

Molecular phylogenies of algal genes identified in *Ciona intestinalis*. Numbers above branches show bootstrap support values inferred from maximum likelihood and distance analyses, respectively. Asterisks indicate values lower than 50%. Other bootstrap values below 50% in both methods were not shown. Red: tunicates; green: Plantae; blue: cyanobacteria; pink: other plastid-bearing eukaryotes. The alignment data are available on request.

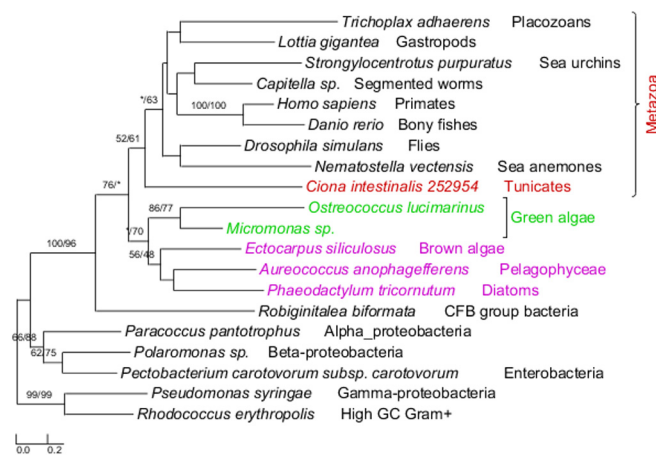


Figure S1. Molecular phylogeny of aminoglycoside phosphotransferase.

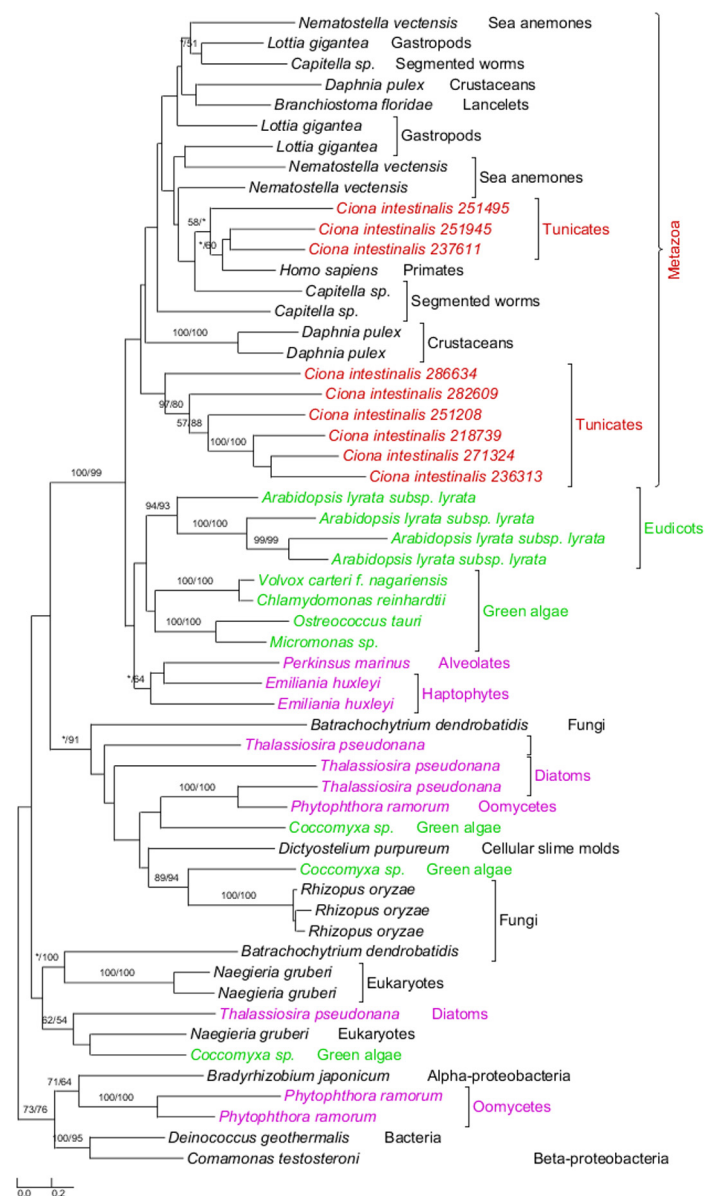


Figure S2. Molecular phylogeny of solute carrier family 22. Only nine of the 27 *Ciona* genes belonging to this subfamily are included here. Additional analyses indicated that all the 27 *Ciona* genes form a monophyletic group with other animal sequences.

