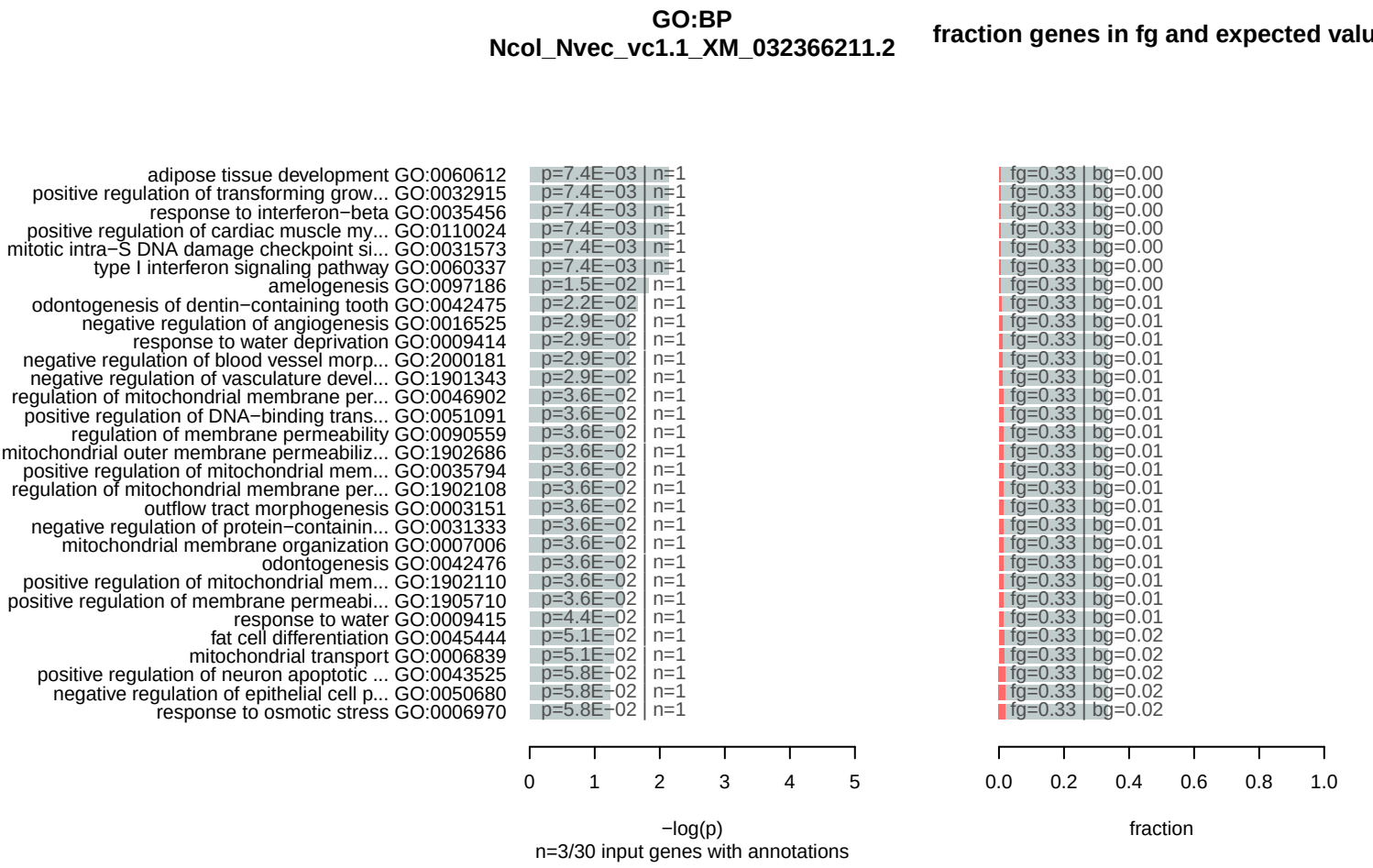
GO:BP
Ncol_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
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positive regulation of transforming grow... GO:0032915 p=7.4E−03 n=1 fg=0.33 bg=0.00
response to interferon−beta GO:0035456 p=7.4E−03 n=1 fg=0.33 bg=0.00
positive regulation of cardiac muscle my... GO:0110024 p=7.4E−03 n=1 fg=0.33 bg=0.00
mitotic intra−S DNA damage checkpoint si... GO:0031573 p=7.4E−03 n=1 fg=0.33 bg=0.00
type I interferon signaling pathway GO:0060337 p=7.4E−03 n=1 fg=0.33 bg=0.00
amelogenesis GO:0097186 p=1.5E−02 n=1 fg=0.33 bg=0.00
odontogenesis of dentin−containing tooth GO:0042475 p=2.2E−02 n=1 fg=0.33 bg=0.01
negative regulation of angiogenesis GO:0016525 p=2.9E−02 n=1 fg=0.33 bg=0.01
response to water deprivation GO:0009414 p=2.9E−02 n=1 fg=0.33 bg=0.01
negative regulation of blood vessel morp... GO:2000181 p=2.9E−02 n=1 fg=0.33 bg=0.01
negative regulation of vasculature devel... GO:1901343 p=2.9E−02 n=1 fg=0.33 bg=0.01
regulation of mitochondrial membrane per... GO:0046902 p=3.6E−02 n=1 fg=0.33 bg=0.01
positive regulation of DNA−binding trans... GO:0051091 p=3.6E−02 n=1 fg=0.33 bg=0.01
regulation of membrane permeability GO:0090559 p=3.6E−02 n=1 fg=0.33 bg=0.01
mitochondrial outer membrane permeabiliz... GO:1902686 p=3.6E−02 n=1 fg=0.33 bg=0.01
positive regulation of mitochondrial mem... GO:0035794 p=3.6E−02 n=1 fg=0.33 bg=0.01
regulation of mitochondrial membrane per... GO:1902108 p=3.6E−02 n=1 fg=0.33 bg=0.01
outflow tract morphogenesis GO:0003151 p=3.6E−02 n=1 fg=0.33 bg=0.01
negative regulation of protein−containin... GO:0031333 p=3.6E−02 n=1 fg=0.33 bg=0.01
mitochondrial membrane organization GO:0007006 p=3.6E−02 n=1 fg=0.33 bg=0.01
odontogenesis GO:0042476 p=3.6E−02 n=1 fg=0.33 bg=0.01
positive regulation of mitochondrial mem... GO:1902110 p=3.6E−02 n=1 fg=0.33 bg=0.01
positive regulation of membrane permeabi... GO:1905710 p=3.6E−02 n=1 fg=0.33 bg=0.01
response to water GO:0009415 p=4.4E−02 n=1 fg=0.33 bg=0.01
fat cell differentiation GO:0045444 p=5.1E−02 n=1 fg=0.33 bg=0.02
mitochondrial transport GO:0006839 p=5.1E−02 n=1 fg=0.33 bg=0.02
positive regulation of neuron apoptotic ... GO:0043525 p=5.8E−02 n=1 fg=0.33 bg=0.02
negative regulation of epithelial cell p... GO:0050680 p=5.8E−02 n=1 fg=0.33 bg=0.02
response to osmotic stress GO:0006970 p=5.8E−02 n=1 fg=0.33 bg=0.02
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−log(p)
n=3/30 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
cAMP response element binding GO:0035497 p=2.7E−03 n=1 fg=1.00 bg=0.00
cAMP response element binding protein bi... GO:0008140 p=2.7E−03 n=1 fg=1.00 bg=0.00
histone acetyltransferase activity GO:0004402 p=5.5E−03 n=1 fg=1.00 bg=0.01
transcription coactivator activity GO:0003713 p=3.8E−02 n=1 fg=1.00 bg=0.04
transcription coregulator activity GO:0003712 p=6.9E−02 n=1 fg=1.00 bg=0.07
chromatin binding GO:0003682 p=7.1E−02 n=1 fg=1.00 bg=0.07
DNA−binding transcription activator acti... GO:0001228 p=7.4E−02 n=1 fg=1.00 bg=0.07
DNA−binding transcription activator acti... GO:0001216 p=7.4E−02 n=1 fg=1.00 bg=0.07
protein heterodimerization activity GO:0046982 p=1.1E−01 n=1 fg=1.00 bg=0.11
kinase binding GO:0019900 p=1.2E−01 n=1 fg=1.00 bg=0.12
protein kinase binding GO:0019901 p=1.2E−01 n=1 fg=1.00 bg=0.12
DNA−binding transcription factor activit... GO:0000981 p=1.3E−01 n=1 fg=1.00 bg=0.13
DNA−binding transcription factor activit... GO:0003700 p=1.6E−01 n=1 fg=1.00 bg=0.16
protein dimerization activity GO:0046983 p=1.8E−01 n=1 fg=1.00 bg=0.18
transcription regulator activity GO:0140110 p=1.8E−01 n=1 fg=1.00 bg=0.18
enzyme binding GO:0019899 p=2.5E−01 n=1 fg=1.00 bg=0.25
double−stranded DNA binding GO:0003690 p=1.0E+00 n=1 fg=1.00 bg=0.09
N−acyltransferase activity GO:0016410 p=1.0E+00 n=1 fg=1.00 bg=0.01
peptide N−acetyltransferase activity GO:0034212 p=1.0E+00 n=1 fg=1.00 bg=0.01
catalytic activity GO:0003824 p=1.0E+00 n=1 fg=1.00 bg=0.40
acetyltransferase activity GO:0016407 p=1.0E+00 n=1 fg=1.00 bg=0.01
sequence−specific DNA binding GO:0043565 p=1.0E+00 n=1 fg=1.00 bg=0.10
DNA−binding transcription factor binding GO:0140297 p=1.0E+00 n=1 fg=1.00 bg=0.02
cis−regulatory region sequence−specific ... GO:0000987 p=1.0E+00 n=1 fg=1.00 bg=0.05
binding GO:0005488 p=1.0E+00 n=1 fg=1.00 bg=0.76
peptide−lysine−N−acetyltransferase activ... GO:0061733 p=1.0E+00 n=1 fg=1.00 bg=0.01
molecular_function GO:0003674 p=1.0E+00 n=1 fg=1.00 bg=1.00
protein binding GO:0005515 p=1.0E+00 n=1 fg=1.00 bg=0.60
nucleic acid binding GO:0003676 p=1.0E+00 n=1 fg=1.00 bg=0.18
DNA binding GO:0003677 p=1.0E+00 n=1 fg=1.00 bg=0.14
0 1 2 3 4 5
−log(p)
n=1/30 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 DNA damage GO:0090734 p=1.5E−02 n=1 fg=0.33 bg=0.00
site of double−strand break GO:0035861 p=1.5E−02 n=1 fg=0.33 bg=0.00
Cul3−RING ubiquitin ligase complex GO:0031463 p=1.5E−02 n=1 fg=0.33 bg=0.00
mitochondrion GO:0005739 p=1.6E−02 n=2 fg=0.67 bg=0.08
cullin−RING ubiquitin ligase complex GO:0031461 p=3.0E−02 n=1 fg=0.33 bg=0.01
outer membrane GO:0019867 p=4.4E−02 n=1 fg=0.33 bg=0.01
organelle outer membrane GO:0031968 p=4.4E−02 n=1 fg=0.33 bg=0.01
mitochondrial outer membrane GO:0005741 p=4.4E−02 n=1 fg=0.33 bg=0.01
mitochondrial membrane GO:0031966 p=1.0E−01 n=1 fg=0.33 bg=0.03
ubiquitin ligase complex GO:0000151 p=1.1E−01 n=1 fg=0.33 bg=0.04
postsynaptic specialization GO:0099572 p=1.1E−01 n=1 fg=0.33 bg=0.04
postsynaptic density GO:0014069 p=1.1E−01 n=1 fg=0.33 bg=0.04
mitochondrial envelope GO:0005740 p=1.2E−01 n=1 fg=0.33 bg=0.04
asymmetric synapse GO:0032279 p=1.4E−01 n=1 fg=0.33 bg=0.05
neuron to neuron synapse GO:0098984 p=1.5E−01 n=1 fg=0.33 bg=0.05
intracellular protein−containing complex GO:0140535 p=1.7E−01 n=1 fg=0.33 bg=0.06
transferase complex GO:1990234 p=2.0E−01 n=1 fg=0.33 bg=0.07
envelope GO:0031975 p=2.0E−01 n=1 fg=0.33 bg=0.07
organelle envelope GO:0031967 p=2.0E−01 n=1 fg=0.33 bg=0.07
chromosome GO:0005694 p=2.0E−01 n=1 fg=0.33 bg=0.07
postsynapse GO:0098794 p=2.2E−01 n=1 fg=0.33 bg=0.08
catalytic complex GO:1902494 p=2.5E−01 n=1 fg=0.33 bg=0.09
neuronal cell body GO:0043025 p=3.0E−01 n=1 fg=0.33 bg=0.11
cell body GO:0044297 p=3.2E−01 n=1 fg=0.33 bg=0.12
synapse GO:0045202 p=3.9E−01 n=1 fg=0.33 bg=0.15
somatodendritic compartment GO:0036477 p=4.0E−01 n=1 fg=0.33 bg=0.15
bounding membrane of organelle GO:0098588 p=4.0E−01 n=1 fg=0.33 bg=0.15
nucleus GO:0005634 p=4.4E−01 n=2 fg=0.67 bg=0.46
neuron projection GO:0043005 p=4.6E−01 n=1 fg=0.33 bg=0.19
cell junction GO:0030054 p=4.6E−01 n=1 fg=0.33 bg=0.19
0 1 2 3 4 5
−log(p)
n=3/30 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction