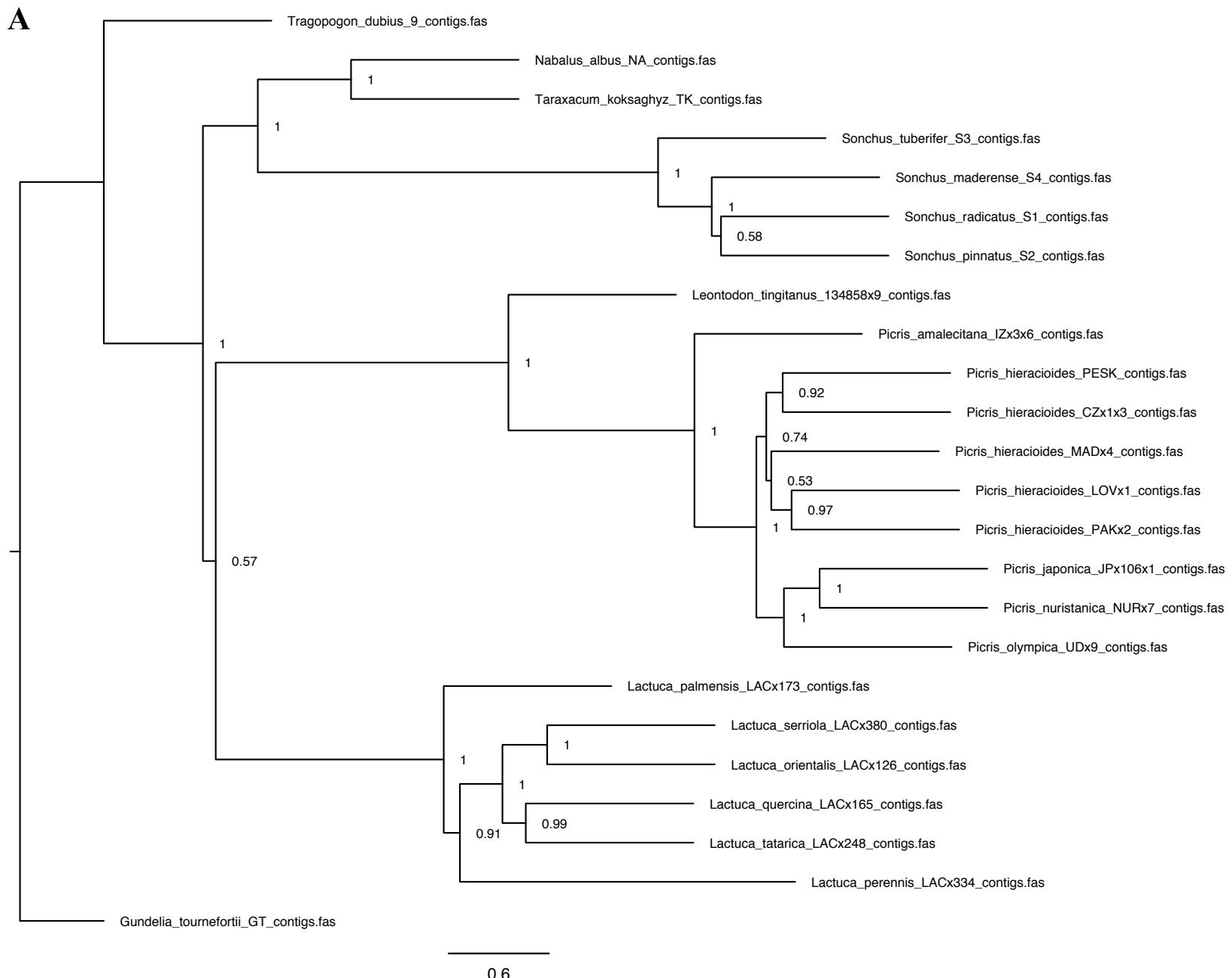


Appendix S13. ASTRAL species tree and RAxML-NG tree with partitioning based on the Tribe-exon-shrunken data set and ASTRAL species tree of the tribe-supercontig-complete data set. (A) ASTRAL tree of the tribe-exon-shrunken data set and RAxML analyses (with partitioning and substitution models) of the tribe-exon-shrunken data set. (B) ASTRAL tree of the tribe-supercontig data set. Scale bars indicate the expected number of nucleotide substitutions per site. In the ASTRAL trees, the numbers on nodes indicate posterior probability values and on the ML trees the numbers indicate percentage bootstrap support.



B