

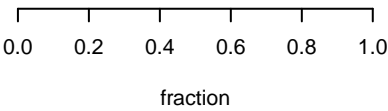
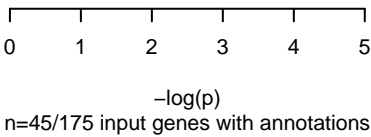
GO:BP
Elav_Nvec_vc1.1_XM_032387281.2

fraction genes in fg and expected value

regulation of intracellular pH	GO:0051453
intracellular transport	GO:0046907
regulation of alpha-beta T cell activati...	GO:0046634
hormone biosynthetic process	GO:0042446
regulation of cell adhesion	GO:0030155
establishment or maintenance of cell pol...	GO:0007163
regulation of vesicle-mediated transport	GO:0060627
intracellular protein transport	GO:0006886
positive regulation of cell-cell adhesio...	GO:0022409
regulation of lymphocyte differentiation	GO:0045619
response to antineoplastic agent	GO:0097327
megakaryocyte differentiation	GO:0030219
amide transport	GO:0042886
peptide transport	GO:0015833
regulation of intracellular transport	GO:0032386
positive regulation of regulated secreto...	GO:1903307
vacuolar acidification	GO:0007035
positive regulation of lymphocyte differ...	GO:0045621
ketone biosynthetic process	GO:0042181
energy coupled proton transmembrane tran...	GO:0015988
cellular hormone metabolic process	GO:0034754
negative regulation of DNA metabolic pro...	GO:0051053
actin cortical patch localization	GO:0051666
type 2 immune response	GO:0042092
transferrin transport	GO:0033572
demethylation	GO:0070988
lysine transport	GO:0015819
basic amino acid transport	GO:0015802
regulation of interleukin-4 production	GO:0032673
DNA demethylation	GO:0080111

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p=2.0E-03	n=17
p=4.7E-03	n=3
p=4.7E-03	n=3
p=5.9E-03	n=7
p=6.3E-03	n=6
p=6.7E-03	n=8
p=6.9E-03	n=9
p=1.1E-02	n=3
p=1.1E-02	n=3
p=1.1E-02	n=3
p=1.1E-02	n=3
p=1.1E-02	n=14
p=1.1E-02	n=14
p=1.2E-02	n=6
p=1.2E-02	n=2
p=1.2E-02	n=2
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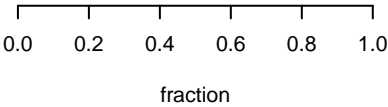
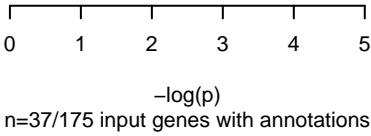
GO:MF
Elav_Nvec_vc1.1_XM_032387281.2

fraction genes in fg and expected value

magnesium ion binding	GO:0000287
growth factor receptor binding	GO:0070851
ATP hydrolysis activity	GO:0016887
ATP binding	GO:0005524
catalytic activity, acting on a nucleic ...	GO:0140640
catalytic activity, acting on DNA	GO:0140097
ATPase activity, coupled to transmembran...	GO:0044769
proton transmembrane transporter activit...	GO:0015078
proton-transporting ATPase activity, rot...	GO:0046961
pyrophosphate hydrolysis-driven proton t...	GO:0009678
gamma-tubulin binding	GO:0043015
helicase activity	GO:0004386
ATP-dependent activity, acting on RNA	GO:0008186
tubulin binding	GO:0015631
protein serine/threonine kinase activity	GO:0004674
GTPase binding	GO:0051020
HMG box domain binding	GO:0071837
phosphotyrosine residue binding	GO:0001784
cytokine receptor binding	GO:0005126
phosphatidylinositol binding	GO:0035091
protein domain specific binding	GO:0019904
small GTPase binding	GO:0031267
protein phosphorylated amino acid bindin...	GO:0045309
receptor tyrosine kinase binding	GO:0030971
protein kinase activity	GO:0004672
enzyme regulator activity	GO:0030234
nucleoside-triphosphatase regulator acti...	GO:0060589
ATP-dependent activity, acting on DNA	GO:0008094
dioxygenase activity	GO:0051213
epidermal growth factor receptor binding	GO:0005154

p=4.3E-04	n=4
p=9.7E-04	n=3
p=5.5E-03	n=6
p=8.4E-03	n=5
p=8.4E-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
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p=2.8E-02	n=2
p=2.8E-02	n=2
p=3.3E-02	n=4
p=3.3E-02	n=5
p=5.0E-02	n=5
p=5.3E-02	n=2
p=5.3E-02	n=2
p=5.3E-02	n=2
p=6.7E-02	n=4
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p=8.2E-02	n=4
p=8.3E-02	n=2
p=8.3E-02	n=2
p=8.3E-02	n=5
p=8.4E-02	n=7
p=9.6E-02	n=5
p=1.0E-01	n=1
p=1.0E-01	n=1
p=1.0E-01	n=1

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GO:CC
Elav_Nvec_vc1.1_XM_032387281.2

fraction genes in fg and expected value

intracellular membrane-bounded organelle	GO:0043231
plasma membrane proton-transporting V-ty...	GO:0033181
proton-transporting two-sector ATPase co...	GO:0016469
proton-transporting V-type ATPase comple...	GO:0033176
vacuolar proton-transporting V-type ATPa...	GO:0016471
cell tip	GO:0051286
cell pole	GO:0060187
perinuclear region of cytoplasm	GO:0048471
vacuolar membrane	GO:0005774
vesicle	GO:0031982
storage vacuole	GO:0000322
fungal-type vacuole	GO:0000324
fungal-type vacuole membrane	GO:0000329
cytoplasmic vesicle	GO:0031410
intracellular vesicle	GO:0097708
endosome membrane	GO:0010008
cytoplasm	GO:0005737
endosome	GO:0005768
late endosome	GO:0005770
Golgi trans cisterna	GO:0000138
acetyltransferase complex	GO:1902493
protein acetyltransferase complex	GO:0031248
histone acetyltransferase complex	GO:0000123
nucleus	GO:0005634
lytic vacuole membrane	GO:0098852
endomembrane system	GO:0012505
microtubule cytoskeleton	GO:0015630
Golgi cisterna	GO:0031985
cell division site	GO:0032153
cytoplasmic vesicle membrane	GO:0030659

p=4.0E-03	n=39
p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.3E-02	n=8
p=2.2E-02	n=4
p=2.2E-02	n=14
p=3.1E-02	n=2
p=3.1E-02	n=2
p=3.1E-02	n=2
p=3.3E-02	n=13
p=3.3E-02	n=13
p=4.0E-02	n=4
p=4.2E-02	n=36
p=5.7E-02	n=7
p=5.8E-02	n=2
p=5.8E-02	n=2
p=5.8E-02	n=2
p=5.8E-02	n=2
p=5.8E-02	n=2
p=5.9E-02	n=25
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p=6.9E-02	n=20
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fg=0.16	bg=0.10

