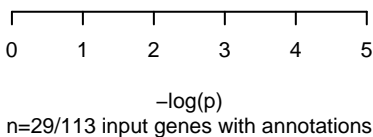
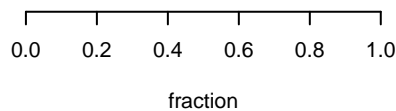


GO:BP
Ncol_Nvec_vc1.1_XM_001626384.3

fraction genes in fg and expected value

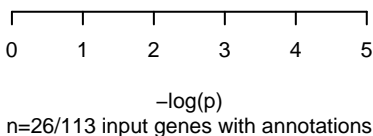
negative regulation of myeloid leukocyte...	GO:0002762	p=2.4E-03	n=2
positive regulation of gluconeogenesis	GO:0045722	p=4.9E-03	n=2
negative regulation of tyrosine phosphor...	GO:0042532	p=4.9E-03	n=2
glucose homeostasis	GO:0042593	p=7.3E-03	n=4
cellular response to insulin stimulus	GO:0032869	p=9.6E-03	n=4
lipid modification	GO:0030258	p=1.1E-02	n=3
pronephric glomerulus development	GO:0039021	p=1.6E-02	n=1
uridine transport	GO:0015862	p=1.6E-02	n=1
pyrimidine nucleoside transport	GO:0015864	p=1.6E-02	n=1
regulation of activation of Janus kinase...	GO:0010533	p=1.6E-02	n=1
adenine transport	GO:0015853	p=1.6E-02	n=1
pyrimidine nucleobase transport	GO:0015855	p=1.6E-02	n=1
abducens nerve morphogenesis	GO:0021598	p=1.6E-02	n=1
abducens nerve formation	GO:0021599	p=1.6E-02	n=1
cellular response to thyroxine stimulus	GO:0097069	p=1.6E-02	n=1
negative regulation of activation of Jan...	GO:1902569	p=1.6E-02	n=1
abducens nerve development	GO:0021560	p=1.6E-02	n=1
regulation of phosphatidylcholine biosyn...	GO:2001245	p=1.6E-02	n=1
negative regulation of phosphatidylcholi...	GO:2001246	p=1.6E-02	n=1
pupariation	GO:0035073	p=1.6E-02	n=1
protein localization to cleavage furrow	GO:1905345	p=1.6E-02	n=1
rhombomere 5 development	GO:0021571	p=1.6E-02	n=1
rhombomere 6 development	GO:0021572	p=1.6E-02	n=1
positive regulation of ligase activity	GO:0051351	p=1.6E-02	n=1
regulation of platelet-derived growth fa...	GO:2000586	p=1.6E-02	n=1
negative regulation of platelet-derived ...	GO:2000587	p=1.6E-02	n=1
protein localization to cell division si...	GO:0072741	p=1.6E-02	n=1
regulation of glutamate-cysteine ligase ...	GO:0035227	p=1.6E-02	n=1
negative regulation of vascular endothel...	GO:0030948	p=1.6E-02	n=1
positive regulation of glutamate-cystein...	GO:0035229	p=1.6E-02	n=1

[illegible]

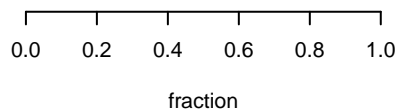
GO:MF
Ncol_Nvec_vc1.1_XM_001626384.3

fraction genes in fg and expected value

thiolester hydrolase activity	GO:0016790	p=1.3E-02	n=2
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159	p=1.6E-02	n=1
glutamate-cysteine ligase catalytic subu...	GO:0035226	p=1.6E-02	n=1
long-chain fatty acid binding	GO:0036041	p=1.6E-02	n=1
nucleoside transmembrane transporter act...	GO:0005337	p=1.6E-02	n=1
stearic acid binding	GO:0070540	p=1.6E-02	n=1
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597	p=1.6E-02	n=1
1-alkylglycerophosphocholine O-acyltra...	GO:0047191	p=1.6E-02	n=1
icosanoid binding	GO:0050542	p=1.6E-02	n=1
icosatetraenoic acid binding	GO:0050543	p=1.6E-02	n=1
arachidonic acid binding	GO:0050544	p=1.6E-02	n=1
fatty acid binding	GO:0005504	p=3.2E-02	n=1
non-membrane spanning protein tyrosine p...	GO:0004726	p=3.2E-02	n=1
long-chain fatty acyl-CoA binding	GO:0036042	p=3.2E-02	n=1
1-acylglycerophosphocholine O-acyltra...	GO:0047184	p=3.2E-02	n=1
STAT family protein binding	GO:0097677	p=3.2E-02	n=1
chloride channel inhibitor activity	GO:0019869	p=3.2E-02	n=1
2-acylglycerol-3-phosphate O-acyltra...	GO:0047144	p=3.2E-02	n=1
O-acetyltransferase activity	GO:0016413	p=3.2E-02	n=1
glutamate-cysteine ligase activity	GO:0004357	p=3.2E-02	n=1
1-alkylglycerophosphocholine O-acetyltra...	GO:0047192	p=3.2E-02	n=1
fatty acid ligase activity	GO:0015645	p=3.2E-02	n=1
galactosylgalactosylxylosylprotein 3-bet...	GO:0015018	p=3.2E-02	n=1
neurotransmitter:sodium symporter activi...	GO:0005328	p=3.2E-02	n=1
syntaxin binding	GO:0019905	p=4.1E-02	n=2
phosphatidylinositol-4,5-bisphosphate ph...	GO:0106019	p=4.8E-02	n=1
1-acylglycerol-3-phosphate O-acyltra...	GO:0003841	p=4.8E-02	n=1
carbonate dehydratase activity	GO:0004089	p=4.8E-02	n=1
fatty-acyl-CoA binding	GO:0000062	p=4.8E-02	n=1
acid-amino acid ligase activity	GO:0016881	p=4.8E-02	n=1



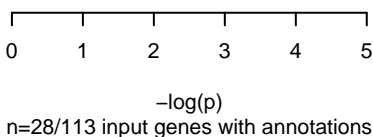
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GO:CC
Ncol_Nvec_vc1.1_XM_001626384.3

fraction genes in fg and expected value

translation preinitiation complex	GO:0070993	p=1.5E-02	n=1
eukaryotic 43S preinitiation complex	GO:0016282	p=1.5E-02	n=1
late endosome membrane	GO:0031902	p=2.1E-02	n=2
lysosomal membrane	GO:0005765	p=2.7E-02	n=3
Lewy body	GO:0097413	p=3.1E-02	n=1
phagophore assembly site membrane	GO:0034045	p=3.1E-02	n=1
eukaryotic translation initiation factor...	GO:0005850	p=3.1E-02	n=1
multi-eIF complex	GO:0043614	p=3.1E-02	n=1
glutamate-cysteine ligase complex	GO:0017109	p=3.1E-02	n=1
sarcoplasmic reticulum membrane	GO:0033017	p=3.1E-02	n=1
lytic vacuole membrane	GO:0098852	p=3.4E-02	n=3
endoplasmic reticulum-Golgi intermediate...	GO:0005793	p=3.7E-02	n=2
intrinsic component of mitochondrial out...	GO:0031306	p=4.6E-02	n=1
integral component of mitochondrial oute...	GO:0031307	p=4.6E-02	n=1
U2-type prespliceosome	GO:0071004	p=4.6E-02	n=1
phagophore assembly site	GO:0000407	p=4.6E-02	n=1
azurophil granule	GO:0042582	p=5.2E-02	n=2
primary lysosome	GO:0005766	p=5.2E-02	n=2
dendrite cytoplasm	GO:0032839	p=6.1E-02	n=1
spliceosome	GO:0071010	p=6.1E-02	n=1
vacuolar membrane	GO:0005774	p=6.8E-02	n=3
septin cytoskeleton	GO:0032156	p=7.5E-02	n=1
immunological synapse	GO:0001772	p=7.5E-02	n=1
early endosome	GO:0005769	p=8.8E-02	n=3
sarcoplasm	GO:0016528	p=8.9E-02	n=1
sarcoplasmic reticulum	GO:0016529	p=8.9E-02	n=1
nuclear inner membrane	GO:0005637	p=1.0E-01	n=1
neuron projection cytoplasm	GO:0120111	p=1.0E-01	n=1
integral component of mitochondrial memb...	GO:0032592	p=1.2E-01	n=1
azurophil granule membrane	GO:0035577	p=1.2E-01	n=1

[illegible]