

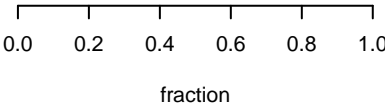
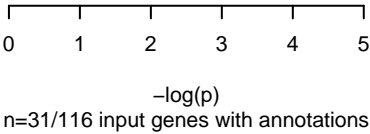
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032380001.2

fraction genes in fg and expected value

cell differentiation involved in kidney ...	GO:0061005
peristalsis	GO:0030432
cellular response to acid chemical	GO:0071229
cellular response to pH	GO:0071467
digestive system process	GO:0022600
polyol catabolic process	GO:0046174
nephron tubule development	GO:0072080
negative regulation of T cell proliferat...	GO:0042130
protein homotrimerization	GO:0070207
response to glucose	GO:0009749
positive regulation of organelle organiz...	GO:0010638
positive regulation of multicellular org...	GO:0040018
response to amino acid	GO:0043200
embryo development	GO:0009790
actin filament polymerization	GO:0030041
cellular response to toxic substance	GO:0097237
positive regulation of supramolecular fi...	GO:1902905
female meiotic nuclear division	GO:0007143
aspartate family amino acid metabolic pr...	GO:0009066
epithelial cell differentiation involved...	GO:0035850
regulation of actin cytoskeleton organiz...	GO:0032956
cellular response to monosaccharide stim...	GO:0071326
cellular response to hexose stimulus	GO:0071331
cellular response to glucose stimulus	GO:0071333
positive regulation of actin filament po...	GO:0030838
regulation of gluconeogenesis	GO:0006111
regulation of actin filament-based proce...	GO:0032970
positive regulation of cytoskeleton orga...	GO:0051495
cellular response to carbohydrate stimul...	GO:0071322
cellular glucose homeostasis	GO:0001678

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p=1.2E-02	n=2
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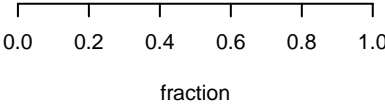
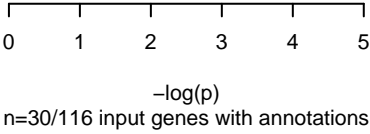
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032380001.2

fraction genes in fg and expected value

manganese ion binding	GO:0030145
oxidoreductase activity, acting on NAD(P...	GO:0016651
phosphotransferase activity, phosphate g...	GO:0016776
protein-disulfide reductase (NAD(P)) act...	GO:0047134
nucleobase-containing compound kinase ac...	GO:0019205
GDP binding	GO:0019003
GPI-anchor transamidase activity	GO:0003923
N-acetylglucosamine-1-phosphodiester alp...	GO:0003944
translation elongation factor binding	GO:0061770
thioredoxin-disulfide reductase activity	GO:0004791
inositol monophosphate 3-phosphatase act...	GO:0052832
tyrosyl-RNA phosphodiesterase activity	GO:0036317
lithium ion binding	GO:0031403
acid-sensing ion channel activity	GO:0044736
inositol monophosphate 1-phosphatase act...	GO:0008934
5'-tyrosyl-DNA phosphodiesterase activit...	GO:0070260
pyruvate dehydrogenase (acetyl-transferr...	GO:0004740
selenium binding	GO:0008430
actin binding	GO:0003779
magnesium ion binding	GO:0000287
purine ribonucleoside triphosphate bindi...	GO:0035639
actin filament binding	GO:0051015
single-stranded DNA binding	GO:0003697
core promoter sequence-specific DNA bind...	GO:0001046
omega peptidase activity	GO:0008242
asparaginase activity	GO:0004067
threonine-type peptidase activity	GO:0070003
STAT family protein binding	GO:0097677
guanylate kinase activity	GO:0004385
inositol monophosphate 4-phosphatase act...	GO:0052833

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p=2.2E-02	n=3
p=2.6E-02	n=3
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032380001.2

fraction genes in fg and expected value

PML body	GO:0016605
CHOP-C/EBP complex	GO:0036488
mitochondrial pyruvate dehydrogenase com...	GO:0005967
TORC2 complex	GO:0031932
cuticular plate	GO:0032437
actin-based cell projection	GO:0098858
adherens junction	GO:0005912
microvillus	GO:0005902
lateral loop	GO:0043219
eukaryotic translation initiation factor...	GO:0005850
caspase complex	GO:0008303
NELF complex	GO:0032021
node of Ranvier	GO:0033268
GPI-anchor transamidase complex	GO:0042765
TOR complex	GO:0038201
filamentous actin	GO:0031941
nuclear stress granule	GO:0097165
TORC1 complex	GO:0031931
oxidoreductase complex	GO:1990204
condensed chromosome, centromeric region	GO:0000779
pyruvate dehydrogenase complex	GO:0045254
MPP7-DLG1-LIN7 complex	GO:0097025
myelin sheath abaxonal region	GO:0035748
spindle	GO:0005819
eukaryotic translation initiation factor...	GO:0005851
aggresome	GO:0016235
intrinsic component of the cytoplasmic s...	GO:0031235
unconventional myosin complex	GO:0016461
actin filament	GO:0005884
myosin complex	GO:0016459

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