fraction genes in fg and expected val

GO term	p-value	n	fg	bg
action potential GO:0001508	p=8.6E−05	n=7	fg=0.10	bg=0.02
behavioral response to nicotine GO:0035095	p=5.0E−04	n=3	fg=0.04	bg=0.00
regulation of heart rate GO:0002027	p=8.7E−04	n=5	fg=0.07	bg=0.01
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868	p=1.4E−03	n=2	fg=0.03	bg=0.00
regulation of backward locomotion GO:0043058	p=1.6E−03	n=3	fg=0.04	bg=0.00
sensory processing GO:0050893	p=1.6E−03	n=3	fg=0.04	bg=0.00
neuron remodeling GO:0016322	p=1.7E−03	n=5	fg=0.07	bg=0.01
inorganic ion transmembrane transport GO:0098660	p=1.8E−03	n=12	fg=0.17	bg=0.07
regulation of synapse organization GO:0050807	p=2.6E−03	n=8	fg=0.12	bg=0.04
segment specification GO:0007379	p=3.7E−03	n=3	fg=0.04	bg=0.00
regulation of forward locomotion GO:0043059	p=4.2E−03	n=2	fg=0.03	bg=0.00
ventricular compact myocardium morphogen... GO:0003223	p=4.2E−03	n=2	fg=0.03	bg=0.00
somite rostral/caudal axis specification GO:0032525	p=4.2E−03	n=2	fg=0.03	bg=0.00
adult walking behavior GO:0007628	p=5.2E−03	n=3	fg=0.04	bg=0.01
olfactory behavior GO:0042048	p=5.9E−03	n=4	fg=0.06	bg=0.01
regulation of axon guidance GO:1902667	p=5.9E−03	n=4	fg=0.06	bg=0.01
regulation of axon extension involved in... GO:0048841	p=7.0E−03	n=3	fg=0.04	bg=0.01
nervous system process involved in regul... GO:0001976	p=8.1E−03	n=2	fg=0.03	bg=0.00
positive regulation of axon extension in... GO:0048691	p=8.1E−03	n=2	fg=0.03	bg=0.00
female genitalia development GO:0030540	p=8.1E−03	n=2	fg=0.03	bg=0.00
detection of chemical stimulus involved ... GO:0050911	p=8.1E−03	n=2	fg=0.03	bg=0.00
positive regulation of smooth muscle con... GO:0045987	p=8.1E−03	n=2	fg=0.03	bg=0.00
positive regulation of sensory perceptio... GO:1904058	p=8.1E−03	n=2	fg=0.03	bg=0.00
regulation of neurotransmitter secretion GO:0046928	p=8.3E−03	n=4	fg=0.06	bg=0.01
branching involved in ureteric bud morph... GO:0001658	p=9.1E−03	n=3	fg=0.04	bg=0.01
potassium ion transmembrane transport GO:0071805	p=1.1E−02	n=4	fg=0.06	bg=0.01
associative learning GO:0008306	p=1.2E−02	n=5	fg=0.07	bg=0.02
retina development in camera−type eye GO:0060041	p=1.3E−02	n=5	fg=0.07	bg=0.02
regulation of synapse structural plastic... GO:0051823	p=1.3E−02	n=2	fg=0.03	bg=0.00
gamma−aminobutyric acid signaling pathwa... GO:0007214	p=1.3E−02	n=2	fg=0.03	bg=0.00

