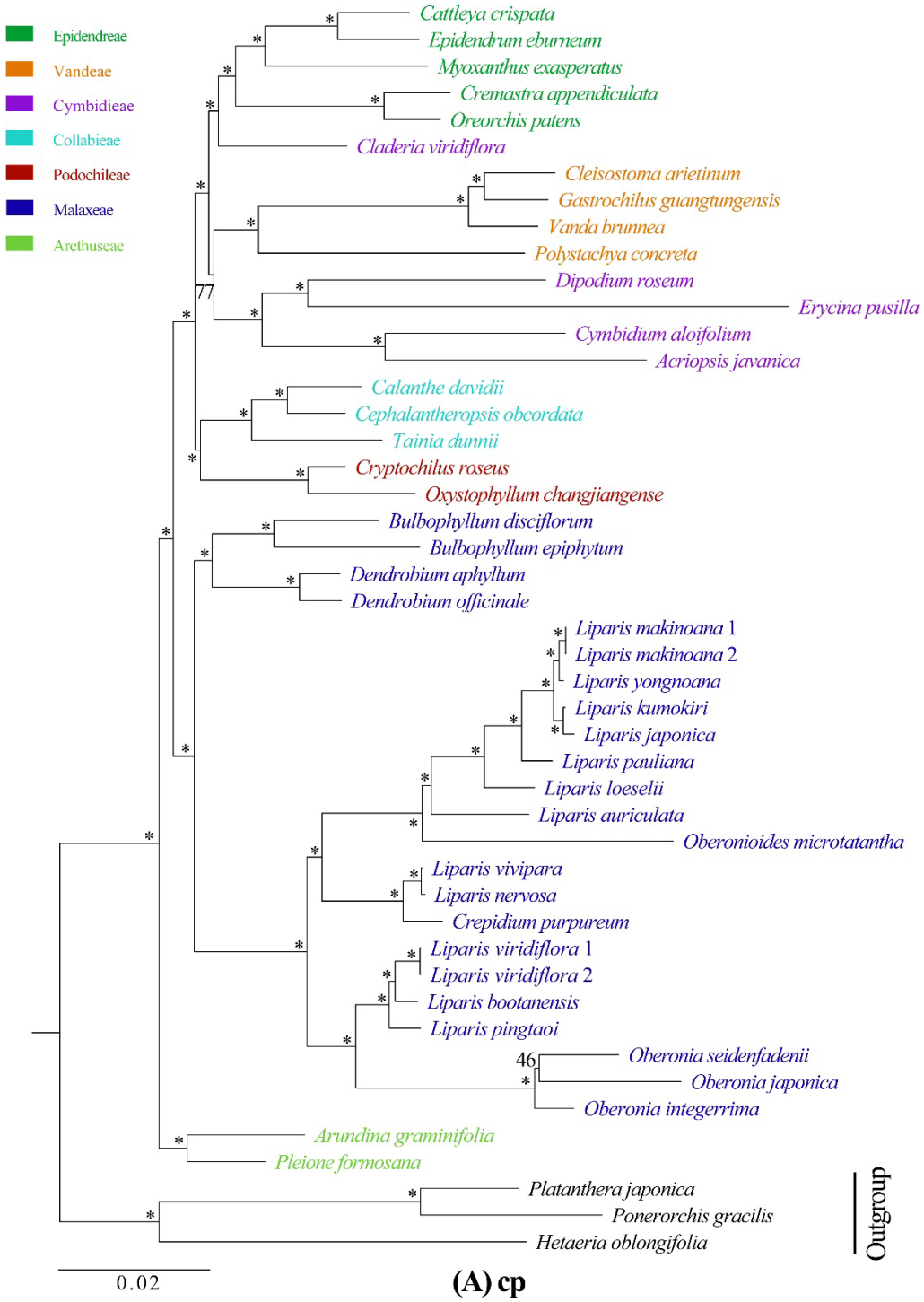
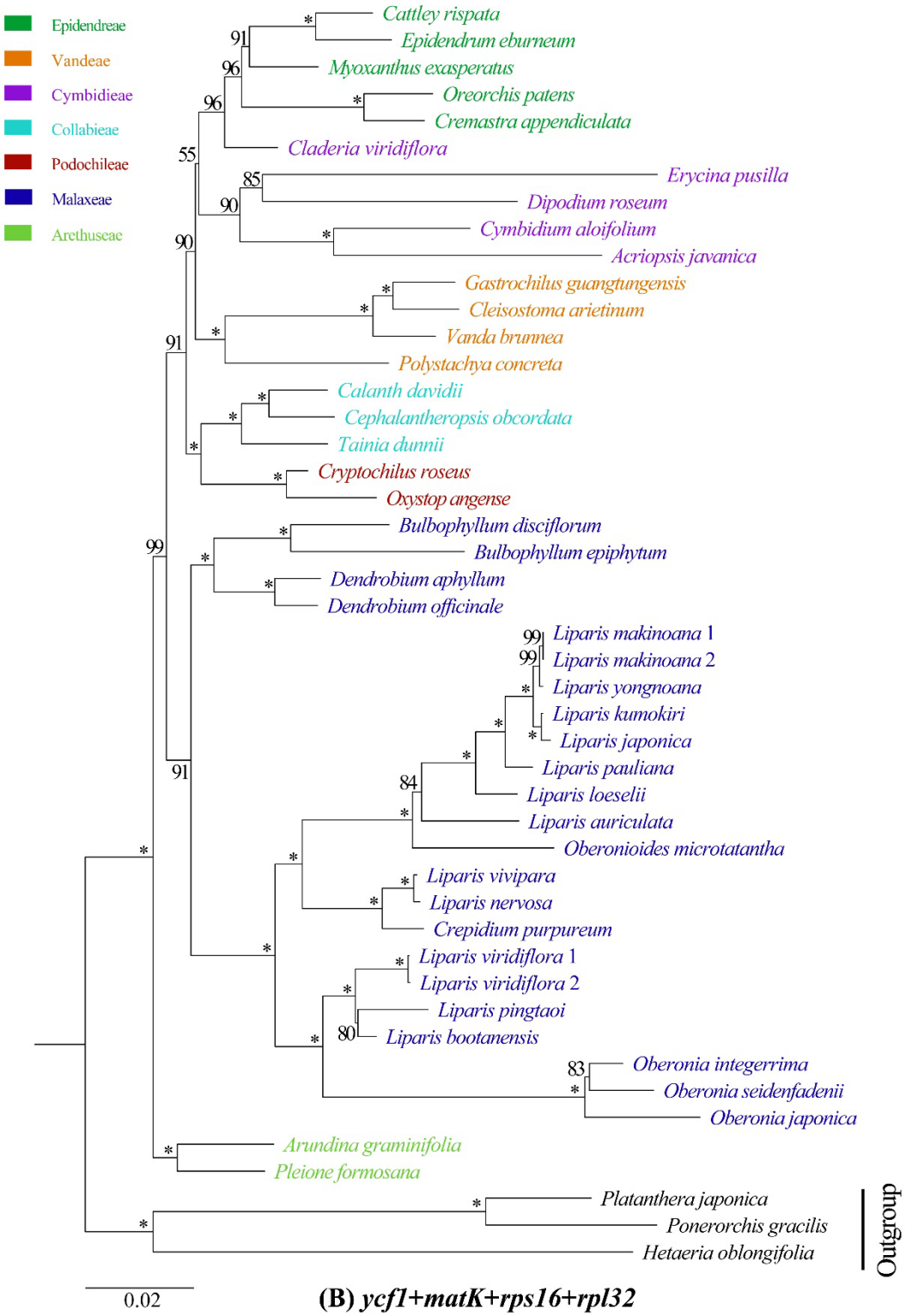
Supplementary Figure





(B) *ycf1+matK+rps16+rpl32*

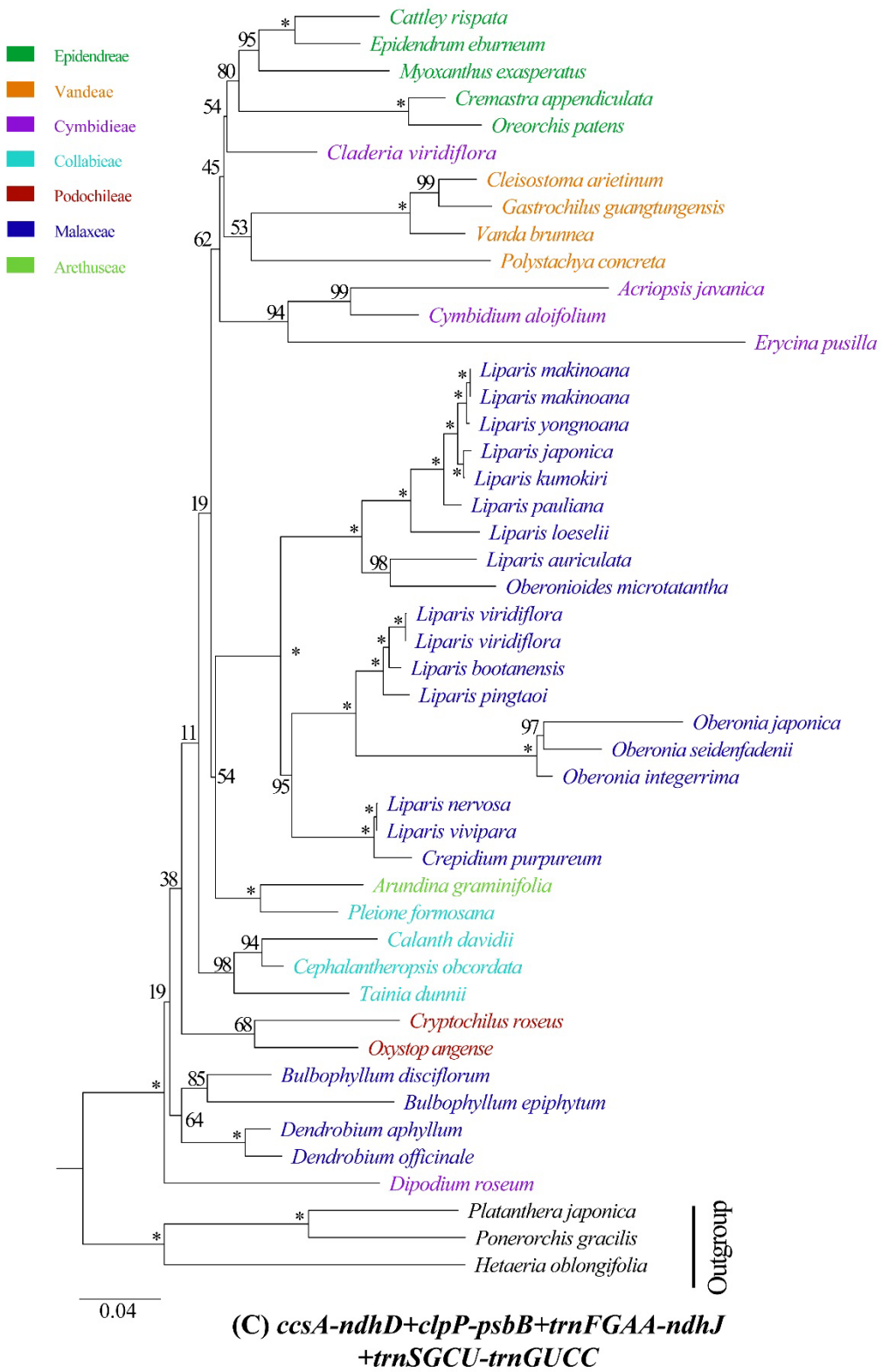


Figure S1. Phylogenetic tree of Epidendroideae obtained viamaximum likelihood (ML) analysis based on the whole plastome (A), the top-four protein-coding genes hotspots (*ycf1*, *matK*, *rps16*, and *rpl32*) (B) and the top-four intergenic regions hotspots (*ccsA-ndhD*, *clpP-psbB*, *trnF*^{GAA}*-ndhJ*, and *trnS*^{GCU}*-trnG*^{UCC}) (C). Numbers near the nodes are bootstrap percentages for ML analysis. An asterisk (*) indicates the node has 100% bootstrap probability.