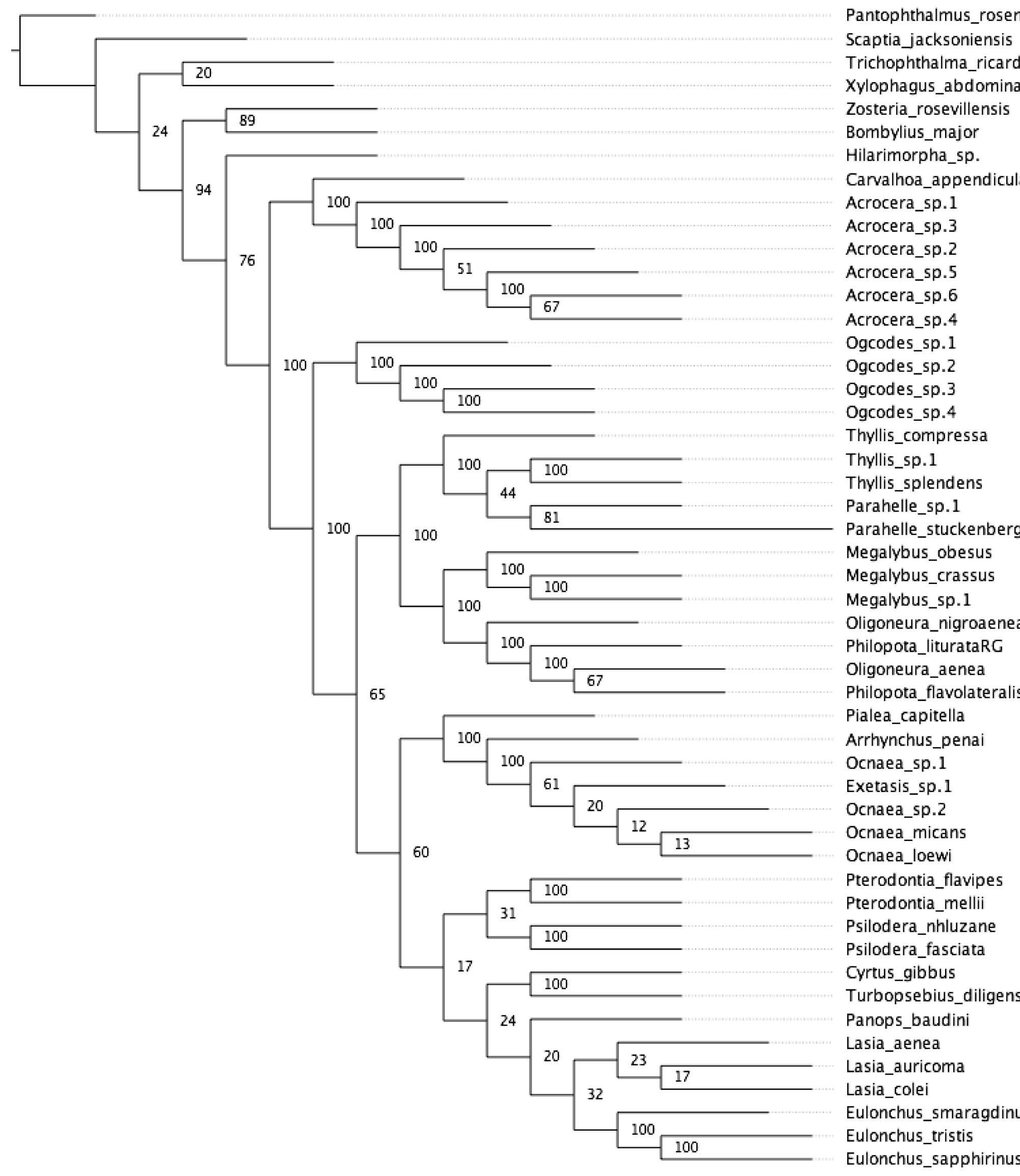
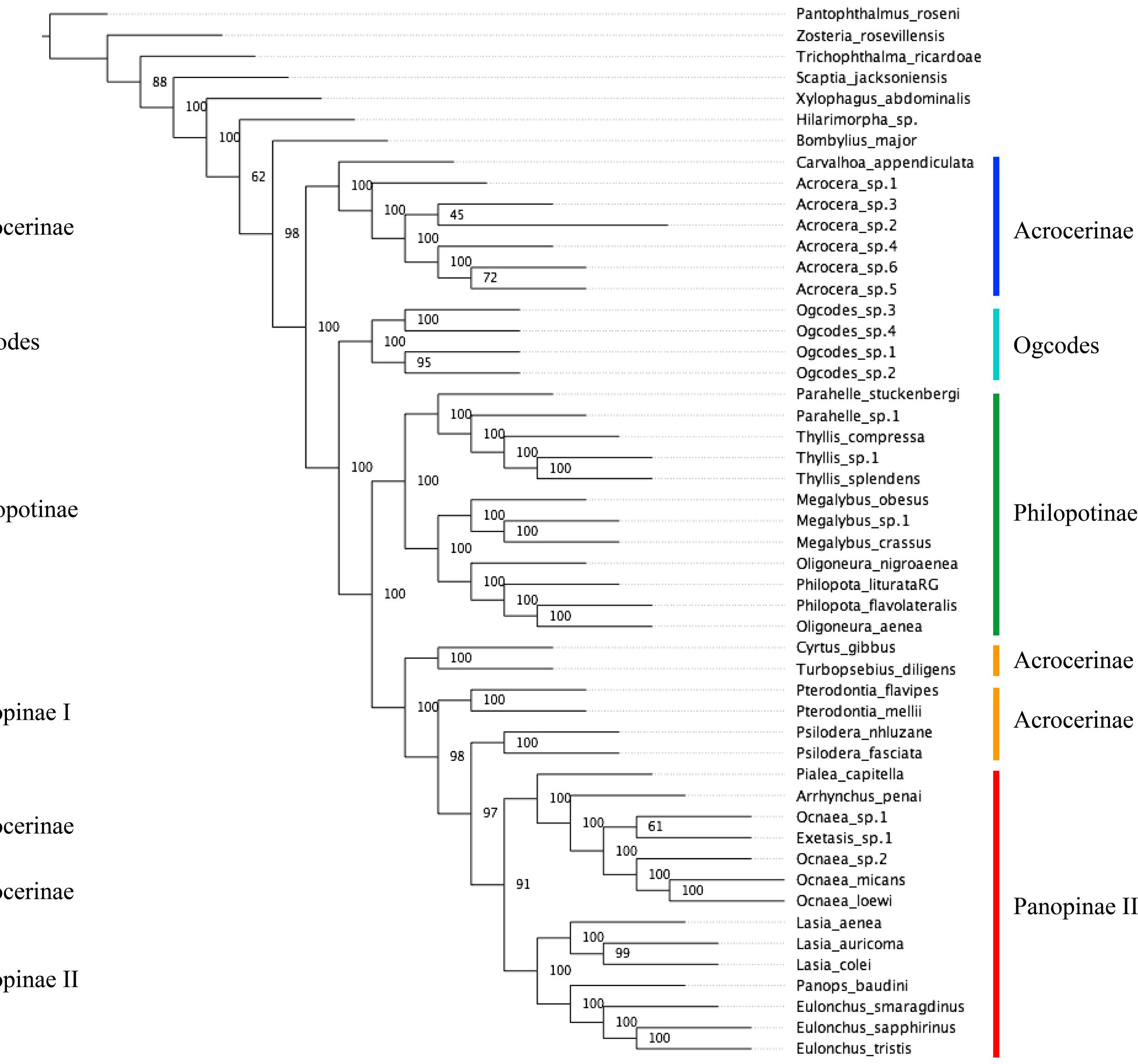


Supplementary