

Supplementary material

Table S1: All clusters regarding functional annotation analysis are presented

| Annotation Cluster 1 | Pathways Enrichment Score: 2.05 | P value | Benjamini |
|-----------------------------|--|-----------------------|------------------------|
| INTERPRO | Neurotransmitter-gated ion-channel, conserved site | 8.80×10^{-4} | 6.00×10^{-2} |
| INTERPRO | Neurotransmitter-gated ion-channel transmembrane domain | 1.00×10^{-3} | 6.00×10^{-2} |
| INTERPRO | Neurotransmitter-gated ion-channel | 1.00×10^{-3} | 6.00×10^{-2} |
| INTERPRO | Neurotransmitter-gated ion-channel ligand binding | 1.00×10^{-3} | 6.00×10^{-2} |
| INTERPRO | Nicotinic acetylcholine receptor | 2.40×10^{-3} | 1.20×10^{-1} |
| UP_KEYWORDS | Synapse | 2.80×10^{-3} | 2.20×10^{-1} |
| UP_KEYWORDS | Ion channel | 2.90×10^{-3} | 2.20×10^{-1} |
| UP_KEYWORDS | Ligand-gated ion channel | 3.90×10^{-3} | 2.20×10^{-1} |
| GOTERM_MF_DIRECT | acetylcholine receptor activity | 4.20×10^{-3} | 3.50×10^{-1} |
| GOTERM_MF_DIRECT | acetylcholine-activated cation-selective channel activity | 4.20×10^{-3} | 3.50×10^{-1} |
| INTERPRO | Nicotinic acetylcholine-gated receptor, transmembrane domain | 4.30×10^{-3} | 1.70×10^{-1} |
| GOTERM_CC_DIRECT | acetylcholine-gated channel complex | 4.30×10^{-3} | 6.10×10^{-10} |
| GOTERM_MF_DIRECT | acetylcholine binding | 5.30×10^{-3} | 3.50×10^{-1} |
| UP_KEYWORDS | Postsynaptic cell membrane | 5.50×10^{-3} | 2.30×10^{-1} |
| GOTERM_BP_DIRECT | neuromuscular synaptic transmission | 5.50×10^{-3} | 1.00×10^{00} |
| GOTERM_MF_DIRECT | ligand-gated ion channel activity | 1.00×10^{-2} | 4.90×10^{-1} |
| GOTERM_BP_DIRECT | synaptic transmission, cholinergic | 1.10×10^{-2} | 1.00×10^{00} |
| Annotation Cluster 2 | Pathways Enrichment Score: 1.93 | P value | Benjamini |
| KEGG_PATHWAY | Renin-angiotensin system | 4.60×10^{-6} | 3.60×10^{-4} |
| GOTERM_BP_DIRECT | proteolysis | 2.00×10^{-2} | 1.00×10^{00} |
| GOTERM_MF_DIRECT RT | metallopeptidase activity | 4.60×10^{-2} | 1.00×10^{00} |
| UP_KEYWORDS | Protease | 6.30×10^{-2} | 8.00×10^{-1} |
| Annotation Cluster 3 | Pathways Enrichment Score: 0.83 | P value | Benjamini |
| UP_KEYWORDS | Zinc | 4.50×10^{-1} | 1.00×10^{00} |
| GOTERM_MF_DIRECT | zinc ion binding | 2.20×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Metal-binding | 3.60×10^{-1} | 1.00×10^{00} |
| INTERPRO | Zinc finger C2H2-type/integrase DNA binding domain | 7.90×10^{-1} | 1.00×10^{00} |
| SMART | ZnF C2H2 | 7.90×10^{-1} | 1.00×10^{00} |
| INTERPRO | Zinc finger, C2H2-like | 8.20×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Zinc-finger | 8.40×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | metal ion-binding site: Zinc; catalytic | 0.092 | 1 |
| INTERPRO | Zinc finger, C2H2 | 8.40×10^{-1} | 1.00×10^{00} |

(Continued)

