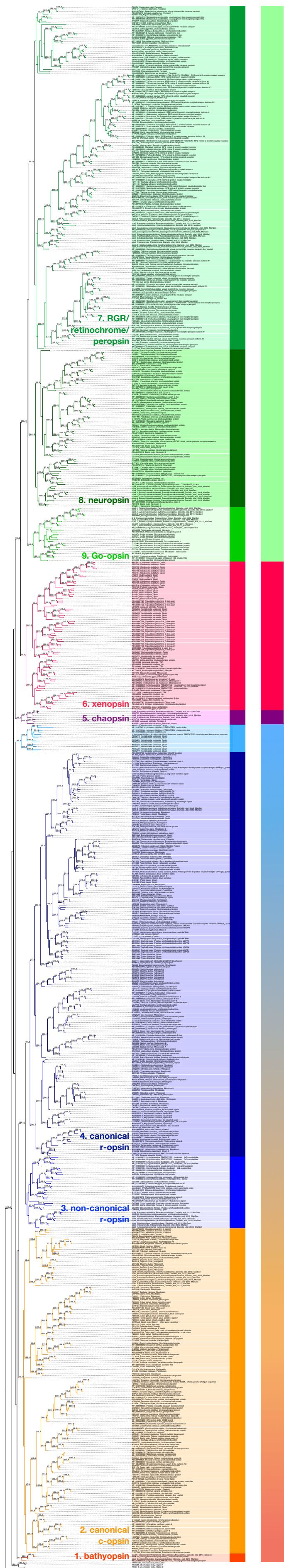
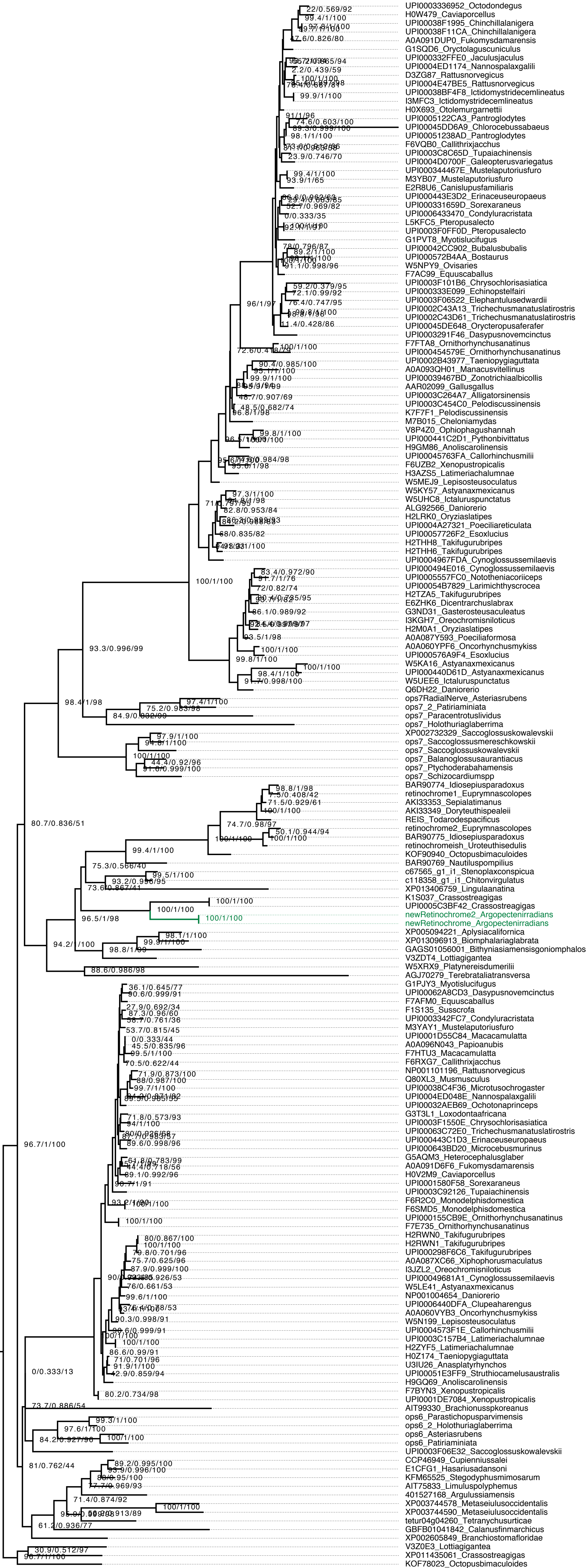


Supplemental Figure S1: IQ-TREE opsin phylogeny of 769 protein sequences from 14 animal phyla. We used the LG+F+R8 substitution model implemented in IQ-TREE 1.4.0 (Nguyen et al. 2014). UFBoot supports are displayed above their corresponding branches, and SH-aLRT and aBayes single branch test values are displayed below their corresponding branch. Nine bilaterian opsin paralogs are labeled with a Arabic numeral and name corresponding to the text and main figures. Four eumetazoan opsin paralogs are labeled with a Roman numeral and name corresponding with the text and main figures.



Supplemental Figure S2: NOTUNG reconciled opsin phylogeny of 769 protein sequences from 14 animal phyla. The 9 bilaterian opsin paralogs are labeled with a Arabic numeral and name corresponding to the text and main figures. The 4 eumetazoan opsin paralogs are labeled with a Roman numeral and name corresponding with the text and main figures. UFBBoot supports are displayed for well-supported branches (above 95%). Branches with less than 95% UFBBoot support were allowed to be rearranged by NOTUNG. Rearranged nodes are marked with an 'R'.



Supplemental Figure S3: IQ-TREE RGR/peropsin/retinochrome opsin phylogeny including two *Argopecten irradians* retinochromes. We added a previously excluded *A. irradians* retinochromes to an alignment of RGR/peropsin/retinochrome sequences. The added sequences are highlighted in green, and fall sister to other bivalve retinochrome-like sequences as expected, and with high support from UFBoot, aLRT and aBayes tests.