

Supplementary figures for: **Blaimer et al. 2018. Paleotropical diversification dominates the evolution of the hyperdiverse ant tribe Crematogastrini (Hymenoptera: Formicidae). Insect Systematics and Diversity.**

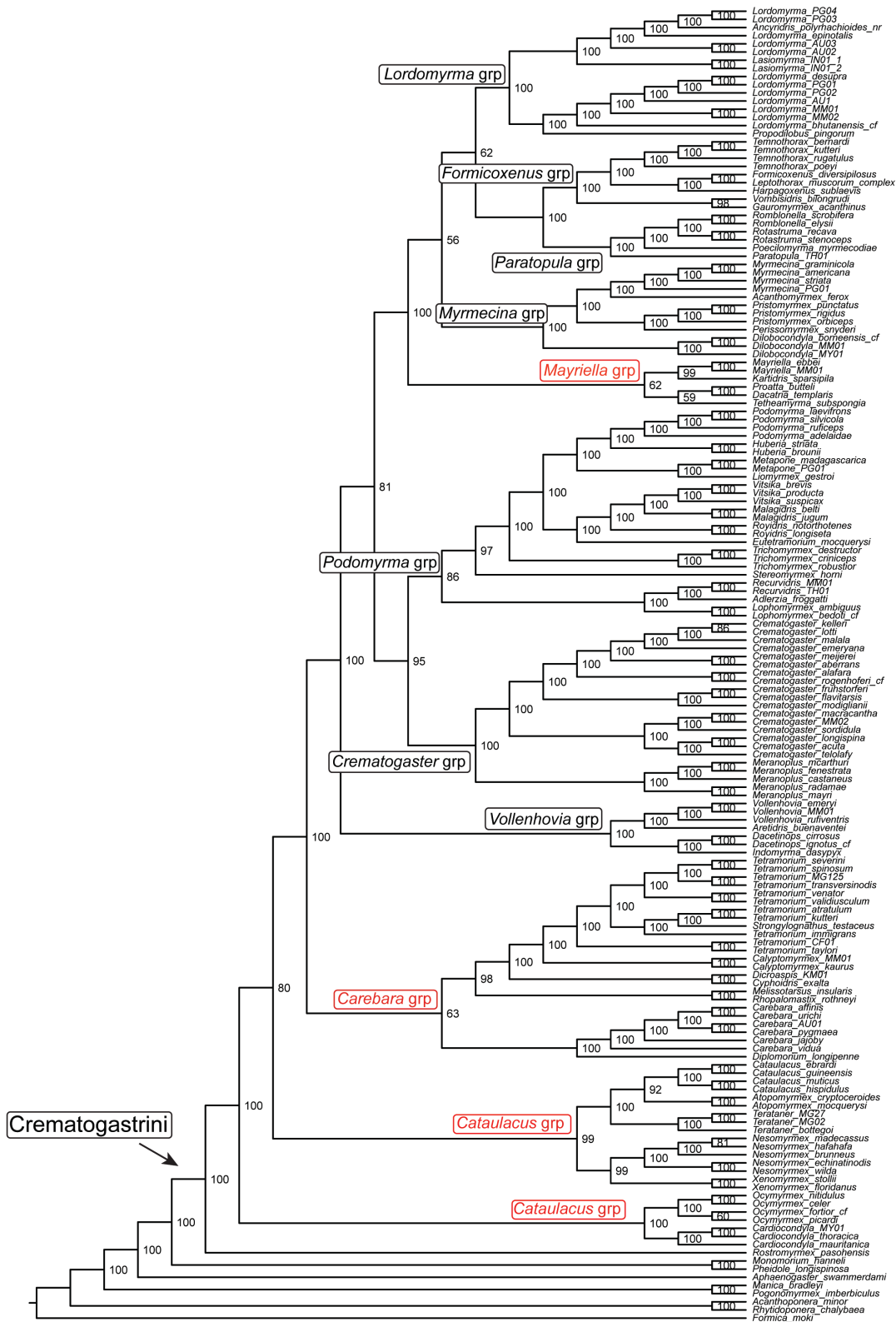


Figure S1: Cladogram from concatenated unpartitioned maximum likelihood analysis. Based on best tree and bootstrap searches (N=100) in RAxML v8.2.7. The ten major genus-groups are indicated and clade names in red highlight conflicts regarding the assembly of these clades with respect to analyses presented in Figs 1 and 2.

