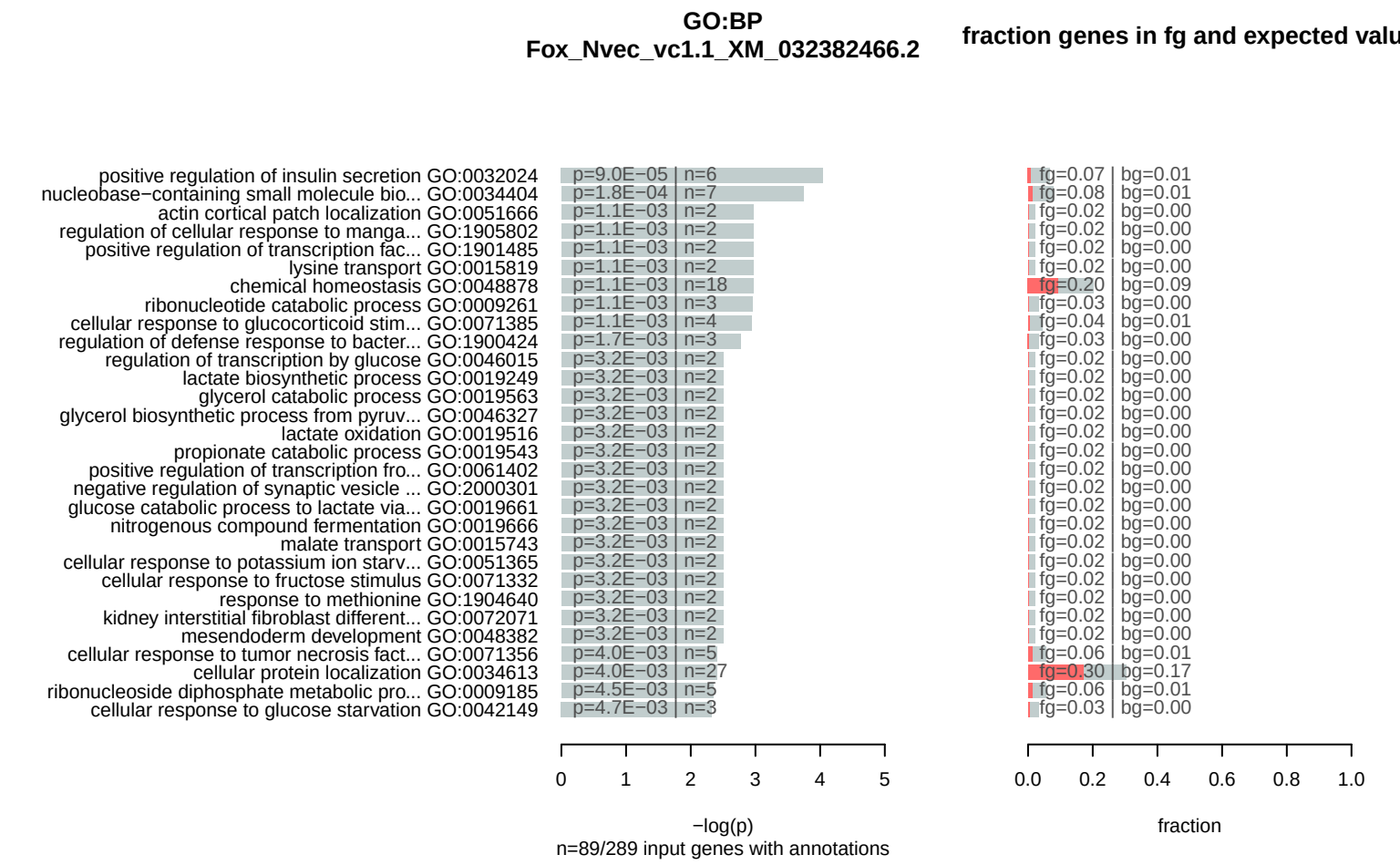
GO:BP
Fox_Nvec_vc1.1_XM_032382466.2
fraction genes in fg and expected valu
positive regulation of insulin secretion GO:0032024 p=9.0E−05 n=6 fg=0.07 bg=0.01
nucleobase−containing small molecule bio... GO:0034404 p=1.8E−04 n=7 fg=0.08 bg=0.01
actin cortical patch localization GO:0051666 p=1.1E−03 n=2 fg=0.02 bg=0.00
regulation of cellular response to manga... GO:1905802 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of transcription fac... GO:1901485 p=1.1E−03 n=2 fg=0.02 bg=0.00
lysine transport GO:0015819 p=1.1E−03 n=2 fg=0.02 bg=0.00
chemical homeostasis GO:0048878 p=1.1E−03 n=18 fg=0.20 bg=0.09
ribonucleotide catabolic process GO:0009261 p=1.1E−03 n=3 fg=0.03 bg=0.00
cellular response to glucocorticoid stim... GO:0071385 p=1.1E−03 n=4 fg=0.04 bg=0.01
regulation of defense response to bacter... GO:1900424 p=1.7E−03 n=3 fg=0.03 bg=0.00
regulation of transcription by glucose GO:0046015 p=3.2E−03 n=2 fg=0.02 bg=0.00
lactate biosynthetic process GO:0019249 p=3.2E−03 n=2 fg=0.02 bg=0.00
glycerol catabolic process GO:0019563 p=3.2E−03 n=2 fg=0.02 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=3.2E−03 n=2 fg=0.02 bg=0.00
lactate oxidation GO:0019516 p=3.2E−03 n=2 fg=0.02 bg=0.00
propionate catabolic process GO:0019543 p=3.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of transcription fro... GO:0061402 p=3.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of synaptic vesicle ... GO:2000301 p=3.2E−03 n=2 fg=0.02 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=3.2E−03 n=2 fg=0.02 bg=0.00
nitrogenous compound fermentation GO:0019666 p=3.2E−03 n=2 fg=0.02 bg=0.00
malate transport GO:0015743 p=3.2E−03 n=2 fg=0.02 bg=0.00
cellular response to potassium ion starv... GO:0051365 p=3.2E−03 n=2 fg=0.02 bg=0.00
cellular response to fructose stimulus GO:0071332 p=3.2E−03 n=2 fg=0.02 bg=0.00
response to methionine GO:1904640 p=3.2E−03 n=2 fg=0.02 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=3.2E−03 n=2 fg=0.02 bg=0.00
mesendoderm development GO:0048382 p=3.2E−03 n=2 fg=0.02 bg=0.00
cellular response to tumor necrosis fact... GO:0071356 p=4.0E−03 n=5 fg=0.06 bg=0.01
cellular protein localization GO:0034613 p=4.0E−03 n=27 fg=0.30 bg=0.17
ribonucleoside diphosphate metabolic pro... GO:0009185 p=4.5E−03 n=5 fg=0.06 bg=0.01
cellular response to glucose starvation GO:0042149 p=4.7E−03 n=3 fg=0.03 bg=0.00
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−log(p)
n=89/289 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
GTP binding GO:0005525 p=3.1E−03 n=6 fg=0.07 bg=0.02
oxidoreductase activity, acting on the C... GO:0016899 p=3.3E−03 n=2 fg=0.03 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=3.3E−03 n=2 fg=0.03 bg=0.00
inosine kinase activity GO:0008906 p=3.3E−03 n=2 fg=0.03 bg=0.00
purine ribonucleoside binding GO:0032550 p=3.9E−03 n=6 fg=0.07 bg=0.02
DNA binding domain binding GO:0050692 p=6.5E−03 n=2 fg=0.03 bg=0.00
lactate dehydrogenase activity GO:0004457 p=6.5E−03 n=2 fg=0.03 bg=0.00
nucleobase−containing compound kinase ac... GO:0019205 p=6.5E−03 n=3 fg=0.04 bg=0.01
epinephrine binding GO:0051379 p=1.1E−02 n=2 fg=0.03 bg=0.00
poly(A) binding GO:0008143 p=1.1E−02 n=2 fg=0.03 bg=0.00
nucleoside diphosphate kinase activity GO:0004550 p=1.1E−02 n=2 fg=0.03 bg=0.00
catecholamine binding GO:1901338 p=1.1E−02 n=2 fg=0.03 bg=0.00
single−stranded RNA binding GO:0003727 p=1.2E−02 n=4 fg=0.05 bg=0.01
poly−purine tract binding GO:0070717 p=1.5E−02 n=2 fg=0.03 bg=0.00
protein binding GO:0005515 p=1.8E−02 n=57 fg=0.71 bg=0.59
p53 binding GO:0002039 p=1.8E−02 n=3 fg=0.04 bg=0.01
cytoskeletal protein binding GO:0008092 p=2.2E−02 n=12 fg=0.15 bg=0.08
4−hydroxy−2−oxoglutarate aldolase activi... GO:0008700 p=3.4E−02 n=1 fg=0.01 bg=0.00
adiponectin binding GO:0055100 p=3.4E−02 n=1 fg=0.01 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=3.4E−02 n=1 fg=0.01 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=3.4E−02 n=1 fg=0.01 bg=0.00
SUMO polymer binding GO:0032184 p=3.4E−02 n=1 fg=0.01 bg=0.00
protein−membrane adaptor activity GO:0043495 p=3.4E−02 n=1 fg=0.01 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=3.4E−02 n=1 fg=0.01 bg=0.00
uridine−diphosphatase activity GO:0045134 p=3.4E−02 n=1 fg=0.01 bg=0.00
histone deacetylase regulator activity GO:0035033 p=3.4E−02 n=1 fg=0.01 bg=0.00
AMP deaminase activity GO:0003876 p=3.4E−02 n=1 fg=0.01 bg=0.00
inorganic phosphate transmembrane transp... GO:0005315 p=3.4E−02 n=1 fg=0.01 bg=0.00
nuclear progesterone receptor binding GO:0033142 p=3.4E−02 n=1 fg=0.01 bg=0.00
