

Figure 1

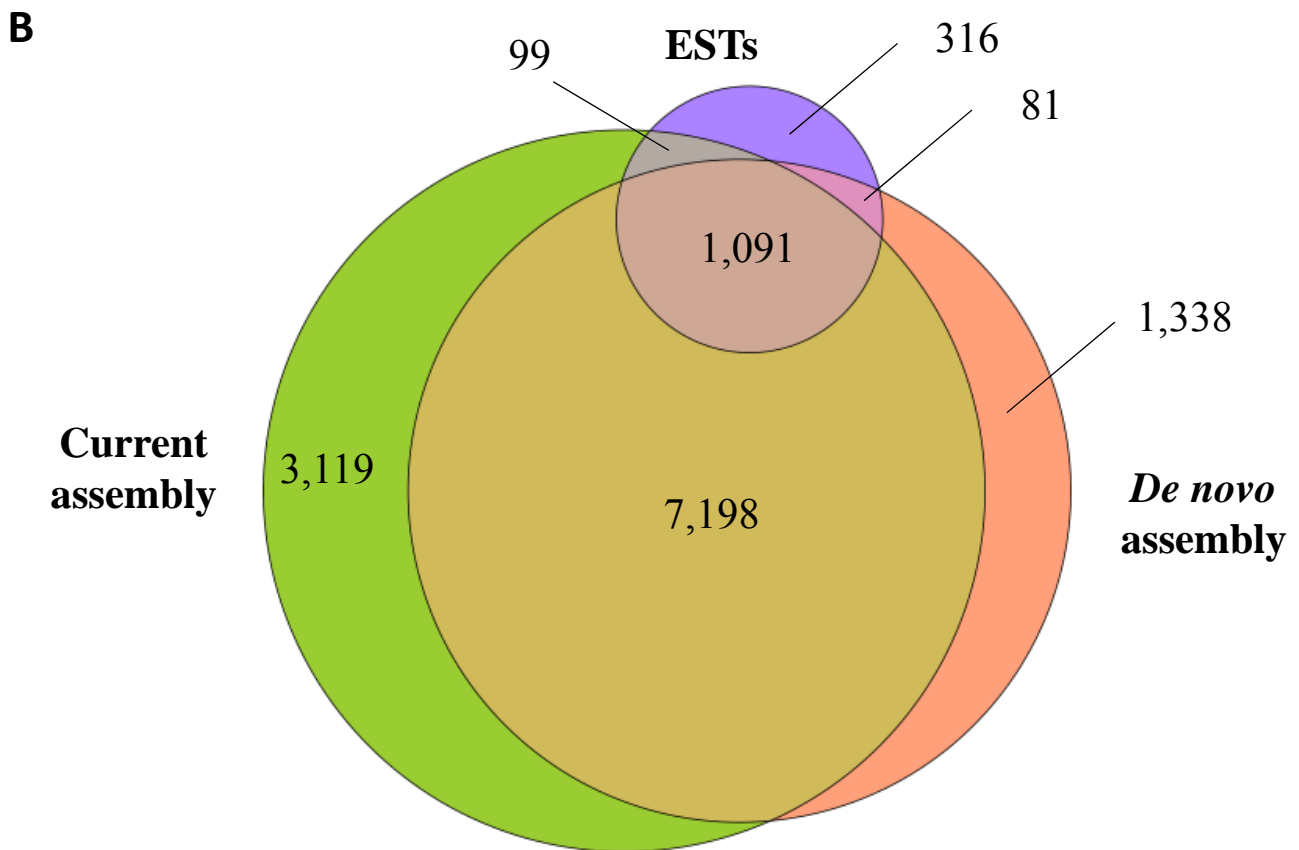
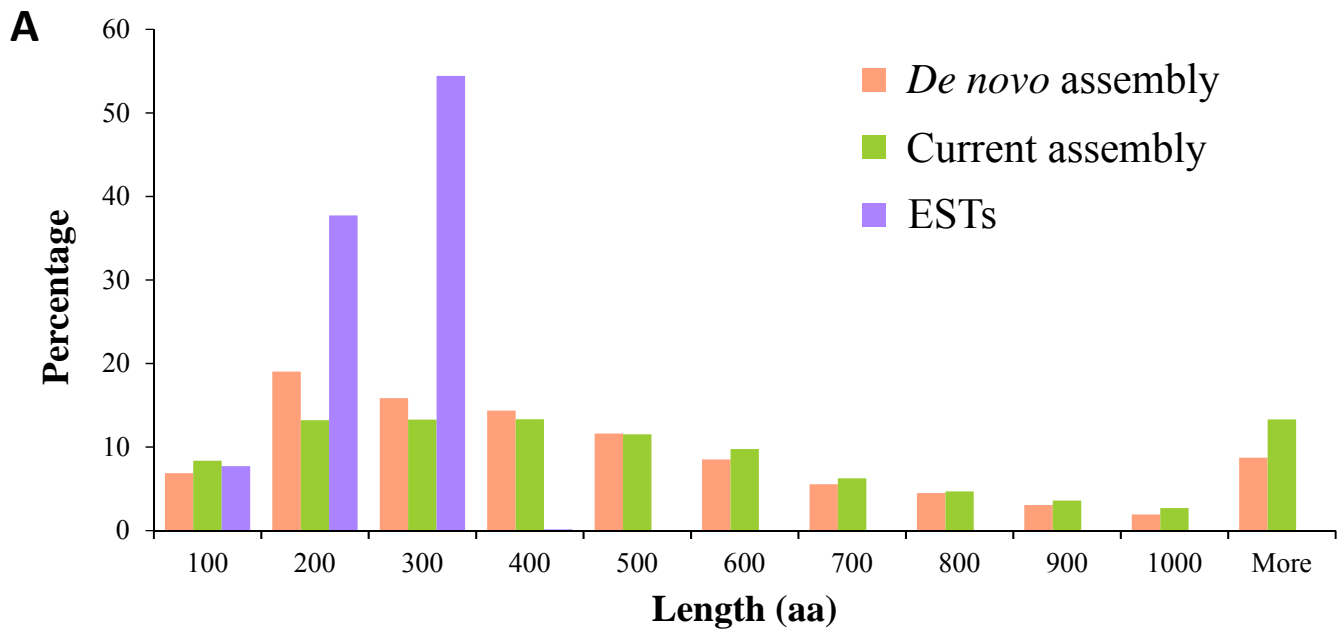


