



Supplementary Materials for

Title: Attenuated evolution of mammals through the Cenozoic

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This PDF file includes:

Materials and Methods
Figs. S1 to S8
Tables S1 to S2

Other Supplementary Materials for this manuscript include the following:

Data S1

Materials and Methods

Specimens

Our dataset samples 322 crown and stem placental mammals, including 207 extant and 115 extinct species (data S1). Sampling includes 123 (of ~127) extant placental families and an additional 58 wholly extinct families, with multiple subfamilies sampled for most large clades. Sampling was selected to cover the full phylogenetic, ecological, and morphological breadth of living and extinct placentals, with sampling of fossil specimens limited to those that are known from well-preserved complete crania. Because of the requirement for skulls that are undeformed in 3D, we were only able to sample Cenozoic representatives of “Cretaceous lineages”, i.e. wholly extinct, likely stem lineages that the fossil record supports unambiguously as having diverged in the Cretaceous, such as leptictids and cimolestids (23). Within these limitations of requiring undeformed 3D specimens, we made great efforts to sample the full breadth of extinct placental lineages, particularly those that appear proximal to the K/Pg mass extinction. Full details of specimens are included in data S1. 3D scans of specimens were obtained from micro-CT and surface scanning at 25 international institutions. Surface scans were obtained with a FARO Edge Arm and Laser Line Probe, a Creaform Go!SCAN 20, a Creaform Go!SCAN 50, or a Breuckmann StereoSCAN3D white light fringed surface scanner. A minimum of 0.2mm resolution was used for all but the largest specimens, i.e., those with crania over a metre in length, which were scanned with 0.5mm resolution with the Creaform GoScan 50. Additional specimen scans were sourced from public repositories, including Phenome10k, Digimorph, and Morphosource. Specimen locations and, if applicable, scan sources, are provided in data S1. Micro-CT scans were processed with Avizo Lite 8.0 (FEI Visualisation), and all surface and micro-CT scans were processed in Geomagic Wrap 2017 (3D Systems) prior to collection of morphometric data. All scans are available for download on Phenome10k (subject to institutional permissions).

Morphometric data

3D landmark and semi-landmark data were collected for the left side of the skull using Stratovan Checkpoint. 66 landmarks were selected to represent points of unambiguous Type I and Type II homology. 69 semi-landmark curves were then placed that connected landmarks and largely follow the sutures of cranial bones (Fig. S1, Table S1). The lacrimal, which variably has a facial aspect, was included with the maxilla when present on the facial surface. Variably present bones, including the premaxilla, nasal, and jugal, were treated as zero-area structures when absent, following the protocol in (24). Landmarks and semi-landmarks were imported into R for analysis using the ‘SURGE’ package (github.com/rnfelice/SURGE), where curves were resampled to a common number of semi-landmarks and slid to minimize bending energy with the ‘Morpho’ v. 2.8 package (25). A full description of landmarks and curves is provided in Table S1 and Fig. S1. Following sliding, morphometric data were mirrored using midline landmarks with the ‘paleomorph’ package and then subjected to Generalized Procrustes Analysis in the ‘geomorph’ package v. 4.0 (26). Mirrored landmarks were then removed, leaving a total of 757 3D landmarks and sliding semi-landmarks. Centroid size output from the Procrustes superimposition was used as a proxy for body size in further analyses. Shape data are available at https://github.com/anjoswami/Goswami_et_al_Placental_evolution_2022.

Ecological and life history traits

Ecological and life history data were collected from the published literature for the following categories: Diet, Locomotion, Habitat, Development, Social Structure, and Activity Pattern (27–59). Published reconstructions were used to score diet and locomotion for extinct taxa, while all six traits were scored for extant taxa. Given the taxonomic breadth of this dataset, inevitable uncertainties on ecology and life history for rare species, and the need for a minimum of five species in each bin for statistical analyses, we used relatively broad categories for diet, locomotion, and habitat. Development and social structure were treated as binary traits, while activity pattern used four distinct states. Details of traits and references are provided in data S1.

Phylogeny

While molecular data has largely resolved the higher-level topology of placental mammals and there are detailed morphological phylogenies available for many extinct placental clades, there is continuing debate over the positions of some entirely extinct clades within Placentalia. There is also extensive debate over the root age of the crown group, with persistent gaps between paleontological and molecular data. For example, the most recent molecular analyses of placental phylogeny (15) provide a distribution of trees that vary in root age from 70 Ma to over 100 Ma, whereas no unambiguous crown placental fossils predate the end-Cretaceous mass extinction that occurred 66 million years ago (9, 13, 23). The timing of origin for Placentalia and the positions of the earliest post-Cretaceous lineages are clearly critical for placing the radiation in the appropriate environmental and evolutionary context, and the lack of resolution in this area is a key factor in the exclusion of fossil taxa from most analyses of mammal diversification.

In the absence of a well-resolved phylogenetic hypothesis that samples all living and extinct taxa in our dataset and constrained to a reasonably narrow range of root ages, we constructed an extensive range of alternative phylogenies that capture the impact of this phylogenetic uncertainty on our results. To do so, we started with the maximum credibility consensus tree from the most recent species-level molecular analysis of placental relationship, which samples all of our extant sample, as well as some recently extinct species (15). We then used a suite of recent morphological phylogenetic analyses (13, 23, 60–90) that include our fossil sample to place the extinct taxa within the molecular tree, generating three alternative composite topologies that capture the major points of uncertainty in the relationships of early placentals, particularly the potentially paraphyletic cimolestids and amblyopods. We focused the alternative topologies on these problematic branches near the base of Placentalia, as they encompass contentious members of the wastebasket taxon “Condylarthra” or are variably considered to be stem or early crown placentals. Most of the other fossil taxa in our sample are better resolved in terms of phylogenetic affiliations, with remaining uncertainty largely involving within-group relationships that should have little impact on rate estimations at this level of sampling.

A notable large group with considerable ongoing debate in their phylogenetic affinities are the South American Native Ungulates (SANUs), here represented by three of the five large orders: Notoungulata, Litopterna, and Astrapotheria. Recent analyses support Notoungulata and Litopterna as allied with Perissodactyla (67), and Astrapotheria has also been supported in a close relationship with Notoungulata (66). Other SANU clades have been supported outside of Laurasiatheria, meaning that SANUs is potentially polyphyletic [see discussion in (60)]. Treating this group as monophyletic could exaggerate evolutionary rates from the (incorrectly

reconstructed) ancestral node to the base of each SANU clade. Because the sample of 8 SANU taxa here don't include some of the more enigmatic taxa and are better supported in an affiliation with Perissodactyla, this effect is unlikely to have impacted our results. Nonetheless, it is important to remember that uncertainty in the phylogenetic positions of extinct mammals remains a continuing hindrance to the integration of fossil data into macroevolutionary analyses, despite the quality of the Cenozoic mammal fossil record, and that this issue will only be resolved through continuing dedicated systematic analysis.

As noted above, uncertainty in the topology of the placental tree is matched by uncertainty in estimating the timing of placental divergences. We first attempted to date the trees generated as described above using a fossilized birth-death approach, but this approach consistently generated trees with unambiguously incorrect divergence estimates. To circumvent this issue and capture the uncertainty in the root age of the placental tree, we first drew a set of node-dated trees from the posterior distribution of (15) that had the same topology as the MCC tree. We then binned these trees into six 5-million year bins (70-75Ma, 75-80Ma, 80-85Ma, 85-90Ma, 90-95Ma, and 95-100Ma). We then took our three composite topologies and grafted the extinct taxa onto all of the trees across six bins, with the node age for fossil branch divergences randomly selected from within each third of the parent branch (resulting in three alternative divergence estimates for each node leading to an extinct branch for each topology). This process generated 419,400 alternative trees, which we subsampled to 1800 trees, 100 for each of the six 5-million-year root age bin for each of the three topologies. These 1800 trees form the basis of the following analyses and cover broadly much of the immense range of continued uncertainty in the placental tree. Code for grafting trees is available at <https://github.com/rnfelice>.

Cranial shape variation

To examine the overall pattern of cranial variation across placentals, we conducted a principal components analysis using Procrustes-aligned 3D landmarks data in 'geomorph'. We reconstructed wireframe models for the minimum and maximum shapes on the first four principal components, which together account for 64.5% of the total variation in the dataset. We projected the first three components into a morphospace (Fig. 1) and generated density contours to identify concentrations of cranial morphology by estimating 3D Gaussian kernel density using the `gaussian_kde` function in SciPy (91). We further generated plots of PC1 and 2 (Fig. 1) and PC3 and 4 (Fig. S2) to highlight the distributions of ordinal and superordinal level clades and extinct and extant taxa. We also conducted a phylogenetic PCA in 'geomorph' and extracted the pPC scores for the components which combined explain 95% of the total variation in the dataset (67 components for the tree figured in Fig. 2). Finally, we estimated the ancestral shape for the placental MRCA and each superordinal MRCA by maximum likelihood in the R package 'Rphylopars' v0.2.11 (92) and warped a reference mesh (*Vulpes pallida*) to the target shape to produce 3d models of the ancestral estimates in 'Morpho'. Using alternative reference meshes, including unusual forms such as the armadillo (*Oryzomys azer*) had no impact on results.

Macroevolutionary modelling

We assessed 10 alternative evolutionary models (variable- and single-rate models for Brownian motion, Ornstein-Uhlenbeck, and BM with lambda, kappa, or delta tree transformations) for cranial evolution with a reversible-jump Markov Chain Monte Carlo (MCMC) algorithm implemented in BayesTraits v. 3 (<http://www.evolution.rdg.ac.uk/>) (5), using phylogenetic PC

scores as input data. Because initial tests demonstrated that a run of 1,000,000,000 iterations were required to achieve convergence in parameter value estimates, we ran analyses on a subset of one randomly sampled tree from each topology and root age bin, for a total of 18 alternative trees. We used a burn-in of 500,000,000 and sampled every 5,000 trees, resulting in a posterior distribution of 100,000 trees from 1,000,000,000 iterations. Trace plots were examined to ensure that the chains reached stationarity after burn-in. Convergence of the chains was assessed using Gelman and Rubin's convergence diagnostic implemented in the R package 'coda' v.0.19-3.

Bayes Factor supported the variable rates Brownian Motion model with a lambda tree transformation as the best fit model for all 18 phylogenetic frameworks (Fig. S3). The lambda transformation effectively lengthens terminal branches, thereby accommodating error due to within-species variation and artefacts such as measurement error, which can be important factors in evolutionary modelling (26). Lambda values range from 0.629 to 0.741 across all phylogenetic frameworks, with the lowest values for those trees with the youngest root ages (70-75 Mya) and the highest values for those with the oldest root ages (95-100 Mya). We plotted mean per-branch rates on each tree and summarized by the branch-specific average rate and the posterior probability of rate shifts estimated from the posterior samples using the 'BTRTools' R package v.0.0.0.9000 (<https://github.com/hferg/btrtools/tree/master/R>). Rate shifts with a probability greater than 0.5 are indicated on Fig. S4. We binned rates by geological time and plotted their pattern through time for the 18 alternative trees (results for the six trees for Topology 2 shown in Fig. 3). We then extracted rates for the terminal branches and plotted them by clade to assess differences in mean rate across clades (Fig. 3, Fig. S5), with the distributions representing the variation in rates across branches within each tree for the mean tree of the posterior distribution of 100,000 trees.

Ecological and life history associations with cranial evolution

We assessed the association of life history and ecological traits on cranial variation and evolutionary rates using the 'mvMORPH' package v 1.1.4 (93). We conducted Type II phylogenetic MANOVAs (phylogenetic regressions) on the Procrustes coordinates with log centroid size and each of the six factors as predictors. We conducted one analysis of size, diet, and locomotion for the full dataset of living and extinct species ($n = 322$) and a second one of all six factors for just the extant taxa ($n = 207$). Multivariate phylogenetic linear models with Pagel's lambda by penalized likelihood were fit using "mvgl", with significance assessed using the "manova.gls" function with Pillai's statistic and 1000 permutations. Using Pagel's lambda corresponds to fitting a phylogenetic mixed model which allows accounting for departure from Brownian motion and usually provides increased flexibility in estimating the error structure (94–97). Some of these factors may interact, e.g. social structure and development, or locomotion and habitat, but because many, possibly the majority, of intersecting bins do not have any representatives (e.g., there are no volant bulk invertivores, or aquatic social insectivores), we limited analyses of factor interactions to size with all other factors. Because the MANOVAs and permutation tests took multiple weeks for each analysis to run on a dataset of this size, even on the Crop Diversity Bioinformatics High Performance Computing cluster, we performed analyses on the same subset of 18 trees as used in the BayesTraits analyses above, allowing us to assess the effect of phylogenetic uncertainties on our results (Table S2).

Finally, we used the state-specific Brownian motion (BMM) model in the ‘mvglS’ function in *mvMORPH* to estimate rates of evolution for each ecological and life history state. The reconstructed histories for each category were estimated with stochastic character mapping across the full sample of 1800 trees using an ‘ARD’ model in the R package *phytools* v. 0.7-70. We performed model fitting by jointly estimating the contribution of measurement error and intra-specific variation, which is flexible to departures from Brownian motion. Results were binned by tree topology and root age estimate to again assess the impact of phylogenetic uncertainty on results (Fig. 4, Fig. S6).

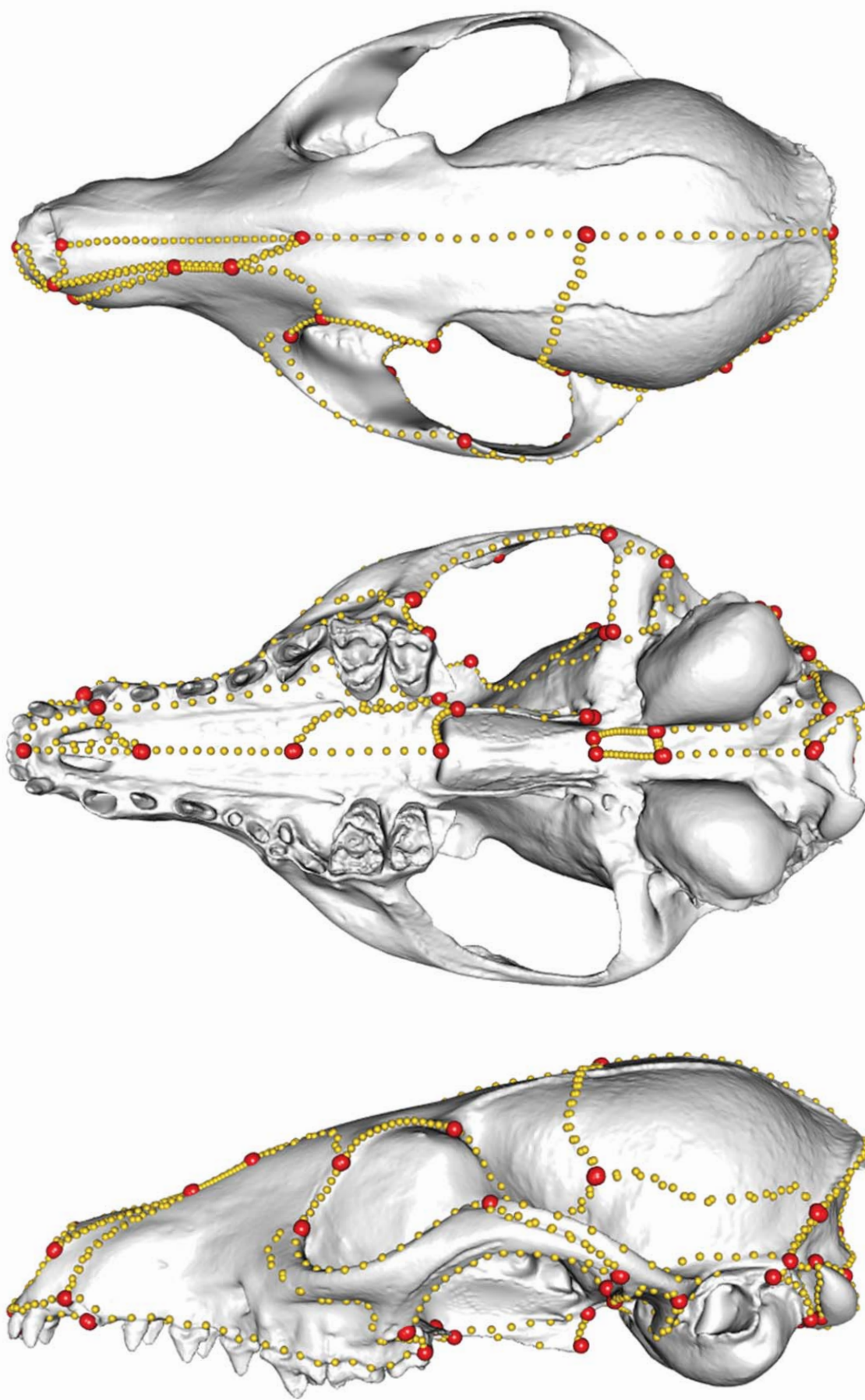


Fig. S1. Landmarks (red) and sliding semi-landmarks (gold) shown on *Vulpes pallida* in dorsal, ventral, and lateral views (top to bottom)

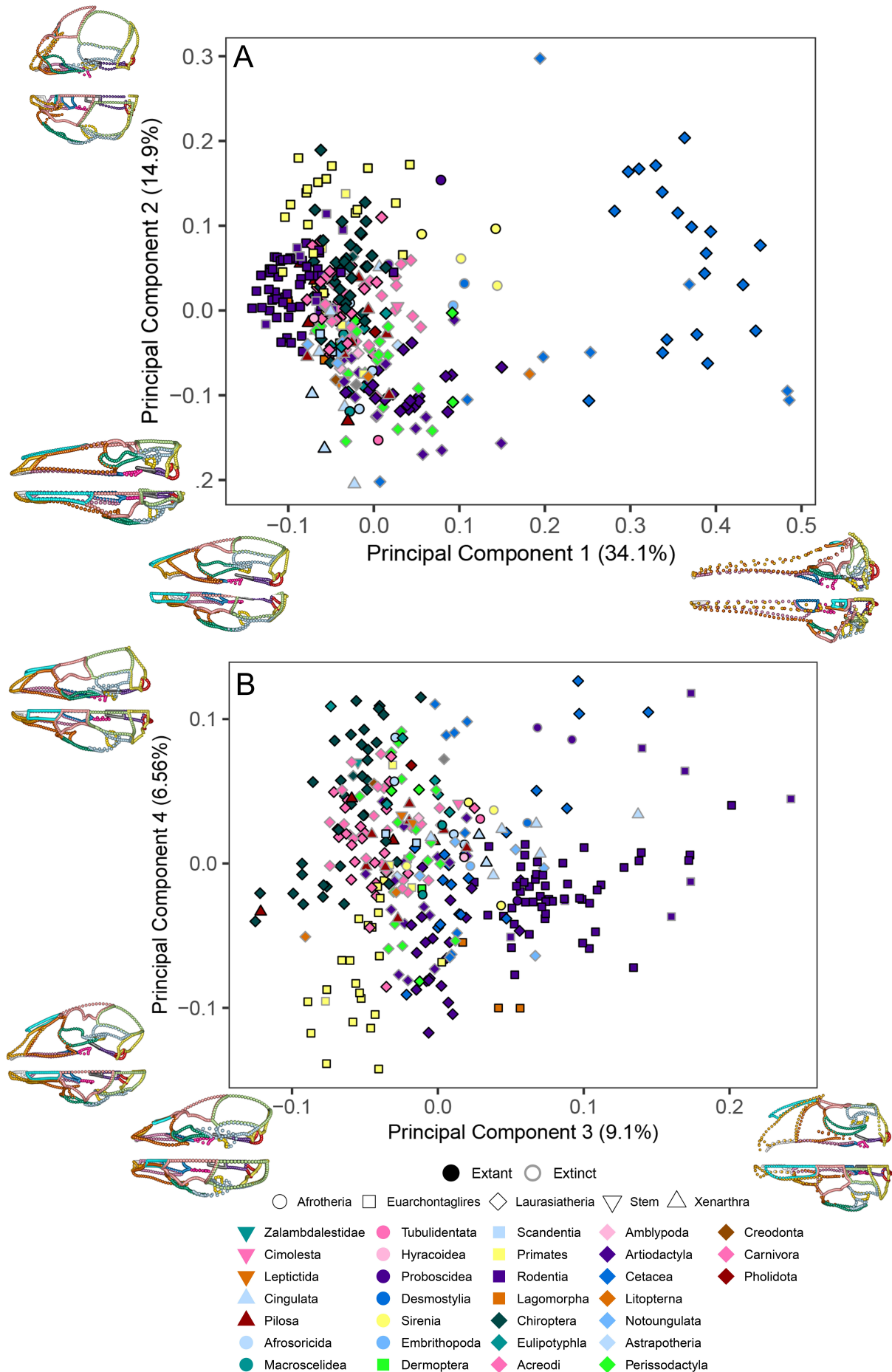


Fig. S2. Morphospace and wireframes for A) PC1 and 2 and B) PC3 and 4, using a color-blind palette for taxon symbols. Interactive morphospaces produced with Plotly (Montreal, Quebec) are available at https://github.com/anjgoswami/Goswami_et_al_Placental_evolution_2022.

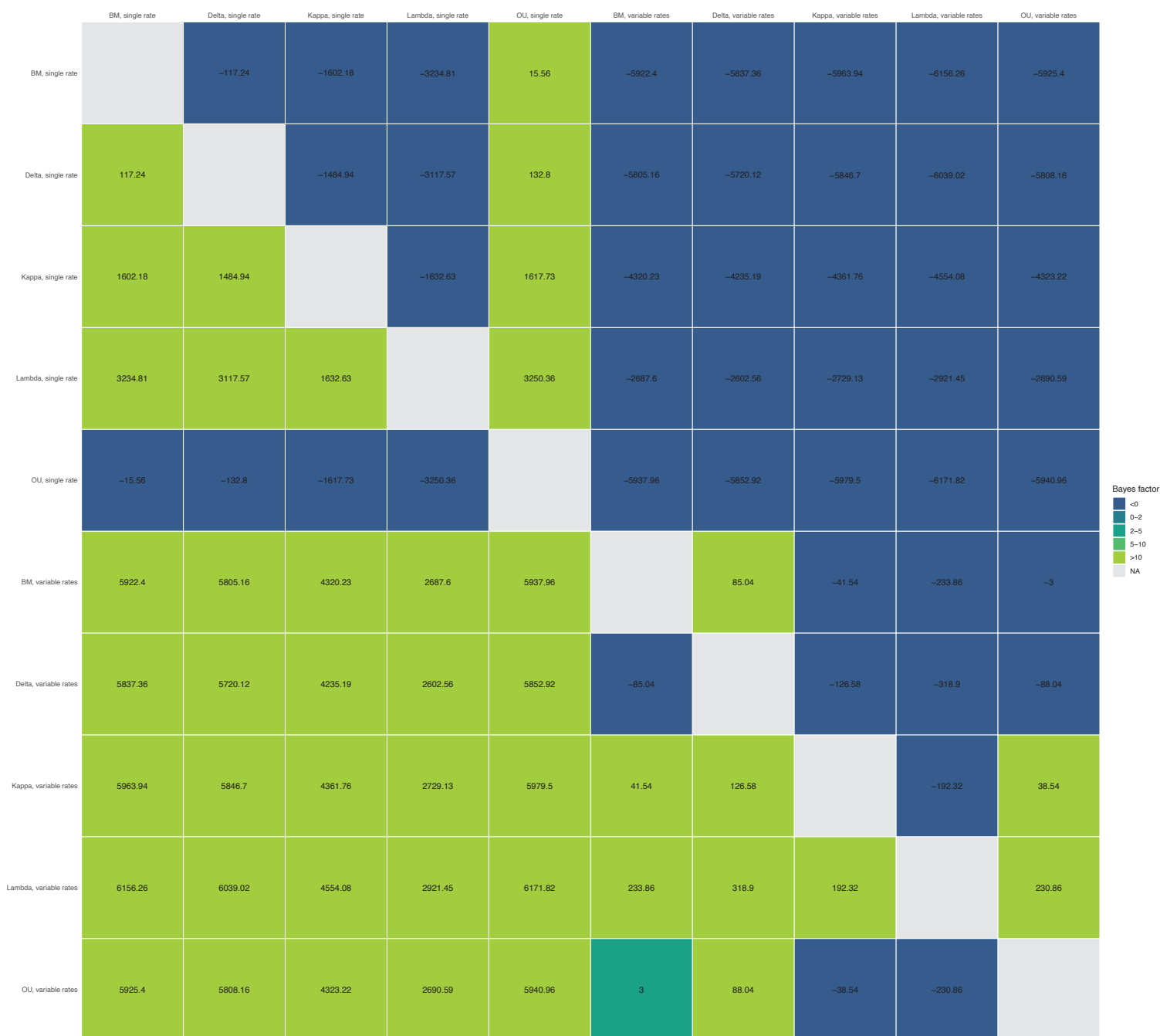


Fig. S3. A) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 1, Root Age = 70-75Ma.

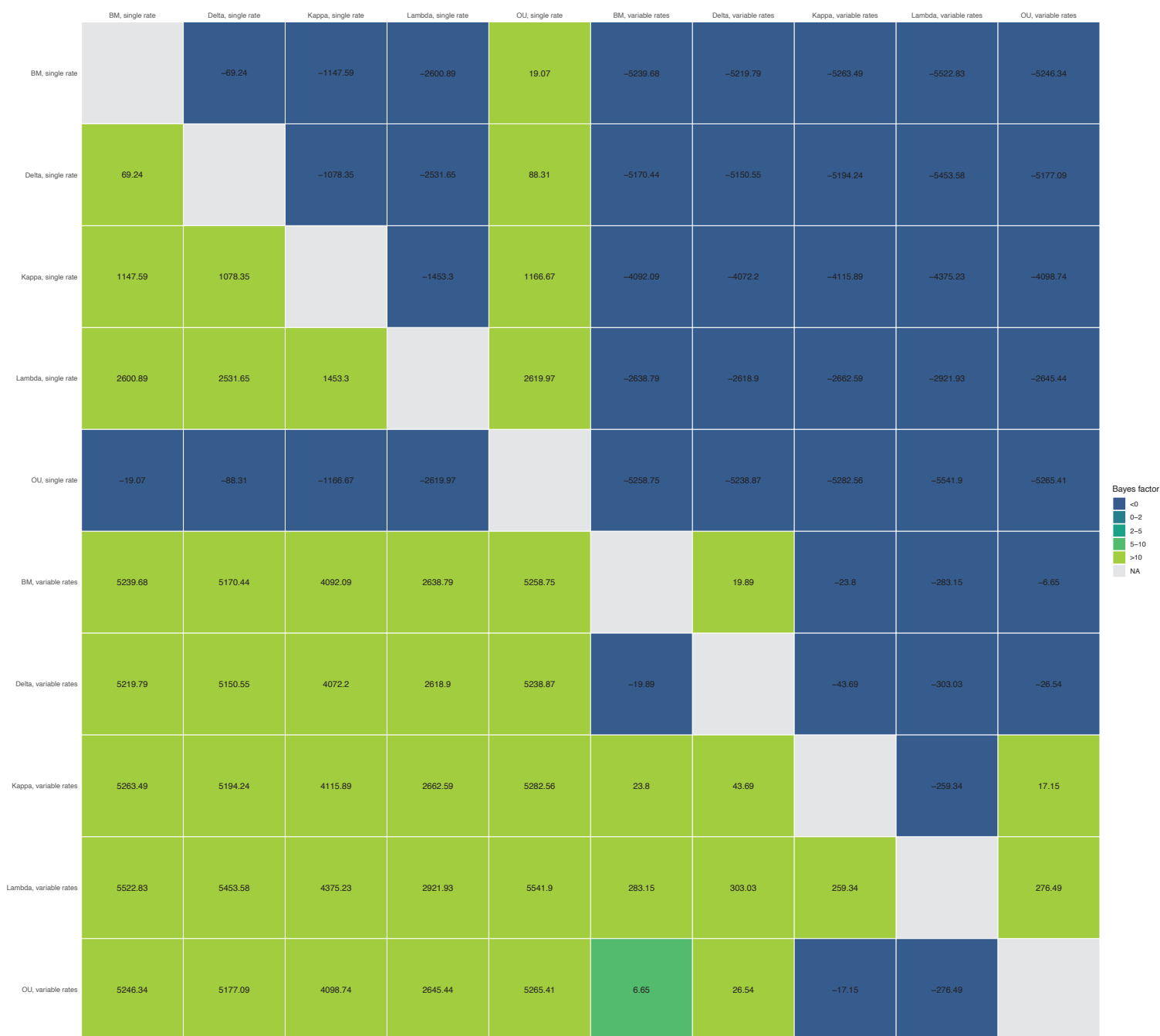


Fig. S3. B) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 1, Root Age = 75-80Ma.

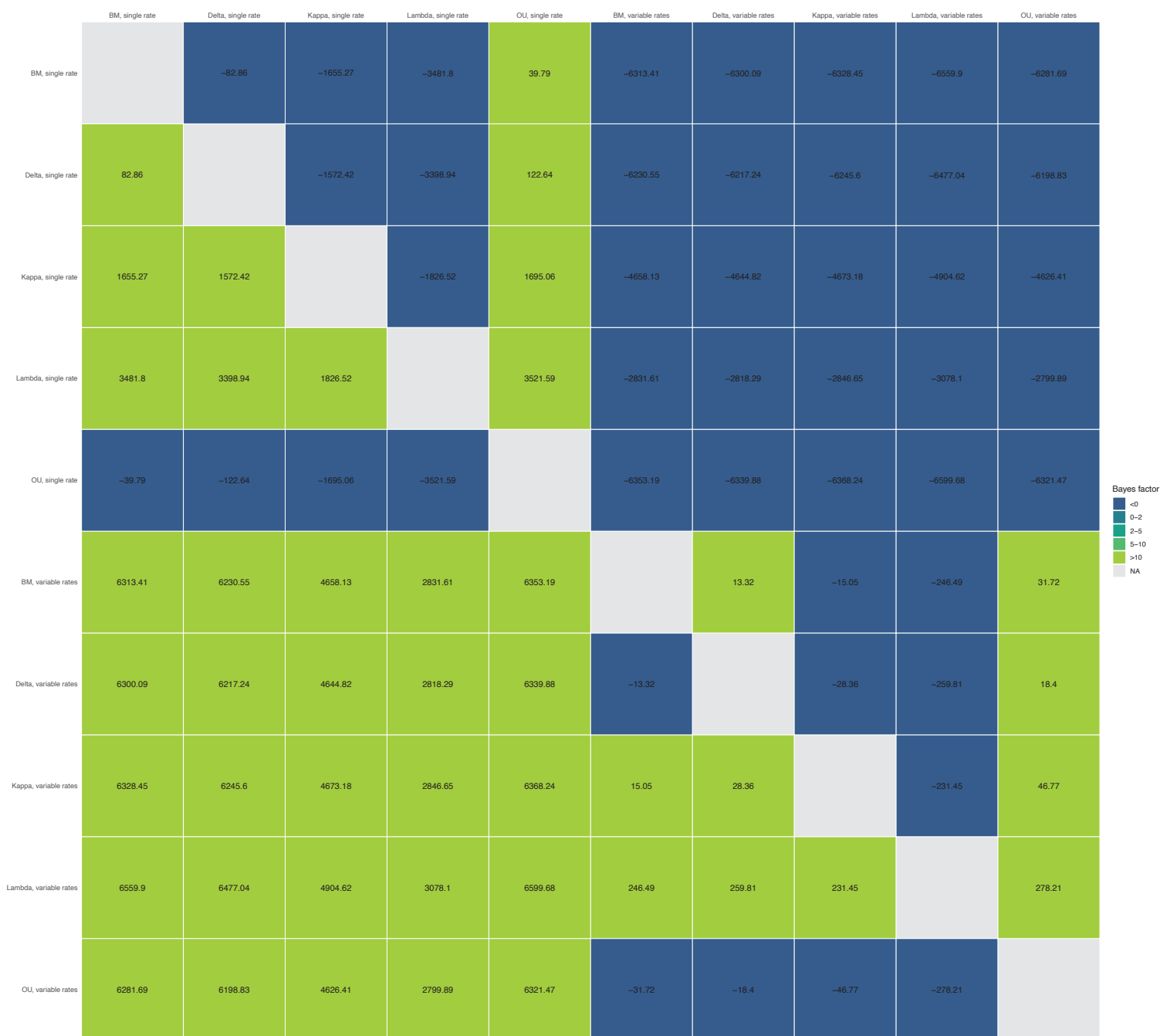


Fig. S3. C) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 1, Root Age = 80-85Ma.

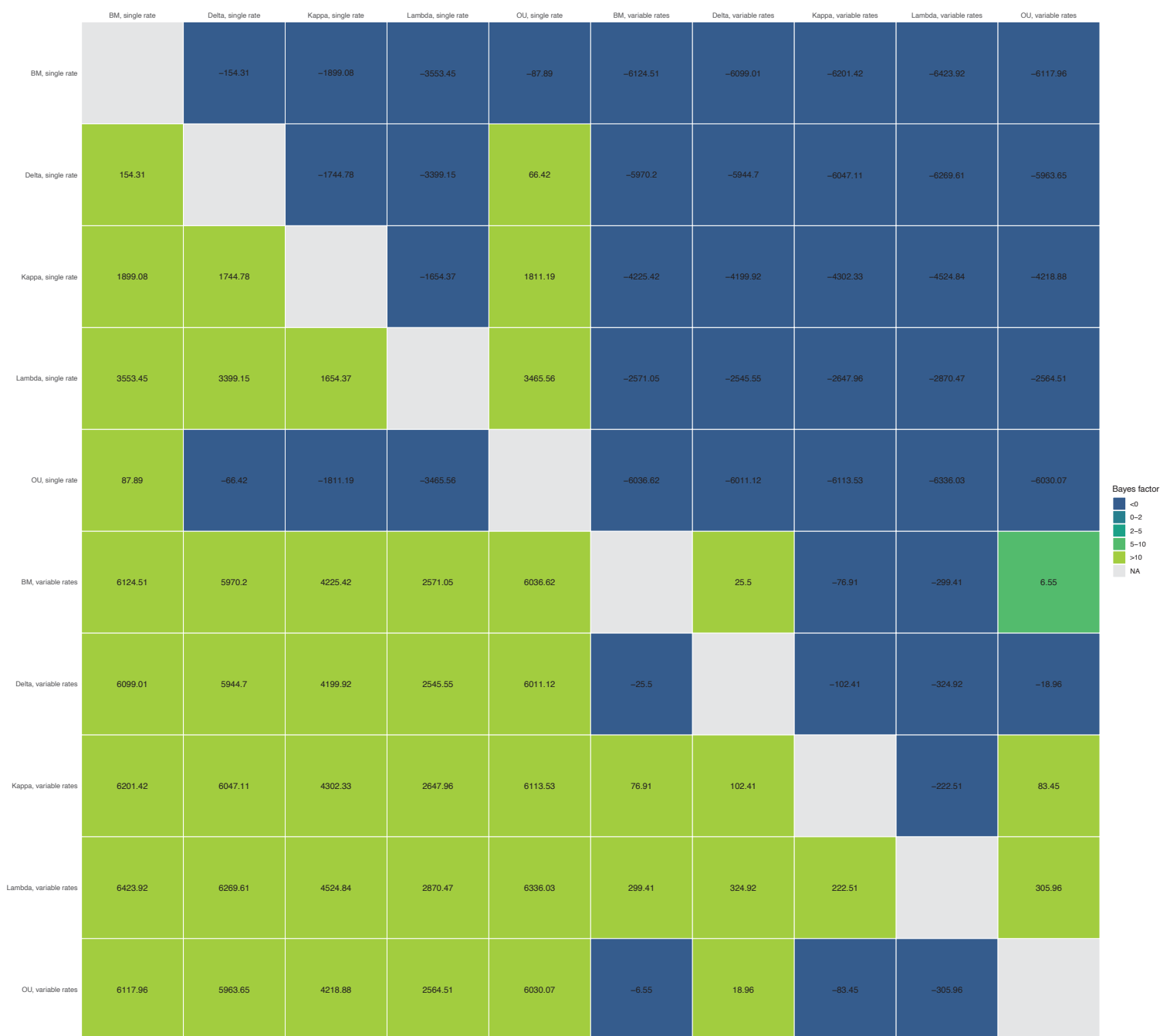


Fig. S3. D) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 1, Root Age = 85-90Ma.

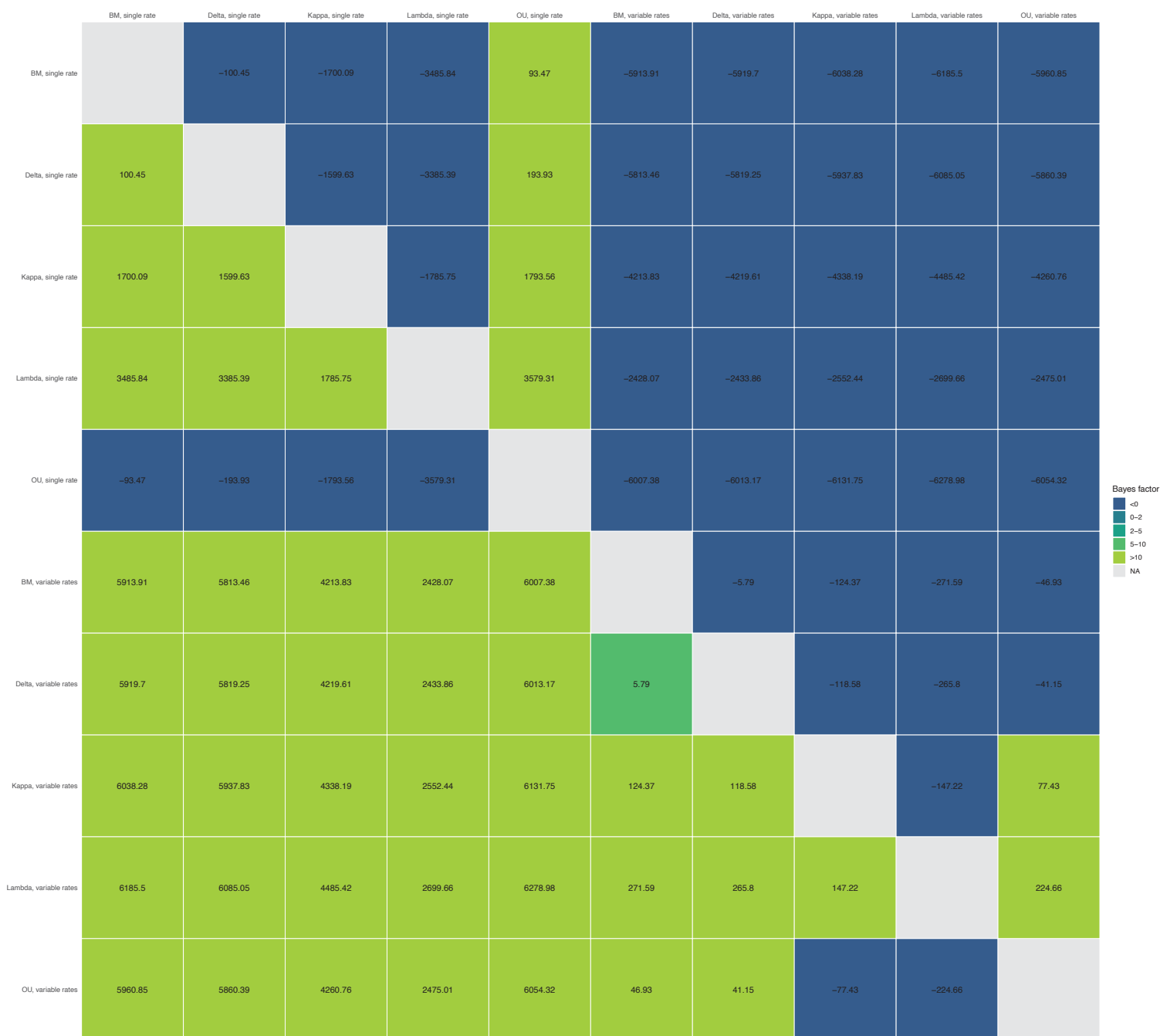


Fig. S3. E) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 1, Root Age = 90-95Ma.

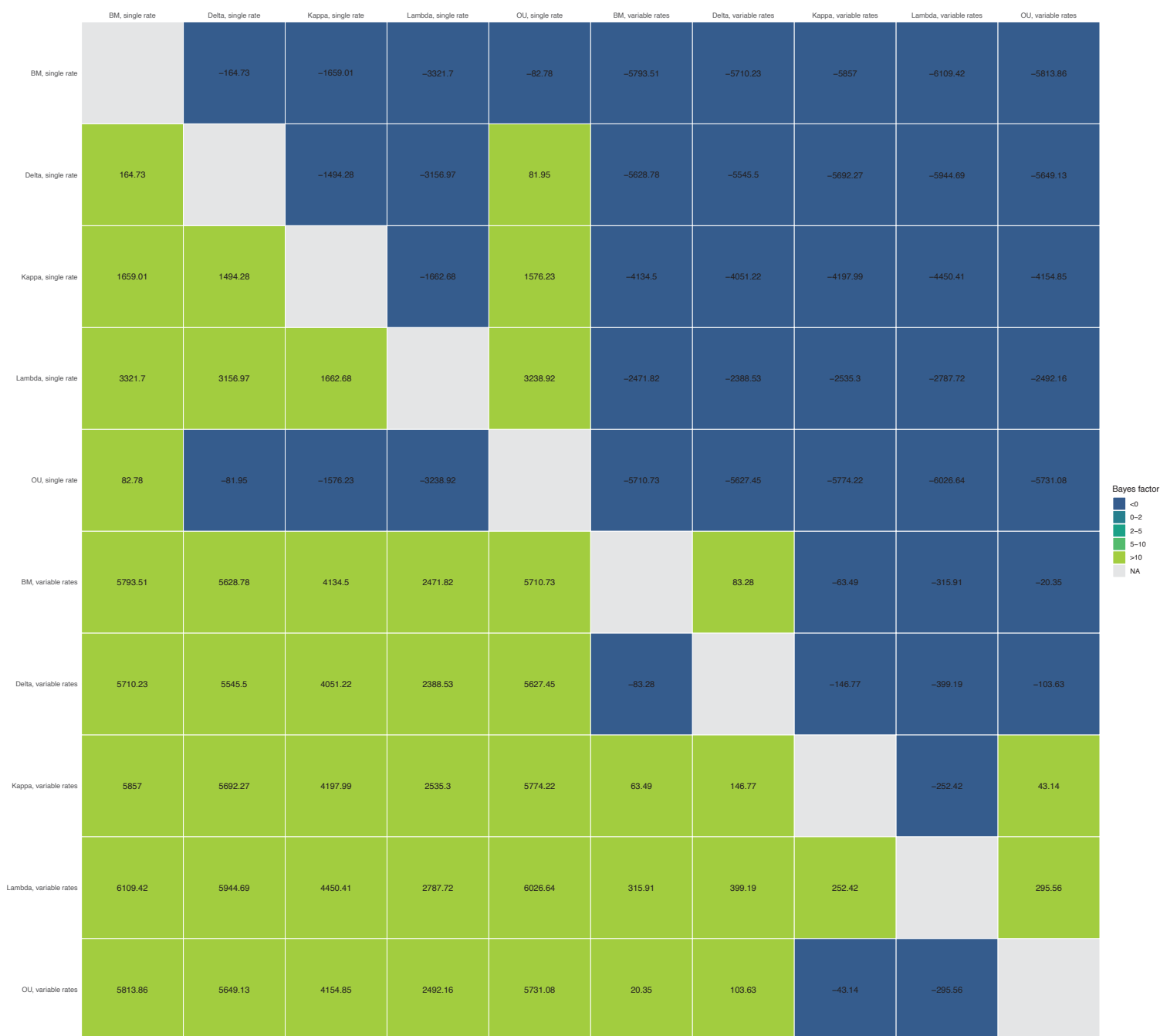


Fig. S3. F) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 1, Root Age = 95-100Ma.

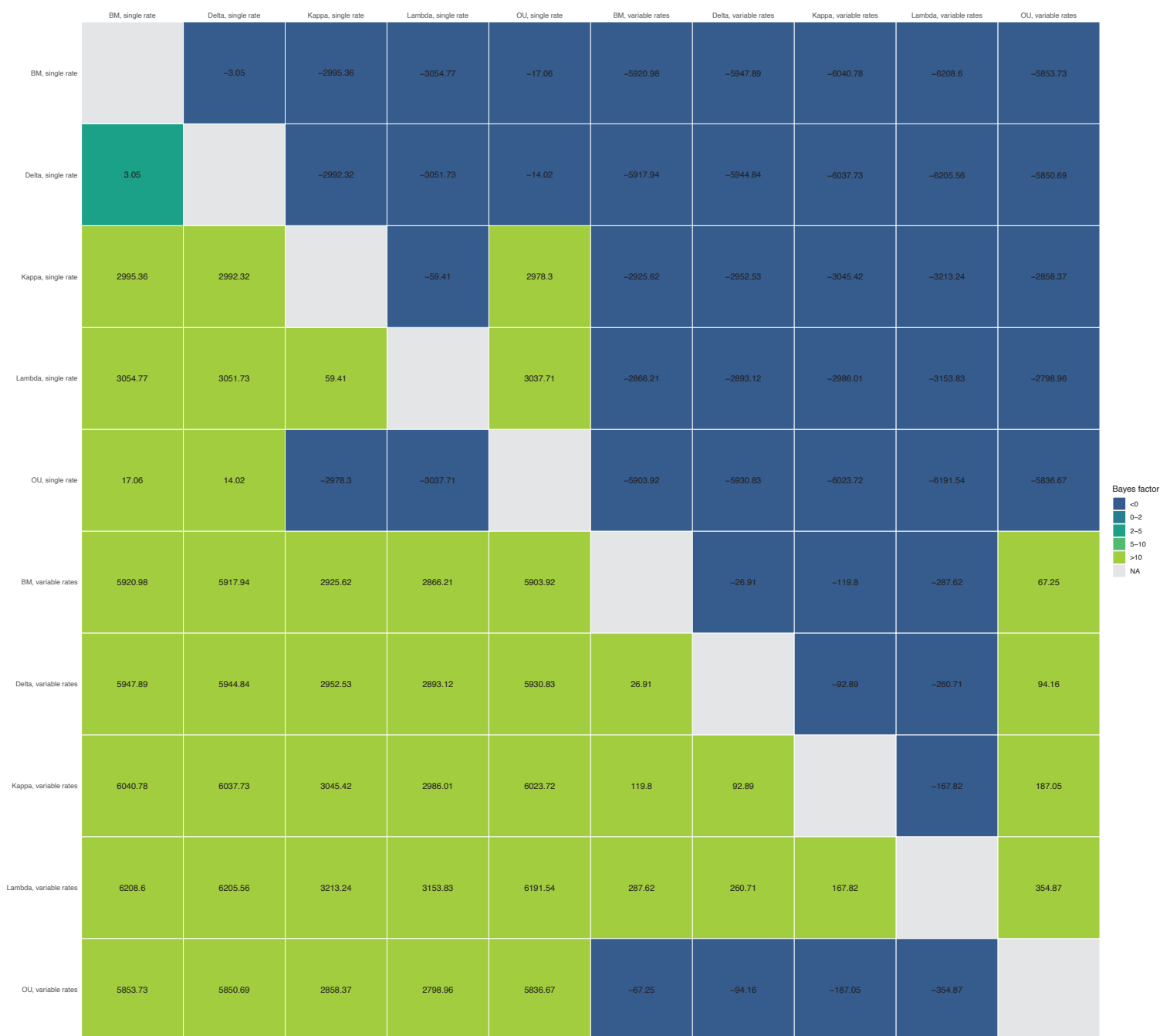


Fig. S3. G) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 2, Root Age = 70-75Ma.

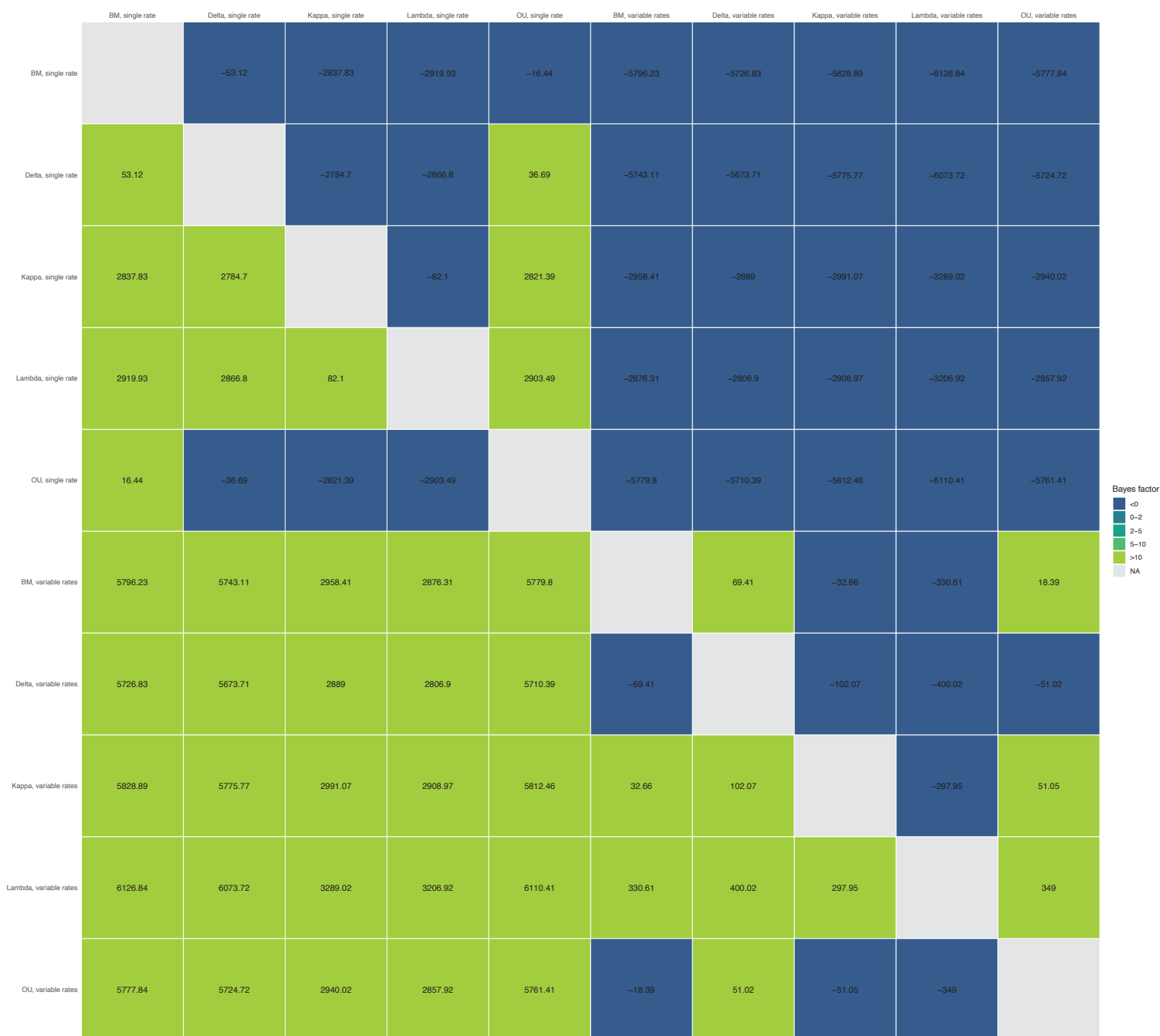


Fig. S3. H) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 2, Root Age = 75-80Ma.

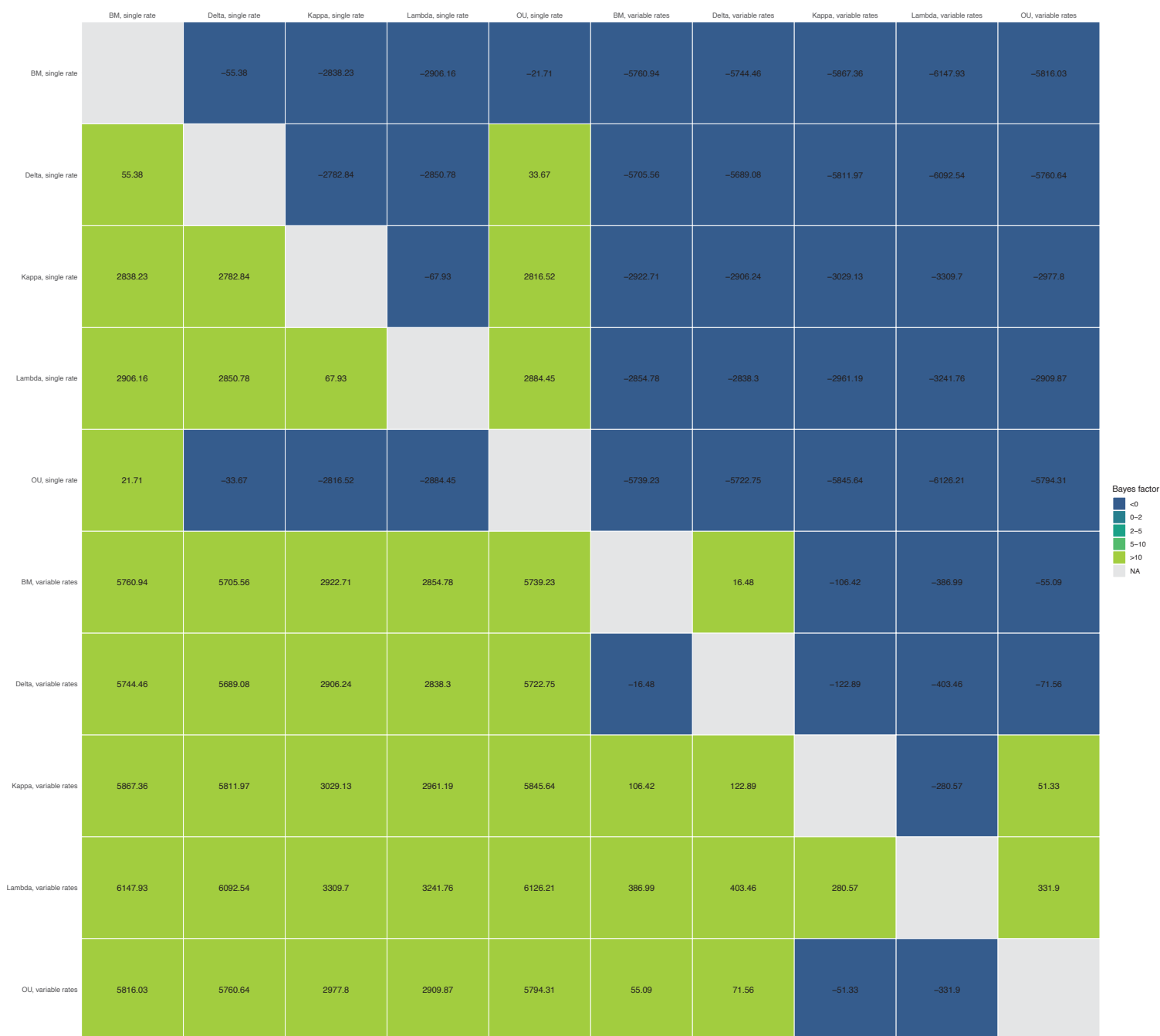


Fig. S3. I) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 2, Root Age = 80-85Ma.

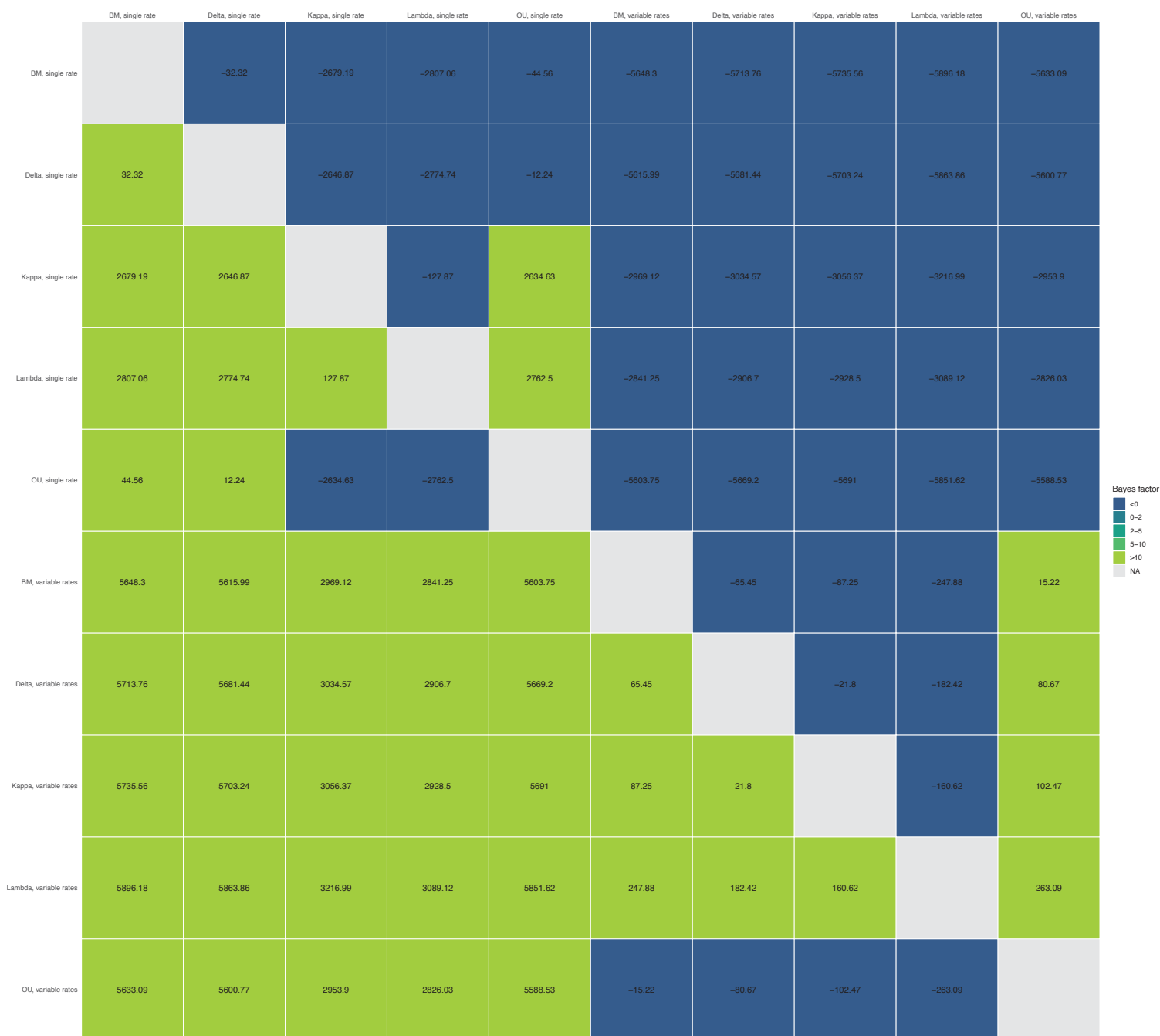


Fig. S3. J) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 2, Root Age = 85-90Ma.

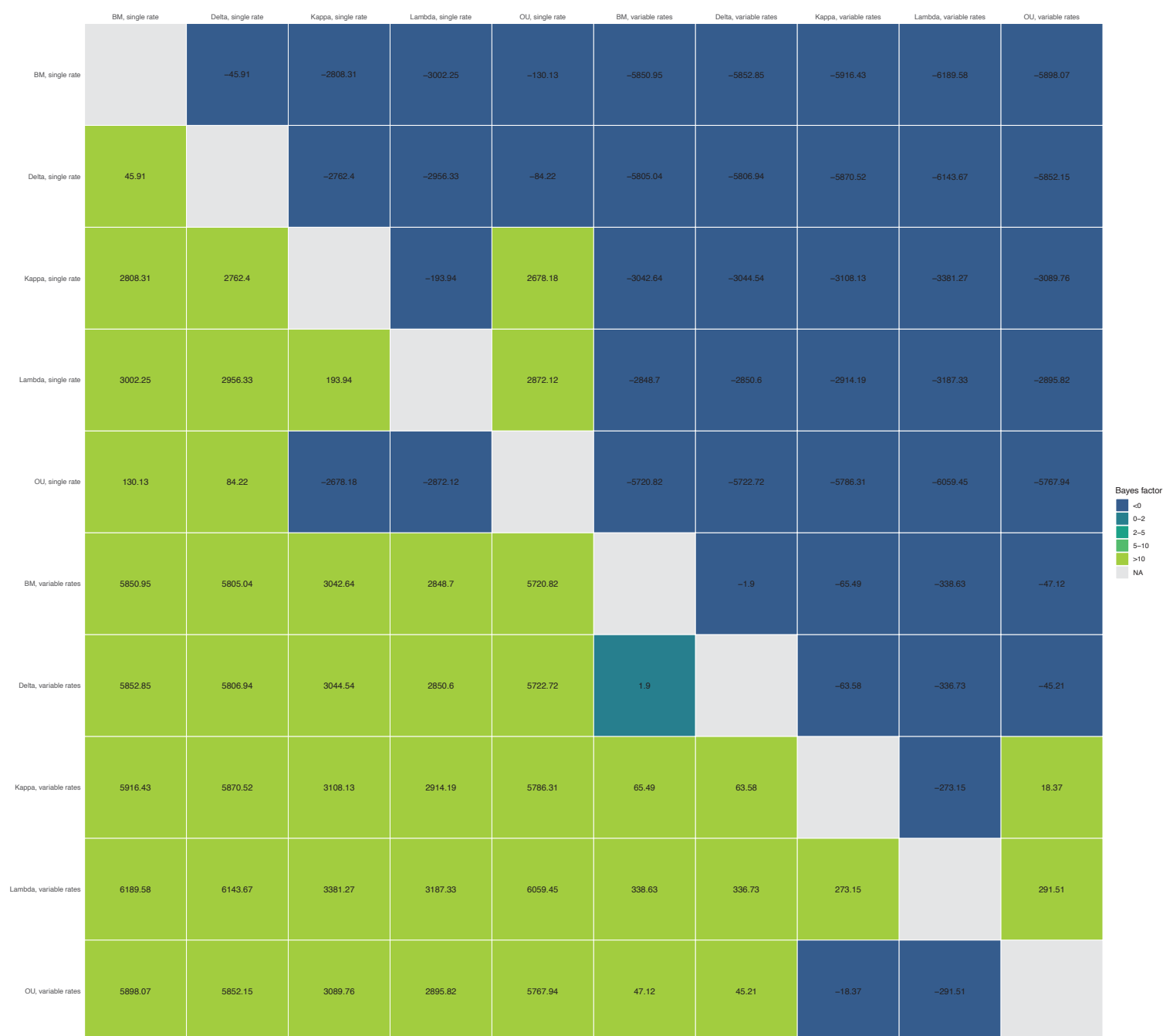


Fig. S3. K) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 2, Root Age = 90-95Ma.

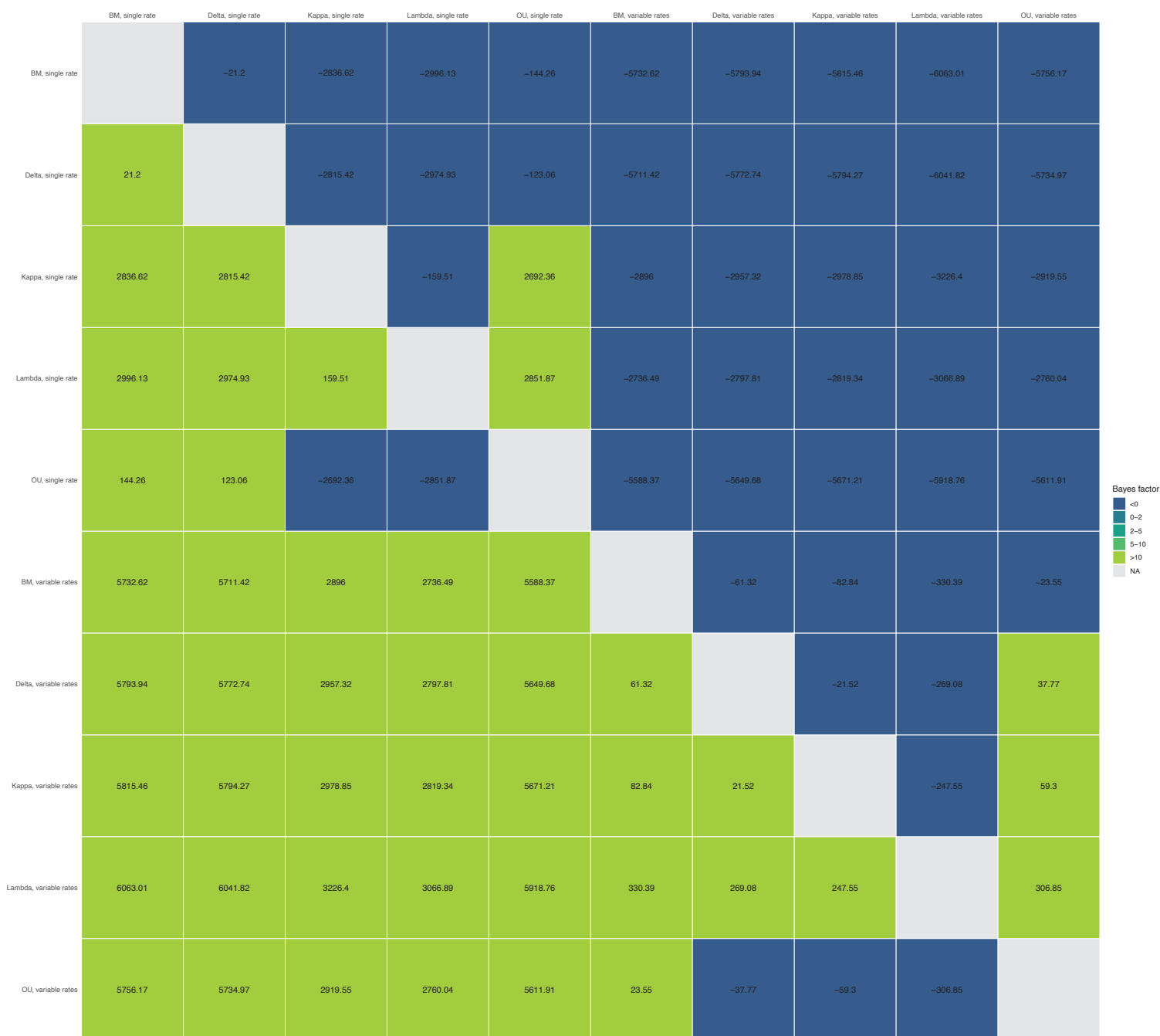


Fig. S3. L) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 2, Root Age = 95-100Ma.

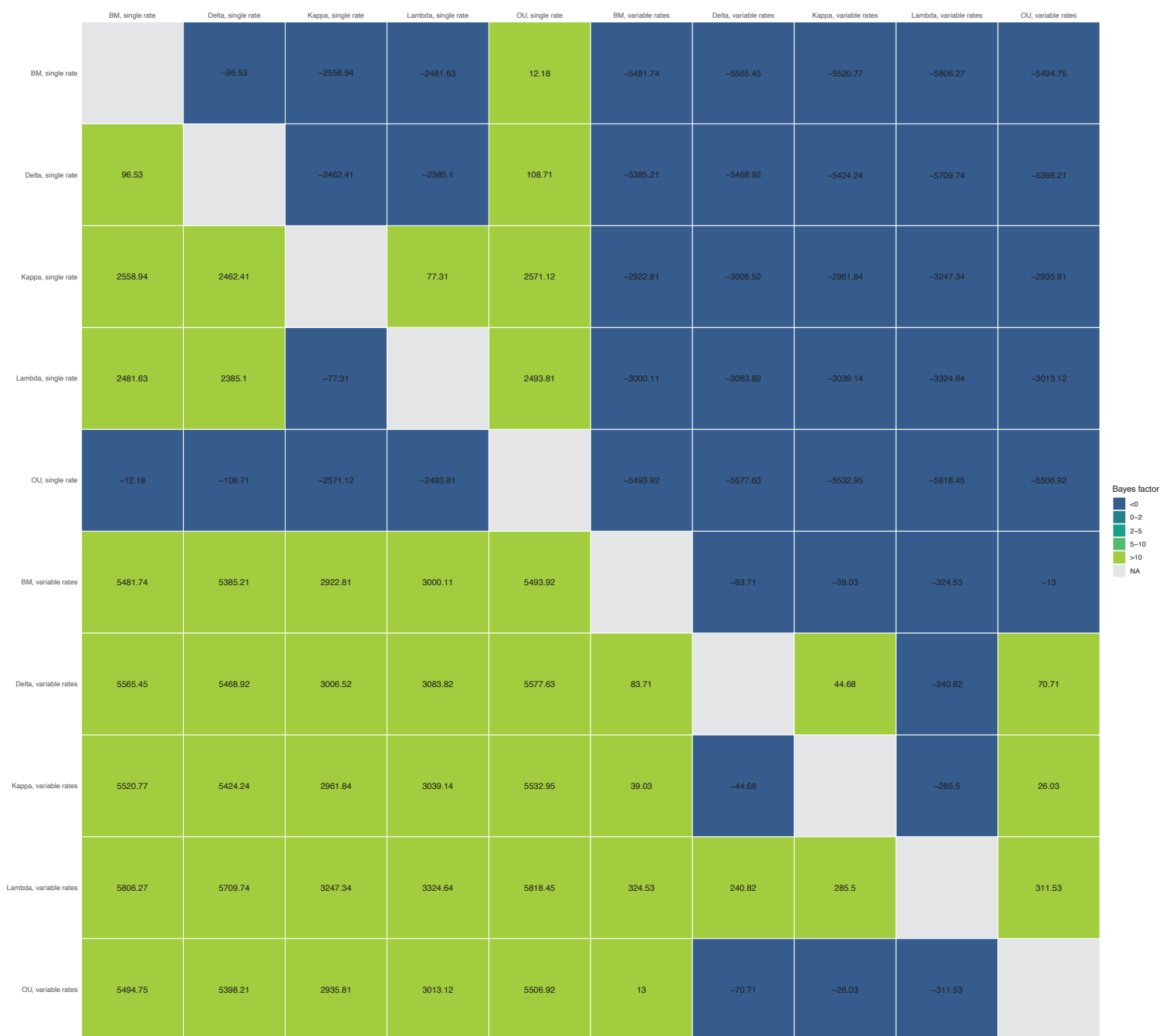


Fig. S3. M) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 3, Root Age = 70-75Ma.

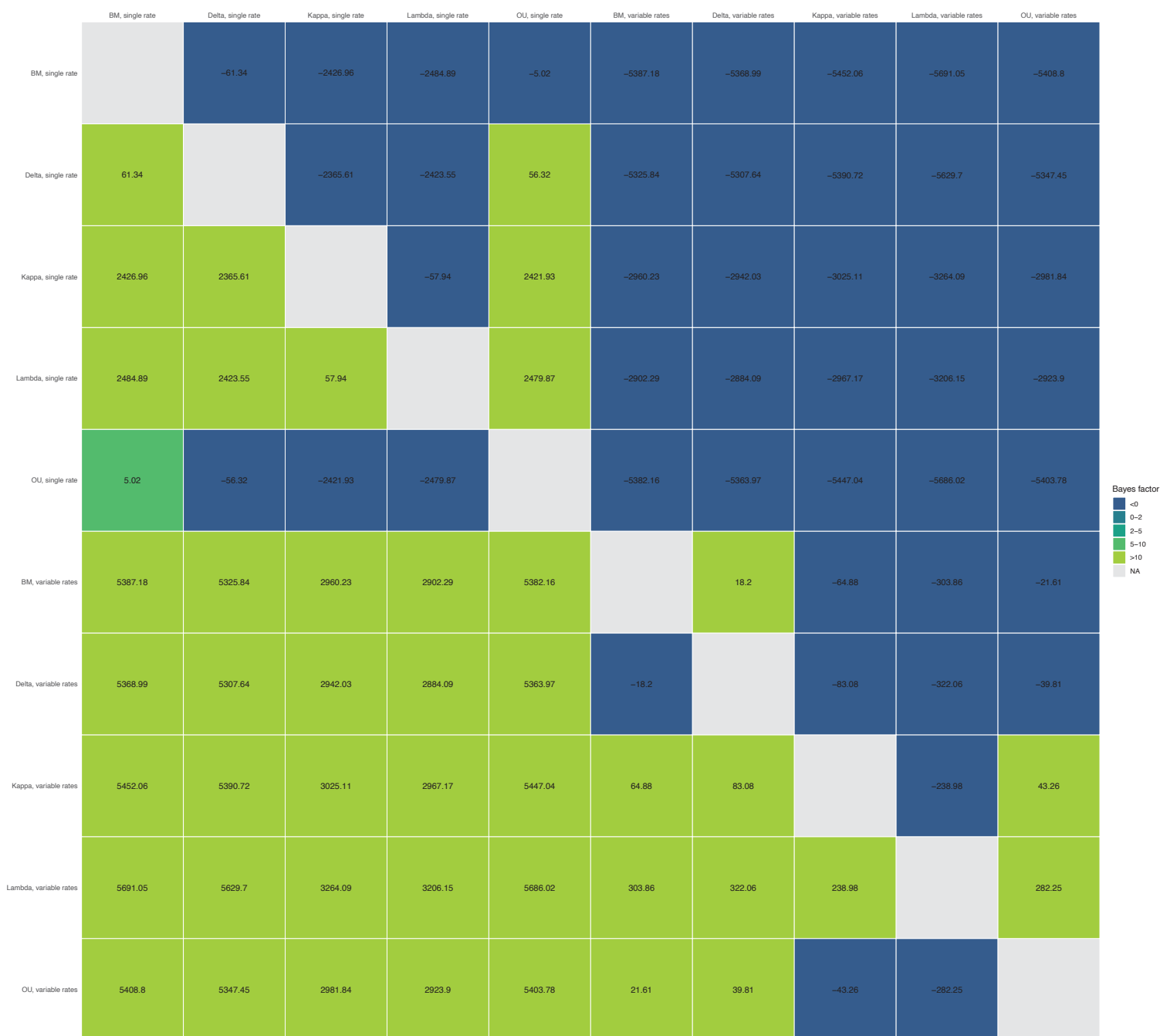


Fig. S3. N) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 3 Root Age = 75-80Ma.

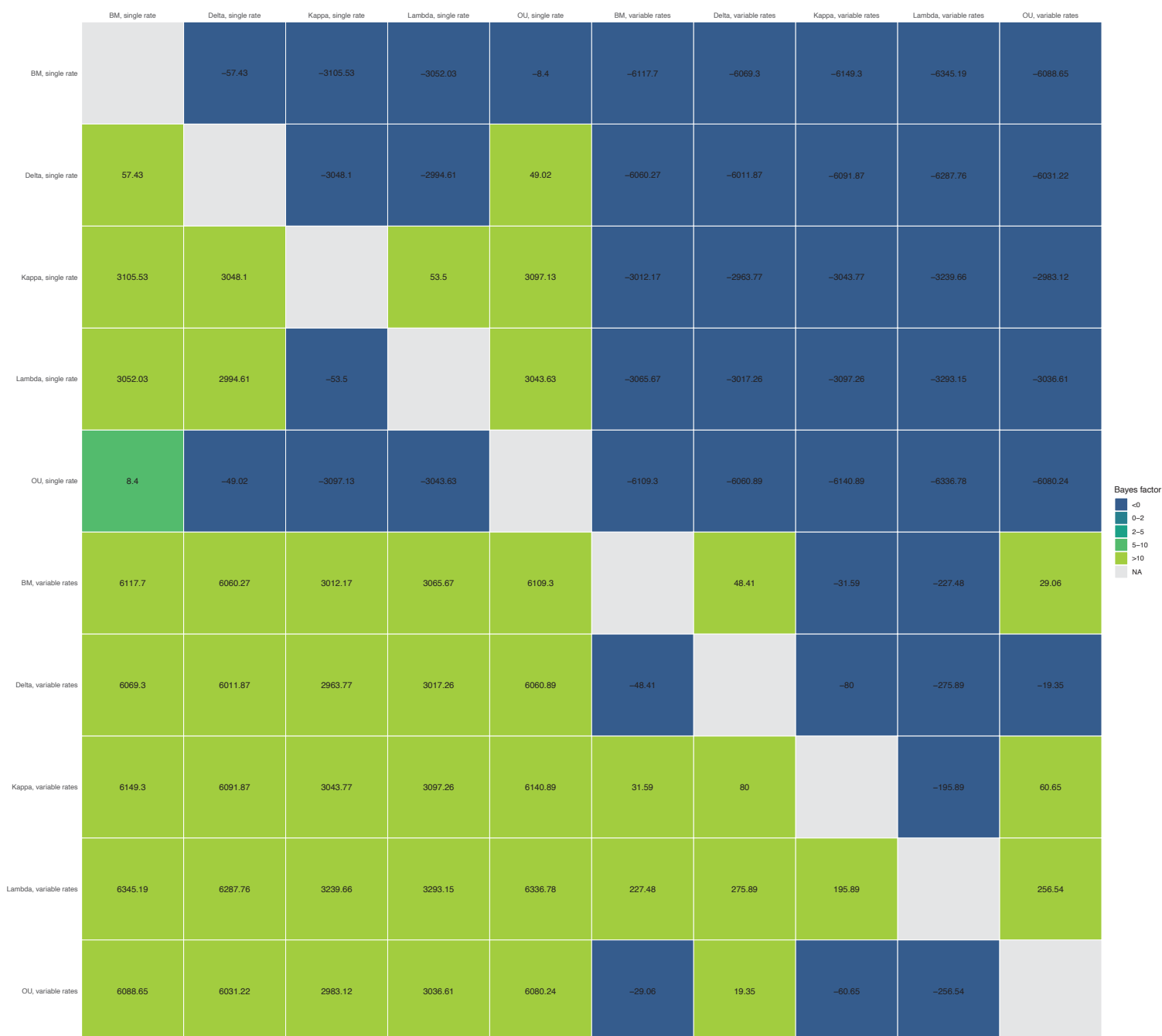


Fig. S3. O) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 3, Root Age = 80-85Ma.

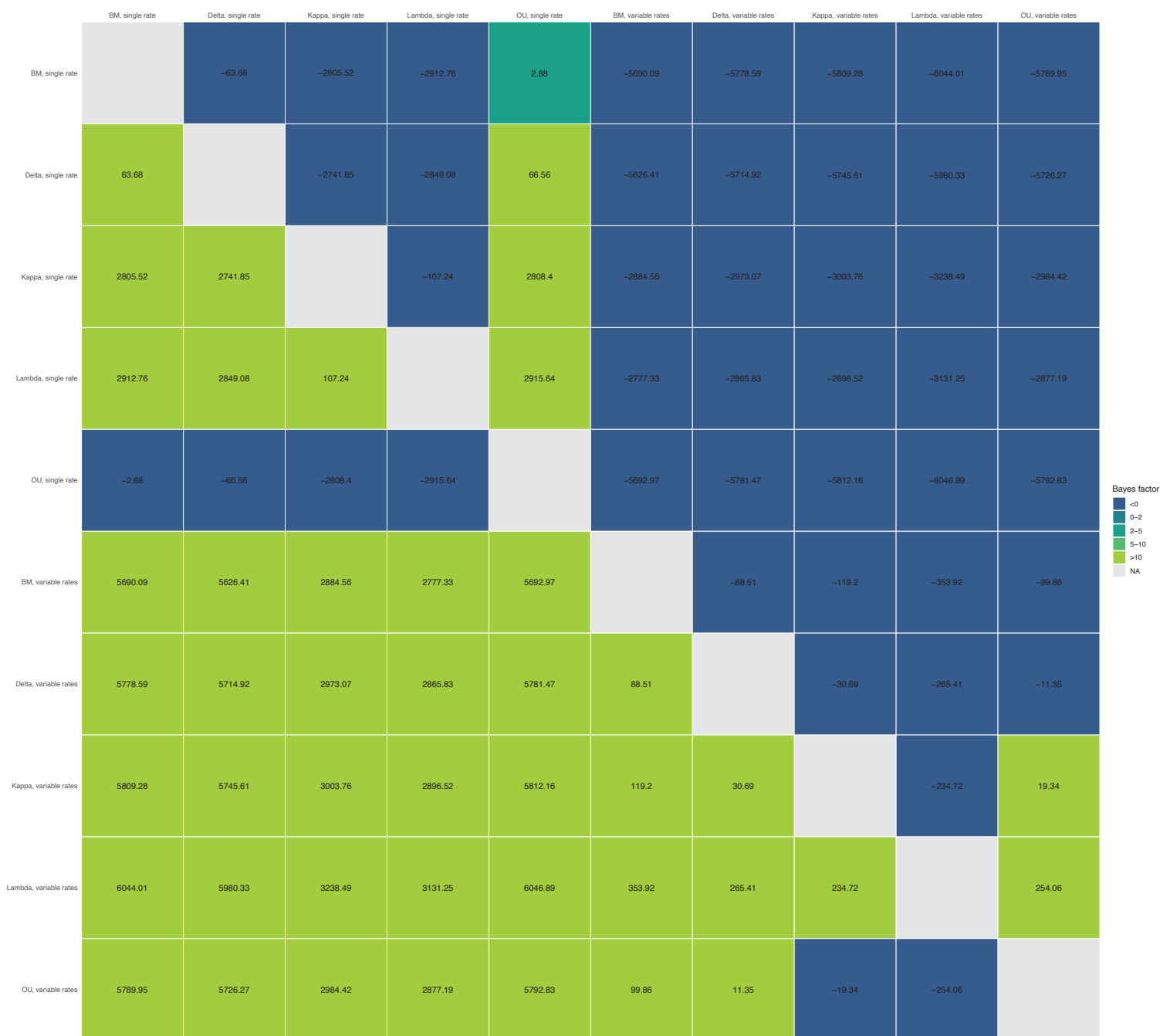


Fig. S3. P) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 3, Root Age = 85-90Ma.

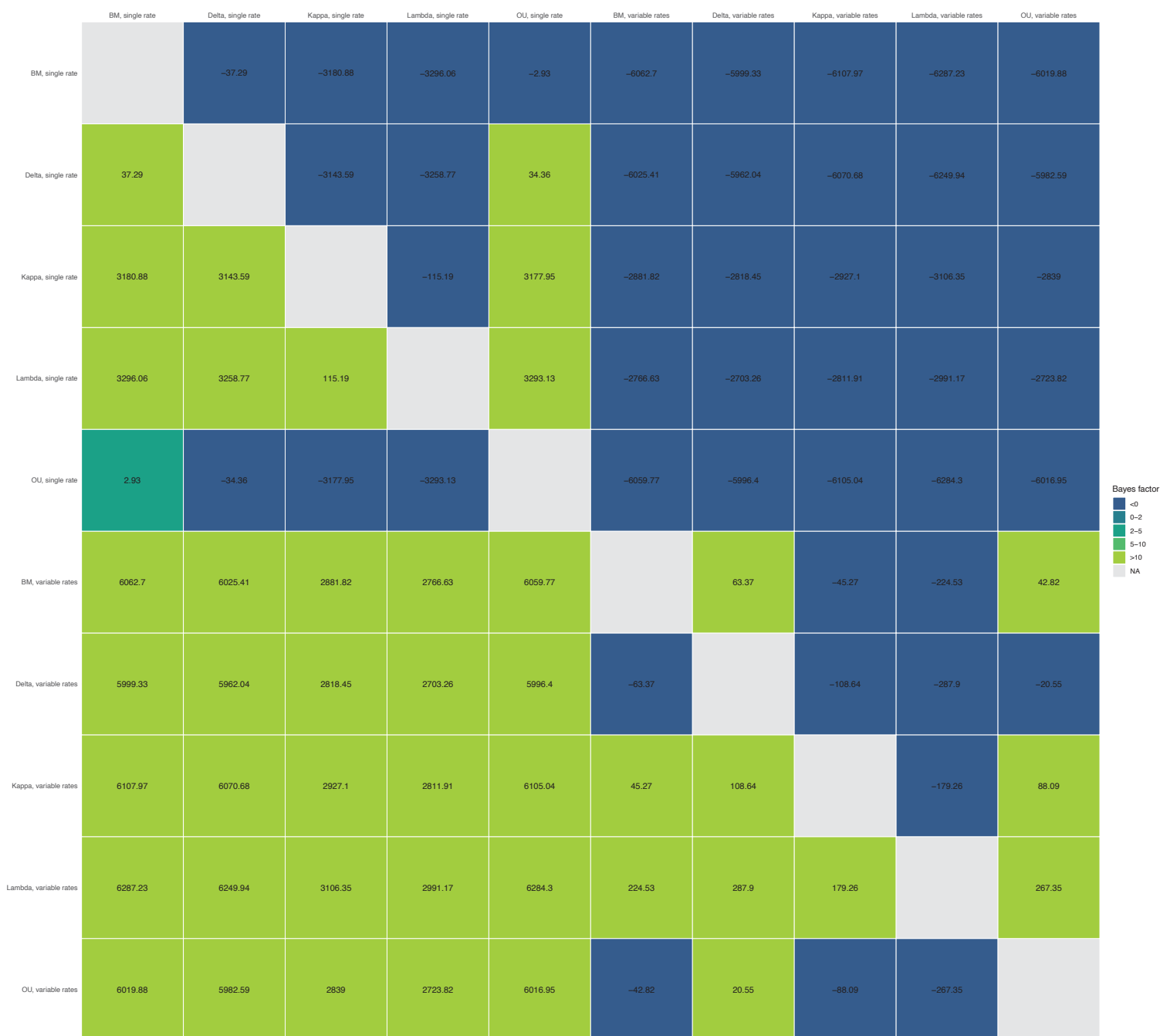


Fig. S3. Q) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 3, Root Age = 90-95Ma.

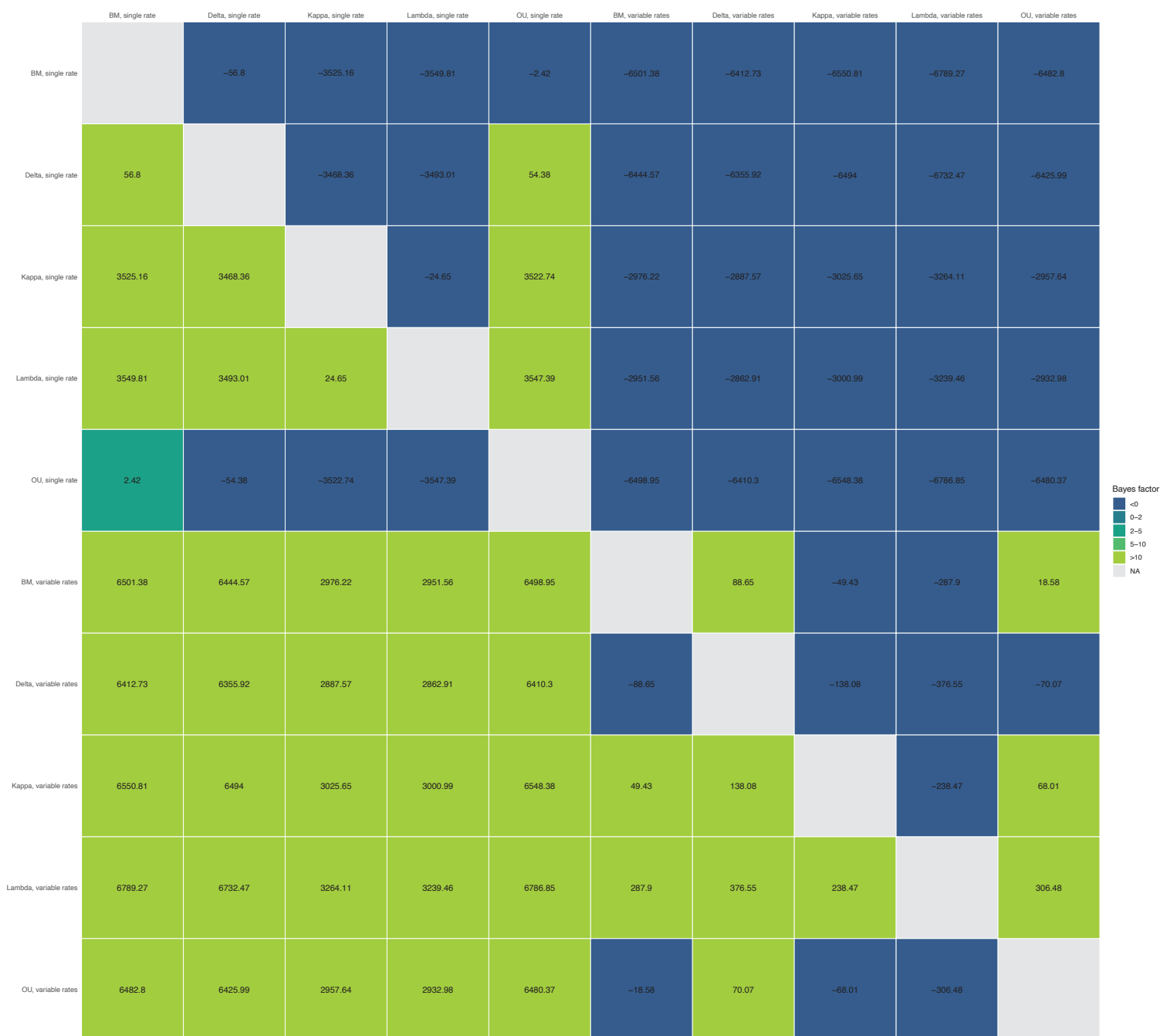


Fig. S3. R) Bayes Factor comparisons for 10 alternative evolutionary models for Tree Topology 3, Root Age = 95-100Ma.

Tree Topology 1: Root Age = 70 - 75 Ma

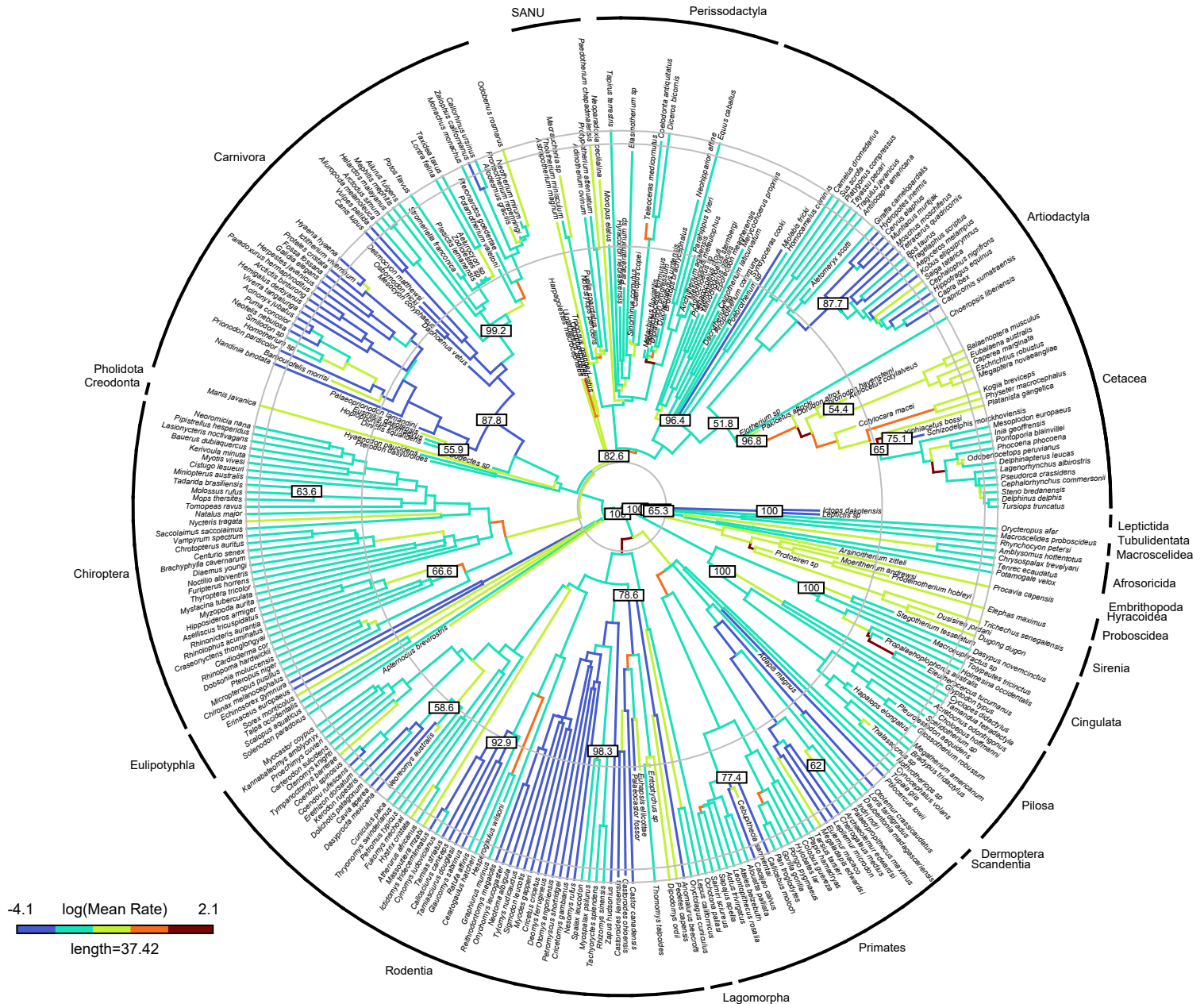


Fig. S4. A) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 1, Root Age = 70-75Ma.

Tree Topology 1: Root Age = 75 - 80 Ma

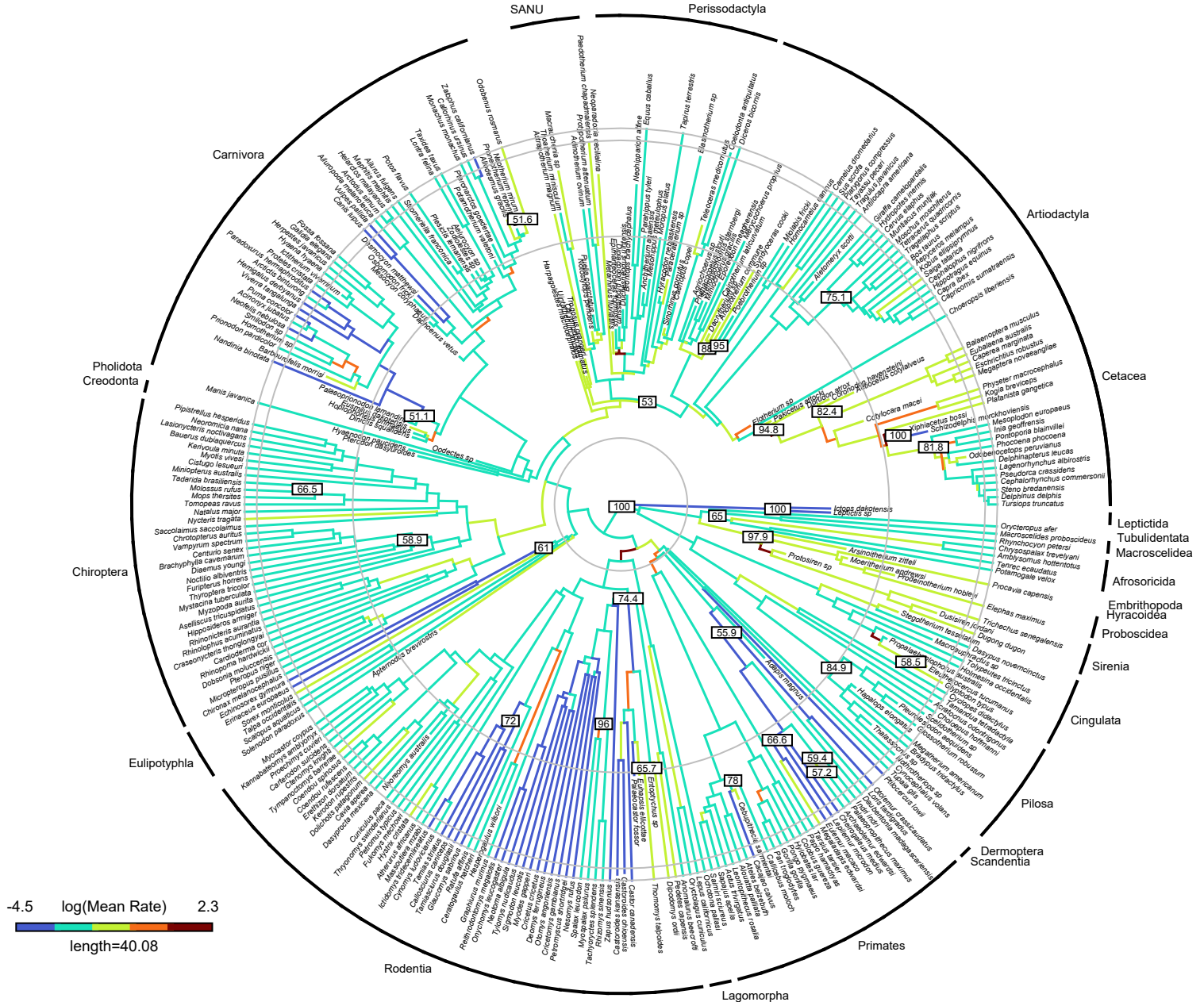


Fig. S4. B) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 1, Root Age = 75-80Ma.

Tree Topology 1: Root Age = 80 - 85 Ma

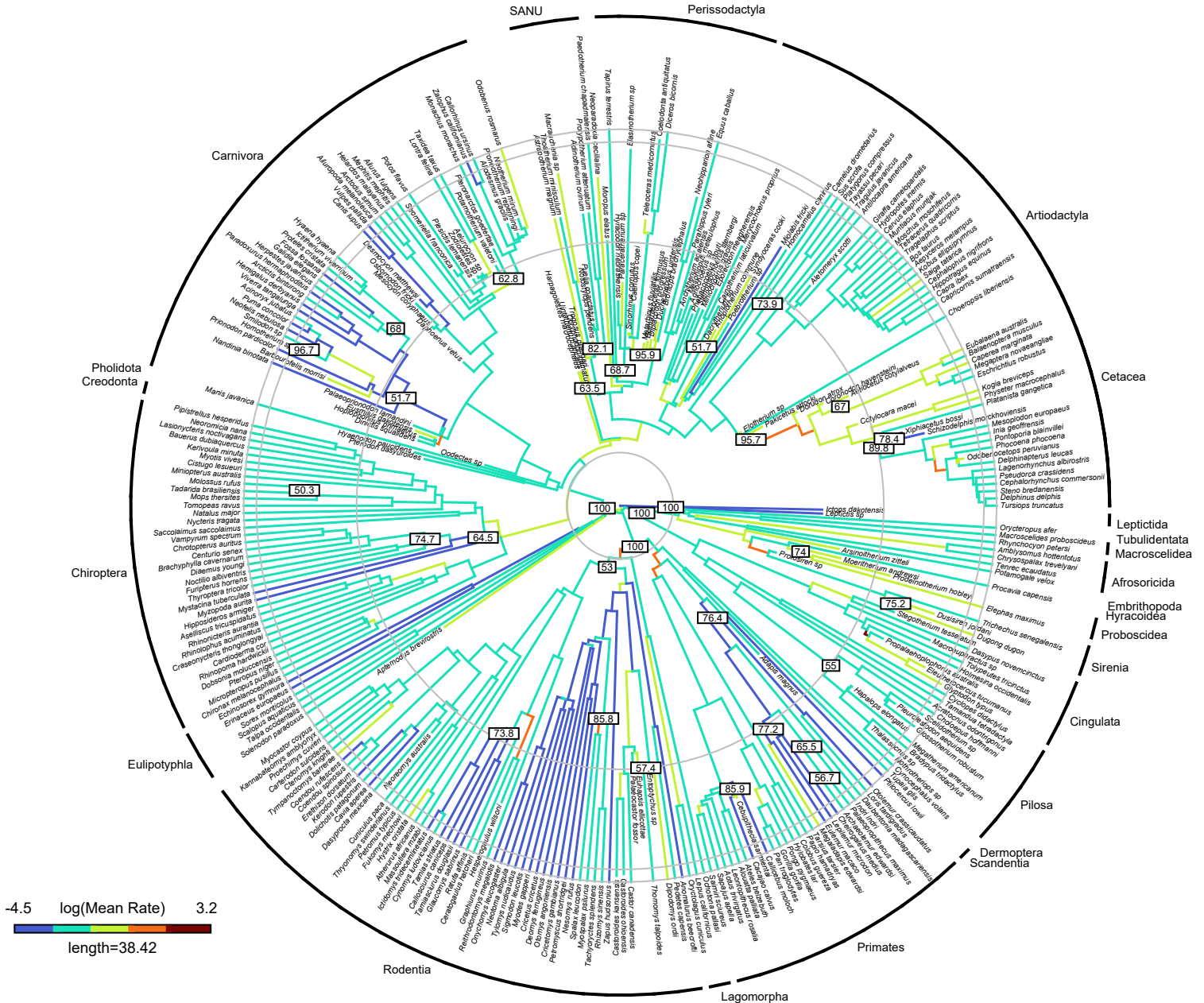
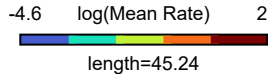


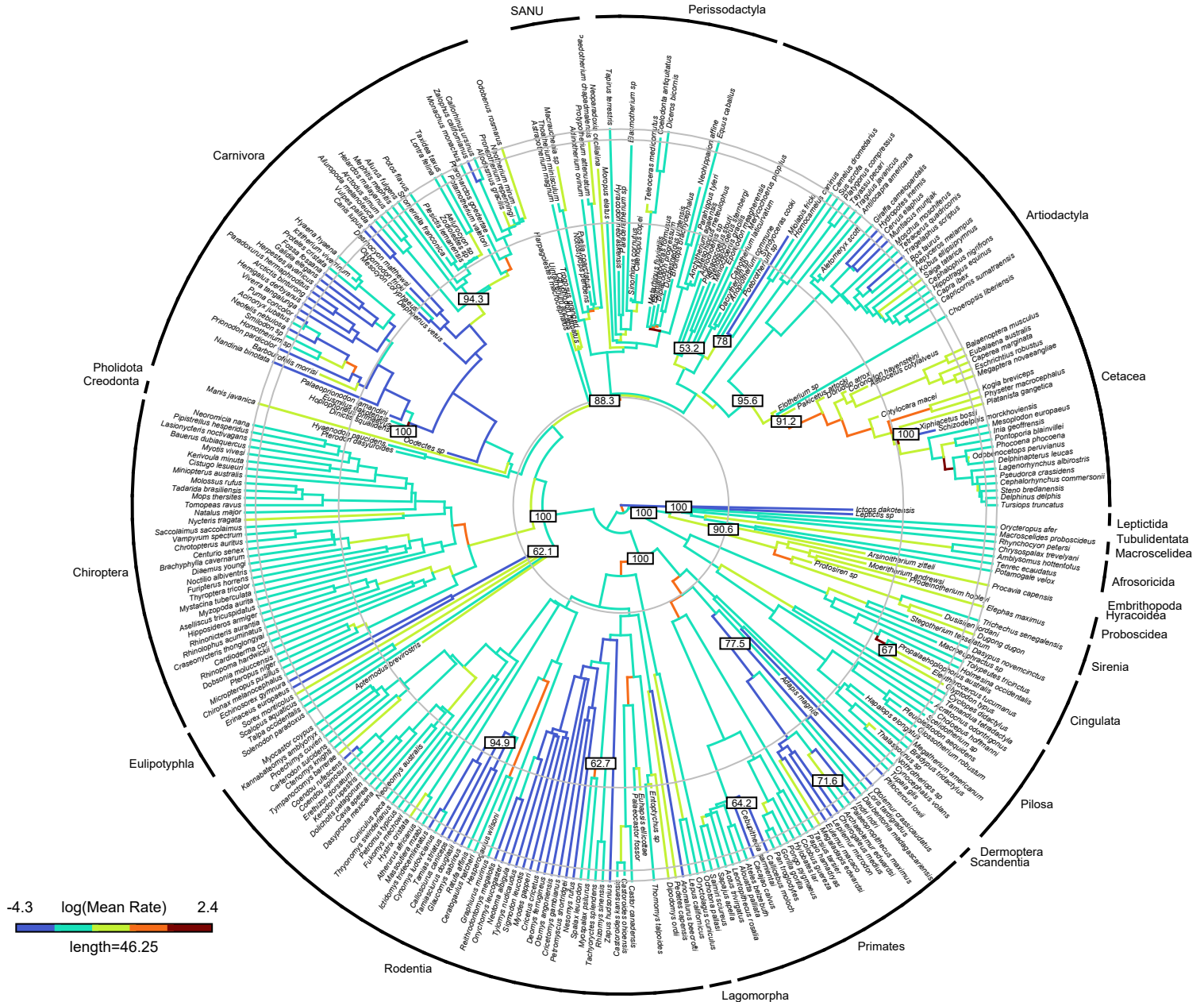
Fig. S4. C) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 1, Root Age = 80-85 Ma.

SANU Perissodactyla



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Tree Topology 1: Root Age = 90 - 95 Ma



Tree Topology 2: Root Age = 80 - 85 Ma

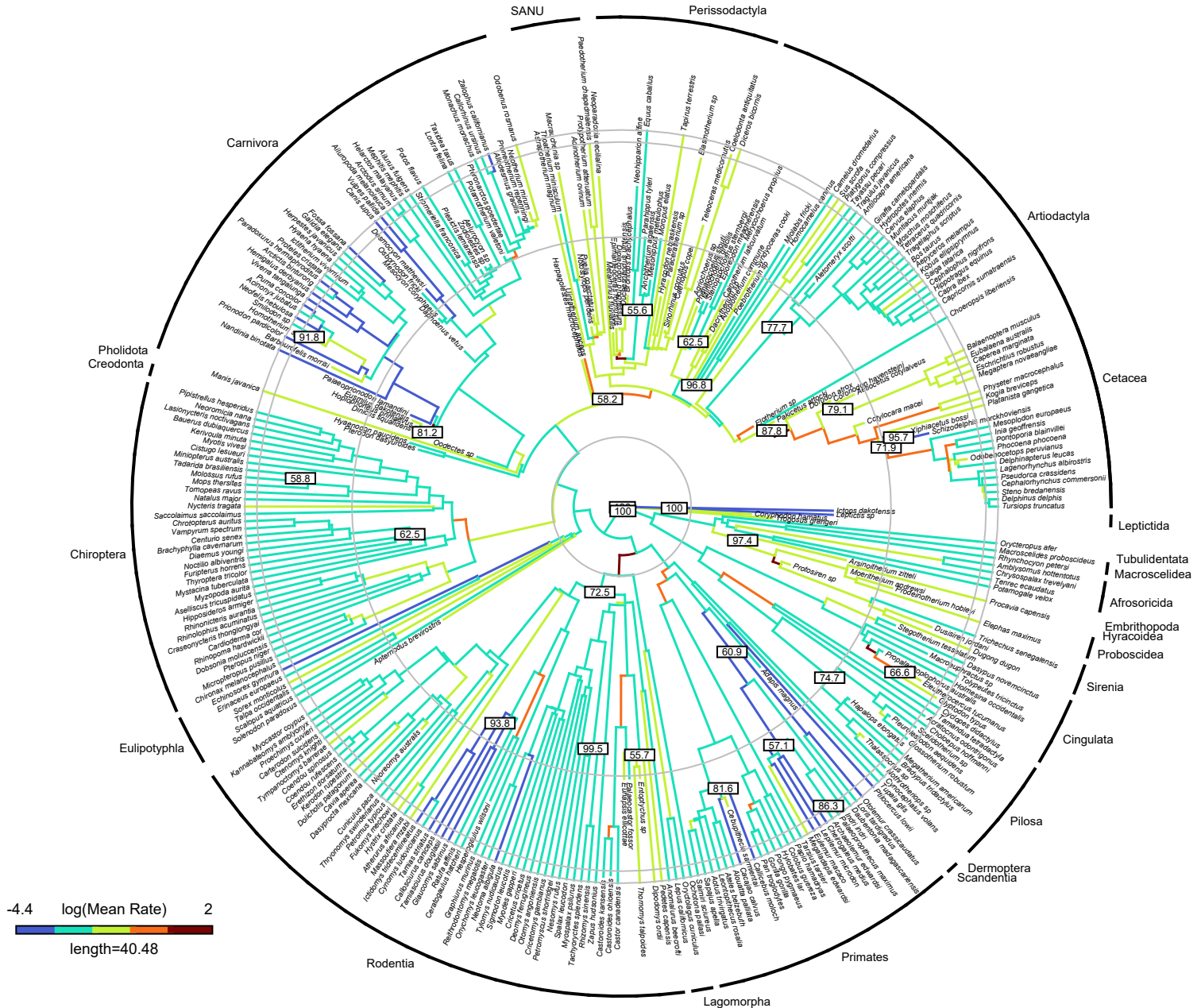


Fig. S4.1) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 2, Root Age = 80-85 Ma.

Tree Topology 2: Root Age = 85 - 90 Ma

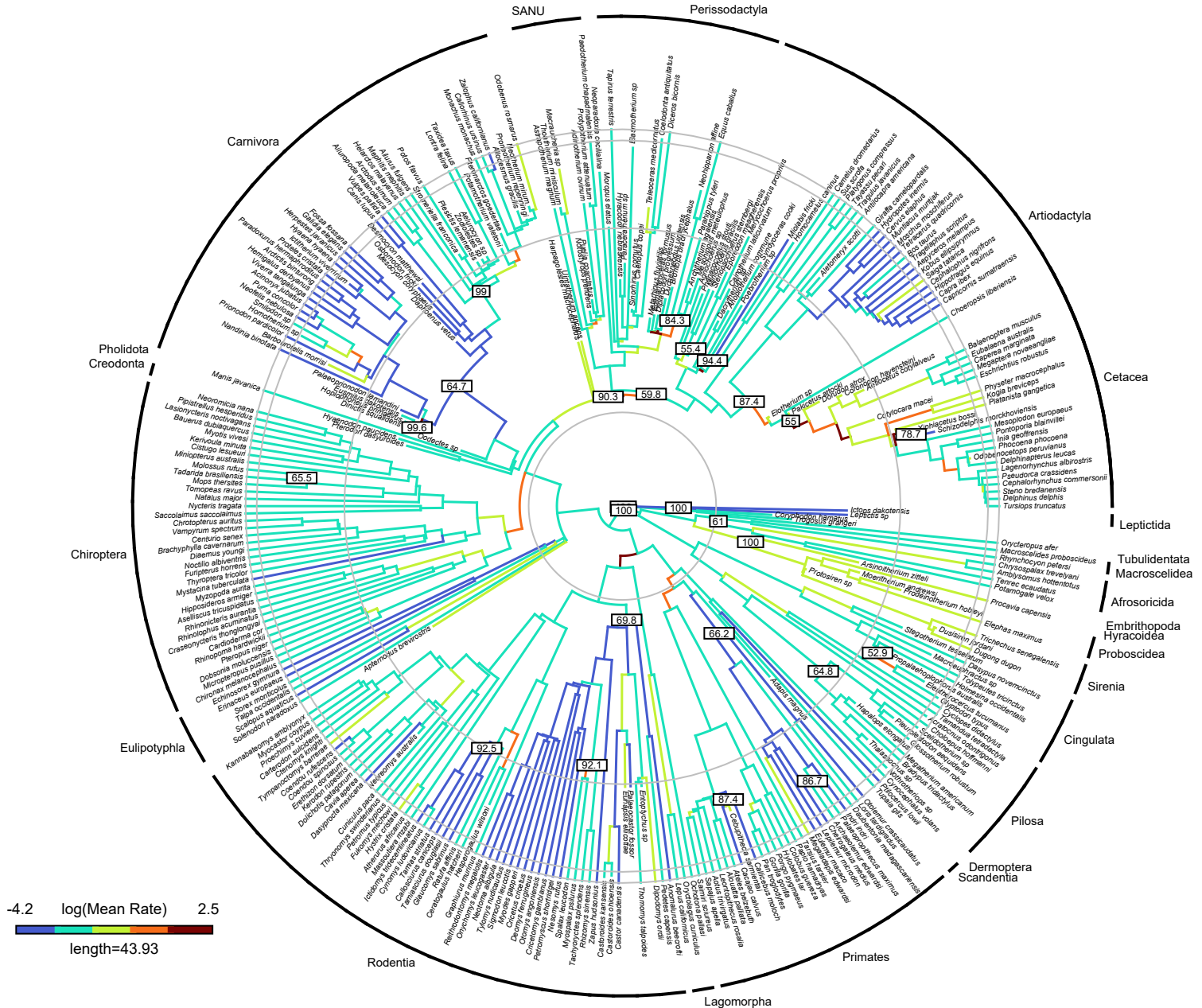


Fig. S4. J) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 2, Root Age = 85-90Ma.

Tree Topology 2: Root Age = 90 - 95 Ma

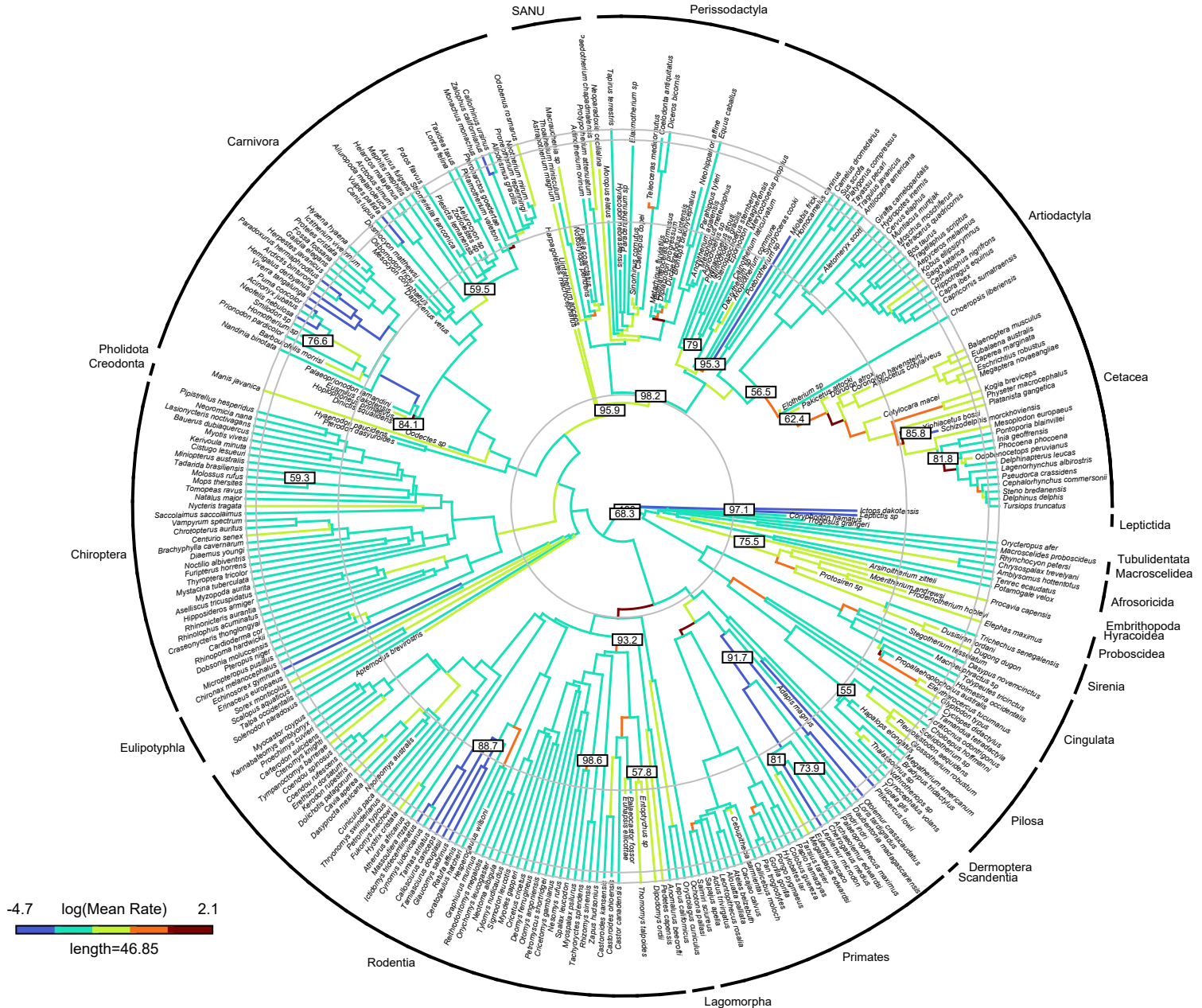


Fig. S4. K) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 2, Root Age = 90-95Ma.

