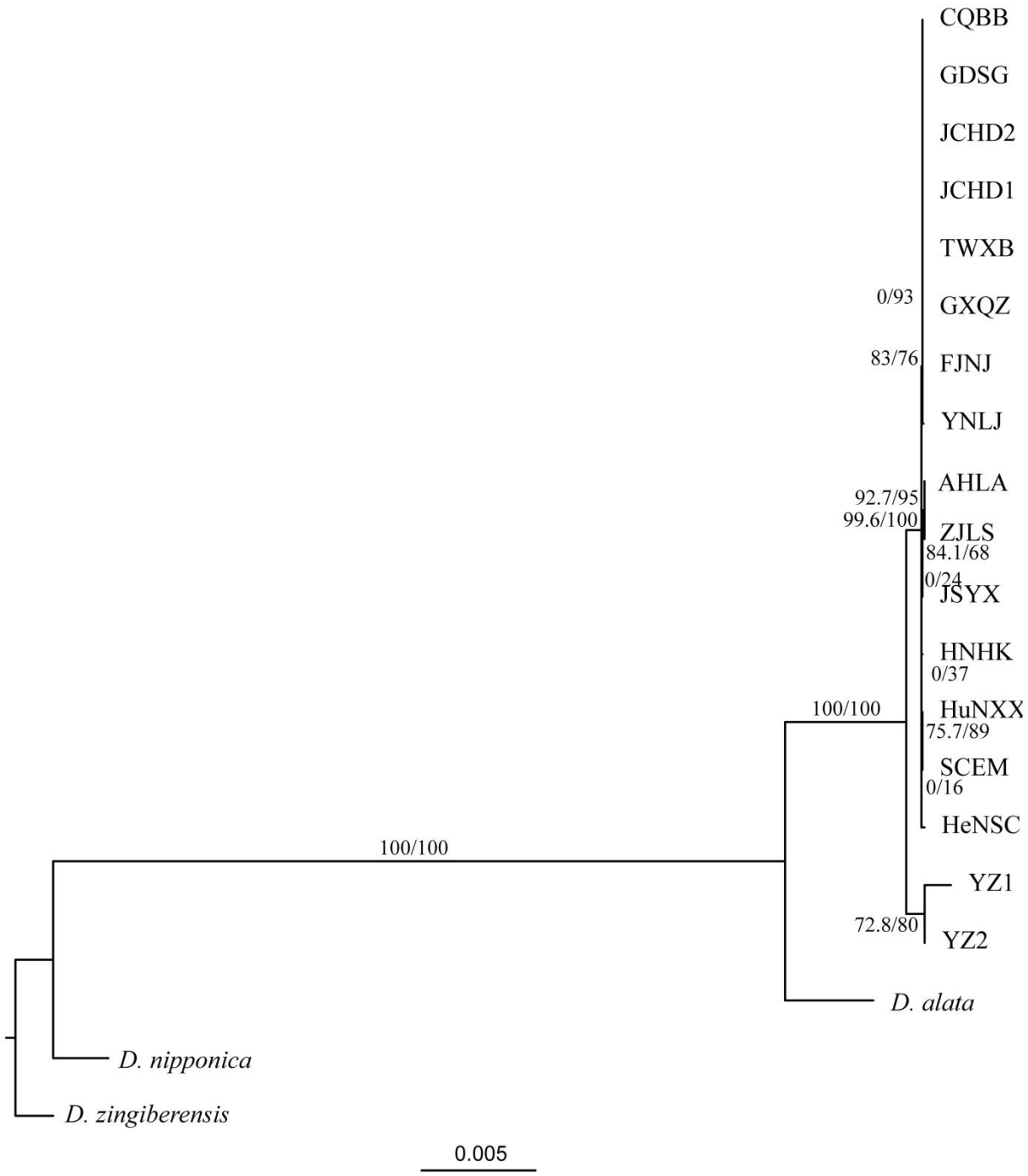


Supplementary Fig. S3 Maximum likelihood phylogenetic tree based on 79 concatenated plastome amino acid sequences. Branch values indicate ultrafast bootstrap SH-aLRT / UFBoot support. The tree was rooted with *D. zingiberensis*. The scale bar represents 0.005 amino acid substitutions per site.