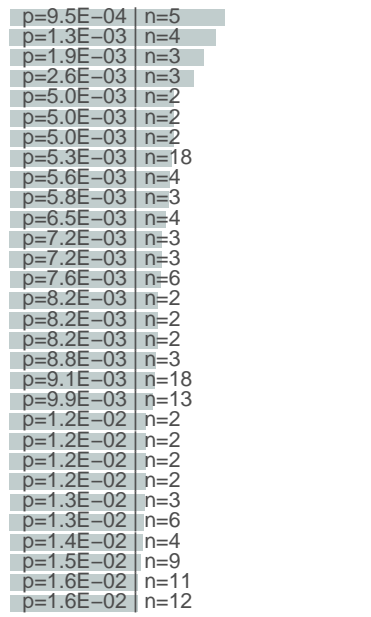


GO:BP
Elav_Nvec_vc1.1_XM_001636155.3

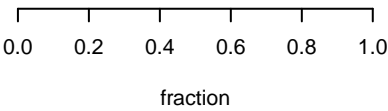
fraction genes in fg and expected value

negative regulation of cell growth	GO:0030308
mRNA polyadenylation	GO:0006378
regulation of oxidative stress–induced n...	GO:1903203
visual learning	GO:0008542
negative regulation of epithelial to mes...	GO:0010719
neuroblast migration	GO:0097402
regulation of long–term neuronal synapti...	GO:0048169
regulation of cell differentiation	GO:0045595
transition metal ion homeostasis	GO:0055076
response to cold	GO:0009409
regulation of lipid biosynthetic process	GO:0046890
negative regulation of oxidative stress–...	GO:1903202
negative regulation of cellular response...	GO:1900408
regulation of Wnt signaling pathway	GO:0030111
positive regulation of G2/M transition o...	GO:0010971
mRNA transcription	GO:0009299
response to iron ion	GO:0010039
cellular response to hydrogen peroxide	GO:0070301
regulation of multicellular organismal d...	GO:2000026
negative regulation of cellular macromol...	GO:2000113
endoplasmic reticulum calcium ion homeos...	GO:0032469
positive regulation of receptor signalin...	GO:0046427
regulation of epidermal cell differentia...	GO:0045604
positive regulation of receptor signalin...	GO:1904894
positive regulation of insulin secretion	GO:0032024
muscle organ development	GO:0007517
positive regulation of protein secretion	GO:0050714
negative regulation of transcription by ...	GO:0000122
negative regulation of transcription, DN...	GO:0045892
regulation of cell development	GO:0060284



–log(p)
n=54/211 input genes with annotations

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fg=0.04	bg=0.00
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fg=0.07	bg=0.01
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fg=0.07	bg=0.01
fg=0.06	bg=0.01
fg=0.11	bg=0.03
fg=0.04	bg=0.00
fg=0.04	bg=0.00
fg=0.04	bg=0.01
fg=0.33	bg=0.19
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fg=0.06	bg=0.01
fg=0.11	bg=0.04
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fg=0.22	bg=0.11

