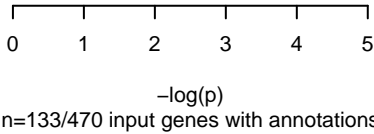


GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_032363603.2

fraction genes in fg and expected value

humoral immune response	GO:0006959	p=5.0E-04	n=6
sympathetic nervous system development	GO:0048485	p=2.1E-03	n=3
regulation of cellular macromolecule bio...	GO:2000112	p=2.4E-03	n=47
ganglion morphogenesis	GO:0061552	p=2.4E-03	n=2
trigeminal nerve morphogenesis	GO:0021636	p=2.4E-03	n=2
intermembrane lipid transfer	GO:0120009	p=2.4E-03	n=2
negative regulation of pancreatic juice ...	GO:0090188	p=2.4E-03	n=2
nephric duct formation	GO:0072179	p=2.4E-03	n=2
positive regulation of transcription by ...	GO:0045944	p=3.1E-03	n=21
transmembrane transport	GO:0055085	p=3.2E-03	n=24
negative regulation of Notch signaling p...	GO:0045746	p=5.4E-03	n=5
ventral spinal cord development	GO:0021517	p=5.5E-03	n=3
positive regulation of peptidyl-lysine a...	GO:2000758	p=5.5E-03	n=3
cellular response to staurosporine	GO:0072734	p=7.0E-03	n=2
single stranded viral RNA replication vi...	GO:0039692	p=7.0E-03	n=2
maintenance of lens transparency	GO:0036438	p=7.0E-03	n=2
positive regulation of cysteine-type end...	GO:2001269	p=7.0E-03	n=2
response to UV-C	GO:0010225	p=7.0E-03	n=2
regulation of nephron tubule epithelial ...	GO:0072182	p=7.0E-03	n=2
somite specification	GO:0001757	p=7.0E-03	n=2
negative regulation of response to exter...	GO:0032102	p=7.4E-03	n=8
potassium ion transport	GO:0006813	p=8.4E-03	n=6
nitrogen compound metabolic process	GO:0006807	p=9.0E-03	n=107
neuroepithelial cell differentiation	GO:0060563	p=9.0E-03	n=5
motor neuron axon guidance	GO:0008045	p=1.0E-02	n=4
signal transduction in absence of ligand	GO:0038034	p=1.0E-02	n=4
extrinsic apoptotic signaling pathway in...	GO:0097192	p=1.0E-02	n=4
negative regulation of autophagy	GO:0010507	p=1.1E-02	n=5
thymus development	GO:0048538	p=1.1E-02	n=3
cell differentiation in spinal cord	GO:0021515	p=1.1E-02	n=3

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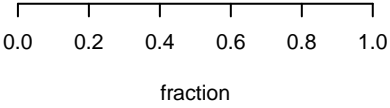
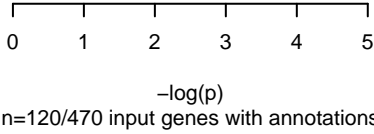


GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_032363603.2

fraction genes in fg and expected value

transcription coregulator activity	GO:0003712	p=2.2E-03	n=14
serine hydrolase activity	GO:0017171	p=2.3E-03	n=4
inositol bisphosphate phosphatase activi...	GO:0016312	p=2.5E-03	n=2
cysteine-type endopeptidase activity inv...	GO:0097200	p=2.5E-03	n=2
mRNA binding	GO:0003729	p=3.8E-03	n=10
transcription coactivator activity	GO:0003713	p=1.4E-02	n=9
xylosyltransferase activity	GO:0042285	p=1.4E-02	n=2
C2H2 zinc finger domain binding	GO:0070742	p=1.4E-02	n=2
UDP-xylosyltransferase activity	GO:0035252	p=1.4E-02	n=2
methyl-CpG binding	GO:0008327	p=1.4E-02	n=2
serine-type peptidase activity	GO:0008236	p=1.5E-02	n=3
serine-type endopeptidase activity	GO:0004252	p=1.5E-02	n=3
DNA-binding transcription factor activit...	GO:0003700	p=1.9E-02	n=15
nuclear receptor coactivator activity	GO:0030374	p=2.0E-02	n=3
sequence-specific DNA binding	GO:0043565	p=2.0E-02	n=14
DNA-binding transcription factor activit...	GO:0000981	p=2.1E-02	n=13
RNA polymerase II complex binding	GO:0000993	p=2.3E-02	n=2
cadherin binding	GO:0045296	p=3.1E-02	n=3
E-box binding	GO:0070888	p=3.1E-02	n=3
aspartic-type endopeptidase activity	GO:0004190	p=3.3E-02	n=2
aspartic-type peptidase activity	GO:0070001	p=3.3E-02	n=2
lipid transfer activity	GO:0120013	p=3.3E-02	n=2
molecular function inhibitor activity	GO:0140678	p=3.7E-02	n=3
DNA-binding transcription repressor acti...	GO:0001227	p=4.4E-02	n=4
DNA-binding transcription repressor acti...	GO:0001217	p=4.4E-02	n=4
HMG box domain binding	GO:0071837	p=4.5E-02	n=2
protein tyrosine/serine/threonine phosph...	GO:0008138	p=4.5E-02	n=2
chloride channel regulator activity	GO:0017081	p=4.5E-02	n=2
semaphorin receptor activity	GO:0017154	p=5.1E-02	n=1
SET domain binding	GO:0070984	p=5.1E-02	n=1

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GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_032363603.2

fraction genes in fg and expected value

caveola	GO:0005901	p=4.7E-03	n=5
mitochondrial crista	GO:0030061	p=7.2E-03	n=2
exon-exon junction complex	GO:0035145	p=1.4E-02	n=2
flotillin complex	GO:0016600	p=1.4E-02	n=2
nuclear speck	GO:0016607	p=2.2E-02	n=9
Derlin-1 retrotranslocation complex	GO:0036513	p=3.3E-02	n=2
chaperone complex	GO:0101031	p=4.4E-02	n=2
mitochondrial proton-transporting ATP sy...	GO:0000276	p=5.0E-02	n=1
SAM complex	GO:0001401	p=5.0E-02	n=1
DSIF complex	GO:0032044	p=5.0E-02	n=1
TSC1-TSC2 complex	GO:0033596	p=5.0E-02	n=1
semaphorin receptor complex	GO:0002116	p=5.0E-02	n=1
proton-transporting ATP synthase complex...	GO:0045263	p=5.0E-02	n=1
proton-transporting ATP synthase, centra...	GO:0045269	p=5.0E-02	n=1
serine-type peptidase complex	GO:1905286	p=5.0E-02	n=1
mitochondrial proton-transporting ATP sy...	GO:0005756	p=5.0E-02	n=1
signal recognition particle, endoplasmic...	GO:0005786	p=5.0E-02	n=1
death-inducing signaling complex	GO:0031264	p=5.0E-02	n=1
serine-type endopeptidase complex	GO:1905370	p=5.0E-02	n=1
methionyl glutamyl tRNA synthetase compl...	GO:0017102	p=5.0E-02	n=1
signal recognition particle	GO:0048500	p=5.0E-02	n=1
synaptic cleft	GO:0043083	p=5.0E-02	n=1
nucleus	GO:0005634	p=5.1E-02	n=77
contractile ring	GO:0070938	p=5.7E-02	n=2
transcription regulator complex	GO:0005667	p=5.9E-02	n=9
myelin sheath	GO:0043209	p=6.6E-02	n=5
replication fork	GO:0005657	p=6.6E-02	n=3
sperm principal piece	GO:0097228	p=7.1E-02	n=2
fusome	GO:0045169	p=7.1E-02	n=2
fibrillar center	GO:0001650	p=8.0E-02	n=4

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