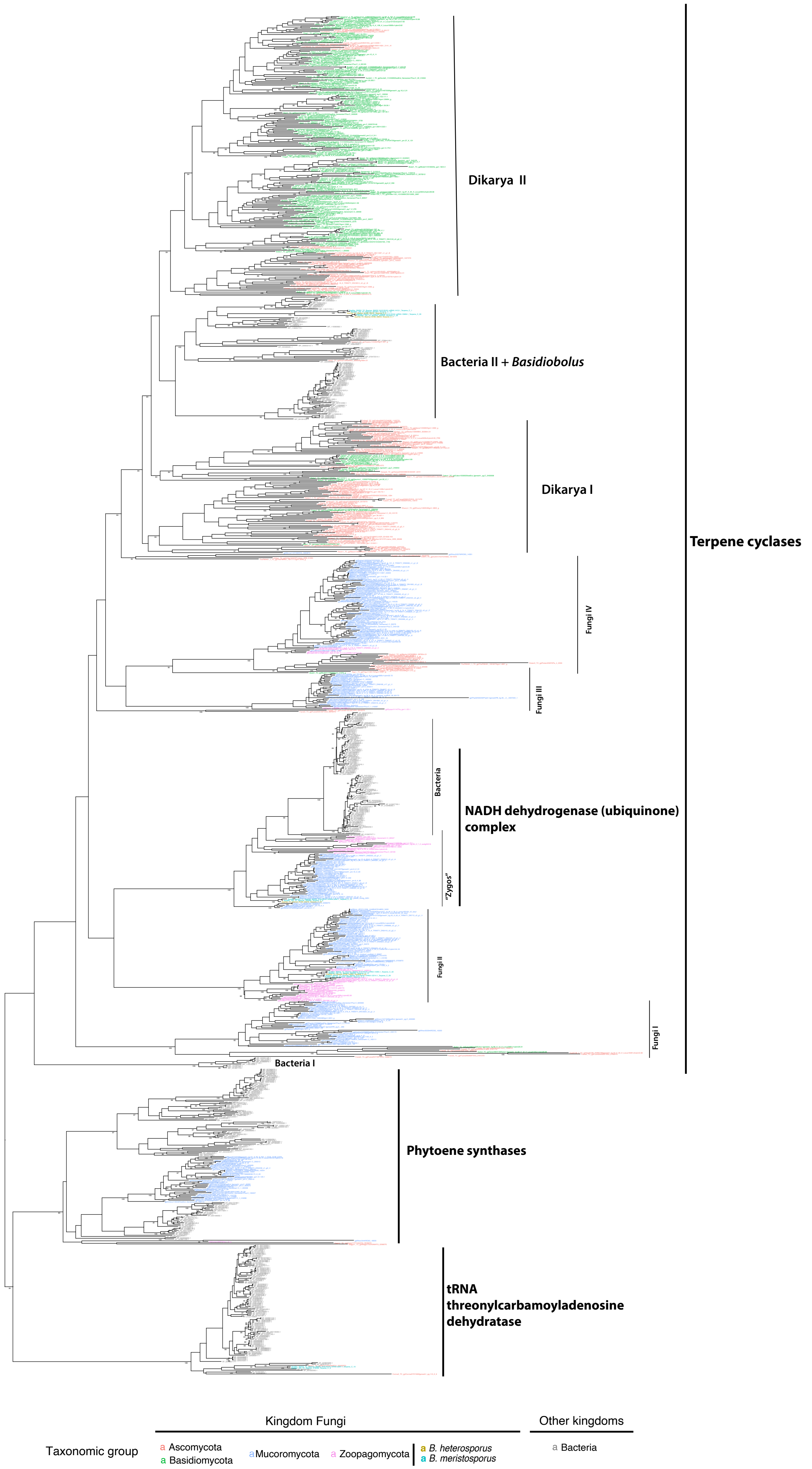


Supplementary Figure 7. Maximum likelihood tree reconstruction using the predicted terpene cyclase (TC) core genes from Zoopagomycota and Mucoromycota genomes. The maximum likelihood phylogenetic was reconstructed using the predicted TC domains for the genomes of interest. Numbers above each branch represent bootstrap values after 1,000 replicates when support is greater than 70%.