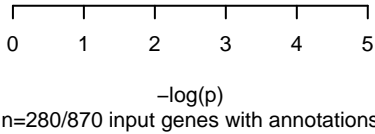


GO:BP
Ncol_Nvec_vc1.1_XM_032378312.2

fraction genes in fg and expected value

positive regulation of viral life cycle	GO:1903902	p=9.3E-04	n=7
germline cell cycle switching, mitotic t...	GO:0051729	p=1.1E-03	n=3
interleukin-2-mediated signaling pathway	GO:0038110	p=1.1E-03	n=3
regulation of oxidative stress-induced n...	GO:1903376	p=1.1E-03	n=3
oocyte development	GO:0048599	p=1.7E-03	n=15
regulation of biological process involve...	GO:0043903	p=1.9E-03	n=12
viral budding via host ESCRT complex	GO:0039702	p=1.9E-03	n=5
metaphase plate congression	GO:0051310	p=2.0E-03	n=7
neuroblast fate determination	GO:0007400	p=3.1E-03	n=4
ERAD pathway	GO:0036503	p=3.1E-03	n=9
positive regulation of angiogenesis	GO:0045766	p=3.6E-03	n=8
chemokine-mediated signaling pathway	GO:0070098	p=4.1E-03	n=3
regulation of protein complex stability	GO:0061635	p=4.1E-03	n=3
negative regulation of anoikis	GO:2000811	p=4.1E-03	n=3
negative regulation of endoplasmic retic...	GO:1902236	p=4.1E-03	n=3
ATF6-mediated unfolded protein response	GO:0036500	p=4.1E-03	n=3
inner mitochondrial membrane organizatio...	GO:0007007	p=5.0E-03	n=5
positive regulation of viral genome repl...	GO:0045070	p=5.0E-03	n=5
regulation of fibroblast proliferation	GO:0048145	p=5.2E-03	n=7
negative regulation of glucose transmemb...	GO:0010829	p=5.6E-03	n=4
septum digestion after cytokinesis	GO:0000920	p=5.6E-03	n=4
B cell homeostasis	GO:0001782	p=5.6E-03	n=4
stem cell fate determination	GO:0048867	p=5.6E-03	n=4
negative regulation of oxidative stress-...	GO:1902176	p=5.6E-03	n=4
peptidyl-amino acid modification	GO:0018193	p=6.0E-03	n=43
multivesicular body assembly	GO:0036258	p=7.4E-03	n=5
non-motile cilium assembly	GO:1905515	p=8.8E-03	n=7
maintenance of protein location in cell	GO:0032507	p=8.8E-03	n=7
mitochondrial fusion	GO:0008053	p=9.4E-03	n=4
negative regulation of peptidyl-serine p...	GO:0033137	p=9.4E-03	n=4

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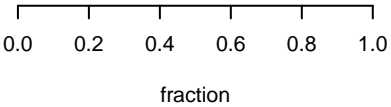
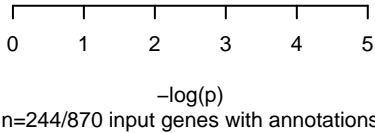


