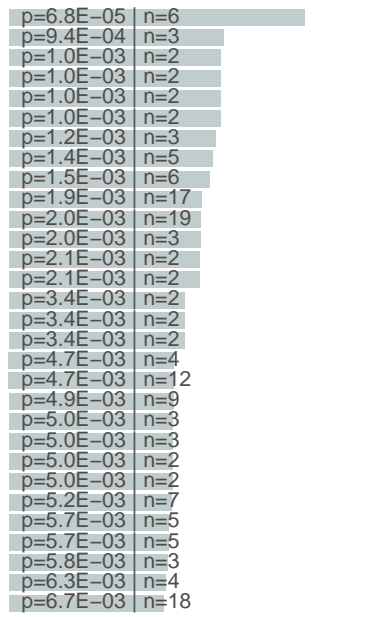


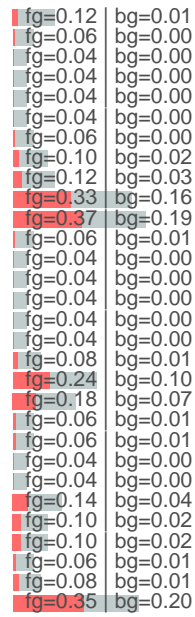
GO:BP
Elav_Nvec_vc1.1_XM_032383641.2

cell fate determination	GO:0001709
mitochondrion distribution	GO:0048311
cartilage morphogenesis	GO:0060536
protein kinase C-activating G protein-co...	GO:0007205
cellular response to hepatocyte growth f...	GO:0035729
cellular response to X-ray	GO:0071481
regulation of synaptic transmission, glu...	GO:0051966
skeletal system morphogenesis	GO:0048705
regulation of neuron apoptotic process	GO:0043523
multi-organism reproductive process	GO:0044703
regulation of cellular protein metabolic...	GO:0032268
regulation of fat cell differentiation	GO:0045598
semicircular canal development	GO:0060872
negative regulation of extrinsic apoptot...	GO:2001240
nephron tubule epithelial cell different...	GO:0072160
polarity specification of anterior/poste...	GO:0009949
calcium-mediated signaling using intrace...	GO:0035584
embryonic skeletal system development	GO:0048706
positive regulation of catalytic activit...	GO:0043085
positive regulation of intracellular sig...	GO:1902533
locomotor rhythm	GO:0045475
regulation of cardiac muscle tissue deve...	GO:0055024
positive regulation of neuron migration	GO:2001224
otic vesicle morphogenesis	GO:0071600
developmental maturation	GO:0021700
regulation of animal organ morphogenesis	GO:2000027
negative regulation of neuron death	GO:1901215
outflow tract morphogenesis	GO:0003151
immune response-activating cell surface ...	GO:0002429
organic substance transport	GO:0071702



0 1 2 3 4 5
-log(p)
n=51/182 input genes with annotations

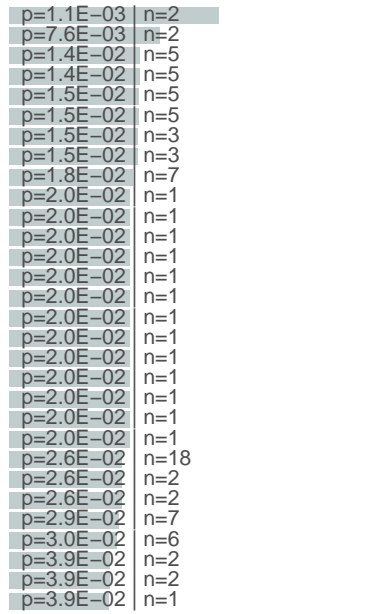
fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0
fraction

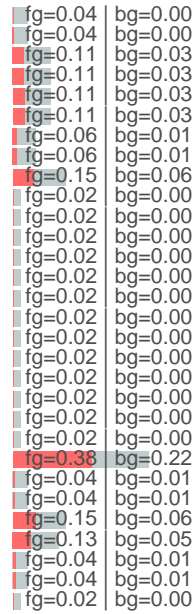
GO:MF
Elav_Nvec_vc1.1_XM_032383641.2

caspase binding	GO:0089720
HMG box domain binding	GO:0071837
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
cis-regulatory region sequence-specific ...	GO:0000987
RNA polymerase II cis-regulatory region ...	GO:0000978
DNA-binding transcription repressor acti...	GO:0001227
DNA-binding transcription repressor acti...	GO:0001217
double-stranded DNA binding	GO:0003690
glutamate-cysteine ligase catalytic subu...	GO:0035226
interleukin-2 receptor binding	GO:0005134
cysteine desulfurase activity	GO:0031071
S-adenosyl-L-methionine transmembrane tr...	GO:0000095
heparan sulfate N-acetylglucosaminyltran...	GO:0042328
poly(G) binding	GO:0034046
protein tyrosine phosphatase activity, m...	GO:0030946
inorganic diphosphatase activity	GO:0004427
glucuronosyl-N-acetylglucosaminyl-proteo...	GO:0050508
N-acetylglucosaminyl-proteoglycan 4-beta...	GO:0050509
acid sphingomyelin phosphodiesterase act...	GO:0061750
arylsulfamidase activity	GO:0004061
glucose-6-phosphate dehydrogenase activi...	GO:0004345
enzyme binding	GO:0019899
protein tyrosine phosphatase activity	GO:0004725
histone acetyltransferase binding	GO:0035035
sequence-specific DNA binding	GO:0043565
sequence-specific double-stranded DNA bi...	GO:1990837
growth factor receptor binding	GO:0070851
protein tyrosine kinase binding	GO:1990782
A2A adenosine receptor binding	GO:0031687



0 1 2 3 4 5
-log(p)
n=47/182 input genes with annotations

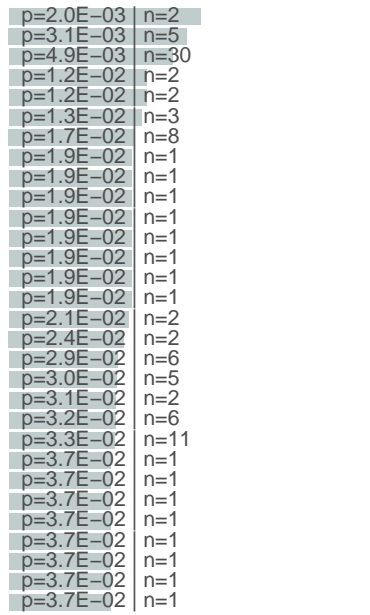
fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0
fraction

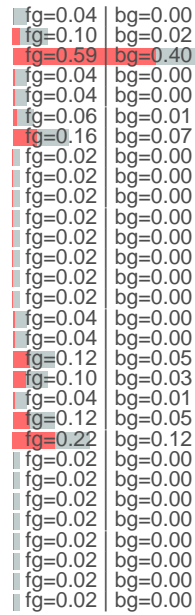
GO:CC
Elav_Nvec_vc1.1_XM_032383641.2

eukaryotic translation initiation factor...	GO:0071541
site of polarized growth	GO:0030427
cytosol	GO:0005829
microbody lumen	GO:0031907
peroxisomal matrix	GO:0005782
ATPase complex	GO:1904949
axon	GO:0030424
internode region of axon	GO:0033269
anterior cell cortex	GO:0061802
sperm individualization complex	GO:0070864
investment cone	GO:0070865
Schmidt-Lanterman incisure	GO:0043220
cerebellar mossy fiber	GO:0044300
compact myelin	GO:0043218
ATF4-CREB1 transcription factor complex	GO:1990589
Golgi trans cisterna	GO:0000138
cytoplasmic microtubule	GO:0005881
nuclear chromosome	GO:0000228
cell cortex	GO:0005938
Golgi medial cisterna	GO:0005797
chromatin	GO:0000785
neuron projection	GO:0043005
growing cell tip	GO:0035838
L-cysteine desulfurase complex	GO:1990221
G protein-coupled receptor complex	GO:0097648
lateral loop	GO:0043219
glutamate-cysteine ligase complex	GO:0017109
extrinsic component of Golgi membrane	GO:0090498
Ku70:Ku80 complex	GO:0043564
ESCRT IV complex	GO:1990621



0 1 2 3 4 5
-log(p)
n=51/182 input genes with annotations

fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0
fraction