

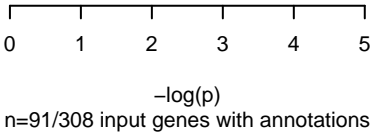
GO:BP
Ncol_Nvec_vc1.1_XM_032374041.2

fraction genes in fg and expected value

positive regulation of vascular endothel...	GO:0010575
production of miRNAs involved in gene si...	GO:0035196
antigen processing and presentation of e...	GO:0019886
positive regulation of vascular endothel...	GO:0030949
negative regulation of chromatin binding	GO:0035562
regulation of transcription from RNA pol...	GO:0061418
defense response to bacterium	GO:0042742
B cell homeostasis	GO:0001782
post-translational protein modification	GO:0043687
muscle cell cellular homeostasis	GO:0046716
dopaminergic neuron differentiation	GO:0071542
mitochondrion localization	GO:0051646
histone H3-K36 methylation	GO:0010452
pancreatic juice secretion	GO:0030157
3'-UTR-mediated mRNA destabilization	GO:0061158
actin filament severing	GO:0051014
negative regulation of miRNA-mediated ge...	GO:0060965
hypoxia-inducible factor-1alpha signalin...	GO:0097411
COPII-coated vesicle cargo loading	GO:0090110
regulation of oxidative stress-induced n...	GO:1903376
connective tissue replacement	GO:0097709
protein lipidation	GO:0006497
response to nitrogen compound	GO:1901698
cell morphogenesis involved in neuron di...	GO:0048667
mRNA transcription by RNA polymerase II	GO:0042789
neural fold formation	GO:0001842
cellular response to insulin-like growth...	GO:1990314
negative regulation of adaptive immune r...	GO:0002823
eIF2alpha phosphorylation in response to...	GO:0036492
regulation of sodium ion transmembrane t...	GO:1902305

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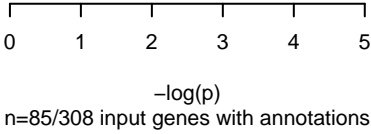
GO:MF
Ncol_Nvec_vc1.1_XM_032374041.2

fraction genes in fg and expected value

miRNA binding	GO:0035198
protein-cysteine S-palmitoyltransferase ...	GO:0019706
histone methyltransferase activity (H3-K...	GO:0046975
histone methyltransferase activity (H3-K...	GO:0042800
long-chain fatty acyl-CoA binding	GO:0036042
ion channel regulator activity	GO:0099106
translation repressor activity	GO:0030371
metal ion binding	GO:0046872
transition metal ion binding	GO:0046914
eukaryotic initiation factor eIF2 bindin...	GO:0071074
calcium channel regulator activity	GO:0005246
translation initiation factor binding	GO:0031369
gamma-tubulin binding	GO:0043015
transmembrane transporter activity	GO:0022857
zinc ion binding	GO:0008270
nuclear receptor activity	GO:0004879
insulin receptor binding	GO:0005158
ligand-activated transcription factor ac...	GO:0098531
DNA-binding transcription factor activit...	GO:0000981
channel activity	GO:0015267
passive transmembrane transporter activi...	GO:0022803
Hsp90 protein binding	GO:0051879
DNA-binding transcription factor activit...	GO:0003700
CoA carboxylase activity	GO:0016421
methionine-R-sulfoxide reductase activit...	GO:0070191
purine-specific nucleoside:sodium sympor...	GO:0015390
benzodiazepine receptor binding	GO:0030156
nucleobase:cation symporter activity	GO:0015391
histone methyltransferase activity (H3-K...	GO:0046976
glutaminase activity	GO:0004359

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p=7.3E-03	n=2
p=8.1E-03	n=16
p=1.2E-02	n=11
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p=1.7E-02	n=2
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p=2.4E-02	n=8
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p=2.5E-02	n=10
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GO:CC
Ncol_Nvec_vc1.1_XM_032374041.2

fraction genes in fg and expected value

manchette	GO:0002177
proteasome regulatory particle	GO:0005838
actin filament	GO:0005884
perinuclear endoplasmic reticulum	GO:0097038
endoplasmic reticulum	GO:0005783
ficolin-1-rich granule	GO:0101002
cell junction	GO:0030054
cytoplasmic ubiquitin ligase complex	GO:0000153
Cul2-RING ubiquitin ligase complex	GO:0031462
proteasome regulatory particle, base sub...	GO:0008540
dynactin complex	GO:0005869
ficolin-1-rich granule lumen	GO:1904813
supramolecular complex	GO:0099080
dendritic spine	GO:0043197
neuron spine	GO:0044309
P-body	GO:0000932
actin rod	GO:0031002
plasmodesma	GO:0009506
chloroplast	GO:0009507
symplast	GO:0055044
centralspindlin complex	GO:0097149
apoplast	GO:0048046
syntrophin complex	GO:0016013
autosome	GO:0030849
cofilin-actin rod	GO:0090732
tubulin folding cofactor complex	GO:1990727
plastid	GO:0009536
melanosome	GO:0042470
integral component of endoplasmic reticu...	GO:0030176
synapse	GO:0045202

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