Tree Topology 3: Root Age = 70 - 75 Ma

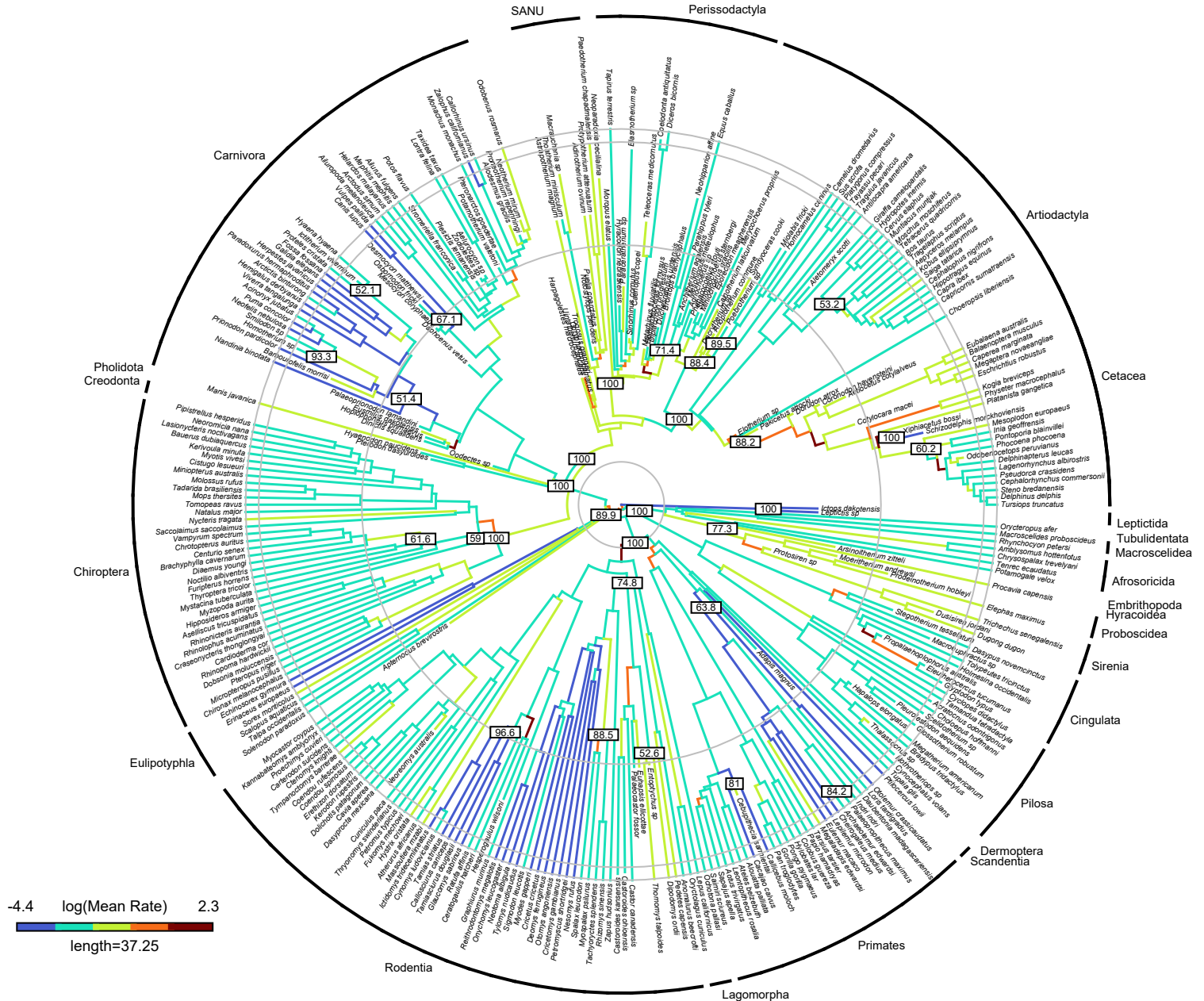


Fig. S4. M) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 3, Root Age = 70-75Ma.

Tree Topology 3: Root Age = 75 - 80 Ma

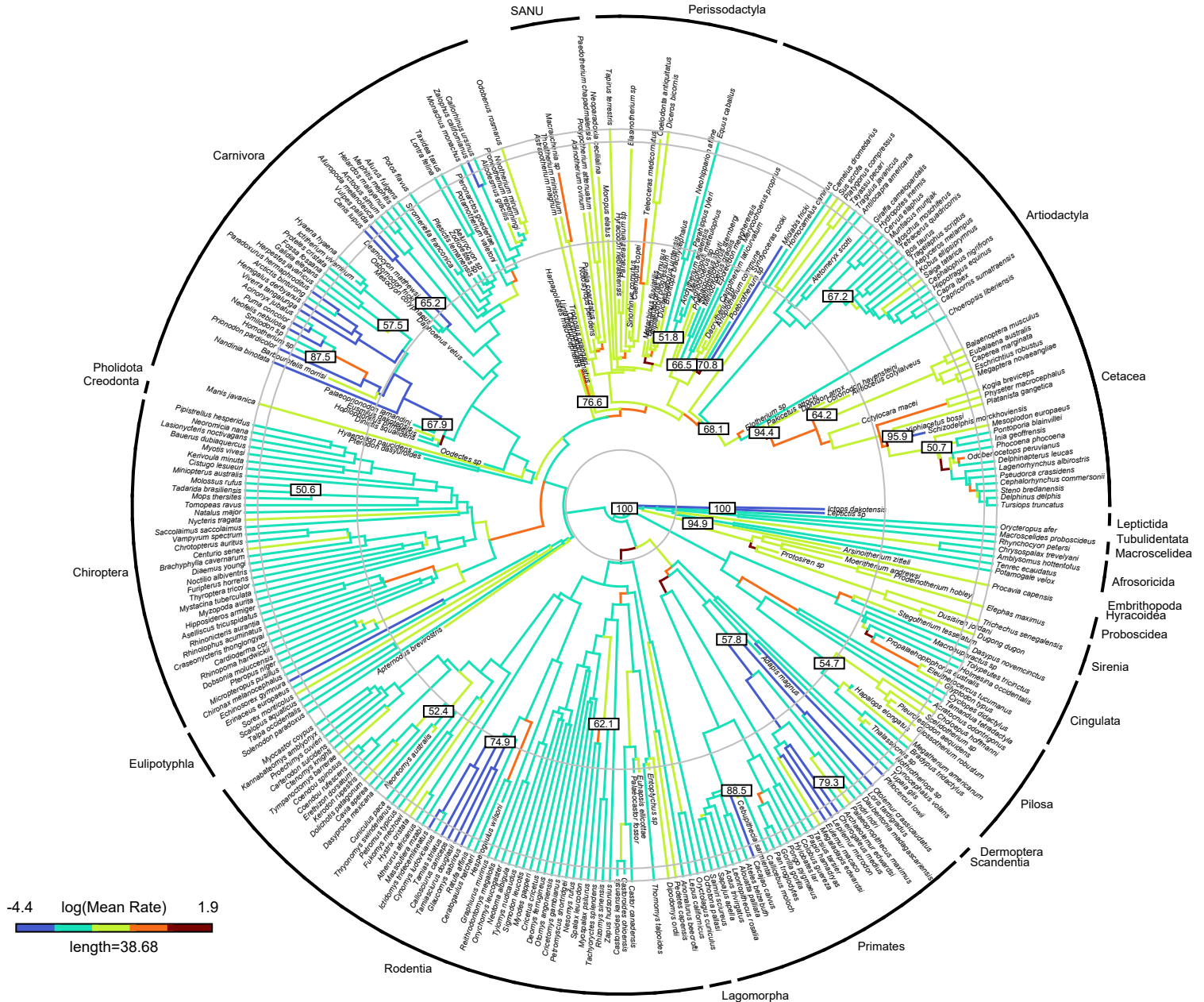


Fig. S4. N) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 3, Root Age = 75-80Ma.

Tree Topology 3: Root Age = 80 - 85 Ma

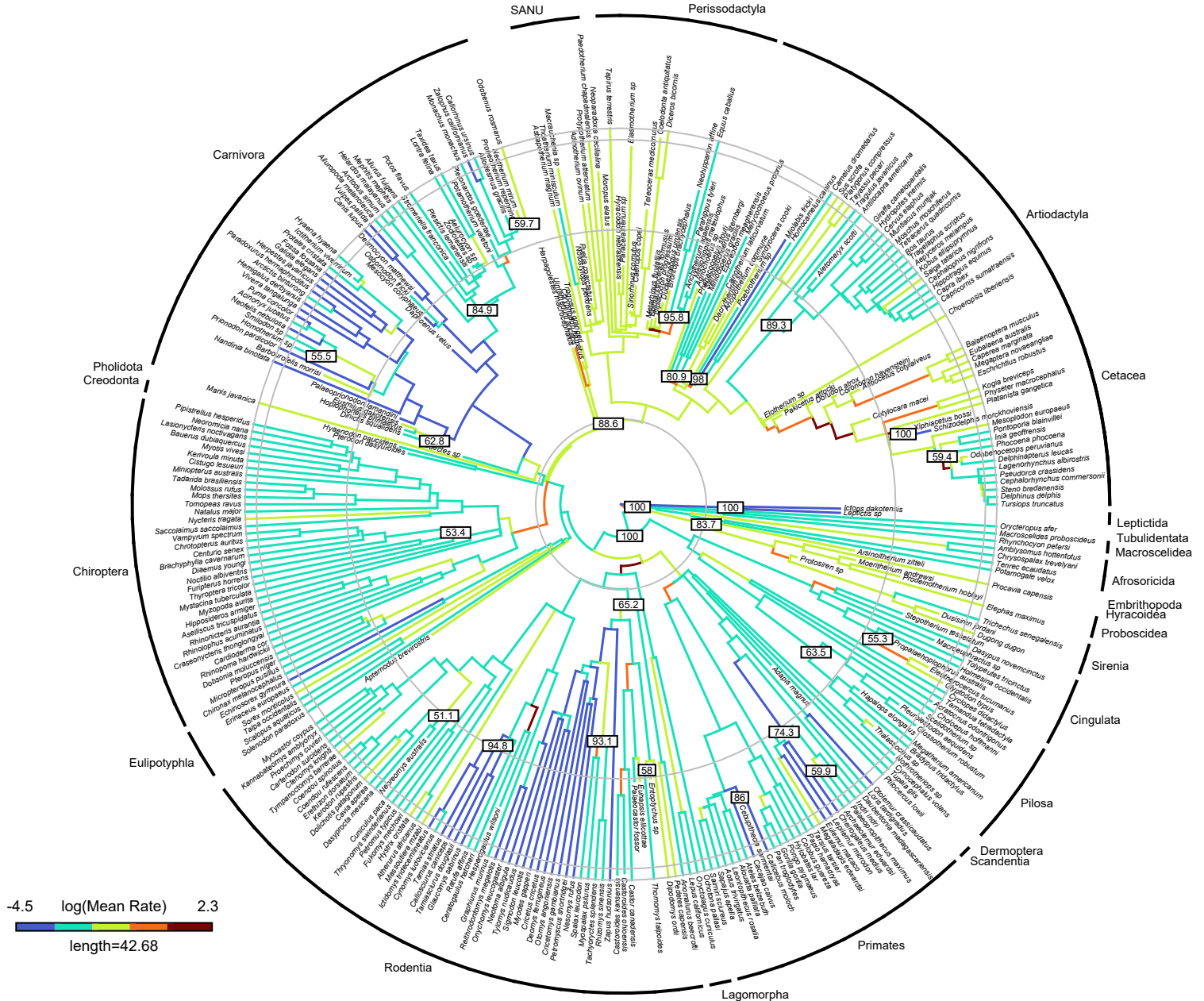


Fig. S4. O) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 3, Root Age = 80-85Ma.

Tree Topology 3: Root Age = 85 - 90 Ma

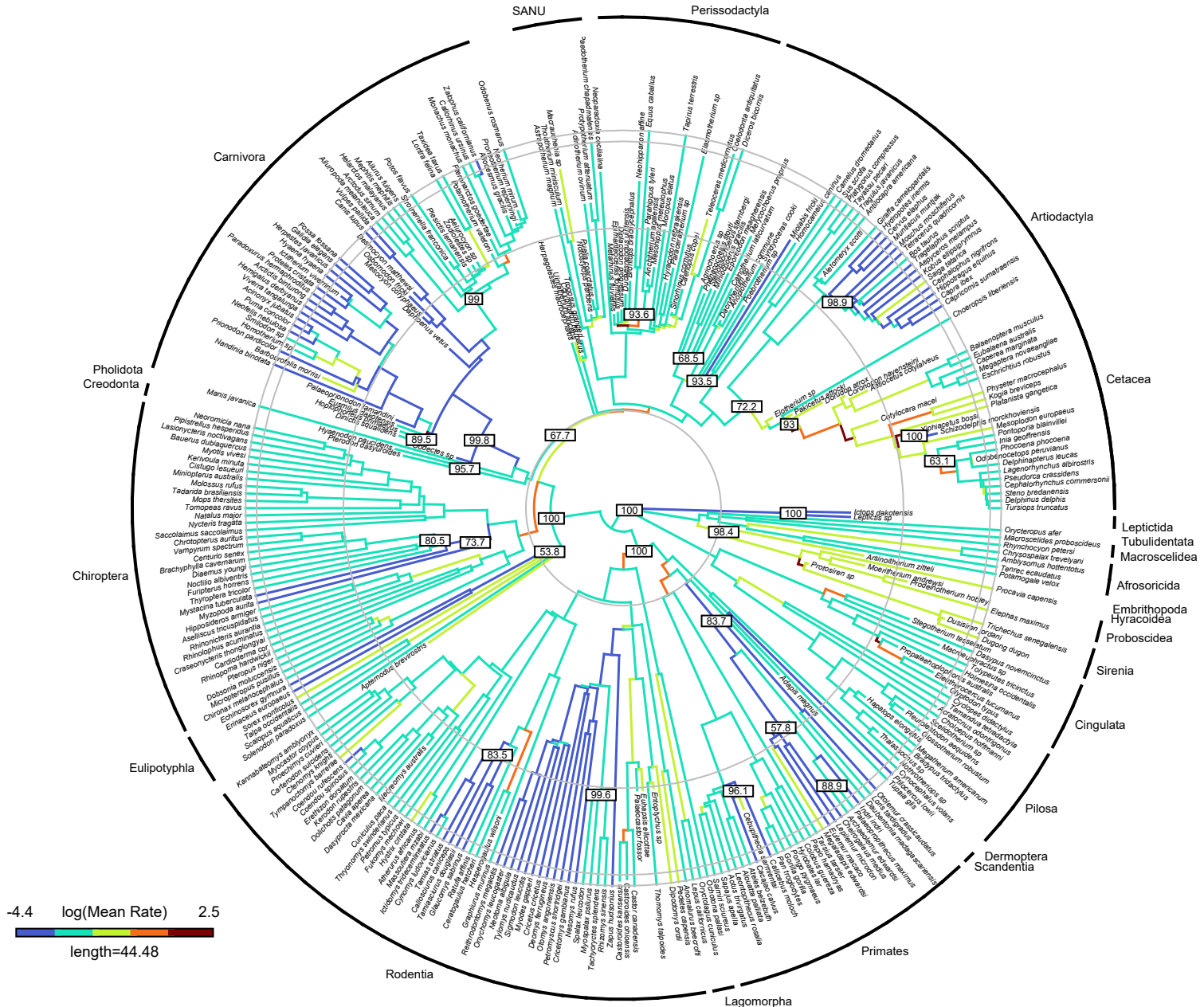


Fig. S4. P) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 3, Root Age = 85-90Ma.

Tree Topology 3: Root Age = 95 - 100 Ma

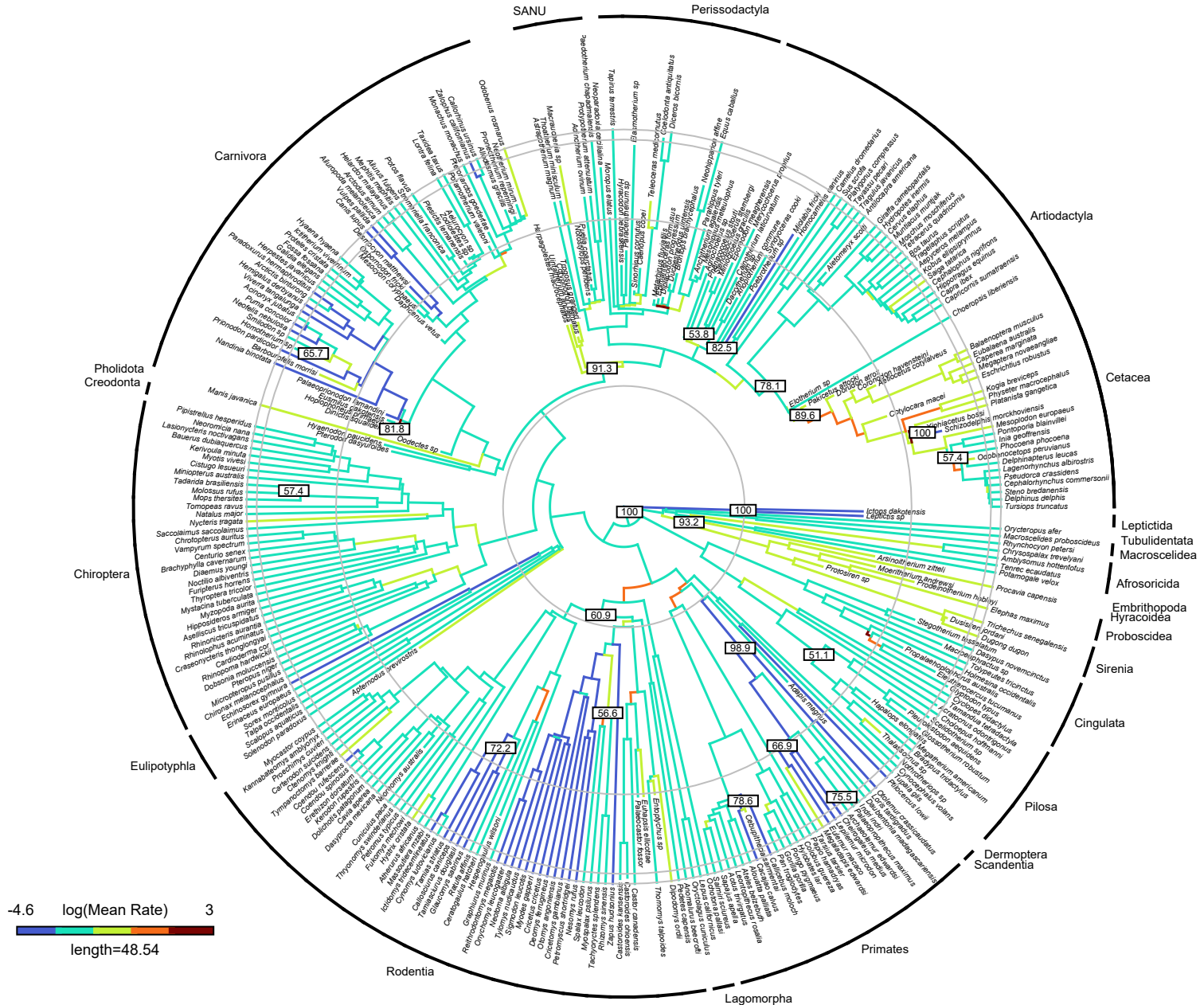


Fig. S4. R) Estimated branch-specific rates of cranial evolution using a variable-rates Brownian motion model with a lambda tree transformation for Tree Topology 3, Root Age = 95-100Ma.

Tree Topology 1: Root Age 70–75 Ma

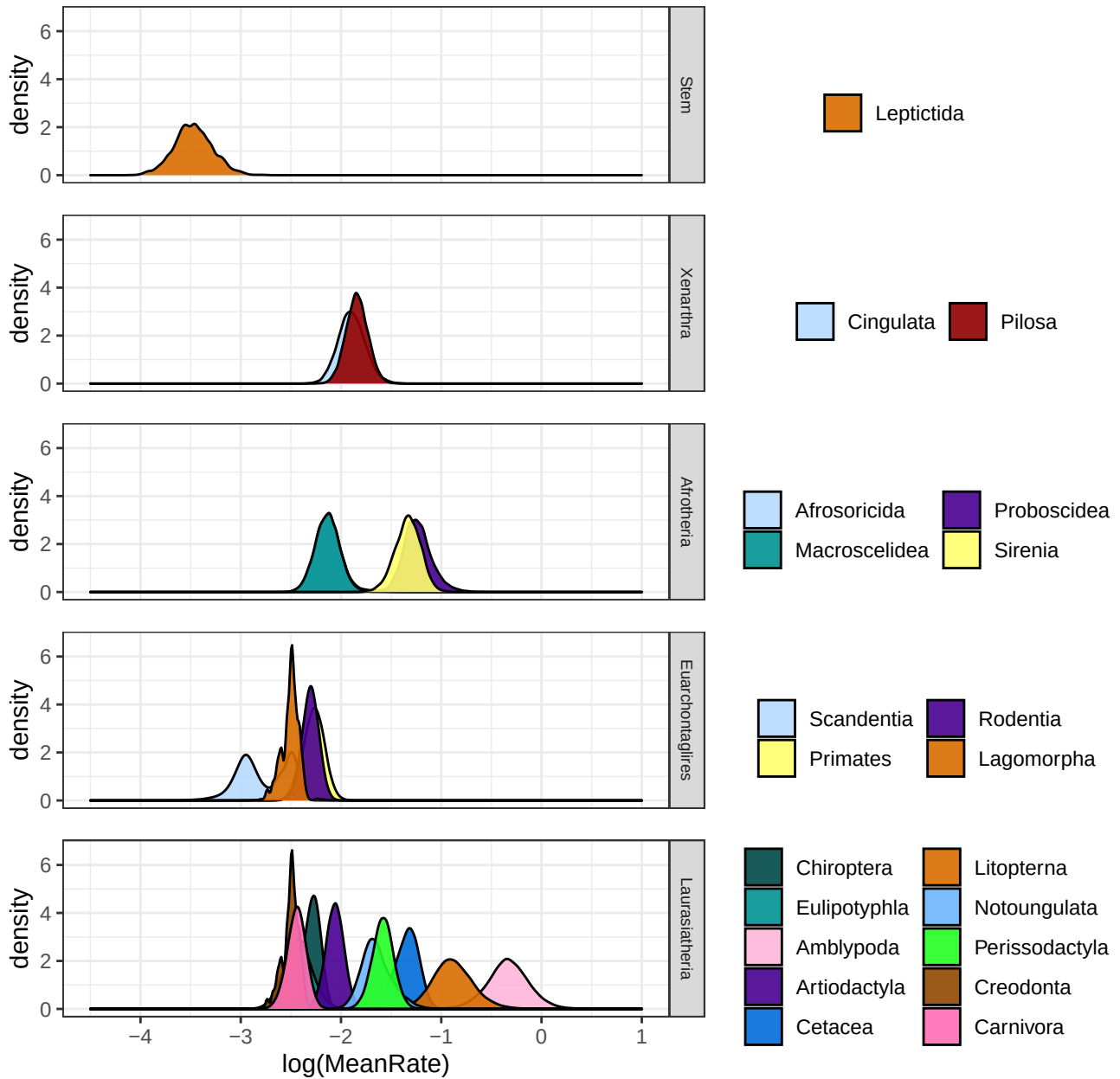


Fig. S5. A) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 1, Root Age = 70-75Ma.

Tree Topology 1: Root Age 75–80 Ma

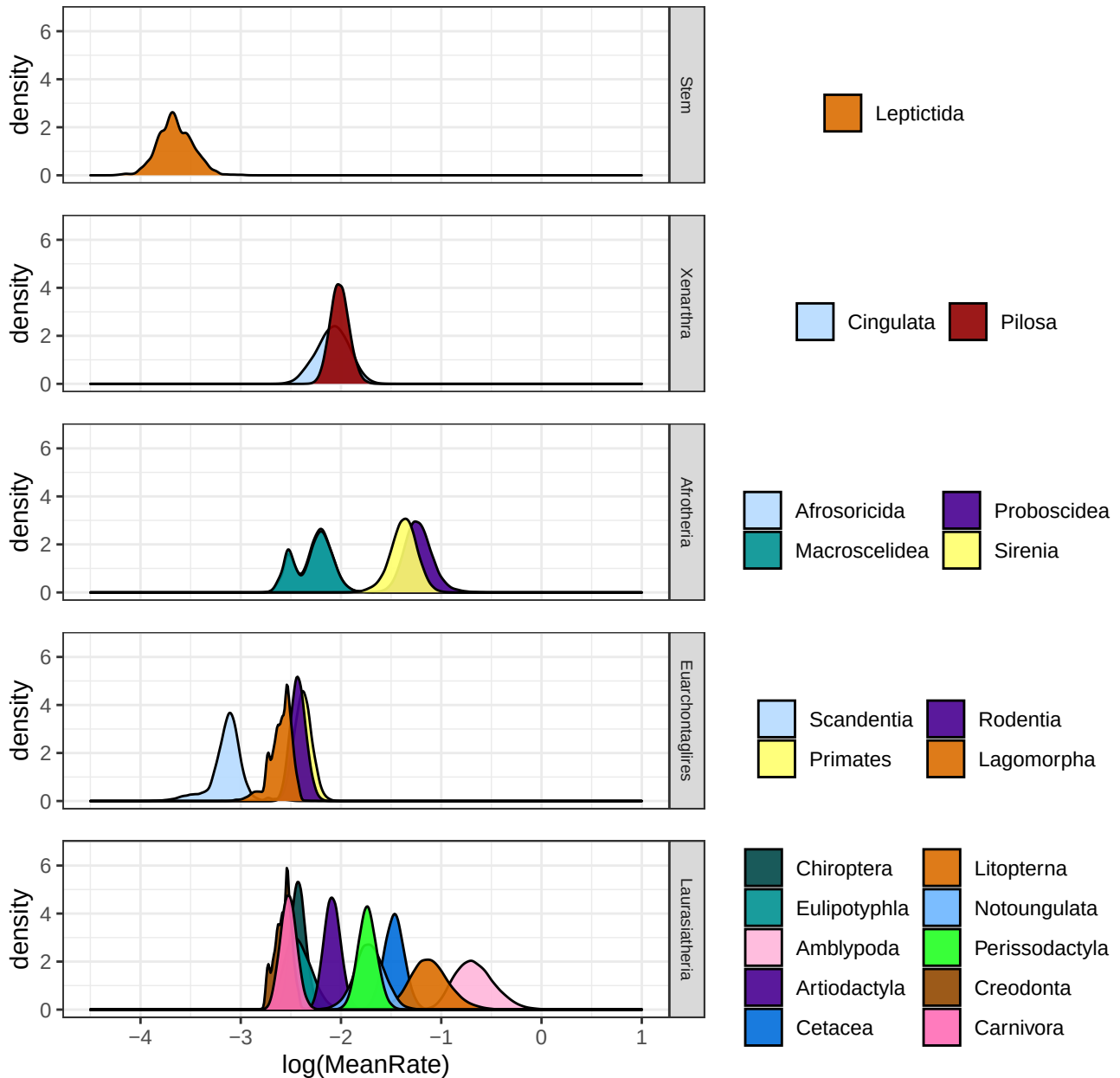


Fig. S5. B) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 1, Root Age = 75-80Ma.

Tree Topology 1: Root Age 80–85 Ma

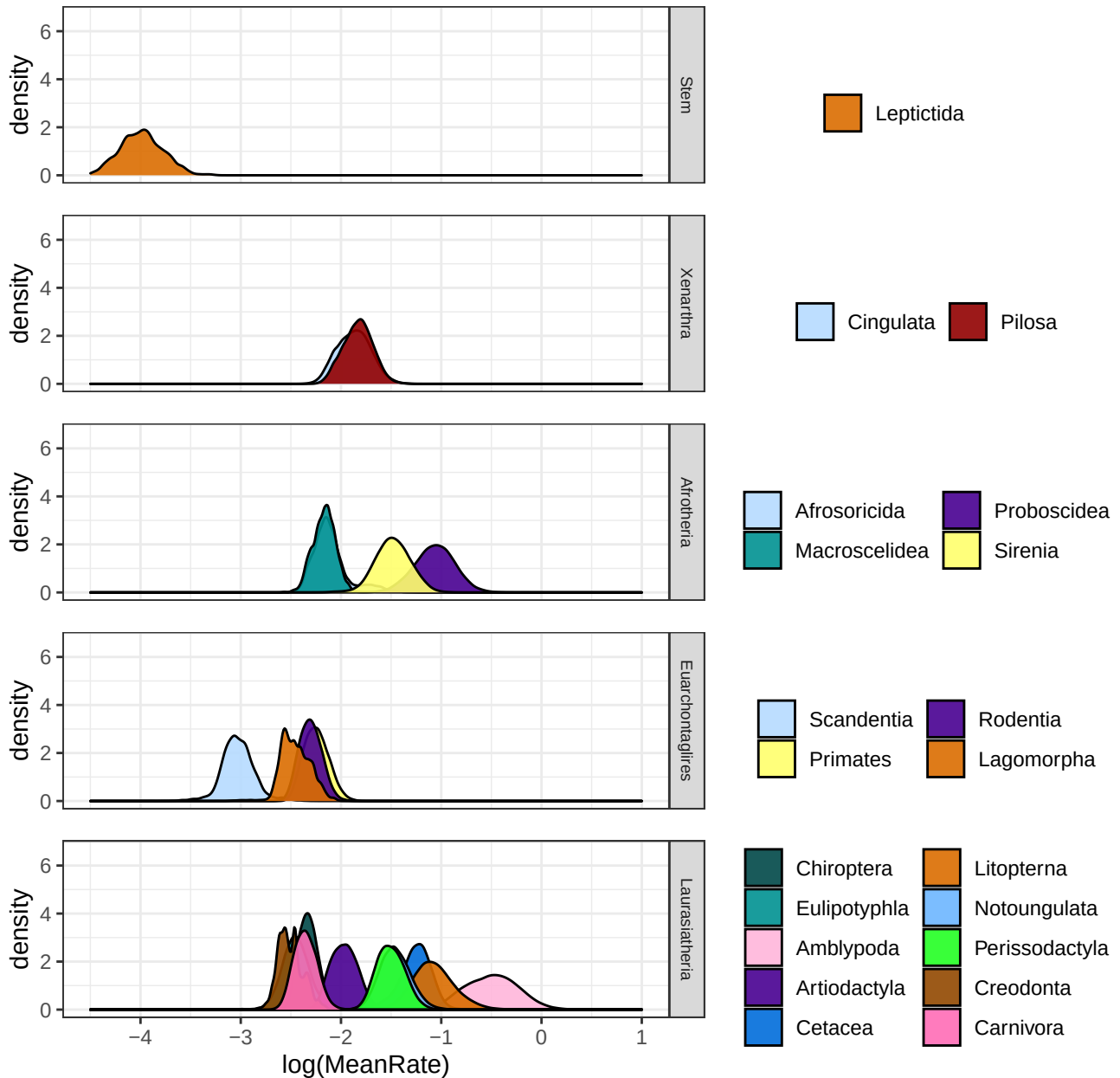


Fig. S5. C) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 1, Root Age = 80-85Ma.

Tree Topology 1: Root Age 85–90 Ma

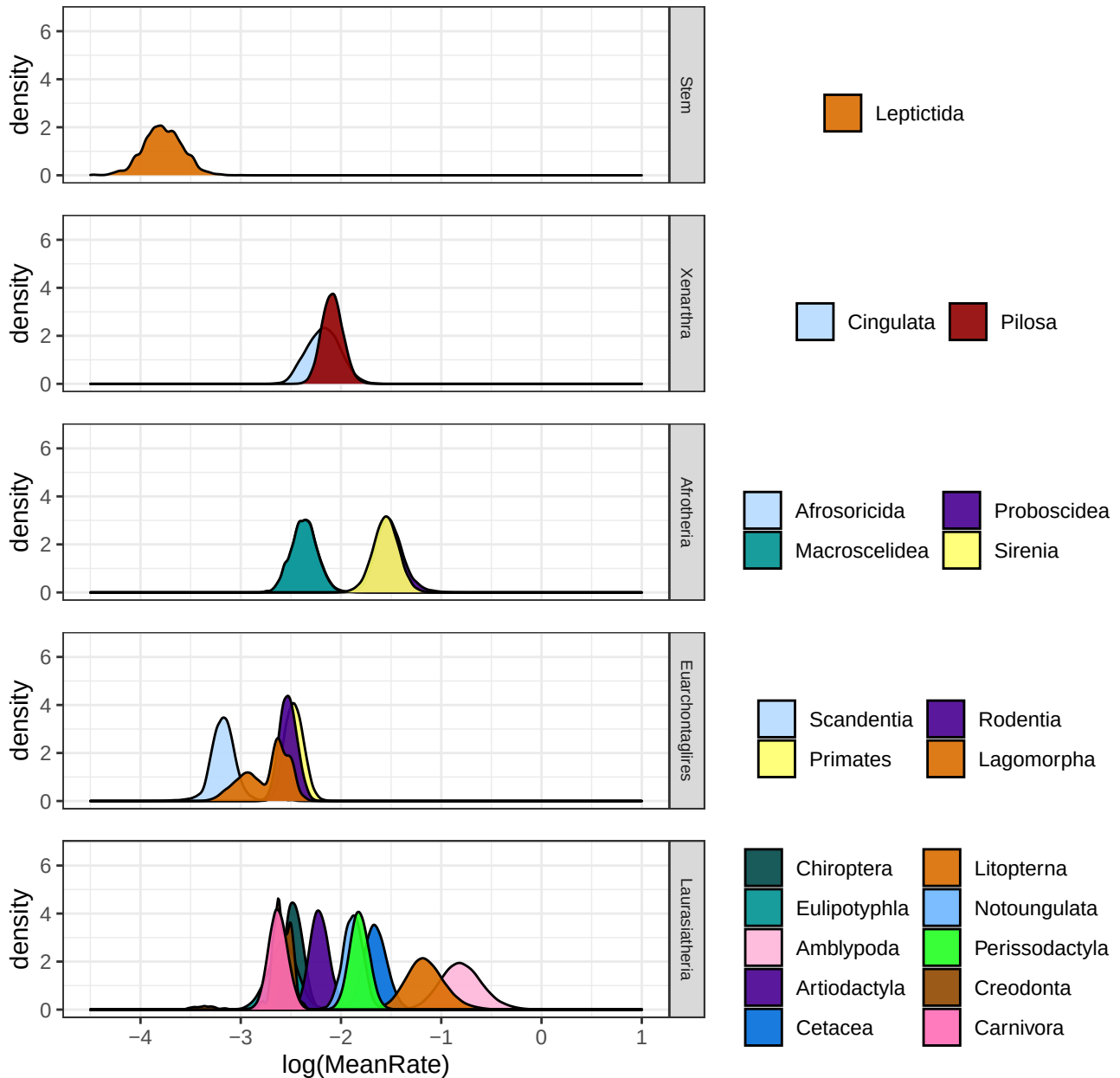


Fig. S5. D) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 1, Root Age = 85-90Ma.

Tree Topology 1: Root Age 90–95 Ma

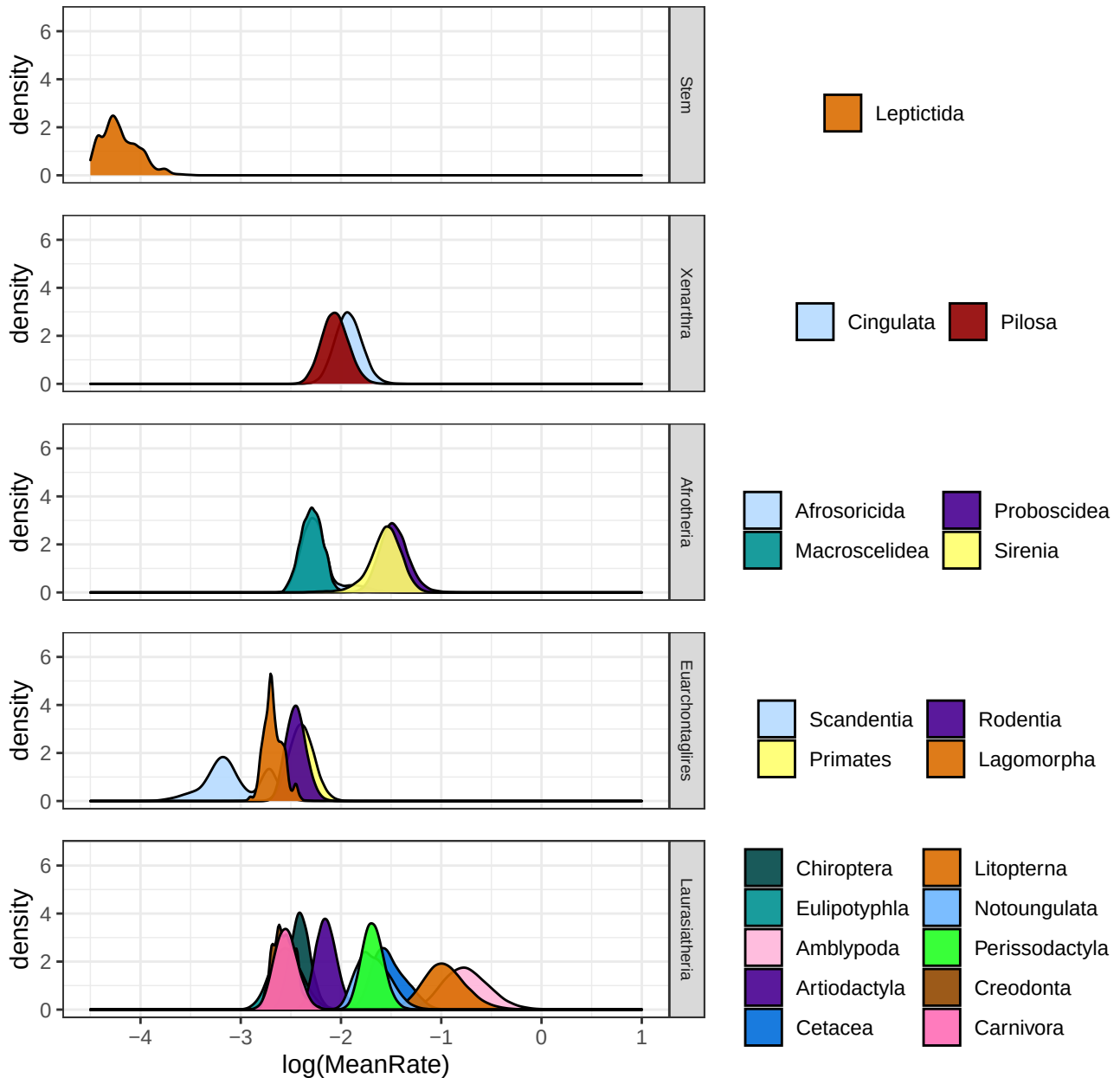


Fig. S5. E) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 1, Root Age = 90-95Ma.

Tree Topology 1: Root Age 95–100 Ma

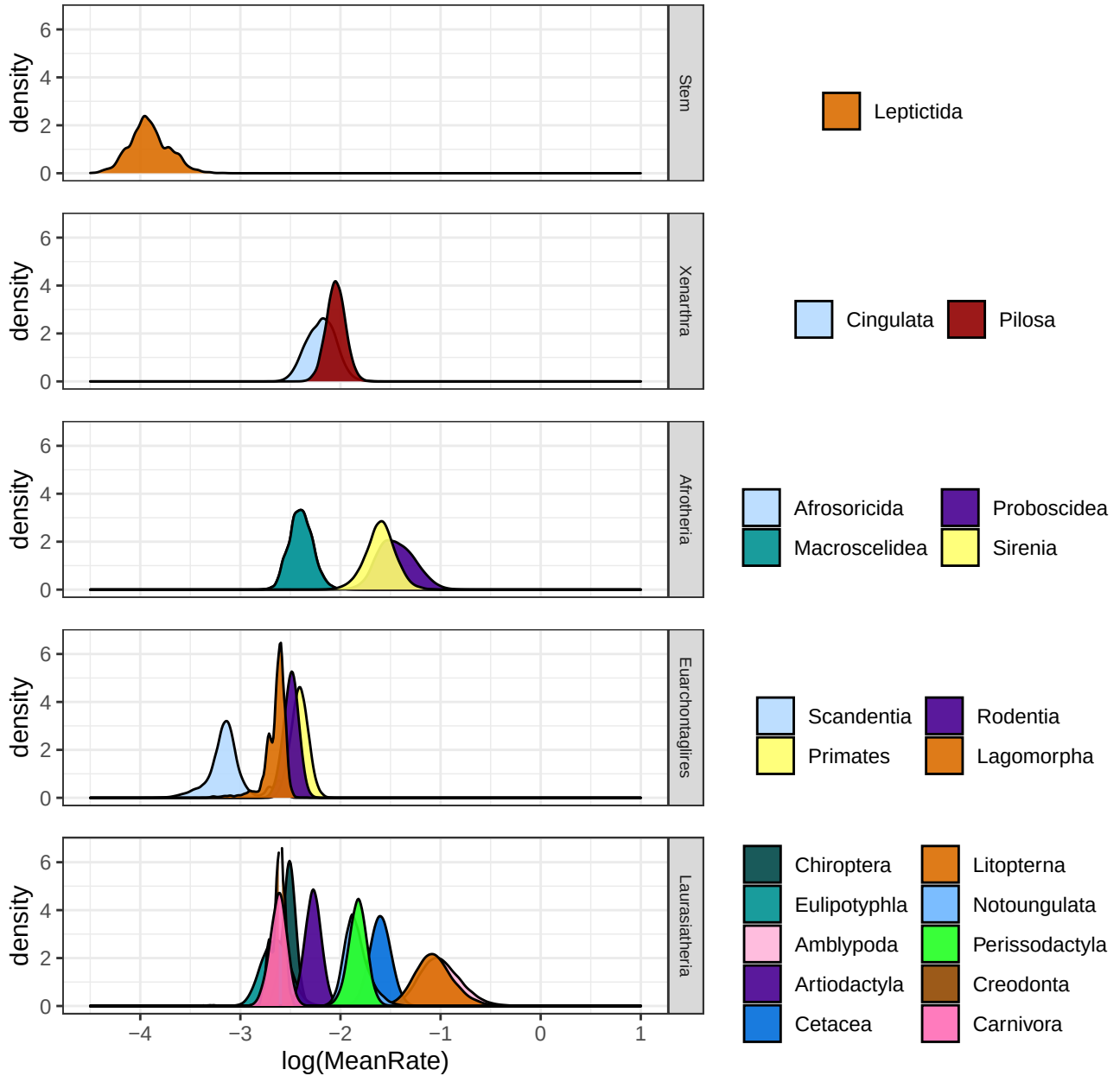


Fig. S5. F) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 1, Root Age = 95-100Ma.

Tree Topology 2: Root Age 70–75 Ma

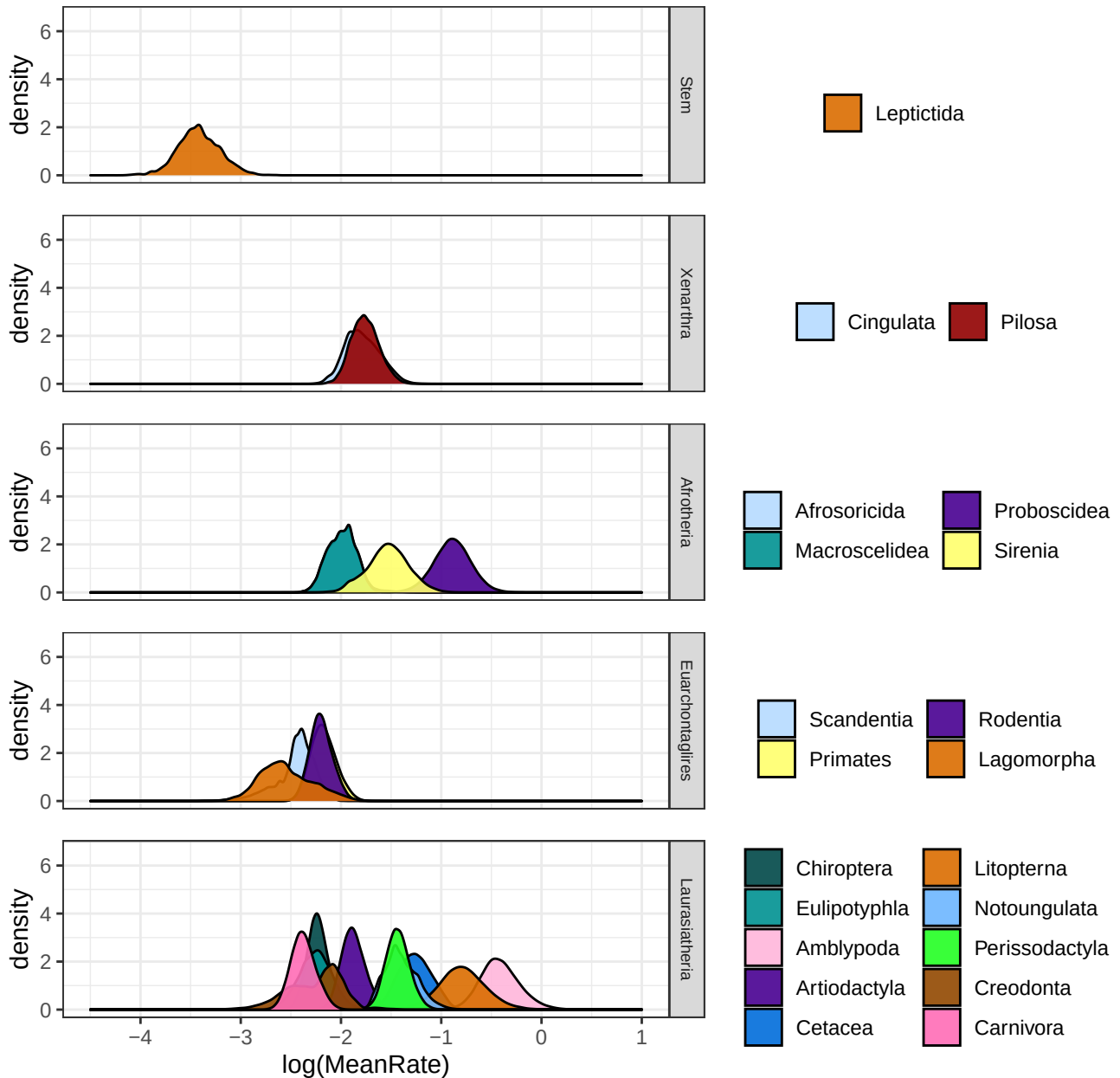


Fig. S5. G) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 2, Root Age = 70-75Ma.

Tree Topology 2: Root Age 75–80 Ma

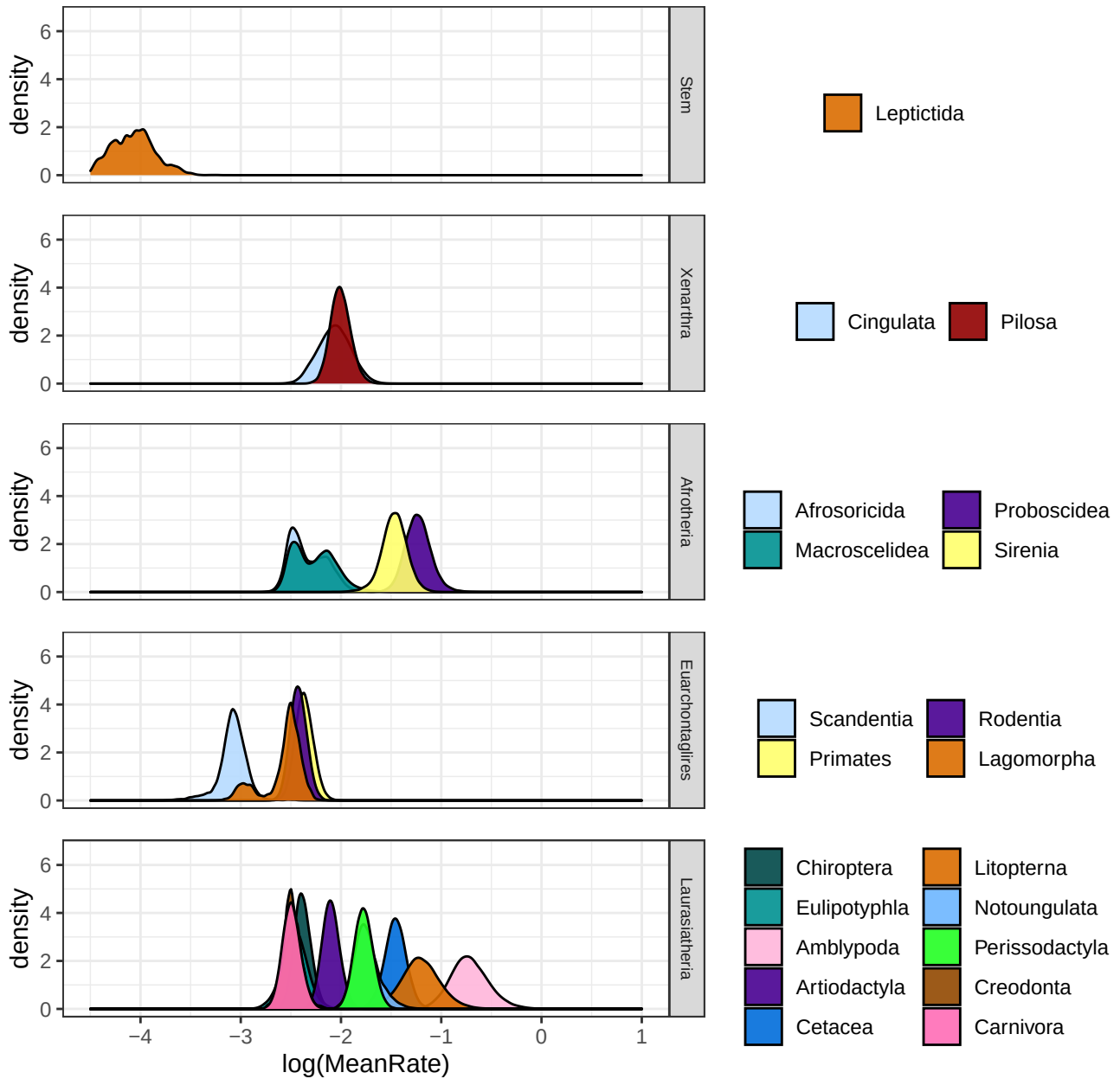


Fig. S5. H) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 2, Root Age = 75-80Ma.

Tree Topology 2: Root Age 80–85 Ma

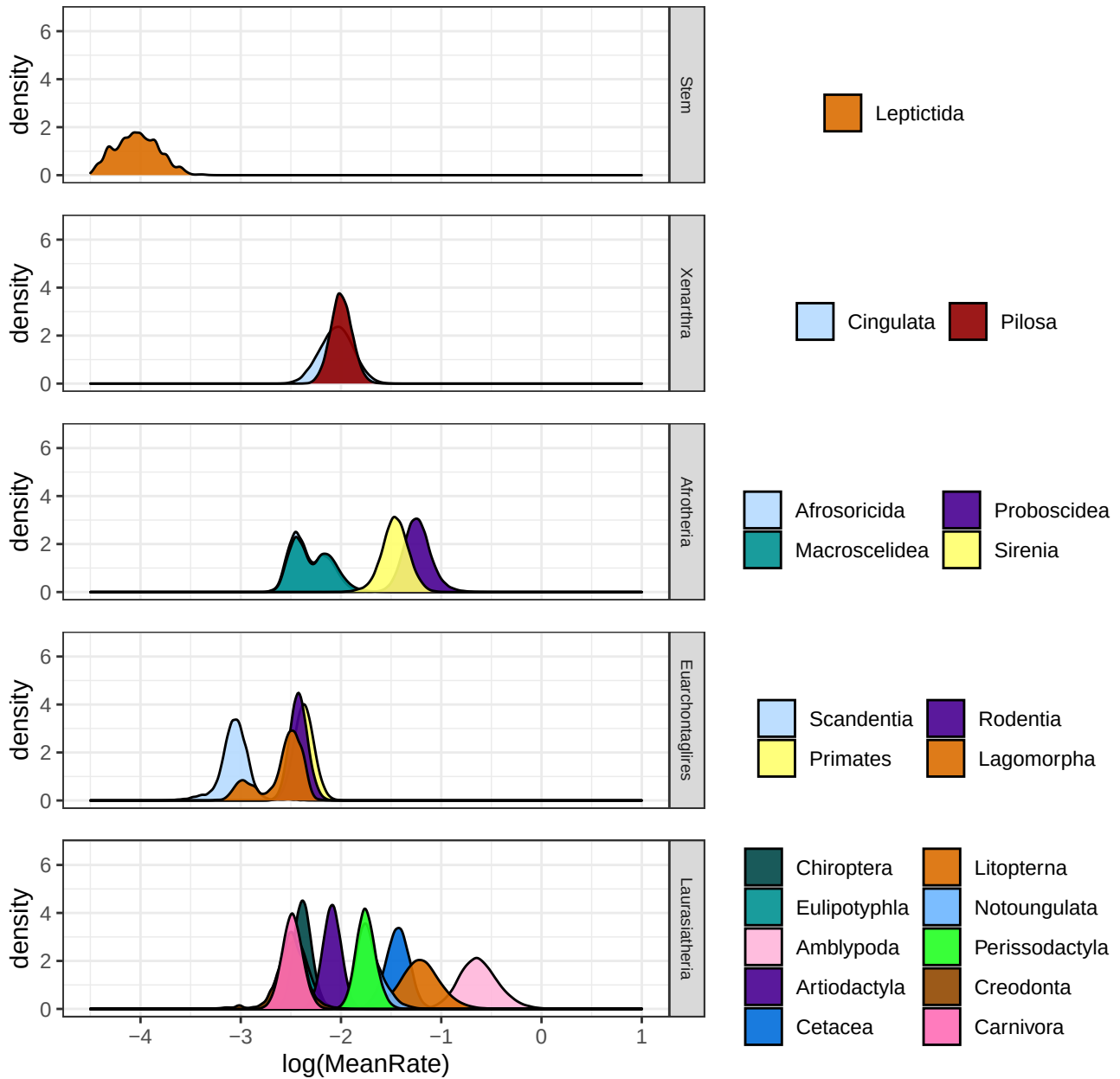


Fig. S5. i) Rates of evolution for terminal branches, subsetted into placental orders, for Tree Topology 2, Root Age = 80-85Ma.

Tree Topology 2: Root Age 85–90 Ma

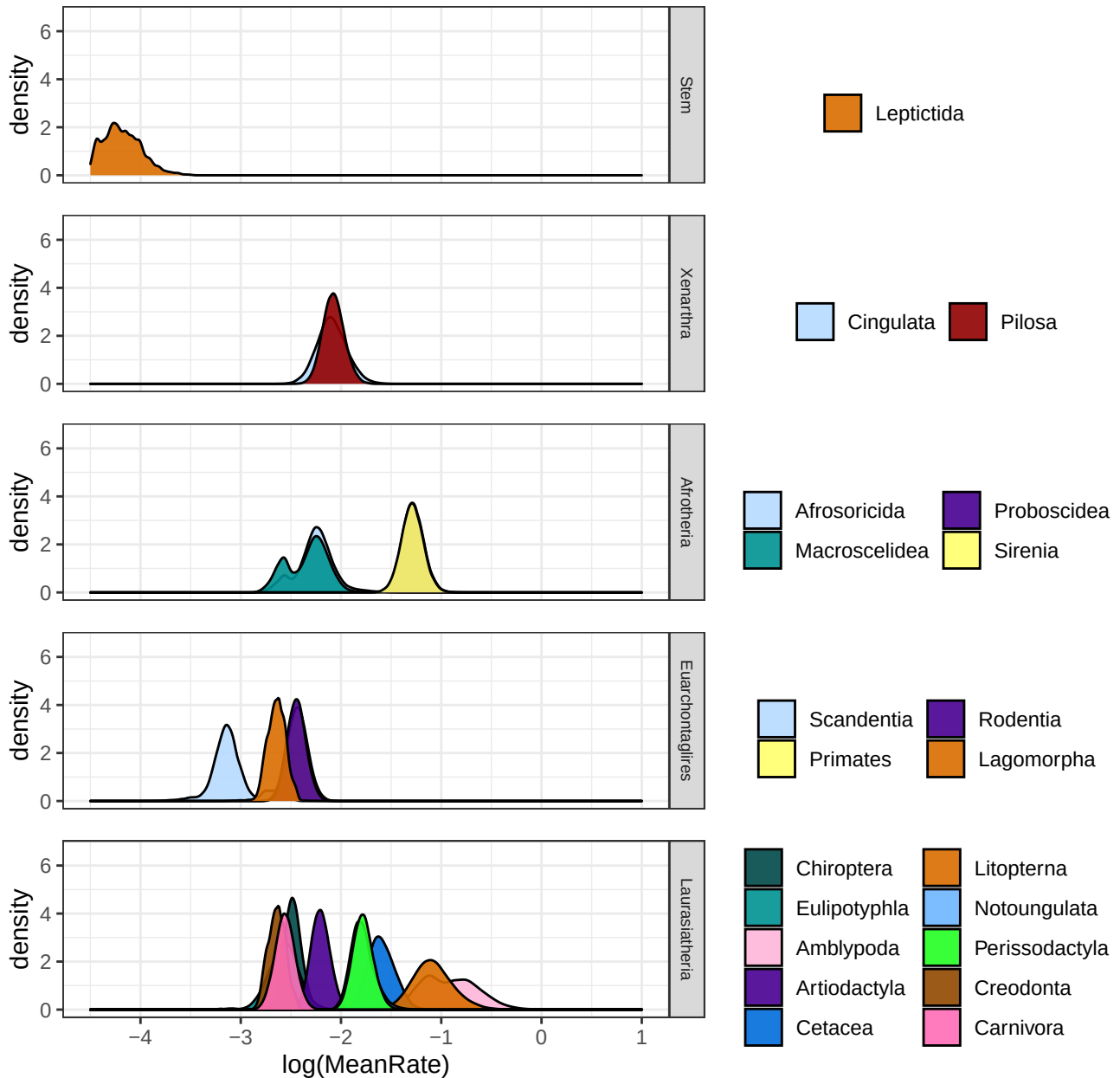


Fig. S5. J) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 2, Root Age = 85-90Ma.

Tree Topology 2: Root Age 90–95 Ma

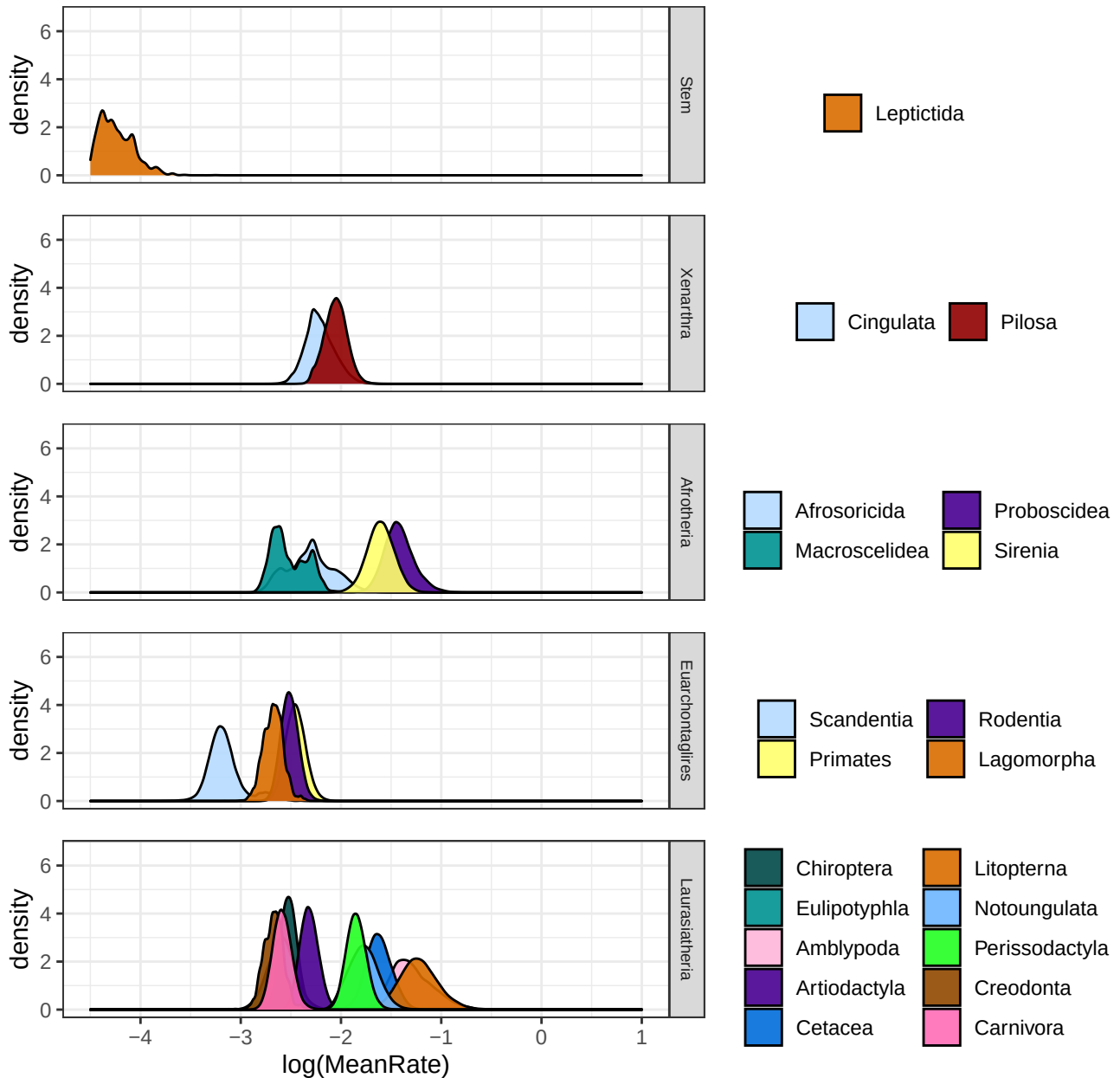


Fig. S5. K) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 2, Root Age = 90-95Ma.

Tree Topology 2: Root Age 95–100 Ma

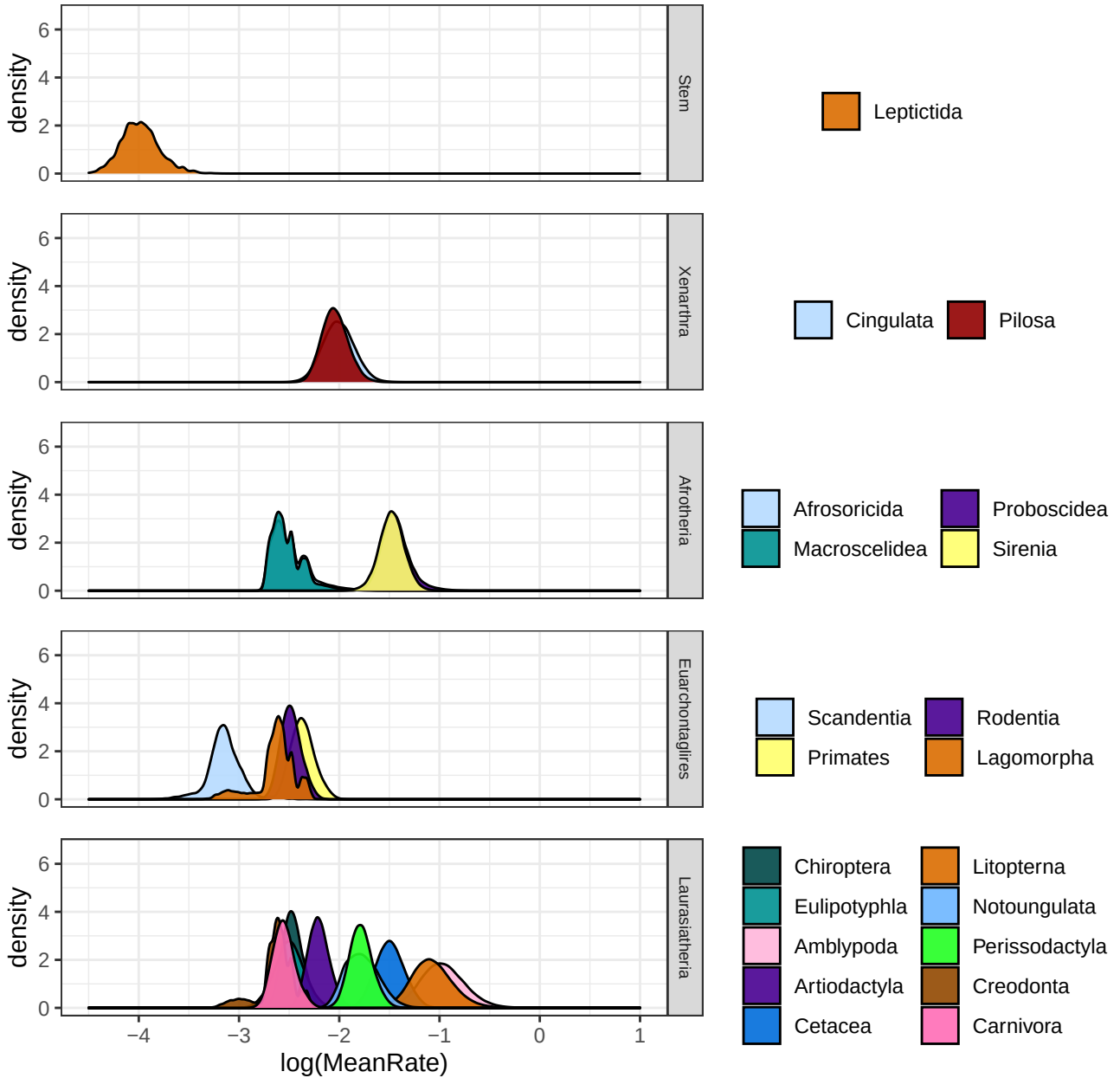


Fig. S5. L) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 2, Root Age = 95-100Ma.

Tree Topology 3: Root Age 70–75 Ma

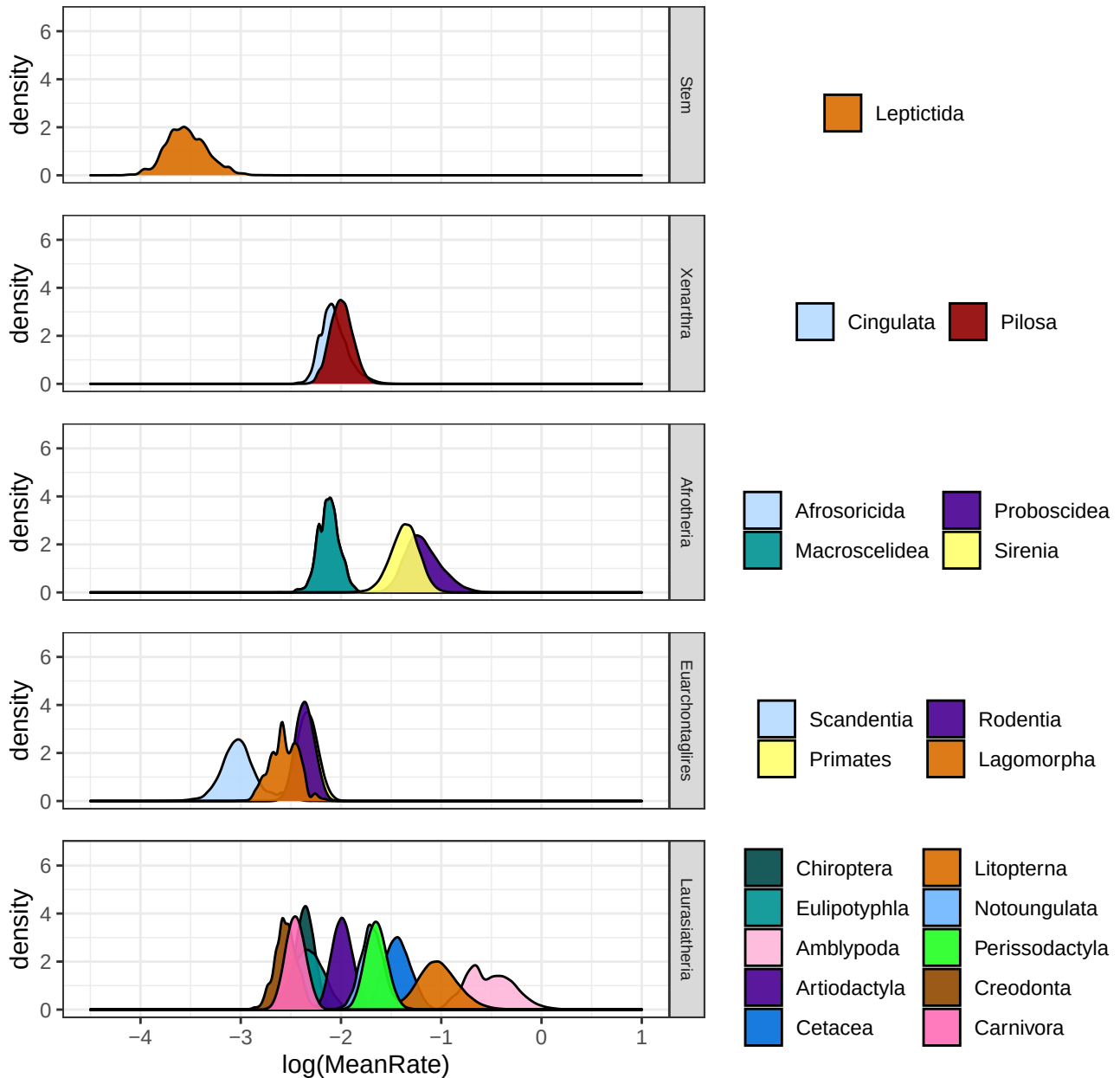


Fig. S5. M) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 3, Root Age = 70-75Ma.

Tree Topology 3: Root Age 75–80 Ma

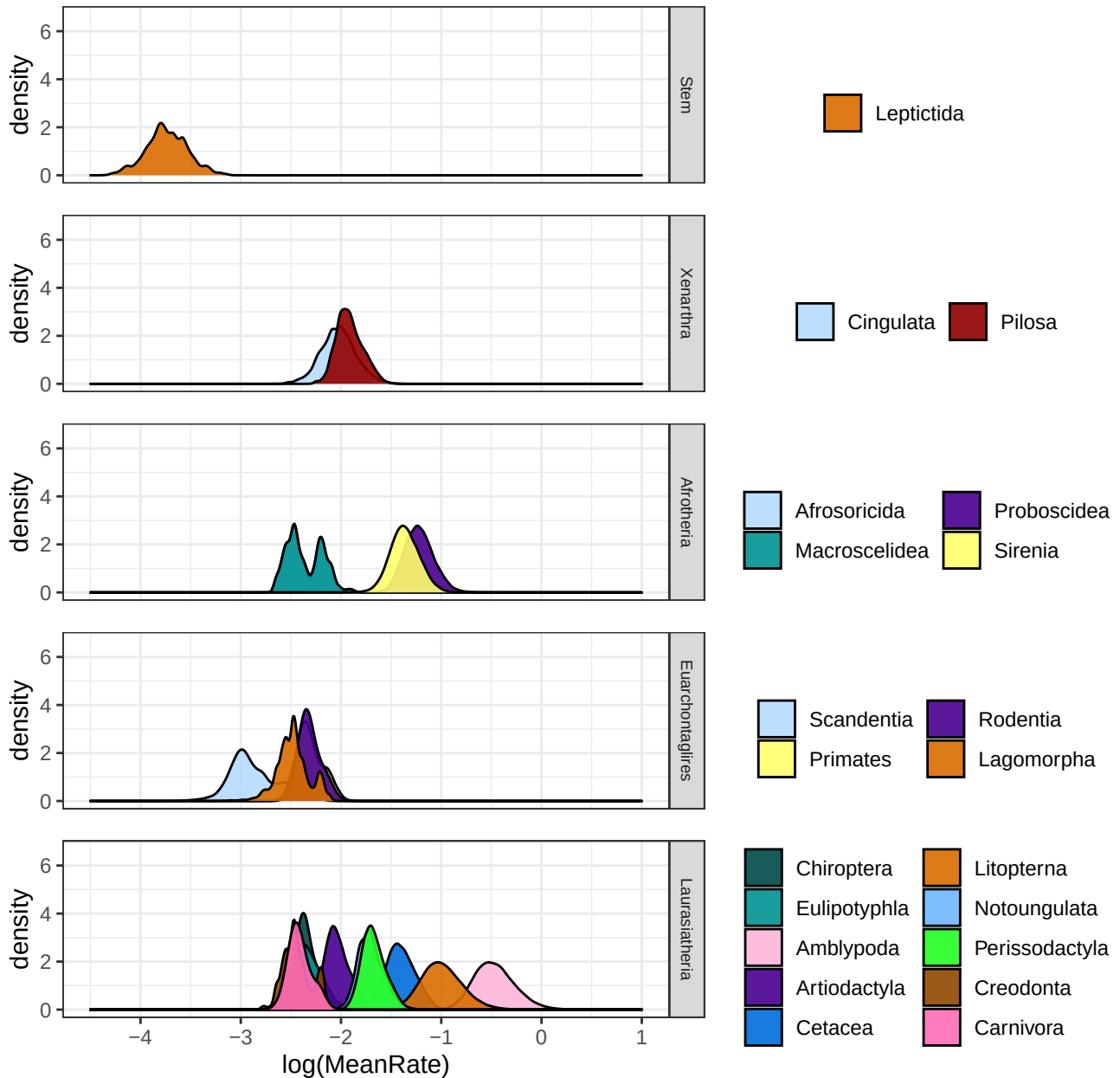


Fig. S5. N) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 3, Root Age = 75-80Ma.

Tree Topology 3: Root Age 80–85 Ma

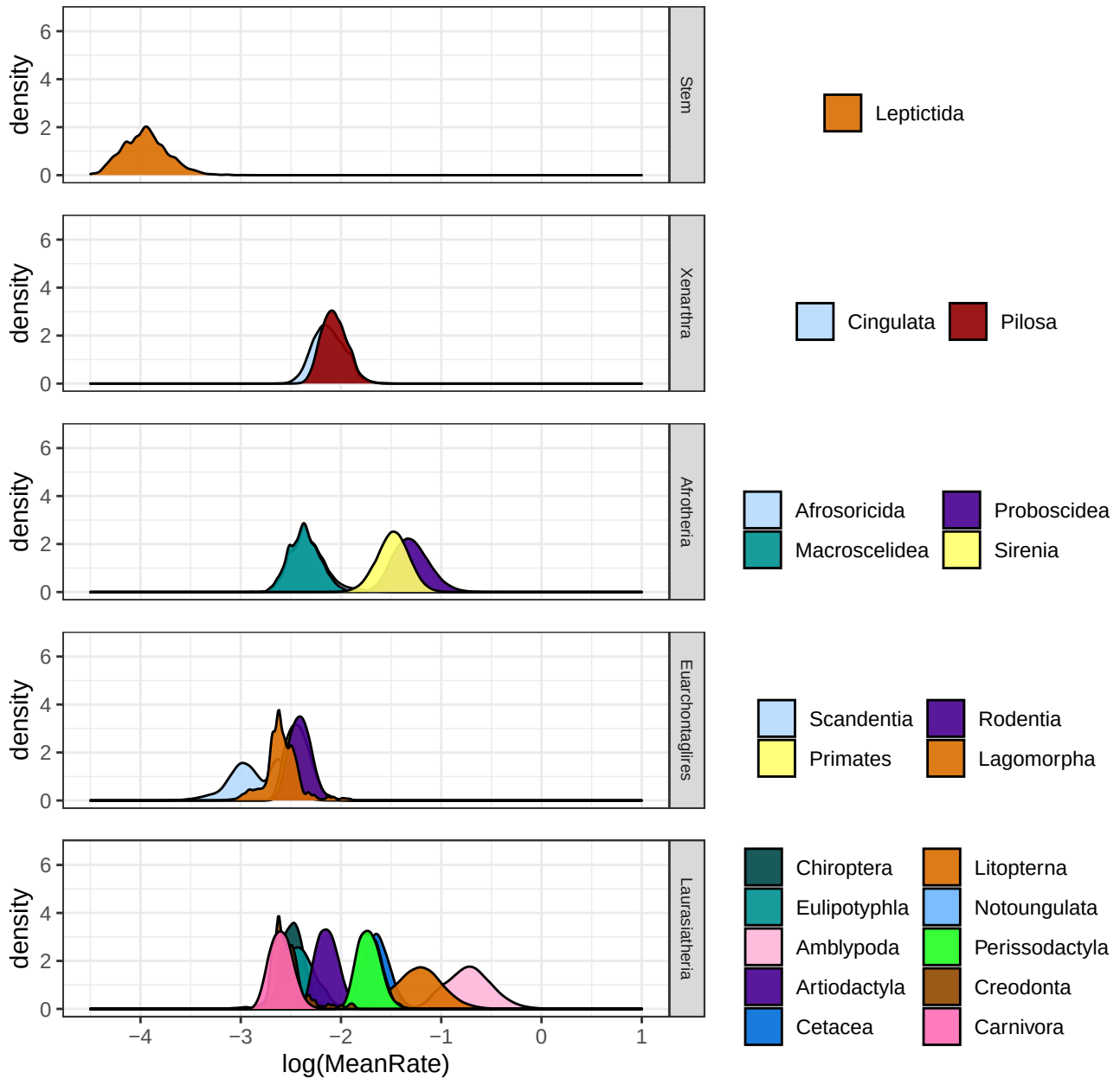


Fig. S5. O) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 3, Root Age = 80-85Ma.

