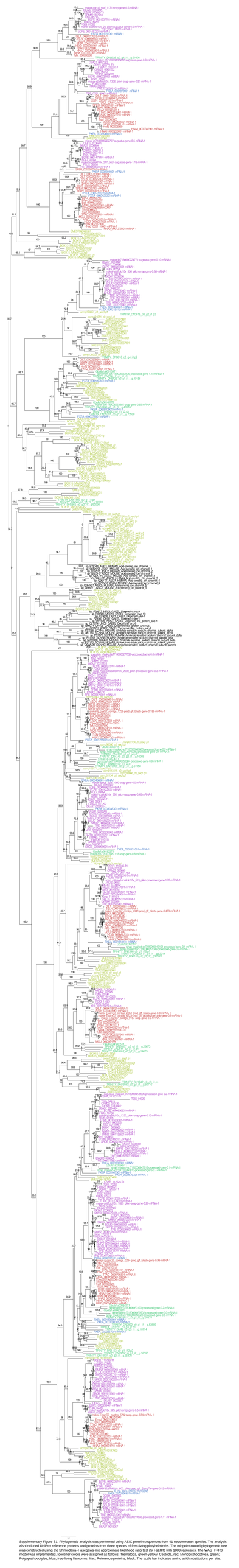
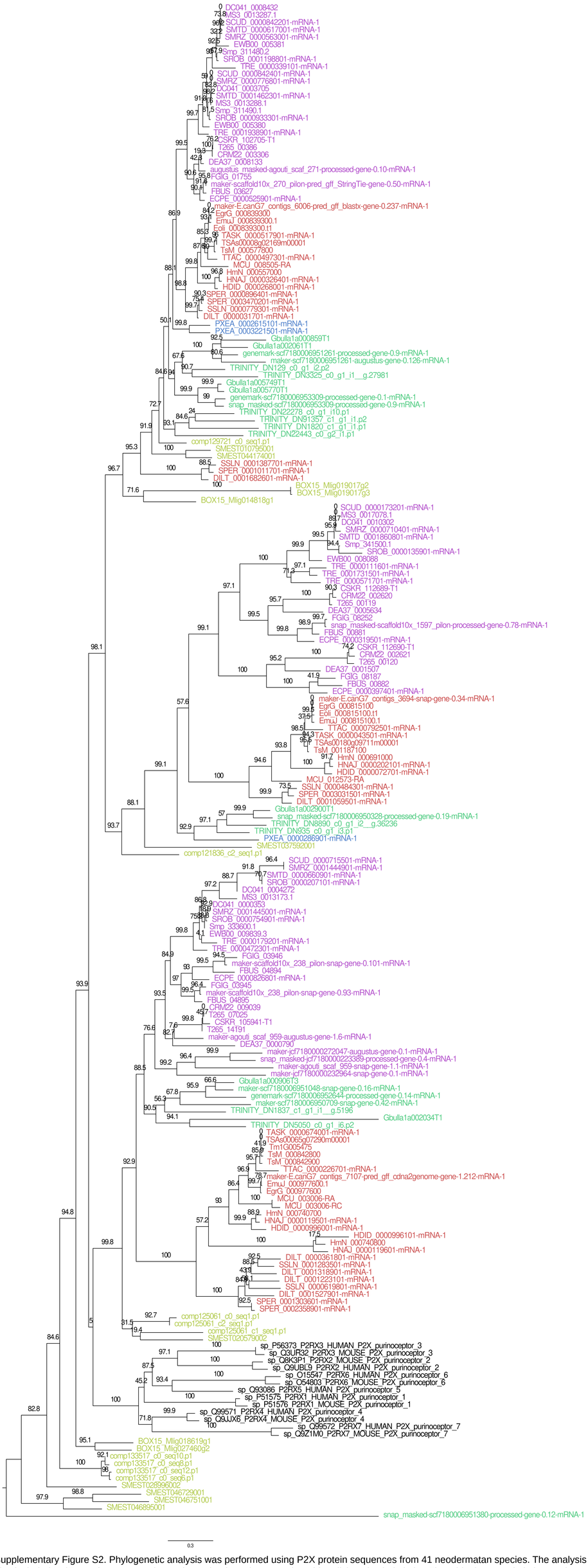
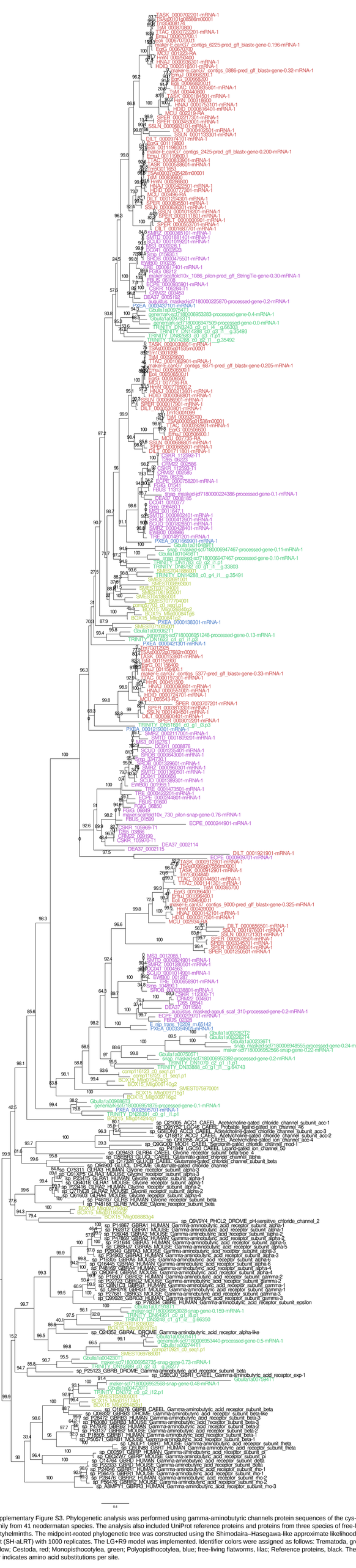


Supplementary Figure S1. Phylogenetic analysis was performed using ASIC protein sequences from 41 neodermatan species. The analysis also included UniProt reference proteins and proteins from three species of free-living platyhelminths. The midpoint-rooted phylogenetic tree was constructed using the Shimodaira-Hasegawa-like approximate likelihood ratio test (SH-aLRT) with 1000 replicates. The WAG+F+R8 model was implemented. Identifier colors were assigned as follows: Trematoda, green-yellow; Cestoda, red; Monopisthocotylea, green; Polyopisthocotylea, blue; free-living flatworms, lilac. Reference proteins, black. The scale bar indicates amino acid substitutions per site.



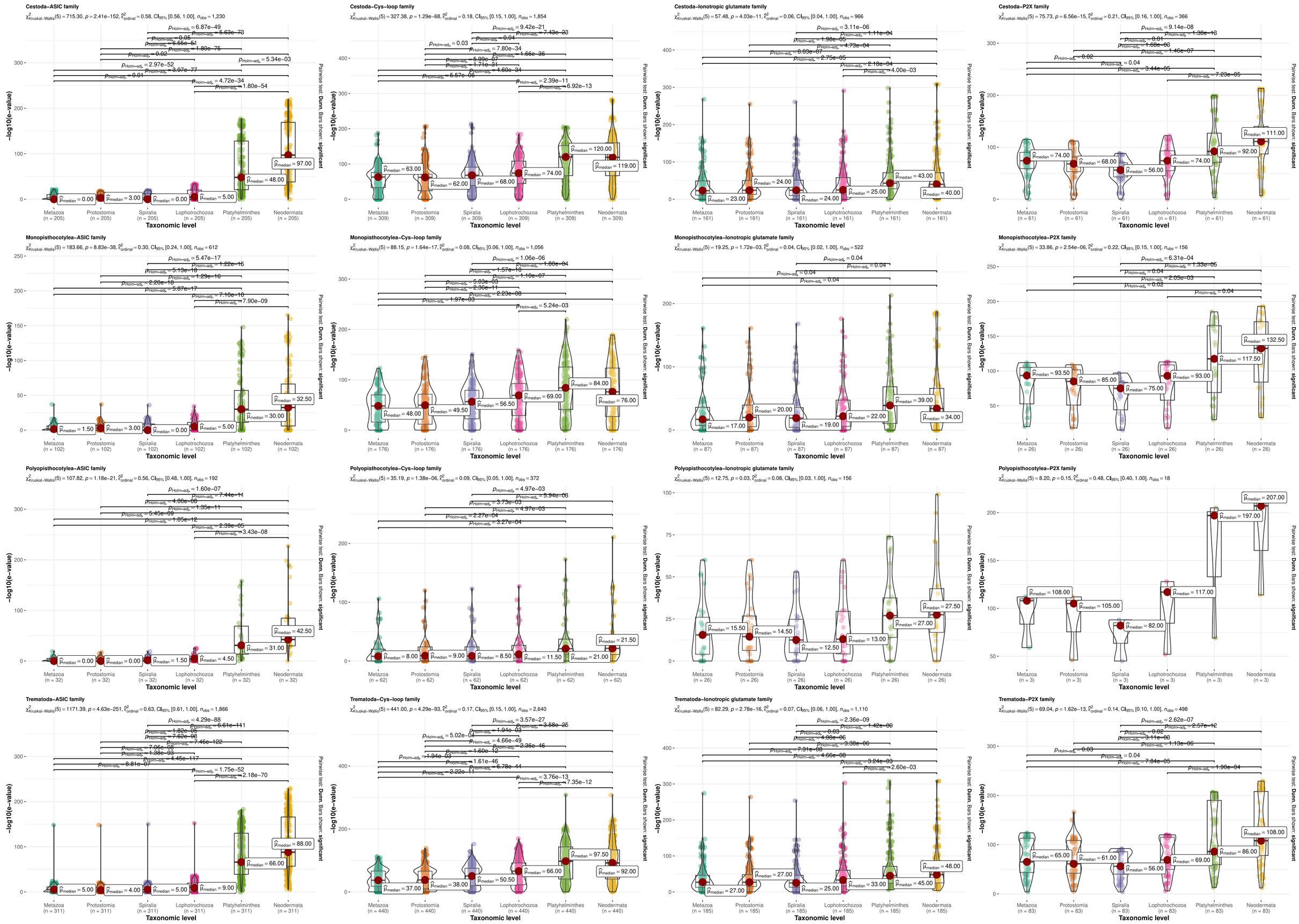
Supplementary Figure S2. Phylogenetic analysis was performed using P2X protein sequences from 41 neodermatan species. The analysis also included UniProt reference proteins and proteins from three species of free-living platyhelminths. The midpoint-rooted phylogenetic tree was constructed using the Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) with 1000 replicates. The WAG+F+R7 model was implemented. Identifier colors were assigned as follows: Trematoda, green-yellow; Cestoda, red; Monopisthocotylea, green; Polyopisthocotylea, blue; free-living flatworms, lilac; Reference proteins, black. The scale bar indicates amino acid substitutions per site.



Supplementary Figure S3. Phylogenetic analysis was performed using gamma-aminobutyric channels protein sequences of the cys-loop family from 41 neodermatan species. The analysis also included UniProt reference proteins and proteins from three species of free-living platyhelminths. The midpoint-rooted phylogenetic tree was constructed using the Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) with 1000 replicates. The LG+R9 model was implemented. Identifier colors were assigned as follows: Trematoda, green-yellow; Cestoda, red; Monopisthocotylea, green; Polyopisthocotylea, blue; free-living flatworms, lilac; Reference proteins, black. The scale bar indicates amino acid substitutions per site.

Supplementary Figure S4. Phylogenetic analysis was performed using acetylcholine channels protein sequences of the cys-loop family from Ctenophora, Cnidaria, Porifera, Placozoa, Mesozoa, Orthonectida, Rhombozoa, Platyhelminthes, Annelida, Mollusca, Nematoda, Nematomorpha, Tardigrada, Onychophora, Arthropoda, Chaetognatha, Hemichordata, Echinodermata, Urochordata, Cephalochordata, Vertebrata. The midpoint rooted phylogenetic tree was constructed using the Maximum Likelihood method implemented in the Jtreeprime-like approximate likelihood ratio test (SH-aLRT) with 1000 replicates. The LG+G4 model was implemented. Identifier colors were assigned as follows: Trematoda, green-yellow; Cestoda, red; Monogenea/Aspidogastrea, green; Polypodiozoa/Myxozoa, blue; free-living flatworms, lilac; Reference proteins, black. The scale bar indicates amino acid substitutions per site.

Supplementary Figure S5. Phylogenetic analysis was performed using iGluR protein sequences from 41 neodermatan species. The analysis also included UniProt reference proteins and proteins from three species of free-living platyhelminths. The midpoint-rooted phylogenetic tree was constructed using the Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) with 1000 replicates. The LG+R6 model was implemented. Identifier colors were assigned as follows: Turquoise, green-yellow; Cyan, dark-blue; Monogenophoridea, green; Polyopisthocotylea, blue; free-living flatworms, lilac; Reference proteins, black. The scale bar indicates amino acid substitutions per site.



Supplementary Figure S6. Box-and-violin plots showing the distribution of e-values of Neodermata LGICs found in pairwise sequence alignments against LGICs from different taxa. Box elements show the median and the upper and lower quartiles. Red dots display the median. The Kruskal-Wallis statistic and the corresponding p-values are shown. P-values obtained from the post-hoc Dunn test were corrected using the Holm method for pairwise comparisons. Bars show significant comparisons (p-values < 0.05).