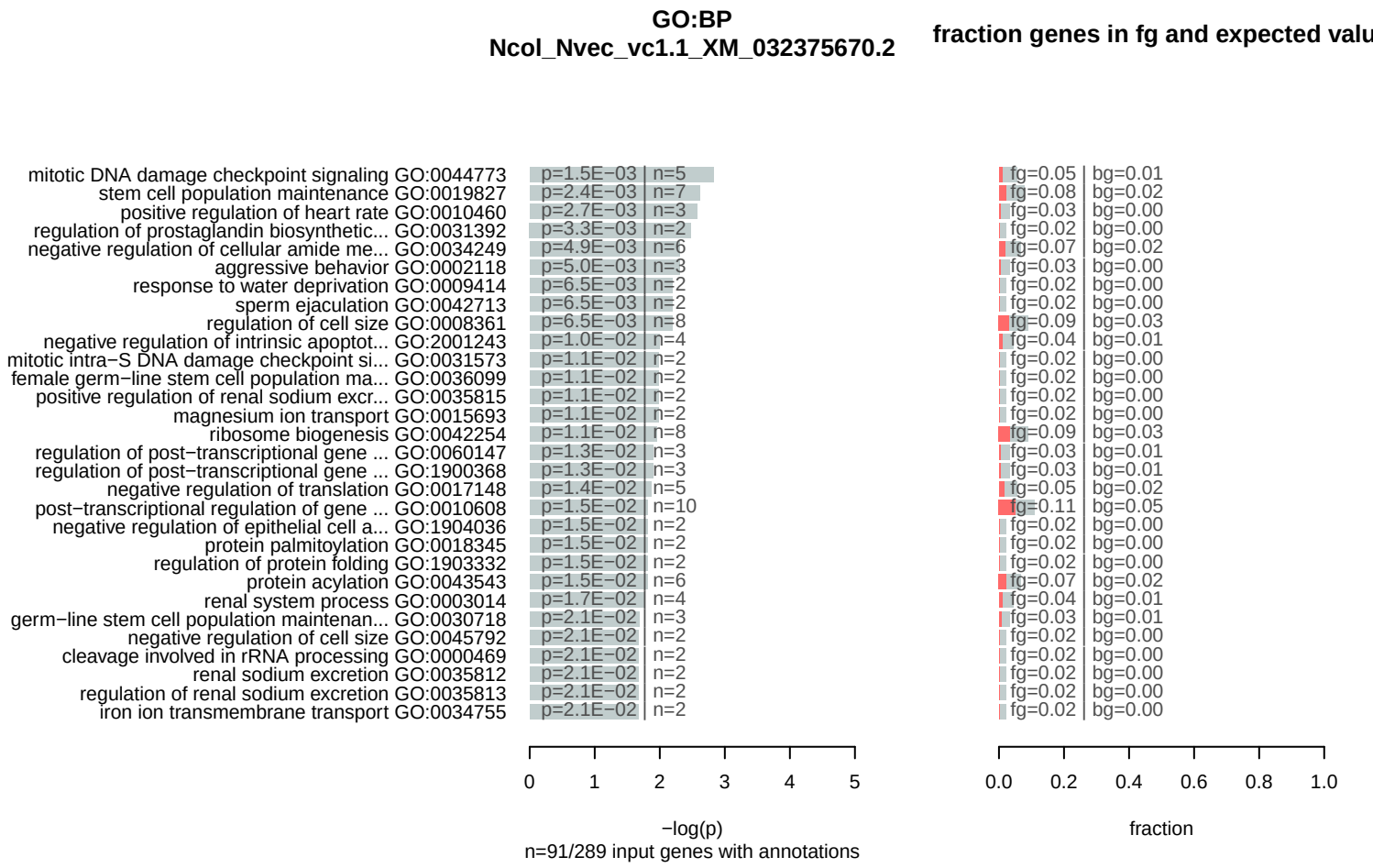
GO:BP
Ncol_Nvec_vc1.1_XM_032375670.2
fraction genes in fg and expected valu
mitotic DNA damage checkpoint signaling GO:0044773 p=1.5E−03 n=5 fg=0.05 bg=0.01
stem cell population maintenance GO:0019827 p=2.4E−03 n=7 fg=0.08 bg=0.02
positive regulation of heart rate GO:0010460 p=2.7E−03 n=3 fg=0.03 bg=0.00
regulation of prostaglandin biosynthetic... GO:0031392 p=3.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of cellular amide me... GO:0034249 p=4.9E−03 n=6 fg=0.07 bg=0.02
aggressive behavior GO:0002118 p=5.0E−03 n=3 fg=0.03 bg=0.00
response to water deprivation GO:0009414 p=6.5E−03 n=2 fg=0.02 bg=0.00
sperm ejaculation GO:0042713 p=6.5E−03 n=2 fg=0.02 bg=0.00
regulation of cell size GO:0008361 p=6.5E−03 n=8 fg=0.09 bg=0.03
negative regulation of intrinsic apoptot... GO:2001243 p=1.0E−02 n=4 fg=0.04 bg=0.01
mitotic intra−S DNA damage checkpoint si... GO:0031573 p=1.1E−02 n=2 fg=0.02 bg=0.00
female germ−line stem cell population ma... GO:0036099 p=1.1E−02 n=2 fg=0.02 bg=0.00
positive regulation of renal sodium excr... GO:0035815 p=1.1E−02 n=2 fg=0.02 bg=0.00
magnesium ion transport GO:0015693 p=1.1E−02 n=2 fg=0.02 bg=0.00
ribosome biogenesis GO:0042254 p=1.1E−02 n=8 fg=0.09 bg=0.03
regulation of post−transcriptional gene ... GO:0060147 p=1.3E−02 n=3 fg=0.03 bg=0.01
regulation of post−transcriptional gene ... GO:1900368 p=1.3E−02 n=3 fg=0.03 bg=0.01
negative regulation of translation GO:0017148 p=1.4E−02 n=5 fg=0.05 bg=0.02
post−transcriptional regulation of gene ... GO:0010608 p=1.5E−02 n=10 fg=0.11 bg=0.05
negative regulation of epithelial cell a... GO:1904036 p=1.5E−02 n=2 fg=0.02 bg=0.00
protein palmitoylation GO:0018345 p=1.5E−02 n=2 fg=0.02 bg=0.00
regulation of protein folding GO:1903332 p=1.5E−02 n=2 fg=0.02 bg=0.00
protein acylation GO:0043543 p=1.5E−02 n=6 fg=0.07 bg=0.02
renal system process GO:0003014 p=1.7E−02 n=4 fg=0.04 bg=0.01
germ−line stem cell population maintenan... GO:0030718 p=2.1E−02 n=3 fg=0.03 bg=0.01
negative regulation of cell size GO:0045792 p=2.1E−02 n=2 fg=0.02 bg=0.00
cleavage involved in rRNA processing GO:0000469 p=2.1E−02 n=2 fg=0.02 bg=0.00
renal sodium excretion GO:0035812 p=2.1E−02 n=2 fg=0.02 bg=0.00
regulation of renal sodium excretion GO:0035813 p=2.1E−02 n=2 fg=0.02 bg=0.00
iron ion transmembrane transport GO:0034755 p=2.1E−02 n=2 fg=0.02 bg=0.00
