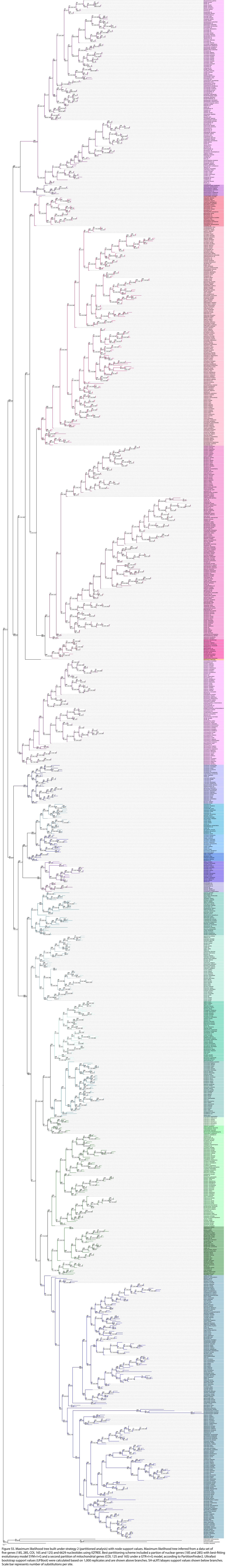
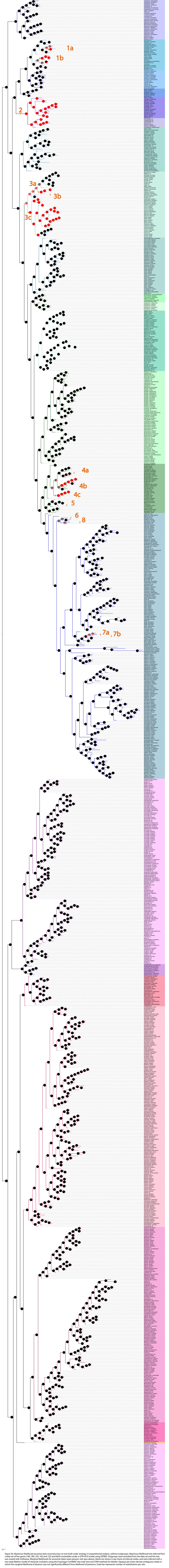
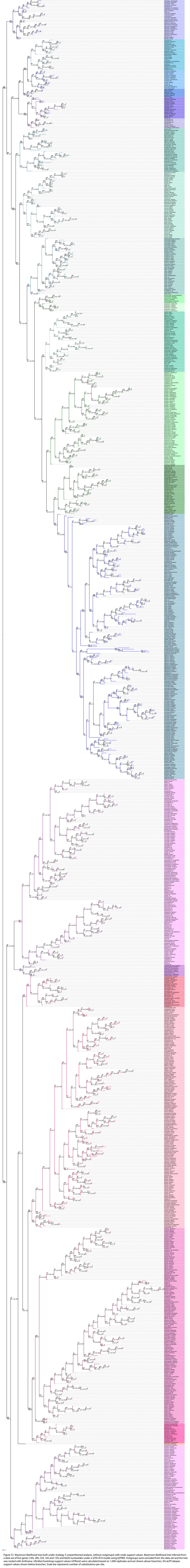


Figure S4. Maximum likelihood ancestral state reconstruction on tree built under strategy 2 (partitioned analysis). Maximum likelihood tree inferred from a data set of five genes (185, 285, COI, 16S and 12S) and 6629 nucleotides using iOTREE. Best partitioning scheme included a partition of nuclear genes (185 and 285) with best-fitting evolutionary model SYM+H+G and a second partition of mitochondrial genes (COI, 12S and 16S) under a GTR+I+G model, according to PartitionFinder2. Marginal likelihoods for ancestral states (eyes present, red; eyes absent, black) are shown in pie charts at internal nodes, and were inferred with a two-state Markov model of character evolution using the R package "corHMM" (see main text and STAR methods for details). Opaque pie charts denote ambiguous nodes in which the marginal likelihood of absence was not significantly different from likelihood of presence. Scale bar represents number of substitutions per site.







