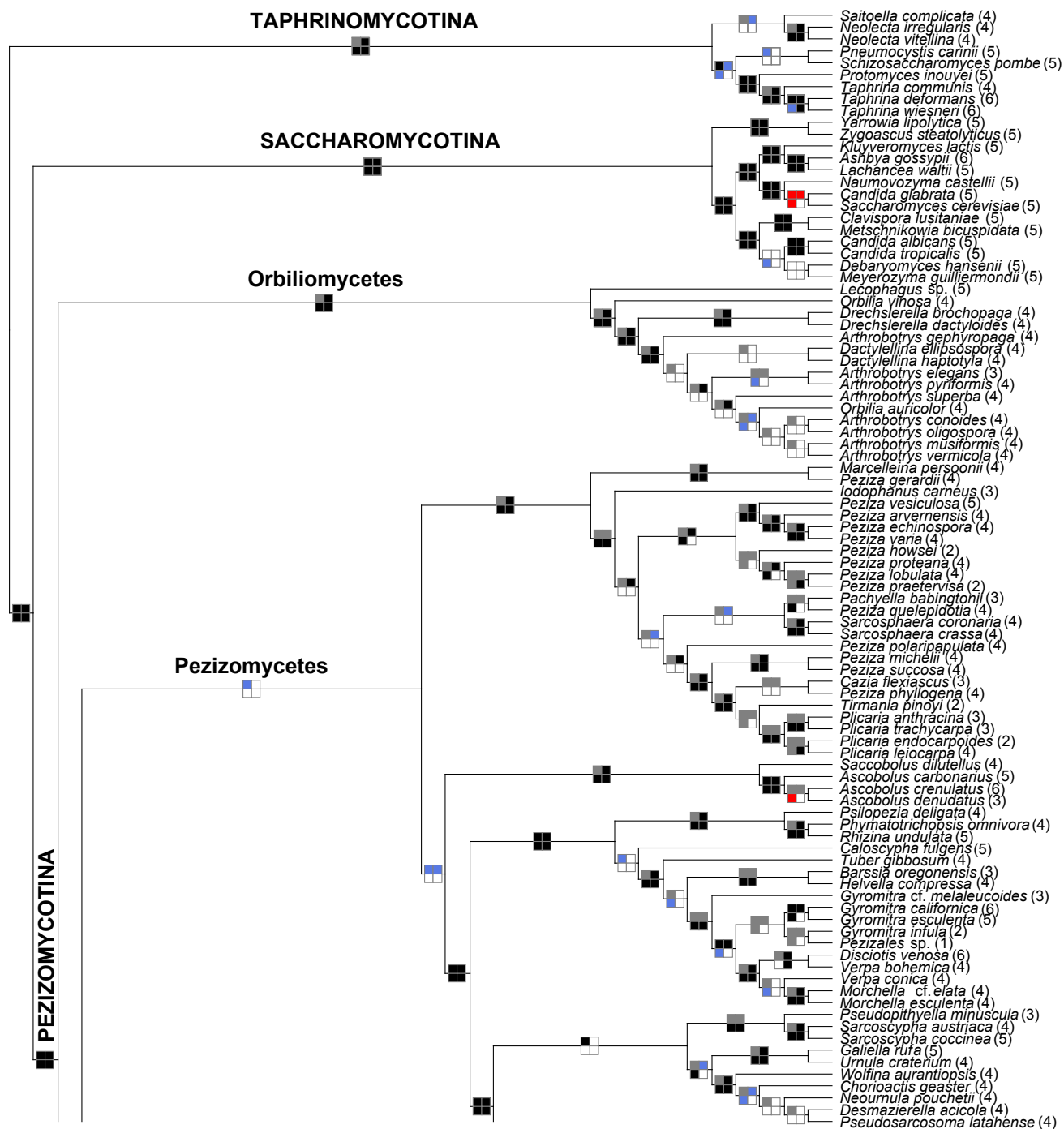
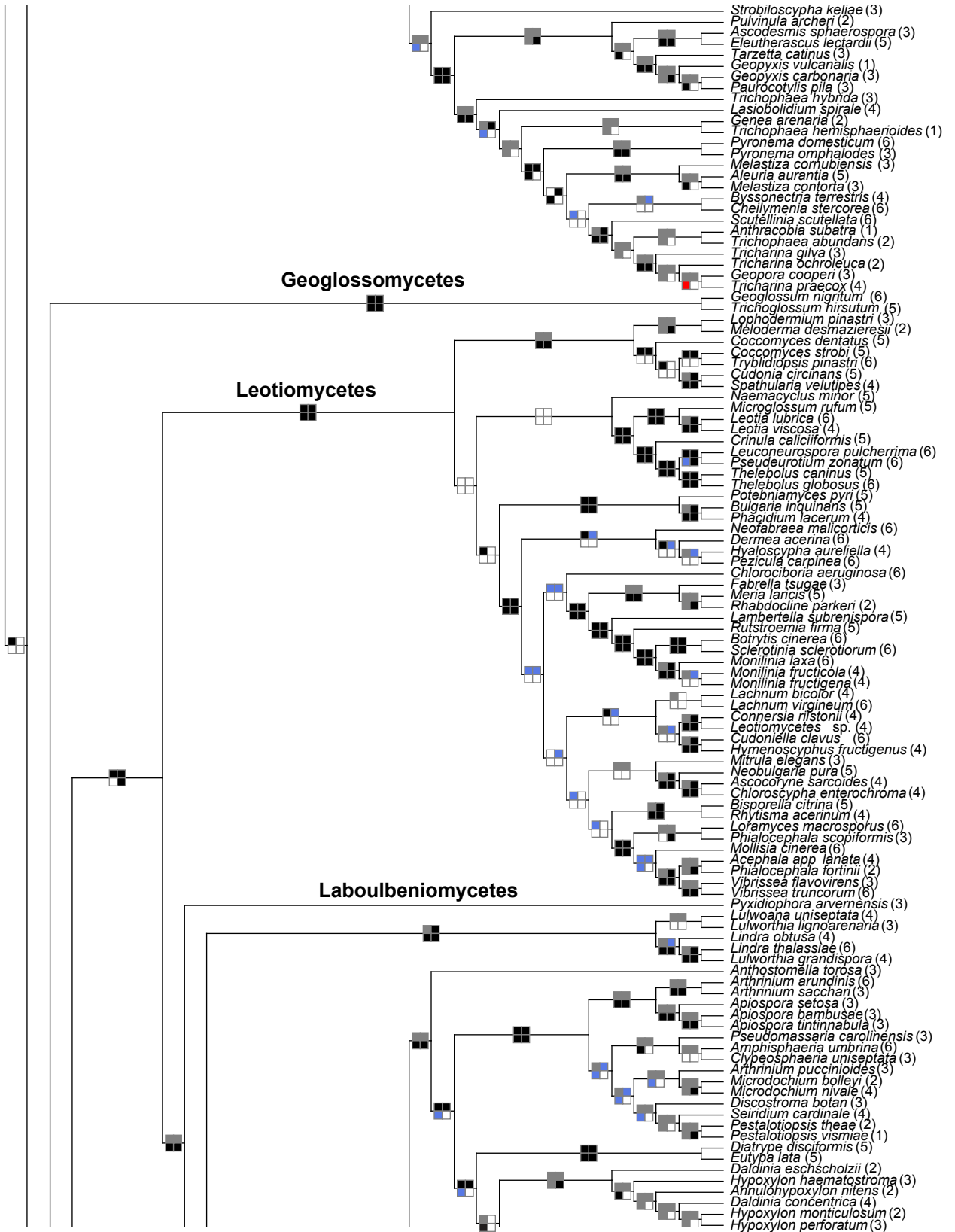


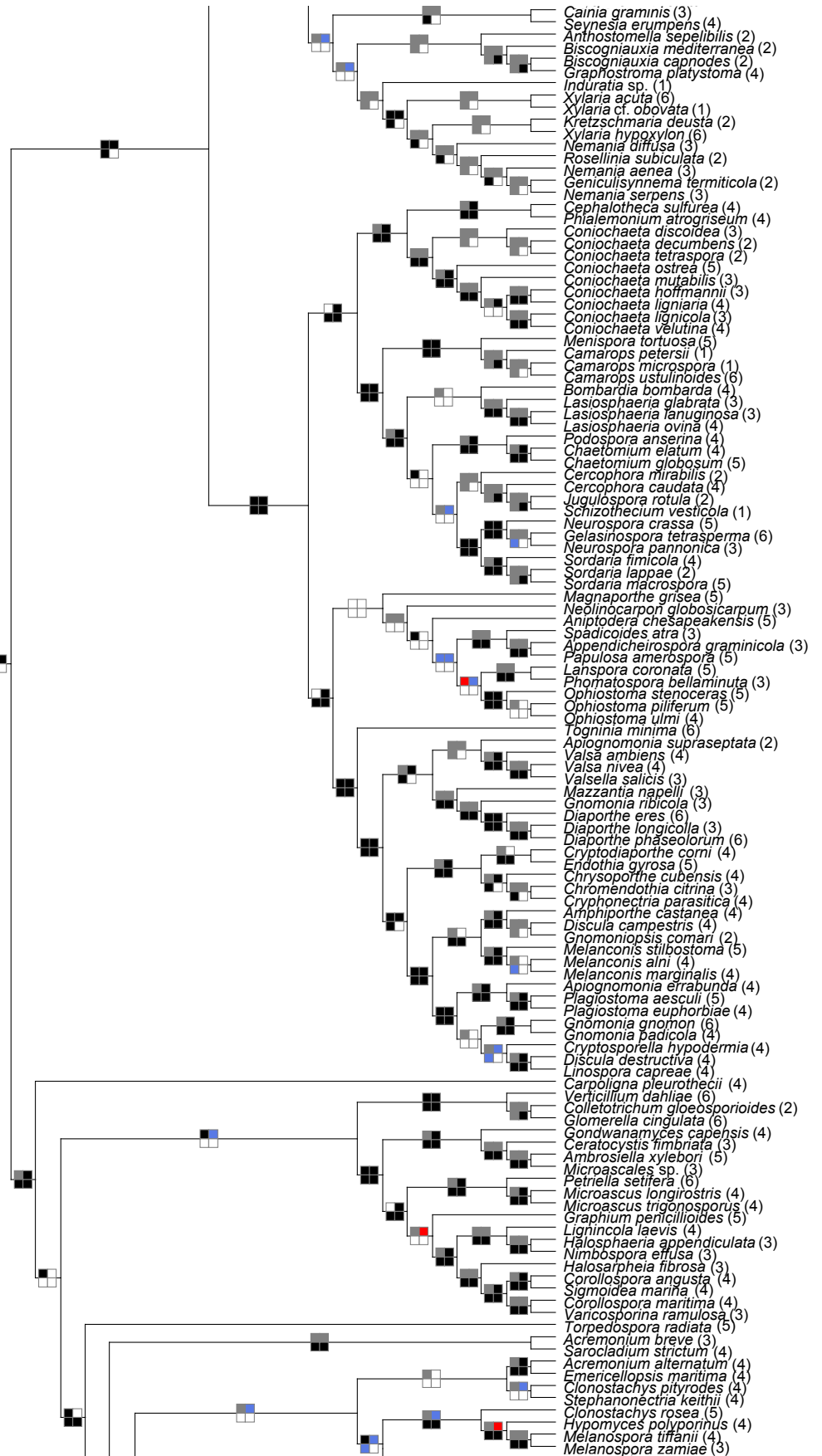
Threshold values (BS %)			
6+5-gene	70	70	6+5+4-gene
6+5+4+3-gene	70	70	6+5+4+3+2+1-gene

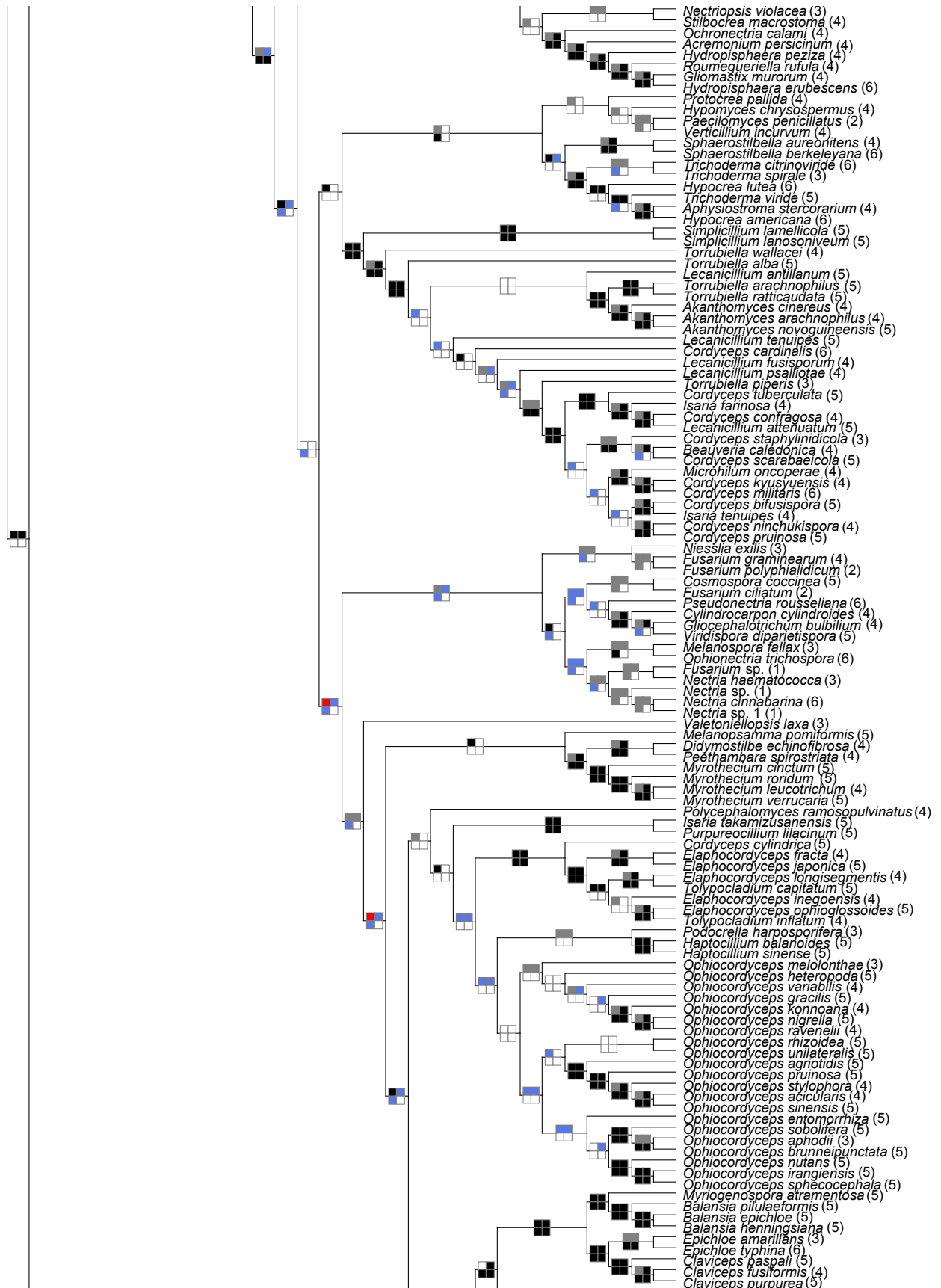


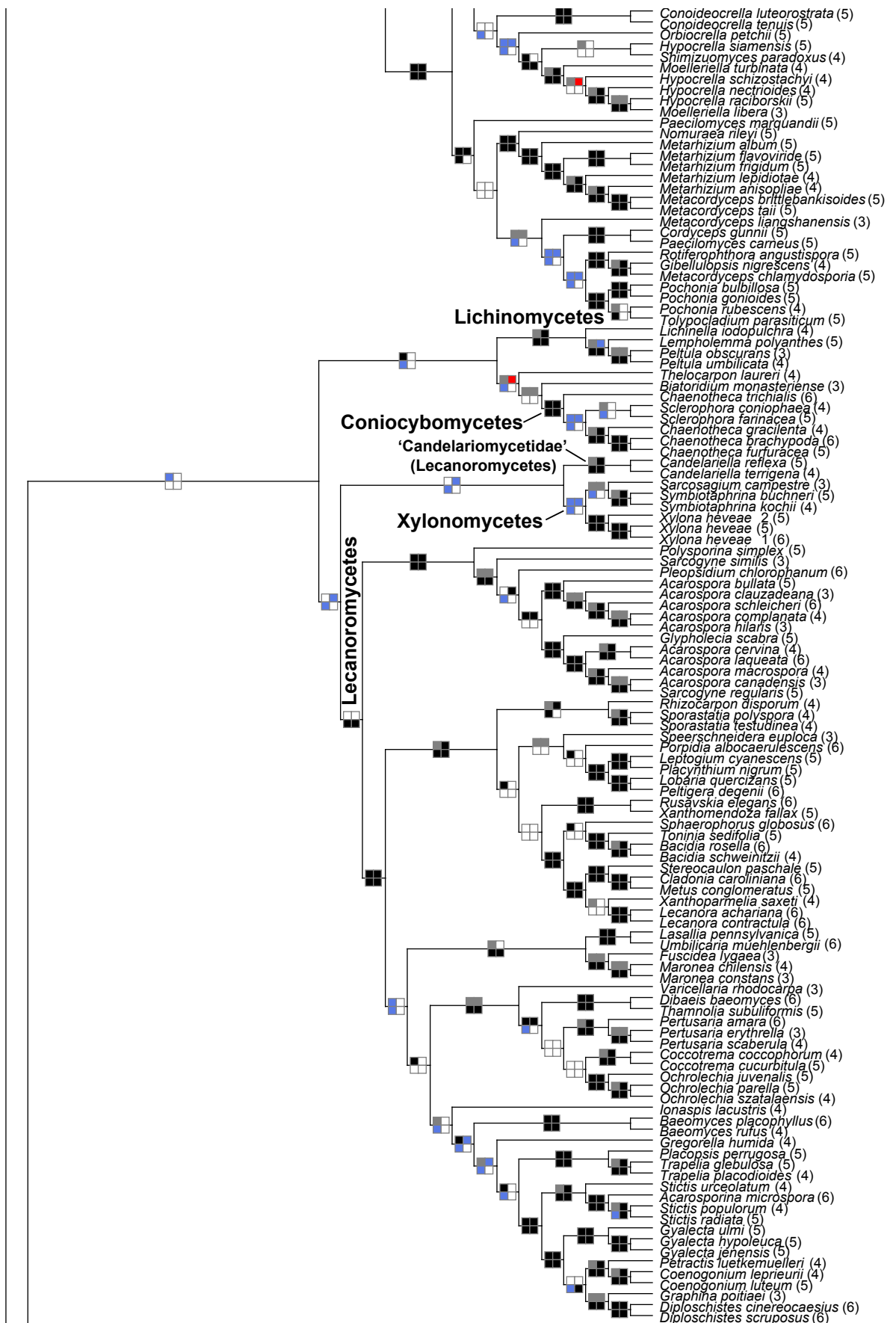


LEOTIOMYCETA

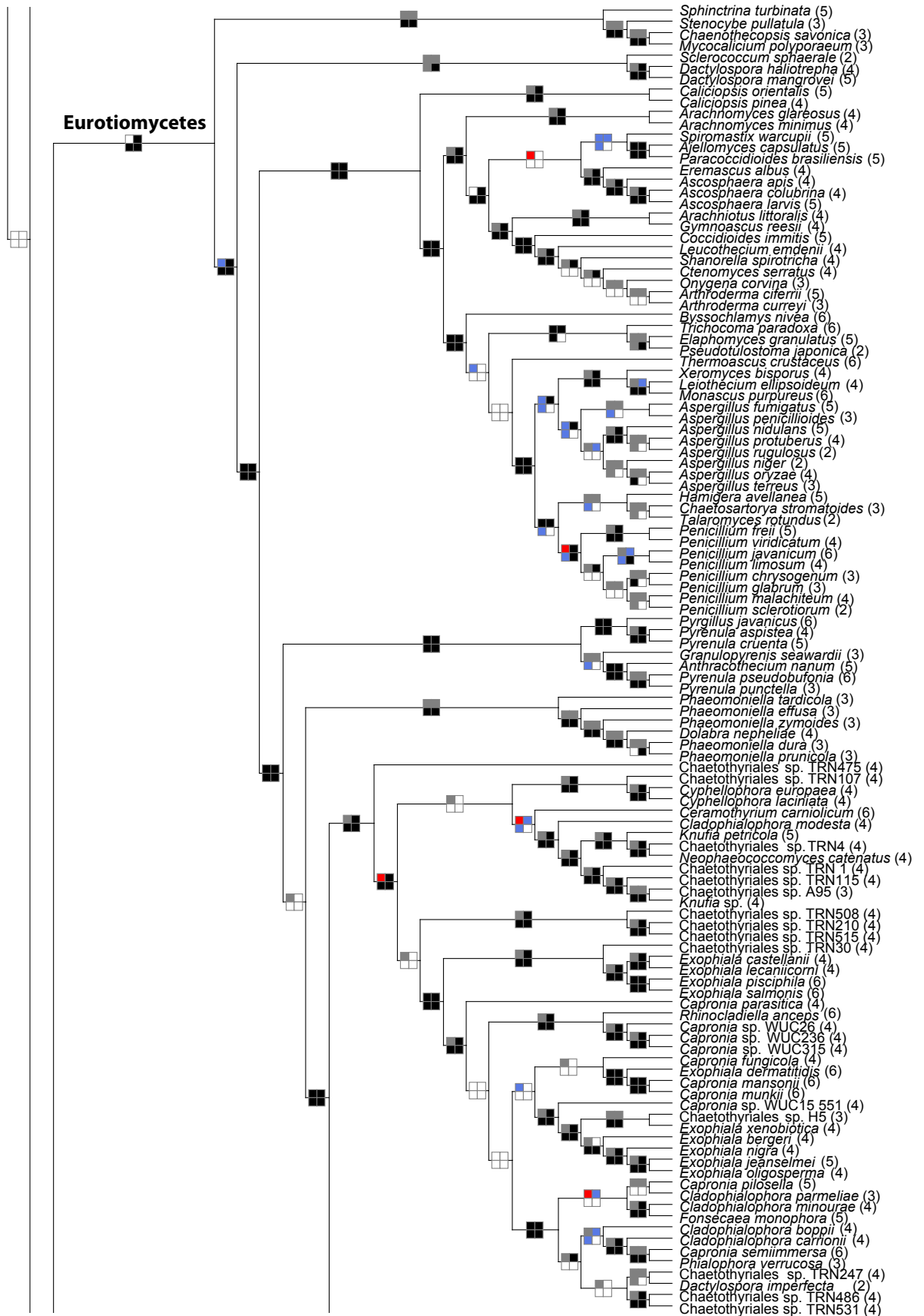