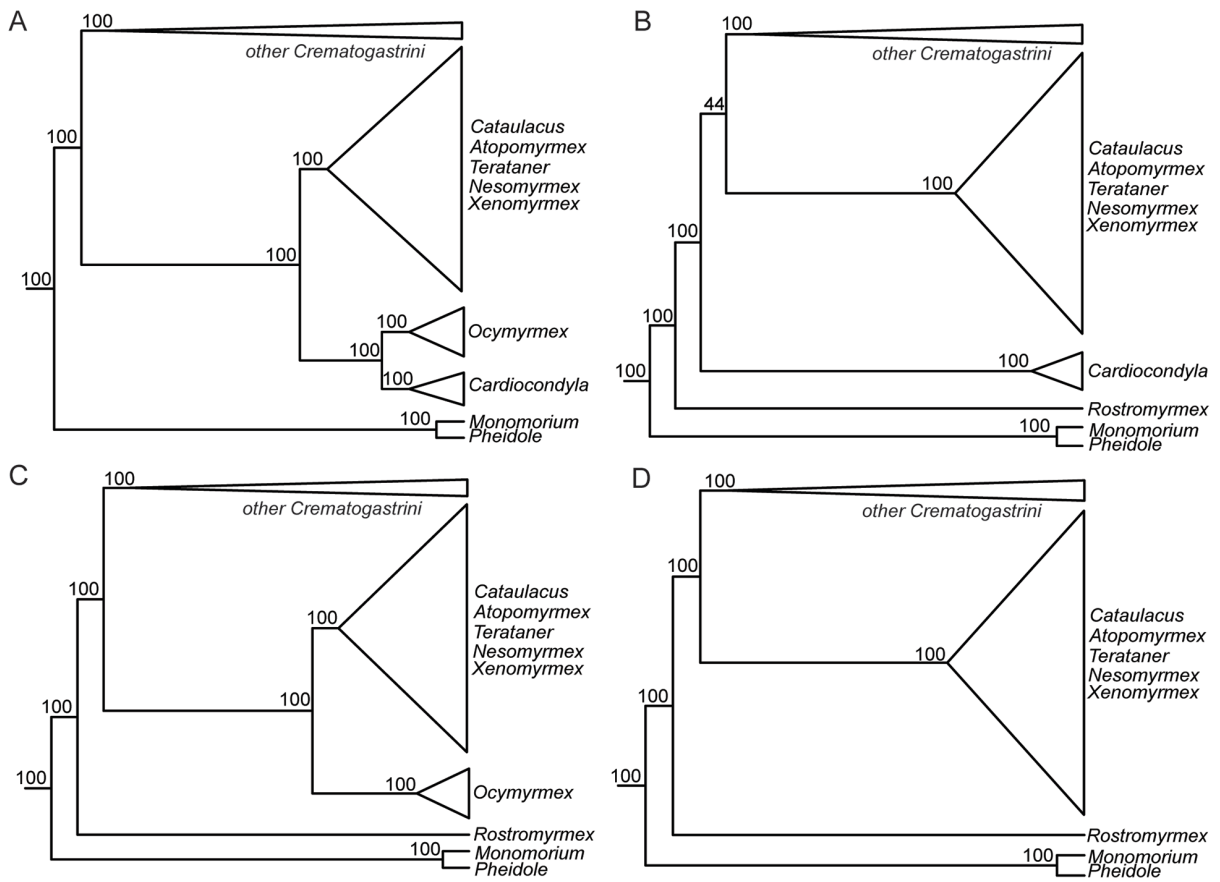


Figure S2: Schematic relationships within Crematogastrini when excluding long-branched taxa. All panels based on concatenated, partitioned maximum-likelihood analyses including best-tree and bootstrap (N=100) searches in RAxML v8.2.7. *A) Rostrormymex* excluded, *B) Cardiocondyla* excluded, *C) Ocymymex* excluded, *D) Cardiocondyla* and *Ocymymex* excluded.

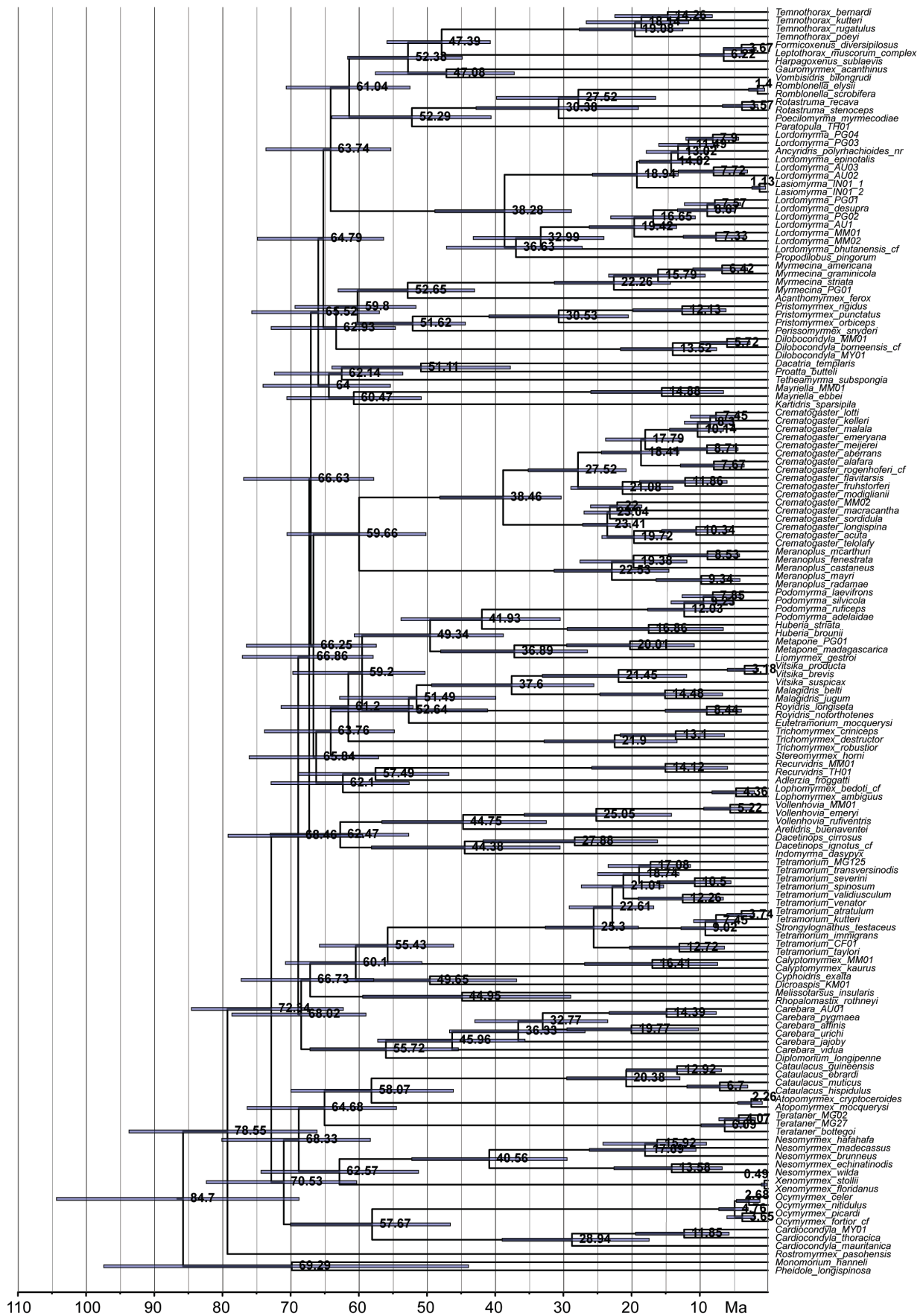


Figure S3: BEAST2 chronogram based on the 50-best-CP topology. Node ages are given as median heights; node error bars represent the 95% highest posterior density (HPD) interval.

