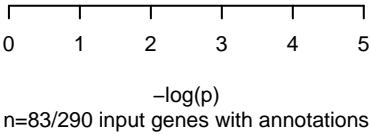


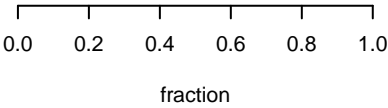
GO:BP
Ncol_Nvec_vc1.1_XM_001626384.3

fraction genes in fg and expected value

negative regulation of ATP-dependent act...	GO:0032780	p=5.4E-03	n=2
regulation of vascular endothelial growt...	GO:0030947	p=5.4E-03	n=2
brain development	GO:0007420	p=7.9E-03	n=13
cellular response to hormone stimulus	GO:0032870	p=1.1E-02	n=11
regulation of protein polyubiquitination	GO:1902914	p=1.3E-02	n=2
regulation of locomotion	GO:0040012	p=1.4E-02	n=13
carbohydrate homeostasis	GO:0033500	p=1.5E-02	n=6
locomotion	GO:0040011	p=1.5E-02	n=22
cellular response to peptide hormone sti...	GO:0071375	p=1.6E-02	n=7
mitochondrial translational termination	GO:0070126	p=1.6E-02	n=3
negative regulation of extrinsic apoptot...	GO:2001237	p=1.6E-02	n=3
cellular response to insulin stimulus	GO:0032869	p=1.7E-02	n=6
positive regulation of gluconeogenesis	GO:0045722	p=1.8E-02	n=2
negative regulation of oxidoreductase ac...	GO:0051354	p=1.8E-02	n=2
mitochondrial translational elongation	GO:0070125	p=1.9E-02	n=3
positive regulation of carbohydrate meta...	GO:0045913	p=1.9E-02	n=3
cellular response to organonitrogen comp...	GO:0071417	p=1.9E-02	n=10
cellular process involved in reproductio...	GO:0022412	p=2.1E-02	n=16
positive regulation of small molecule me...	GO:0062013	p=2.3E-02	n=4
negative regulation of tyrosine phosphor...	GO:0042532	p=2.3E-02	n=2
imaginal disc growth	GO:0007446	p=2.3E-02	n=2
translational termination	GO:0006415	p=2.5E-02	n=3
negative regulation of apoptotic signal...	GO:2001234	p=2.5E-02	n=5
cell migration	GO:0016477	p=2.7E-02	n=15
response to insulin	GO:0032868	p=2.8E-02	n=6
sensory system development	GO:0048880	p=2.9E-02	n=11
male meiosis cytokinesis	GO:0007112	p=2.9E-02	n=2
negative regulation of myeloid leukocyte...	GO:0002762	p=2.9E-02	n=2
positive regulation of ATP biosynthetic ...	GO:2001171	p=2.9E-02	n=2
phosphatidic acid biosynthetic process	GO:0006654	p=2.9E-02	n=2



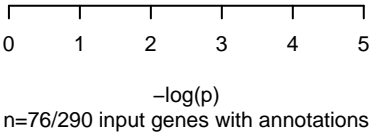
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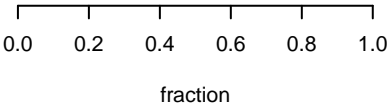
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Ncol_Nvec_vc1.1_XM_001626384.3

fraction genes in fg and expected value

1-acylglycerol-3-phosphate O-acyltransfe...	GO:0003841	p=1.4E-02	n=2
acetyltransferase activity	GO:0016407	p=1.8E-02	n=3
ligand-activated transcription factor ac...	GO:0098531	p=1.9E-02	n=2
chloride channel regulator activity	GO:0017081	p=1.9E-02	n=2
acylglycerol O-acyltransferase activity	GO:0016411	p=1.9E-02	n=2
nuclear receptor activity	GO:0004879	p=1.9E-02	n=2
lysophosphatidic acid acyltransferase ac...	GO:0042171	p=2.5E-02	n=2
cullin family protein binding	GO:0097602	p=2.5E-02	n=2
lysophospholipid acyltransferase activit...	GO:0071617	p=2.5E-02	n=2
acyltransferase activity, transferring g...	GO:0016747	p=2.6E-02	n=4
peptide transmembrane transporter activi...	GO:1904680	p=3.2E-02	n=2
acyltransferase activity	GO:0016746	p=3.2E-02	n=4
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159	p=3.2E-02	n=1
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597	p=3.2E-02	n=1
G-protein beta-subunit binding	GO:0031681	p=3.2E-02	n=1
mitochondrial ribosome binding	GO:0097177	p=3.2E-02	n=1
glutamate-cysteine ligase catalytic subu...	GO:0035226	p=3.2E-02	n=1
phosphoglycerate mutase activity	GO:0004619	p=3.2E-02	n=1
RNA-3'-phosphate cyclase activity	GO:0003963	p=3.2E-02	n=1
calcium-dependent outer dynein arm bindi...	GO:0120152	p=3.2E-02	n=1
[3-methyl-2-oxobutanoate dehydrogenase (...	GO:0047323	p=3.2E-02	n=1
arginine kinase activity	GO:0004054	p=3.2E-02	n=1
icosanoid binding	GO:0050542	p=3.2E-02	n=1
icosatetraenoic acid binding	GO:0050543	p=3.2E-02	n=1
arachidonic acid binding	GO:0050544	p=3.2E-02	n=1
F-box domain binding	GO:1990444	p=3.2E-02	n=1
phosphotransferase activity, nitrogenous...	GO:0016775	p=3.2E-02	n=1
1-alkylglycerophosphocholine O-acyltrans...	GO:0047191	p=3.2E-02	n=1
stearic acid binding	GO:0070540	p=3.2E-02	n=1
O-acyltransferase activity	GO:0008374	p=3.9E-02	n=2



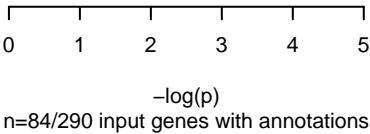
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GO:CC
Ncol_Nvec_vc1.1_XM_001626384.3

fraction genes in fg and expected value

Lewy body	GO:0097413	p=9.6E-04	n=2
U2-type prespliceosome	GO:0071004	p=9.0E-03	n=2
eukaryotic 43S preinitiation complex	GO:0016282	p=3.1E-02	n=1
FANCM-MHF complex	GO:0071821	p=3.1E-02	n=1
NatA complex	GO:0031415	p=3.1E-02	n=1
organellar large ribosomal subunit	GO:0000315	p=4.4E-02	n=2
mitochondrial large ribosomal subunit	GO:0005762	p=4.4E-02	n=2
integral component of mitochondrial memb...	GO:0032592	p=5.2E-02	n=2
intrinsic component of mitochondrial mem...	GO:0098573	p=5.2E-02	n=2
lysosomal membrane	GO:0005765	p=6.0E-02	n=4
transcription factor TFIIC complex	GO:0000127	p=6.1E-02	n=1
dihydrolipoyl dehydrogenase complex	GO:0045240	p=6.1E-02	n=1
mitochondrial alpha-ketoglutarate dehydr...	GO:0005947	p=6.1E-02	n=1
Parkin-FBXW7-Cul1 ubiquitin ligase compl...	GO:1990452	p=6.1E-02	n=1
glutamate-cysteine ligase complex	GO:0017109	p=6.1E-02	n=1
translation preinitiation complex	GO:0070993	p=6.1E-02	n=1
RNA polymerase III transcription regulat...	GO:0090576	p=6.1E-02	n=1
N-terminal protein acetyltransferase com...	GO:0031414	p=6.1E-02	n=1
azurophil granule	GO:0042582	p=6.5E-02	n=3
primary lysosome	GO:0005766	p=6.5E-02	n=3
germ cell nucleus	GO:0043073	p=7.7E-02	n=2
lytic vacuole membrane	GO:0098852	p=8.1E-02	n=4
perinuclear region of cytoplasm	GO:0048471	p=8.8E-02	n=9
transcription regulator complex	GO:0005667	p=8.8E-02	n=6
RSC-type complex	GO:0016586	p=9.0E-02	n=1
tricarboxylic acid cycle enzyme complex	GO:0045239	p=9.0E-02	n=1
EARP complex	GO:1990745	p=9.0E-02	n=1
SWI/SNF complex	GO:0016514	p=9.0E-02	n=1
Fanconi anaemia nuclear complex	GO:0043240	p=9.0E-02	n=1
GARP complex	GO:0000938	p=9.0E-02	n=1



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