

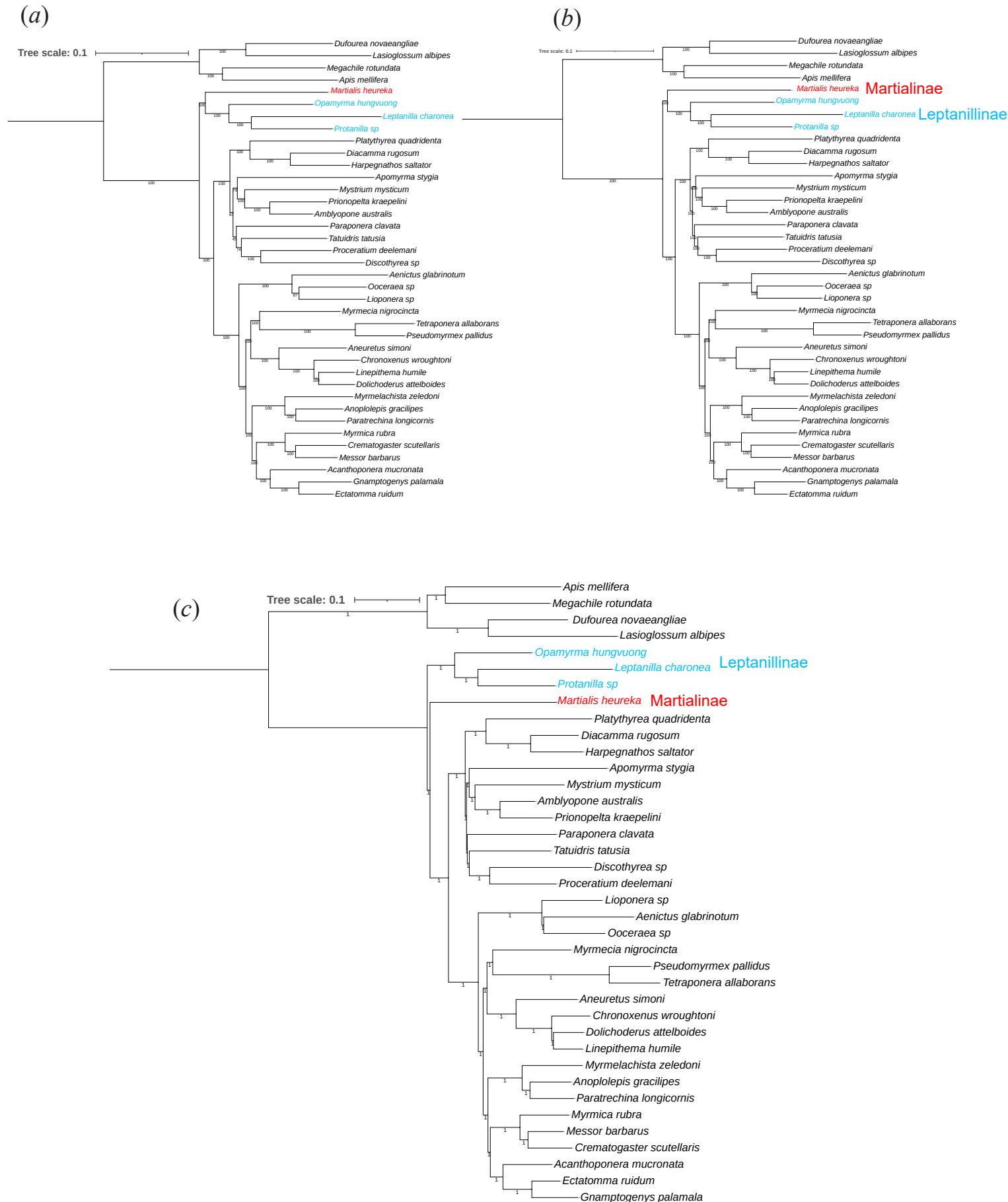


Figure S1. Phylogenomic analyses of filtered nuclear genomic 4,151-gene dataset (Matrix 1) from Romiguier et al. (2022). (a) Under the LG4X+R model in IQ-TREE. (b) Under the LG+C20+F+G model in IQ-TREE (PMSF, LG4X+R tree as guide tree). (c) Preferred topology under the site-heterogeneous CAT-GTR+G4 model in PhyloBayes: Burnin = 470 samples; Total number of cycles = 1424; Bpcomp maxdiff = 0; Trace-comp minimal overall effsize = 52.

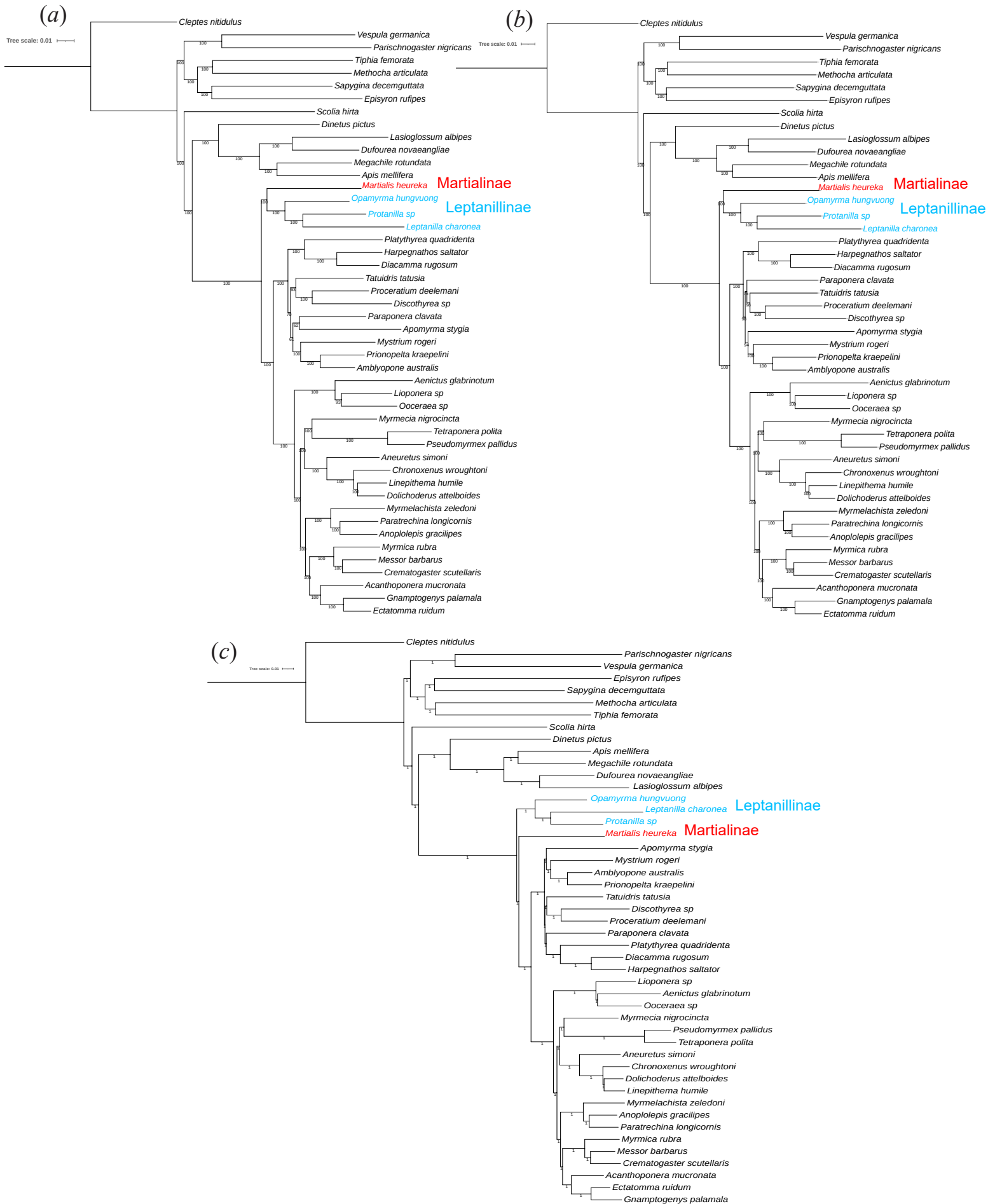


Figure S2. Phylogenomic analyses of filtered nuclear genomic 2,343-gene dataset (Matrix 2) from Romiguier et al. (2022). (a) Under the LG4X+R model in IQ-TREE. (b) Under the LG+C20+F+G model in IQ-TREE (PMSF, LG4X+R tree as guide tree). (c) Preferred topology under the site-heterogeneous CAT-GTR+G4 model in PhyloBayes: Bpcomp maxdiff/meandiff = 0.

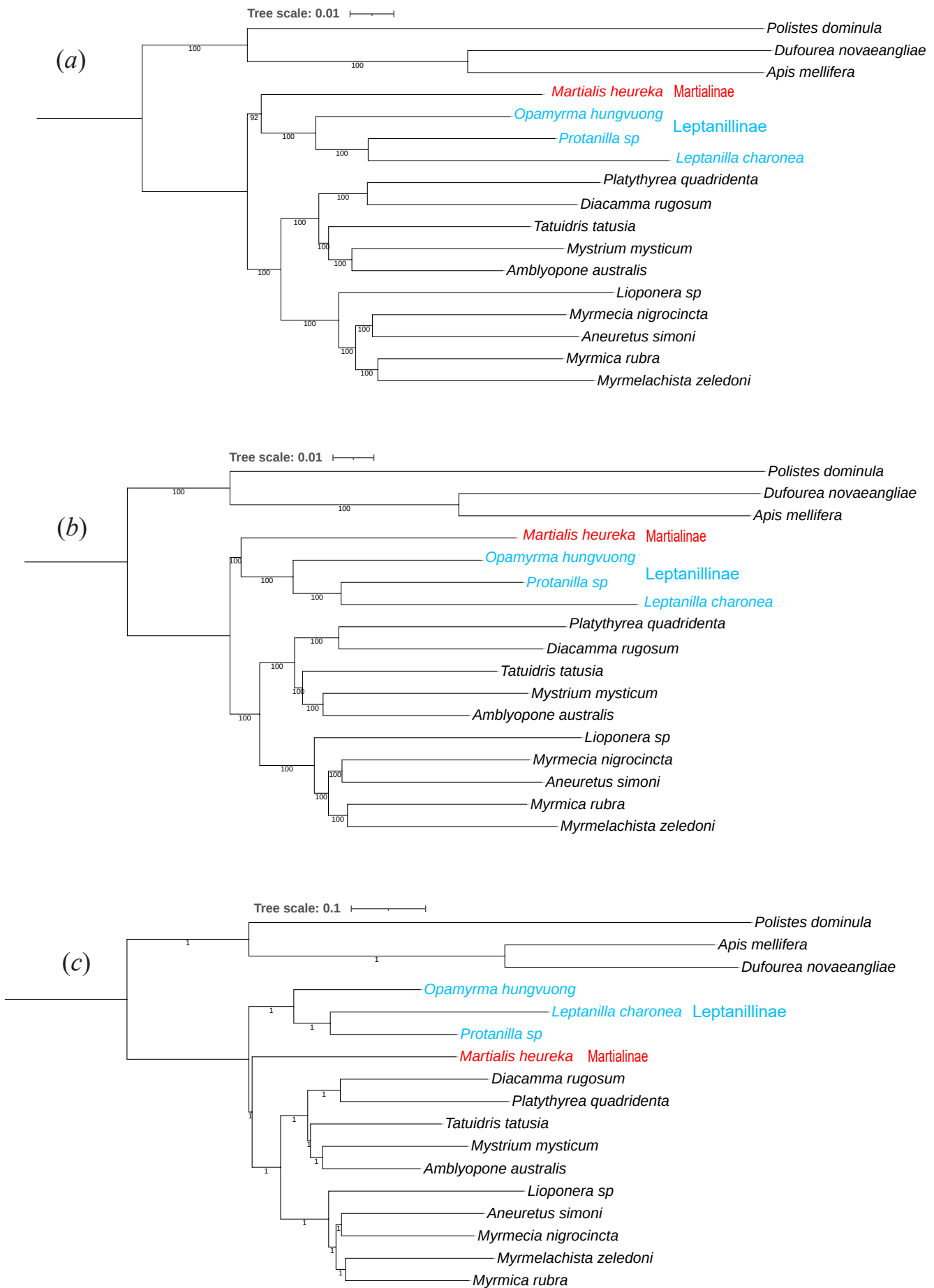


Figure S4. Phylogenomic analyses of subsampled (alignments not trimmed) nuclear genomic 4,151-gene dataset (Matrix 4) from Romiguier et al. (2022). (a) Under the LG4X+R model in IQ-TREE. (b) Under the LG+C20+F+G model in IQ-TREE (PMSF, LG4X+R tree as guide tree). (c) Preferred topology under the site-heterogeneous CAT-GTR+G4 model in PhyloBayes: Burnin = 350 samples; Total number of cycles = 1055; Bpcomp maxdiff = 0; Tracecomp minimal overall effsize = 54.

