

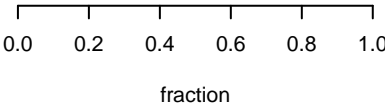
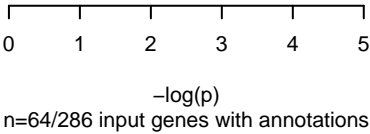
GO:BP
Ncol_Nvec_vc1.1_XM_032361814.2

fraction genes in fg and expected value

detection of external stimulus	GO:0009581
detection of abiotic stimulus	GO:0009582
retina vasculature morphogenesis in came...	GO:0061299
sensory perception	GO:0007600
regulated exocytosis	GO:0045055
regulation of heart rate	GO:0002027
toxin transport	GO:1901998
cellular response to calcium ion	GO:0071277
positive regulation of axon extension in...	GO:0048842
response to hepatocyte growth factor	GO:0035728
dendrite arborization	GO:0140059
photoreceptor cell fate commitment	GO:0046552
inorganic ion transmembrane transport	GO:0098660
cation transmembrane transport	GO:0098655
regulation of membrane potential	GO:0042391
regulation of synapse structural plastic...	GO:0051823
gamma-aminobutyric acid signaling pathwa...	GO:0007214
response to hypoxia	GO:0001666
calcium-mediated signaling	GO:0019722
detection of light stimulus	GO:0009583
response to decreased oxygen levels	GO:0036293
detection of stimulus involved in sensor...	GO:0050906
cranial nerve structural organization	GO:0021604
negative regulation of calcium-mediated ...	GO:0050849
vascular endothelial growth factor signa...	GO:0038084
branched-chain amino acid metabolic proc...	GO:0009081
branched-chain amino acid catabolic proc...	GO:0009083
actin cytoskeleton reorganization	GO:0031532
regulation of calcium ion transport into...	GO:0010522
detection of mechanical stimulus	GO:0050982

p=2.6E-03	n=6
p=3.3E-03	n=6
p=3.6E-03	n=2
p=3.7E-03	n=10
p=4.8E-03	n=10
p=5.4E-03	n=4
p=5.6E-03	n=3
p=5.6E-03	n=3
p=7.0E-03	n=2
p=7.0E-03	n=2
p=7.0E-03	n=2
p=7.3E-03	n=3
p=9.3E-03	n=10
p=1.0E-02	n=10
p=1.1E-02	n=7
p=1.1E-02	n=2
p=1.1E-02	n=2
p=1.2E-02	n=7
p=1.2E-02	n=5
p=1.3E-02	n=4
p=1.3E-02	n=7
p=1.5E-02	n=4
p=1.7E-02	n=2
p=1.7E-02	n=2
p=1.7E-02	n=2
p=1.7E-02	n=2
p=1.7E-02	n=2
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fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.05	bg=0.01
fg=0.05	bg=0.01
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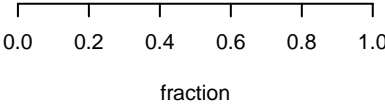
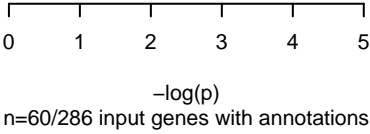
GO:MF
Ncol_Nvec_vc1.1_XM_032361814.2

fraction genes in fg and expected value

ion gated channel activity	GO:0022839
high voltage-gated calcium channel activ...	GO:0008331
peroxidase activity	GO:0004601
phosphatidylinositol binding	GO:0035091
acyltransferase activity, transferring g...	GO:0016747
calcium-dependent phospholipid binding	GO:0005544
phosphatidylethanolamine binding	GO:0008429
ammonium ion binding	GO:0070405
acetyltransferase activity	GO:0016407
transmitter-gated ion channel activity	GO:0022824
transmitter-gated channel activity	GO:0022835
anion channel activity	GO:0005253
chloride channel activity	GO:0005254
ion channel activity	GO:0005216
voltage-gated anion channel activity	GO:0008308
voltage-gated chloride channel activity	GO:0005247
phospholipase activity	GO:0004620
quaternary ammonium group binding	GO:0050997
phosphatidylcholine binding	GO:0031210
phosphatidylinositol phosphate binding	GO:1901981
chloride transmembrane transporter activ...	GO:0015108
phosphoprotein binding	GO:0051219
lipase activity	GO:0016298
identical protein binding	GO:0042802
phosphatidylinositol bisphosphate bindin...	GO:1902936
glycogen binding	GO:2001069
semaphorin receptor activity	GO:0017154
[phosphorylase] phosphatase activity	GO:0050196
C-acetyltransferase activity	GO:0016453
acetyl-CoA C-acetyltransferase activity	GO:0003985

p=7.3E-04	n=7
p=1.4E-03	n=2
p=4.1E-03	n=2
p=6.4E-03	n=6
p=6.7E-03	n=4
p=8.0E-03	n=2
p=8.0E-03	n=2
p=8.8E-03	n=3
p=1.1E-02	n=3
p=1.3E-02	n=2
p=1.3E-02	n=2
p=1.7E-02	n=3
p=1.7E-02	n=3
p=1.7E-02	n=8
p=1.9E-02	n=2
p=1.9E-02	n=2
p=2.0E-02	n=3
p=2.6E-02	n=2
p=2.6E-02	n=2
p=2.7E-02	n=4
p=2.8E-02	n=3
p=3.2E-02	n=3
p=3.2E-02	n=3
p=3.4E-02	n=16
p=3.7E-02	n=3
p=3.8E-02	n=1
p=3.8E-02	n=1
p=3.8E-02	n=1
p=3.8E-02	n=1

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GO:CC
Ncol_Nvec_vc1.1_XM_032361814.2

fraction genes in fg and expected value

ficolin-1-rich granule membrane	GO:0101003
presynapse	GO:0098793
apical plasma membrane	GO:0016324
integral component of synaptic vesicle m...	GO:0030285
side of membrane	GO:0098552
ion channel complex	GO:0034702
cell surface	GO:0009986
voltage-gated calcium channel complex	GO:0005891
extrinsic component of cytoplasmic side ...	GO:0031234
cytoplasmic side of plasma membrane	GO:0009898
organelle membrane contact site	GO:0044232
cytoplasmic side of membrane	GO:0098562
calcium channel complex	GO:0034704
cell projection membrane	GO:0031253
L-type voltage-gated calcium channel com...	GO:1990454
UBC13-UEV1A complex	GO:0035370
semaphorin receptor complex	GO:0002116
extrinsic component of plasma membrane	GO:0019897
cation channel complex	GO:0034703
lysosome	GO:0005764
brush border	GO:0005903
leading edge membrane	GO:0031256
lytic vacuole	GO:0000323
plasma membrane protein complex	GO:0098797
vacuolar membrane	GO:0005774
cell periphery	GO:0071944
cell body fiber	GO:0070852
acetylcholine-gated channel complex	GO:0005892
outer kinetochore	GO:0000940
transcription factor AP-1 complex	GO:0035976

p=7.8E-04	n=3
p=2.3E-03	n=12
p=3.1E-03	n=8
p=5.7E-03	n=3
p=7.4E-03	n=7
p=7.6E-03	n=4
p=8.1E-03	n=7
p=1.1E-02	n=2
p=1.4E-02	n=3
p=1.5E-02	n=5
p=1.7E-02	n=2
p=2.3E-02	n=5
p=2.3E-02	n=2
p=2.8E-02	n=6
p=3.5E-02	n=1
p=3.5E-02	n=1
p=3.5E-02	n=1
p=3.6E-02	n=3
p=3.6E-02	n=3
p=4.9E-02	n=7
p=5.0E-02	n=3
p=5.6E-02	n=3
p=5.9E-02	n=7
p=6.5E-02	n=5
p=6.5E-02	n=5
p=6.8E-02	n=28
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p=7.0E-02	n=1

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