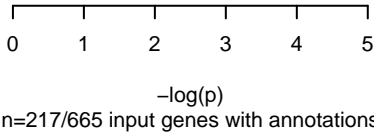


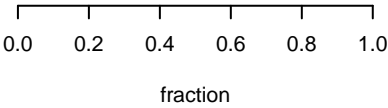
GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_032372114.2

fraction genes in fg and expected value

tRNA aminoacylation for protein translat...	GO:0006418	p=3.5E-03	n=5
olfactory behavior	GO:0042048	p=4.3E-03	n=7
neuron remodeling	GO:0016322	p=4.3E-03	n=7
protein targeting to membrane	GO:0006612	p=5.4E-03	n=10
photoreactive repair	GO:0000719	p=6.4E-03	n=2
negative regulation of viral transcripti...	GO:0032897	p=6.4E-03	n=2
phosphatidylcholine catabolic process	GO:0034638	p=6.4E-03	n=2
base-excision repair, gap-filling	GO:0006287	p=6.4E-03	n=2
regulation of organelle assembly	GO:1902115	p=8.0E-03	n=11
amide transport	GO:0042886	p=8.0E-03	n=47
secretory granule organization	GO:0033363	p=1.2E-02	n=4
microtubule cytoskeleton organization in...	GO:1902850	p=1.3E-02	n=11
cellular macromolecule localization	GO:0070727	p=1.5E-02	n=55
cellular protein localization	GO:0034613	p=1.5E-02	n=54
peptide transport	GO:0015833	p=1.5E-02	n=45
nuclear export	GO:0051168	p=1.6E-02	n=11
axis elongation	GO:0003401	p=1.6E-02	n=4
centrosome separation	GO:0051299	p=1.6E-02	n=4
catabolic process	GO:0009056	p=1.8E-02	n=60
somatic muscle development	GO:0007525	p=1.8E-02	n=5
mesonephric duct development	GO:0072177	p=1.8E-02	n=2
dense core granule maturation	GO:1990502	p=1.8E-02	n=2
negative regulation of cell maturation	GO:1903430	p=1.8E-02	n=2
early endosome to recycling endosome tra...	GO:0061502	p=1.8E-02	n=2
positive regulation of apoptotic process...	GO:1904747	p=1.8E-02	n=2
extracellular exosome assembly	GO:0071971	p=1.8E-02	n=2
regulation of extracellular exosome asse...	GO:1903551	p=1.8E-02	n=2
dorsal closure, amnioserosa morphology c...	GO:0046664	p=1.8E-02	n=2
maintenance of protein location in nucle...	GO:0051457	p=2.1E-02	n=3
ruffle assembly	GO:0097178	p=2.1E-02	n=3



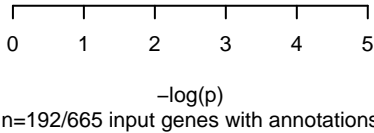
fg=0.02	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.05	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.05	bg=0.02
fg=0.22	bg=0.16
fg=0.02	bg=0.00
fg=0.05	bg=0.02
fg=0.25	bg=0.18
fg=0.25	bg=0.17
fg=0.21	bg=0.15
fg=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.21
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=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



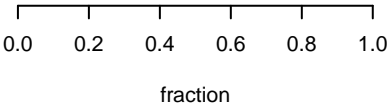
GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_032372114.2

fraction genes in fg and expected value

calcium-independent phospholipase A2 act...	GO:0047499	p=6.5E-03	n=2
lipid phosphatase activity	GO:0042577	p=6.5E-03	n=2
steroid dehydrogenase activity	GO:0016229	p=6.5E-03	n=2
small GTPase binding	GO:0031267	p=9.8E-03	n=16
catalytic activity, acting on a tRNA	GO:0140101	p=1.2E-02	n=7
aminoacyl-tRNA ligase activity	GO:0004812	p=1.2E-02	n=4
amide transmembrane transporter activity	GO:0042887	p=1.2E-02	n=4
ligase activity, forming carbon-oxygen b...	GO:0016875	p=1.2E-02	n=4
GTPase activity	GO:0003924	p=1.3E-02	n=9
DNA photolyase activity	GO:0003913	p=1.9E-02	n=2
deoxyribodipyrimidine photo-lyase activi...	GO:0003904	p=1.9E-02	n=2
1-acylglycerophosphocholine O-acyltransf...	GO:0047184	p=1.9E-02	n=2
tRNA binding	GO:0000049	p=1.9E-02	n=5
protein-macromolecule adaptor activity	GO:0030674	p=2.5E-02	n=10
molecular adaptor activity	GO:0060090	p=2.5E-02	n=10
ubiquitin-like protein binding	GO:0032182	p=3.4E-02	n=5
microtubule plus-end binding	GO:0051010	p=3.5E-02	n=2
O-acyltransferase activity	GO:0008374	p=4.1E-02	n=3
GTPase activating protein binding	GO:0032794	p=4.1E-02	n=3
kinesin binding	GO:0019894	p=4.3E-02	n=4
general transcription initiation factor ...	GO:0140296	p=5.2E-02	n=4
JUN kinase binding	GO:0008432	p=5.6E-02	n=2
protein kinase A regulatory subunit bind...	GO:0034237	p=5.6E-02	n=2
translation regulator activity	GO:0045182	p=5.9E-02	n=6
G protein-coupled peptide receptor activ...	GO:0008528	p=6.7E-02	n=3
peptide receptor activity	GO:0001653	p=6.7E-02	n=3
structural constituent of cytoskeleton	GO:0005200	p=6.7E-02	n=3
translation factor activity, RNA binding	GO:0008135	p=7.1E-02	n=5
gamma-tubulin binding	GO:0043015	p=7.9E-02	n=2
DNA-(apurinic or apyrimidinic site) endo...	GO:0003906	p=7.9E-02	n=2



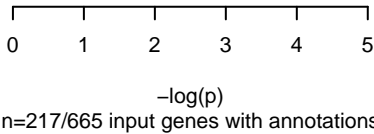
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.08	bg=0.04
fg=0.04	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.05	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.05	bg=0.03
fg=0.05	bg=0.03
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.02	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=0.03	bg=0.01
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_032372114.2

fraction genes in fg and expected value

Golgi medial cisterna	GO:0005797	p=4.9E-03	n=5
gamma-tubulin complex	GO:0000930	p=6.4E-03	n=2
mitotic spindle midzone	GO:1990023	p=8.5E-03	n=3
spindle pole	GO:0000922	p=1.2E-02	n=8
SAGA-type complex	GO:0070461	p=2.1E-02	n=3
cytosol	GO:0005829	p=2.6E-02	n=101
cytoplasm	GO:0005737	p=3.3E-02	n=184
SAGA complex	GO:0000124	p=3.5E-02	n=2
subapical complex	GO:0035003	p=3.5E-02	n=2
integral component of peroxisomal membra...	GO:0005779	p=3.5E-02	n=2
intrinsic component of peroxisomal membr...	GO:0031231	p=3.5E-02	n=2
COPI-coated vesicle membrane	GO:0030663	p=3.5E-02	n=2
Golgi-associated vesicle	GO:0005798	p=4.2E-02	n=7
transcription repressor complex	GO:0017053	p=5.1E-02	n=4
cytoplasmic side of apical plasma membra...	GO:0098592	p=5.5E-02	n=2
Golgi cis cisterna	GO:0000137	p=5.5E-02	n=2
nuclear proteasome complex	GO:0031595	p=5.5E-02	n=2
phagophore assembly site	GO:0000407	p=5.5E-02	n=2
guanyl-nucleotide exchange factor comple...	GO:0032045	p=5.5E-02	n=2
cis-Golgi network	GO:0005801	p=6.0E-02	n=4
Golgi-associated vesicle membrane	GO:0030660	p=6.0E-02	n=4
perinuclear region of cytoplasm	GO:0048471	p=6.1E-02	n=20
Golgi trans cisterna	GO:0000138	p=6.6E-02	n=3
polytene chromosome puff	GO:0005703	p=6.6E-02	n=3
spindle microtubule	GO:0005876	p=7.1E-02	n=4
intercellular bridge	GO:0045171	p=7.1E-02	n=4
transport vesicle membrane	GO:0030658	p=7.1E-02	n=6
spindle	GO:0005819	p=7.5E-02	n=14
postsynapse of neuromuscular junction	GO:0098975	p=7.8E-02	n=2
sperm midpiece	GO:0097225	p=7.8E-02	n=2



fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.04	bg=0.01
fg=0.01	bg=0.00
fg=0.47	bg=0.40
fg=0.85	bg=0.80
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=0.02
fg=0.02	bg=0.01
fg=0.09	bg=0.06
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=0.03	bg=0.01
fg=0.06	bg=0.03
fg=0.01	bg=0.00
fg=0.01	bg=0.00