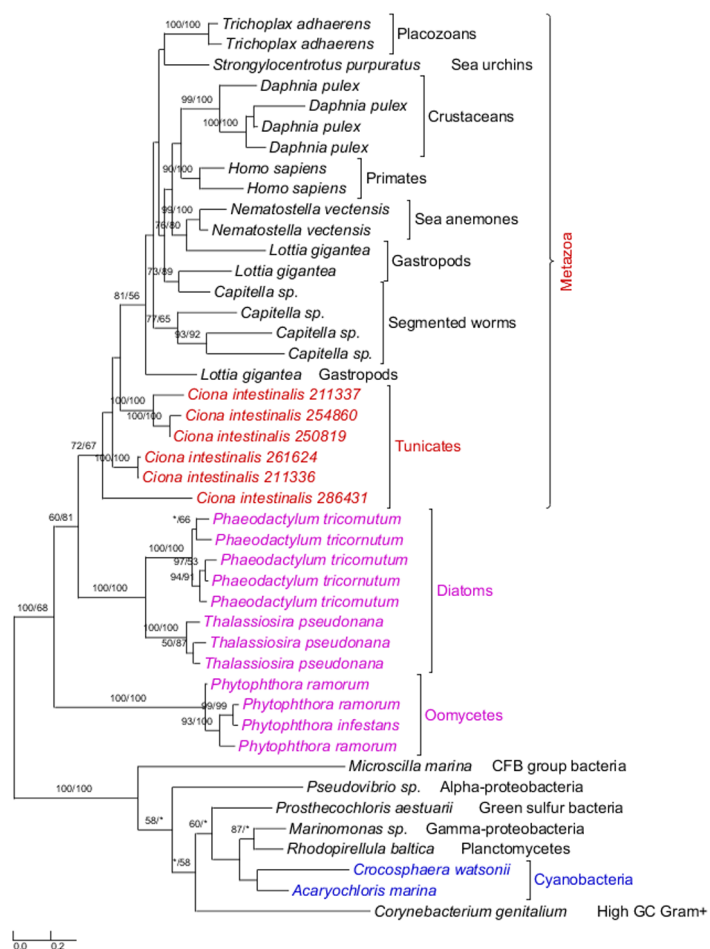


Figure S3. Molecular phylogeny of solute carrier family 34.

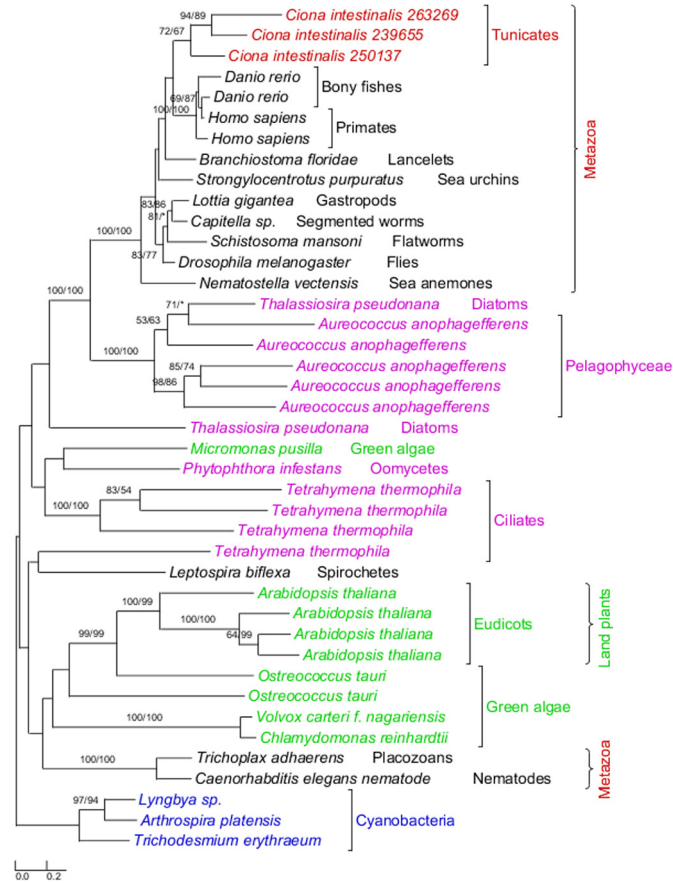


Figure S4. Molecular phylogeny of potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2.

