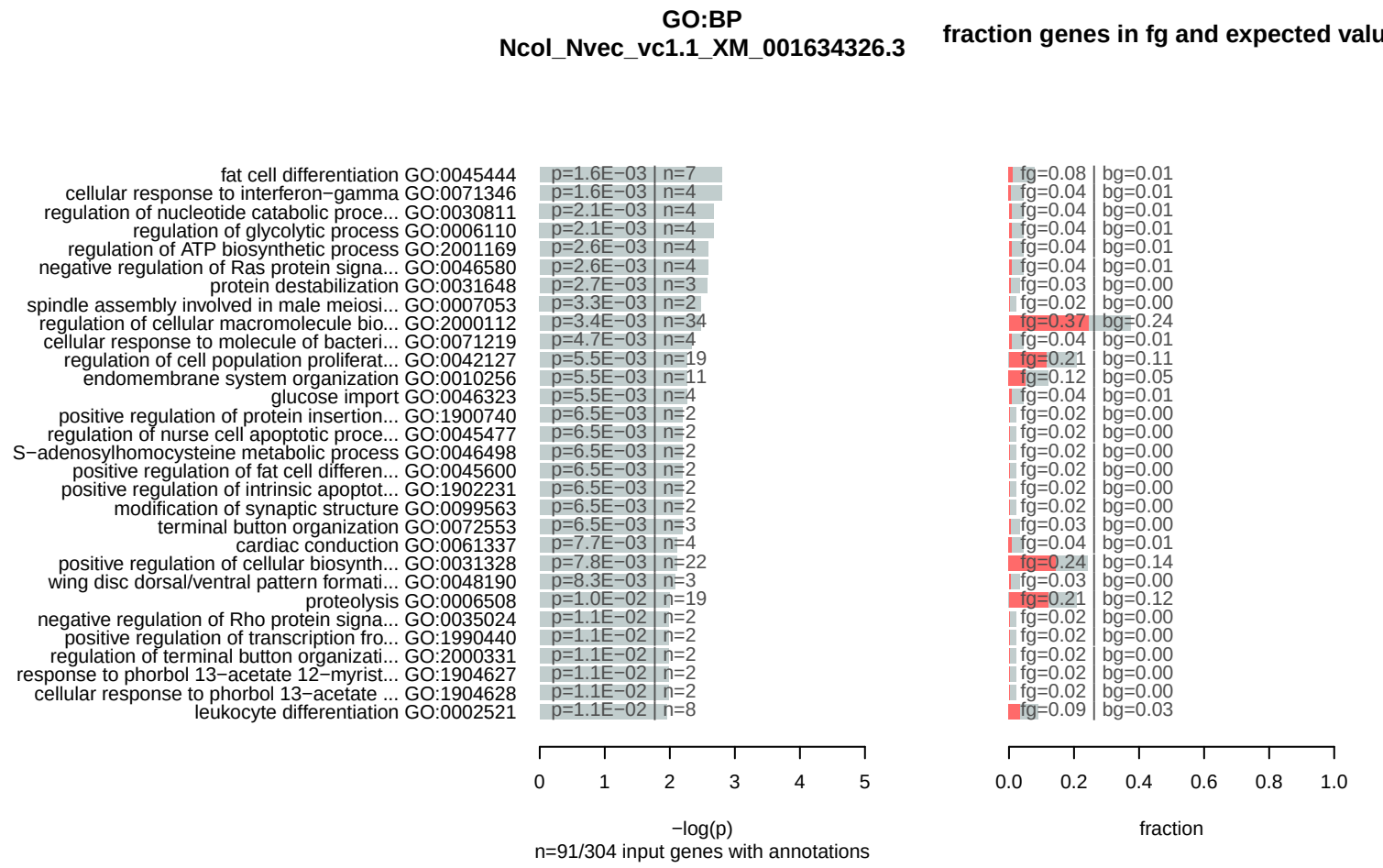
GO:BP
Ncol_Nvec_vc1.1_XM_001634326.3
fraction genes in fg and expected valu
fat cell differentiation GO:0045444 p=1.6E−03 n=7 fg=0.08 bg=0.01
cellular response to interferon−gamma GO:0071346 p=1.6E−03 n=4 fg=0.04 bg=0.01
regulation of nucleotide catabolic proce... GO:0030811 p=2.1E−03 n=4 fg=0.04 bg=0.01
regulation of glycolytic process GO:0006110 p=2.1E−03 n=4 fg=0.04 bg=0.01
regulation of ATP biosynthetic process GO:2001169 p=2.6E−03 n=4 fg=0.04 bg=0.01
negative regulation of Ras protein signa... GO:0046580 p=2.6E−03 n=4 fg=0.04 bg=0.01
protein destabilization GO:0031648 p=2.7E−03 n=3 fg=0.03 bg=0.00
spindle assembly involved in male meiosi... GO:0007053 p=3.3E−03 n=2 fg=0.02 bg=0.00
regulation of cellular macromolecule bio... GO:2000112 p=3.4E−03 n=34 fg=0.37 bg=0.24
cellular response to molecule of bacteri... GO:0071219 p=4.7E−03 n=4 fg=0.04 bg=0.01
regulation of cell population proliferat... GO:0042127 p=5.5E−03 n=19 fg=0.21 bg=0.11
endomembrane system organization GO:0010256 p=5.5E−03 n=11 fg=0.12 bg=0.05
glucose import GO:0046323 p=5.5E−03 n=4 fg=0.04 bg=0.01
positive regulation of protein insertion... GO:1900740 p=6.5E−03 n=2 fg=0.02 bg=0.00
regulation of nurse cell apoptotic proce... GO:0045477 p=6.5E−03 n=2 fg=0.02 bg=0.00
S−adenosylhomocysteine metabolic process GO:0046498 p=6.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of fat cell differen... GO:0045600 p=6.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of intrinsic apoptot... GO:1902231 p=6.5E−03 n=2 fg=0.02 bg=0.00
modification of synaptic structure GO:0099563 p=6.5E−03 n=2 fg=0.02 bg=0.00
terminal button organization GO:0072553 p=6.5E−03 n=3 fg=0.03 bg=0.00
cardiac conduction GO:0061337 p=7.7E−03 n=4 fg=0.04 bg=0.01
positive regulation of cellular biosynth... GO:0031328 p=7.8E−03 n=22 fg=0.24 bg=0.14
wing disc dorsal/ventral pattern formati... GO:0048190 p=8.3E−03 n=3 fg=0.03 bg=0.00
proteolysis GO:0006508 p=1.0E−02 n=19 fg=0.21 bg=0.12
negative regulation of Rho protein signa... GO:0035024 p=1.1E−02 n=2 fg=0.02 bg=0.00
positive regulation of transcription fro... GO:1990440 p=1.1E−02 n=2 fg=0.02 bg=0.00
regulation of terminal button organizati... GO:2000331 p=1.1E−02 n=2 fg=0.02 bg=0.00
response to phorbol 13−acetate 12−myrist... GO:1904627 p=1.1E−02 n=2 fg=0.02 bg=0.00
