

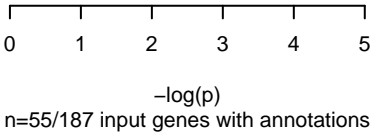
GO:BP
Elav_Nvec_vc1.1_XM_001634160.3

fraction genes in fg and expected value

establishment of mitotic spindle orienta...	GO:0000132
energy coupled proton transmembrane tran...	GO:0015988
cellular response to glucagon stimulus	GO:0071377
adherens junction assembly	GO:0034333
proton-transporting two-sector ATPase co...	GO:0070071
oocyte microtubule cytoskeleton organiza...	GO:0016325
cellular response to glucose stimulus	GO:0071333
transferrin transport	GO:0033572
positive regulation of peptide hormone s...	GO:0090277
activation of phospholipase C activity	GO:0007202
activation of protein kinase A activity	GO:0034199
establishment or maintenance of polarity...	GO:0016332
alcohol biosynthetic process	GO:0046165
innate immune response-activating signal...	GO:0002758
response to cycloheximide	GO:0046898
basal protein localization	GO:0045175
response to antipsychotic drug	GO:0097332
response to clozapine	GO:0097338
protein secretion	GO:0009306
regulation of angiogenesis	GO:0045765
transforming growth factor beta receptor...	GO:0007179
asymmetric protein localization involved...	GO:0045167
regulation of meiotic cell cycle process...	GO:1903538
regulation of T cell differentiation in ...	GO:0033081
NADH regeneration	GO:0006735
response to fungicide	GO:0060992
syncytium formation by plasma membrane f...	GO:0000768
response to xenobiotic stimulus	GO:0009410
cell-substrate junction assembly	GO:0007044
cell-substrate junction organization	GO:0150115

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p=1.9E-03	n=3
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p=3.1E-03	n=4
p=4.8E-03	n=3
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p=6.2E-03	n=8
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p=9.3E-03	n=3
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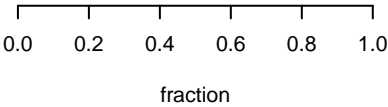
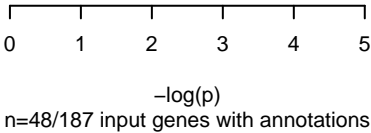
GO:MF
Elav_Nvec_vc1.1_XM_001634160.3

fraction genes in fg and expected value

protein-disulfide reductase (NAD(P)) act...	GO:0047134
vinculin binding	GO:0017166
proton-transporting ATPase activity, rot...	GO:0046961
protein kinase A binding	GO:0051018
oxidoreductase activity, acting on NAD(P...	GO:0016651
manganese ion transmembrane transporter ...	GO:0005384
phosphoglycerate kinase activity	GO:0004618
UDP-N-acetylglucosamine-dolichyl-phospha...	GO:0003975
selenium binding	GO:0008430
[phosphorylase] phosphatase activity	GO:0050196
nickel cation transmembrane transporter ...	GO:0015099
BH4 domain binding	GO:0051435
1-alkylglycerophosphocholine O-acyltrans...	GO:0047191
netrin receptor activity	GO:0005042
glycogen binding	GO:2001069
diacylglycerol binding	GO:0019992
mitochondrial ribosome binding	GO:0097177
cyclic nucleotide-dependent protein kina...	GO:0004690
cAMP-dependent protein kinase activity	GO:0004691
cobalt ion transmembrane transporter act...	GO:0015087
neurotrophin TRK receptor binding	GO:0005167
neurotrophin TRKA receptor binding	GO:0005168
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159
phosphatidylinositol phospholipase C act...	GO:0004435
neuropilin binding	GO:0038191
thioredoxin-disulfide reductase activity	GO:0004791
Roundabout binding	GO:0048495
myosin II binding	GO:0045159
ubiquitin protein ligase binding	GO:0031625
ubiquitin-like protein ligase binding	GO:0044389

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p=5.6E-02	n=5

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GO:CC
Elav_Nvec_vc1.1_XM_001634160.3

fraction genes in fg and expected value

vacuolar proton-transporting V-type ATPa...	GO:0016471
nucleotide-activated protein kinase comp...	GO:0031588
cAMP-dependent protein kinase complex	GO:0005952
germinal vesicle	GO:0042585
integral component of organelle membrane	GO:0031301
cell-cell junction	GO:0005911
plasma membrane proton-transporting V-ty...	GO:0033181
apicolateral plasma membrane	GO:0016327
integral component of mitochondrial memb...	GO:0032592
axonal growth cone	GO:0044295
intrinsic component of mitochondrial mem...	GO:0098573
plasma membrane raft	GO:0044853
apical junction complex	GO:0043296
plasma membrane region	GO:0098590
plasma membrane	GO:0005886
phagocytic vesicle membrane	GO:0030670
integral component of endoplasmic reticu...	GO:0030176
intrinsic component of endoplasmic retic...	GO:0031227
Ric1-Rgp1 guanyl-nucleotide exchange fac...	GO:0034066
internode region of axon	GO:0033269
smooth septate junction	GO:0005920
anterior cell cortex	GO:0061802
Schmidt-Lanterman incisure	GO:0043220
compact myelin	GO:0043218
FACT complex	GO:0035101
M band	GO:0031430
Golgi apparatus	GO:0005794
ciliary base	GO:0097546
endoplasmic reticulum membrane	GO:0005789
transcription elongation factor complex	GO:0008023

p=7.2E-04	n=3
p=2.4E-03	n=2
p=2.4E-03	n=2
p=4.7E-03	n=2
p=5.1E-03	n=7
p=7.8E-03	n=7
p=1.1E-02	n=2
p=1.6E-02	n=2
p=2.0E-02	n=2
p=2.0E-02	n=2
p=2.0E-02	n=2
p=2.1E-02	n=3
p=2.1E-02	n=3
p=2.5E-02	n=10
p=2.5E-02	n=21
p=2.6E-02	n=2
p=2.8E-02	n=4
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