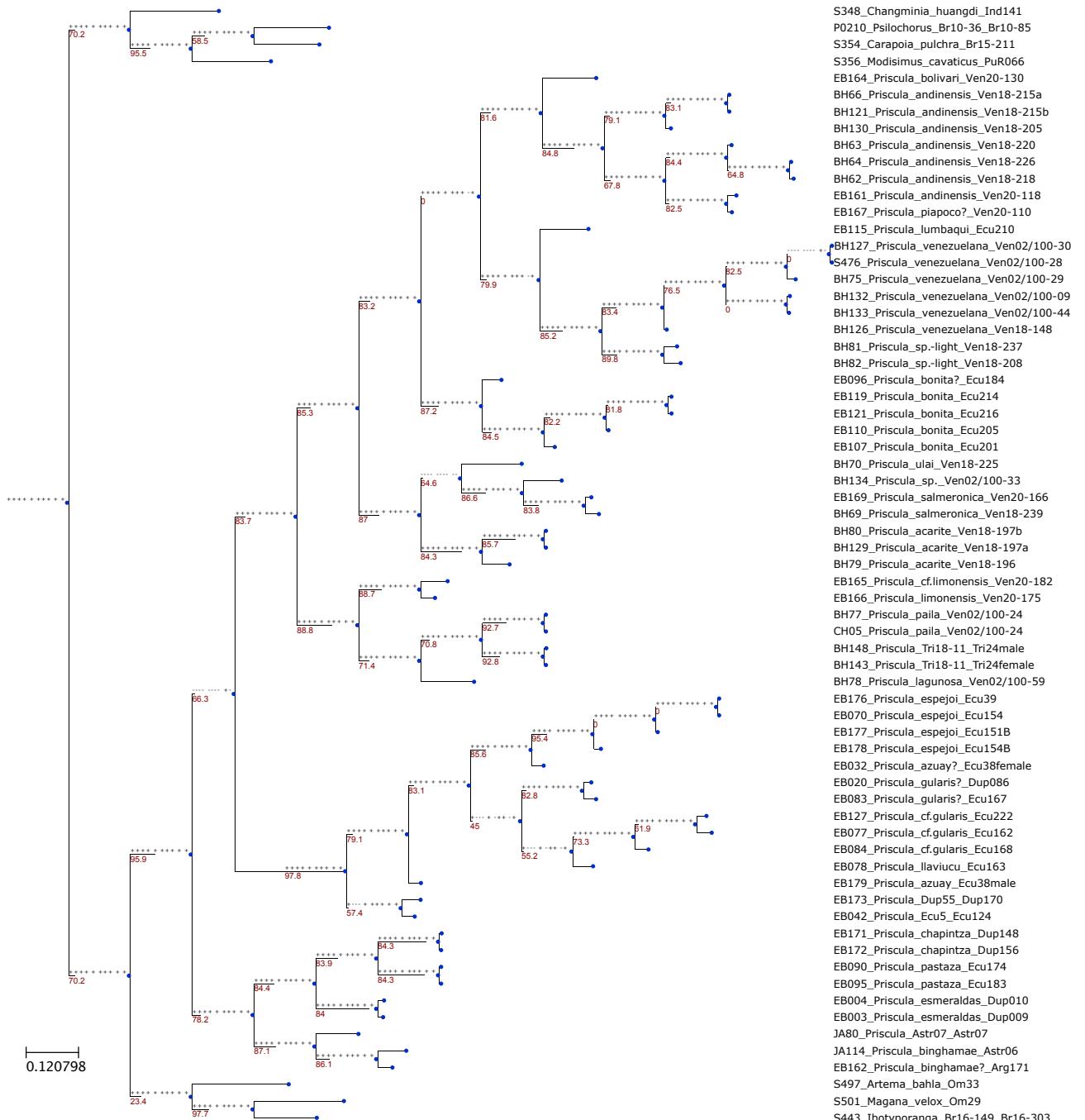**Figure S3.** Summary tree of all trees constructed from partitioned analyses. All trees were constructed from the same gene set but with different multiple-sequence-alignment (MSA) trimming strategies or from the untrimmed MSA using IQ-TREE. The Gblocks tree was used as the reference tree. The trees (query trees) from other MSA-trimming strategies were compared to the reference tree, with '+' or '-' indicating that the query trees agree or disagree, respectively with the branching events of the reference tree. Numbers on the branches are SH-aLRT support (%). For the partitioned analyses, the initial partition was locus-wise, but subsequently the best partitioning scheme was determined by allowing the merge of different loci (-m MFP+MERGE); at the same time, the best-fit model of each partition was also determined. The best partitioning scheme and the best-fit model of each partition of the reference tree: (1) CO1 partition: TIM3+F+I+G4; (2) H3+18S+28S partition: TN +F+G4; (3) 12S+16S partition: GTR+F+G4. https://doi.org/10.5852/ejt.2023.909.2351.10267