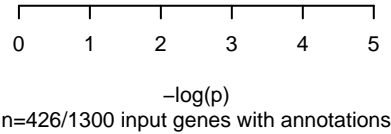


GO:BP
Ncol_Nvec_vc1.1_XM_032364331.2

fraction genes in fg and expected value

base-excision repair	GO:0006284	p=3.6E-03	n=8
type B pancreatic cell apoptotic process	GO:0097050	p=3.9E-03	n=3
regulation of RNA stability	GO:0043487	p=4.0E-03	n=12
regulation of endoplasmic reticulum unfo...	GO:1900101	p=5.9E-03	n=6
cellular modified amino acid biosyntheti...	GO:0042398	p=7.9E-03	n=8
intracellular estrogen receptor signalin...	GO:0030520	p=9.5E-03	n=6
regulation of ubiquitin-protein transfer...	GO:0051438	p=9.5E-03	n=6
anaphase-promoting complex-dependent cat...	GO:0031145	p=9.5E-03	n=6
virion assembly	GO:0019068	p=9.5E-03	n=6
regulation of mRNA stability	GO:0043488	p=1.0E-02	n=10
regulation of centrosome duplication	GO:0010824	p=1.1E-02	n=7
ribonucleoside diphosphate metabolic pro...	GO:0009185	p=1.2E-02	n=11
carbohydrate phosphorylation	GO:0046835	p=1.2E-02	n=5
signal transduction in response to DNA d...	GO:0042770	p=1.2E-02	n=16
negative regulation of centrosome duplic...	GO:0010826	p=1.4E-02	n=3
establishment of melanosome localization	GO:0032401	p=1.4E-02	n=3
melanosome transport	GO:0032402	p=1.4E-02	n=3
ubiquitin recycling	GO:0010992	p=1.4E-02	n=3
deadenylation-dependent decapping of nuc...	GO:0000290	p=1.4E-02	n=3
S-adenosylhomocysteine metabolic process	GO:0046498	p=1.4E-02	n=3
pigment granule transport	GO:0051904	p=1.4E-02	n=3
establishment of pigment granule localiz...	GO:0051905	p=1.4E-02	n=3
positive regulation of ubiquitin-protein...	GO:0051443	p=1.4E-02	n=4
positive regulation of mRNA catabolic pr...	GO:0061014	p=1.5E-02	n=8
mRNA destabilization	GO:0061157	p=1.5E-02	n=8
RNA destabilization	GO:0050779	p=1.5E-02	n=8
nuclear-transcribed mRNA catabolic proce...	GO:0000288	p=1.5E-02	n=7
regulation of mRNA catabolic process	GO:0061013	p=1.7E-02	n=10
telomere organization	GO:0032200	p=1.8E-02	n=13
telomere maintenance	GO:0000723	p=1.8E-02	n=13

fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.04	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.03	bg=0.02
fg=0.03	bg=0.02

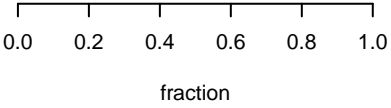
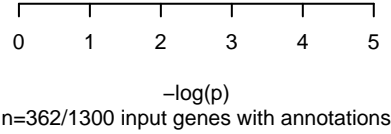


GO:MF
Ncol_Nvec_vc1.1_XM_032364331.2

fraction genes in fg and expected value

protein serine/threonine kinase activato...	GO:0043539	p=3.5E-03	n=3
catalytic activity, acting on RNA	GO:0140098	p=6.5E-03	n=25
cytochrome-c oxidase activity	GO:0004129	p=1.3E-02	n=3
oxidoreductase activity, acting on a hem...	GO:0016675	p=1.3E-02	n=3
carbohydrate kinase activity	GO:0019200	p=1.3E-02	n=4
ribonuclease activity	GO:0004540	p=1.5E-02	n=9
nuclease activity	GO:0004518	p=1.7E-02	n=13
high voltage-gated calcium channel activ...	GO:0008331	p=2.3E-02	n=2
deNEDDylase activity	GO:0019784	p=2.3E-02	n=2
glycolipid mannosyltransferase activity	GO:0004376	p=2.3E-02	n=2
single-stranded DNA helicase activity	GO:0017116	p=2.3E-02	n=2
L-malate dehydrogenase activity	GO:0030060	p=2.3E-02	n=2
2 iron, 2 sulfur cluster binding	GO:0051537	p=2.3E-02	n=2
ISG15 transferase activity	GO:0042296	p=2.3E-02	n=2
U1 snRNA binding	GO:0030619	p=2.3E-02	n=2
aspartic endopeptidase activity, intrame...	GO:0042500	p=2.3E-02	n=2
oxidoreduction-driven active transmembra...	GO:0015453	p=3.4E-02	n=6
signaling receptor complex adaptor activ...	GO:0030159	p=3.6E-02	n=4
pre-mRNA binding	GO:0036002	p=3.6E-02	n=4
calcium-dependent protein binding	GO:0048306	p=3.6E-02	n=5
SNAP receptor activity	GO:0005484	p=3.6E-02	n=5
RNA helicase activity	GO:0003724	p=4.5E-02	n=6
MAP kinase kinase activity	GO:0004708	p=5.0E-02	n=3
snRNP binding	GO:0070990	p=5.0E-02	n=3
translation factor activity, RNA binding	GO:0008135	p=5.2E-02	n=8
ATP-dependent activity, acting on RNA	GO:0008186	p=5.7E-02	n=6
oxidoreductase activity, acting on CH-OH...	GO:0016614	p=6.1E-02	n=7
primary active transmembrane transporter...	GO:0015399	p=6.1E-02	n=11
nucleotidyltransferase activity	GO:0016779	p=6.3E-02	n=10
carbohydrate phosphatase activity	GO:0019203	p=6.3E-02	n=2

fg=0.01	bg=0.00
fg=0.07	bg=0.04
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.04	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.01
fg=0.01	bg=0.01
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.03	bg=0.02
fg=0.03	bg=0.02
fg=0.01	bg=0.00



GO:CC
Ncol_Nvec_vc1.1_XM_032364331.2

fraction genes in fg and expected value

catalytic complex	GO:1902494	p=1.3E-02	n=76
transferase complex	GO:1990234	p=1.7E-02	n=47
nuclear protein-containing complex	GO:0140513	p=1.8E-02	n=64
L-cysteine desulfurase complex	GO:1990221	p=2.5E-02	n=2
DNA replication preinitiation complex	GO:0031261	p=2.5E-02	n=2
extrinsic component of mitochondrial inn...	GO:0031314	p=2.5E-02	n=2
GIN5 complex	GO:0000811	p=2.5E-02	n=2
ESCRT I complex	GO:0000813	p=2.5E-02	n=2
eukaryotic translation elongation factor...	GO:0005853	p=2.5E-02	n=2
collagen and cuticulin-based cuticle ext...	GO:0060102	p=2.5E-02	n=2
TORC2 complex	GO:0031932	p=2.5E-02	n=2
translation preinitiation complex	GO:0070993	p=2.5E-02	n=2
protein-containing complex	GO:0032991	p=2.7E-02	n=200
cullin-RING ubiquitin ligase complex	GO:0031461	p=3.0E-02	n=12
telomerase holoenzyme complex	GO:0005697	p=3.1E-02	n=3
azurophilic granule membrane	GO:0035577	p=4.0E-02	n=4
peroxisomal matrix	GO:0005782	p=4.0E-02	n=4
microbody lumen	GO:0031907	p=4.0E-02	n=4
dendrite terminus	GO:0044292	p=5.4E-02	n=3
nucleoplasm	GO:0005654	p=5.5E-02	n=138
ubiquitin ligase complex	GO:0000151	p=5.5E-02	n=19
intracellular anatomical structure	GO:0005622	p=5.9E-02	n=410
intracellular protein-containing complex	GO:0140535	p=6.1E-02	n=45
intracellular organelle lumen	GO:0070013	p=6.2E-02	n=193
organelle lumen	GO:0043233	p=6.2E-02	n=193
membrane-enclosed lumen	GO:0031974	p=6.2E-02	n=193
integral component of cytoplasmic side o...	GO:0071458	p=6.7E-02	n=2
Flemming body	GO:0090543	p=6.7E-02	n=2
eukaryotic translation initiation factor...	GO:0005850	p=6.7E-02	n=2
TOR complex	GO:0038201	p=6.7E-02	n=2

fg=0.18	bg=0.14
fg=0.11	bg=0.08
fg=0.15	bg=0.12
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.47	bg=0.42
fg=0.03	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.32	bg=0.29
fg=0.04	bg=0.03
fg=0.96	bg=0.94
fg=0.11	bg=0.08
fg=0.45	bg=0.42
fg=0.45	bg=0.42
fg=0.45	bg=0.42
fg=0.45	bg=0.42
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00

