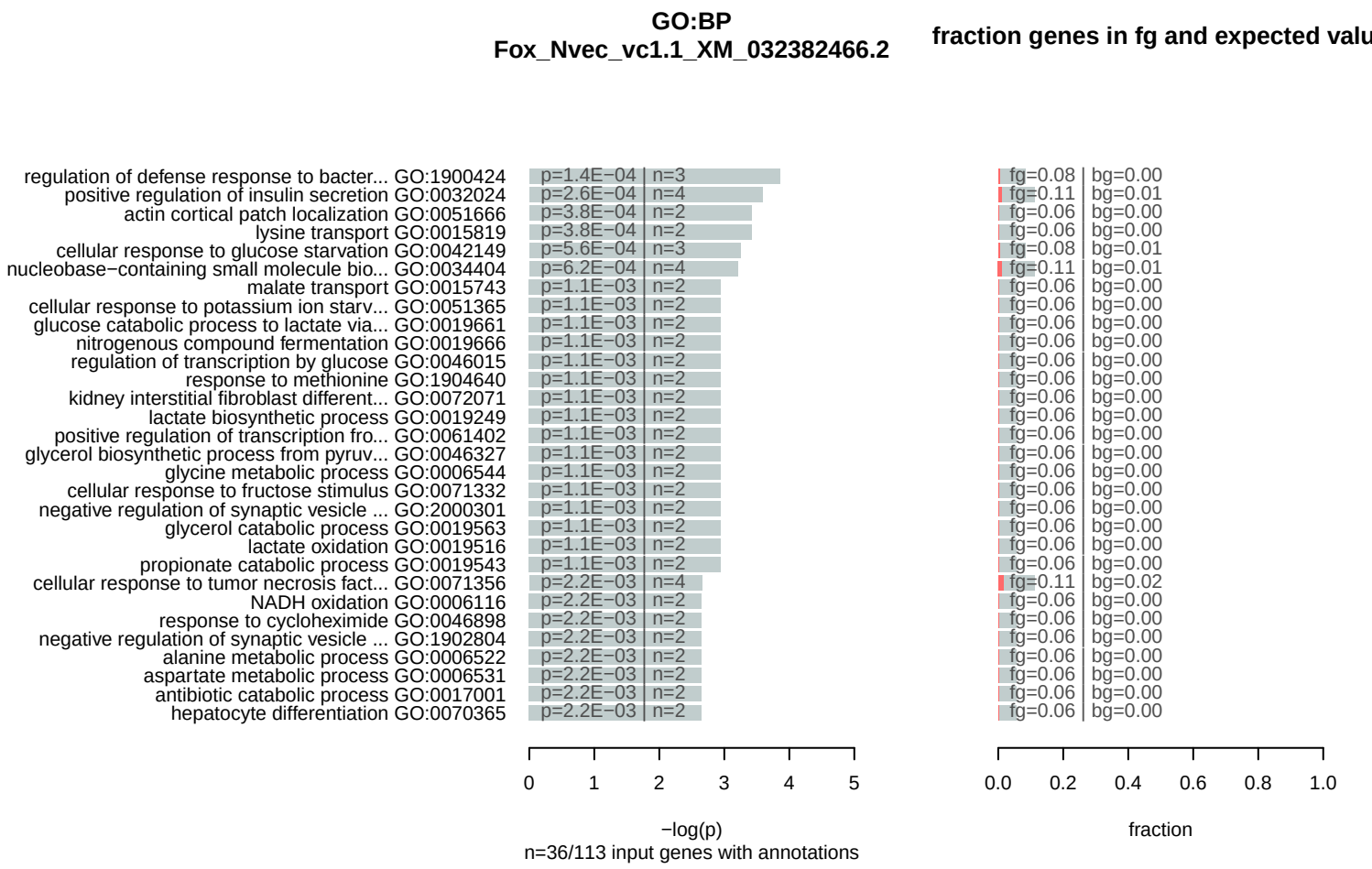
GO:BP
Fox_Nvec_vc1.1_XM_032382466.2
fraction genes in fg and expected valu
regulation of defense response to bacter... GO:1900424 p=1.4E−04 n=3 fg=0.08 bg=0.00
positive regulation of insulin secretion GO:0032024 p=2.6E−04 n=4 fg=0.11 bg=0.01
actin cortical patch localization GO:0051666 p=3.8E−04 n=2 fg=0.06 bg=0.00
lysine transport GO:0015819 p=3.8E−04 n=2 fg=0.06 bg=0.00
cellular response to glucose starvation GO:0042149 p=5.6E−04 n=3 fg=0.08 bg=0.01
nucleobase−containing small molecule bio... GO:0034404 p=6.2E−04 n=4 fg=0.11 bg=0.01
malate transport GO:0015743 p=1.1E−03 n=2 fg=0.06 bg=0.00
cellular response to potassium ion starv... GO:0051365 p=1.1E−03 n=2 fg=0.06 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=1.1E−03 n=2 fg=0.06 bg=0.00
nitrogenous compound fermentation GO:0019666 p=1.1E−03 n=2 fg=0.06 bg=0.00
regulation of transcription by glucose GO:0046015 p=1.1E−03 n=2 fg=0.06 bg=0.00
response to methionine GO:1904640 p=1.1E−03 n=2 fg=0.06 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=1.1E−03 n=2 fg=0.06 bg=0.00
lactate biosynthetic process GO:0019249 p=1.1E−03 n=2 fg=0.06 bg=0.00
positive regulation of transcription fro... GO:0061402 p=1.1E−03 n=2 fg=0.06 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=1.1E−03 n=2 fg=0.06 bg=0.00
glycine metabolic process GO:0006544 p=1.1E−03 n=2 fg=0.06 bg=0.00
cellular response to fructose stimulus GO:0071332 p=1.1E−03 n=2 fg=0.06 bg=0.00
negative regulation of synaptic vesicle ... GO:2000301 p=1.1E−03 n=2 fg=0.06 bg=0.00
glycerol catabolic process GO:0019563 p=1.1E−03 n=2 fg=0.06 bg=0.00
lactate oxidation GO:0019516 p=1.1E−03 n=2 fg=0.06 bg=0.00
propionate catabolic process GO:0019543 p=1.1E−03 n=2 fg=0.06 bg=0.00
cellular response to tumor necrosis fact... GO:0071356 p=2.2E−03 n=4 fg=0.11 bg=0.02
NADH oxidation GO:0006116 p=2.2E−03 n=2 fg=0.06 bg=0.00
response to cycloheximide GO:0046898 p=2.2E−03 n=2 fg=0.06 bg=0.00
negative regulation of synaptic vesicle ... GO:1902804 p=2.2E−03 n=2 fg=0.06 bg=0.00
alanine metabolic process GO:0006522 p=2.2E−03 n=2 fg=0.06 bg=0.00
aspartate metabolic process GO:0006531 p=2.2E−03 n=2 fg=0.06 bg=0.00
antibiotic catabolic process GO:0017001 p=2.2E−03 n=2 fg=0.06 bg=0.00
hepatocyte differentiation GO:0070365 p=2.2E−03 n=2 fg=0.06 bg=0.00
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−log(p)
n=36/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032382466.2
fraction genes in fg and expected valu
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=1.2E−03 n=2 fg=0.06 bg=0.00
DNA binding domain binding GO:0050692 p=1.2E−03 n=2 fg=0.06 bg=0.00
lactate dehydrogenase activity GO:0004457 p=1.2E−03 n=2 fg=0.06 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=1.2E−03 n=2 fg=0.06 bg=0.00
inosine kinase activity GO:0008906 p=1.2E−03 n=2 fg=0.06 bg=0.00
GTP binding GO:0005525 p=2.2E−03 n=4 fg=0.12 bg=0.02
purine ribonucleoside binding GO:0032550 p=2.2E−03 n=4 fg=0.12 bg=0.02
nucleoside diphosphate kinase activity GO:0004550 p=2.3E−03 n=2 fg=0.06 bg=0.00
protein−macromolecule adaptor activity GO:0030674 p=2.4E−03 n=5 fg=0.16 bg=0.03
epinephrine binding GO:0051379 p=3.8E−03 n=2 fg=0.06 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=7.7E−03 n=2 fg=0.06 bg=0.00
GDP binding GO:0019003 p=1.6E−02 n=2 fg=0.06 bg=0.01
nuclease inhibitor activity GO:0140721 p=2.0E−02 n=1 fg=0.03 bg=0.00
adipokinetic hormone receptor activity GO:0097003 p=2.0E−02 n=1 fg=0.03 bg=0.00
adiponectin binding GO:0055100 p=2.0E−02 n=1 fg=0.03 bg=0.00
interleukin−5 receptor binding GO:0005137 p=2.0E−02 n=1 fg=0.03 bg=0.00
protein−membrane adaptor activity GO:0043495 p=2.0E−02 n=1 fg=0.03 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.0E−02 n=1 fg=0.03 bg=0.00
endoribonuclease inhibitor activity GO:0060698 p=2.0E−02 n=1 fg=0.03 bg=0.00
AMP deaminase activity GO:0003876 p=2.0E−02 n=1 fg=0.03 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=2.0E−02 n=1 fg=0.03 bg=0.00
ribonuclease inhibitor activity GO:0008428 p=2.0E−02 n=1 fg=0.03 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=2.0E−02 n=1 fg=0.03 bg=0.00
GMP binding GO:0019002 p=2.0E−02 n=1 fg=0.03 bg=0.00
identical protein binding GO:0042802 p=3.1E−02 n=10 fg=0.31 bg=0.17
protein heterodimerization activity GO:0046982 p=3.4E−02 n=5 fg=0.16 bg=0.06
protein N−terminus binding GO:0047485 p=3.5E−02 n=2 fg=0.06 bg=0.01
actin filament binding GO:0051015 p=3.5E−02 n=2 fg=0.06 bg=0.01
manganese ion binding GO:0030145 p=3.5E−02 n=2 fg=0.06 bg=0.01
calcium−dependent protein kinase regulat... GO:0010858 p=4.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=32/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032382466.2
fraction genes in fg and expected valu
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=4.1E−04 n=4 fg=0.12 bg=0.01
COPII−coated ER to Golgi transport vesic... GO:0030134 p=1.5E−03 n=3 fg=0.09 bg=0.01
fungal−type vacuole membrane GO:0000329 p=2.0E−03 n=2 fg=0.06 bg=0.00
cell tip GO:0051286 p=2.0E−03 n=2 fg=0.06 bg=0.00
cell division site GO:0032153 p=2.4E−03 n=3 fg=0.09 bg=0.01
cis−Golgi network GO:0005801 p=2.9E−03 n=3 fg=0.09 bg=0.01
integral component of endoplasmic reticu... GO:0030176 p=6.4E−03 n=4 fg=0.12 bg=0.02
endoplasmic reticulum−Golgi intermediate... GO:0033116 p=1.1E−02 n=2 fg=0.06 bg=0.01
dense core granule GO:0031045 p=1.9E−02 n=1 fg=0.03 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=1.9E−02 n=1 fg=0.03 bg=0.00
dense core granule membrane GO:0032127 p=1.9E−02 n=1 fg=0.03 bg=0.00
actin cortical patch GO:0030479 p=1.9E−02 n=1 fg=0.03 bg=0.00
microvesicle GO:1990742 p=1.9E−02 n=1 fg=0.03 bg=0.00
endocytic patch GO:0061645 p=1.9E−02 n=1 fg=0.03 bg=0.00
interleukin−5 receptor complex GO:0005895 p=1.9E−02 n=1 fg=0.03 bg=0.00
transport vesicle membrane GO:0030658 p=1.9E−02 n=3 fg=0.09 bg=0.02
cytoplasm GO:0005737 p=2.0E−02 n=33 fg=0.97 bg=0.80
lytic vacuole GO:0000323 p=2.5E−02 n=7 fg=0.21 bg=0.06
Golgi−associated vesicle GO:0005798 p=2.8E−02 n=3 fg=0.09 bg=0.02
intrinsic component of membrane GO:0031224 p=3.0E−02 n=13 fg=0.38 bg=0.17
actin−based cell projection GO:0098858 p=3.0E−02 n=3 fg=0.09 bg=0.02
lysosome GO:0005764 p=3.1E−02 n=5 fg=0.15 bg=0.05
extracellular vesicle GO:1903561 p=3.5E−02 n=2 fg=0.06 bg=0.01
extracellular membrane−bounded organelle GO:0065010 p=3.5E−02 n=2 fg=0.06 bg=0.01
extracellular organelle GO:0043230 p=3.5E−02 n=2 fg=0.06 bg=0.01
filopodium GO:0030175 p=3.5E−02 n=2 fg=0.06 bg=0.01
preribosome, small subunit precursor GO:0030688 p=3.7E−02 n=1 fg=0.03 bg=0.00
early phagosome GO:0032009 p=3.7E−02 n=1 fg=0.03 bg=0.00
phagophore assembly site membrane GO:0034045 p=3.7E−02 n=1 fg=0.03 bg=0.00
U2AF complex GO:0089701 p=3.7E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=34/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction