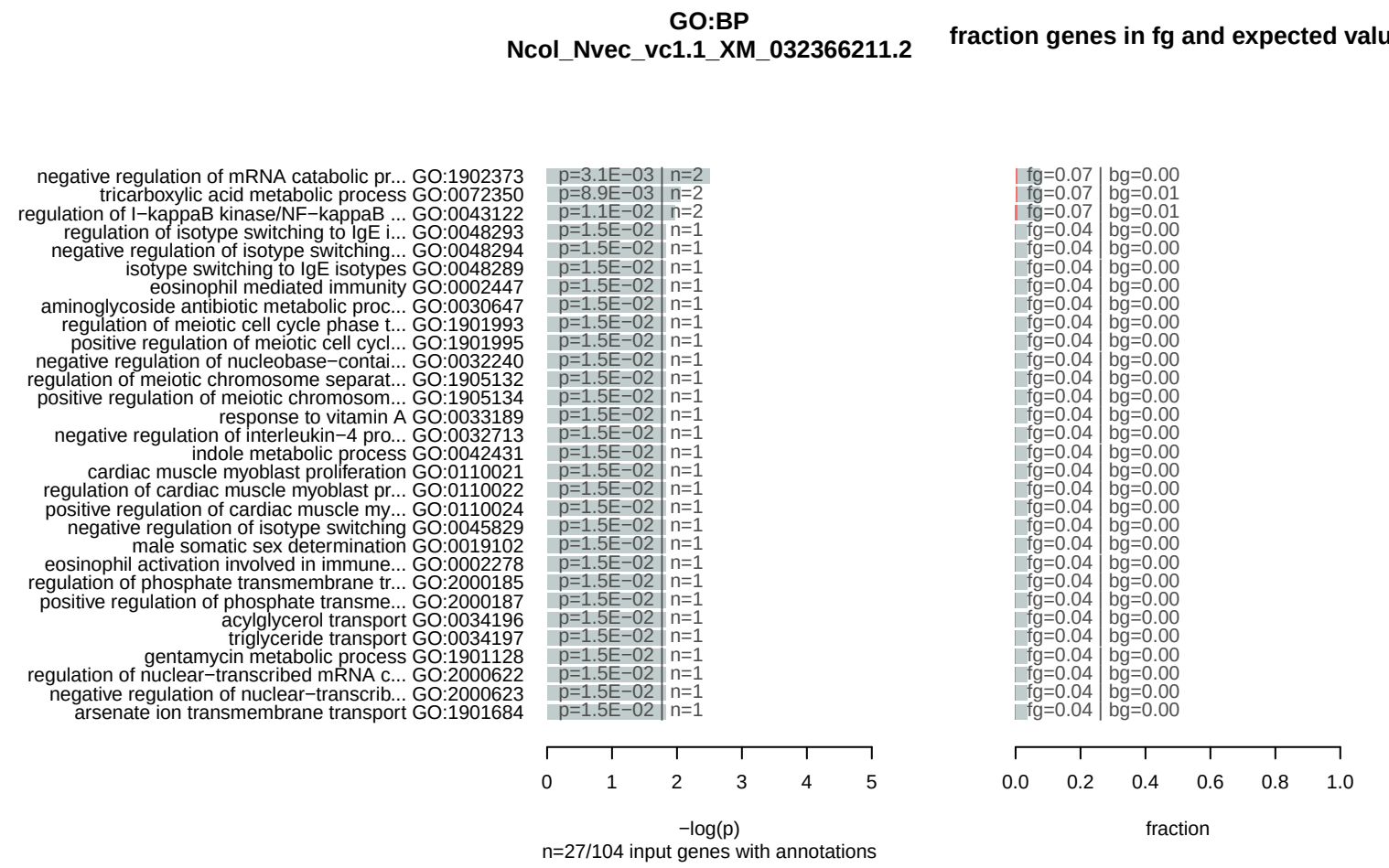
GO:BP
Ncol_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
negative regulation of mRNA catabolic pr... GO:1902373 p=3.1E−03 n=2 fg=0.07 bg=0.00
tricarboxylic acid metabolic process GO:0072350 p=8.9E−03 n=2 fg=0.07 bg=0.01
regulation of I−kappaB kinase/NF−kappaB ... GO:0043122 p=1.1E−02 n=2 fg=0.07 bg=0.01
regulation of isotype switching to IgE i... GO:0048293 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of isotype switching... GO:0048294 p=1.5E−02 n=1 fg=0.04 bg=0.00
isotype switching to IgE isotypes GO:0048289 p=1.5E−02 n=1 fg=0.04 bg=0.00
eosinophil mediated immunity GO:0002447 p=1.5E−02 n=1 fg=0.04 bg=0.00
aminoglycoside antibiotic metabolic proc... GO:0030647 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of meiotic cell cycle phase t... GO:1901993 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of meiotic cell cycl... GO:1901995 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of nucleobase−contai... GO:0032240 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of meiotic chromosome separat... GO:1905132 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of meiotic chromosom... GO:1905134 p=1.5E−02 n=1 fg=0.04 bg=0.00
response to vitamin A GO:0033189 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of interleukin−4 pro... GO:0032713 p=1.5E−02 n=1 fg=0.04 bg=0.00
indole metabolic process GO:0042431 p=1.5E−02 n=1 fg=0.04 bg=0.00
cardiac muscle myoblast proliferation GO:0110021 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of cardiac muscle myoblast pr... GO:0110022 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of cardiac muscle my... GO:0110024 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of isotype switching GO:0045829 p=1.5E−02 n=1 fg=0.04 bg=0.00
male somatic sex determination GO:0019102 p=1.5E−02 n=1 fg=0.04 bg=0.00
eosinophil activation involved in immune... GO:0002278 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of phosphate transmembrane tr... GO:2000185 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of phosphate transme... GO:2000187 p=1.5E−02 n=1 fg=0.04 bg=0.00
acylglycerol transport GO:0034196 p=1.5E−02 n=1 fg=0.04 bg=0.00
triglyceride transport GO:0034197 p=1.5E−02 n=1 fg=0.04 bg=0.00