Figure 2

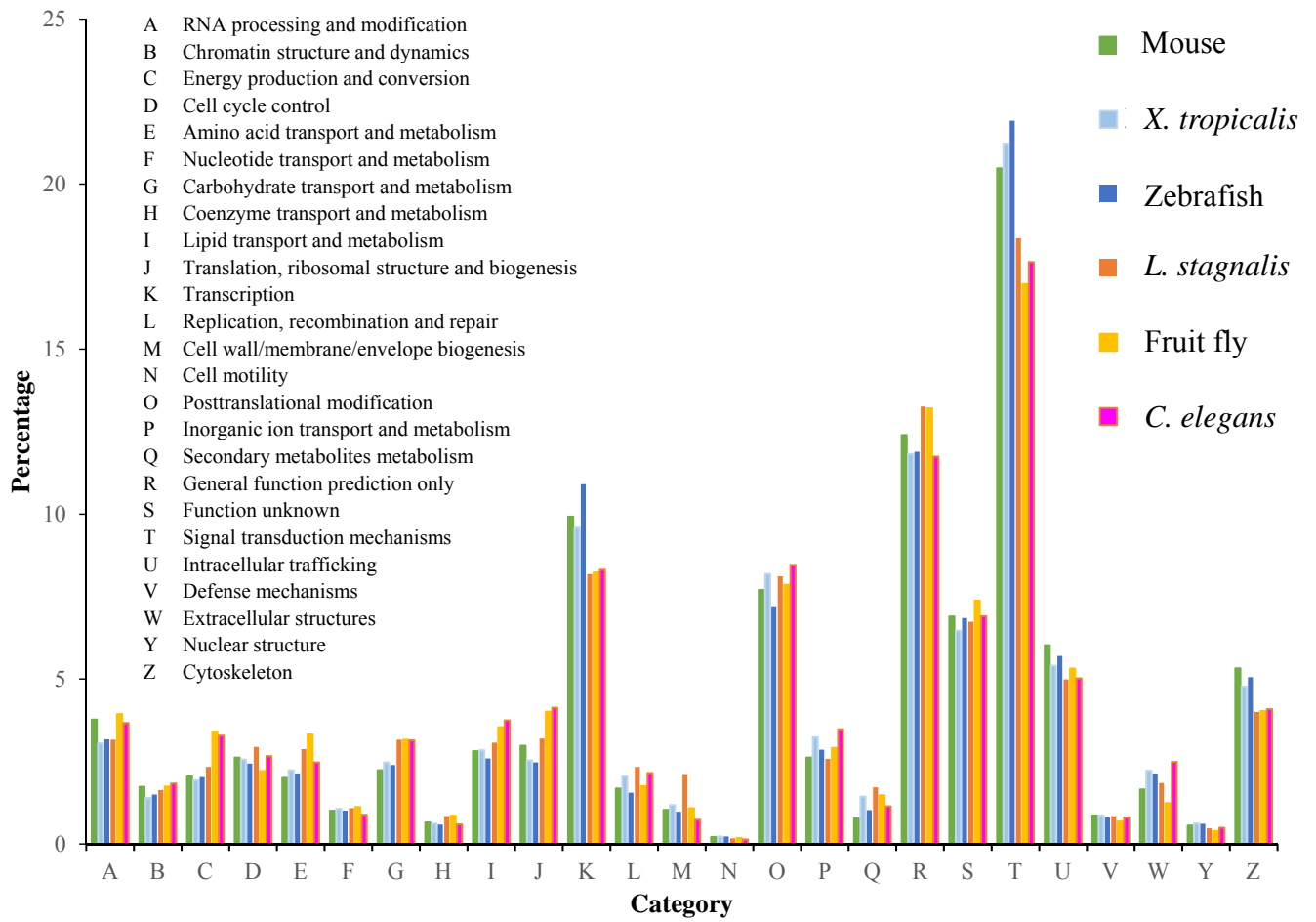


Figure 3

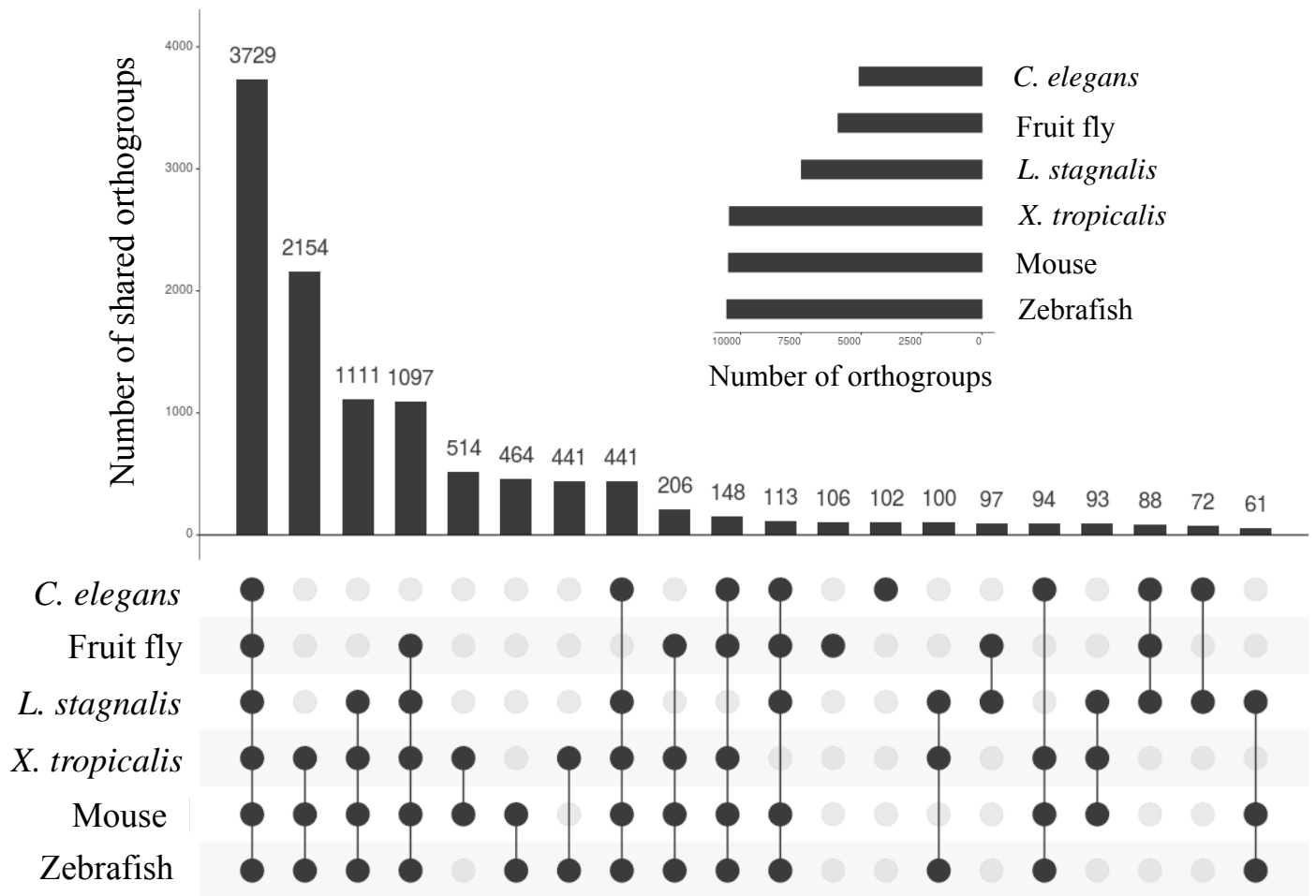
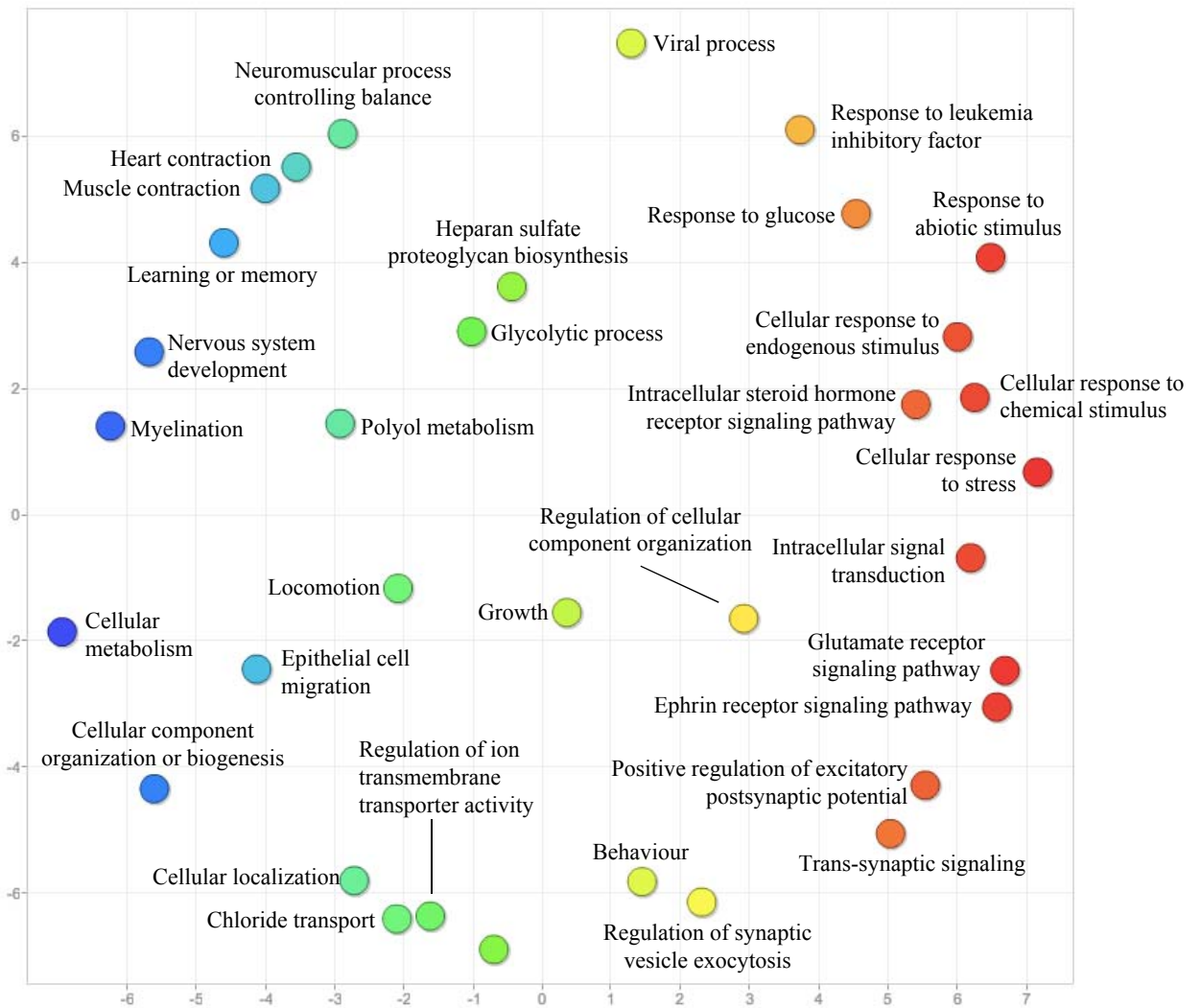
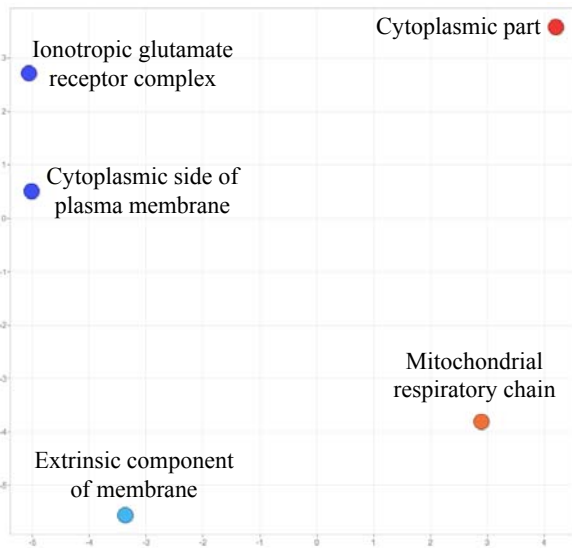


