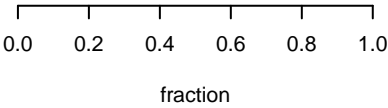
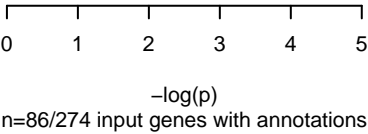


GO:BP
Ncol_Nvec_vc1.1_XM_032384126.2

fraction genes in fg and expected value

positive regulation of sodium-dependent ...	GO:2000120	p=1.0E-03	n=2
chromatin organization	GO:0006325	p=1.1E-03	n=15
cellular response to dsRNA	GO:0071359	p=2.3E-03	n=3
regulation of cell-cell adhesion mediate...	GO:2000047	p=2.9E-03	n=2
cellular response to 2,3,7,8-tetrachloro...	GO:1904613	p=2.9E-03	n=2
negative regulation of proteasomal ubiqu...	GO:0032435	p=5.6E-03	n=3
regulation of fibroblast apoptotic proce...	GO:2000269	p=5.8E-03	n=2
histone H3-K36 demethylation	GO:0070544	p=5.8E-03	n=2
canonical glycolysis	GO:0061621	p=5.8E-03	n=2
mitotic spindle midzone assembly	GO:0051256	p=5.8E-03	n=2
response to mercury ion	GO:0046689	p=5.8E-03	n=2
positive regulation of histone H3-K9 ace...	GO:2000617	p=5.8E-03	n=2
regulation of photoreceptor cell differe...	GO:0046532	p=7.1E-03	n=3
negative regulation of intracellular tra...	GO:0032387	p=7.3E-03	n=4
intracellular signal transduction	GO:0035556	p=9.2E-03	n=26
box C/D snoRNP assembly	GO:0000492	p=9.4E-03	n=2
aorta morphogenesis	GO:0035909	p=9.4E-03	n=2
regulation of brood size	GO:0060378	p=9.4E-03	n=2
establishment of endothelial barrier	GO:0061028	p=9.4E-03	n=2
chromatin remodeling	GO:0006338	p=1.0E-02	n=6
regulation of skeletal muscle tissue dev...	GO:0048641	p=1.1E-02	n=3
negative regulation of peptidase activit...	GO:0010466	p=1.3E-02	n=3
negative regulation of endopeptidase act...	GO:0010951	p=1.3E-02	n=3
cell-cell signaling involved in cell fat...	GO:0045168	p=1.4E-02	n=2
female germ-line stem cell asymmetric di...	GO:0048132	p=1.4E-02	n=2
lateral inhibition	GO:0046331	p=1.4E-02	n=2
production of miRNAs involved in gene si...	GO:0035196	p=1.4E-02	n=2
hindlimb morphogenesis	GO:0035137	p=1.4E-02	n=2
divalent inorganic anion homeostasis	GO:0072505	p=1.4E-02	n=2
trivalent inorganic anion homeostasis	GO:0072506	p=1.4E-02	n=2

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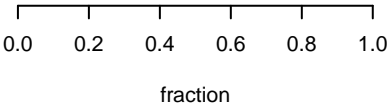
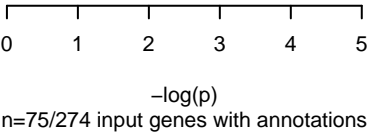


GO:MF
Ncol_Nvec_vc1.1_XM_032384126.2

fraction genes in fg and expected value

TPR domain binding	GO:0030911	p=9.9E-04	n=2
oxidoreductase activity, acting on the C...	GO:0016647	p=2.9E-03	n=2
histone H3-methyl-lysine-36 demethylase ...	GO:0051864	p=5.7E-03	n=2
TFIID-class transcription factor complex...	GO:0001094	p=9.3E-03	n=2
anion binding	GO:0043168	p=1.1E-02	n=17
core promoter sequence-specific DNA bind...	GO:0001046	p=1.8E-02	n=3
transferase activity, transferring nitro...	GO:0016769	p=1.9E-02	n=2
protein tyrosine/serine/threonine phosph...	GO:0008138	p=1.9E-02	n=2
helicase activity	GO:0004386	p=2.1E-02	n=4
phosphatidylinositol biphosphate phosph...	GO:0034593	p=2.4E-02	n=2
RNA polymerase II core promoter sequence...	GO:0000979	p=2.4E-02	n=2
G-protein alpha-subunit binding	GO:0001965	p=2.4E-02	n=2
endopeptidase inhibitor activity	GO:0004866	p=2.4E-02	n=2
peptidase inhibitor activity	GO:0030414	p=2.4E-02	n=2
Notch binding	GO:0005112	p=2.4E-02	n=2
cis-regulatory region sequence-specific ...	GO:0000987	p=2.9E-02	n=6
RNA polymerase II cis-regulatory region ...	GO:0000978	p=2.9E-02	n=6
signaling receptor binding	GO:0005102	p=3.0E-02	n=13
alpha-tubulin binding	GO:0043014	p=3.1E-02	n=2
glyceraldehyde-3-phosphate dehydrogenase...	GO:0043891	p=3.2E-02	n=1
spermine:oxygen oxidoreductase (spermidi...	GO:0052901	p=3.2E-02	n=1
N1-acetylspermidine:oxygen oxidoreductas...	GO:0052904	p=3.2E-02	n=1
signal recognition particle binding	GO:0005047	p=3.2E-02	n=1
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597	p=3.2E-02	n=1
light-activated ion channel activity	GO:0010461	p=3.2E-02	n=1
propionyl-CoA carboxylase activity	GO:0004658	p=3.2E-02	n=1
7S RNA binding	GO:0008312	p=3.2E-02	n=1
acyltransferase activity, acyl groups co...	GO:0046912	p=3.2E-02	n=1
glucose-1,6-bisphosphate synthase activi...	GO:0047933	p=3.2E-02	n=1
histone kinase activity (H3-T3 specific)	GO:0072354	p=3.2E-02	n=1

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GO:CC
Ncol_Nvec_vc1.1_XM_032384126.2

fraction genes in fg and expected value

mitotic spindle	GO:0072686	p=9.4E-04	n=6
R2TP complex	GO:0097255	p=2.8E-03	n=2
histone methyltransferase complex	GO:0035097	p=4.2E-03	n=4
mitotic spindle midzone	GO:1990023	p=1.3E-02	n=2
germinal vesicle	GO:0042585	p=1.8E-02	n=2
microvillus membrane	GO:0031528	p=1.8E-02	n=2
female germ cell nucleus	GO:0001674	p=2.4E-02	n=2
microvillus	GO:0005902	p=2.6E-02	n=3
peroxisomal matrix	GO:0005782	p=3.0E-02	n=2
MLL1 complex	GO:0071339	p=3.0E-02	n=2
H4 histone acetyltransferase complex	GO:1902562	p=3.0E-02	n=2
microbody lumen	GO:0031907	p=3.0E-02	n=2
sperm connecting piece	GO:0097224	p=3.1E-02	n=1
signal recognition particle, endoplasmic...	GO:0005786	p=3.1E-02	n=1
rhabdomere microvillus	GO:0035996	p=3.1E-02	n=1
rhabdomere microvillus membrane	GO:0035997	p=3.1E-02	n=1
BAT3 complex	GO:0071818	p=3.1E-02	n=1
AP-4 adaptor complex	GO:0030124	p=3.1E-02	n=1
rhabdomere membrane	GO:0033583	p=3.1E-02	n=1
centralspindlin complex	GO:0097149	p=3.1E-02	n=1
signal recognition particle	GO:0048500	p=3.1E-02	n=1
ER membrane insertion complex	GO:0072379	p=3.1E-02	n=1
DNA polymerase III, core complex	GO:0044776	p=3.1E-02	n=1
translation release factor complex	GO:0018444	p=3.1E-02	n=1
CHOP-C/EBP complex	GO:0036488	p=3.1E-02	n=1
nuclear pore cytoplasmic filaments	GO:0044614	p=3.1E-02	n=1
cytoplasmic periphery of the nuclear por...	GO:1990723	p=3.1E-02	n=1
adherens junction	GO:0005912	p=3.3E-02	n=5
MLL1/2 complex	GO:0044665	p=4.4E-02	n=2
midbody	GO:0030496	p=4.6E-02	n=4

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