cellular response to phorbol 13−acetate ... GO:1904628 p=1.1E−02 n=2 fg=0.02 bg=0.00
leukocyte differentiation GO:0002521 p=1.1E−02 n=8 fg=0.09 bg=0.03
0 1 2 3 4 5
−log(p)
n=91/304 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001634326.3
fraction genes in fg and expected valu
histone deacetylase binding GO:0042826 p=1.2E−03 n=5 fg=0.06 bg=0.01
E−box binding GO:0070888 p=9.3E−03 n=3 fg=0.04 bg=0.01
eukaryotic initiation factor eIF2 bindin... GO:0071074 p=9.8E−03 n=2 fg=0.03 bg=0.00
translation elongation factor activity GO:0003746 p=2.0E−02 n=2 fg=0.03 bg=0.00
transferase activity, transferring nitro... GO:0016769 p=2.0E−02 n=2 fg=0.03 bg=0.00
transcription regulator activity GO:0140110 p=2.1E−02 n=14 fg=0.18 bg=0.10
Hsp90 protein binding GO:0051879 p=2.5E−02 n=3 fg=0.04 bg=0.01
Notch binding GO:0005112 p=2.6E−02 n=2 fg=0.03 bg=0.00
ubiquitin−like protein ligase activity GO:0061659 p=2.8E−02 n=6 fg=0.08 bg=0.03
ubiquitin protein ligase activity GO:0061630 p=2.8E−02 n=6 fg=0.08 bg=0.03
transcription corepressor activity GO:0003714 p=3.0E−02 n=4 fg=0.05 bg=0.02
glyceraldehyde−3−phosphate dehydrogenase... GO:0043891 p=3.3E−02 n=1 fg=0.01 bg=0.00
Rho GDP−dissociation inhibitor binding GO:0051022 p=3.3E−02 n=1 fg=0.01 bg=0.00
NAD−dependent histone deacetylase activi... GO:0046969 p=3.3E−02 n=1 fg=0.01 bg=0.00
apolipoprotein receptor binding GO:0034190 p=3.3E−02 n=1 fg=0.01 bg=0.00
apolipoprotein A−I receptor binding GO:0034191 p=3.3E−02 n=1 fg=0.01 bg=0.00
deubiquitinase activator activity GO:0035800 p=3.3E−02 n=1 fg=0.01 bg=0.00
protein−L−isoaspartate (D−aspartate) O−m... GO:0004719 p=3.3E−02 n=1 fg=0.01 bg=0.00
elongation factor−2 kinase activity GO:0004686 p=3.3E−02 n=1 fg=0.01 bg=0.00
class II DNA−(apurinic or apyrimidinic s... GO:0052720 p=3.3E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=3.3E−02 n=1 fg=0.01 bg=0.00
RNA guanylyltransferase activity GO:0008192 p=3.3E−02 n=1 fg=0.01 bg=0.00
tRNA guanylyltransferase activity GO:0008193 p=3.3E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.3E−02 n=1 fg=0.01 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=3.3E−02 n=1 fg=0.01 bg=0.00
protein carboxyl O−methyltransferase act... GO:0051998 p=3.3E−02 n=1 fg=0.01 bg=0.00
phorbol ester receptor activity GO:0001565 p=3.3E−02 n=1 fg=0.01 bg=0.00
NAD−dependent histone deacetylase activi... GO:0017136 p=3.3E−02 n=1 fg=0.01 bg=0.00
small protein activating enzyme binding GO:0044388 p=3.3E−02 n=1 fg=0.01 bg=0.00
C−methyltransferase activity GO:0008169 p=3.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=77/304 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001634326.3
fraction genes in fg and expected valu
nuclear body GO:0016604 p=3.1E−03 n=13 fg=0.14 bg=0.06
myelin sheath GO:0043209 p=3.3E−03 n=6 fg=0.07 bg=0.02
cytoplasmic ribonucleoprotein granule GO:0036464 p=1.4E−02 n=6 fg=0.07 bg=0.02
ribonucleoprotein granule GO:0035770 p=1.8E−02 n=6 fg=0.07 bg=0.02
nuclear protein−containing complex GO:0140513 p=1.9E−02 n=18 fg=0.20 bg=0.12
storage vacuole GO:0000322 p=2.2E−02 n=2 fg=0.02 bg=0.00
nuclear speck GO:0016607 p=2.3E−02 n=7 fg=0.08 bg=0.03
growth cone GO:0030426 p=2.8E−02 n=5 fg=0.05 bg=0.02
Golgi−associated vesicle lumen GO:0070931 p=3.4E−02 n=1 fg=0.01 bg=0.00
Cdc73/Paf1 complex GO:0016593 p=3.4E−02 n=1 fg=0.01 bg=0.00
XPC complex GO:0071942 p=3.4E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=3.4E−02 n=1 fg=0.01 bg=0.00
checkpoint clamp complex GO:0030896 p=3.4E−02 n=1 fg=0.01 bg=0.00
SUMO activating enzyme complex GO:0031510 p=3.4E−02 n=1 fg=0.01 bg=0.00
PR−DUB complex GO:0035517 p=3.4E−02 n=1 fg=0.01 bg=0.00
CHOP−C/EBP complex GO:0036488 p=3.4E−02 n=1 fg=0.01 bg=0.00
nucleotide−excision repair complex GO:0000109 p=3.4E−02 n=1 fg=0.01 bg=0.00
nuclear pore inner ring GO:0044611 p=3.4E−02 n=1 fg=0.01 bg=0.00
site of polarized growth GO:0030427 p=3.5E−02 n=5 fg=0.05 bg=0.02
supramolecular complex GO:0099080 p=6.0E−02 n=12 fg=0.13 bg=0.08
type I terminal bouton GO:0061174 p=6.1E−02 n=2 fg=0.02 bg=0.00
midbody GO:0030496 p=6.1E−02 n=4 fg=0.04 bg=0.02
chromosome GO:0005694 p=6.4E−02 n=13 fg=0.14 bg=0.09
extrinsic component of Golgi membrane GO:0090498 p=6.7E−02 n=1 fg=0.01 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=6.7E−02 n=1 fg=0.01 bg=0.00
protein−lipid complex GO:0032994 p=6.7E−02 n=1 fg=0.01 bg=0.00
NSL complex GO:0044545 p=6.7E−02 n=1 fg=0.01 bg=0.00
GAIT complex GO:0097452 p=6.7E−02 n=1 fg=0.01 bg=0.00
BBSome GO:0034464 p=6.7E−02 n=1 fg=0.01 bg=0.00
glycine cleavage complex GO:0005960 p=6.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=92/304 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction