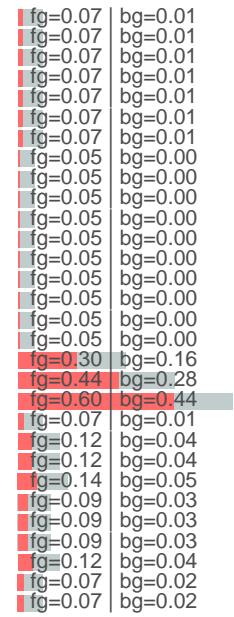
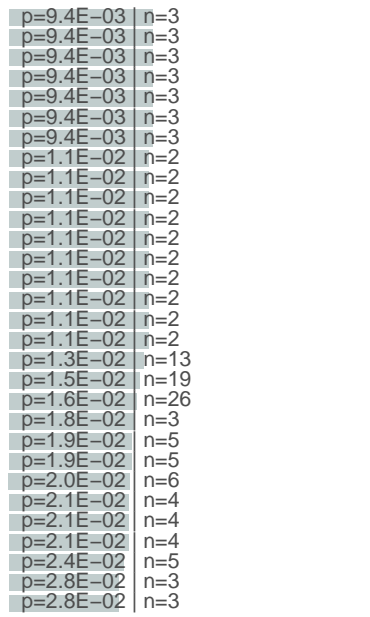


GO:BP
Ncol_Nvec_vc1.1_XM_032361906.2

fraction genes in fg and expected value

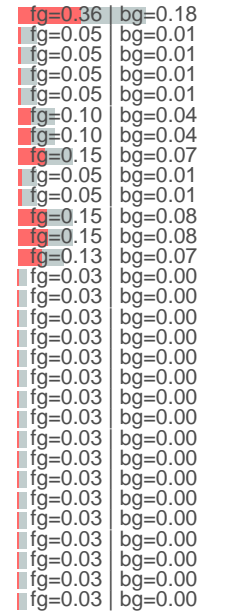
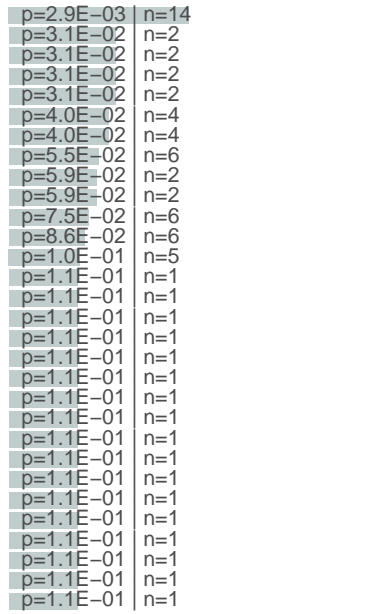
monosaccharide biosynthetic process	GO:0046364	p=9.4E-03	n=3
regulation of microtubule-based movement	GO:0060632	p=9.4E-03	n=3
regulation of focal adhesion assembly	GO:0051893	p=9.4E-03	n=3
oocyte axis specification	GO:0007309	p=9.4E-03	n=3
regulation of axon extension involved in...	GO:0048841	p=9.4E-03	n=3
positive regulation of axon extension	GO:0045773	p=9.4E-03	n=3
regulation of adherens junction organiza...	GO:1903391	p=9.4E-03	n=3
lactate metabolic process	GO:0006089	p=1.1E-02	n=2
protein localization to nuclear envelope	GO:0090435	p=1.1E-02	n=2
cell redox homeostasis	GO:0045454	p=1.1E-02	n=2
positive regulation of actin cytoskeleto...	GO:2000251	p=1.1E-02	n=2
regulation of actin cytoskeleton reorgan...	GO:2000249	p=1.1E-02	n=2
oocyte dorsal/ventral axis specification	GO:0007310	p=1.1E-02	n=2
positive regulation of axon extension in...	GO:0048842	p=1.1E-02	n=2
positive regulation of filopodium assemb...	GO:0051491	p=1.1E-02	n=2
regulation of filopodium assembly	GO:0051489	p=1.1E-02	n=2
filopodium assembly	GO:0046847	p=1.1E-02	n=2
positive regulation of response to stimu...	GO:0048584	p=1.3E-02	n=13
cellular localization	GO:0051641	p=1.5E-02	n=19
organonitrogen compound metabolic proces...	GO:1901564	p=1.6E-02	n=26
regulation of axon guidance	GO:1902667	p=1.8E-02	n=3
carboxylic acid biosynthetic process	GO:0046394	p=1.9E-02	n=5
organic acid biosynthetic process	GO:0016053	p=1.9E-02	n=5
monocarboxylic acid metabolic process	GO:0032787	p=2.0E-02	n=6
cellular modified amino acid metabolic p...	GO:0006575	p=2.1E-02	n=4
positive regulation of epithelial cell m...	GO:0010634	p=2.1E-02	n=4
positive regulation of cytoskeleton orga...	GO:0051495	p=2.1E-02	n=4
response to starvation	GO:0042594	p=2.4E-02	n=5
pyruvate metabolic process	GO:0006090	p=2.8E-02	n=3
sulfur compound biosynthetic process	GO:0044272	p=2.8E-02	n=3



GO:MF
Ncol_Nvec_vc1.1_XM_032361906.2

fraction genes in fg and expected value

catalytic activity, acting on a protein	GO:0140096	p=2.9E-03	n=14
protein-disulfide reductase activity	GO:0015035	p=3.1E-02	n=2
disulfide oxidoreductase activity	GO:0015036	p=3.1E-02	n=2
thiolester hydrolase activity	GO:0016790	p=3.1E-02	n=2
oxidoreductase activity, acting on a sul...	GO:0016667	p=3.1E-02	n=2
ubiquitin-like protein ligase binding	GO:0044389	p=4.0E-02	n=4
ubiquitin protein ligase binding	GO:0031625	p=4.0E-02	n=4
phosphotransferase activity, alcohol gro...	GO:0016773	p=5.5E-02	n=6
lysophospholipase activity	GO:0004622	p=5.9E-02	n=2
isomerase activity	GO:0016853	p=5.9E-02	n=2
kinase activity	GO:0016301	p=7.5E-02	n=6
transferase activity, transferring phosp...	GO:0016772	p=8.6E-02	n=6
protein kinase activity	GO:0004672	p=1.0E-01	n=5
vascular endothelial growth factor bindi...	GO:0038085	p=1.1E-01	n=1
1-alkyl-2-acetylglycerophosphocholine es...	GO:0003847	p=1.1E-01	n=1
cAMP response element binding	GO:0035497	p=1.1E-01	n=1
dystroglycan binding	GO:0002162	p=1.1E-01	n=1
phosphofructokinase activity	GO:0008443	p=1.1E-01	n=1
semaphorin receptor activity	GO:0017154	p=1.1E-01	n=1
dipeptidase activity	GO:0016805	p=1.1E-01	n=1
selenium binding	GO:0008430	p=1.1E-01	n=1
glucosylceramidase activity	GO:0004348	p=1.1E-01	n=1
fructose-6-phosphate binding	GO:0070095	p=1.1E-01	n=1
fructose-2,6-bisphosphate 2-phosphatase ...	GO:0004331	p=1.1E-01	n=1
phosphatidylserine binding	GO:0001786	p=1.1E-01	n=1
modified amino acid binding	GO:0072341	p=1.1E-01	n=1
pyruvate dehydrogenase (acetyl-transferr...	GO:0004740	p=1.1E-01	n=1
intramolecular oxidoreductase activity, ...	GO:0016864	p=1.1E-01	n=1
peptidyl-prolyl cis-trans isomerase acti...	GO:0003755	p=1.1E-01	n=1
protein disulfide isomerase activity	GO:0003756	p=1.1E-01	n=1



GO:CC
Ncol_Nvec_vc1.1_XM_032361906.2

fraction genes in fg and expected value

site of DNA damage	GO:0090734	p=1.2E-02	n=2
site of double-strand break	GO:0035861	p=1.2E-02	n=2
axonal growth cone	GO:0044295	p=3.3E-02	n=2
cytoplasm	GO:0005737	p=3.4E-02	n=37
growth cone	GO:0030426	p=4.3E-02	n=4
site of polarized growth	GO:0030427	p=5.5E-02	n=4
cytoplasmic microtubule	GO:0005881	p=6.1E-02	n=2
nucleolus	GO:0005730	p=7.9E-02	n=5
intermediate filament cytoskeleton	GO:0045111	p=9.5E-02	n=2
voltage-gated calcium channel complex	GO:0005891	p=9.5E-02	n=2
endoplasmic reticulum subcompartment	GO:0098827	p=1.1E-01	n=6
polymeric cytoskeletal fiber	GO:0099513	p=1.1E-01	n=3
preribosome, small subunit precursor	GO:0030688	p=1.1E-01	n=1
sorting endosome	GO:0097443	p=1.1E-01	n=1
cell body fiber	GO:0070852	p=1.1E-01	n=1
centrosomal corona	GO:0031592	p=1.1E-01	n=1
L-type voltage-gated calcium channel com...	GO:1990454	p=1.1E-01	n=1
anchored component of plasma membrane	GO:0046658	p=1.1E-01	n=1
cortical microtubule cytoskeleton	GO:0030981	p=1.1E-01	n=1
microtubule plus-end	GO:0035371	p=1.1E-01	n=1
core-binding factor complex	GO:0016513	p=1.1E-01	n=1
integrator complex	GO:0032039	p=1.1E-01	n=1
semaphorin receptor complex	GO:0002116	p=1.1E-01	n=1
spindle microtubule	GO:0005876	p=1.1E-01	n=1
6-phosphofructo-2-kinase/fructose-2,6-bi...	GO:0043540	p=1.1E-01	n=1
Seh1-associated complex	GO:0035859	p=1.1E-01	n=1
ER to Golgi transport vesicle membrane	GO:0012507	p=1.1E-01	n=1
U2-type spliceosomal complex	GO:0005684	p=1.1E-01	n=1
kinetochore microtubule	GO:0005828	p=1.1E-01	n=1
U2 snRNP	GO:0005686	p=1.1E-01	n=1

