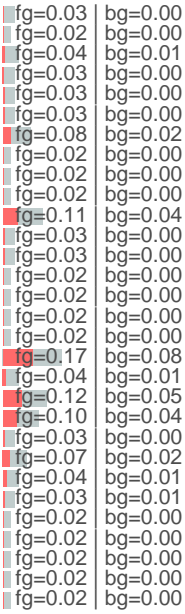
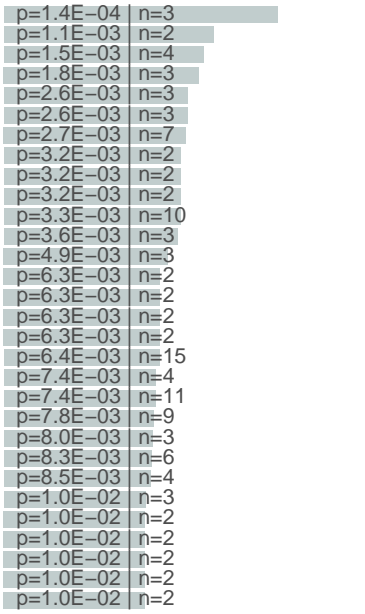


GO:BP
Elav_Nvec_vc1.1_XM_032375280.2

fraction genes in fg and expected value

negative regulation of long-term synapti... GO:1900272
regulation of G protein-coupled receptor... GO:1904020
autophagosome maturation GO:0097352
germ-line cyst formation GO:0048134
regulation of epidermal growth factor-ac... GO:0007176
actin filament depolymerization GO:0030042
response to ketone GO:1901654
deoxynucleotide transport GO:0030302
pyrimidine nucleotide import into mitoch... GO:1990519
regulation of receptor binding GO:1900120
regulation of protein catabolic process GO:0042176
positive regulation of epidermal growth ... GO:0045742
membrane protein ectodomain proteolysis GO:0006509
regulation of spontaneous synaptic trans... GO:0150003
sensory neuron axon guidance GO:0097374
regulation of protein localization to ce... GO:1904776
mitochondrial transcription GO:0006390
negative regulation of protein metabolic... GO:0051248
negative regulation of Notch signaling p... GO:0045746
positive regulation of catabolic process GO:0009896
negative regulation of nervous system de... GO:0051961
regulation of epithelial to mesenchymal ... GO:0010717
protein acetylation GO:0006473
regulation of nematode larval developmen... GO:0061062
exit from mitosis GO:0010458
female germ-line cyst formation GO:0048135
suckling behavior GO:0001967
germarium-derived female germ-line cyst ... GO:0030727
establishment or maintenance of polarity... GO:0016334
collateral sprouting GO:0048668



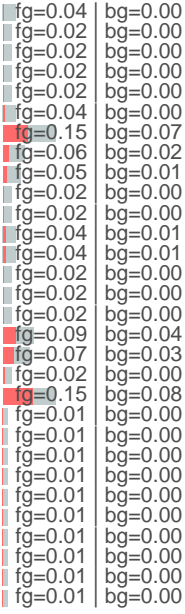
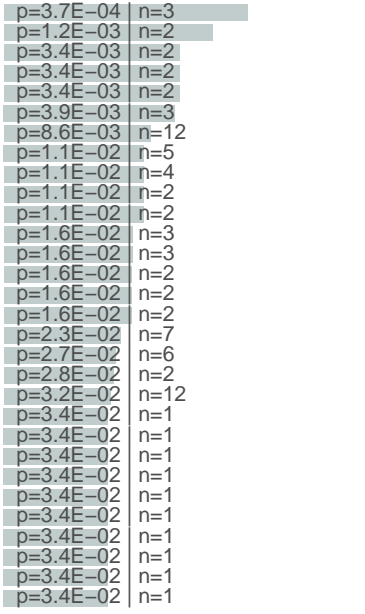
-log(p)
n=90/330 input genes with annotations