gentamycin metabolic process GO:1901128 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of nuclear−transcribed mRNA c... GO:2000622 p=1.5E−02 n=1 fg=0.04 bg=0.00
negative regulation of nuclear−transcrib... GO:2000623 p=1.5E−02 n=1 fg=0.04 bg=0.00
arsenate ion transmembrane transport GO:1901684 p=1.5E−02 n=1 fg=0.04 bg=0.00
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n=27/104 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
DNA topoisomerase binding GO:0044547 p=1.4E−02 n=1 fg=0.05 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=1.4E−02 n=1 fg=0.05 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004473 p=1.4E−02 n=1 fg=0.05 bg=0.00
phosphate ion binding GO:0042301 p=1.4E−02 n=1 fg=0.05 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=1.4E−02 n=1 fg=0.05 bg=0.00
phosphoric diester hydrolase activity GO:0008081 p=2.4E−02 n=2 fg=0.09 bg=0.01
malate dehydrogenase activity GO:0016615 p=2.7E−02 n=1 fg=0.05 bg=0.00
malic enzyme activity GO:0004470 p=2.7E−02 n=1 fg=0.05 bg=0.00
cAMP response element binding protein bi... GO:0008140 p=2.7E−02 n=1 fg=0.05 bg=0.00
histone methyltransferase activity (H3−K... GO:0042800 p=2.7E−02 n=1 fg=0.05 bg=0.00
phosphate ion transmembrane transporter ... GO:0015114 p=2.7E−02 n=1 fg=0.05 bg=0.00
histone methyltransferase activity (H3−K... GO:0046975 p=2.7E−02 n=1 fg=0.05 bg=0.00
single−stranded DNA endodeoxyribonucleas... GO:0000014 p=2.7E−02 n=1 fg=0.05 bg=0.00
cAMP response element binding GO:0035497 p=4.1E−02 n=1 fg=0.05 bg=0.00
calcium−dependent protein serine/threoni... GO:0009931 p=4.1E−02 n=1 fg=0.05 bg=0.00
NAD binding GO:0051287 p=4.1E−02 n=1 fg=0.05 bg=0.00
pyrimidine nucleotide transmembrane tran... GO:0015218 p=4.1E−02 n=1 fg=0.05 bg=0.00
calcium−dependent protein kinase activit... GO:0010857 p=4.1E−02 n=1 fg=0.05 bg=0.00
WW domain binding GO:0050699 p=4.1E−02 n=1 fg=0.05 bg=0.00
NADP binding GO:0050661 p=4.1E−02 n=1 fg=0.05 bg=0.00
sodium ion binding GO:0031402 p=4.1E−02 n=1 fg=0.05 bg=0.00
histone acetyltransferase activity GO:0004402 p=4.1E−02 n=1 fg=0.05 bg=0.00
histone−lysine N−methyltransferase activ... GO:0018024 p=4.1E−02 n=1 fg=0.05 bg=0.00
peptide−lysine−N−acetyltransferase activ... GO:0061733 p=5.4E−02 n=1 fg=0.05 bg=0.00
peptide N−acetyltransferase activity GO:0034212 p=5.4E−02 n=1 fg=0.05 bg=0.00
ubiquitin protein ligase binding GO:0031625 p=5.7E−02 n=3 fg=0.14 bg=0.04