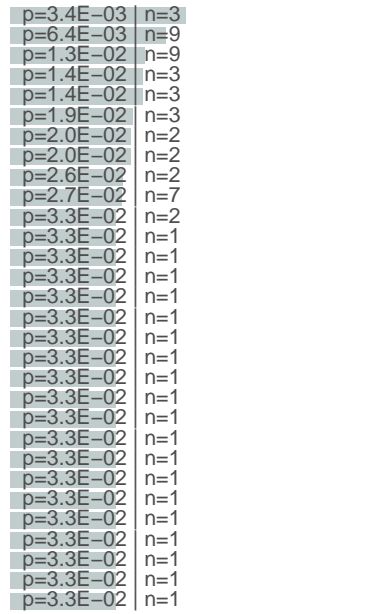


fraction

GO:MF
Elav_Nvec_vc1.1_XM_001636155.3

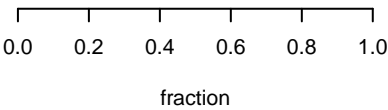
fraction genes in fg and expected value

histone acetyltransferase binding	GO:0035035
DNA–binding transcription factor activit...	GO:0000981
transcription factor binding	GO:0008134
Hsp90 protein binding	GO:0051879
core promoter sequence–specific DNA bind...	GO:0001046
histone deacetylase binding	GO:0042826
polyubiquitin modification–dependent pro...	GO:0031593
polynucleotide adenyllyltransferase activ...	GO:0004652
hormone binding	GO:0042562
protein heterodimerization activity	GO:0046982
adenyllyltransferase activity	GO:0070566
adipokinetic hormone receptor activity	GO:0097003
pyrroline–5–carboxylate reductase activi...	GO:0004735
cobalt ion binding	GO:0050897
uridyllyltransferase activity	GO:0070569
RNA uridyllyltransferase activity	GO:0050265
chondroitin–glucuronate 5–epimerase acti...	GO:0047757
acetylcholine receptor regulator activit...	GO:0030548
acetylcholine receptor activator activit...	GO:0030549
TFIIIF–class transcription factor complex...	GO:0001096
N–acetylglucosamine–1–phosphodiester alp...	GO:0003944
translation elongation factor binding	GO:0061770
adiponectin binding	GO:0055100
G–protein beta–subunit binding	GO:0031681
calcitonin family binding	GO:0097644
neurotransmitter receptor regulator acti...	GO:0099602
amylin binding	GO:0097645
glycolipid transfer activity	GO:0017089
heparan sulfate binding	GO:1904399
K48–linked polyubiquitin modification–de...	GO:0036435



–log(p)
n=52/211 input genes with annotations

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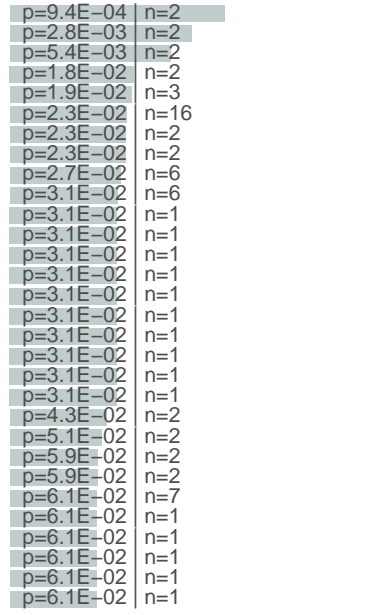


fraction

GO:CC
Elav_Nvec_vc1.1_XM_001636155.3

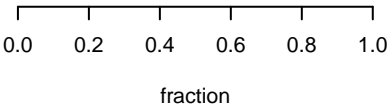
fraction genes in fg and expected value

growth cone filopodium	GO:1990812
growth cone lamellipodium	GO:1990761
spindle midzone	GO:0051233
vacuolar proton–transporting V–type ATPa...	GO:0016471
lipid droplet	GO:0005811
intrinsic component of membrane	GO:0031224
proton–transporting two–sector ATPase co...	GO:0016469
proton–transporting V–type ATPase comple...	GO:0033176
integral component of organelle membrane	GO:0031301
intrinsic component of organelle membran...	GO:0031300
chromaffin granule	GO:0042583
chromaffin granule membrane	GO:0042584
amyloid–beta complex	GO:0106003
core–binding factor complex	GO:0016513
intermediate–density lipoprotein particl...	GO:0034363
high–density lipoprotein particle	GO:0034364
lipoprotein particle	GO:1990777
plasma lipoprotein particle	GO:0034358
triglyceride–rich plasma lipoprotein par...	GO:0034385
endosome to plasma membrane transport ve...	GO:0070381
integral component of Golgi membrane	GO:0030173
intrinsic component of Golgi membrane	GO:0031228
transcription repressor complex	GO:0017053
COPII–coated ER to Golgi transport vesic...	GO:0030134
nuclear body	GO:0016604
extrinsic component of endoplasmic retic...	GO:0042406
endosome lumen	GO:0031904
ciliary rootlet	GO:0035253
spanning component of plasma membrane	GO:0044214
platelet alpha granule membrane	GO:0031092



–log(p)
n=56/211 input genes with annotations

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fraction