

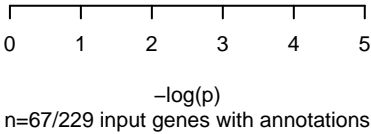
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032386243.2

fraction genes in fg and expected value

positive regulation of insulin secretion	GO:0032024
metal ion transport	GO:0030001
synaptic vesicle docking	GO:0016081
S-adenosylmethionine cycle	GO:0033353
regulation of intrinsic apoptotic signal...	GO:1902253
localization within membrane	GO:0051668
aspartate family amino acid metabolic pr...	GO:0009066
negative regulation of intrinsic apoptot...	GO:2001243
S-adenosylhomocysteine metabolic process	GO:0046498
L-cysteine metabolic process	GO:0046439
cellular response to stress	GO:0033554
cellular response to peptide hormone sti...	GO:0071375
import into cell	GO:0098657
regulation of terminal button organizati...	GO:2000331
epithelial fluid transport	GO:0042045
tracheal outgrowth, open tracheal system	GO:0007426
response to salt stress	GO:0009651
digestive system process	GO:0022600
neural tube closure	GO:0001843
DNA methylation	GO:0006306
cellular response to chemical stimulus	GO:0070887
cellular modified amino acid catabolic p...	GO:0042219
response to fructose	GO:0009750
negative regulation of Ras protein signa...	GO:0046580
phototransduction	GO:0007602
response to insulin	GO:0032868
regulation of leukocyte mediated cytox...	GO:0001910
negative regulation of DNA damage respon...	GO:0043518
cellular response to parathyroid hormone...	GO:0071374
regulation of calcium ion import	GO:0090279

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p=6.0E-04	n=12
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p=1.8E-03	n=2
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p=2.9E-03	n=11
p=3.4E-03	n=4
p=3.4E-03	n=4
p=3.5E-03	n=2
p=3.5E-03	n=2
p=4.5E-03	n=23
p=5.1E-03	n=7
p=5.1E-03	n=9
p=5.8E-03	n=2
p=5.8E-03	n=2
p=5.8E-03	n=2
p=6.5E-03	n=3
p=6.6E-03	n=4
p=7.4E-03	n=4
p=7.7E-03	n=3
p=8.3E-03	n=26
p=8.5E-03	n=2
p=8.5E-03	n=2
p=9.1E-03	n=3
p=9.1E-03	n=3
p=1.0E-02	n=6
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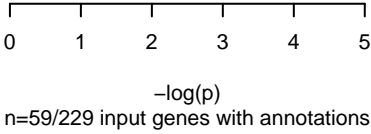
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032386243.2

fraction genes in fg and expected value

caspase binding	GO:0089720
neurexin family protein binding	GO:0042043
chloride channel inhibitor activity	GO:0019869
insulin-like growth factor receptor bind...	GO:0005159
amidine-lyase activity	GO:0016842
protein-macromolecule adaptor activity	GO:0030674
transporter activity	GO:0005215
carboxy-lyase activity	GO:0016831
metal ion transmembrane transporter acti...	GO:0046873
passive transmembrane transporter activi...	GO:0022803
channel activity	GO:0015267
alpha-tubulin binding	GO:0043014
transmembrane transporter activity	GO:0022857
phosphotransferase activity, phosphate g...	GO:0016776
inorganic cation transmembrane transport...	GO:0022890
opsin binding	GO:0002046
polyamine binding	GO:0019808
light-activated ion channel activity	GO:0010461
tricarboxylate secondary active transmem...	GO:0005371
dimethylglycine dehydrogenase activity	GO:0047865
phosphoglycerate dehydrogenase activity	GO:0004617
gamma-glutamylaminocyclotransferase acti...	GO:0061929
V2 vasopressin receptor binding	GO:0031896
platelet activating factor receptor bind...	GO:0031859
[3-methyl-2-oxobutanoate dehydrogenase (...]	GO:0047323
pyrimidine nucleotide binding	GO:0019103
putrescine binding	GO:0019810
type 2A serotonin receptor binding	GO:0031826
follicle-stimulating hormone receptor bi...	GO:0031762
methionine-tRNA ligase activity	GO:0004825

p=1.8E-03	n=2
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p=3.5E-03	n=2
p=3.8E-03	n=6
p=1.1E-02	n=12
p=1.5E-02	n=2
p=1.7E-02	n=6
p=1.8E-02	n=6
p=1.8E-02	n=6
p=2.0E-02	n=2
p=2.1E-02	n=10
p=2.4E-02	n=2
p=2.4E-02	n=7
p=2.5E-02	n=1
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p=2.5E-02	n=1
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032386243.2

fraction genes in fg and expected value

NuRD complex	GO:0016581
plasma membrane	GO:0005886
plasma membrane protein complex	GO:0098797
microvillus membrane	GO:0031528
aminoacyl-tRNA synthetase multienzyme co...	GO:0017101
basal plasma membrane	GO:0009925
basolateral plasma membrane	GO:0016323
terminal bouton	GO:0043195
extracellular exosome	GO:0070062
nuclear lamina	GO:0005652
extracellular membrane-bounded organelle	GO:0065010
extracellular organelle	GO:0043230
extracellular vesicle	GO:1903561
rhabdomere	GO:0016028
interleukin-5 receptor complex	GO:0005895
apical cytoplasm	GO:0090651
endocytic vesicle lumen	GO:0071682
pinosome	GO:0044352
macropinosome	GO:0044354
podocyte foot	GO:0098846
rhabdomere membrane	GO:0033583
rhabdomere microvillus	GO:0035996
rhabdomere microvillus membrane	GO:0035997
basal part of cell	GO:0045178
cytoplasmic vesicle membrane	GO:0030659
type I terminal bouton	GO:0061174
vesicle	GO:0031982
vesicle membrane	GO:0012506
endocytic vesicle	GO:0030139
endosome	GO:0005768

p=3.5E-03	n=2
p=6.9E-03	n=25
p=1.1E-02	n=6
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.8E-02	n=5
p=1.8E-02	n=5
p=1.8E-02	n=4
p=1.8E-02	n=3
p=1.9E-02	n=2
p=2.0E-02	n=3
p=2.0E-02	n=3
p=2.0E-02	n=3
p=2.4E-02	n=2
p=2.5E-02	n=1
p=2.5E-02	n=1
p=2.5E-02	n=1
p=2.5E-02	n=1
p=2.5E-02	n=1
p=2.5E-02	n=1
p=2.5E-02	n=1
p=2.5E-02	n=1
p=2.5E-02	n=1
p=3.0E-02	n=5
p=3.4E-02	n=9
p=3.4E-02	n=2
p=3.7E-02	n=17
p=3.8E-02	n=9
p=4.6E-02	n=4
p=4.6E-02	n=9

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