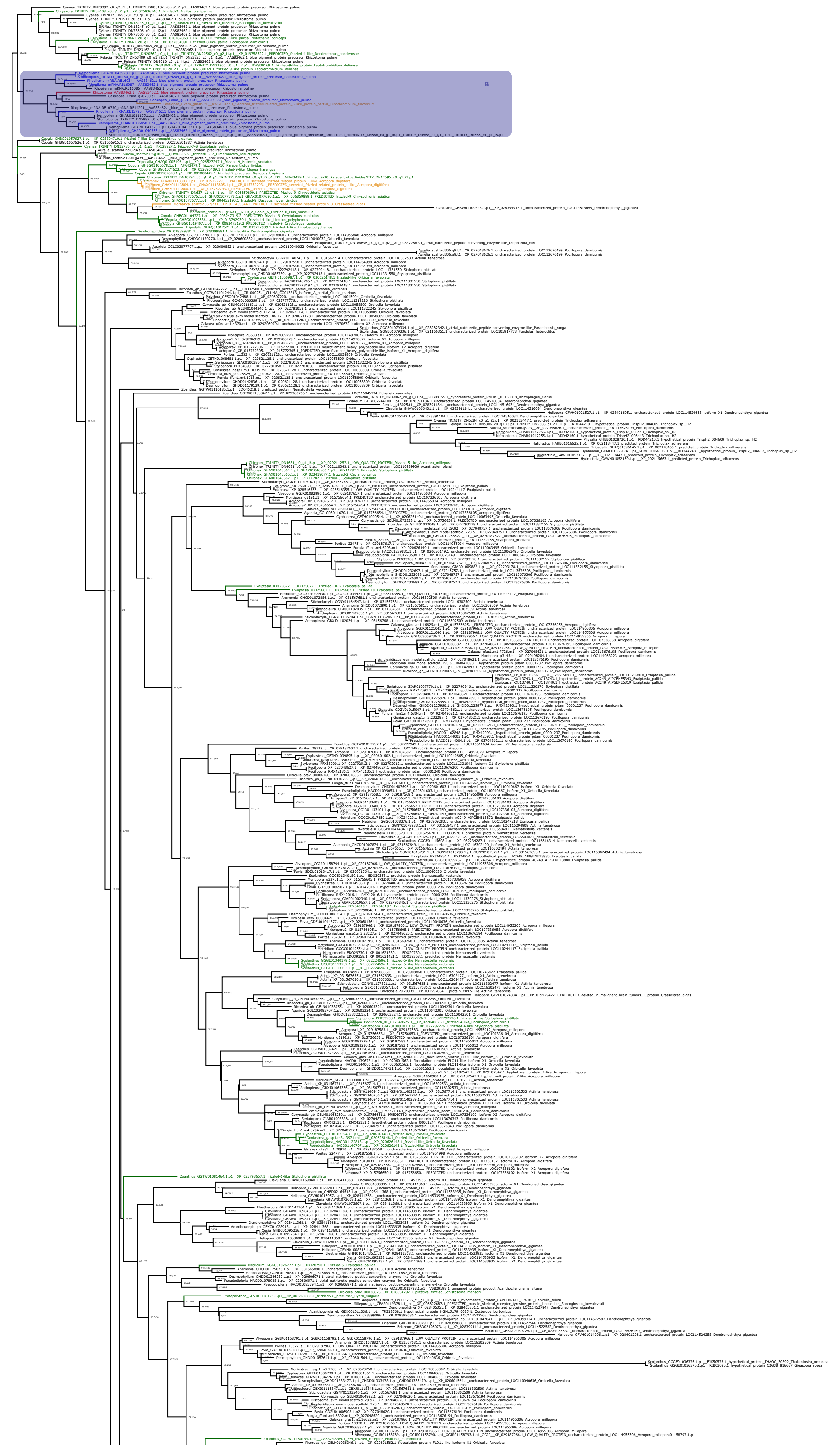

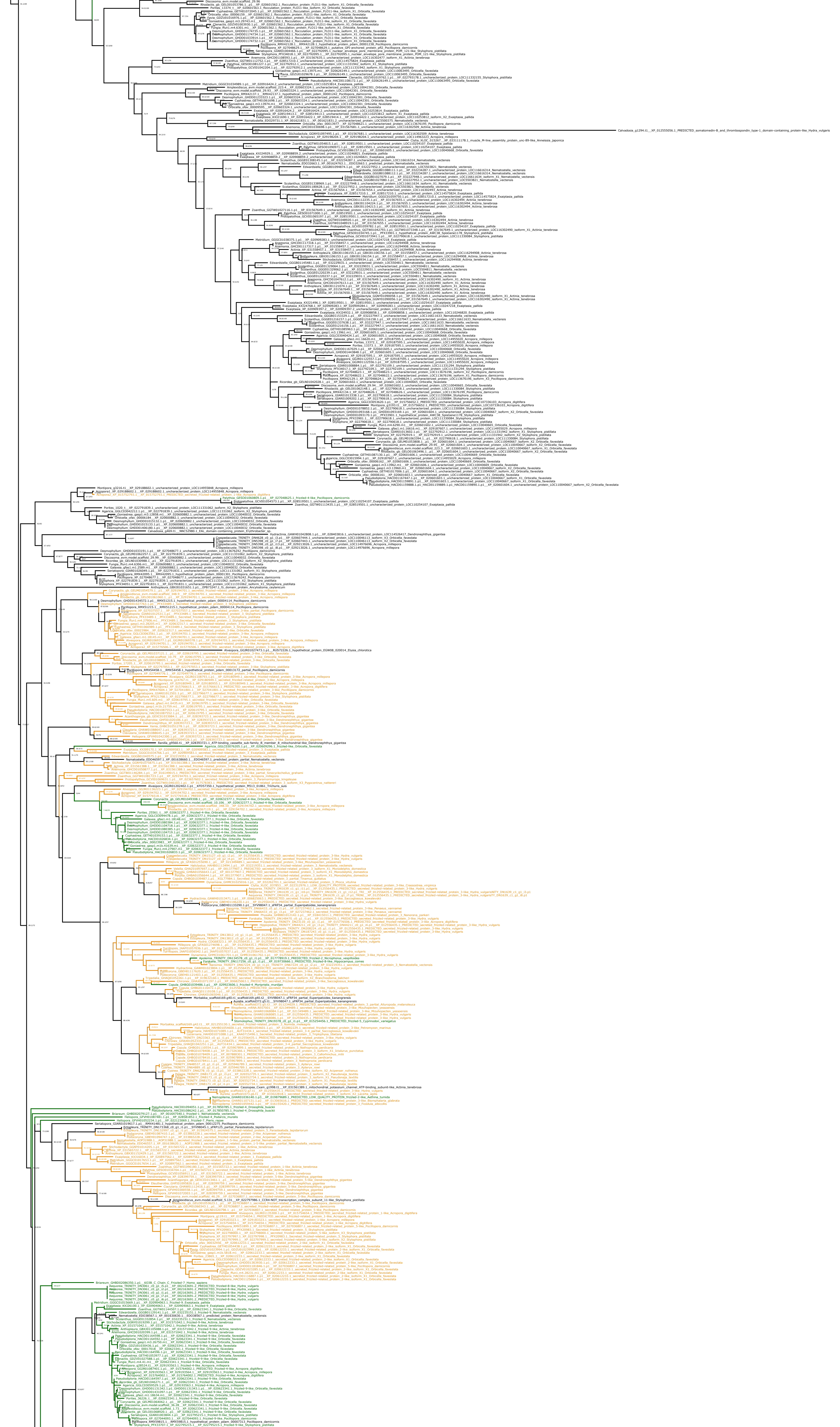

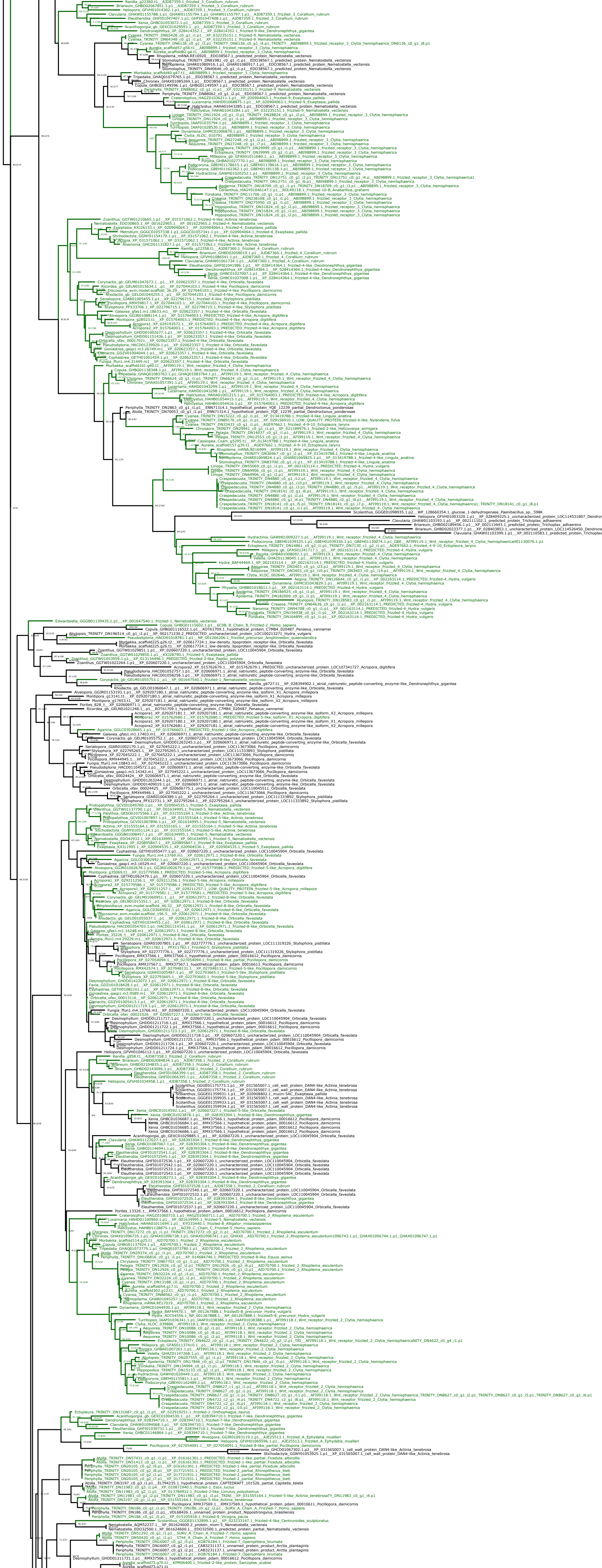

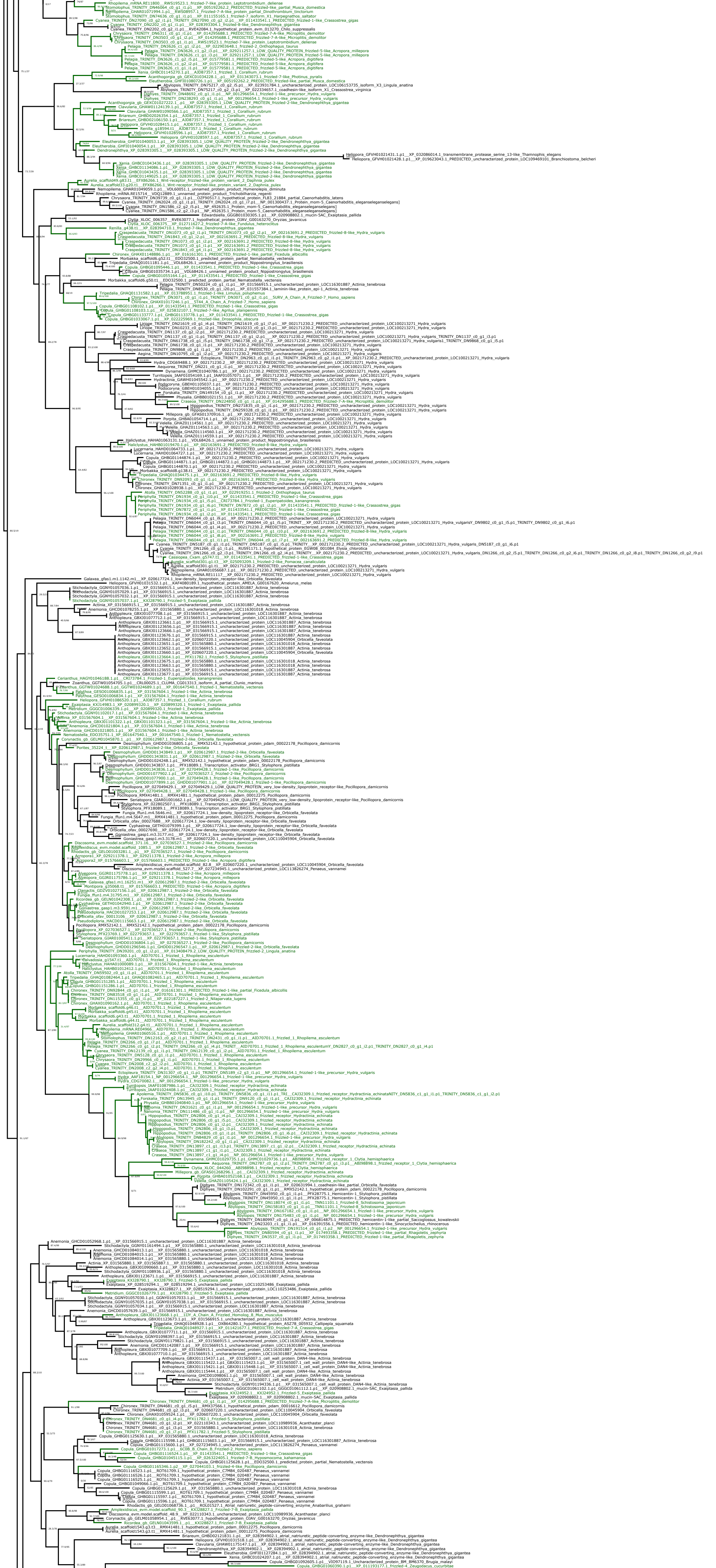

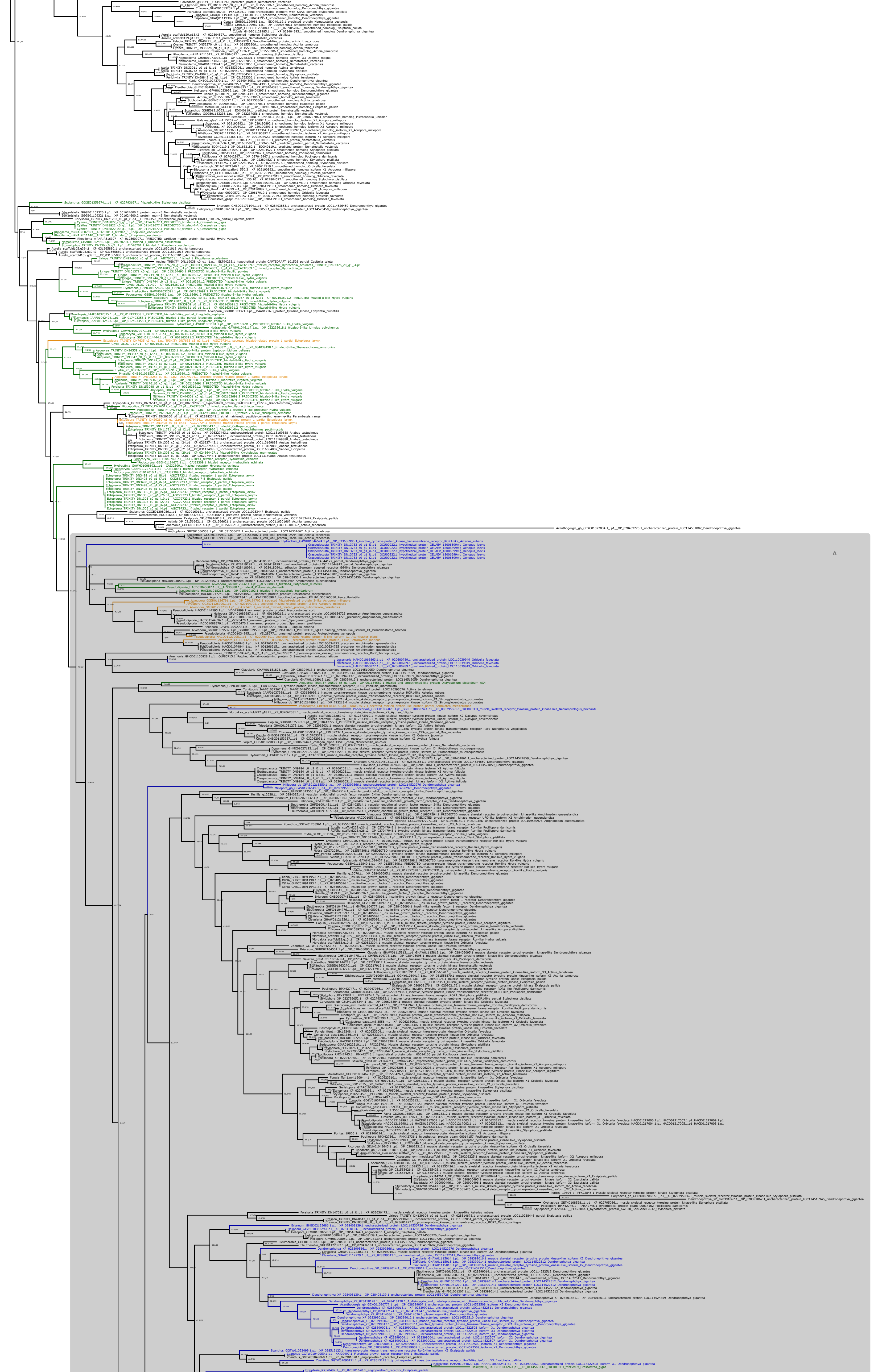

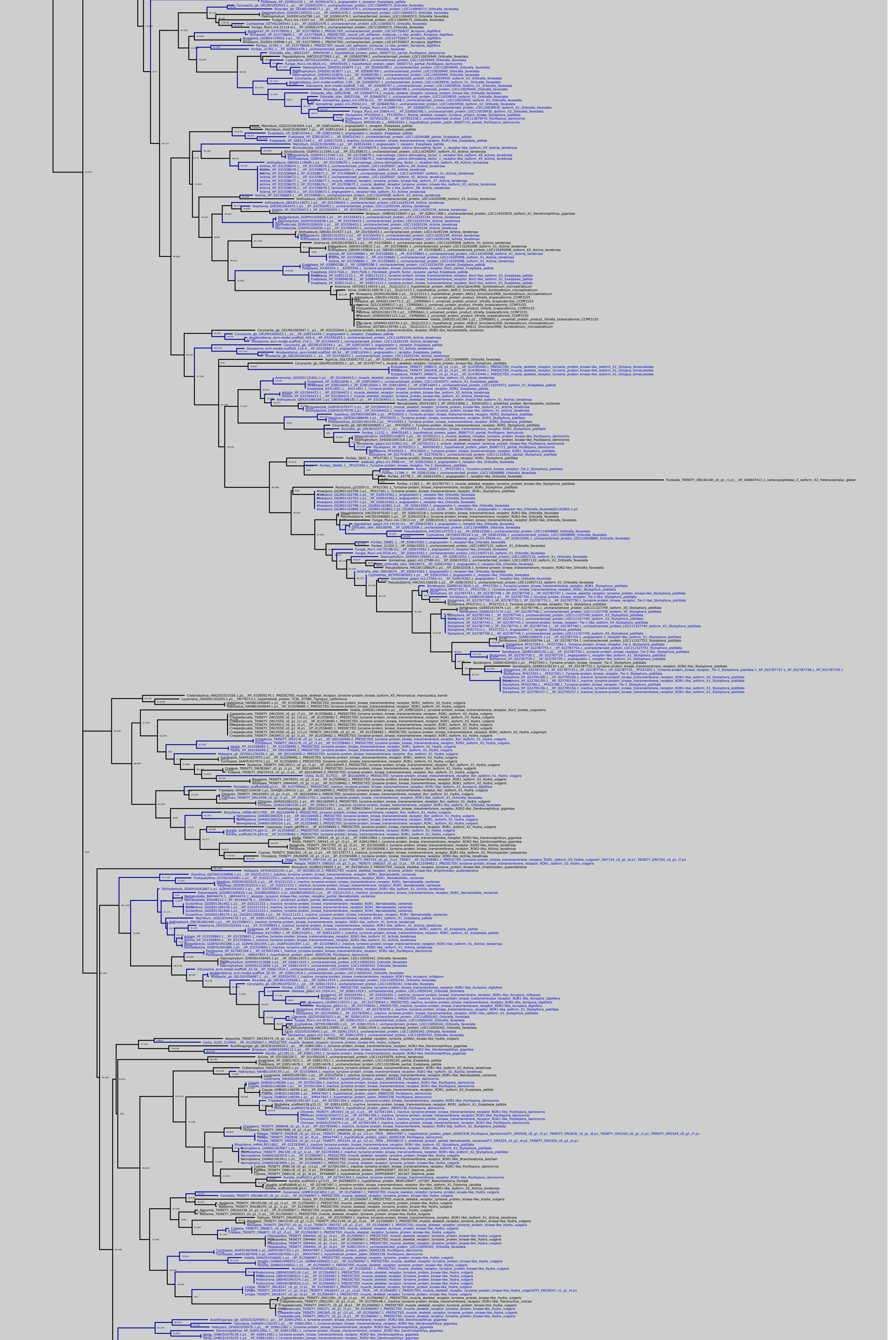

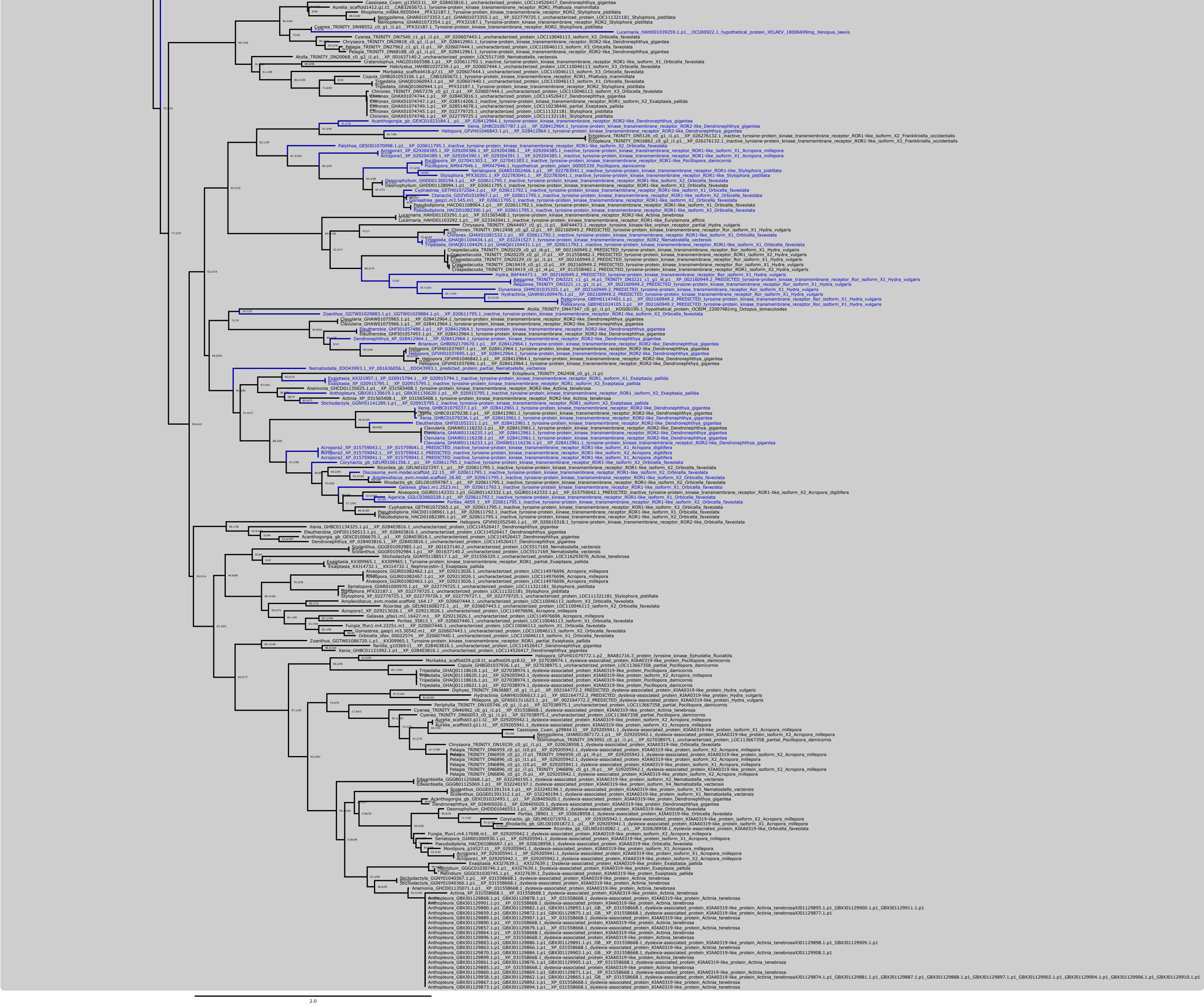

Supplementary Figure 1. Maximum likelihood phylogenetic relationships between cnidarian Fz-CRD, with the best BLAST hit for each sequence listed next to the gene identifier. Green and orange terminals represent sequences that retrieved Fz-like genes or SFRP-like genes (respectively) as best BLAST hit. 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 KR domain (blue terminals). The remaining proteins with both domains are present in clade B (highlighted in blue), which includes the pigment precursor rpulFKz1 (red terminal). Numbers on nodes represent ultrafast bootstrap resampling frequencies and SH-aLRT. Scale bar represents the number of amino acid substitutions per site.