Tree Topology 3: Root Age 85–90 Ma

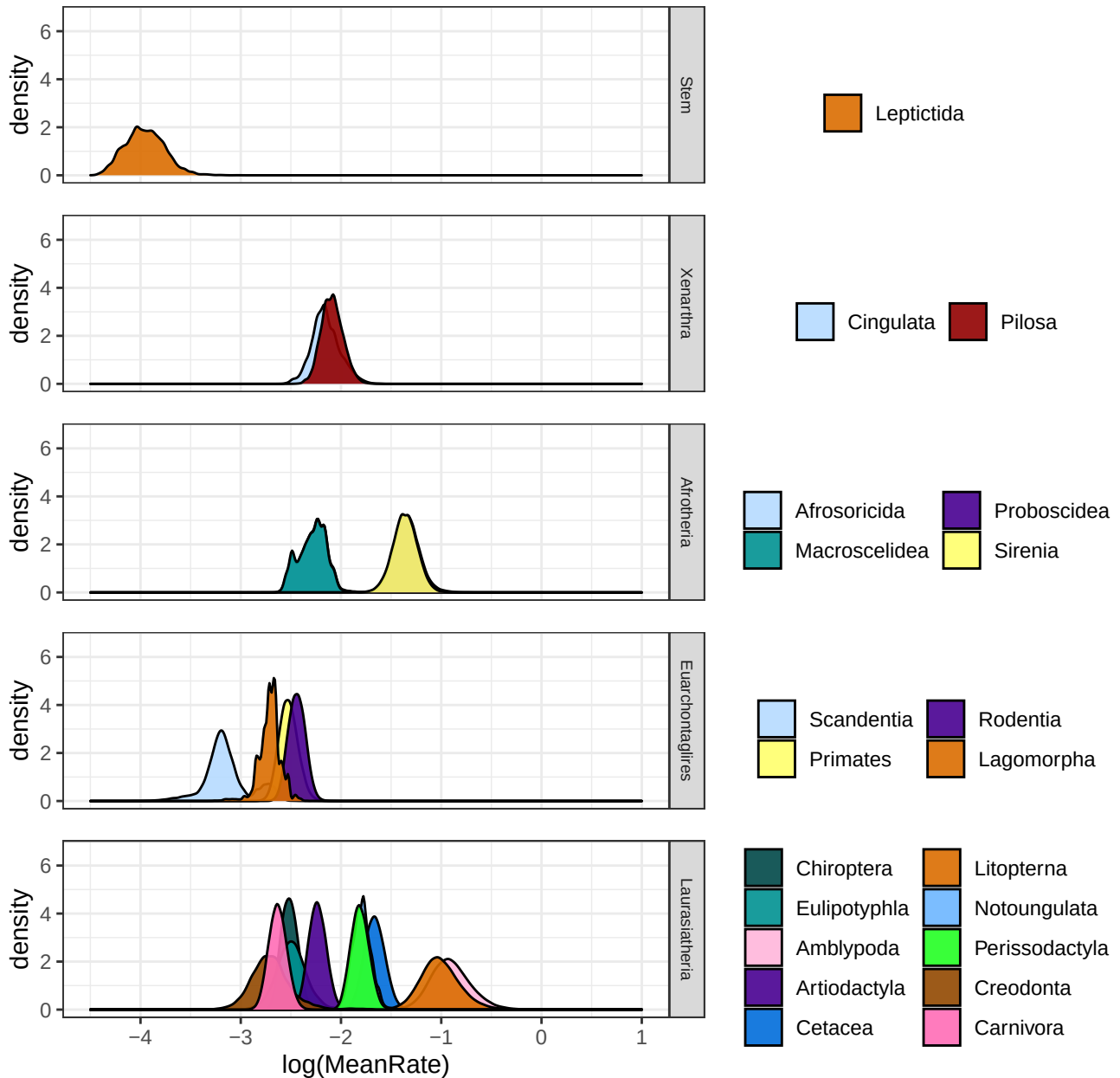


Fig. S5. P) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 3, Root Age = 85-90Ma.

Tree Topology 3: Root Age 90–95 Ma

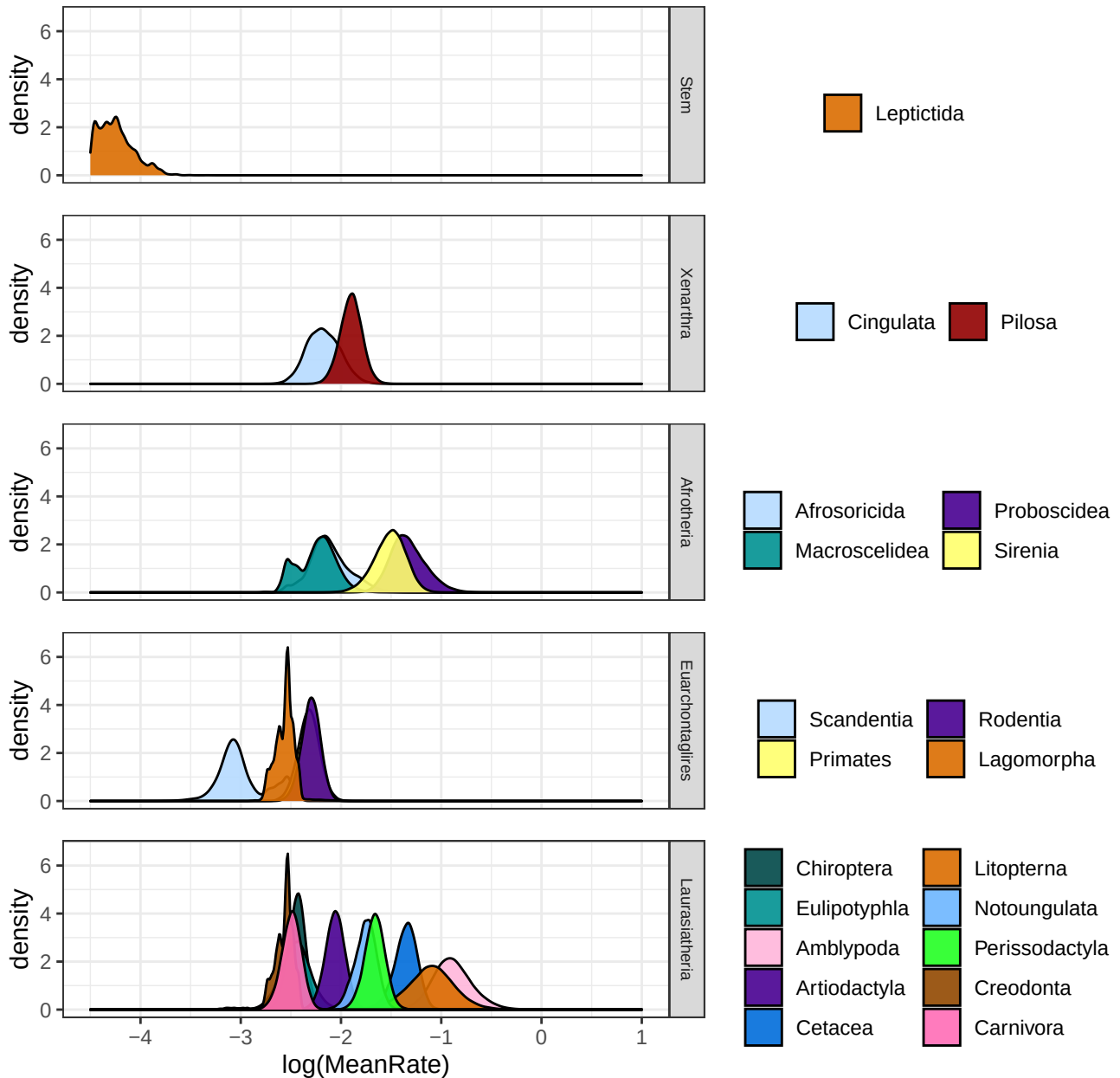


Fig. S5. Q) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 3, Root Age = 90-95Ma.

Tree Topology 3: Root Age 95–100 Ma

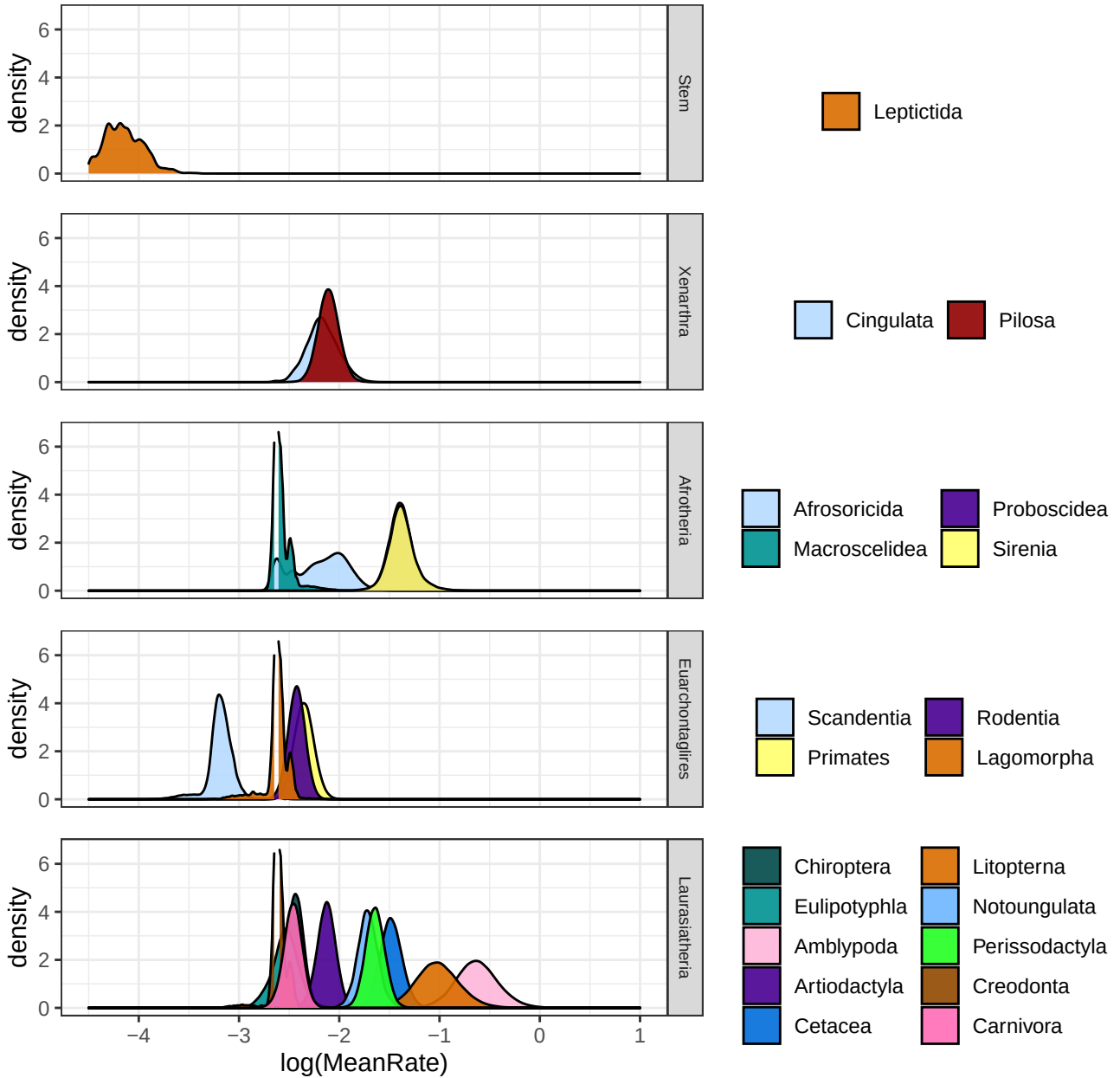


Fig. S5. R) Rates of evolution for terminal branches, subsetting into placental orders, for Tree Topology 3, Root Age = 95-100Ma.

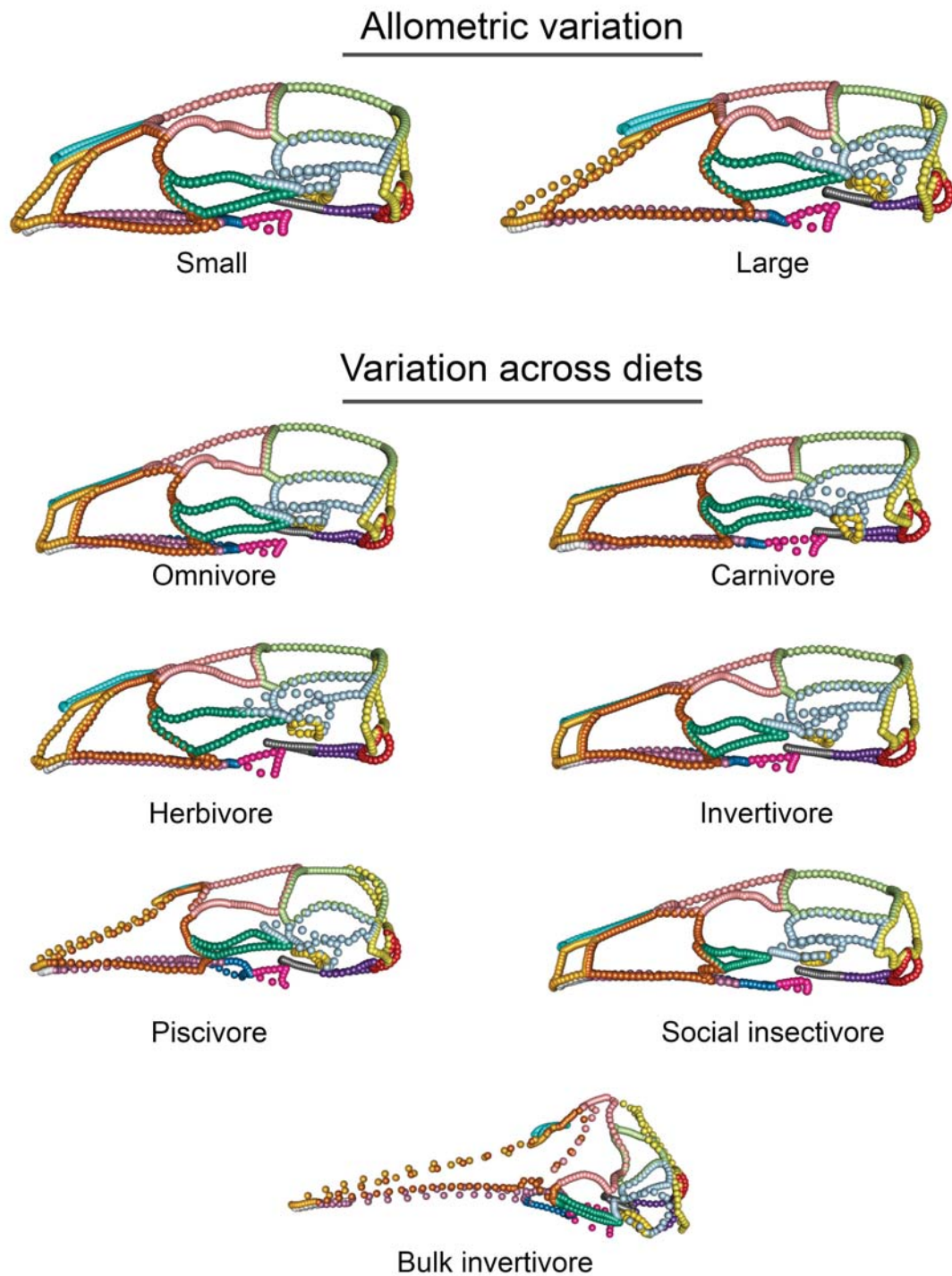


Fig. S6. Shape variation associated with allometry and phylogenetic mean shapes for each dietary category.

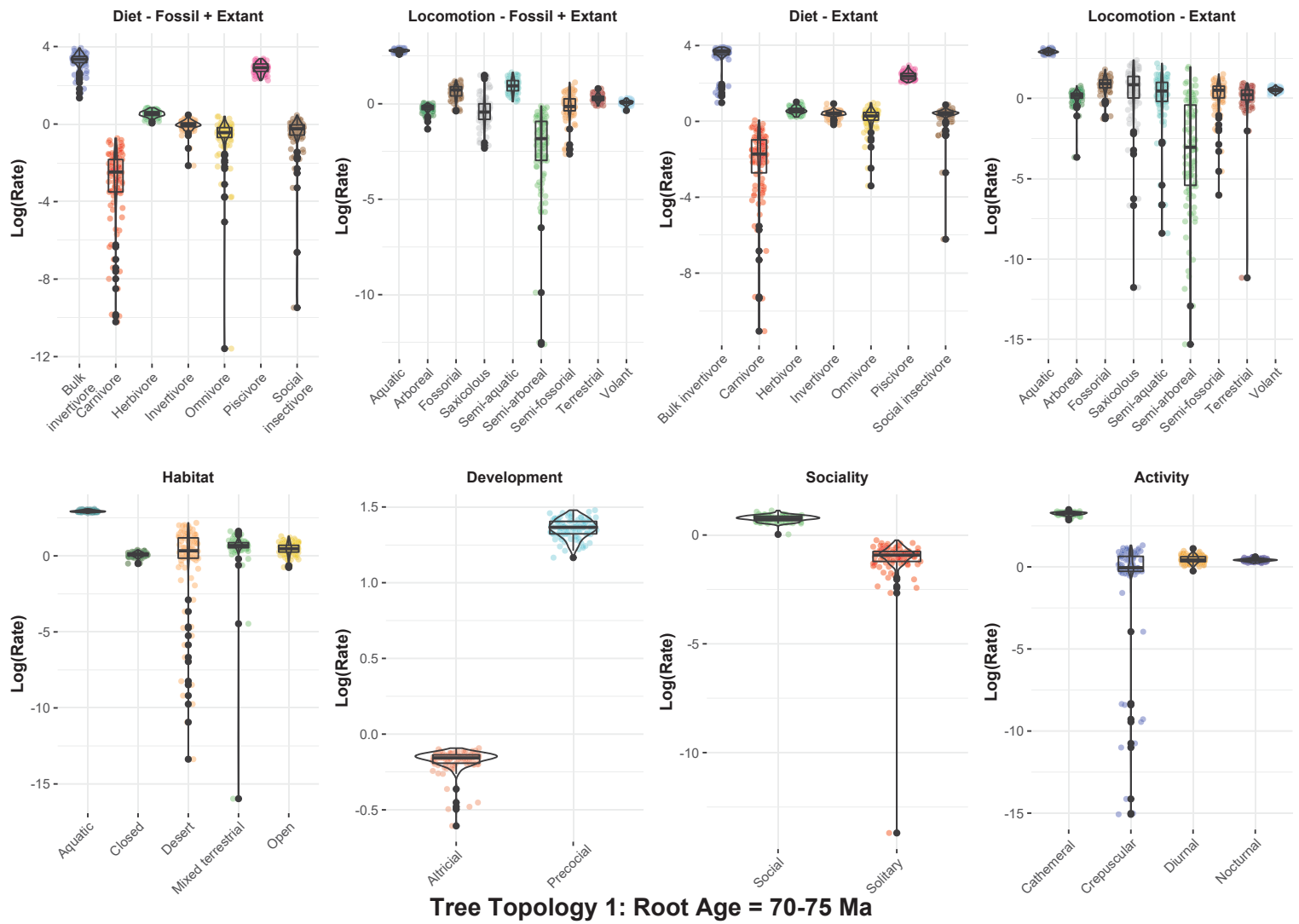


Fig. S7. A) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 1, Root Age = 70-75Ma.

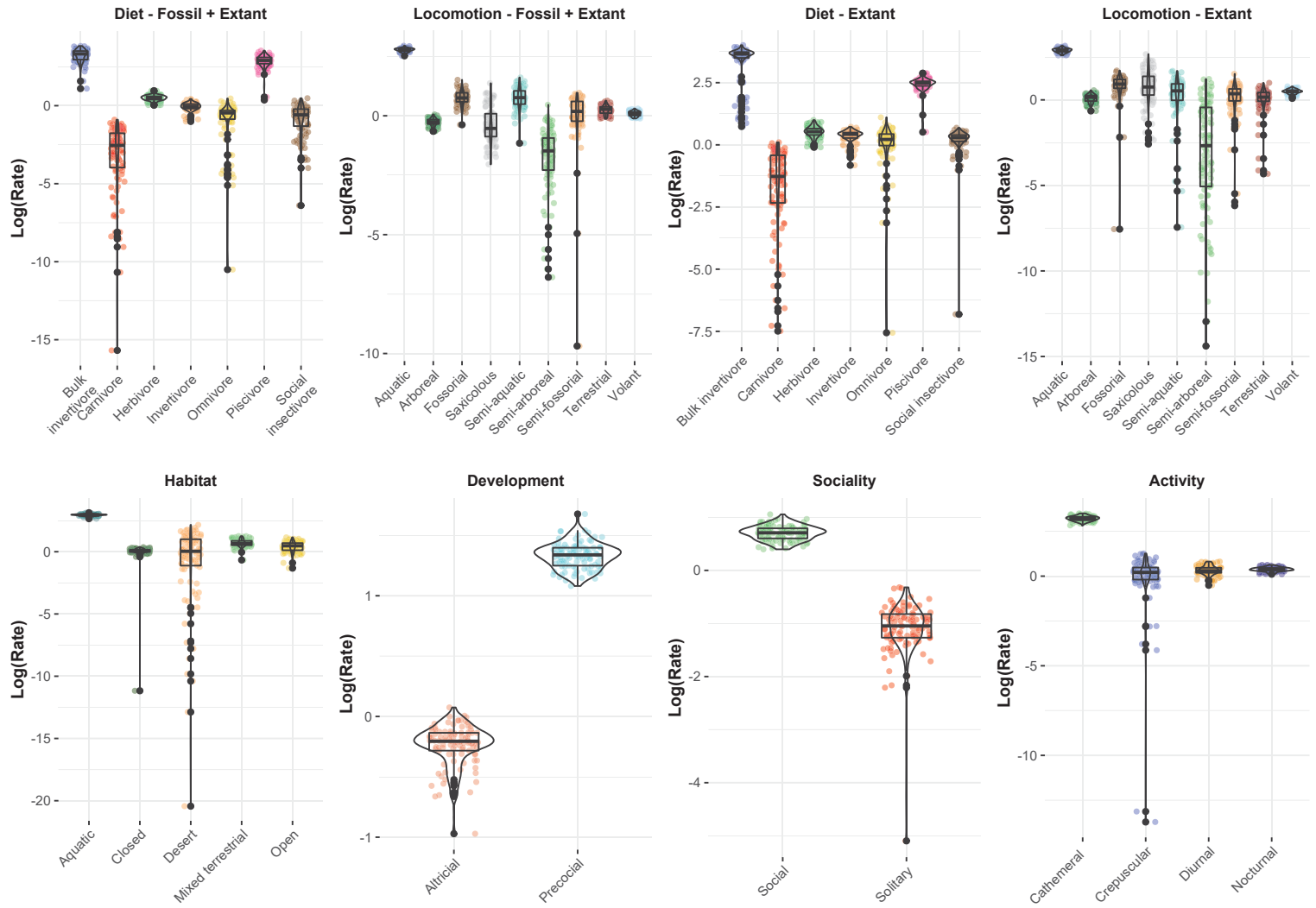


Fig. S7. B) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 1, Root Age = 75-80Ma.

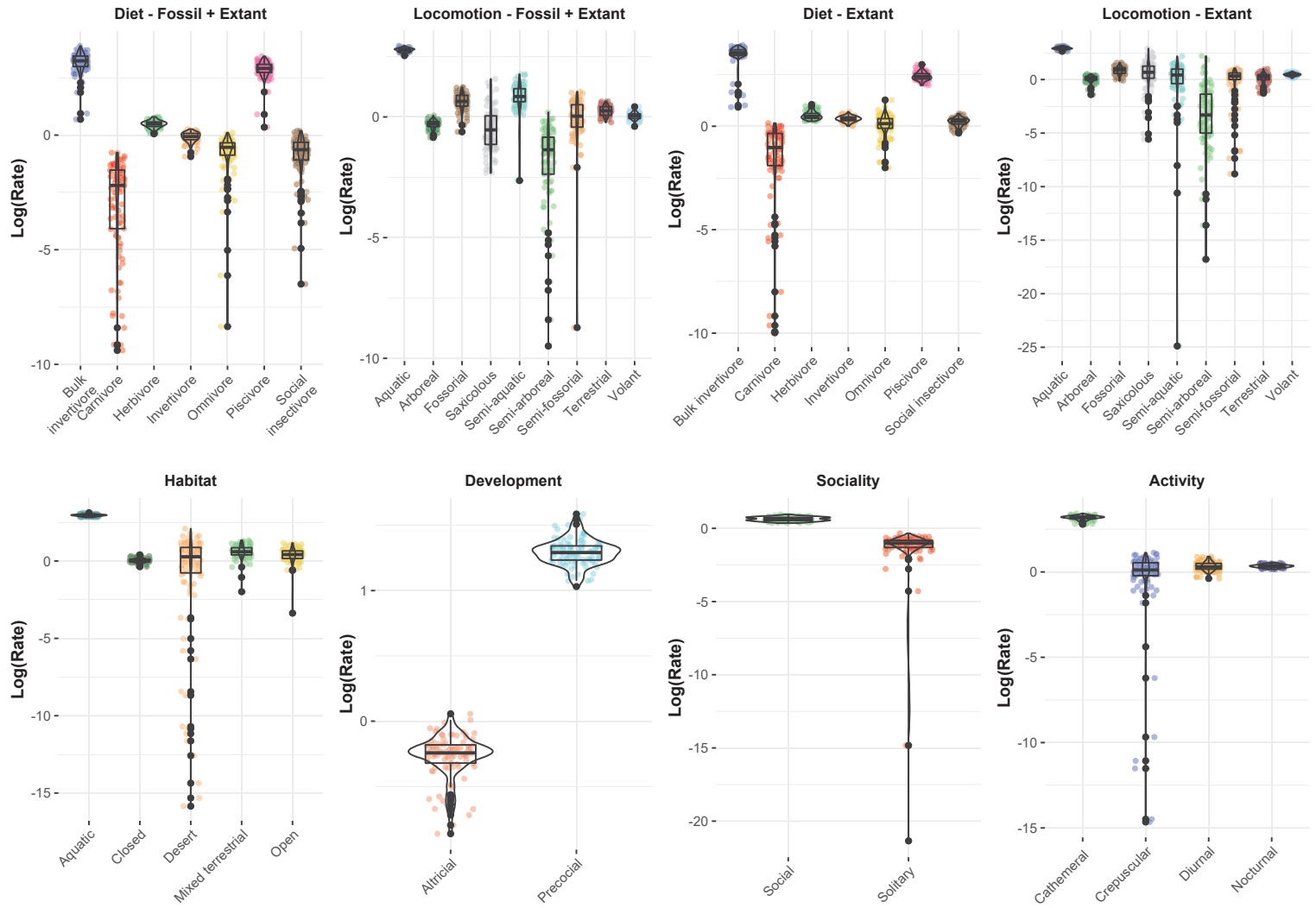


Fig. S7. C) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 1, Root Age = 80-85Ma.

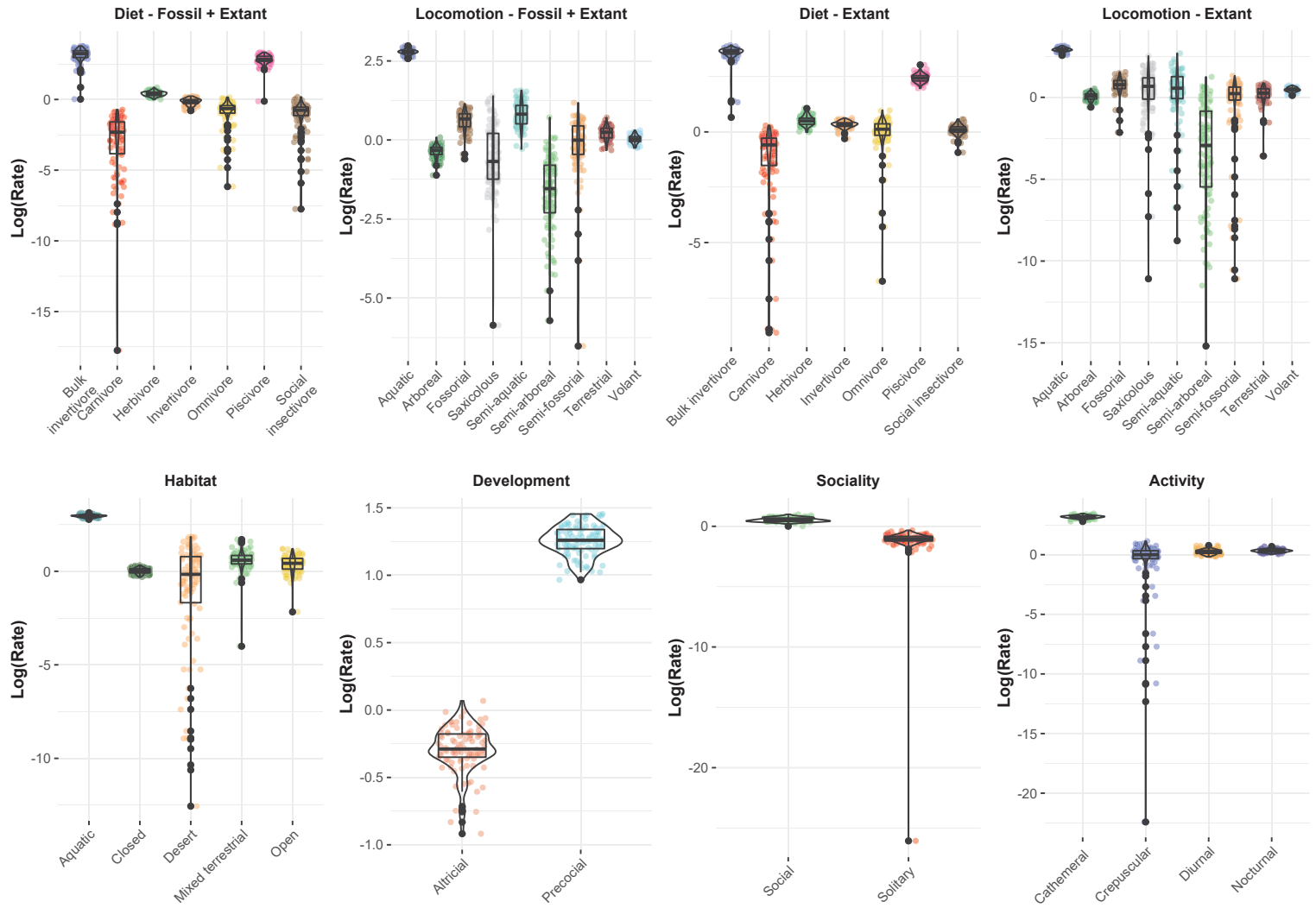


Fig. S7. D) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 1, Root Age = 85-90Ma.

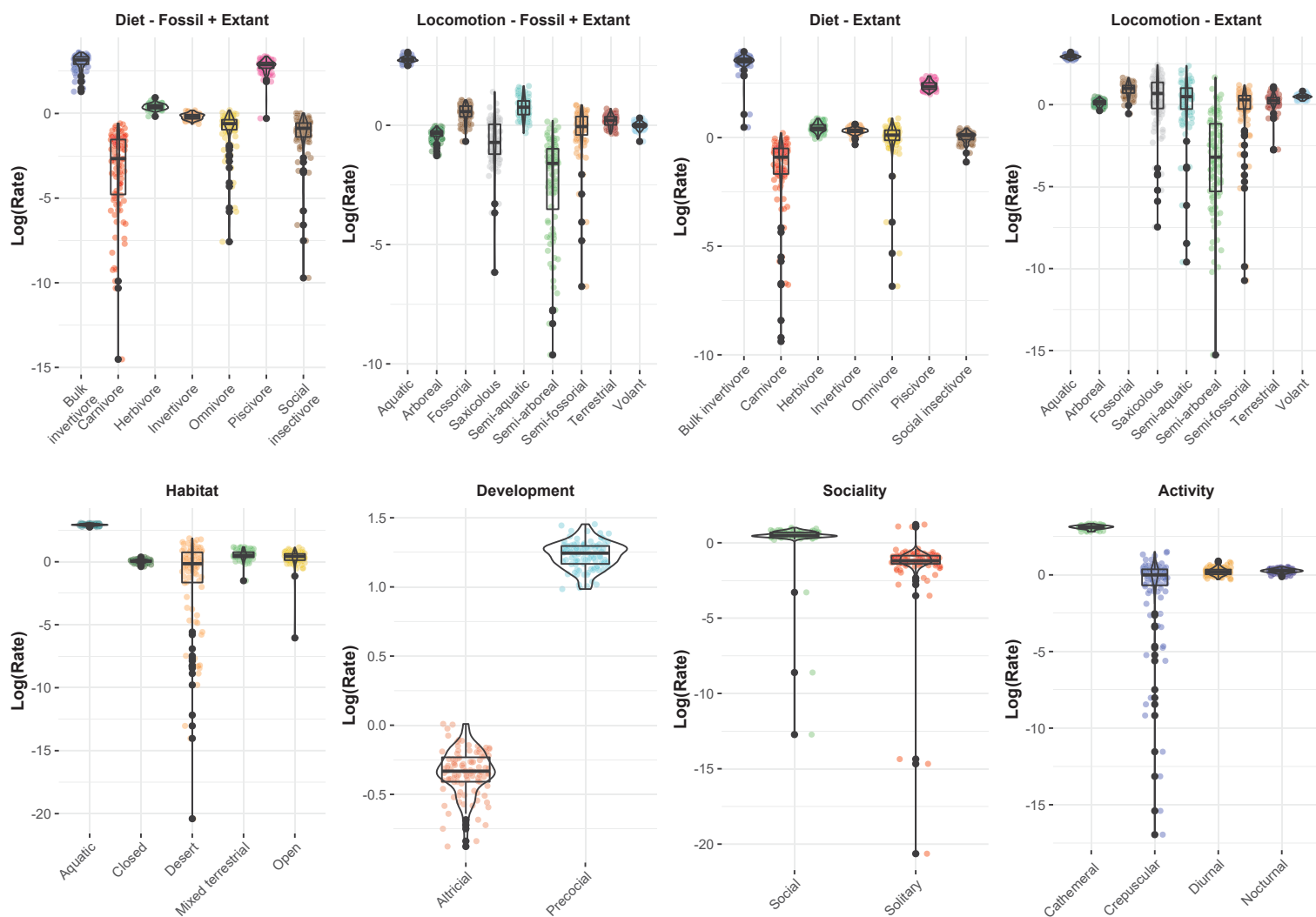


Fig. S7. E) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 1, Root Age = 90-95Ma.

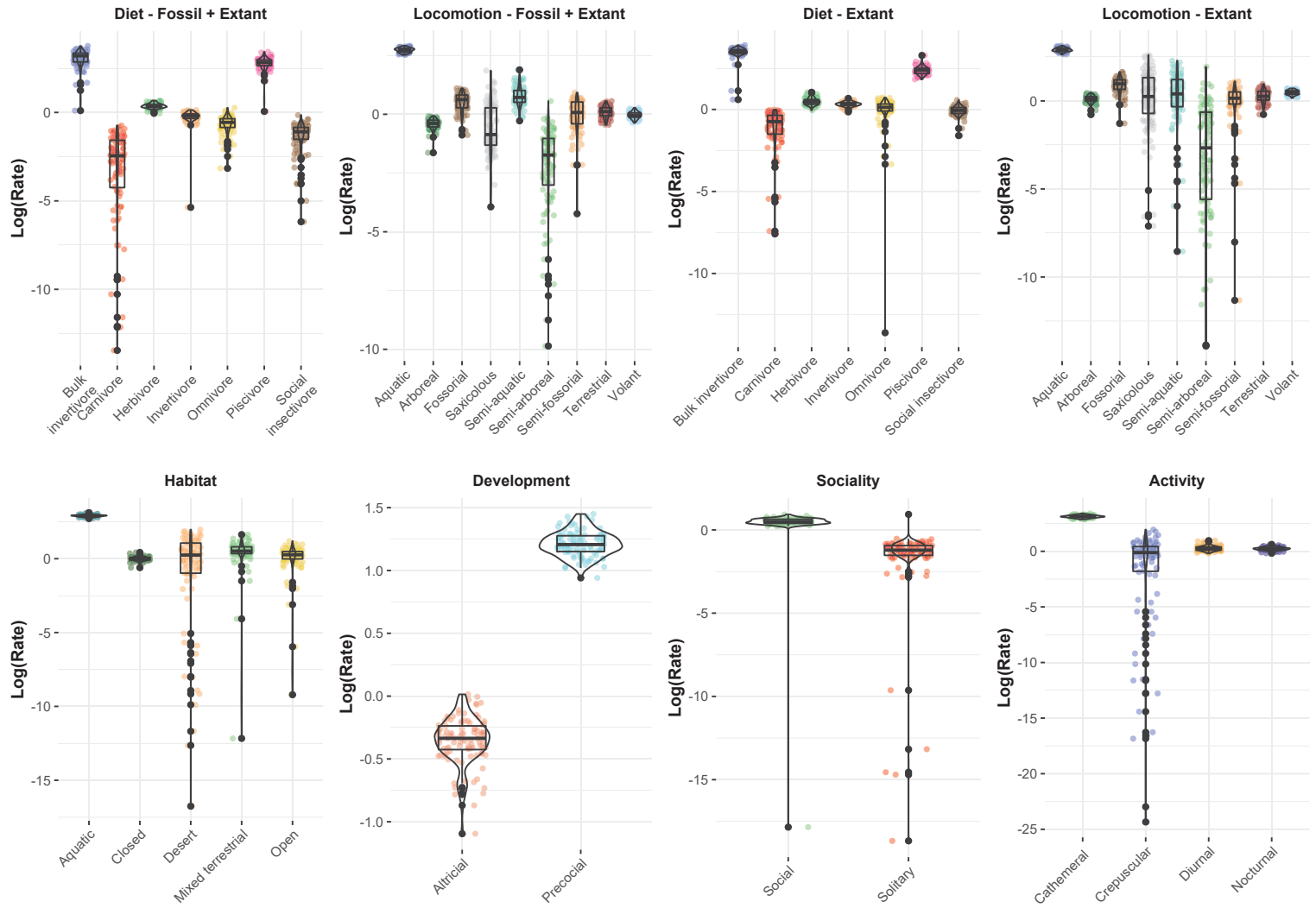


Fig. S7. F) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 1, Root Age = 95-100Ma.