Table S1: *Continued*

| Annotation Cluster 3 | Pathways Enrichment Score: 0.83 | P value | Benjamini |
|----------------------|--|-----------------------|-----------------------|
| Annotation Cluster 4 | Pathways Enrichment Score: 0.59 | P value | Benjamini |
| GOTERM_CC DIRECT | postsynaptic membrane | 1.10×10^{-2} | 7.80×10^{-1} |
| UP_KEYWORDS | Ion transport | 1.30×10^{-2} | 3.90×10^{-1} |
| GOTERM_BP_DIRECT | Ion transport | 1.70×10^{-2} | 1.00×10^{00} |
| GOTERM_BP DIRECT | cation transmembrane transport | 1.80×10^{-2} | 1.00×10^{00} |
| UP_KEYWORDS | Transport | 2.20×10^{-2} | 4.20×10^{-1} |
| GOTERM_CC DIRECT | cell junction | 4.10×10^{-2} | 1.00×10^{00} |
| UP_KEYWORDS | cell junction | 5.00×10^{-2} | 7.10×10^{-1} |
| KEGG PATHWAY | Neuroactive ligand-receptor interaction | 1.70×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Receptor | 2.00×10^{-1} | 1.00×10^{00} |
| GOTERM_BP_DIRECT | chemical synaptic transmission | 2.80×10^{-1} | 1.00×10^{00} |
| Annotation Cluster 5 | Pathways Enrichment Score: 0.55 | P value | Benjamini |
| GOTERM_CC_DIRECT | integral component of plasma membrane | 7.00×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Ion channel | 2.90×10^{-3} | 2.20×10^{-1} |
| UP_KEYWORDS | Ion channel | 1.30×10^{-2} | 3.90×10^{-1} |
| UP_KEYWORDS | Chloride channel | 1.70×10^{-2} | 4.20×10^{-1} |
| UP_KEYWORDS | Chloride | 3.40×10^{-2} | 5.20×10^{-1} |
| GOTERM_BP_DIRECT | chloride transmembrane transport | 6.00×10^{-2} | 1.00×10^{00} |
| UP_SEQ_FEATURE | metal ion-binding site: Zinc; catalytic | 9.20×10^{-2} | 1.00×10^{00} |
| UP_KEYWORDS | Metalloprotease | 1.20×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Hydrolase | 3.40×10^{-1} | 1.00×10^{00} |
| GOTERM_BP_DIRECT | positive regulation of GTPase activity | 2.20×10^{-1} | 1.00×10^{00} |
| Annotation Cluster 6 | Pathways Enrichment Score: 0.37 | P value | Benjamini |
| UP_SEQ FEATURE | domain:PH | 2.50×10^{-1} | 1.00×10^{00} |
| INTERPRO | Pleckstrin homology-like domain | 2.50×10^{-1} | 1.00×10^{00} |
| SMART | PH | 2.60×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | transmembrane region | 1.20×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Transmembrane helix | 2.80×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Membrane | 1.80×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | topological domain:Cytoplasmic | 2.80×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Transmembrane | 2.80×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | topological domain: Extracellular | 3.00×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | glycosylation site: N-linked (GlcNAc...) | 3.00×10^{-1} | 1.00×10^{00} |
| GOTERM_CC DIRECT | integral component of membrane | 4.70×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Glycoprotein | 5.30×10^{-1} | 1.00×10^{00} |
| Annotation Cluster 7 | Pathways Enrichment Score: 0.11 | P value | Benjamini |
| UP_KEYWORDS | Calmodulin-binding | 2.20×10^{-2} | 4.20×10^{-1} |

(Continued)

Table S1: Continued

| Annotation Cluster 7 | Pathways Enrichment Score: 0.11 | P value | Benjamini |
|----------------------|---|-----------------------|-----------------------|
| GOTERM_MF DIRECT | calmodulin binding | 4.50×10^{-2} | 1.00×10^{00} |
| INTERPRO | Serine/threonine-protein kinase, active site | 3.70×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | binding site:ATP | 3.80×10^{-1} | 1.00×10^{00} |
| SMART | S TKC | 4.00×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Serine/threonine-protein kinase | 4.60×10^{-1} | 1.00×10^{00} |
| INTERPRO | Protein kinase, ATP binding site | 4.60×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | nucleotide phosphate-binding region: ATP | 5.50×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Methylation | 5.60×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | domain:Protein kinase | 5.60×10^{-1} | 1.00×10^{00} |
| GOTERM_BP_DIRECT | protein phosphorylation | 5.90×10^{-1} | 1.00×10^{00} |
| INTERPRO | Protein kinase, catalytic domain | 6.00×10^{-1} | 1.00×10^{00} |
| INTERPRO | Protein kinase-like domain | 6.40×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | ATP-binding | 6.50×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Nucleotide-binding | 7.20×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | active site:Proton acceptor | 7.50×10^{-1} | 1.00×10^{00} |
| GOTERM MF DIRECT | ATP-binding | 7.60×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Kinase | 7.90×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | glycosylation site:N-linked (GlcNAc...) | 3.00×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Signal | 3.70×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | signal peptide | 4.50×10^{-1} | 1.00×10^{00} |
| UP_SEQ_FEATURE | disulfide bond | 4.80×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Disulfide bond | 6.10×10^{-1} | 1.00×10^{00} |
| GOTERM_CC DIRECT | extracellular space | 6.60×10^{-1} | 1.00×10^{00} |
| GOTERM_CC_DIRECT | extracellular region | 8.00×10^{-1} | 1.00×10^{00} |
| UP_KEYWORDS | Secreted | 9.00×10^{-1} | 1.00×10^{00} |