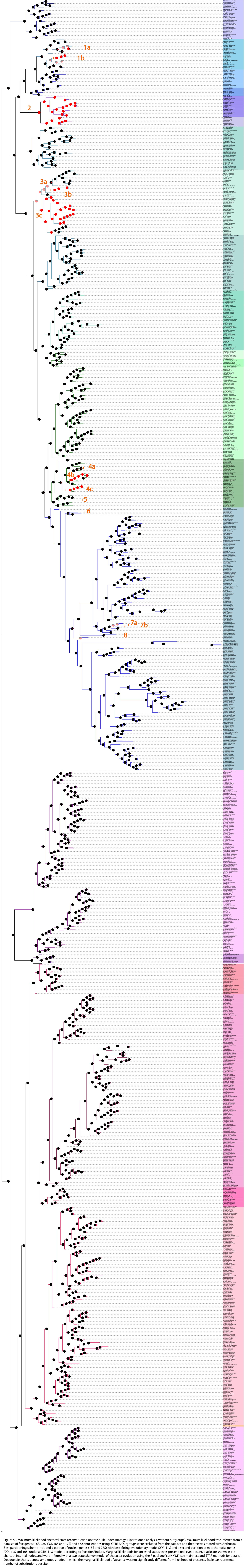


Figure S8. Maximum likelihood ancestral state reconstruction on tree built under strategy 4 (partitioned analysis, without outgroups). Maximum likelihood tree inferred from a data set of five genes (18S, 28S, COI, 16S and 12S) and 6629 nucleotides using IQTREE. Outgroups were excluded from the data set and the tree was rooted with Anthozoa. Best partitioning scheme included a part of nuclear genes (18S and 28S) with best-fitting evolutionary model SYM+H+G and a second partition of mitochondrial genes (COI, 12S and 16S) under a GTR+H+G model, according to PartitionFinder2. Marginal likelihoods for ancestral states (eyes present, red; eyes absent, black) are shown in pie charts at internal nodes, and were inferred with a two-state Markov model of character evolution using the R package "coRHM" (see main text and STAR methods for details). Opaque pie charts denote ambiguous nodes in which the marginal likelihood of absence was not significantly different from likelihood of presence. Scale bar represents number of substitutions per site.

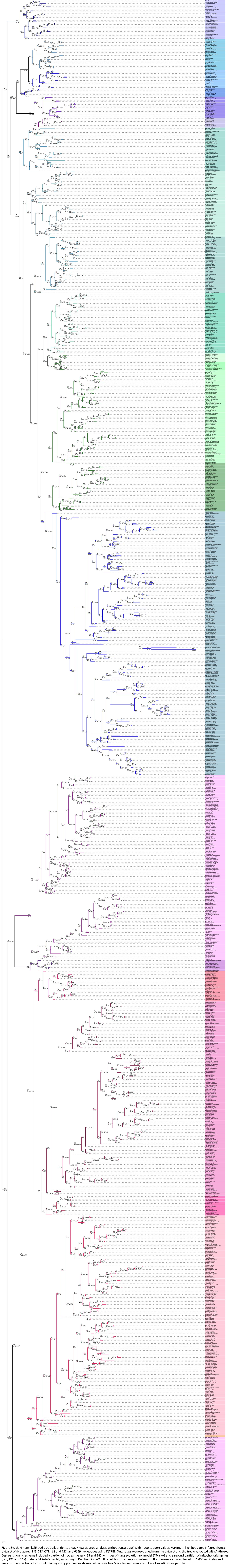


Figure S9. Maximum likelihood tree built under strategy 4 (partitioned analysis, without outgroups) with node support values. Maximum likelihood tree inferred from a data set of five genes (18S, 28S, COI, 16S and 12S) and 6629 nucleotides using IQTREE. Outgroups were excluded from the data set and the tree was rooted with Anthozoa. Best partitioning scheme included a partion 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.

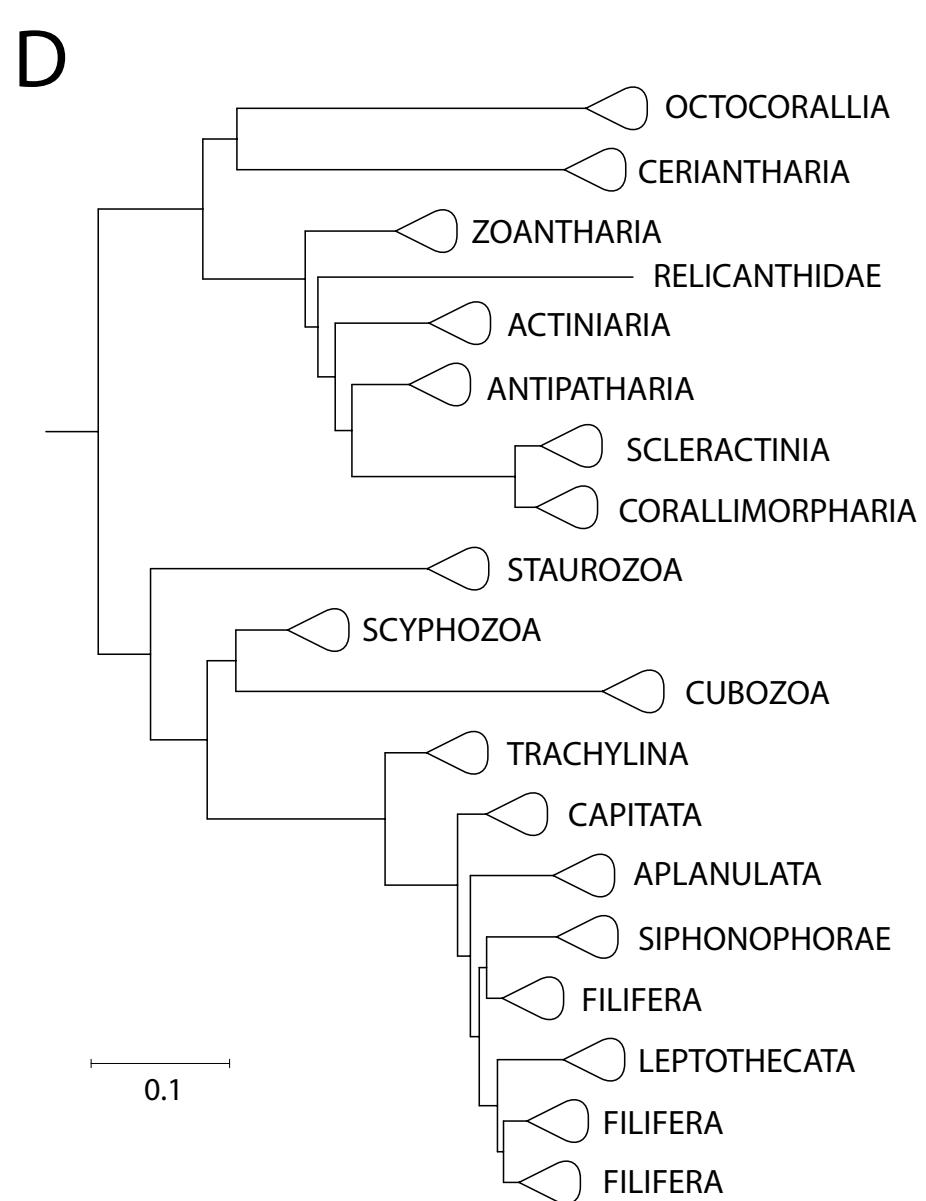
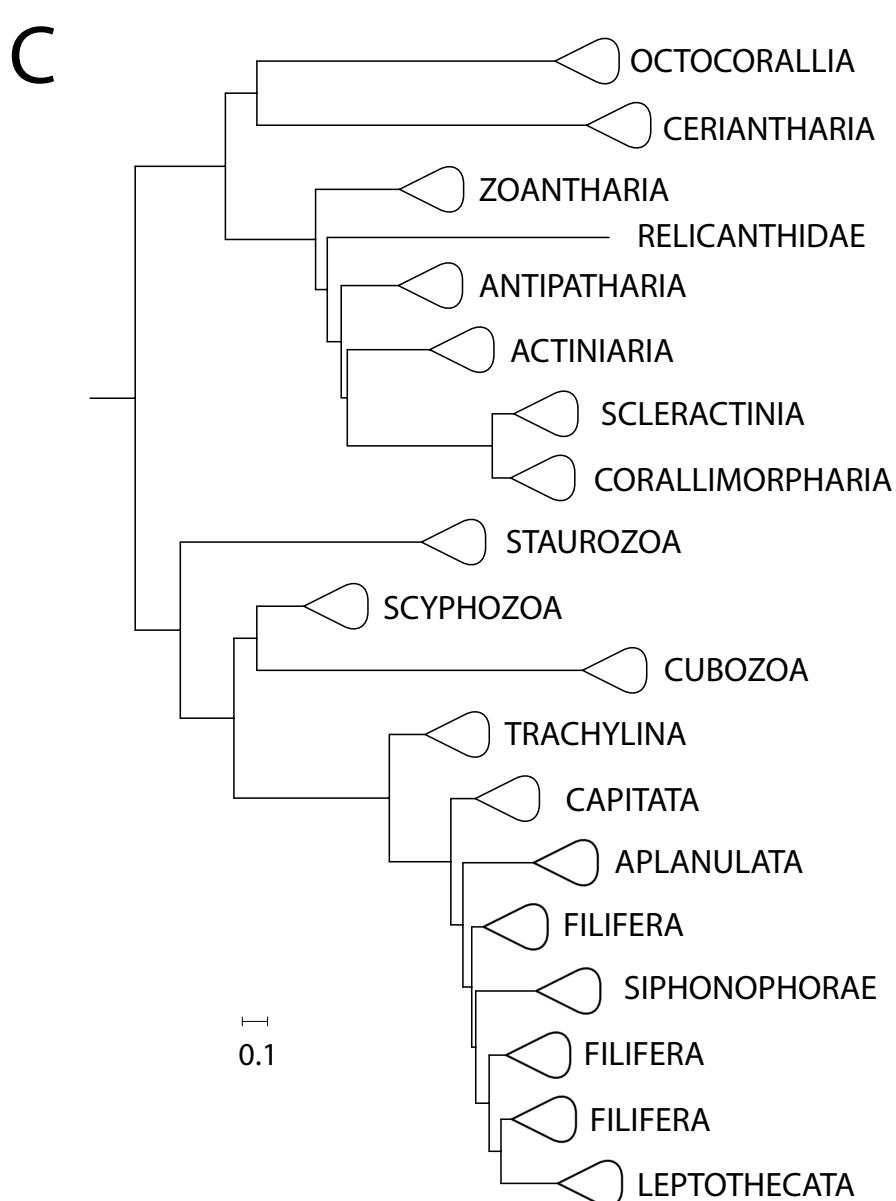
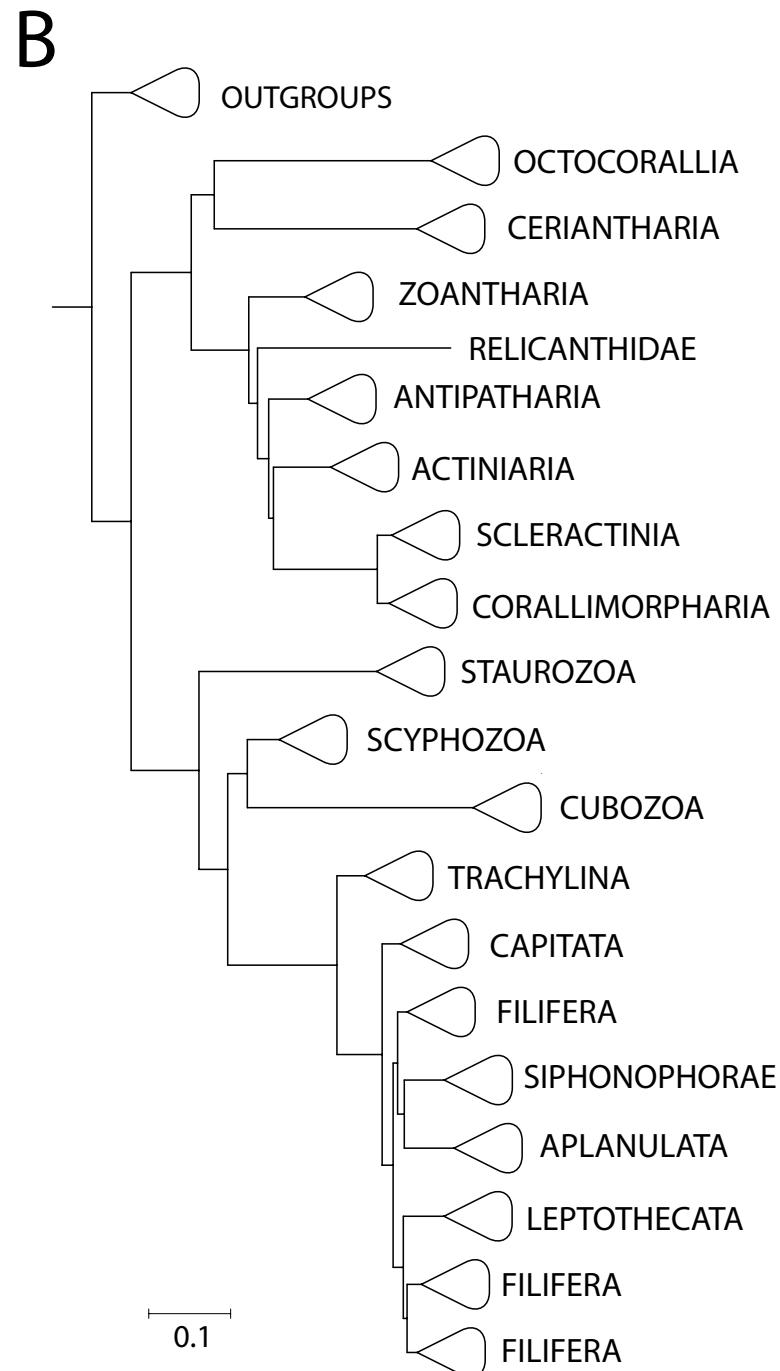
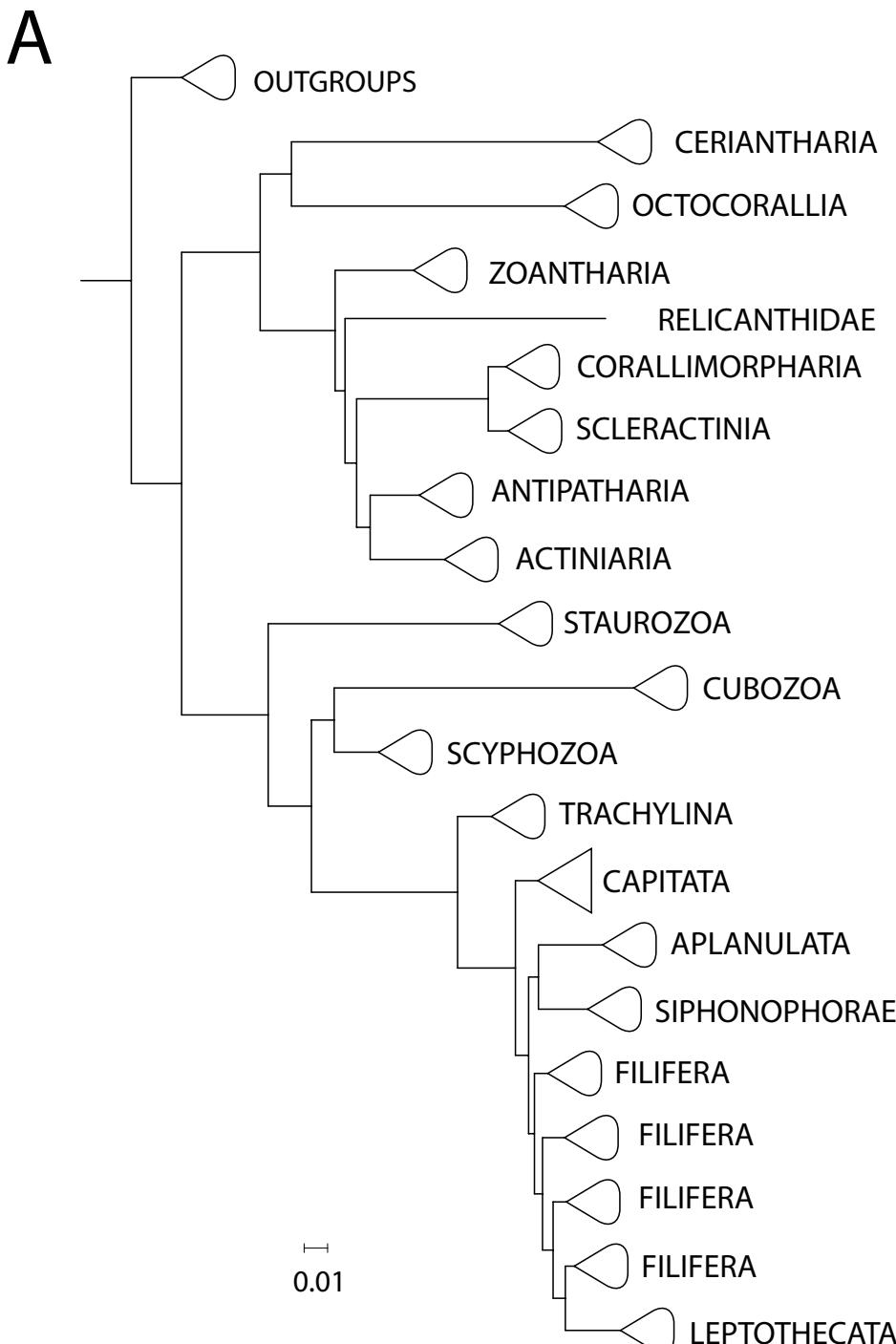


Figure S9. Summary Maximum Likelihood trees from phylogenetic analyses using strategies 1-4 (panels A-D). A: strategy 1, B: strategy 2, C: strategy 3, D: strategy 4. See STAR methods for details. Scale bar denotes number of nucleotide substitutions per site.



Figure S11. Parsimony ancestral state reconstruction. Character optimization under accelerated transformation criteria indicates 10 transitions from eyes absent (white lines) to eyes present (black lines), as shown in magenta numbers. Under a delayed transformation criteria, parsimony indicates there could be 16 eye origins, as shown in green numbers. Ambiguous nodes are represented with black and white colored branches. Grey lines represent unknown states.

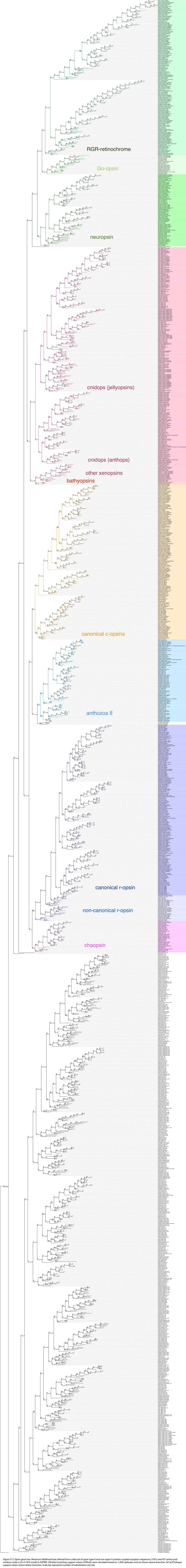


Figure S12. Opsin gene tree. Maximum likelihood tree inferred from a data set of opsin type-II and non-opsin G-protein coupled receptors sequences (1591) and 457 amino acid residues under a LG+F+R10 model in IQTREE. Ultrafast bootstrap support values (UFboot) were calculated based on 1,000 replicates and are shown above branches. Scale bar represents number of substitutions per site.