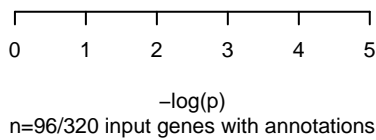


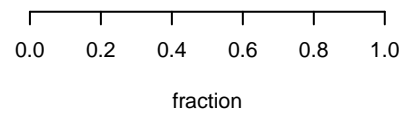
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Ncol\_Nvec\_vc1.1\_XM\_001624046.3

fraction genes in fg and expected value

positive regulation of inclusion body as...	GO:0090261	p=1.3E-03	n=2
motor neuron axon guidance	GO:0008045	p=3.1E-03	n=4
cell junction maintenance	GO:0034331	p=3.1E-03	n=3
regulation of cell-cell adhesion mediate...	GO:0033632	p=3.7E-03	n=2
cysteine biosynthetic process	GO:0019344	p=3.7E-03	n=2
nuclear-transcribed mRNA catabolic proce...	GO:0000291	p=4.4E-03	n=3
cellular response to cadmium ion	GO:0071276	p=4.4E-03	n=3
response to folic acid	GO:0051593	p=7.2E-03	n=2
deadenylation-dependent decapping of nuc...	GO:0000290	p=7.2E-03	n=2
serine family amino acid catabolic proce...	GO:0009071	p=7.2E-03	n=2
male anatomical structure morphogenesis	GO:0090598	p=7.9E-03	n=4
regulation of photoreceptor cell differe...	GO:0046532	p=9.6E-03	n=3
adherens junction maintenance	GO:0034334	p=1.2E-02	n=2
regulation of development, heterochronic	GO:0040034	p=1.2E-02	n=2
intracellular signal transduction	GO:0035556	p=1.2E-02	n=28
nematode male tail tip morphogenesis	GO:0045138	p=1.2E-02	n=3
response to antibiotic	GO:0046677	p=1.3E-02	n=9
RNA methylation	GO:0001510	p=1.4E-02	n=4
endosomal transport	GO:0016197	p=1.7E-02	n=7
cell-cell junction maintenance	GO:0045217	p=1.7E-02	n=2
negative regulation of double-strand bre...	GO:2000780	p=1.7E-02	n=2
C4-dicarboxylate transport	GO:0015740	p=1.7E-02	n=2
torso signaling pathway	GO:0008293	p=1.7E-02	n=2
imaginal disc morphogenesis	GO:0007560	p=1.7E-02	n=9
post-embryonic animal organ morphogenesi...	GO:0048563	p=1.9E-02	n=9
cAMP-mediated signaling	GO:0019933	p=2.3E-02	n=4
positive regulation of gluconeogenesis	GO:0045722	p=2.3E-02	n=2
negative regulation of DNA repair	GO:0045738	p=2.3E-02	n=2
NADH regeneration	GO:0006735	p=2.3E-02	n=2
cellular response to arsenic-containing ...	GO:0071243	p=2.3E-02	n=2



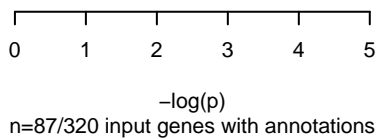
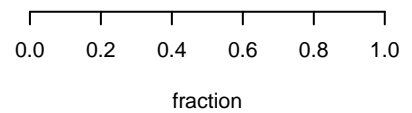
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**GO:MF**  
**Ncol\_Nvec\_vc1.1\_XM\_001624046.3**

fraction genes in fg and expected value

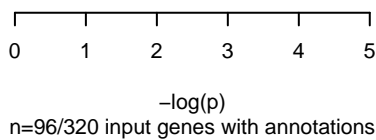
cystathionine beta-synthase activity	GO:0004122	p=1.3E-03	n=2
cysteine synthase activity	GO:0004124	p=1.3E-03	n=2
RNA 7-methylguanosine cap binding	GO:0000340	p=3.9E-03	n=2
DNA binding domain binding	GO:0050692	p=7.6E-03	n=2
RNA methyltransferase activity	GO:0008173	p=8.8E-03	n=4
intracellular ligand-gated ion channel a...	GO:0005217	p=1.1E-02	n=3
S-adenosylmethionine-dependent methyltra...	GO:0008757	p=1.6E-02	n=5
tRNA (guanine) methyltransferase activit...	GO:0016423	p=1.8E-02	n=2
damaged DNA binding	GO:0003684	p=2.2E-02	n=3
calcium-release channel activity	GO:0015278	p=2.5E-02	n=2
protein tyrosine/serine/threonine phosph...	GO:0008138	p=2.5E-02	n=2
rRNA methyltransferase activity	GO:0008649	p=2.5E-02	n=2
catalytic activity, acting on a rRNA	GO:0140102	p=2.5E-02	n=2
pyridoxal phosphate binding	GO:0030170	p=3.2E-02	n=2
vitamin B6 binding	GO:0070279	p=3.2E-02	n=2
ligand-gated cation channel activity	GO:0090904	p=3.5E-02	n=3
Hsp90 protein binding	GO:0051879	p=3.5E-02	n=3
RNA cap binding	GO:0000339	p=3.6E-02	n=3
nitrite reductase (NO-forming) activity	GO:0050421	p=3.7E-02	n=1
heteroduplex DNA loop binding	GO:0000404	p=3.7E-02	n=1
double-strand/single-strand DNA junction...	GO:0000406	p=3.7E-02	n=1
phosphatidylinositol 3-kinase catalytic...	GO:0036313	p=3.7E-02	n=1
rRNA (cytosine) methyltransferase activi...	GO:0016434	p=3.7E-02	n=1
volume-sensitive chloride channel activi...	GO:0072320	p=3.7E-02	n=1
rRNA (cytosine-C5-)-methyltransferase ac...	GO:0009383	p=3.7E-02	n=1
8-oxo-7,8-dihydroguanine DNA N-glycosyla...	GO:0034039	p=3.7E-02	n=1
adenylsulfatase activity	GO:0047627	p=3.7E-02	n=1
2',3'-cyclic GMP-AMP synthase activity	GO:0061501	p=3.7E-02	n=1
pseudophosphatase activity	GO:0001691	p=3.7E-02	n=1
rRNA (guanosine-2'-O-)-methyltransferase...	GO:0070039	p=3.7E-02	n=1

[illegible]

GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_001624046.3

fraction genes in fg and expected value

P-body	GO:0000932	p=5.6E-03	n=4
RNA cap binding complex	GO:0034518	p=7.2E-03	n=2
messenger ribonucleoprotein complex	GO:1990124	p=1.2E-02	n=2
cell cortex	GO:0005938	p=1.7E-02	n=8
mitochondrial intermembrane space	GO:0005758	p=3.2E-02	n=3
protein phosphatase 4 complex	GO:0030289	p=3.6E-02	n=1
Kibra-Ex-Mer complex	GO:0036375	p=3.6E-02	n=1
steroid hormone aporeceptor complex	GO:0005831	p=3.6E-02	n=1
MutSbeta complex	GO:0032302	p=3.6E-02	n=1
integral component of lysosomal membrane	GO:1905103	p=3.6E-02	n=1
cytoskeleton of presynaptic active zone	GO:0048788	p=3.6E-02	n=1
retromer, cargo-selective complex	GO:0030906	p=3.6E-02	n=1
presynaptic active zone cytoplasmic complex...	GO:0098831	p=3.6E-02	n=1
cell cortex region	GO:0099738	p=3.6E-02	n=3
late endosome membrane	GO:0031902	p=3.6E-02	n=3
endosome	GO:0005768	p=3.8E-02	n=12
nuclear replisome	GO:0043601	p=3.8E-02	n=2
replisome	GO:0030894	p=3.8E-02	n=2
filopodium	GO:0030175	p=4.1E-02	n=3
late endosome	GO:0005770	p=5.3E-02	n=5
pronucleus	GO:0045120	p=5.6E-02	n=2
nuclear body	GO:0016604	p=6.3E-02	n=10
ruffle membrane	GO:0032587	p=6.6E-02	n=2
actin cytoskeleton	GO:0015629	p=6.6E-02	n=6
katanin complex	GO:0008352	p=7.0E-02	n=1
intrinsic component of vacuolar membrane	GO:0031310	p=7.0E-02	n=1
lkappaB kinase complex	GO:0008385	p=7.0E-02	n=1
nuclear stress granule	GO:0097165	p=7.0E-02	n=1
Sin3 complex	GO:0016580	p=7.0E-02	n=1
presynaptic cytoskeleton	GO:0099569	p=7.0E-02	n=1



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