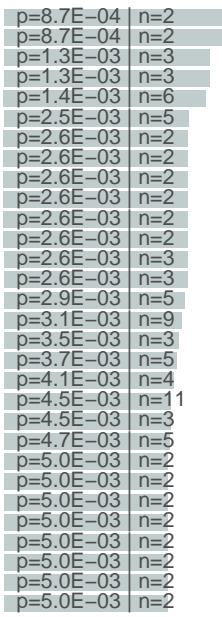


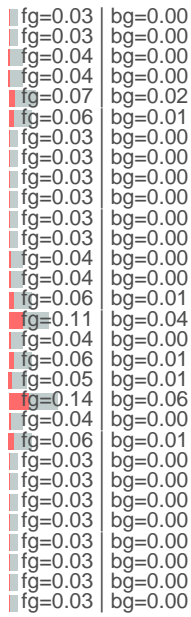
GO:BP
Elav_Nvec_vc1.1_XM_048722721.1

fraction genes in fg and expected value

platelet activating factor biosynthetic ... GO:0006663
nephric duct formation GO:0072179
heart valve morphogenesis GO:0003179
ventral spinal cord development GO:0021517
neuron migration GO:0001764
cellular response to tumor necrosis fact... GO:0071356
regulation of nephron tubule epithelial ... GO:0072182
negative regulation of interleukin-2 pro... GO:0032703
negative regulation of blood vessel endo... GO:0043537
cardiac ventricle formation GO:0003211
phosphatidylcholine acyl-chain remodelin... GO:0036151
phosphatidylglycerol acyl-chain remodeli... GO:0036148
cell differentiation in spinal cord GO:0021515
negative regulation of exocytosis GO:0045920
renal tubule morphogenesis GO:0061333
neutrophil degranulation GO:0043312
aminoglycan catabolic process GO:0006026
negative regulation of defense response GO:0031348
regulation of response to drug GO:2001023
negative regulation of intracellular sig... GO:1902532
autonomic nervous system development GO:0048483
regulation of G1/S transition of mitotic... GO:2000045
lymphoid progenitor cell differentiation GO:0002320
uterus development GO:0060065
metanephric renal vesicle morphogenesis GO:0072283
positive regulation of mesonephros devel... GO:0061213
cardiac right ventricle morphogenesis GO:0003215
norepinephrine metabolic process GO:0042415
positive regulation of urine volume GO:0035810
ubiquitin recycling GO:0010992



0 1 2 3 4 5
-log(p)
n=80/283 input genes with annotations

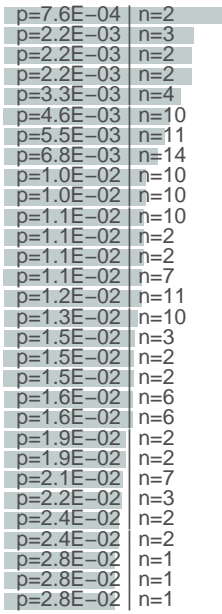


0.0 0.2 0.4 0.6 0.8 1.0
fraction

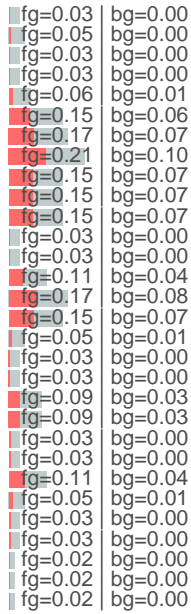
GO:MF
Elav_Nvec_vc1.1_XM_048722721.1

fraction genes in fg and expected value

1-alkylglycerophosphocholine O-acetyltra... GO:0047192
beta-catenin binding GO:0008013
1-acylglycerophosphocholine O-acyltransf... GO:0047184
2-acylglycerol-3-phosphate O-acyltransfe... GO:0047144
cytokine receptor binding GO:0005126
purine ribonucleoside triphosphate bindi... GO:0035639
DNA-binding transcription factor activit... GO:0003700
small molecule binding GO:0036094
ribonucleotide binding GO:0032553
purine ribonucleotide binding GO:0032555
transcription factor binding GO:0008134
tumor necrosis factor receptor binding GO:0005164
1-acylglycerol-3-phosphate O-acyltransfe... GO:0003841
ubiquitin-like protein ligase binding GO:0044389
carbohydrate derivative binding GO:0097367
purine nucleotide binding GO:0017076
carbohydrate binding GO:0030246
acylglycerol O-acyltransferase activity GO:0016411
HMG box domain binding GO:0071837
DNA-binding transcription activator acti... GO:0001228
DNA-binding transcription activator acti... GO:0001216
tumor necrosis factor receptor superfami... GO:0032813
outward rectifier potassium channel acti... GO:0015271
ATP binding GO:0005524
voltage-gated cation channel activity GO:0022843
monosaccharide binding GO:0048029
neurotransmitter binding GO:0042165
neuropilin binding GO:0038191
1-alkenylglycerophosphocholine O-acyltra... GO:0047159
MDM2/MDM4 family protein binding GO:0097371



0 1 2 3 4 5
-log(p)
n=66/283 input genes with annotations

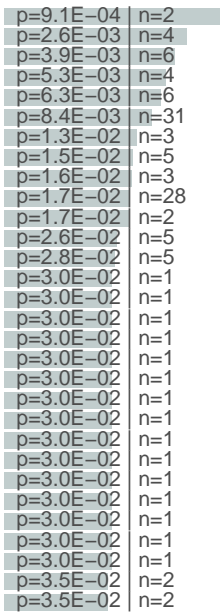


0.0 0.2 0.4 0.6 0.8 1.0
fraction

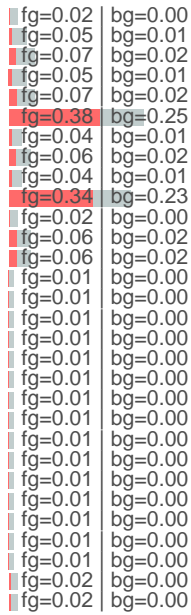
GO:CC
Elav_Nvec_vc1.1_XM_048722721.1

fraction genes in fg and expected value

Lewy body GO:0097413
lysosomal lumen GO:0043202
secretory granule membrane GO:0030667
lipid droplet GO:0005811
myofibril GO:0030016
cell periphery GO:0071944
actomyosin GO:0042641
sarcomere GO:0030017
A band GO:0031672
plasma membrane GO:0005886
cytosolic proteasome complex GO:0031597
asymmetric synapse GO:0032279
neuron to neuron synapse GO:0098984
host cell nuclear part GO:0044094
DNA ligase III-XRCC1 complex GO:0070421
host cell part GO:0033643
host intracellular part GO:0033646
host intracellular organelle GO:0033647
host intracellular membrane-bounded orga... GO:0033648
host cell nucleus GO:0042025
L-type voltage-gated calcium channel com... GO:1990454
host intracellular region GO:0043656
host cell PML body GO:0075341
host cell GO:0043657
acrosomal membrane GO:0002080
outer acrosomal membrane GO:0002081
other organism part GO:0044217
host cellular component GO:0018995
stress fiber GO:0001725
potassium channel complex GO:0034705



0 1 2 3 4 5
-log(p)
n=82/283 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0
fraction