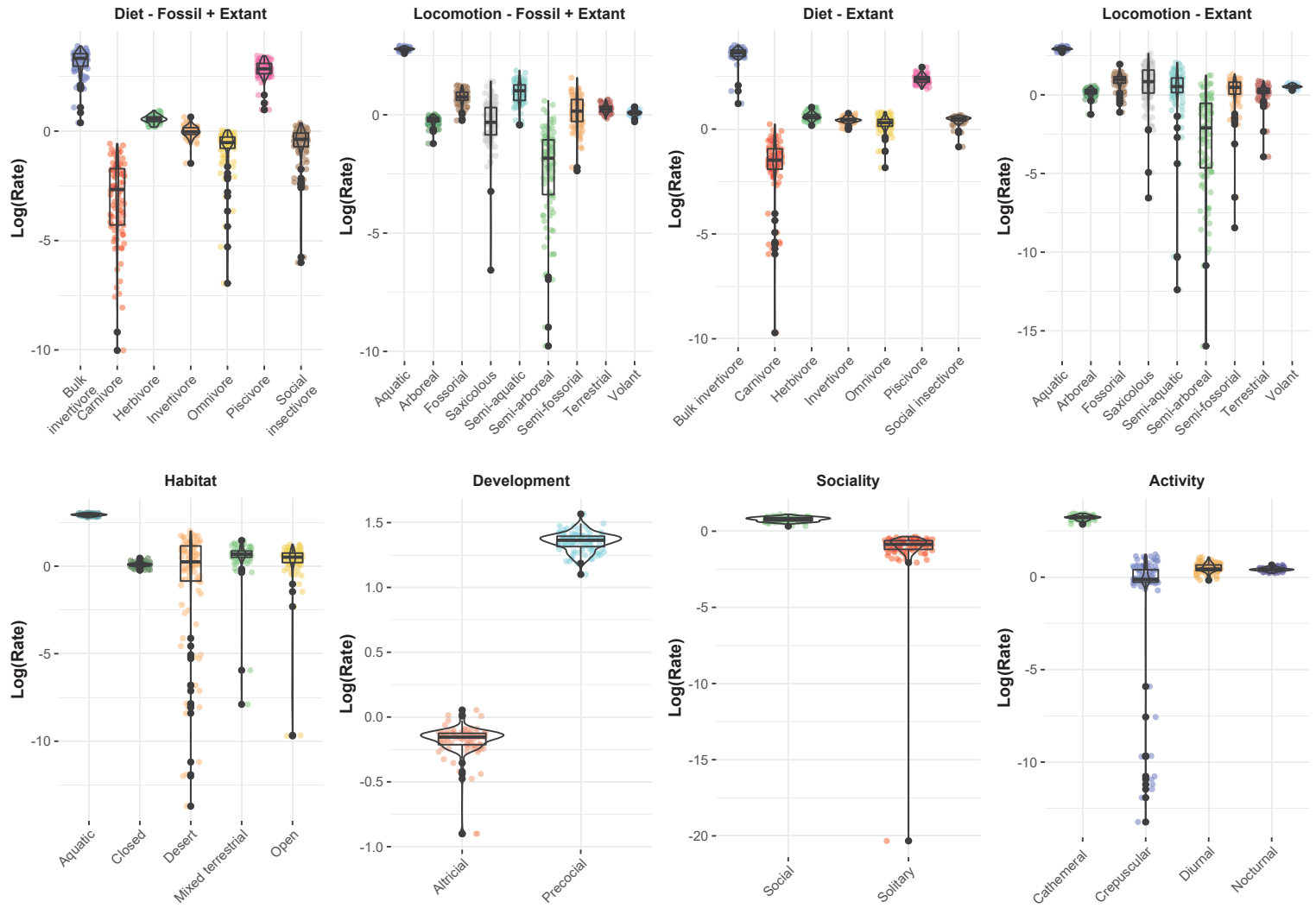


Fig. S7. G) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 2, Root Age = 70-75Ma.

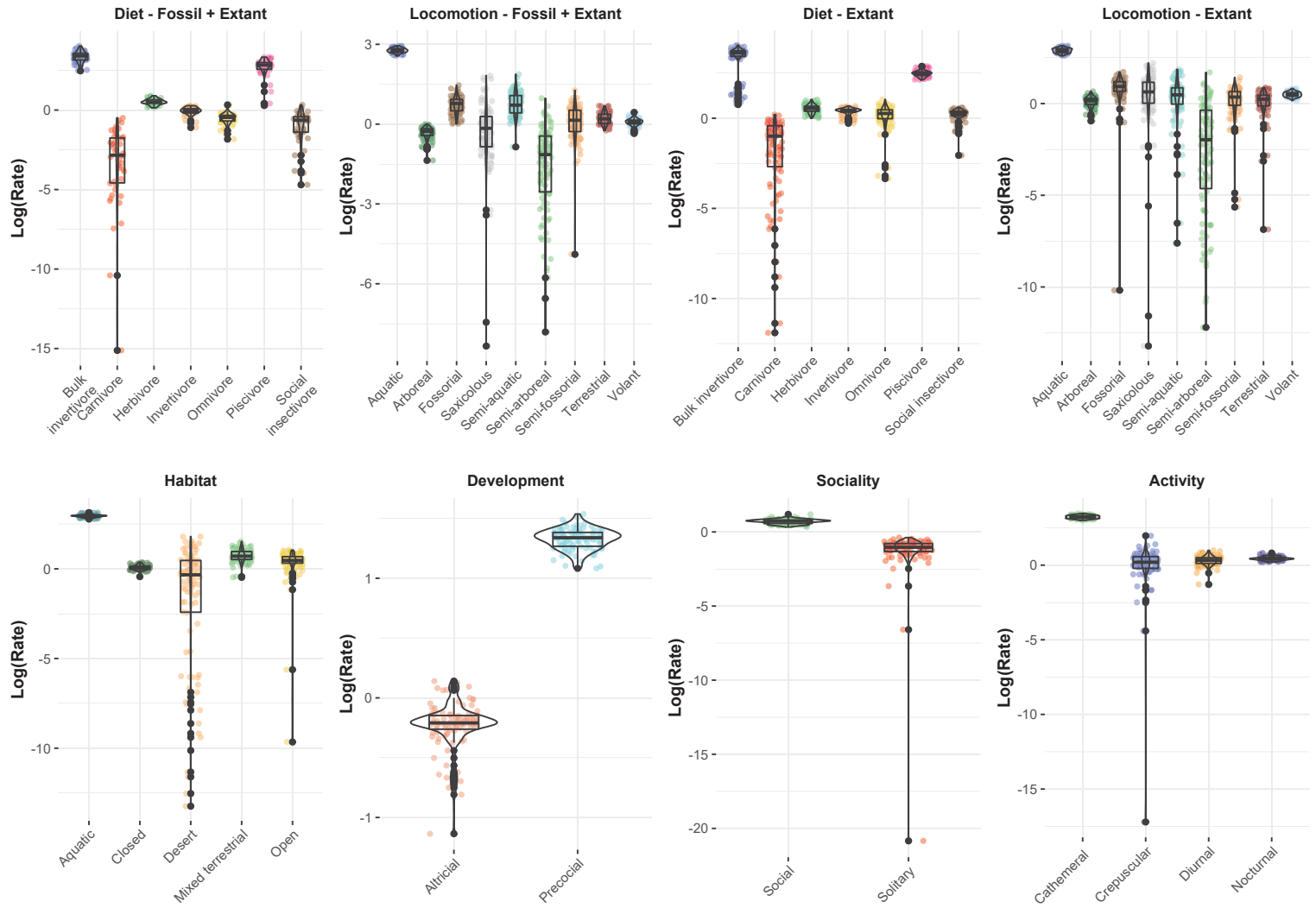


Fig. S7. H) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 2, Root Age = 75-80Ma.

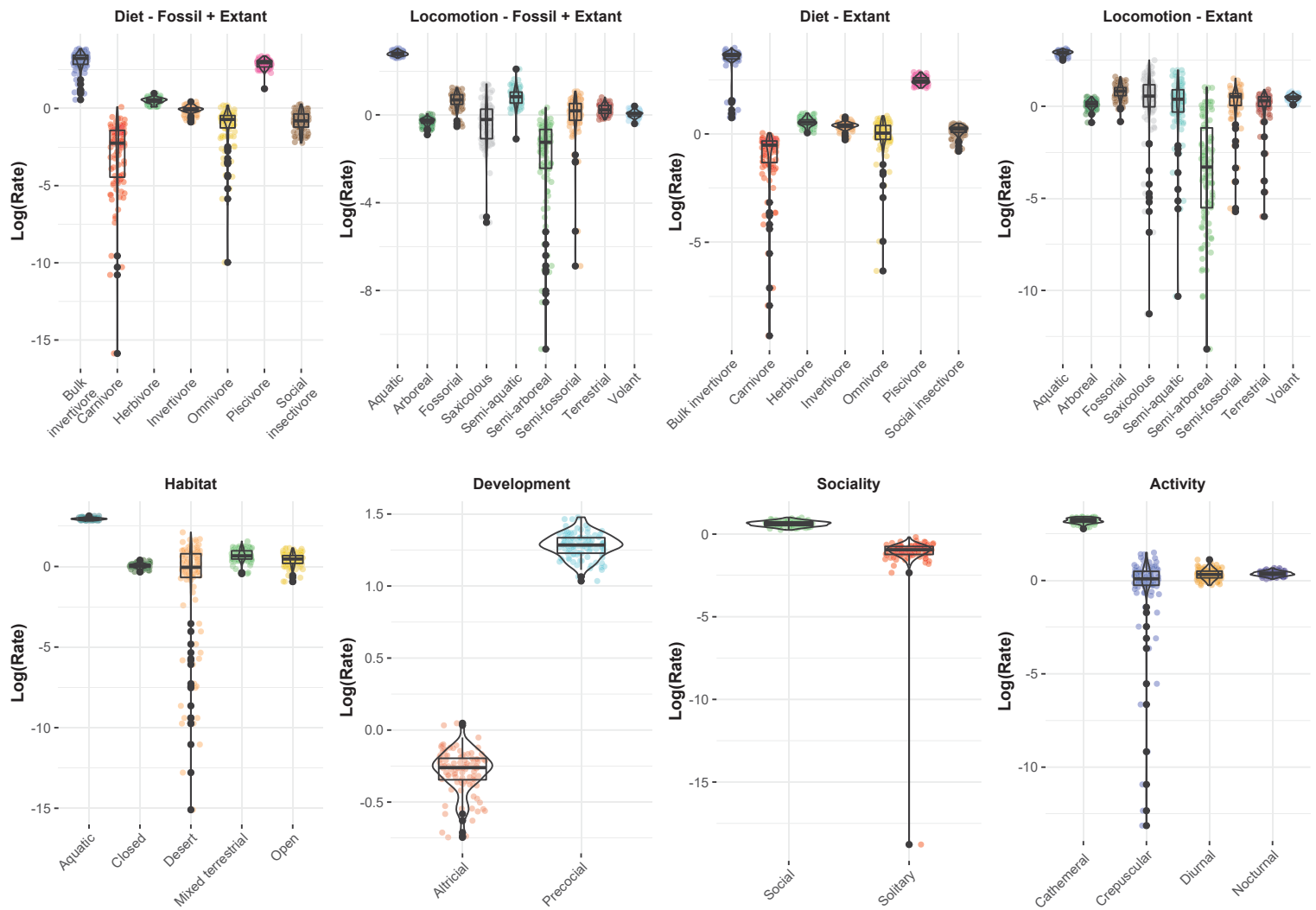


Fig. S7. I) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 2, Root Age = 80-85Ma.

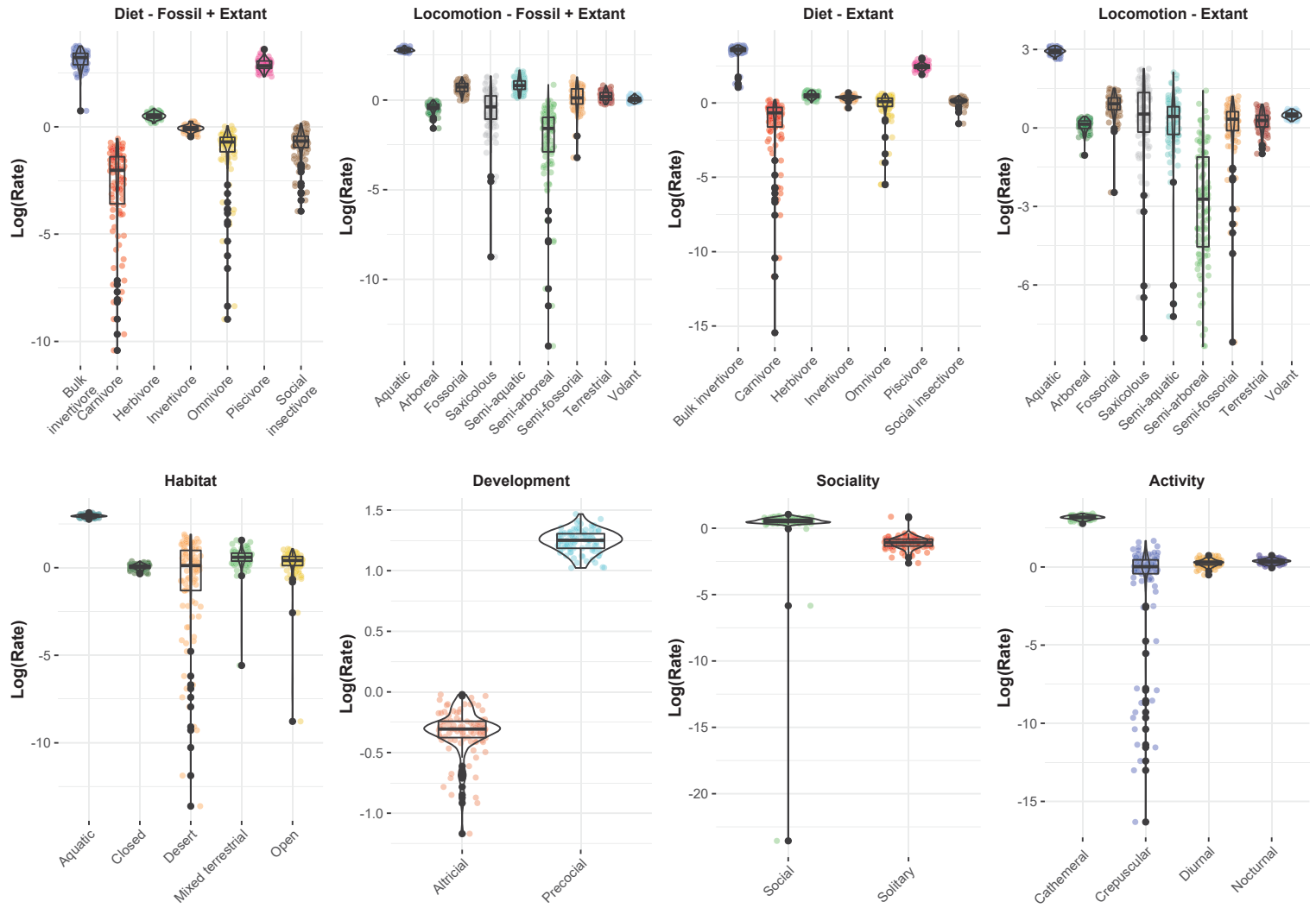


Fig. S7. J) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 2, Root Age = 85-90Ma.

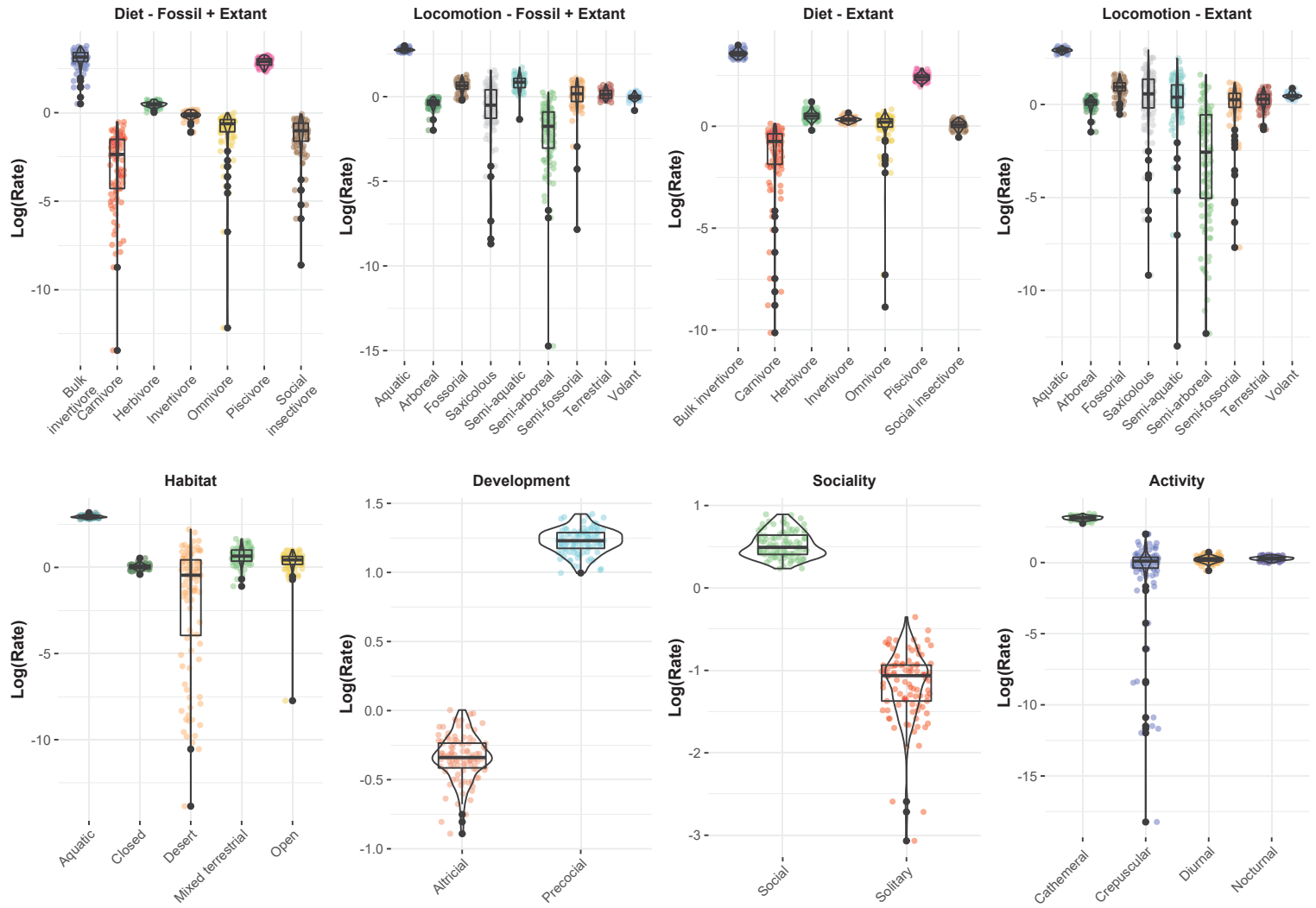


Fig. S7. K) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 2, Root Age = 90-95Ma.

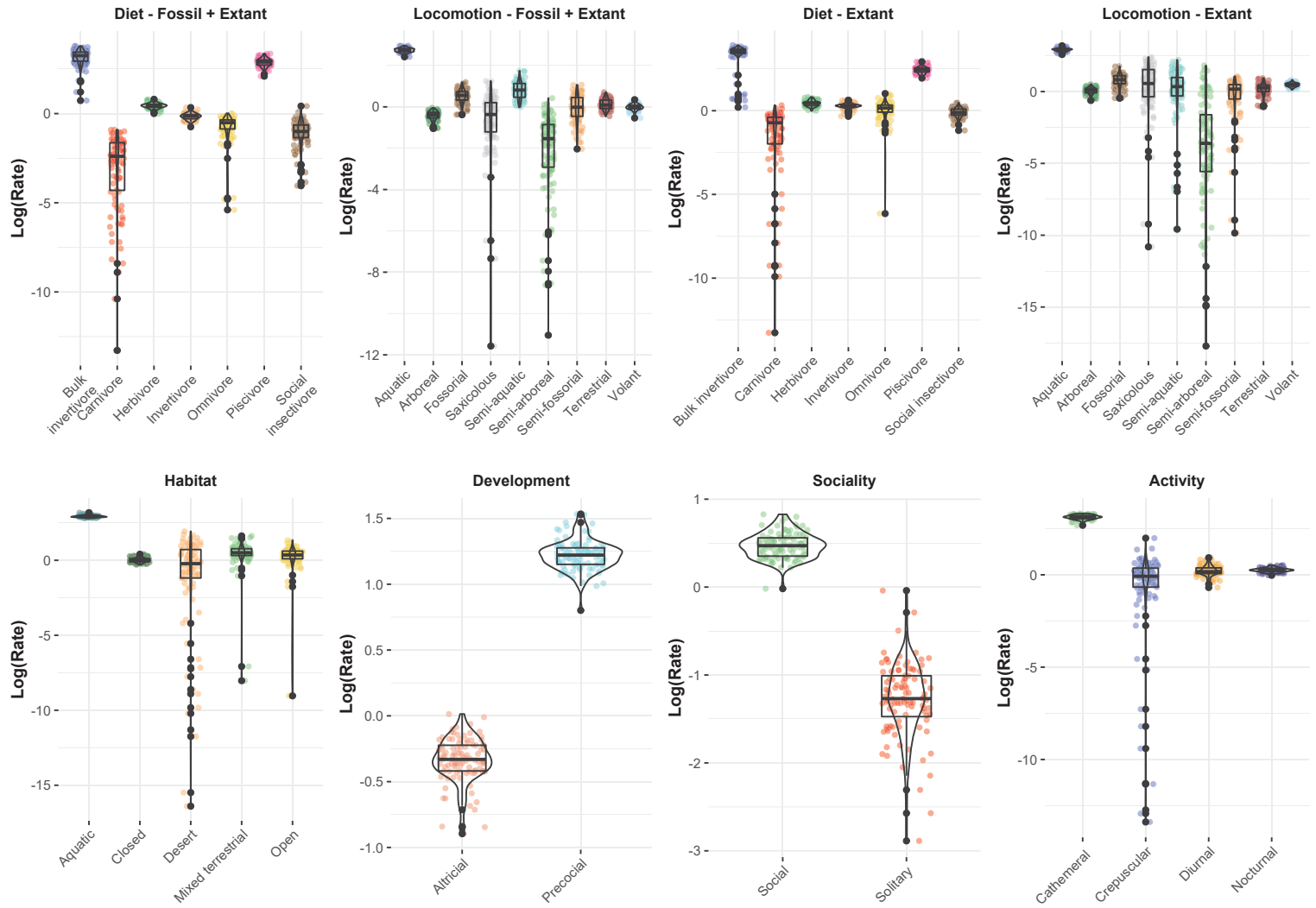


Fig. S7. L) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 2, Root Age = 95-100Ma.

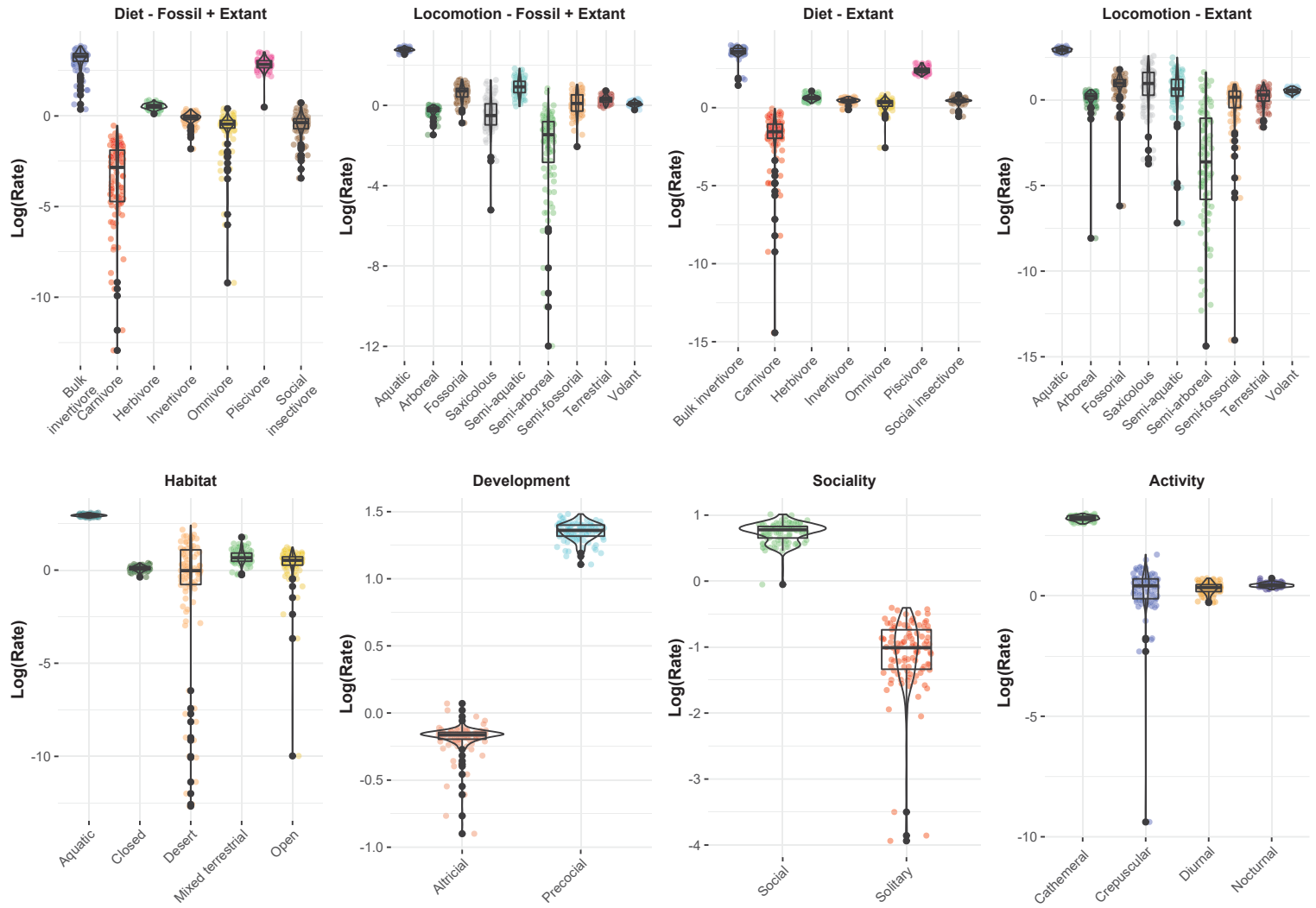


Fig. S7. M) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 3, Root Age = 70-75Ma.

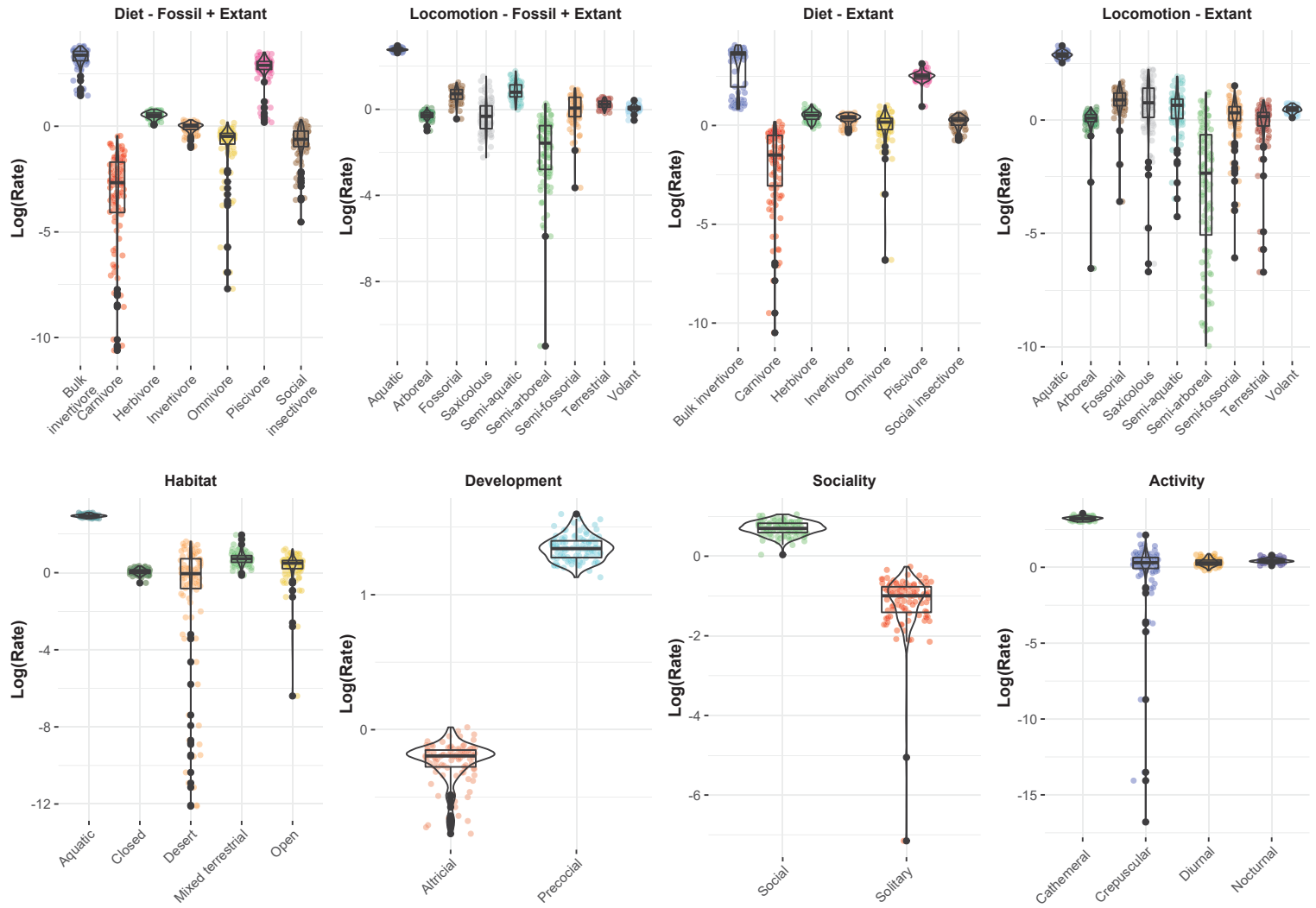


Fig. S7. N) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 3, Root Age = 75-80Ma.

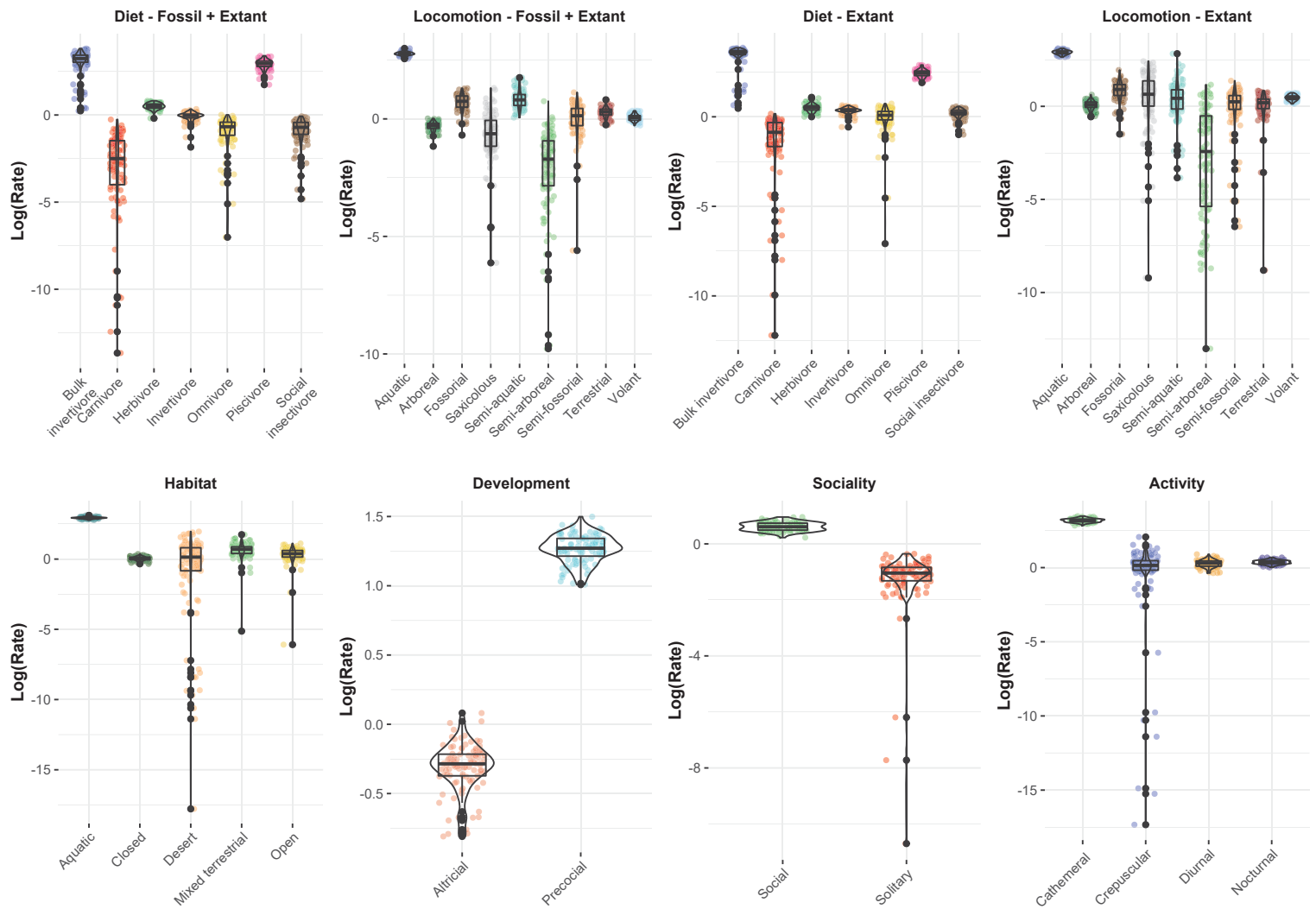


Fig. S7. O) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 3, Root Age = 80-85Ma.

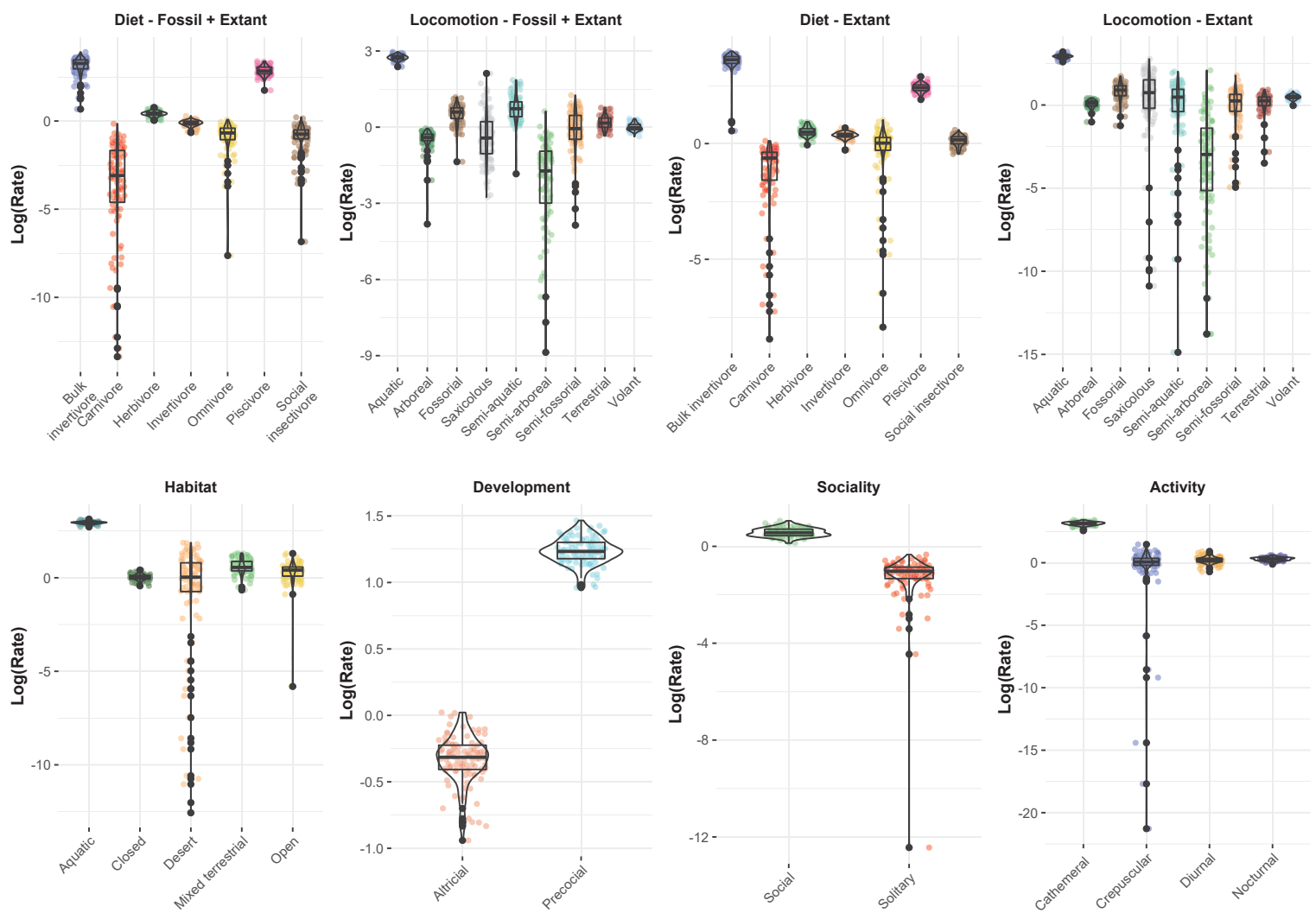


Fig. S7. P) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 3, Root Age = 85-90Ma.

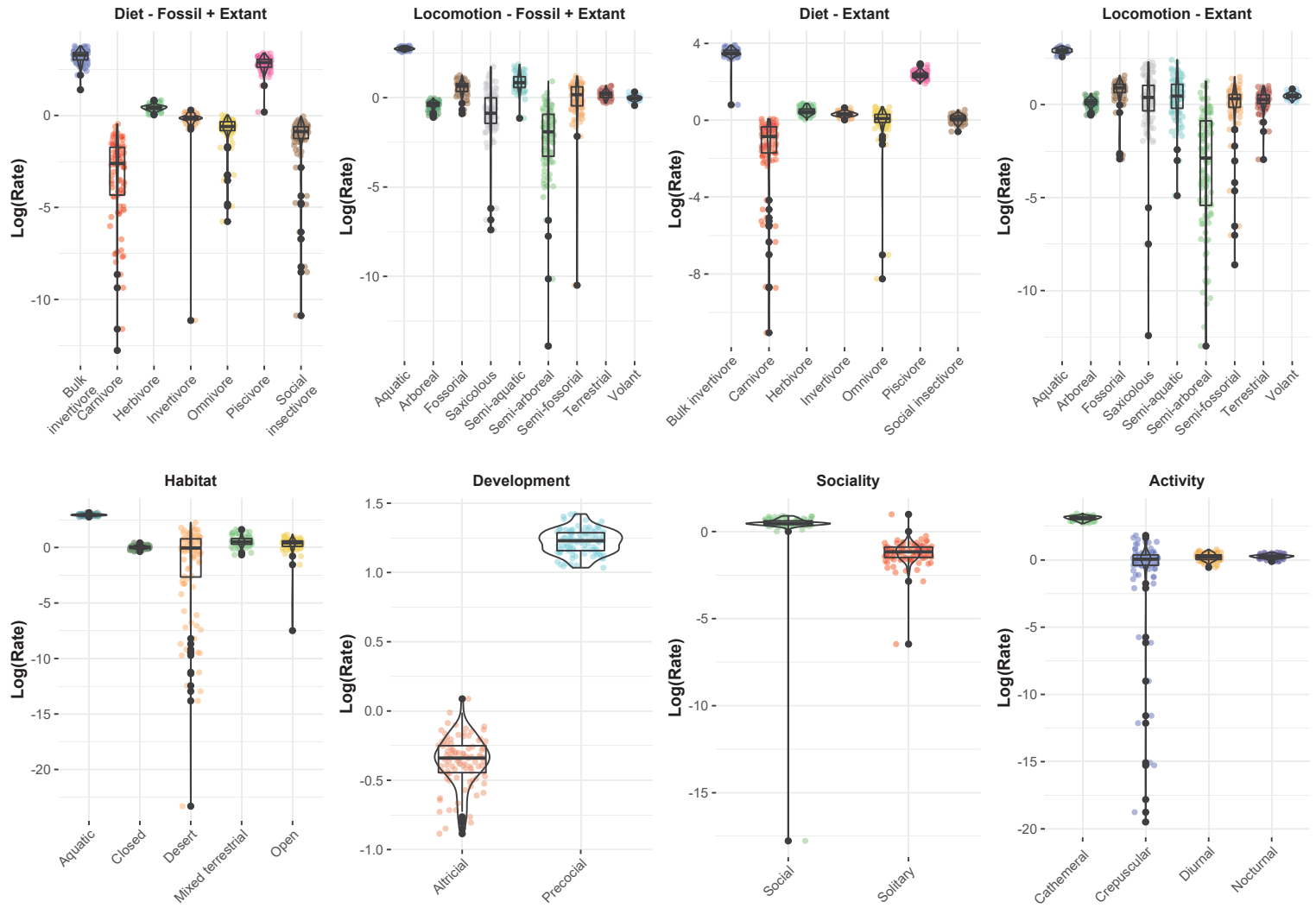


Fig. S7. Q) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 3, Root Age = 90-95Ma.

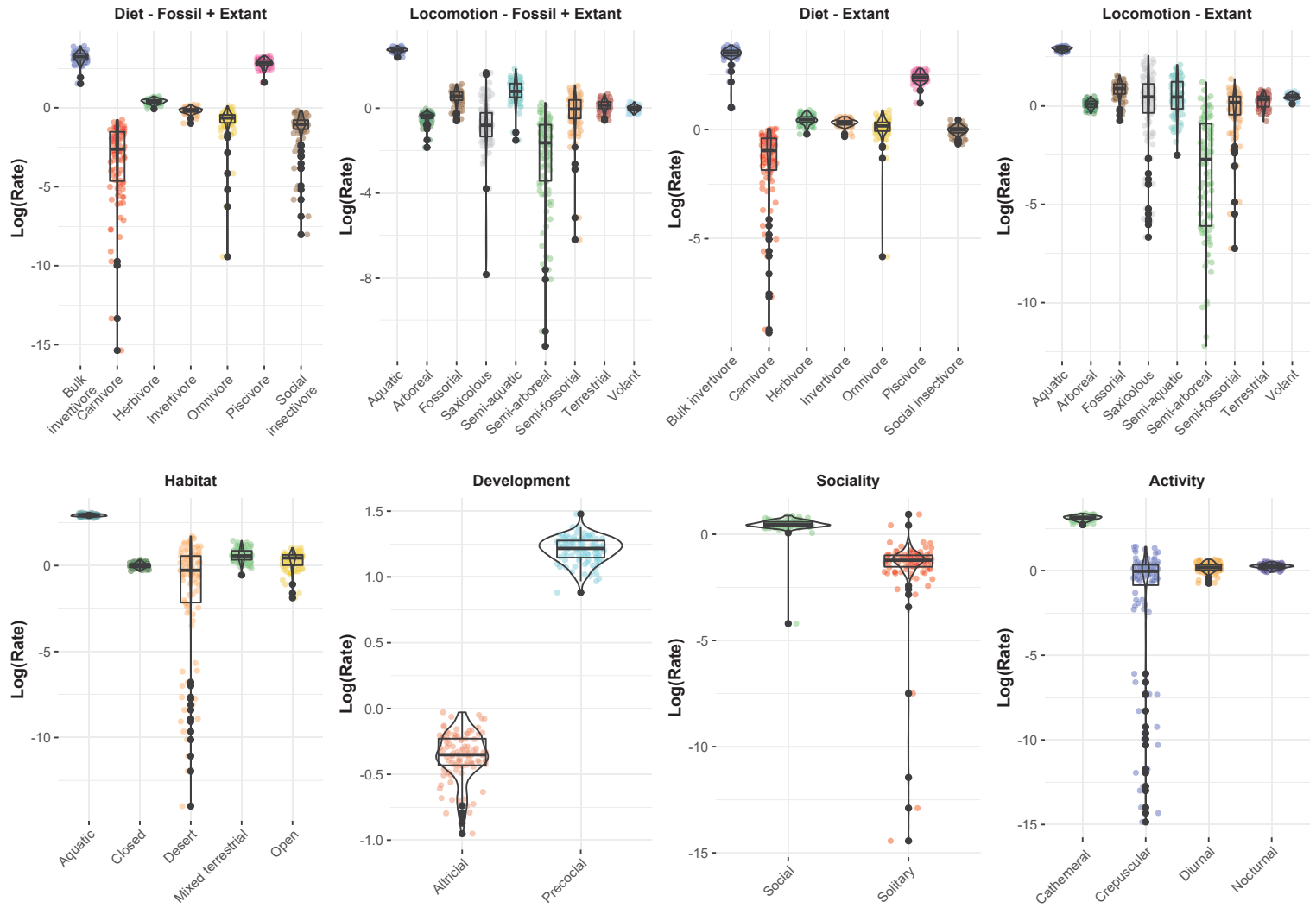


Fig. S7. R) Rates of evolution based on ecological and life history traits for placentals for Tree Topology 3, Root Age = 95-100Ma.

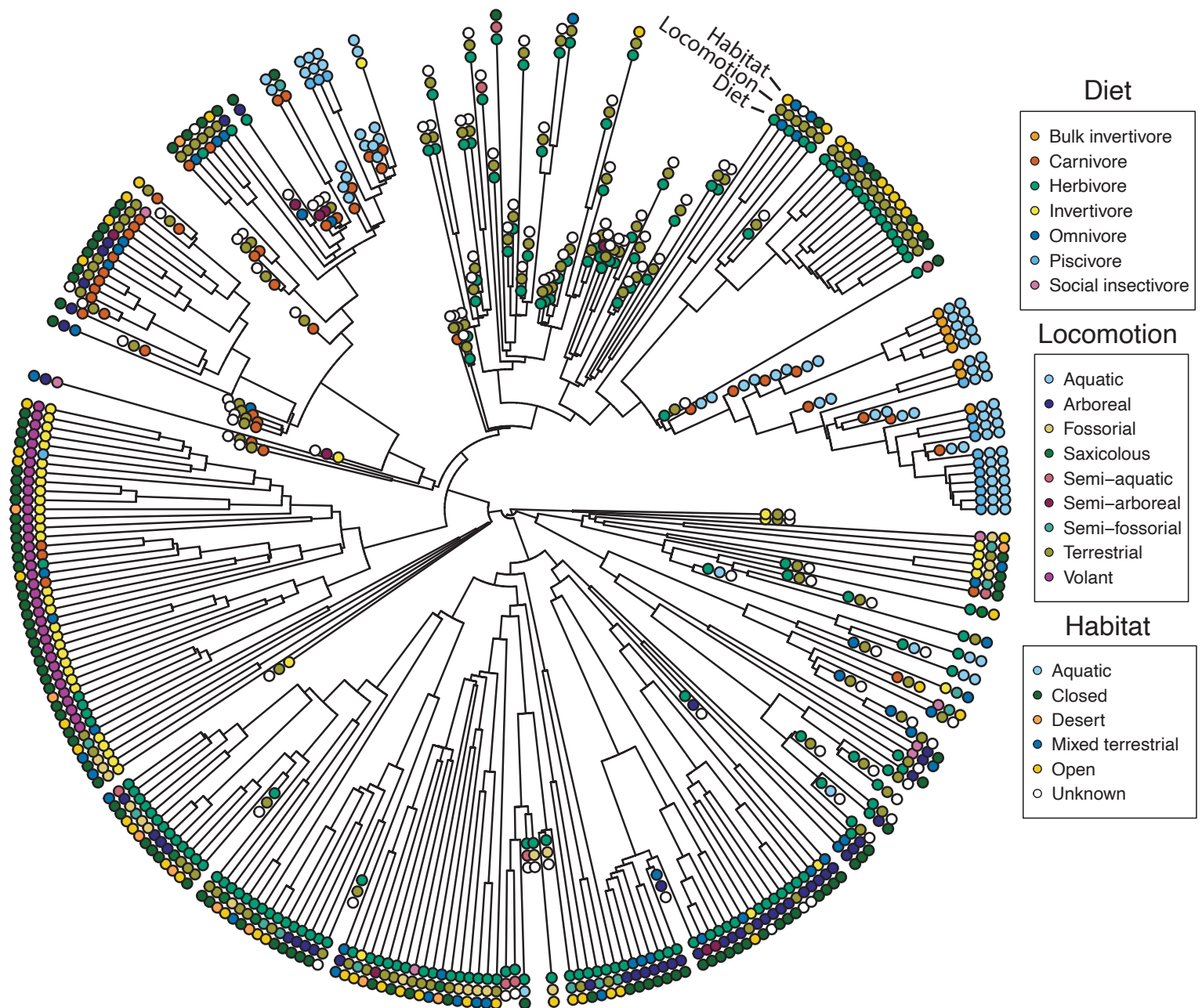


Fig. S8. A) Trait distributions for ecological traits, shown on Tree Topology 2, Root Age 80-85 Ma. Habitat traits are unknown for extinct taxa. Details of traits and references are provided in Table S1. Tree topology with species names is provided in Figure S4.

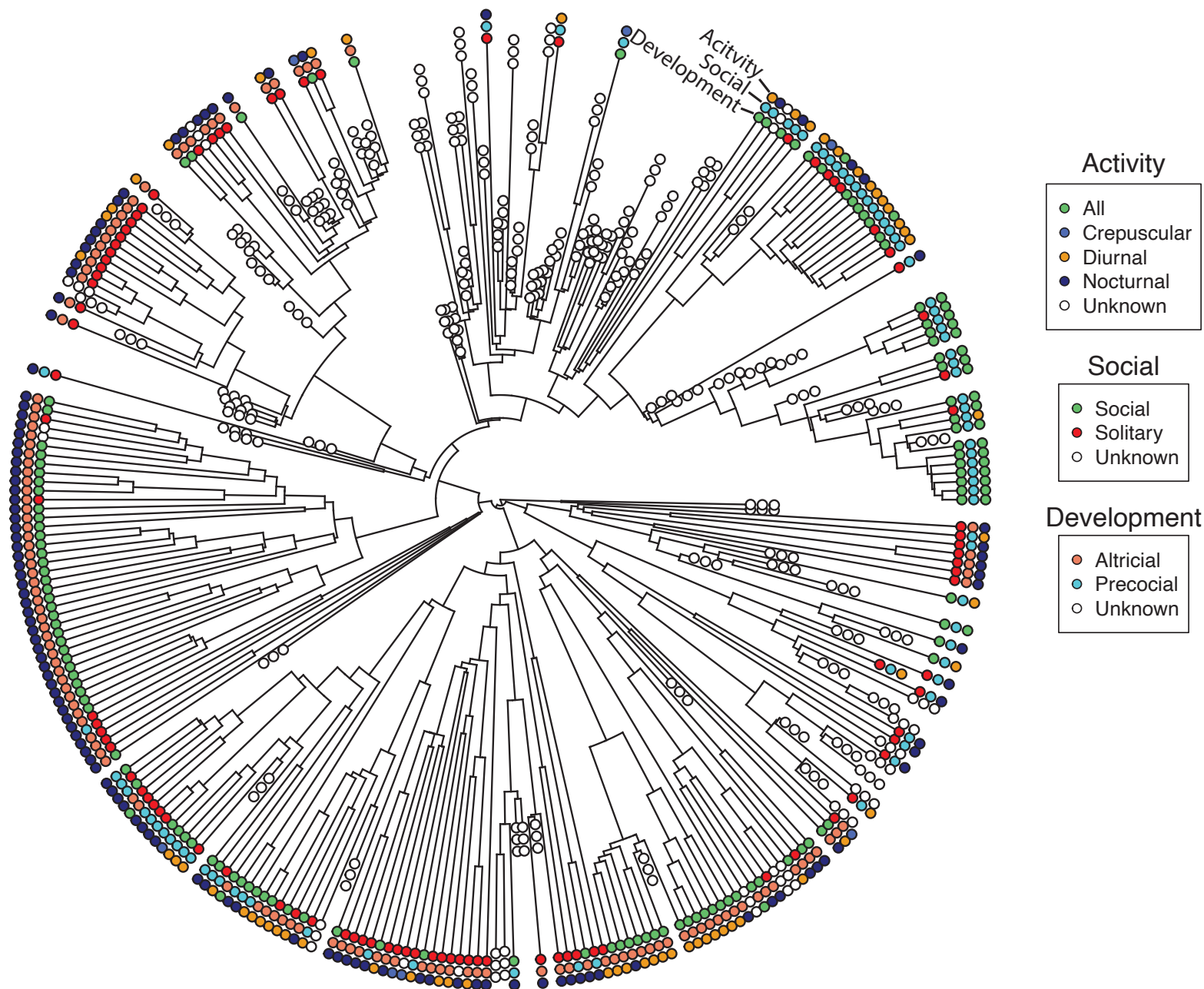


Fig. S8. B) Trait distributions for life history traits, shown on Tree Topology 2, Root Age 80-85 Ma. Traits are unknown for extinct taxa. Details of traits and references are provided in Table S1. Tree topology with species names is provided in Figure S4.

Table S1. Details of landmarks and curve sliding semi-landmarks.

Landmarks	Description	Element colour in Figure 1
1	Nasal: anteromedial	Turquoise
2	Nasal: anterolateral suture with premaxilla	
3	Nasal: posterolateral suture with frontal	
4	Nasal: posteromedial suture with frontal	
5	Premaxilla: anteromedial tip of rostrum,	Orange
6	Premaxilla: anterodorsal suture with nasal	
7	Premaxilla: posterodorsal suture with nasal and maxilla	
8	Premaxilla: posterolateral suture with maxilla, along tooth row	Dark orange
9	Maxilla: anterolateral suture with premaxilla, along tooth row	
10	Maxilla: anterodorsal suture with nasal and premaxilla	
11	Maxilla: posterodorsal/medial suture with nasal and frontal	
12	Maxilla/Lacrimal: posterodorsal junction with frontal along the orbit	
13	Maxilla: suture with jugal along the orbit	
14	Maxilla: ventral suture with jugal along the	
15	Maxilla: posterior end of tooth row	Green
16	Jugal: suture with maxilla along the orbit	
17	Jugal: ventral suture with maxilla along the zygomatic arch	
18	Jugal: posteroventral suture with squamosal	Pink
19	Frontal: anteromedial suture with nasal	
20	Frontal: posteromedial suture with parietal	
21	Frontal: posterolateral suture with parietal	
22	Frontal: postorbital process/bar tip	
23	Frontal: anterolateral suture with maxilla on orbit	
24	Frontal: anterodorsal suture with nasal and	Light green
25	Parietal: anteromedial suture with frontal	
26	Parietal: posteromedial suture with supraoccipital	
27	Parietal: posterolateral suture with squamosal and occipital	
28	Parietal: anterolateral suture with squamosal	
29	Parietal: anterolateral suture with frontal	
30	Squamosal: anterodorsal suture with parietal	Light blue
31	Squamosal: anteromedial junction of vault and zygomatic arch	
32	Squamosal: anterodorsal suture with jugal	
33	Squamosal: posteroventral/lateral suture with jugal	

34	Squamosal: anteromedial edge of glenoid	Yellow
35	Squamosal: posterolateral edge of glenoid	
36	Squamosal: posterolateral suture with occipital	Light blue
37	Squamosal: posterodorsal suture with parietal and occipital	
38	Posteromedial margin of skull roof	Pale yellow
39	Supraoccipital: anteromedial suture with parietal	
40	Occipital: opisthion	
41	Occipital condyle: dorsomedial	Red
42	Occipital condyle: dorsolateral	
43	Paraoccipital process	Pale yellow
44	Occipital: ventrolateral suture with squamosal	
45	Occipital: dorsolateral suture with squamosal and parietal	
46	Occipital condyle: ventrolateral	Red
47	Occipital condyle: ventromedial	
48	Basioccipital: basion	Purple
49	Basioccipital: anteromedial with basisphenoid	
50	Basioccipital: anterolateral with basisphenoid	
51	Basisphenoid: anteromedial with presphenoid	Dark grey
52	Basisphenoid: anterolateral with presphenoid	
53	Basisphenoid: posterolateral with basioccipital	
54	Basisphenoid: posteromedial suture with basioccipital	
55	Palatine: posteromedial	Blue
56	Palatine: anteromedial suture with maxilla	
57	Palatine: posteromedial suture with pterygoid	
58	Palatine: posteriolateral suture with maxilla	Hot pink
59	Pterygoid: posterior process	
60	Pterygoid: posterodorsal suture	Rose
61	Maxilla (ventral): posteromedial suture with palatine	
62	Maxilla (ventral): anteromedial suture with premaxilla	
63	Maxilla (ventral): anterolateral suture with premaxilla along tooth row	Light grey
64	Premaxilla (ventral): posteromedial suture with maxilla (or foramen)	
65	Premaxilla (ventral): anteromedial edge,	
66	Premaxilla (ventral): posterolateral suture with maxilla, along tooth row	

Curves	Description	From landmark	To landmark
1	Nasal: midline	1	4
2	Nasal: posterior	4	3
3	Nasal: lateral	3	2
4	Nasal: anterior	2	1
5	Premaxilla: anterior	5	6
6	Premaxilla: dorsal	6	7
7	Premaxilla: posterior	7	8
8	Premaxilla: lateral (ventral margin)	8	5
9	Maxilla: anterior	9	10
10	Maxilla: dorsal	10	11
11	Maxilla: posterodorsal to orbit	11	12
12	Maxilla: orbit	12	13
13	Maxilla: orbit to zygomatic	13	14
14	Maxilla: posteroventral	14	15
15	Maxilla: tooth row	15	9
16	Jugal: dorsal	16	18
17	Jugal: ventral	18	17
18	Jugal: anterior	17	16
19	Frontal: anteromedial	19	24
20	Frontal: anterolateral	24	23
21	Frontal: orbit	23	22
22	Frontal: postorbital process to vault along orbit	22	21
23	Frontal: posterior	21	20
24	Frontal: midline	20	19
25	Parietal: midline	25	26
26	Parietal: posterior	26	27
27	Parietal: lateral	27	28
28	Parietal: squamosal to frontal (where separated)	28	29
29	Parietal: anterolateral to midline	29	25
30	Glenoid: anterior	34	35
31	Glenoid: posterior	35	34
32	Squamosal: ventral zygomatic	32	33
33	Squamosal: dorsal zygomatic	33	32
34	Squamosal: anterior vault	31	30
35	Squamosal: dorsal vault	30	37
36	Squamosal: posterior vault	37	36
37	Squamosal: ventral vault	36	31
38	Supra/Occipital: midline to foramen magnum	39	40
39	Foramen magnum: dorsal	40	41
40	Exoccipital: dorsal	41	42
41	Occipital: dorsolateral to paraoccipital process	42	43
42	Occipital: paraoccipital to ventrolateral occipital	43	44

43	Occipital: ventrolateral to suture with squamosal	44	45
44	Supra/Occipital: dorsal	45	39
45	Exoccipital: medial	41	46
46	Exoccipital: ventral	46	47
47	Exoccipital: lateral	47	42
48	Basioccipital: midline	48	49
49	Basioccipital: anterior	49	50
50	Basioccipital: lateral	50	47
51	Basioccipital: posterior	47	48
52	Basisphenoid: midline	54	51
53	Basisphenoid: anterior	51	52
54	Basisphenoid: lateral	52	54
55	Basisphenoid: posterior	53	54
56	Palatine: midline	55	56
57	Palatine: lateral	56	58
58	Palatine: posterolateral to pterygoid	58	57
59	Palatine: pterygoid to posteromedial	57	55
60	Pterygoid: suture with palatine to process	57	59
61	Pterygoid: posterior	59	60
62	Pterygoid: dorsal	60	57
63	Maxilla (ventral): midline	61	62
64	Maxilla (ventral): anterior	62	63
65	Maxilla (ventral): lateral	63	58
66	Maxilla (ventral):posterior	58	61
67	Premaxilla (ventral): posterior	64	66
68	Premaxilla (ventral): lateral	66	65
69	Premaxilla (ventral): medial	65	64

Phylogenetic Regressions: Tree Topology 1, Extant Taxa only								Factors					
	Size	Diet	Locomotion	Habitat	Development	Activity	Social	Size:Diet	Size:Loc	Size:Hab	Size:Act	Size:Dev	Size:Soc
Tree Topology 1: Root Age 70-75													
Pillai's Test Statistic	0.979	5.562	7.313	3.688	2.761	1.853	1.838	5.608	6.441	2.764	2.783	1.873	1.871
SES	4.353	2.025	1.289	0.975	0.900	0.427	0.267	1.695	0.656	0.213	0.555	0.742	0.454
P value	0.001	0.008	0.081	0.155	0.174	0.382	0.476	0.023	0.268	0.457	0.305	0.243	0.362
Tree Topology 1: Root Age 75-80													
Pillai's Test Statistic	0.982	5.612	7.391	3.726	2.791	1.866	1.859	5.655	6.502	2.795	2.809	1.886	1.889
SES	4.695	2.622	2.073	1.619	1.525	0.726	0.679	2.438	1.498	0.911	1.139	1.156	0.878
P value	0.001	0.002	0.006	0.034	0.050	0.232	0.254	0.002	0.059	0.176	0.110	0.109	0.170
Tree Topology 1: Root Age 80-85													
Pillai's Test Statistic	0.981	5.608	7.381	3.718	2.783	1.866	1.851	5.645	6.493	2.786	2.804	1.884	1.880
SES	4.271	2.630	1.930	1.471	1.283	0.783	0.481	2.170	1.273	0.705	0.964	1.042	0.625
P value	0.001	0.002	0.011	0.056	0.085	0.215	0.329	0.008	0.086	0.252	0.156	0.146	0.291
Tree Topology 1: Root Age 85-90													
Pillai's Test Statistic	0.981	5.610	7.391	3.718	2.782	1.872	1.854	5.646	6.497	2.785	2.804	1.887	1.880
SES	4.219	2.593	2.064	1.430	1.236	0.844	0.540	2.095	1.365	0.668	0.968	1.170	0.613
P value	0.001	0.001	0.010	0.061	0.096	0.186	0.322	0.004	0.071	0.273	0.161	0.097	0.291
Tree Topology 1: Root Age 90-95													
Pillai's Test Statistic	0.983	5.641	7.436	3.739	2.799	1.882	1.863	5.670	6.535	2.802	2.819	1.896	1.887
SES	4.438	3.026	2.520	1.869	1.674	1.038	0.717	2.573	1.922	1.083	1.289	1.405	0.820
P value	0.001	0.001	0.002	0.012	0.033	0.133	0.232	0.001	0.019	0.131	0.071	0.049	0.203
Tree Topology 1: Root Age 95-100													
Pillai's Test Statistic	0.982	5.619	7.412	3.722	2.786	1.876	1.854	5.647	6.507	2.789	2.808	1.890	1.879
SES	4.447	2.795	2.249	1.555	1.382	0.996	0.535	2.211	1.537	0.712	1.099	1.258	0.562
P value	0.001	0.001	0.002	0.049	0.056	0.140	0.336	0.006	0.061	0.253	0.125	0.075	0.310

Table S2. A) Phylogenetic regressions of ecological, developmental, and social traits on skull shape, assessed with extant taxa only (all factors), for Tree Topology 1.

Phylogenetic Regressions: Tree Topology 1, Full Dataset					
	Factors				
	Size	Diet	Locomotion	Size:Diet	Size:Loc
Tree Topology 1: Root Age 70-75					
Pillai's Test Statistic	0.974	5.387	7.059	5.289	7.006
SES	6.540	3.703	2.767	1.204	0.979
P value	0.001	0.001	0.003	0.109	0.177
Tree Topology 1: Root Age 75-80					
Pillai's Test Statistic	0.974	5.387	7.083	5.296	7.043
SES	6.717	3.626	2.985	1.356	1.378
P value	0.001	0.001	0.002	0.077	0.075
Tree Topology 1: Root Age 80-85					
Pillai's Test Statistic	0.974	5.413	7.069	5.305	7.001
SES	7.303	4.170	2.686	1.282	0.685
P value	0.001	0.001	0.002	0.091	0.264
Tree Topology 1: Root Age 85-90					
Pillai's Test Statistic	0.975	5.452	7.103	5.406	7.074
SES	6.909	4.584	2.808	2.483	1.364
P value	0.001	0.001	0.001	0.005	0.074
Tree Topology 1: Root Age 90-95					
Pillai's Test Statistic	0.974	5.416	7.110	5.339	7.090
SES	6.696	4.080	3.160	1.651	1.861
P value	0.001	0.001	0.002	0.040	0.033
Tree Topology 1: Root Age 95-100					
Pillai's Test Statistic	0.975	5.419	7.103	5.371	7.082
SES	6.980	4.037	3.043	2.167	1.689
P value	0.001	0.001	0.001	0.017	0.043

Table S2. B) Phylogenetic regressions of ecological, developmental, and social traits on skull shape, assessed with full dataset (for diet, locomotion, and size only), for Tree Topology 1.

Phylogenetic Regressions: Tree Topology 2, Extant Taxa only													
	Factors												
	Size	Diet	Locomotion	Habitat	Development	Activity	Social	Size:Diet	Size:Loc	Size:Hab	Size:Act	Size:Dev	Size:Soc
Tree Topology 2: Root Age 70-75													
Pillai's Test Statistic	0.981	5.605	7.381	3.715	2.781	1.867	1.851	5.642	6.492	2.783	2.803	1.885	1.879
SES	4.542	2.606	1.948	1.362	1.251	0.753	0.465	2.052	1.290	0.634	0.942	1.122	0.621
P value	0.001	0.001	0.014	0.069	0.084	0.231	0.373	0.009	0.091	0.279	0.171	0.112	0.297
Tree Topology 2: Root Age 75-80													
Pillai's Test Statistic	0.980	5.584	7.336	3.704	2.774	1.858	1.847	5.629	6.467	2.777	2.794	1.879	1.878
SES	4.364	2.427	1.525	1.146	1.134	0.553	0.452	2.008	1.017	0.504	0.801	0.975	0.600
P value	0.001	0.001	0.048	0.120	0.123	0.329	0.375	0.012	0.161	0.329	0.218	0.176	0.294
Tree Topology 2: Root Age 80-85													
Pillai's Test Statistic	0.980	5.584	7.331	3.706	2.777	1.856	1.849	5.633	6.469	2.780	2.796	1.879	1.882
SES	4.506	2.377	1.490	1.336	1.249	0.553	0.477	2.022	1.027	0.645	0.881	0.960	0.643
P value	0.001	0.001	0.040	0.075	0.100	0.328	0.343	0.013	0.148	0.277	0.188	0.168	0.269
Tree Topology 2: Root Age 85-90													
Pillai's Test Statistic	0.981	5.596	7.382	3.715	2.784	1.866	1.851	5.643	6.490	2.786	2.806	1.885	1.883
SES	4.573	2.402	1.958	1.411	1.418	0.786	0.503	2.160	1.268	0.762	0.970	1.141	0.673
P value	0.001	0.002	0.006	0.070	0.063	0.225	0.344	0.004	0.097	0.249	0.167	0.110	0.250
Tree Topology 2: Root Age 90-95													
Pillai's Test Statistic	0.981	5.608	7.379	3.725	2.790	1.866	1.856	5.650	6.496	2.792	2.809	1.885	1.885
SES	4.588	2.586	1.906	1.530	1.465	0.770	0.568	2.249	1.443	0.889	1.102	1.134	0.771
P value	0.001	0.001	0.010	0.050	0.058	0.238	0.306	0.005	0.068	0.195	0.123	0.105	0.227
Pillai's Test Statistic	0.980	5.583	7.344	3.674	2.751	1.866	1.830	5.595	6.437	2.750	2.774	1.877	1.850
SES	4.320	2.323	1.616	0.740	0.660	0.709	0.093	1.444	0.549	-0.139	0.356	0.766	-0.022
P value	0.001	0.003	0.033	0.244	0.283	0.238	0.546	0.062	0.323	0.605	0.379	0.223	0.590

Table S2. C) Phylogenetic regressions of ecological, developmental, and social traits on skull shape, assessed with extant taxa only (all factors), for Tree Topology 2.

Phylogenetic Regressions: Tree Topology 2, Full Dataset					
	Factors				
	Size	Diet	Locomotion	Size:Diet	Size:Loc
Tree Topology 2: Root Age 70-75					
Pillai's Test Statistic	0.975	5.383	7.049	5.291	7.011
SES	6.888	3.629	2.481	1.185	0.965
P value	0.001	0.001	0.004	0.112	0.165
Tree Topology 2: Root Age 75-80					
Pillai's Test Statistic	0.974	5.383	7.044	5.298	7.044
SES	6.785	3.404	2.442	1.273	1.351
P value	0.001	0.001	0.007	0.092	0.087
Tree Topology 2: Root Age 80-85					
Pillai's Test Statistic	0.974	5.383	7.045	5.298	7.044
SES	6.879	3.478	2.474	1.243	1.410
P value	0.001	0.001	0.003	0.103	0.074
Tree Topology 2: Root Age 85-90					
Pillai's Test Statistic	0.974	5.424	7.097	5.315	7.018
SES	7.167	3.979	3.222	1.422	0.894
P value	0.001	0.001	0.001	0.061	0.186
Tree Topology 2: Root Age 90-95					
Pillai's Test Statistic	0.974	5.383	7.058	5.350	7.061
SES	6.756	3.711	2.549	1.928	1.622
P value	0.001	0.001	0.005	0.011	0.050
Tree Topology 2: Root Age 95-100					
Pillai's Test Statistic	0.975	5.401	7.092	5.305	7.030
SES	6.880	3.723	3.091	1.323	1.182
P value	0.001	0.001	0.001	0.093	0.113

Table S2. D) Phylogenetic regressions of ecological, developmental, and social traits on skull shape, assessed with full dataset (for diet, locomotion, and size only), for Tree Topology 2.

Phylogenetic Regressions: Tree Topology 3, Extant Taxa only

	Factors												
	Size	Diet	Locomotion	Habitat	Development	Activity	Social	Size:Diet	Size:Loc	Size:Hab	Size:Act	Size:Dev	Size:Soc
Tree Topology 3: Root Age 70-75													
Pillai's Test Statistic	0.979	5.566	7.315	3.692	2.763	1.853	1.839	5.614	6.443	2.767	2.785	1.873	1.871
SES	4.321	2.112	1.345	1.057	0.852	0.531	0.255	1.794	0.633	0.243	0.615	0.745	0.501
P value	0.001	0.004	0.069	0.141	0.190	0.330	0.481	0.018	0.287	0.440	0.300	0.234	0.348
Tree Topology 3: Root Age 75-80													
Pillai's Test Statistic	0.982	5.625	7.416	3.729	2.792	1.876	1.857	5.659	6.516	2.794	2.813	1.892	1.883
SES	4.505	2.859	2.315	1.696	1.515	0.974	0.584	2.318	1.617	0.838	1.148	1.303	0.684
P value	0.001	0.001	0.006	0.028	0.046	0.142	0.299	0.004	0.039	0.206	0.105	0.076	0.272
Tree Topology 3: Root Age 80-85													
Pillai's Test Statistic	0.982	5.615	7.408	3.729	2.795	1.869	1.859	5.651	6.505	2.797	2.814	1.887	1.890
SES	4.467	2.735	2.294	1.692	1.587	0.833	0.683	2.326	1.488	1.026	1.227	1.197	0.826
P value	0.001	0.002	0.003	0.031	0.036	0.195	0.258	0.004	0.053	0.146	0.099	0.102	0.192
Tree Topology 3: Root Age 85-90													
Pillai's Test Statistic	0.979	5.564	7.336	3.688	2.763	1.857	1.838	5.608	6.445	2.765	2.786	1.875	1.869
SES	4.440	2.170	1.549	1.024	0.864	0.584	0.221	1.701	0.676	0.194	0.558	0.829	0.440
P value	0.001	0.009	0.041	0.154	0.208	0.300	0.473	0.028	0.245	0.458	0.319	0.219	0.372
Tree Topology 3: Root Age 90-95													
Pillai's Test Statistic	0.981	5.590	7.367	3.709	2.778	1.861	1.847	5.630	6.477	2.780	2.799	1.880	1.879
SES	4.511	2.481	1.821	1.277	1.181	0.619	0.397	2.008	1.126	0.525	0.952	0.902	0.606
P value	0.001	0.002	0.010	0.083	0.103	0.287	0.388	0.009	0.118	0.332	0.176	0.176	0.296
Tree Topology 3: Root Age 95-100													
Pillai's Test Statistic	0.981	5.609	7.385	3.717	2.784	1.867	1.853	5.641	6.490	2.786	2.806	1.885	1.879
SES	4.465	2.680	2.035	1.400	1.337	0.741	0.484	2.205	1.238	0.640	1.077	1.095	0.594
P value	0.001	0.002	0.007	0.078	0.082	0.233	0.347	0.004	0.104	0.277	0.125	0.113	0.300

Table S2. E) Phylogenetic regressions of ecological, developmental, and social traits on skull shape, assessed with extant taxa only (all factors), for Tree Topology 3.

Phylogenetic Regressions: Tree Topology 3, Full Dataset					
	Factors				
	Size	Diet	Locomotion	Size:Diet	Size:Loc
Tree Topology 3: Root Age 70-75					
Pillai's Test Statistic	0.974	5.385	7.060	5.291	7.003
SES	6.761	3.812	2.763	1.260	0.961
P value	0.001	0.001	0.001	0.095	0.153
Tree Topology 3: Root Age 75-80					
Pillai's Test Statistic	0.974	5.426	7.083	5.370	7.053
SES	6.533	3.719	2.791	2.284	1.427
P value	0.001	0.001	0.001	0.006	0.061
Tree Topology 3: Root Age 80-85					
Pillai's Test Statistic	0.975	5.406	7.119	5.349	7.067
SES	6.533	3.980	3.359	1.973	1.645
P value	0.001	0.001	0.001	0.018	0.040
Tree Topology 3: Root Age 85-90					
Pillai's Test Statistic	0.974	5.409	7.106	5.301	7.030
SES	6.896	3.980	3.325	1.295	1.187
P value	0.001	0.001	0.001	0.090	0.114
Tree Topology 3: Root Age 90-95					
Pillai's Test Statistic	0.974	5.436	7.116	5.356	7.061
SES	6.914	4.065	3.268	1.896	1.466
P value	0.001	0.001	0.001	0.015	0.062
Tree Topology 3: Root Age 95-100					
Pillai's Test Statistic	0.974	5.418	7.082	5.361	7.041
SES	6.626	4.212	2.957	2.015	1.244
P value	0.001	0.001	0.001	0.009	0.103

Table S2. F) Phylogenetic regressions of ecological, developmental, and social traits on skull shape, assessed with full dataset (for diet, locomotion, and size only), for Tree Topology 3.

Data S1. (separate file)

Specimen details and species trait data.