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n=91/289 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032375670.2
fraction genes in fg and expected valu
cAMP response element binding GO:0035497 p=3.5E−03 n=2 fg=0.02 bg=0.00
iron ion transmembrane transporter activ... GO:0005381 p=6.8E−03 n=2 fg=0.02 bg=0.00
U1 snRNP binding GO:1990446 p=6.8E−03 n=2 fg=0.02 bg=0.00
histone acetyltransferase activity GO:0004402 p=1.6E−02 n=2 fg=0.02 bg=0.00
peptide−lysine−N−acetyltransferase activ... GO:0061733 p=2.2E−02 n=2 fg=0.02 bg=0.00
polynucleotide adenylyltransferase activ... GO:0004652 p=2.2E−02 n=2 fg=0.02 bg=0.00
peptide N−acetyltransferase activity GO:0034212 p=2.2E−02 n=2 fg=0.02 bg=0.00
core promoter sequence−specific DNA bind... GO:0001046 p=2.2E−02 n=3 fg=0.04 bg=0.01
acetyltransferase activity GO:0016407 p=2.2E−02 n=3 fg=0.04 bg=0.01
ubiquitin−like protein ligase binding GO:0044389 p=3.4E−02 n=7 fg=0.09 bg=0.04
acyltransferase activity, transferring g... GO:0016747 p=3.4E−02 n=4 fg=0.05 bg=0.02
glycogen (starch) synthase activity GO:0004373 p=3.5E−02 n=1 fg=0.01 bg=0.00
histone pre−mRNA stem−loop binding GO:0071207 p=3.5E−02 n=1 fg=0.01 bg=0.00
malate dehydrogenase (NADP+) activity GO:0046554 p=3.5E−02 n=1 fg=0.01 bg=0.00
netrin receptor activity GO:0005042 p=3.5E−02 n=1 fg=0.01 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=3.5E−02 n=1 fg=0.01 bg=0.00
adiponectin binding GO:0055100 p=3.5E−02 n=1 fg=0.01 bg=0.00
guanyl nucleotide exchange factor inhibi... GO:1990624 p=3.5E−02 n=1 fg=0.01 bg=0.00
polynucleotide 5'−phosphatase activity GO:0004651 p=3.5E−02 n=1 fg=0.01 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=3.5E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.5E−02 n=1 fg=0.01 bg=0.00
polynucleotide phosphatase activity GO:0098518 p=3.5E−02 n=1 fg=0.01 bg=0.00
gamma−glutamylaminecyclotransferase acti... GO:0061929 p=3.5E−02 n=1 fg=0.01 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=3.5E−02 n=1 fg=0.01 bg=0.00
glycogen synthase activity, transferring... GO:0061547 p=3.5E−02 n=1 fg=0.01 bg=0.00
DNA end binding GO:0045027 p=3.5E−02 n=1 fg=0.01 bg=0.00
cobalt ion transmembrane transporter act... GO:0015087 p=3.5E−02 n=1 fg=0.01 bg=0.00
RNA polymerase I general transcription i... GO:0001181 p=3.5E−02 n=1 fg=0.01 bg=0.00
