



Figure S5. Maximum likelihood tree built under nucleotide 2 (partitioned) with node support values. Maximum likelihood tree inferred from a data set of five genes (18S, 28S, COI, 16S and 12S) and 6629 nucleotide partitions using IQ-TREE. 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 (COI, 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/abeyes support values shown below branches. Scale bar represents number of substitutions per site.