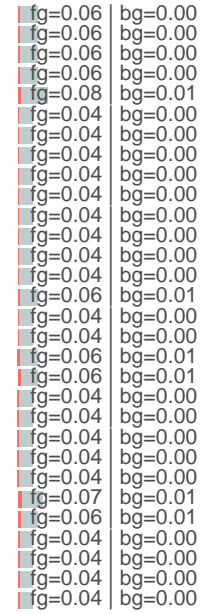
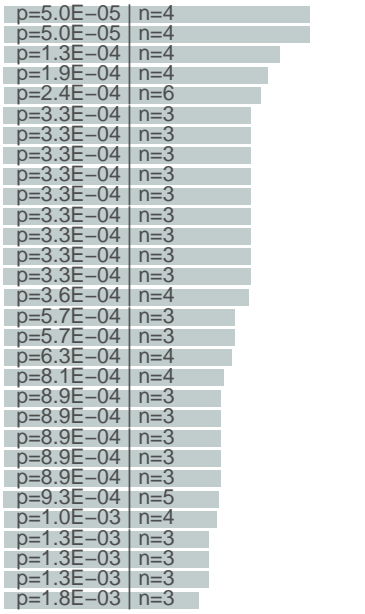


GO:BP
Ncol_Nvec_vc1.1_XM_001637272.3

fraction genes in fg and expected value

neuronal signal transduction	GO:0023041
detection of mechanical stimulus involve...	GO:0050976
startle response	GO:0001964
sensory perception of taste	GO:0050909
negative regulation of cytosolic calcium...	GO:0051481
membrane repolarization during bundle of...	GO:0086050
membrane repolarization during SA node c...	GO:0086052
positive regulation of voltage-gated pot...	GO:1903818
membrane repolarization during atrial ca...	GO:0098914
optic nerve structural organization	GO:0021633
mating behavior, sex discrimination	GO:0048047
proboscis extension reflex	GO:0007637
regulation of atrial cardiac muscle cell...	GO:0060372
behavioral response to ether	GO:0048150
response to hyperoxia	GO:0055093
membrane hyperpolarization	GO:0060081
cellular response to magnesium ion	GO:0071286
positive regulation of peptidyl-serine p...	GO:0033138
neuronal action potential	GO:0019228
regulation of dopamine secretion	GO:0014059
positive regulation of myoblast prolifer...	GO:2000288
negative regulation of calcium-mediated ...	GO:0050849
potassium ion homeostasis	GO:0055075
detection of mechanical stimulus involve...	GO:0050966
hippocampus development	GO:0021766
cellular response to dopamine	GO:1903351
regulation of circadian sleep/wake cycle...	GO:0045188
regulation of synaptic activity	GO:0060025
positive regulation of circadian sleep/w...	GO:0045938
regulation of heart rate by cardiac cond...	GO:0086091



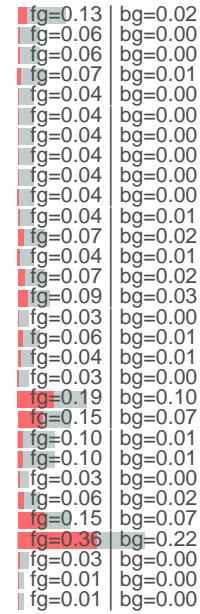
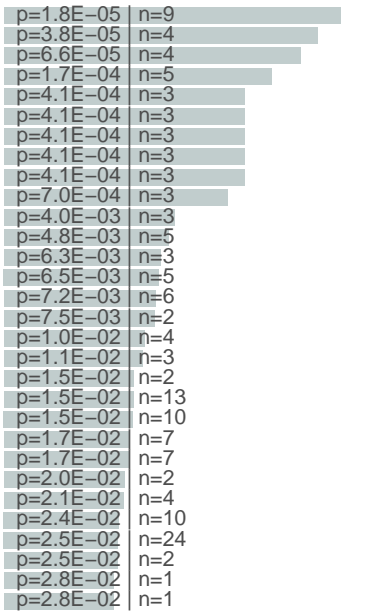
-log(p)
n=71/269 input genes with annotations

fraction

GO:MF
Ncol_Nvec_vc1.1_XM_001637272.3

fraction genes in fg and expected value

ion gated channel activity	GO:0022839
outward rectifier potassium channel acti...	GO:0015271
alpha-actinin binding	GO:0051393
scaffold protein binding	GO:0097110
delayed rectifier potassium channel acti...	GO:0005251
voltage-gated potassium channel activity...	GO:0086087
voltage-gated potassium channel activity...	GO:0086089
intracellular cyclic nucleotide activate...	GO:0005221
voltage-gated potassium channel activity...	GO:0086090
potassium channel inhibitor activity	GO:0019870
disordered domain specific binding	GO:0097718
calcium ion transmembrane transporter ac...	GO:0015085
ubiquitin conjugating enzyme binding	GO:0031624
hormone receptor binding	GO:0051427
protein-macromolecule adaptor activity	GO:0030674
acetylcholine receptor binding	GO:0033130
calcium channel activity	GO:0005262
kinesin binding	GO:0019894
dopamine receptor binding	GO:0050780
transcription regulator activity	GO:0140110
protein kinase binding	GO:0019901
voltage-gated ion channel activity	GO:0005244
voltage-gated channel activity	GO:0022832
cargo receptor activity	GO:0038024
nuclear receptor binding	GO:0016922
kinase binding	GO:0019900
enzyme binding	GO:0019899
neurotransmitter transmembrane transport...	GO:0005326
neuropilin binding	GO:0038191
platelet activating factor receptor bind...	GO:0031859



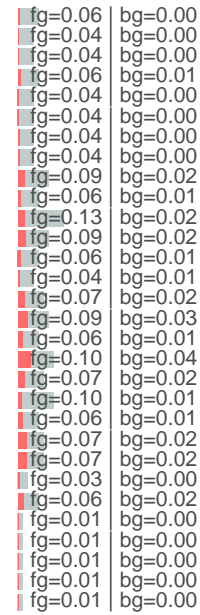
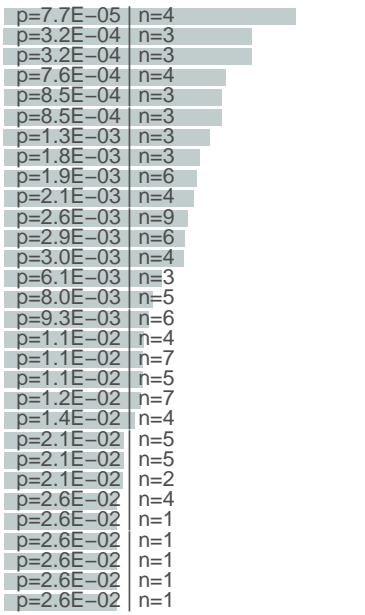
-log(p)
n=67/269 input genes with annotations

fraction

GO:CC
Ncol_Nvec_vc1.1_XM_001637272.3

fraction genes in fg and expected value

voltage-gated potassium channel complex	GO:0008076
intracellular canalliculus	GO:0046691
juxtaparanode region of axon	GO:0044224
neuronal cell body membrane	GO:0032809
paranode region of axon	GO:0033270
integral component of postsynaptic membr...	GO:0099055
integral component of presynaptic membra...	GO:0099056
striated muscle dense body	GO:0055120
dendritic spine	GO:0043197
dendritic shaft	GO:0043198
transmembrane transporter complex	GO:1902495
asymmetric synapse	GO:0032279
perikaryon	GO:0043204
intercalated disc	GO:0014704
sarcomere	GO:0030017
basal part of cell	GO:0045178
Z disc	GO:0030018
cell leading edge	GO:0031252
lamellipodium	GO:0030027
ion channel complex	GO:0034702
I band	GO:0031674
basal plasma membrane	GO:0009925
basolateral plasma membrane	GO:0016323
melanosome	GO:0042470
myelin sheath	GO:0043209
actin cortical patch	GO:0030479
NLS-dependent protein nuclear import com...	GO:0042564
ER membrane insertion complex	GO:0072379
endocytic patch	GO:0061645
palmitoyltransferase complex	GO:0002178



-log(p)
n=70/269 input genes with annotations

fraction