Figure 4

A



B



C

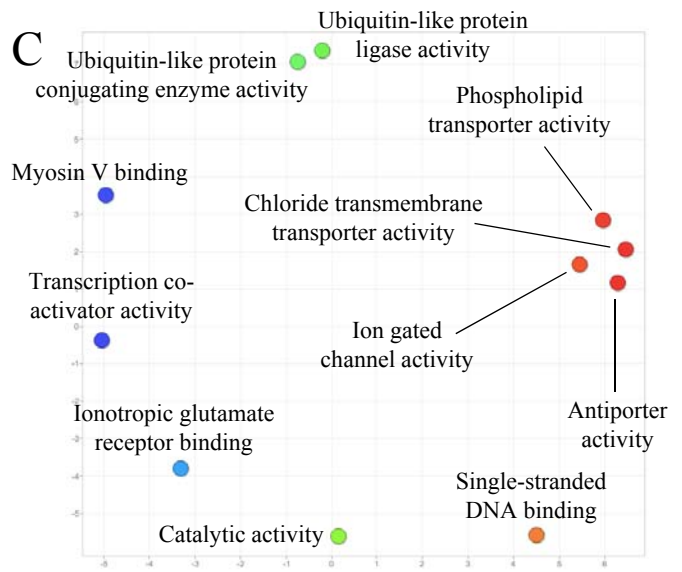
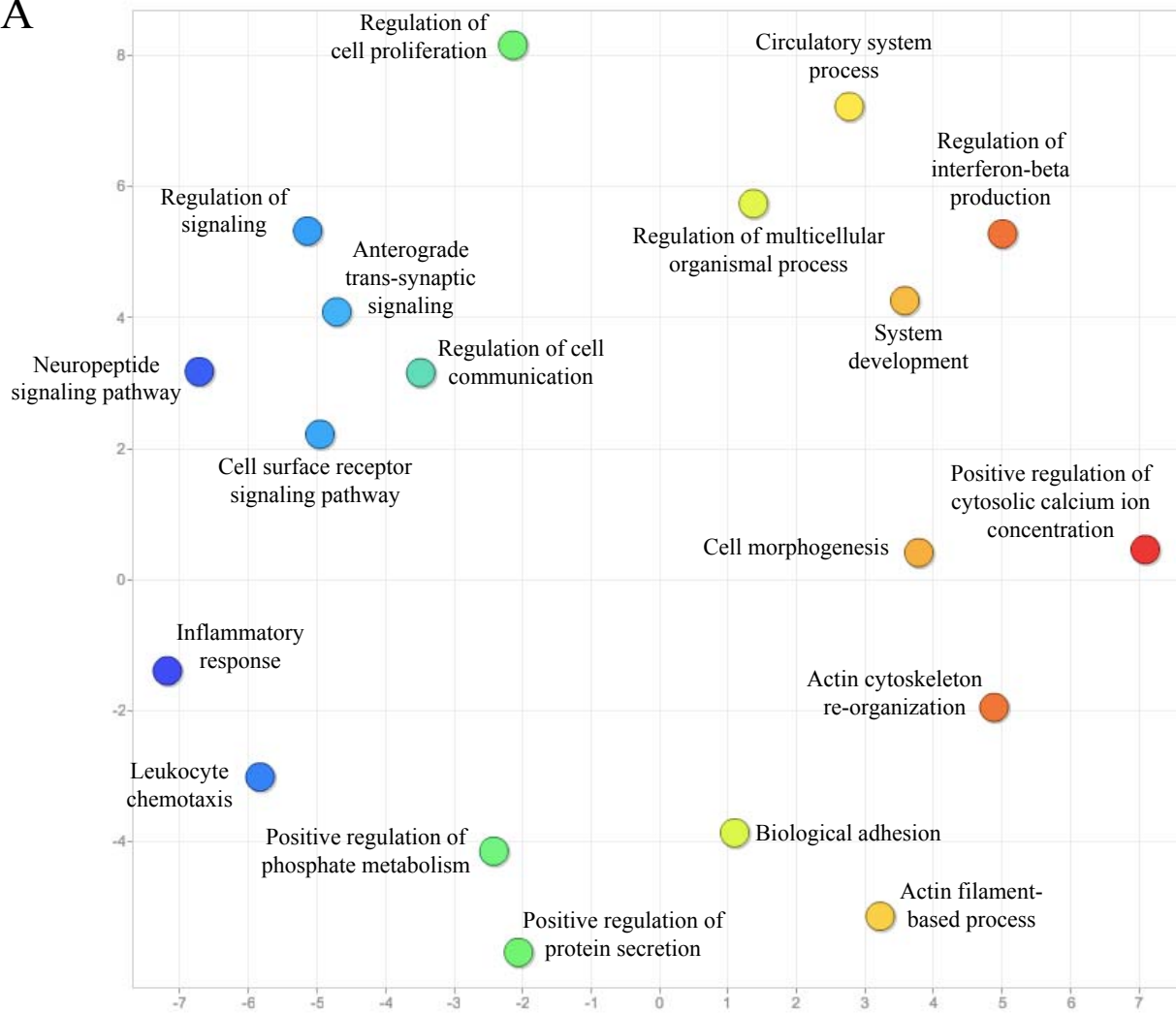
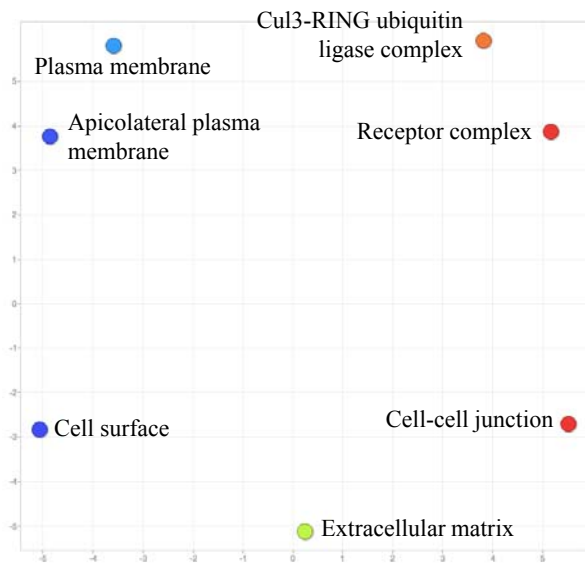


