

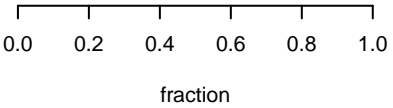
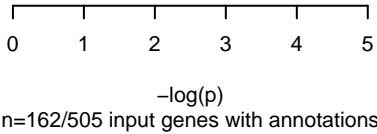
GO:BP
Ncol_Nvec_vc1.1_XM_032376926.2

fraction genes in fg and expected value

vesicle budding from membrane	GO:0006900
response to water deprivation	GO:0009414
central nervous system development	GO:0007417
locomotory behavior	GO:0007626
spleen development	GO:0048536
response to starvation	GO:0042594
embryonic ectodermal digestive tract mor...	GO:0048613
vesicle transport along actin filament	GO:0030050
regulation of store-operated calcium ent...	GO:2001256
positive regulation of transforming grow...	GO:0032915
positive regulation of gastrulation	GO:2000543
positive regulation of prostaglandin bio...	GO:0031394
thrombopoietin-mediated signaling pathwa...	GO:0038163
endoplasmic reticulum to Golgi vesicle-m...	GO:0006888
regulation of cellular catabolic process	GO:0031329
protein localization to cell surface	GO:0034394
histone H3-K9 methylation	GO:0051567
heparan sulfate proteoglycan biosynthesi...	GO:0015012
positive regulation of organic acid tran...	GO:0032892
positive regulation of transcription of ...	GO:0007221
mitochondrial DNA metabolic process	GO:0032042
endoplasmic reticulum organization	GO:0007029
carbohydrate derivative biosynthetic pro...	GO:1901137
glomerulus development	GO:0032835
regulation of cell maturation	GO:1903429
negative regulation of inclusion body as...	GO:0090084
actin nucleation	GO:0045010
negative regulation of protein localizat...	GO:2000009
fatty-acyl-CoA biosynthetic process	GO:0046949
histone H3-K9 trimethylation	GO:0036124

p=4.7E-04	n=7
p=8.1E-04	n=3
p=1.7E-03	n=27
p=1.9E-03	n=16
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p=2.2E-03	n=12
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p=3.6E-03	n=2
p=3.6E-03	n=2
p=3.6E-03	n=2
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p=3.6E-03	n=2
p=3.6E-03	n=2
p=3.6E-03	n=2
p=3.9E-03	n=8
p=4.3E-03	n=24
p=5.8E-03	n=4
p=6.2E-03	n=3
p=6.2E-03	n=3
p=6.2E-03	n=3
p=6.2E-03	n=3
p=6.2E-03	n=3
p=6.8E-03	n=5
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p=8.4E-03	n=5
p=9.5E-03	n=3
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fg=0.01	bg=0.00
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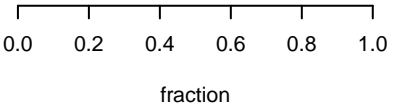
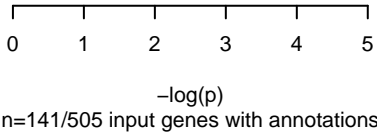
GO:MF
Ncol_Nvec_vc1.1_XM_032376926.2

fraction genes in fg and expected value

ribosome binding	GO:0043022
proteasome binding	GO:0070628
catalytic activity, acting on a glycopro...	GO:0140103
transporter activity	GO:0005215
beta-1,3-galactosyltransferase activity	GO:0048531
peptidase activator activity involved in...	GO:0016505
cysteine-type endopeptidase activator ac...	GO:0008656
triglyceride lipase activity	GO:0004806
transmembrane transporter activity	GO:0022857
low-density lipoprotein particle recepto...	GO:0050750
lipoprotein particle receptor binding	GO:0070325
transcription coregulator binding	GO:0001221
inorganic molecular entity transmembrane...	GO:0015318
UDP-glycosyltransferase activity	GO:0008194
small GTPase binding	GO:0031267
ion transmembrane transporter activity	GO:0015075
single-stranded DNA binding	GO:0003697
active ion transmembrane transporter act...	GO:0022853
protein heterodimerization activity	GO:0046982
transcription coactivator binding	GO:0001223
glucuronosyltransferase activity	GO:0015020
dynactin binding	GO:0034452
cysteine-type endopeptidase regulator ac...	GO:0043028
active transmembrane transporter activit...	GO:0022804
peptidase regulator activity	GO:0061134
secondary active transmembrane transport...	GO:0015291
acid-sensing ion channel activity	GO:0044736
nerve growth factor binding	GO:0048406
L-proline transmembrane transporter acti...	GO:0015193
L-tryptophan transmembrane transporter a...	GO:0015196

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p=3.6E-03	n=3
p=5.1E-03	n=24
p=9.3E-03	n=3
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p=1.0E-02	n=2
p=1.0E-02	n=2
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p=1.3E-02	n=3
p=1.3E-02	n=3
p=1.3E-02	n=3
p=1.5E-02	n=16
p=1.9E-02	n=5
p=2.1E-02	n=12
p=2.3E-02	n=16
p=2.6E-02	n=5
p=2.6E-02	n=7
p=2.8E-02	n=14
p=3.1E-02	n=2
p=4.5E-02	n=2
p=4.5E-02	n=2
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GO:CC
Ncol_Nvec_vc1.1_XM_032376926.2

fraction genes in fg and expected value

cell body fiber	GO:0070852
basal dendrite	GO:0097441
Golgi membrane	GO:0000139
post-mRNA release spliceosomal complex	GO:0071014
transport vesicle membrane	GO:0030658
apical dendrite	GO:0097440
Golgi apparatus subcompartment	GO:0098791
oligosaccharyltransferase complex	GO:0008250
actin cap	GO:0030478
FAR/SIN/STRIPAK complex	GO:0090443
endoplasmic reticulum membrane	GO:0005789
integral component of endoplasmic reticu...	GO:0030176
nuclear outer membrane-endoplasmic retic...	GO:0042175
endoplasmic reticulum subcompartment	GO:0098827
intrinsic component of endoplasmic retic...	GO:0031227
Golgi stack	GO:0005795
alpha DNA polymerase:primase complex	GO:0005658
Golgi-associated vesicle membrane	GO:0030660
integral component of organelle membrane	GO:0031301
actin-based cell projection	GO:0098858
integral component of membrane	GO:0016021
XY body	GO:0001741
microvillus	GO:0005902
intrinsic component of membrane	GO:0031224
intrinsic component of organelle membran...	GO:0031300
Golgi cisterna	GO:0031985
filopodium tip	GO:0032433
exocytic vesicle membrane	GO:0099501
organelle subcompartment	GO:0031984
transcription elongation factor complex	GO:0008023

p=7.8E-04	n=3
p=7.8E-04	n=3
p=9.2E-04	n=18
p=3.5E-03	n=2
p=5.1E-03	n=7
p=6.0E-03	n=3
p=7.1E-03	n=19
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p=1.0E-02	n=2
p=1.1E-02	n=20
p=1.3E-02	n=8
p=1.3E-02	n=20
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p=2.3E-02	n=4
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p=2.9E-02	n=7
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