Figure 1. Multi-species coalescent topologies in ASTRAL.



0.6

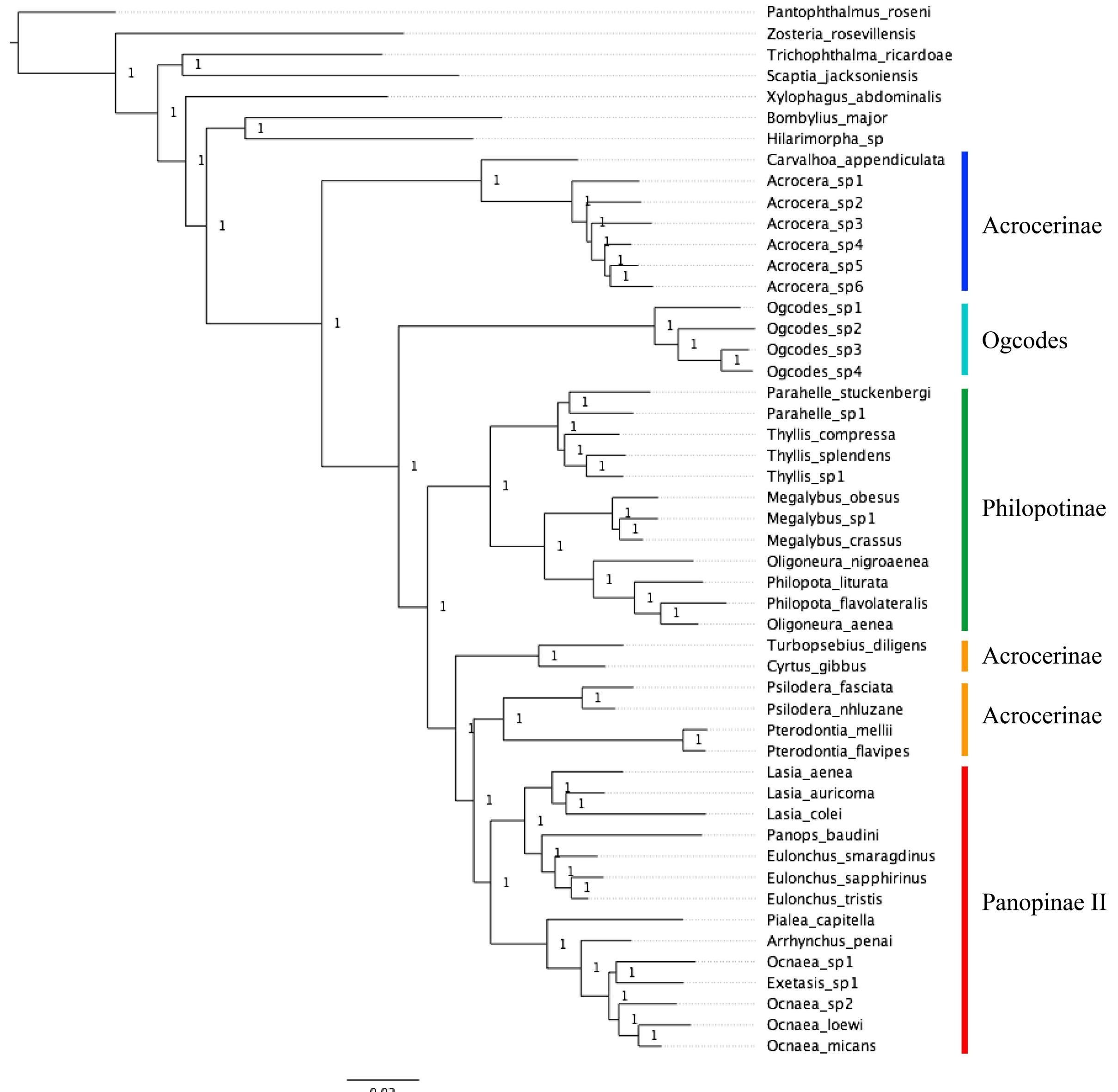
