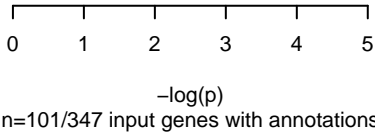


GO:BP
Ncol_Nvec_vc1.1_XM_001639547.3

fraction genes in fg and expected value

adherens junction maintenance	GO:0034334	p=6.4E-04	n=3
negative regulation of extrinsic apoptot...	GO:2001240	p=3.1E-03	n=2
positive regulation of secondary heart f...	GO:0072513	p=3.1E-03	n=2
energy coupled proton transmembrane tran...	GO:0015988	p=5.0E-03	n=3
regulation of heart morphogenesis	GO:2000826	p=5.0E-03	n=3
cell cycle G1/S phase transition	GO:0044843	p=6.3E-03	n=7
larval development	GO:0002164	p=6.7E-03	n=12
ectodermal placode development	GO:0071696	p=7.6E-03	n=3
phosphatidylserine metabolic process	GO:0006658	p=8.9E-03	n=2
trigeminal ganglion development	GO:0061551	p=8.9E-03	n=2
facial nerve morphogenesis	GO:0021610	p=8.9E-03	n=2
insulin receptor signaling pathway	GO:0008286	p=9.7E-03	n=6
ERK1 and ERK2 cascade	GO:0070371	p=1.1E-02	n=5
transferrin transport	GO:0033572	p=1.1E-02	n=3
G1/S transition of mitotic cell cycle	GO:0000082	p=1.3E-02	n=6
MAPK cascade	GO:0000165	p=1.4E-02	n=13
nematode larval development	GO:0002119	p=1.5E-02	n=9
artery morphogenesis	GO:0048844	p=1.5E-02	n=3
negative regulation of G2/M transition o...	GO:0010972	p=1.5E-02	n=3
somatic sex determination	GO:0018993	p=1.7E-02	n=2
cellular response to arsenic-containing ...	GO:0071243	p=1.7E-02	n=2
SCF complex assembly	GO:0010265	p=1.7E-02	n=2
antimicrobial peptide biosynthetic proce...	GO:0002777	p=1.7E-02	n=2
positive regulation of steroid biosynthe...	GO:0010893	p=1.7E-02	n=2
negative regulation of B cell activation	GO:0050869	p=1.7E-02	n=2
regulation of antimicrobial peptide bios...	GO:0002805	p=1.7E-02	n=2
dendrite arborization	GO:0140059	p=1.7E-02	n=2
immune system process	GO:0002376	p=1.8E-02	n=28
cellular iron ion homeostasis	GO:0006879	p=2.0E-02	n=3
cellular response to amino acid stimulus	GO:0071230	p=2.6E-02	n=3

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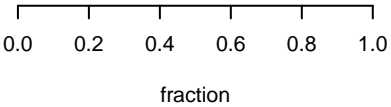
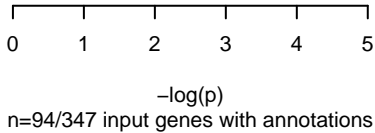


GO:MF
Ncol_Nvec_vc1.1_XM_001639547.3

fraction genes in fg and expected value

hydrolase activity, acting on ester bond...	GO:0016788	p=9.5E-03	n=13
RNA polymerase activity	GO:0097747	p=1.9E-02	n=2
5'-3' RNA polymerase activity	GO:0034062	p=1.9E-02	n=2
lipase activity	GO:0016298	p=2.2E-02	n=4
intramolecular oxidoreductase activity, ...	GO:0016864	p=3.1E-02	n=2
vascular endothelial growth factor-activ...	GO:0005021	p=3.1E-02	n=2
flavin adenine dinucleotide binding	GO:0050660	p=3.1E-02	n=2
protein disulfide isomerase activity	GO:0003756	p=3.1E-02	n=2
transaminase activity	GO:0008483	p=3.1E-02	n=2
ribonuclease activity	GO:0004540	p=4.5E-02	n=3
CoA carboxylase activity	GO:0016421	p=5.9E-02	n=1
open rectifier potassium channel activit...	GO:0005252	p=5.9E-02	n=1
MDM2/MDM4 family protein binding	GO:0097371	p=5.9E-02	n=1
vascular endothelial growth factor bindi...	GO:0038085	p=5.9E-02	n=1
tRNA-intron endonuclease activity	GO:0000213	p=5.9E-02	n=1
oxidoreductase activity, acting on singl...	GO:0016702	p=5.9E-02	n=1
TFIIIF-class transcription factor complex...	GO:0001096	p=5.9E-02	n=1
endoribonuclease activity, producing 3'-...	GO:0016892	p=5.9E-02	n=1
endonuclease activity, active with eithe...	GO:0016894	p=5.9E-02	n=1
rRNA primary transcript binding	GO:0042134	p=5.9E-02	n=1
branched-chain-amino-acid transaminase a...	GO:0004084	p=5.9E-02	n=1
butyryl-CoA dehydrogenase activity	GO:0004085	p=5.9E-02	n=1
protein tyrosine phosphatase activity, m...	GO:0030946	p=5.9E-02	n=1
oxidoreductase activity, acting on the C...	GO:0052890	p=5.9E-02	n=1
L-alanine:2-oxoglutarate aminotransferas...	GO:0004021	p=5.9E-02	n=1
translation termination factor activity	GO:0008079	p=5.9E-02	n=1
6-phosphogluconolactonase activity	GO:0017057	p=5.9E-02	n=1
alanine-oxo-acid transaminase activity	GO:0047635	p=5.9E-02	n=1
hedgehog receptor activity	GO:0008158	p=5.9E-02	n=1
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597	p=5.9E-02	n=1

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GO:CC
Ncol_Nvec_vc1.1_XM_001639547.3

fraction genes in fg and expected value

proton-transporting V-type ATPase comple...	GO:0033176	p=7.7E-03	n=3
vacuolar lumen	GO:0005775	p=1.3E-02	n=5
ficolin-1-rich granule	GO:0101002	p=1.5E-02	n=5
Cul2-RING ubiquitin ligase complex	GO:0031462	p=1.7E-02	n=2
intracellular vesicle	GO:0097708	p=3.0E-02	n=26
cytoplasmic vesicle	GO:0031410	p=3.0E-02	n=26
vesicle	GO:0031982	p=3.2E-02	n=27
secretory vesicle	GO:009503	p=3.9E-02	n=13
ficolin-1-rich granule membrane	GO:0101003	p=4.0E-02	n=2
plasma membrane proton-transporting V-ty...	GO:0033181	p=4.0E-02	n=2
secretory granule	GO:0030141	p=4.0E-02	n=10
extracellular region	GO:0005576	p=4.4E-02	n=12
vacuolar proton-transporting V-type ATPa...	GO:0016471	p=5.4E-02	n=2
collagen-containing extracellular matrix	GO:0062023	p=5.4E-02	n=2
RNA-directed RNA polymerase complex	GO:0031379	p=5.6E-02	n=1
telomerase holoenzyme complex	GO:0005697	p=5.6E-02	n=1
tRNA-intron endonuclease complex	GO:0000214	p=5.6E-02	n=1
mitochondrial DNA-directed RNA polymeras...	GO:0034245	p=5.6E-02	n=1
collagen and cuticulin-based cuticle ext...	GO:0060102	p=5.6E-02	n=1
podocyte foot	GO:0098846	p=5.6E-02	n=1
semaphorin receptor complex	GO:0002116	p=5.6E-02	n=1
nuclear RNA-directed RNA polymerase comp...	GO:0031380	p=5.6E-02	n=1
cullin-RING ubiquitin ligase complex	GO:0031461	p=6.0E-02	n=4
mitochondrial matrix	GO:0005759	p=6.1E-02	n=8
tertiary granule	GO:0070820	p=7.5E-02	n=3
lysosomal lumen	GO:0043202	p=7.5E-02	n=3
extracellular space	GO:0005615	p=8.2E-02	n=6
mediator complex	GO:0016592	p=8.6E-02	n=2
vacuole	GO:0005773	p=8.7E-02	n=11
presynapse	GO:0098793	p=9.6E-02	n=9

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