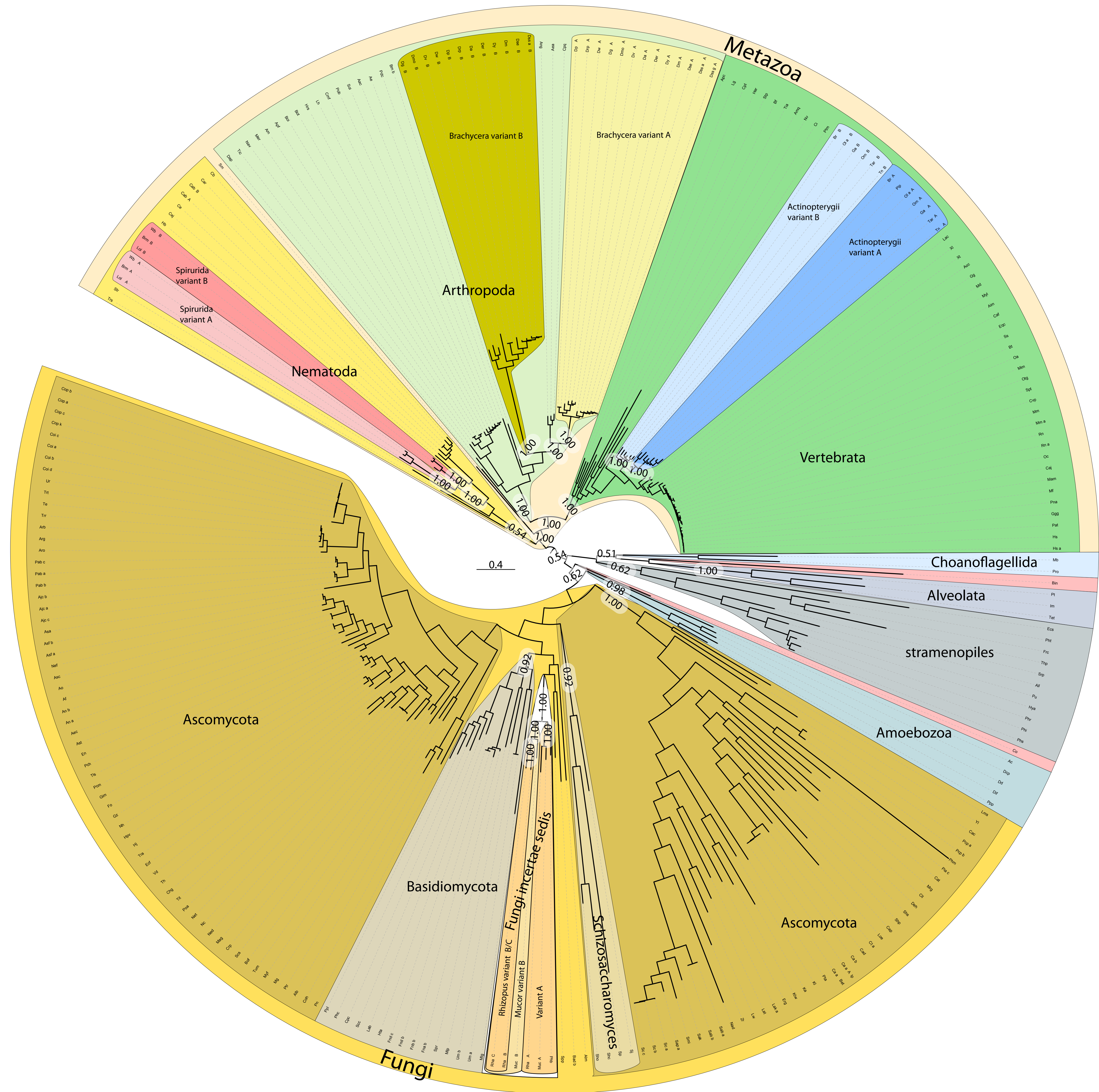




Phylogenetic tree of the dynactin1 subunit

The phylogenetic tree of the dynactin1 from Bayesian inference (MrBayes) using the JTT model. The unrooted tree was drawn with iTOL and branches were coloured according to taxonomic distributions and taxon-specific dynactin1 duplications. Posterior probability support values are only given for some major branches due to space limitations. For the extended tree including the posterior probability values for all branches see Additional File 1. The scale bar represents amino acid substitutions per site.