UDP−N−acetylglucosamine−dolichyl−phospha... GO:0003975 p=3.5E−02 n=1 fg=0.01 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=3.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=82/289 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032375670.2
fraction genes in fg and expected valu
activating signal cointegrator 1 complex GO:0099053 p=1.2E−03 n=2 fg=0.02 bg=0.00
commitment complex GO:0000243 p=1.1E−02 n=2 fg=0.02 bg=0.00
U4/U6 x U5 tri−snRNP complex GO:0046540 p=1.1E−02 n=2 fg=0.02 bg=0.00
U1 snRNP GO:0005685 p=1.1E−02 n=2 fg=0.02 bg=0.00
U2−type prespliceosome GO:0071004 p=1.1E−02 n=2 fg=0.02 bg=0.00
spliceosomal tri−snRNP complex GO:0097526 p=1.6E−02 n=2 fg=0.02 bg=0.00
prespliceosome GO:0071010 p=2.2E−02 n=2 fg=0.02 bg=0.00
INO80−type complex GO:0097346 p=2.2E−02 n=2 fg=0.02 bg=0.00
spliceosomal snRNP complex GO:0097525 p=2.3E−02 n=3 fg=0.03 bg=0.01
fibrillar center GO:0001650 p=2.6E−02 n=4 fg=0.04 bg=0.01
anaphase−promoting complex GO:0005680 p=2.9E−02 n=2 fg=0.02 bg=0.00
small nuclear ribonucleoprotein complex GO:0030532 p=3.5E−02 n=3 fg=0.03 bg=0.01
ectoplasm GO:0043265 p=3.5E−02 n=1 fg=0.01 bg=0.00
Dsl1/NZR complex GO:0070939 p=3.5E−02 n=1 fg=0.01 bg=0.00
fungal biofilm matrix GO:0062040 p=3.5E−02 n=1 fg=0.01 bg=0.00
biofilm matrix GO:0062039 p=3.5E−02 n=1 fg=0.01 bg=0.00
histone pre−mRNA 3'end processing comple... GO:0071204 p=3.5E−02 n=1 fg=0.01 bg=0.00
NLS−dependent protein nuclear import com... GO:0042564 p=3.5E−02 n=1 fg=0.01 bg=0.00
9+2 non−motile cilium GO:0097732 p=3.5E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=3.5E−02 n=1 fg=0.01 bg=0.00
kinocilium GO:0060091 p=3.5E−02 n=1 fg=0.01 bg=0.00
nuclear exosome (RNase complex) GO:0000176 p=3.5E−02 n=1 fg=0.01 bg=0.00
sarcoplasmic reticulum lumen GO:0033018 p=3.5E−02 n=1 fg=0.01 bg=0.00
centriolar satellite GO:0034451 p=3.7E−02 n=2 fg=0.02 bg=0.00
Sm−like protein family complex GO:0120114 p=5.4E−02 n=3 fg=0.03 bg=0.01
precatalytic spliceosome GO:0071011 p=6.3E−02 n=2 fg=0.02 bg=0.00
nucleocytoplasmic transport complex GO:0031074 p=6.8E−02 n=1 fg=0.01 bg=0.00
nuclear SCF ubiquitin ligase complex GO:0043224 p=6.8E−02 n=1 fg=0.01 bg=0.00
exoribonuclease complex GO:1905354 p=6.8E−02 n=1 fg=0.01 bg=0.00
U4 snRNP GO:0005687 p=6.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=94/289 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction