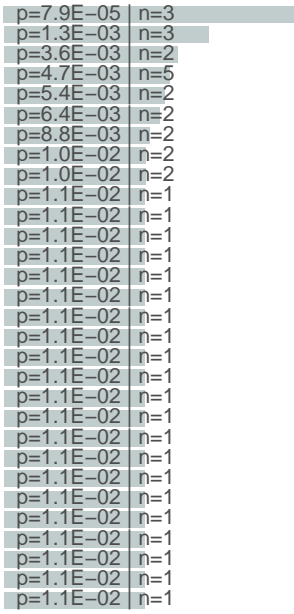


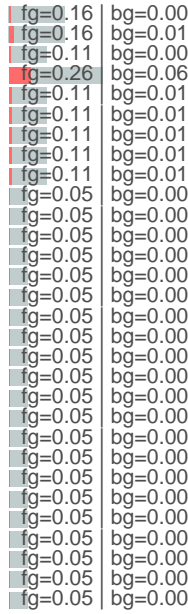
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_048724605.1

fraction genes in fg and expected value

receptor catabolic process	GO:0032801
bone mineralization	GO:0030282
negative regulation of protein localizat...	GO:1905476
spermatogenesis	GO:0007283
regulation of mitochondrial membrane per...	GO:1902108
negative regulation of small molecule me...	GO:0062014
regulation of type I interferon producti...	GO:0032479
negative regulation of carbohydrate meta...	GO:0045912
regulation of mitochondrial membrane pot...	GO:0051881
regulation of receptor clustering	GO:1903909
negative regulation of double-strand bre...	GO:2001033
regulation of hyaluronan biosynthetic pr...	GO:1900125
negative regulation of hyaluronan biosyn...	GO:1900126
microspike assembly	GO:0030035
multinuclear osteoclast differentiation	GO:0072674
osteoclast fusion	GO:0072675
establishment of protein localization to...	GO:0090152
hepatocyte apoptotic process	GO:0097284
regulation of skeletal muscle acetylchol...	GO:1904393
negative regulation of skeletal muscle a...	GO:1904394
formate transport	GO:0015724
oxalate transport	GO:0019532
skeletal muscle acetylcholine-gated chan...	GO:0071340
cellular response to interleukin-11	GO:0071348
hyaluronan biosynthetic process	GO:0030213
transcription initiation from mitochondr...	GO:0006391
multicellular organism adhesion	GO:0022608
multicellular organism adhesion to subst...	GO:0022609
positive regulation of mRNA 3'-end proce...	GO:0031442
sulfate transmembrane transport	GO:1902358



0 1 2 3 4 5  
-log(p)  
n=19/61 input genes with annotations

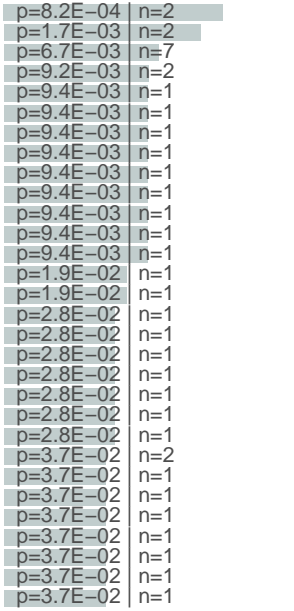


0.0 0.2 0.4 0.6 0.8 1.0  
fraction

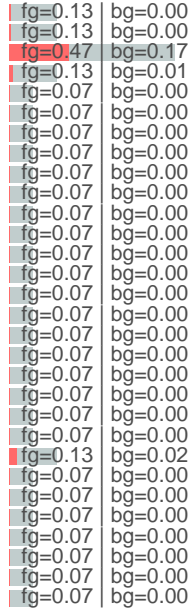
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_048724605.1

fraction genes in fg and expected value

arrestin family protein binding	GO:1990763
polyubiquitin modification-dependent pro...	GO:0031593
identical protein binding	GO:0042802
single-stranded DNA binding	GO:0003697
oxalate transmembrane transporter activi...	GO:0019531
3'-5'-exodeoxyribonuclease activity	GO:0008296
sulfate transmembrane transporter activi...	GO:0015116
MutLalpha complex binding	GO:0032405
MutSalpha complex binding	GO:0032407
formate transmembrane transporter activi...	GO:0015499
CXCR chemokine receptor binding	GO:0045236
translation elongation factor binding	GO:0061770
clathrin light chain binding	GO:0032051
STAT family protein binding	GO:0097677
sequence-specific single stranded DNA bi...	GO:0098847
DNA-directed 5'-3' RNA polymerase activi...	GO:0003899
ankyrin binding	GO:0030506
pre-mRNA 3'-splice site binding	GO:0030628
Wnt-activated receptor activity	GO:0042813
K63-linked polyubiquitin modification-de...	GO:0070530
bicarbonate transmembrane transporter ac...	GO:0015106
RNA polymerase II intronic transcription...	GO:0001162
heat shock protein binding	GO:0031072
anion:anion antiporter activity	GO:0015301
inorganic anion exchanger activity	GO:0005452
5'-3' RNA polymerase activity	GO:0034062
solute:anion antiporter activity	GO:0140323
nucleoside diphosphate kinase activity	GO:0004550
actin monomer binding	GO:0003785
protein phosphatase inhibitor activity	GO:0004864



0 1 2 3 4 5  
-log(p)  
n=15/61 input genes with annotations

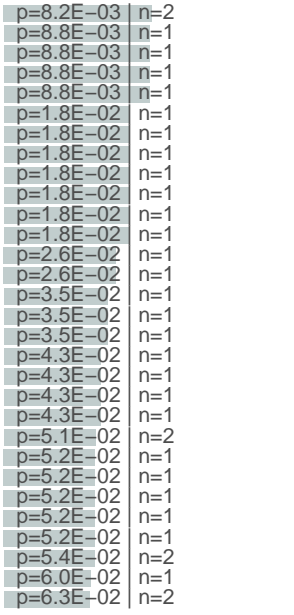


0.0 0.2 0.4 0.6 0.8 1.0  
fraction

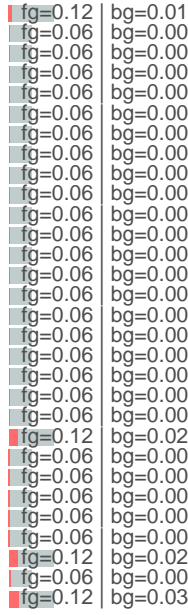
GO:CC  
Elav\_Nvec\_vc1.1\_XM\_048724605.1

fraction genes in fg and expected value

filopodium	GO:0030175
mitotic spindle microtubule	GO:1990498
outer dynein arm	GO:0036157
mitochondrial DNA-directed RNA polymeras...	GO:0034245
sperm cytoplasmic droplet	GO:0097598
clathrin complex	GO:0071439
GATOR2 complex	GO:0061700
ESCRT I complex	GO:0000813
U2AF complex	GO:0089701
Seh1-associated complex	GO:0035859
nuclear stress granule	GO:0097165
sorting endosome	GO:0097443
endolysosome membrane	GO:0036020
endolysosome	GO:0036019
Myb complex	GO:0031523
aggresome	GO:0016235
intrinsic component of the cytoplasmic s...	GO:0031235
mitotic spindle pole	GO:0097431
filopodium membrane	GO:0031527
sperm fibrous sheath	GO:0035686
sperm principal piece	GO:0097228
cytoplasmic side of plasma membrane	GO:0009898
mitochondrial nucleoid	GO:0042645
nucleoid	GO:0009295
proteasome regulatory particle, base sub...	GO:0008540
pronucleus	GO:0045120
clathrin-coated endocytic vesicle membra...	GO:0030669
lysosomal membrane	GO:0005765
PML body	GO:0016605
lytic vacuole membrane	GO:0098852



0 1 2 3 4 5  
-log(p)  
n=16/61 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0  
fraction