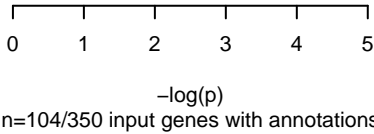


GO:BP
Ncol_Nvec_vc1.1_XM_032384965.2

fraction genes in fg and expected value

regulation of mitochondrial membrane pot...	GO:0051881	p=1.2E-03	n=5
Golgi to transport vesicle transport	GO:0055108	p=1.5E-03	n=2
liver morphogenesis	GO:0072576	p=1.5E-03	n=2
regulation of R7 cell differentiation	GO:0045676	p=1.7E-03	n=3
regulation of viral life cycle	GO:1903900	p=2.2E-03	n=5
protein polymerization	GO:0051258	p=2.2E-03	n=8
locomotion	GO:0040011	p=2.6E-03	n=29
dephosphorylation	GO:0016311	p=2.6E-03	n=11
imaginal disc growth	GO:0007446	p=2.7E-03	n=3
viral RNA genome replication	GO:0039694	p=2.7E-03	n=3
deoxynucleotide transport	GO:0030302	p=4.3E-03	n=2
pyrimidine nucleotide import into mitoch...	GO:1990519	p=4.3E-03	n=2
neuron projection development	GO:0031175	p=5.4E-03	n=21
negative regulation of nucleobase-contai...	GO:0045934	p=5.6E-03	n=21
regulation of cellular catabolic process	GO:0031329	p=5.8E-03	n=17
intracellular receptor signaling pathway	GO:0030522	p=6.7E-03	n=7
regulation of DNA repair	GO:0006282	p=6.8E-03	n=5
mitochondrion distribution	GO:0048311	p=7.3E-03	n=3
protein sumoylation	GO:0016925	p=7.3E-03	n=3
positive regulation of ion transport	GO:0043270	p=7.4E-03	n=7
protein localization to membrane	GO:0072657	p=7.8E-03	n=12
developmental process involved in reprod...	GO:0003006	p=8.2E-03	n=26
negative regulation of extrinsic apoptot...	GO:2001240	p=8.4E-03	n=2
cellular response to forskolin	GO:1904322	p=8.4E-03	n=2
glomerulus morphogenesis	GO:0072102	p=8.4E-03	n=2
mitochondrial transcription	GO:0006390	p=8.4E-03	n=2
negative regulation of mitochondrial fus...	GO:0010637	p=8.4E-03	n=2
epithelial cell maturation	GO:0002070	p=8.4E-03	n=2
negative regulation of cellular protein ...	GO:0032269	p=9.1E-03	n=16
axonemal dynein complex assembly	GO:0070286	p=9.5E-03	n=3

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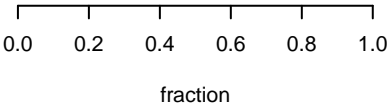
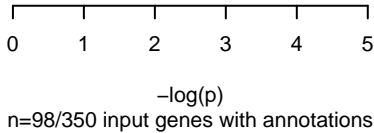


