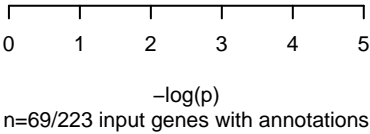


GO:BP
Ncol_Nvec_vc1.1_XM_032373497.2

Golgi ribbon formation	GO:0090161
3'-UTR-mediated mRNA destabilization	GO:0061158
histone H4-K20 trimethylation	GO:0034773
modulation of process of another organis...	GO:0035821
purine nucleobase biosynthetic process	GO:0009113
'de novo' IMP biosynthetic process	GO:0006189
regulation of miRNA metabolic process	GO:2000628
negative regulation of neurogenesis	GO:0050768
cell migration in hindbrain	GO:0021535
positive regulation of autophagy	GO:0010508
regulation of TORC1 signaling	GO:1903432
modulation by host of symbiont process	GO:0051851
regulation of macroautophagy	GO:0016241
positive regulation of macroautophagy	GO:0016239
peptidyl-lysine dimethylation	GO:0018027
sperm flagellum assembly	GO:0120316
sperm axoneme assembly	GO:0007288
protein modification process	GO:0036211
cellular protein modification process	GO:0006464
negative regulation of neuron differenti...	GO:0045665
intracellular signal transduction	GO:0035556
protein ubiquitination	GO:0016567
regulation of cardiac muscle cell apopto...	GO:0010665
intrinsic apoptotic signaling pathway in...	GO:0042771
signal transduction by p53 class mediato...	GO:0072331
protein polyubiquitination	GO:0000209
intrinsic apoptotic signaling pathway by...	GO:0072332
Rab protein signal transduction	GO:0032482
modulation by host of viral transcriptio...	GO:0043921
negative regulation by host of viral tra...	GO:0043922

p=3.0E-04	n=3
p=1.9E-03	n=2
p=1.9E-03	n=2
p=2.4E-03	n=4
p=3.7E-03	n=2
p=3.7E-03	n=2
p=3.7E-03	n=2
p=4.6E-03	n=7
p=9.0E-03	n=2
p=9.1E-03	n=4
p=9.9E-03	n=3
p=9.9E-03	n=3
p=1.1E-02	n=5
p=1.1E-02	n=3
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.2E-02	n=2
p=1.4E-02	n=31
p=1.4E-02	n=31
p=1.5E-02	n=5
p=1.5E-02	n=23
p=1.6E-02	n=10
p=1.6E-02	n=2
p=1.6E-02	n=2
p=1.8E-02	n=5
p=1.9E-02	n=6
p=2.0E-02	n=3
p=2.1E-02	n=2
p=2.1E-02	n=2
p=2.1E-02	n=2



fraction genes in fg and expected value

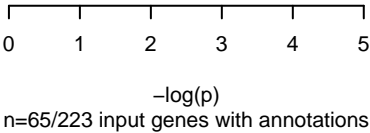
fg=0.04	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.06	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.10	bg=0.03
fg=0.03	bg=0.00
fg=0.06	bg=0.01
fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.07	bg=0.02
fg=0.04	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.45	bg=0.30
fg=0.45	bg=0.30
fg=0.07	bg=0.02
fg=0.33	bg=0.19
fg=0.14	bg=0.07
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.07	bg=0.02
fg=0.09	bg=0.03
fg=0.04	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00



GO:MF
Ncol_Nvec_vc1.1_XM_032373497.2

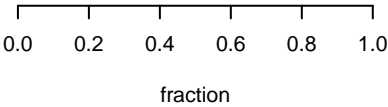
phosphatidylinositol-4,5-bisphosphate ph...	GO:0106019
cyclosporin A binding	GO:0016018
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
amidophosphoribosyltransferase activity	GO:0004044
phosphoribosylaminoimidazole carboxylase...	GO:0004638
phosphoribosylaminoimidazolesuccinocarbo...	GO:0004639
semaphorin receptor binding	GO:0030215
MAP kinase kinase kinase activity	GO:0008349
protein-L-isoaspartate (D-aspartate) O-m...	GO:0004719
carboxyl-O-methyltransferase activity	GO:0010340
beta-1,3-galactosyl-O-glycosyl-glycoprot...	GO:0047223
hedgehog receptor activity	GO:0008158
protein carboxyl O-methyltransferase act...	GO:0051998
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597
dolichyl-phosphate beta-glucosyltransfer...	GO:0004581
cis-trans isomerase activity	GO:0016859
peptidyl-prolyl cis-trans isomerase acti...	GO:0003755
GTP binding	GO:0005525
calmodulin binding	GO:0005516
purine ribonucleoside binding	GO:0032550
ribonucleoside binding	GO:0032549
GTPase activity	GO:0003924
purine nucleoside binding	GO:0001883
guanyl ribonucleotide binding	GO:0032561
guanyl nucleotide binding	GO:0019001
nucleoside binding	GO:0001882
SNAP receptor activity	GO:0005484
mRNA binding	GO:0003729
DNA ligase (ATP) activity	GO:0003910