GO:MF
Ncol_Nvec_vc1.1_XM_032378312.2

fraction genes in fg and expected value

RNA polymerase binding	GO:0070063	p=1.0E-03	n=6
gamma-tubulin binding	GO:0043015	p=1.4E-03	n=4
poly(U) RNA binding	GO:0008266	p=9.1E-03	n=4
transition metal ion binding	GO:0046914	p=9.3E-03	n=24
ubiquitin-like protein transferase activ...	GO:0019787	p=9.6E-03	n=20
oxidoreductase activity, acting on NAD(P...	GO:0016655	p=1.0E-02	n=5
zinc ion binding	GO:0008270	p=1.0E-02	n=18
NAD-dependent protein deacetylase activi...	GO:0034979	p=1.1E-02	n=2
BH3 domain binding	GO:0051434	p=1.1E-02	n=2
inositol monophosphate 4-phosphatase act...	GO:0052833	p=1.1E-02	n=2
inositol monophosphate phosphatase activ...	GO:0052834	p=1.1E-02	n=2
nucleotide binding	GO:0000166	p=1.1E-02	n=30
nucleoside phosphate binding	GO:1901265	p=1.1E-02	n=30
ubiquitin-like protein ligase activity	GO:0061659	p=1.3E-02	n=14
ubiquitin protein ligase activity	GO:0061630	p=1.3E-02	n=14
catalytic activity, acting on a protein	GO:0140096	p=1.4E-02	n=64
cis-trans isomerase activity	GO:0016859	p=1.4E-02	n=4
peptidyl-prolyl cis-trans isomerase acti...	GO:0003755	p=1.4E-02	n=4
ubiquitin-protein transferase activity	GO:0004842	p=1.5E-02	n=19
small molecule binding	GO:0036094	p=1.7E-02	n=36
oxidoreduction-driven active transmembra...	GO:0015453	p=2.4E-02	n=5
p53 binding	GO:0002039	p=2.4E-02	n=5
organic cyclic compound binding	GO:0097159	p=2.6E-02	n=86
cholesterol binding	GO:0015485	p=2.8E-02	n=3
inositol phosphate phosphatase activity	GO:0052745	p=2.8E-02	n=3
NADH dehydrogenase (quinone) activity	GO:0050136	p=2.8E-02	n=4
NAD(P)H dehydrogenase (quinone) activity	GO:0003955	p=2.8E-02	n=4
SH2 domain binding	GO:0042169	p=2.8E-02	n=4
NADH dehydrogenase (ubiquinone) activity	GO:0008137	p=2.8E-02	n=4
ATP binding	GO:0005524	p=2.9E-02	n=17

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GO:CC
Ncol_Nvec_vc1.1_XM_032378312.2

fraction genes in fg and expected value

P-body	GO:0000932	p=9.4E-04	n=8
mitochondrial protein-containing complex	GO:0098798	p=5.6E-03	n=14
germ plasm	GO:0060293	p=6.5E-03	n=6
intracellular non-membrane-bounded organ...	GO:0043232	p=8.6E-03	n=119
t-UTP complex	GO:0034455	p=1.1E-02	n=2
ribonucleoprotein complex	GO:1990904	p=1.2E-02	n=37
90S preribosome	GO:0030686	p=1.6E-02	n=4
P granule	GO:0043186	p=2.2E-02	n=5
endoplasmic reticulum-Golgi intermediate...	GO:0005793	p=3.0E-02	n=6
apical dendrite	GO:0097440	p=3.1E-02	n=3
cytosolic proteasome complex	GO:0031597	p=3.1E-02	n=3
endoplasmic reticulum chaperone complex	GO:0034663	p=3.2E-02	n=2
endoplasmic reticulum exit site	GO:0070971	p=3.2E-02	n=2
Bcl-2 family protein complex	GO:0097136	p=3.2E-02	n=2
small-subunit processome	GO:0032040	p=3.2E-02	n=4
catalytic step 2 spliceosome	GO:0071013	p=3.7E-02	n=6
endoplasmic reticulum lumen	GO:0005788	p=3.9E-02	n=8
endoplasmic reticulum	GO:0005783	p=4.0E-02	n=48
nucleus	GO:0005634	p=4.0E-02	n=159
smooth endoplasmic reticulum	GO:0005790	p=4.3E-02	n=4
contractile ring	GO:0070938	p=4.6E-02	n=3
inner mitochondrial membrane protein com...	GO:0098800	p=4.9E-02	n=7
fibrillar center	GO:0001650	p=5.7E-02	n=7
intracellular organelle lumen	GO:0070013	p=5.7E-02	n=134
membrane-enclosed lumen	GO:0031974	p=5.7E-02	n=134
organelle lumen	GO:0043233	p=5.7E-02	n=134
recycling endosome	GO:0055037	p=5.8E-02	n=9
nuclear protein-containing complex	GO:0140513	p=5.9E-02	n=43
mitochondrial intermembrane space protei...	GO:0042719	p=6.0E-02	n=2
endoplasmic reticulum quality control co...	GO:0044322	p=6.0E-02	n=2

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