−log(p)
n=69/354 input genes with annotations

fraction

fraction genes in fg and expected valu

GO term	p-value	n	fg	bg
ion gated channel activity GO:0022839	p=1.9E−05	n=9	fg=0.15	bg=0.03
high voltage−gated calcium channel activ... GO:0008331	p=1.5E−03	n=2	fg=0.03	bg=0.00
methylated histone binding GO:0035064	p=2.7E−03	n=3	fg=0.05	bg=0.01
promoter−specific chromatin binding GO:1990841	p=4.0E−03	n=3	fg=0.05	bg=0.01
voltage−gated potassium channel activity GO:0005249	p=5.6E−03	n=3	fg=0.05	bg=0.01
DNA−binding transcription factor activit... GO:0000981	p=6.8E−03	n=10	fg=0.16	bg=0.07
extracellularly glutamate−gated chloride... GO:0008068	p=8.5E−03	n=2	fg=0.03	bg=0.00
ion channel regulator activity GO:0099106	p=1.2E−02	n=4	fg=0.06	bg=0.02
glutamate binding GO:0016595	p=1.4E−02	n=2	fg=0.03	bg=0.00
transmitter−gated ion channel activity GO:0022824	p=1.4E−02	n=2	fg=0.03	bg=0.00
transmitter−gated channel activity GO:0022835	p=1.4E−02	n=2	fg=0.03	bg=0.00
channel regulator activity GO:0016247	p=1.6E−02	n=4	fg=0.06	bg=0.02
extracellular ligand−gated ion channel a... GO:0005230	p=1.9E−02	n=4	fg=0.06	bg=0.01
1−alkenylglycerophosphocholine O−acyltra... GO:0047159	p=3.9E−02	n=1	fg=0.02	bg=0.00
glucuronosyl−N−acetylgalactosaminyl−prot... GO:0047238	p=3.9E−02	n=1	fg=0.02	bg=0.00
glycogen binding GO:2001069	p=3.9E−02	n=1	fg=0.02	bg=0.00
S100 protein binding GO:0044548	p=3.9E−02	n=1	fg=0.02	bg=0.00
glutamate 5−kinase activity GO:0004349	p=3.9E−02	n=1	fg=0.02	bg=0.00
rRNA primary transcript binding GO:0042134	p=3.9E−02	n=1	fg=0.02	bg=0.00
[phosphorylase] phosphatase activity GO:0050196	p=3.9E−02	n=1	fg=0.02	bg=0.00
open rectifier potassium channel activit... GO:0005252	p=3.9E−02	n=1	fg=0.02	bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395	p=3.9E−02	n=1	fg=0.02	bg=0.00
acetate ester transmembrane transporter ... GO:1901375	p=3.9E−02	n=1	fg=0.02	bg=0.00
C−acetyltransferase activity GO:0016453	p=3.9E−02	n=1	fg=0.02	bg=0.00
acetylcholine transmembrane transporter ... GO:0005277	p=3.9E−02	n=1	fg=0.02	bg=0.00
amino acid kinase activity GO:0019202	p=3.9E−02	n=1	fg=0.02	bg=0.00
delta1−pyrroline−5−carboxylate synthetas... GO:0017084	p=3.9E−02	n=1	fg=0.02	bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985	p=3.9E−02	n=1	fg=0.02	bg=0.00
intracellular sodium activated potassium... GO:0005228	p=3.9E−02	n=1	fg=0.02	bg=0.00
acetyl−CoA C−acyltransferase activity GO:0003988	p=3.9E−02	n=1	fg=0.02	bg=0.00

−log(p)
n=62/354 input genes with annotations

fraction

fraction genes in fg and expected valu

GO term	p-value	n	fg	bg
voltage−gated potassium channel complex GO:0008076	p=4.1E−03	n=3	fg=0.04	bg=0.00
ion channel complex GO:0034702	p=1.4E−02	n=6	fg=0.08	bg=0.01
voltage−gated calcium channel complex GO:0005891	p=1.4E−02	n=2	fg=0.03	bg=0.00
neuron projection membrane GO:0032589	p=1.9E−02	n=3	fg=0.04	bg=0.01
calcium channel complex GO:0034704	p=2.8E−02	n=2	fg=0.03	bg=0.00
L−type voltage−gated calcium channel com... GO:1990454	p=3.9E−02	n=1	fg=0.01	bg=0.00
9+2 non−motile cilium GO:0097732	p=3.9E−02	n=1	fg=0.01	bg=0.00
smooth muscle contractile fiber GO:0030485	p=3.9E−02	n=1	fg=0.01	bg=0.00
syntrophin complex GO:0016013	p=3.9E−02	n=1	fg=0.01	bg=0.00
kinocilium GO:0060091	p=3.9E−02	n=1	fg=0.01	bg=0.00
synapse GO:0045202	p=4.2E−02	n=12	fg=0.17	bg=0.10
plasma membrane protein complex GO:0098797	p=4.7E−02	n=8	fg=0.11	bg=0.03
integral component of membrane GO:0016021	p=6.6E−02	n=19	fg=0.27	bg=0.16
PcG protein complex GO:0031519	p=6.6E−02	n=2	fg=0.03	bg=0.01
leading edge membrane GO:0031256	p=7.2E−02	n=3	fg=0.04	bg=0.01
cation channel complex GO:0034703	p=7.3E−02	n=5	fg=0.07	bg=0.01
mitochondrial crista GO:0030061	p=7.7E−02	n=1	fg=0.01	bg=0.00
pleated septate junction GO:0005919	p=7.7E−02	n=1	fg=0.01	bg=0.00
acetylcholine−gated channel complex GO:0005892	p=7.7E−02	n=1	fg=0.01	bg=0.00
cell junction GO:0030054	p=8.7E−02	n=14	fg=0.20	bg=0.13
presynapse GO:0098793	p=8.9E−02	n=7	fg=0.10	bg=0.05
transmembrane transporter complex GO:1902495	p=9.4E−02	n=6	fg=0.08	bg=0.02
intrinsic component of membrane GO:0031224	p=9.4E−02	n=19	fg=0.27	bg=0.17
integral component of plasma membrane GO:0005887	p=1.0E−01	n=11	fg=0.15	bg=0.08
neuronal cell body membrane GO:0032809	p=1.0E−01	n=2	fg=0.03	bg=0.01
transporter complex GO:1990351	p=1.1E−01	n=6	fg=0.08	bg=0.02
postsynaptic membrane GO:0045211	p=1.1E−01	n=3	fg=0.04	bg=0.02
glycogen granule GO:0042587	p=1.1E−01	n=1	fg=0.01	bg=0.00
muscle cell projection GO:0036194	p=1.1E−01	n=1	fg=0.01	bg=0.00
muscle cell projection membrane GO:0036195	p=1.1E−01	n=1	fg=0.01	bg=0.00

−log(p)
n=71/354 input genes with annotations

fraction