Figure 5

A



B



C

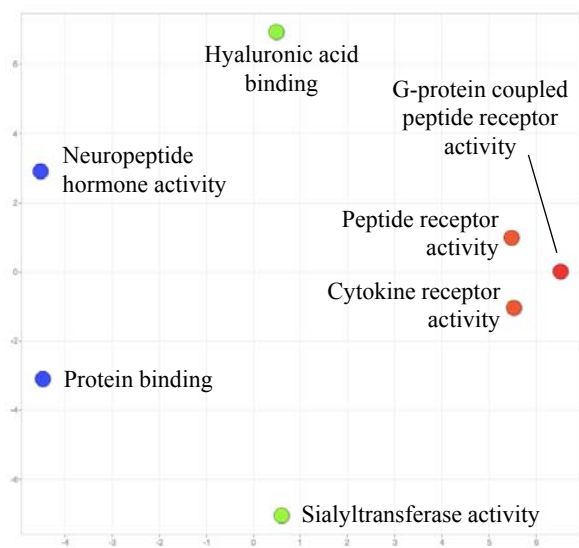


Figure 6

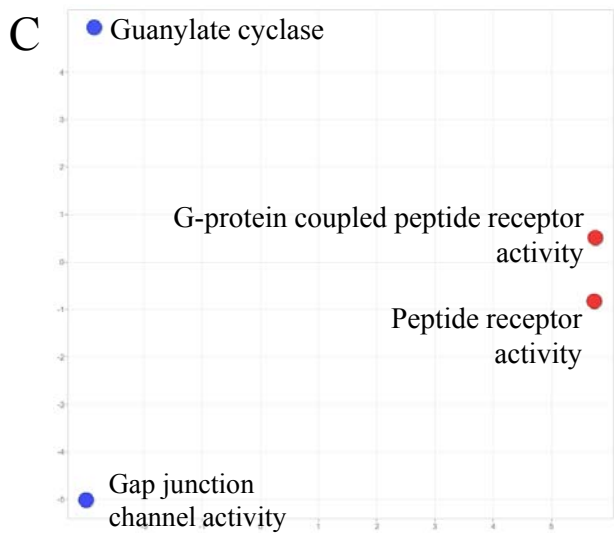
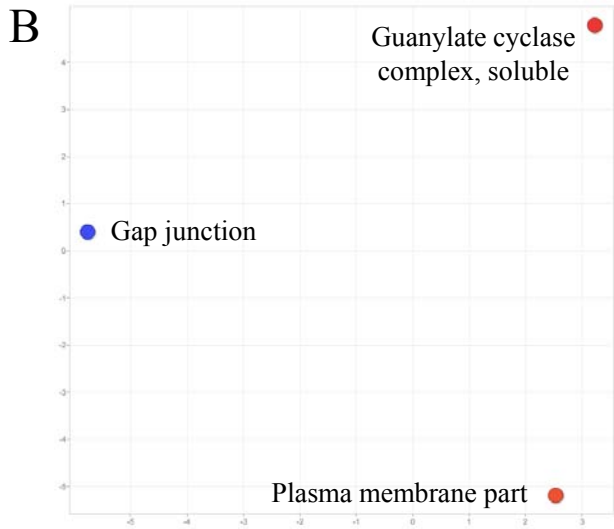
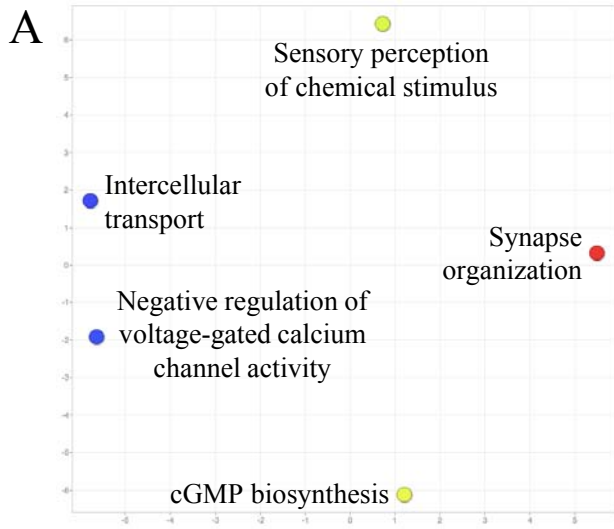


Figure 7

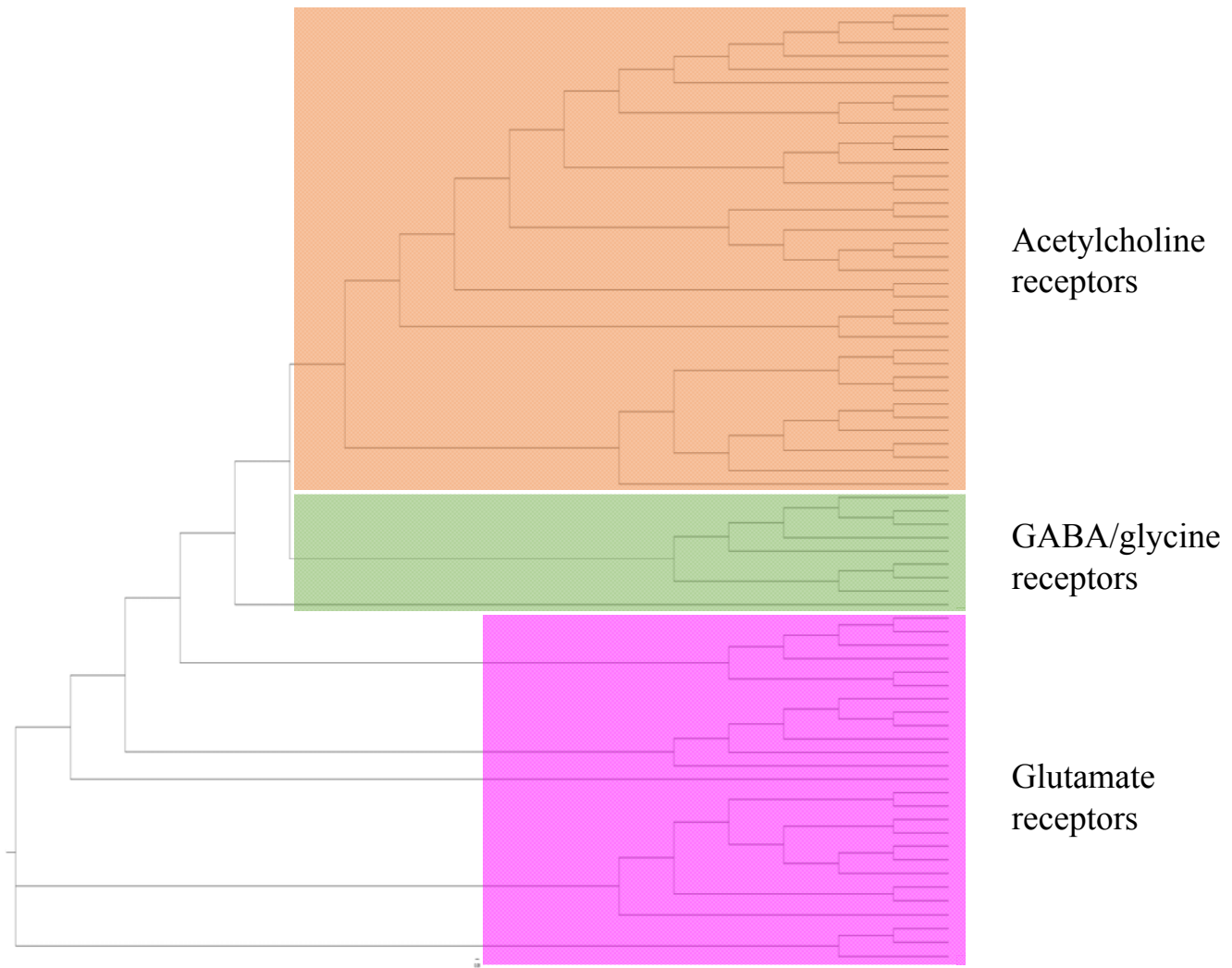
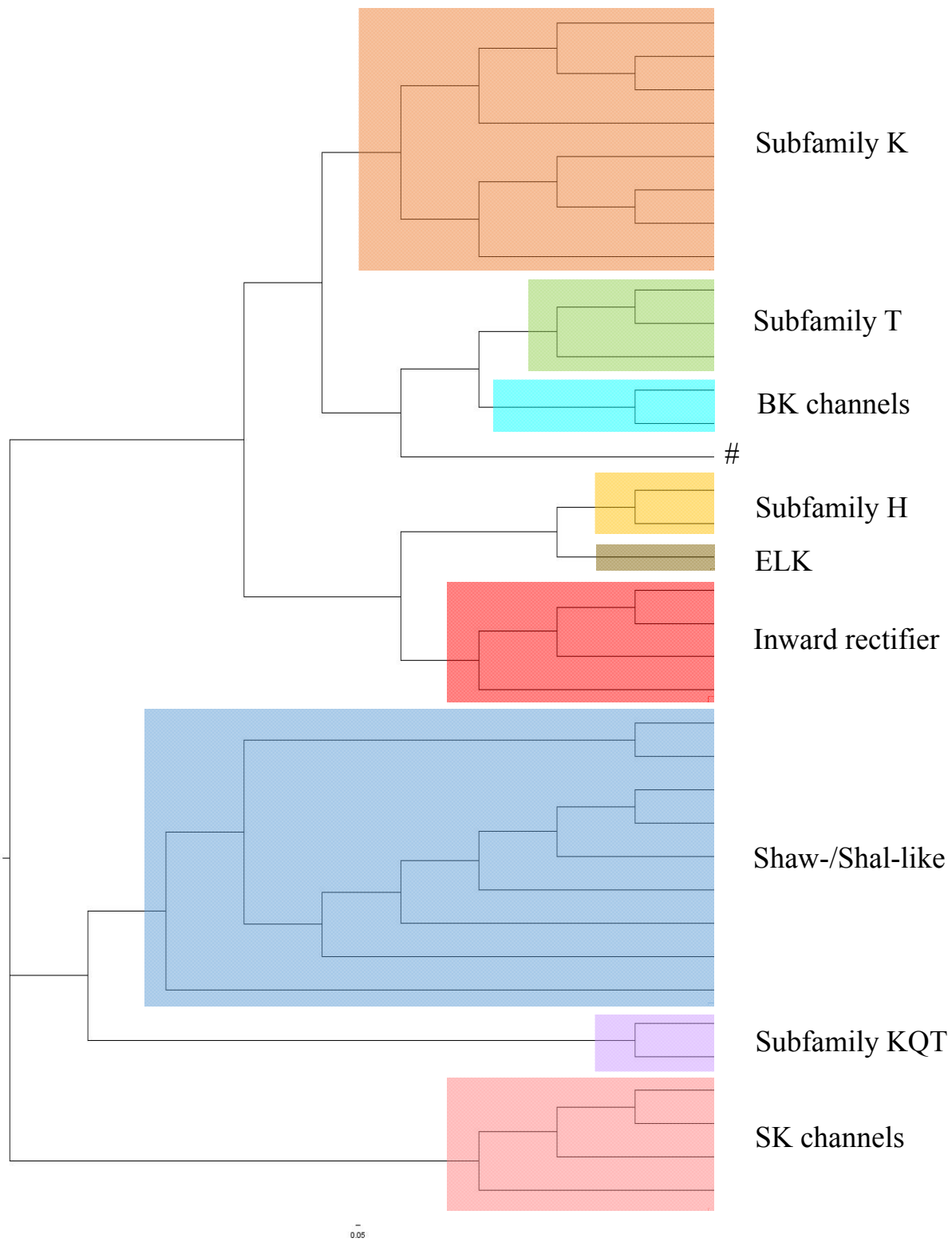


Figure 8



Contains InterPro signature of voltage-gated K⁺ channel.

