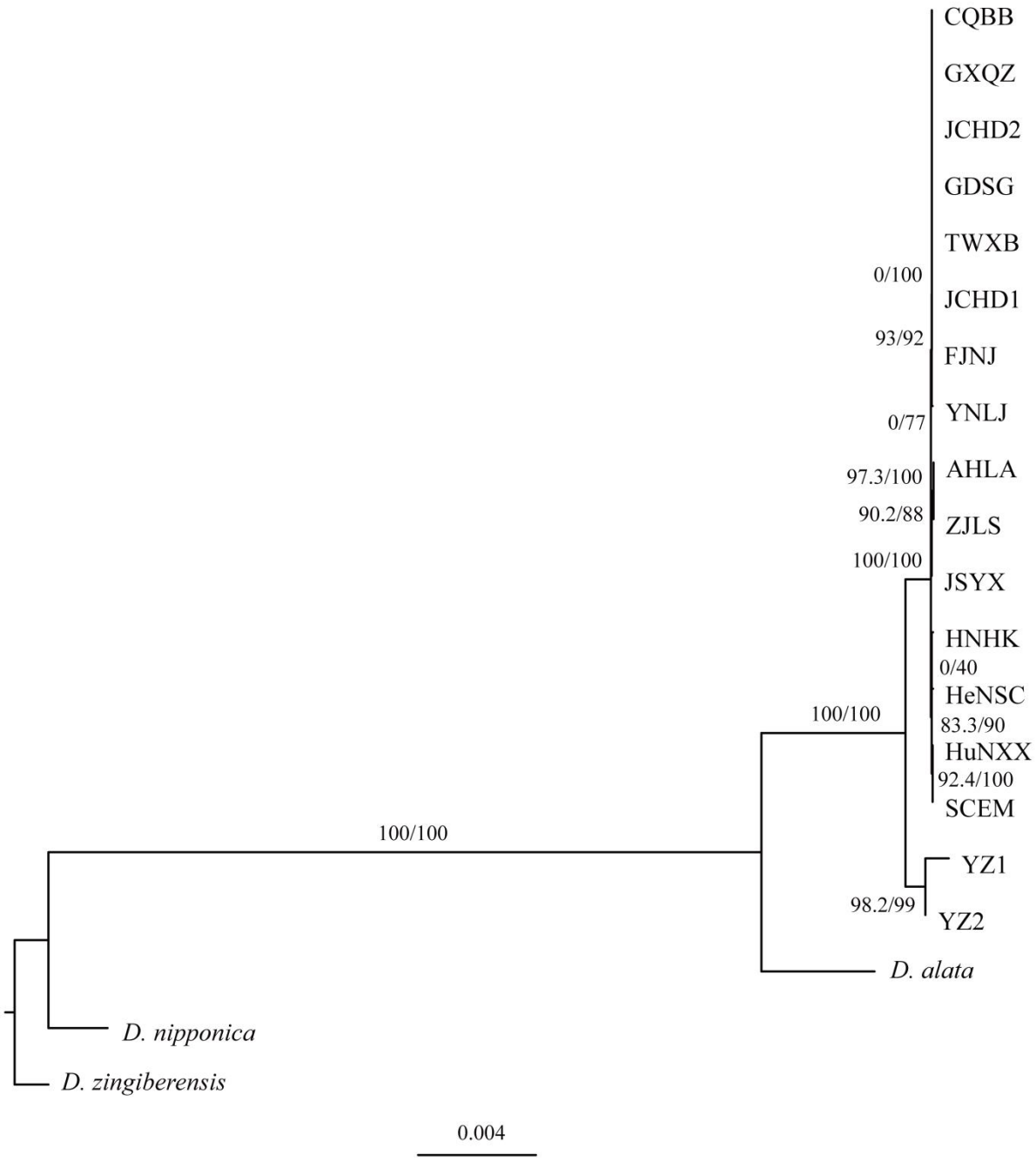
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Supplementary Fig. S2 Maximum likelihood phylogenetic tree based on 79 concatenated plastome coding sequence (CDS) genes. Branch values indicate ultrafast bootstrap SH-aLRT / UFBoot support. The tree was rooted with *D. zingiberensis*. The scale bar represents 0.004 nucleotide substitutions per site.