Amino acids



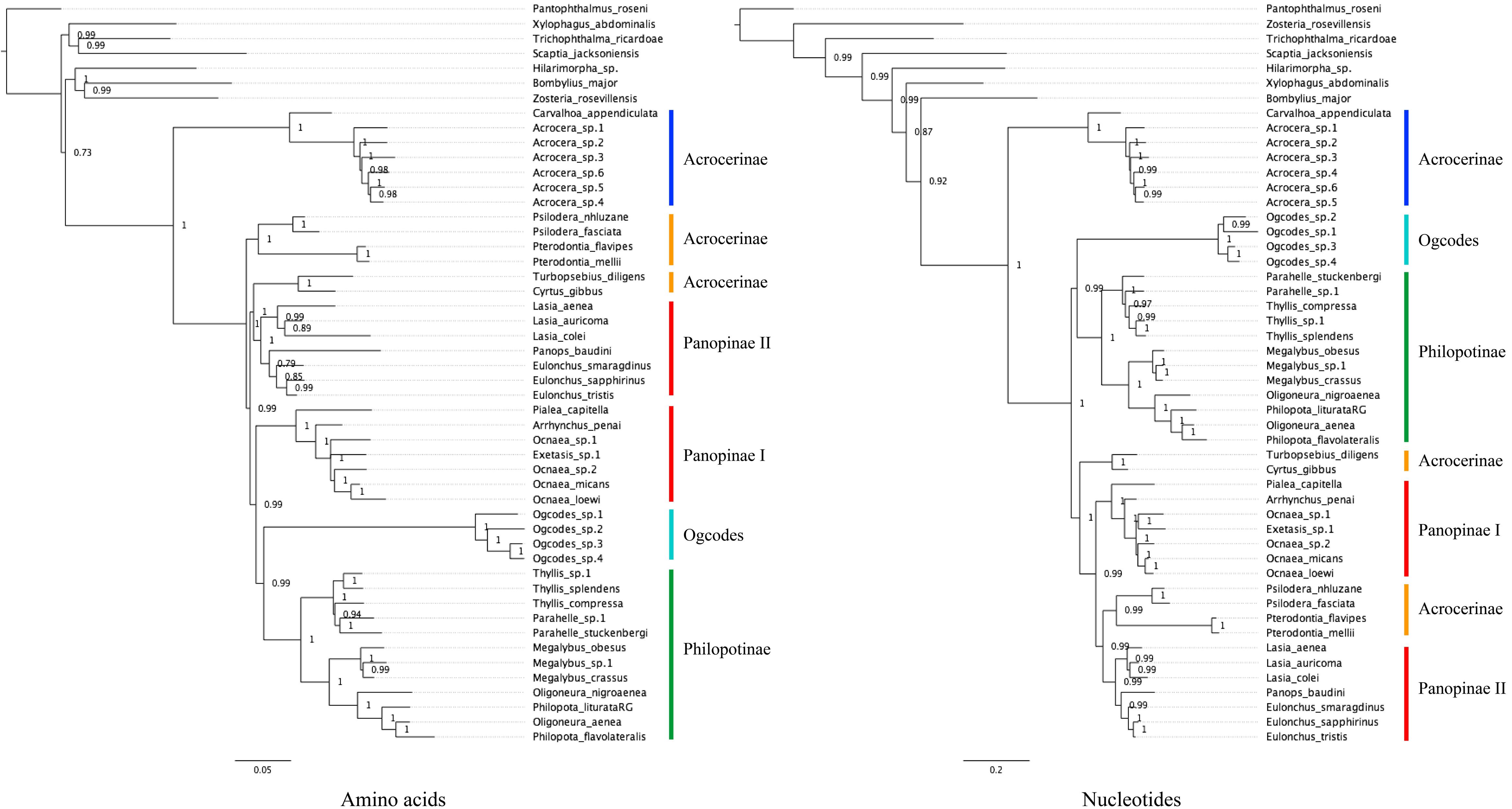
0.7

Nucleotides

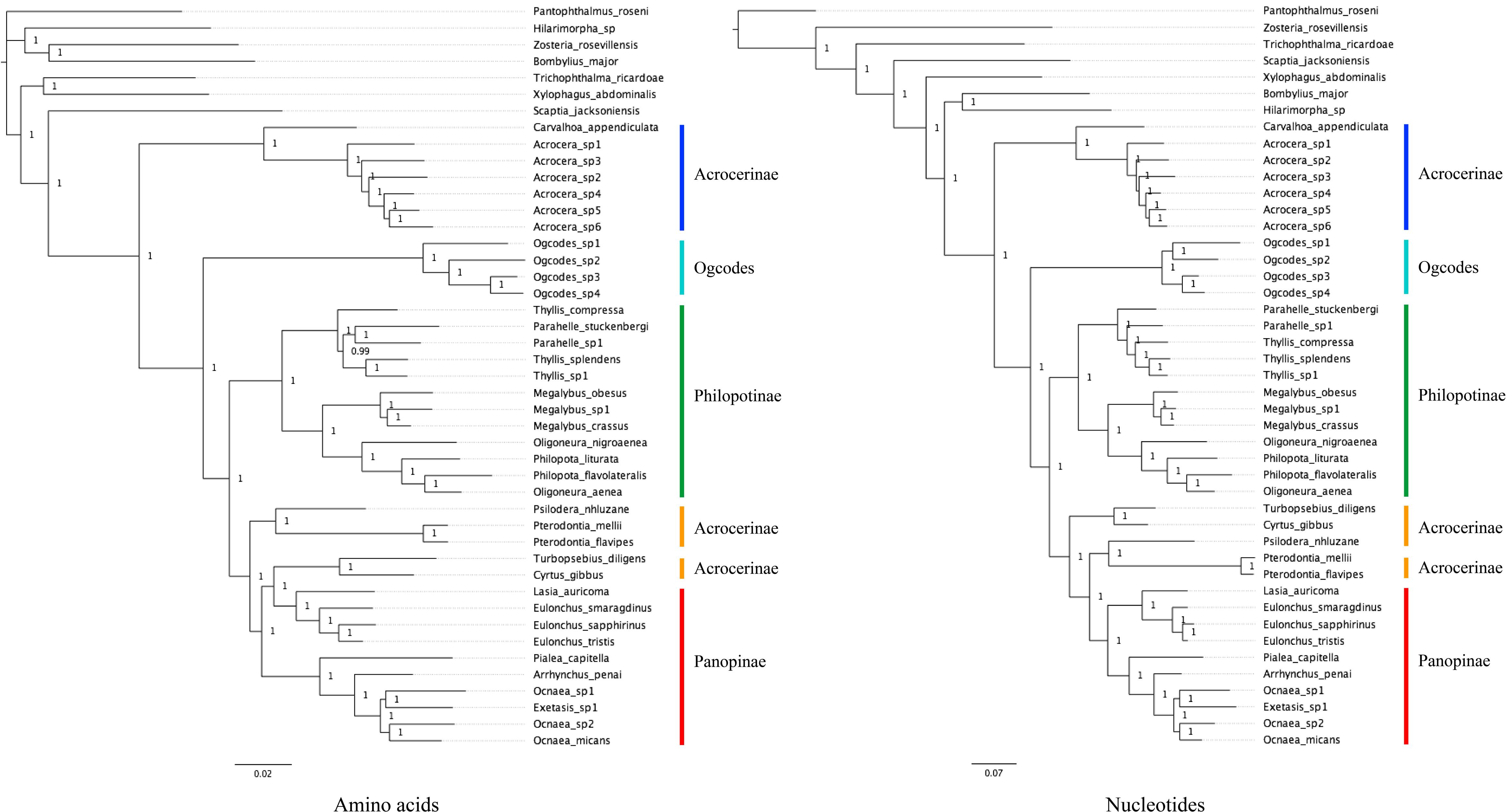
Supplementary Figure 2. Topology based on nucleotides excluding third codon positions.



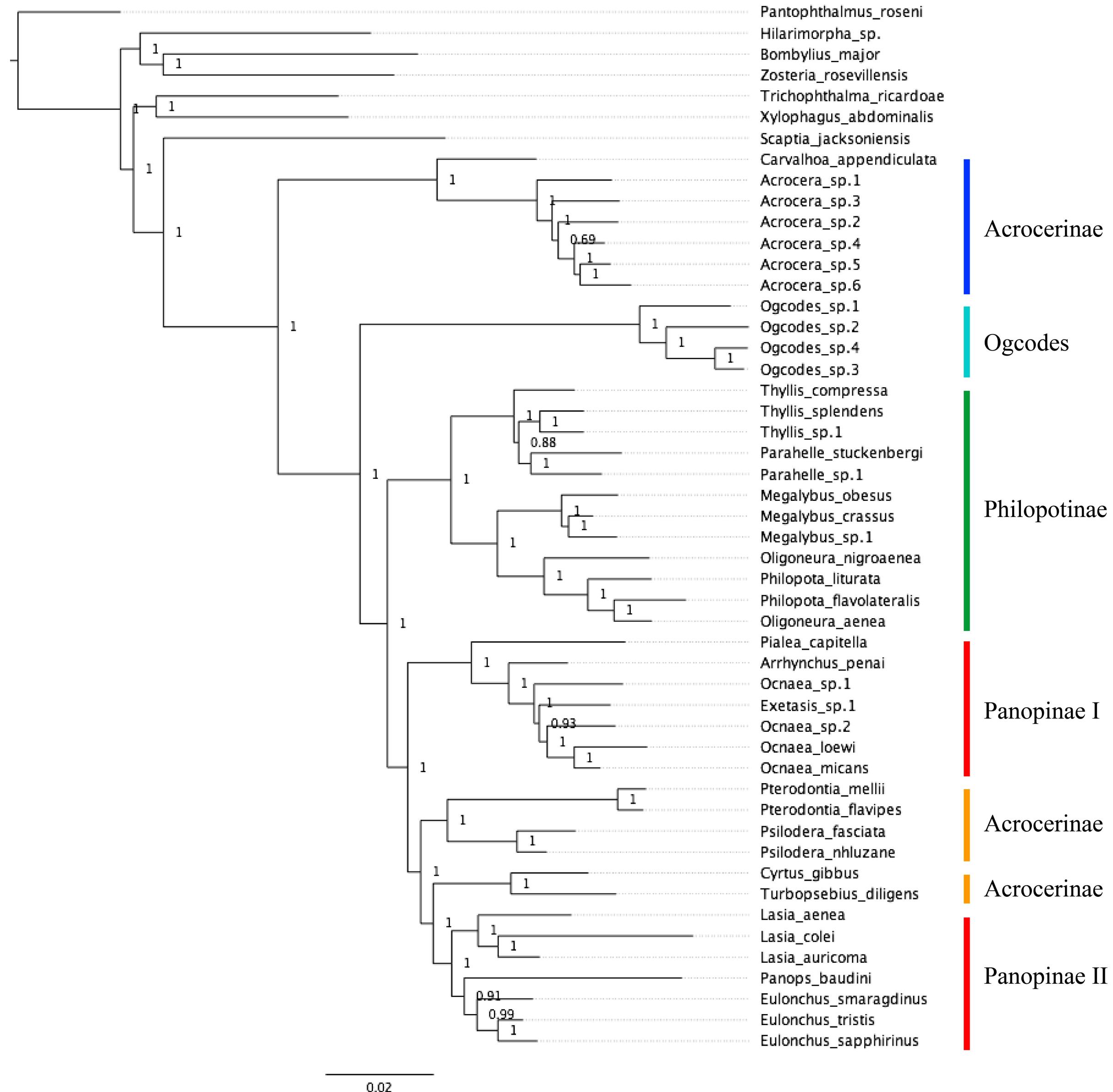
Supplementary Figure 3. Topologies under the CAT-GTR-G mixture model of base substitution in PhyloBayes.



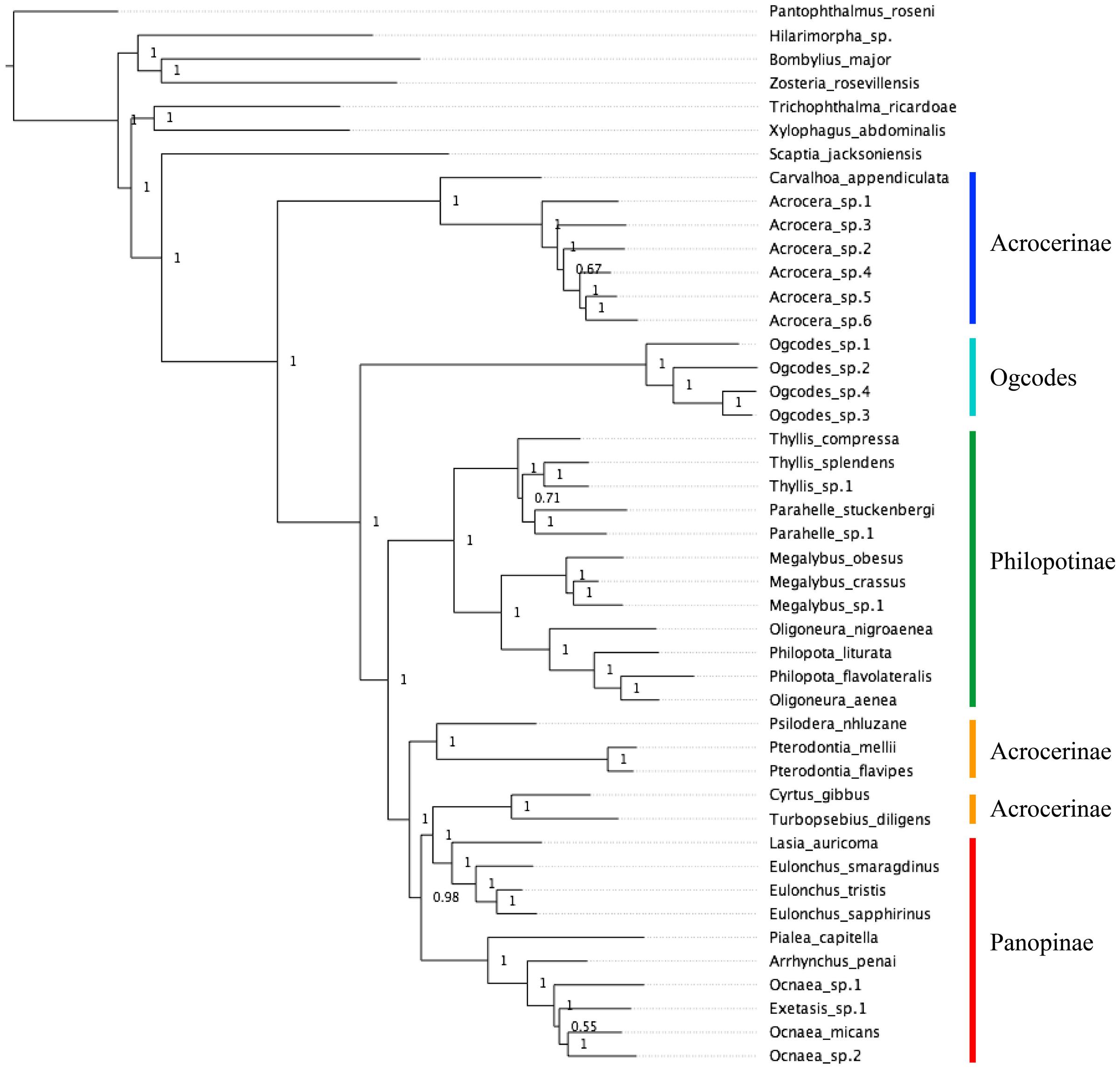
Supplementary Figure 4. Topologies