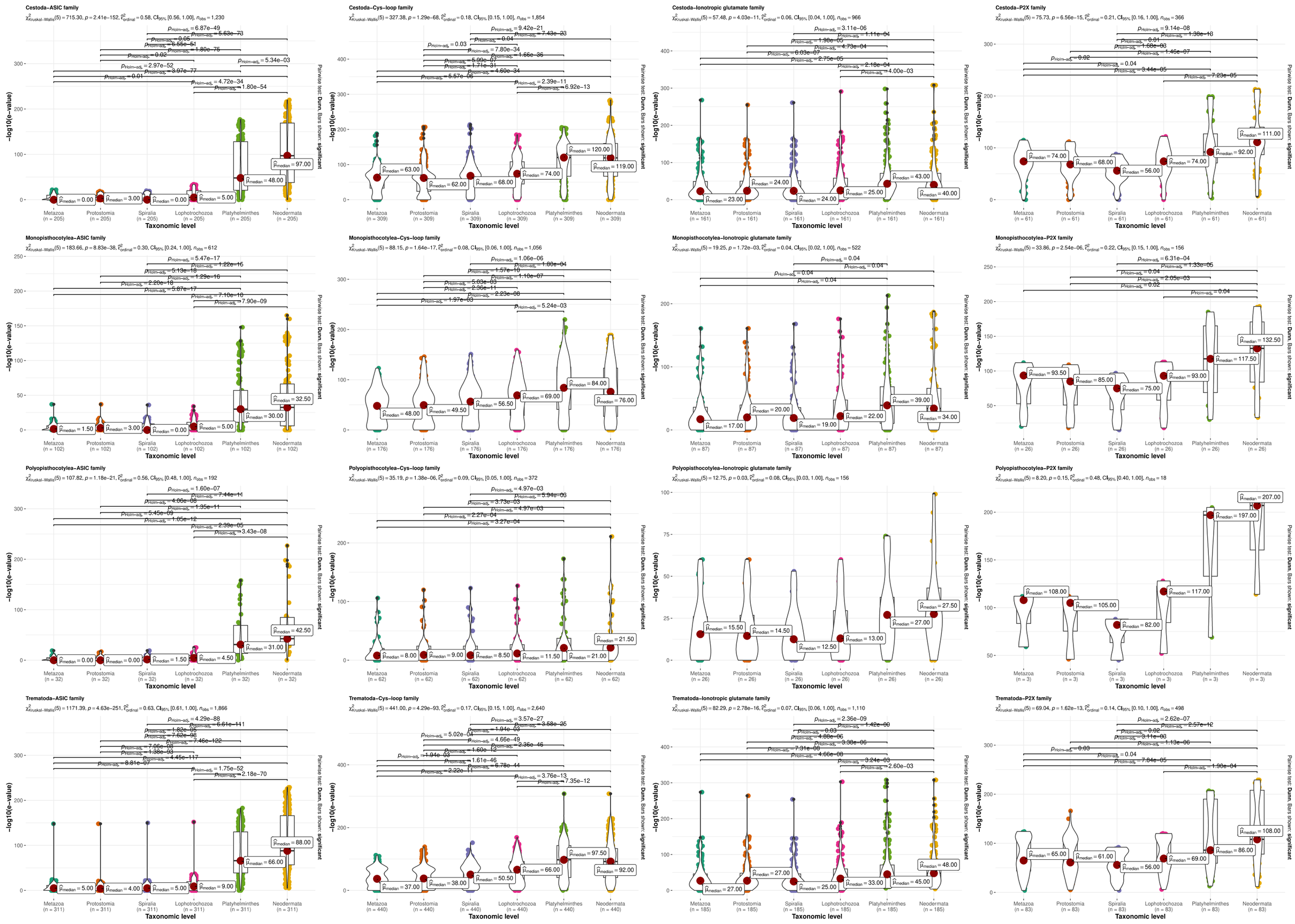
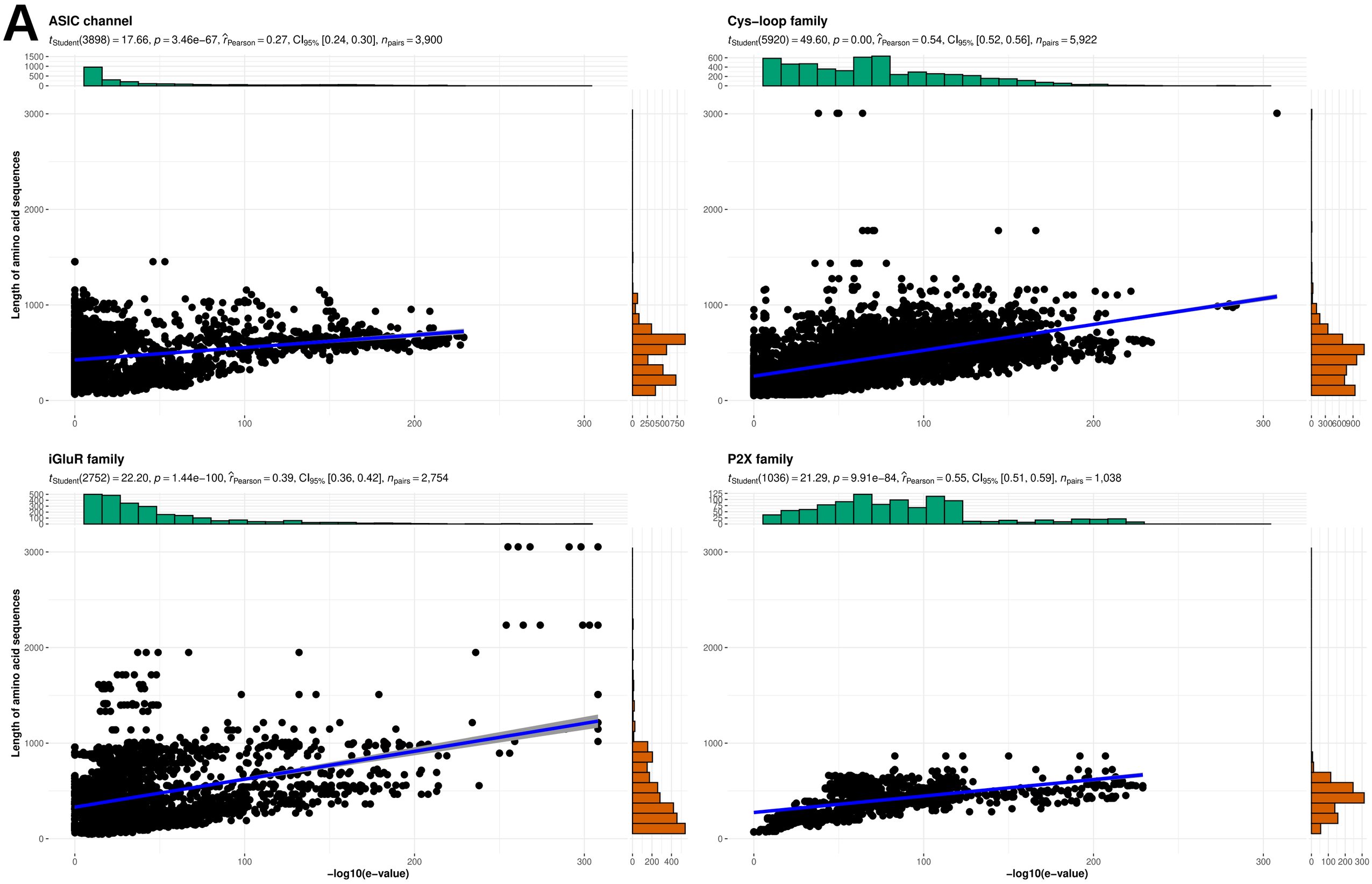
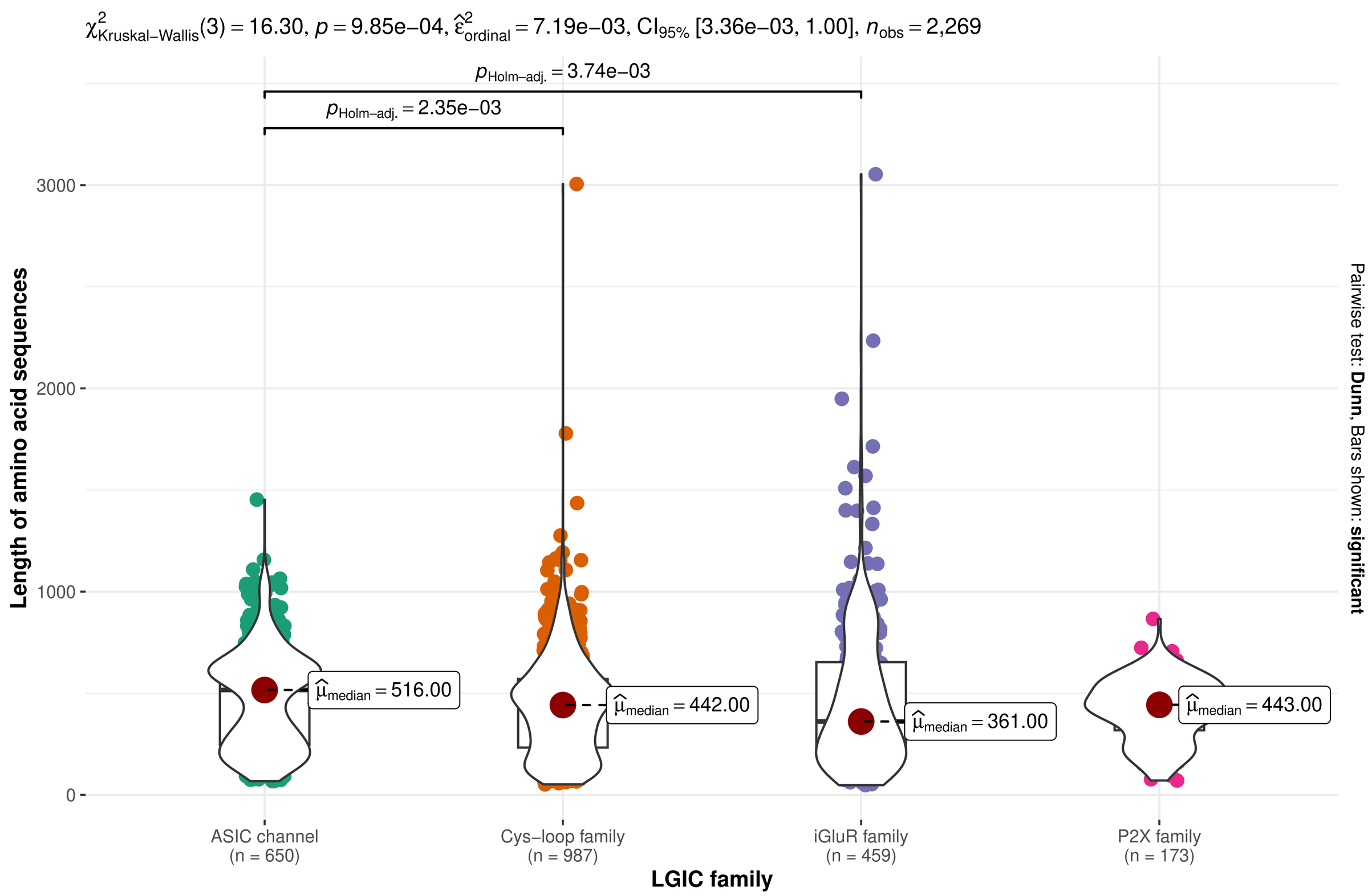
