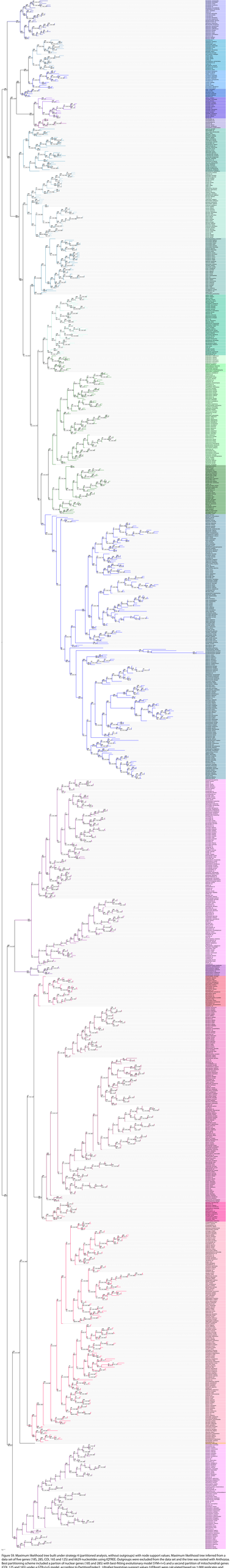

Figure 59. Maximum likelihood tree built under strategy 4 (partitioned analysis, without outgroups) with node support values. Maximum likelihood tree inferred from a data set of five genes (18S, 28S, COI, 16S and 12S) and 6629 nucleotides using IQTREE. Outgroups were excluded from the data set and the tree was rooted with Ambosia. Best partitioning scheme included a partition of nuclear genes (18S and 28S) with best-fitting evolutionary model SYM+I+G and a second partition of mitochondrial genes (16S, 12S and 16S) under a GTR+I+G model, according to PartitionFinder2. Ultrafast bootstrap support values (UFBoot) were calculated based on 1,000 replicates and are shown above branches. SH-aLRT/aBayes support values shown below branches. Scale bar represents number of substitutions per site.