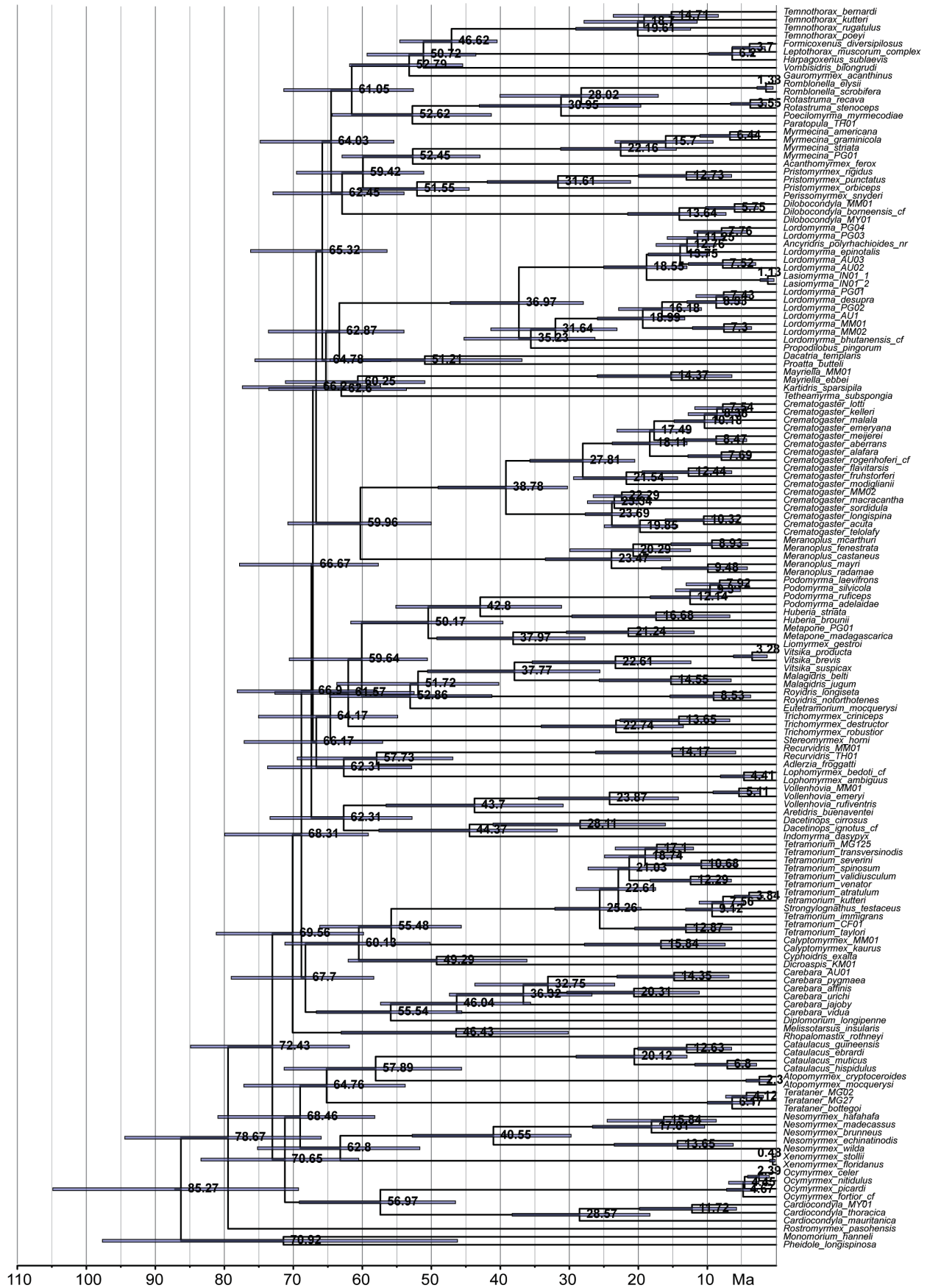


Figure S4: BEAST2 chronogram based on the 50-best-ST topology. Node ages are given as median heights; node error bars represent the 95% highest posterior density (HPD) interval.

