

Supplementary Information for

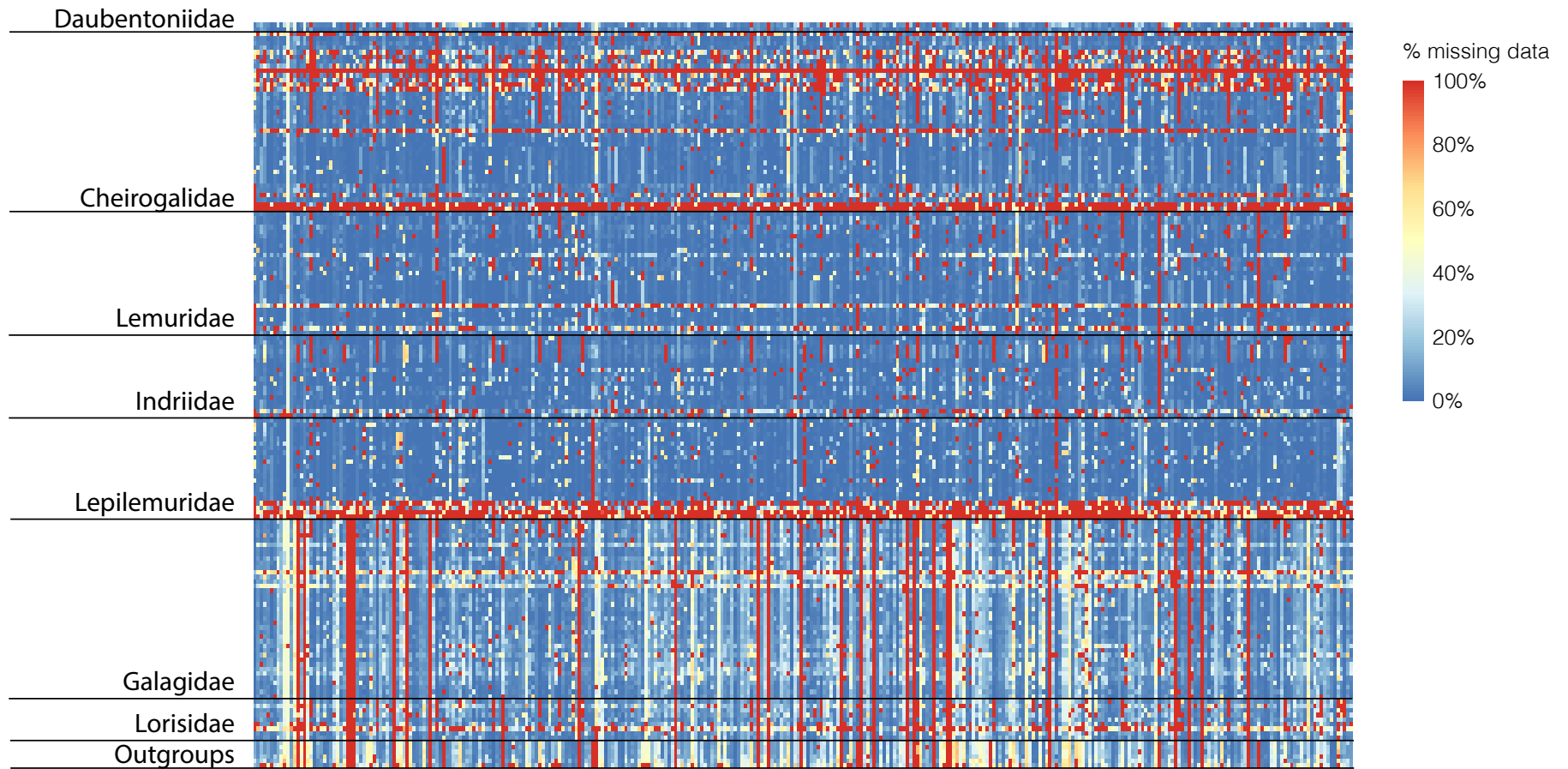
Multiple bursts of speciation in Madagascar's endangered lemurs

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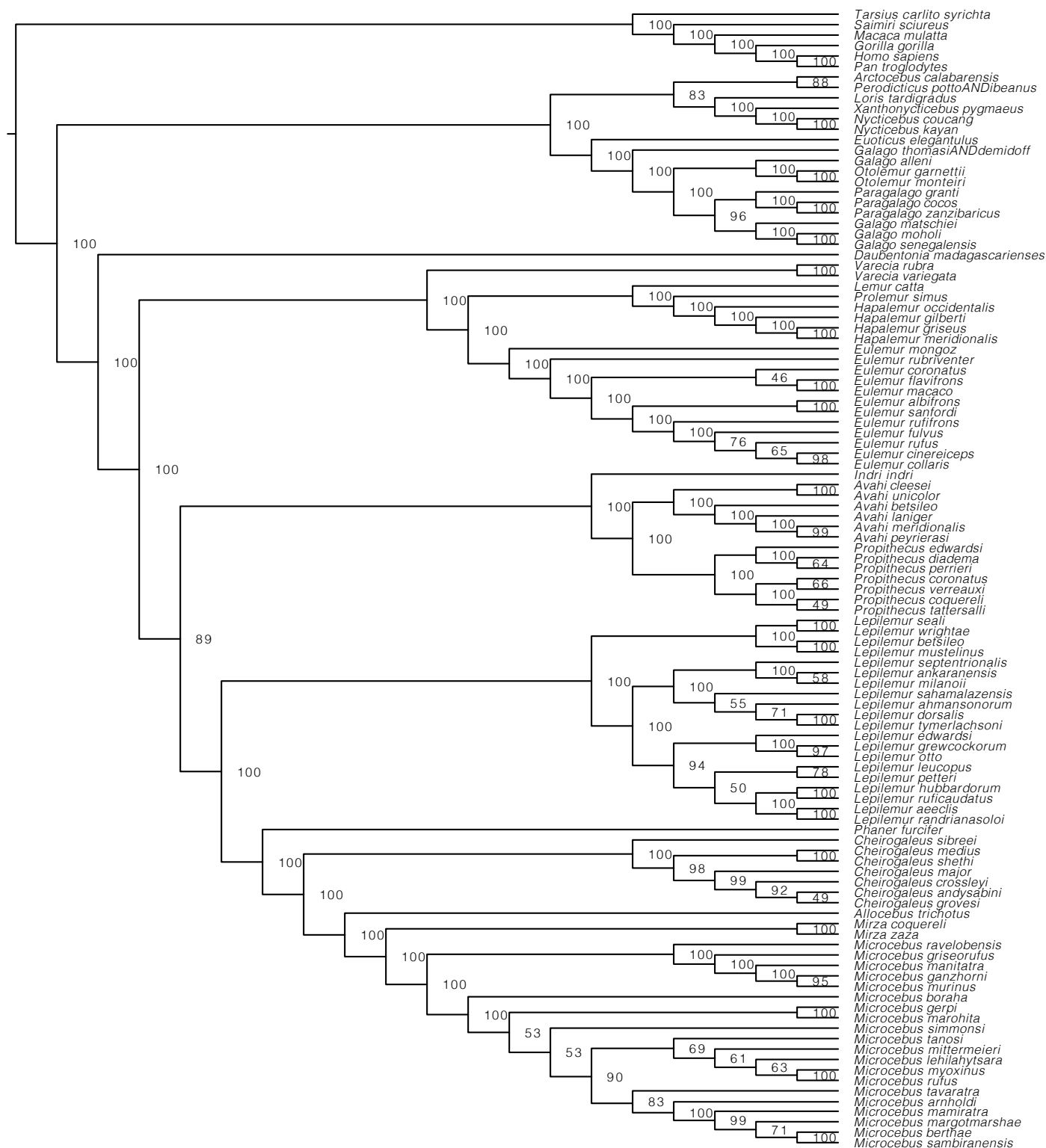
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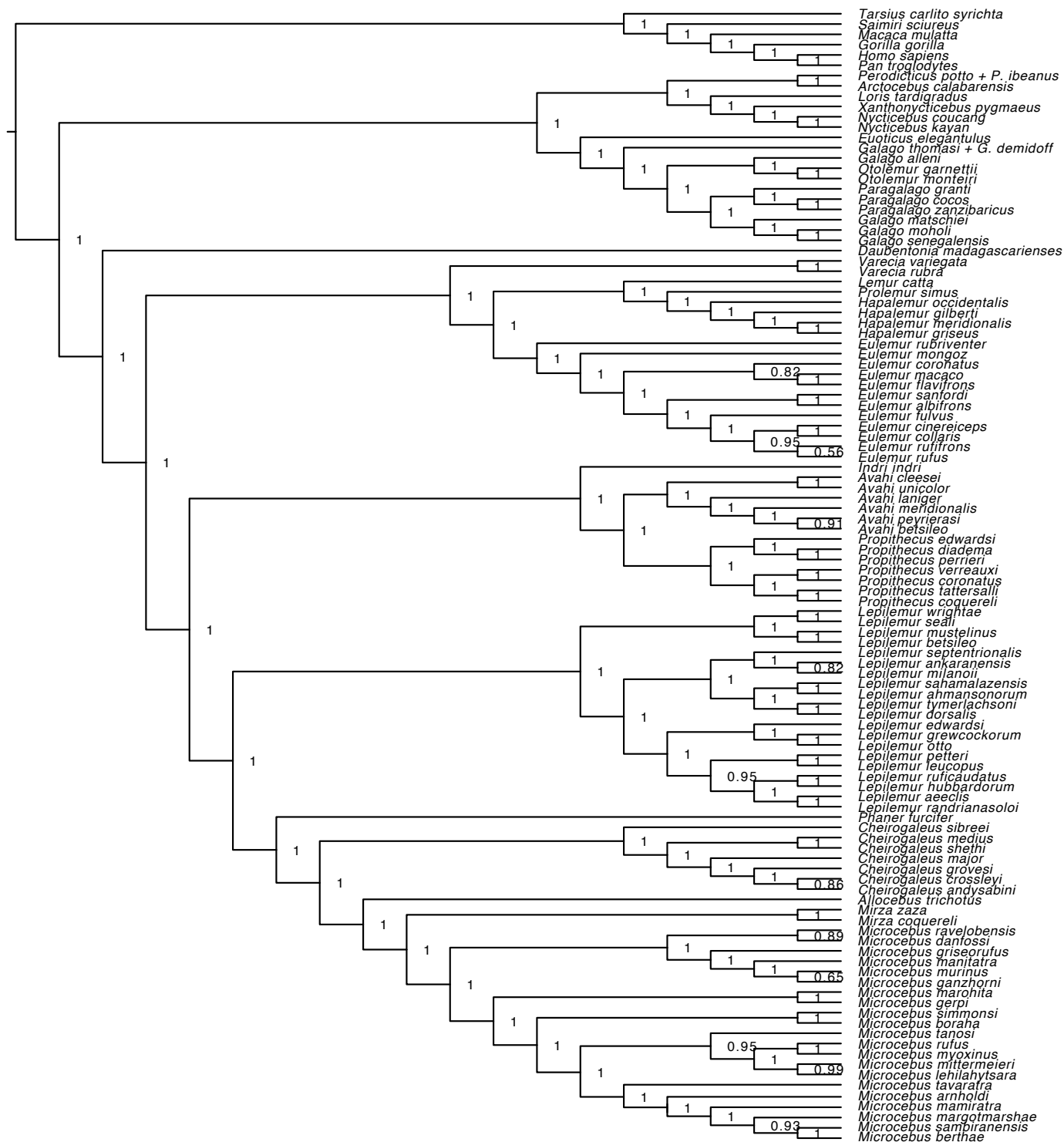
Supplementary Figures 1-18



Supplementary Figure 1. A visualization of the amount missing data in our nuclear dataset. Each row in the matrix represents an individual and each column represents a locus. Cells are colored according to the amount of missing data for in each alignment, along a gradient from blue (0% missing data) to red (100% missing data). The effects of missing data on our phylogenetic analyses were explored (see Methods and Figs. S12-S17). Family names for groups of individuals are shown to the left of the matrix. Source data for this figure can be found in Supplementary Data 12.

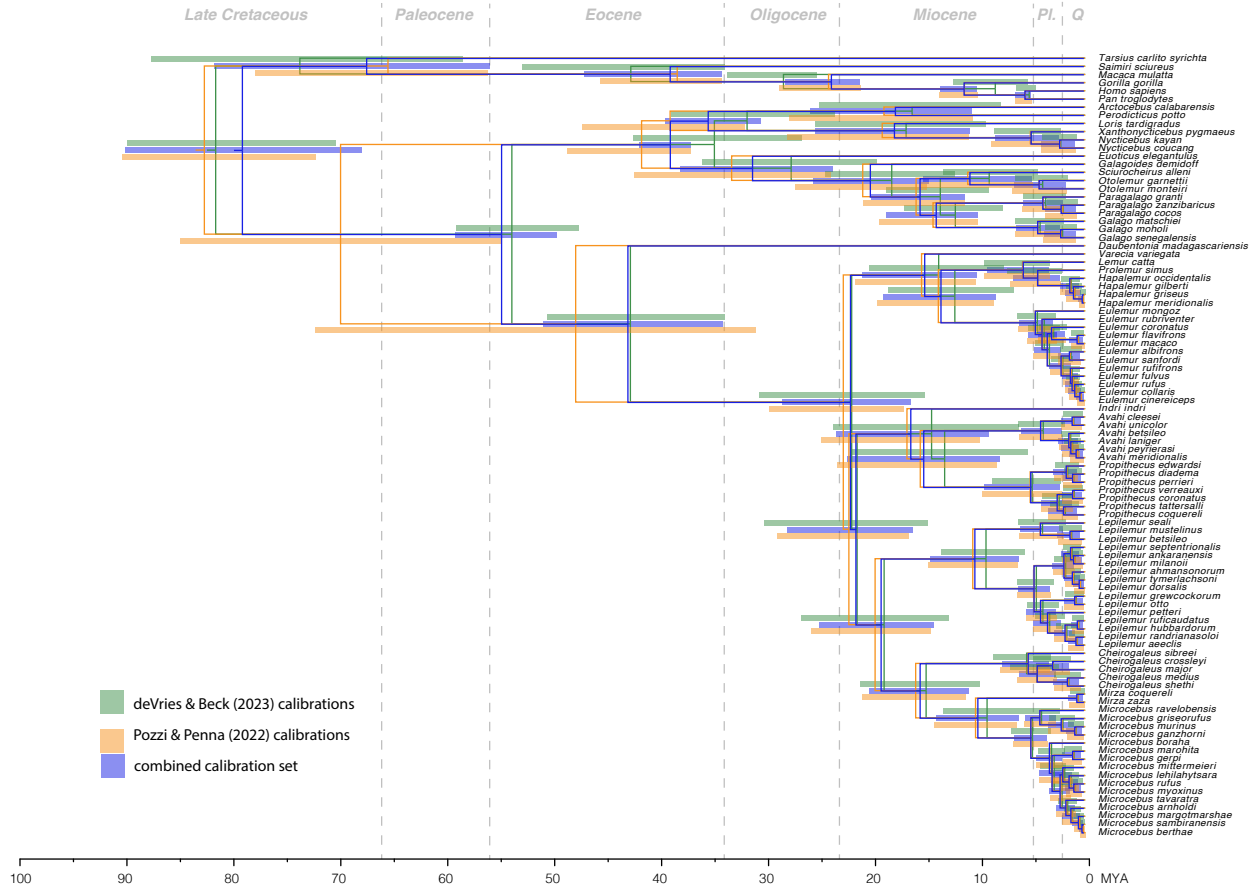


Supplementary Figure 2. A species tree of strepsirrhine primates estimated using SVDQuartets. Node support values were estimated using 1000 bootstrap replicates. Branch lengths are not scaled.

