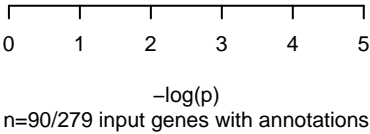


GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_032372078.2

fraction genes in fg and expected value

negative regulation of response to gamma...	GO:2001229	p=1.1E-03	n=2
positive regulation of tooth mineralizat...	GO:0070172	p=1.1E-03	n=2
anterior neuropore closure	GO:0021506	p=1.1E-03	n=2
positive regulation of odontogenesis	GO:0042482	p=1.1E-03	n=2
positive regulation of inclusion body as...	GO:0090261	p=1.1E-03	n=2
specification of segmental identity, abd...	GO:0007385	p=1.1E-03	n=2
pyrimidine ribonucleotide metabolic proc...	GO:0009218	p=1.1E-03	n=3
defense response to Gram-negative bacter...	GO:0050829	p=1.4E-03	n=5
organic substance biosynthetic process	GO:1901576	p=1.5E-03	n=55
glutathione metabolic process	GO:0006749	p=1.5E-03	n=4
pyrimidine ribonucleoside metabolic proc...	GO:0046131	p=1.8E-03	n=3
response to ethanol	GO:0045471	p=3.0E-03	n=7
long-chain fatty acid catabolic process	GO:0042758	p=3.2E-03	n=2
ubiquitin-independent protein catabolic ...	GO:0090611	p=3.2E-03	n=2
negative regulation of fibroblast prolifer...	GO:0048147	p=3.6E-03	n=3
embryonic body morphogenesis	GO:0010172	p=4.5E-03	n=4
hormone metabolic process	GO:0042445	p=4.8E-03	n=5
secretion by cell	GO:0032940	p=4.8E-03	n=19
response to amyloid-beta	GO:1904645	p=4.9E-03	n=3
anatomical structure maturation	GO:0071695	p=5.7E-03	n=9
regulation of apoptotic DNA fragmentatio...	GO:1902510	p=6.3E-03	n=2
cornea development in camera-type eye	GO:0061303	p=6.3E-03	n=2
establishment of vesicle localization	GO:0051650	p=7.5E-03	n=8
positive regulation of telomere maintena...	GO:0032212	p=8.0E-03	n=3
monovalent inorganic anion homeostasis	GO:0055083	p=8.0E-03	n=3
cellular response to oxidative stress	GO:0034599	p=9.8E-03	n=7
exit from mitosis	GO:0010458	p=1.0E-02	n=3
response to lipid	GO:0033993	p=1.0E-02	n=12
basement membrane organization	GO:0071711	p=1.0E-02	n=2
pyrimidine ribonucleotide biosynthetic p...	GO:0009220	p=1.0E-02	n=2

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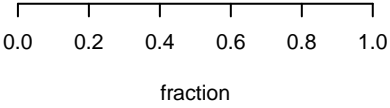
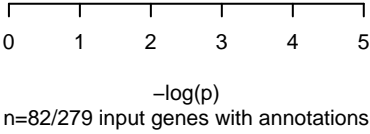


GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_032372078.2

fraction genes in fg and expected value

antioxidant activity	GO:0016209	p=8.9E-03	n=3
ammonium ion binding	GO:0070405	p=8.9E-03	n=3
calmodulin binding	GO:0005516	p=1.1E-02	n=4
actin filament binding	GO:0051015	p=1.1E-02	n=4
ATPase-coupled cation transmembrane tran...	GO:0019829	p=1.3E-02	n=3
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=1.6E-02	n=3
cysteine-type endopeptidase regulator ac...	GO:0043028	p=1.6E-02	n=2
phosphatidylcholine binding	GO:0031210	p=2.2E-02	n=2
rRNA binding	GO:0019843	p=2.6E-02	n=3
Notch binding	GO:0005112	p=2.9E-02	n=2
identical protein binding	GO:0042802	p=3.4E-02	n=21
nicotinate-nucleotide adenyllyltransferas...	GO:0004515	p=3.5E-02	n=1
glutathione-disulfide reductase (NADPH) ...	GO:0004362	p=3.5E-02	n=1
tRNA-intron endonuclease activity	GO:0000213	p=3.5E-02	n=1
cis-stilbene-oxide hydrolase activity	GO:0033961	p=3.5E-02	n=1
proteinase activated receptor binding	GO:0031871	p=3.5E-02	n=1
TFIIIF-class transcription factor complex...	GO:0001096	p=3.5E-02	n=1
juvenile hormone epoxide hydrolase activ...	GO:0008096	p=3.5E-02	n=1
5'-deoxyribose-5-phosphate lyase activit...	GO:0051575	p=3.5E-02	n=1
endoribonuclease activity, producing 3'-...	GO:0016892	p=3.5E-02	n=1
proton-transporting ATP synthase activit...	GO:0046933	p=3.5E-02	n=1
CDP-diaclylglycerol-serine O-phosphatidyl...	GO:0003882	p=3.5E-02	n=1
CTP synthase activity	GO:0003883	p=3.5E-02	n=1
uridine-diphosphatase activity	GO:0045134	p=3.5E-02	n=1
P-type calcium transporter activity invo...	GO:0086039	p=3.5E-02	n=1
dystroglycan binding	GO:0002162	p=3.5E-02	n=1
nicotinamide-nucleotide adenyllyltransfer...	GO:0000309	p=3.5E-02	n=1
5-oxoprolinase (ATP-hydrolyzing) activit...	GO:0017168	p=3.5E-02	n=1
selenodiglutathione-disulfide reductase ...	GO:0098622	p=3.5E-02	n=1
polypeptide N-acetylgalactosaminyltransf...	GO:0004653	p=3.5E-02	n=1

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GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_032372078.2

fraction genes in fg and expected value

intercalary heterochromatin	GO:0005725	p=3.1E-03	n=2
PRC1 complex	GO:0035102	p=3.1E-03	n=2
smooth endoplasmic reticulum	GO:0005790	p=7.6E-03	n=3
side of membrane	GO:0098552	p=8.6E-03	n=8
centrosome	GO:0005813	p=1.4E-02	n=10
transcription repressor complex	GO:0017053	p=1.9E-02	n=3
excitatory synapse	GO:0060076	p=2.0E-02	n=2
organelle subcompartment	GO:0031984	p=2.0E-02	n=18
organellar ribosome	GO:0000313	p=2.2E-02	n=3
mitochondrial ribosome	GO:0005761	p=2.2E-02	n=3
intracellular vesicle	GO:0097708	p=2.4E-02	n=21
cytoplasmic vesicle	GO:0031410	p=2.4E-02	n=21
contractile ring	GO:0070938	p=2.6E-02	n=2
nuclear outer membrane-endoplasmic retic...	GO:0042175	p=2.8E-02	n=12
spindle	GO:0005819	p=2.9E-02	n=7
coated membrane	GO:0048475	p=2.9E-02	n=3
membrane coat	GO:0030117	p=2.9E-02	n=3
cytoplasmic side of plasma membrane	GO:0009898	p=3.0E-02	n=5
endoplasmic reticulum lumen	GO:0005788	p=3.1E-02	n=4
microtubule organizing center	GO:0005815	p=3.1E-02	n=11
calcium channel complex	GO:0034704	p=3.3E-02	n=2
nucleoid	GO:0009295	p=3.3E-02	n=2
COPI-coated vesicle	GO:0030137	p=3.3E-02	n=2
mitochondrial nucleoid	GO:0042645	p=3.3E-02	n=2
chromaffin granule	GO:0042583	p=3.3E-02	n=1
chromaffin granule membrane	GO:0042584	p=3.3E-02	n=1
mitochondrial proton-transporting ATP sy...	GO:0005754	p=3.3E-02	n=1
cortical microtubule	GO:0055028	p=3.3E-02	n=1
centrosomal corona	GO:0031592	p=3.3E-02	n=1
intrinsic component of autophagosome mem...	GO:0097636	p=3.3E-02	n=1

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