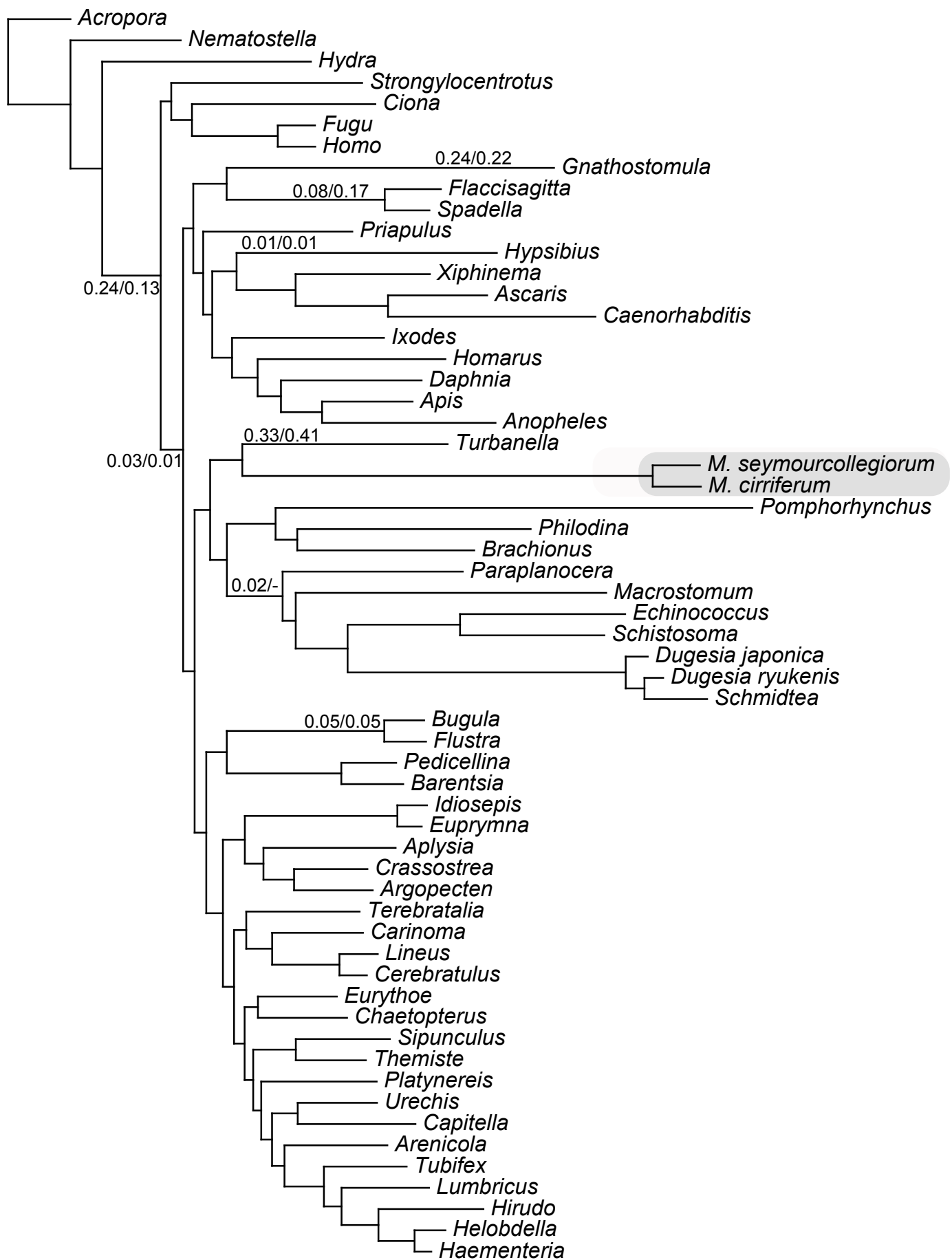




Suppl. Fig. 1: Branch attachment frequency (BAF) of the partition jackknifing analysis mapped on the best ML-tree from the concatenated RP-dataset. BAF's are given at the node, whereas the first number indicates the frequency a clade has been recovered in the 100 35-gene replicates and the second indicates the frequency for the 50-gene-replicates.



Suppl. Fig. 3: Bayesian inference of the mtDNA-dataset based on the site-heterogeneous CAT-model using Phylobayes v2.1C. Posterior probabilities are given at the nodes.