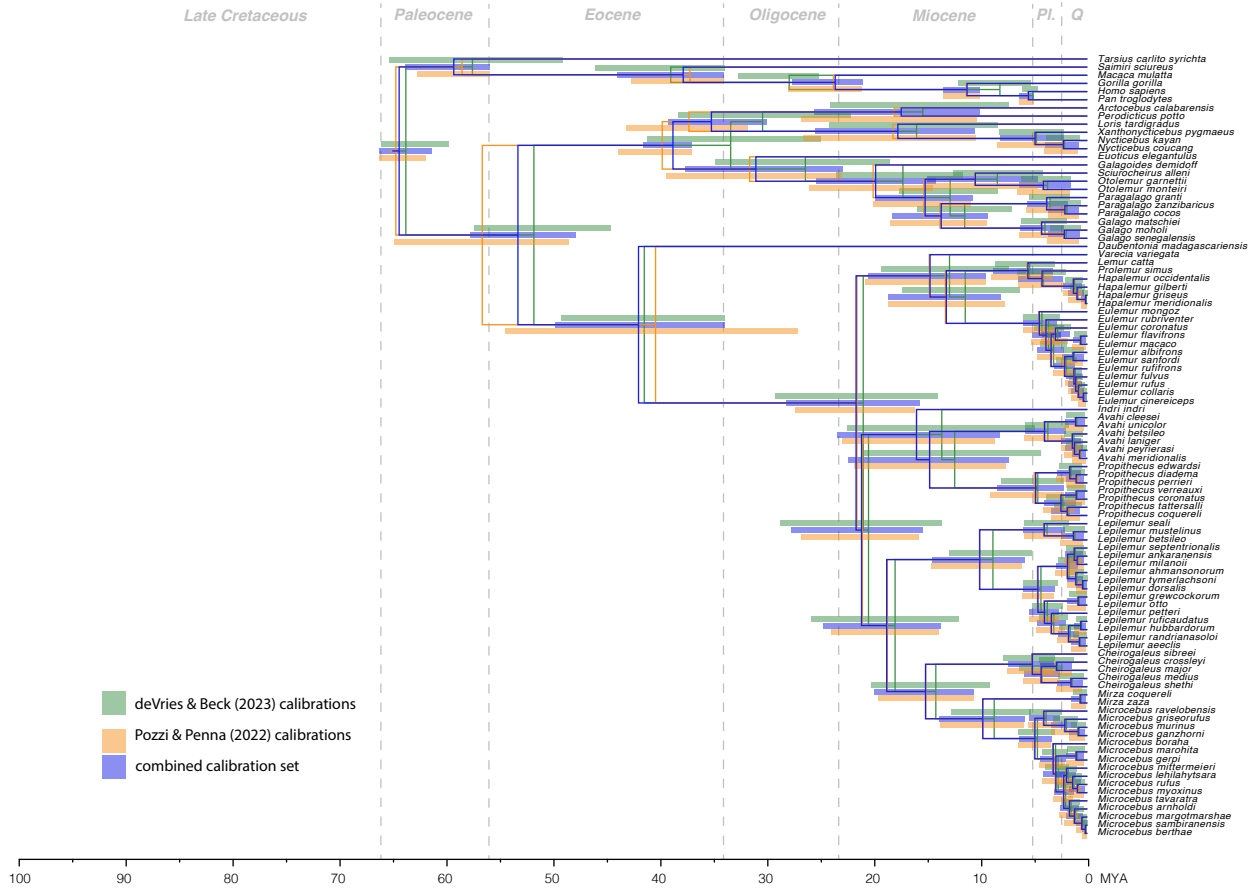


Supplementary Figure 3. A species tree of strepsirrhine primates estimated using ASTRAL. Node support values represent support for the quadripartition, or the fraction of induced quartet trees in the input set of gene trees that are also in the species tree. Branch lengths are not scaled.

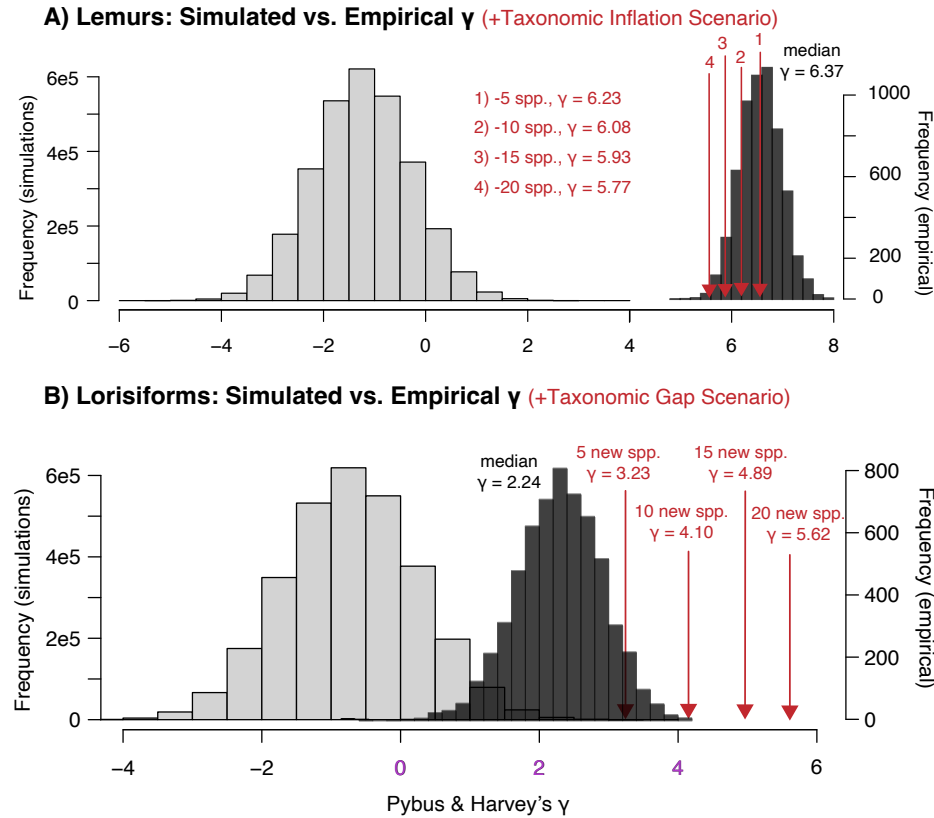
A. Time-Calibrated Species Tree (soft maximum on root)



B. Time-Calibrated Species Tree (hard maximum on root = 66.059 mya)

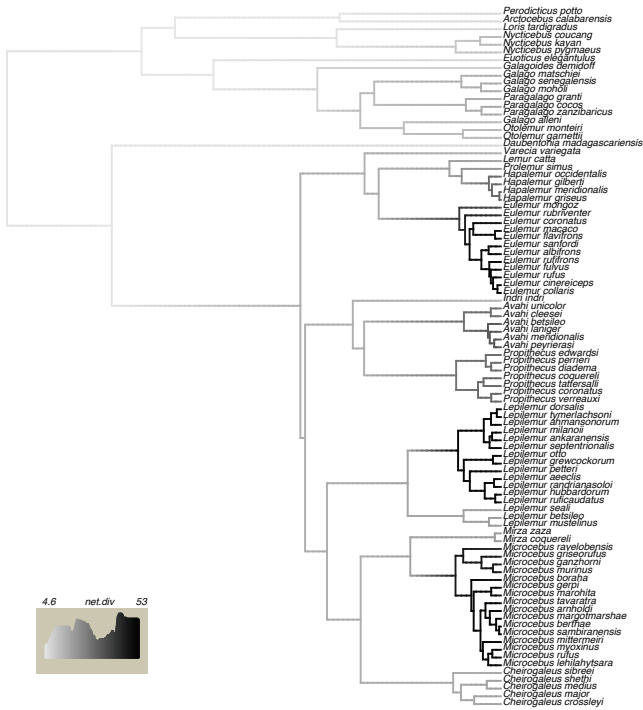


Supplementary Figure 4 (previous page). Time-calibrated phylogenies of Strepsirrhini, as estimated using MCMCTree. Trees are colored according to the fossil set used for calibration, and the top set of trees were estimated using a soft maximum prior on the root node whereas the bottom set of trees were estimated using a hard maximum prior on the root node (Supplementary Data 3). Nodes are shown as median ages with 95% highest posterior density intervals indicated by colored bars.

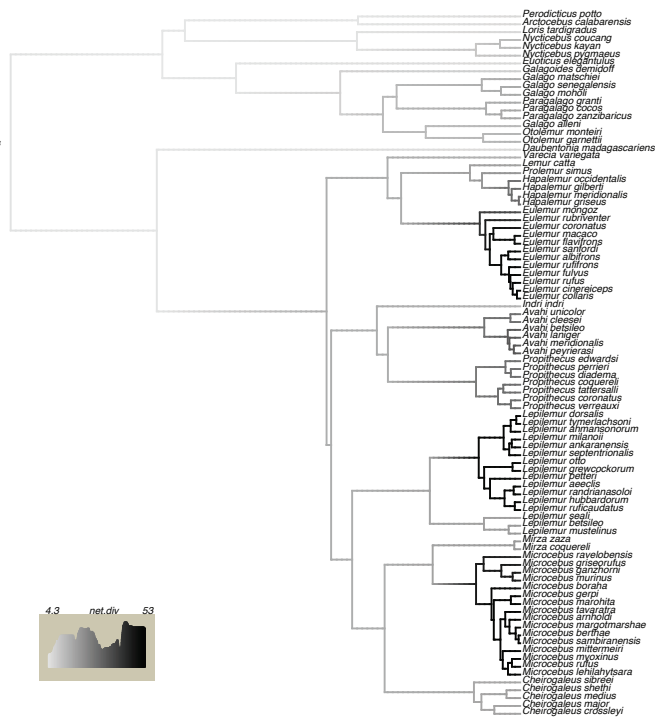


Supplementary Figure 5. Estimates of Pybus and Harvey's γ for lemurs (A) and lorisiforms (B). The dark gray vertical bars show the distribution of γ calculated across 6000 empirical trees (i.e., the set of 1000 stochastically resolved trees from TACT for each of the six time-calibrated phylogenies shown in Supplementary Figure 4). The light gray vertical bars show the distribution of γ simulated under a pure-birth speciation model for trees of the same species richness. We simulated 500 trees for each of the 6000 empirical trees (hence the difference in magnitude of the y axis for the simulated and empirical values). The red arrows indicate median values of γ calculated under a scenario of taxonomic inflation (lemurs; panel A) or taxonomic gap (lorisiforms; panel B). Under a taxonomic inflation scenario, 5, 10, 15, or 20 species were randomly pruned from the lemur phylogeny; under a taxonomic gap scenario, 5, 10, 15, or 20 new species were randomly added to the lorisiform phylogeny.

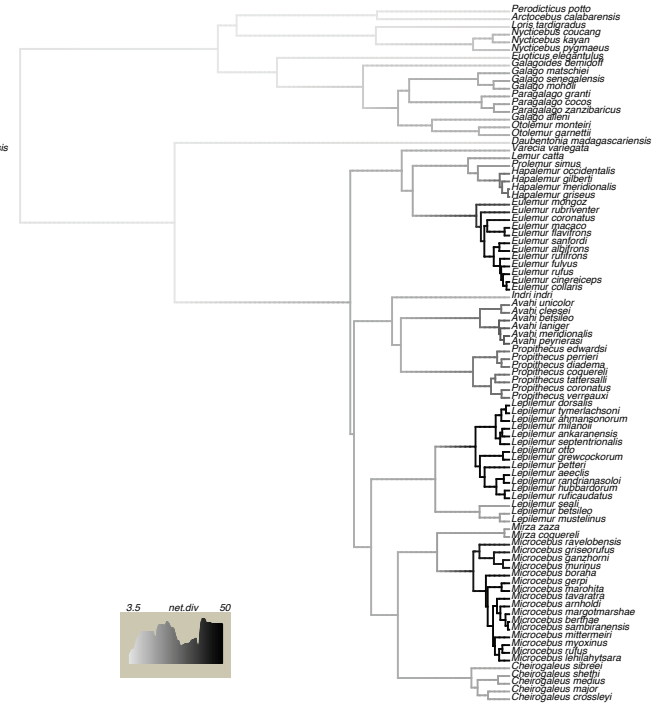
A. Combined fossil set with hard root



B. Pozzi & Penna fossil set with hard root

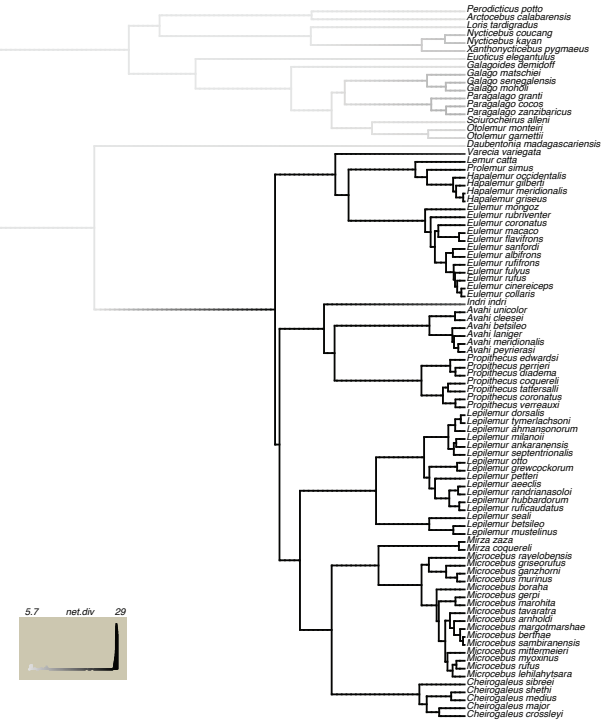


C. Pozzi & Penna fossil set with soft root

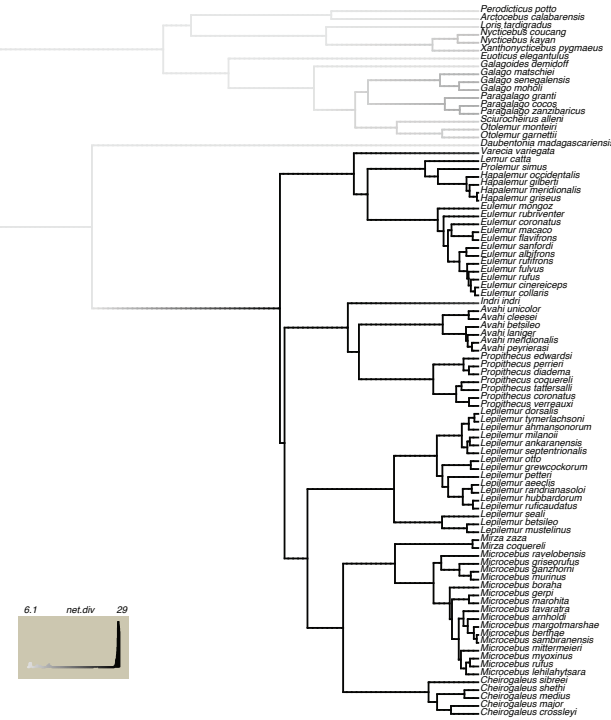


Supplementary Figure 6. Time-calibrated phylogenies of Strepsirrhini with branches colored according to diversification rate (net species per million years), as estimated using a three-rate model in MiSSE. A three-rate model was the best-supported model under three fossil calibration regimes (Supplementary Data 3): the combined fossil set with a soft root (A), the combined fossil set with a hard root (B), and the Pozzi and Penna fossil set with a hard root (C). See Supplementary Data 6 for MiSSE model test results.

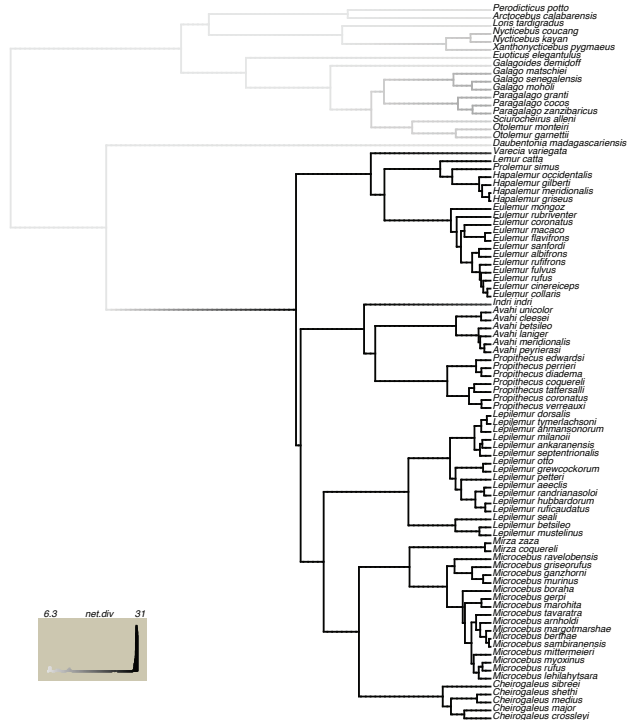
A. Combined fossil set with soft root



B. de Vries & Beck fossil set with soft root

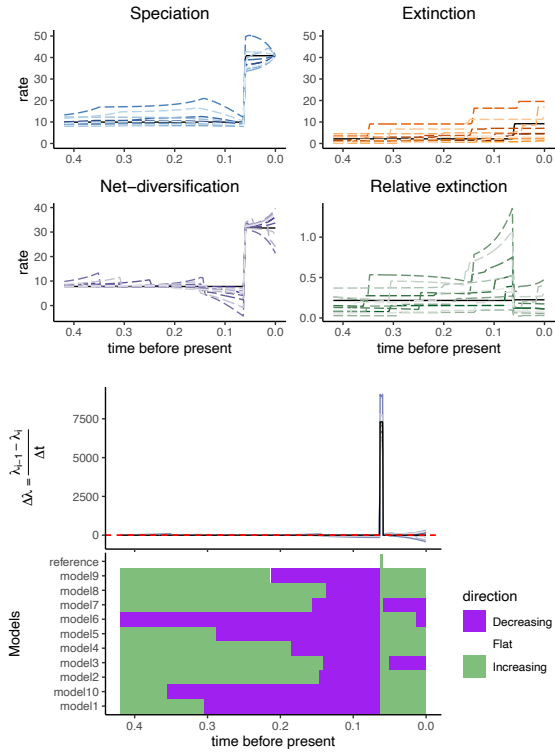


C. de Vries & Beck fossil set with hard root

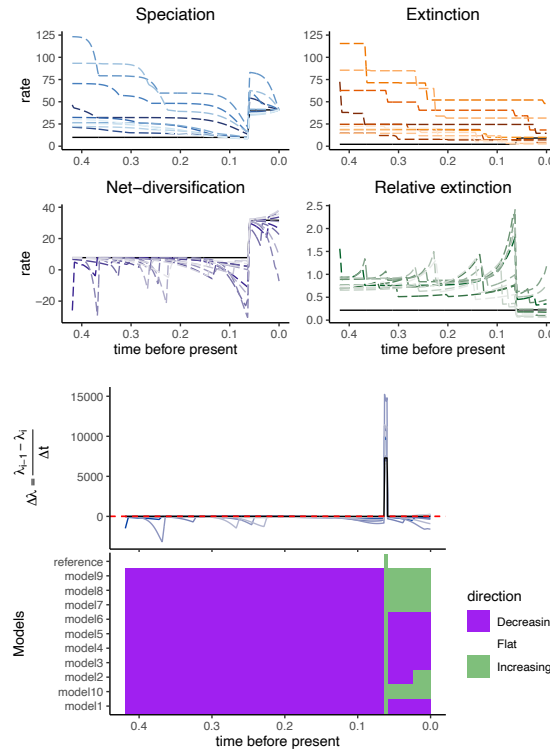


Supplementary Figure 7. Time-calibrated phylogenies of Strepsirrhini with branches colored according to diversification rate (net species per million years), as estimated using a two-rate model in MiSSE. A two-rate model was the best-supported model under three fossil calibration regimes (Supplementary Data 3): the de Vries and Beck fossil set with a soft root (A), the de Vries and Beck fossil set with a hard root (B), and the Pozzi and Penna fossil set with a soft root (C). See Supplementary Data 6 for MiSSE model test results.

