

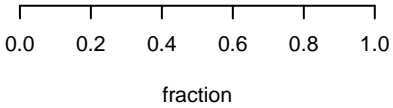
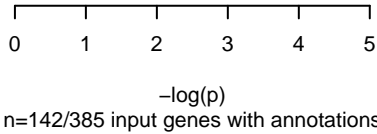
GO:BP
Elav_Nvec_vc1.1_XM_032366797.2

fraction genes in fg and expected value

response to bronchodilator	GO:0097366
autophagosome maturation	GO:0097352
GTP metabolic process	GO:0046039
membrane organization	GO:0061024
regulation of oskar mRNA translation	GO:0046011
regulation of deacetylase activity	GO:0150065
negative regulation of molecular functio...	GO:0044362
determination of digestive tract left/ri...	GO:0071907
intracellular estrogen receptor signalin...	GO:0030520
guanosine-containing compound metabolic ...	GO:1901068
response to amine	GO:0014075
cellular response to estradiol stimulus	GO:0071392
dendritic spine development	GO:0060996
molybdopterin cofactor biosynthetic proc...	GO:0032324
cellular response to nitric oxide	GO:0071732
maintenance of presynaptic active zone s...	GO:0048790
positive regulation of long-term synapti...	GO:1900454
learning or memory	GO:0007611
regulation of synapse assembly	GO:0051963
transport	GO:0006810
intracellular transport	GO:0046907
nucleobase-containing small molecule bio...	GO:0034404
regulation of filopodium assembly	GO:0051489
regulation of histone deacetylation	GO:0031063
proximal/distal axis specification	GO:0009946
neuroblast proliferation	GO:0007405
positive regulation of anion transport	GO:1903793
regulation of dendritic spine morphogene...	GO:0061001
regulation of synaptic assembly at neuro...	GO:0008582
salivary gland development	GO:0007431

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p=3.6E-03	n=4
p=4.3E-03	n=3
p=4.3E-03	n=3
p=4.3E-03	n=3
p=5.9E-03	n=5
p=8.0E-03	n=2
p=8.0E-03	n=2
p=8.0E-03	n=2
p=8.0E-03	n=2
p=9.1E-03	n=13
p=9.8E-03	n=8
p=1.0E-02	n=66
p=1.0E-02	n=38
p=1.3E-02	n=6
p=1.5E-02	n=4
p=1.5E-02	n=2
p=1.5E-02	n=2
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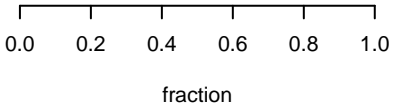
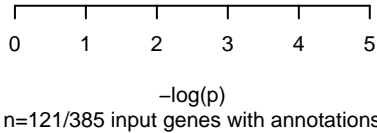
GO:MF
Elav_Nvec_vc1.1_XM_032366797.2

fraction genes in fg and expected value

protein phosphatase 1 binding	GO:0008157
sulfurtransferase activity	GO:0016783
cation channel activity	GO:0005261
mitogen-activated protein kinase binding	GO:0051019
nuclear estrogen receptor binding	GO:0030331
GTPase binding	GO:0051020
potassium ion transmembrane transporter ...	GO:0015079
potassium channel activity	GO:0005267
actin binding	GO:0003779
small GTPase binding	GO:0031267
hormone receptor binding	GO:0051427
pyrophosphate hydrolysis-driven proton t...	GO:0009678
intramolecular oxidoreductase activity, ...	GO:0016864
ATPase activity, coupled to transmembran...	GO:0044769
MAP kinase kinase activity	GO:0004708
proton-transporting ATPase activity, rot...	GO:0046961
protein disulfide isomerase activity	GO:0003756
transcription coregulator activity	GO:0003712
protein phosphatase regulator activity	GO:0019888
transcription coactivator activity	GO:0003713
mRNA 3'-UTR binding	GO:0003730
MAP kinase activity	GO:0004707
inositol phosphate phosphatase activity	GO:0052745
signaling receptor binding	GO:0005102
polyamine binding	GO:0019808
transmembrane receptor protein phosphata...	GO:0019198
oxidoreductase activity, acting on NAD(P...	GO:0050664
importin-alpha family protein binding	GO:0061676
myosin II binding	GO:0045159
oxidative DNA demethylase activity	GO:0035516

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p=5.1E-03	n=5
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p=1.7E-02	n=11
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p=3.7E-02	n=11
p=3.8E-02	n=3
p=4.0E-02	n=8
p=4.5E-02	n=3
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p=4.6E-02	n=2
p=4.9E-02	n=18
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GO:CC
Elav_Nvec_vc1.1_XM_032366797.2

fraction genes in fg and expected value

plasma membrane region	GO:0098590
presynaptic active zone	GO:0048786
midbody	GO:0030496
endolysosome membrane	GO:0036020
transport vesicle	GO:0030133
mediator complex	GO:0016592
cell cortex	GO:0005938
asymmetric synapse	GO:0032279
synaptic vesicle	GO:0008021
protein phosphatase type 1 complex	GO:0000164
presynaptic membrane	GO:0042734
neuron to neuron synapse	GO:0098984
synaptic membrane	GO:0097060
late endosome	GO:0005770
cortical cytoskeleton	GO:0030863
perikaryon	GO:0043204
neuronal cell body	GO:0043025
exocytic vesicle	GO:0070382
postsynaptic density	GO:0014069
cation channel complex	GO:0034703
cytoplasmic region	GO:0099568
presynaptic active zone membrane	GO:0048787
microvillus membrane	GO:0031528
apicolateral plasma membrane	GO:0016327
cytoplasmic side of dendritic spine plas...	GO:1990780
spectrin	GO:0008091
cytoskeleton of presynaptic active zone	GO:0048788
spectrosome	GO:0045170
smooth septate junction	GO:0005920
microvesicle	GO:1990742

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p=6.6E-03	n=7
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p=2.4E-02	n=7
p=2.4E-02	n=7
p=2.4E-02	n=2
p=2.6E-02	n=5
p=2.6E-02	n=7
p=2.8E-02	n=7
p=2.8E-02	n=7
p=2.8E-02	n=4
p=3.3E-02	n=4
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