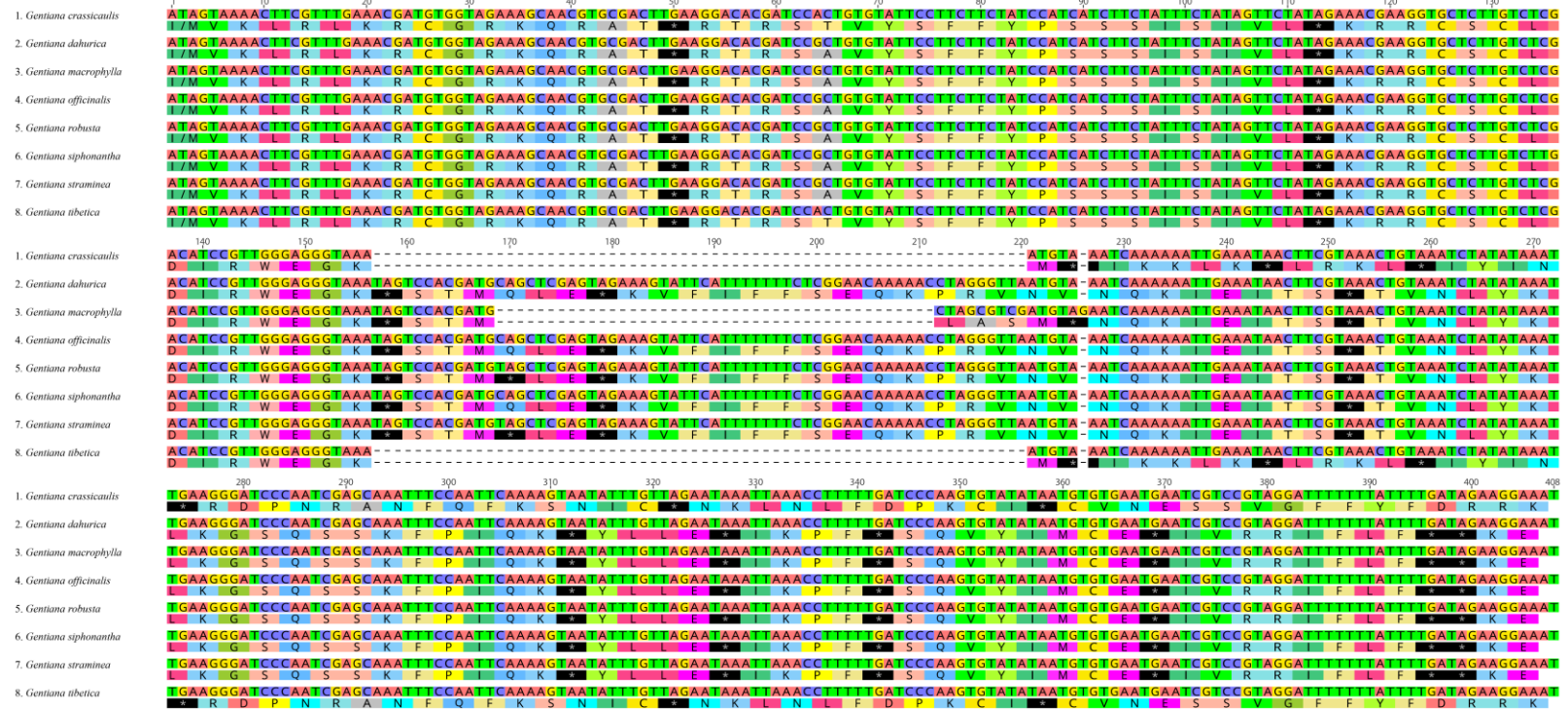**Figure S1.*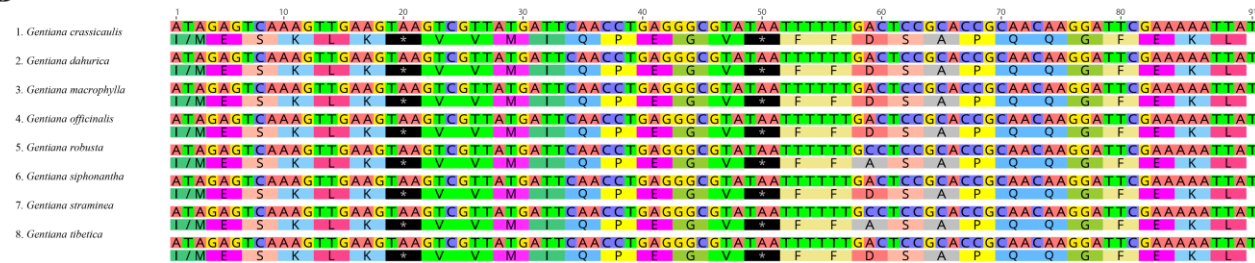* Alignment of two pseudogenes in the eight *Gentiana* species chloroplast genome. (**A**) *rps16*. (**B**) *infA*. The black box with an asterisk represents stop codons.
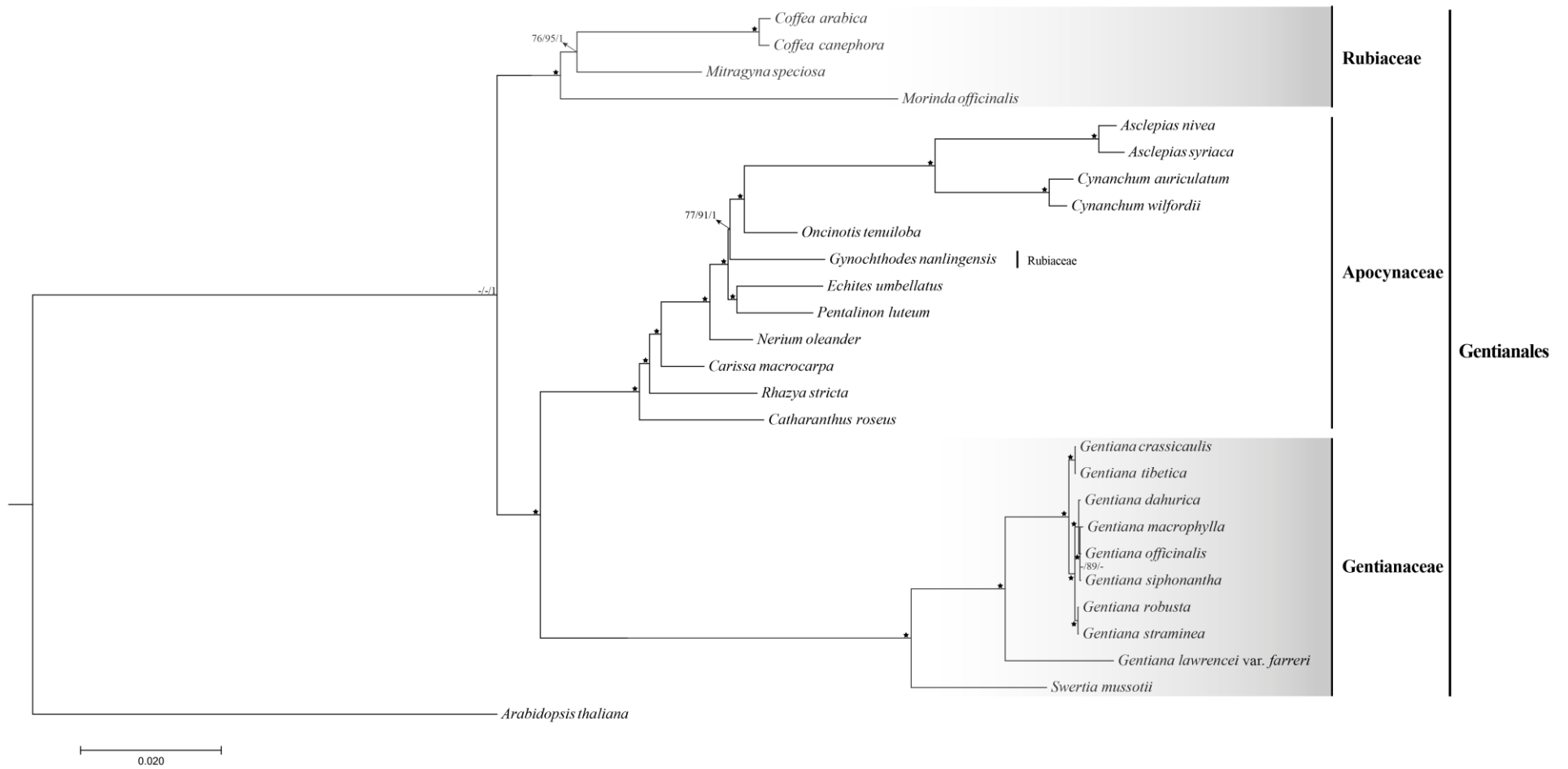
Figure S2. Phylogenetic relationships of species belong to *Gentiana* sect. *Cruciata* inferred from MP/ML/BI analysis based on 70 shared PCGs. The numbers associated with each node are bootstrap support and posterior probability values, and the symbol ★ in the phylogenetic tree indicated that the support value of branch is 100/100/1.0.

Figure S3. Phylogenetic relationships of species belong to *Gentiana* sect. *Cruciata* inferred from MP/ML/BI analysis based on TMCRs of chloroplast genomes. The numbers associated with each node are bootstrap support and posterior probability values, and the symbol ★ in the phylogenetic tree indicated that the sup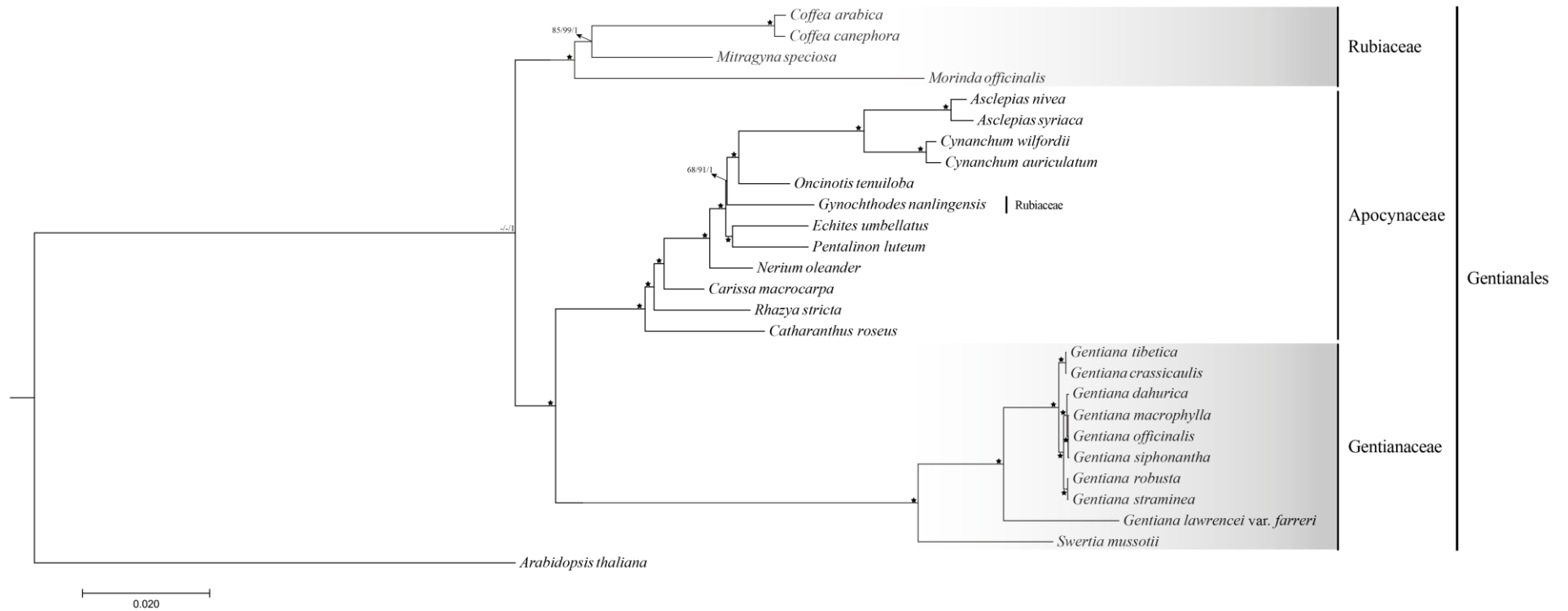port value of branch is 100/100/1.0.