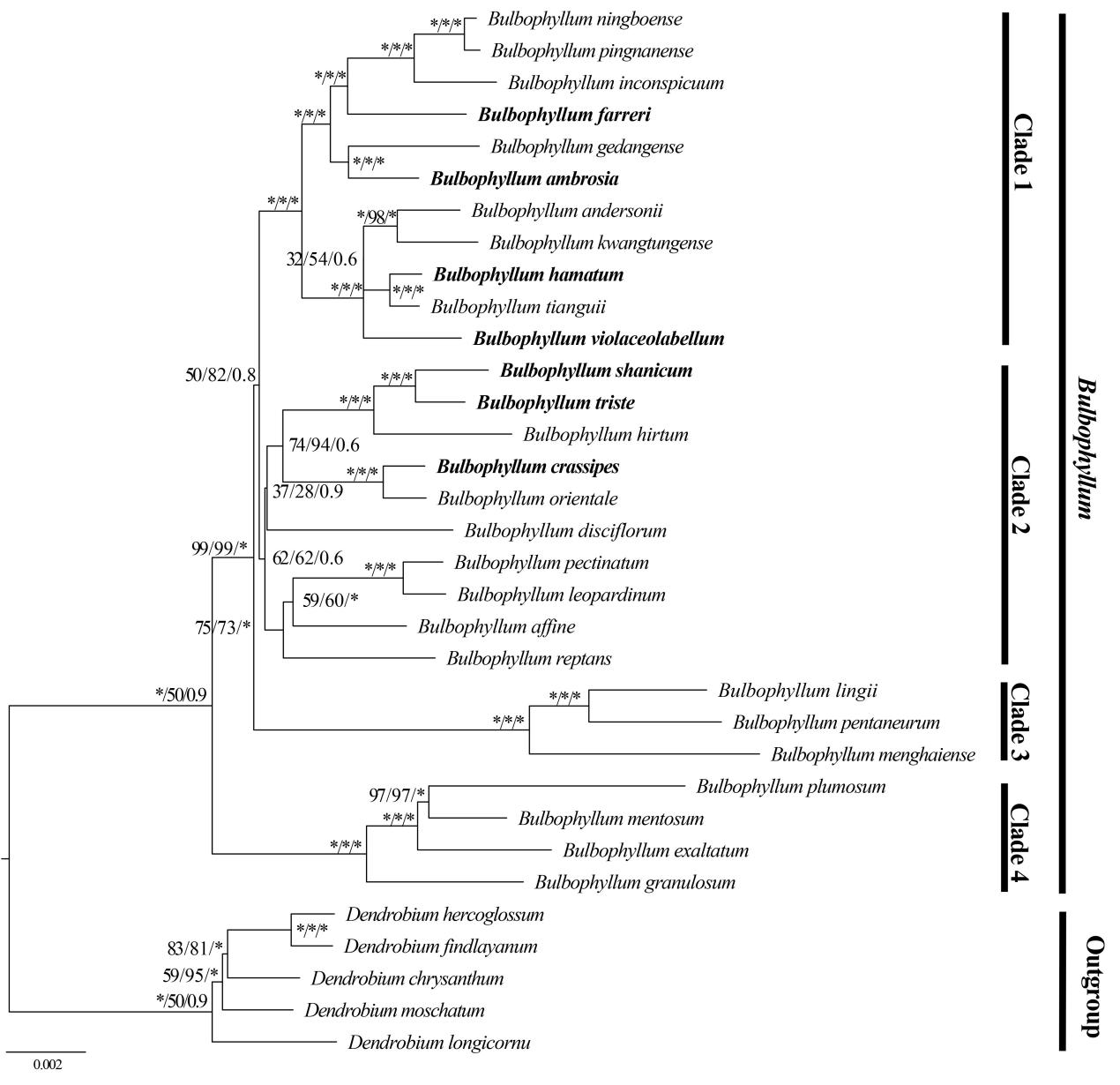
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**Supplementary** **Figure S1** The phylogenetic tree of 28 *Bulbophyllum* species and five outgroups obtained by maximum-likelihood analysis based on concatenated 68 protein-coding genes. The numbers near the nodes are bootstrap percentages and Bayesian posterior probabilities (BPML, BPMP, PP), \*node is 100 bootstrap percentage or 1.00 posterior probability.