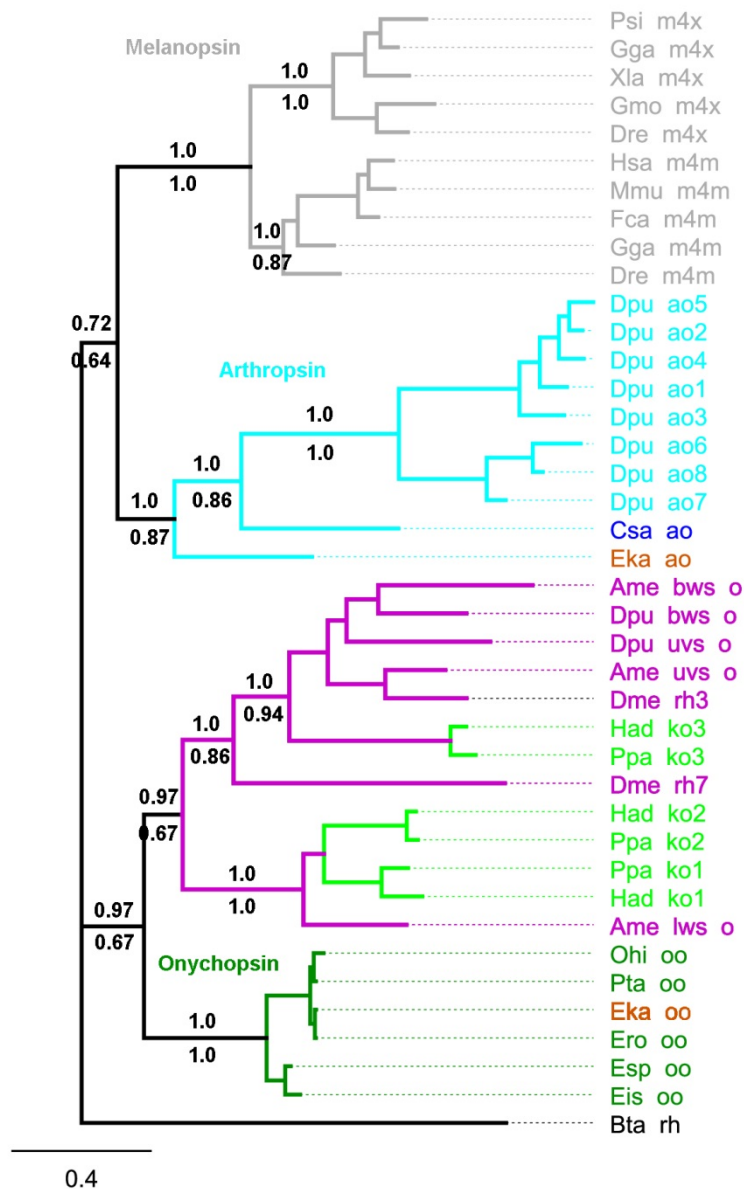




Additional figure S1 Phylogenetic reconstruction of c r-opsins. The tree is from Bayesian likelihood analysis using MrBayes with a WAG distribution model of amino acid substitutions, half compatibility consensus from 1,100,000 replicates. The numbers above the branches are posterior probabilities from Bayesian analysis and the number below branches are bootstrap support from a maximum likelihood analysis with PhyML with 100 replicates. Opsin sequences were aligned with clustalW and regions outside of the 7 transmembrane domains were excluded. Bta rh (*Bos taurus*) rhodopsin was used as an outgroup. *C. saiei* and *E. kanangrensis* protein names are coloured blue and brown respectively. Scale bar show substitutions per site. Species included in the analysis are a subset of the species used in figure 1. See figure 1 for abbreviations.