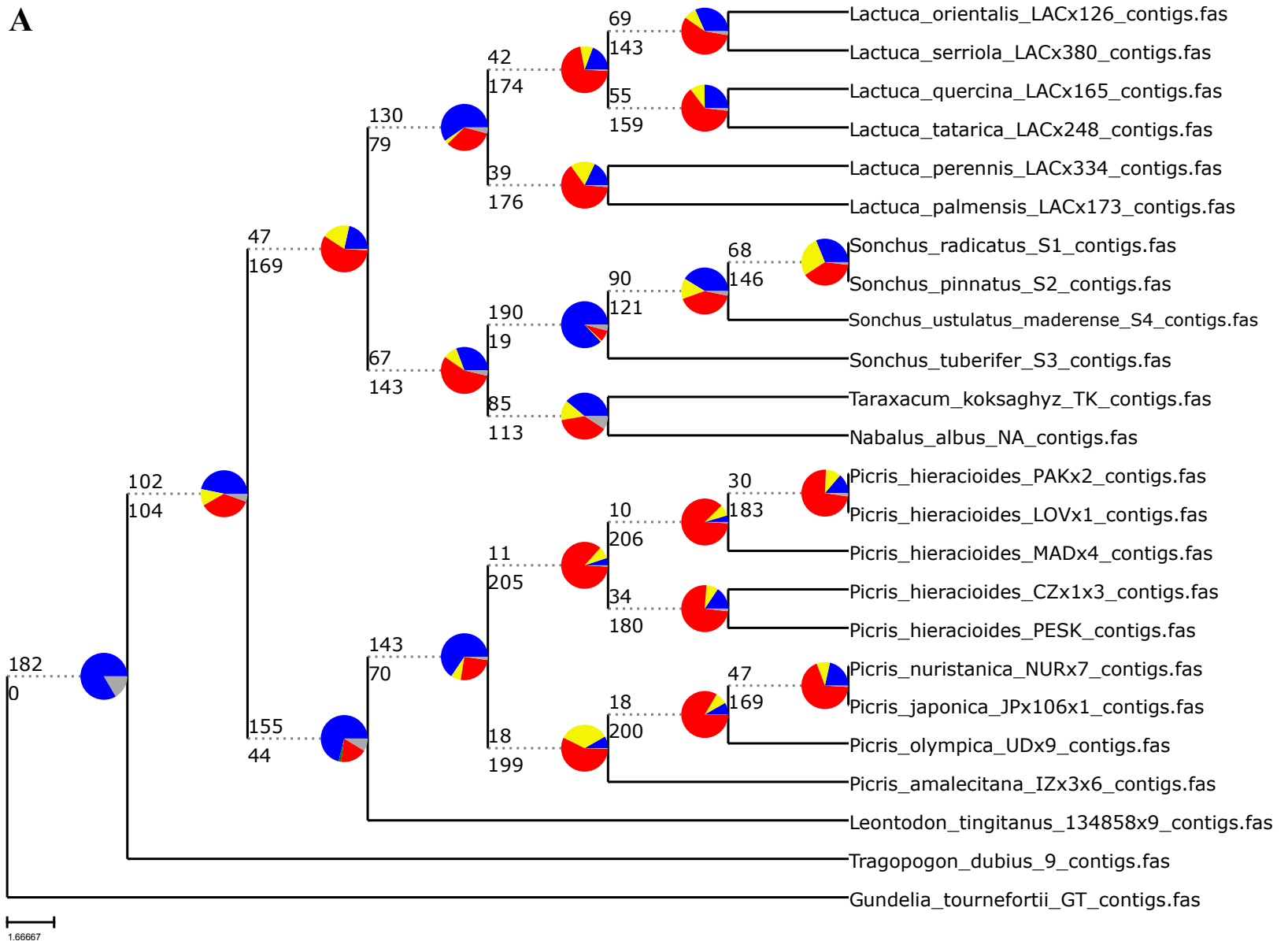


Appendix S15. Summaries of conflicting and concordant gene trees from phyparts with the tribe-exon-complete ASTRAL species trees and supercontig maximum likelihood (ML) and ASTRAL trees. (A) phyparts analyses of the RAxML-NG species tree from the tribe-exon-complete data set. (B) phyparts analyses of the ASTRAL species tree from the tribe-exon-complete data set. (C) phyparts analyses of the RAxML-NG species tree from the tribe-exon-shrunken data set (201 gene trees with outgroup). (D) phyparts analyses of the RAxML-NG species tree from the tribe-exon-shrunken data set (139 gene trees with outgroup). For each branch, the top number indicates the number of gene trees concordant with the ML tree at that node and the bottom number indicates the number of gene trees in conflict with that node. The pie charts present the proportion of gene trees that support that clade (blue), the proportion that support the main alternative topology for that clade (yellow), the proportion that support the remaining alternatives topologies (red), and the proportion that inform (conflict or support) that clade that have <50% bootstrap support (gray). The scale bars in each tree correspond to expected number of nucleotide substitutions per site.



B