GO:MF
Ncol_Nvec_vc1.1_XM_032384965.2

fraction genes in fg and expected value

DNA-binding transcription repressor acti...	GO:0001227	p=6.3E-04	n=6
DNA replication origin binding	GO:0003688	p=1.7E-03	n=2
channel regulator activity	GO:0016247	p=3.1E-03	n=6
pyrimidine nucleotide transmembrane tran...	GO:0015218	p=5.0E-03	n=2
RNA polymerase II transcription regulato...	GO:0000977	p=6.7E-03	n=10
cis-regulatory region sequence-specific ...	GO:0000987	p=1.1E-02	n=8
RNA polymerase II cis-regulatory region ...	GO:0000978	p=1.1E-02	n=8
ion channel regulator activity	GO:0099106	p=1.2E-02	n=5
potassium channel regulator activity	GO:0015459	p=1.5E-02	n=3
sodium channel regulator activity	GO:0017080	p=1.6E-02	n=2
RNA polymerase II-specific DNA-binding t...	GO:0061629	p=2.0E-02	n=6
histone deacetylase binding	GO:0042826	p=2.0E-02	n=4
myosin binding	GO:0017022	p=2.0E-02	n=4
1-acylglycerol-3-phosphate O-acyltransfe...	GO:0003841	p=2.3E-02	n=2
aryl hydrocarbon receptor binding	GO:0017162	p=2.3E-02	n=2
cyclase activity	GO:0009975	p=2.3E-02	n=2
mRNA 3'-UTR binding	GO:0003730	p=2.6E-02	n=3
transcription factor binding	GO:0008134	p=2.7E-02	n=12
DNA-binding transcription factor binding	GO:0140297	p=2.8E-02	n=6
single-stranded DNA binding	GO:0003697	p=3.0E-02	n=4
chromatin binding	GO:0003682	p=3.0E-02	n=10
DNA-binding transcription activator acti...	GO:0001228	p=3.1E-02	n=7
DNA-binding transcription activator acti...	GO:0001216	p=3.1E-02	n=7
acylglycerol O-acyltransferase activity	GO:0016411	p=3.1E-02	n=2
nuclear receptor activity	GO:0004879	p=3.1E-02	n=2
chloride channel regulator activity	GO:0017081	p=3.1E-02	n=2
adenylate cyclase binding	GO:0008179	p=3.1E-02	n=2
ubiquitin-specific protease binding	GO:1990381	p=3.1E-02	n=2
ligand-activated transcription factor ac...	GO:0098531	p=3.1E-02	n=2
phosphatase activity	GO:0016791	p=3.3E-02	n=6

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GO:CC
Ncol_Nvec_vc1.1_XM_032384965.2

fraction genes in fg and expected value

Lewy body	GO:0097413	p=1.6E-03	n=2
myelin sheath abaxonal region	GO:0035748	p=4.6E-03	n=2
microvillus	GO:0005902	p=8.6E-03	n=4
integral component of mitochondrial oute...	GO:0031307	p=9.0E-03	n=2
supramolecular complex	GO:0099080	p=1.1E-02	n=16
postsynaptic density	GO:0014069	p=1.3E-02	n=6
intrinsic component of the cytoplasmic s...	GO:0031235	p=1.5E-02	n=2
contractile fiber	GO:0043292	p=1.9E-02	n=7
somatodendritic compartment	GO:0036477	p=1.9E-02	n=16
postsynaptic specialization	GO:0099572	p=1.9E-02	n=6
asymmetric synapse	GO:0032279	p=2.3E-02	n=6
neuron to neuron synapse	GO:0098984	p=2.5E-02	n=6
neuron projection	GO:0043005	p=2.6E-02	n=20
dendrite	GO:0030425	p=2.8E-02	n=12
dendritic tree	GO:0097447	p=3.0E-02	n=12
immunological synapse	GO:0001772	p=3.8E-02	n=2
sperm connecting piece	GO:0097224	p=4.0E-02	n=1
Ndc80 complex	GO:0031262	p=4.0E-02	n=1
XPC complex	GO:0071942	p=4.0E-02	n=1
apicomedial cortex	GO:0106037	p=4.0E-02	n=1
Sec61 translocon complex	GO:0005784	p=4.0E-02	n=1
alpha-heterochromatin	GO:0005723	p=4.0E-02	n=1
FANCM-MHF complex	GO:0071821	p=4.0E-02	n=1
NMS complex	GO:0031617	p=4.0E-02	n=1
AP-4 adaptor complex	GO:0030124	p=4.0E-02	n=1
inner kinetochore	GO:0000939	p=4.0E-02	n=1
translocon complex	GO:0071256	p=4.0E-02	n=1
condensin complex	GO:0000796	p=4.0E-02	n=1
CHOP-C/EBP complex	GO:0036488	p=4.0E-02	n=1
nucleotide-excision repair complex	GO:0000109	p=4.0E-02	n=1

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