Figure 9



Figure 10

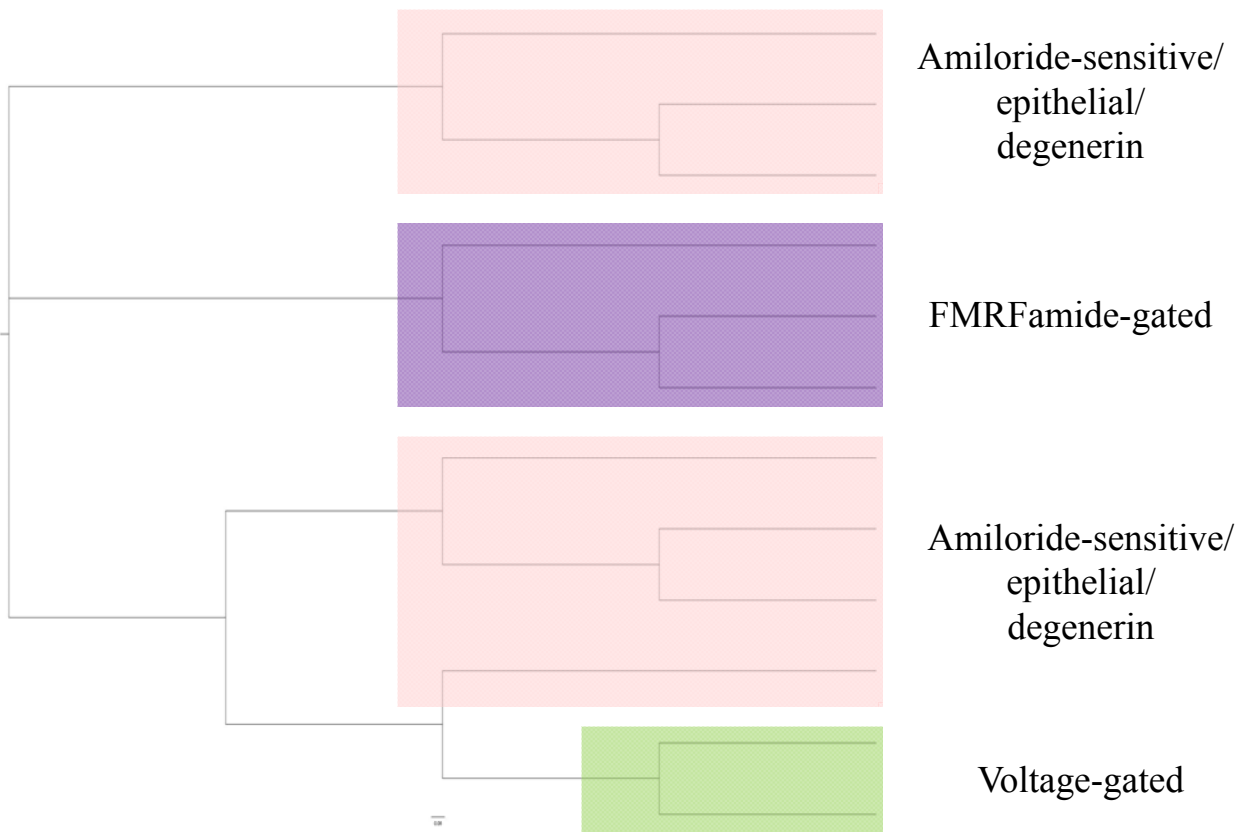


Figure 11

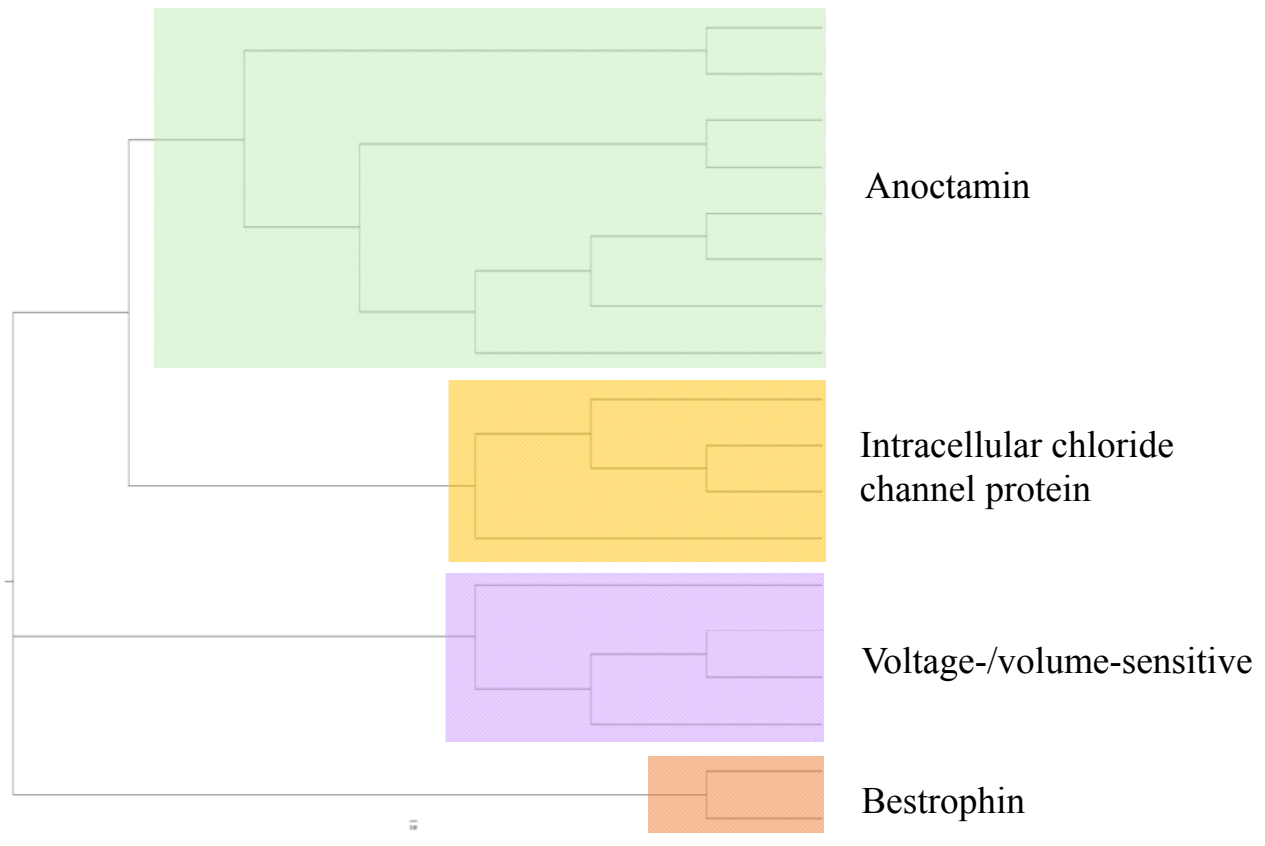


Figure 12

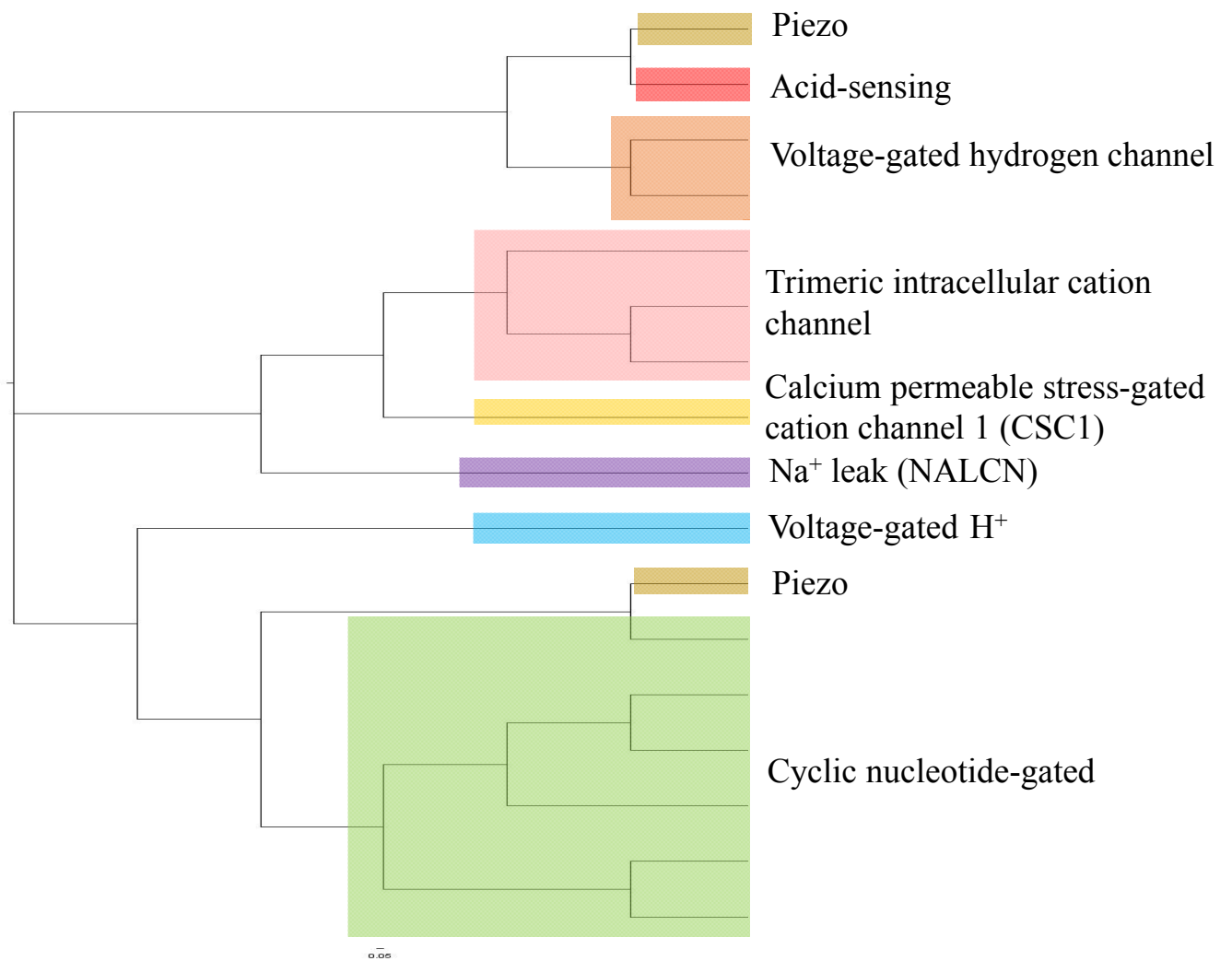


Figure 13

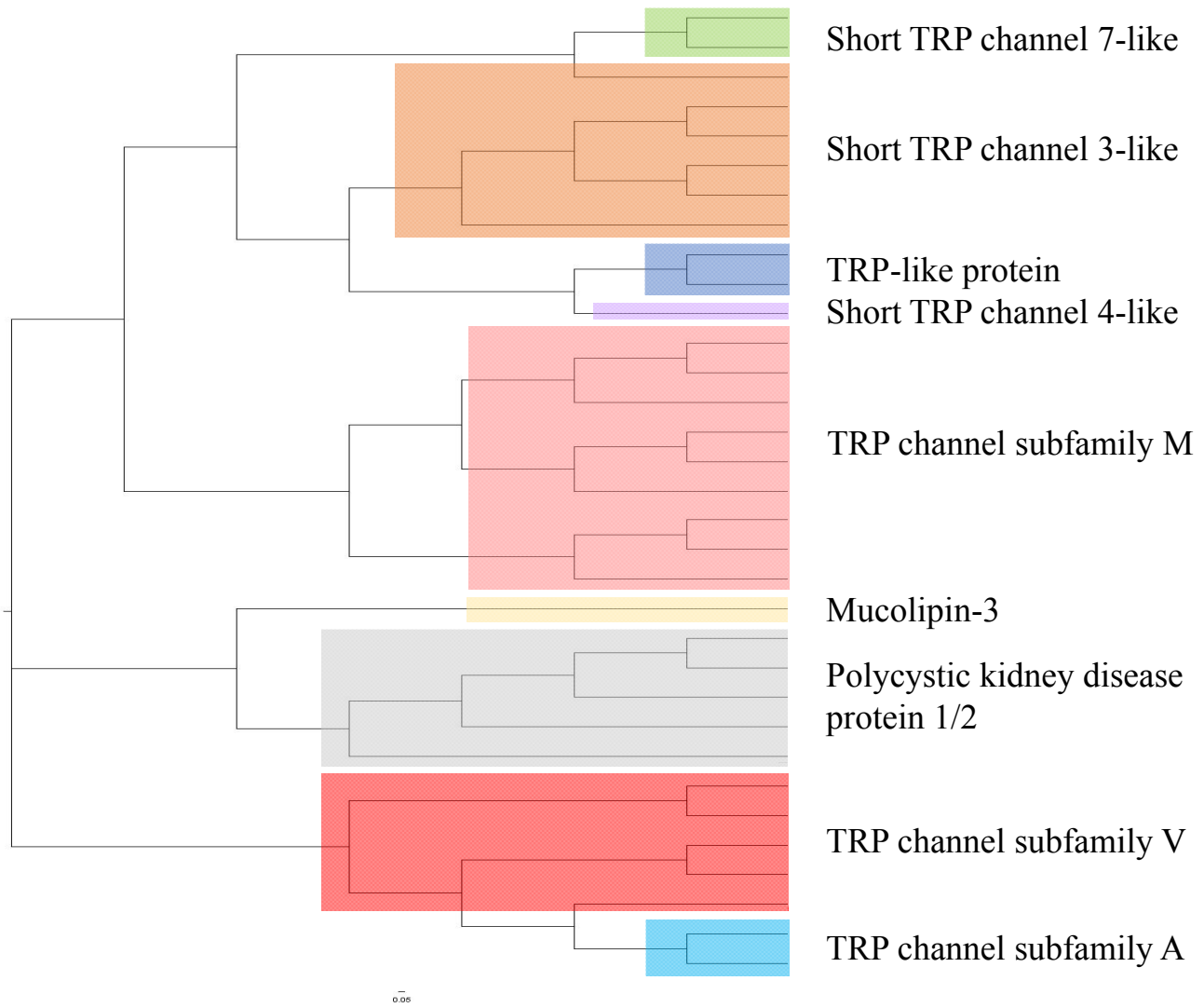


Figure 14

A

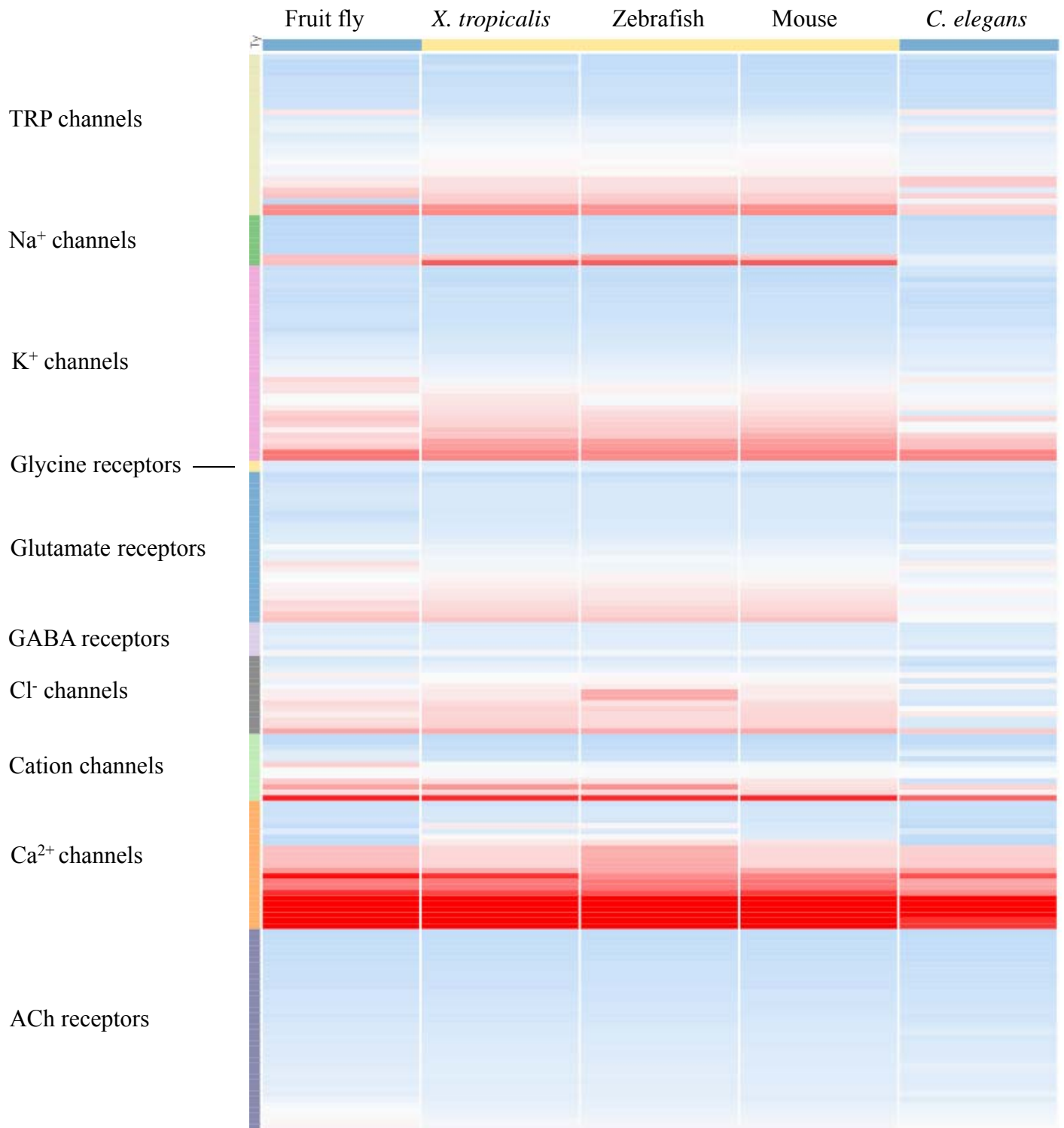
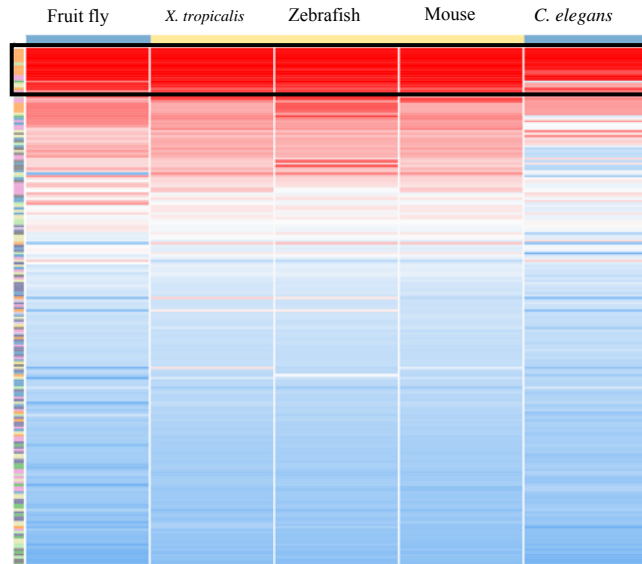


Figure 15

B1



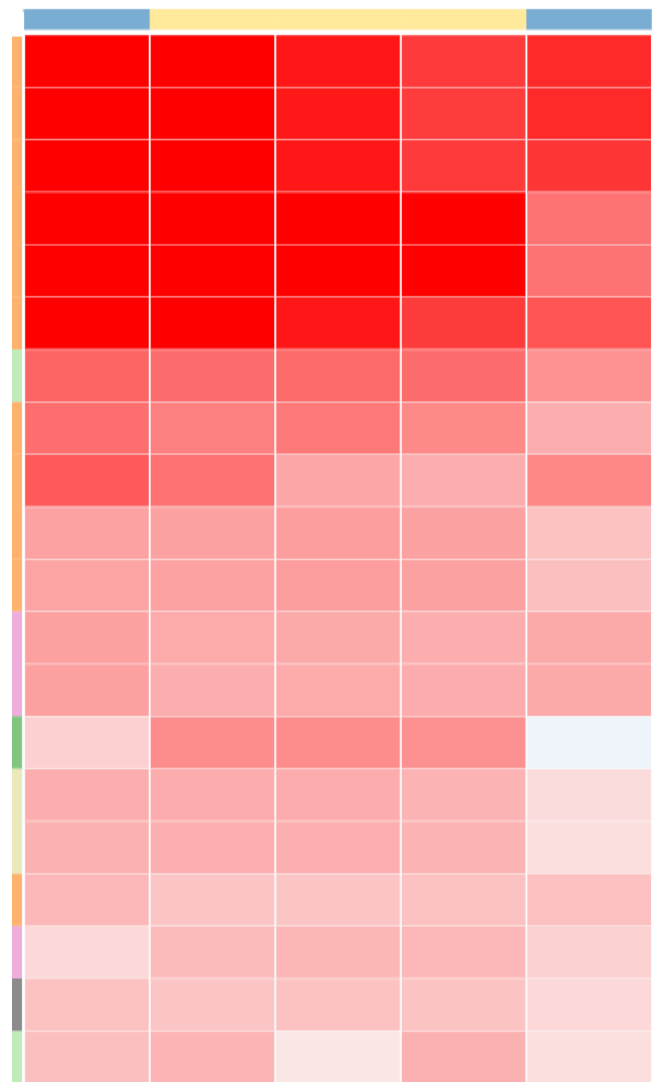
B2 **Transcript ID**

evgLocus_Trinity_AG_97056
 evgLocus_Trinity_GG_DRR_44867
 evgLocus_Trinity_AH_95415
 evgLocus_Trinity_GG_DRR_35036
 evgLocus_Stringtie_DRR_40665
 evgLocus_FX_16361
 evgLocus_Trinity_AH_67380
 evgLocus_scallop_AG_4605
 evgLocus_Trinity_GG_DRR_44870
 evgLocus_Trinity_GG_DRR_50598
 evgLocus_Strawberry_DRR_59689
 evgLocus_Strawberry_DRR_58351
 evgLocus_strawberry_AE_56499
 evgLocus_Trinity_GG_DRR_14950
 evgLocus_Trinity_GG_DRR_79297
 evgLocus_Scallop_AE_2814
 evgLocus_FX_17353
 evgLocus_FX_19780
 evgLocus_Trinity_AE_85637
 evgLocus_FX_16447

Annotation

Ryanodine receptor
 Inositol 1,4,5-trisphosphate receptor type 1
 Ryanodine receptor
 NALCN
 Voltage-dependent L-type calcium channel alpha-1 subunit
 Ryanodine receptor
 Voltage-dependent non-L-type calcium channel alpha-1 subunit
 Calcium-activated potassium channel slowpoke-like
 Voltage-gated sodium channel alpha subunit
 Transient receptor potential cation channel subfamily M member 1-like
 Voltage-dependent non-L-type calcium channel alpha-1 subunit
 Potassium channel subfamily T member 2
 H(+)/Cl(-) exchange transporter 3-like
 Piezo-type mechanosensitive ion channel component 2-like

Fruit fly *X. tropicalis* Zebrafish Mouse *C. elegans*



Ca²⁺ channels Cation channels K⁺ channels Na⁺ channels TRP channels Cl⁻ channels

Figure 15

Table 1. BLAST hit of the top 20 expressed transcripts in the *L. stagnalis* CNS.

Accession	Gene name	Species	Identity (%)	Description
BAW32915.1	Cytochrome c oxidase subunit I, partial (mitochondrion)	<i>Ringicula cf. pilula</i>	84	Energy production
AAB29129.1	preproLYCP	<i>Lymnaea stagnalis</i>	99.1	
P42579.1	Sodium-influx-stimulating peptide Predicted signaling peptide	<i>Lymnaea stagnalis</i>	100	Neuropeptide signaling
P80090.2	Molluscan insulin-related peptide 3	<i>Lymnaea stagnalis</i>	99.2	
ABV22501.1	Myoglobin Predicted signaling peptide	<i>Biomphalaria tenagophila</i>	69.5	Oxygen transport Neuropeptide signaling
P58154.1	Acetylcholine-binding protein Predicted signaling peptide	<i>Lymnaea stagnalis</i>	98.3	Synaptic transmission Neuropeptide signaling
P42577.2	Soma ferritin	<i>Lymnaea stagnalis</i>	100	Metal ion homeostasis
YP_006665701.1	Cytochrome c oxidase subunit III (mitochondrion)	<i>Galba pervia</i>	85	Energy production
AAD02473.1	Cardioexcitatory peptide precursor	<i>Lymnaea stagnalis</i>	94.1	Neuropeptide signaling
AAS20460.1	Granularin Predicted signaling peptide	<i>Lymnaea stagnalis</i>	100	Defense response Neuropeptide signaling
P48416.1	Cytochrome P450	<i>Lymnaea stagnalis</i>	96.3	Oxidoreductase activity
XP_012943264.1	PREDICTED: uncharacterized protein LOC106013068	<i>Aplysia californica</i>	45.2	
P06308.2	Ovulation prohormone Predicted signaling peptide	<i>Lymnaea stagnalis</i>	87.4	Neuropeptide signaling
ARS01367.1	Ffamide 2 Predicted signaling peptide	<i>Deroceras reticulatum</i>	58.2	

Table 2. BUSCO analyses of protein-coding sequences identified in the published EST library and *de novo* assembly, the current assembly and combined set.

	Complete (single-copy)	Complete (duplicated)	Fragmented	Missing
Current assembly	803 (82.1%)	104 (10.6%)	3 (0.3%)	68 (7.0%)
<i>De novo</i> assembly	885 (90.5%)	10 (1.0%)	13 (1.3%)	70 (7.2%)
EST library	124 (12.7%)	7 (0.72%)	61 (6.2%)	786 (80.4%)
Combined	907 (92.7%)	34 (3.5%)	3 (0.3%)	34 (3.5%)