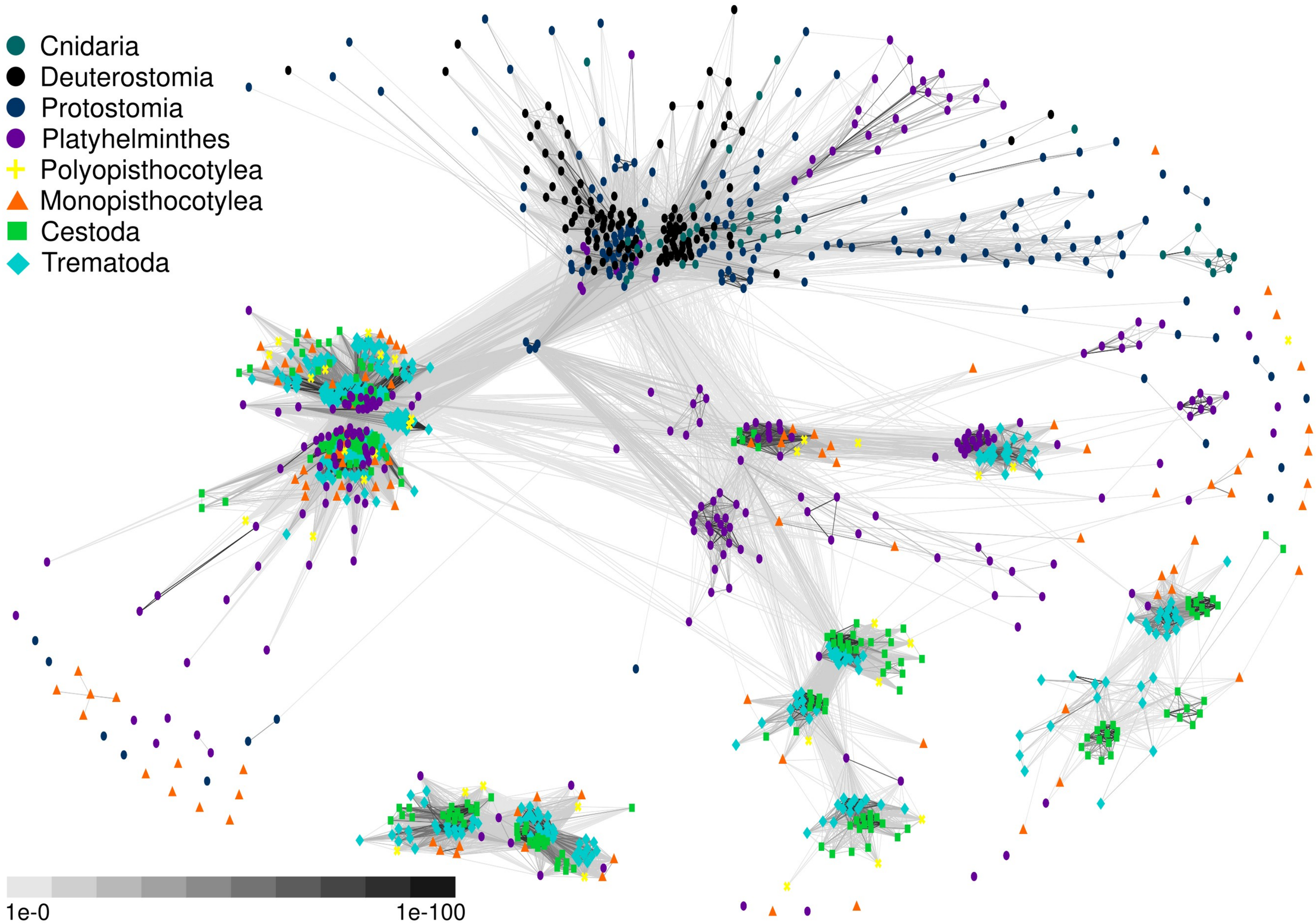


Supplementary Figure S1. Box-and-violin plots showing the distribution of e-values of Neodermata LGICs found in pairwise sequence alignments against LGICs from different taxa. Box elements show the median and the upper and lower quartiles. Red dots display the median. The Kruskal-Wallis statistic and 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).