SNARE binding GO:0000149 p=6.3E−02 n=2 fg=0.09 bg=0.02
dynactin binding GO:0034452 p=6.7E−02 n=1 fg=0.05 bg=0.00
nucleotide transmembrane transporter act... GO:0015215 p=6.7E−02 n=1 fg=0.05 bg=0.00
alkali metal ion binding GO:0031420 p=6.7E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=22/104 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
site of double−strand break GO:0035861 p=5.3E−03 n=2 fg=0.08 bg=0.00
ubiquitin ligase complex GO:0000151 p=1.1E−02 n=4 fg=0.15 bg=0.03
eukaryotic 43S preinitiation complex GO:0016282 p=1.4E−02 n=1 fg=0.04 bg=0.00
Dsl1/NZR complex GO:0070939 p=1.4E−02 n=1 fg=0.04 bg=0.00
translation preinitiation complex GO:0070993 p=1.4E−02 n=1 fg=0.04 bg=0.00
endosome GO:0005768 p=2.2E−02 n=6 fg=0.23 bg=0.09
eukaryotic translation initiation factor... GO:0005850 p=2.9E−02 n=1 fg=0.04 bg=0.00
VCB complex GO:0030891 p=2.9E−02 n=1 fg=0.04 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=2.9E−02 n=1 fg=0.04 bg=0.00
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synaptic vesicle membrane GO:0030672 p=2.9E−02 n=2 fg=0.08 bg=0.01
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perinuclear region of cytoplasm GO:0048471 p=3.6E−02 n=5 fg=0.19 bg=0.07
microtubule cytoskeleton GO:0015630 p=3.8E−02 n=6 fg=0.23 bg=0.10
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pseudopodium GO:0031143 p=4.3E−02 n=1 fg=0.04 bg=0.00
zymogen granule membrane GO:0042589 p=4.3E−02 n=1 fg=0.04 bg=0.00
kinetochore microtubule GO:0005828 p=4.3E−02 n=1 fg=0.04 bg=0.00
cullin−RING ubiquitin ligase complex GO:0031461 p=5.6E−02 n=2 fg=0.08 bg=0.02
microvillus membrane GO:0031528 p=5.6E−02 n=1 fg=0.04 bg=0.00
Cul2−RING ubiquitin ligase complex GO:0031462 p=5.6E−02 n=1 fg=0.04 bg=0.00
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autolysosome GO:0044754 p=7.0E−02 n=1 fg=0.04 bg=0.00
Cul3−RING ubiquitin ligase complex GO:0031463 p=7.0E−02 n=1 fg=0.04 bg=0.00
transport vesicle membrane GO:0030658 p=7.2E−02 n=2 fg=0.08 bg=0.02
clathrin−coated vesicle GO:0030136 p=7.6E−02 n=2 fg=0.08 bg=0.02
Cajal body GO:0015030 p=8.3E−02 n=1 fg=0.04 bg=0.00
cytoplasmic ubiquitin ligase complex GO:0000153 p=8.3E−02 n=1 fg=0.04 bg=0.00
microtubule organizing center GO:0005815 p=8.9E−02 n=4 fg=0.15 bg=0.07
0 1 2 3 4 5
−log(p)
n=26/104 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction