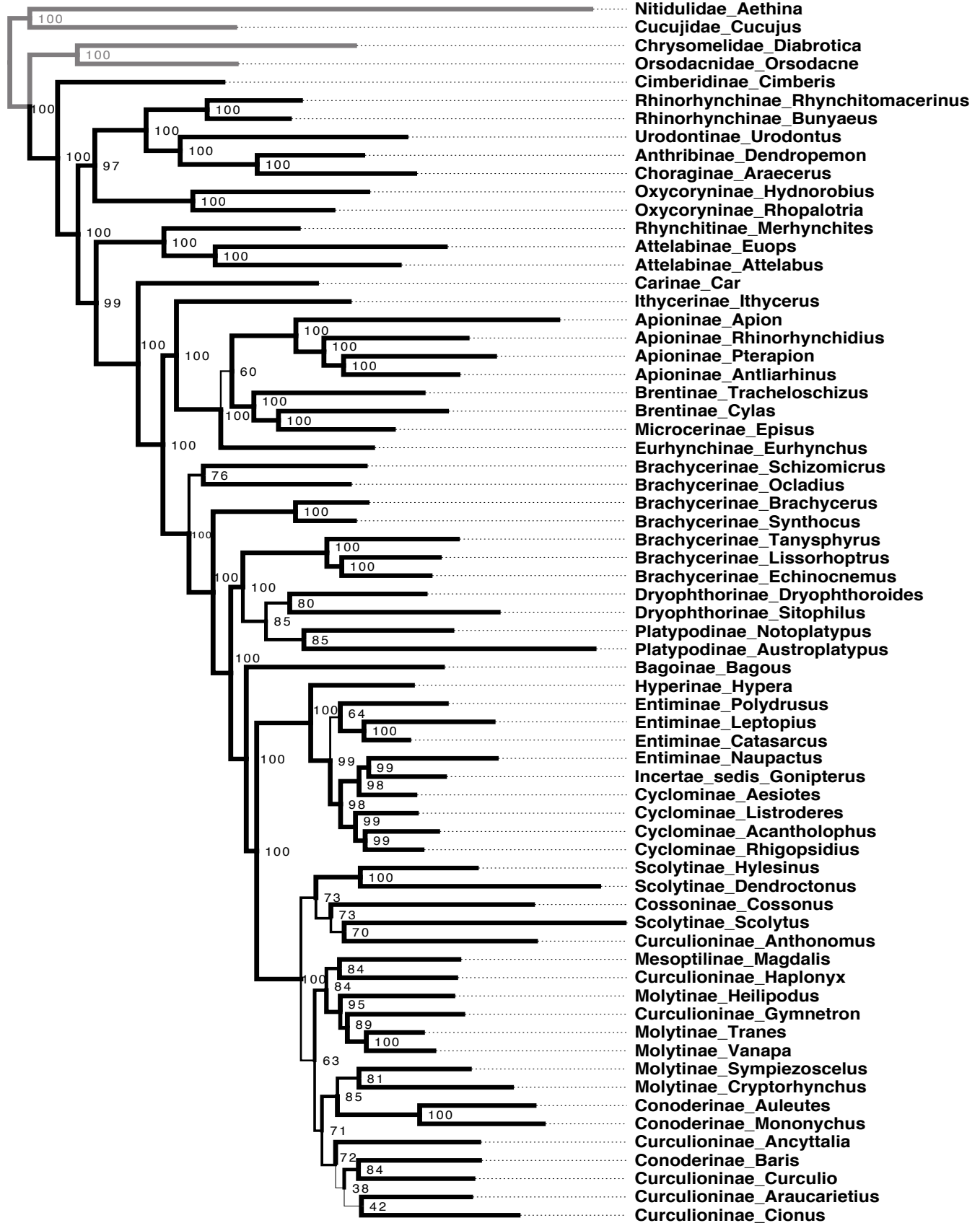
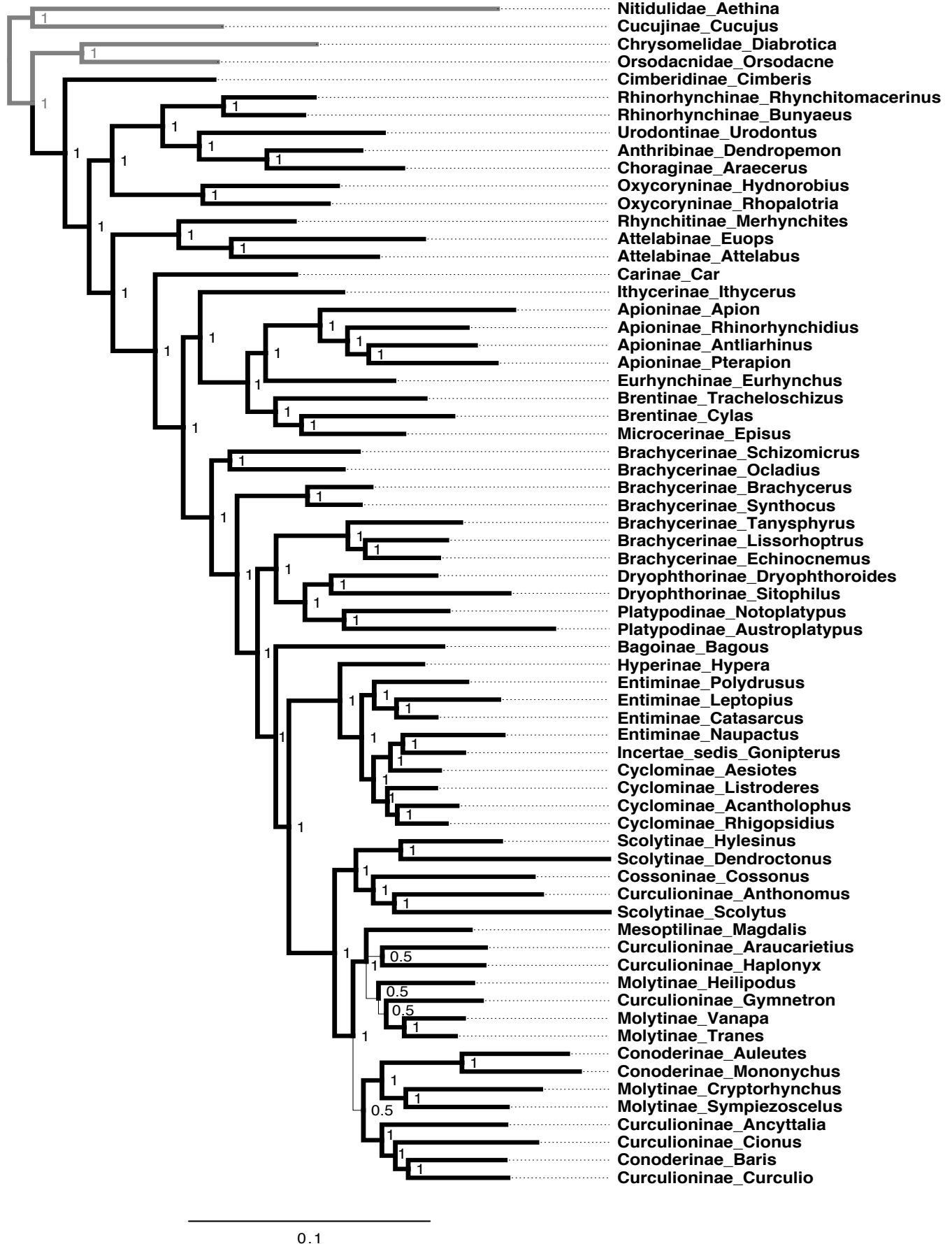


Supplementary figure S1. Phylogenetic tree based on a maximum likelihood analysis of non-partitioned nucleotide sequence data (all codons; C123), with ML bootstrap support values plotted to the right of the nodes they refer to.



Supplementary figure S2. Phylogenetic tree based on a maximum likelihood analysis of non-partitioned amino acid sequence data, with ML bootstrap values plotted to the right of the nodes they refer to.

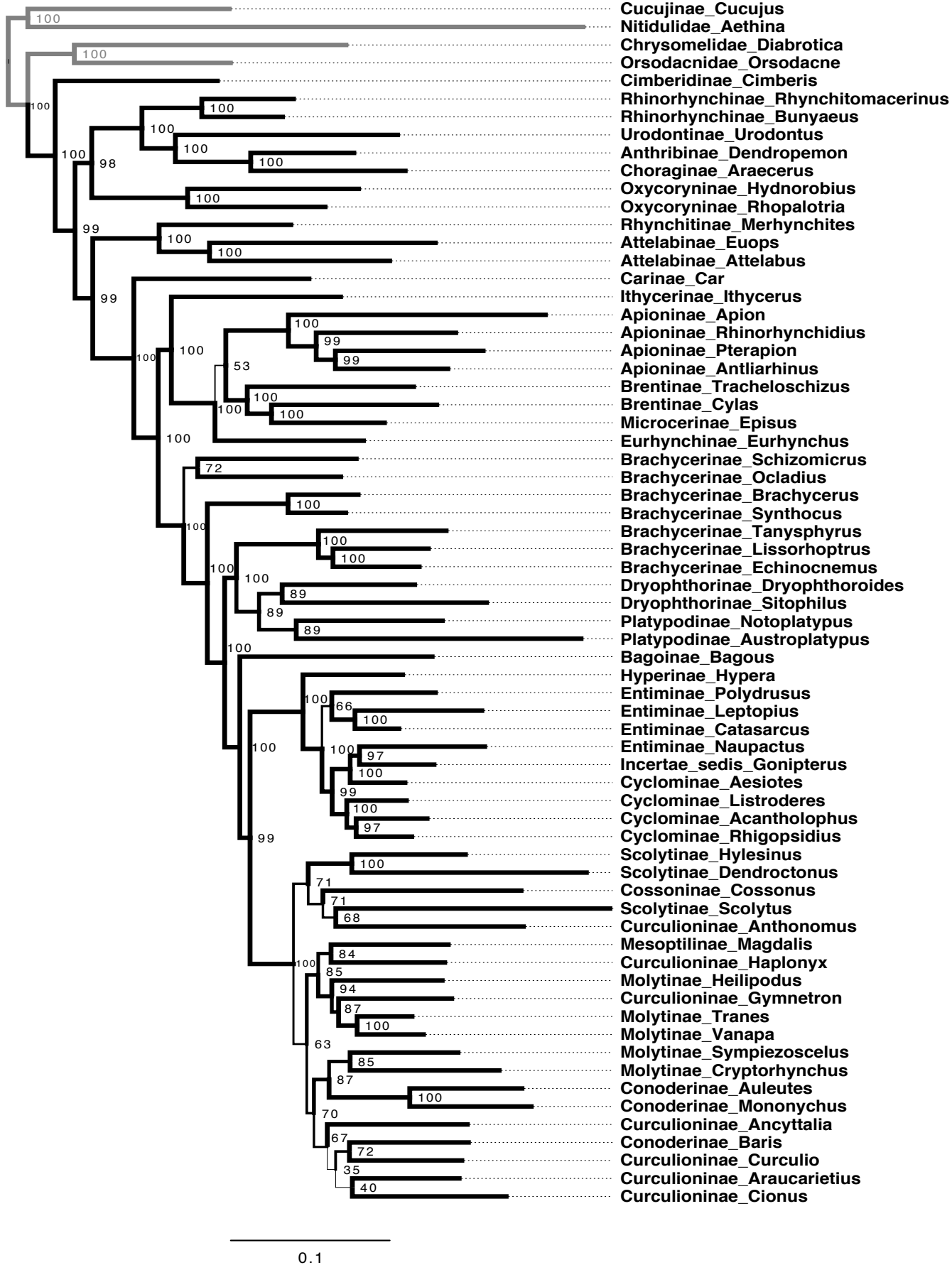




Supplementary figure S4. Phylogenetic tree based on a Bayesian analysis of non-partitioned amino acid sequence data, with posterior probability values plotted to the right of the nodes they refer to.



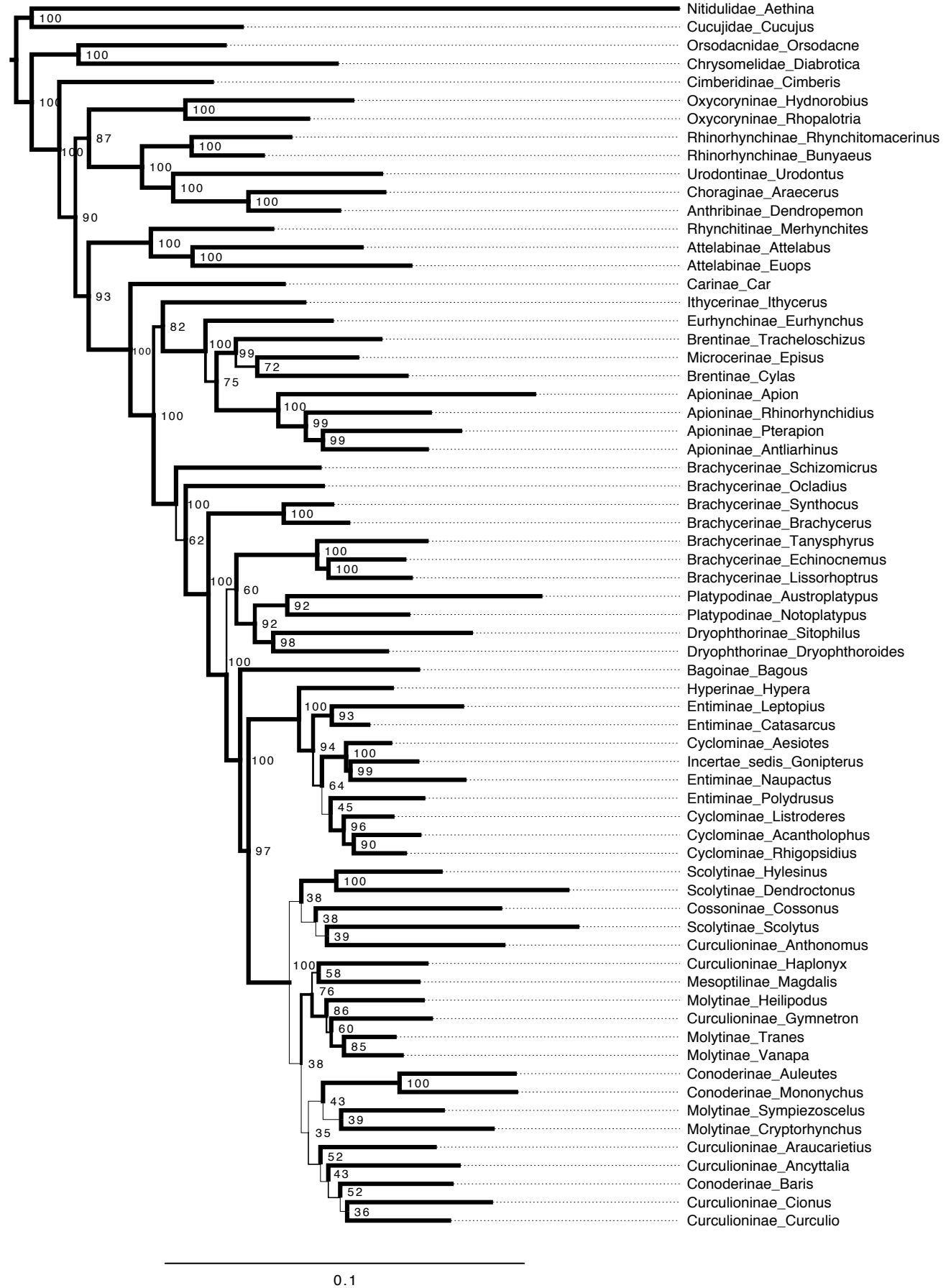
Supplementary figure S5. Phylogenetic tree based on a maximum likelihood analysis of partitioned nucleotide sequence data (all codons; C123), with ML bootstrap support values plotted to the right of the nodes they refer to.



Supplementary figure S6. Phylogenetic tree based on a maximum likelihood analysis of partitioned amino acid sequence data, with ML bootstrap values plotted to the right of the nodes they refer to. (See also Fig. 1 in paper).



Supplementary figure S7. Phylogenetic tree based on a maximum likelihood analysis (GTR+I+G) of first codon positions (C1), with bootstrap values plotted to the right of the nodes they refer to.

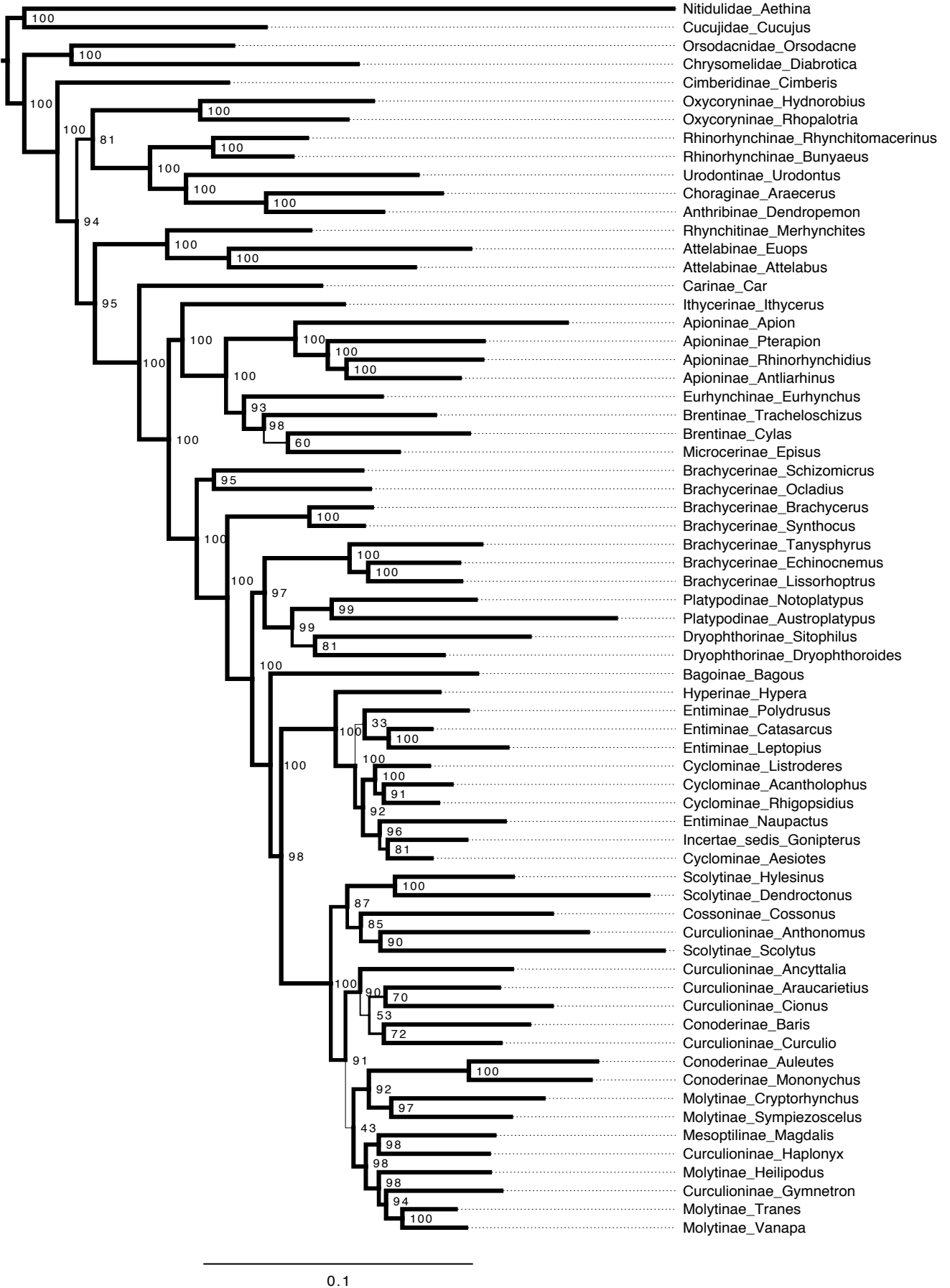


Supplementary figure S8. Phylogenetic tree based on a maximum likelihood analysis (GTR+I+G) of second codon positions (C2), with bootstrap values plotted to the right of the nodes they refer to.

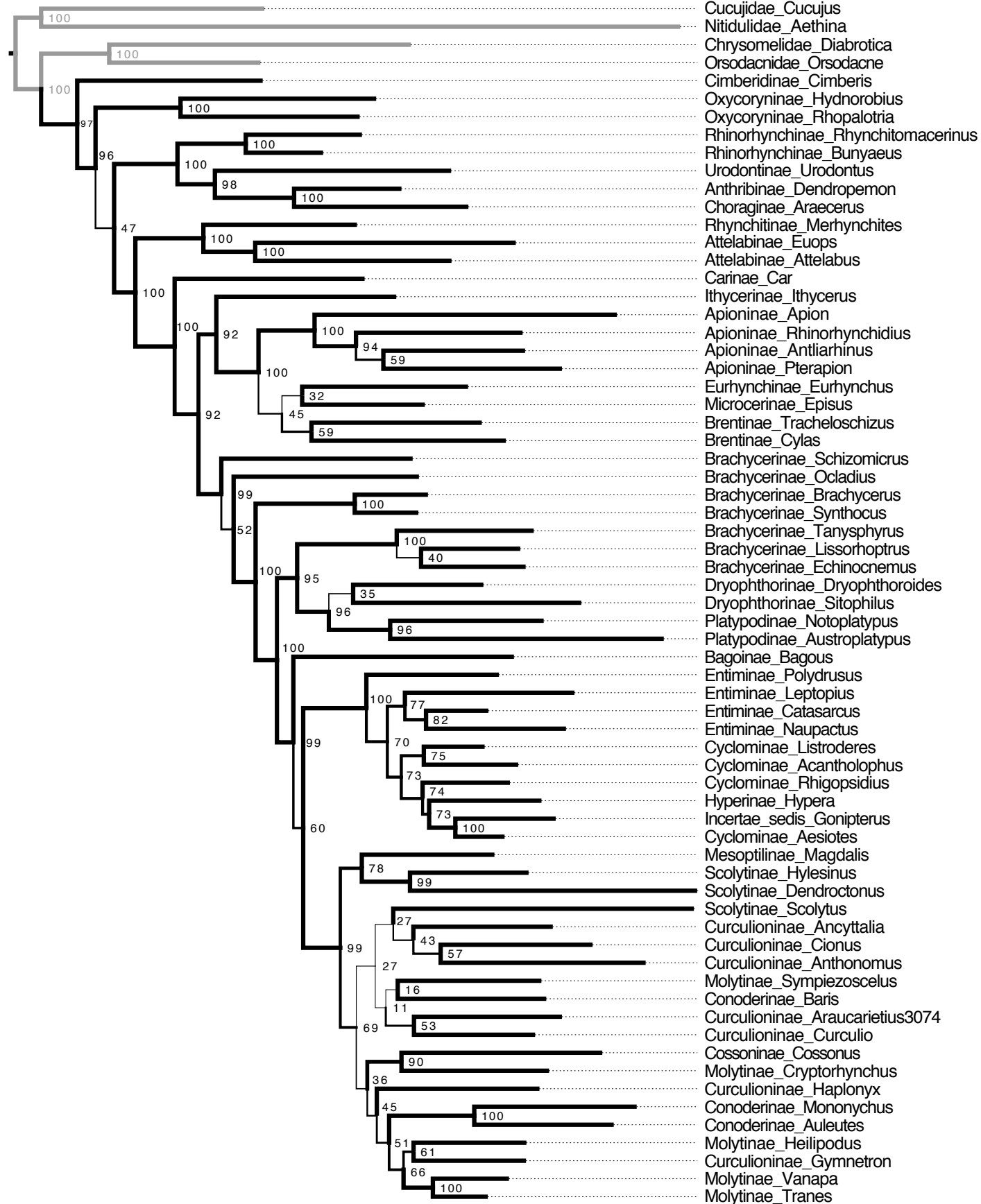




Supplementary figure S9. Phylogenetic tree based on a maximum likelihood analysis (GTR+I+G) of third codon positions (C3), with bootstrap values plotted to the right of the nodes they refer to.



Supplementary figure S10. Phylogenetic tree based on a maximum likelihood analysis (GTR+I+G) of first and second codon positions (C12), with bootstrap values plotted to the right of the nodes they refer to.

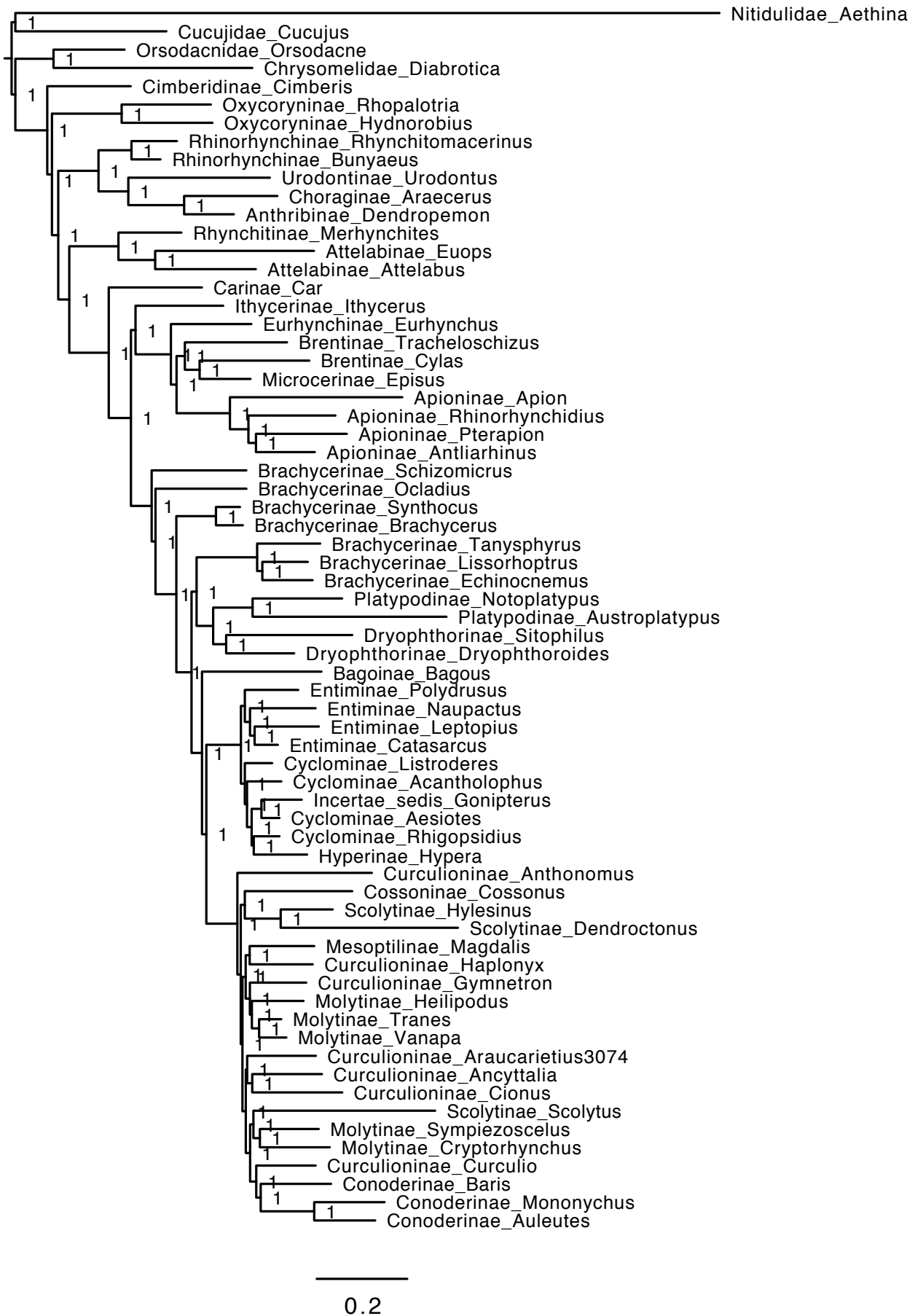


0.1

Supplementary figure S11. Phylogenetic tree based on a maximum likelihood analysis of non-partitioned 6 Dayhoff recoded amino acid data, with bootstrap values plotted to the right of the nodes they refer to.



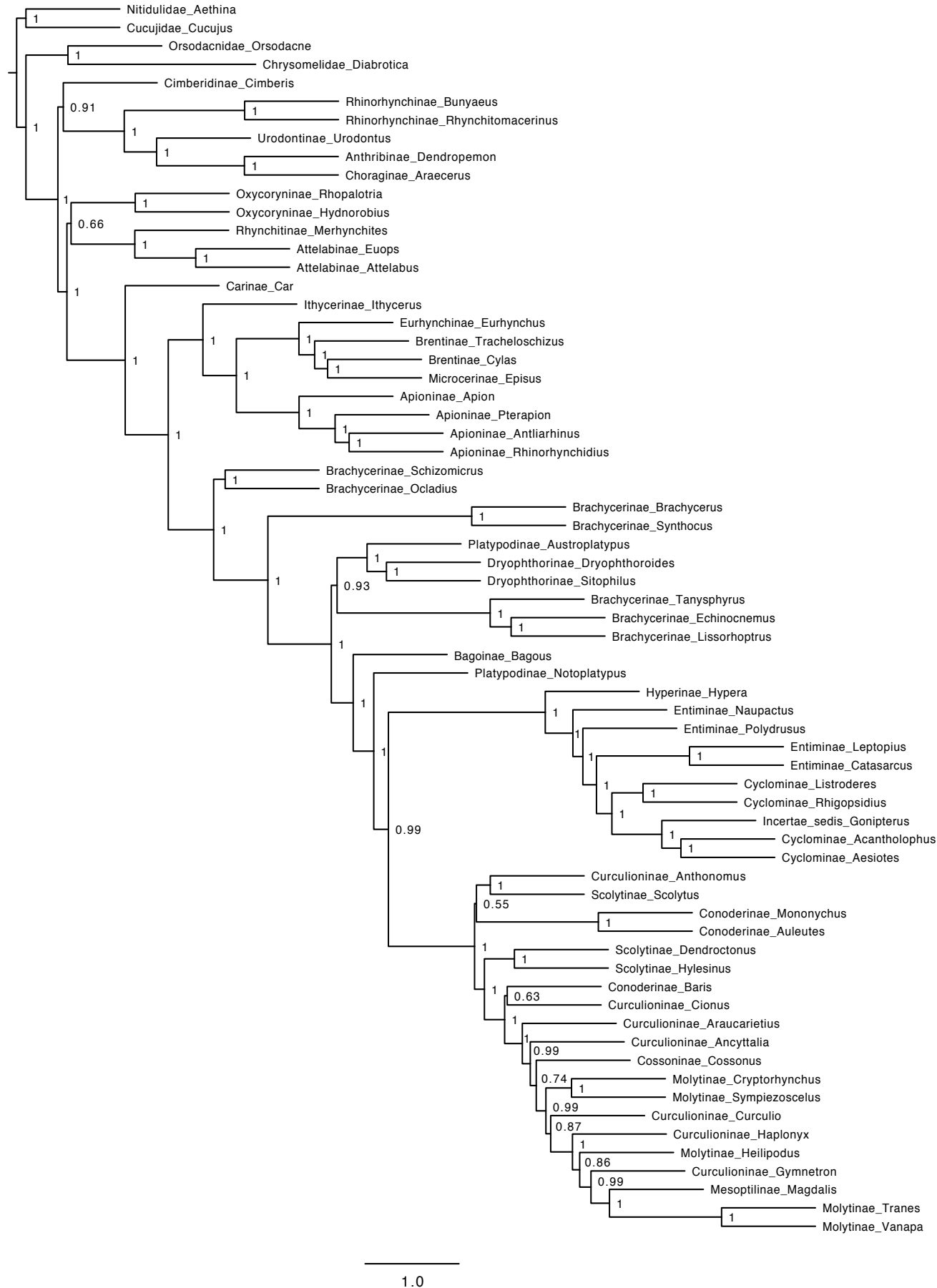
Supplementary figure S12. Posterior consensus tree derived from a Phylobayes analysis (CAT-GTR) of non-partitioned amino acid data, with posterior probability values plotted to the right of the nodes they refer to.



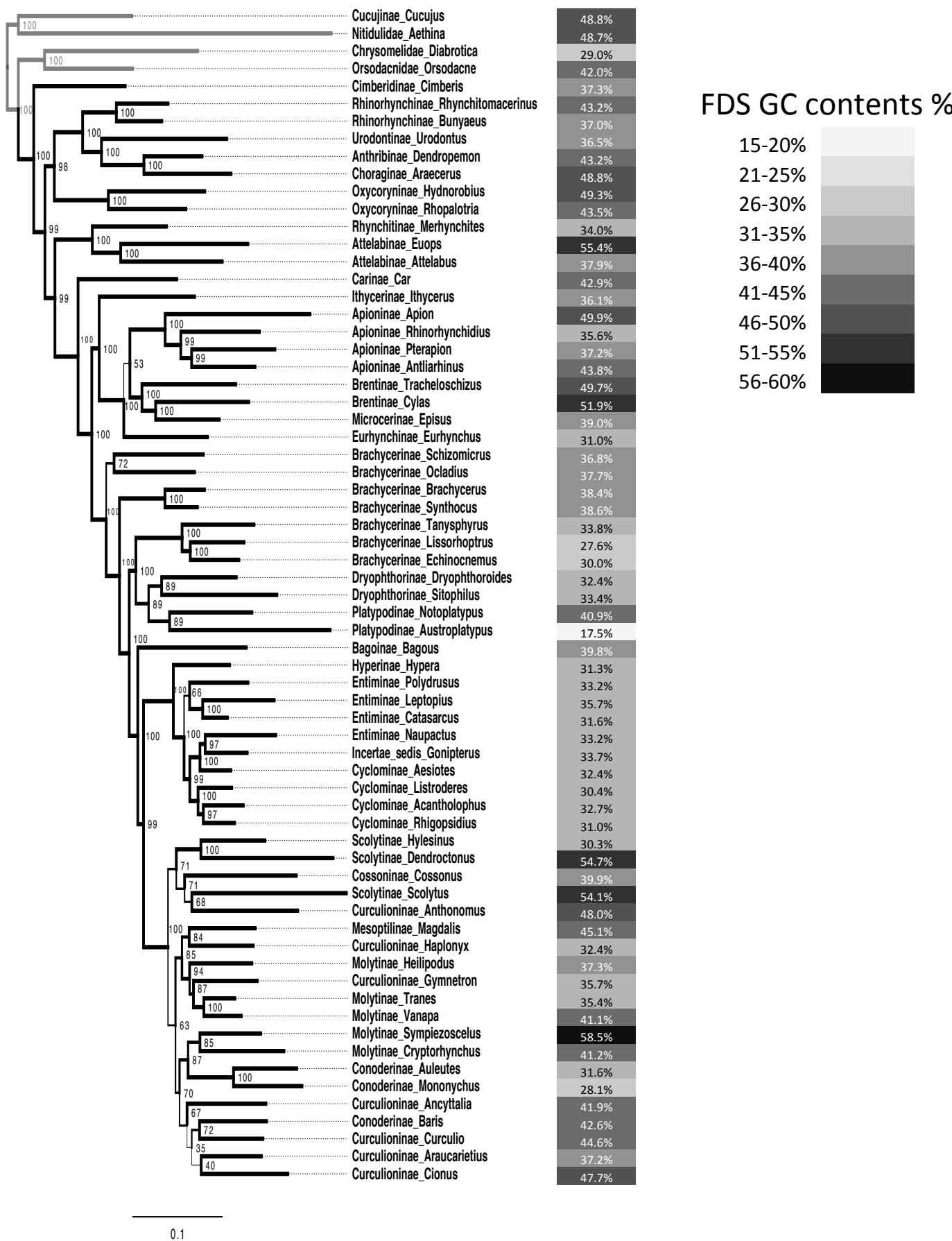
Supplementary figure S13. Posterior consensus tree derived from a Phylobayes analysis (CAT-GTR) of non-partitioned nucleotide data, with posterior probability values plotted to the right of the nodes they refer to.



Supplementary figure S14. Coalescent species tree generated from a binned and weighted ASTRAL analysis of amino acid data, with support values plotted to the right of the nodes they refer to.

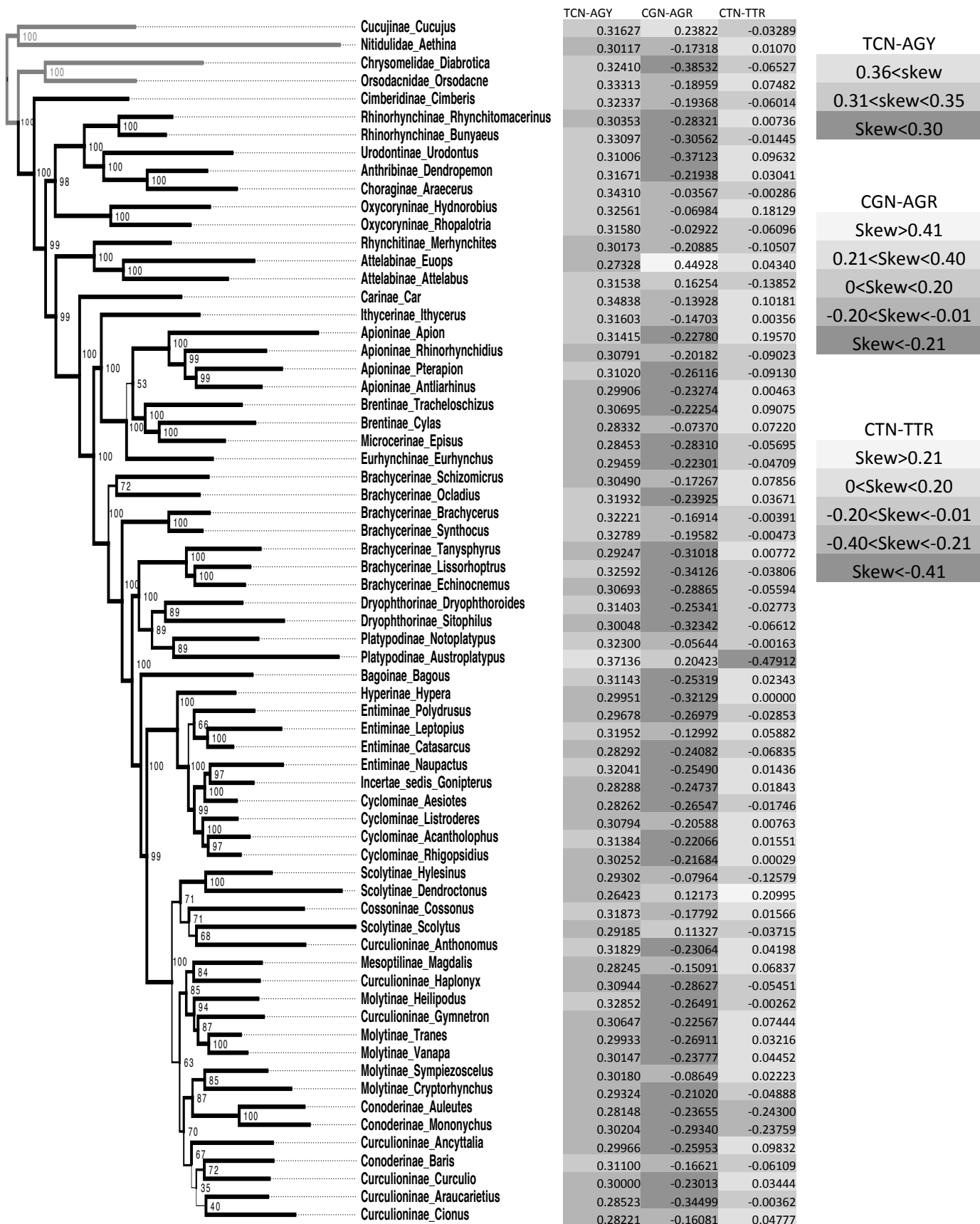


Supplementary figure S15. Coalescent species tree generated from a binned and weighted ASTRAL analysis of nucleotide data, with support values plotted to the right of the nodes they refer to.



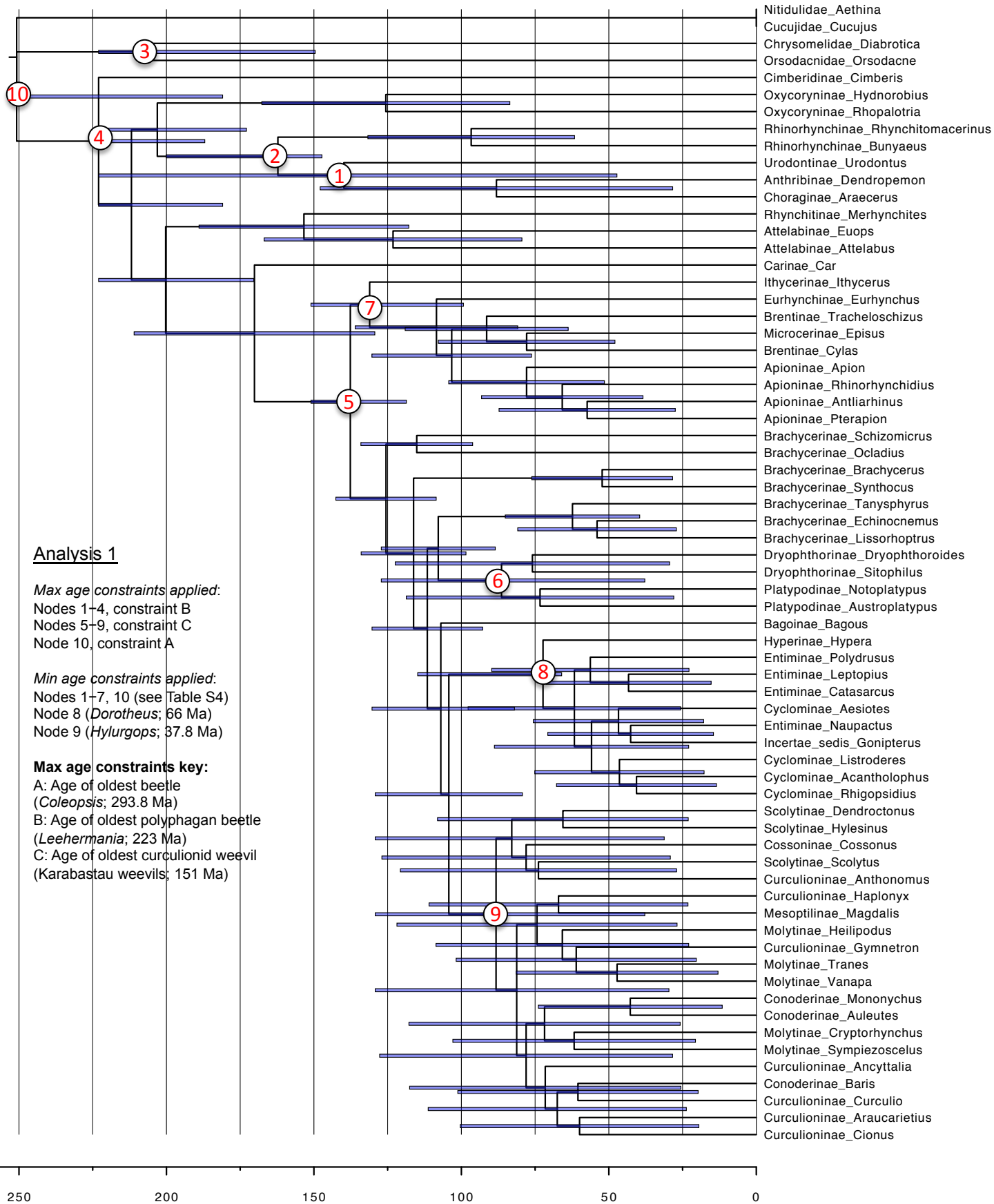
Supplementary figure S16. Four-fold degenerate sites (FDS) GC content mapped onto the phylogenetic tree based on a maximum likelihood analysis of partitioned amino acid data (as shown in Supplementary figure S6).



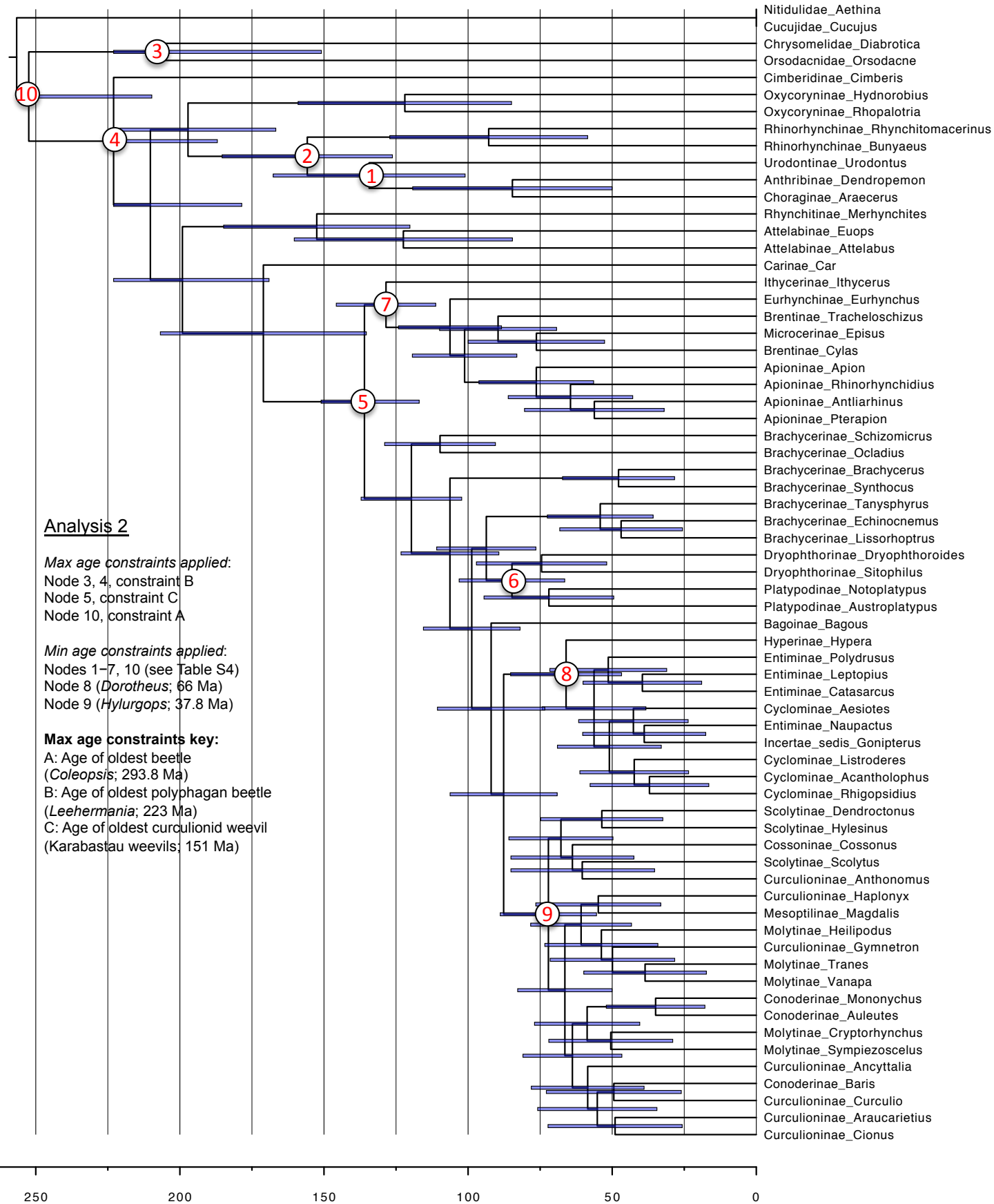


0.1

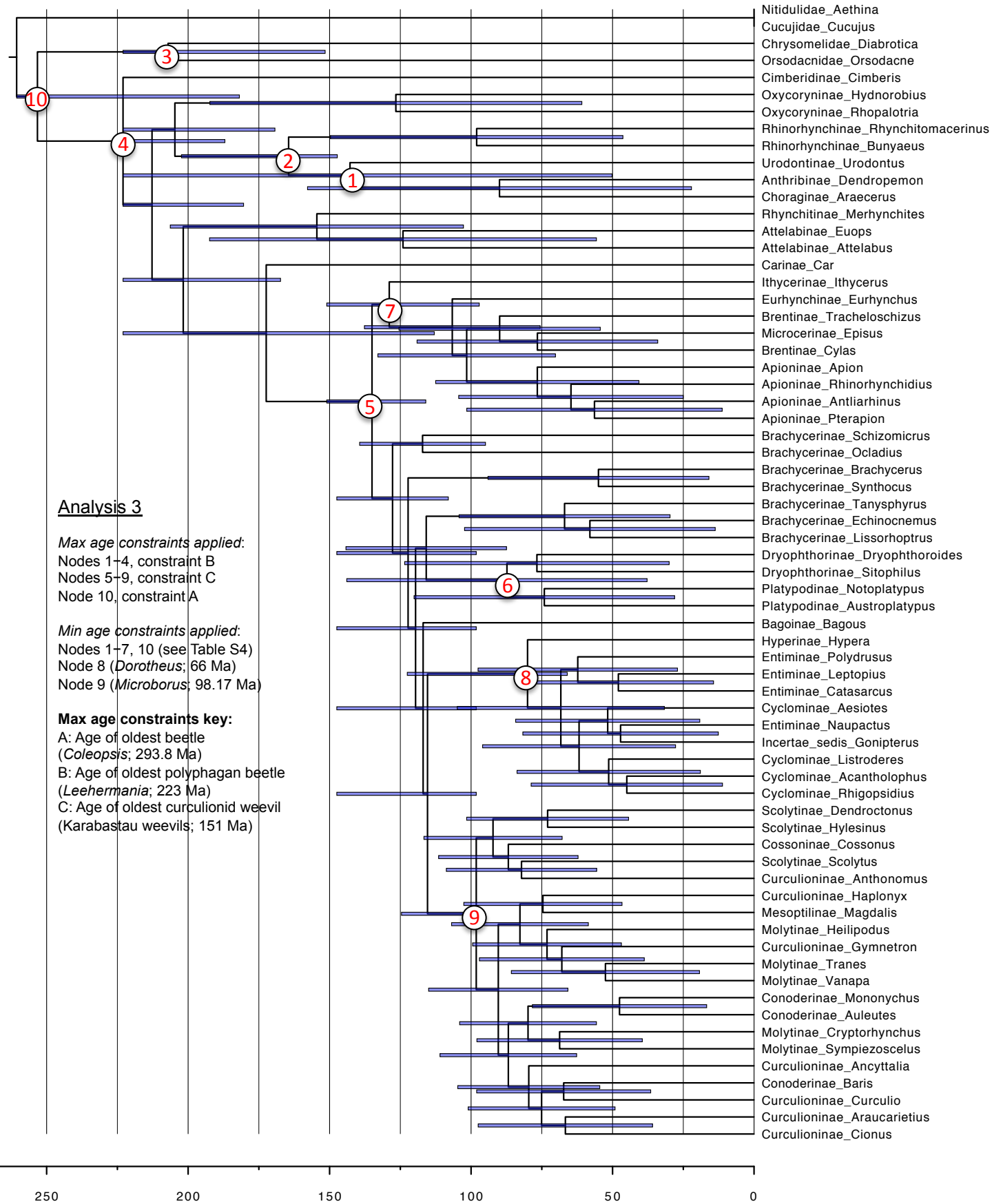
Supplementary figure S17. Skew values for the codon sets of serine (TCN/AGY), arginine (CGN/AGR), and leucine (CTN/TTR) plotted onto the phylogenetic tree based on a maximum likelihood analysis of partitioned amino acid data (shown in Supplementary figure S6). See text (main paper and Supplementary Materials) for details.



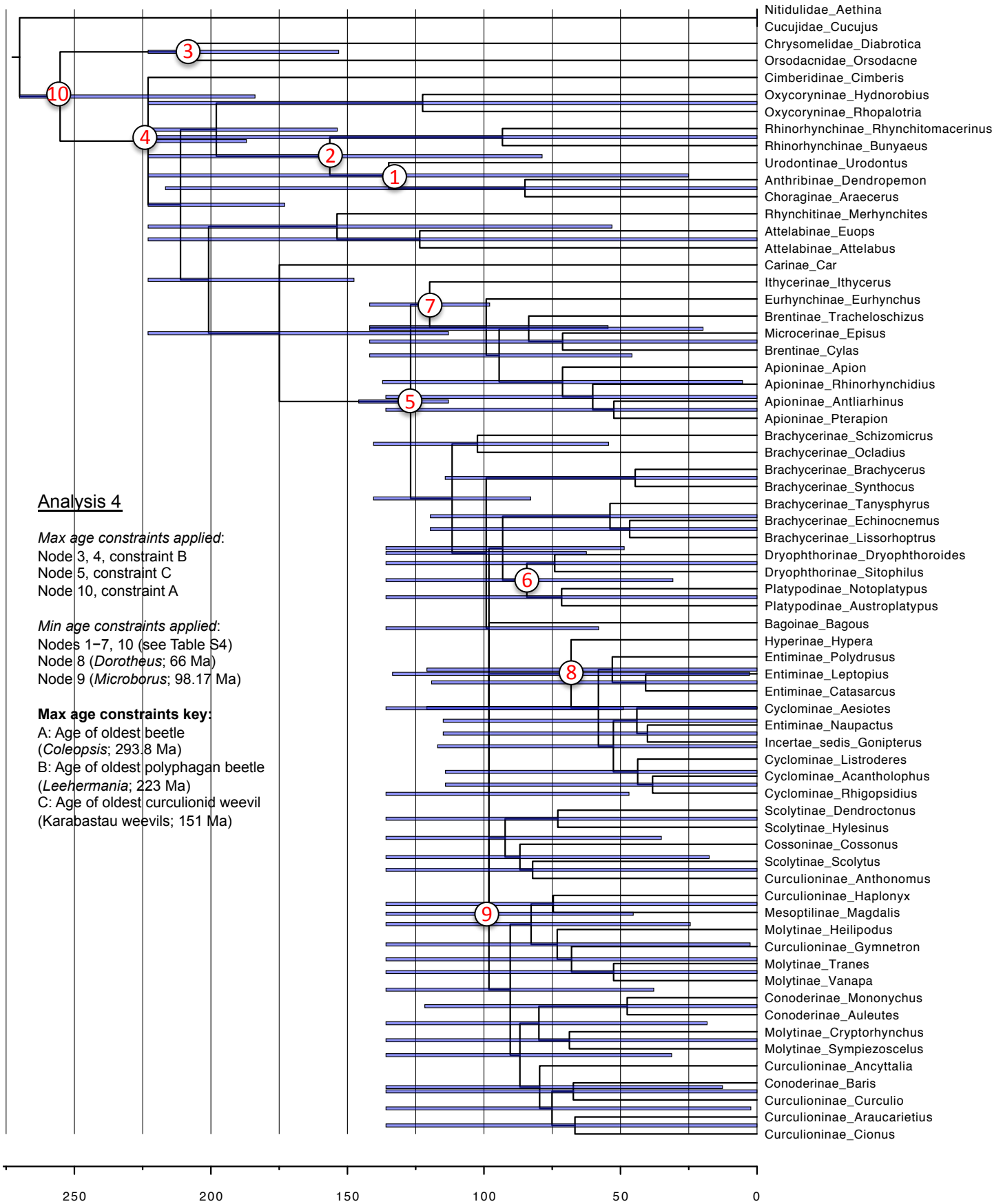
Supplementary figure S18. Chronogram showing divergence time estimation. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.



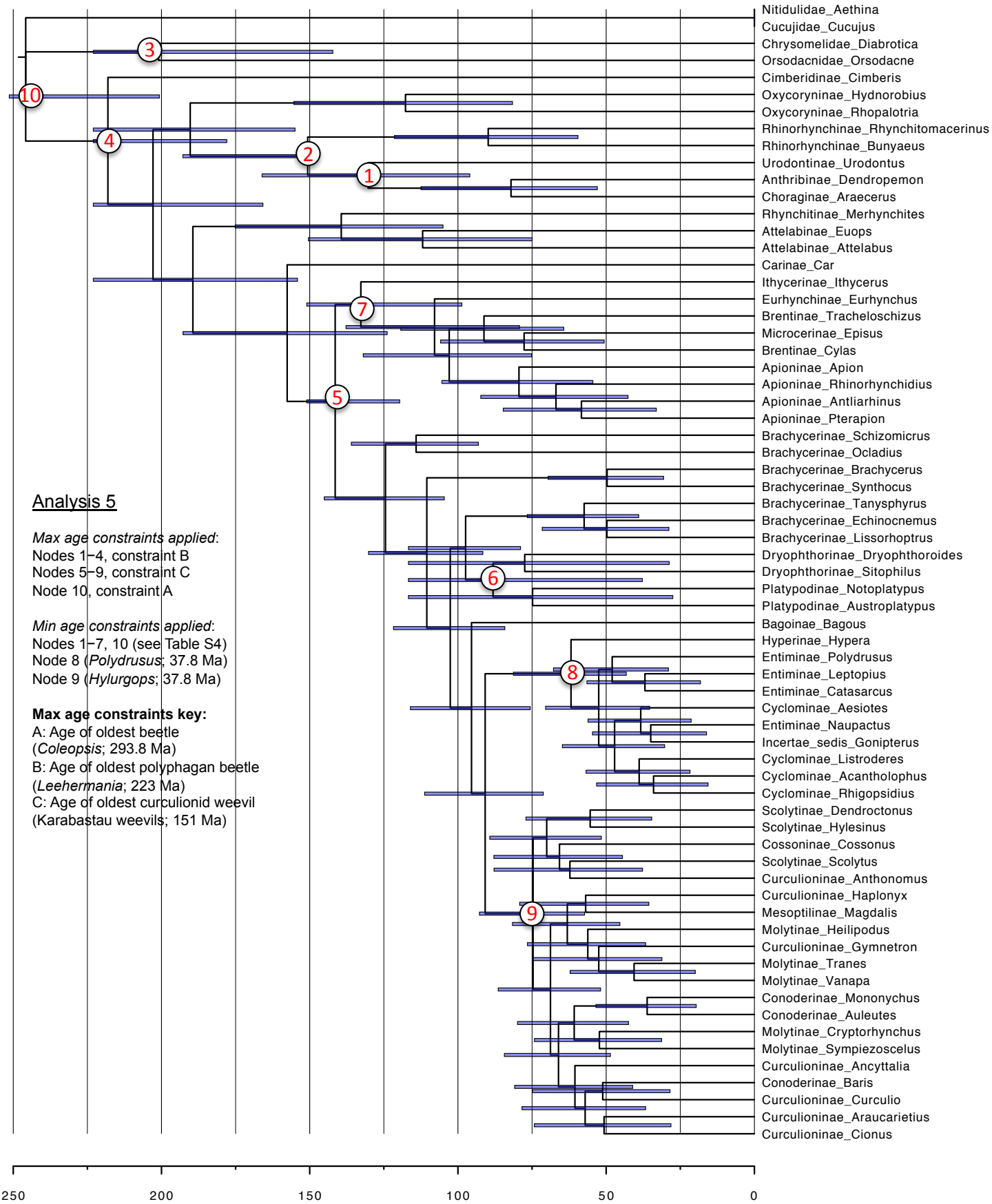
Supplementary figure S19. Chronogram showing divergence times. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.



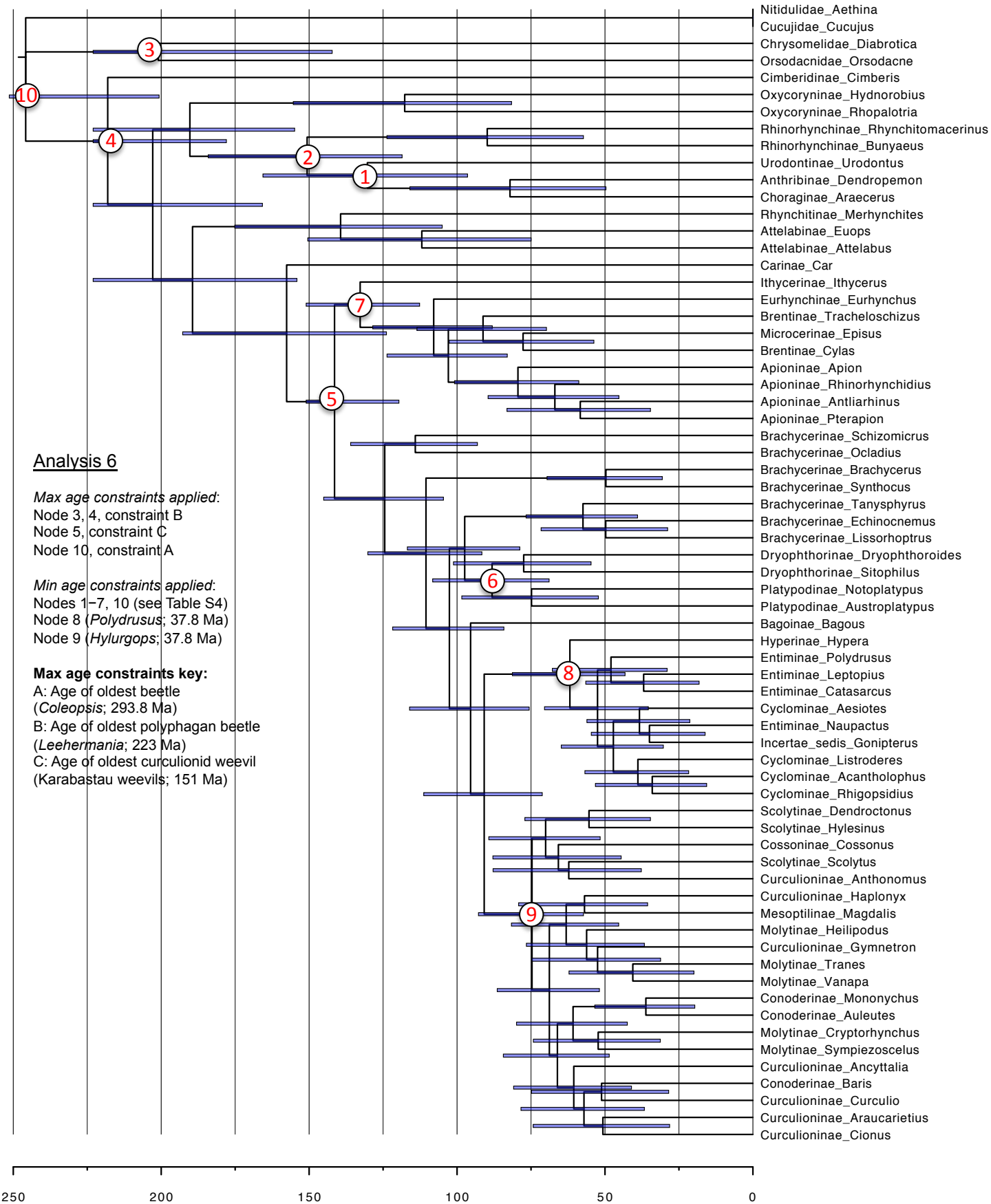
Supplementary figure S20. Chronogram showing divergence time estimation. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.



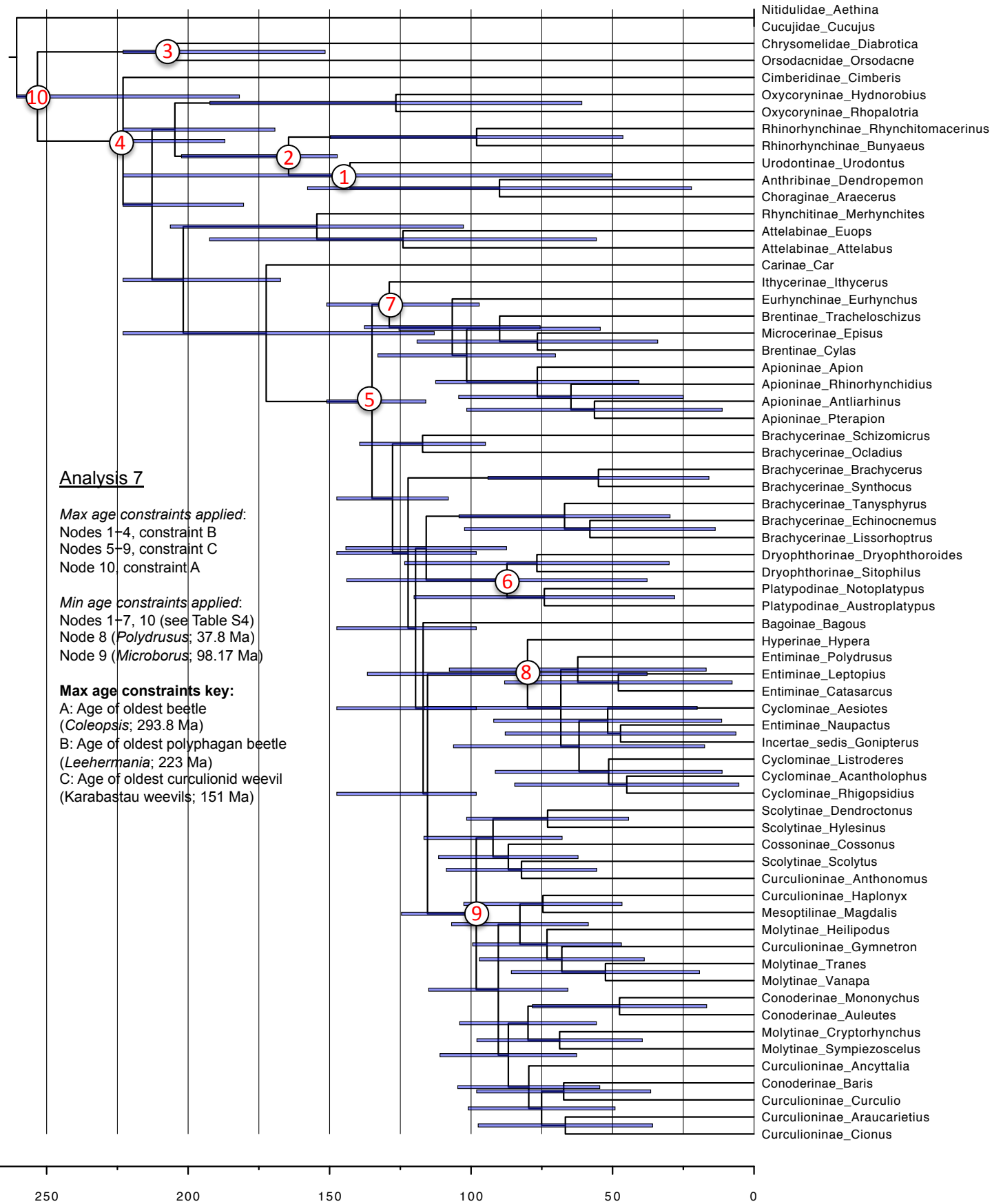
Supplementary figure S21. Chronogram showing divergence time estimation. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.



Supplementary figure S22. Chronogram showing divergence time estimation. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.

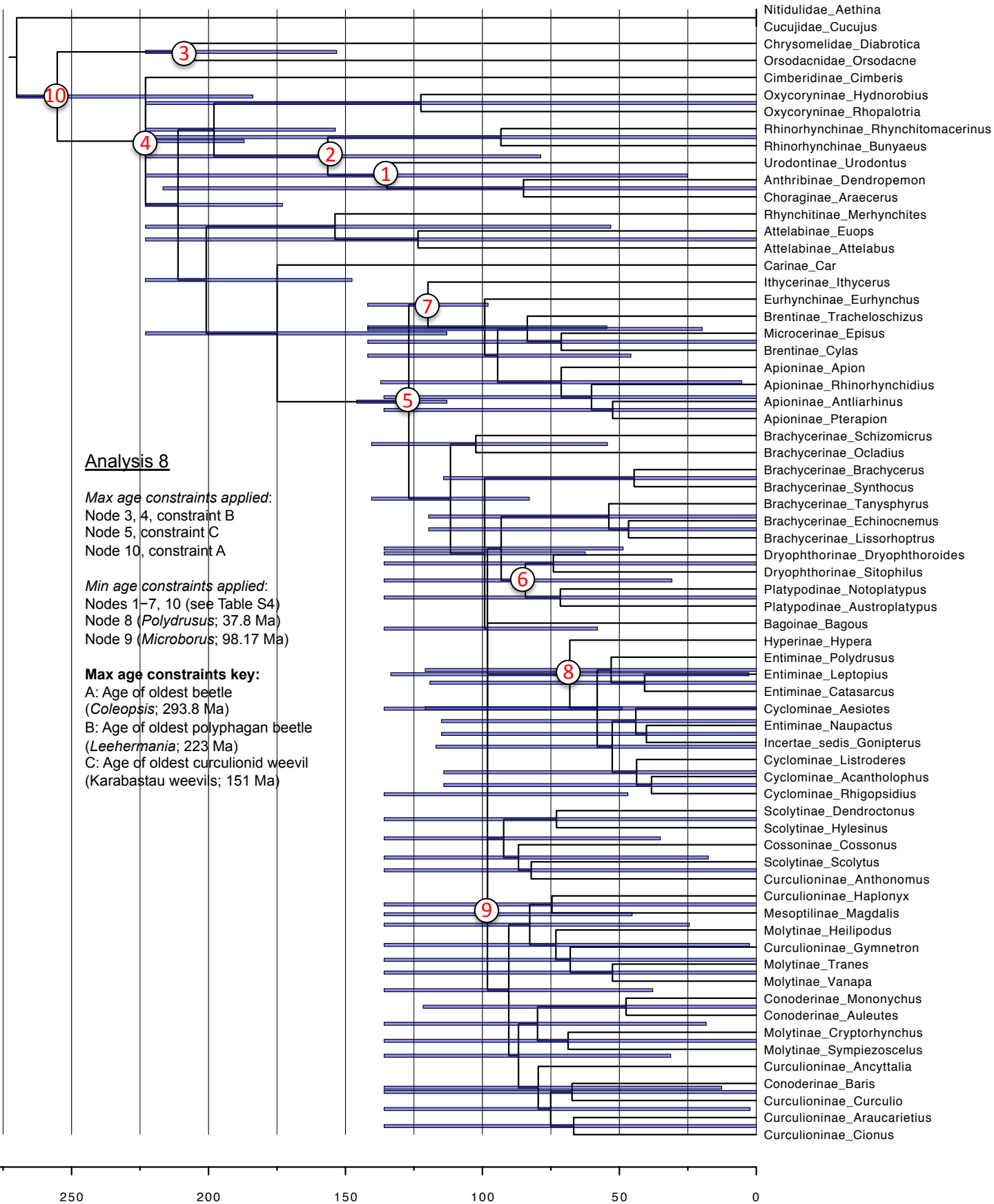


Supplementary figure S23. Chronogram showing divergence time estimation. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.



Supplementary figure S24. Chronogram showing divergence time estimation. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.





Supplementary figure S25. Chronogram showing divergence time estimation. RelTime estimates of lineage divergence were generated using the tree shown in Supplementary fig. S6 (partitioned amino acid data). The time scale is given on the x axis (Ma). The blue bars at nodes are the 95% confidence intervals of the age estimates.