

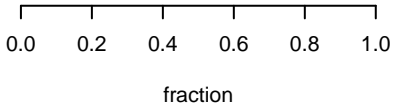
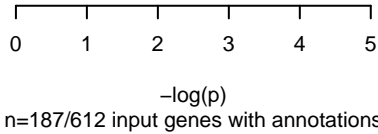
GO:BP
Elav_Nvec_vc1.1_XM_001625700.3

fraction genes in fg and expected value

melanization defense response	GO:0035006
positive regulation of neuron projection...	GO:0010976
protein import into nucleus	GO:0006606
dendrite morphogenesis	GO:0048813
collateral sprouting	GO:0048668
exonucleolytic catabolism of deadenylate...	GO:0043928
positive regulation of neuron differenti...	GO:0045666
cellular response to biotic stimulus	GO:0071216
nucleus localization	GO:0051647
positive regulation of gene expression	GO:0010628
intracellular transport	GO:0046907
positive regulation of protein localizat...	GO:1903078
positive regulation of neurogenesis	GO:0050769
somatic muscle development	GO:0007525
head development	GO:0060322
nervous system development	GO:0007399
regulation of endocytosis	GO:0030100
regulation of intracellular protein tran...	GO:0033157
exploration behavior	GO:0035640
mitotic G2 DNA damage checkpoint signali...	GO:0007095
negative regulation of Rho protein signa...	GO:0035024
production of miRNAs involved in gene si...	GO:0035196
negative regulation of hydrogen peroxide...	GO:1903206
negative regulation of cellular response...	GO:2001039
positive regulation of transcription, DN...	GO:0045893
cytoskeleton organization	GO:0007010
histone H4 acetylation	GO:0043967
phototransduction	GO:0007602
regulation of cellular response to manga...	GO:1905802
negative regulation of cell killing	GO:0031342

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p=1.5E-03	n=15
p=2.3E-03	n=9
p=3.7E-03	n=14
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p=4.0E-03	n=3
p=4.0E-03	n=17
p=4.9E-03	n=7
p=5.2E-03	n=6
p=5.2E-03	n=43
p=5.3E-03	n=58
p=5.5E-03	n=4
p=7.0E-03	n=19
p=7.1E-03	n=5
p=7.6E-03	n=26
p=8.1E-03	n=72
p=8.5E-03	n=13
p=9.0E-03	n=11
p=9.2E-03	n=3
p=9.2E-03	n=3
p=9.2E-03	n=3
p=9.2E-03	n=3
p=9.2E-03	n=3
p=9.6E-03	n=33
p=1.0E-02	n=34
p=1.0E-02	n=5
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p=1.1E-02	n=2
p=1.1E-02	n=2

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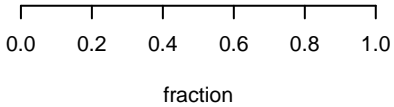
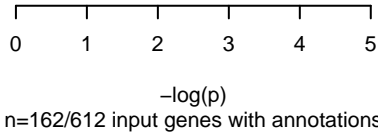
GO:MF
Elav_Nvec_vc1.1_XM_001625700.3

fraction genes in fg and expected value

cysteine-type endopeptidase regulator ac...	GO:0043028
heterocyclic compound binding	GO:1901363
R-SMAD binding	GO:0070412
insulin-like growth factor binding	GO:0005520
angiotensin receptor binding	GO:0031701
type 1 angiotensin receptor binding	GO:0031702
cysteine-type endopeptidase inhibitor ac...	GO:0043027
phosphatidylinositol-3,5-bisphosphate bi...	GO:0080025
protein kinase B binding	GO:0043422
binding	GO:0005488
organic cyclic compound binding	GO:0097159
kinase binding	GO:0019900
anion binding	GO:0043168
carbohydrate derivative binding	GO:0097367
ion binding	GO:0043167
oxidoreductase activity, acting on the C...	GO:0016645
transcription regulatory region nucleic ...	GO:0001067
phosphatidylinositol-3,4,5-trisphosphate...	GO:0005547
peptidase regulator activity	GO:0061134
small molecule binding	GO:0036094
nucleic acid binding	GO:0003676
polynucleotide adenyllyltransferase activ...	GO:0004652
ATPase-coupled cation transmembrane tran...	GO:0019829
transcription factor binding	GO:0008134
peptidase activator activity involved in...	GO:0016505
retinoid binding	GO:0005501
cysteine-type endopeptidase activator ac...	GO:0008656
bHLH transcription factor binding	GO:0043425
cysteine-type endopeptidase inhibitor ac...	GO:0004869
isoprenoid binding	GO:0019840

p=4.8E-04	n=4
p=8.8E-03	n=57
p=8.9E-03	n=3
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.2E-02	n=138
p=1.2E-02	n=57
p=1.3E-02	n=21
p=1.4E-02	n=30
p=1.4E-02	n=21
p=1.4E-02	n=45
p=1.6E-02	n=3
p=1.7E-02	n=17
p=1.9E-02	n=4
p=1.9E-02	n=4
p=2.4E-02	n=24
p=2.4E-02	n=41
p=2.7E-02	n=3
p=2.7E-02	n=4
p=2.7E-02	n=19
p=2.9E-02	n=2
p=2.9E-02	n=2
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p=2.9E-02	n=2

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GO:CC
Elav_Nvec_vc1.1_XM_001625700.3

fraction genes in fg and expected value

recycling endosome membrane	GO:0055038
cytosol	GO:0005829
neuron projection	GO:0043005
nuclear lumen	GO:0031981
synapse	GO:0045202
nuclear membrane	GO:0031965
cytoplasmic ribonucleoprotein granule	GO:0036464
extrinsic component of Golgi membrane	GO:0090498
COPII vesicle coat	GO:0030127
cleavage furrow	GO:0032154
nucleoplasm	GO:0005654
P-body	GO:0000932
MLL1/2 complex	GO:0044665
acetyltransferase complex	GO:1902493
ruffle	GO:0001726
histone acetyltransferase complex	GO:0000123
protein acetyltransferase complex	GO:0031248
subrhabdomeral cisterna	GO:0016029
endoplasmic reticulum cisternal network	GO:0071781
smooth endoplasmic reticulum cisterna	GO:0120082
synaptic membrane	GO:0097060
microtubule	GO:0005874
early endosome	GO:0005769
azurophil granule membrane	GO:0035577
rhabdomere	GO:0016028
specific granule membrane	GO:0035579
ficolin-1-rich granule	GO:0101002
non-membrane-bounded organelle	GO:0043228
intracellular non-membrane-bounded organ...	GO:0043232
chromatin	GO:0000785

p=8.6E-04	n=5
p=1.9E-03	n=89
p=3.9E-03	n=38
p=8.1E-03	n=72
p=8.3E-03	n=28
p=8.6E-03	n=9
p=9.4E-03	n=10
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.3E-02	n=4
p=1.7E-02	n=62
p=2.2E-02	n=5
p=2.5E-02	n=3
p=2.8E-02	n=5
p=2.8E-02	n=5
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p=2.8E-02	n=5
p=2.8E-02	n=2
p=2.8E-02	n=2
p=2.8E-02	n=2
p=3.0E-02	n=9
p=3.5E-02	n=7
p=3.7E-02	n=12
p=3.8E-02	n=3
p=3.8E-02	n=3
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p=4.9E-02	n=69
p=5.0E-02	n=13

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