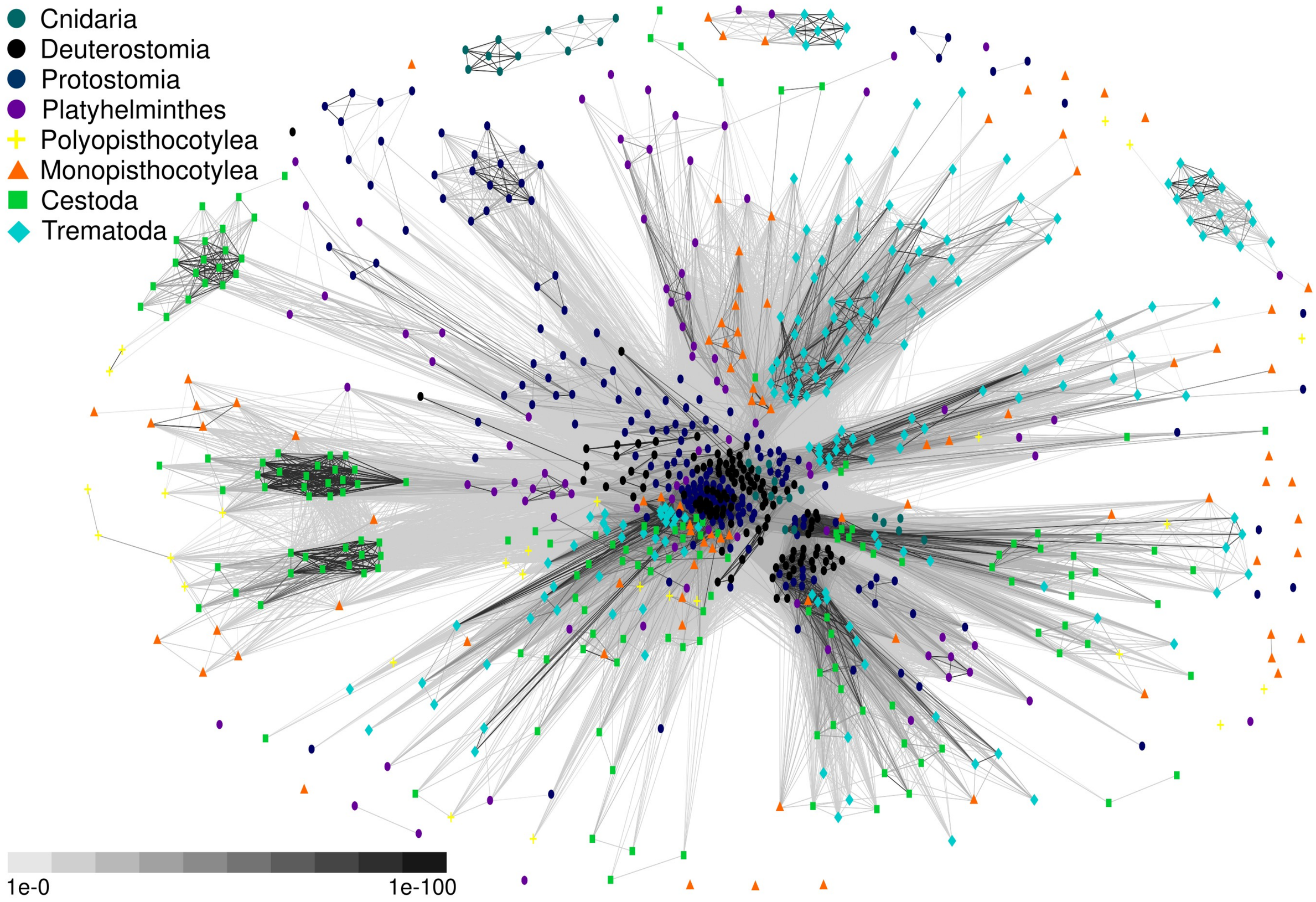




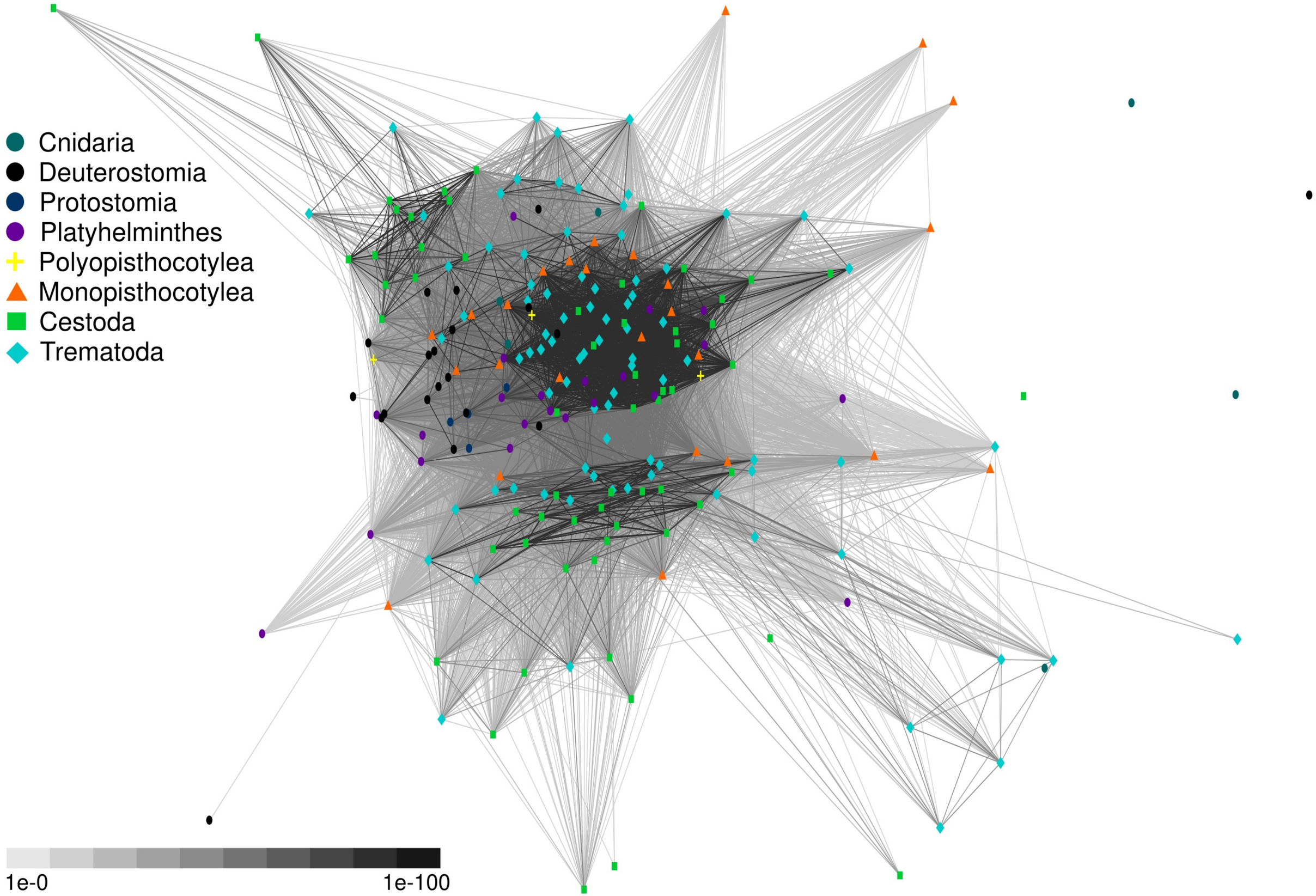
Supplementary Figure S2. A) Correlation analysis between sequence length and -log10(e-value) using the Pearson correlation coefficient. The proteins from the ASIC and iGluR families showed a weak correlation, while proteins from the P2X and cys-loop families exhibit a moderate correlatio. B) Comparative analysis of sequence lengths among LGIC families. Box-and-violin plots show the distribution of sequence lengths of each LGIC family of Neodermata. 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. Adjusted p-values < 0.05 were considered significant.



Supplementary Figure S3. Nodes correspond to individual channel sequences corresponding to ASIC family and are colored by taxon as indicated by the legend. Edges correspond to BLAST connections with p-values < 1e-15.



Supplementary Figure S4. Nodes correspond to individual channel sequences corresponding to the iGluR family and are colored by taxon as indicated by the legend. Edges correspond to BLAST connections with p-values < 1e-20.



Supplementary Figure S5. Nodes correspond to individual channel sequences corresponding to the P2X family and are colored by taxon as indicated by the legend. Edges correspond to BLAST connections with p-values < 1e-30.

Taxon (ID in the tree)
Platyhelminthes
Lophotrochozoa
Protostomia
Ecdysozoa
Deuterostomia
Chordata
Cephalochordata
Tunicata
Vertebrata
Cyclostomata
Gnathostomata
Chondrichthyes
Osteichthyes
Actinopterygii
Sarcopterygii
Tetrapoda
Amphibia
Reptilia
Aves
Mammalia
Eutheria
Primates
Homo sapiens (Human, human)
Pan paniscus (Bonobo, Pygmy chimpanzee)
Pan troglodytes (Chimpanzee, Common chimpanzee)
Gorilla gorilla (Western lowland gorilla, Gorilla)
Pongo abelii (Sumatran orangutan, Orangutan)
Pongo pygmaeus (Bornean orangutan, Orangutan)
Hylobates (Gibbons, Lesser apes)
Nomascus (Crested gibbons)
Macaca (Macaques, Macaques)
Papio (Baboons, Baboons)
Chlorocebus (Green monkeys, Vervets)
Rhinopithecus (Snub-nosed monkeys, Snub-nosed monkeys)
Colobus (Colobus, Colobus)
Pan (Chimpanzees, Chimpanzees)
Gorilla (Gorillas, Gorillas)
Pongo (Orangutans, Orangutans)
Hylobates (Gibbons, Gibbons)
Nomascus (Crested gibbons,

Taxon (ID in the tree)
Cestoda (Cestoda)
Trematoda
Echinococcus granulosus (Cestoda, Echinococcus)
Fasciola hepatica (Trematoda, Fasciolidae)
Schistosoma japonicum (Trematoda, Schistosomatidae)
Echinostoma (Trematoda, Echinostomatidae)
Platyhelminthes
Lophotrochozoa
Lophotrochozoa sensu Pla. (Protostomia, Lop*)
Platyhelminthes sensu Nematodoxoa (Bilateria, Platy*)
Platyhelminthes
Neodermata
Cestoda (Neodermata, Cestoda*)
Trematoda (Neodermata, Trematoda*)
Monogenea (Neodermata, Monogenea*)
Schistosoma mansoni Cys. (Trematoda*, Schistosomatidae

A
B
C
Taxon (ID in the tree)
Cnidaria (Cnidaria_7)
Chordata (Ciona_Ciona_robusta)
Protostomia
Lophotrochozoa
Ecdysozoa (Pteros_ecdy)
Deuterostomia
Ambulacraria (Ambulacraria_1)
Echinodermata (Strongylo_purpu)
Chordata (Ciona_Ciona_robusta)
Vertebrata (Homo_sapiens)
Neuronal
Non-neuronal
GABA_alpha_gamma_Anth_Cnid_Cryp
GABA_alpha_gamma_Ecdy_Eco_Pep_Nem
GABA_alpha_delta
GABA_Cat
GABA_Inv_Mol_Ann
GABA_beta_delta_Chor
GABA_alpha_delta_Cryp_Cnid
GABA_Vert
GABA_Inv_Ecdy
GABA_Inv_Lo
Glycine_receptor_like_Ecdy
Glycine_receptor_like
Glycine_receptor_like_Cnid
Glycine_receptor_like_Lo
Cys-loop_Cryp
Anionic_ACC_channel_Cele
Monoamine-gated_channels_Cnid
GRC_Cele
Cys-loop_Cnid
Cys-loop_Lo
Cys-loop_Ecdy
Cys-loop_Vert
GluCl_Ecdy_Nem (Ecdy_Nem_Pep_Vert)
GluCl_Lo
Nematode_Strongy_Ostertagia0007071
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-1
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-2
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-3
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-4
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-5
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-6
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-7
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-8
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-9
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-10
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-11
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Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-15
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Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-18
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-19
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-20
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-21
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-22
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-23
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-24
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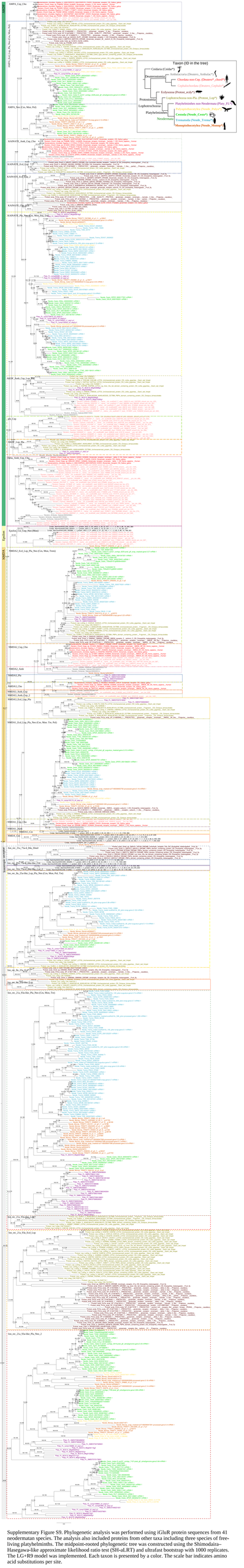
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-26
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-27
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-28
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-29
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-30
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-31
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-32
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-33
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-34
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-35
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-36
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-37
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-38
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-39
Nematode_Caenorhabditis_elegans_protein-of-unknown-function-DUF3646-2-mRNA-40


Taxon (ID in the tree)
Ciliata (Ciliate*)
Deuterostoma
Bilateria (Deuteros_Ambulac*)
Chordata non-Cep. (Deuteros_chord*)
Cephalochordata (Deuteros_Cephala*)
Ecdysozoa (Protost_ecdy*)
Protostomia
Lophotrochozoa non-Pla. (Protost_Lopho*)
Platyhelminthes non-Neodermata (Platy_Non*)
Lophotrochozoa
Platyhelminthes
Parapolyscelis/Acoela (Neode_Para*)
Cestoda (Neode_Cesto*)
Trematoda (Neode_Trema*)
Neodermata
Monopisthocotyla (Neode_Mono*)
AMPA_Cep_Chu
AMPA_Ecd_Lop_Pla_Neo (Ecs, Mon, Pol)
AMPA_Neo (Ecs, Mon, Pol)
KAINATE_Arth_Cep_Chu
KAINATE_Ecd_Lop
KAINATE_Pla
KAINATE_Pla_Neo(Ecs, Mon, Pol)
KAINATE_Pla_Neo(Ecs, Mon, Trem)
AKAP_Arth_Cep_Lop_Pla
Chu_Cep
AMPA_Lop_Pla
Hom_Arth_Cep_Chu
Epithelial
NMDA1
Epithelial_Lop_Neo(Mon)
NMDA1_Ecd_Lop_Pla_Neo (Ecs, Mon, Trem)
NMDA1_Cep_Chu
NMDA1_Arth
NMDA1_Pla
NMDA1_Arth_Ecd
NMDA1_Arth_Cep_J
NMDA1_Ecd_Lop_Pla
NMDA1_Ecd_Lop_Pla_Neo (Ecs, Mon, Trem, Pol)
NMDA1_Chu
NMDA1_Arth_Cep
NMDA1_Arth_Ecd
NMDA1_Cep
NMDA1_Cep_J
Ion_tra_Cep_Chu_Ecd_Pla_Hom
Ion_tra_Ecd_Lop_Pla_Neo (Ecs, Mon, Pol, Trem)
Ion_tra_Cep_Chu_Ecd_Lop
Ion_tra_Ecd_Lop_Pla_Neo (Ecs, Mon, Trem)
Ion_tra_Cep_Chu_Ecd_Lop
Ion_tra_Ecd_Lop_Pla_Neo (Ecs, Mon, Pol)
Ion_tra_Ecd_Lop_Pla_Neo (Ecs, Mon, Trem)
Ion_tra_Ecd_Lop_Pla_Neo (Ecs, Mon, Pol, Trem)
Ion_tra_Ecd_Lop_Pla_Neo (Ecs, Mon, Trem)
Ion_tra_Ecd_Lop_Pla_Neo (Ecs, Mon, Pol

Supplementary Figure S10. Phylogenetic analysis was performed using P2X protein sequences from 41 neodermatan species. The analysis also included proteins from other taxa including three species of free-living platyhelminths. The midpoint-rooted phylogenetic tree was constructed using the Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) and ultrafast bootstrap with 1000 replicates. The WAG+F+R7 model was implemented. Each taxon is presented by a color. The scale bar indicates amino acid substitutions per site.