

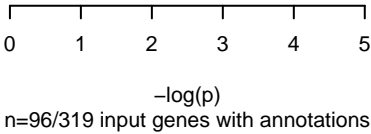
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032377390.2

fraction genes in fg and expected value

response to inorganic substance	GO:0010035
detection of endogenous stimulus	GO:0009726
response to mechanical stimulus	GO:0009612
response to reactive oxygen species	GO:0000302
cellular response to lipid	GO:0071396
central nervous system development	GO:0007417
positive regulation of cholesterol trans...	GO:0032376
metanephric ascending thin limb developm...	GO:0072218
metanephric distal tubule development	GO:0072235
presynaptic active zone organization	GO:1990709
cellular response to organic cyclic comp...	GO:0071407
protein-containing complex assembly	GO:0065003
wing disc dorsal/ventral pattern formati...	GO:0048190
positive regulation of cholesterol metab...	GO:0090205
intracellular sterol transport	GO:0032366
intracellular cholesterol transport	GO:0032367
regulation of hydrogen peroxide-induced ...	GO:1903205
negative regulation of hydrogen peroxide...	GO:1903206
regulation of imaginal disc growth	GO:0045570
foam cell differentiation	GO:0090077
regulation of cellular response to drug	GO:2001038
negative regulation of cellular response...	GO:2001039
negative regulation of response to react...	GO:1901032
multicellular organismal process	GO:0032501
forebrain development	GO:0030900
regulation of cellular response to stres...	GO:0080135
response to anesthetic	GO:0072347
negative regulation of developmental pro...	GO:0051093
regulation of synapse assembly	GO:0051963
cellular amino acid biosynthetic process	GO:0008652

p=3.4E-04	n=15
p=1.3E-03	n=2
p=2.0E-03	n=8
p=3.9E-03	n=7
p=5.3E-03	n=10
p=6.7E-03	n=17
p=7.2E-03	n=2
p=7.2E-03	n=2
p=7.2E-03	n=2
p=7.2E-03	n=2
p=7.8E-03	n=11
p=9.1E-03	n=25
p=9.6E-03	n=3
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=67
p=1.2E-02	n=9
p=1.4E-02	n=13
p=1.4E-02	n=4
p=1.4E-02	n=14
p=1.6E-02	n=6
p=1.6E-02	n=4

fg=0.16	bg=0.06
fg=0.02	bg=0.00
fg=0.08	bg=0.02
fg=0.07	bg=0.02
fg=0.10	bg=0.04
fg=0.18	bg=0.09
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.11	bg=0.05
fg=0.26	bg=0.16
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.70	bg=0.54
fg=0.09	bg=0.04
fg=0.14	bg=0.07
fg=0.04	bg=0.01
fg=0.15	bg=0.08
fg=0.06	bg=0.02
fg=0.04	bg=0.01



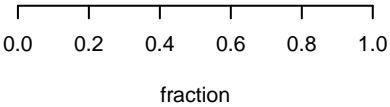
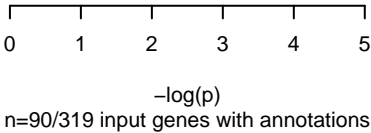
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032377390.2

fraction genes in fg and expected value

mitogen-activated protein kinase p38 bin...	GO:0048273
signaling receptor complex adaptor activ...	GO:0030159
ankyrin binding	GO:0030506
double-stranded RNA binding	GO:0003725
clathrin binding	GO:0030276
lipid binding	GO:0008289
JUN kinase binding	GO:0008432
AP-2 adaptor complex binding	GO:0035612
transaminase activity	GO:0008483
oxidoreductase activity, acting on the C...	GO:0016646
calcium ion binding	GO:0005509
phospholipid binding	GO:0005543
BH domain binding	GO:0051400
mitogen-activated protein kinase kinase ...	GO:0031434
phosphatase inhibitor activity	GO:0019212
transferase activity, transferring nitro...	GO:0016769
cholesterol binding	GO:0015485
potassium channel activity	GO:0005267
transmembrane transporter binding	GO:0044325
active transmembrane transporter activit...	GO:0022804
protein domain specific binding	GO:0019904
transmembrane transporter activity	GO:0022857
transcription coregulator activity	GO:0003712
outward rectifier potassium channel acti...	GO:0015271
sterol binding	GO:0032934
phosphoprotein binding	GO:0051219
neuropilin binding	GO:0038191
protein-arginine omega-N asymmetric meth...	GO:0035242
vascular endothelial growth factor recep...	GO:0043184
S-adenosyl-L-methionine transmembrane tr...	GO:0000095

p=1.4E-03	n=2
p=3.8E-03	n=3
p=8.1E-03	n=2
p=1.1E-02	n=3
p=1.1E-02	n=3
p=1.3E-02	n=10
p=1.3E-02	n=2
p=1.3E-02	n=2
p=1.3E-02	n=2
p=1.3E-02	n=2
p=1.7E-02	n=6
p=1.7E-02	n=8
p=1.9E-02	n=2
p=1.9E-02	n=2
p=2.6E-02	n=2
p=2.6E-02	n=2
p=2.6E-02	n=2
p=2.9E-02	n=3
p=2.9E-02	n=3
p=3.0E-02	n=7
p=3.1E-02	n=13
p=3.2E-02	n=13
p=3.4E-02	n=9
p=3.4E-02	n=2
p=3.4E-02	n=2
p=3.8E-02	n=3
p=3.8E-02	n=1
p=3.8E-02	n=1
p=3.8E-02	n=1

fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.11	bg=0.05
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.07	bg=0.02
fg=0.09	bg=0.04
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.08	bg=0.03
fg=0.14	bg=0.08
fg=0.14	bg=0.08
fg=0.10	bg=0.05
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032377390.2

fraction genes in fg and expected value

neuromuscular junction	GO:0031594
presynaptic membrane	GO:0042734
cytoplasmic side of membrane	GO:0098562
dendritic spine membrane	GO:0032591
growth cone lamellipodium	GO:1990761
sarcomere	GO:0030017
cytoplasmic side of plasma membrane	GO:0009898
postsynaptic membrane	GO:0045211
methylosome	GO:0034709
presynaptic periaxial zone	GO:0036062
neuronal cell body membrane	GO:0032809
cell periphery	GO:0071944
A band	GO:0031672
cell body membrane	GO:0044298
neuronal cell body	GO:0043025
main axon	GO:0044304
spectrosome	GO:0045170
AP-4 adaptor complex	GO:0030124
dendritic spine head	GO:0044327
spectrin	GO:0008091
anchored component of the cytoplasmic si...	GO:0098753
polycystin complex	GO:0002133
cytoplasmic side of dendritic spine plas...	GO:1990780
hippocampal mossy fiber to CA3 synapse	GO:0098686
fusome	GO:0045169
I band	GO:0031674
presynaptic active zone	GO:0048786
stress fiber	GO:0001725
contractile actin filament bundle	GO:0097517
cell cortex	GO:0005938

p=3.8E-03	n=6
p=5.8E-03	n=5
p=6.1E-03	n=7
p=7.3E-03	n=2
p=7.3E-03	n=2
p=7.4E-03	n=6
p=1.2E-02	n=6
p=1.2E-02	n=5
p=1.2E-02	n=2
p=1.2E-02	n=2
p=2.1E-02	n=3
p=2.3E-02	n=37
p=2.5E-02	n=3
p=2.5E-02	n=3
p=2.7E-02	n=11
p=2.9E-02	n=3
p=3.6E-02	n=1
p=3.6E-02	n=1
p=3.6E-02	n=1
p=3.6E-02	n=1
p=3.6E-02	n=1
p=3.6E-02	n=1
p=3.9E-02	n=2
p=4.2E-02	n=4
p=4.7E-02	n=3
p=4.8E-02	n=2
p=4.8E-02	n=2
p=5.0E-02	n=7

fg=0.06	bg=0.02
fg=0.05	bg=0.01
fg=0.07	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.05	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.38	bg=0.25
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.11	bg=0.06
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.04	bg=0.01
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.07	bg=0.03