high−affinity inorganic phosphate:sodium... GO:0005316 p=3.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=80/289 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
cis−Golgi network GO:0005801 p=3.0E−03 n=4 fg=0.04 bg=0.01
cell division site GO:0032153 p=3.0E−03 n=4 fg=0.04 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=4.8E−03 n=14 fg=0.16 bg=0.07
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=6.3E−03 n=4 fg=0.04 bg=0.01
fungal−type vacuole GO:0000324 p=1.0E−02 n=2 fg=0.02 bg=0.00
fungal−type vacuole membrane GO:0000329 p=1.0E−02 n=2 fg=0.02 bg=0.00
dendrite cytoplasm GO:0032839 p=1.0E−02 n=2 fg=0.02 bg=0.00
COPII−coated ER to Golgi transport vesic... GO:0030134 p=1.2E−02 n=3 fg=0.03 bg=0.01
cell tip GO:0051286 p=1.5E−02 n=2 fg=0.02 bg=0.00
plasma membrane bounded cell projection ... GO:0032838 p=1.6E−02 n=5 fg=0.06 bg=0.02
lytic vacuole GO:0000323 p=2.1E−02 n=9 fg=0.10 bg=0.05
storage vacuole GO:0000322 p=2.1E−02 n=2 fg=0.02 bg=0.00
cell pole GO:0060187 p=2.1E−02 n=2 fg=0.02 bg=0.00
integral component of endoplasmic reticu... GO:0030176 p=3.2E−02 n=5 fg=0.06 bg=0.02
microvesicle GO:1990742 p=3.3E−02 n=1 fg=0.01 bg=0.00
AMPA glutamate receptor complex GO:0032281 p=3.3E−02 n=1 fg=0.01 bg=0.00
intrinsic component of autophagosome mem... GO:0097636 p=3.3E−02 n=1 fg=0.01 bg=0.00
integral component of autophagosome memb... GO:0097637 p=3.3E−02 n=1 fg=0.01 bg=0.00
endocytic patch GO:0061645 p=3.3E−02 n=1 fg=0.01 bg=0.00
centralspindlin complex GO:0097149 p=3.3E−02 n=1 fg=0.01 bg=0.00
dense core granule membrane GO:0032127 p=3.3E−02 n=1 fg=0.01 bg=0.00
actin cortical patch GO:0030479 p=3.3E−02 n=1 fg=0.01 bg=0.00
interleukin−5 receptor complex GO:0005895 p=3.3E−02 n=1 fg=0.01 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=3.3E−02 n=1 fg=0.01 bg=0.00
stereocilia ankle link GO:0002141 p=3.3E−02 n=1 fg=0.01 bg=0.00
stereocilia ankle link complex GO:0002142 p=3.3E−02 n=1 fg=0.01 bg=0.00
stereocilia coupling link GO:0002139 p=3.3E−02 n=1 fg=0.01 bg=0.00
SUMO−targeted ubiquitin ligase complex GO:0033768 p=3.3E−02 n=1 fg=0.01 bg=0.00
USH2 complex GO:1990696 p=3.3E−02 n=1 fg=0.01 bg=0.00
DSIF complex GO:0032044 p=3.3E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=90/289 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction