

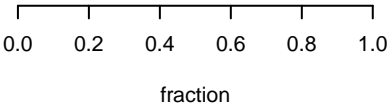
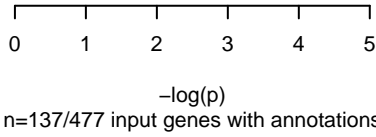
GO:BP
Elav_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

negative regulation of endothelial cell ...	GO:2000352
positive regulation of endocytosis	GO:0045807
head involution	GO:0008258
Rho protein signal transduction	GO:0007266
gonad morphogenesis	GO:0035262
activation of protein kinase activity	GO:0032147
regulation of establishment of cell pola...	GO:2000114
regulation of neuron differentiation	GO:0045664
cleavage furrow ingression	GO:0036090
chemical synaptic transmission	GO:0007268
negative regulation of transcription by ...	GO:0000122
positive regulation of peptidase activit...	GO:0010952
positive regulation of angiogenesis	GO:0045766
neuroepithelial cell differentiation	GO:0060563
negative regulation of cell junction ass...	GO:1901889
regulation of neuron projection developm...	GO:0010975
neuron projection morphogenesis	GO:0048812
metal ion export	GO:0070839
brain segmentation	GO:0035284
export across plasma membrane	GO:0140115
positive regulation of cytosolic calcium...	GO:0007204
positive regulation of transcription fro...	GO:0006990
response to tunicamycin	GO:1904576
positive regulation of cellular amide me...	GO:0034250
dendrite development	GO:0016358
positive regulation of transcription by ...	GO:0045944
regulation of animal organ morphogenesis	GO:2000027
cell morphogenesis involved in neuron di...	GO:0048667
positive regulation of protein localizat...	GO:1903829
macrophage differentiation	GO:0030225

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p=6.2E-04	n=9
p=6.6E-04	n=4
p=8.6E-04	n=7
p=8.7E-04	n=5
p=1.0E-03	n=10
p=1.0E-03	n=4
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p=1.2E-03	n=3
p=1.2E-03	n=18
p=1.3E-03	n=19
p=1.3E-03	n=8
p=1.5E-03	n=6
p=1.9E-03	n=6
p=1.9E-03	n=6
p=1.9E-03	n=16
p=2.1E-03	n=22
p=2.3E-03	n=3
p=2.3E-03	n=3
p=2.3E-03	n=3
p=2.4E-03	n=8
p=2.6E-03	n=2
p=2.6E-03	n=2
p=2.9E-03	n=7
p=3.4E-03	n=12
p=3.4E-03	n=23
p=3.5E-03	n=9
p=3.6E-03	n=23
p=3.7E-03	n=13
p=3.9E-03	n=3

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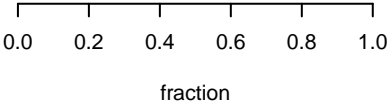
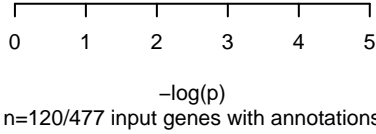
GO:MF
Elav_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

DNA-binding transcription activator acti...	GO:0001228
acetylcholine receptor binding	GO:0033130
transcription coactivator binding	GO:0001223
protein domain specific binding	GO:0019904
potassium channel regulator activity	GO:0015459
mRNA 3'-UTR binding	GO:0003730
triglyceride lipase activity	GO:0004806
ligand-gated calcium channel activity	GO:0099604
RNA polymerase II transcription regulato...	GO:0000977
DNA binding	GO:0003677
cis-regulatory region sequence-specific ...	GO:0000987
RNA polymerase II cis-regulatory region ...	GO:0000978
molecular function regulator activity	GO:0098772
transcription coregulator binding	GO:0001221
scaffold protein binding	GO:0097110
sequence-specific double-stranded DNA bi...	GO:1990837
enzyme inhibitor activity	GO:0004857
ion channel inhibitor activity	GO:0008200
enzyme activator activity	GO:0008047
enzyme regulator activity	GO:0030234
arrestin family protein binding	GO:1990763
14-3-3 protein binding	GO:0071889
ephrin receptor binding	GO:0046875
transcription cis-regulatory region bind...	GO:0000976
protein serine/threonine kinase activity	GO:0004674
intracellular ligand-gated ion channel a...	GO:0005217
channel inhibitor activity	GO:0016248
transcription regulatory region nucleic ...	GO:0001067
peptidase regulator activity	GO:0061134
calcium channel regulator activity	GO:0005246

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p=3.1E-03	n=4
p=7.1E-03	n=4
p=7.4E-03	n=2
p=8.5E-03	n=3
p=1.0E-02	n=11
p=1.2E-02	n=23
p=1.2E-02	n=9
p=1.2E-02	n=9
p=1.4E-02	n=24
p=1.4E-02	n=5
p=1.6E-02	n=4
p=1.7E-02	n=12
p=1.7E-02	n=7
p=2.0E-02	n=3
p=2.1E-02	n=11
p=2.2E-02	n=18
p=2.3E-02	n=2
p=2.3E-02	n=2
p=2.3E-02	n=2
p=2.4E-02	n=11
p=2.4E-02	n=10
p=2.5E-02	n=3
p=2.5E-02	n=3
p=2.9E-02	n=12
p=3.1E-02	n=3
p=3.1E-02	n=3

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GO:CC
Elav_Nvec_vc1.1_XM_032367127.2

fraction genes in fg and expected value

chromatin	GO:0000785
terminal bouton	GO:0043195
transcription regulator complex	GO:0005667
postsynaptic membrane	GO:0045211
cell leading edge	GO:0031252
dendrite	GO:0030425
COPII-coated ER to Golgi transport vesic...	GO:0030134
skeletal muscle myofibril	GO:0098723
ciliary rootlet	GO:0035253
cell projection membrane	GO:0031253
cell-cell junction	GO:0005911
anchoring junction	GO:0070161
integral component of organelle membrane	GO:0031301
main axon	GO:0044304
subs synaptic reticulum	GO:0071212
actin-based cell projection	GO:0098858
intrinsic component of organelle membran...	GO:0031300
neuron spine	GO:0044309
dendritic spine	GO:0043197
Golgi-associated vesicle	GO:0005798
integral component of endoplasmic reticu...	GO:0030176
type I terminal bouton	GO:0061174
endoplasmic reticulum	GO:0005783
protein phosphatase type 1 complex	GO:0000164
photoreceptor inner segment	GO:0001917
intrinsic component of endoplasmic retic...	GO:0031227
leading edge membrane	GO:0031256
endomembrane system	GO:0012505
membrane raft	GO:0045121
membrane microdomain	GO:0098857

p=8.4E-04	n=16
p=1.0E-03	n=8
p=1.8E-03	n=13
p=3.6E-03	n=7
p=3.8E-03	n=12
p=4.6E-03	n=17
p=6.3E-03	n=4
p=8.0E-03	n=2
p=8.0E-03	n=2
p=1.1E-02	n=10
p=1.2E-02	n=12
p=1.2E-02	n=12
p=1.2E-02	n=11
p=1.5E-02	n=4
p=1.5E-02	n=2
p=1.6E-02	n=7
p=1.7E-02	n=11
p=1.8E-02	n=7
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p=2.2E-02	n=3
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