fraction

GO:MF
Elav_Nvec_vc1.1_XM_032375280.2

fraction genes in fg and expected value

ephrin receptor binding GO:0046875
apolipoprotein binding GO:0034185
neurexin family protein binding GO:0042043
pyrimidine nucleotide transmembrane tran... GO:0015218
mRNA regulatory element binding translat... GO:0000900
frizzled binding GO:0005109
protein kinase binding GO:0019901
calcium ion transmembrane transporter ac... GO:0015085
actin filament binding GO:0051015
P-type calcium transporter activity GO:0005388
acetylcholine receptor binding GO:0033130
protein tyrosine kinase binding GO:1990782
growth factor receptor binding GO:0070851
coreceptor activity GO:0015026
proteoglycan binding GO:0043394
dynein heavy chain binding GO:0045504
metal ion transmembrane transporter acti... GO:0046873
amide binding GO:0033218
snRNA binding GO:0017069
protein domain specific binding GO:0019904
CCR chemokine receptor binding GO:0048020
phosphatidylcholine transporter activity GO:0008525
myosin II binding GO:0045159
protein phosphatase 5 binding GO:1990634
tRNA 2'-phosphotransferase activity GO:0000215
testosterone 17-beta-dehydrogenase (NADP... GO:0047045
mono-olein transacylation activity GO:0051264
diolein transacylation activity GO:0051265
ACP phosphopantetheine attachment site b... GO:0044620
phosphopantetheine binding GO:0031177



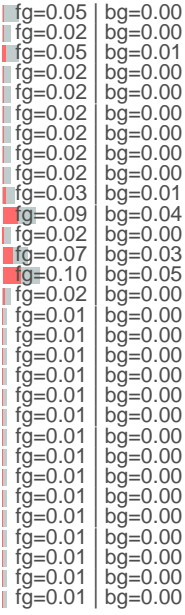
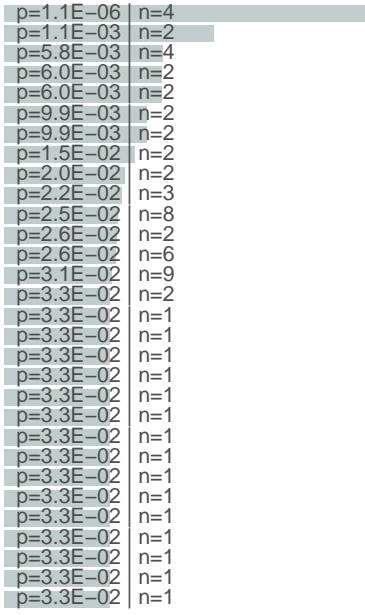
-log(p)
n=81/330 input genes with annotations

fraction

GO:CC
Elav_Nvec_vc1.1_XM_032375280.2

fraction genes in fg and expected value

growth cone lamellipodium GO:1990761
growth cone filopodium GO:1990812
presynaptic active zone GO:0048786
dendritic spine membrane GO:0032591
integral component of luminal side of en... GO:0071556
presynaptic periaxial zone GO:0036062
kinetochore microtubule GO:0005828
voltage-gated calcium channel complex GO:0005891
axonemal dynein complex GO:0005858
main axon GO:0044304
mitochondrial inner membrane GO:0005743
aggresome GO:0016235
basal part of cell GO:0045178
cytoplasmic region GO:0099568
calcium channel complex GO:0034704
cytoplasmic side of dendritic spine plas... GO:1990780
endosome to plasma membrane transport ve... GO:0070381
lipoprotein particle GO:1990777
cytoplasmic periphery of the nuclear por... GO:1990723
cortical microtubule cytoskeleton GO:0030981
interleukin-5 receptor complex GO:0005895
amyloid-beta complex GO:0106003
cortical microtubule plus-end GO:1903754
nuclear pore cytoplasmic filaments GO:0044614
cyclin E1-CDK2 complex GO:0097134
cyclin E2-CDK2 complex GO:0097135
centrosomal corona GO:0031592
smooth septate junction GO:0005920
cytoplasmic microtubule plus-end GO:1904511
cortical microtubule GO:0055028



-log(p)
n=88/330 input genes with annotations

fraction