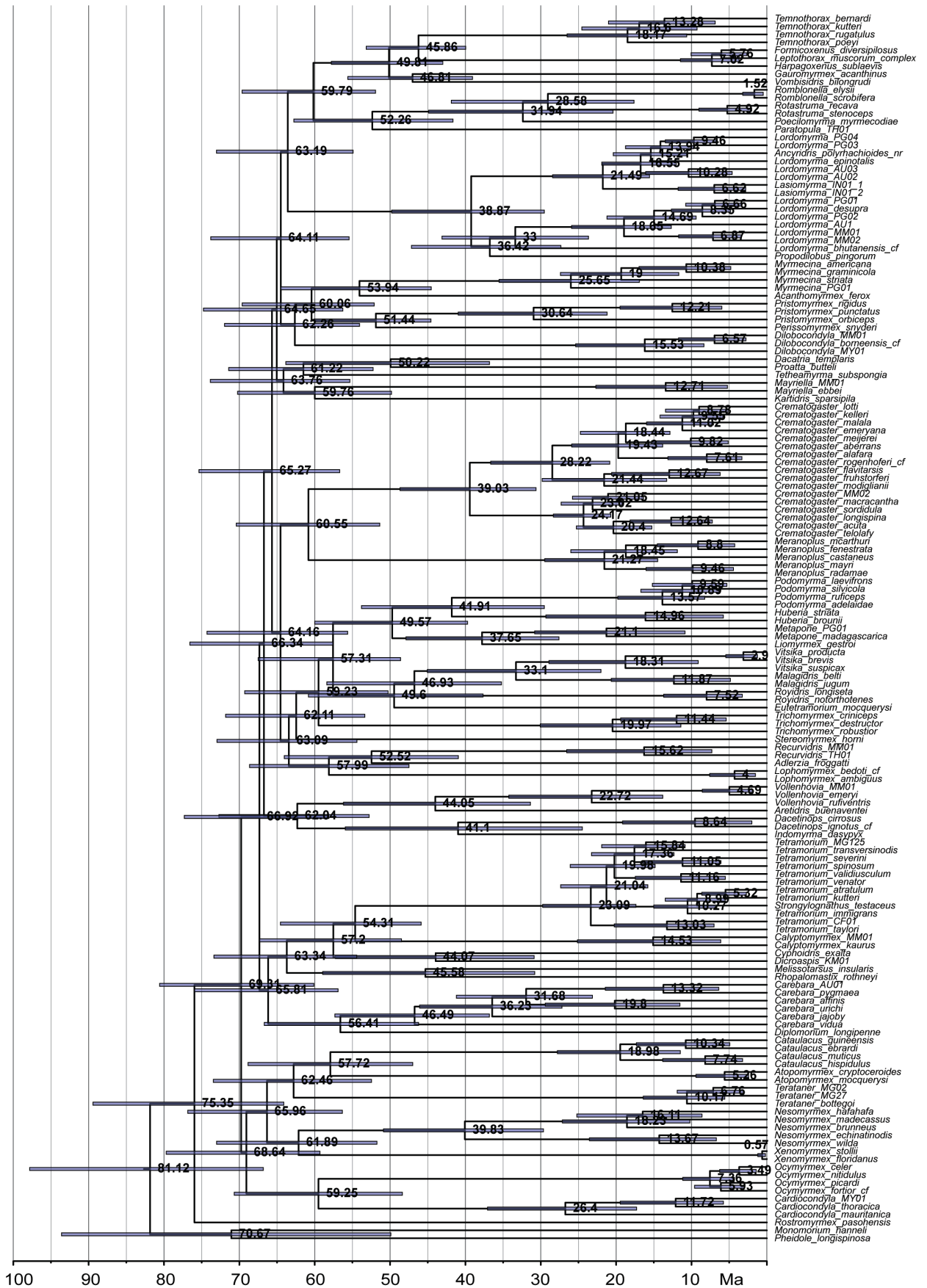


Figure S5: BEAST2 chronogram based on the 50-random-1 topology. Node ages are given as median heights; node error bars represent the 95% highest posterior density (HPD) interval.

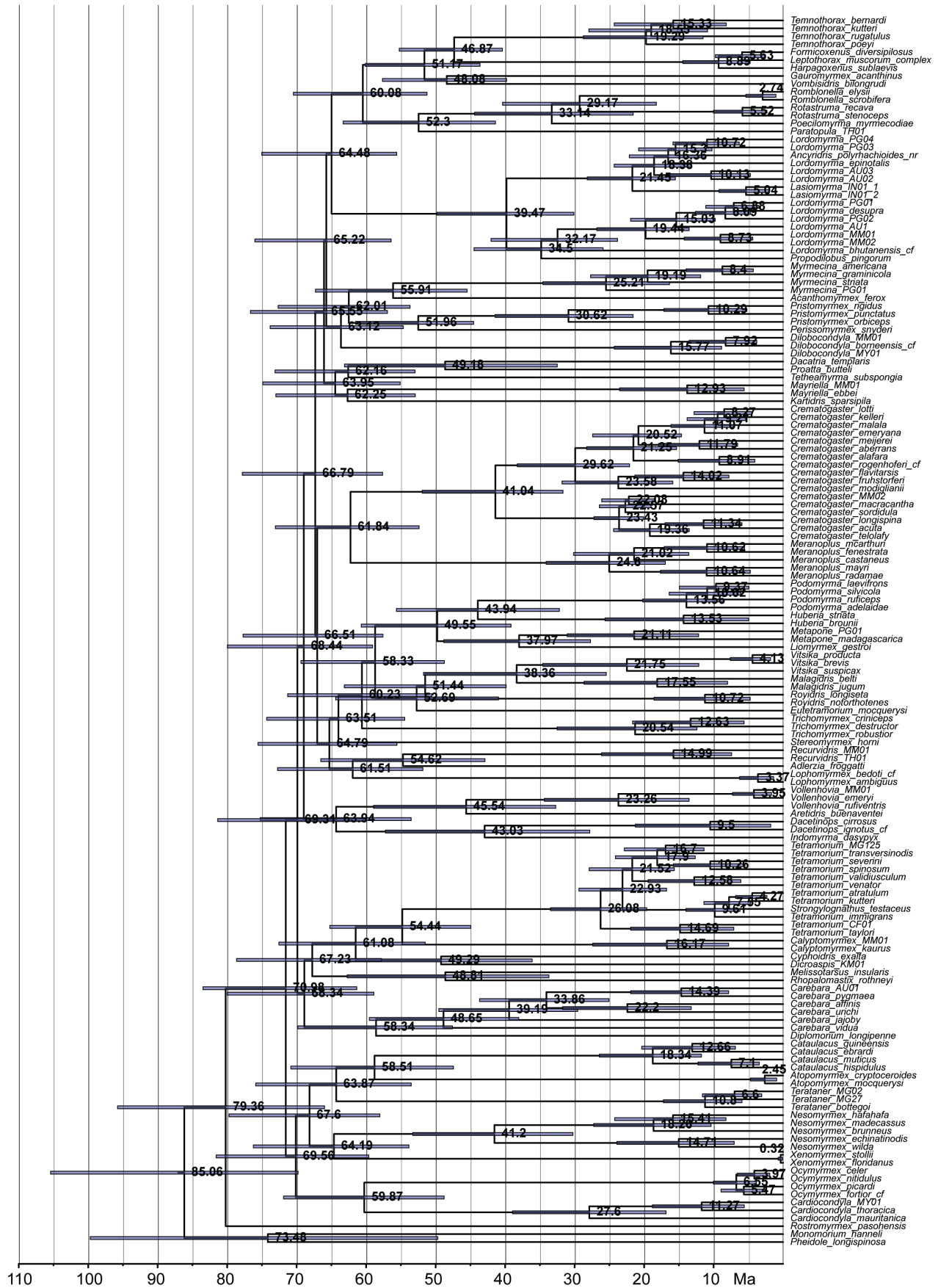


Figure S6: BEAST2 chronogram based on the 50-random-2 topology. Node ages are given as median heights; node error bars represent the 95% highest posterior density (HPD) interval.

