



Figure S12. Opson gene tree. Maximum likelihood tree inferred from a data set of opson 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; SH-aLRT/abayes support values shown below branches. Scale bar represents number of substitutions per site.