



Figure S7. 28S phylogenetic analysis under parsimony as the optimality criterion. Numbers at nodes indicate Goodman-Bremer support values and colored circles represent bootstrap resampling frequencies (black = ≥ 95 , grey = ≥ 75 , absent = < 75). Scale bar represents the number of nucleotide transformations. Table S4 contains further details on sequences used to reconstruct this phylogeny.