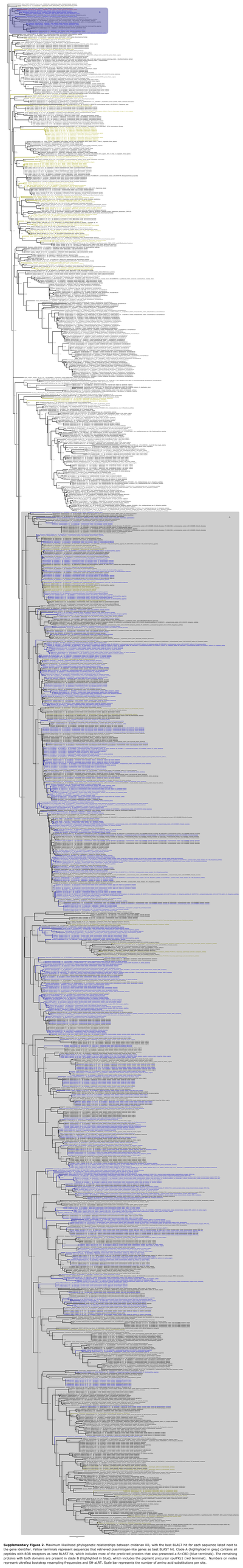

Supplementary Figure 2. Maximum likelihood phylogenetic relationships between cnidarian KR, with the best BLAST hit for each sequence listed next to the gene identifier. Yellow terminals represent sequences that retrieved plasminogen-like genes as best BLAST hit. Clade A (highlighted in grey) contains all peptides with ROR receptors as best BLAST hit, which includes most of the predicted proteins that also presented a Fz-CRD (Fzd terminal). The remaining proteins with both domains are present in clade B (highlighted in blue), which includes the pigment precursor cipsRPx1 (red terminal). Numbers on nodes represent ultrafast bootstrap resampling frequencies and SH-aLRT. Scale bar represents the number of amino acid substitutions per site.