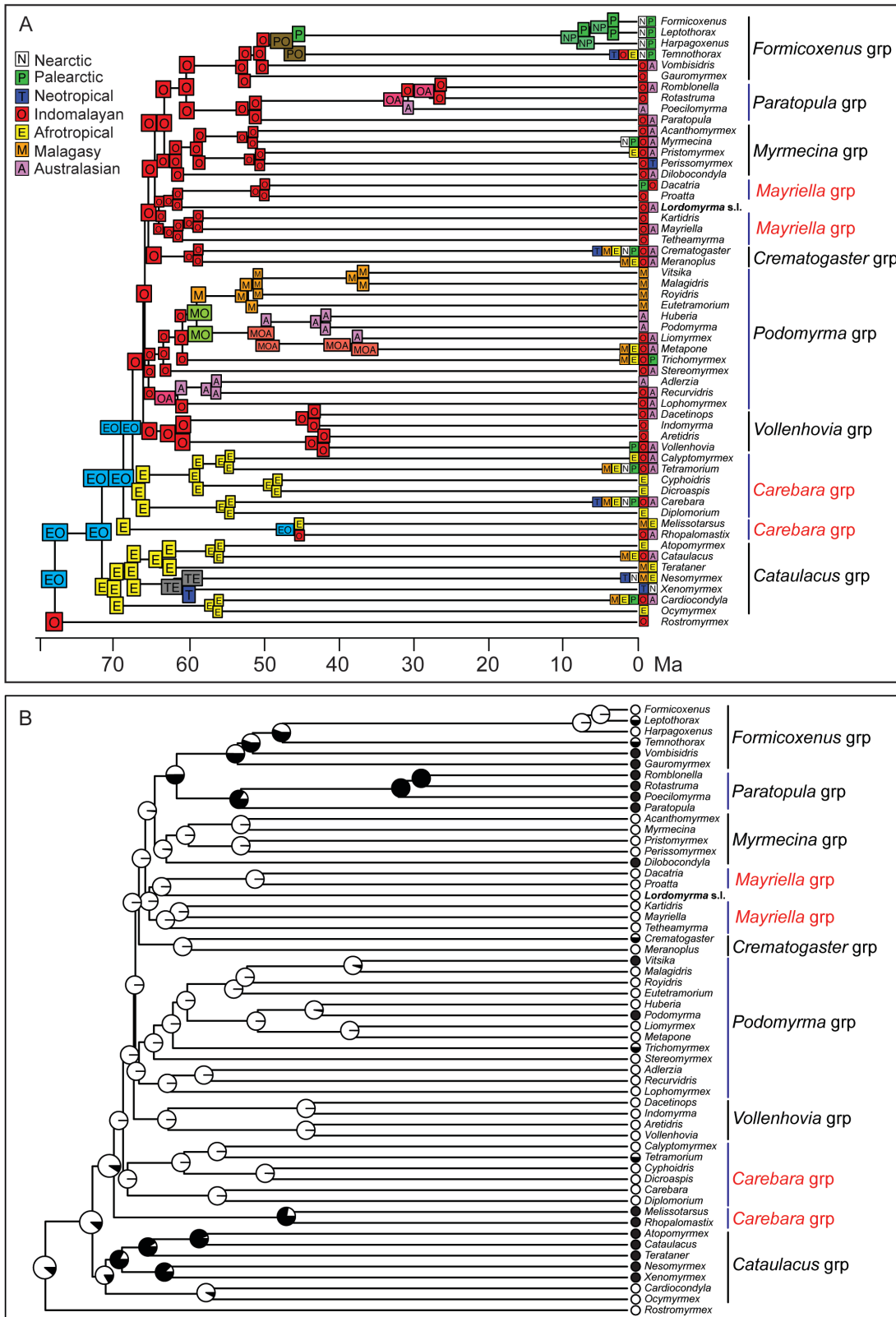


Figure S7: The evolution of biogeography (A) and nesting preference (B) in Crematogastrini based on the species-tree topology. Reconstructions are based on a modified chronogram from the 50-best-ST analysis in BEAST2, from which all but one representative species per genus, as well as the outgroups, have been pruned. A) Biogeographic reconstructions with BioGeoBEARS under the DEC model. N=Nearctic, T=Neotropical, P=Palearctic, E=Afrotropical, M=Malagasy, O=Indomalayan and A=Australasian. B) Nesting preference reconstructed under the ER model with rayDISC in corHMM. Black=arboreal nesting; white=ground nesting. See Supp. Table S3 for geographic distributions and trait data for each genus.

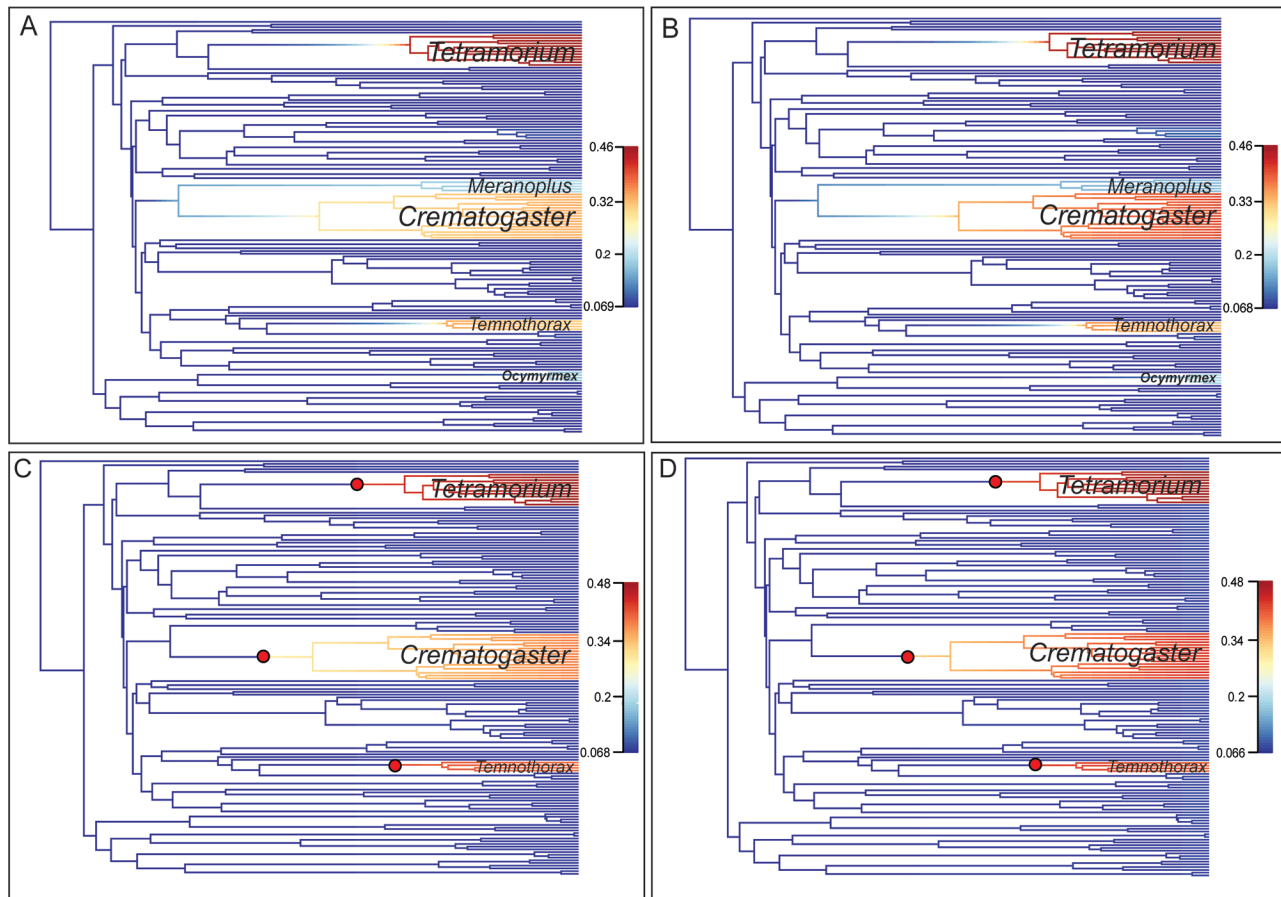


Figure S8: Diversification of Crematogastrini based on the species-tree topology. BMM analyses based on the chronogram resulting from the 50-best-ST analysis with BEAST2, using clade-specific sampling probabilities to account for incomplete sampling based either on species estimates only or including species and subspecies. Panels show *A*) mean phylorate plots based on species only; *B*) mean phylorate plots based on species and subspecies; *C*) best shift configuration based on species only; *D*) best shift configuration based on species and subspecies. Supp. Table S5 lists diversity estimates per genus including and excluding subspecies.

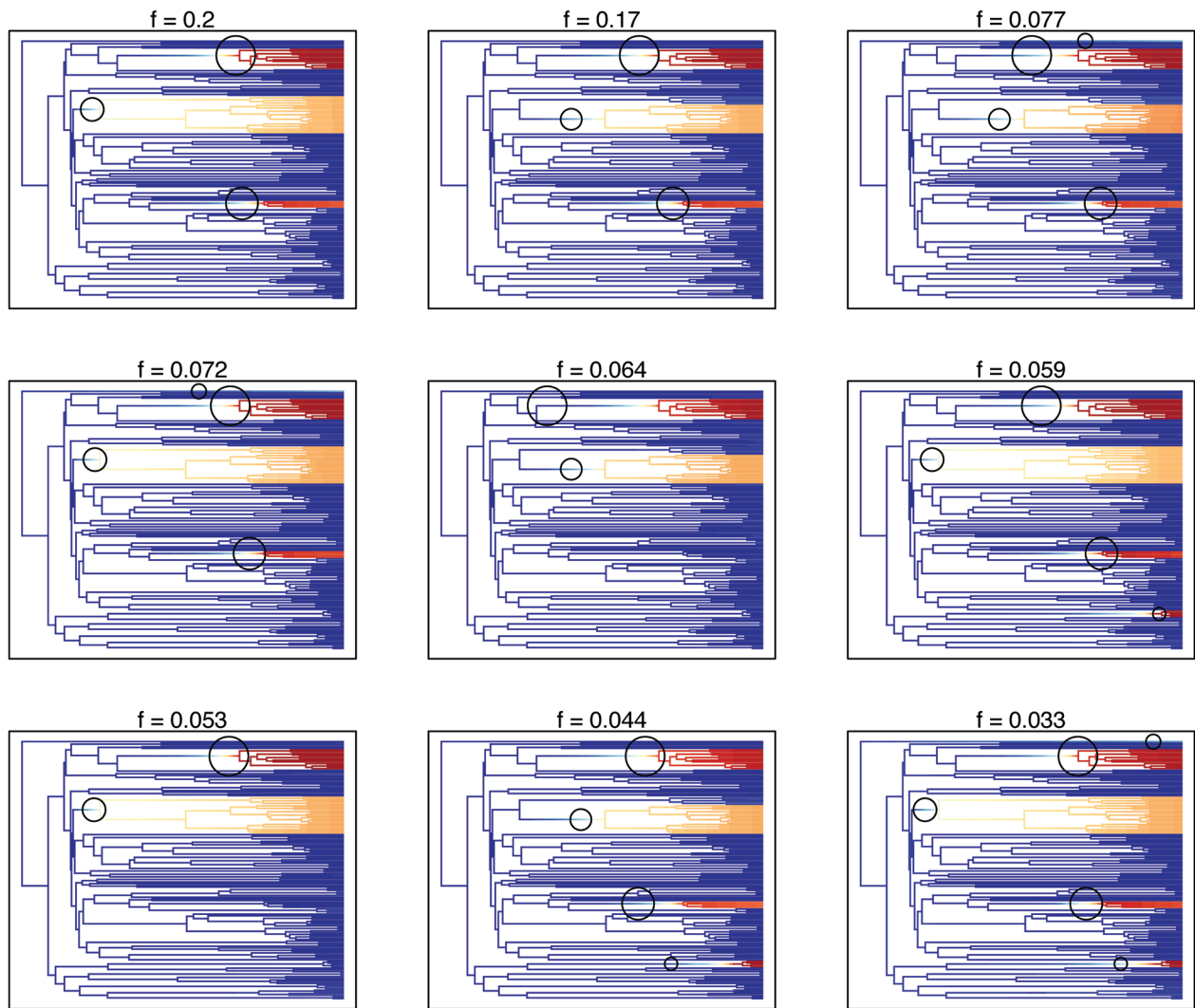


Figure S9: 95% credible shift set for BAMM analyses based on 50-best-CP topology and species-only estimates.

