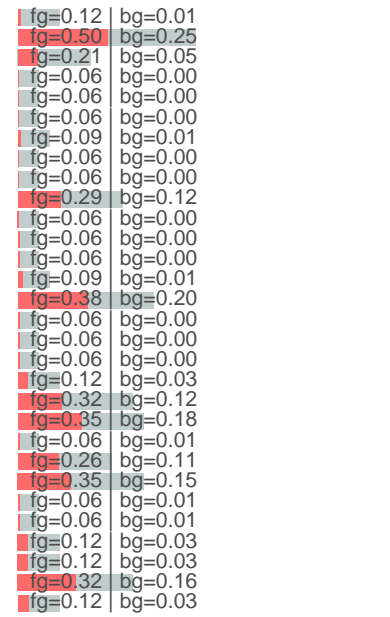
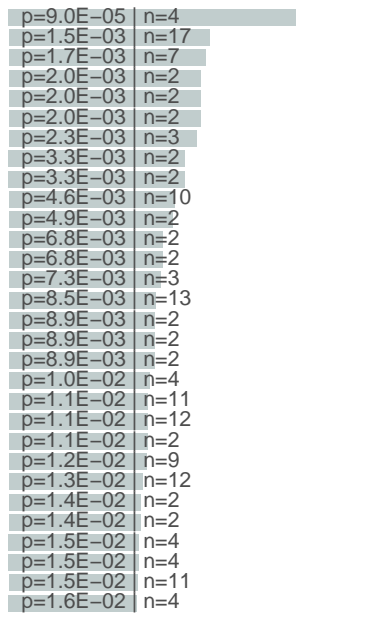


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001640781.3

fraction genes in fg and expected value

protein K48-linked ubiquitination	GO:0070936
regulation of cellular macromolecule bio...	GO:2000112
negative regulation of cell population p...	GO:0008285
embryonic hindlimb morphogenesis	GO:0035116
cardiac right ventricle morphogenesis	GO:0003215
negative regulation of endoplasmic retic...	GO:1902236
cardiac septum morphogenesis	GO:0060411
endoplasmic reticulum mannose trimming	GO:1904380
aorta morphogenesis	GO:0035909
positive regulation of transcription, DN...	GO:0045893
positive regulation of dendrite extensio...	GO:1903861
negative regulation of oxidative stress-...	GO:1903204
heart valve morphogenesis	GO:0003179
ubiquitin-dependent ERAD pathway	GO:0030433
cell surface receptor signaling pathway	GO:0007166
negative regulation of actin filament bu...	GO:0032232
startle response	GO:0001964
glial cell proliferation	GO:0014009
cellular response to topologically incor...	GO:0035967
negative regulation of signal transducti...	GO:0009968
transcription by RNA polymerase II	GO:0006366
regulation of tumor necrosis factor-medi...	GO:0010803
regulation of cell development	GO:0060284
negative regulation of response to stimu...	GO:0048585
adult walking behavior	GO:0007628
walking behavior	GO:0090659
imaginal disc-derived wing morphogenesis	GO:0007476
response to topologically incorrect prot...	GO:0035966
regulation of transcription by RNA polym...	GO:0006357
wing disc morphogenesis	GO:0007472



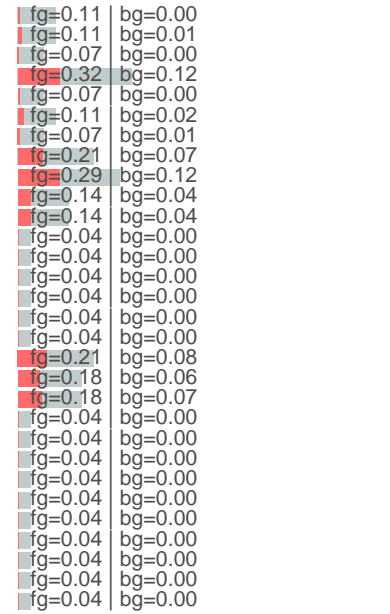
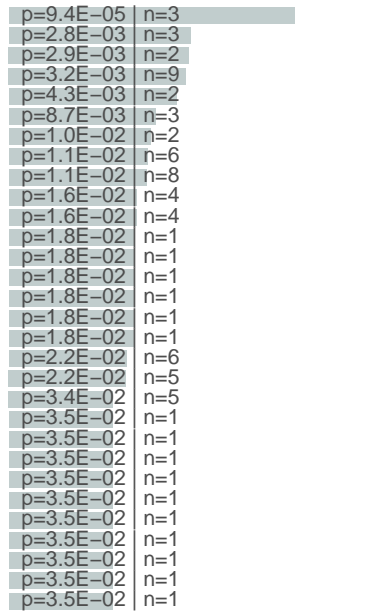
-log(p)  
n=34/124 input genes with annotations

fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001640781.3

fraction genes in fg and expected value

ubiquitin-specific protease binding	GO:1990381
p53 binding	GO:0002039
phospholipase binding	GO:0043274
transcription regulator activity	GO:0140110
beta-catenin binding	GO:0008013
chaperone binding	GO:0051087
ubiquitin binding	GO:0043130
sequence-specific DNA binding	GO:0043565
DNA binding	GO:0003677
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
K48-linked polyubiquitin modification-de...	GO:0036435
racemase and epimerase activity, acting ...	GO:0016857
dynein light intermediate chain binding	GO:0051959
chondroitin-glucuronate 5-epimerase acti...	GO:0047757
F-box domain binding	GO:1990444
non-tyrosine kinase fibroblast growth fa...	GO:0001571
DNA-binding transcription factor activit...	GO:0003700
transcription coregulator activity	GO:0003712
double-stranded DNA binding	GO:0003690
vinculin binding	GO:0017166
beta-2 adrenergic receptor binding	GO:0031698
cAMP-dependent protein kinase inhibitor ...	GO:0004862
phosphatidylinositol-5-phosphate binding	GO:0010314
cAMP-dependent protein kinase regulator ...	GO:0008603
BAT3 complex binding	GO:1904288
racemase and epimerase activity	GO:0016854
protein kinase A catalytic subunit bindi...	GO:0034236
LIM domain binding	GO:0030274
armadillo repeat domain binding	GO:0070016



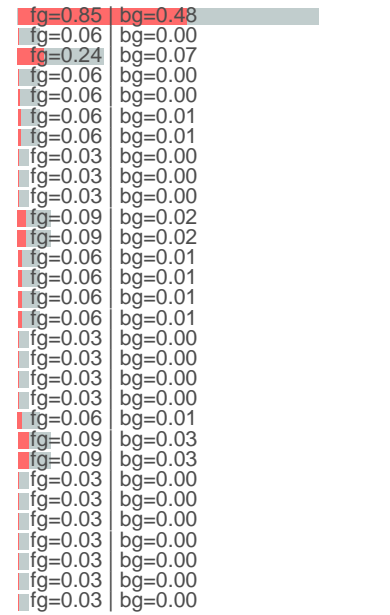
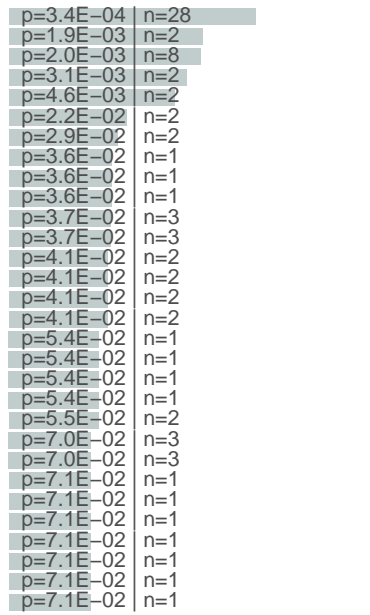
-log(p)  
n=28/124 input genes with annotations

fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001640781.3

fraction genes in fg and expected value

nucleus	GO:0005634
zonula adherens	GO:0005915
nucleolus	GO:0005730
MLL1 complex	GO:0071339
Derlin-1 retrotranslocation complex	GO:0036513
cortical actin cytoskeleton	GO:0030864
cortical cytoskeleton	GO:0030863
NSL complex	GO:0044545
Parkin-FBXW7-Cul1 ubiquitin ligase compl...	GO:1990452
Lewy body	GO:0097413
intrinsic component of endoplasmic retic...	GO:0031227
integral component of endoplasmic reticu...	GO:0030176
acetyltransferase complex	GO:1902493
histone acetyltransferase complex	GO:0000123
cell-substrate junction	GO:0030055
protein acetyltransferase complex	GO:0031248
cAMP-dependent protein kinase complex	GO:0005952
Hrd1p ubiquitin ligase ERAD-L complex	GO:0000839
spot adherens junction	GO:0005914
nucleotide-activated protein kinase comp...	GO:0031588
plasma membrane raft	GO:0044853
membrane microdomain	GO:0098857
membrane raft	GO:0045121
aggresome	GO:0016235
germinal vesicle	GO:0042585
ER ubiquitin ligase complex	GO:0000835
Hrd1p ubiquitin ligase complex	GO:0000836
SAGA complex	GO:0000124
endoplasmic reticulum quality control co...	GO:0044322
intrinsic component of the cytoplasmic s...	GO:0031235



-log(p)  
n=33/124 input genes with annotations

fraction