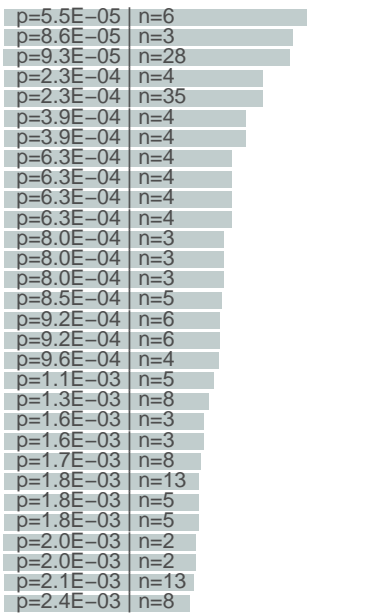


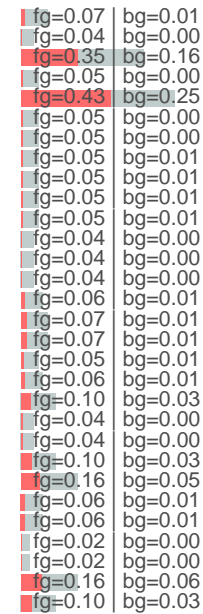
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032373618.2

fraction genes in fg and expected value

somatic stem cell population maintenance	GO:0035019
stem cell fate specification	GO:0048866
positive regulation of gene expression	GO:0010628
developmental induction	GO:0031128
regulation of cellular macromolecule bio...	GO:2000112
cellular response to glucose starvation	GO:0042149
segment polarity determination	GO:0007367
artery morphogenesis	GO:0048844
cellular response to cAMP	GO:0071320
cellular response to retinoic acid	GO:0071300
epidermis morphogenesis	GO:0048730
lens morphogenesis in camera-type eye	GO:0002089
cellular response to ethanol	GO:0071361
Kupffer's vesicle development	GO:0070121
non-canonical Wnt signaling pathway	GO:0035567
transforming growth factor beta receptor...	GO:0007179
regulation of organ growth	GO:0046620
regulation of hematopoietic stem cell di...	GO:1902036
epithelial to mesenchymal transition	GO:0001837
regulation of animal organ morphogenesis	GO:2000027
endodermal cell fate commitment	GO:0001711
positive regulation of transcription of ...	GO:0007221
imaginal disc-derived wing morphogenesis	GO:0007476
embryonic organ development	GO:0048568
kidney morphogenesis	GO:0060993
positive regulation of canonical Wnt sig...	GO:0090263
endothelial tube morphogenesis	GO:0061154
neuroblast fate specification	GO:0014018
positive regulation of programmed cell d...	GO:0043068
dorsal/ventral pattern formation	GO:0009953



0 1 2 3 4 5  
-log(p)  
n=81/296 input genes with annotations

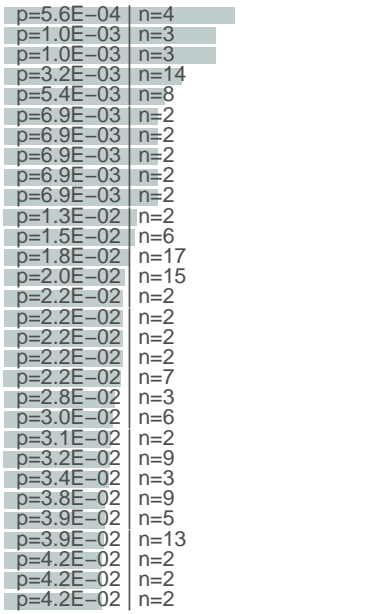


0.0 0.2 0.4 0.6 0.8 1.0  
fraction

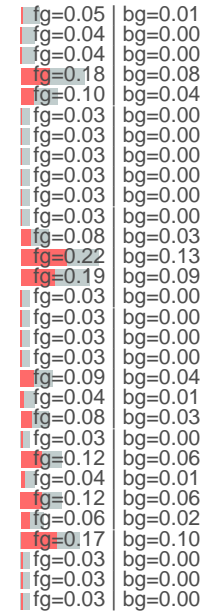
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032373618.2

fraction genes in fg and expected value

transcription coregulator binding	GO:0001221
calcium-release channel activity	GO:0015278
Wnt-protein binding	GO:0017147
DNA-binding transcription factor activit...	GO:0003700
RNA polymerase II cis-regulatory region ...	GO:0000978
oxidoreductase activity, acting on the C...	GO:0016899
DNA binding domain binding	GO:0050692
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613
lactate dehydrogenase activity	GO:0004457
inosine kinase activity	GO:0008906
nucleoside diphosphate kinase activity	GO:0004550
ion gated channel activity	GO:0022839
protein dimerization activity	GO:0046983
protein domain specific binding	GO:0019904
cysteine-type endopeptidase regulator ac...	GO:0043028
transcription coactivator binding	GO:0001223
epinephrine binding	GO:0051379
catecholamine binding	GO:1901338
transcription coactivator activity	GO:0003713
SMAD binding	GO:0046332
mRNA binding	GO:0003729
mitogen-activated protein kinase kinase ...	GO:0031434
protein heterodimerization activity	GO:0046982
transmembrane transporter binding	GO:0044325
transcription coregulator activity	GO:0003712
GTPase activator activity	GO:0005096
small molecule binding	GO:0036094
nuclear estrogen receptor binding	GO:0030331
adrenergic receptor binding	GO:0031690
protein-disulfide reductase (NAD(P)) act...	GO:0047134



0 1 2 3 4 5  
-log(p)  
n=78/296 input genes with annotations

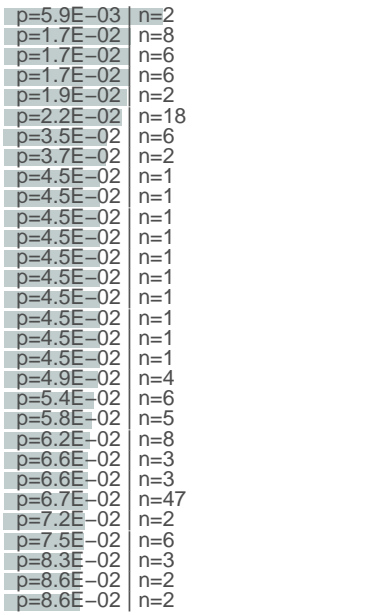


0.0 0.2 0.4 0.6 0.8 1.0  
fraction

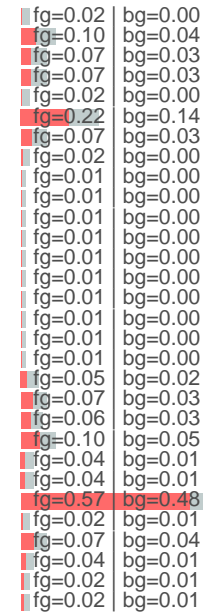
GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032373618.2

fraction genes in fg and expected value

beta-catenin-TCF complex	GO:1990907
cell cortex	GO:0005938
basal plasma membrane	GO:0009925
basolateral plasma membrane	GO:0016323
sensory dendrite	GO:0071683
mitochondrion	GO:0005739
basal part of cell	GO:0045178
calcium channel complex	GO:0034704
beta-catenin-TCF7L2 complex	GO:0070369
post-mRNA release spliceosomal complex	GO:0071014
apoptosome	GO:0043293
beta-catenin destruction complex	GO:0030877
catenin-TCF7L2 complex	GO:0071664
smooth septate junction	GO:0005920
polycystin complex	GO:0002133
fascia adherens	GO:0005916
Scrib-APC-beta-catenin complex	GO:0034750
catenin complex	GO:0016342
receptor complex	GO:0043235
nuclear speck	GO:0016607
cytoplasmic side of membrane	GO:0098562
cytoplasmic region	GO:0099568
plasma membrane raft	GO:0044853
cation channel complex	GO:0034703
nucleus	GO:0005634
cytoplasmic stress granule	GO:0010494
side of membrane	GO:0098552
ion channel complex	GO:0034702
ciliary base	GO:0097546
lateral plasma membrane	GO:0016328



0 1 2 3 4 5  
-log(p)  
n=82/296 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0  
fraction