SORDARIOMYCETES

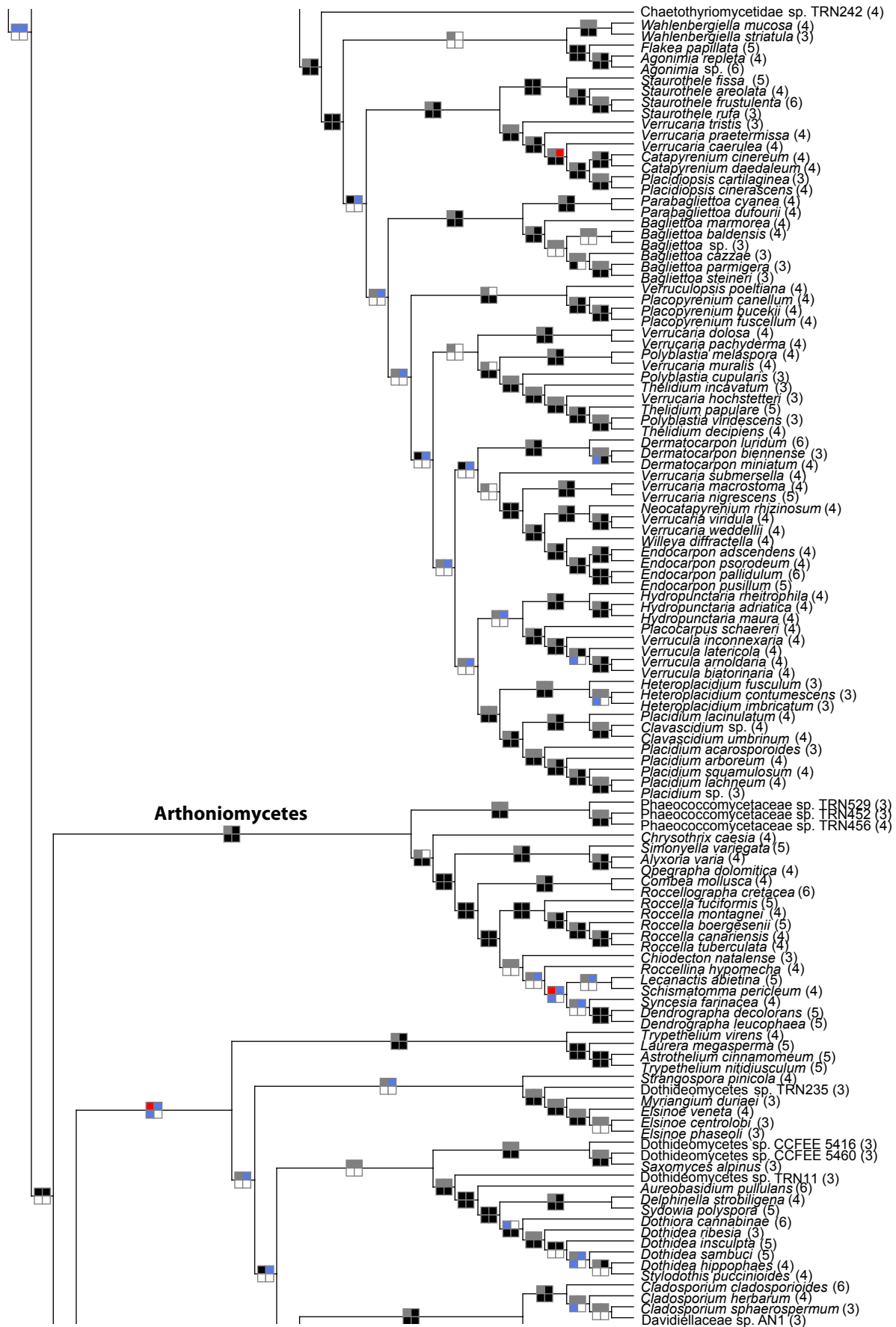




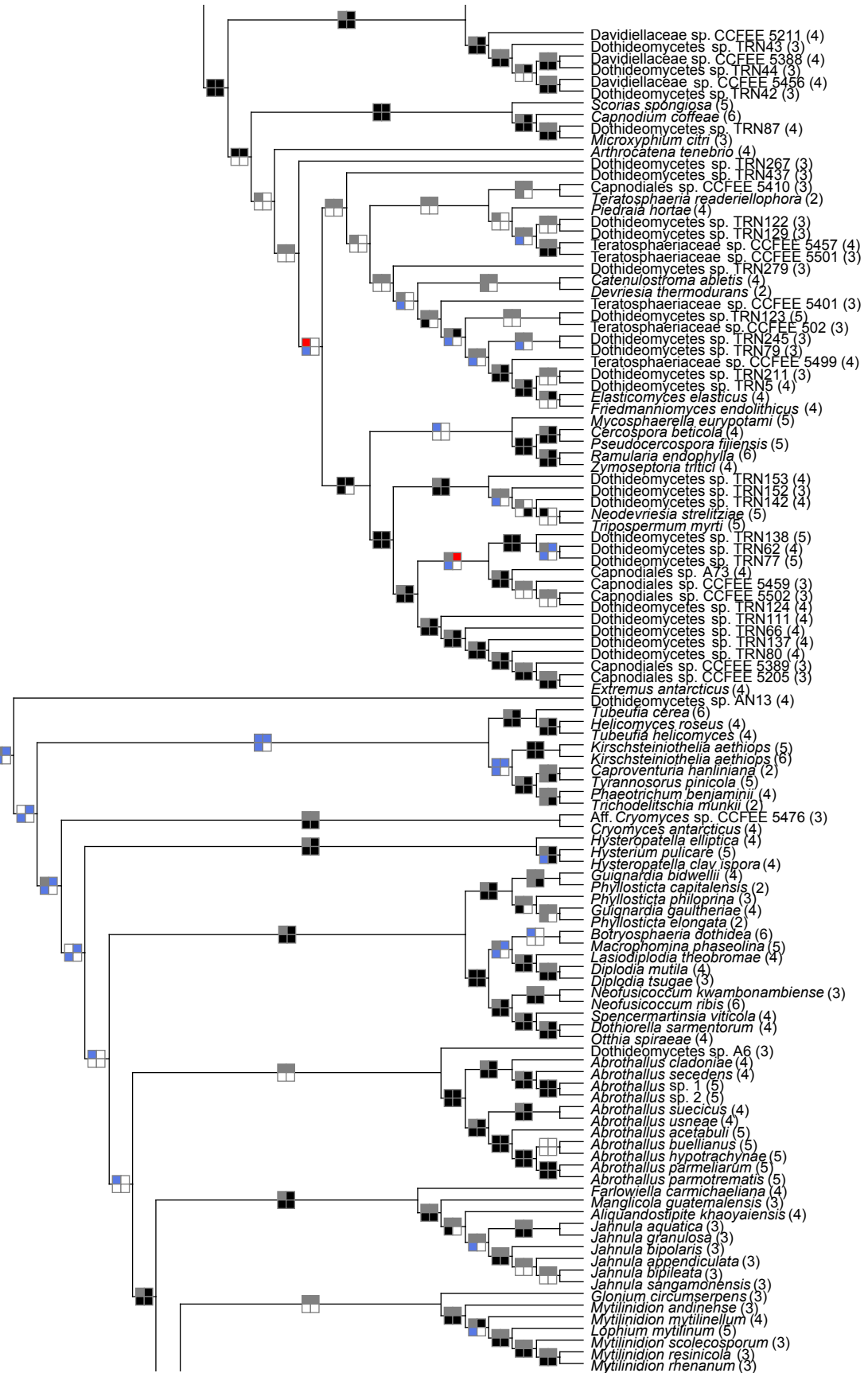




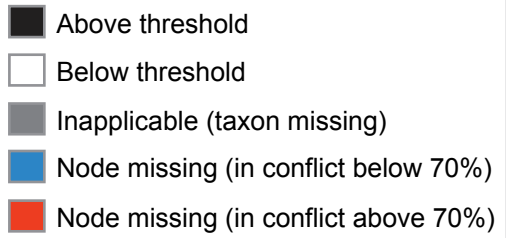
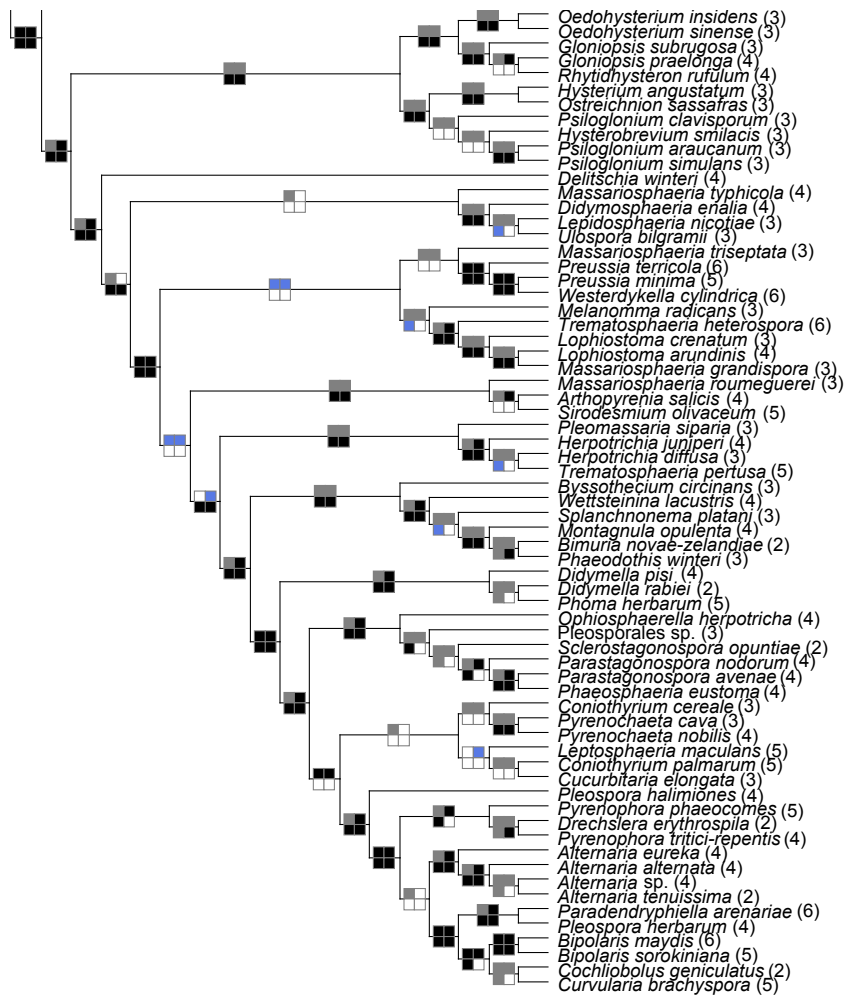




# Dothideomycetes







Threshold values (BS %)			
6+5-gene	70	70	6+5+4-gene
6+5+4+3-gene	70	70	6+5+4+3+2+1-gene

SUPPLEMENTARY FIGURE S1. Six-locus (nr5.8S, nrLSU, nrSSU, mtSSU, *RPB1*, *RPB2*; entire supermatrix) phylogenetic tree of 979 OTU representing all 13 classes of the Pezizomycotina, 12 subclasses, 61 orders, 175 families and 496 genera (classification follows GenBank) using RAxML-HPC2 version 7.2.8 (Stamatakis 2006; Stamatakis et al. 2008) as implemented on the CIPRES portal (Miller et al. 2010). Optimal tree and bootstrap searches were conducted with the rapid hill-climbing algorithm for 1000 replicates with GTRGAMMA substitution model (Rodriguez et al. 1990). Data subsets were established using PartitionFinder (greedy algorithm to explore all the nucleotide substitution models under BIC selection criterion; Lanfear et al. 2012). The four-box grid associated with each internode indicates maximum likelihood bootstrap support based on a cumulative supermatrix approach (Miadlikowska et al. 2014) including taxa with at least five of six genes (6+5-gene dataset), at least four genes (6+5+4-gene dataset), at least three genes (6+5+4+3-gene dataset) and the entire supermatrix, i.e., including taxa with at least one of the six genes (6+5+4+3+2+1-gene dataset). These bootstrap values are reported using the Hypha module (Oliver et al. 2013) of Mesquite (Maddison and Maddison 2011). Black boxes indicate bootstrap support above 70%; white boxes indicate bootstrap support below 70%; grey boxes indicate cases where internodal support is not applicable due to at least one of the (usually two) immediately downstream branches being absent (due to missing taxa); blue and red boxes indicate internodes that were not recovered and for which alternative relationships involving taxa from these clades were found at bootstrap support below (blue) and above 70% (red). Numbers in parentheses after taxon names indicate the number of genes in our supermatrix for each OTU (Supplementary Table S1). This tree is displayed online by T-BAS and used to

phylogenetically place unknowns and/or download alignments. The entire supermatrix (6+5+4+3+2+1-gene dataset) was deposited in TreeBASE (<http://purl.org/phylo/treebase/phylows/study/TB2:S20206>).