

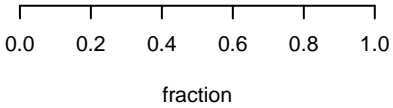
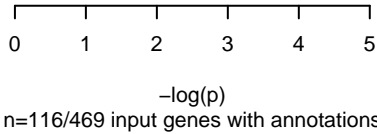
GO:BP
Elav_Nvec_vc1.1_XM_001635374.3

fraction genes in fg and expected value

negative regulation of multicellular org...	GO:0051241
ommatidial rotation	GO:0016318
positive regulation of fertilization	GO:1905516
response to metal ion	GO:0010038
anatomical structure formation involved ...	GO:0048646
homophilic cell adhesion via plasma memb...	GO:0007156
glomerulus morphogenesis	GO:0072102
regulation of myeloid cell differentiati...	GO:0045637
regulation of cell communication	GO:0010646
homeostasis of number of cells	GO:0048872
positive regulation of gene expression	GO:0010628
signal transduction	GO:0007165
negative regulation of developmental pro...	GO:0051093
regulation of signaling	GO:0023051
regulation of neurogenesis	GO:0050767
cell-cell signaling	GO:0007267
cellular response to glucose stimulus	GO:0071333
nucleotide transmembrane transport	GO:1901679
regulation of protein homodimerization a...	GO:0043496
male courtship behavior	GO:0008049
heart looping	GO:0001947
response to anesthetic	GO:0072347
mitochondrial genome maintenance	GO:0000002
protein homotetramerization	GO:0051289
mesenchyme development	GO:0060485
cellular response to steroid hormone sti...	GO:0071383
regulation of cellular component organiz...	GO:0051128
nephron tubule development	GO:0072080
regulation of system process	GO:0044057
actin filament-based process	GO:0030029

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p=7.6E-05	n=4
p=2.6E-04	n=3
p=9.0E-04	n=12
p=9.7E-04	n=24
p=9.7E-04	n=3
p=9.7E-04	n=3
p=9.8E-04	n=8
p=1.4E-03	n=49
p=1.4E-03	n=10
p=1.6E-03	n=31
p=1.8E-03	n=64
p=1.8E-03	n=20
p=1.9E-03	n=49
p=2.1E-03	n=22
p=2.1E-03	n=29
p=2.2E-03	n=7
p=2.3E-03	n=3
p=2.3E-03	n=3
p=2.3E-03	n=6
p=2.4E-03	n=5
p=2.5E-03	n=6
p=2.5E-03	n=4
p=2.5E-03	n=4
p=2.7E-03	n=7
p=3.0E-03	n=8
p=3.1E-03	n=41
p=3.1E-03	n=6
p=3.2E-03	n=15
p=3.2E-03	n=17

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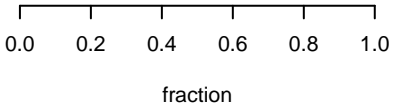
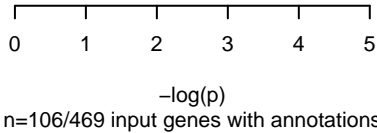
GO:MF
Elav_Nvec_vc1.1_XM_001635374.3

fraction genes in fg and expected value

RNA polymerase II cis-regulatory region ...	GO:0000978
calcium-activated potassium channel acti...	GO:0015269
nucleotide transmembrane transporter act...	GO:0015215
high voltage-gated calcium channel activ...	GO:0008331
low voltage-gated calcium channel activi...	GO:0008332
DNA-binding transcription activator acti...	GO:0001228
protein heterodimerization activity	GO:0046982
cytoskeletal protein binding	GO:0008092
voltage-gated ion channel activity	GO:0005244
transcription factor binding	GO:0008134
ATP binding	GO:0005524
pyrimidine nucleotide transmembrane tran...	GO:0015218
minor groove of adenine-thymine-rich DNA...	GO:0003680
voltage-gated cation channel activity	GO:0022843
transcription coactivator activity	GO:0003713
actin filament binding	GO:0051015
sodium ion transmembrane transporter act...	GO:0015081
purine ribonucleoside triphosphate bindi...	GO:0035639
E-box binding	GO:0070888
transcription coregulator binding	GO:0001221
protein domain specific binding	GO:0019904
actin binding	GO:0003779
identical protein binding	GO:0042802
voltage-gated sodium channel activity	GO:0005248
histone acetyltransferase binding	GO:0035035
voltage-gated potassium channel activity	GO:0005249
ubiquitin conjugating enzyme binding	GO:0031624
modification-dependent protein binding	GO:0140030
ion gated channel activity	GO:0022839
voltage-gated calcium channel activity	GO:0005245

p=2.3E-04	n=12
p=2.9E-04	n=3
p=2.6E-03	n=3
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p=4.4E-03	n=2
p=5.7E-03	n=10
p=6.2E-03	n=13
p=7.7E-03	n=16
p=9.2E-03	n=8
p=9.8E-03	n=15
p=1.2E-02	n=10
p=1.3E-02	n=2
p=1.3E-02	n=2
p=1.3E-02	n=7
p=1.4E-02	n=9
p=1.4E-02	n=4
p=1.4E-02	n=4
p=1.7E-02	n=12
p=1.8E-02	n=3
p=1.8E-02	n=3
p=1.8E-02	n=17
p=1.9E-02	n=6
p=2.3E-02	n=26
p=2.4E-02	n=2
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p=3.3E-02	n=4
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p=3.7E-02	n=5

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GO:CC
Elav_Nvec_vc1.1_XM_001635374.3

fraction genes in fg and expected value

voltage-gated calcium channel complex	GO:0005891
nuclear speck	GO:0016607
presynaptic active zone	GO:0048786
external side of plasma membrane	GO:0009897
basolateral plasma membrane	GO:0016323
caveola	GO:0005901
dendrite	GO:0030425
dendritic tree	GO:0097447
XY body	GO:0001741
Myb complex	GO:0031523
presynaptic periaxial zone	GO:0036062
transcription regulator complex	GO:0005667
cell pole	GO:0060187
postsynapse of neuromuscular junction	GO:0098975
anchoring junction	GO:0070161
cell-cell junction	GO:0005911
coated vesicle	GO:0030135
adherens junction	GO:0005912
plasma membrane raft	GO:0044853
COPII-coated ER to Golgi transport vesic...	GO:0030134
acrosomal vesicle	GO:0001669
clathrin-coated vesicle	GO:0030136
cell leading edge	GO:0031252
RNA polymerase II transcription regulato...	GO:0090575
molybdopterin synthase complex	GO:0019008
transverse filament	GO:0000802
lamellipodium membrane	GO:0031258
Flemming body	GO:0090543
RSC-type complex	GO:0016586
CCAAT-binding factor complex	GO:0016602

p=8.5E-05	n=4
p=4.2E-04	n=12
p=6.9E-04	n=6
p=3.7E-03	n=5
p=9.9E-03	n=8
p=1.7E-02	n=4
p=2.0E-02	n=15
p=2.0E-02	n=15
p=2.4E-02	n=2
p=2.4E-02	n=2
p=2.4E-02	n=2
p=2.6E-02	n=10
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p=4.2E-02	n=7
p=4.3E-02	n=6
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p=4.9E-02	n=3
p=5.4E-02	n=2
p=5.5E-02	n=2
p=5.9E-02	n=8
p=6.1E-02	n=5
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