

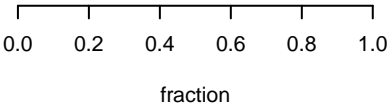
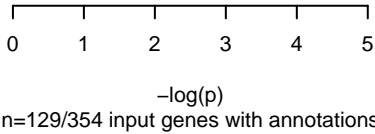
GO:BP
Elav_Nvec_vc1.1_XM_001634460.3

fraction genes in fg and expected value

cellular response to parathyroid hormone...	GO:0071374
nurse cell apoptotic process	GO:0045476
response to cycloheximide	GO:0046898
negative regulation of vascular associat...	GO:1904753
negative regulation of oogenesis	GO:1905880
negative regulation of fat cell prolifer...	GO:0070345
regulation of bicoid mRNA localization	GO:0008359
aflatoxin catabolic process	GO:0046223
phosphatidylcholine catabolic process	GO:0034638
response to fungicide	GO:0060992
cellular response to glucagon stimulus	GO:0071377
response to xenobiotic stimulus	GO:0009410
encapsulation of foreign target	GO:0035010
heparan sulfate proteoglycan metabolic p...	GO:0030201
lactate biosynthetic process	GO:0019249
nuclear body organization	GO:0030575
regulation of transcription by glucose	GO:0046015
glycerol catabolic process	GO:0019563
lactate oxidation	GO:0019516
propionate catabolic process	GO:0019543
oxalate transport	GO:0019532
glucose catabolic process to lactate via...	GO:0019661
nitrogenous compound fermentation	GO:0019666
glycerol biosynthetic process from pyruv...	GO:0046327
response to methionine	GO:1904640
kidney interstitial fibroblast different...	GO:0072071
formate transport	GO:0015724
malate transport	GO:0015743
cellular response to potassium ion starv...	GO:0051365
cellular response to fructose stimulus	GO:0071332

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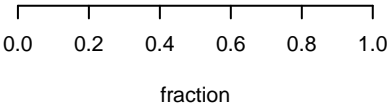
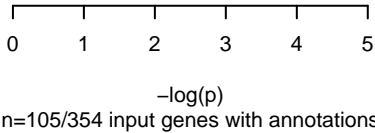
GO:MF
Elav_Nvec_vc1.1_XM_001634460.3

fraction genes in fg and expected value

calcium-independent phospholipase A2 act...	GO:0047499
anion:anion antiporter activity	GO:0015301
inorganic anion exchanger activity	GO:0005452
oxidoreductase activity, acting on the C...	GO:0016899
oxalate transmembrane transporter activi...	GO:0019531
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613
sulfate transmembrane transporter activi...	GO:0015116
inosine kinase activity	GO:0008906
formate transmembrane transporter activi...	GO:0015499
DNA-binding transcription repressor acti...	GO:0001227
DNA binding domain binding	GO:0050692
lactate dehydrogenase activity	GO:0004457
proteasome-activating activity	GO:0036402
nucleobase-containing compound kinase ac...	GO:0019205
ubiquitin-like protein ligase binding	GO:0044389
JUN kinase binding	GO:0008432
epinephrine binding	GO:0051379
nucleoside diphosphate kinase activity	GO:0004550
catecholamine binding	GO:1901338
TBP-class protein binding	GO:0017025
bicarbonate transmembrane transporter ac...	GO:0015106
growth factor receptor binding	GO:0070851
ubiquitin protein ligase binding	GO:0031625
sequence-specific DNA binding	GO:0043565
HMG box domain binding	GO:0071837
general transcription initiation factor ...	GO:0140296
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159
testosterone 17-beta-dehydrogenase (NADP...	GO:0047045
L-ornithine transmembrane transporter ac...	GO:0000064
heparanase activity	GO:0030305

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p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.4E-02	n=3
p=1.6E-02	n=9
p=1.8E-02	n=2
p=1.8E-02	n=2
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p=2.2E-02	n=3
p=2.6E-02	n=2
p=3.1E-02	n=3
p=3.2E-02	n=8
p=3.5E-02	n=12
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GO:CC
Elav_Nvec_vc1.1_XM_001634460.3

fraction genes in fg and expected value

nuclear proteasome complex	GO:0031595
mitochondrial intermembrane space	GO:0005758
proteasome regulatory particle	GO:0005838
proteasome accessory complex	GO:0022624
Golgi medial cisterna	GO:0005797
proteasome regulatory particle, base sub...	GO:0008540
axolemma	GO:0030673
cytosolic proteasome complex	GO:0031597
germinal vesicle	GO:0042585
piP-body	GO:0071547
microvesicle	GO:1990742
dense core granule membrane	GO:0032127
chromosome passenger complex	GO:0032133
TSC1-TSC2 complex	GO:0033596
meiotic spindle midzone	GO:1990385
inner kinetochore	GO:0000939
gamma DNA polymerase complex	GO:0005760
alpha-heterochromatin	GO:0005723
axon hillock	GO:0043203
female germ cell nucleus	GO:0001674
anchored component of membrane	GO:0031225
chromocenter	GO:0010369
intercellular bridge	GO:0045171
Golgi apparatus subcompartment	GO:0098791
leading edge membrane	GO:0031256
polysomal ribosome	GO:0042788
activating signal cointegrator 1 complex	GO:0099053
Rb-E2F complex	GO:0035189
GIN5 complex	GO:0000811
extrinsic component of Golgi membrane	GO:0090498

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p=2.0E-03	n=5
p=1.7E-02	n=3
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