

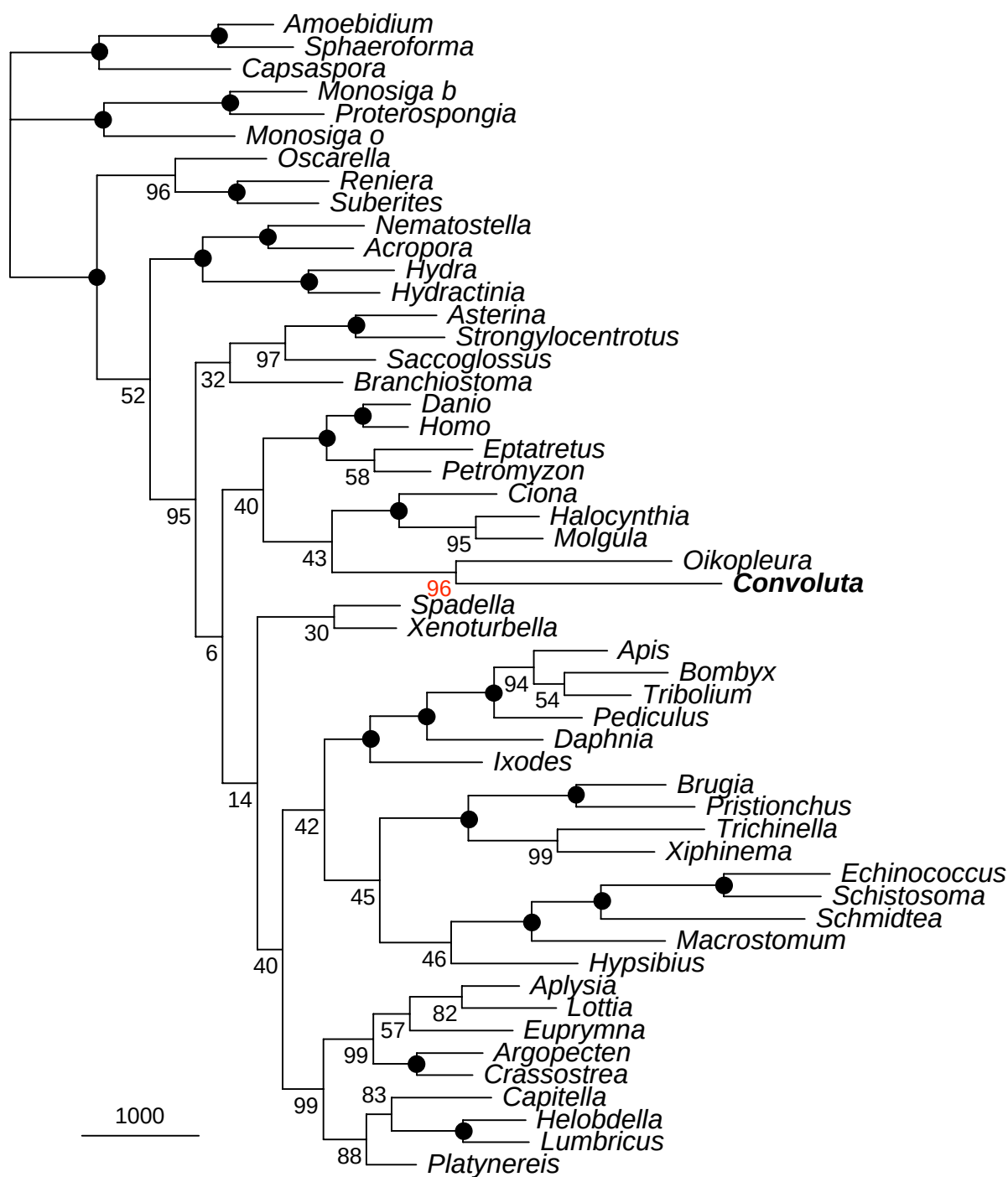


Figure S1: Maximum parsimony tree inferred from 11,959 unambiguously aligned amino acid positions with PAUP. The robustness of the phylogenetic inference was estimated by 1000 bootstrap replicates. Nodes supported by 100% bootstrap are denoted by black circles while lower values are given explicitly. The scale bar indicates the number of changes.