

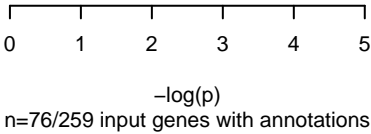
GO:BP
Ncol_Nvec_vc1.1_XM_048728976.1

fraction genes in fg and expected value

chloride transmembrane transport	GO:1902476
pH reduction	GO:0045851
positive regulation of heart rate invol...	GO:0001988
negative gravitaxis	GO:0048060
endothelial cell morphogenesis	GO:0001886
positive regulation of secondary heart f...	GO:0072513
negative regulation of extrinsic apoptot...	GO:2001240
positive regulation of CoA-transferase a...	GO:1905920
positive regulation of acetylcholine bio...	GO:1905923
generation of ovulation cycle rhythm	GO:0060112
sensory processing	GO:0050893
regulation of heart morphogenesis	GO:2000826
regulation of membrane potential	GO:0042391
neuron fate commitment	GO:0048663
regulation of amyloid fibril formation	GO:1905906
rhabdomere morphogenesis	GO:0061541
ocellus photoreceptor cell development	GO:0042463
dopamine biosynthetic process	GO:0042416
negative regulation of amyloid-beta form...	GO:1902430
regulation of norepinephrine secretion	GO:0014061
ocellus morphogenesis	GO:0048816
anterior head segmentation	GO:0035288
diet induced thermogenesis	GO:0002024
positive regulation of branching involve...	GO:0090190
sevenless signaling pathway	GO:0045500
retina vasculature morphogenesis in came...	GO:0061299
anterior region determination	GO:0007355
negative regulation of ryanodine-sensiti...	GO:0060315
negative regulation of interleukin-1 bet...	GO:0032691
midbrain-hindbrain boundary development	GO:0030917

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p=3.3E-03	n=7
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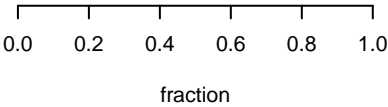
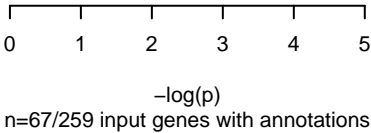
GO:MF
Ncol_Nvec_vc1.1_XM_048728976.1

fraction genes in fg and expected value

protein disulfide isomerase activity	GO:0003756
voltage-gated chloride channel activity	GO:0005247
ion gated channel activity	GO:0022839
acetylcholine-gated cation-selective cha...	GO:0022848
acetylcholine receptor activity	GO:0015464
glutathione peroxidase activity	GO:0004602
D3 dopamine receptor binding	GO:0031750
D4 dopamine receptor binding	GO:0031751
acetylcholine binding	GO:0042166
D2 dopamine receptor binding	GO:0031749
toxic substance binding	GO:0015643
chloride channel regulator activity	GO:0017081
ammonium ion binding	GO:0070405
transcription coactivator binding	GO:0001223
ubiquitin-ubiquitin ligase activity	GO:0034450
adenylate cyclase binding	GO:0008179
phosphatase regulator activity	GO:0019208
identical protein binding	GO:0042802
neurotransmitter transmembrane transport...	GO:0005326
ligand-gated anion channel activity	GO:0099095
protein serine/threonine kinase inhibito...	GO:0030291
G protein-coupled receptor binding	GO:0001664
extracellular ligand-gated ion channel a...	GO:0005230
passive transmembrane transporter activi...	GO:0022803
channel activity	GO:0015267
Notch binding	GO:0005112
hormone binding	GO:0042562
CXCR chemokine receptor binding	GO:0045236
acetate ester transmembrane transporter ...	GO:1901375
protein tyrosine phosphatase activity, m...	GO:0030946

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p=1.2E-02	n=3
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p=2.3E-02	n=3
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p=3.9E-02	n=10
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GO:CC
Ncol_Nvec_vc1.1_XM_048728976.1

fraction genes in fg and expected value

Cul3-RING ubiquitin ligase complex	GO:0031463
extracellular space	GO:0005615
acetylcholine-gated channel complex	GO:0005892
external side of plasma membrane	GO:0009897
muscle cell projection membrane	GO:0036195
lysosomal lumen	GO:0043202
axolemma	GO:0030673
azurophil granule lumen	GO:0035578
membrane raft	GO:0045121
membrane microdomain	GO:0098857
neuron projection membrane	GO:0032589
extracellular exosome	GO:0070062
extracellular membrane-bounded organelle	GO:0065010
extracellular organelle	GO:0043230
extracellular vesicle	GO:1903561
Cul4-RING E3 ubiquitin ligase complex	GO:0080008
postsynaptic membrane	GO:0045211
endoplasmic reticulum lumen	GO:0005788
dendritic shaft	GO:0043198
postsynapse	GO:0098794
stereocilium	GO:0032420
stereocilium bundle	GO:0032421
striated muscle dense body	GO:0055120
equatorial microtubule organizing center	GO:0000923
syntrophin complex	GO:0016013
interleukin-5 receptor complex	GO:0005895
nuclear SCF ubiquitin ligase complex	GO:0043224
gamma-tubulin complex	GO:0000930
Cul5-RING ubiquitin ligase complex	GO:0031466
Cul7-RING ubiquitin ligase complex	GO:0031467

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p=1.6E-03	n=2
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p=4.8E-03	n=2
p=5.1E-03	n=4
p=1.5E-02	n=2
p=1.7E-02	n=3
p=1.9E-02	n=6
p=1.9E-02	n=6
p=2.1E-02	n=3
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p=3.0E-02	n=2
p=3.2E-02	n=4
p=3.2E-02	n=4
p=3.4E-02	n=3
p=3.5E-02	n=7
p=3.9E-02	n=2
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