

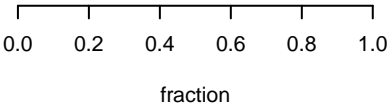
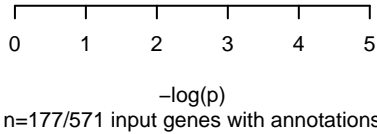
GO:BP
Elav_Nvec_vc1.1_XM_032377897.2

fraction genes in fg and expected value

melanosome transport	GO:0032402
Fc-gamma receptor signaling pathway invo...	GO:0038096
SRP-dependent cotranslational protein ta...	GO:0006614
tissue homeostasis	GO:0001894
regulation of organelle transport along ...	GO:1902513
microtubule anchoring at centrosome	GO:0034454
positive regulation of anion transmembra...	GO:1903961
negative regulation of transcription fro...	GO:1990441
positive regulation of bone resorption	GO:0045780
positive regulation of bone remodeling	GO:0046852
adipose tissue development	GO:0060612
positive regulation of T cell proliferat...	GO:0042102
cytoplasmic translation	GO:0002181
ephrin receptor signaling pathway	GO:0048013
regulation of hemocyte differentiation	GO:0045610
positive regulation of JUN kinase activi...	GO:0043507
nuclear-transcribed mRNA catabolic proce...	GO:0000184
pseudouridine synthesis	GO:0001522
positive regulation of phosphatidylinosi...	GO:0014068
energy coupled proton transmembrane tran...	GO:0015988
response to unfolded protein	GO:0006986
regulation of Notch signaling pathway	GO:0008593
cell-substrate junction assembly	GO:0007044
vesicle-mediated transport to the plasma...	GO:0098876
chaperone-mediated protein folding	GO:0061077
endocytic recycling	GO:0032456
response to interleukin-2	GO:0070669
regulation of amino acid transmembrane t...	GO:1903789
protein transport within plasma membrane	GO:0099632
neurotransmitter receptor transport	GO:0099637

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p=4.3E-03	n=2
p=4.3E-03	n=2
p=4.8E-03	n=3
p=4.8E-03	n=3
p=5.8E-03	n=9
p=5.8E-03	n=4
p=5.8E-03	n=4
p=6.3E-03	n=5
p=7.6E-03	n=7
p=8.0E-03	n=3
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p=8.4E-03	n=9
p=9.4E-03	n=9
p=9.8E-03	n=5
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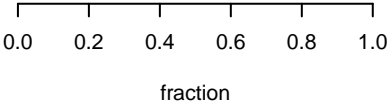
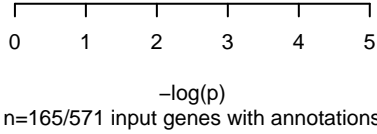
GO:MF
Elav_Nvec_vc1.1_XM_032377897.2

fraction genes in fg and expected value

mitogen-activated protein kinase kinase ...	GO:0031435
signaling adaptor activity	GO:0035591
phosphotyrosine residue binding	GO:0001784
structural molecule activity	GO:0005198
ephrin receptor binding	GO:0046875
NADPH binding	GO:0070402
SH2 domain binding	GO:0042169
nucleoside-triphosphatase regulator acti...	GO:0060589
telomerase RNA binding	GO:0070034
LIM domain binding	GO:0030274
GTPase regulator activity	GO:0030695
structural constituent of ribosome	GO:0003735
enzyme binding	GO:0019899
signaling receptor complex adaptor activ...	GO:0030159
macrolide binding	GO:0005527
FK506 binding	GO:0005528
MAP-kinase scaffold activity	GO:0005078
protein kinase B binding	GO:0043422
small GTPase binding	GO:0031267
ATPase binding	GO:0051117
JUN kinase binding	GO:0008432
5S rRNA binding	GO:0008097
NF-kappaB binding	GO:0051059
pentosyltransferase activity	GO:0016763
guanyl-nucleotide exchange factor activi...	GO:0005085
histone acetyltransferase activity	GO:0004402
dynactin binding	GO:0034452
tumor necrosis factor receptor binding	GO:0005164
extracellular matrix binding	GO:0050840
phosphatidylinositol 3-kinase binding	GO:0043548

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p=4.8E-03	n=2
p=7.2E-03	n=4
p=7.9E-03	n=15
p=9.4E-03	n=3
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p=1.4E-02	n=13
p=1.5E-02	n=9
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p=2.6E-02	n=2
p=2.6E-02	n=2
p=2.6E-02	n=2
p=2.6E-02	n=2
p=3.0E-02	n=13
p=4.1E-02	n=5
p=4.2E-02	n=2
p=4.2E-02	n=2
p=4.2E-02	n=2
p=4.6E-02	n=3
p=5.5E-02	n=6
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GO:CC
Elav_Nvec_vc1.1_XM_032377897.2

fraction genes in fg and expected value

cytosolic large ribosomal subunit	GO:0022625
plasma membrane proton-transporting V-ty...	GO:0033181
cytoplasmic side of plasma membrane	GO:0009898
vacuolar proton-transporting V-type ATPa...	GO:0000221
EARP complex	GO:1990745
GARP complex	GO:0000938
proton-transporting V-type ATPase, V1 do...	GO:0033180
lipid droplet	GO:0005811
Golgi cisterna	GO:0031985
basolateral plasma membrane	GO:0016323
basal plasma membrane	GO:0009925
filamentous actin	GO:0031941
intracellular anatomical structure	GO:0005622
endosome	GO:0005768
telomerase holoenzyme complex	GO:0005697
Golgi cis cisterna	GO:0000137
proton-transporting two-sector ATPase co...	GO:0033178
actin cytoskeleton	GO:0015629
basal part of cell	GO:0045178
extrinsic component of cytoplasmic side ...	GO:0031234
exocytic vesicle	GO:0070382
sno(s)RNA-containing ribonucleoprotein c...	GO:0005732
eukaryotic translation initiation factor...	GO:0005852
axon cytoplasm	GO:1904115
dendrite terminus	GO:0044292
focal adhesion	GO:0005925
phagolysosome	GO:0032010
protein farnesyltransferase complex	GO:0005965
Yb body	GO:0070725
anchored component of synaptic vesicle m...	GO:0098993

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p=4.9E-03	n=3
p=8.0E-03	n=9
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p=2.5E-02	n=175
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p=3.8E-02	n=2
p=3.8E-02	n=2
p=3.8E-02	n=2
p=3.9E-02	n=10
p=4.2E-02	n=9
p=4.6E-02	n=4
p=5.4E-02	n=8
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