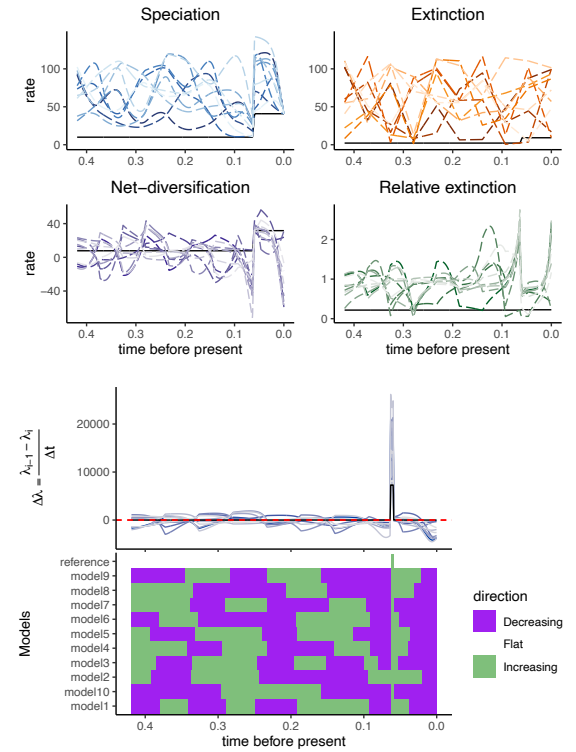
A. Alternative diversification models within the congruence class where extinction has been *increasing over time*



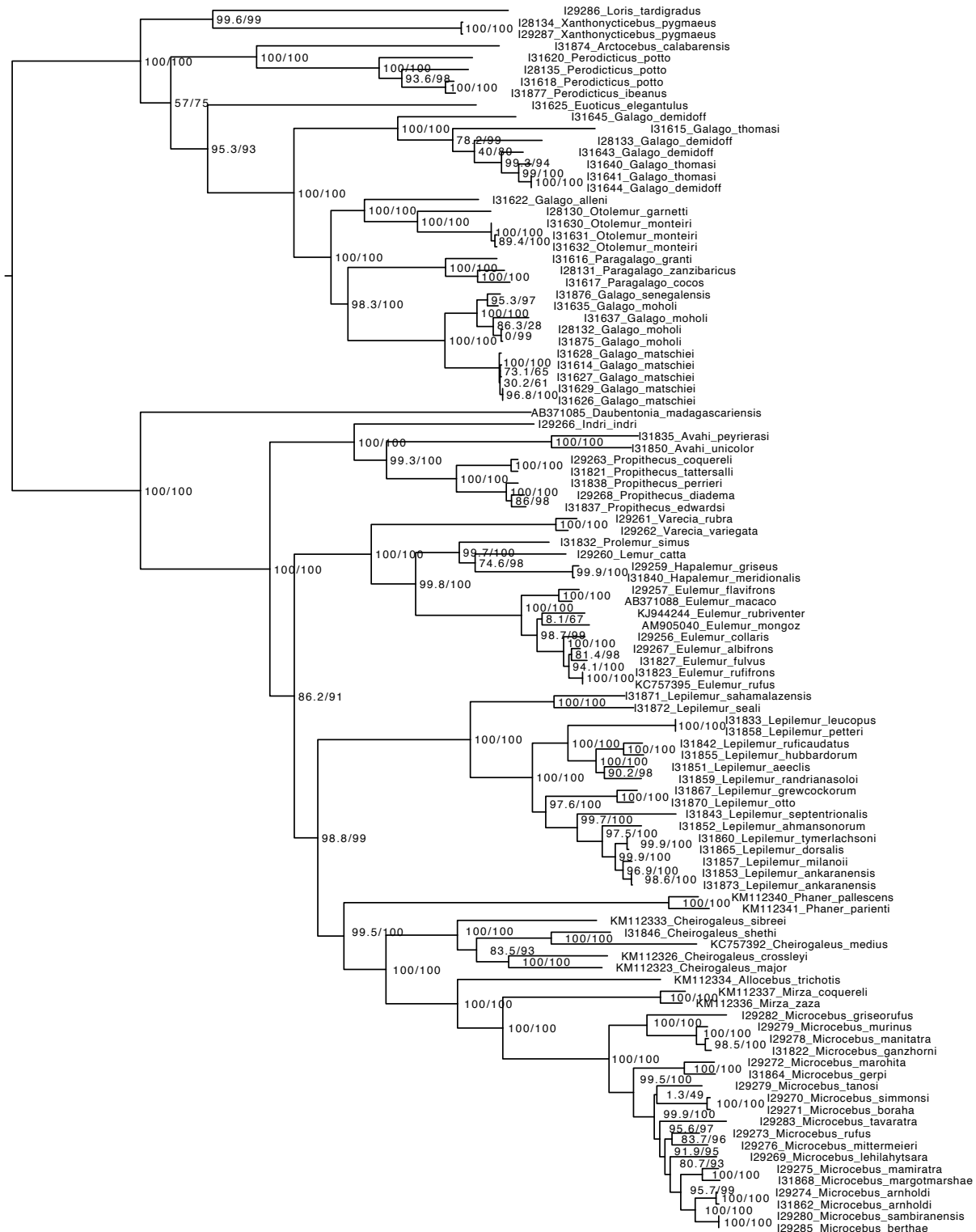
B. Alternative diversification models within the congruence class where extinction has been *decreasing over time*



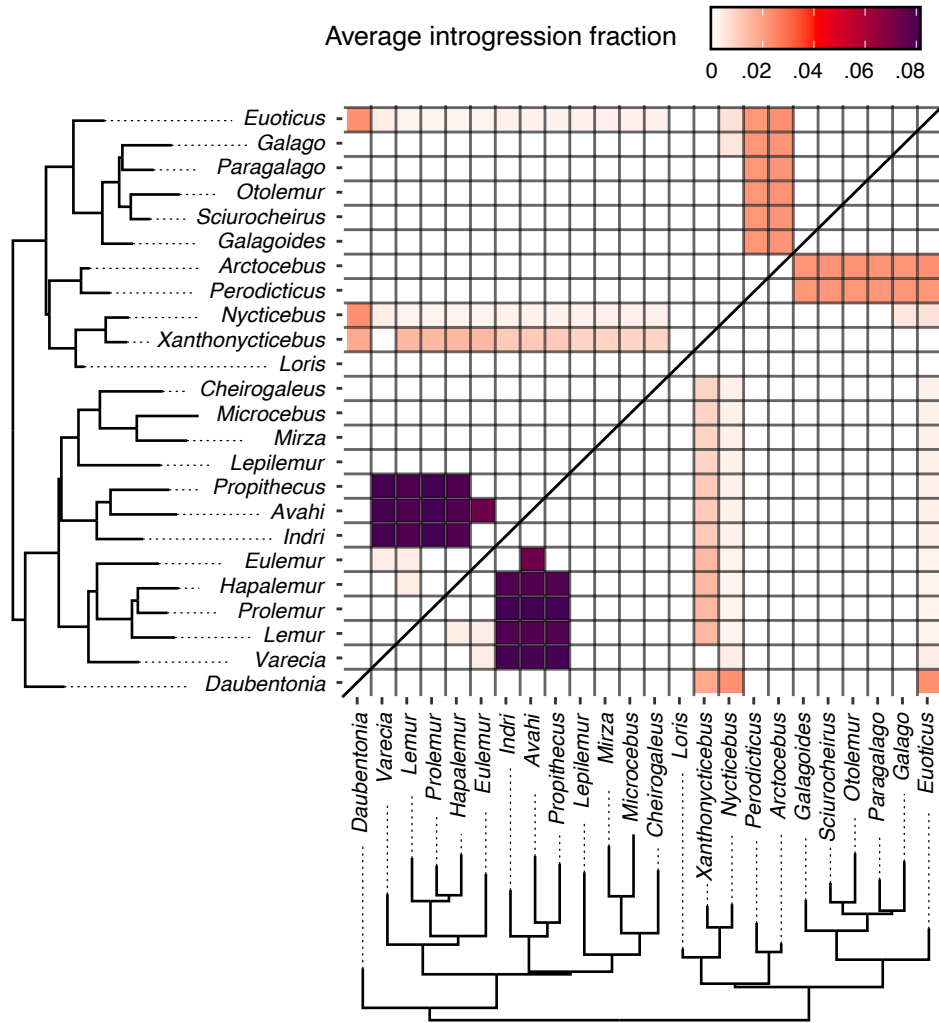
C. Alternative diversification models within the congruence class where extinction has been *fluctuating randomly over time*



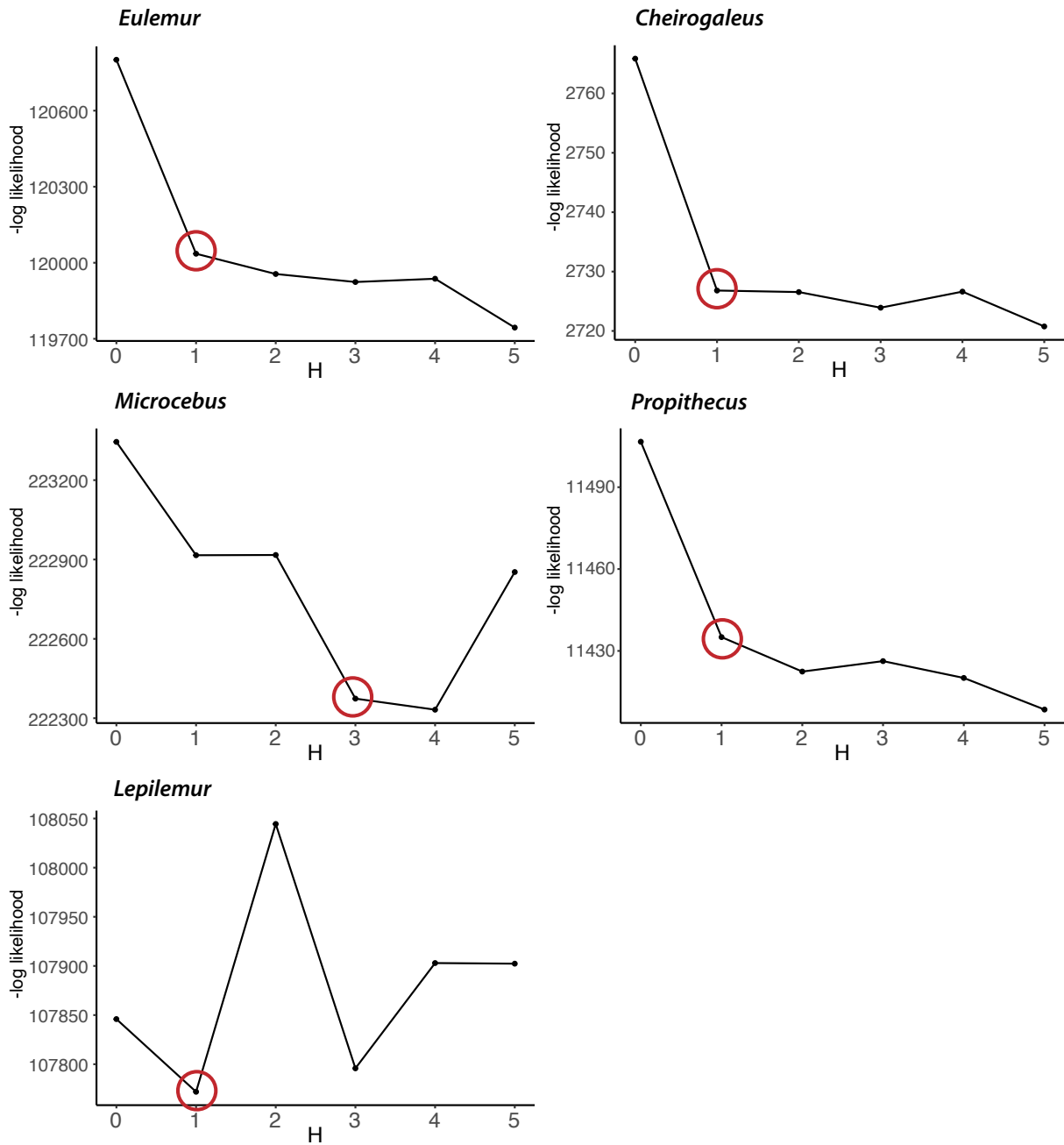
Supplementary Figure 8. An exploration of alternative strepsirrhine diversification models contained in the congruence class. We used CRABS to generate 30 congruent scenarios: 10 scenarios where extinction has been increasing over time (A), 10 where extinction has been decreasing over time (B), and 10 where extinction has fluctuated randomly over time (C). In the top three rows of plots, the black line is the empirical model and each colored line represents a different congruent model. The net diversification rates and relative extinction rates result from the speciation and extinction rate functions. In the bottom plots, each row represents a different model and the overall trend in speciation rate (increasing, decreasing, or flat) is shown. Note that despite a great degree of variation in trend, all 30 models show one period of increased speciation rates at the same interval around 6 MYA (time units: 1 = 100 MYA).



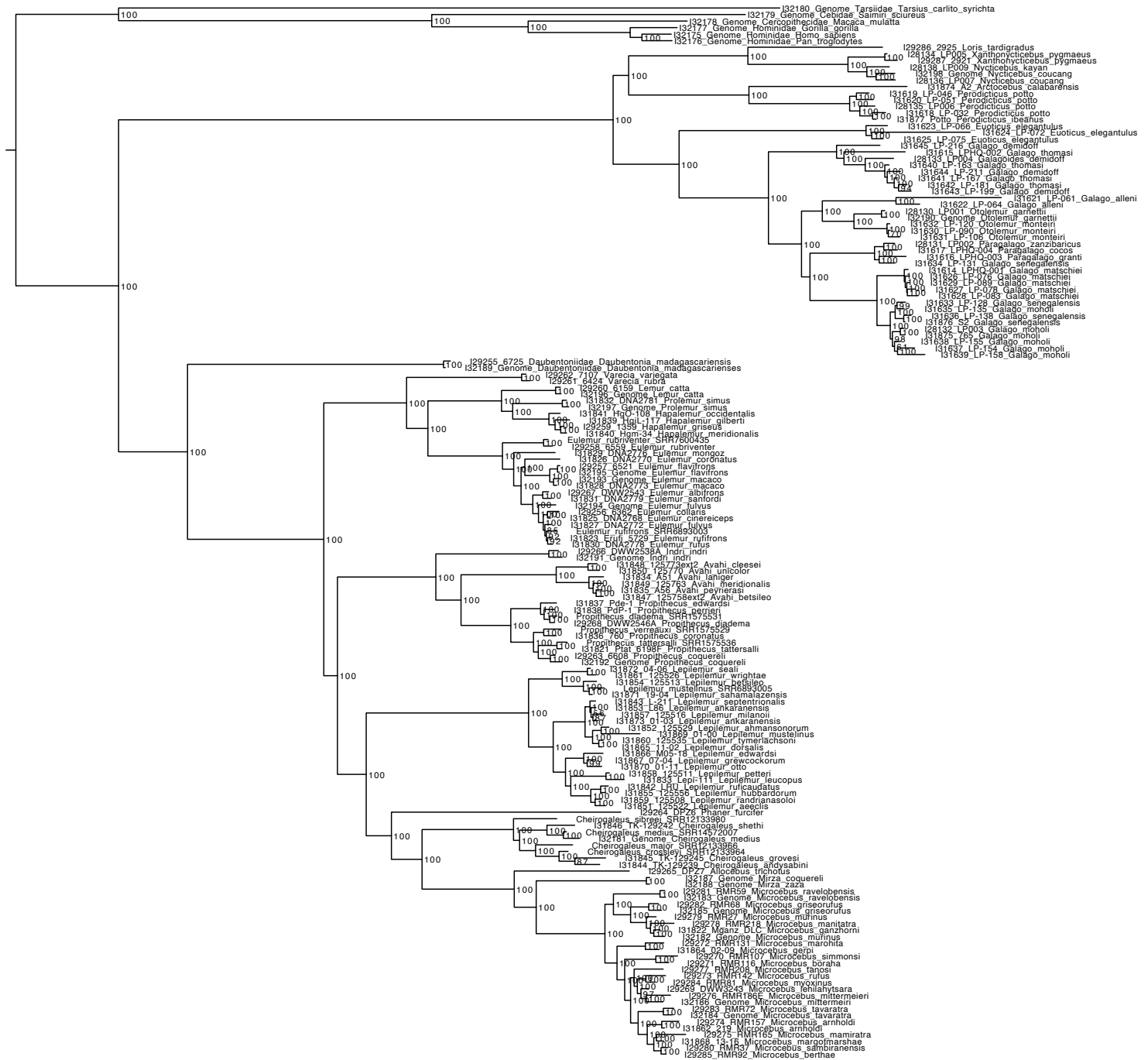
Supplementary Figure 9. A mitochondrial phylogeny estimated using IQTree. Node support values are from 1000 ultrafast bootstrap replicates (before the slash) 1000 replicates of the Shimodaira-Hasegawa approximate likelihood ratio test (SH-aLRT; after the slash). Tip labels correspond to the individuals listed in Supplementary Data 1. Note that only 104 individuals had sufficient mitochondrial data to be harvested from our sequencing runs.



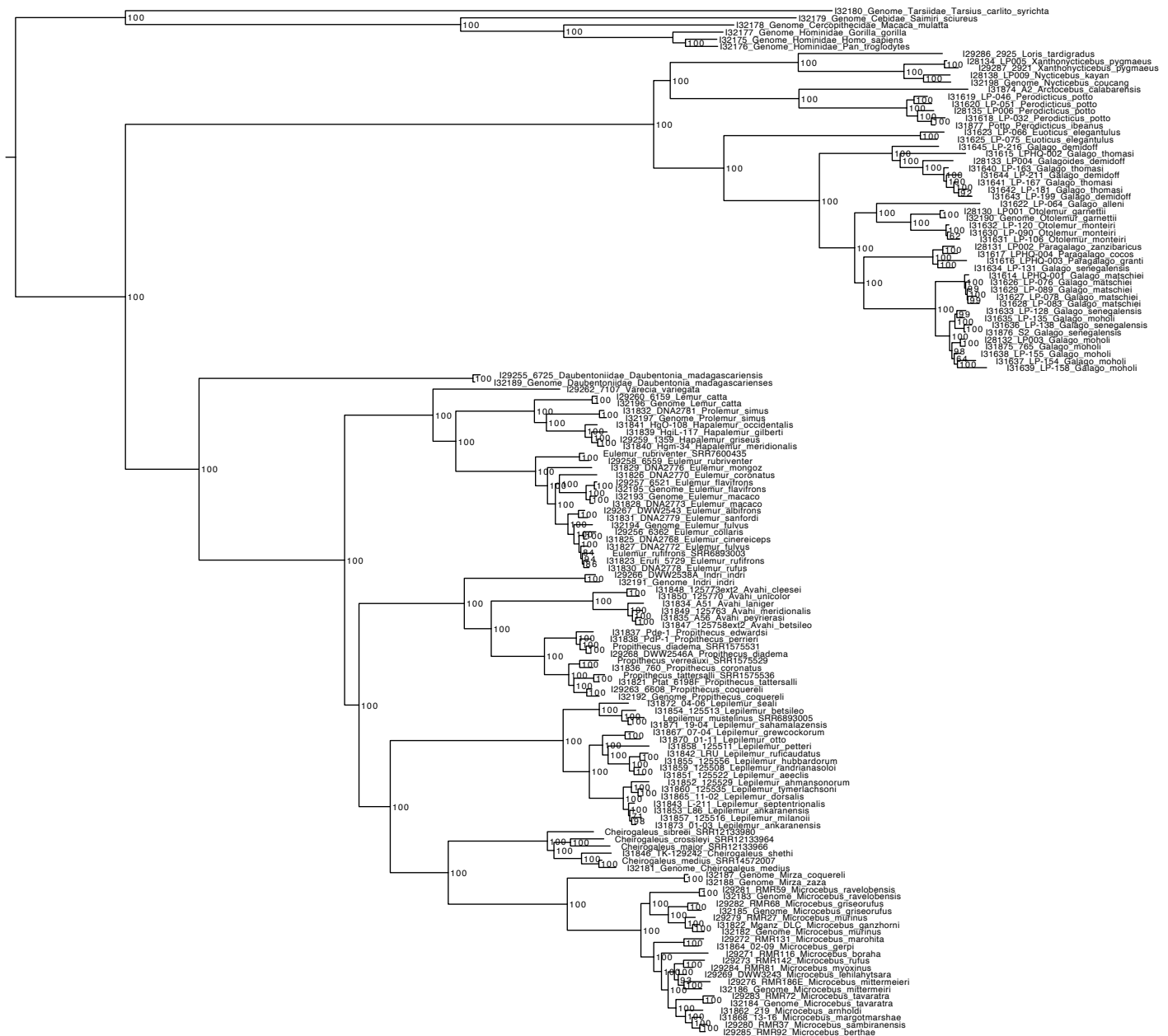
Supplementary Figure 10. Fraction of introgressed loci between each strepsirrhine genus pair (ranging from zero, lighter colors, to 0.08, darker colors), as estimated by QuiBL. A value of zero has been assigned to all instances of non-significant introgression.



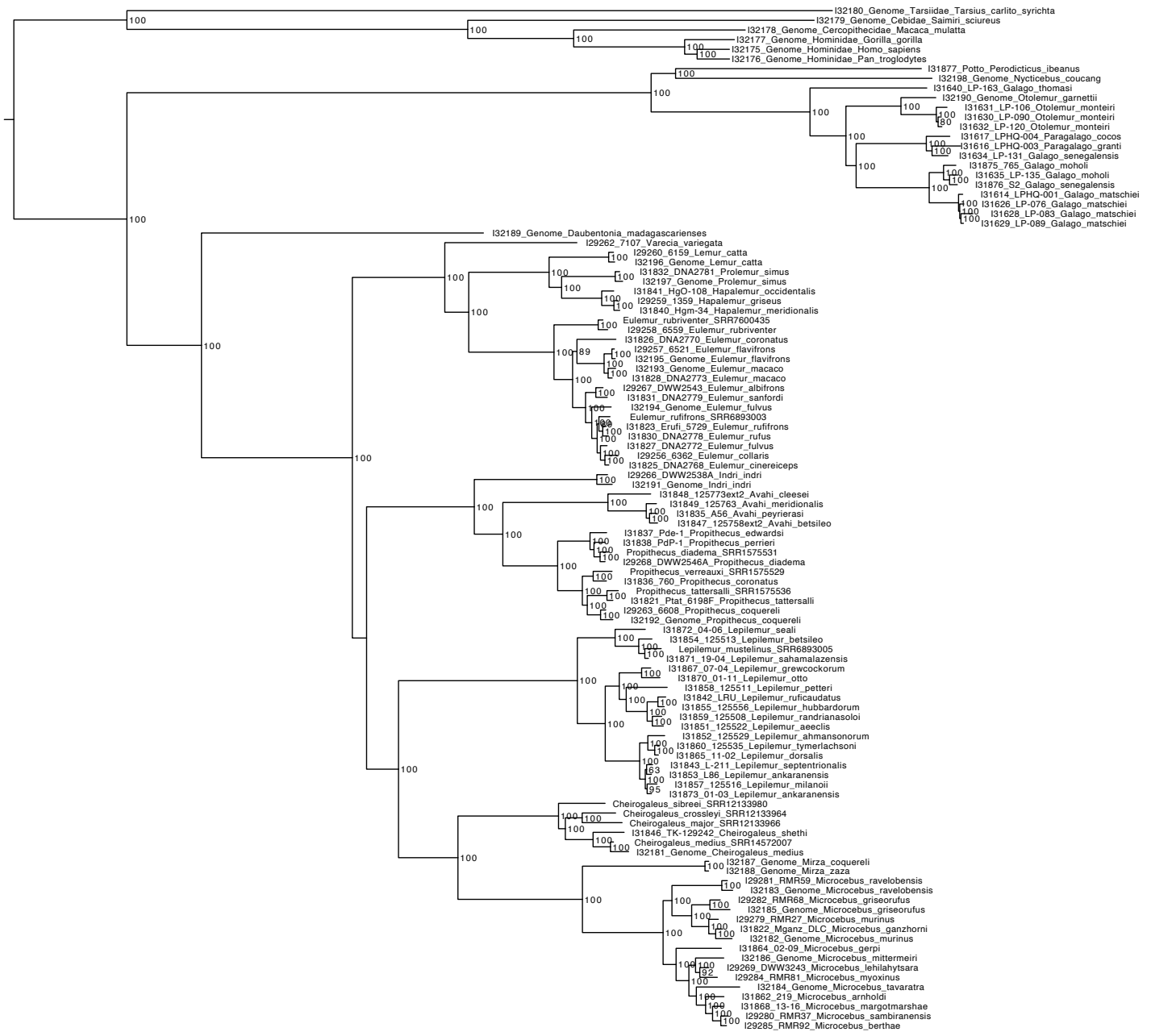
Supplementary Figure 11. Model test results for the PhyloNet analyses of five lemur genera. For each genus, models containing between zero and five reticulations (H) were explored. Models were selected by plotting the change in negative log-likelihood scores ($-\log\text{lik}$) across increasing model complexity (i.e., number of H), and choosing the least-complex model beyond which the $-\log\text{lik}$ did not substantially improve. These “best” models are indicated by red circles here and are shown in the main text (Fig. 4). Source data for these plots can be found in Supplementary Data 13.



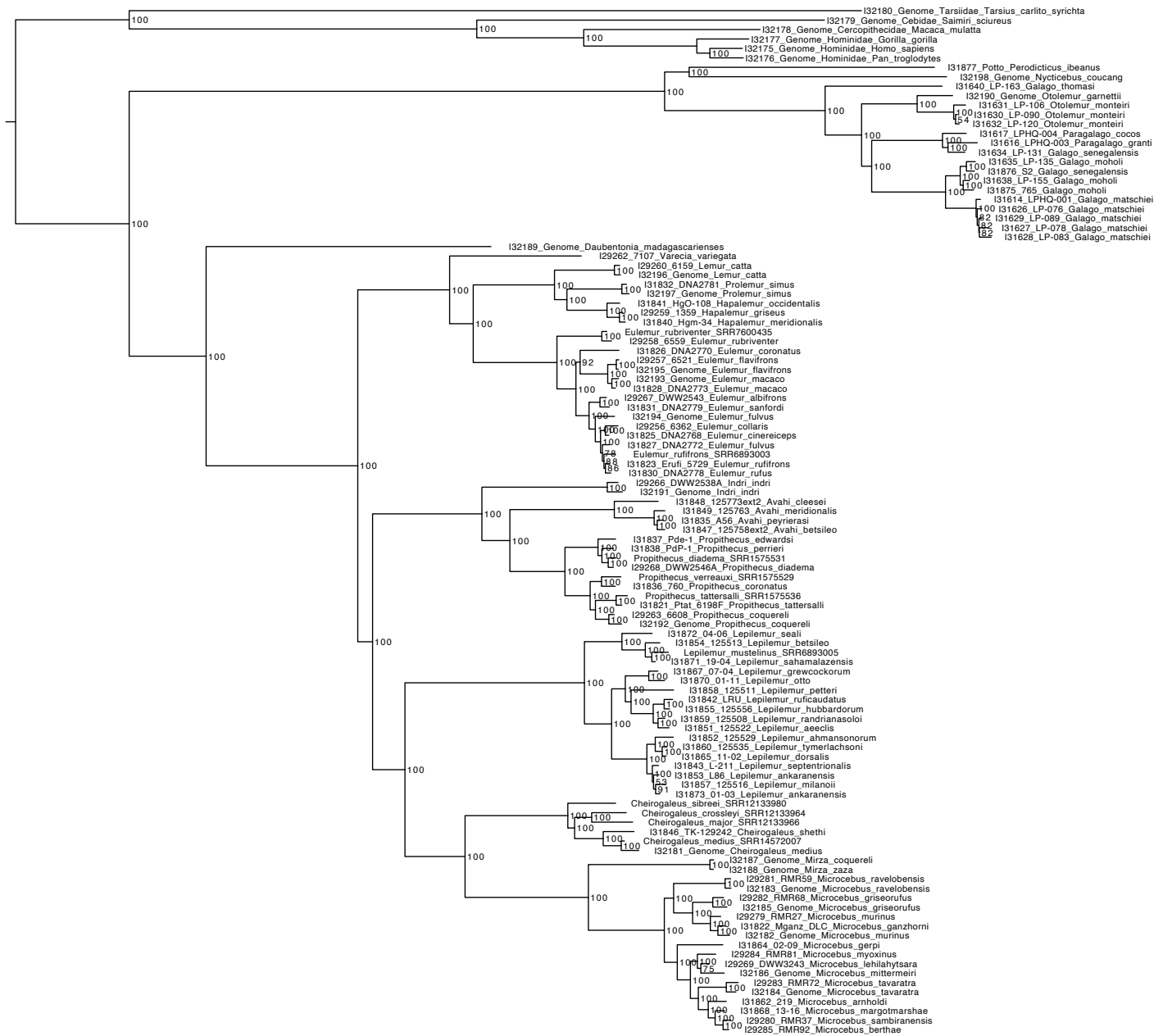
Supplementary Figure 13. A nuclear phylogeny estimated in IQTree using all individuals but dropping the 37 loci that failed to sequence in loriforms and outgroups. Formatting follows Fig. S12.



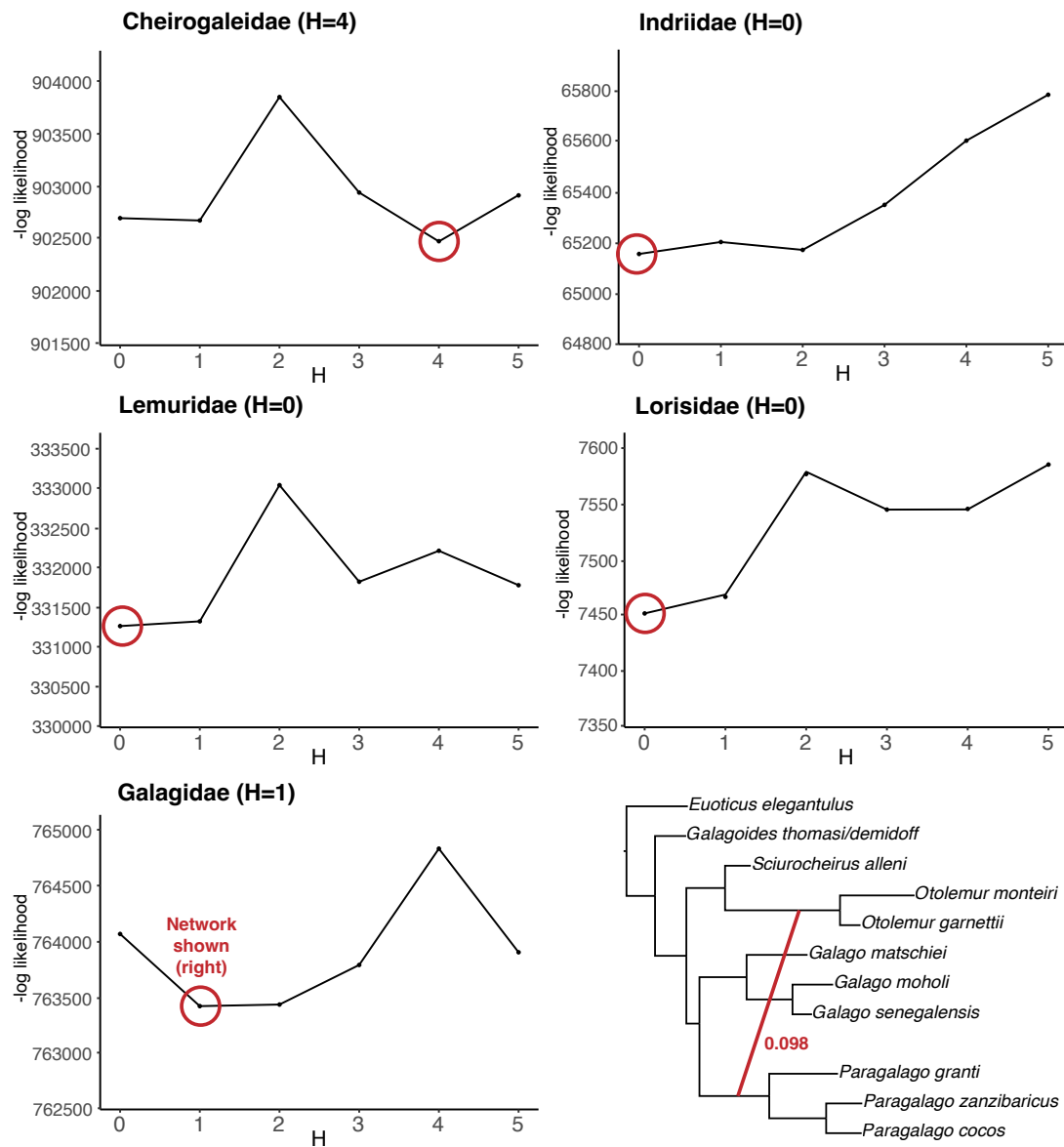
Supplementary Figure 15. A nuclear phylogeny estimated in IQTree using all individuals with <50% missing data and dropping the 37 loci that failed to sequence in loriforms and outgroups. Formatting follows Fig. S12.



Supplementary Figure 16. A nuclear phylogeny estimated in IQTree using all loci and all individuals with <20% missing data. Formatting follows Fig. S12.



Supplementary Figure 17. A nuclear phylogeny estimated in IQTree using all individuals with <20% missing data and dropping the 37 loci that failed to sequence in lorises and outgroups. Formatting follows Fig. S12.



Supplementary Figure 18. Model test results for the PhyloNet analyses of each strepsirrhine Family, which was performed in order to determine whether any additional taxa should be scored as “hybridizing” in our HiSSE analysis. For each Family, models containing between zero and five reticulations (H) were explored. Models were selected by plotting the change in negative log-likelihood scores ($-\loglik$) across increasing model complexity (i.e., number of H), and choosing the least-complex model beyond which the $-\loglik$ did not substantially improve. These “best” models are indicated by red circles. Networks with $H > 0$ were only detected in two analyses: Cheirogaleidae ($H=4$) and Galagidae ($H=1$). The top network for Galagidae is shown, although the single reticulation detected in this analysis did not result in any changes to our HiSSE scoring matrix. The top network for Cheirogaleidae is not shown, as the four reticulations detected from this Family are already shown in Fig. 4 in the main text (one reticulation in *Cheirogaleus* and three in *Microcebus*). Source data for these plots can be found in Supplementary Data 13.