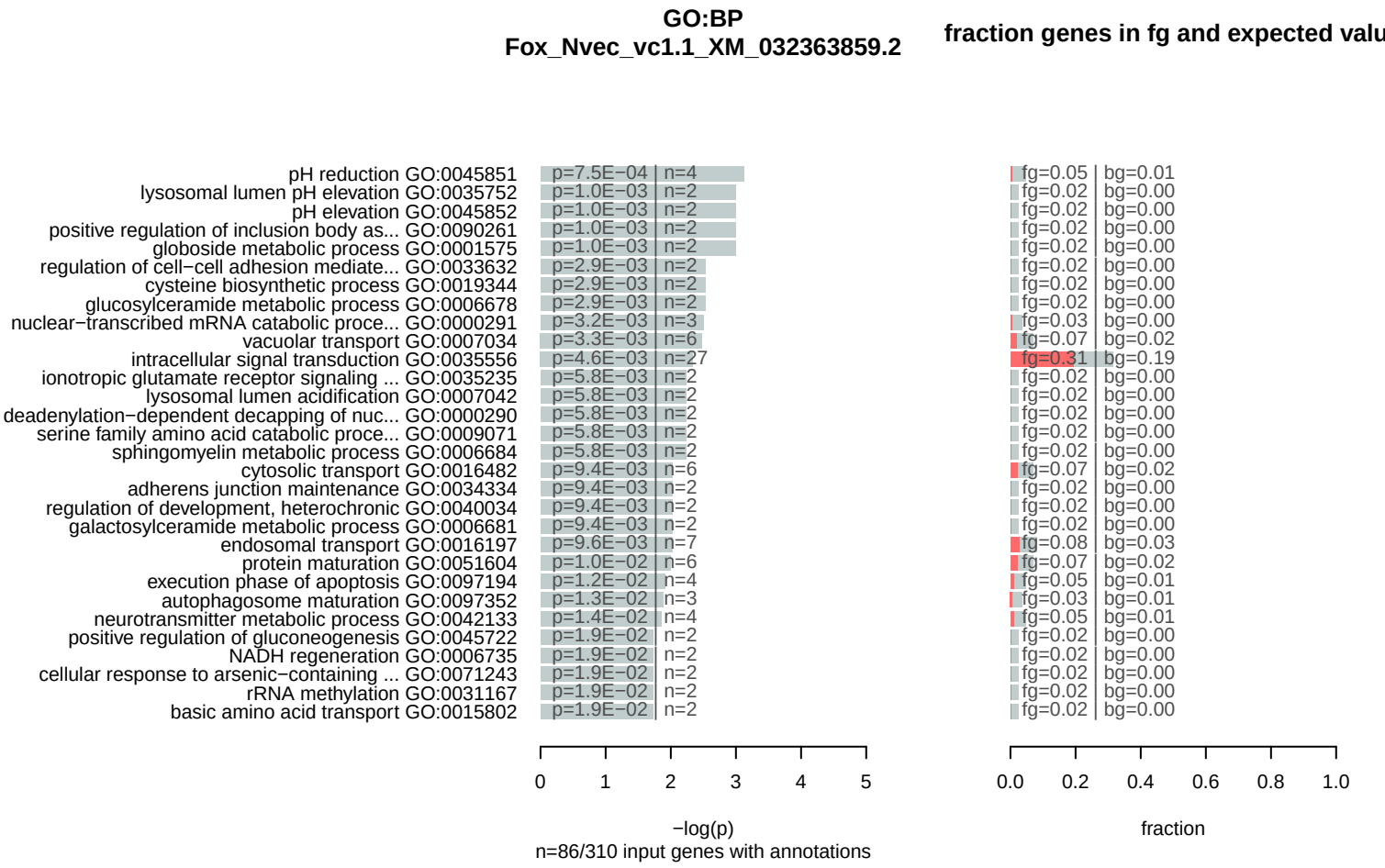
GO:BP
Fox_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
pH reduction GO:0045851 p=7.5E−04 n=4 fg=0.05 bg=0.01
lysosomal lumen pH elevation GO:0035752 p=1.0E−03 n=2 fg=0.02 bg=0.00
pH elevation GO:0045852 p=1.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of inclusion body as... GO:0090261 p=1.0E−03 n=2 fg=0.02 bg=0.00
globoside metabolic process GO:0001575 p=1.0E−03 n=2 fg=0.02 bg=0.00
regulation of cell−cell adhesion mediate... GO:0033632 p=2.9E−03 n=2 fg=0.02 bg=0.00
cysteine biosynthetic process GO:0019344 p=2.9E−03 n=2 fg=0.02 bg=0.00
glucosylceramide metabolic process GO:0006678 p=2.9E−03 n=2 fg=0.02 bg=0.00
nuclear−transcribed mRNA catabolic proce... GO:0000291 p=3.2E−03 n=3 fg=0.03 bg=0.00
vacuolar transport GO:0007034 p=3.3E−03 n=6 fg=0.07 bg=0.02
intracellular signal transduction GO:0035556 p=4.6E−03 n=27 fg=0.31 bg=0.19
ionotropic glutamate receptor signaling ... GO:0035235 p=5.8E−03 n=2 fg=0.02 bg=0.00
lysosomal lumen acidification GO:0007042 p=5.8E−03 n=2 fg=0.02 bg=0.00
deadenylation−dependent decapping of nuc... GO:0000290 p=5.8E−03 n=2 fg=0.02 bg=0.00
serine family amino acid catabolic proce... GO:0009071 p=5.8E−03 n=2 fg=0.02 bg=0.00
sphingomyelin metabolic process GO:0006684 p=5.8E−03 n=2 fg=0.02 bg=0.00
cytosolic transport GO:0016482 p=9.4E−03 n=6 fg=0.07 bg=0.02
adherens junction maintenance GO:0034334 p=9.4E−03 n=2 fg=0.02 bg=0.00
regulation of development, heterochronic GO:0040034 p=9.4E−03 n=2 fg=0.02 bg=0.00
galactosylceramide metabolic process GO:0006681 p=9.4E−03 n=2 fg=0.02 bg=0.00
endosomal transport GO:0016197 p=9.6E−03 n=7 fg=0.08 bg=0.03
protein maturation GO:0051604 p=1.0E−02 n=6 fg=0.07 bg=0.02
execution phase of apoptosis GO:0097194 p=1.2E−02 n=4 fg=0.05 bg=0.01
autophagosome maturation GO:0097352 p=1.3E−02 n=3 fg=0.03 bg=0.01
neurotransmitter metabolic process GO:0042133 p=1.4E−02 n=4 fg=0.05 bg=0.01
positive regulation of gluconeogenesis GO:0045722 p=1.9E−02 n=2 fg=0.02 bg=0.00
NADH regeneration GO:0006735 p=1.9E−02 n=2 fg=0.02 bg=0.00
cellular response to arsenic−containing ... GO:0071243 p=1.9E−02 n=2 fg=0.02 bg=0.00
rRNA methylation GO:0031167 p=1.9E−02 n=2 fg=0.02 bg=0.00
basic amino acid transport GO:0015802 p=1.9E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=86/310 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
1−phosphatidylinositol binding GO:0005545 p=1.1E−03 n=2 fg=0.03 bg=0.00
cystathionine beta−synthase activity GO:0004122 p=1.1E−03 n=2 fg=0.03 bg=0.00
cysteine synthase activity GO:0004124 p=1.1E−03 n=2 fg=0.03 bg=0.00
RNA 7−methylguanosine cap binding GO:0000340 p=3.1E−03 n=2 fg=0.03 bg=0.00
calcium−release channel activity GO:0015278 p=2.0E−02 n=2 fg=0.03 bg=0.00
rRNA methyltransferase activity GO:0008649 p=2.0E−02 n=2 fg=0.03 bg=0.00
catalytic activity, acting on a rRNA GO:0140102 p=2.0E−02 n=2 fg=0.03 bg=0.00
methyltransferase activity GO:0008168 p=2.1E−02 n=5 fg=0.06 bg=0.02
transferase activity, transferring one−c... GO:0016741 p=2.5E−02 n=5 fg=0.06 bg=0.02
pyridoxal phosphate binding GO:0030170 p=2.6E−02 n=2 fg=0.03 bg=0.00
vitamin B6 binding GO:0070279 p=2.6E−02 n=2 fg=0.03 bg=0.00
ubiquitin−like protein ligase activity GO:0061659 p=2.9E−02 n=6 fg=0.08 bg=0.03
ubiquitin protein ligase activity GO:0061630 p=2.9E−02 n=6 fg=0.08 bg=0.03
RNA cap binding GO:0000339 p=3.2E−02 n=3 fg=0.04 bg=0.00
nitrite reductase (NO−forming) activity GO:0050421 p=3.3E−02 n=1 fg=0.01 bg=0.00
heteroduplex DNA loop binding GO:0000404 p=3.3E−02 n=1 fg=0.01 bg=0.00
double−strand/single−strand DNA junction... GO:0000406 p=3.3E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=3.3E−02 n=1 fg=0.01 bg=0.00
volume−sensitive chloride channel activi... GO:0072320 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
adenosine−phosphate deaminase activity GO:0047623 p=3.3E−02 n=1 fg=0.01 bg=0.00
adenylylsulfatase activity GO:0047627 p=3.3E−02 n=1 fg=0.01 bg=0.00
2',3'−cyclic GMP−AMP synthase activity GO:0061501 p=3.3E−02 n=1 fg=0.01 bg=0.00
AMP deaminase activity GO:0003876 p=3.3E−02 n=1 fg=0.01 bg=0.00
rRNA (guanosine−2'−O−)−methyltransferase... GO:0070039 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
DNA insertion or deletion binding GO:0032135 p=3.3E−02 n=1 fg=0.01 bg=0.00
intracellular phosphatidylinositol−3,5−b... GO:0097682 p=3.3E−02 n=1 fg=0.01 bg=0.00
cyclic GMP−AMP synthase activity GO:0140699 p=3.3E−02 n=1 fg=0.01 bg=0.00
centromeric DNA binding GO:0019237 p=3.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=78/310 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
late endosome GO:0005770 p=2.4E−03 n=7 fg=0.08 bg=0.02
P−body GO:0000932 p=4.1E−03 n=4 fg=0.05 bg=0.01
RNA cap binding complex GO:0034518 p=6.0E−03 n=2 fg=0.02 bg=0.00
synaptic vesicle GO:0008021 p=8.9E−03 n=6 fg=0.07 bg=0.02
messenger ribonucleoprotein complex GO:1990124 p=9.9E−03 n=2 fg=0.02 bg=0.00
MCM complex GO:0042555 p=1.5E−02 n=2 fg=0.02 bg=0.00
microvillus membrane GO:0031528 p=2.0E−02 n=2 fg=0.02 bg=0.00
actin−based cell projection GO:0098858 p=2.4E−02 n=5 fg=0.06 bg=0.02
cell cortex region GO:0099738 p=2.9E−02 n=3 fg=0.03 bg=0.01
late endosome membrane GO:0031902 p=2.9E−02 n=3 fg=0.03 bg=0.01
integral component of endoplasmic reticu... GO:0030176 p=3.0E−02 n=5 fg=0.06 bg=0.02
nuclear replisome GO:0043601 p=3.3E−02 n=2 fg=0.02 bg=0.00
replisome GO:0030894 p=3.3E−02 n=2 fg=0.02 bg=0.00
protein phosphatase 4 complex GO:0030289 p=3.3E−02 n=1 fg=0.01 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=3.3E−02 n=1 fg=0.01 bg=0.00
steroid hormone aporeceptor complex GO:0005831 p=3.3E−02 n=1 fg=0.01 bg=0.00
MutSbeta complex GO:0032302 p=3.3E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=3.3E−02 n=1 fg=0.01 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=3.3E−02 n=1 fg=0.01 bg=0.00
retromer, cargo−selective complex GO:0030906 p=3.3E−02 n=1 fg=0.01 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=3.3E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=3.3E−02 n=1 fg=0.01 bg=0.00
filopodium GO:0030175 p=3.3E−02 n=3 fg=0.03 bg=0.01
intrinsic component of endoplasmic retic... GO:0031227 p=3.6E−02 n=5 fg=0.06 bg=0.02
pronucleus GO:0045120 p=4.8E−02 n=2 fg=0.02 bg=0.00
early endosome GO:0005769 p=5.4E−02 n=6 fg=0.07 bg=0.03
DNA polymerase complex GO:0042575 p=5.6E−02 n=2 fg=0.02 bg=0.00
ruffle membrane GO:0032587 p=5.6E−02 n=2 fg=0.02 bg=0.00
katanin complex GO:0008352 p=6.4E−02 n=1 fg=0.01 bg=0.00
intrinsic component of vacuolar membrane GO:0031310 p=6.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=88/310 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction