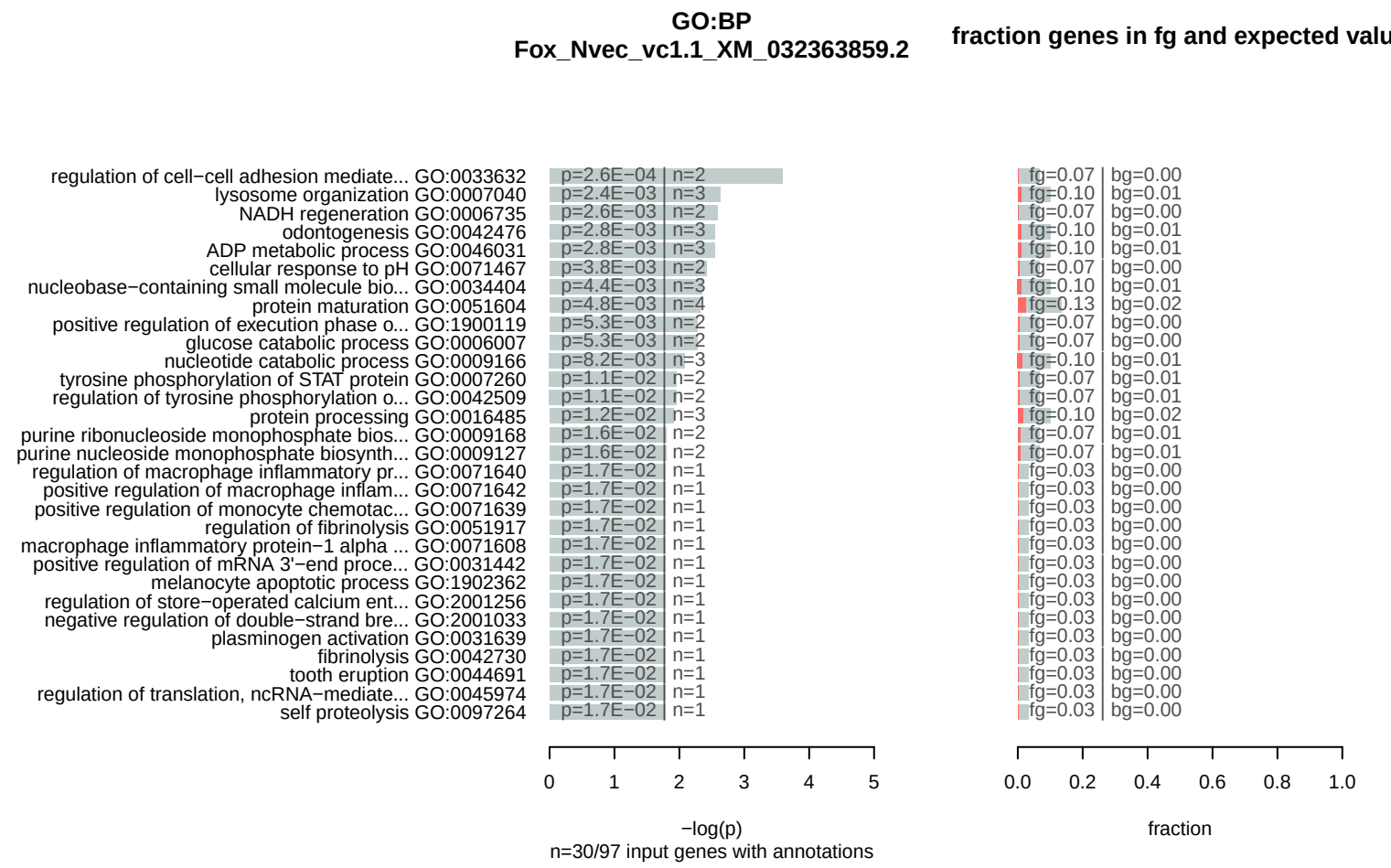
GO:BP
Fox_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
regulation of cell−cell adhesion mediate... GO:0033632 p=2.6E−04 n=2 fg=0.07 bg=0.00
lysosome organization GO:0007040 p=2.4E−03 n=3 fg=0.10 bg=0.01
NADH regeneration GO:0006735 p=2.6E−03 n=2 fg=0.07 bg=0.00
odontogenesis GO:0042476 p=2.8E−03 n=3 fg=0.10 bg=0.01
ADP metabolic process GO:0046031 p=2.8E−03 n=3 fg=0.10 bg=0.01
cellular response to pH GO:0071467 p=3.8E−03 n=2 fg=0.07 bg=0.00
nucleobase−containing small molecule bio... GO:0034404 p=4.4E−03 n=3 fg=0.10 bg=0.01
protein maturation GO:0051604 p=4.8E−03 n=4 fg=0.13 bg=0.02
positive regulation of execution phase o... GO:1900119 p=5.3E−03 n=2 fg=0.07 bg=0.00
glucose catabolic process GO:0006007 p=5.3E−03 n=2 fg=0.07 bg=0.00
nucleotide catabolic process GO:0009166 p=8.2E−03 n=3 fg=0.10 bg=0.01
tyrosine phosphorylation of STAT protein GO:0007260 p=1.1E−02 n=2 fg=0.07 bg=0.01
regulation of tyrosine phosphorylation o... GO:0042509 p=1.1E−02 n=2 fg=0.07 bg=0.01
protein processing GO:0016485 p=1.2E−02 n=3 fg=0.10 bg=0.02
purine ribonucleoside monophosphate bios... GO:0009168 p=1.6E−02 n=2 fg=0.07 bg=0.01
purine nucleoside monophosphate biosynth... GO:0009127 p=1.6E−02 n=2 fg=0.07 bg=0.01
regulation of macrophage inflammatory pr... GO:0071640 p=1.7E−02 n=1 fg=0.03 bg=0.00
positive regulation of macrophage inflam... GO:0071642 p=1.7E−02 n=1 fg=0.03 bg=0.00
positive regulation of monocyte chemotac... GO:0071639 p=1.7E−02 n=1 fg=0.03 bg=0.00
regulation of fibrinolysis GO:0051917 p=1.7E−02 n=1 fg=0.03 bg=0.00
macrophage inflammatory protein−1 alpha ... GO:0071608 p=1.7E−02 n=1 fg=0.03 bg=0.00
positive regulation of mRNA 3'−end proce... GO:0031442 p=1.7E−02 n=1 fg=0.03 bg=0.00
melanocyte apoptotic process GO:1902362 p=1.7E−02 n=1 fg=0.03 bg=0.00
regulation of store−operated calcium ent... GO:2001256 p=1.7E−02 n=1 fg=0.03 bg=0.00
negative regulation of double−strand bre... GO:2001033 p=1.7E−02 n=1 fg=0.03 bg=0.00
plasminogen activation GO:0031639 p=1.7E−02 n=1 fg=0.03 bg=0.00
fibrinolysis GO:0042730 p=1.7E−02 n=1 fg=0.03 bg=0.00
tooth eruption GO:0044691 p=1.7E−02 n=1 fg=0.03 bg=0.00
regulation of translation, ncRNA−mediate... GO:0045974 p=1.7E−02 n=1 fg=0.03 bg=0.00
self proteolysis GO:0097264 p=1.7E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=30/97 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
1−phosphatidylinositol binding GO:0005545 p=3.0E−04 n=2 fg=0.07 bg=0.00
calcium−release channel activity GO:0015278 p=2.9E−03 n=2 fg=0.07 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=5.9E−03 n=2 fg=0.07 bg=0.00
metalloendopeptidase activity GO:0004222 p=7.8E−03 n=2 fg=0.07 bg=0.01
protein self−association GO:0043621 p=1.5E−02 n=2 fg=0.07 bg=0.01
inositol 1,3,4,5 tetrakisphosphate bindi... GO:0043533 p=1.8E−02 n=1 fg=0.04 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=1.8E−02 n=1 fg=0.04 bg=0.00
intracellular phosphatidylinositol−3,5−b... GO:0097682 p=1.8E−02 n=1 fg=0.04 bg=0.00
translation elongation factor binding GO:0061770 p=1.8E−02 n=1 fg=0.04 bg=0.00
N−acetylglucosamine−1−phosphodiester alp... GO:0003944 p=1.8E−02 n=1 fg=0.04 bg=0.00
AMP deaminase activity GO:0003876 p=1.8E−02 n=1 fg=0.04 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=1.8E−02 n=1 fg=0.04 bg=0.00
leucine zipper domain binding GO:0043522 p=1.8E−02 n=1 fg=0.04 bg=0.00
integrin binding GO:0005178 p=1.8E−02 n=2 fg=0.07 bg=0.01
UDP−galactose transmembrane transporter ... GO:0005459 p=3.5E−02 n=1 fg=0.04 bg=0.00
exogenous protein binding GO:0140272 p=3.5E−02 n=1 fg=0.04 bg=0.00
phosphatidylinositol−3,5−bisphosphate bi... GO:0080025 p=3.5E−02 n=1 fg=0.04 bg=0.00
calcium−induced calcium release activity GO:0048763 p=3.5E−02 n=1 fg=0.04 bg=0.00
phosphotransferase activity, carboxyl gr... GO:0016774 p=3.5E−02 n=1 fg=0.04 bg=0.00
NAADP−sensitive calcium−release channel ... GO:0072345 p=3.5E−02 n=1 fg=0.04 bg=0.00
STAT family protein binding GO:0097677 p=3.5E−02 n=1 fg=0.04 bg=0.00
virus receptor activity GO:0001618 p=3.5E−02 n=1 fg=0.04 bg=0.00
store−operated calcium channel activity GO:0015279 p=3.5E−02 n=1 fg=0.04 bg=0.00
N4−(beta−N−acetylglucosaminyl)−L−asparag... GO:0003948 p=3.5E−02 n=1 fg=0.04 bg=0.00
LRR domain binding GO:0030275 p=3.5E−02 n=1 fg=0.04 bg=0.00
sequence−specific single stranded DNA bi... GO:0098847 p=3.5E−02 n=1 fg=0.04 bg=0.00
dipeptidyl−peptidase activity GO:0008239 p=3.5E−02 n=1 fg=0.04 bg=0.00
protease binding GO:0002020 p=3.8E−02 n=2 fg=0.07 bg=0.01
oxidoreductase activity, acting on NAD(P... GO:0016651 p=4.7E−02 n=2 fg=0.07 bg=0.01
phosphatidylinositol bisphosphate bindin... GO:1902936 p=4.7E−02 n=2 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=28/97 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
integral component of endoplasmic reticu... GO:0030176 p=4.6E−03 n=4 fg=0.13 bg=0.02
serine/threonine protein kinase complex GO:1902554 p=1.2E−02 n=2 fg=0.06 bg=0.01
ruffle membrane GO:0032587 p=1.2E−02 n=2 fg=0.06 bg=0.01
cytoplasmic vesicle GO:0031410 p=1.5E−02 n=11 fg=0.35 bg=0.18
intracellular vesicle GO:0097708 p=1.5E−02 n=11 fg=0.35 bg=0.18
cytoskeleton of presynaptic active zone GO:0048788 p=1.7E−02 n=1 fg=0.03 bg=0.00
apical cytoplasm GO:0090651 p=1.7E−02 n=1 fg=0.03 bg=0.00
integral component of lysosomal membrane GO:1905103 p=1.7E−02 n=1 fg=0.03 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=1.7E−02 n=1 fg=0.03 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=1.7E−02 n=1 fg=0.03 bg=0.00
vesicle GO:0031982 p=2.2E−02 n=11 fg=0.35 bg=0.19
protein kinase complex GO:1902911 p=2.3E−02 n=2 fg=0.06 bg=0.01
plasma membrane GO:0005886 p=2.3E−02 n=14 fg=0.45 bg=0.27
extrinsic component of cytoplasmic side ... GO:0031234 p=2.6E−02 n=2 fg=0.06 bg=0.01
cortical cytoskeleton GO:0030863 p=2.6E−02 n=2 fg=0.06 bg=0.01
secretory vesicle GO:0099503 p=2.6E−02 n=6 fg=0.19 bg=0.08
early endosome GO:0005769 p=2.8E−02 n=4 fg=0.13 bg=0.04
extrinsic component of membrane GO:0019898 p=3.3E−02 n=3 fg=0.10 bg=0.02
cytoplasmic side of plasma membrane GO:0009898 p=3.3E−02 n=3 fg=0.10 bg=0.02
sarcoplasmic reticulum membrane GO:0033017 p=3.4E−02 n=1 fg=0.03 bg=0.00
presynaptic cytoskeleton GO:0099569 p=3.4E−02 n=1 fg=0.03 bg=0.00
IkappaB kinase complex GO:0008385 p=3.4E−02 n=1 fg=0.03 bg=0.00
nuclear stress granule GO:0097165 p=3.4E−02 n=1 fg=0.03 bg=0.00
intrinsic component of vacuolar membrane GO:0031310 p=3.4E−02 n=1 fg=0.03 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=3.4E−02 n=1 fg=0.03 bg=0.00
Nebenkern GO:0016006 p=3.4E−02 n=1 fg=0.03 bg=0.00
mitochondrial derivative GO:0016007 p=3.4E−02 n=1 fg=0.03 bg=0.00
integral component of vacuolar membrane GO:0031166 p=3.4E−02 n=1 fg=0.03 bg=0.00
cell cortex region GO:0099738 p=3.7E−02 n=2 fg=0.06 bg=0.01
ruffle GO:0001726 p=3.7E−02 n=2 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=31/97 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction