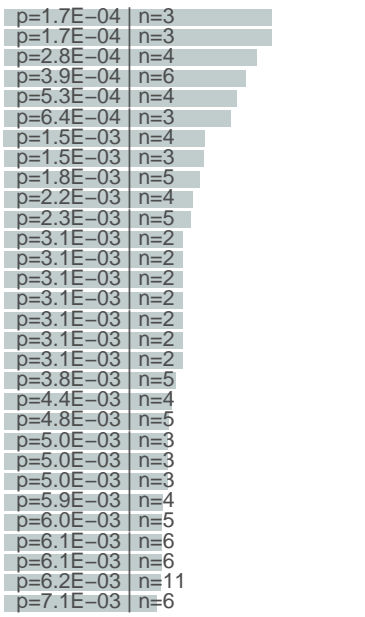


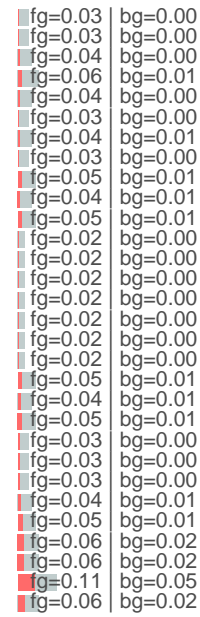
GO:BP
Ncol_Nvec_vc1.1_XM_032378312.2

fraction genes in fg and expected value

interleukin-2-mediated signaling pathway	GO:0038110
negative regulation of anoikis	GO:2000811
negative regulation of peptidyl-serine p...	GO:0033137
positive regulation of angiogenesis	GO:0045766
B cell homeostasis	GO:0001782
chemokine-mediated signaling pathway	GO:0070098
positive regulation of response to endop...	GO:1905898
fluid transport	GO:0042044
vascular endothelial growth factor recep...	GO:0048010
bone resorption	GO:0045453
regulation of carbohydrate biosynthetic ...	GO:0043255
positive regulation of cell adhesion med...	GO:0033630
positive regulation of nitric-oxide synt...	GO:0051000
positive regulation of apoptotic process...	GO:1904747
hypoxia-inducible factor-1alpha signalin...	GO:0097411
positive thymic T cell selection	GO:0045059
negative regulation of bone mineralizati...	GO:0030502
regulation of transforming growth factor...	GO:0032909
regulation of calcium-mediated signaling	GO:0050848
positive regulation of intrinsic apoptot...	GO:2001244
endosome organization	GO:0007032
positive regulation of fibroblast prolif...	GO:0048146
protein peptidyl-prolyl isomerization	GO:0000413
positive regulation of alpha-beta T cell...	GO:0046635
protein K48-linked ubiquitination	GO:0070936
antigen receptor-mediated signaling path...	GO:0050851
regulation of cellular carbohydrate meta...	GO:0010675
B cell activation	GO:0042113
response to peptide hormone	GO:0043434
regulation of peptidyl-tyrosine phosphor...	GO:0050730



-log(p)
n=101/368 input genes with annotations

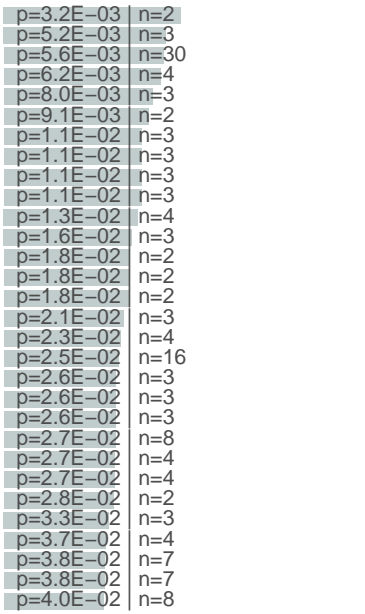


fraction

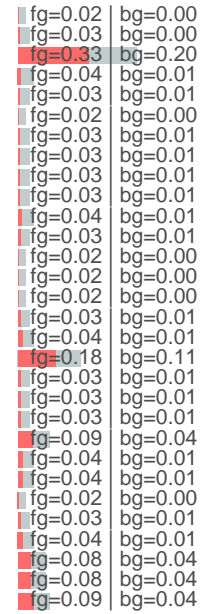
GO:MF
Ncol_Nvec_vc1.1_XM_032378312.2

fraction genes in fg and expected value

BH3 domain binding	GO:0051434
peptidyl-prolyl cis-trans isomerase acti...	GO:0003755
catalytic activity, acting on a protein	GO:0140096
oxidoreduction-driven active transmembra...	GO:0015453
RNA polymerase core enzyme binding	GO:0043175
protein transmembrane transporter activi...	GO:0008320
NAD(P)H dehydrogenase (quinone) activity	GO:0003955
oxidoreductase activity, acting on NAD(P...	GO:0016655
NADH dehydrogenase (ubiquinone) activity	GO:0008137
NADH dehydrogenase (quinone) activity	GO:0050136
p53 binding	GO:0002039
NADH dehydrogenase activity	GO:0003954
sterol transporter activity	GO:0015248
phosphatidylinositol phosphate 5-phospha...	GO:0034595
non-membrane spanning protein tyrosine k...	GO:0004715
ubiquitin conjugating enzyme activity	GO:0061631
oxidoreductase activity, acting on NAD(P...	GO:0016651
protein-containing complex binding	GO:0044877
receptor tyrosine kinase binding	GO:0030971
integrin binding	GO:0005178
ubiquitin-like protein conjugating enzym...	GO:0061650
ubiquitin protein ligase binding	GO:0031625
electron transfer activity	GO:0009055
acyltransferase activity, transferring g...	GO:0016747
inositol phosphate phosphatase activity	GO:0052745
acetyltransferase activity	GO:0016407
acyltransferase activity	GO:0016746
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
ubiquitin-like protein ligase binding	GO:0044389



-log(p)
n=90/368 input genes with annotations

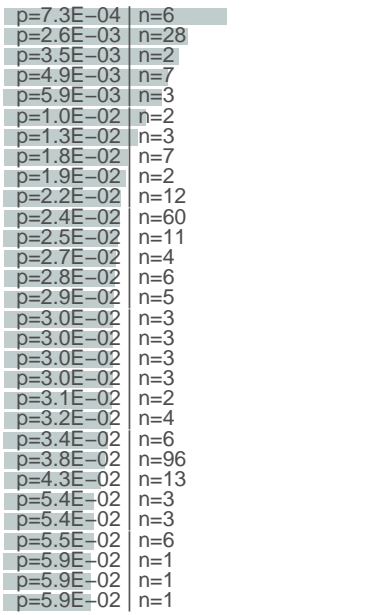


fraction

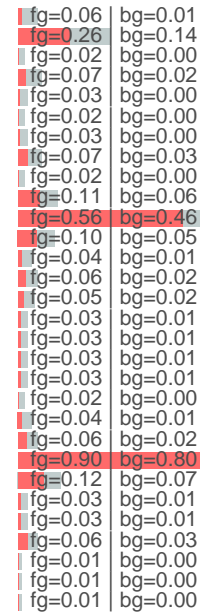
GO:CC
Ncol_Nvec_vc1.1_XM_032378312.2

fraction genes in fg and expected value

endoplasmic reticulum-Golgi intermediate...	GO:0005793
endoplasmic reticulum	GO:0005783
endoplasmic reticulum chaperone complex	GO:0034663
mitochondrial protein-containing complex	GO:0098798
apical dendrite	GO:0097440
Bcl-2 family protein complex	GO:0097136
endoplasmic reticulum-Golgi intermediate...	GO:0033116
endocytic vesicle	GO:0030139
intrinsic component of the cytoplasmic s...	GO:0031235
mitochondrial envelope	GO:0005740
membrane	GO:0016020
mitochondrial membrane	GO:0031966
oxidoreductase complex	GO:1990204
transporter complex	GO:1990351
endoplasmic reticulum lumen	GO:0005788
NADH dehydrogenase complex	GO:0030964
mitochondrial respiratory chain complex ...	GO:0005747
smooth endoplasmic reticulum	GO:0005790
respiratory chain complex I	GO:0045271
septin cytoskeleton	GO:0032156
inner mitochondrial membrane protein com...	GO:0098800
cytoplasmic side of plasma membrane	GO:0009898
cytoplasm	GO:0005737
perinuclear region of cytoplasm	GO:0048471
extrinsic component of cytoplasmic side ...	GO:0031234
respiratory chain complex	GO:0098803
cytoplasmic side of membrane	GO:0098562
rough endoplasmic reticulum lumen	GO:0048237
insulin-responsive compartment	GO:0032593
FHF complex	GO:0070695



-log(p)
n=107/368 input genes with annotations



fraction