resulting from the exclusion of five taxa with high levels of missing data.



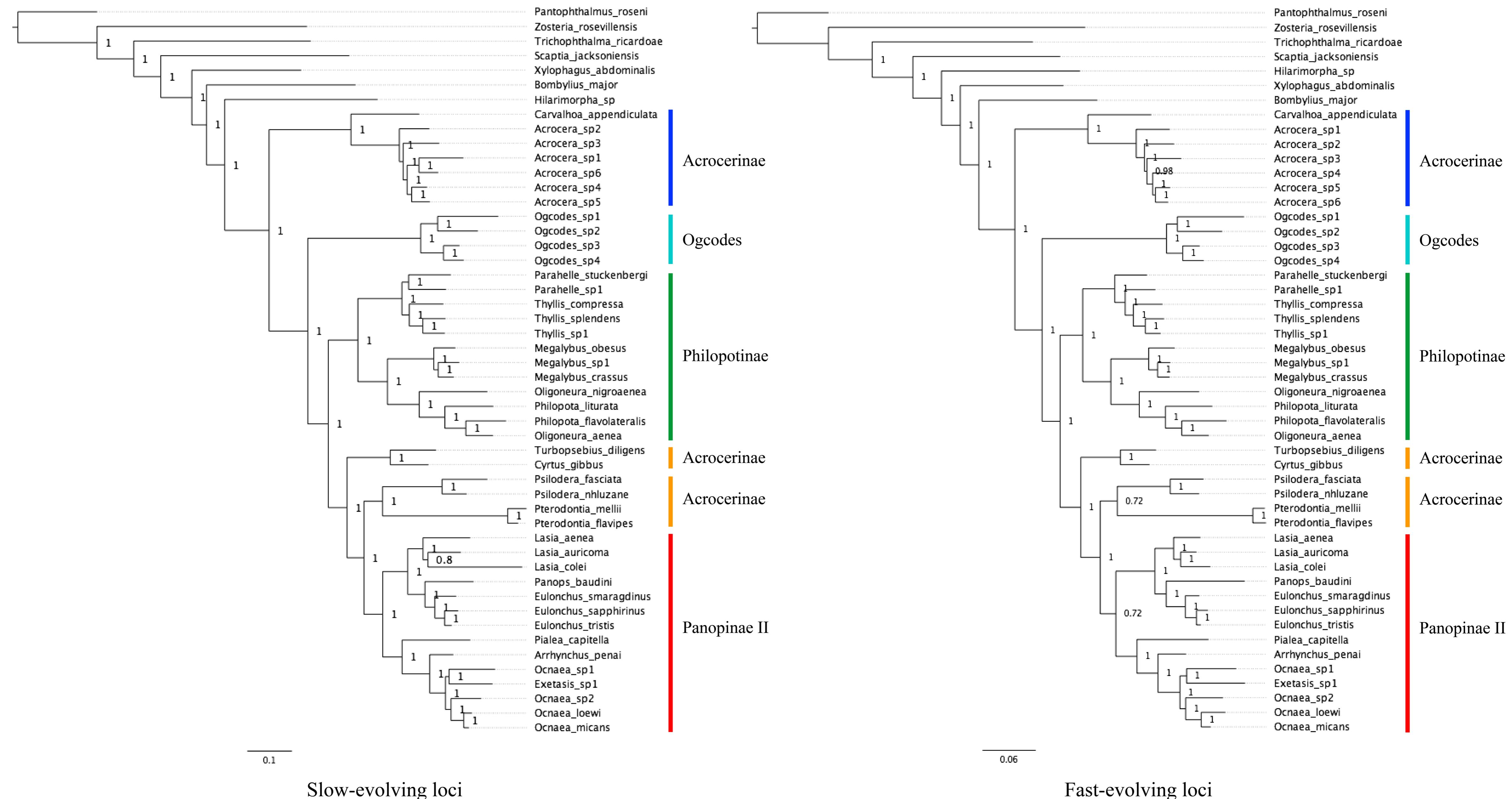
Supplementary Figure 5. Topology based on the degenerated nucleotide dataset using the *degen1* coding approach.



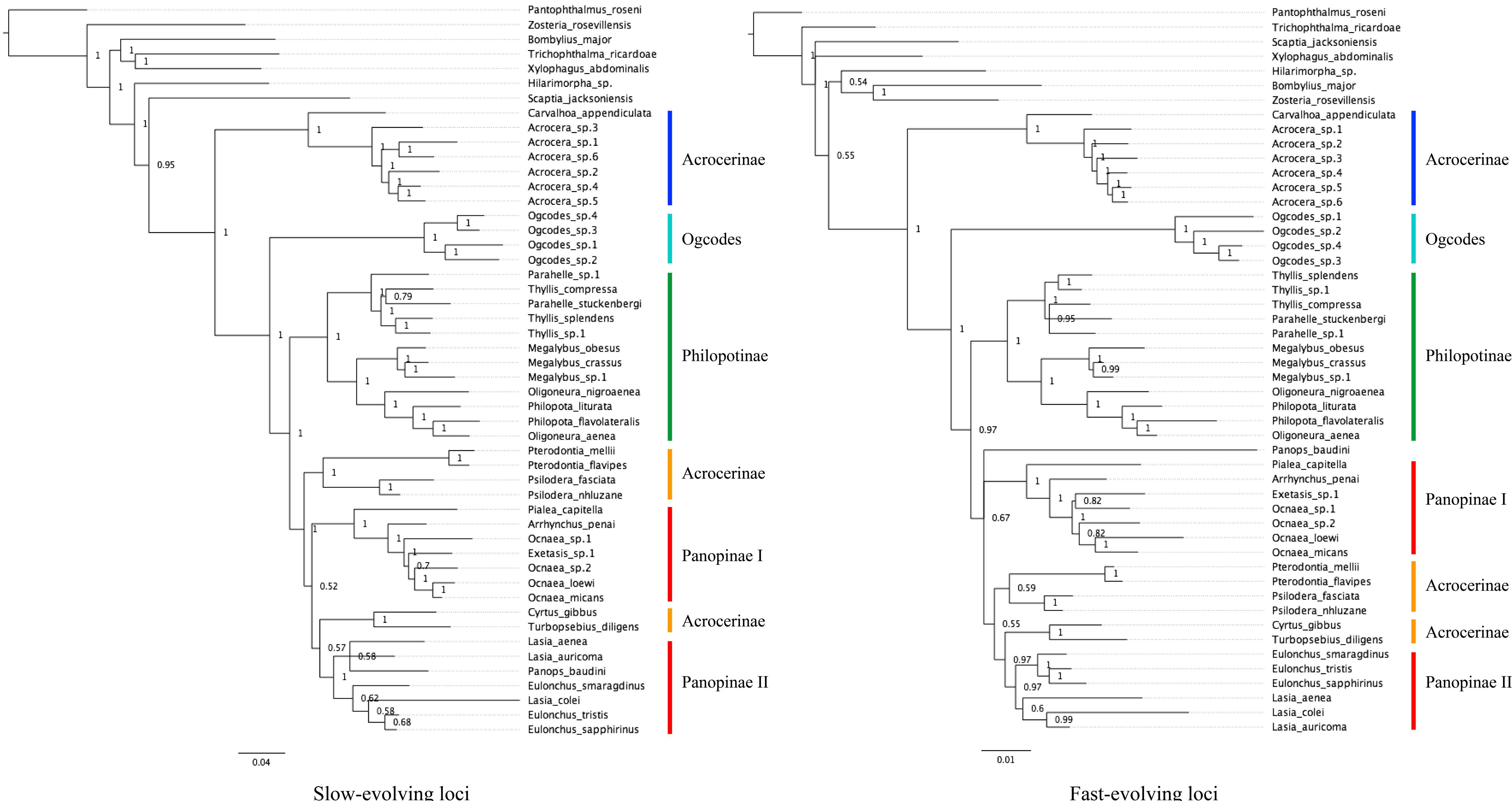
Supplementary Figure 6. Topology based on the degenerated nucleotide dataset using the *degen1* coding approach excluding five taxa with high levels of missing data.



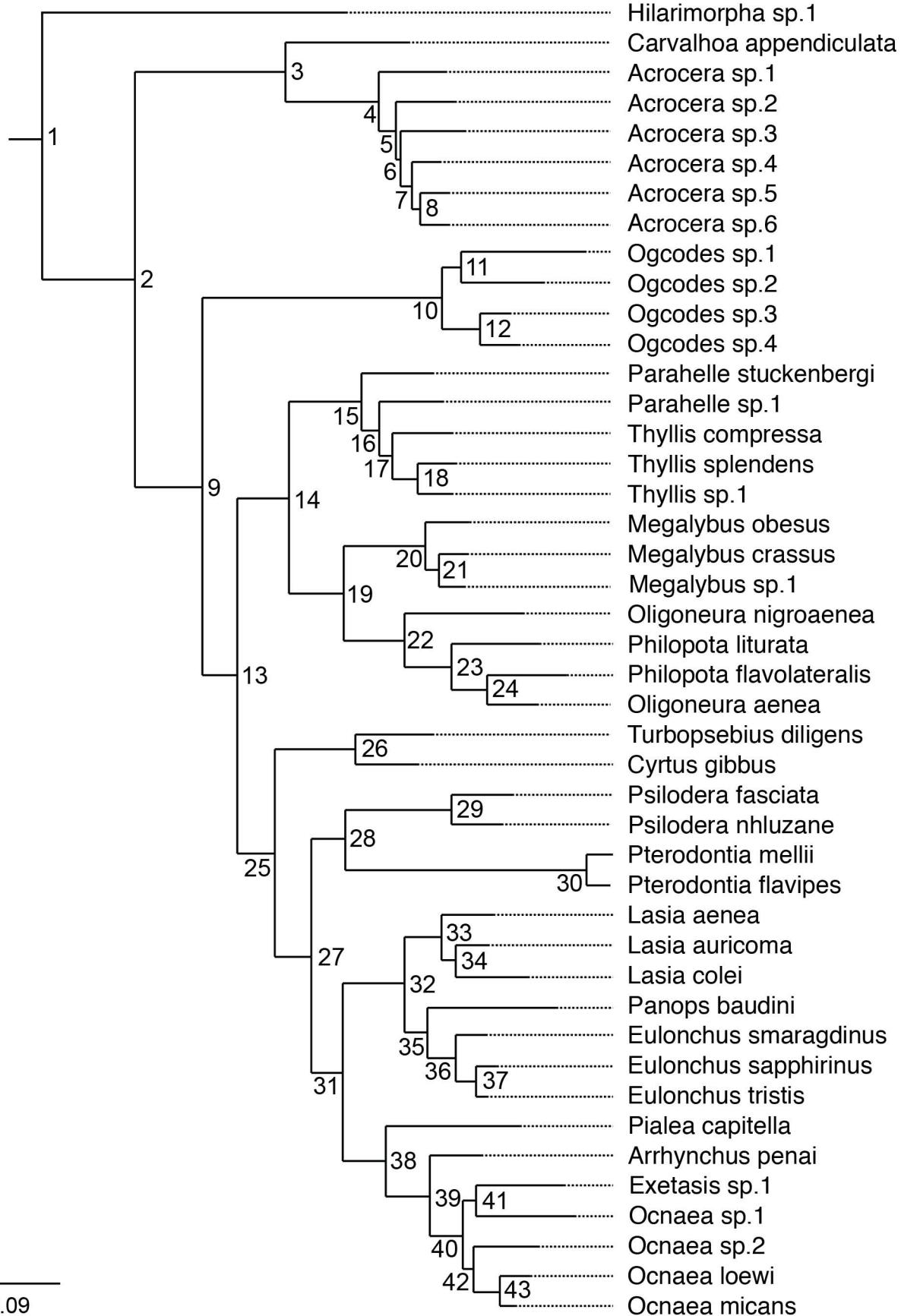
Supplementary Figure 7. Variation in tree topology attributable to mutation rate heterogeneity based on nucleotides. Topologies were generated based on the slowest third (left) and fastest third (right) of loci, which were ranked by average branch length on the original tree (as a proxy for mutation rate).



Supplementary Figure 8. Variation in tree topology attributable to mutation rate heterogeneity based on amino acids. Topologies were generated based on the slowest third (left) and fastest third (right) of loci, which were ranked by average branch length on the original tree (as a proxy for mutation rate).



Supplementary Figure 9. Chronogram based on nucleotides with numbered nodes.



Supplementary Figure 10. Proportion of variable sites in the original and degenerated nucleotide datasets for the whole alignment, and first, second and third codon positions only.

