

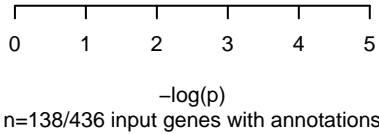
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_048732532.1

fraction genes in fg and expected value

Golgi to endosome transport	GO:0006895
podosome assembly	GO:0071800
regulation of NMDA receptor activity	GO:2000310
positive regulation of vascular associat...	GO:1904754
actomyosin contractile ring assembly	GO:0000915
cholesterol biosynthetic process	GO:0006695
progesterone receptor signaling pathway	GO:0050847
regulation of germinal center formation	GO:0002634
negative regulation of lipid kinase acti...	GO:0090219
female gonad development	GO:0008585
actin cytoskeleton reorganization	GO:0031532
T cell activation involved in immune res...	GO:0002286
positive regulation of substrate adhesio...	GO:1900026
regulation of glutamate receptor signali...	GO:1900449
regulation of cell junction assembly	GO:1901888
regulation of Rho protein signal transdu...	GO:0035023
dendrite morphogenesis	GO:0048813
regulation of cellular macromolecule bio...	GO:2000112
regulation of lamellipodium assembly	GO:0010591
B cell homeostasis	GO:0001782
regulation of embryonic cell shape	GO:0016476
ribonucleoprotein complex assembly	GO:0022618
axonogenesis	GO:0007409
activation of immune response	GO:0002253
establishment of cell polarity	GO:0030010
T cell differentiation	GO:0030217
Rac protein signal transduction	GO:0016601
epithelial cell morphogenesis	GO:0003382
myeloid dendritic cell activation	GO:0001773
negative regulation of CD4-positive, alp...	GO:0043371

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p=2.3E-03	n=4
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p=2.6E-03	n=2
p=2.7E-03	n=5
p=3.4E-03	n=5
p=3.9E-03	n=3
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p=3.9E-03	n=3
p=4.2E-03	n=10
p=4.4E-03	n=4
p=5.1E-03	n=10
p=5.5E-03	n=47
p=5.7E-03	n=4
p=6.1E-03	n=3
p=6.1E-03	n=3
p=6.2E-03	n=9
p=6.4E-03	n=16
p=6.7E-03	n=10
p=6.7E-03	n=8
p=7.1E-03	n=8
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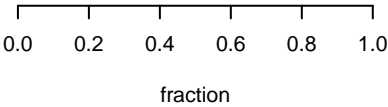
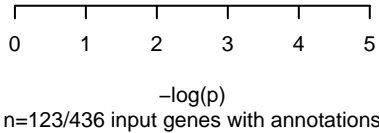
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_048732532.1

fraction genes in fg and expected value

guanyl-nucleotide exchange factor activi...	GO:0005085
small GTPase binding	GO:0031267
mRNA binding	GO:0003729
actin binding	GO:0003779
miRNA binding	GO:0035198
L-histidine transmembrane transporter ac...	GO:0005290
SH3 domain binding	GO:0017124
molecular adaptor activity	GO:0060090
protein-macromolecule adaptor activity	GO:0030674
profilin binding	GO:0005522
amide transmembrane transporter activity	GO:0042887
GTP binding	GO:0005525
double-stranded RNA binding	GO:0003725
purine ribonucleoside binding	GO:0032550
ribonucleoside binding	GO:0032549
translation regulator activity	GO:0045182
proline-rich region binding	GO:0070064
aspartic-type endopeptidase activity	GO:0004190
aspartic-type peptidase activity	GO:0070001
purine nucleoside binding	GO:0001883
GTPase activity	GO:0003924
nucleoside binding	GO:0001882
guanyl ribonucleotide binding	GO:0032561
guanyl nucleotide binding	GO:0019001
actin filament binding	GO:0051015
protein heterodimerization activity	GO:0046982
ribosomal small subunit binding	GO:0043024
phosphatidylcholine binding	GO:0031210
MAP kinase kinase kinase activity	GO:0004709
single-stranded RNA binding	GO:0003727

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p=8.0E-03	n=5
p=1.3E-02	n=8
p=1.3E-02	n=8
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p=2.4E-02	n=6
p=2.7E-02	n=3
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_048732532.1

fraction genes in fg and expected value

sperm annulus	GO:0097227
septin complex	GO:0031105
septin ring	GO:0005940
actin filament bundle	GO:0032432
actomyosin contractile ring	GO:0005826
cytoplasmic side of membrane	GO:0098562
cleavage furrow	GO:0032154
polysome	GO:0005844
cytoplasmic region	GO:0099568
neuron projection	GO:0043005
stress fiber	GO:0001725
contractile actin filament bundle	GO:0097517
myofilament	GO:0036379
striated muscle thin filament	GO:0005865
Cajal body	GO:0015030
cytoplasmic side of plasma membrane	GO:0009898
midbody	GO:0030496
myelin sheath	GO:0043209
guanyl-nucleotide exchange factor comple...	GO:0032045
protein phosphatase type 2A complex	GO:0000159
Prp19 complex	GO:0000974
podosome	GO:0002102
nuclear speck	GO:0016607
catalytic step 2 spliceosome	GO:0071013
cell cortex	GO:0005938
axon	GO:0030424
filopodium tip	GO:0032433
Derlin-1 retrotranslocation complex	GO:0036513
sarcomere	GO:0030017
euchromatin	GO:0000791

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p=4.2E-03	n=4
p=5.9E-03	n=5
p=7.3E-03	n=14
p=7.8E-03	n=26
p=1.2E-02	n=3
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p=1.4E-02	n=2
p=1.4E-02	n=2
p=1.5E-02	n=3
p=1.7E-02	n=7
p=2.1E-02	n=6
p=2.1E-02	n=6
p=2.3E-02	n=2
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