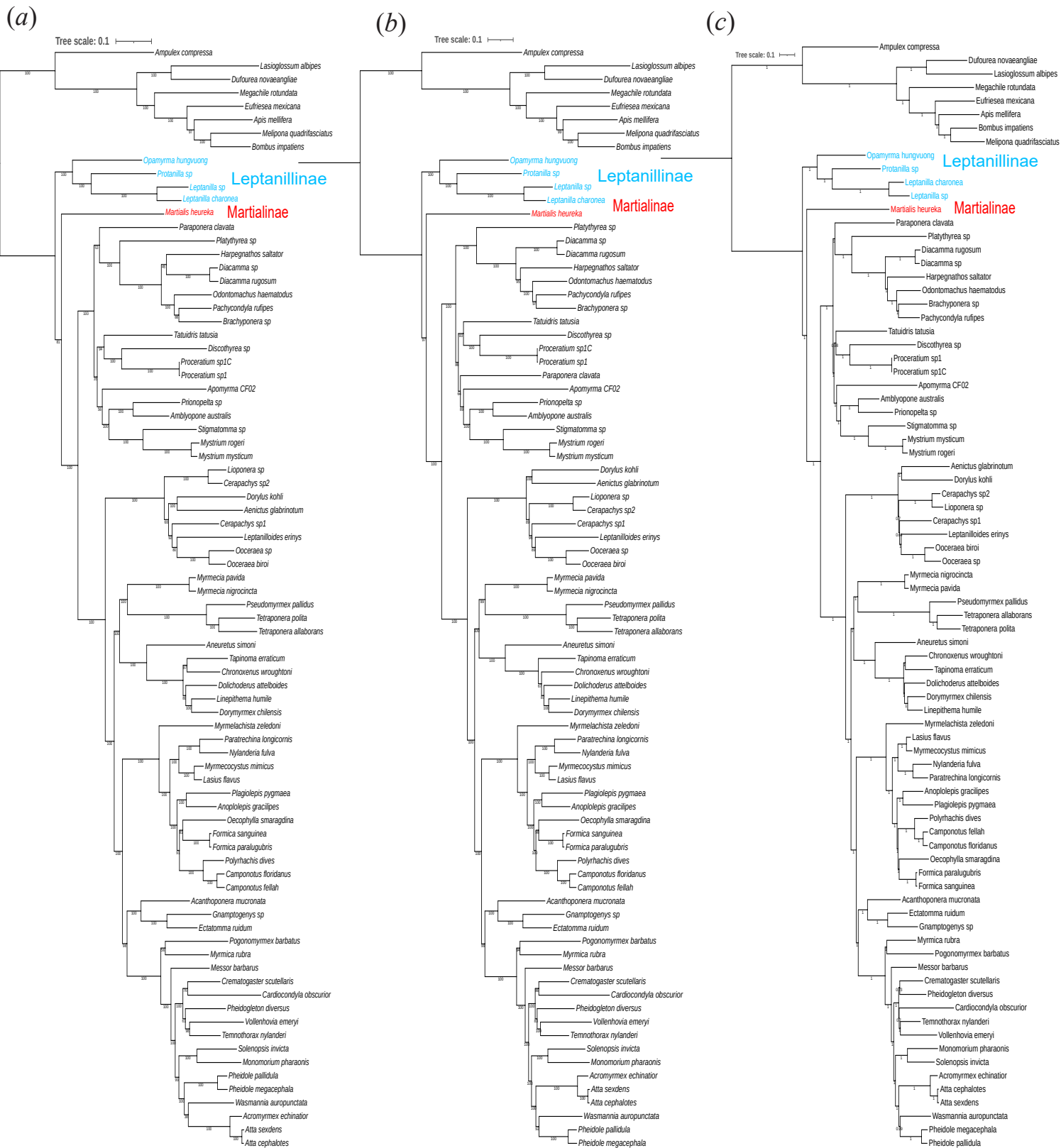


Figure S5. Phylogenomic analyses of trimmed nuclear genomic 4,151-gene dataset (Matrix 5) from Romiguier et al. (2022). (a) Under the LG4X+R model in IQ-TREE. (b) Under the LG+C20+F+G model in IQ-TREE (PMSF model not used). (c) Under the site-heterogeneous CAT-GTR+G4 model in PhyloBayes: Burnin = 600 samples; Total number of cycles = 2065; Bpcomp maxdiff = 0.17; Tracecomp minimal overall effsize = 250.

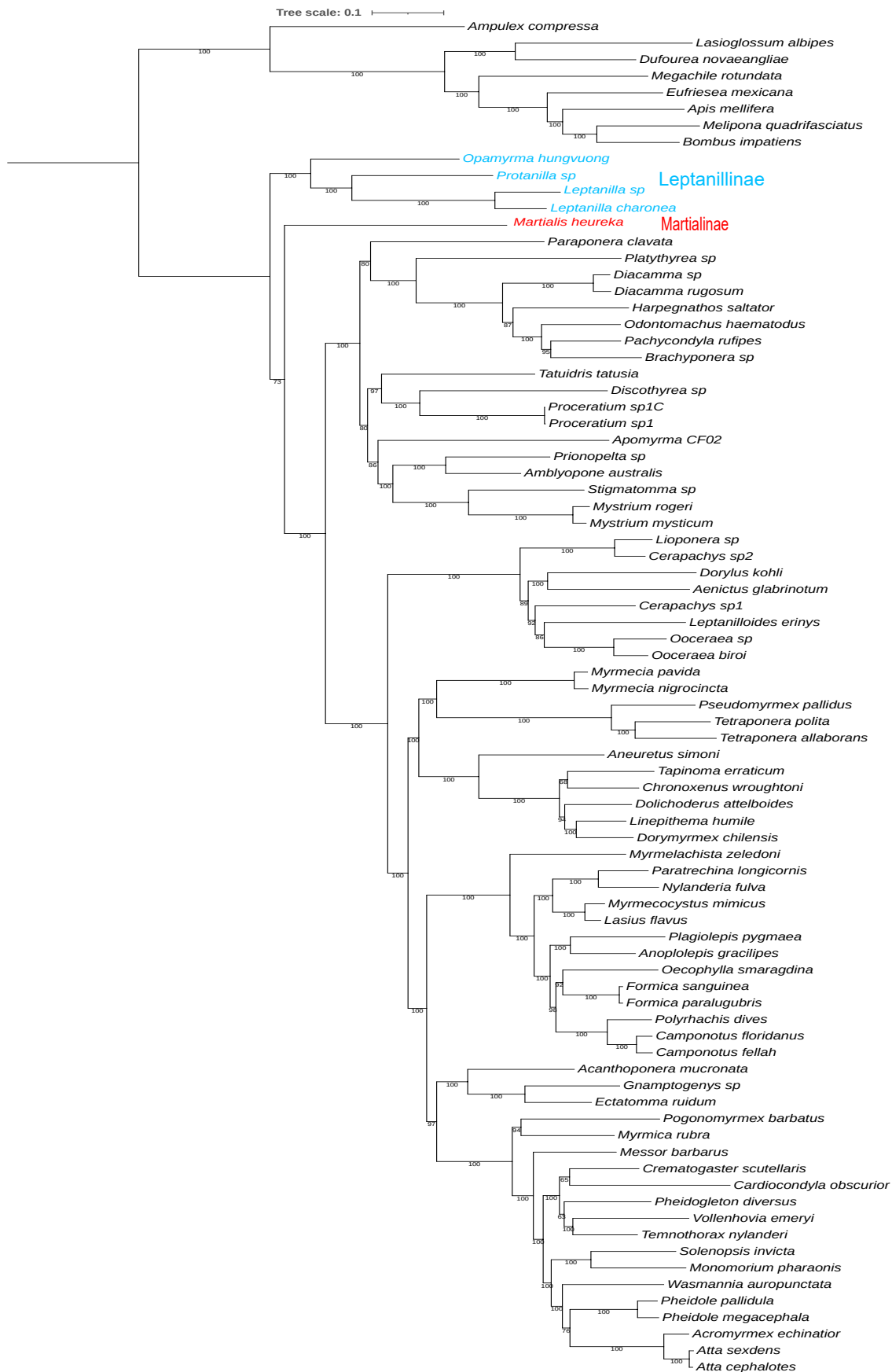


Figure S6. Phylogenomic analyses of trimmed nuclear genomic 4,151-gene dataset (Matrix 5) from Romiguier et al. (2022). Under the heterotachous GHOST (LG+FO*H4) model in IQ-TREE.