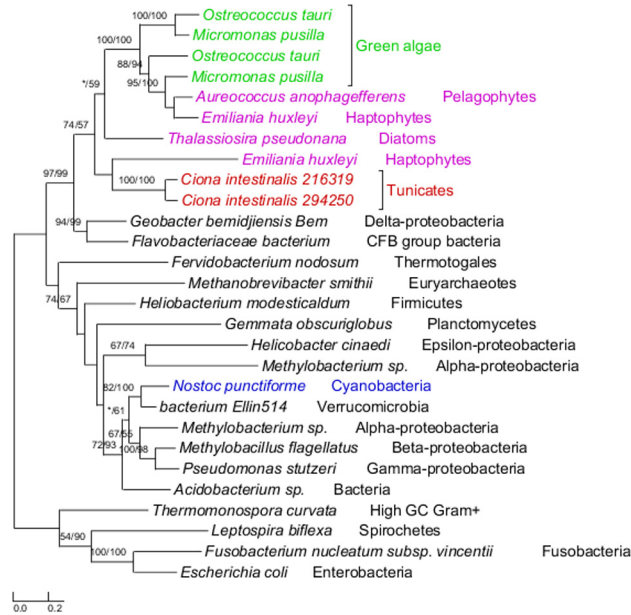


Figure S5. Molecular phylogeny of UDP galactopyranose mutase.

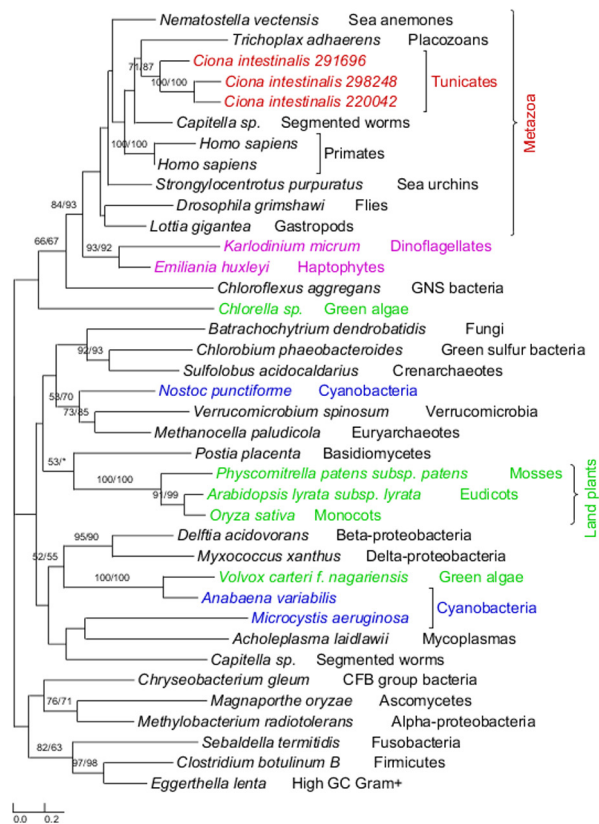


Figure S6. Molecular phylogeny of biphenyl/valacyclovir hydrolase.

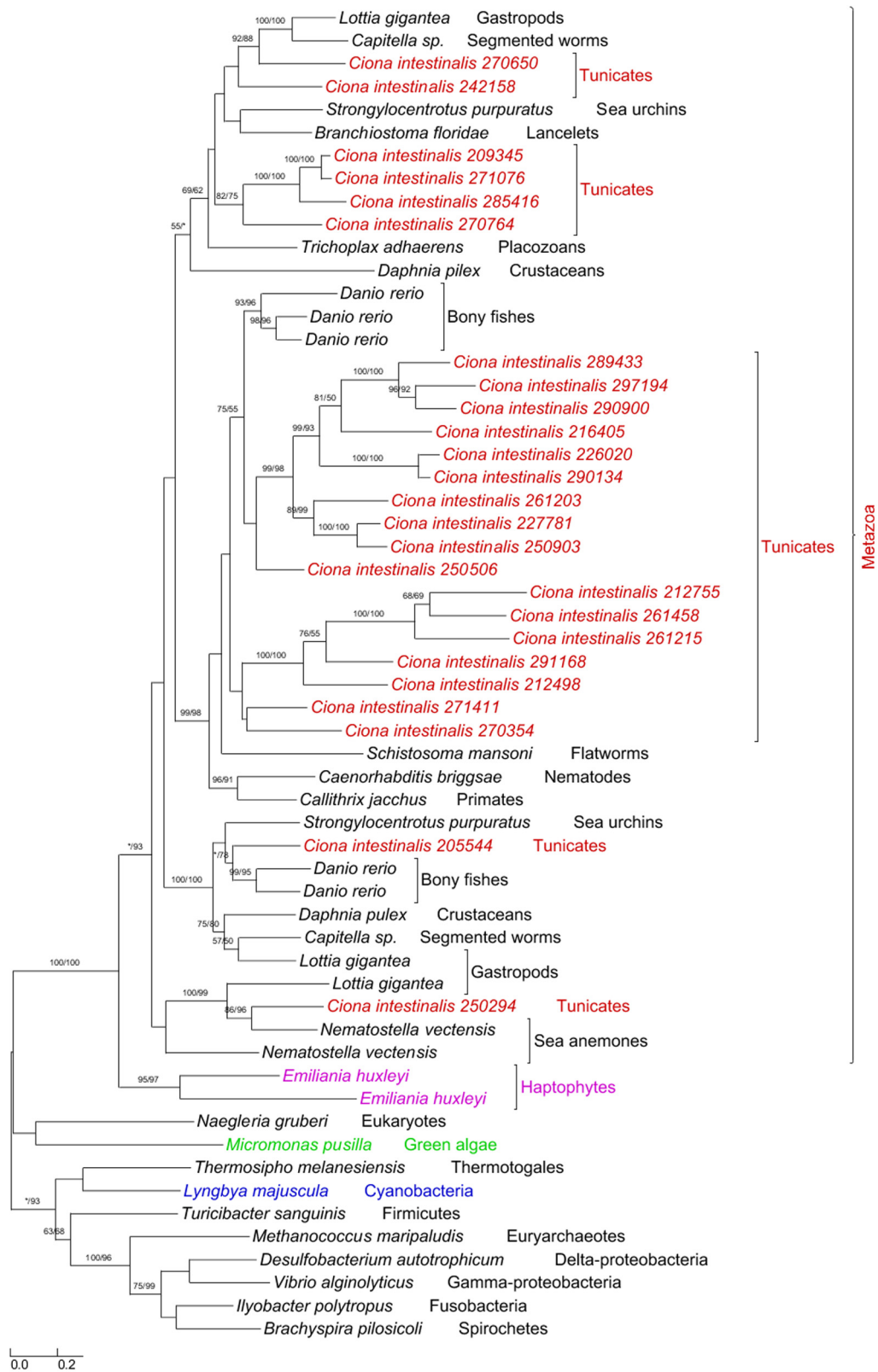


Figure S7. Molecular phylogeny of solute carrier family 6. Only 25 of the 31 *Ciona* genes belonging to this subfamily are included here. The missing 6 genes have extremely high similarity with some of the included genes.

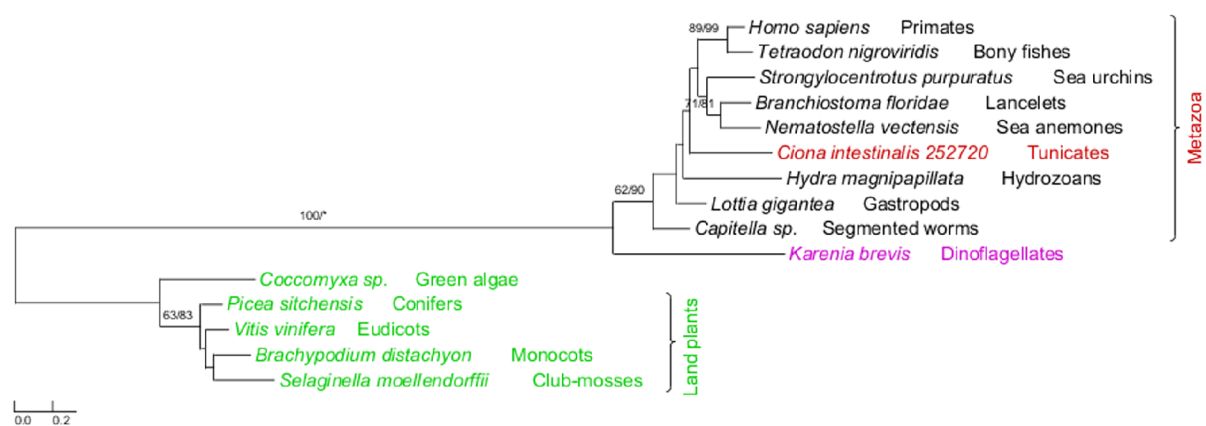


Figure S8. Molecular phylogeny of alkylation repair homolog 5