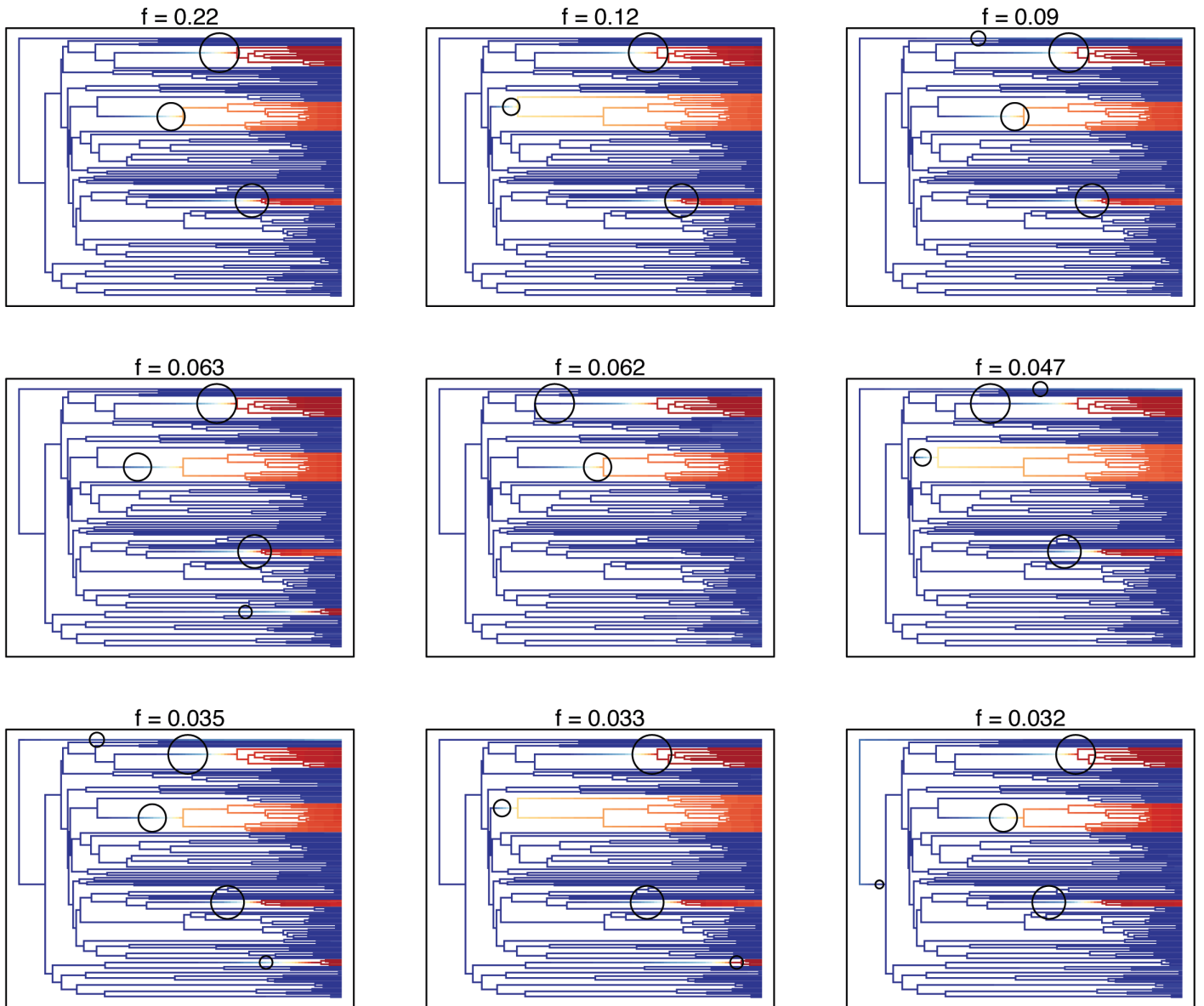


Figure S10: 95% credible shift set for BAMM analyses based on 50-best-CP topology and species and subspecies estimates.

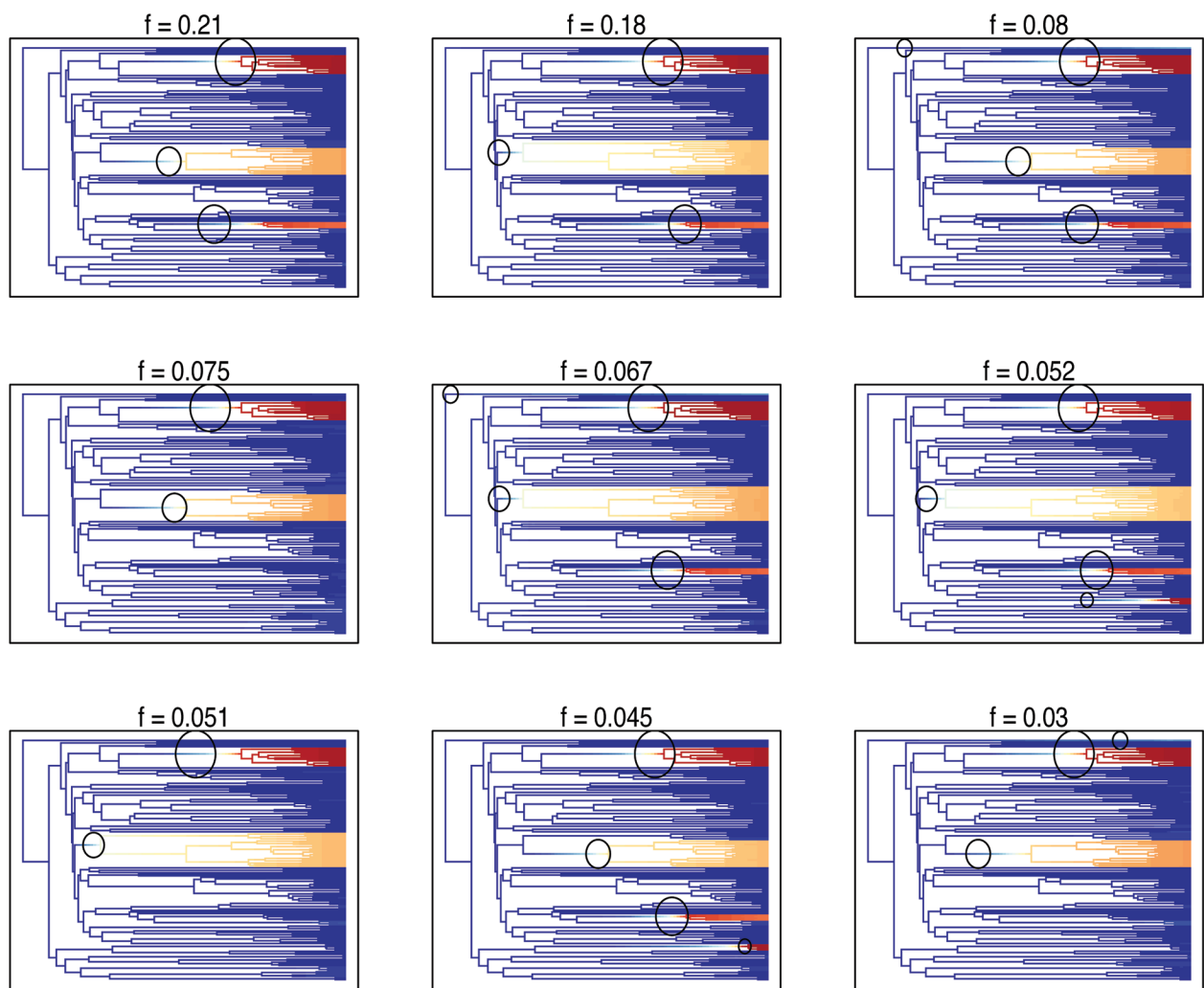


Figure S11: 95% credible shift set for BAMM analyses based on 50-best-ST topology and species-only estimates.

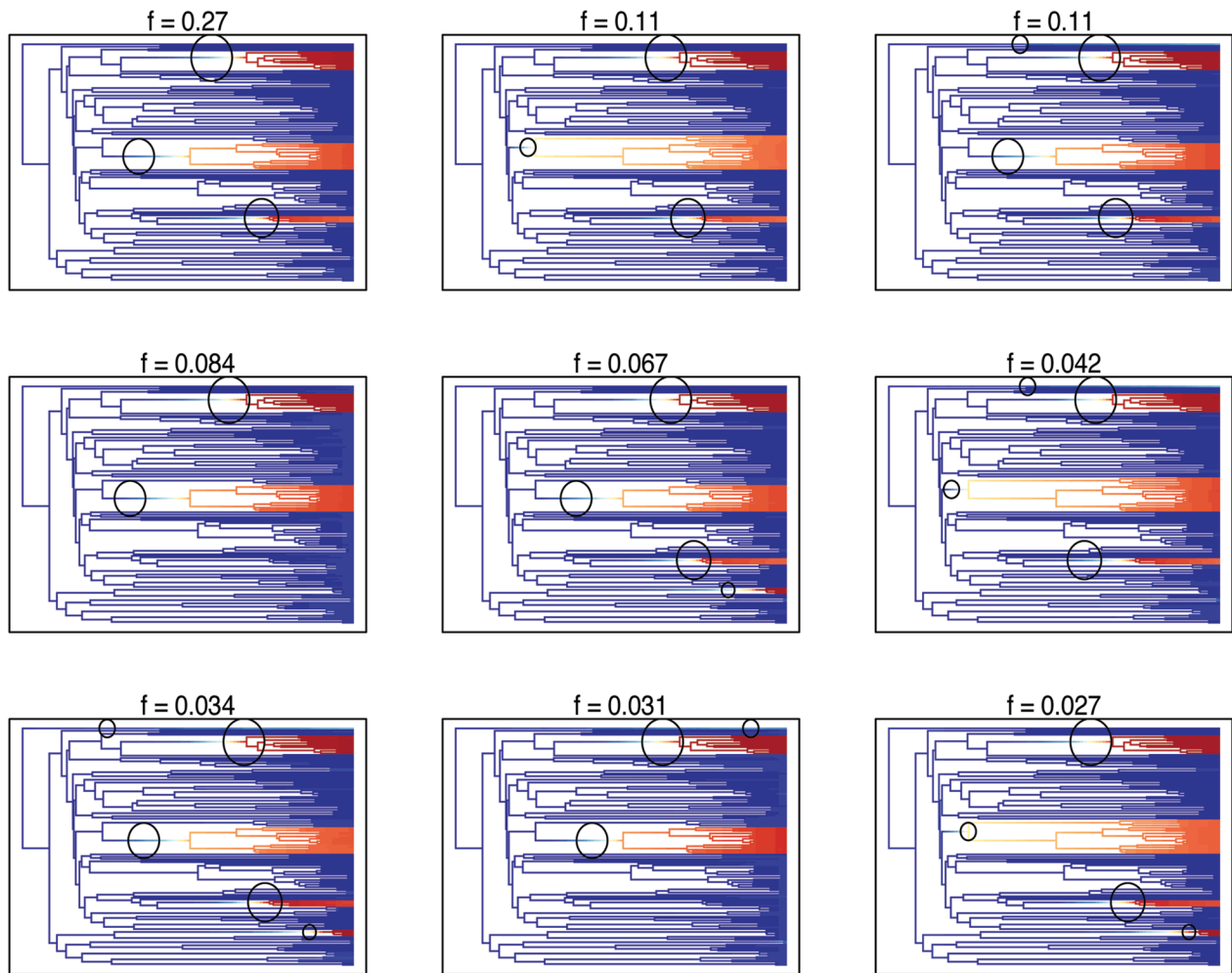


Figure S12: 95% credible shift set for BAMM analyses based on 50-best-ST topology and species and subspecies estimates.