p=7.0E-03	n=2
p=1.0E-02	n=2
p=1.3E-02	n=6
p=1.3E-02	n=6
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.7E-02	n=1
p=2.9E-02	n=2
p=2.9E-02	n=2
p=3.1E-02	n=4
p=3.3E-02	n=3
p=3.6E-02	n=4
p=3.6E-02	n=4
p=4.1E-02	n=4
p=4.1E-02	n=4
p=4.3E-02	n=4
p=4.3E-02	n=4
p=4.3E-02	n=4
p=4.8E-02	n=2
p=5.2E-02	n=5
p=5.4E-02	n=1



fraction genes in fg and expected value

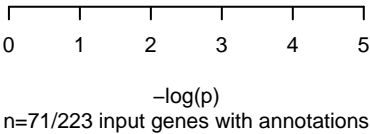
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.09	bg=0.03
fg=0.09	bg=0.03
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.06	bg=0.02
fg=0.05	bg=0.01
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.06	bg=0.02
fg=0.03	bg=0.01
fg=0.08	bg=0.03
fg=0.02	bg=0.00



GO:CC
Ncol_Nvec_vc1.1_XM_032373497.2

condensed nuclear chromosome	GO:0000794
phagophore assembly site	GO:0000407
Prp19 complex	GO:0000974
trans-Golgi network	GO:0005802
cytoplasmic ubiquitin ligase complex	GO:0000153
condensed chromosome, centromeric region	GO:0000779
U2-type catalytic step 2 spliceosome	GO:0071007
melanosome	GO:0042470
catalytic step 2 spliceosome	GO:0071013
heterochromatin	GO:0000792
DNA ligase III-XRCC1 complex	GO:0070421
postsynaptic cytoskeleton	GO:0099571
postsynaptic actin cytoskeleton	GO:0098871
polytene chromosome band	GO:0005704
KICSTOR complex	GO:0140007
sarcoplasmic reticulum lumen	GO:0033018
pigment granule	GO:0048770
phagocytic vesicle	GO:0045335
vesicle	GO:0031982
chromosome, centromeric region	GO:0000775
transport vesicle	GO:0030133
mediator complex	GO:0016592
cytoplasmic stress granule	GO:0010494
Golgi trans cisterna	GO:0000138
intracellular vesicle	GO:0097708
cytoplasmic vesicle	GO:0031410
Golgi apparatus subcompartment	GO:0098791
integral component of Golgi membrane	GO:0030173
trans-Golgi network membrane	GO:0032588
SMAD protein complex	GO:0071141

p=3.7E-03	n=4
p=6.5E-03	n=2
p=6.5E-03	n=2
p=1.1E-02	n=6
p=1.3E-02	n=2
p=1.7E-02	n=4
p=1.7E-02	n=2
p=2.2E-02	n=2
p=2.4E-02	n=3
p=2.4E-02	n=3
p=2.6E-02	n=1
p=2.6E-02	n=1
p=2.6E-02	n=1
p=2.6E-02	n=1
p=2.6E-02	n=1
p=2.6E-02	n=1
p=2.7E-02	n=2
p=2.9E-02	n=3
p=3.3E-02	n=18
p=3.3E-02	n=4
p=3.4E-02	n=6
p=3.8E-02	n=2
p=3.8E-02	n=2
p=3.8E-02	n=2
p=3.8E-02	n=2
p=3.9E-02	n=17
p=3.9E-02	n=17
p=4.0E-02	n=9
p=4.4E-02	n=2
p=5.0E-02	n=3
p=5.2E-02	n=1



fraction genes in fg and expected value

fg=0.06	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.08	bg=0.03
fg=0.03	bg=0.00
fg=0.06	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.04	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=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.00
fg=0.08	bg=0.03
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.24	bg=0.15
fg=0.24	bg=0.15
fg=0.13	bg=0.07
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.01	bg=0.00

