

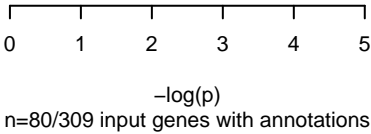
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032367127.2

fraction genes in fg and expected value

regulation of neurogenesis	GO:0050767
regulation of neuron differentiation	GO:0045664
negative regulation of endothelial cell ...	GO:2000352
Rho protein signal transduction	GO:0007266
positive regulation of cytosolic calcium...	GO:0007204
positive regulation of endothelial cell ...	GO:0010595
positive regulation of angiogenesis	GO:0045766
regulation of animal organ morphogenesis	GO:2000027
positive regulation of cellular componen...	GO:0051130
pituitary gland development	GO:0021983
positive regulation of protein kinase B ...	GO:0051897
cellular response to catecholamine stimu...	GO:0071870
positive regulation of growth rate	GO:0040010
kidney morphogenesis	GO:0060993
neuroepithelial cell differentiation	GO:0060563
embryonic hemopoiesis	GO:0035162
positive regulation of transcription fro...	GO:0006990
response to tunicamycin	GO:1904576
compartment pattern specification	GO:0007386
cellular response to estrogen stimulus	GO:0071391
T cell cytokine production	GO:0002369
positive regulation of transcription by ...	GO:0045944
membrane repolarization during cardiac m...	GO:0086013
regulation of establishment of cell pola...	GO:2000114
positive regulation of peptidyl-lysine a...	GO:2000758
adenylate cyclase-modulating G protein-c...	GO:0007188
regulation of neuron projection developm...	GO:0010975
positive regulation of cysteine-type end...	GO:0043280
regulation of blood vessel endothelial c...	GO:0043535
tissue morphogenesis	GO:0048729

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p=1.3E-04	n=17
p=3.2E-04	n=3
p=3.4E-04	n=6
p=7.4E-04	n=7
p=8.0E-04	n=5
p=1.0E-03	n=5
p=1.2E-03	n=8
p=1.3E-03	n=20
p=1.3E-03	n=4
p=1.3E-03	n=4
p=1.4E-03	n=5
p=1.5E-03	n=3
p=1.7E-03	n=5
p=1.7E-03	n=5
p=1.9E-03	n=4
p=1.9E-03	n=2
p=1.9E-03	n=2
p=1.9E-03	n=2
p=1.9E-03	n=2
p=2.3E-03	n=18
p=2.5E-03	n=3
p=2.5E-03	n=3
p=2.5E-03	n=3
p=2.7E-03	n=5
p=2.7E-03	n=12
p=3.2E-03	n=5
p=3.3E-03	n=4
p=3.3E-03	n=20

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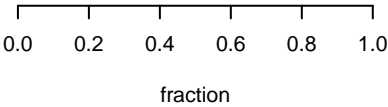
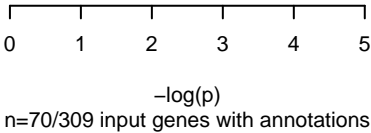
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032367127.2

fraction genes in fg and expected value

acetylcholine receptor binding	GO:0033130
transcription coactivator binding	GO:0001223
potassium channel regulator activity	GO:0015459
DNA-binding transcription activator acti...	GO:0001228
ligand-gated calcium channel activity	GO:0099604
scaffold protein binding	GO:0097110
protein domain specific binding	GO:0019904
enzyme inhibitor activity	GO:0004857
NAD binding	GO:0051287
triglyceride lipase activity	GO:0004806
calcium channel regulator activity	GO:0005246
RNA polymerase II transcription regulato...	GO:0000977
transcription coregulator activity	GO:0003712
intracellular ligand-gated ion channel a...	GO:0005217
ion gated channel activity	GO:0022839
transcription coregulator binding	GO:0001221
peptidase regulator activity	GO:0061134
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
protein heterodimerization activity	GO:0046982
14-3-3 protein binding	GO:0071889
calcium-release channel activity	GO:0015278
arrestin family protein binding	GO:1990763
enzyme activator activity	GO:0008047
transmembrane transporter binding	GO:0044325
endopeptidase inhibitor activity	GO:0004866
peptidase activator activity	GO:0016504
HMG box domain binding	GO:0071837

p=3.2E-04	n=3
p=7.6E-04	n=3
p=9.0E-04	n=4
p=1.0E-03	n=9
p=1.5E-03	n=3
p=4.2E-03	n=4
p=4.6E-03	n=14
p=5.3E-03	n=6
p=5.6E-03	n=2
p=5.6E-03	n=2
p=5.6E-03	n=3
p=6.3E-03	n=9
p=7.0E-03	n=10
p=7.8E-03	n=3
p=8.7E-03	n=6
p=1.0E-02	n=5
p=1.0E-02	n=3
p=1.1E-02	n=7
p=1.1E-02	n=7
p=1.2E-02	n=4
p=1.2E-02	n=4
p=1.7E-02	n=9
p=1.7E-02	n=2
p=1.7E-02	n=2
p=1.8E-02	n=8
p=2.5E-02	n=3
p=2.5E-02	n=2
p=2.5E-02	n=2
p=2.5E-02	n=2

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032367127.2

fraction genes in fg and expected value

postsynaptic membrane	GO:0045211
cell projection membrane	GO:0031253
dendritic spine	GO:0043197
transcription regulator complex	GO:0005667
COPII-coated ER to Golgi transport vesic...	GO:0030134
membrane raft	GO:0045121
terminal bouton	GO:0043195
leading edge membrane	GO:0031256
Golgi-associated vesicle	GO:0005798
actin-based cell projection	GO:0098858
subs synaptic reticulum	GO:0071212
integral component of organelle membrane	GO:0031301
neuronal cell body membrane	GO:0032809
intrinsic component of organelle membran...	GO:0031300
chromatin	GO:0000785
neuronal cell body	GO:0043025
cell leading edge	GO:0031252
cell body membrane	GO:0044298
intrinsic component of plasma membrane	GO:0031226
cytoplasmic vesicle membrane	GO:0030659
anchoring junction	GO:0070161
cell-cell junction	GO:0005911
caveola	GO:0005901
filopodium	GO:0030175
cell-cell contact zone	GO:0044291
main axon	GO:0044304
vesicle membrane	GO:0012506
nucleus	GO:0005634
dendrite	GO:0030425
dendritic tree	GO:0097447

p=2.9E-04	n=7
p=7.0E-04	n=10
p=1.8E-03	n=7
p=2.1E-03	n=10
p=2.2E-03	n=4
p=2.3E-03	n=8
p=3.2E-03	n=6
p=4.6E-03	n=5
p=5.0E-03	n=6
p=5.8E-03	n=6
p=1.2E-02	n=2
p=2.1E-02	n=8
p=2.4E-02	n=3
p=2.4E-02	n=8
p=2.7E-02	n=8
p=2.7E-02	n=11
p=2.8E-02	n=10
p=2.8E-02	n=3
p=3.1E-02	n=12
p=3.1E-02	n=12
p=3.1E-02	n=8
p=3.1E-02	n=8
p=3.4E-02	n=3
p=3.4E-02	n=3
p=3.4E-02	n=3
p=3.4E-02	n=3
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p=3.6E-02	n=15

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