACACGCTAGCCATCATCCCAATCATCGCAAAACAACACCACCCACGAGCAACAGAAGCCTCAACA
X.vigilis          TAGCCTGAGTCGGCCTGGAAATTAACACACTAGCCATCCTCCCAATCATTTCAAAACCCCACCACCCTCGAGCAACAGAAGCCATAACA
C.polyzonus        TAGCCTGAGCAGGACTAGAAATTAACACCCTGGCAATTATCCCGATCATAACAAAACCCCACCACCCCCGAGCAACAGAAGCAGCAACC
Zonosaurus.sp.     TAGCCTGAACTGGCTTAGAAATTAACACCCTAGCGATCATCCCGATAATAGCAAAAAAACATCACCCCCGAGCCACTGAAGCCGCAACA
Dibamus            TCGCTTGAATCGGCCTAGAACTTAATACCCTAGCCATTATTCCTGTTATTGCCAAACATCACCACCCACGATCCACAGAAGCCGCAACC

Index1             55555555555555555555555555555555555555555555555555555555555555555666666666666666666666666
Index2             33333444444444455555555556666666666777777777788888888889999999999000000000011111111112222
Index3             56789012345678901234567890123456789012345678901234567890123456789012345678901234567890123
Qualifiers1        .........................................................................................
Qualifiers2        1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1.
A.mississippiensis AAATATTTTCTCACCCAGGCAATAGCATCTGCATTAATTATCTTTTCAGGAACACTAAATTACGAAATGACAGGAAGCTGCCAAATTGT
G.gallus           AAATATTTCCTCACCCAATCAACTGCATCAGCCCTAATCCTCTTCTCGAGCATAACCAACGCCTGATCCACCGGACAATGAGACATTAC
C.mydas            AAATATTTTCTAACACAAGCAACTGCCTCAACACTAATCCTATTCTCCAGCATTATTAATGCCTGAATACTAGGCCAATGAGATATTAC
S.punctatus        AAATATTTCATGACACAAGCCGCCGCCTCAGCCATATTAATCTTCGCAAGCACCATTAATGCTTGACAAACTGCCCAATGAGACATTTC
B.theili           AAATACTTCCTAGTACAATCTATTGCCTCAGCAGTAATAATATTCTCAGGAACACTAAATGCCATACAAACCGGACAATGAGACATCTC
C.rudis            AAATACTTTTTAACCCAAACAATTGCCTCAACTATAATGCTATTTTCAGGAACAATTAACGCTATTCAAACAGGACAATGAGATATTTC
C.brevicornis      AAATACTTCCTCACCCAAGCAATCGCTTCAACCTTAATACTATTTTCAAGCACAGTCAACACCATTCAAACAGGACAGTGAGATATCTC
C.salinarum        AAATACTTCTTAACCCAAGCAATTGCCTCCGCACTCATCCTATTTTCCAGCACACTAAATGCCTGACAAACCGGCTCATGAGACATTAC
P.leusterii        AAATACTTCCTCACCCAAGCAACAGCCTCCTCCATTATATTGCTCGCCAGCACAATAAATGTCTGACAAACAGGCTCATGAGATATTAC
P.cocincinus       AAATACTTATTGACCCAAGCAATCGCCTCAGCTATCATACTACTCTCAAGCTCATTAAATGCCTGACAAACGGGACTTTGAGACATTAC
Hydrosaurus.sp.    AAGTACTTCCTAACTCAATCAATCGCCTCATCAATCCTACTATTCTCAAGCATTACAAACGCCTGACTAACCGGACACTGAAACATCAC
C.calotes          AAATATTTCCTAACACAAGCAACCGCATCATGCTTACTTCTACTAGCCGGAACCTCAAATGCATGATTAACCGGAACTTGAGACATCAC
J.tricarinata      AAATACTTCCTAACGCAAGCCATCGCCTCCTGCCTCATATTATCTTCCAGCATTGCCAGCGCCTGACAAACTGGAAGCTGAGACATTAC
P.raddei           AAATACTTTCTAACGCAAGCTATTGCATCCTCAATAATATTACTATCAAGCACAATCAATGCCTGACAAACAGGTAATTGAGACATCTT
L.belliana         AAATACTTCCTGACACAAGCCATTGCCTCAACCCTAGTTATATTTTCAAGCACAATAAATGCCTGAGAGACAGGACAATGGCACCTCAC
U.acanthinurus     AAATACTTCCTAACACAAGCAATCGCCTCCGCCCTCCTTCTATTTTCAAGCACAATAAACGCATGACAAACAGGACAATGAGACACAAC
A.paternus         AAATATTTTCTTACACAAGCTGCAGCCTCTGCCTTAATTTTATTTTCTAGTATAACCAATGCATGACATACGGGATCTTGAGACATTAC
P.mcallii          AAATATTTCTTAACACAAGCAGCCGCCTCCGCCACAATCCTGTTTGCAAGCACAACAAACGCCTGACAAACAGGAACCTGAGACATTAC
Sauromalus.obesus  AAATACTTCCTAACACAAGCAGCCGCGTCCGCCATACTCCTATTCTCCAGCACAATAAACGCATGACAAACTGGAACATGAGACATCAC
Hoplocercus.sp.    AAATACTTCCTAACACAAGCAGCAGCCTCCGCCCTACTTCTATTCTCCAGCTCCATTAATGCATGAAAAATAGGAACTTGAGATATTAC
E.laticeps         AAGTACTTCCTGACACAAGCAACAGCCTCCGCCCTAATTCTCTTCTCAAGTTCACTAAACGCCTGAAAAACAGGAACCTGAGACATCAC
P.somuncurensis    AAATATTTCCTAACACAAGCTGCTGCATCAGCCCTAATTCTATTCTCAAGCACAATAAATGCCTGACAAACTGGATCCTGAAACATCAC
L.pictus           AAATATTTCCTAACACAGGCAGCCGCCTCAGCAATCATCCTATTTTCAAGCACAATTAATGCTTGACAAACCGGAACTTGAGACATTAT
U.flaviceps        AAGTACTTTTTAACCCAAGCTGCTGCCTCCGCCTTGATCCTATTCTCCAGCACTATAAACGCACAACTAACAGGATCATGAGACATCAC
S.crassicaudatus   AAATATTTCTTACACAAGCAACAGCCTCCGCCATAATCCTATTCTCCAGCATAATCAACGCATGACAATCAGGAATATGAAACATTAC
L.carinatus        AAATACTTCTTAACCCAAGCAGCCGCCTCGGCCCTAATCCTATTCTCAAGTACAATTAATGCCTGACACTCAGGAACCTGAGACATTAC
B.plumifrons       AAATACTTCCTAACACAAGCAGCAGCCTCCGCCCTGATCCTATTTTCCAGCACAATCAATGCCTGAAAATCGGGCACATGAGACATTAC
G.wislizenii       AAATACTTTTTAACACAAGCAGCTGCCTCCGCCCTCATCTTATTCTCAAGCACAATCAACGCATGAGACACAGGAACATGAAACATTTT
O.cuvieri          AAATATTTCTTAACACAAGCAGCCGCCTCAGCCACAATCCTCTTCTCAAGCACATTAAACGCCTGACAAACAGGCTCATGAGACATTAC
O.attenuatus       AAATACTTCCTAACACAAGCAGCAGCATCTGCCCTAATCCTGTTCTCTAGCGTAGTAAACGCCCAGGCAACAGGCCAATGAAGCATCTT
E.panamintina      AAATACTTTTTAACACAAGCAGCAGCATCCGCCCTAATCCTGTTTGCCAGCATTACAAATGCCCAAACCACAGGCCAATGAAATATTTT
C.enneagrammus     AAATACTTTTTAACACAAGCCGCAGCATCTGCCTTAATCCTATTCTCAAGCATAATTAATGCACTATACACCGGCCAATGAAATATTAT
A.pulchra          AAATACTTCCTTACACAAGCCACAGCTTCAGCACTTATCCTATTCTCAAGCCTAATCAACGCCCAAACTACAGGTCAATGAAACATCCT
H.suspectum        AAATACTTCTTAATTCAAGCTGGTGCCTCAGCCATAATTTTATTTTCCAGTATTATTAATGCATGATTTATAGGACAATGAGATATTCT
X.grandis          AAGTACTTCCTCACACAAGCTGCTGCCTCCTCATTAATTCTGTTCGCAAGTATCTTAAATGCCCAACCCTCAGGACAATGAGACATTAT
V.griseus          AAATACTTCCTAATCCAAGCCGCTACCTCCGCACTAATCCTATTTTCCAGCACTATCAATGCACTCTTCCACGGAACATGAGACATTAC
L.borneensis       AAATATTTCCTCGTCCAAGCCGCTGCATCATCAATAGTCCTATTTTCTGCACTAATTAATGCACAATCCACGGGATTGTGGGACATCAC
S.crocodilurus     AAATATTTTCTCACCCAAGCCGCAGCCTCTGCCCTAATCTTGTTTTCAAGTTCAATCAATGCACAACACGCAGGCCTATGGGATATTAC
D.semicarinatus    AAATATTACCTAATCCAAACCATAGCCTCCACCTCTATACTATTTGCAGCCACAACAAATGCCTTAAACACCTCAAACTGAGAAACCCA
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R.braminus         AAATACTTCCTAACACAAGCCATAGCCTCAGCAATAATTTTATTTGCAGCTACAATAAATGCCTCTAATACCGGACAATGAGAAATCAA
C.ruffus           AAATACTTCCTAACCCAAACCATAGCCTCAATAACCATACTATTCGCCGCAACAATAAACGCCCTAAACACCTCAAACTGAGAAATCAC
Agkistrodon.sp.    AAGTACTTCCTAACACAAACCCTTGCCTCCATAGCCATCCTATTCGCAACGACCATAAATGCACTTAACACCTCAAACTGAGAAATTAC
E.grammica         AAATACTTTATCATTCAAGCAACAGCATCCACCATCATCCTATTCTCAAGCACATTTAATGCTTGACACACCGGAATCTGAGACATCAC
B.biporus          AAATATTTCCTTATTCAAACCGCAGCCTCAACCACACTTCTATTCGCGAGCACAACAAACGCCTGAATCACAGGCCAATGATCCATCAA
T.weigmanni        AAGTACTTTCTTATCCAGGCCGCGGCCTCCAGCATACTACTCTTAGCCAGCATTATTAATGCACAAATAACTAGTCAATGAGATATCAC
A.xera             AAATACTTCCTAACTCAAACAGCTGCGTCAATCGTACTACTATTAGCCATCACCATAAACGCCCACACCACCGGCCAATGAGACATCAC
C.tigris           AAATACTTTTTAGCGCAAACAGGGGCATCACTATTAATACTATTTGCAAGCTCAATCAACGCATGATATCTGGGAACATGAGATATCAC
L.parietale        AAATATTTCCTCGCCCAAGCAGGCGCTTCAATACTTATATTATTTTCAAGCACCATAAACGCCTGAAACACAAACACCTGAGATATCAC
E.turkmenicus      AAATACTTCCTCACCCAAACAGCAGCTTCCACCCTAATCCTACTTTCAAGTACACTTAATGCCTGAACAACAGGACAATGAACCATTAC
S.shrevei          AAATACTTCCTAGTCCAAGCAATTTCAGCCGCACTAATCCTCCTAGCCAGCACTATCAACGCCTGACAAACCGGCCAATGAACCATTTT
T.przewalskii      AAATATTTCCTAATCCAGGCTGCTGCCGCAGCACCAATCCTATTCGCAAGCACACTTAATGCCTGAACTTCCGGCCAATGATCAATTCT
G.gecko            AAATACTTTCTCATTCAAGCCATGGCCGCTGCCCTAATCATGTTCGCTAGCACCTTAAACGCCTGACAGACCGGACATTGATCAATTAC
P.lindneri         AAATACTTCCTAACCCAAGCCACCGCCTCCGCCGTAATTCTATTCTCAAGCTCCATGAATGCCTGAAAGAATGGACAATGAGACATCAC
Cr.ocellatus       AAATATTTTTTAACTCAAGCCACAGCCTCCGCAATAATTTTATTCGCAAGCTCAATAAACGCCTGAAAAACAGGACAATGAGATATCTC
L.jicari           AAATACTTTTTCACACAAGCTGCCGCCTCCGCCCTAATCGTCTTTGCAACCACAATTAACGCCTGAAAAACGGGACAATGAGACATCTC
M.aurata           AAATATTTCCTCACCCAAGCTACAGCCTCTGCTATAATTCTTTTCGCCAGCACAACAAATGCATGAACAACCGGAACATGAGACATCTC
C.robustus         AAGTACTTTCTAATCCAGGCAGCAGCCTCCGCCACAGTCCTATTTGCCAGCACCACAAACGCCTGAACAACAGGAACATGAGACATCAC
S.sikkimensis      AAGTACTTCCTAATTCAAGCTGCTGCCTCAGCCACCGTACTGTTTTCTAGTGTAATCAATGCCTGATCTACAGGAACCTGAGATATTTC
E.inexpectatus     AAGTACTTCCTCACACAAGCCGCCGCTTCCGCCACAATCCTATTCGCCAGCACAATTAATGCCTGAACATCGGGCTCCTGAGACATTTC
E.skiltonianus     AAGTATTTTCTCACACAAGCCGCTGCCTCCGCCACAGTTTTATTCGCTAGCACCATCAATGCTTGATCAACAGGAACATGGGACATTTT
E.anthracinus      AAATATTTCCTCACACAAGCTGCAGCCTCCGCCACAGTACTATTCTCCAGCACTATTAATGCTTGATCAACAGGAACATGAGACATCAC
S.anguineus        AAATATTTCTTAACCCAAGCTGCAGCATCAGCCACAGTATTATTTTCAAGCACCATTAACGCTTGAGCCACCGGCACCTGAGACATCAC
P.eggeli           AAATATTTCCTAACACAAGCAGCAGCATCCGCCACAATCTTATTTTCAAGCACTATTAACGCCTGAGCCACCAGCACCTGAGATATCCT
F.polylepis        AAATATTTCCTAACCCAAGCCGCCGCATCCGCCACAGTCCTATTTGCAAGCTCAATCAATGCCCTCTCTACTGGATCATGAGATATCAC
Ch.ocellatus       AAATACTTCCTCACCCAAGCTGCCGCCTCAGCCATAGTCTTATTCTCAAGCACAACCAACGCCTGATCAACCGGCACATGAGACATTAC
A.meleagris        AAATACTTCTTGACACAAGCAGCAGCATCAGCAATGATCATATTCTCAGCCACAATAAATGCCTGATCAACAGGAACATGAGATATTAC
T.lomii            AAATACTTCCTAACACAAGCAGCAGCATCAGCAATAATCCTATTTTCTGCCACAATAAACGCCTGATCTACAGGAACATGAGATATCAC
T.gariepensis      AAATACTTTCTAACACAAGCAGCAGCATCAGCAATAATCCTATTCTCAGCCACAATAAACGCCTGATCCACAGGAACATGAGACATTAC
X.vigilis          AAATACTTCTTAACCCAAACAGCAGCCTCAACTATAATTTTATTTGCAAGTACACTAAATGCATGACACTCAGGACAATGAAACATTAT
C.polyzonus        AAGTATTTCCTCACACAAGCAGCTGCCTCTGCCATAATTCTCCTTGCAAGTTCCATCAACGCCTGGCACACAGGACAATGAGACATCAC
Zonosaurus.sp.     AAATACTTCCTAACCCAAGCAGCTGCCTCCGCAATAATTCTATTTTCTAGCTCTATTAACGCCTGGTATTCAGGACAGTGGGACATCAC
Dibamus            AAATACTTTCTCACACAGGCCGCCGCATCCGCCCTAATCTTATTCTCGAGCACCATAAACGCCTGACACTCAGGACAGTGAGACATCAC

Index1             66666666666666666666666666666666666666666666666666666666666666666666666666667777777777777
Index2             22222233333333334444444444555555555566666666667777777777888888888899999999990000000000111
Index3             45678901234567890123456789012345678901234567890123456789012345678901234567890123456789012
Qualifiers1        .........................................................................................
Qualifiers2        .1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1
A.mississippiensis AGAATTAACAAACTTAACTTCAATAATTGTGCTAACCCTTGCCCTATTTATTAAAGTGGGATTAGTACCATTTCACTTCTGAGTACCAG
G.gallus           ACAACTAAACCACCCGACATCATGCCTAATATTAACAATAGCAATCGCAATCAAATTAGGACTAGTCCCATTCCACTTCTGATTCCCAG
C.mydas            ACAAATATCAAACAACACATCATGCACAATTCTTACTACCGCCCTAGCCATCAAACTAGGACTCGCCCCATTCCACTTTTGACTACCAG
S.punctatus        ATTACTCACACCCTCAACACCAATAATAATATTAACACTAGCTATTACCATAAAACTAGGCTTGGCCCCATTCCACTTCTGATTACCAG
B.theili           ACAACTAACAAACAAATATGCTAACATTACACTTATACTAGCCATACTAATAAAAATTGGAGCAGCACCAATCTATTTTTGACTACCAG
C.rudis            CCAACTAACAGACAAATATGCCTGCACAATCCTCCTCATTGCCATAACAATAAAAATTGGAGCCGCCCCAATTTTCTTTTGATTACCAG
C.brevicornis      ACAAATAACAGATAAATACGCCTGTACAATACTATTATTAGCCATAACAATAAAAATTGGAGCAGCTCCAATTTATTTCTGACTACCAG
C.salinarum        ACAACTC---AACGAGACCTGTTCAACTTTAATAATTCCCGCCCTAGCAATAAAAATAGGAGCCGCCCCCGCCCACCTATGATTACCAG
P.leusterii        ACAACTCAATAATGAATTATCTTGCATCCTGATTACCTCAGCCCTAGTAATAAAAACAGGGGCCGCCCCAGCTCATTTCTGACTACCAG
P.cocincinus       ACAACTAACCAACGAACTCTCCTGCACCATGATAACCCTCGCCATCACAATCAAAATCGGCGCCGCCCCGGCTCACTTTTGACTACCAG
Hydrosaurus.sp.    ATTAATACAAAATGAATATGCCTGCTTATTTATAACCATCTCCCTAGCAATAAAAATAGGCGCCGCCCCATTACACTTTTGACTCCCAG
C.calotes          ACAAATATCAAACAAATTAACATCCACCATCATACTTATTGCCCTCACCATAAAAATAGGAACTGTACCAACCCACTTCTGACTCCCAG
J.tricarinata      ACAAATAACTAACAAATACTCATCCACAGTAATAGCCATCGCCCTCACAATAAAAATAGGCTCAGTTCCACTACACTTCTGACTTCCAG
P.raddei           AGAACTCAAAAACAAATTCTCCACAACAATTATAACCCTGTCCCTATTAATAAAAATAGGAGCCGCCCCCGTTCACTTTTGACTCCCAG
L.belliana         ACAACTATCAAACAACTACGCCTGTATCATAATAACTATTGCCCTAATAATTAAAGTAGGCACTGCCCCCATGCACTTCTGACTACCAG
U.acanthinurus     CCAGATAGACAACAAATACGCCTGCACAATCATAGCAATTGCCCTTGCCATAAAACTAGGAGCAGCCCCATTCCACTTCTGATTACCAG
A.paternus         TCAAATATTATTTTCTCCATCAAACACCATGCTAACCATAGCCCTAGCCATAAAACTAGGGTTAGCTCCACTTCACTTCTGGCTACCAG
P.mcallii          TAATATAACAAGCCTTACCGCAAACACACTCCTTACCATAGCCCTTGCAATAAAGCTAGGCCTTGCCCCAATACATTTTTGACTTCCAG
Sauromalus.obesus  ACAACTCACAAACCCCATAGCCACCATCCTACTCACAATGGCCCTAGCCACCAAACTAGGCTTGGCTCCAATGCACTTCTGACTTCCAG
Hoplocercus.sp.    TCAAATAACAGACCCACATGCAAACATCCTACTAACCTCCGCCCTCGCCATAAAACTGGGGCTCACCCCAATACATTTTTGACTTCCAG
E.laticeps         CCAAATAACAAGTCCAACTGCAAACACATTATTGATCACCGCCCTTGCTCTAAAACTAGGACTAGCTCCAATACATTTCTGACTCCCAG
P.somuncurensis    ACAACAAATCACAACACTACCAAGTATCCTCCTAACCATAGCCTTAGCAATAAAACTTGGCTTAGCCCCAACCCATTTCTGATTAACAG
L.pictus           ACAACTCACCAACCCAATAGCATCAATCCTACTAACCATAGCCCTCGCTATAAAACTAGGACTTGCCCCAGCCCACTTCTGACTTACCG
U.flaviceps        CCATCTCACTTCTATACAATCAGCCACCTTACTTACAATAGCACTAGCCATAAAACTAGGTCTCGCACCCACACATTTCTGACTCCCCG
S.crassicaudatus   CCAGCCATTAAGCCCAACATCCTCCATCCTACTTACAATCGCCCTAATAATAAAACTAGGTCTCGCCCCAGCTCACTTTTGACTACCAG
L.carinatus        ACAAACAACTAATAATATATCAAACATTCTACTAACAACAGCCTTAGCCATAAAACTAGGCCTAGCACCCACACACTTCTGACTACCAG
B.plumifrons       CCAAATAACAGACACAACATCAAACATCCTTCTAACCTCAGCCCTAGCAATAAAACTAGGAATAGCACCAATACATTTCTGACTTCCAG
G.wislizenii       ATCAATAACCAACCAACAAGCCAACATTCTATTAACCGCAGCCCTGGCCATAAAACTAGGTCTCGCACCCATACATTTTTGACTACCAG
O.cuvieri          CCAAATAAATTATATTCCATCCAACATTTTACTAACACTAGCACTTGCCATAAAACTAGGTCTCGCCCCCACTCACTTCTGACTACCAG
O.attenuatus       ACAACTAGAAGACCCCTCAGCCCAAACACTCCTAACAATGGCCCTAGCAATAAAACTAGGACTGGCACCAGCTCACTTCTGACTACCAG
E.panamintina      ACAACTAGAAAACCCCCTAGCCCAAACACTACTCACAATTGCACTAGCCATAAAACTAGGACTAGCACCGACCCATTTCTGACTGCCAG
C.enneagrammus     ACAACTAGAAAGTCCACTAGCCCAAATCCTACTAACCATAGCACTTGCCATAAAACTAGGGTTAGCACCAGCACACTTCTGACTACCAG
A.pulchra          GCAACTAGAACACCCCATTGCCCAAGTCCTTCTAACAATAGCACTAGCAATAAAACTAGGCCTTTCACCTGCACACTTCTGACTACCAG
H.suspectum        ACAACTATCAGACCCATTAGCTAAAACTCTACTTACAATTGCACTAATAATAAAACTAGGACTAACCCCCCTTCACTTCTGATTCCCTG
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X.grandis           ACAACTATCAGACCCCTTAGCTAAAGTGCTATTCACCATAGCCCTTGCCATAAAACTGGGCCTCTCCCCAACCCACTTCTGATTGCCAG
V.griseus           ACAACTCTCAGACAGTCTGGCCAAAATTATGCTAACTATCGCCCTCGCCACTAAACTAGGCCTCGCCCCCATACACTTCTGACTCCCAG
L.borneensis        ACAGCTCTCAAACGAAGCTGCAAAAATCATACTAACAACTGCACTCTCCATAAAACTAGGACTGGTCCCAATACACTTCTGATTACCAG
S.crocodilurus      ACAGCTCACAGATCCACAAGCAAAAATCCTCCTAACTCTAGCTCTTTCAATAAAACTGGGATTAGTTCCCCTACACTTCTGACTACCAG
D.semicarinatus     TCTCACAACAGAACCAATAGCAACAACTATTATTACACTAGCCCTCATAATAAAAATGGCAGCTGCCCCATTCCACTCCTGACTCCCAA
R.braminus          GGACTGCCCCCTACAAACTTCAACAATAATTCTATCGACAGCCCTTCTCATAAAACTTGGCTCAGCCCCATTCCACTTTTGAGTGCCTG
C.ruffus            ACTCATAACCGACAACACAATACTAGCCCTAATAACACTAGCCCTAATAATAAAAATTGCAGCAGCCCCCTTCCACTTTTGATTACCAG
Agkistrodon.sp.     TCTCACAACAGAAACCACAACTATAAAAATCATTACATTGGCCCTATTAATAAAAATAGCTGCAGCGCCGTTCCACTTCTGACTCCCAG
E.grammica          TCAACTATCCACATTTCCTACTACTGTGATACTAACAATTGCACTAACCATAAAACTAGGACTAGCACCCATACATTTCTGACTTCCCG
B.biporus           CCAACTAACCCTGTGCCCAACAAACGTAATTATAACATTAGCCCTACTAATAAAACTAGGTGTCGCCCCAGTACATGCATGACTCCCCG
T.weigmanni         ACAACTAACCACACAACCTGCAATTACCATACTAACTCTAGCCCTTATAATAAAACTAGGTGTAGCCCCAATACATAGCTGATTACCAG
A.xera              TCAAACTACGACCCAACCTGCACTAACCATGCTAACACTAGCCTTGGCAATAAAACTTGGCATCGCACCCCTCCATGCTTGACTACCAG
C.tigris            CCAACTCACAAACCAAATATCCTGCACCTTACTAACTATTGCCCTTTGCATAAAAATCGGCCTAACCCCAATACACCTATGACTACCAG
L.parietale         CCAACTAACCAACCCCTACGCATGCACACTACTAACCACTGCACTCTGTATAAAAATAGGGCTCGCCCCATTACACCTCTGACTACCTG
E.turkmenicus       CGAACTTCATCATCCACTAGCAATAATAATACTTACTTTGGCCGTAGCCATAAAACTAGGACTAGCACCCACCCACTTCTGGCTACCAG
S.shrevei           AACCACTACATCAACCTTCGCAACAATTATCCTAACCCTTGCCCTAACCATAAAACTCGGCCTCGCCCCCACCCACTTCTGATACCCTG
T.przewalskii       CCACCCAACCTCCCTACCTGCAACCCTATTAATGCTAGTTGCCCTAGCTATAAAGCTAGGACTAGCCCCGGTACACGCCTGATATCCAG
G.gecko             AAATACAACCAACATAGTCACAATCACTATAATTACCCTAGCACTTTTATTTAAATTAGGTGCAGCCCCAATACACGCATGATACCCAG
P.lindneri          CCAAACAAATACACCAGAATTCACCATAATACTAACTTTGGCCCTAGCCATAAAACTAGGATTAGCACCATTTCACTTCTGATTGCCCG
Cr.ocellatus        TCAACTATCAACAACCAGTGCAACCATAATACTTACTCTAGCCCTGGCCACAAAATTAGGGTTGGGTCCAATCCACTTCTGATTGCCAG
L.jicari            TCAAATTTTCCTCCCTGAAACATCCACCATCATTACACTAGCAATTGCTATAAAACTAGGACTAGCCCCCTTCCACTTTTGACTGCCTG
M.aurata            ACAACTAACAAACCAGCCATCTTGCATTCTACTAACAATAGCACTCTCAATAAAACTAGGACTTGCCCCACTACACTTCTGATTACCAG
C.robustus          ACAACTAACTAATCAACCATCCTGCATTCTTCTAACCATGGCCCTATCAATAAAACTGGGCCTAGCCCCCCTACACTTCTGACTACCAG
S.sikkimensis       ACAGCTCACAAATCAACCAGCCTCTATTATATTAACCATAGCCCTATCAATAAAACTTGGCTTAGCCCCCCTACACTTTTGACTCCCAG
E.inexpectatus      ACAACTAACAAGCCTACCCGCATGCACCCTTCTAACAATAGCACTATCAATAAAATTAGGACTCGCCCCCCTTCATTTCTGACTACCAG
E.skiltonianus      ACAGCTAACAAACCAACCCGCATGTATCATACTAACGATAGCGTTATCAATAAAACTAGGACTAGCCCCATTACACTTCTGATTGCCAG
E.anthracinus       CCAATTAACCAACCAACCAGCATGTATCACACTAACAATAGCACTGTCCATAAAACTAGGGCTCGCCCCACTTCACTTTTGGCTACCAG
S.anguineus         CCAAATAACACACCAGCCAGCCTGTATTCTACTAACCACAGCCCTTTCAATAAAACTGGGACTCGCCCCACTTCATTTCTGGCTCCCAG
P.eggeli            GCAAATAACGGACCCCGCAGCCTGCATCATTCTAACTATAGCCCTGGCCATAAAACTCGGACTTGCCCCCCTCCATTTCTGGTTGCCAG
F.polylepis         CCAGCTAACCAACCAACCGGCATGCATTCTACTAACAATAGCACTAGCAATAAAACTGGGACTAGCCCCAATACACTTCTGACTGCCAG
Ch.ocellatus        ACAAATTACCAACCAAGAAGCCTGTATTATATTAACAGTAGCTCTATCAATAAAACTAGGACTAGCCCCGCTACACTTCTGATTACCAG
A.meleagris         CCAACTAACAAACAATACAGCGTGCATCACATTAACAATGGCCCTATCAATAAAACTAGGCATCGCACCACTGCACTTCTGACTACCAG
T.lomii             ACAACTAACAAACAACACAGCGTGCACTACACTAACAATTGCCCTATCAATAAAACTTGGAATTGCCCCATTACACTTCTGACTACCAG
T.gariepensis       ACAACTAACAAACAACACAGCATGCATCACACTAACAATAGCACTATCAATAAAACTAGGAATTGCGCCACTACACTTCTGACTACCAG
X.vigilis           ACAACTAACAACGGAACCCGCTTCCACTGTACTAACCCTAGCCCTAACCATAAAACTAGGATTAGCCCCAGTACACTTTTGACTACCAG
C.polyzonus         ACAACTAACGAACCAACTATCCTCTACCCTAATAACCGCAGCCTTAGCTATAAAACTAGGCCTTGCCCCTACACACTTTTGACTACCAG
Zonosaurus.sp.      TAATATTACAAATGAACCCGCCTCAATCCTATTAACAATCGCACTTGCCATAAAACTAGGACTCGCCCCCCTCCACTTCTGACTGCCTG
Dibamus             ACAACTAACCTATCAACCAGCCTGCATCACCATCACCATGGCCCTAGCCATAAAACTAGGATTAGCACCCCTACATTTTTGACTTCCAG

Index1              77777777777777777777777777777777777777777777777777777777777777777777777777777777777777788
Index2              11111112222222222333333333344444444445555555555666666666677777777778888888888999999999900
Index3              34567890123456789012345678901234567890123456789012345678901234567890123456789012345678901
Qualifiers1         .........................................................................................
Qualifiers2         ..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..
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G.gallus            AAGTACTCCAAGGCTCCTCCCTAATCACTGCCCTACTACTCTCCACCCTAATAAAACTCCCCCAATCACACTCCTCCTCCTAACATCA
C.mydas             AAGTAATACAAGGAACTTCCACAACAACAGCTCTAATCTTAGTTACCTGACAAAAACTAGCCCCACTATCATTACTAATAATAACCTCC
S.punctatus         AAGTATCATTAGGAACAACCAACTCAGTTATATTAATTATCACAACATGACAAAAACTGGCCCCACTAGCCATCATTATTCTATTACAT
B.theili            AAGTAATACAAGGTACAACAATAAAAACAGCCTTAATTATTGCCACATGACAAAAAATTGCCCCAATTACCCTACTCTATATAACATTC
C.rudis             AAGTTATACAAGGTTCTACAACAATAACCGCCCTAATTATTGCCTCATGACAAAAAATTGCCCCAATTTCACTTCTCTTTATAACCTAC
C.brevicornis       AAGTTATACAAGGAACCACAACAATAACAGCCATAATTATTGCCTCATGACAAAAAATTGCCCCCATTACTATTTTATTCATAACCTAT
C.salinarum         AAGTACTCCAAGGAACCACTATCACCACCGCTCTACTAGTCACAACCTGACAGAAAATCGCCCCCATCACACTACTATACACAATTTCA
P.leusterii         AAGTATTACAAGGATCCACCCTTACCACTGCTCTCCTAATAACAACCTGACAGAAAATTGCCCCAATTACACTGCTATACACAATCTCA
P.cocincinus        AAGTGATACAAGGAACCACAATTCCAATCGCCCTACTAATAGCAACCCTACAAAAAATCCCACCACTTACACTCCTATATATAATAGCC
Hydrosaurus.sp.     AAGTAGTCCAAGGCTCAACTCTTTCTTCAGCCTTACTTATTACAACCTGACAAAAAATCGCCCCAATTGTACTAATATACATAACATCA
C.calotes           AGGTACTTCAAGGCAGCACACTACTAACCGCCCTACTAATTTCAACATGACAAAAAATTGCCCCTATAACACTTTTGTTCCTCATATCA
J.tricarinata       AAGTAATACAGGGCAGCACACTATACACCACCTTAGTAATCTCAACATGACAAAAACTAGCCCCCTTCGCCCTACTTTATTTCATATCA
P.raddei            AAGTATTACAAGGAACAACACTACAAACAGCACTACTTATCACAACATGACAAAAACTTGCCCCCATCTCATTAATATACATAATCTCA
L.belliana          AAGTTCTACAAGGCTCAACAATGCAAACAGCTCTCCTAATCACAACCTGACAAAAAATCGCCCCCATCACACTACTGTACTCAATAGCA
U.acanthinurus      AAGTACTACAAGGCTCTACCATACAAACTTCTTTACTAATCCTGACCTGACAAAAAATTGCCCCAATTGCACTACTATACACAACAGCC
A.paternus          AAGTAATTCAAGGATCAACAATACTAACTGCCTTTATTATTACTACATGACAAAAACTAGCCCCAATATCTCTAATTTTTTTAACTATA
P.mcallii           AAGTCCTACAAGGCTCCACCATTAAAACTGCCTTAATTATTACAACATGGCAAAAACTTGCCCCAATCGCTCTAATCCTTATAGTGTCT
Sauromalus.obesus   AAGTCCTCCAAGGCTCAACAATAAAAACAGCCCTCATCATCACCACATGACAAAAACTTGCCCCTATGGCACTAATCTACCTAACAGCC
Hoplocercus.sp.     AAGTACTACAGGGCTCCACAATAAAAACGGCCCTCATCATTAGCACATGACAAAAACTTGCACCAATAACACTAATCCTTTTAACAGCA
E.laticeps          AAGTACTTCAAGGCTCCACAATAAAAACAGCACTAATCATTAGCACCTGACAAAAACTAGCCCCAATAACACTAATCTTCCTAACAATA
P.somuncurensis     AGGTCATACAAGGCTCAACCACAGTAACCGCAATAATTGTTGCAACTTGACAAAAAATAGCCCCAATGGCCCTAATTATTACCACAATA
L.pictus            AAGTAATACAAGGAACAACAACAGAAACAGCAATAATCATCGCAACATGACAAAAATTAGCCCCAATAGCAATTATCTTTTTAACCGCT
U.flaviceps         AAGTTCTGCAAGGATCCACAATACTTTCAGCATTAATTATTACCACCTGACAAAAACTAGCCCCAATAACACTTCTATATTTAACAGTA
S.crassicaudatus    AAGTCCTACAAGGCACCACAACACCCACCGCCCTAATTATTAGCACCTGACAAAAACTAGCTCCAATAGCCCTAATTTACCTCACAGCA
L.carinatus         AAGTCCTACAAGGGACCTCGATGATAACAGCCCTAATTATCAGCACCTGACAAAAACTAGCACCAATAGCCCTTATCGTACTAACAAAC
B.plumifrons        AGGTTCTACAAGGATCAACTATAAAAACAGCCCTAATCATTACCACATGACAAAAACTAGCCCCAATAGCCCTTATAACCCTGACAGCA
G.wislizenii        AAGTACTACAAGGCTCAACAATAAAAACAGCACTCATCATTAGTACTTGACAAAAACTAGCCCCCATAGCCCTAATATACCTCACAATC
O.cuvieri           AAGTACTCCAAGGATCAACCATAAAAACCGCCCTAATCATTACCACCTGACAAAAACTGGCTCCAATAGCCTTAATTTACCAAACAATA
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O.attenuatus       AAGTACTACAAGGATCATCATTTAAAATCGGCCTGATCATTATTACATGACAAAAACTAGCCCCAATAACCCTACTCCTTCTAACATGA
E.panamintina      AAGTATTACAAGGCACATCATTCAAAACCACCCTAATCATCATCACCTGACAAAAACTGGCCCCAATAACACTCATATTACTAACATGG
C.enneagrammus     AAGTCCTACAAGGGGCCTCCCTAAAAACAACACTAATCATTGTGACCTGACAAAAACTAGCACCAATAGCACTTCTCTTCCTAACATGA
A.pulchra          AAGTACTACAAGGCTCATCATTAAAAACCACCCTAATCATTATCACTTGACAGAAACTAGCCCCAACAACAATCCTCTTCTTAACATGA
H.suspectum        AAGTTCTTCAAGGATCATCACTTACAACAGCACTAATCTTAGCCACATGACAAAAACTTGCACCAATGACCCTCCTTTATATAACAGCA
X.grandis          AAGTACTTCAGGGCTCCCCCCTTAAAACCTCACTAATCATTGTTACTTGACAAAAACTAGCACCAATAACACTTCTCTATCTCACATAC
V.griseus          AAGTACTTCAAGGAGTACCAATACTCACAGCACTTATCATTACCACCTGACAAAAAATCGCCCCAATATCACTCCTCATCATAACCTCA
L.borneensis       AAGTCCTCCAAGCCATGCCCATTTTAACCATATTAATTATTACAACCTGACAAAAACTTGCCCCAACAACCCTGCTCCTATTAATCTGA
S.crocodilurus     AAGTATTACAAGGCACATCCTTCCCAGTTATACTCATTATTATTACATGACAGAAACTAGCACCCATCACCATCCTCTACCTTACATTT
D.semicarinatus    GCGTATCACAAGGCACAACAACCCTAACAACCCTAACCATCCTAACCTGACAAAAAATTGCCCCACTAACAATTCTATTAACCACCCAT
R.braminus         AAGTACTTCAAGGCTCGCAAATAAAAACAGGACTAGTAATCCTCACCTGGCAAAAACTTGCACCAATAGCCCTTATTTTATCAATGGGA
C.ruffus           AAGTATCACAAGGAACAACCACCCTAACAAGCTTAACAATCCTCACATGACAAAAACTAGCACCACTATCAATCCTACTTACCCTGTCC
Agkistrodon.sp.    AAGTGGCACAAGGCGCTACAACGCTAACAACCCTGACAATCCTAACTTGACAGAAAATTGCCCCCCTCACCATCCTTATAGTCAACCAT
E.grammica         AAGTAATACAAGGTGTTACCCTTTCATCAGCCCTAATTATTACAACATGACAAAAACTACCCCCCATAACTCTACTCTATTTAACTACT
B.biporus          AAGTCATGCAAGGCGCCTCAACTACCATAGCACTAATCATGGCCACATGACAAAAACTAGCCCCGTTCATCCTACTCTACACAATTTCA
T.weigmanni        AAATCATACAAGGGACAACTACACAAATAGCACTAGTAGTAGCCACCTGACAAAAACTGGCCCCTATTGCTCTACTTTTTTCCACCGCA
A.xera             AAGTAATACAAGGGACCACCCTTAAAATAGCCCTCATCATGGCAACATGACAAAAACTTGCCCCCTTTACCCTATTATACACGCTAGCC
C.tigris           AAGTAATACAAGGAACAACCCTAAAAATAGCCCTCATCATTGCAACCTGACAAAAACTAGCTCCTATAAGCCTTATTTTAATAACATCT
L.parietale        ACACTATGCAAGGCACACCACTAAGCACCAGCTTTATTATTGCCACATGACAAAAGCTCGCCCCAATAGGGCTTATTATTATAACCCAC
E.turkmenicus      AGGTGATACAAGGAACGACAATTAAAACAGCACTACTTCTCACAACTTGACAAAAAATTGCCCCATTGACATTTATTTATTTAACATCA
S.shrevei          AAGTAATTCAAGGATCAACAATCACCACAGCCTTAATTCTATCTACATGACAAAAACTAGCCCCCCTCACACTAATATACATAACCCTC
T.przewalskii      AAGTACTTCAAGGCACTACTCTTACAACTGCACTACTTATAGCTACATGACAAAAACTTGCCCCATTAGCTCTGCTACTTATAATATAC
G.gecko            AAATCCTACAAGGCTCAACCTTAACAACAGCCATGATTCTAACAACATGACAAAAATTAGCACCAATAACCCTACTCTACATAATTAGC
P.lindneri         AAGTATTACAAGGCTCAACTCTACTAACTGCTACTATCATTTCAACCTGACAAAAACTAGCCCCAACTACTCTACTATACTTGAACATC
Cr.ocellatus       AAGTTTTACAAGGATCAACACTATTTATCGCTATAATTATTTCTACCTGACAAAAATTGGCCCCCATAGCCCTCCTCTTATAACCAATA
L.jicari           AGGTACTTCAAGGCTCCTCCCTCCCAATCGCAATATTAATCTCAACCTGACAAAAACTAGCCCCAACTGCCCTCCTTTTTATAACTATT
M.aurata           AGGTTTTACAAGGGACCTCAATAAAAACAGCACTCATCATTGCAACATGACAAAAACTAGCACCAATAACCCTACTCTACCTGACATAC
C.robustus         AAGTACTCCAGGGCACAACCATAAAAACAGCACTAATCATTGCTACATGACAAAAGCTAGCCCCAATAGCCCTACTTTACTTAACCCAT
S.sikkimensis      AAGTACTTCAGGGCACTTCCCTAAAAACAGCATTAATTATCACAACCTGACAAAAACTGGCCCCCCTAGCCCTTCTATTTTTAACCCAC
E.inexpectatus     AGGTCCTACAGGGCACCCCATTAACAACAGCACTAATCATTGTAACATGACAAAAACTAGCCCCCCTCACACTACTATACCTGACACAA
E.skiltonianus     AAGTCCTACAGGGCACCTCATTAAAAACAGCACTAATTATTGTAACCTGACAGAAACTTGCCCCATTAGCCCTACTATACCTCACACAA
E.anthracinus      AAGTACTACAAGGTACGCCACTAAAAACAGCATTAATTATTGTTACATGACAAAAACTAGCCCCCCTAACATTACTGTACCTCACACAA
S.anguineus        AAGTACTACAAGGGACATCACTAAAAACAGCCATAATTATTACAACATGACAAAAACTTGCCCCAATTGCCCTACTATACCTCACCCAT
P.eggeli           AAGTACTACAAGGCTCCTCCCTAAAAACAGCCTTAATTATTACAACATGACAAAAACTCGCCCCAATTACCCTACTGTACCTCGCCCAA
F.polylepis        AAGTTCTACAAGGCTCAACCCTAATCACCGCAATAGTTGTTACAACATGACAAAAACTAGCCCCACTGTCCCTACTATTCTTAACACAA
Ch.ocellatus       AAGTACTCCAAGGATCAACCTTAAGCACAGCCCTGATTATTACCACCTGACAAAAACTCGCCCCACTAGCACTATTATACCTTACACAA
A.meleagris        AAGTATTACAAGGCTCTACACTAAAAACAGCCCTAATCATCACAACATGACAAAAACTCGCCCCAATAGCACTAATATACATAACACAC
T.lomii            AAGTACTACAAGGATCAACACTAAAAACAGCCCTCATTATCACGACATGACAAAAACTTGCCCCAATAGCACTACTATTCATAACACAC
T.gariepensis      AAGTACTACAAGGATCAACACTAAAAACAGCCCTCATTATCACAACTTGACAAAAACTTGCCCCAATAACACTAATATTTATAACACAC
X.vigilis          AAGTAATACAAGGTTCAACTATTATAACAGCCATAATCCTTACTACATGACAAAAACTTGCACCAATAACAATCCTAATCATAACCCAC
C.polyzonus        AAGTAATACAAGGAACAACAATAAAAACAGCAATAATCATCACAACCTGAATAAAACTGGCCCCAATATCTCTTCTTCTATTAATCCAC
Zonosaurus.sp.     AAGTACTACAAGGCACAACACTAACAACCGCAATAATTATTACAACATGACAAAAACTAGCCCCAATAACCCTCCTAATTCTTACACAA
Dibamus            AGGTCCTTCAAGGAGCCTCCATAATAACCGCCATACTTATCACCACATGACAAAAGCTCGCTCCAATAGCCCTGATCTTCATAACATCA

Index1             88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
Index2             00000000111111111122222222223333333333444444444455555555556666666666777777777788888888889
Index3             23456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
Qualifiers1        .........................................................................................
Qualifiers2        1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1.
A.mississippiensis CCCCTTATCAACTTTGAATTAACCTCTGTAGTAGCTACTTTATCTTCCCTTGTTGCAGGCTGAATGGGACTAAACCAAACTCAAGTACG
G.gallus           CAGTCTCTTAATACCACCTTACTCACCCTCCTAGCAATCTCCTCCACCCTAATCGGAGGCTGAATGGGCCTAAACCAAACACAAACACG
C.mydas            CAATCCCTAAACACACCACTACTACTAATACTAGGACTAACATCTACCCTAATTGGCGGATGAAACGGATTAAACCAAACCCAACTACG
S.punctatus        AACTCATTAAATCATCACTTATTGACCAGCCTCGGTCTTTTATCTATGGTAGTTGGGGGGTGAGGAGGAATGAACCAATTACAAATTCG
B.theili           AACAACATACCACAAAAATTTATAATTATCCTAGGAACCATATCTCTTATTATTGGTGGCTTAGGCGGAATTAATCAAACACAACTCCG
C.rudis            AACCATCTACCCTCAAAAATTATTATAATTATTGGAATTACATCAATTGTAATTGGAGGATGAGGAGGCATCAACCAAACACAACTACG
C.brevicornis      AACAATATACCACCAAAAATTATAATAACAATTGGAATTATATCAACAATCATTGGAGGCTGAGGAAGCATTAACCAAACACAACTACG
C.salinarum        AATAATACCAAGTCAAACATACTACTTATAATCGGACTACTATCCATCCTAATTGGGGGCTGAGGTGGAATCAACCAAACACAACTACG
P.leusterii        AATCACATTCAGTCAAACATTACACTCCCAGTAGGCCTGCTTTCCATCCTAGTGGGAGGATGAGGAGGGATCAACCAGACACAACTACG
P.cocincinus       AACCACACAAAACCCAACATCACACTCACACTAGGTATGCTATCAATCCTAGCAGGAGGATGAGGTGGCATTAACCAAACACAACTTCG
Hydrosaurus.sp.    AACCACCTACCACCAAACACTCTAATAACAATCGGCGCCCTCTCAATCCTAGTCGGGGGTGCAGGCGGAATAAACCAAACCCAACTACG
C.calotes          AACAACACCCAACCAACCTTCACACTGATATTAGGCCTTCTTTCAACCGCCTTTGGCGGATGGGGCGGTATAAACCAAACACAATTGCG
J.tricarinata      AACCACATACAACCCGTTATTATCTTAACACTTGGAATCCTATCAACAACATTCGGAGGCTGAGGGGGAATAAATCAAACCCAACTACG
P.raddei           AACAACACCCAGCCTACCATTTTAATGCTCACAGGACTCCTGTCAATAATTATTGGAGGATGAGGCGGTGTAAACCAAACACAACTGCG
L.belliana         AACCACCTCCCAACAAAAATAACAATAACGCTAGGCATCCTGTCCACACTAATTGGTGGCTGAGGGGGAATCAACCAAACCCAAACCCG
U.acanthinurus     CCACATCTCCCCCAAAAAATCATACTAACAATTGGCATCATGTCTACAATAGTGGGCGGTTTTGGGGGACTAAACCAAACCCAACTACG
A.paternus         AATAGTATGTCCACAACAATTCTTCTACTAATGGGAGTCTTATCCTCACTTGTTGGTGGTTGAGGGGGGTTGAACCAAACACAGACCCG
P.mcallii          AATAACCTATCCCCAACAACCCTTCTAACAATAGCCATAATCTCAACCCTCTTAGGGGGTTGAGCCGGACTTAACCAAACCCAAACCCG
Sauromalus.obesus  AACAACCTATCTACCCCCACCCTCCTAACAATAGCCATCCTATCCACCCTACTAGGTGGCTGAGGTGGACTAAACCAAACCCAAACCCG
Hoplocercus.sp.    AACAACCTTTCAACTCCAATATTACTAACCATAGGAGTACTATCTGCTTTAACCGGCGGCTGAGGAGGACTAAACCAAACACAAACTCG
E.laticeps         AACAACCTACCTACAACAATTTTATTAACAACAGGAGCCATCTCTGCCCTAATCGGCGGATGAGCCGGACTAAACCAAACACAAACTCG
P.somuncurensis    AATAACCTATCACCAACAACCATATTAATCCTAGCCTCCACATCTACCATTATTGGCGGCTGAGGCGGACTAAACCAAACCCAACTACG
L.pictus           AACTCCCTAACACCAACAATTCTATTAACAATAGGCATACTCTCCGCCGCCATCGGGGGCTGAGGTGGACTAAACCAAACTCAAATACG
U.flaviceps        AACAACATACCAACAGTACTTCTCTTAAGTCTTGGAATCTTATCCACACTAATTGGAGGCTGAGGCGGTCTCAACCAAACACAGACACG
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S.crassicaudatus   AACAACCTATCACCCACCACCCTAATCCTAATAGGAACCCTCTCCACATGGATCGGAGGCTGAGGCGGACTTAACCAAACACAAACACG
L.carinatus        AATAACTTATCTTCAACCGTGCTGATAACAATAGGTATTTTATCTGCCATCATTGGGGGCTGAGGCGGACTAAACCAGACCCAAACACG
B.plumifrons       AACAACCTCTCCATAACCACCCTAATCTTAATGGGCATTTTATCCGCCATAGTCGGAGGATGGGGGGCCTCAACCAAACTCAAACCCG
G.wislizenii       AATAACTTATCCCCAACAATCCTCCTAATAATAGGCCTTCTTTCAACAACTATCGGCGGCTGAGGCGGCCTAAACCAAACACAACTACG
O.cuvieri          AACAACCTATCACCAACATTACTATTTATACTAGCAATAATCTCAACCTTACTCGGCGGATGAGGCGGACTAAACCAAACCCAACTGCG
O.attenuatus       AACCAAACCTCTATGATTACCATCACAATAATGGGTCTCCTATCAGTAATTATCGGCGGGTTTGGCGGATTAAATCAAACGCAGCTCCG
E.panamintina      AACCAAACCTCCATACTAACAATTACAATGATAGGAGCCCTATCAGTAGTAATCGGAGGACTCGGCGGACTAAACCAAACGCAACTACG
C.enneagrammus     AACCAAACTTCAACACTTACTATTTCAACAATAGGGGCCCTCTCCGTTCTAGTTGGAGGACTAGGTGGACTCAACCAAACGCAACTCCG
A.pulchra          AACCAGATATCCACACTTACAATCACAACAATAGGAATCCTGTCAGTGCTAACAGGCGGCCTAGGCGGCCTAAACCAAACACAACTACG
H.suspectum        CACCAGATCTCAACAACTATTCTTTTAATTATTGGAACCATATCAACAATTGTAGGCGGCCTAGGCGGACTAAACCAAACACAGCTACG
X.grandis          AATCAAACCTCAACACCAACCCTAATTACAATTGGCATCATCTCCGTACTAGTTGGGGGGTTAGGGGGCCTAAACCAGACACAACTGCG
V.griseus          AAACTCATCCCCACCCCCATCACCCTCACCATAGGACTTACATCAACAATCGTGGGGGGATTAGCCGGCCTCAACCAGACCCAGCTTCG
L.borneensis       GACCAGATTCCCACCTACCCTATTGCCACAATCGGCTGGCTATCCATCCTTATCGGAGGACTTGGCGGCTTAAACCAAACACAGTTACG
S.crocodilurus     AACCAAATTTCCTCTATCACGTTACTAACAATAAGCACACTATCAATCATCTTAGGAGGACTATGAGGCCTAAACCAAACCCAACTCCG
D.semicarinatus    AATAAAACAAATATTACCCTAATCCTACTATCCGCAATACTATCCATCACAATAGGAGGCCTTGGAAGCCTTAACCAAACCCAACTACG
R.braminus         GACGCACTAAACCAAAAGGTTTTAATTACCTCAGCAATTTTCTCAATTCTSCTTGGGGGCTGAGGTGGATTAAACCAAACTCAACTACG
C.ruffus           AACAAAATCAACCAAACCATCCTTCTATCCATAGCAATCCTATCAATCACAGTTGGAGGCTTAGGAGGCCTCAACCAAACACAACTACG
Agkistrodon.sp.    AACAACACCAACCTAACAATCCTAAGCTCCTCAGCAATCTTATCTGTGCTAGTAGGGGGACTGGGCGGACTTAACCAAACCCAACTCCG
E.grammica         CCCAACCTCCCAACTCCAGTTCTACTTATATTAGCTATAACTTCAACAGTAGTTGGAGGTTGATCAGGGCTCAACCAAACCCAAATACG
B.biporus          AACAACACGTACACAACACTACTCCTCCCACTGGCACTGCTATCAACTACACTTGGAGGCTGAGGCGGACTAAACCAGACACAAATCCG
T.weigmanni        CACACACTACACACACCAACAATCCTAGGACTAGCTCTTCTATCAACCCTAATTGGTGGATGAGGCGGCCTAAATCAAACACAACTGCG
A.xera             CACATATTACACACCCCCACCATTATAATACTAGCAACCATCTCCATCTTGCTGGGCGGCTGAGCCGGCCTAAACCAAACACAACTCCG
C.tigris           AACAGCCACTCAAAATTTATATTAATATCAATAGCAGCACTATCCATTGTTATTGGTGGGTGAGGCGGATTAAATCAAACACAACTACG
L.parietale        AATAGCCATTCAAAACTAATATTATTAACAATAGCATCAGCATCAATCTTTATTGGCGGCTGGGGGGGCCTAAACCAAACGCAATTACG
E.turkmenicus      AACCATCTCTCAACTAAAATATTATTTACCTTAGGTCTCCTATCCGTAATATTAGGTGGAATCACAGGACTAAACCAAACACAAACCCG
S.shrevei          CACCAACTACCAACAGCAATCATCCTCCTAATCGGACTCACCTCTGCCTTAATCGGGGGCTGAGCAGGCCTAAATCAAACCCAAATACG
T.przewalskii      AACCACCTACCACAAAATACCCTACTCACACTCGGTCTTCTTTCCGCCTGTATCGGCGGATGAGCAGGCCTCAACCAAACACAAACACG
G.gecko            CCCCATCTCCCCCAACAGCTCATTCTTGTAACAGGACTTCTCTCAGCTCTAGTAGGCGGCTGGTCAGGACTAAATCAAACCCAAACTCG
P.lindneri         AACAATCTTAATCAACTAACACTAATAATCTTAGGACTATTTTCAGCCCTGCTAGGCGGATGACTCGGGGTAAACCAAACACAAACCCG
Cr.ocellatus       AATAGCCTAAACCAACAAGTACTGATAACTCTTGGTCTAATATCAGCCTTCTTAGGAGGATGACTAGGACTAAACCAAACACAAACCCG
L.jicari           AATAACCTAAACCAAAACATTCTAATTCTTCTAGGACTTATTTCAACCCTTATCGGAGGATGAATGGGACTAAACCAAACCCAAACACG
M.aurata           AACTCAATCAACTCTACAATCCTACTAACAATAGGAATACTATCAGCTCTAACGGGCGGATGGGGCGGCCTAAACCAGACACAAACACG
C.robustus         CAGTCACTGCACCCAATGACACTACTAACAATAGGCCTTTTATCTACCTTAGTTGGCGGTTGAGGTGGACTAAACCAAACACAAACACC
S.sikkimensis      CACTCATTACACCCAACAACCCTACTAACAATAGGGCTCCTATCAACACTAATCGGGGGTTGAGGCGGCCTAAACCAGACACAAACACG
E.inexpectatus     AACTCACTATGCACAACAACACTACTAATAATAGGGCTACTATCAACTTTAACCGGGGGCTGAGGCGGACTTAACCAAACACAAACACG
E.skiltonianus     AATTCACTGTGCACAACAACACTATTAATAATAGGACTACTATCGACCCTGTTTGGGGGCTGGGGCGGATTAAATCAAACACAAACACG
E.anthracinus      AATTCACTGTCTACAACAACCCTCYTAACAATAGGACTACTATCAACCCTAATCGGGGGCTGAGGGGGATTAAATCAAACACAAACACG
S.anguineus        AACTCAATCAACACAACAATTCTACTTACACTAGGATTACTATCCACTGTAATTGGGGGGTGAGGAGGCTTAAACCAAACACAGATACG
P.eggeli           AACTCAATCAACACCCCCGCCCTATTAACACTAGGACTTATATCTACAGTAATTGGGGGCTGAGGCGGCCTTAACCAAACACAAATACG
F.polylepis        AGCTCCCTCAACCCCCACGCCCTTCTGACACTTGGAATCTTTTCCACCATCCTAGGAGGATGAGGCGGACTCAACCAAACACAAATACG
Ch.ocellatus       AACTCATTAAACACACCCATACTATTAACGATAGCAGTCCTATCAACAATCACCGGAGGTTGAGGGGGCCTTAACCAAACACAAATACG
A.meleagris        AATTCCATCAACCCAGAATTACTCCTAACTATGGGAATTTTATCCACAATAATCGGCGGATGAGGAGGACTAAACCAAACCCAACTACG
T.lomii            AACTCCATCCACCCTGAACTACTACTAACTATAGGAATTTTGTCCACAGTCATCGGAGGATGGGGGGGCCTAAACCAAACCCAATTACG
T.gariepensis      AACTCAATTCACCCAGAACTACTACTAACAATAGGAATTATATCAACAATCACCGGCGGATGAGGCGGACTAAACCAGACCCAACTACG
X.vigilis          CAAAACTTACCTACAACAATTCTACTAACAATCGGCATCATCTCCTCATTATGAGGAGGATGAGCAGGACTAAACCAAACACAGCTCCG
C.polyzonus        ACCTCCCTAAACCACCATATTCTACTATCCCTAGGCGCACTATCTATTTTAGTCGGAGGGTGGGGAGGATTAAACCAAACACAAATCCG
Zonosaurus.sp.     CATAAACTTAACTCTACATTACTAATAACCCTCGGAATCCTATCAATCCTAGTTGGCGGCTGAGGAGGACTAAATCAAACACAACTACG
Dibamus            AACCACCTATCAACAATAACCCTATTAACATTAGGACTAGCCTCAACAATAATTGGGGGCTGAGGCGGCCTAAACCAAACGCAACTTCG

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Index2             99999999900000000001111111111222222222233333333334444444444555555555566666666667777777777
Index3             12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789
Qualifiers1        .........................................................................................
Qualifiers2        .1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1
A.mississippiensis AAAATTAATAGCACTATCGTCCATTGCCCAAATAGCATGAATTATCGTAATTATTAAATACGCACCATCACTAGCCATCCTAACCTTCT
G.gallus           AAAAATCCTAGCCTTCTCATCCATCTCCCATTTAGGATGAATAATTATAATTATCTCCTATAACCCACAACTCACTATTCTCACCTTCA
C.mydas            AAAAATCATAGCATTCTCCTCCATCGCCCATCTAGGATGAATAATTACAATCCTTACTTTATCCCCCAAACTTATATTATTTACATTCT
S.punctatus        AAAAATTATAGCATACTCCTCAATCGCCCATATAGGATGAGTAGTTATAATTTTACCAAAAGCCCCAGACCTATCCCTACTGTACCTTA
B.theili           AAAACTAATAGCCTACTCATCACTAACCAACCTAGGCTGAACAGTGATAATTTTTTCAATATTCCCACACACCGCAGTACTTAACATTG
C.rudis            AAAATTAATAGCATATTCATCAATTTCAAACATTGGATGAACAATAGTAATTTTCACAATTTCCCCACATACAGCAGTACTAAATATTG
C.brevicornis      AAAACTAATAGCATACTCATCAATTACAAACCTGGGATGAACTATAATTATTTTTACAACTTCACCACACACTGCTACACTCAACATTG
C.salinarum        AAAAATAATAGCCTACTCATCAACCGCCCACTTAGGATGAACAATTACAACAATATCAGTCATACCAAACATTGCACTACTAAACATTA
P.leusterii        AAAAATAATAGCCTACTCGTCAATCGCTCACCTTGGATGGACAATAACTGCAATTTCGATCACACCCAACATTGCTCTACTAAACATTT
P.cocincinus       AAAAATAATAGCCTACTCATCAATCACCCACCTCGGATGAACAATAACAGCAATTTCAATTTCCCCAAATATTGCCATATTAAATATTA
Hydrosaurus.sp.    AAAAATAATAGCATACTCATCAATCGCCCACATTGGATGAACAATACTGGCAATAGCCACAGCACCCAATATTTCCATACTAAATATTG
C.calotes          AAAAATAATAGCCTACTCATCAATTGCAAACATAGGCTGGACTATTATTATTCTTACCCACGAACCAAAAGCATCAATAATCAACATCT
J.tricarinata      AAAAATAATAGCCTACTCATCAATTACCAACGTAGGTTGAACACTGATGACCCTTACATCAGAACCAAATACATCTGCAATCAACATTA
P.raddei           CAAAACAATAGCTTACTCATCAATTAACAACCTAGGTTGAACTATTATAATTATATCCCTCTCTCCCAATATAGCAATCATAAATATCT
L.belliana         AAAACTCCTAGCCTACTCCTCCATCGCCCACATAGGATGAACTCTAATAATTATTACCATCTCACCAAACATCGCCGTACTCAATATCA
U.acanthinurus     AAAAATCTTAGCCTACTCATCAATCTCAAACTTAGGATGAACCGTATCAGCCATGACACTAGCACCAAACATTGCAATCTTAAACATCC
A.paternus         AAAAATCATAGCATACTCATCAATTGCCCACCTCGGATGAATAGCTACAATTTCATCTATTATAACAAACATCTTAATTTTAAACCTAA
P.mcallii          AAAGATTATAGCATACTCATCAATTGCACATCTAGGCTGAATGGCCGCAATTACCACAATTATACCTACTATCCTTACACTTAACCTAA
Sauromalus.obesus  AAAAATCATAGCATACTCATCAATCGCCCACCTAGGCTGAATAGCAGCAATCACCCCCATATTAACAAACATCCTAACTCTAAACCTAA
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Hoplocercus.sp.    AAAAATTATGGCCTACTCATCCATCGCCCACTTAGGCTGAATAGTCACAATTGTCACAACACTAACAAACATCACAACCCTCGCCCTAG
E.laticeps         AAAAATCATAGCTTACTCATCAATCGCCCACCTTGGCTGAATAGTCACAGTCGCTACCACATTAACAAACATAATAACAGTTGCCCTTA
P.somuncurensis    AAAAATTATAGCCTATTCATCAATCGCACATCTAGGCTGAATAGCTGCAATCTCAACTATCATAACAAACATTTTAACACTCAACTTAC
L.pictus           AAAAATCCTAGCCTACTCATCAATCGCCCACCTAGGCTGAATAGCCGCCATCTCAACCATAATAACTAACATCCTTACACTAAACCTAA
U.flaviceps        AAAAATTATAGCCTATTCATCAATTGCCCATCTTGGCTGAATTACAGCCGTCTCCCAAATACAAACCAACATCTTATGCCTCAATCTAA
S.crassicaudatus   CAAGCTAATAGCCTACTCATCAATCGCCCACTTTGGATGAATAATAACAATTACCCCGATACTAACCAACATCATACTCCTAAACCTCA
L.carinatus        AAAAATCATAGCATACTCATCCATCGCACACCTAGGCTGAATGGCAATCATCACCCCACTAATAACTAACCTACTCATTTTAAACCTAA
B.plumifrons       AAAACTAATAGCATATTCCTCAATCGCACACCTAGGATGAATGGCTACAATCTCAACAATAATAACAAACATCATAGTCTTAAACCTAT
G.wislizenii       AAAAATCATAGCCTACTCATCAATCGCACATCTAGGCTGAATCGCAGCAATTGGCCCAATAATAACTAACATCATAACCCTGAACCTAG
O.cuvieri          GAAAATTATAGCATACTCATCAATTGCCCATCTTGGTTGAATAGCAGCAATCATACCTATCATGCCTAACATTCTAATCTTAAACCTCA
O.attenuatus       AAAAATCATCGCATTCTCCTCAATCTCCCACCTAGGATGAATGGCCACAATTATTACAAAATCCAATAAATTAGCTCTTCTAAACCTAA
E.panamintina      AAAAATCATCGCATTTTCCTCAATCGCCCATCTCGGATGAATAGCAACAATTATCACTAAATCCAACAAACTGGCCCTTCTCAACCTCA
C.enneagrammus     AAAAATCATTGCATTCTCATCAATTGCACACTTAGGATGGATAGCTACCATCATTCCAAAATCCCACAAACTTGCCCTATTAAACCTCA
A.pulchra          AAAAATTATGGCCTTCTCATCTATCGCCCACCTAGGATGAATGGCCACAATCATCACCAAATCCAACAAACTAGCCTTCCTAAACCTAA
H.suspectum        AAAAATAATAGCATTCTCCTCAATTGCCCACTTAGGTTGAATAACAGCAGTTATCACATTATCTACAAACCTAGCAATATTTAACCTAG
X.grandis          AAAAATATTAGCCTTCTCCTCAATTTCACATCTCGGATGAATAGCCACAATTATAACTACAAACCCTAACCTTTCCCTACTAAGTCTAG
V.griseus          AAAAATAATAGCCTTCTCCTCAATCGCCCACCTAGGTTGAATGACTGTAATCATTACAATTACCCCAAGCCTCTCACTATTTAATCTAA
L.borneensis       AAAAATAATAGCCTACTCCTCCATCGCCCACGTAGGGTGGACAGTAACAATCCTTACAATTTCCCCAAGCGTTGCCCTATTTAGCCTCG
S.crocodilurus     AAAAATTCTAGCATTCTCCTCCATCGCCCACTTAGGCTGAATAACAGCAGTTCTAACAATATCACCAAACCTTGCCCTCTTTAACCTCA
D.semicarinatus    AAAACTAATAGCCTTCTCATCAATCGCTCACACGGGCTGAATCATAGCAACTATCACAATAGCACCAAAAATCTCAACCTTAACCTTCA
R.braminus         AAAGCTAATAGCCTTCTCATCAATCTCACACATAGGATGAATCTTACTCACAGTCGGACTAGCCCCGAAAACATCAGCCTTCGCTTTAA
C.ruffus           AAAAATCATAGCCTTTTCATCAATCGCTCACACAGGATGAATTCTATCAACAATAGTAATCGCACCAAATATCTCAACACTAACCCTAA
Agkistrodon.sp.    AAAATTAATAGCCTTCTCATCCATCGCCCACACAGGCTGAATCCTCGCAACCATTACCCTAGCACCGAACATCTCCACTTTAACCTTCT
E.grammica         CAAAATCATAGCCTATTCATCAATTGCACACCTAGGATGGATAGTCGCAGTACTTTCCCTATCGCAAAACCTCCTATTATTTACATTAC
B.biporus          AAAGATAATGGCATTCTCCTCAATCGCCCACCTAGGCTGAGCTATCGCCACATTAACATTCAACCAAATACTCCCGCTACTAACACTAG
T.weigmanni        AAAACTAATAGCCTTTTCATCAATTGCCCACCTAGGCTGAATCATCTCAATAATACCGCTAAACATAAGCCTAACTATAATTACACTAA
A.xera             CAAATTAATAGCCTTTTCATCAATCGCACACCTAGGCTGAATCATCGCTGTCCTAACCACAAACAAGCACATTGCATTAATCACACTAG
C.tigris           AAAAATCATAGCCTATTCCTCAATCGCAAACATAGGGTGAATAGTTATTATTTTACAACAAGCACCGAAACTTACAACACTTACCCTGA
L.parietale        AAAACTCCTAGCCTACTCTTCCATCGCCAATATAGGATGAATAGTTATTATTGTTTCAACAACCCCAAAACTTACCTCAATAACACTAA
E.turkmenicus      AAAAATTATAGCGTACTCTTCCATTGCACACATAGGCTGACTCACAATAATCCTCACATTAAATCTCAATCTTATAACTTTCACCCTTA
S.shrevei          AAAAATCATAGCATTCTCGTCCATTGCCCACATAGGCTGACTAATAGCCGCTATAACTCTCAACTACAACCTAACAACACTAACCCTAA
T.przewalskii      AAAAATCATAGCATTTTCTTCAATTGCCCACATAGGATGACTATTAACCGCCCTAATTCTTAGCCAAAGCCTAACAACCCTTACCCTCC
G.gecko            AAAAATCATAGCCTTCTCATCAATTGCACACATAGGATGGCTCATTATCGCCCTGCACTTGAGCCTTACCCTCACAACAACAACACTTT
P.lindneri         AAAGATCATAGCATTTTCATCAATCGCCCACATAGGATGAATCTTTATAGCACTAACAATAAACCCAAATATAACATTACTAACCCTAA
Cr.ocellatus       AAAAATCATAGCATTTTCCTCTATCGCTCACATAGGCTGACTTTTTATAGCTTTAACAACCTCTCCTAACCTAACCATTCTCACCCTAA
L.jicari           AAAAATCATAGCATTCTCATCTATCGCCCACATGGGATGAATGTTCACATCCCTAGCTCTTACCCCCTACCTTTCATTACTAATTCTTT
M.aurata           AAAAATCATGGCATTTTCATCAATCGCACACCTCGGATGAATAGCAAGCATTCTAACACTCAACCCAAACATCCTTATTCTAAACCTAC
C.robustus         GAAAAATCTAGCATACTCATCGATTGCCCACCTAGGTTGAATAGCCTCAATCCTAACACTAGCCCCAAACATCATACTACTAAACCTCG
S.sikkimensis      AAAAATCATAGCATATTCATCAATTGCCCATCTCGGATGAATAGCCACAATCCTTACAATAGCCCCAGACATTATAGTCCTGAACCTAA
E.inexpectatus     AAAAATCATAGCATTCTCATCAATCGCCCACCTAGGATGAATAGCAACAATCCTAACACTAGCCCCAAACATTATACTGCTAAACTTAA
E.skiltonianus     AAAAATCATAGCATTTTCATCAATCGCACATCTAGGATGAATAGCAACAGTCCTAACCCTCGCCACAAACATCATACTACTAAACCTAA
E.anthracinus      AAAAATTATAGCATTTTCATCAATCGCCCACCTAGGTTGAATAGCAACAATCTTAACACTCGCCACAAATATCCTGCTACTAAACCTAG
S.anguineus        AAAAATTATAGCATACTCATCAATCGCACACCTAGGATGGATGGCTGCTGTACTGACACTTGCCCCAAACATTTTACTACTTAATCTAA
P.eggeli           AAAAATCATAGCATTCTCATCAGTTGCACACCTAGGCTGAATAGTAGCCGTACTAACACTAGCCCCAAACATTATACTTCTAAACCTAA
F.polylepis        AAAAATTATGGCATACTCATCAATCGCACACTTAGGATGAATGGTCTCAGTACTGGCAGTGGCACCAAACATCATACTCCTGACTCTTT
Ch.ocellatus       GAAAATTATAGCATTTTCATCCATTGCCCACCTCGGCTGAATAGCAGCAATCCTAACAATCAACCCTGACATAATACTACTAACCCTAG
A.meleagris        AAAAATCATAGCATTTTCATCAATCGCACACCTCGGATGAATGGCATCAATCCTAACCATGGCACCAAACATCATACTACTAAACCTGA
T.lomii            AAAAATCATAGCCTTCTCATCAATCGCCCACCTTGGATGAATAACATCAATCCTGACCTTGGCACCAAACATTATACTACTAAACCTAG
T.gariepensis      AAAAATTATAGCATTTTCATCAATCGCCCATCTTGGATGAATAGCATCAATCTTAACCCTGGCACCAAACATTATACTACTAAACCTGG
X.vigilis          TAAAATCCTAGCATATTCTTCAATTGCACACCTAGGATGAATCTATGTAGCTATTTCAATGGACGAAACAATCACAATTTTAACCCTGC
C.polyzonus        TAAAATCATAGGATTCTCATCAATCTCCCACTTGGGCTGAATAACAATTGTCATCACCCTATCCCCTTCCCTAGCTCTCTTAAACCTAA
Zonosaurus.sp.     AAAAATCATAGCTTTTTCCTCAATCGCCCACCTTGGATGAATGGTAACCGTACTAACCCTAATGCCAACACTCACTATTATTAATCTCA
Dibamus            CAAACTGATGGCATTCTCATCCATCGCCAATCTTGGTTGAATAGCAACAATTTCAACCATCGCCCCAAATATTATGCTACTTAACCTAG

Index0             00000000000000000000111111111111111111111111111111111111111111111111111111111111111111111
Index1             99999999999999999999000000000000000000000000000000000000000000000000000000000000000000000
Index2             88888888889999999999000000000011111111112222222222333333333344444444445555555555666666666
Index3             01234567890123456789012345678901234567890123456789012345678901234567890123456789012345678
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Qualifiers2        ..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..
A.mississippiensis ACATCTACTCCACCACCATCTCCGCTACACTGTTAACACTAGACAAAATATCAACAACCTCCATTAAATACCTCATTATTTCTTTTTCA
G.gallus           TCCTCTACACAATTATGACCTCAACTGTATTCCTATCCCTAGCCCAAATCAAAGTCCTAAAACTGTCAACACTACTCATCTCATGAACT
C.mydas            ACACCTACATCATCATAACCTCAACAATATTCCTAATAATTAAACTCCTAAAAACAAACAAAATCTCCACAATAATAACATCATGAACA
S.punctatus        TACTATATATTATGTTAAACCTCACAATATTCTTAATTATTATTTCCACCGCCCTAACCAAGCTGACAAGCCTTTTTTCAACACAAAAC
B.theili           CTACCTATATTATTATATCAATCCCCACCTTCTTTTTAATAGAAAAAATAATACTAAAAACACTACAAAATATAACAACTGCATGAACA
C.rudis            TTATCTACATAATTATGCTAATTCCAACATTTACACTCATTAAAAAAATATCTTTAAAAACACTTCAAGACTCAACAACTACATGAACA
C.brevicornis      TCATCTACATAATTATACTTATTCCATCATTCATACTTATTAAAAAAATATCCATAAAAACACTACGAGACTCAACAACCACATGAACG
C.salinarum        CTATTTACATGATAATATCCACCCCACTATTCCTCCTACTATCATCTACATCATCAAAAACCCTACAAACTATAACAACCCACTGATCA
P.leusterii        TAATCTATATAACCATTTCTACCCCATTCTTTCTATTACTCACAACCACGTCATCCAAAACCCTACAAGCCATAACAACAACCTGATCC
P.cocincinus       TCATCTACATAACCATCTCCACCCCAGTATTCCTACTTCTTTCAGCCACATCAACCAAAACCCTACAAGCCACAACAAACACCTGATCT
Hydrosaurus.sp.    TTATCTACATGATTATAACTGCCCCAACATTCTTACTACTAATACAAACAACTACTAAAACCCTACAAGATATTACAACCACATGAACC
C.calotes          TTACCTACATTATCCTAACAATCCCAACATTTTTATTAATAGCACTGACATCAACAAAAACCCTTCAAAACATAACAACAATATGATCA
J.tricarinata      TAACATATATTCTCCTGATAATCCCGACATTCCTTCTCATAATTCTAACAACAACCAAGACATTACAAAATATATCAACCACTTGAACC
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P.raddei           CCACATACATTATTATGACCACCCCAATTTTCTTAATGATAACAAACACATCAATAAAAACACTACAAAATTTATCAACAGCATGAACA
L.belliana         TAATCTATATCATCATAACAACACCAACATTTCTACTCCTAATTCAACTATCACTAAAAACCCTAAAAGATTCATCCACCGCATGAACA
U.acanthinurus     TCATCTACATCCTACTATCAACACCCACCCTTCTCCTATTAATAACAACGTCAACAAAAACCTTAAAAGACACCACAACCATATGAACA
A.paternus         CTATTTACCTAATTATAACAACTTCCATATTTTTTTCCCTAATTATTTCTAAGTCAAAAACAATCCAAAACACAGCGGAGACCTGAACA
P.mcallii          TGTTATACTTATTAATAACAACCTCAATATTTTATATCCTTATTTTACTTAATTCAAAAAACATCAAAGATATAGCAGCATCAGCAACA
Sauromalus.obesus  TCATCTACCTAATCATAACAACAGCAATATTCTACATACTCATTCTCTCAAAAACAAAAACCATCCAAGACACCACAACAATCTGAACA
Hoplocercus.sp.    CCATATACTTATTTATAACAACGTGCATATTTTCCACACTAATTTTATCAAAATCAAAAACAATTCAAGACACAACCACATCATGAACA
E.laticeps         TAATGTACCTACTAATAACAACCACCATATTCTCAACTCTTATCCTATCAAAGTCAAAAACAATCCAAAACACAGCCACCTCATGAACA
P.somuncurensis    TAGTTTACCTAACAATAACAATTACTATATTCCTCTTAATGAGTTTATCAAATTCAAAAACCATCCAAGACATAACAACAACATCAGCA
L.pictus           TTATTTATCTATTAATAACAACATCTATATTTTCCATCATAATTATAATAAAATCAAAAACAATCCAAGACCTAACACTATCATGATCT
U.flaviceps        TACTTTATCTAATTTTTACTACCACAATATTTCTAACCCTCATTATATCCAACTCAAAGACTATCAAAGACACAACAACCCTATGAACG
S.crassicaudatus   TAATCTACACCCTCATAACCACCTCCCTATTCATAACACTAATCCTAACCAAATCAAAAACCCTACAAAATATAACAACAACATGAACC
L.carinatus        TCATATATCTACTTATAACGACATCAACATTCTTAACCCTTACATTTTCAAAATCAAAAACATTACAAGATATCGCCACACTATGAGCC
B.plumifrons       TTATGTACCTTGCCATAACAACCTCAATATTCTTCATACTTATCTTATCAAAATCCAACACCATCCAAGACACAGCAACTGCCTGAACC
G.wislizenii       TAATCTACATTACCATAACAACCTCCATATTCTCCATATTACTCATAACCCAATCAAAAACCATCCAAGACACAACAATATCTTGAACC
O.cuvieri          TCATTTATCTCCTAATAACAACATCAATATTTACAACACTTATTTTATCAAAATCAAAAACCATCCAAGACACAATAACCTCATGAACA
O.attenuatus       TTATATACATTCTAATCTCAACCCCTATAATATTGTCACTACTACTAGCCTCAACTAAAACCACCCAAGACCTGACAACAATATGAATA
E.panamintina      CCCTCTATATCCTTATCTCAACCCCTCTAATATTATCATTAATTTTTACCTCAATAAAAACCACTCAAGATCTGACAACTTCATGAACA
C.enneagrammus     GCATCTACATTATTATCTCAATTCCACTCATGATGTCCCTGATCTTTTTTTACGCAAAAACAGCCCTTGATCTTACAACTACATGAATT
A.pulchra          TAATCTACATTATAATCTCCTCCCCCCTAATACTAACACTAATCCTCTTCTCTACAAAAACGGTCCCTGATCTTACAACCACATGAACA
H.suspectum        TCATTTATATCCTTATTACAACTAACACATTTATAATCTTTATTTCTCTATCAACGAAAACAATTAAAGACATAGGAACAACATTAAAC
X.grandis          CAGTATATATCCTTATCACCACCCCAACATTCCTATCCATAATCCTCTTAACAACCAAAACAATTAAAGACCTAGGGGCCTCATGAACA
V.griseus          CCCTATACATCACCCTCACATCTTCAGCAATACTTGCTATACACATTACATCATCAAAAACACTTCAAAACACAGCCCTCAGCTCCACA
L.borneensis       CCCTTTACATCCTAATAACAACCCCCACCATCTTAATTATGCACATCTCACTTTCAAAAACTATTAAAGATACAACAACCATCACAACA
S.crocodilurus     CTCTCTACATTACTATTACACTAGCCCTTCTTAGCCAACTAACTTTTTCCTCAGCAAAAACGATCCAAGACACAGGAACTATATGAACT
D.semicarinatus    CAATTTACATCATAACCACCATCCCCACATTTCTACTAATCAACACTACAATATCAATAACAATCAAAGACCTAGGAACCATGTGAACC
R.braminus         TAGTTTATATTCTATTAACGACCCCCCTTTTCTTATCGATACTTATGCTCCAATCAAAAACTATTAAAGACGTAGGCACAGCCTGAAAC
C.ruffus           CCGTATACATCCTAACCACCATCCCAATCTTCATCCTACTAAACTCGACCTCAACCATAACAATCAAAGACATAGGAACAATATGAACA
Agkistrodon.sp.    TAGTCTACACGACAACTACCACCCCAATTTTCCTCATACTAAGCACGTCATCAACAACAACTATTAAAGATATAGGAACCATATGAACA
E.grammica         TTATTTATATCCTCATAACCTCTTCTATGTTTTTAATTCTCATTACCTCTTCATCAAAAACATCTAAAGACCTAGGACAGCTTTGATCA
B.biporus          CCATATACATCATCATAACCTGATCAATATTCTCACTCATACAAACGACACACACAAAAACACTCAAGGACACCTCCACAGCCTGATCT
T.weigmanni        CTCTATACATTATTATAACAACAACAATATTTATAGCAATATCCCTAACTAACACGAAATCACTTAAAGATATCACCACAACATGGAAC
A.xera             CTCTATACATCTGCATAACAACCACAATATTTACCACCATGCTACCAACCGACATAAAATCACTACAAGACACCGCCACAAGCTGAACA
C.tigris           TCATTTATATTATTATAACCACCACAATATTTATAACCCTTACCCCCCAAAAAACCAAAACAATTAAAACAATTGGAACAACATGGACC
L.parietale        TTTTATACATTATAATACTTACGGCCCTCTTTAGCATAATAATTTCACATAAAACCAACACTATTAAAACTATCAGCGAAACCTGAACC
E.turkmenicus      TACTCTATATCACAATAACTACATCTTCATTTATAATTCTACTAATATCAGAATCAAAAACAATAACTGACTTAGGACTTGCCTGAACG
S.shrevei          CAATCTACATCACCATAACAACTGCCATATTCACCACACTCTCACACACCATAATAAAAACCCTCCCAGACCTGGGAACATCATGAACC
T.przewalskii      TCATCTACATACTAATAACTACAGCCATATTTCTAACACTAATCTTCACCACAACAAAAACCATTACTGACCTCGGCACAACCTGAACC
G.gecko            TAATTTATATTACTATAACCTCAACCATATTTTTAGCACTTAACACAATAACAATCAAAACTCTCACCGATATAGGCCTTGCCTGATCC
P.lindneri         TTATCTACCTAATCCTATCCACAGCCATATTCACTGCCCTCATAACAACTTCATCCAAAACCCTACTAGATCTAGGCACCTCTTGGCCA
Cr.ocellatus       TTACATATATTATTATAACAACAGCAATATTTACTACACTGTTAATAACTACATCAAAAACCCTAATAGACCTCGGAACAACCCCCTTA
L.jicari           TAACCTACCTAATCCTAACCTCAGCAACCTTCATAGCCCTCCTTTCAACAACATCAAAAACCCTTCACGACCTGGGCACAAGCTGAACA
M.aurata           TACTATACATTATTATAACCACCCCAATGTTCTTAATGTTAGAACTAACCACATCAAAAACAATTAAAGACCTCACAACATCATGAACC
C.robustus         GATTATACCCTACTAATAACCACATCCCATTCTTAGCACTAATATTTTCATCATCAAAAACAATTAAAGACTTAACTATAGCATGAGCT
S.sikkimensis      CTATTTACCTATTAATAACACTATCAACATTCACCATATTCATCTTCTCTTCATCCAAAACCACTAAAGACCTTACAACATCATGAACC
E.inexpectatus     CACTTTACATCATAATAACCACCTCGATATTTTTACTACTAATCACCACCTCAGCCAAAACTATTCAAGACCTAACAACTCTGTGAGCG
E.skiltonianus     CACTTTACATCCTAATAACCACCGCAACATTCCTACTACTAATAACCACCTCAACCAAAACCATTCAAGACCTAACAACAACATGAACA
E.anthracinus      CACTCTATATCCTAATGACCGCCTCAACATTCCTGCTACTAATGAGCACTTCAGCCAAAACTACCCAAGACCTAGCAACAATGTGAATA
S.anguineus        CACTCTACATTATCATAACCATCTCACTATTCCTCCTACTAATAACAACCATTTCAAAAACAATCCAAGATCTTTCATCAACCTGACTA
P.eggeli           CACTATATGTTCTAATAACCGCTTCCACCTTTCTACTATTAACCCTATCCTCATCAAAAACAATCCAAGACTTAACATCATCCTGAGTA
F.polylepis        TAATCTACATTATAATAACCTCCACAATATTCTTAACCCTACTATTTACCGCATCAAAAACAATCAAAGACCTATCAACATCCTGAGCA
Ch.ocellatus       CACTTTACATCTTAATAACAACCTCAACATTCATAATATTAACATTTTCCTCATCAAAAACAATTAAAGACTTAACAGCTTCATGAATA
A.meleagris        CCCTATACCTAACAATAACCACCTCAATATTCTTAATACTACTGTATACATCATCAAAAACAATCAAAGACCTAACAACATCACGAATA
T.lomii            CACTATACCTAACAATGACTACCTCCATATTTTTAATATTACTATATACAGCATCAAAAACAATCAAAGACCTAACAACATCACGAATA
T.gariepensis      CACTATACCTGACAATAACAACCTCCACATTCCTACTTCTACTATATACATCATCAAAAACAATCAAGGACCTAACAACATCACGAATA
X.vigilis          TCATTTACATTTTACTCACCTCTCTAATCTTTTTATCCATAAACACTAGCCACTCAAAGACAATAAAAGACATAGCTACAACATGAACA
C.polyzonus        CAGTATACCTTATTATTACCCTAACTATGTTTCTCCTGCTAATCTCAACCCAAGCAAAGACAGCCCAAAATATGACAACT---TGGACA
Zonosaurus.sp.     TTATCTATATCGCTATAACACTAACAACATTCCTCCTGCTAATCATAATAAACTCAAAAACAATCCAAAACATAACAACAGCCTGAATG
Dibamus            CCATCTACATTACAATAACAATGCCAGTTTTCATTGCACTAATCTTTTCCTCATCAAAAACGATCAAGGACCTTGGAAACTCTTGAACA

Index0             11111111111111111111111111111111111111111111111111111111111111111111111111111111111111111
Index1             00000000000000000000000000000001111111111111111111111111111111111111111111111111111111111
Index2             67777777777888888888899999999990000000000111111111122222222223333333333444444444455555555
Index3             90123456789012345678901234567890123456789012345678901234567890123456789012345678901234567
Qualifiers1        .........................................................................................
Qualifiers2        1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1.
A.mississippiensis AAATCCCCAATCACCACCACCATCCTGATAATTTCCCTCCTATCACTATCCGGCCTCCCACCCCTAGCCGGCTTTATACCAAAATGATT
G.gallus           AAAACCCCAATACTAAATGCAACTGTAATACTAACCCTCCTCTCCCTAGCTGGCCTCCCACCATTAACCGGCTTCATGCCAAAATGACT
C.mydas            AAACTCCCAACCATAAACACCCTAATAATACTAACCCTCATATCACTCGCAGGCCTACCACCACTAACAGGATTCATACCAAAATGATT
S.punctatus        AAATCATTCCCCATAATAATCTTGATAGCCCTAACCCTGCTTTCAATAGGAGGCCTACCACCCATAACAGGATTTTTACCAAAATGATT
B.theili           ACATCAACCACAGCAAACATTTTACTAACACTAATATTTTTATCACTAAGCGGACTACCACCACTTACAGGATTTATACCAAAACTATT
C.rudis            TCATCCCCAATAACTAGTGTTATACTCACACTAATACTACTTTCACTAAGCGGACTTCCCCCTATAACAGGATTTACCCCAAAACTTTT
C.brevicornis      ACATCCCCAATAGCAAACACCCTATTAACCCTAATACTTCTTTCACTAAGTGGACTCCCACCACTCACAGGCTTTACCCCAAAACTTTT
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C.salinarum        CACTCTCCAACAGCCGCTATCATTCTTTCACTCATTTTTCTTTCCATAGCAGGCTTACCCCCACTAACAGGATTTACACCAAAACTACT
P.leusterii        CACTCACCAGCCGCTGCCACCCTCCTAATGTTACTACTTCTCTCTATAGCGGGTCTCCCTCCACTAACAGGGTTCACACCAAAATTACT
P.cocincinus       ATCTCACCAACCGCCGCCTTCCTAATGACACTTATACTACTATCACTAGCAGGCCTTCCACCCCTTGCCGGATTTACACCAAAACTAGC
Hydrosaurus.sp.    ACAACTCCAGCAGCAACCATAACACTGACAATACTACTCCTATCACTAGGAGGCCTCCCTCCATTAACAGGGTTCATTCCAAAATTACT
C.calotes          ACCTCCCCACTAGCAACCACAACAATAGCTCTACTCCTGCTATCAACAGCCGGGTTACCCCCACTCACCGGCTTTTTACCAAAATTAAT
J.tricarinata      ACATCTCCAACTGCAACCACAACACTAACAATCTTATTGCTCTCAACAGCCGGACTTCCACCACTCACCGGGTTTTTACCAAAACTACT
P.raddei           ACCTCTACAACAACAACTTTCTCGATTTCCCTTTTAATACTATCAACCAGCGGCTTACCGCCATTCACAGGATTCATACCAAAGATACT
L.belliana         ACAACCCCA---ATAATCATCCTCCTAATACCAATTATAATATCACTAGGAGGACTACCCCCACTAACAGGATTCACACCAAAACTCTT
U.acanthinurus     ACAACACCAACAATCAGCACACTACTAGCCCTACTACTACTATCGACAGGCGGACTCCCACCATTCACCGGATTCCTACCAAAACTACT
A.paternus         TTTTCACCCATACTAACGATTATAATAATACTTTCACTTCTTTCACTAGGGGGACTACCACCACTAACTGGATTTGTACCAAAGTGGCT
P.mcallii          ACCTCCCCAACAACTACCACCCTTGCCATATTAATCCTACTATCCCTAGGCGGACTTCCCCCCCTAACCGGCTTTCTACCAAAATGACT
Sauromalus.obesus  TCCTCCCCCACACTAACCATCATAATAATACTGACACTACTATCGCTAGGAGGCCTTCCCCCCCTAACTGGGTTTATACCAAAATGACT
Hoplocercus.sp.    ACCTCCCCCACTCTAGTTATCACCACAATATTTACCCTACTATCCCTAGGGGGCCTCCCCCCACTATCAGGGTTCCTCCCAAAATGAAT
E.laticeps         ACGTCCCCAACATTAATTATTATAATAATACTCACCCTCCTCTCCCTAGGTGGACTCCCCCCACTGTCAGGCTTCCTACCAAAATGACT
P.somuncurensis    ACATCCCCAACAATAACCATCATTATTTCCATAACACTACTCTCACTCGGCGGACTTCCCCCACTTACCGGCTTTTTACCAAAATGACT
L.pictus           TCATCCCCAATTACTACCGTTCTAACAGCTATAACCCTCCTATCCCTAGGAGGCCTCCCTCCACTAACAGGATTTATACCAAAATGACT
U.flaviceps        ACCTCCCCCGCTTTAACAATCACGATGGCCCTCACACTTATTTCACTAGGGGGACTCCCCCCCATATCCGGCTTTATTCCAAAGTGGCT
S.crassicaudatus   CTATCACCTGCACTAACCACAATTGCCCTACTAACACTACTCTCACTAGGAGGCCTACCCCCACTCTCAGGATTTATACCAAAATGACT
L.carinatus        TTATCTCCTACACTAATAATTATAACGATACTAGCCCTCCTATCACTAGGAGGACTCCCACCATTGACAGGATTTATTCCAAAGTGACT
B.plumifrons       ACATCACCAACCACAACTCTCATAATAATACTCACACTACTCTCTCTTGGGGGCCTCCCTCCACTAACAGGCTTCATCCCAAAATGACT
G.wislizenii       TCCTCCCCAACTGCTACAATTACTATAATACTTACACTACTATCCTTAGGCGGCCTGCCACCATTATCCGGATTTATACCAAAATGACT
O.cuvieri          TATTCCCCAATACTAGCCACAACAATAATACTAACGCTCCTTTCCTTAGGTGGCCTCCCCCCACTTACAGGATTTCTGCCCAAATGGCT
O.attenuatus       ACCTCCCCAATACTAACCCCACTCACCATAATAACCCTCCTATCACTAGGAGGCCTGCCCCCACTATCAGGATTTATGCCTAAATGACT
E.panamintina      ACATCACCCATACTCTCTTCACTAACAATAATAACACTTCTATCCTTAGGAGGACTTCCCCCACTCACAGGCTTCTTGCCAAAATGACT
C.enneagrammus     ACTTCCCCTATATTAACTGCCCTGACAATAATAACCCTACTATCCTTGGGGGGTCTCCCCCCTTTAACTGGCTTCATTCCAAAATGACT
A.pulchra          ACATCACCACTCTTAACCACACTTACCATAACAACCCTCCTGTCACTAGGAGGCCTACCCCCACTAACCGGATTCCTACCAAAATGACT
H.suspectum        ACAACACCTATACTAGCTACAATACTAATAATTGTCCTCTTATCAATAGGAGGCCTTCCACCACTATCTGGGTTCCTGCCAAAATGGCT
X.grandis          ACCTCCCCAACCCTAATCTCATTAACAATAATACTCCTATTATCCCTAGGAGGACTCCCCCCCCTAACCGGGTTCCTACCAAAATGGCT
V.griseus          CACTCACCCCTCATAGCCAGCCTCTTCCTACTATCCCTTCTCTCACTCGGAGGACTTCCCCCCCTATCAGGATTCTCCCCTAAATGACT
L.borneensis       ACACTCCCCCCCCTCACAACCCTTTTCGCAGCCTCACTACTCTCACTAGGAGGGCTACCTCCACTAACAGGATTTTTGCCAAAATGACT
S.crocodilurus     ACATCCCCCATACTTATGCCCACTACTATACTTACACTTCTATCCCTAGGAGGTCTTCCTCCACTGACAGGCTTTTTACCAAAGTGACT
D.semicarinatus    AACTCCCCATACACCATAACTATCCTATCTATAACCATCCTATCTATAGGAGGACTACCGCCCCTATCAGGATTCATACCAAAATGGTT
R.braminus         TCCTCAACCCACACCTCCTCTATTATACTTCTAACTCTTATATCCATCGCAGGGTTACCACCAATAACCGGCTTTGCCCCAAAATGACT
C.ruffus           ACATCCCCACAACTGACATCAGCCATTACACTTACAATCCTATCACTAAGCGGCCTACCACCACTAACAGGATTCATGCCCAAATGACT
Agkistrodon.sp.    GCCTCCCCCTATCTAACCTTAATTATACTAACAACAATCCTATCCTTAACTGGCCTTCCTCCCCTCACAGGGTTTATACCAAAATGACT
E.grammica         ACCTCCCCAACTATTACATCAATTTCCCTAATTACCCTTATCTCACTAGGAGGTCTACCCCCGCTCATTGGATTCTTACCAAAATGACT
B.biporus          ACAACCCCACATGCAATGATAATATTACTAATAACACTTCTCTCACTTGGCGGACTACCGCCACTATCAGGCTTCATACCAAAGCTACT
T.weigmanni        AGCATCCCATCAACAATAGTCCTACTACTACTCACACTTATCTCACTAGGAGGCCTACCCCCCCTCTCCGGCTTCATACTAAAATGGCT
A.xera             ACCGCCCCTCCAATAATACTAACAGCCCTCCTAACACTCATCTCCCTTGGCGGACTACCCCCAACCACGGGCTTCCTAATAAAATGGTT
C.tigris           CTGTCACCCCCACTAACAATCATTACAATACTCACACTGACATCTCTAGGAGGTCTCCCACCAATAACAGGATTTATGCCAAAATGACT
L.parietale        TTGTCCCCAGCAATAATAACAATATTACTTCTAATTCTCATCTCATTAGGAGGCCTTCCACCAATAACCGGATTTTTACCAAAATGATT
E.turkmenicus      ACTTCCCCAACATCCATACTCTTACTAATACTATCTCTTCTCTCACTAGGAGGACTTCCACCACTATCAGGATTTATACCAAAACTACT
S.shrevei          CGCAACCCAACGCTACTATCCATAACCATACTCACCGCCATGTCCCTCGGAGGACTCCCCCCAATAACCGGCTTCACACCAAAGTGACT
T.przewalskii      AACAGCCCCACACTCCTCACCATTTCAATAATCATCCTAATATCACTAGGAGGCCTACCCCCACTAACAGGATTTATACCAAAATGACT
G.gecko            CAATCCCCTTCACTCATAACAATAGTAATAATTTCCATTATATCACTAGGAGGGCTACCCCCATTAACAGGCTTCCTGCCAAAATGACT
P.lindneri         AAAACCCCGCCCCTAATAATAATAACCATACTCACCCTTATATCCTTAGGAGGACTACCTCCACTAACTGGCTTTATTCCTAAATGATT
Cr.ocellatus       CAATCCCCCACCCTCCTCACATTTTCCATACTAATCTTAATATCCCTAGGAGGATTACCCCCCCTTACAGGATTCGTACCAAAATGACT
L.jicari           ATCTCTCCCCCCTTACTCGCAATCACAATATTAACCCTATTATCACTAGGCGGACTACCCCCACTAACCGGCTTCCTCCCTAAATGATT
M.aurata           ATCTCCCCACCCATAACCGCCACAATAATAGCTCTGCTAATATCACTAGGTGGCCTCCCACCCCTAACAGGATTTATGCCTAAATGACT
C.robustus         ATTTCCCCAACTACAGCAGCCCTTATATTAACCCTACTTATGTCCATAGGAGGCCTCCCCCCACTAACTGGCTTTATACCAAAATGGTT
S.sikkimensis      ATCTCCCCCCTACTAACCGCCTCAATACTAATTTTACTAATATCAATAGGGGGGCTCCCCCCTCTTTCAGGCTTTATACCAAAATGATT
E.inexpectatus     ATCTCACCTACAATATCAGCCCTAGCCCTAACACTACTTATATCACTAGCCGGCCTGCCCCCCTTTACTGGCTTCATGCCAAAATGACT
E.skiltonianus     ATTTCGCCCACTACAACAGCCCTTATGCTCATATTGCTCATATCCTTAGCTGGCCTACCCCCATTTACCGGCTTCACACCAAAATGGCT
E.anthracinus      GTCTCACCCACAATATCAGCCCTCATACTAATACTACTCATATCACTAGCCGGCCTACCCCCATTTACCGGGTTCATGCCAAAATGACT
S.anguineus        TCCTCCCCAACAACAACAGCCTTTACACTTATTCTACTTATATCCCTAGGTGGACTGCCACCTCTCACAGGATTTATACCAAAATGATT
P.eggeli           ACCGCCCCAACAACAACCACCTTCATACTTATCCTACTAATATCCCTGGGCGGCTTACCCCCACTTACAGGGTTTATACCAAAATGACT
F.polylepis        ATCTCACCAACAATAACAACCCTCTCACTCATTCTACTAATATCCCTCGGAGGACTCCCACCCCTAACCGGATTCATACCAAAATGATT
Ch.ocellatus       ATTTCACCAACAACAACAGTACTCATACTTATAGTCCTAATATCACTTGGCGGCCTTCCCCCTCTCACAGGATTCATACCAAAATGACT
A.meleagris        ATTACTCCAGTAACAACAACCTTATTACTAATATTATTAATATCACTGGGAGGCCTACCCCCACTAACAGGATTTATGCCAAAATGGTT
T.lomii            ATCACACCAATAACAACAACAACACTACTAACGCTACTAATATCACTAGGAGGCCTACCACCACTAACAGGATTCATACCAAAATGACT
T.gariepensis      ATCACACCAACAACAGCAACAATAACACTAACACTATTAATATCACTTGGAGGCCTACCCCCACTAACAGGATTCATGCCAAAATGATT
X.vigilis          CTTTCCCCCACCCTCACTACCTTTATACTATTAACATTATTGTCTCTAGGAGGCCTACCACCATTAACAGGATTTCTACCAAAATGATT
C.polyzonus        ACCACTCCAATCACCCCTGCCTTAACTACACTAACACTATTATCCCTAGGCGGACTACCCCCACTCACAGGATTTTTACCAAAATGATT
Zonosaurus.sp.     ACCTCCCCAACACTCTCCACCATTACTATAATAACCTTGCTATCACTAAGCGGACTTCCCCCTTTAACAGGATTTTTACCAAAATGGTT
Dibamus            ACATCCATAACCTCCACAACATTAATAATGCTCGCTATCATGTCTCTAGGGGGCCTACCACCTTTGACTGGCTTCATGCCAAAATGGCT

Index0             11111111111111111111111111111111111111111111111111111111111111111111111111111111111111111
Index1             11111111111111111111111111111111111111111122222222222222222222222222222222222222222222222
Index2             55666666666677777777778888888888999999999900000000001111111111222222222233333333334444444
Index3             89012345678901234567890123456789012345678901234567890123456789012345678901234567890123456
Qualifiers1        .........................................................................................
Qualifiers2        .1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..---1..1..1..1..1..1..1..1
A.mississippiensis AACAATCAACCAACTCCTCGCAGAAAAAGCAATTTGAATTGCACTATTAATACTAATTACATCC---CTTCTAAGTCTATTCTTCTATC
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G.gallus           CATTATCCAAGAACTAACCAAACAAGAAATAACCCCAATAGCCACAATCATCACAATACTATCA---CTCCTAAGCCTATTCTTCTACC
C.mydas            AATCCTCCAAGAATTAACCAAACAACACATAACCATCATAGCCACTATAATAGCCATACTCTCA---CTCTTAACCCTATTCTTTTATC
S.punctatus        AATTCTACAAGAACTAATCTACCAACACCAAACACAAATGGCCACTCTAGCATCCTTATCCACC---TTGCTCAGCCTCTTCTTTTATC
B.theili           AATCTTAAATGAACTAGTAACACAAAGCCTAACACTAATTGCAACTACAGTGGCCATCTTCTCA---TTACTTAACCTATTTTTTTATA
C.rudis            AATCCTTAATGAACTAATTACACAAAACCTAACACCCATTGCAACAACAATGGCTATAATATCA---CTTATTAGCCTGTTTTTTTATA
C.brevicornis      AATTTTAAATGAACTAATCTTACAAAACTTAACACCAACTGCAACAACAATAGCAATAGTGTCA---CTAATTAGCTTATTTTTTTATG
C.salinarum        AATCCTAGATAATCTAGTAGCACACAAATTAACAACATTAGCCACAATAATAGCCCTATTATCC---CTCCTAAGTCTAGTGTTTTACC
P.leusterii        AATTCTAGACAAATTAGTAGCACACAAACTAACCCCAATTGCCACGACTCTCGCCCTGCTCTCC---CTTCTCAGCCTAATCTTTTACC
P.cocincinus       AATCTTAAATATCCTCGTAACATATAAACTAACCCCCCTAGCCATAATCATTGCTCTATCCTCC---CTATTAAGCCTACTTTTTTATC
Hydrosaurus.sp.    AATCCTCAACGAGCTAATCATGCAAAAACTAACCCCACTAGCAACCTTAATAGCACTCACATCC---CTACTAAGCCTATTATTCTACC
C.calotes          TATTATAAATGAATTAGTAATTCAAAACCTTACCACTCTAGCTACACTAACAATAATAACCTCC---TTACTTAGCCTATCATTCTACT
J.tricarinata      AATTTTAAACGAACTAGTAACACAAAAACTCACACCCATTGCCGTCATTTCCACAATGACCACC---CTATTGAACTTAACCTTTTACC
P.raddei           AATCCTAAATGAACTTATTTTACAAAAACTTACTACACTGGCAACCTTAGCAATCATAACATCA---CTAATTAGTTTACTGTTTTACC
L.belliana         GATCCTAAATGAAATAGTAACACAAAAAATAACCCCCCTAGCAACCATCGCCGCCCTGGCATCA---CTATTAAGCCTTGTATTTTACC
U.acanthinurus     AATCATAAACGAGTTCTTAATACAAAATCTAACACCCATAGGAATCCTCATAGCCATGACATCA---CTACTCAACCTAATATACTACC
A.paternus         AGTTATAGAAGAATTAATTTTACAAAATTTTAATCTTCCAGCTATTTTAATAGCTATATCTTCC---CTACTAAGCCTATTTTTTTACC
P.mcallii          AATTCTTGAAGAATTAATTGTACAAAACCTAACCCCCACAGCAATAATTCTAGTACTATCAGCA---CTACTAAGCCTATTTTTTTATT
Sauromalus.obesus  CATCTTAGAAGAACTAGTCATACAAAACCTAACCACAATAGCAACCATACTCGCCCTCTCCGCA---CTACTGAGCCTATTCTTCTACC
Hoplocercus.sp.    AATCCTAGAAGAACTAATCTCACAAAACCTATCTCCACTAGCAACAACCATTGCTATATCCTCC---CTACTCAGCCTATTCTTTTACC
E.laticeps         TATCCTAGAAGAACTTATTACACAAAACTTCATCCCTACAGCAATCACTATTGCTCTATCCTCT---CTACTAAGCCTATTCTTTTACC
P.somuncurensis    TATCCTAGAAGAATTAACAATACAAAACCTAACTCCAACAGCAACAATTCTTGCCATTTCGGCT---TTACTCAGTCTATATTTTTACC
L.pictus           AATCATTGAAGAATTAACCCTACAAAACCTAGCACCAATAGCAACCGTACTAGCCATATCATCC---CTGCTTAGCCTATACTTCTACT
U.flaviceps        AGTAATAGAAGAATTAACCAATCAAAACCTAATACTAATTACAACTTTACTAGCCCTTTCATCA---CTACTAAGCCTCTTTTTTTACC
S.crassicaudatus   CATCCTTAACGAACTAATCAACCAGAACCTCATCATCGTATCTGCCCTCCTAGCAATATCCACC---CTCCTTAGCTTATTCTTCTACC
L.carinatus        TGTCTTACAAGAACTAACAACACAAAACATAACTATAATAGCCACTATCATAGCACTATCAGCC---CTCCTTAGCCTCTTCTTCTACT
B.plumifrons       AATCCTAGAAGAACTGACAATACAAAACATAACCCCCACAGCAACCATTCTAGCATTATCCTCT---CTACTAAGCCTTTACTTTTATC
G.wislizenii       AATCCTAGAAGAACTGACAACACAAAACCTTGCCCCAATAGCCACACTCCTAGCCATCACATCC---CTACTAAGTCTATTCTTTTACC
O.cuvieri          TATCATAGAAGAACTAACCCTACAAAGTTTAATCCCAATTACAACCTTATTAGCCATAGCCTCA---TTACTCAGCCTATTCTTCTATC
O.attenuatus       AACCCTAGAAGAACTACTAACACAAAACATAGCCCCCCTAGCAATTGCACTAGCCATGTCCTCA---CTTCTAAGCCTTCTATTCTACC
E.panamintina      CACTCTAGAAGAACTATTAACACAAAACATAACCCCTTTAGCCACAATCCTGGCTATAACAACA---CTACTCAGCCTATTTTTCTACA
C.enneagrammus     AACACTAGAAGAATTACTATCACAAGACATAACACTCCTTGCCACCCTCTTAGCCCTTACTACC---CTACTCAGCCTATTCTTCTACT
A.pulchra          AATCCTAGAAGAACTTCTAAAACAAAACATAACCTTGCTAGCCACTCTAATAACCATAATAACC---CTCATAAGCCTATTCTTCTACC
H.suspectum        TATTTTACAAGAACTAACAACCCAAAACCTATTACCAGTAGCCATTCTTATAGCTATAGCTACG---CTCCTCAATCTATTCTTCTACC
X.grandis          AATTCTACAAGAACTCACAATTAACAACACAATTGTCATAGCAACAGGAATGGCACTAATAACC---CTCCTAAACCTTTTCTTCTACT
V.griseus          CATCCTCCAAGAACTAATCCTCCACAACCTCACCCCCTTAGCCACAGCAATAGCTATCACAACC---CTCCTTAGCCTAATATTCTATC
L.borneensis       CATTCTGCAAGAATTAGCCCTACAAAACCTAGCCCCACTCGCAACAACTATAGCAGTACTGACC---CTTTTCAGCCTCTTCTTCTACT
S.crocodilurus     TATTTTAAAAGAACTAATTACACAAAACATGACACCTCTAGCAACTACTCTAGCACTAGCAACA---CTAACTAGCCTATTCTTCTACC
D.semicarinatus    AATCTTAAATAATCTAATTTCAATAAACATAATTACAGAAGCAACCCTAATAGCCATAGCCTCA---CTACTCAGCCTATACGTATATA
R.braminus         TATCCTAAAAGAGTTAACACACCATAGTATGATCCTCCTAGCAACAACAGCTGCTATCTTATCA---ACCCTGAGCCTTTTCTTTTACC
C.ruffus           AATTGTAAATAAAATAATAACATTCAACATAACTATTGAAGCTACAATCATAGCCATAATATCC---CTACTAAGCCTCTATATATATC
Agkistrodon.sp.    TATTCTTAATAAAATAACCACCTTCAACCTAACCACAGAAGCCACCCTCATAGCCATATCCTCC---CTACCAAGCCTATACCTATACA
E.grammica         CATCTTAACAGAACTAACAACCAACCACCTTACTCCCCTAGCAGTCCTCCTCGCCCTATCCTCT---CTCCTCAGCCTAATATTTTACA
B.biporus          AATCCTAAAAGACCTAGTAGAAACCAACCTTGCCTTCACCGCCACAGCCATAGCAATTACCTCC---CTCCTCAGCCTGGCATTCTATG
T.weigmanni        CATCCTAAAAGAACTAGTCTTTACAGACCTTTCCATTACCGCTACACTCATGGCACTGGCCTCG---CTACTAAGTCTAATATTCTATA
A.xera             CATCCTAAAAGAACTCACCTTTATGAACCTCCAAATTATTGCCACACTAATAGCCACAGCCTCC---CTACTAAGCCTCCTTTTCTACA
C.tigris           TATTCTAGAAACATTATTACTAGAAAATATAACCACATTAGCAACACTCACTGCAATAGCAACA---CTCCTAAGCCTATTTTTTTACT
L.parietale        AATTTTAAACGAGTTAATTACAGAAACATACACCACAATCGCAACACTTATTGCTATAGCAACA---CTCCTAAGCCTTTTCTTTTACC
E.turkmenicus      TATTCTAAAAGAAATAACAATACTAAACATAATCTCCACAAGCACAATCTTAGCCCTATCTGCC---CTCCCAAGTTTATTCTTCTACC
S.shrevei          AATCACAAAAGAACTAATTGAAGCCACACTCTCACCAGCCGCCACAATACTTATCCTAACCAGC---CTACCAAGCCTATTTTTCTACA
T.przewalskii      TATCATTAAAGAACTCACTGCCCTCCAACTTACCCCACTAGCTACTGCCCTCGCCATAGCAAGC---CTCCCAAGCCTCTTCTTTTACA
G.gecko            AATTCTAAGTGCCCTCTGCCAAAATAATCTTATTCAACTAAGTGTCCTTCTAGCAGCAGCGAGT---TTACCAAGCCTATTTTTCTACA
P.lindneri         GATTCTAAAAGAACTTATACAAAATAATTTAACCACAATCAGTATCATAATAGCCCTATCCACC---CTGCCCAGCTTATTCTTCTACC
Cr.ocellatus       AATCCTAACAGAACTTACCACAATAAACCTCCCCCTAATCAGCACACTCATAGCCATATCCACC---CTCCCTAGTCTATTCTTCTACC
L.jicari           AGTGTTAAAAGAACTAGTCACCATAAACTTCATCACTCTCAGTGTCCTAATAGCCCTATCCACC---CTCCCTAGTCTATTCTTCTATC
M.aurata           AGTCCTACAAGAACTAACAACACATAACCTAACCATAACCGCAACAATTATAGTATTATCCGCA---CTACTCAGCTTATTTTTTTACT
C.robustus         AATCTTACAAAACCTAACTACACACAACCTCCAAACAATAGCAACAATCATTGCATTATCCGCC---CTTCTAAGCCTGTTCTTCTACC
S.sikkimensis      AATTTTACAAGAGCTGACCTCCCATAACCTTACTATAATAGCAACAACGCTAGCCCTCTCAGCC---CTGCTCAGTTTATTCTTCTACC
E.inexpectatus     AATCTTACAAGAATTAACAACACACAACCTCTGCACAATCGCAACCATAATAGCACTATCCGCC---CTACTAAGCCTATTCTTCTACC
E.skiltonianus     CATCTTACAAGAATTAACAACACACAACCTCTGTATAACCGCAACAATAATGGCACTGTCCGCC---CTATTAAGCCTATTCTTCTACC
E.anthracinus      GATCCTACAAGAATTAACAACACACAACCTCTGCACAACCGCAACAATACTAGCGCTATCCGCC---CTACTAAGCCTATTCTTCTATC
S.anguineus        AATCTTACAAGAACTAACTACCCATAATCTAGCCTTACCCGCCATAATTATGGCCATATCCGCC---CTGCTAAGCCTATTCTTTTATT
P.eggeli           TATCCTACAAGAACTAACCACACACAACCTATCCCTGCCAGCCACAATCATAGCCCTCTCCGCC---CTGTTAAGCTTATTTTTTTACC
F.polylepis        AATCTTACAGGAACTAACAACACACAGCCTCTCAACAACAGCGACCATCCTGGCCCTCTCCGCA---CTCCTCAGCTTATTTTTTTATC
Ch.ocellatus       AATTCTACAAGAACTAACAACACACAGCCTATCCACAACCGCAACAATTATAGCAATATCCGCA---TTACTTAGCTTATTCTTTTACC
A.meleagris        AATTCTACAAGAACTAGTAACATATAACCTAACCCCAATAGCAACATTAATAGCACTATCAGCA---CTACTAAGCCTATACTTCTACC
T.lomii            AATCCTGCAAGAACTAACAACACACAACCTAACCACAATAGCAACACTAATAGCACTATCAGCA---CTACTAAGCCTATACTTTTACC
T.gariepensis      AATCCTCCAAGAACTAGTAACACACCACCTAACCACAATAGCCACACTAATAGCACTATCAGCA---CTACTAAGCCTATATTTTTACT
X.vigilis          AATTTTACAAGAACTTACAACCCACCACTTAACACCTATCGCCACCCTCCTCGCTTTCTCAACC---CTGCTAAGCCTCTTTTTTTACC
C.polyzonus        TATCCTACAAGAACTAATTACCCAACAATCCACATTTATCGCCACAGTTGCGGCAATATCTTCC---CTCCTAAACCTATTCTTCTACC
Zonosaurus.sp.     AATCTTACAAGAACTGGTAGTCCAACACATAACGCCTCTAGCAACAATTATATCAATCTCAACA---CTTCTCAGCCTCTTCTTCTACC
Dibamus            CATCCTACAAGAAATGATCAACCAACACCTCGCTCCCATAGCGACGGCTATTGCCATCTCCGCA---CTACTTAGCTTATTCTTCTACA

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Index2             44455555555556666666666777777777788888888889999999999000000000011111111112222222222333333
Index3             78901234567890123456789012345678901234567890123456789012345678901234567890123456789012345
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A.mississippiensis TCCGACTATGATACAACTCCTCATCAACTATGCCACCAAGCACTACCAACACAACCCGCCTCTGACGAAAATCTACCCCCCAAAGTAAC
G.gallus           TCCGACTTGCATACCACTCAACAATCACACTCCCCCCAACTCATCAAACCACATAAAACTCTGACGAACTAACAAAACCCTAAACACC
C.mydas            TACGAGTCTCATACTATGCAACCATTACATTACCACCAAACTCAACTAACTATTCACAACAATGACGCCACAAAAACAACCAGAAACCC
S.punctatus        TCCGCCTAGTATTCAACGCATTTCTAACCACTCCACCAAACACCTCAAATGTGACAAAAAACTGACGAAACCAAACCAACCACCACATT
B.theili           TACGAACAACCTACATCATAACAATAACCACCCCCCCATCATCCTCCACAATTATAACAAAATGACGCCACAAACCGCACTATCACAAA
C.rudis            CACGAACAACCTATATTACTACAATAACCACACCCCCCATCACAACATTAATAGTAACAAAATGACGACTTACTTTACCACAACTAAAA
C.brevicornis      TACGAACAACCTACATTACCACAATAACTACCCCCCCCATCCTATCTCCAACCACAATAAAATGACGCCTCAATCAACCACAACAAAAA
C.salinarum        TACGCACAACATACCTGTTAACCTTAACAGCCCCACCAACTACAGCCCAATCAATAACCATATGACGACTAAAACCA---CACTACAAC
P.leusterii        TACGCACGGCATACCTCCTAACCTCAACAGCCCCGCCTACCACAACTCAAGCTACCACACTCTGACGACTAAAAAACCACCACAACCAA
P.cocincinus       TACGAACCACATATATCCTCACCTCAGCAACCCCCCCCATCACAACCCAATCAACTACACTATGACGCGCAAAAACCAACCACAACCAA
Hydrosaurus.sp.    TACGAACAACCTACCTAATTACCATAACAACCGCACCAACAACAACCACCTCCCAAATAAAATGACGAATCCCAAATCACAACTACCTA
C.calotes          TACGAACCACCTACCTGACAACACTTCTAAACCCACCAAACTCCTCTACATCAACAACAAAATGACGCCAAAAAATAAACAAAAACAAA
J.tricarinata      TGCGAACAGCATACATGACAACATTACTTAACTCTCCTGCCTCTGCCACATCAACAATAAAATGACGACAGAACCCTAATAAAATCAAA
P.raddei           TACGAATCGCCTACTTAACCATAATACTTACATCCCCAATAACAACCTCATCATCAACAAAATGACGAACCCAAAACCAAAAATCACAA
L.belliana         TTCGAATAGCCTACCTAACAACAATAACTCTACCTCCAATCACAACAACCTCAACAATAAAATGACGCCTGACAACAAAACATCTATCC
U.acanthinurus     TACGAATTGTTTACCTAACATCCATAACAACCCCCCCAATCACCTTCCCAATAACAATAAAATGACGTCTAAAACAGCACCAACCTTCC
A.paternus         TTCGAATTTCCTACACAGCCACACTCTCACTATCACCTAATACAACTCAAATAAAATTCAAATGACGATTTTATCCAAAAACTACAACC
P.mcallii          TACGCTTAAGCTATTCATCCACAATTACCCTCGCACCAAACACAACAACAACCAAACATAAATGACGATTTAAACCGGCCCCCAACTCA
Sauromalus.obesus  TACGACTAACTTACACAACCACAATAACACTAGCCCCCACCACAACAACCACCCACCATAAATGACGATTCAAACCCACCTCCACCACA
Hoplocercus.sp.    TACGACTAGCTTACACAGCAACACTAACAACCTCCCCCAACACAACACAAACTAATCACAAATGACGATTCAAACCATCAACCTCCAAC
E.laticeps         TACGACTCACATACACAGCTGCACTAACAACCTCCCCCAACACAATCCAAACCAAACATAAATGACGACTTAAACCCAACACCTCAAAT
P.somuncurensis    TTCGACTAACATATACATCAACACTTACACTACCACCATACATAACACTAACCCAACACAAATGACGTTTCAAACCCCACTCAACAACA
L.pictus           TACGATTAACATACACCTCAACATTAACTCTTTCACCAAACTCCACAACAACTAAACACAAATGACGTTTCAAAACGAAATCCCCCTCA
U.flaviceps        TCCGATTAACGTATACAACTACACTCACACTCGCCCCAAACACAACAACCTCCAAACACACATGACGATTCAAACCAAACACCCCAACA
S.crassicaudatus   TCCGCCTCACATACATTACAGCCCTCACCCTACCACCAAACACCCCCAACACCACCTACAAATGACGATTCATACCCCCCATACCACTC
L.carinatus        TACGCCTAACATACATTATAACCCTAACCACCCCACCAAACACAACAACATTCAAGCACAAATGACGATTTAATTACACAAATAATACT
B.plumifrons       TACGAATTGCCTACACAACAACACTTACAACCTCTCCTAACACAACACCCACAAAACATAAATGACGATTTAAACCAACACCAACAACA
G.wislizenii       TTCGACTAACTTACACCACAACCCTAACACTATCACCAAATCCATCCATAACCTTCCATAAATGACGATTCAAATCCAAAACTCCAATA
O.cuvieri          TCCGACTAACCTACACAACATCTCTAACCCTATCCCCAAACACAACCTCATCCCAACACAAATGACGATTTAAATCAATGCAAACACCC
O.attenuatus       TACGACTATCCTACTCTCTCTCCATAACCATCTCACCGAGCCCAACAAAAGCTACAAGCAAATGACGACTAAAACCTAACACCACAGCC
E.panamintina      TACGACTCTCTTACTCACTATCCATAACAATCTCCCCTAGTCCAACAAAAATTACAAGCAAGTGACGACTAAAAACTAAAACATCAACC
C.enneagrammus     TACGCCTATCCTACTCCCTATCTATTACCATTGCCCCAAACTCAACTAAATCATCCAGCAAATGACGACTACAACCATCAACCCTAACA
A.pulchra          TTCGTCTGTCCTACACCCTTTCAGTAACCATCACCCCAACACCAACCATAACTACAAACAAATGACGAATTAAACCAAACATAACAACA
H.suspectum        TACGACTGGCATATACAACAGCCCTCACCCTACCCCCAAACGCAATAGGAGTATTAAACAATTGACGATTTAAAGCAAAATCAACAAGC
X.grandis          TACGACTAACTTATACTATAACCCTAACCCTCACCCCAAATGTCACTACCAATACCAGCAAGTGACGGTTTAATACAACCCAAACCACC
V.griseus          TACGAACCACTTATATTTCAACTATAACTCTTCCCCCCCTTACCACCCAAACCAAGCACACATGACGCCTAAAACCTAACCCCAACACC
L.borneensis       TACGGCTCATGTACACCTCTGCAATAACCCTGTCTCCAAACACCACCCCCTCAAAAAACAAATGACGACTTAAAACCAACCTAAACACG
S.crocodilurus     TTCGACTAGCCTATACTACAAGTATAACTCTAAACCCAAATACAACCGCAATCGAAAATAAATGACGATTTAAAACTAAGTCCAATACA
D.semicarinatus    TGCGACTAACATATATATCATCAATAACACTATCACCCCACACTACAACCATACCATTAAAATGACGGACATCAAATAAAAAACATCCT
R.braminus         TACACCTTTCCTACTCAACAGCCATAACCACCCCACCAAATACAGTTTAATAACACAAAAATGACGTTTTTCCCCAAAAAACACTCC
C.ruffus           TACGACTAACATACATCTTCTCTATAACCCTAACACCACACACTAACACCATAACAATAAAATGACGAACAAACCACAAAACACAACCA
Agkistrodon.sp.    TCCGCCTAACCTATATCCTAACCATAACACTACCTCCCCACACATCCACCACACAAATAAAATGACGTACACCACACAAAAAACTCCCC
E.grammica         TACGATTAACATACACAACAACACTTACAATTTCCCCGAACACAACTAACTCCATGATAAAATGACGATTCAAGCTAGCTAAACCACTC
B.biporus          TACGCCTGGCGTACACCACATCCCTAACTATCGCCCCCACCACAACTACAACAAAAATCAACTGACGAATACCCCCAAACCGCCGCACA
T.weigmanni        TTCGCCTGGGATATCTGACCTCACTCACTATTTCACCTAATACCAACATGATAGAAACAAAATGACGCCTAAAACCCAACCACCACACA
A.xera             TCCGCATCACATATGTAATAACCCTAACAATTTCCCCAACCACACCCCCAATAAAACTAAAATGACGACTACCCACGCCTACCAACACA
C.tigris           TACGACTATTTTACTCAACAACCATAATAGTTTTTCCAAACACAACAAACACAACACAAAAATGACGACTCCAAACAAAAACCATACTA
L.parietale        TTCGCCTCTTCTACGCAACAACCATAACGATCTCCCCAAACGCCACCACCAACGAACAAAAATGACGCCAAACAACACAAAATGTGTAT
E.turkmenicus      TACGACTATCCTACCTAATACTAATAACTATCCCCCCAACCACAACAACAACAGAACATAAATGACGACACAAAAATAATACCCTAAAA
S.shrevei          TCCGCCTAGCATACTTCACTACCCTAACCACTCCACCAAGCAACATAAACTATAAACTCACCTGACGATTTAAAAACCACACGCCCACA
T.przewalskii      TCCGAATGGCATACTTCACCACGCTAACAACACCCCCAACCACCACAACTACAGAACAAAAATGACGCCACACTCCTCAAACACTCCCC
G.gecko            CCCGCATGGCCTACTTCACTGTACTCACCATCCCACCTAACACAACAAGTACACACCTCAAATGACGATTCAAACCCAAATTAACCTGT
P.lindneri         TTCGAATATCCCACATAACTTCCCTAACTTTACCGCCTGAAACAATCAATACAAAACACAAATGACGATTTAAAACCCCTAAAATAAAC
Cr.ocellatus       TACGTATATCACATATAACCACCCTAACTCTCACTCCTAAAACTTCTACTATACTATACAAATGACGATTCAAACCTCAATCAAATCCA
L.jicari           TCCGAATATCTCACATAACAACACTAACCCTCCCACCAAGCACAACAAGCACCAGCCACGAATGACGATTTAAAACCCGCAACATCATA
M.aurata           TACGACTATCCTATACCTCCACACTAACCGTATACCCCACTACAACCAAAAGTAGTTACAAATGACGATTCCAACCGAAATTAACCACA
C.robustus         TACGACTATCGTACGCAACAGCACTTACCTTATACCCAACAACCACACAAAACAAACTCAAATGACGATTTCAACCAAAACTAAAAACC
S.sikkimensis      TACGACTATCGTATATAACAGCCCTCACTCTCTCCCCAACCACCACACAAAATAAACTAAAATGGCGACTCCAGCCGAGCCTAAAAACA
E.inexpectatus     TACGACTATCATACATCTCAACCCTAACCCTCGCCCTAACCCCAACACAGAGCACACACAAATGACGATTCAAGCCAAACACA---ACA
E.skiltonianus     TACGACTATCCTATGCCTCAACCCTAACCCTCGCCCAAAACCCAGTACAAAGCTCACACAAATGACGATTCCAACCGACCACAAAAACA
E.anthracinus      TACGACTATCATATATTTCAACCCTAACCCTCACCCTGAACTCAACACAAACCCCCCACAAATGACGGTTTCAACCAAGCACAAAAACA
S.anguineus        TACGTCTATCATACACAACGGCCCTAACTATATTCCCAAGTCCCCCACAAAACTCATATAAATGACGATTTAAAACAAACCAAAAAACA
P.eggeli           TCCGCCTCTCCTACGTAACCACTCTTACCCTATTCCCAAGCCCCTTACAAAACTTTCACAAATGACGATTTCAACCAAAATCAAAAACC
F.polylepis        TCCGACTATCTTACACCGCAACCCTCACCGTCTTCCCAACCCCAATACAAGTCTCATACAAATGACGGCTCCAACCAAAAACAAAAACA
Ch.ocellatus       TACGACTCACATATACTACCTCCCTAACCATATTCCCGACCCCGACACAATCAACACACAAATGACGATTCCAACCAAAATCAAAAACC
A.meleagris        TCCGATTAACATACGCAACAACACTAACACTATTCCCAACCACCAACAACACAACACACAAATGACGATTTAAACCAAAACACAAAACA
T.lomii            TACGACTAACATACACAACAACACTAACACTATTTCCAACCACAAATAACACAACACACAAATGACGGTTTAAACCAAAACACAAAACA
T.gariepensis      TACGACTAACATACACAACAACACTTACACTATTCCCAACCACCAACAACACAACACATAAATGACGATTTAAACCAAAACACAAAACA
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X.vigilis          TACGACTTTCTTATACTACAACAATCACACTACACCCCAACCCAACCACAATATCAAACAAATGGCGACAAAAAAAATATAAACACTCA
C.polyzonus        TACGACTATCCTACATCACCACCCTTACCACCTCACCAAACACCACCACCCTCTCCAACAAATGACGATTCAAACTTCTCTCAAAACCC
Zonosaurus.sp.     TTCGACTGTCCTACACCACAACACTAACCATTCAACCAAACATAACCTCACCTTCACAAAAATGACGATTTAAACCAAACAACCAAACA
Dibamus            TACGAATGACTTACACCATAACCCTTACTCTGCCTCCTAACTCGATCAACTCAAAATACAATTGACGATTCAAACCAACAATAAAAACT

Index0             11111111111111111111111111111111111111111111111111111111111111111111111111111111111111111
Index1             33333333333333333333333333333333333333333333333333333333333333334444444444444444444444444
Index2             33334444444444555555555566666666667777777777888888888899999999990000000000111111111122222
Index3             67890123456789012345678901234567890123456789012345678901234567890123456789012345678901234
Qualifiers1        ....................................................................................TRP..
Qualifiers2        1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1..1.....AA>>>
A.mississippiensis TTTACCATCAACCTCCTCACCATAGCGACCACCACTCTCCTACTATCAACCACACTAATGAAAGCAATTACT------TAA---AAGAA
G.gallus           CCCACCGCCATTCTAACTGCGCTATCAACCACCCTATTGCCCCTTTCC---CCCCTAATTATTACCATACTA------T-----AGAAA
C.mydas            TACCTAGCCCTACTAACTACACTATCAATTTCCATACTTCCAATCACACCAACCCTACTAACCATACCA---------T-----AGAAA
S.punctatus        TTACTCCCACAACTAATAATCTTGTCCTTAATATTACTTATTATTACCCCACTAGTTATTAGCCTATTT---------TA----AGAAA
B.theili           CTCCTATCAACATTAATCATTGTATCACTTATAAACATCCCACTACTTCCAACCATTACAGCCATTACAACCACAATCT-----AGGAA
C.rudis            CTGACATCCGTATTAATTACCCTATCACTCATAACTCTTCCTCTCACACCAATCCTAACATCCATAAAC---------T-----AGGAA
C.brevicornis      CTAATATCACTATTTATCCCCTTGTCCCTAATAGCACTACCACTTATACCAATTTTAACATCTATGACC---------T-----AGGAG
C.salinarum        CAAACCACAGCACTACTAACCCCAATTGCCTTATTTAATATTACAATCTTACCTGCTATACTAATA------------T-----AGGGA
P.leusterii        CTAACAACAACCATAGCCCCAATCGCCCTCTTCAACATCACAATCTTACCGGCCCTCTTAATA---------------T-----AGGGA
P.cocincinus       CTCACAACAATCCTAGCCCCAATAGCCCTATTTAACATGACAATAATACCCGCTTTAATTTCA---------------T-----AGAGA
Hydrosaurus.sp.    CTAACACCAGCTACCACCCCAACAGCCCTAGCCTCCACCCCAGCAACCCCCTCCCTCATCATA---------------T-----AGAAG
C.calotes          ACTATGAGTATCCTACCAACTGCCCTAACATCAACCATAGTAATACCAGCACTAATTCCC------------------TAACC-AGGAA
J.tricarinata      CCAACAATACTAGCCCCAACCGCTATTGCCAGCACGACAGCCCTACCAATAGTCATCCCA------------------T-----AGGAA
P.raddei           TTAGCAACAATAATAGCTCCAGTAGCACTATTCATTGCCCACCTAATTCCAGCAATCCCATTC---------------AG----AGAAG
L.belliana         CTTCCATTAGCAATCACCATAACAATAACCATAATAAGCCTCCCTATAACCCCTACATTTATCCCA------------T-----AAGGA
U.acanthinurus     GCCACAATCGCCACACTGACCACAACCGCCCTATTGATGACCCCAACAGCCCCAATAATTACAATT------------TA----CGAAG
A.paternus         ACCTTAACCTCTTCCACCACAACAATAACAATCTTCCTCCTACCACTTACACCCATAATTTTATTA------------T-----AAAAA
P.mcallii          ACACTACTTACAATAACCTTACCAATATCATTATTAATACTCCCAATTACCCCAACAATGTGC---------------T-----AGAAA
Sauromalus.obesus  ACCCTACTAACCACCACCCTACCCCTCACACTAATAATACTACCCATAACCCCCATAACACTTCTA------------TAAT--AGAAG
Hoplocercus.sp.    TTACTACTAACAACCTCATCCTCATTAATAACAATAGTACTACCACTTACCCCAATCCTATTATAC------------TA----AGGAA
E.laticeps         ATTACACTATCCTTCACTATTCCAATAACAACAATAATACTACCACTTTCACCACTAATCATAAAC------------T-----AGGAA
P.somuncurensis    ATACTCTCTATTACCACCCCAGCTACACTCATAATACTACCTATAACCCCCCTACTACTACCA---------------T-----AGGAA
L.pictus           CTCCTACTTACAACTTCATTACCAGCCACCATCCTATTCCTACCAATAACCCCCCTAATCTTAGCC------------TA----AAGAG
U.flaviceps        AATCTAATAACAACCCTAACCCCAATCTCCCTATTCCTCCTACCAATGACCCCACTACTACTA---------------TA----AGAAA
S.crassicaudatus   CTTCTAACCTCCACACTCCCAATGACCCTACTAATACTCCCAATCACCCCAATCATAACCCAA---------------T-----AGAAA
L.carinatus        AATCCACTGTCTATCACTCTAACCATGTCAATTCTACTACTGCCAATTACACCTTTAATTCTGATA------------T-----AGGGA
B.plumifrons       ACCCCTCTAACCCTGGCCCTCCCCCTATCACTCTTTATACTCCCAATTACCCCACTAATCTTGTCA------------T-----AAAAA
G.wislizenii       TTAATTACCATAACCCTCCCAGCCTCTACTATAATTCTCCCACTAACCCCAATAATTTTACTC---------------T-----AGAAA
O.cuvieri          CTATTACTGAGCATAACTGCCCCAATAACCATCTTAATACTACCAATCTCCCCACTAATCCTACAA------------TAAC--AGAAA
O.attenuatus       CTACTACTACCAACCACCCTCCCACCATCAATCCTGGCTCTGCCATTAACCCCCCTATTAAAACCA------------TAGCACAGAAA
E.panamintina      TTACTACTCTCAACAACCCTCCCAATATCCATCATAGGACTACCTCTCGTACCACTAATAAAACCA------------TAAC--AGAAA
C.enneagrammus     ACCACATTATCAACAATAACCCCCCTCGTACTAGCCTCACTACCCCTATTACCCCTAATGAAACCA------------TAAC--AGAAA
A.pulchra          CCCCTACTATCAACAGCACTCCCCATCTCACTAATAGCACTACCACTAATACCGCTCATCAAACCC------------TA----AGGGG
H.suspectum        CTTCTACTAACCACGACCTTTCCACTCTCCATTATAATAACACCTCTGATACCCATCATTCAGCTA------------TAAC--AGAAA
X.grandis          CCCCTAATAACAACAGGAATCTCATTATCACTACTTGCCCTCCCACTAATACCCCTAGTACTG---------------TAAC--AGAAA
V.griseus          TCCCCACTATCCACCTCAATCCCGATTTCACTCCTCCTTCTGCCAATCACACCCCACCTCACTCAG------------TAA---AGAAA
L.borneensis       ACCCTGATCTCAATTTTACTCCCAACAACTACCCTCGCCCTGCCAATACTCCCACTAATAGGC---------------T-----AGAAA
S.crocodilurus     ATATTTTTAACAATAACAAGCCCATTAGCCCTCTTAATAATCCCAATTACACCCTTTATCATCCCA------------TAAC--AGAAG
D.semicarinatus    ATAGGAACCTCAATACTAACAATAATAACAATACTTCTTCTACCCCTATCACCAAATATA------------------T-----AGAAG
R.braminus         TCCTGATTCCCCCTCCTAGCATCAACAACCATCTTGTTACTTCCGCTAACCCCCGCACTTCTA---------------T-----AGGAG
C.ruffus           ACCATCACATCCACACTAATAATCTCCTCCATCATAATACTGCCAATAACACCAACACTT------------------TAG---AGAAA
Agkistrodon.sp.    CAATTCTCAACTACACTAGCAACCATAATAGTCTTACTCCTACCACTCTCACCAAGCATG------------------T-----AGGAA
E.grammica         AACAAAATTCCAATAATTACCACCCTTCTTATTATTACCCCGATTCTTCCACTAATTTCCCCT---------------T-----AGAAA
B.biporus          ATGCACACAGCGGCCACCATCACACTAACTACAATACTACTCCTACTCACACCAATCCTCGCCCTATGC---------T-----AGAAG
T.weigmanni        GCCGGTATCACCACTACCATAGCAATAACAATCATACTACTACCACTAATACCCGTACTAATCACCCAT---------T-----AGAAA
A.xera             CTCATGTACATAACCATCCCAATTACCGTAATGGCCTTACCACTGACTCCCCTACTAATCACAAAT------------TA----AGAGA
C.tigris           ATCATAACACTAACTACCCCAACAGCCCTTATACTATTACCAATTCTCCCACTAATAAACCCA---------------TA----AGAAA
L.parietale        ATAATAACACTATTAGTACCCCCAACACTTCTTCTTCTACCAATATTAACACCCGTTTTATCA---------------T-----AGAAA
E.turkmenicus      ATCACTACCCAATTATTTATTATTACCACTACGCTCCTACCAATTACCCCCCTAGTTAATAAAATTTTG---------TAAT--AGAAA
S.shrevei          GAACTAGCCCCAACACTTACCCTAGCAACACTTCTACTACCAATCACACCCATCATCTACTACACCCCC---------T-----AGAAA
T.przewalskii      CCACTACCACTAACTATGACCCTAGCCACACTCGCCCTACCAATTACACCACTACTATATCACTCCCTC---------T-----AGAGA
G.gecko            GGCCTTACAACCACTGTAACAACAACACTAATACTCCTCACCCTCACCCCTCTACTAATCACCACA------------T-----AGAAA
P.lindneri         CCCATTCTACCTCAATTATCCTATCAAACACACTACTTCCCAATCACCCCTCTAATCATAAACTTTTGC---------TAAC--AGAAA
Cr.ocellatus       CTCATCCCTACAACTATTTTAGCTACCATATTACTACCACTAACCCCATTAATCAATAATCTCTAC------------T-----AGAAA
L.jicari           CCAATCACCCCCACTATTATTATTGCAACAATAGCCCTACCAATTTCCCCACTCGTCTTAAACCTTTAT---------TAAC--AGAAA
M.aurata           ATACCAATTATAGCCCCCACAGTACTATCATTGCTTCTTCTCCCAATAACCCCAATATTTTACCAA------------TAAAT-AAAAG
C.robustus         GCCGTACTTACTACAACAATAACCCTATCAATACTACTACTACCAATTACCCCCGCCCTCATT---------------TA----AGAGA
S.sikkimensis      ACAATTCTAACCACAACACTAGTTCTATCCACAATACTTTTACCAATTACCCCAACACTTATC---------------T-----AGGGA
E.inexpectatus     ACCCCAATAACCCCCACAATCATCCTGTCTACCCTTCTCCTACCAACCACACCACTACTAATC---------------TAA---AGAAA
E.skiltonianus     ACCCCAATAGCCACCACAATCATTTTGTCAACCCTCCTCCTACCAATCACACCAATATTTATC---------------TAA---AGAGG
E.anthracinus      GCCACAACAACCACTCTAATTGCCCTATCAACCCTTCTCCTACCAATCACACCCATATTTATC---------------TAA---AGAAA
S.anguineus        ACCTCAATAAGCATAACAATCCTCCTATCCACCGCCTTACTTCCAATCACTCCTATATTAATTATA------------T-----AGAAA
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P.eggeli             ACCCCAATAAGCATAATAATCCTTTTATCCACACTTGCCCTGCCCATCACCCCAATACTAATTATA------------T-----AGGAG
F.polylepis          ACACTCTTAAGCATAGCAATAATGCTCTCACTCCTTTCCCTGCCAATAACCCCAACATTCACC---------------TAACA-AAGGA
Ch.ocellatus         AACCTAATAATCACCACAACCATCTTATCCACACTAATCCTCCCAATTACCCCAATATTTATTATT------------T-----AGAAG
A.meleagris          TCACCACTATCAACAATAATAATCACATCAATATTACTACTACCAATCACCCCAATACTAATATACACAACA------T-----AGAAG
T.lomii              CCACCACTATCAACAATAATAACCATATCAACAATACTTCTACCAATCACCCCAATACTCATATACACAACA------T-----AGAAG
T.gariepensis        CCACCACTATCAACAACAATAATCGCATCAATAATACTCTTACCAATTACCCCAATACTAATATGCACAACA------T-----AGAAG
X.vigilis            AAACTAATCTCAACTATAATACCAGTTACAACTACCATAATCCCAATATCACCAATTATACTC---------------T-----AGAGA
C.polyzonus          ATAACAATAATTATATTCATTCTCTCTACCCTCGCTCTACCAATAACCTTTACCCTCGCC------------------T-----AGAAG
Zonosaurus.sp.       GCTCTGATAGTGAGCCTCTCAATCCTATCACTACTCCTACTCCCAATCACCCCAACAACA------------------T-----AGAAG
Dibamus              ACCCTAATTTCAACAACCCTAATACTAGCCCTATGCCTACTCCCATCAACCCACTTAATAACC---------------T-----AGAAA

Index0               11111111111111111111111111111111111111111111111111111111111111111111111111111111111111111
Index1               44444444444444444444444444444444444444444444444444444444444444444444444444455555555555555
Index2               22222333333333334444444444555555555566666666667777777777888888888899999999990000000000111
Index3               56789012345678901234567890123456789012345678901234567890123456789012345678901234567890123
Qualifiers1          .......................................................................TRP..........ALA...
Qualifiers2          >>..D>>>...........D>>>.AC>>>..COD..AC>>>.....T>>>>........T>>>>AA>>>>>*..........*<<<<<
A.mississippiensis   ATTAGGTTTAAATTCCA---AGCCGAGGGCCTTCAAAGCCCTAAAT-GGGAGTAAACAACCCCCCATTTCTTGATT-------TAAGGT
G.gallus             CTTAGGATTAACTGTCACCAAACCAAAGGCCTTCAAAGCCTTAAAT-AAGAGTTAAACT-CTCTTAGTTTCTGCCCAAC----TAAGAC
C.mydas              CTTAGGATCAAAACCTATCAAACCAGGGGCCTTCAAAGCCCCAAAT-AAGAGATAAAAC-CTCTTAGTTTCTG----------TAAGAC
S.punctatus          TTTAGGATATATA-------AACCAGGGGCCTTCAAAGCCCCAAAA-AAGAGACAT----CTCTTAATTTCTGA---------GGAAAC
B.theili             CTTAGGATATATTA------AACCAGTGGCCTTCAAAACCACTAAA-AAGAGTACCAC--CTCTTAGTTCCTC----------TAAAGC
C.rudis              CTTAGGATAATTTA------AACCCGAGGCCTTCAAAGCCTCTAAA-AAGAGATTTAAC-CTCTTAGCTCCTGACAC------GAAAGC
C.brevicornis        CTTAGGATAAACATA-----AACCCGGAGCCTTCAAAGCCCCAAAC-AAGAGCCCAGAC-CTCTTAGCTCCTGCCAACAACA-TAAAGC
C.salinarum          CTTAGGATTACATA------AACCGAGAGCCTTCAAAGCCCTAAAT-AAGAGTTATACC-CTCTTAGCCCCTGC---------TAAAAC
P.leusterii          CTTAGGATAAATTTTA----AACCAAGGGCCTTCAAAGCCCTAAAT-AAGAGCCACGCC-CTCTTAGTCCTTGGC--------TAAAAC
P.cocincinus         CTTAGGATAGCTCA------AACCGAGGGCCTTCAAAGCCCTAAAC-AAGAGACCACC--CTCTTAGCCTCTGCA--------TAAAAC
Hydrosaurus.sp.      CTTAGGTTAACCCTATCA--AACCTGAAGCCTTCAAAGCTTCGAAC-AAGAGTACCCACACTCTTAGCATCTGCCAC------TAAAAC
C.calotes            CTTAGGAATACACTTA----AACCGGAGGCCTTCAAAGCCTAAAAC-AAGAGATAC----CTCTTAGTACCTGT---------TAAAAC
J.tricarinata        CTTAGGACTAATATA-----AACCAAAGGCCTTCAAAGCCTTAAAC-AAGAGATCCAC--CTCTTAGTACCTGAT--------TAAAAC
P.raddei             CTTAGGATTAAATCTTA---AACCAGTGGCCTTCAACACCACAAAT-AAGGGCGAA----CCCTTAGCTTCTG-----------AAGAC
L.belliana           TTTAGGATAACATCA-----AACCAAGGGCCTTCAAAGTCCTAAAT-AAGAGACTGAC--CTCTTAATCCTTGACC-------TAAAAC
U.acanthinurus       CTTAGGATTATCACCA----AACCGAGGGCCTTCAAAGCCCTAAAA-AAGAGTGCCAAC-CTCTTAGCTTCTGCTCAA-----TAAAAC
A.paternus           CTTAGGATCAAATA------AACCAAGGGCCTTCAAAGCCCAAAAT-ATGGGTTAAACA-CCCATAGTTTTTG----------TAAGAC
P.mcallii            CTTAGGATAACACTA-----AACCAAGAGCCTTCAAAGCTCTAAAC-AGGGGCTAAAC--CCCCTAGTTTCTGT---------TAAGAC
Sauromalus.obesus    CTTAGGATAAACCA------AACCAAGGACCTTCAAAGTCCAAAAT-AGGAGTGAAACC-CCCCTAGCTTCTGC---------CAAGAC
Hoplocercus.sp.      CTTAGGATAAACACA-----AACCAAGAGCCTTCAAAGCTCAAAAT-ACGGGCGCAACC-CCCGTAGTCCCTGC---------TAAAAC
E.laticeps           CTTAGGATAAACTA------AACCAAGAGCCTTCAAAGCCCAAAAT-AGGGGCGAAACC-CCCCTAGATCCTGC---------TAAGAC
P.somuncurensis      TTTAGGATAACATA------AACCATGGACCTTCAAAGCCCAAAAC-AGAGGTGCAACC-CCACTAATTCCTGA---------TAAGAC
L.pictus             TTTAGGATAATTTACA----AACCATAGACCTTCAAAGTCTAAAAA-AAAGGTGCAAAC-CCTCTAACTCTTGA---------TAAGAC
U.flaviceps          CTTAGGATAATGTA------AACCAAGGACCTTCAAAGCCCTAAAT-AGGGAAGAATC--CCCCTAGTTTCTG----------CAAAAC
S.crassicaudatus     CTTAGGATAACACA------AACCAAGAGCCTTCAAAGCCCAAAAT-AGAGACAAACC--CCTCTAGTTTCTGC---------TAAGAC
L.carinatus          CTTAGGATAATATTA-----AACCAAGGGCCTTCAAAGCCCAAAAC-AGGAGTGAAACC-CCCCTAGCCCCTGA---------TAAGAC
B.plumifrons         CTTAGGATAACTTA------AACCATGGGCCTTCAAAGCCCAAAAC-AGGGATGAAACC-ACCCTAGTTTTTGCAC-------TAAAAC
G.wislizenii         CTTAGGATTAAACA------AACCAAGGGCCTTCAAATCCCAAAAC-AGGAGTGAAAAC-CCCCTAGTTTCTGAAT-------TAAAAC
O.cuvieri            CTTAGGTTAACTCA------AACCAAGGGCCTTCAAAGCCCTAAACGAAGCCAAGC----CCCTTAGTTCCTGC---------CAAGAC
O.attenuatus         TTTAGGTTAATACCA-----AACCGAGGGCCTTCAAAGCCCTAAAT-AGAGAATAAACT-TCCCTAATTTCTGAT--------CAAGAC
E.panamintina        TTTAGGTTACATA-------AACCAAGGGCCTTCAAAGCCCTAAAC-AAGGAACAC----TCCTTAATTTCTGA---------TAAGAT
C.enneagrammus       CTTAAGTTACCACTA-----AACTAAGAACCTTCAAAGTTCTAAAC-AGGGACTAAA---CCCCTAGTTTCTGCT--------TAAGAC
A.pulchra            CTTAGGATAATCTTA-----AACCAAGAGCCTTCAAAACTCTAAAT-AAGGGCCCATAA-CCCTTAGCCCCTG----------AAAAAC
H.suspectum          TTTAGGATCACCATTA----AACCGAGGACCTTCAAAGCCCTAAAC-AAGAGTAATA---CTCTTAATTTCTGG---------AAAGAC
X.grandis            CTTAAACTTAACCCCTAA--AGCTAAGAACCTTCAAAGTTCTAGAT-AAGAGTGAAACC-CTCTTAGTTTCTGC---------TTAGGC
V.griseus            TTTAGGTTCATACTTA----AACCAAGAGCCTTCAAAGCCCTAAAA-AAGAGCACAAAC-CTCTTAATTTCTG----------CAAGAC
L.borneensis         CTTAGGTTACTGCCCTA---AACCAAGAGCCTTCAAAGCTCTCAAC-AAGAGTGAAACC-CTCTTAGTTTCT-----------GAAGGC
S.crocodilurus       TTTAAGCTAACAA-------AACTAAGAGCCTTCAAAGTCCTAACT-AGGAGTGAAACC-CTCCTAACTTCTGCT--------TAAAGC
D.semicarinatus      CTTAAGTTATATTA------AACTAGGAACCTTCAAAGTCCCAAAA-AAAGACC------ACTTTAGTTTCTGTT--------TAGAGC
R.braminus           CTTAGGCTATACA-------AACCAAAAGCCTTCAAAGCTTTAAAA-AGGGAACA-----ACCCTAGCTTCT-----------GAGAGC
C.ruffus             CTTAAGTTATACCA------AACTAGAGACCTTCAAAGTCCCCAAA-AAAGACAT-----ACTTTAGTTTCT-----------GAGAGT
Agkistrodon.sp.      CTTAAGTTATATCA------AACTAAGAGCCTTCAAAGCCCCAAAT-AAAGCACA-----ACTTTAGTTTCTG----------CAGAAC
E.grammica           CTTAGGTTAGTCCTAA----AACCAGAAGCCTTCAAAGCCTCAAAC-AGGGTACACATA-TCCCTAGTTTCTGA---------TAAGAC
B.biporus            CTTAGGTTACAAATATCCCAAACCAGGGGCCTTCAAAGCCCCAAAC-AAGATCAAAC---ATCTTAGCTTCTG----------CAAGAC
T.weigmanni          CTTAGGTTAATCTA------AACCTGAAACCTTCAAAGTTTCAAAT-ATGAGCGAAACCACTCTTAGTTTCTG----------TAAAGC
A.xera               CTTAGGTTAACAA-------AACCATGGGCCTTCAAAGCCCAAAAC-AAGAGCGGGA---CTCTTAGTCTCTG----------TAAGAC
C.tigris             TATAGGCTAATTTATCA---AACCATGGGCCTTCAAAGCCCAAATT-GTGAACTA-----CTCACTATTTCTGC---------TAAGAC
L.parietale          TATAGGCTAAACAACA----AACCACGGGCCTTCAAAGCCCAAACT-GTGTTA-------AACACTATTTCTG----------TAAGAC
E.turkmenicus        CTTAGGTTATACTACA----AACCAAGAGCCTTCAAAGCCCTAAAT-AGAGAACGCCACCCCTCTAGTTTCTG-----------AAGGC
S.shrevei            CTTAGGCTAACACCCAA---AACCGCACGCCTTCAAAGCGTGAAAT-ATGTACCA-----CACATAGTTTCTGC----------AAGAC
T.przewalskii        CTTAGGTTAAACA-------AACCAAGGACCTTCAAAGCCCTAAAT-AGAAGCCACAC--CCTCTAGTCTCTGG----------AAGAC
G.gecko              TTTAGGTTAACTAGTAGTA-AACCGAGAGCCTTCAAAGCCCTAAAT-GGGACCCAA----AACCCAATTTCTGCTCGTG-----AGGAT
P.lindneri           CTTAGGTTAACATCA-----AACCAAGGGCCTTCAAAGCCCTAAAC-AGGGGACAAAA--CTCCTAGATTCTG-----------AAGAC
Cr.ocellatus         CTTAGGTTATACCA------AACCCAGGACCTTCAAAGTCCTAAAA-AAGAATACT----CTCTTAGTTTCTG-----------AAGAC
L.jicari             CTTAGGTTAACAACAAA---AACCAAGGGCCTTCAAAGCCCTAAAC-ACGGGGACC----CCCGTAGTTTCTG-----------AAGGC
M.aurata             CTTAGGTTAAAACTA-----AACCAGGGGCCTTCAAAGCCCCAAAT-AAGGACTAACC--CCCTTAGCTTTTGAACT-------AAGAC
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C.robustus         CTTAGGTTAAACCAAA----AACCAGTGGCCTTCAAAGCCACAAAC-AAGAGATCAACC-CTCTTAGTCCCTG-----------AAGGC
S.sikkimensis      CTTAGGCTAAATAA------AACCGGTAACCTTCAAAGCTACAATC-AAGAGTTTAAAC-CTCTTAGCCCCTG-----------AAAGC
E.inexpectatus     CTTAGGTTAACCA-------AACCAGGGGCCTTCAAAGCCCCAAAC-AAGAGCTAGACC-CTCTTAGTTTCTG-----------AAGGC
E.skiltonianus     CTTAAGTTAAACTTA-----AACTAGCGGCCTTCAAAGCCCCAAAC-AAGAGTTAAACC-CTCTTAGCCCCTG-----------AAAGC
E.anthracinus      CTTAGGTTAATTTA------AACCAAAGGCCTTCAAAGCCTTAAAC-AGGGGTTAAACC-CCCCTAGTTTCTG-----------AAGGC
S.anguineus        ATTAAGTTAACCATA-----AACTAATGACCTTCAAAGCCATAAAT-AAGAGTTTAATC-CTCTTAATCTCTG-----------AAAGT
P.eggeli           CTTAGGTTAACCCTCA----AACCAGGGGCCTTCAAAGCCCCAAAC-AAAAGTTAAAAT-CTCTTAGCTCCTGT----------AAGGC
F.polylepis        CTTAGGTTAAACCACCAA--AACCAGGGGCCTTCAAAGCCCCAAAC-AGGAGATAAAAA-CTCTTAGTCCTTG-----------AAGGC
Ch.ocellatus       CTTAGGTTAATATCA-----AACCAGGGGCCTTCAAAGCCCCAAAC-AAGAGTTCAACC-CTTTTAGCTCCTG-----------AAGGC
A.meleagris        CTTACGTTAACAA-------AACCAAGAGCCTTCAAAGCCCTAAAC-AAGAGTGAGACC-CCCTTAGCTTCTGC----------AAGAC
T.lomii            CTTAGGTTAACAA-------AACCAAGAGCCTTCAAAGCCTTAAAT-AAGAGTGAGACC-CCCTTAGCTTCTGC----------AAGAC
T.gariepensis      CTTACGTTAACATA------AACCAAGGGCCTTCAAAGCCCAAAAT-AAGGGTGAAACC-CCCCTAGCTCCTGC----------AAGAC
X.vigilis          CTTAGGATAAGACA------AACCAAGAGCCTTCAAAGCCCAAAAT-AAGAGCTAAGC--CTCTTAGTCTCTG-----------AAGGC
C.polyzonus        CTTAGGATAATTTTATTA--AACCAGGGGCCTTCAAAGCCCAAAAT-GAGAGCGGAACC-CTCTTAGCTTCTGA----------AAGAC
Zonosaurus.sp.     CTTAGGATAATCTTTTA---AACCAAGGACCTTCAAAGTCCTAAAT-AGGAGTTAAAAA-CTCTTAGCTTCTGCCC--------AAGAC
Dibamus            CTTAGGATAGACACA-----AACCAGAGGCCTTCAAAGCCCCAAAC-AAGAGCTCAACA-CTCTTAGTTTCTG-----------AAGAC

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Index1             55555555555555555555555555555555555555555555555555555555555555555555555555555555555555666
Index2             11111122222222223333333333444444444455555555556666666666777777777788888888889999999999000
Index3             45678901234567890123456789012345678901234567890123456789012345678901234567890123456789012
Qualifiers1        ..............................................................ALA........ASN.............
Qualifiers2        AA<<<<T........<<<<T....<<<AC..COD..<<<AC.<<<D......<<<D..<<<<<AA........*<<<<<AA<<<<T...
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G.gallus           CAACAGGACATTAA-CCTGTATCTCCTGAATGCAAATCAGACGCTTTAATT-AAGCTAAGGCCTCTAC-----CTAGACAGATGGGCTT
C.mydas            CTACAGGACCCTAT-CCCATATCTTCTGAATGCAACTCAAACACTTTAATT-AAGCTAAGGCCTT--------CTAGACAAATGGGCCT
S.punctatus        CTGAAAGATTCTTA-CTTTCATAGCCTTAATGCAACTAAGACACTTTTATT-AAGATAAGGCTTC--------CTAAATGAGCAGGCCT
B.theili           TTATTGATACTA---TCAACATCCTCTGAATGCACCCCAGAAACTTTAATT-AAGCTAAAACTTCCA------CAGGACTAGTGGGCCT
C.rudis            TTGTTGAATTA----CCAACATCTCCTGAATGCAACTCAGATACTTTAATT-AAGCTAAAACTTCGTTA----CCGGACCAGTGGGCCT
C.brevicornis      CTGTTGAGACTA---TCAACATCTCCTGAATGCAACTCAGACGCTCTAATT-AAGCTAAGACCTTATATAACACAGGACCAGCGGGCCT
C.salinarum        CTATAGAACTTA---TCTACATCTACTGAATGCAAATCAGACGCTTTAATT-AAACTAAGGCTTC--------AGGAGACAGAGGGCCT
P.leusterii        CTACAGAACTTA---TCTACATCTCCTGACTGCAAATCAGACGCTTTTATT-AAACTAAGGCTTCC-------AGGAGTCAGCGGGCCT
P.cocincinus       CTATAGAACTTA---TCTACATCTTCTGAATGCAACCCAGACATTTTAATT-AAACTAAGGCTTC---------GGAGTTAGAAGGCCT
Hydrosaurus.sp.    CTGTAGTACATT---ACCACATCTTCTGATTGCAACTCAAACGTTTTACTT-AAACTAAGGCCTC--------CAGGACCGGTGGGCCT
C.calotes          CTGCAAGATTTT---CTTACATCACCTGAATGCAACTCAGACACTTTACTT-AAATTAAGGCTTT--------CAGGATTAGTGGGCCT
J.tricarinata      CTGTGAAATTTTA--CTCACATCACCTGAATGCAACTCAAGCACTTTAATT-AAATTAAGGCCTTATTA----CAGGATCAGCGGGTTT
P.raddei           CCATAGGACTTTAA-CCTACATCACCTGTATGCAACTCAGACATTTTAATT-AAAATAAGGCCTA----------AAACCAGCGGGCCT
L.belliana         CTATAGAACTTTAA-TCTATATCATCCAAATGCAACCCGGACACTTTCATT-AAGCTAAGATTTTA-------CAAGACCGGTGGGCCT
U.acanthinurus     CTGTGAAACTCTA--ATCACATCTTCTGGATGCAACCCAAATGTTTTAATTAAAACTAAGGCCTTGCA-----CAGGGCTGGTGGGCTT
A.paternus         TTGTGAAACACTAT-TACACATCTCCTGAATGCAACTCAAGCACTTTTATT-AAGCTAAAGCCTCA-------CTGAATAGGCGGGCTT
P.mcallii          CTGTGAAATACTAA-AACACATCTCCTGAATGCAAATCAGACACTTTAATT-AAGCTAAGGCCTCCT------CTAGATAGGCGGGCTT
Sauromalus.obesus  CTGCGAAACATTAA-AACGCATCTTCTGAATGCAACTCAGACACTTTAATT-AAGCTAAGGCCTCC-------CTAGACAGGCGGGCCT
Hoplocercus.sp.    CTGTGAAATACTA--AACACATCTCCTAAATGCAACTCAGGCACTTTAATT-AAGCTAAGGCCTC--------CTGGACAGGTGGGCCT
E.laticeps         CTGAGAATCATTAA-AACACATCTCCTGATTGCAACTCAGACACTTTAATT-AAGCTAAGGCCTC--------CTAGACAGGTGGGCCT
P.somuncurensis    CTGCGAAATACTAA-TACACATCTCCTGAATGCAACTCAGACACTTTAATT-AAGCTAAGGCCTCA-------CTAGATAGGAGGGCCT
L.pictus           CTGTGTAACTCTAT-AACACATCTCCTGAATGCAACTCAGACACTTTAATT-AAGCTAAGGCCTCC-------CTAGATAGGCGGGCCT
U.flaviceps        CTGCGAAACACTA--AACGCATCTCCTGAATGCAACTCAGACACTTTAATTTAAGCTAAGGTCTC--------CCAAGAGAGTGGGCCT
S.crassicaudatus   CTGTGAAATTCTA--AACACATCTTCTGAATGCAACTCAAACACTTTAACTTAAGCTAAGGCCTCC-------CCAGACAGACGGGCCT
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O.attenuatus       CTGTAAAACTCTAG-TCTACATATTCTGGCTGCAACCCAGACGCTTTAATT-AAGCTAAGGCCTTA-------CTAGATACACGGGCCT
E.panamintina      CTGTAAGAATTTAA-CCTACATCTTCTGACTGCAACCCAGACACTTTAATT-AAGCTAAAACCTCA-------CTAGACAGACGGGCCT
C.enneagrammus     CTGTAAAACTCTAA-TTTACATCACATGACTGCAACTCAAGCACTTTAATT-AAGCTAAGGCCTTA-------CTAGACAAACGGGCCT
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H.suspectum        CTATAAAACTTTAA-TTTATATCCTCTAAATGCAACTTAGATACTTTAATT-AAGCTAAGACCTTA-------CTAGATAGATGGGCCT
X.grandis          CTGTAAAACTCTAA-TTTACATCTTCTGAATGCAACCCAGACACTTTAATT-AAGCTAAAGCCTGCC------CTAAATAAACGGGCCT
V.griseus          CTATAAAACTCTAA-TCTATATCTCCTGAATGCAACTCAGACACTTTCATT-AAGCTAAAGCCTTC-------CTAGATAGACGGGCCT
L.borneensis       CTGTAAAACTCTAA-TTTACATCACCTGAATGCAACTCAAACACTTTCATT-AAGCTAAAGCCTCC-------CTAGATAAACGGGCCT
S.crocodilurus     CCGTAGAA-TTTAA-ACTACATCATCTGAATGCAACCCAGATACTTTAATT-AAGCTAGAACTTA--------CTAGACAAACGGGCCT
D.semicarinatus    TTGCAGAAAC-----ACCACATCTACTGCTTGCAACACAGACATTTTAATT-AAACTAAAGCTCT--------CTAGATTAGCGGGCCT
R.braminus         TTGCGATT-------CACACATCTCCTGCTTGCAAAACAGACACTTTAATT-AAGCTAAAACTCTT-------CTAGGTAGGTGGGCCT
C.ruffus           TTGCAGCAA------CCCACATCTTCTGCTTGCAACACAGACATTTTAATT-AAACTAAAACTCTC-------CTAGAGTAGAAGGTCT
Agkistrodon.sp.    TTACGGTATT-----ACCACATCTCCTGTTTGCAACACAGACATTTTAATT-AAACTAAAGCTCT--------CTAGATTAGCAGGCCT
E.grammica         CTGTATAACCTTGA-TATACATCTCTTGAATGCAACTCAAACACTTTAATT-AAGCTAAGGCCTCTT------CAAGATGGACAGGCTT
B.biporus          TTGTATGCCTTTAG-CATACATCAACTGACTGCAAATCAGCCACTTTAAACTAAGCTAAAGCCTT--------CTGGACCGGCAGGCCT
T.weigmanni        CTGTGCGCAACTAT-CGCACATCATCTGAATGCAACTCAAATACTTTAATT-AAGCTAAAGCCTTA-------CTGAACTGGCAGGCCT
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C.tigris           TTGCGTTATTCA---AACACATCTCCTGAATGCAACTCAGACACTTTAATT-AAGCTAAAGCCTCC-------CTGGATAAGCGGGCCT
L.parietale        TTGTATAT-------AATACATCCCCTGAATGCAACTCAGGCACTTTACTTTAAGCTAAAGCCTCT-------CTGAATAAACGAGCTT
E.turkmenicus      CTAAGTAATTTTTAATACTCATCATCTGAATGCAACCCAAACACTTTAATTTAAGCTAAGACCTCCA-------AAGACCGACGGGCCT
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T.przewalskii      CTGTATTACTCTAA-AATACATCCTCTGAATGCAACTCAAATGCTTTAATT-AAGCTAAGACCTCA-------CTAGACTGACGGGCTT
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P.lindneri         CTGTATAACTCTAA-CATACATCTCCTGAATGCAACTCAGACACTTTAATT-AAGCTAAGACCTCA-------CTAGACCGACGGGCCT
Cr.ocellatus       TTGTATAATTTTAT-TATACATCCACTGAATGCAACTCAGACACTTTAATT-AAGCTAAAGCCTC--------CTAGACTAACGGGCCT
L.jicari           CTGTGAAACCCTAT-CTCACATCCTCTGAATGCAACTCAGACACTTTAATT-AAGCTAAAGCCTCA-------CTAGATCGACGGGCCT
M.aurata           CTGTAAAACTTTAA-TTTACATCTCCTGAATGCAACCCAGACACTTTAATT-AAGCTAAGGCCTC--------CTAGATAGACGGGCCT
C.robustus         CTGTAAAACTTTAA-TTTACATCTCCTAATTGCAAATCAGACACTTTAATT-AAGCTAAAACCTC--------CTAGACAAACGGGCCT
S.sikkimensis      TTGTAAAACTCTAA-TTTACATCTCCTGACTGCAAATCAAGCACTTTTATT-AAGCTAAAACCTC--------CTAGACAGACGGGCCT
E.inexpectatus     CTGTAAAACTCTAA-TTTACATCTTCTGAATGCAACTCAAACACTTTAATT-AAGCTAAAGCCTC--------CTAGATAGACGGGCCT
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F.polylepis        CTGTAAAACTCTAA-TTTACATCAACTGAATGCAACTCAGACACTTTAATT-AAGCTAAGGCCTC--------CCAGATAAACAGGCCT
Ch.ocellatus       CTGTAAAACTCTAA-TTTACATCTCCTGAATGCAACCCAGACACTTTAATT-AAGCTAAAGCCTC--------CCGAATAAACGGGCCT
A.meleagris        TTGTAAAACTCTAA-TTTACATCTCCTAATTGCAACTCAGACACTTTAATT-AAGCCAAAGCCTCA-------CTAGATAGACGGGCCT
T.lomii            TTGTAAAACTTTAA-TTTACATCTCCTAATTGCAACTCAGACACTTTAATT-AAGCCAAAGCCTCA-------CTAGACAGACGGGCCT
T.gariepensis      TTGTAAAACTTTAA-TTTACATCTCCTGACTGCAACTCAGACACTTTAATT-AAGCCAAAGCCTCC-------CTAGACAGACGGGCCT
X.vigilis          CTGTAAAATTTTAA-TTTACATCTACTAACTGCAACTTAGATACTTTAATT-AAGCTAAAACCTCA-------CTAGATAGACGGGCCT
C.polyzonus        TTGTAGAACTTTAC-TCCACATCTTCTGACTGCAACCCAGACACTTTAATT-AAGCTAAAGCCTTA-------CTAGATAGACAGGCCT
Zonosaurus.sp.     TTGTAAAACTCTAC-TTTACAGCTTCTGAATGCAACCCAGACACTTTAATT-AAGCTAAAGCCTTA-------CTAGACAGGCAGGCCT
Dibamus            CTGCGAAACCCTAG-TTCACATCTCCTGAATGCAACTCAAACGCTTTAATT-AAGCTAAGGCCTCC-------CTGGATAAACGGGCCT

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Index1             66666666666666666666666666666666666666666666666666666666666666666666666666666666666666666
Index2             00000001111111111222222222233333333334444444444555555555566666666667777777777888888888899
Index3             34567890123456789012345678901234567890123456789012345678901234567890123456789012345678901
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Qualifiers2        ....<<<<T......<<<AC..COD..<<<AC..<<<D..........<<<D..<<<<<AA.+1ST>>>>>>..........ST->>>>
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C.mydas            CGATCCCATAACAA--TTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCTTTTGCCTA-TTTCCCGCTCTATAAAAAGCGGAAA-
S.punctatus        CGATCCTACAAACT--CTTAGTTAACAGCTAAAC-ACCTTAAACAAC-AGGCTTCCATCTAC--------------------------
B.theili           CGATCCCACAAAA---ACTAGTTAACAGCTAGAC-ACCTAAACCAAC-AGGAATTAATCCACA-------------------------
C.rudis            CGATCCCACATAA---ACTAGTTAACAGCTAACC-GCCCAAACCAGC-GGGCATTAATCCG----ATTTCTCCGTTTTAGAAAGGAG--
C.brevicornis      CGATCCCACAAAA---ACTAGTTAACAGCTAGTC-GCCCAAACCAGC-GGGCATTAATCCA----GTCTCCTTTTGAAAAAAAAGGAGA
C.salinarum        CGATCCCACAACAC--ACTAGTTAACAGCTAGCACGCCTGACCAG---TGGCACTAACTCCTAAA-----------------------
P.leusterii        CGATCCCACACAA---ACTAATTAACAGCTAGTCCGCCCAACCAAC--GGGCATTAACGCCT--------------------------
P.cocincinus       TGATCCTTCACAAC--ACTAGTTAACAGCTAGTTCACCCACCAAT---AGGTACTAACCCCACCCAAC--------------------
Hydrosaurus.sp.    TGATCCCACAATTCA-ACTAGTTAACAGCTAGTG-GCTTCAACCAAT-AAGCATCAGTCCAGAGTGAAATATGCCTCA----------
C.calotes          CGATCCCACGACTT--AACAGTTAACAGCTGAAC-GCCCAATCCAGA-GGGCATCAATCCACTACTCTATTTTAAAAAGAGT-------
J.tricarinata      TGATCCCACATAAT--ATCAGTTAACAGCTGACC-GCCCAACCCAGA-GAGCATTAATCCACTACTCCTTATAAAAAAGGAGT------
P.raddei           TGATCCCGCAAAAT--AATAGTTAACAGCTATTC-ACCTAAAACCAGCAGGCATCGGTTTATTAAATTTGCCCCCAACACAATCCT---
L.belliana         CGATCCCACAAAA---ACTAGTTAACAGCTAGCC-GCTCAAACCAGC-GAGCATCAACCTAACCCGCCCCGTCAAATAAAAACGGGGCG
U.acanthinurus     CGACCCCACAACAC--ACCGGTTAACAGCCGATC-GCCCAAACCAAC-AGGCATCAGCCCA---------------------------
A.paternus         TGATCCCACGACAA--ATTAATTAACAGCTAATT-ACCCAAACCAGC-GGGCTTCTATTCG-CTT-CTCCCGTCGGTGAAGAA-ACGGG
P.mcallii          TGATCCCACGAAAA--TTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCTTCTATCCG-CTT-CTCCCGTGCTTAAAA---ACGGG
Sauromalus.obesus  CGATCCCACAAAAA--ATTAGTTAACAGCTAAAC-GCCCCAGCCAGC-GGGCTTCTGTCCG-CTT-CTCCCGTCTTTTATTG--ACGGG
Hoplocercus.sp.    CGATCCCACAAAA---ATTAGTTAACAGCTAAAC-ACCCAACCCAGC-GGGCTTCTATCCTGCTT-CTCCCGTTAAGAAAAA--ACGGG
E.laticeps         CGATCCCACAAAAA--CTCAGTTAACAGCCAAAC-ACCCAATCCAGT-GGGCTTCTGTCCG-CTT-CTCCCGCTCAGTAA-----AACG
P.somuncurensis    CGATCCCACAAAAA--CTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCTTCTATCCG-CTT-CTCCCGTCGATAAAAA--ACGGG
L.pictus           TGATCCCACAATAA--CTTAGTTAACAGCTAAAC-ACCCAAACCAGC-GGGCTTCTATCCG-CTT-CTCCCGTTGGTAAAA---ACGGG
U.flaviceps        CGATCCCACAAAA---ACTAATTAACAGCTAGCT-GCCCAAACCAGC-GGGCTTCCATCCTGCTT-CTCCCGTCAAGGAAAA--ACGGG
S.crassicaudatus   CGATCCCGTAAAAA--ATTAATTAACAGCTAACC-ACCCAAACCAGC-GGGCTTCTATCTG-CTT-CTCCCGTTGAAAAAAA--ACGGG
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B.plumifrons       TGATCCCACAATTAAACCTAGTTAACAGCTAGGC-ACCCTAGCCAGC-GGGCTTCTGTCCG-CTT-CTCCCGTTGTAGAAGG--ACGGG
G.wislizenii       CGATCCCACAAAAA--CTTAGTTAACAGCTAAGC-ACCCAATCCAGC-GGGCTTCTATCCG-CTT-CTCCCGTTGAAAAAAA--ACGGG
O.cuvieri          TGATCCCACGAACA--ATTAGTTAACAGCTAAAC-ACCCAAACCAGC-GGGCTTCTATCCG-CTT-CTCCCGTTAGTTAAAAA-ACGGG
O.attenuatus       CGATCCCGTAAACA--ATTAATTAACAGCTAATC-ACTCTATCCAGC-GAGCTTCTATCTA-CTTCTCCCGTCTGTATA---AAACGGG
E.panamintina      CGATCCCGTAAACA--GTTAATTAACAGCTAATC-ACTCAATCCAGC-GAGCTTCTATCTA-CTT-CTCCCGTTAGAGAAAAAA-CGGG
C.enneagrammus     CGATCCCGTAAACA--ATTAATTAACAGCTAATT-ACTCAATCCAGC-GAGCTTCTGCCTA-CTTCTCCCGTCTAAAA----AAACGGG
A.pulchra          CGATCCCGTAAACA--ATTAATTAACAGCTAAAC-ACTCTATCCAGC-GAGCTTTTGCCTA-CTTCTCCCGTTAGTAGAAAAAAACGGG
H.suspectum        TGATCCCATAAACA--ATTAATTAACAGCTAACC-GCCCTAACCAGC-GGACTTCTATCTA-CTTCTCCCGCCTCTTA----AAACGGG
X.grandis          CGATCCCGTAAAAT--ATTAATTAACAACTAACC-GCTCTATCCAGC-GAGCTTTTATCTA-CTTCTCCCGTCGATAAA---AAACGGG
V.griseus          CGATCCCGTAACAA--ACTAATTAACAGCTAGCC-GCCCAAACCAGA-GGGCTTCTATCTA-CTTCTCCCGTTTGGGGAAA-AAACGGG
L.borneensis       CGATCCCGTGAAAA--ATTAATTAACAGCTAAAC-ACCCAAACCAGC-GGGCTTCTATCTA-CTTCTCCCGTTTTTAAACGACGGGAG-
S.crocodilurus     CGATCCCGTGACAA--ATTAATTAACAGCTAATT-ACCCTAACCAGC-GGGCTTCTATCTA-CTTCTCCCGTCTAGAGGAG-AAACGGG
D.semicarinatus    CGATCCCACAAAA---ACTAATTAACAGCTAGCT-GTCAAAACCGGC-GGACTTTAATCTAGCTTCTCCGTTTTTGGACGAAAGAAAAA
R.braminus         CGATCCCACAATCA--ACTAATTAACAGCTAGTT-ATCTAGACCAAT-AGACTCATACCTAA--------------------------
C.ruffus           CGATCCCACAAAAA--ACTAGTTAACAACTAGCC-GTCCAAACCAGC-GGACTTTAGTCTA-CTTCTCCGTTTTACGGAAAAAAAACGG
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E.grammica         TGATCCTGCGAAAC--TCTAGTTAACAGCTAAAA-ACCCAACCCAGC-GGGCTTCCATCTTCCTTCCCCCGTTATAAAAA--AAACGGG
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C.tigris           CGATCCCGCGAAAA--TTTAATTAACAGCTAAAA-ACCCAAGCCAGC-GGGCTTTTATCCA--CTTTCCCGTCGCTTTT-ACGACGGGA
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E.turkmenicus      CGATCCCGTAATAT--TTTAGTTAACAACTAAAC-ACCCAATCCAGC-GGACTTCAATCTTT-CTTCTCCCGTTTAAAAAAA--AACGG
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G.gecko            CGATCCTGCAAAAC--ACTAGTTAACAACTAATC-GCCTAAACCAGC-GGGCTTTAGTCTACAGCTTCGTCCCGCTGAG---ACGAGGG
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Cr.ocellatus       CGATCCCGTAAACC--TTTAGTTAACAAACAAAT-ACCCAAACCAGC-GGGCTTTAGTCTA-CTT-CTCCCGTTTGTTGGGGGAAAAAA
L.jicari           TGATCCCGTAACTC--TTTAATTAACAACTAAAT-GCCTAAACCAGC-GGGCTTCAATCTA-CTT-CTCCCGTTAGAAAAAA--ACGGG
M.aurata           CGATCCCGTAAAAC--CTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCTTCTATCCG----TGGC-TTCAAAAAAA---------
C.robustus         CGATCCCGTAAAAT--TTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCTTCTGTCCG---GGCTTTATAAAAAA-----------
S.sikkimensis      CGATCCCGTAAAAT--TTTAATTAACAGCTAAAC-ACCCAATCCAGC-GGGCTTCTGTCCA---GTCTTTTTTTTTAAAAAA-------
E.inexpectatus     TGATCCCGTAAAAT--TTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCCTCTATCCG--CGCTTCTTCTGTTAGAAGAAG-----
E.skiltonianus     TGATCCCGTAAAAT--TTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCCTCTATCCG--CGTCTTCTTCTATTTAGAAGAAG---
E.anthracinus      CGATCCCGTAAAAT--TTTAGTTAACAGCTAAAT-ACCCAATCCAGC-GGGCCTCTATCCG--CGCTTCTTCTATTTAGAAGAAG----
S.anguineus        CGATCCCATAAAAT--TTTAGTTAACAGCTAAAC-ACCCAAACCAGT-GGGCTTCTATCCG---GGCTTTAAAAAAA------------
P.eggeli           CGATCCCGTAAAAT--CTTAGTTAACAGCTAAAC-ACCCAATCCAGC-GGGCTTCTATCCG---GGCTTTAAAAAAA------------
F.polylepis        CGATCCTGTAAAAA--CTTAGTTAACAGCTAAGC-ACCCAATCCAGC-GGGCTTTTATCCG---GGCTTCAAAAAAA------------
Ch.ocellatus       CGATCCCGCAAAAA--CCTAGTTAACAGCTAAGC-GCCCAATCCAGC-GGGCTTCTATCCG---GGCAATAAAAAA-------------
A.meleagris        CGATCCCGTAACAC--CTTAGTTAACAGCTAAGC-ACCCAATCCAGC-GGGCCTCTATCCG---GCTTCTTCTTGTTTAAGAAGAAG--
T.lomii            CGATCCCGTAACAAC-CCTAGTTAACAGCTAAGA-ACCCAATCCAGC-GGGCTTCTGTCCG---GCTTCTTCTTATTTAAGAAGAAG--
T.gariepensis      CGATCCCGCAACAC--CCTAGTTAACAGCTAAGC-ACCCAATCCAGC-GGGCTTCTGTCCG---GCTTCTTCTTGTTTAAGAAGAAG--
X.vigilis          TGATCCCGCAAAAA--GCTAATTAACAATCAACT-GCCAAAACCAAC-AGACTTCTACCTACCATAAC---------------------
C.polyzonus        TTATCCTGTAAACA--ATTAATTAACAGCTAATC-ACCCAATCCAGC-GGGCTTCTATCTA--TCCTTCTCCCGTTCAAAAAAACGGGA
Zonosaurus.sp.     TTATCCTACAAACA--ATTAATTAACAGCTAATC-ACCCAATCCAGC-GGGCTTCTGTCTGGCTTCTCTTTATATAAAAGAG-------
Dibamus            CGATCCCGTAATAA--CTTAGTTAACAGCTAAAC-ACCCTAACCAGC-GGGCTTCTATCCGATTTCGCCCGTAAGAAAAA---ACGGGC

Index0             11111111111111111111111111111111111111111111111111111111111111111111111111111111111111111
Index1             66666666777777777777777777777777777777777777777777777777777777777777777777777777777777777
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Index3             23456789012345678901234567890123456789012345678901234567890123456789012345678901234567890
Qualifiers1        ..OL....CYS.....................................................................CYS......
Qualifiers2        >+4.....*<<<<<AA<<<<T...........<<<<T......<<<AC..COD..<<<AC.<<<D.....<<<D..<<<<<AA......
A.mississippiensis --------AAACCCCAGTACTACTTAA-----AGTACATCT--ACGAATTTGCAATCCGTTATGAATT--TCACTATGAGGCT------
G.gallus           --------AGACCCCGGCACACTTTAG-----TGTACATCA--ACGAGTTTGCAACTCATTATGAACT--TCACTACAGAGTC------
C.mydas            --------AAACCCAGACATCAACAAA-----GATATATCT--TTAAATTTGCAATTTAACGTGAACT--TCACTACAAGGTC------
S.punctatus        --------TAAGCCTGGACTATATTTC-----TAATCTTTC--CTAAGTTTGCAGCTCAGTACTTAA---------CAGGCCT------
B.theili           --------AAGTCTGGGGTACTTTTAT-----CTACCGTGT--CCAAATTTGCACTTCGGAATT------------CCAAACT------
C.rudis            --------AAATCCAGGGTCTTTAT-------AAACCTTAT--ATGGATTTGCACTCCAAAAT-------------CTGGACTGGTTTG
C.brevicornis      C-------AAGTCCAGGGTATTCTA-------CAACCTTAT--CCGAATTTGCACTTCGGGCTT------------CTGGGCTCTCGGC
C.salinarum        --------AGGCCTAAAGGTCTTTTA------AACCAAAA---TCCGATTTGCAATCAAATATTATT---------AGACCAAT-----
P.leusterii        --------AAGGCCTAAGGACTACAT------AGCCCACTA--TCCGATTTGCACTCAGACAACTTATTT------CAAGCCT------
P.cocincinus       --------TAGACCAAAGAGCAGTAA------TACCCATCA--TCTGATTTGCACTCAGAATTTTATT--------TTGGCCT------
Hydrosaurus.sp.    --------TAGGCCTACTGGCTATTTACA---AACCACCAT--CCAAATTTGCACTTTAGATCTATATC-------TAGGCCT------
C.calotes          --------AGACCTAGGAACCAA---------AATTCTTCT--CCAAATTTGCAATTTGGGGTTTTCTT-------CTAGGTC------
J.tricarinata      --------AGACCCAGGAACGTCCA-------AGTTCTTCT--CCAAATTTGCAATTTGTTTTG------------CCGGGTC------
P.raddei           --------TAGACCTACGAAAATCTA------CTTTCAAAA--CTAAACTTGCAATTTAGCATTTCTT--------TAGGCCT------
L.belliana         A-------AAAACCTCAGAGCCTTATGA----GCTCTTAT---TCGAATTTGCAATTCGAAACCTTT---------GAGGCCT------
U.acanthinurus     --------GAAACCCACAAACATACTAA----GTTATTTCT--CCGAATTTGCACTCCGGAACACA----------TGGGTCT------
A.paternus         AG------AAGCCCCGGAGCCTTTAG------GGCTCTTCT--TCAAACTTGCATTTTGATGTGGA----ACACTTCGGGACTTT----
P.mcallii          AG------AAGCCCCGGGACCCTTTCTG----GGTCCTTCT--TCAAACTTGCAATTTGACGTGAG----TCACCCCAGGGCTTT----
Sauromalus.obesus  AG------AAGCCCCGGAGCCTTTAG------GGCTCTTCT--TCAAACTTGCATTTTGACGTGTC----ACACCCCAGGGCTAT----
Hoplocercus.sp.    AG------AAGCCCCGGGACCTCTTAAG----GGTCCTTCT--TCAAACTTGCATTTTGACGTGAA----ACACCCCGGAGCTGTGTTG
E.laticeps         GGAG----AAGCCCCGGGGCCGATTGG-----GGCCCGTTT--TCAAACTTGCATTTTGACGTGTC----ACACCGCGGGGCTTT----
P.somuncurensis    AG------AAGCCCCGGAGCCCCTTTG-----GGCTCATCT--TCAAATTTGCACTTTGATGTGTAA---ACACCACGAAGCTT-----
L.pictus           AG------AAGCCCCGGAGCCTTTTGG-----GGCTCGTCT--TCAAACTTGCATTTTGACGTGTA----ACACCTCGGGACTTAAATA
U.flaviceps        AG------AAGCCCCGGGGCTCTTTAG-----AGCTCTTTT--TCAAATTTGCACTTTGATGTGAA----ACACTTCAGGACTTCTT--
S.crassicaudatus   AG------AAGCCCCGGAGCCCTTTATG----GGCTCGTCT--TCAAACTTGCAATTTGACGTGGCC---TCACCACGGGGCTGT----
L.carinatus        AG------AAGCCCCGGAGCCTTAAAG-----GGCTCATCC--TTAAACTTGCATTTTAATGTGTTGCTTACACTACGGGGCTT-----
B.plumifrons       AG------AAGCCCCGGAGCCTCTTAG-----GGCTCTTCT--TCAAACTTGCAATTTGACATGCTC---ACACCCCAGGGCTGT----
G.wislizenii       AG------AAGCCCCGGAACCCTTTAG-----GGTTCTTCT--TAAAATTTGCAATTTTATGTGATT---ACACCCCAAGGCTTAT---
O.cuvieri          AG------AAGCCCCGGAGCCTATTAG-----GGCTCGTCC--TCGAATTTGCATTTCGATGTGATA---ACACCCCGAGACTTAT---
O.attenuatus       AG------AAGCCCCGGAGATCCTAA------ATCTCAATT--CCAAGTTTGCAACTTGGCGTGTGA---ACACCTCAGAGCCAT----
E.panamintina      AG------AAGTCCCGGAGATCTTAAC-----GTCTCTTTT--CCAGGTTTGCAGCCTGATGTAT-----TTACCTCGGGACCT-----
C.enneagrammus     AG------AAGCCCCGGAAATCTTTCG-----ATTTCTTCT--CAGGGTTTGCAACCCTGTGTGATA---ACACCCCGAGGCT------
A.pulchra          AG------AAGCCCAGGAAATCTTCG------ATTTCGACT--CCAAGTTTGCAACTTGGCGTGTTAA--ACACCACCAGACTTT----
H.suspectum        AG------AAGTTCCGGGGATCTTA-------ACTCCATTT--CCAAGTTTGCAACTTGACGTAATT---CTACTACAGAACTAT----
X.grandis          AG------AAGCCCGGGGGATCTTAAAA----ATCTCGGCT--CCGAGTTTGCAACTCGGCGTGCAGC--GCACTTCAGGACTT-----
V.griseus          AG------AAGCCCAGGGGTAATCC-------TACCCACTC--TCAGATTTGCAATCTGATGACA---------CTCTGAACTGCATCT
L.borneensis       --------AAGTCCAGGGGGAACGC-------ACCCCCTCTT-TCGGAGTTGCAATCCGACGTGAA----ACACTTCTGGACCT-----
S.crocodilurus     AG------AAGTCCGGGAGATCTTAG------ATCTCCTTT--CCAAGTTTGCAACTTGGCGTGAA----ACACTGCCGAACT------
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D.semicarinatus    ACGGAG--AAACCCGGGGCCG-----------CTGCCGACT--TCAGATTTGCAGTCTGACATGTTAC--ACACCTCCGGGTTT-----
R.braminus         --------AAGTCCGAAGCTTA----------AAGCCCTCT--TCAAATTTGCAATTTGACGTGTTAT--ACACCTCCGAACTT-----
C.ruffus           AG------AAGCCCCGGGCGGA----------GGGCCTTCT--TCAGATTTGCAGTCTGACGTGAA----ACACCACGGGGCCT-----
Agkistrodon.sp.    AAACGGAGAAGCCCCGGGCAG-----------AAGGCCGACT-TCAGATTTGCAGTCTGACATGATG---ACACCTCGGAGCTT-----
E.grammica         GG------AAGCCCCGGCACCTTAAT------GGTGCTTCT--CCAAATTTGCATTTTGGCGTAA-----TTACCTCAGGGCTACT---
B.biporus          G-------AAGCTCTGGCCGCTCCG-------GCGGCGTGG--CCAAATTTGCAATTTGGCTCGCA----------CAGAACTACTT--
T.weigmanni        --------AGGAACTGGCCGCGGCCTAC----GCGGCAAGG--CCAAATTTGCAATTTGGCTCGAT----------CAGCACCTCCCT-
A.xera             --------AAGTCCTGGCCGCGCTTCC-----GCGGCGAGG--CCAAATTTGCAATTTGGCTTGACC---------CAGGACCTCGTTT
C.tigris           --------AAGCCCCGGCACTTCTG-------GGTGCTTAT--CCGAATTTGCAGTTCGATTTGTA----------CGGGACTT-----
L.parietale        --------AAGTCCCGGCACTTTTTG------GGTGCGTGC--TCTTGTTTGCAGCTTGAGTCTCT----------CGAGACTT-----
E.turkmenicus      GAG-----AAGCCCCGGCACTTTTA-------GGTGCTTCT--CTAAACTTGCAATTTAGCGTGATC---TCACCCCGGAGCTCT----
S.shrevei          GAG-----AGGCCCCGGCACCTTTATGG----GGTGCGTTG--CCGAATTTGCACTTCGGTGTACT----GACCACGGGGCCT------
T.przewalskii      GAG-----AAGCCCCGGCACCTTTTAG-----GGTGCTGCT--CCAAATTTGCACTTTGGTGTGTGG---CCACCCCAGGGCTT-----
G.gecko            GAC-----GAAGCCCGGGGCACCATTCCG---GGTGCTTGT--TTAAATTTGCACTTTAACCTCGT------CTCCCGGGCTT------
P.lindneri         AG------AAGCCCCGGCACACTTATG-----GGTGCTTTT--TTAAATTTGCAATTTAACGTGATC---ACACCACGGGGCTCTTTT-
Cr.ocellatus       ACGGGAG-AAGTCCCGGCTACCTCTCG-----GTAACGTCT--TTGAATTTGCAATTCAATGTGCAC---GCACTGCAGAACT------
L.jicari           AG------AAGCCCCGGCAACACTTAG-----GGTGCTTGTT-TCAAATTTGCAATTTGACGTGAAT---CACTACTAGGGCTT-----
M.aurata           --------AAGCCCCGAAACGCCTTTAG----GGTTTATCT--CTAGATTTGCACTCTAGCGTGAA----ACACCGCGGGACTT-----
C.robustus         --------AAGCCACGGCACACCCT-------AGTGTGCGTCTCCAGATTTGCACTCTGATGTGAA----ACACCTCATGGCTT-----
S.sikkimensis      --------AAGCCTCGGTACGCCTTTGGG---GGTACGTCT--CTAGATTTGCACTCTAGTGTGAAA---TCACCTCGAGGCTT-----
E.inexpectatus     --------AAGCCCAGGAACGCCTTTTAG---GGTTCTTCT--CAAGATTTGCACTCTTGCGTGGAA---ACACCACAGGGCTT-----
E.skiltonianus     --------AAGCCCAGGAACGCCTTTAG----GGTTCTTCT--CAAGATTTGCACTCTTGCGTGAA----ACACCGCAGGGCTT-----
E.anthracinus      --------AAGCCCAGGAACGCCTTTAG----GGTTCTTTT--CAAGATTTGCACTCTTGCGTGAA----ACACCGCTGGGCTT-----
S.anguineus        --------AAGCCCGGGCACCCTTTTCG----GGTGCGTCT--CTAGATTTGCATTCTAGTGTAAT----ATACCTCCGGAATT-----
P.eggeli           --------AAGCCCGGGCACCCTTTGG-----GGTGCGTCT--CTAGATTTGCATTCTAGCGTAA-----ATACCTCCGGACTT-----
F.polylepis        --------AAGCCCGGGCGCACCTTTG-----GGTGCGCTTCTTCAGATTTGCACTCTGATGTGAA----ACACCTCCGAGCTT-----
Ch.ocellatus       --------AAGCCCGGCATACGTAA-------ATACGCTTCT-CCAGATTTGCACTCTGACGTGGGA---ACCACCACGGACTTATAAC
A.meleagris        --------AAGCCCAGGCACACTACT------CGTGTGCGTTTCTGGATTTGCATTCCAGCGTGAA----CCACCACAGGGCTT-----
T.lomii            --------AAGCCCAGGCACACCTC-------CGTGTGCTTCTCTAGATTTGCACTCTAGCGTGAA----CCACCACAGGGCTT-----
T.gariepensis      --------AAGCCCAGGCACACTCTC------CGTGTGCGTCTCTAGATTTGCACTCTAGCGTGAAC---CCACCACAAGGCTT-----
X.vigilis          --------AAGCCCAGACGCCATTAAA-----GACGTTCTCT-CCAGATTTGCAATCTGGCGCATTTC--ACTTCATAGGCCT------
C.polyzonus        G-------AAGCCCCGGCACACTTTAG-----TGTGCTTCT--TCAAATTTGCAATTTGCTGTGGAGA--TCACCACAGGGCTT-----
Zonosaurus.sp.     --------AAGCCCGGGCATCTATTTCTTGTTATTGCTCCT--CCAAATTTGCAATTTGGCGTGATTT--CCACCTCCGGGCTT-----
Dibamus            G-------AAGCCCTGGACACCTCTCG-----GTGACTTTT--CCAAATTTGCACTTTGATGTGAA----TCACTTCAGGGCT------

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Qualifiers2        ......*<<<<<AA<<<<T........<<<<T.....<<<AC..COD..<<<AC.<<<D........<<<D..<<<<<AA.1..2..3.
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G.gallus           -------GATAAGAAGAGGAATTGAA-CCTCTGTAA-AAAGGACTACAGCCTAACGCTTCAACACT-CAGCCATCTTACCTGTGACCTT
C.mydas            ------TGATAAGAAGAGGAATTAAA-CCTCTGTAA-AAGGGACTACAGCCCAACGCTAATACACT-CAGCCACCTTACC-GTGATT--
S.punctatus        -------GATAAGAAAAGGAATTAAA-CCTTTATAA-ATAGGTCTACAGCCTAACACCTGACACT--CGGCCATCTTACCTTTGCCA--
B.theili           ------TGGGGAGGGTGGGGGTAAG--ACCACTTAA-GCAGATTTACAGCCTGCCGCCTAAAT----CGGCCACCTGACC-ATGTGA--
C.rudis            GGGTTTTGGATAGGGGAGGAA------CCTCCGTCA-ATAAGTTTACAGCTTACCGCCTTCACT---CGGCCACCTAACC-ATGTGA--
C.brevicornis      C-----TGGGGAGGGGGGGAGTTGAA-CCCCCATTA-ATAAGTTTACAGCCTACCGCCTTATACT--CGGCCACCTAACC-ATGTGA--
C.salinarum        -------GTAAAGAAGGGACTTAA---ACCCCATAA-ATGGAATTACAACCCACCGCTTATACTT--CAGCCACCTCTACAATGTCAAC
P.leusterii        -------GTAAAGAGGGGCTAG-----GCCCCATAA-ATGGAATTACAACCCACCACCTATTAACT-CAGCCACCTTTACAATGTCAAC
P.cocincinus       -------GAAAAGAGGGGCCATC----GCCCCATAA-ATGGAGTTACAACCCACCGCTTTAACT---CAGCCATCTCTACAATGTCTAC
Hydrosaurus.sp.    -------GGAAAGAGAGGAACCTATC-TCCCCATAA-ATGGGATTACAACCCATCGCTTACTTT---CAGCCATCTTACC-ATGTCCAC
C.calotes          -------GACCAGGGGGAGCATGC---CTCCCATTA-ATAAGTTTACAGCCTACCGCCTATAT----CAGCCACCTGACC-ATGTCATT
J.tricarinata      -------GGACGGGGGGCCTGC-----GCCCCATGT-GCGAGTTTACAGCCCGCCGCCTAAAT----CAGCCACCTGACC-ATGTCTAC
P.raddei           -------GATAAGAGGAGCCTCACC--ACTCCATAA-ATGGAATTACAAACCACCGCCTAAATT---CAGCCATCTTACC-ATGTCAAC
L.belliana         -------GATAAGAGAGGGAGTTGAA-CCCCCATAAGGTGAACTTACAATTCATCGCCTACCACTT-CAGCCTTCTTACC-ATGTCT--
U.acanthinurus     -------GGAAAGGAGAGGACTTAA--CCTCCATAA-GCAGAATTACAATCCGCCACCTAACACT--CGGCCACCTTACC-ATGATA--
A.paternus         -------GATAAAGAAAGGAATTAAA-CCAATGTAA-ATAGGACTACAGCCTACTGCCTAACACT--CGGCTACTTTACCTGTGTTT--
P.mcallii          -------GATAAAAAGAGGAGTCAAA-CCCCTATGA-ATAGGACTACAGCCTACCACCTAAACGCT-CGGTCATTTTACCTGTGTTT--
Sauromalus.obesus  -------GGTAAAAAAAGGAATTAAA-CCTTCCTGA-ATAGGACTACAGCCTACCACCTAAACGCT-CGGCCATTTTACCTGTGTCA--
Hoplocercus.sp.    T------GGTAAAAGGGACATCTA---ACCCCCTAA-GCAGATTTACAGCCTGCCACCTCTCT----CGGCCATTTTACCCGTGTTT--
E.laticeps         -------GGCAAGAGAGGGGTTCA---ACCTCCTGA-GTAGATTTACAGCCCACCGCCTAAGCGCT-CGGCCATCTTACCTGTGTTC--
P.somuncurensis    -------GATAAAAAGAGGAGTTAAA-CCCCTGTAT-GCAGGTCTACAGCCCGCCGCCTAAACACT-CAGCCATTTTACCCGTGTCC--
L.pictus           TAGCAATGGTAAAAAGAGGAATTAAA-CCCCTGTTG-ATGGGACTACAGCCCACCACCTAAACATT-CGGTCATTTTACCCGTGTCT--
U.flaviceps        -------GATAAAAGGGGGAATTGAG-CCCTCATTA-ATAGATTTACAATCTACCGCCTATCATT--CGGCCATTTTACCCGTGTTC--
S.crassicaudatus   -------GGTAGGGGGAAGACTCTAG-CTTCCGTTG-ATGAATTTACAGATCACCACCTAAACTCT-CGGCCACCTTACCTGTGTTT--
L.carinatus        -------GGTGAAGAGAGGAATTAAA-CCTCCATGA-ATAGGTCTACAGCCTACCGTCTAAACACT-CGACCACTTTACCTGTGTTC--
B.plumifrons       -------GATAAAAAAAGGAATTTAA-CCCCTCTGA-GTAAGACTACAGCCTACCGCCTAAACACT-CGGCCATTTTACCTGTGTCC--
G.wislizenii       -------GGAAAAAAGAGGAGTTGAA-CCCCTGTGA-GTAATTCTACAGACTACCGCCTAACACT--CGGCCATTTTACCAGTGTCT--
O.cuvieri          -------GGTAAAAAAAGGAATTAAA-CCTCTCTCA-ATAGGACTACAGCCTACCGCTTAAACACT-CAGCCATTTTACCTGTGTTT--
O.attenuatus       -------GATAAGAAAGGGAGTCAAA-CCCCTGTTA-GTAGAACTACAGCCTACCGCCTAGGCGCT-CGGCCATCTTACCTGTGACA--
E.panamintina      -------GATAAGAAAAGGAATTTAA-CCTCTATTA-TTAGGACTACAGCCTACCACCTGAACATT-CGGCCATCTTACCTGTGACC--
C.enneagrammus     -------GATAAGAAGAGGAATTAAA-CCCCTATTA-ATAGGACTACAGCCTACCGCCTAAACGCT-CGGCCATCTTACCTGTGACC--
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A.pulchra          -------GATAAGAAAAGGAATTTAA-CCTCTCTAA-ATAGGACTACAGCCTACTGCCTAAACACT-CGACCATCTTACCTGTGACC--
H.suspectum        -------GATAAGAGAGGAATTTA---ACCTCGTTA-GCAAATTTACAATCTGCCGCCTAACTCT--CGGCCATCTTACCTGTGACC--
X.grandis          -------GATAAGAAAAGGAGTTAAA-CCTCTCTTC-ATAGGACTACAGCCTACCGCTATGGACGCTCAGCCATCTTACCTGTGACC--
V.griseus          -------GATAAGGAAGATCTTAC---CTCTTGTGA-GTAAATTTACAATTTACCGCCTACT-----CAGCCACCTTACCCATGACC--
L.borneensis       -------GATAAGGACGGGAATTAAA-CCCACATTA-GCGGGTCTACAGCCCGCCGCTTAAGCACT-CAGCCAACTTACCTGTGACC--
S.crocodilurus     -------GGAAAGAAGAGGAATTAAA-CCCCTGTTA-ATAGGTCTACAGCCTACCGCTAAGCACT--CAGCCACCTTACCTTTGACC--
D.semicarinatus    -------GGTAGCAAGGAATA------TCCTATTA--ATAATTTTACAGATTACCGCCTAAAT----CAGCCATACTACCCGTGTTC--
R.braminus         -------GGTAGAAGGAAACAATA---CTTCCATCT-GTAGGACTACAATCTACCGCTATTT-----CAGCCATTCTACCAGTGTAC--
C.ruffus           -------GGCAGCAAAGGTTAAA----CCCTTATGA-GTAAATTTACAGTTTACCGCTTATAT----CAGCCATACTACCTGTGTTC--
Agkistrodon.sp.    -------GGTAGCAAGGAATT------ACCTGTGT--GTAAATTTACAGTTTACCGCTTAAAT----CAGCCATACTACCAGTGTAC--
E.grammica         -------GATAGGGGGAGTAAC-----CTCCGTAT--TGGGGTTTACAGCCCCACGCCTTACT----CAGCCACCCTACCTGTGTCT--
B.biporus          -------GGTAGAAGAAAGGACTCGAACCTTCGTCA-AAAGGGCTACAACCTTCTGCCTACCCGCT-CAGCCACTCTACCTGTGTCA--
T.weigmanni        -------GATAGGAAAAGGACTCAAA-CCTCTGTAA-AGGGGACTACAGCCCCCTGCTTCACTCT--CAGCCACCCTACCTGTGATA--
A.xera             GTT----GGTAGGCAAAGGACTCTAA-CCTCTGTAC-GGGGGTTTACAGCCCCCCACTTAACACT--CAGCCACCCTACCTGTGACC--
C.tigris           -------GATAAGAGGGGACA------ACCCCGTCG-TCAGGGCTACAACCTGCCGCAATAACT---TTGCTACCTTACCTATGACC--
L.parietale        -------GATAAAAGGAGGTTTT----TTCCGTCG--TCAGGTTTACAATCTGCCGCAAGTCT----TTGCTATTTTACCAATGACC--
E.turkmenicus      -------AGTAAAAAGGGGGACT----TCCCTGTAA-ACGGAGCTACAATCCGCCGCCTATTCT---CGGCCATCTTACCTGTGACA--
S.shrevei          -------GGTAACAAGGGCACGCTCC-CTGTGG----GCGAATTTACAGCTCGCTGCCTACT-----CGGCCATATTACCTGTGACT--
T.przewalskii      -------GATAAGAAGTGGACTTACA-CCCCTGTGT-GCGAGTCTACAGCTCGCTGCCTCATTCT--CGGCCATCTTACCCGTGGCA--
G.gecko            -------AGTAGGAGGGCCTTTA----CCTCCGTTC-ATGAGGCTACAACTCACCGCCTAGTCT---CGGCCACCCTACCTACGATG--
P.lindneri         -------GACAGAAATAGGAATCAAA-CCTACATTA-ACAGGATTACAGCCTGCCGCCTATTTT---CGGCCATTCTACCTGTGATA--
Cr.ocellatus       -------GATAGAAACAGGGTTTAAA-CCCTATGTA-AGCAGGATACAGCCTGCTGCCTAAACACT-CGGCCATTCTACCTGTGATC--
L.jicari           -------GATAGAAAAAGGACTTAAA-CCAATGTAA-TCAGGACTACAGCCTGCCGCCTAACTCT--CGGCCATTCTACCTGTGATA--
M.aurata           -------GATAAGGACGGGGCTCAAC-CCGCCTAT--GCAGGGCTACAACCTGCCGCTTCACT----CAGCCACCTTACCTGTGACC--
C.robustus         -------GATAAGAGCGGGATTAAAACCCGCCTAC--ACAGGGCTACAACCTGCCACCTTCT-----CGGCCATCTTACCTGTGACC--
S.sikkimensis      -------GATAAGGGTGGGACAAC---TCCACGTGC-ACAGGGCTACAACCTGTCGCCTGCT-----CGGCCACCTTACCTGTGACA--
E.inexpectatus     -------GGTAGAGGCGGGACTAACC-CCGCATAA--GCAGGGCTACAACCTGCCACCTGTTT----CGGCCACCCTACCTGTGACT--
E.skiltonianus     -------GATAGGAGCGGAGTGAGC--CCGCATGA--GCAGGGCTACAACCTGCCACCTTTTT----CGGCCATCCTACCTGTGACC--
E.anthracinus      -------GGTAGGGGCAGGATTAAACCCGCCTCT---GCAGGGCTACAACCTGCCGCCTAATTCT--CGGCCACCCTACCTGTGACT--
S.anguineus        -------GATAAGAATAGGATTAAAA-CCTACATAC-ACAGGCATACAACCTCCTTCCTTCT-----CGGCCACCTTACCCGTGATA--
P.eggeli           -------GGTAGGAGTGGGGCTTGACCCACCTGC---ACAGGGCTACAACCTGCCGCCTTCT-----CGGCCATCTTACCCGTGACC--
F.polylepis        -------GATAAAGGTGGGACTAACACCCACGTAA--ATAGGGCTACAACCTACTGCCTTCT-----CGGCCACCTTACCCGTGTCC--
Ch.ocellatus       AAT----GACAAGAGTGGGACTAAAACCCACATAT--ACAGGGCTACAACCTGCCGCCTATTT----CGGCCATCTTACCCGTGACC--
A.meleagris        -------GATAAGAGCGGGGTTAGCACCCGCCTGC--ACAGGGCTACAACCTGCCGCCTACT-----CGGCCATCTTACCCGTGACC--
T.lomii            -------GGTAAGAGCGGGACTACTACCCGCCTGC--ACAGGGCTACAACCTGCCGCCTACT-----CGGCCATCTTACCCGTGACC--
T.gariepensis      -------GGTAAGAGCGGGGTTACTGCCCGCCTAC--ACAGGGCTACAACCTGCCGCCTACT-----CGGCCACCTTACCTGTGACC--
X.vigilis          -------GATAAGAACAGGACTTTAA-CCTGTCTAA-ACGGGGCTACAACCCGCTGCCAAAACACT-CAGCCATCTTACCTGTGACC--
C.polyzonus        -------GATAAGAGTAGGGCTC----CCTACGTCT-TCAGGGCTACAACCTGCCGCCTAAGCT---CGGCCATCTTACCTGTGACC--
Zonosaurus.sp.     -------GATAAGAACGGGAGTCAAA-CCCGCGTTC-ACAGGACTACAGCCTGCCGCTAAACACT--CAGCCATCTTACCTGTGTCC--
Dibamus            -------GGAAAGAAGGGGAATTAAA-CCCCTCTTC-ACAGGGCTACAACCTGCCGCCTGCACACT-CGGCCATCTTACCTGTGACC--

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Index1             8888888888888888888888888
Index2             7777777777888888888899999
Index3             0123456789012345678901234
Qualifiers1        .........................
Qualifiers2        .4..5..6..7..8..9..0..1..
A.mississippiensis -TTCCACCGTTGACTCTTCTCTACT
G.gallus           CATCAACCGATGATTATTCTCAACC
C.mydas            -TTAACTCGCTGATTCTTCTCCACC
S.punctatus        -TACAAACGCTGACTCTACTCAACC
B.theili           -CTCCTTCGATGACTCTTATCAACA
C.rudis            -CTACTCCGTTGATTATTTTCAACA
C.brevicornis      -CTAATTCGTTGACTTCTATCAACA
C.salinarum        TATAAATCGATGATTCTTATCCACA
P.leusterii        CATAAACCGATGACTATTATCAACA
P.cocincinus       CATAAATCGATGACTACTATCAACA
Hydrosaurus.sp.    CATATCACGATGATTATTTTCAACC
C.calotes          CATAACTCGATGACTTTTATCGACC
J.tricarinata      CATAGCCCGATGACTTTTATCGACA
P.raddei           ACTAACTCACTGATTCTTATCAACT
L.belliana         -ATTCGTCGATGATTGTTTTCAACA
U.acanthinurus     -GCCCATCGATGACTCCTATCAACC
A.paternus         -ATTAACCGTTGATTCTTCTCAACC
P.mcallii          -ATTAACCGTTGATTCTTCTCAACC
Sauromalus.obesus  -ATCACCCGTTGATTCTTCTCAACC
Hoplocercus.sp.    -ATTTCCCGTTGACTATTCTCAACC
E.laticeps         -ATCTCTCGTTGACTATTCTCAACT
P.somuncurensis    -ATCAACCGTTGATTCTTCTCAACA
L.pictus           -ATTAATCGTTGATTCTTCTCAACT
U.flaviceps        -CTTAATCGTTGATTCTTCTCAACT
S.crassicaudatus   -ATCAATCGTTGACTTTTCTCAACC
L.carinatus        -ATTACCCGTTGACTATTTTCAACC
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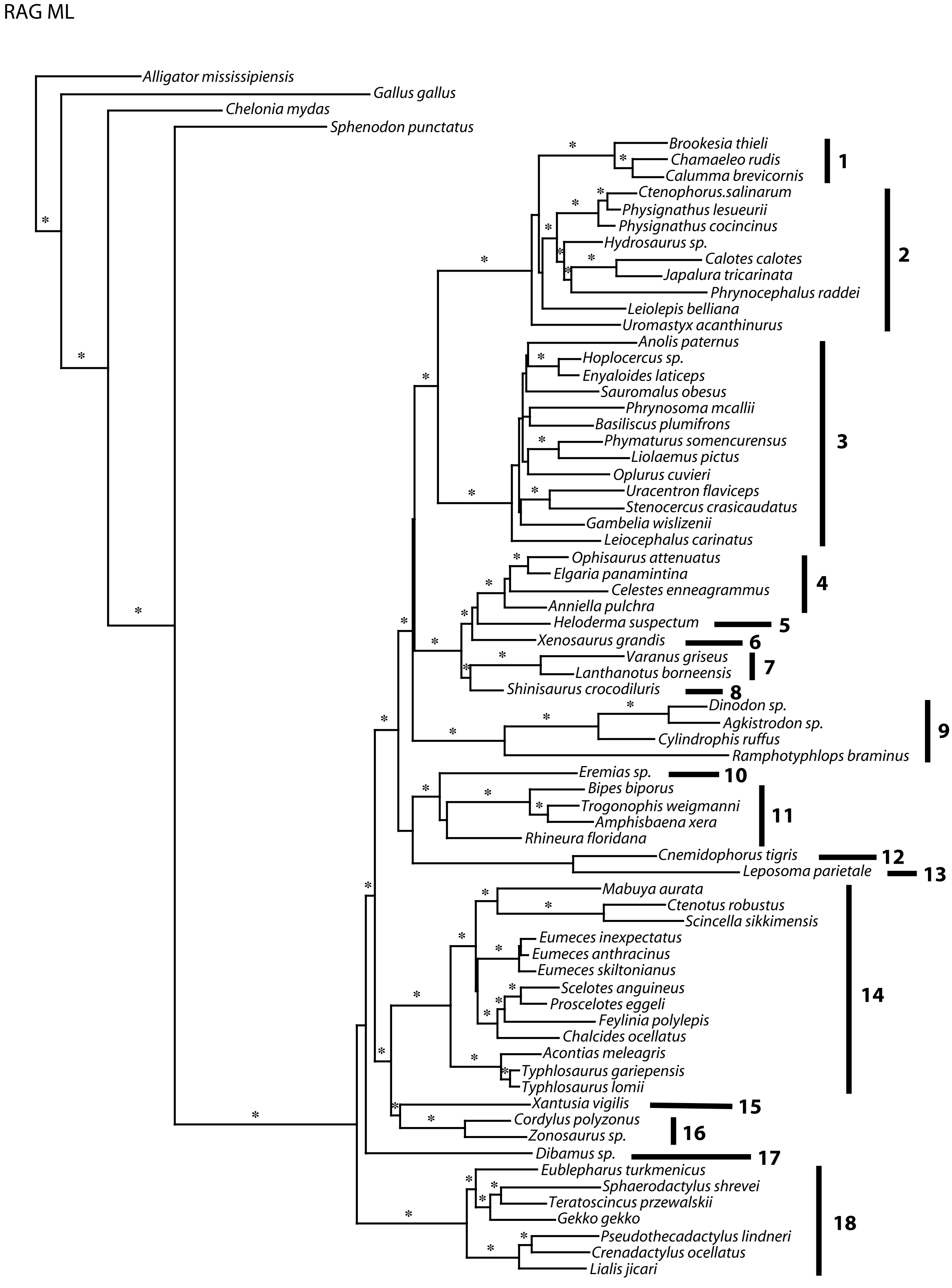
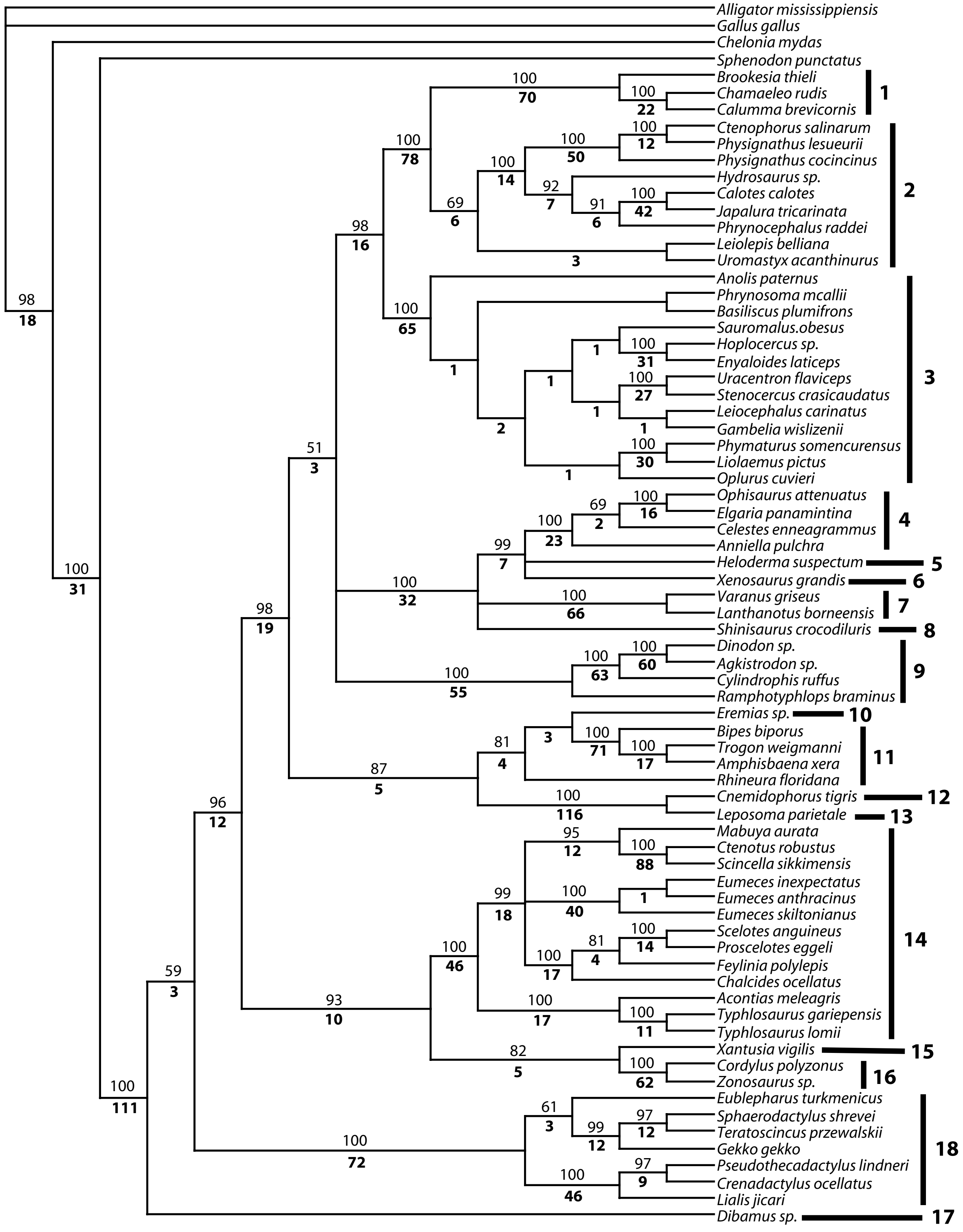
B.plumifrons       -ATCAACCGTTGACTCTTCTCAACT
G.wislizenii       -ATCACCCGTTGATTCTTCTCAACA
O.cuvieri          -ATTAATCGTTGATTTTTCTCAACA
O.attenuatus       -CTAACTCGCTGACTATTTTCTACT
E.panamintina      -ACAACTCGCTGATTATTCTCAACC
C.enneagrammus     -ATAACACGATGACTATTCTCTACA
A.pulchra          -ATCACCCGCTGATTATTCTCAACC
H.suspectum        -ATTACTCGCTGACTCTTTTCAACT
X.grandis          -CTAACTCGATGGTTCTTTTCAACC
V.griseus          -ATCACCCGCTGACTATTCTCCACC
L.borneensis       -ATAACCCGTTGACTCTTCTCCACA
S.crocodilurus     -ATCACTCGCTGATTCTTCTCGACC
D.semicarinatus    -ATCACTCGTTGACTATTCTCGACA
R.braminus         -ATAAACCGTTGACTATTCTCAACT
C.ruffus           -ATCACTCGTTGATTATTCTCAACA
Agkistrodon.sp.    -ATCACCCGTTGACTATTTTCAACA
E.grammica         -CTAATTCGTTGATTTTTTTCAACT
B.biporus          -CTCACCCGTTCATTCTTCTCAACA
T.weigmanni        -CTTACACGTTGATTTTTCTCCACA
A.xera             -CTCACCCGTTGATTTTTCTCTACA
C.tigris           -ATTACTCGTTGATTTTTTTCTACA
L.parietale        -ATTACACGATGATTCTTTTCTACC
E.turkmenicus      -CTTTCCCGTTGACTATTTTCAACA
S.shrevei          -ATCAACCGTTGATTTTTCTCAACA
T.przewalskii      -ATCCCTCGTTGATTCTTCTCAACC
G.gecko            -CTAACACGCTGGTTTTTTTCGACT
P.lindneri         -CTCTCTCGATGATTATTCTCAACA
Cr.ocellatus       -ATTTCTCGTTGACTGTTCTCAACT
L.jicari           -ATTTCTCGTTGATTCTTCTCAACA
M.aurata           -ATTAATCGTTGATTCTTCTCAACC
C.robustus         -ATCAATCGTTGATTCTTCTCAACT
S.sikkimensis      -ATTAATCGTTGATTCTTCTCAACC
E.inexpectatus     -ATCAATCGTTGATTTTTCTCAACC
E.skiltonianus     -ATTAATCGTTGACTTTTCTCAACC
E.anthracinus      -ATTAATCGTTGACTCTTCTCAACC
S.anguineus        -ATTAACCGTTGACTTTTCTCAACC
P.eggeli           -ATCAATCGTTGATTCTTCTCAACC
F.polylepis        -ATCAATCGTTGATTCTTCTCAACC
Ch.ocellatus       -ATCAATCGTTGACTATTCTCAACC
A.meleagris        -ATCAATCGTTGATTCTTCTCAACA
T.lomii            -ATTAACCGTTGATTCTTCTCAACA
T.gariepensis      -ATTAACCGTTGATTTTTCTCGACA
X.vigilis          -ATCACTCGTTGACTTTTCTCAACC
C.polyzonus        -ATCTCCCGCTGATTTTTTTCAACA
Zonosaurus.sp.     -ATCTCCCGCTGATTTTTTTCAACA
Dibamus            -ATCAATCGTTGATTCTTCTCAACC
```

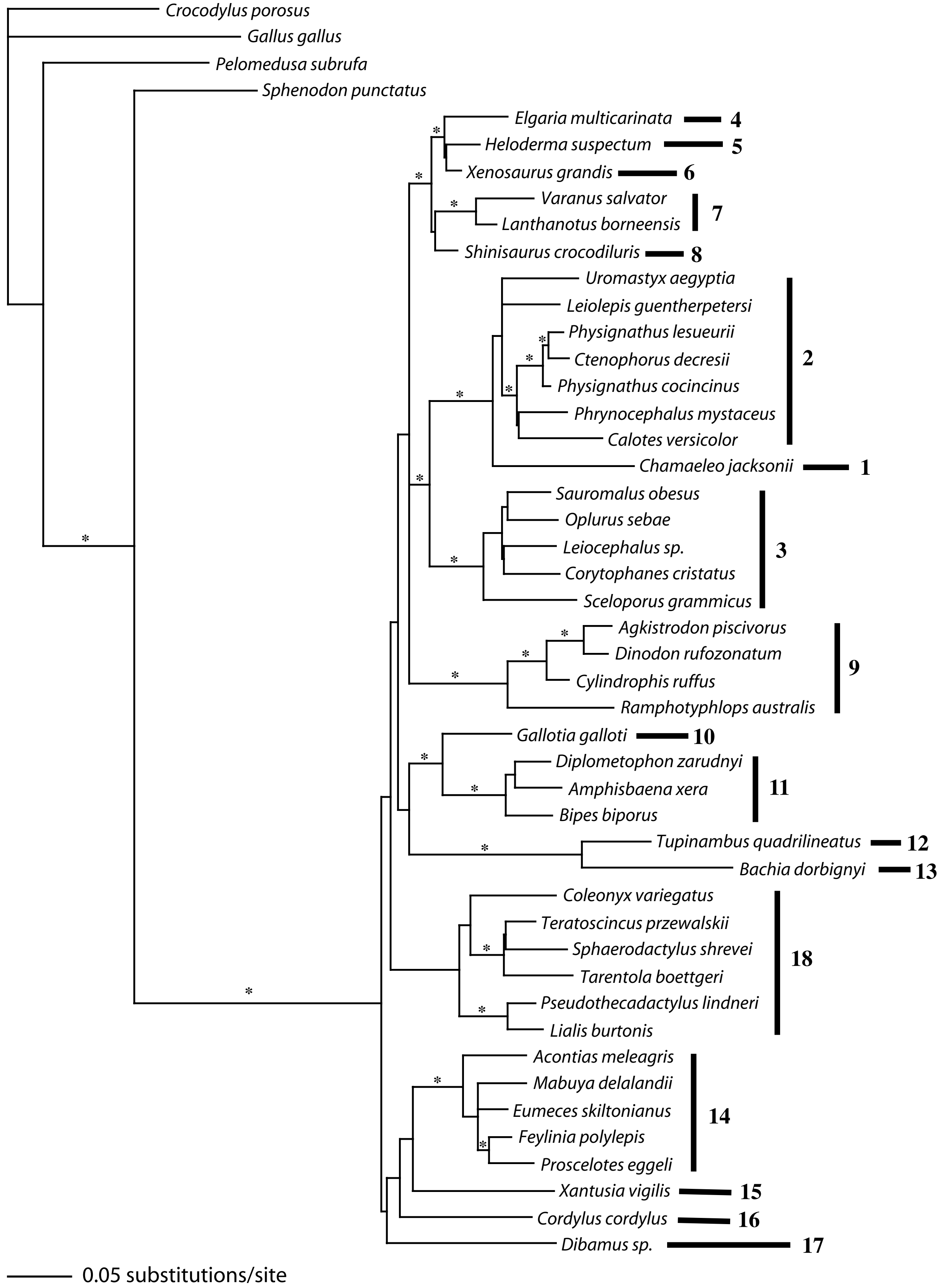
Appendix IV. Separate MP and ML topologies for all analyzed data partitions. All MP topologies have bootstrap and decay values above and below the branches, respectively. All ML topologies have asterisks marking branches supported by posterior probabilities >95% in the Bayesian analyses.


RAG ML
Alligator mississipiensis
Gallus gallus
Chelonia mydas
Sphenodon punctatus
Brookesia thieli
Chamaeleo rudis
Calumma brevicornis
1
Ctenophorus.salinarum
Physignathus lesueurii
Physignathus cocincinus
Hydrosaurus sp.
Calotes calotes
Japalura tricarinata
Phrynocephalus raddei
Leiolepis belliana
Uromastyx acanthinurus
2
Anolis paternus
Hoplocercus sp.
Enyaloides laticeps
Sauromalus obesus
Phrynosoma mcallii
Basiliscus plumifrons
Phymaturus somencurensus
Liolaemus pictus
Oplurus cuvieri
Uracentron flaviceps
Stenocercus crasicaudatus
Gambelia wislizenii
Leiocephalus carinatus
3
Ophisaurus attenuatus
Elgaria panamintina
Celestes enneagrammus
Anniella pulchra
4
Heloderma suspectum
5
Xenosaurus grandis
6
Varanus griseus
Lanthanotus borneensis
7
Shinisaurus crocodiluris
8
Dinodon sp.
Agkistrodon sp.
Cylindrophis ruffus
Ramphotyphlops braminus
9
Eremias sp.
10
Bipes biporus
Trogonophis weigmanni
Amphisbaena xera
Rhineura floridana
11
Cnemidophorus tigris
12
Leposoma parietale
13
Mabuya aurata
Ctenotus robustus
Scincella sikkimensis
Eumeces inexpectatus
Eumeces anthracinus
Eumeces skiltonianus
Scelotes anguineus
Proscelotes eggeli
Feylinia polylepis
Chalcides ocellatus
Acontias meleagris
Typhlosaurus gariepensis
Typhlosaurus lomii
14
Xantusia vigilis
15
Cordylus polyzonus
Zonosaurus sp.
16
Dibamus sp.
17
Eublepharus turkmenicus
Sphaerodactylus shrevei
Teratoscincus przewalskii
Gekko gekko
Pseudothecadactylus lindneri
Crenadactylus ocellatus
Lialis jicari
18
— 0.01 substitutions/site

RAG MP

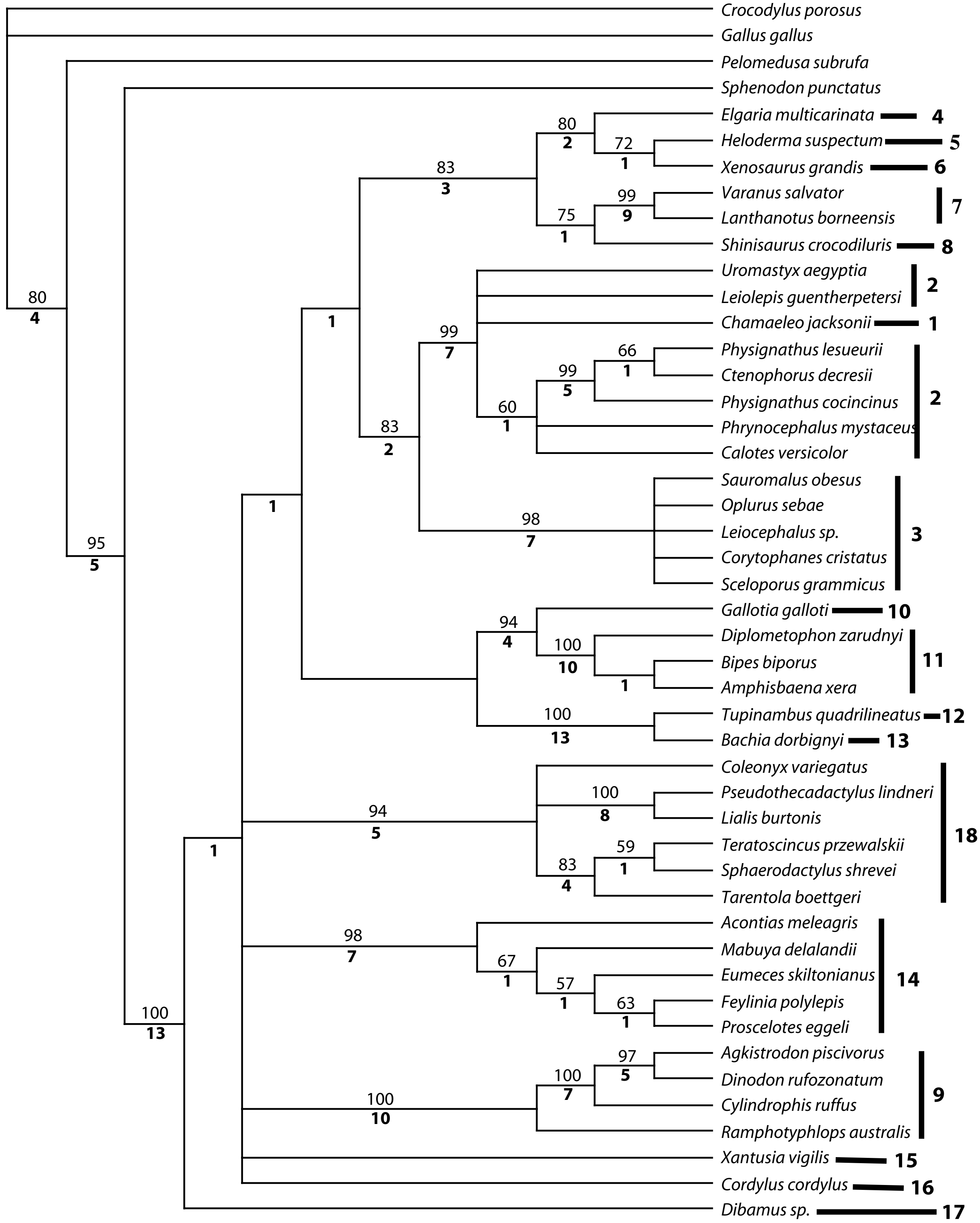

Alligator mississippiensis
Gallus gallus
Chelonia mydas
Sphenodon punctatus
Brookesia thieli
Chamaeleo rudis
Calumma brevicornis
1
Ctenophorus salinarum
Physignathus lesueurii
Physignathus cocincinus
Hydrosaurus sp.
Calotes calotes
Japalura tricarinata
Phrynocephalus raddei
Leiolepis belliana
Uromastyx acanthinurus
2
Anolis paternus
Phrynosoma mcallii
Basiliscus plumifrons
Sauromalus.obesus
Hoplocercus sp.
Enyaloides laticeps
Uracentron flaviceps
Stenocercus crasicaudatus
Leiocephalus carinatus
Gambelia wislizenii
Phymaturus somencurensus
Liolaemus pictus
Oplurus cuvieri
3
Ophisaurus attenuatus
Elgaria panamintina
Celestes enneagrammus
Anniella pulchra
4
Heloderma suspectum
5
Xenosaurus grandis
6
Varanus griseus
Lanthanotus borneensis
7
Shinisaurus crocodiluris
8
Dinodon sp.
Agkistrodon sp.
Cylindrophis ruffus
Ramphotyphlops braminus
9
Eremias sp.
10
Bipes biporus
Trogon weigmanni
Amphisbaena xera
Rhineura floridana
11
Cnemidophorus tigris
12
Leposoma parietale
13
Mabuya aurata
Ctenotus robustus
Scincella sikkimensis
Eumeces inexpectatus
Eumeces anthracinus
Eumeces skiltonianus
Scelotes anguineus
Proscelotes eggeli
Feylinia polylepis
Chalcides ocellatus
Acontias meleagris
Typhlosaurus gariepensis
Typhlosaurus lomii
14
Xantusia vigilis
15
Cordylus polyzonus
Zonosaurus sp.
16
Eublepharus turkmenicus
Sphaerodactylus shrevei
Teratoscincus przewalskii
Gekko gekko
Pseudothecadactylus lindneri
Crenadactylus ocellatus
Lialis jicari
18
Dibamus sp.
17

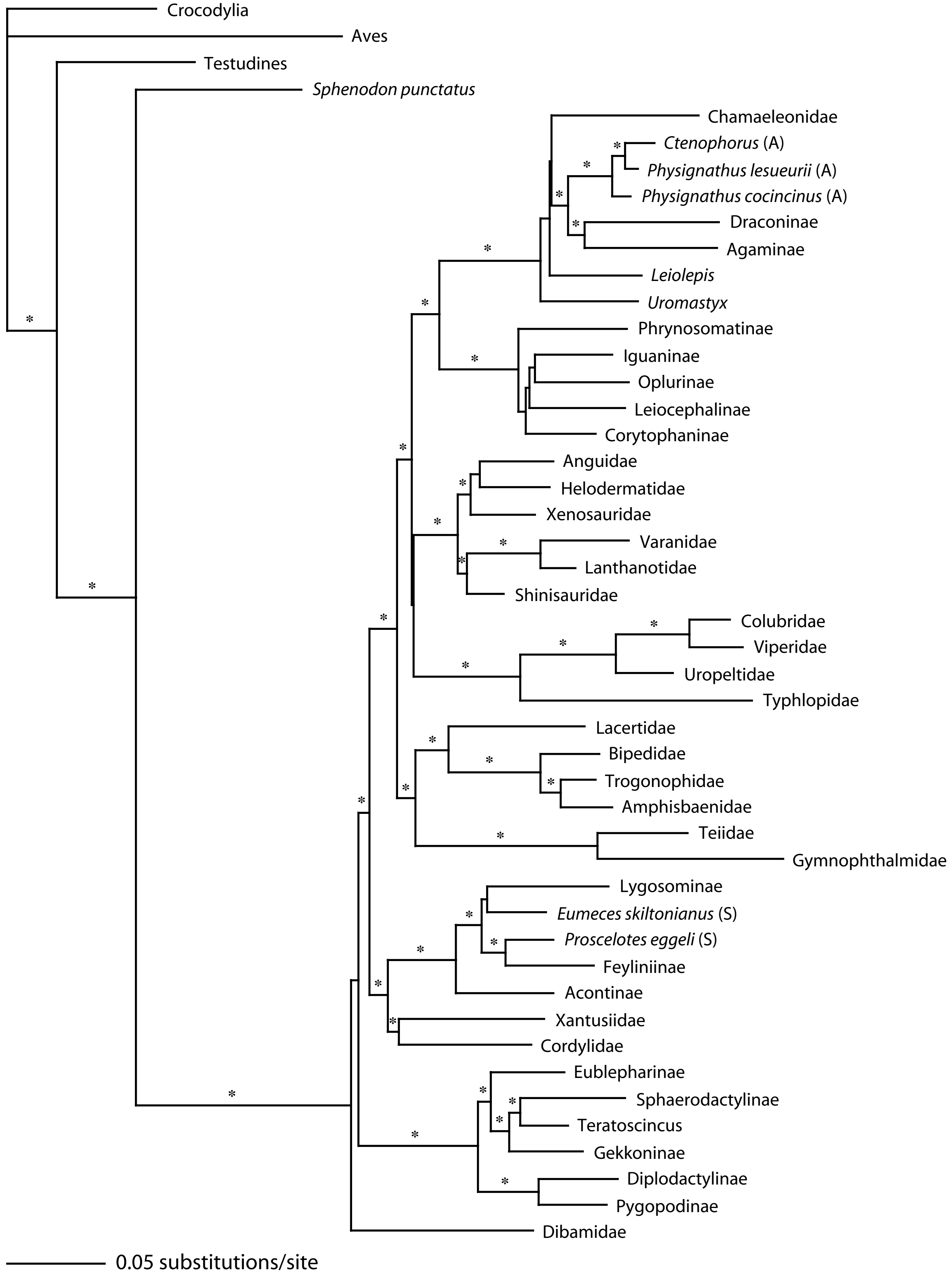
c-mos ML



Crocodylus porosus
Gallus gallus
Pelomedusa subrufa
Sphenodon punctatus
Elgaria multicarinata
4
Heloderma suspectum
5
Xenosaurus grandis
6
Varanus salvator
Lanthanotus borneensis
7
Shinisaurus crocodiluris
8
Uromastyx aegyptia
Leiolepis guentherpetersi
Physignathus lesueurii
Ctenophorus decresii
Physignathus cocincinus
Phrynocephalus mystaceus
Calotes versicolor
2
Chamaeleo jacksonii
1
Sauromalus obesus
Oplurus sebae
Leiocephalus sp.
Corytophanes cristatus
Sceloporus grammicus
3
Agkistrodon piscivorus
Dinodon rufozonatum
Cylindrophis ruffus
Ramphotyphlops australis
9
Gallotia galloti
10
Diplometophon zarudnyi
Amphisbaena xera
Bipes biporus
11
Tupinambus quadrilineatus
12
Bachia dorbignyi
13
Coleonyx variegatus
Teratoscincus przewalskii
Sphaerodactylus shrevei
Tarentola boettgeri
Pseudothecadactylus lindneri
Lialis burtonis
18
Acontias meleagris
Mabuya delalandii
Eumeces skiltonianus
Feylinia polylepis
Proscelotes eggeli
14
Xantusia vigilis
15
Cordylus cordylus
16
Dibamus sp.
17
0.05 substitutions/site

c-mos MP

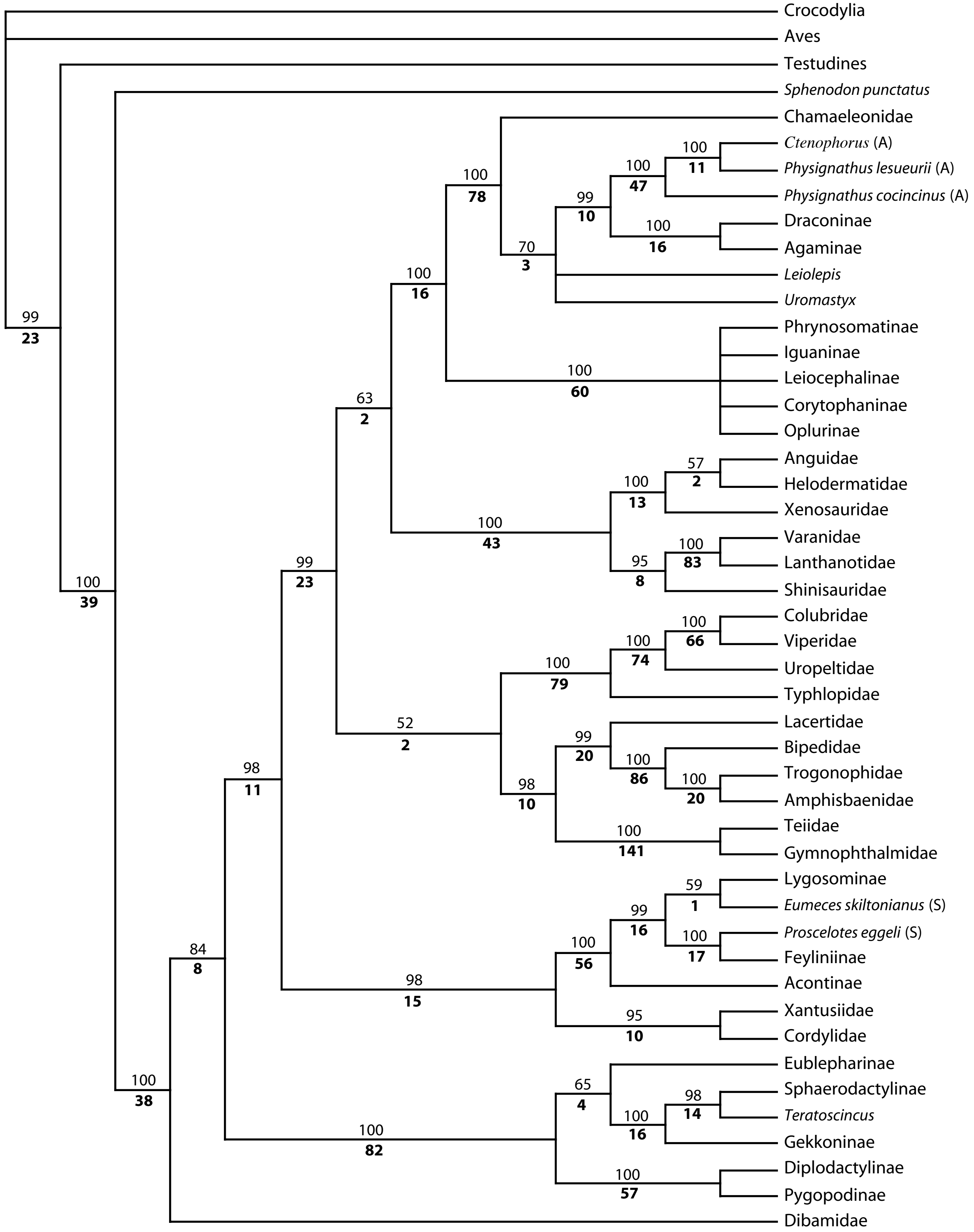

Crocodylus porosus
Gallus gallus
Pelomedusa subrufa
Sphenodon punctatus
Elgaria multicarinata
4
Heloderma suspectum
5
Xenosaurus grandis
6
Varanus salvator
Lanthanotus borneensis
7
Shinisaurus crocodiluris
8
Uromastyx aegyptia
Leiolepis guentherpetersi
2
Chamaeleo jacksonii
1
Physignathus lesueurii
Ctenophorus decresii
Physignathus cocincinus
Phrynocephalus mystaceus
Calotes versicolor
2
Sauromalus obesus
Oplurus sebae
Leiocephalus sp.
Corytophanes cristatus
Sceloporus grammicus
3
Gallotia galloti
10
Diplometophon zarudnyi
Bipes biporus
Amphisbaena xera
11
Tupinambus quadrilineatus
12
Bachia dorbignyi
13
Coleonyx variegatus
Pseudothecadactylus lindneri
Lialis burtonis
Teratoscincus przewalskii
Sphaerodactylus shrevei
Tarentola boettgeri
18
Acontias meleagris
Mabuya delalandii
Eumeces skiltonianus
Feylinia polylepis
Proscelotes eggeli
14
Agkistrodon piscivorus
Dinodon rufozonatum
Cylindrophis ruffus
Ramphotyphlops australis
9
Xantusia vigilis
15
Cordylus cordylus
16
Dibamus sp.
17
80
2
72
1
83
3
99
9
75
1
80
4
1
99
7
66
1
99
5
60
1
83
2
1
98
7
95
5
94
4
100
10
1
100
13
100
8
94
5
83
4
59
1
1
98
7
67
1
57
1
63
1
100
13
97
5
100
7
100
10

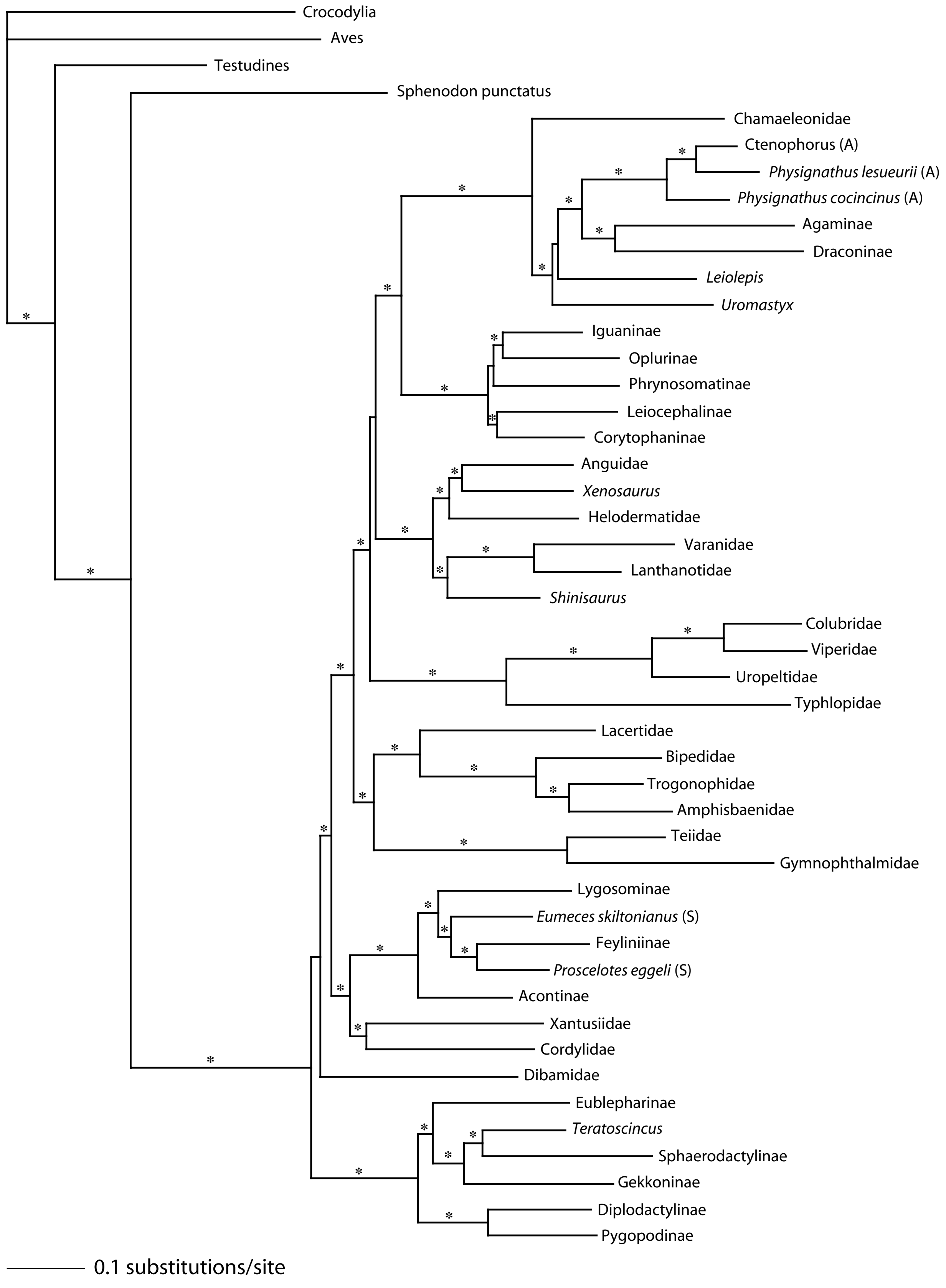


RAG/c-mos ML

Crocodylia
Aves
Testudines
Sphenodon punctatus
Chamaeleonidae
Ctenophorus (A)
Physignathus lesueurii (A)
Physignathus cocincinus (A)
Draconinae
Agaminae
Leiolepis
Uromastyx
Phrynosomatinae
Iguaninae
Oplurinae
Leiocephalinae
Corytophaninae
Anguidae
Helodermatidae
Xenosauridae
Varanidae
Lanthanotidae
Shinisauridae
Colubridae
Viperidae
Uropeltidae
Typhlopidae
Lacertidae
Bipedidae
Trogonophidae
Amphisbaenidae
Teiidae
Gymnophthalmidae
Lygosominae
Eumeces skiltonianus (S)
Proscelotes eggeli (S)
Feyliniinae
Acontinae
Xantusiidae
Cordylidae
Eublepharinae
Sphaerodactylinae
Teratoscincus
Gekkoninae
Diplodactylinae
Pygopodinae
Dibamidae
0.05 substitutions/site

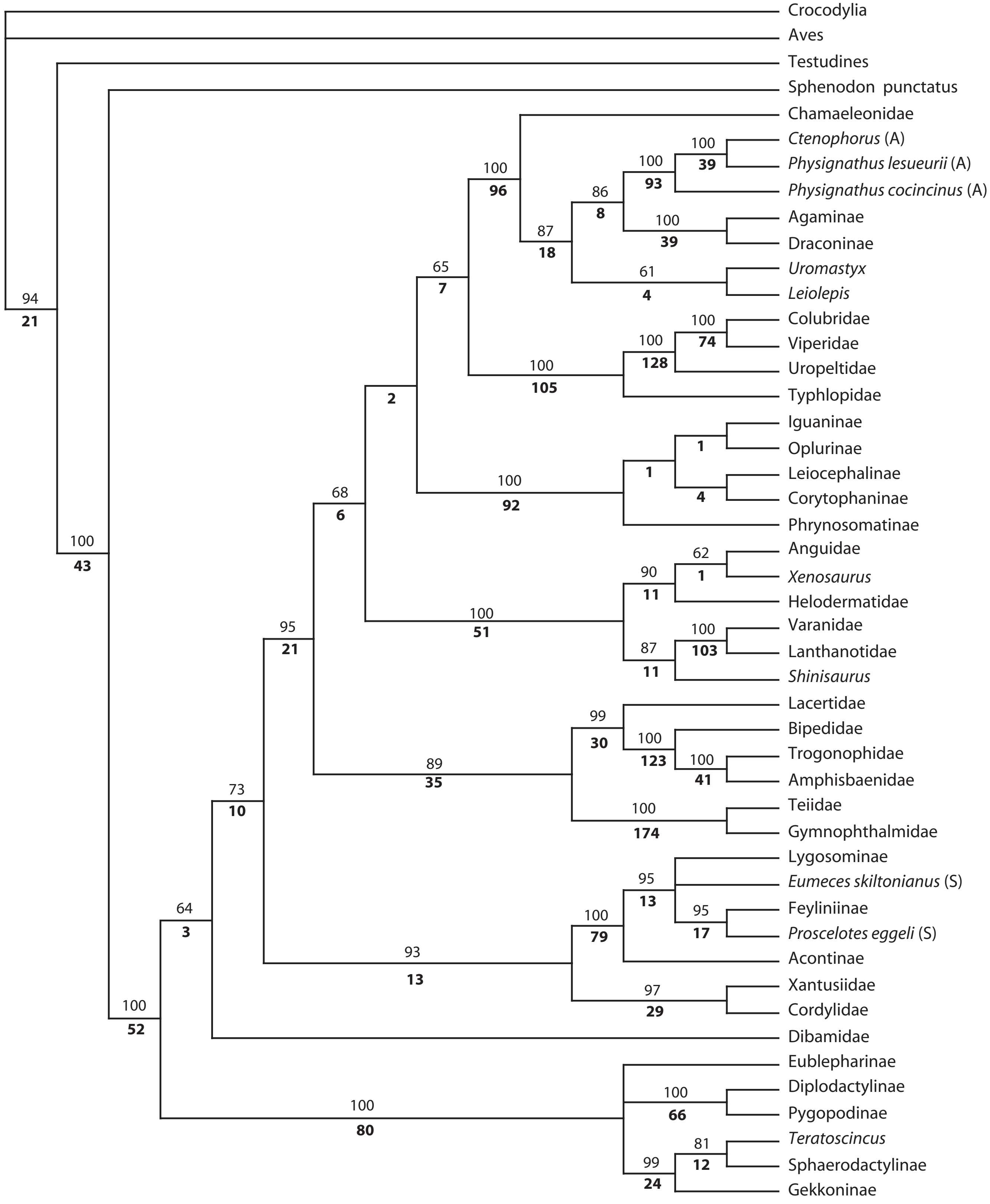
RAG/c-mos MP


Crocodylia
Aves
Testudines
Sphenodon punctatus
Chamaeleonidae
Ctenophorus (A)
Physignathus lesueurii (A)
Physignathus cocincinus (A)
Draconinae
Agaminae
Leiolepis
Uromastyx
Phrynosomatinae
Iguaninae
Leiocephalinae
Corytophaninae
Oplurinae
Anguidae
Helodermatidae
Xenosauridae
Varanidae
Lanthanotidae
Shinisauridae
Colubridae
Viperidae
Uropeltidae
Typhlopidae
Lacertidae
Bipedidae
Trogonophidae
Amphisbaenidae
Teiidae
Gymnophthalmidae
Lygosominae
Eumeces skiltonianus (S)
Proscelotes eggeli (S)
Feyliniinae
Acontinae
Xantusiidae
Cordylidae
Eublepharinae
Sphaerodactylinae
Teratoscincus
Gekkoninae
Diplodactylinae
Pygopodinae
Dibamidae
100 **11**
100 **47**
99 **10**
100 **16**
100 **78**
70 **3**
100 **16**
100 **60**
63 **2**
99 **23**
99 **23**
57 **2**
100 **13**
100 **43**
100 **83**
95 **8**
100 **39**
100 **66**
100 **74**
100 **79**
52 **2**
99 **20**
100 **86**
100 **20**
98 **10**
98 **11**
100 **141**
59 **1**
99 **16**
100 **17**
100 **56**
84 **8**
98 **15**
95 **10**
65 **4**
100 **38**
98 **14**
100 **16**
100 **82**
100 **57**



RAG/c-mos/mtDNA ML

RAG/c-mos/mtDNA MP



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))))),(47,48)))),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))),(47,48)),(((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))))),(47,48))),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))))),(47,48)))),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))),(47,48)),(((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))))),(47,48))),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),((((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))),(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 Variable	No. of Characters Parsimony-Informative	MP tree length	Retention Index[a]	Average pairwise genetic distance[b]
RAG-1	2765	1726	1489	9900	.602	.213 (.149)
1st pos		469	367			
2nd pos		358	256			
3rd pos		899	866			
c-mos	359	237	212	1097	.578	.238 (.169)
1st pos		72	64			
2nd pos		57	42			
3rd pos		120	114			
MtDNA[c]	1497	1254	1137	14328	.396	.905 (.310)
1st pos		295	277			
2nd pos		273	222			
3rd pos		318	311			
tRNA loops		66	51			
tRNA stems		301	275			

[a] Farris 1989.

[b] Average 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.

[c] Third-position transversions excluded.

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

Alternative hypotheses tested[a]	*P*[b]
RAG-1* and *c-mos:	
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 + *Varanus*/*Lanthanotus)*	.0001* (.0008*)
Monophyly of (Lacertidae + Teiioidea) to the exclusion of Amphisbaenia	.044* (.396)
Nonmonophyly of (Lacertidae + Amphisbaenia)	.066 (.198)
Monophyly of Varanoidea (*Heloderma* + *Varanus*/*Lanthanotus*)	.0088* (.0088*)
Monophyly of (*Xenosaurus* + *Shinisaurus*)	.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 + *Varanus* + *Lanthanotus*)	.200 (1.000)
Nonmonophyly of (*Sphaerodactylus* + *Gekko*)	.296 (.592)
Monophyly of (*Xenosaurus* + *Heloderma* + Anguidae)	.278 (.278)
***RAG-1*, *c-mos,* 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-1* 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-1* 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 ≥95% in analyses of both nuclear and mitochondrial DNA. Hatched bars denote branches supported by bootstraps and posterior probabilities ≥95% in the nuclear analysis, and posterior probabilities ≥95% in the mitochondrial analysis. Open bars denote branches supported by bootstraps and posterior probabilities ≥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

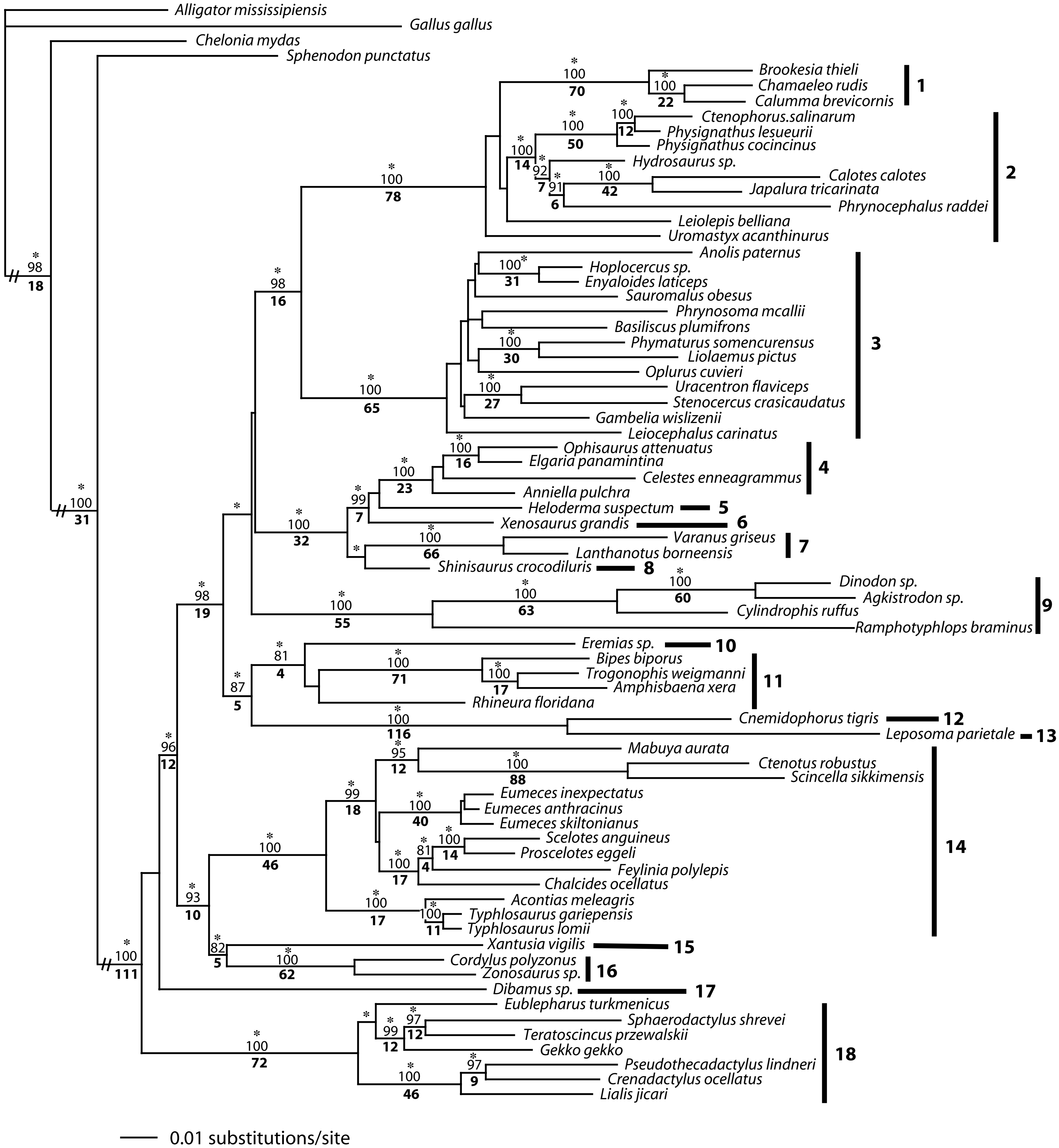


Figure 2. c-mos ML

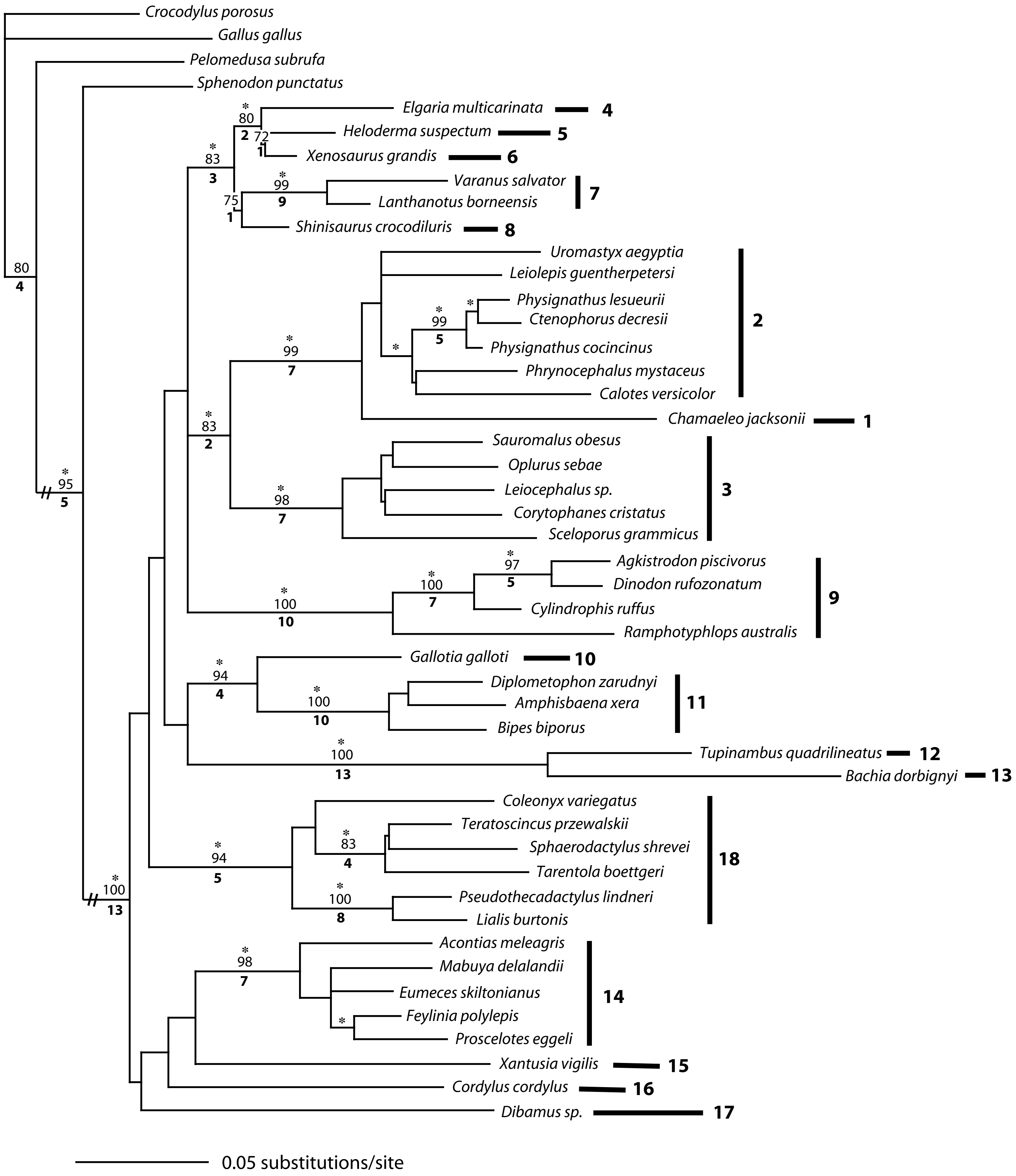


Figure 3. RAG/c-mos ML/MP

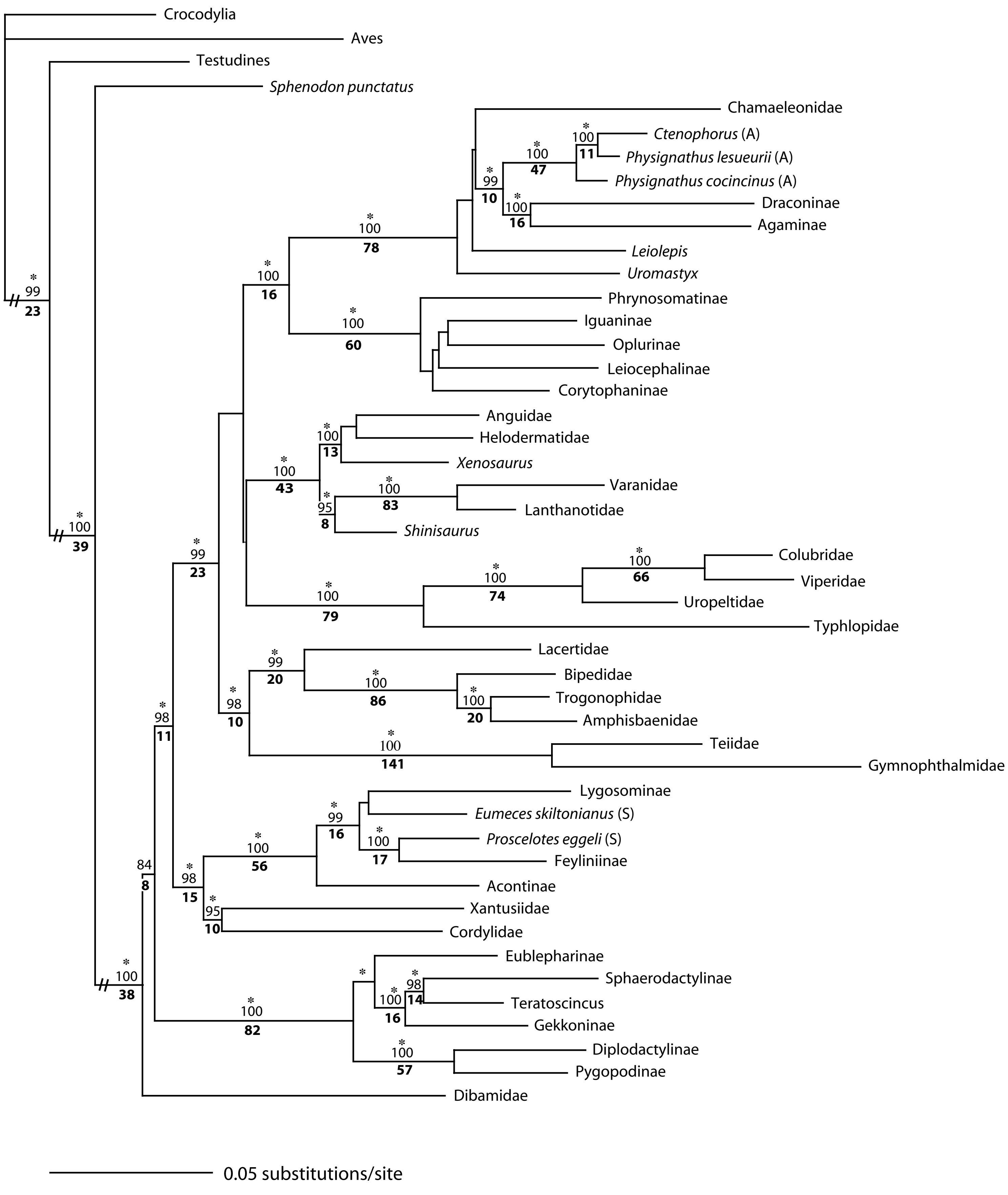


Figure 5. mtDNA MP

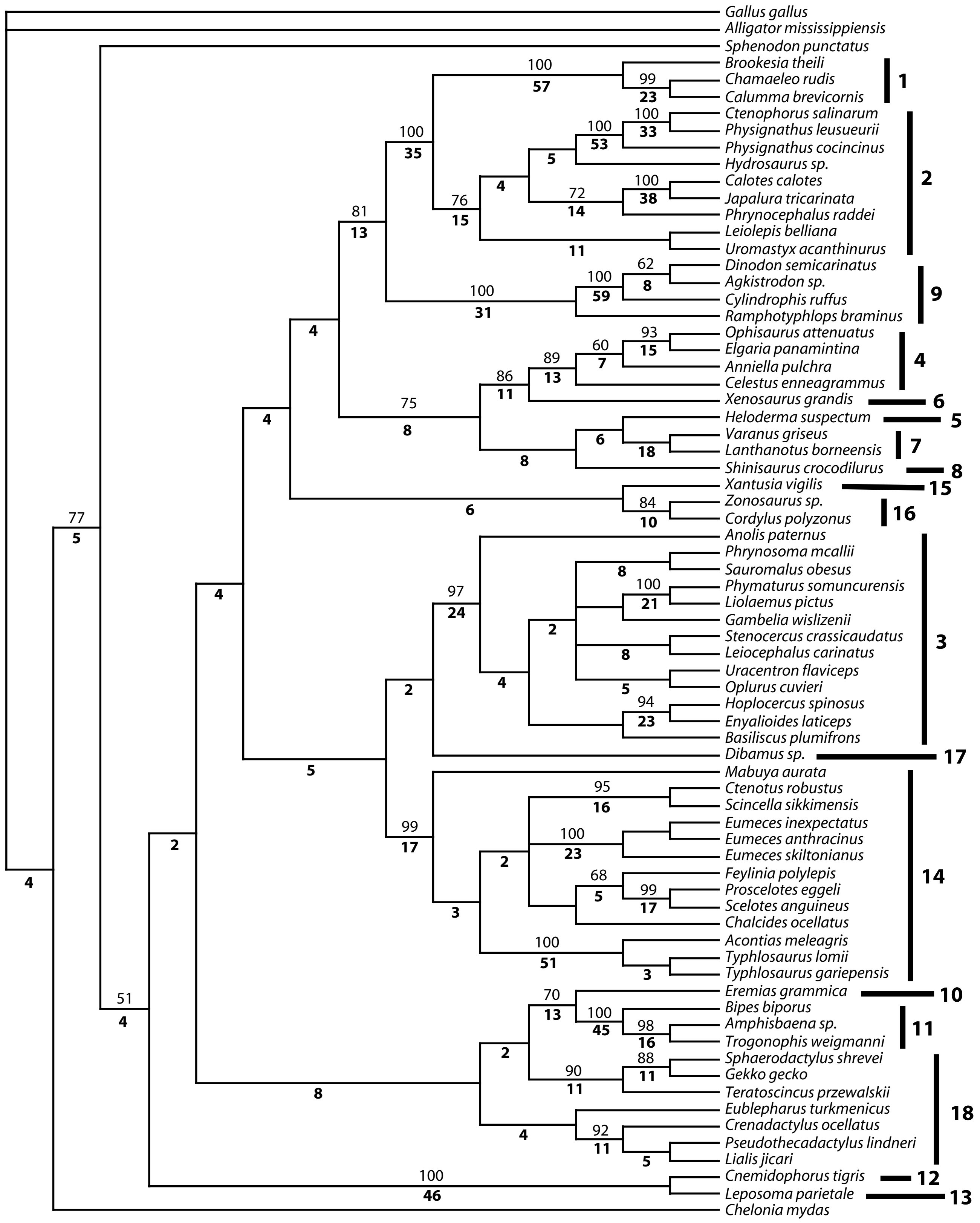


Figure 5. mtDNA ML

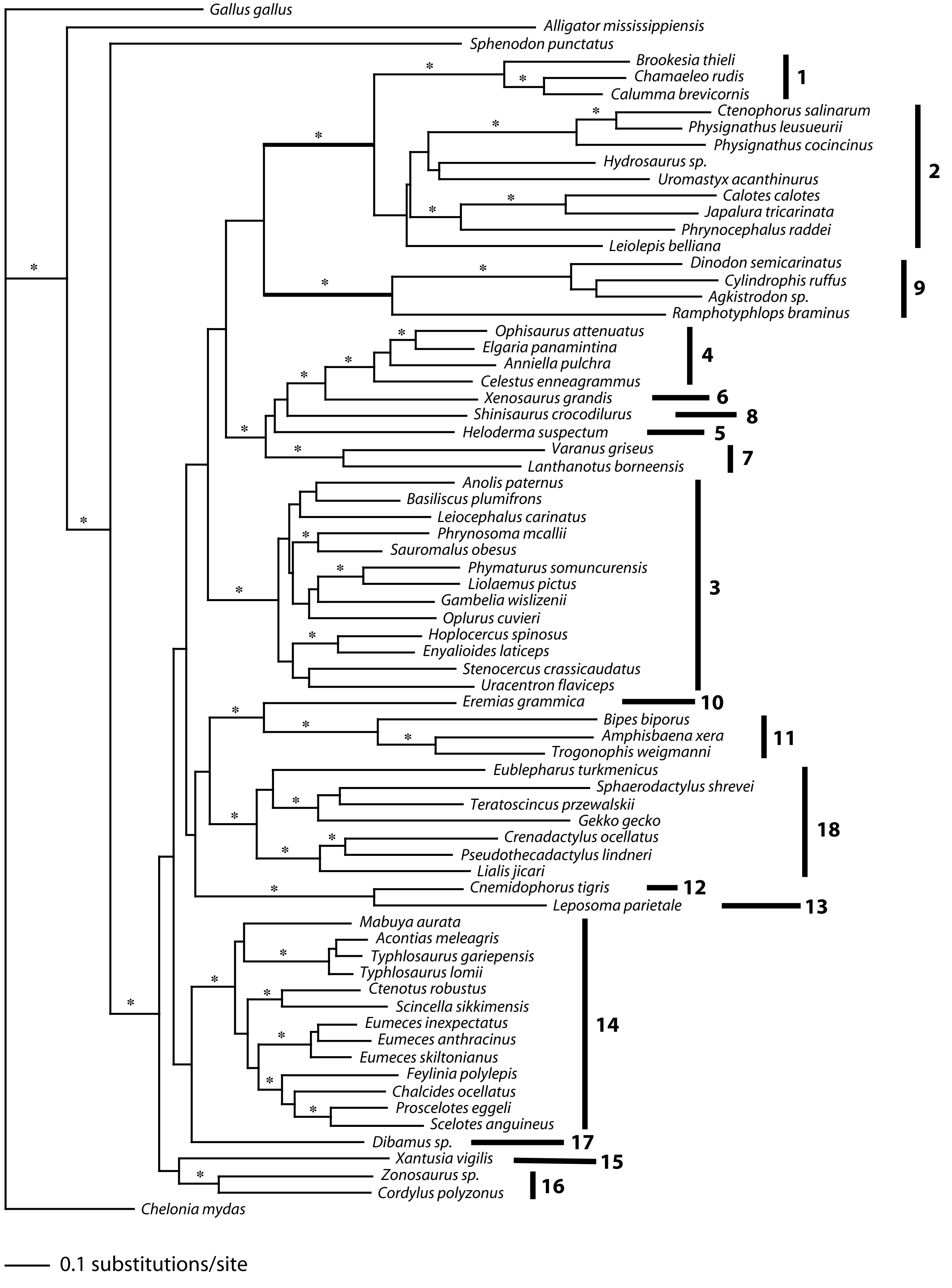


Figure 6. Long Branch Attraction

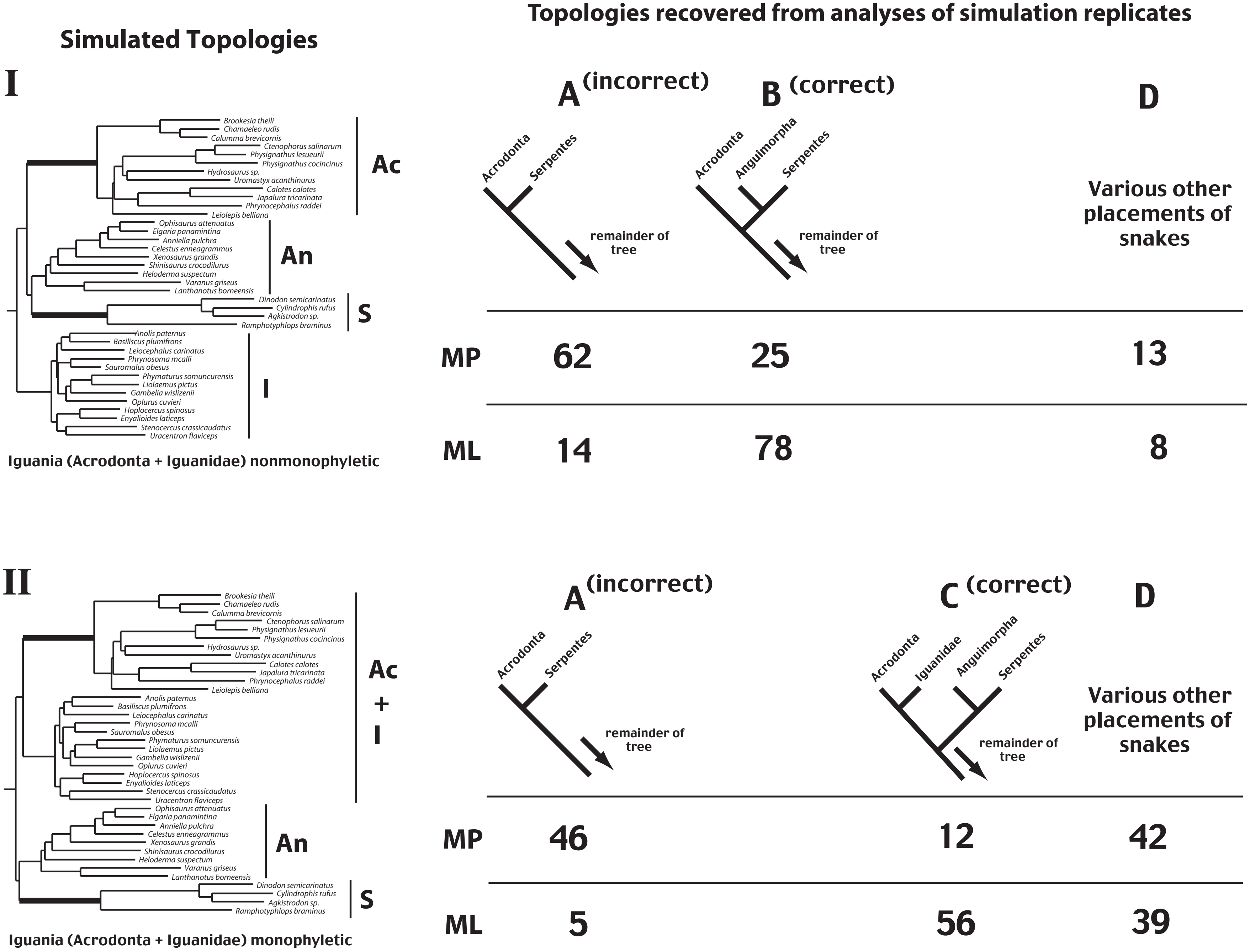


Figure 7. Summary of Squamate Relationships

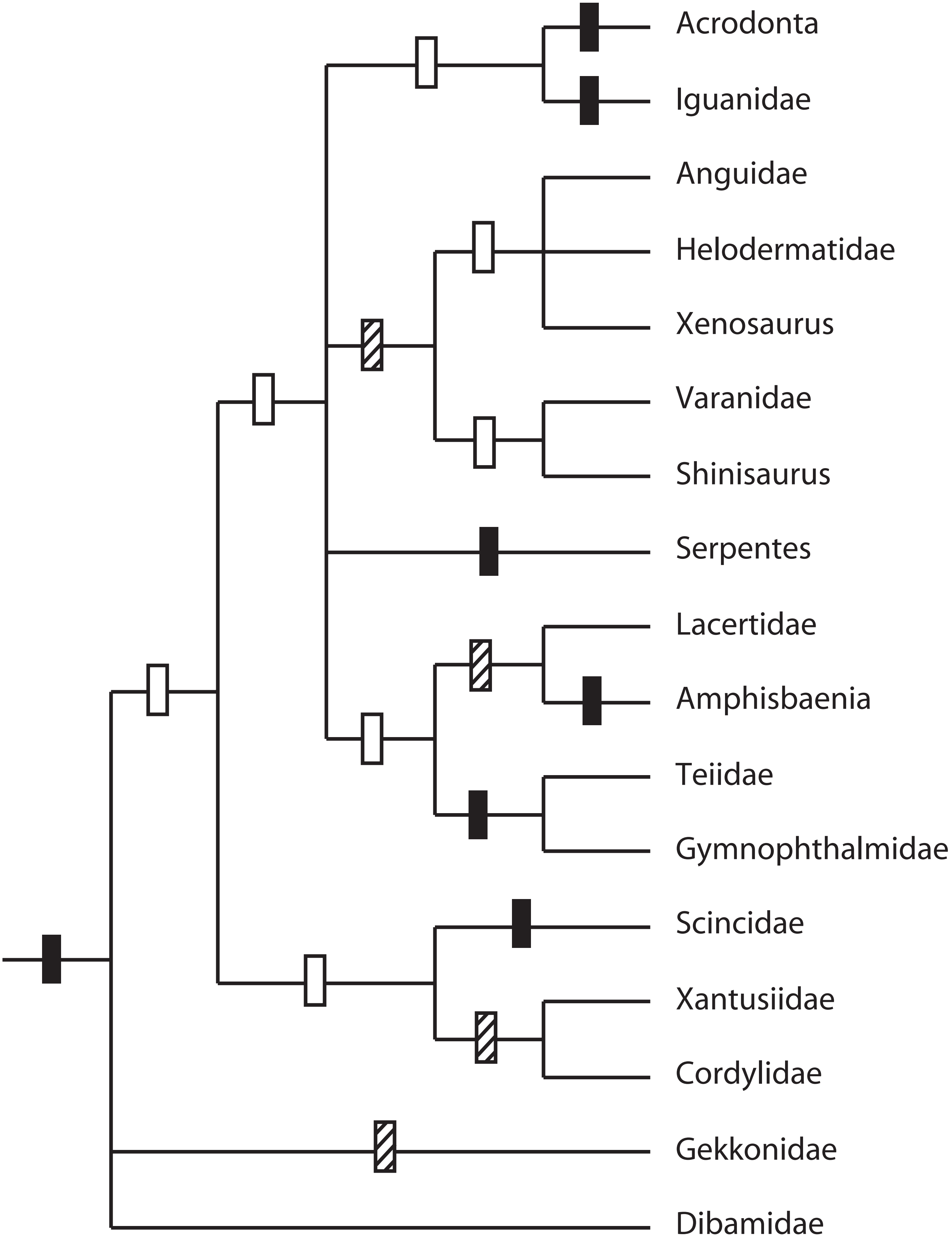


Figure 8. Lee & Caldwell Extant Taxa MP

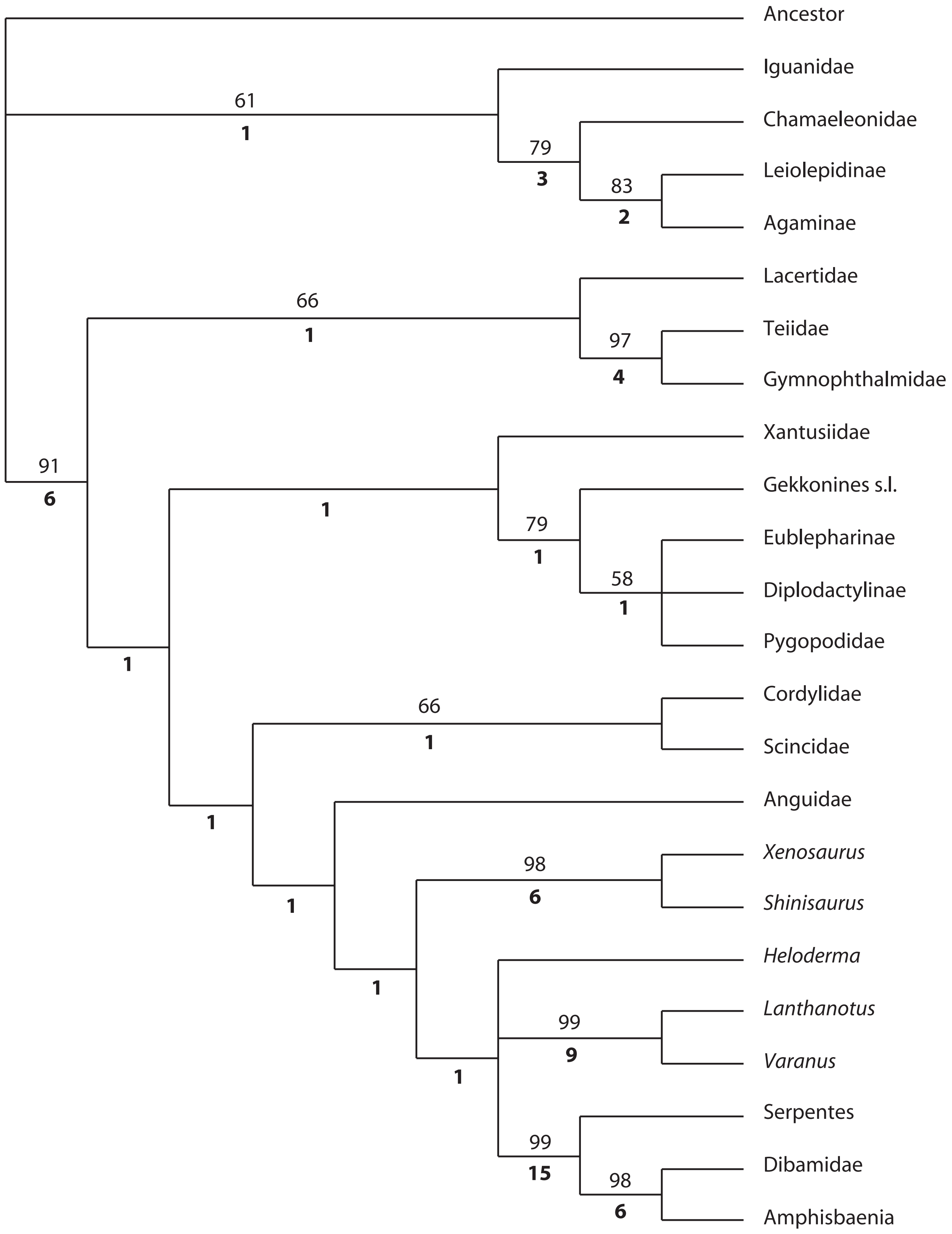
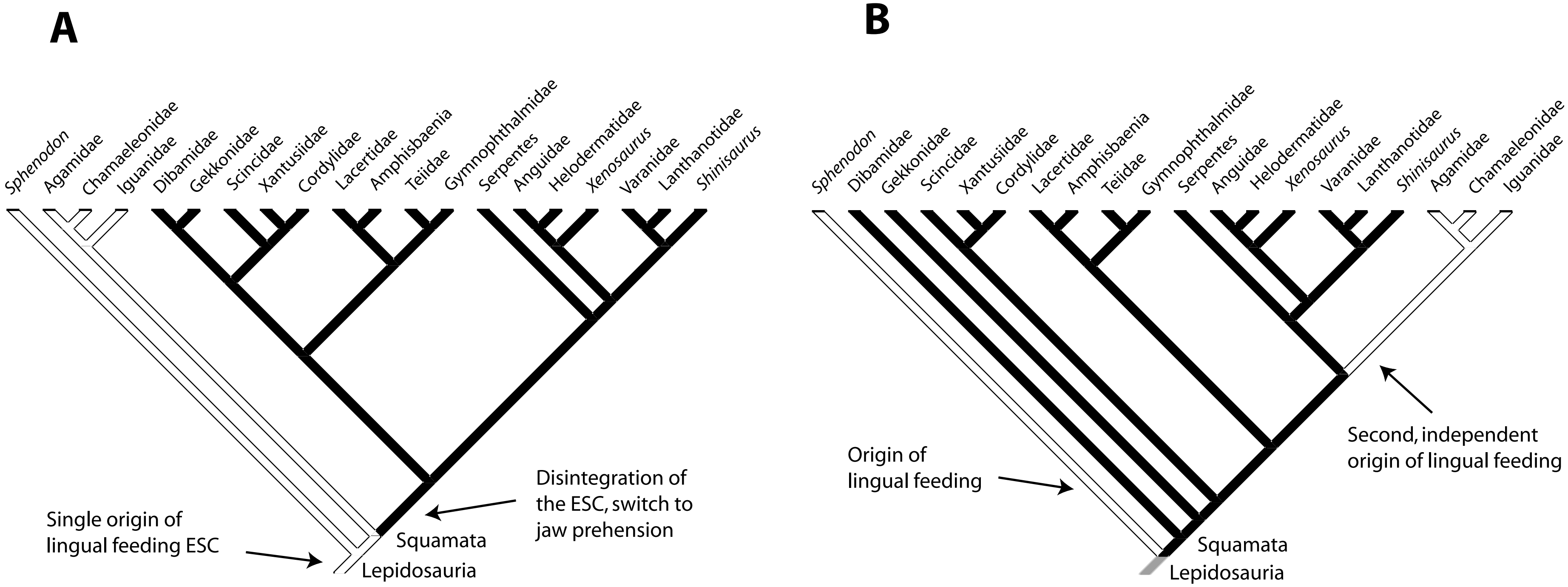


Figure 9. Evolution of Feeding Mode



Single origin of lingual feeding ESC

Disintegration of the ESC, switch to jaw prehension

Origin of lingual feeding

Second, independent origin of lingual feeding