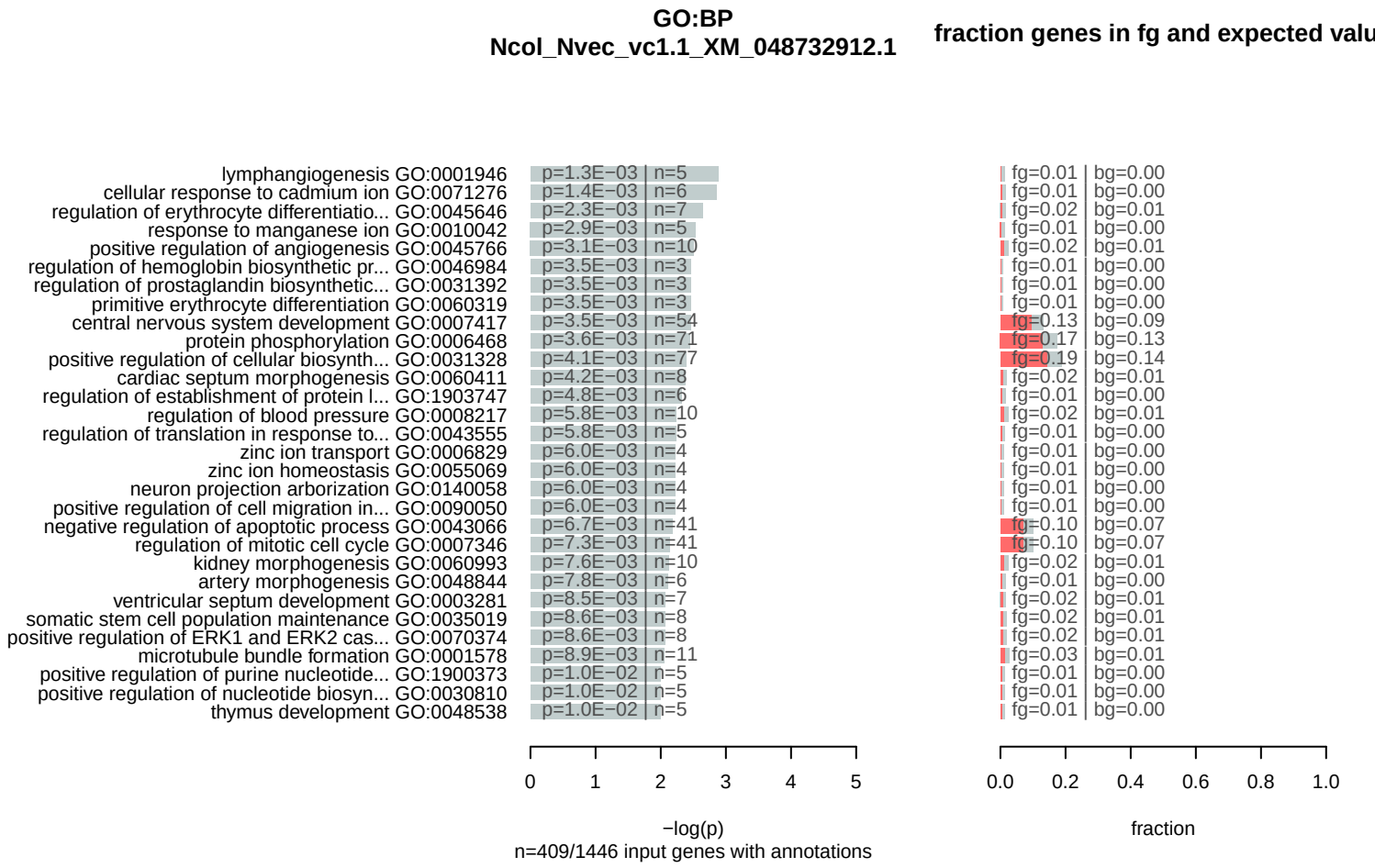
GO:BP
Ncol_Nvec_vc1.1_XM_048732912.1
fraction genes in fg and expected valu
lymphangiogenesis GO:0001946 p=1.3E−03 n=5 fg=0.01 bg=0.00
cellular response to cadmium ion GO:0071276 p=1.4E−03 n=6 fg=0.01 bg=0.00
regulation of erythrocyte differentiatio... GO:0045646 p=2.3E−03 n=7 fg=0.02 bg=0.01
response to manganese ion GO:0010042 p=2.9E−03 n=5 fg=0.01 bg=0.00
positive regulation of angiogenesis GO:0045766 p=3.1E−03 n=10 fg=0.02 bg=0.01
regulation of hemoglobin biosynthetic pr... GO:0046984 p=3.5E−03 n=3 fg=0.01 bg=0.00
regulation of prostaglandin biosynthetic... GO:0031392 p=3.5E−03 n=3 fg=0.01 bg=0.00
primitive erythrocyte differentiation GO:0060319 p=3.5E−03 n=3 fg=0.01 bg=0.00
central nervous system development GO:0007417 p=3.5E−03 n=54 fg=0.13 bg=0.09
protein phosphorylation GO:0006468 p=3.6E−03 n=71 fg=0.17 bg=0.13
positive regulation of cellular biosynth... GO:0031328 p=4.1E−03 n=77 fg=0.19 bg=0.14
cardiac septum morphogenesis GO:0060411 p=4.2E−03 n=8 fg=0.02 bg=0.01
regulation of establishment of protein l... GO:1903747 p=4.8E−03 n=6 fg=0.01 bg=0.00
regulation of blood pressure GO:0008217 p=5.8E−03 n=10 fg=0.02 bg=0.01
regulation of translation in response to... GO:0043555 p=5.8E−03 n=5 fg=0.01 bg=0.00
zinc ion transport GO:0006829 p=6.0E−03 n=4 fg=0.01 bg=0.00
zinc ion homeostasis GO:0055069 p=6.0E−03 n=4 fg=0.01 bg=0.00
neuron projection arborization GO:0140058 p=6.0E−03 n=4 fg=0.01 bg=0.00
positive regulation of cell migration in... GO:0090050 p=6.0E−03 n=4 fg=0.01 bg=0.00
negative regulation of apoptotic process GO:0043066 p=6.7E−03 n=41 fg=0.10 bg=0.07
regulation of mitotic cell cycle GO:0007346 p=7.3E−03 n=41 fg=0.10 bg=0.07
kidney morphogenesis GO:0060993 p=7.6E−03 n=10 fg=0.02 bg=0.01
artery morphogenesis GO:0048844 p=7.8E−03 n=6 fg=0.01 bg=0.00
ventricular septum development GO:0003281 p=8.5E−03 n=7 fg=0.02 bg=0.01
somatic stem cell population maintenance GO:0035019 p=8.6E−03 n=8 fg=0.02 bg=0.01
positive regulation of ERK1 and ERK2 cas... GO:0070374 p=8.6E−03 n=8 fg=0.02 bg=0.01
microtubule bundle formation GO:0001578 p=8.9E−03 n=11 fg=0.03 bg=0.01
positive regulation of purine nucleotide... GO:1900373 p=1.0E−02 n=5 fg=0.01 bg=0.00
positive regulation of nucleotide biosyn... GO:0030810 p=1.0E−02 n=5 fg=0.01 bg=0.00
thymus development GO:0048538 p=1.0E−02 n=5 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
0.0 0.2 0.4 0.6 0.8 1.0
fraction
n=409/1446 input genes with annotations
GO:MF
Ncol_Nvec_vc1.1_XM_048732912.1
fraction genes in fg and expected valu
epoxide hydrolase activity GO:0004301 p=3.5E−03 n=3 fg=0.01 bg=0.00
protein serine/threonine kinase activity GO:0004674 p=4.6E−03 n=25 fg=0.07 bg=0.04
transcription cis−regulatory region bind... GO:0000976 p=7.5E−03 n=27 fg=0.07 bg=0.05
core promoter sequence−specific DNA bind... GO:0001046 p=1.2E−02 n=7 fg=0.02 bg=0.01
zinc ion transmembrane transporter activ... GO:0005385 p=1.2E−02 n=3 fg=0.01 bg=0.00
chloride channel regulator activity GO:0017081 p=1.3E−02 n=4 fg=0.01 bg=0.00
tubulin binding GO:0015631 p=1.4E−02 n=20 fg=0.06 bg=0.03
ATP binding GO:0005524 p=1.5E−02 n=24 fg=0.07 bg=0.04
small molecule binding GO:0036094 p=1.6E−02 n=50 fg=0.14 bg=0.10
ATPase regulator activity GO:0060590 p=1.8E−02 n=6 fg=0.02 bg=0.01
adenyl nucleotide binding GO:0030554 p=1.9E−02 n=27 fg=0.07 bg=0.05
nucleotide binding GO:0000166 p=1.9E−02 n=40 fg=0.11 bg=0.08
nucleoside phosphate binding GO:1901265 p=1.9E−02 n=40 fg=0.11 bg=0.08
nuclear receptor binding GO:0016922 p=2.2E−02 n=11 fg=0.03 bg=0.02
Notch binding GO:0005112 p=2.2E−02 n=4 fg=0.01 bg=0.00
RNA polymerase II−specific DNA−binding t... GO:0061629 p=2.3E−02 n=14 fg=0.04 bg=0.02
gamma−glutamylcyclotransferase activity GO:0003839 p=2.3E−02 n=2 fg=0.01 bg=0.00
armadillo repeat domain binding GO:0070016 p=2.3E−02 n=2 fg=0.01 bg=0.00
DNA binding, bending GO:0008301 p=2.3E−02 n=2 fg=0.01 bg=0.00
calcium−induced calcium release activity GO:0048763 p=2.3E−02 n=2 fg=0.01 bg=0.00
thiopurine S−methyltransferase activity GO:0008119 p=2.3E−02 n=2 fg=0.01 bg=0.00
L−malate dehydrogenase activity GO:0030060 p=2.3E−02 n=2 fg=0.01 bg=0.00
guanylyltransferase activity GO:0070568 p=2.3E−02 n=2 fg=0.01 bg=0.00
general transcription initiation factor ... GO:0140223 p=2.3E−02 n=2 fg=0.01 bg=0.00
adenyl ribonucleotide binding GO:0032559 p=2.5E−02 n=26 fg=0.07 bg=0.05
ion channel regulator activity GO:0099106 p=2.5E−02 n=10 fg=0.03 bg=0.01
S−adenosyl−L−methionine binding GO:1904047 p=2.7E−02 n=3 fg=0.01 bg=0.00
toxic substance binding GO:0015643 p=2.7E−02 n=3 fg=0.01 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=2.8E−02 n=18 fg=0.05 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.8E−02 n=18 fg=0.05 bg=0.03
0 1 2 3 4 5
−log(p)
0.0 0.2 0.4 0.6 0.8 1.0
fraction
n=360/1446 input genes with annotations
GO:CC
Ncol_Nvec_vc1.1_XM_048732912.1
fraction genes in fg and expected valu
Flemming body GO:0090543 p=3.5E−03 n=3 fg=0.01 bg=0.00
spindle pole GO:0000922 p=4.7E−03 n=13 fg=0.03 bg=0.01
rough endoplasmic reticulum membrane GO:0030867 p=6.2E−03 n=4 fg=0.01 bg=0.00
ISWI−type complex GO:0031010 p=6.2E−03 n=4 fg=0.01 bg=0.00
cell body GO:0044297 p=1.1E−02 n=39 fg=0.09 bg=0.07
neuronal cell body GO:0043025 p=1.5E−02 n=35 fg=0.08 bg=0.06
spindle GO:0005819 p=1.8E−02 n=27 fg=0.07 bg=0.03
cytoskeleton GO:0005856 p=2.1E−02 n=80 fg=0.19 bg=0.15
mitotic spindle GO:0072686 p=2.2E−02 n=11 fg=0.03 bg=0.01
actomyosin contractile ring GO:0005826 p=2.3E−02 n=2 fg=0.00 bg=0.00
GAIT complex GO:0097452 p=2.3E−02 n=2 fg=0.00 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=2.3E−02 n=2 fg=0.00 bg=0.00
transcription factor AP−1 complex GO:0035976 p=2.3E−02 n=2 fg=0.00 bg=0.00
Parkin−FBXW7−Cul1 ubiquitin ligase compl... GO:1990452 p=2.3E−02 n=2 fg=0.00 bg=0.00
eukaryotic translation elongation factor... GO:0005853 p=2.3E−02 n=2 fg=0.00 bg=0.00
somatodendritic compartment GO:0036477 p=2.8E−02 n=46 fg=0.11 bg=0.09
MKS complex GO:0036038 p=3.6E−02 n=4 fg=0.01 bg=0.00
integral component of Golgi membrane GO:0030173 p=3.6E−02 n=5 fg=0.01 bg=0.00
midbody GO:0030496 p=3.7E−02 n=14 fg=0.03 bg=0.02
methyltransferase complex GO:0034708 p=4.4E−02 n=9 fg=0.02 bg=0.01
vacuolar lumen GO:0005775 p=4.4E−02 n=9 fg=0.02 bg=0.01
cell projection GO:0042995 p=6.1E+02 n=86 fg=0.21 bg=0.18
ESC/E(Z) complex GO:0035098 p=6.3E+02 n=2 fg=0.00 bg=0.00
RNA N6−methyladenosine methyltransferase... GO:0036396 p=6.3E+02 n=2 fg=0.00 bg=0.00
mRNA editing complex GO:0045293 p=6.3E+02 n=2 fg=0.00 bg=0.00
CHRAC GO:0008623 p=6.3E+02 n=2 fg=0.00 bg=0.00
FAR/SIN/STRIPAK complex GO:0090443 p=6.3E+02 n=2 fg=0.00 bg=0.00
NURF complex GO:0016589 p=6.3E+02 n=2 fg=0.00 bg=0.00
acetylcholine−gated channel complex GO:0005892 p=6.3E+02 n=2 fg=0.00 bg=0.00
eukaryotic translation initiation factor... GO:0005850 p=6.3E+02 n=2 fg=0.00 bg=0.00
0 1 2 3 4 5
−log(p)
0.0 0.2 0.4 0.6 0.8 1.0
fraction
n=412/1446 input genes with annotations