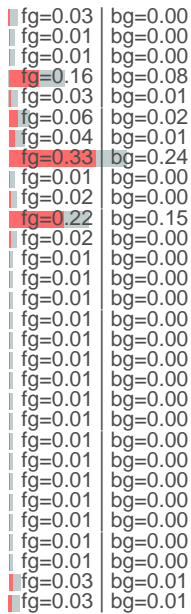
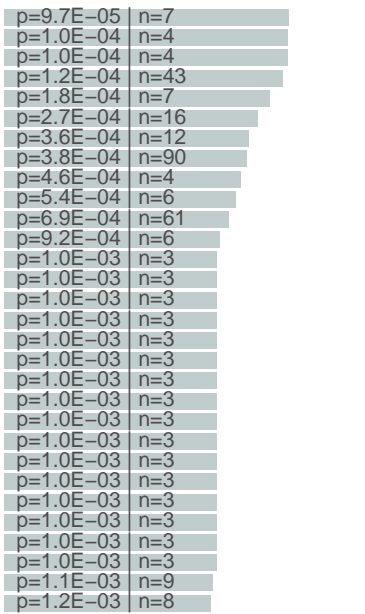


GO:BP
Elav_Nvec_vc1.1_XM_032374853.2

fraction genes in fg and expected value

heart valve morphogenesis	GO:0003179
heart jogging	GO:0003146
alanine metabolic process	GO:0006522
positive regulation of transcription by ...	GO:0045944
cellular response to retinoic acid	GO:0071300
regulation of animal organ morphogenesis	GO:2000027
cellular response to antibiotic	GO:0071236
regulation of cellular macromolecule bio...	GO:2000112
proline metabolic process	GO:0006560
imaginal disc-derived wing vein morphoge...	GO:0008586
positive regulation of gene expression	GO:0010628
cell migration involved in gastrulation	GO:0042074
regulation of nephron tubule epithelial ...	GO:0072182
lactate biosynthetic process	GO:0019249
cellular response to potassium ion starv...	GO:0051365
cellular response to fructose stimulus	GO:0071332
regulation of transcription by glucose	GO:0046015
transdifferentiation	GO:0060290
glycerol catabolic process	GO:0019563
lactate oxidation	GO:0019516
propionate catabolic process	GO:0019543
malate transport	GO:0015743
glucose catabolic process to lactate via...	GO:0019661
nitrogenous compound fermentation	GO:0019666
response to methionine	GO:1904640
glycerol biosynthetic process from pyruv...	GO:0046327
positive regulation of transcription fro...	GO:0061402
kidney interstitial fibroblast different...	GO:0072071
mesoderm formation	GO:0001707
animal organ formation	GO:0048645



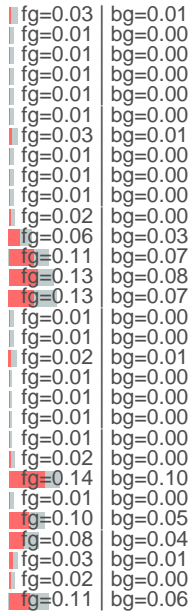
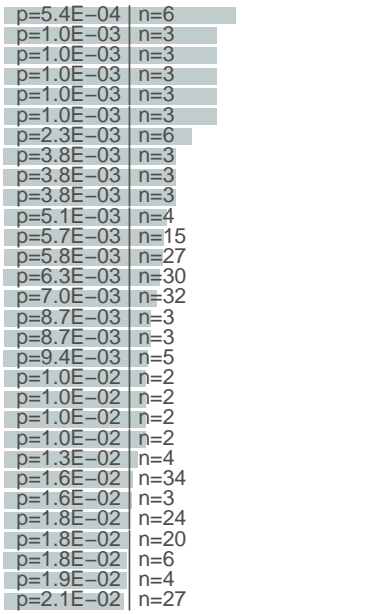
-log(p)
n=272/969 input genes with annotations

fraction

GO:MF
Elav_Nvec_vc1.1_XM_032374853.2

fraction genes in fg and expected value

ion channel inhibitor activity	GO:0008200
oxidoreductase activity, acting on the C...	GO:0016899
chloride channel inhibitor activity	GO:0019869
I-SMAD binding	GO:0070411
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613
inosine kinase activity	GO:0008906
ADP binding	GO:0043531
lactate dehydrogenase activity	GO:0004457
DNA binding domain binding	GO:0050692
regulatory RNA binding	GO:0061980
protein serine/threonine kinase inhibito...	GO:0030291
DNA-binding transcription activator acti...	GO:0001228
protein kinase binding	GO:0019901
cytoskeletal protein binding	GO:0008092
DNA-binding transcription factor activit...	GO:0003700
nucleoside diphosphate kinase activity	GO:0004550
epinephrine binding	GO:0051379
E-box binding	GO:0070888
cargo adaptor activity	GO:0140312
ATP-dependent protein binding	GO:0043008
clathrin adaptor activity	GO:0035615
G protein-coupled serotonin receptor bin...	GO:0031821
beta-catenin binding	GO:0008013
signaling receptor binding	GO:0005102
Wnt-protein binding	GO:0017147
transcription regulatory region nucleic ...	GO:0001067
RNA polymerase II transcription regulato...	GO:0000977
voltage-gated cation channel activity	GO:0022843
voltage-gated potassium channel activity	GO:0005249
DNA-binding transcription factor activit...	GO:0000981



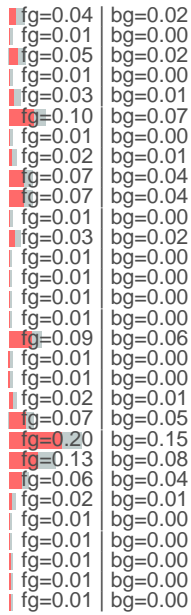
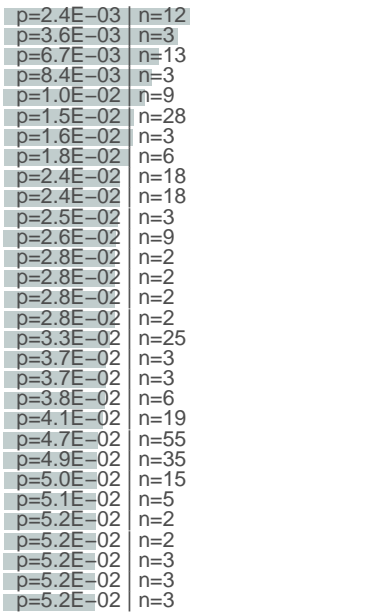
-log(p)
n=239/969 input genes with annotations

fraction

GO:CC
Elav_Nvec_vc1.1_XM_032374853.2

fraction genes in fg and expected value

microtubule	GO:0005874
NuRD complex	GO:0016581
basolateral plasma membrane	GO:0016323
MLL3/4 complex	GO:0044666
mitotic spindle	GO:0072686
intrinsic component of plasma membrane	GO:0031226
nucleosome	GO:0000786
dendritic shaft	GO:0043198
cell-cell junction	GO:0005911
anchoring junction	GO:0070161
chaperone complex	GO:0101031
midbody	GO:0030496
myelin sheath abaxonal region	GO:0035748
beta-catenin-TCF complex	GO:1990907
integral component of nuclear inner memb...	GO:0005639
intrinsic component of nuclear inner mem...	GO:0031229
integral component of plasma membrane	GO:0005887
pericentric heterochromatin	GO:0005721
nuclear inner membrane	GO:0005637
cation channel complex	GO:0034703
nuclear chromosome	GO:0000228
cytoskeleton	GO:0005856
supramolecular complex	GO:0099080
cell surface	GO:0009986
P-body	GO:0000932
nucleotide-activated protein kinase comp...	GO:0031588
eukaryotic translation initiation factor...	GO:0071541
integral component of presynaptic membra...	GO:0099056
integral component of synaptic membrane	GO:0099699
intrinsic component of synaptic membrane	GO:0099240



-log(p)
n=269/969 input genes with annotations

fraction