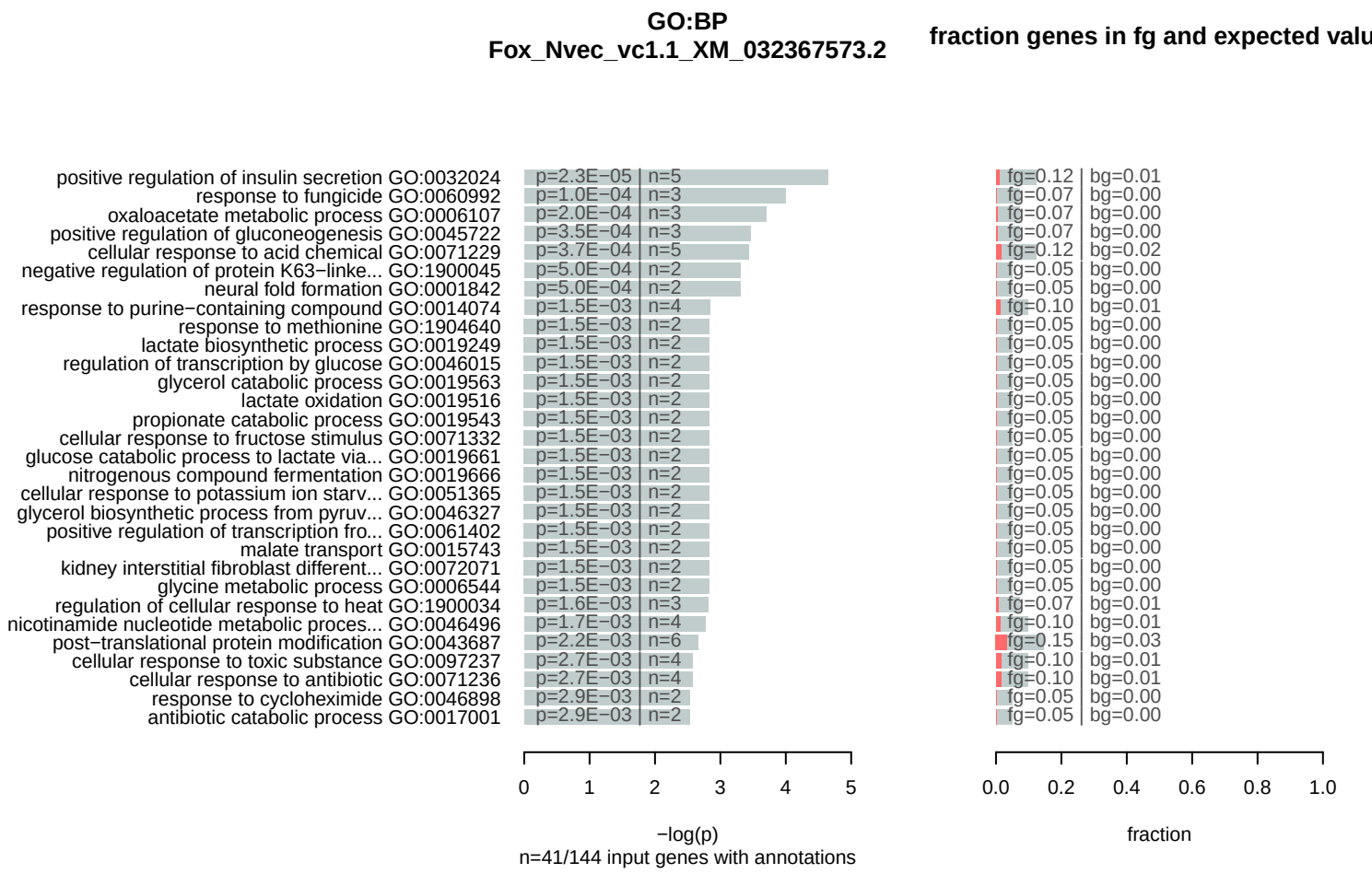
GO:BP
Fox_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
positive regulation of insulin secretion GO:0032024 p=2.3E−05 n=5 fg=0.12 bg=0.01
response to fungicide GO:0060992 p=1.0E−04 n=3 fg=0.07 bg=0.00
oxaloacetate metabolic process GO:0006107 p=2.0E−04 n=3 fg=0.07 bg=0.00
positive regulation of gluconeogenesis GO:0045722 p=3.5E−04 n=3 fg=0.07 bg=0.00
cellular response to acid chemical GO:0071229 p=3.7E−04 n=5 fg=0.12 bg=0.02
negative regulation of protein K63−linke... GO:1900045 p=5.0E−04 n=2 fg=0.05 bg=0.00
neural fold formation GO:0001842 p=5.0E−04 n=2 fg=0.05 bg=0.00
response to purine−containing compound GO:0014074 p=1.5E−03 n=4 fg=0.10 bg=0.01
response to methionine GO:1904640 p=1.5E−03 n=2 fg=0.05 bg=0.00
lactate biosynthetic process GO:0019249 p=1.5E−03 n=2 fg=0.05 bg=0.00
regulation of transcription by glucose GO:0046015 p=1.5E−03 n=2 fg=0.05 bg=0.00
glycerol catabolic process GO:0019563 p=1.5E−03 n=2 fg=0.05 bg=0.00
lactate oxidation GO:0019516 p=1.5E−03 n=2 fg=0.05 bg=0.00
propionate catabolic process GO:0019543 p=1.5E−03 n=2 fg=0.05 bg=0.00
cellular response to fructose stimulus GO:0071332 p=1.5E−03 n=2 fg=0.05 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=1.5E−03 n=2 fg=0.05 bg=0.00
nitrogenous compound fermentation GO:0019666 p=1.5E−03 n=2 fg=0.05 bg=0.00
cellular response to potassium ion starv... GO:0051365 p=1.5E−03 n=2 fg=0.05 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=1.5E−03 n=2 fg=0.05 bg=0.00
positive regulation of transcription fro... GO:0061402 p=1.5E−03 n=2 fg=0.05 bg=0.00
malate transport GO:0015743 p=1.5E−03 n=2 fg=0.05 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=1.5E−03 n=2 fg=0.05 bg=0.00
glycine metabolic process GO:0006544 p=1.5E−03 n=2 fg=0.05 bg=0.00
regulation of cellular response to heat GO:1900034 p=1.6E−03 n=3 fg=0.07 bg=0.01
nicotinamide nucleotide metabolic proces... GO:0046496 p=1.7E−03 n=4 fg=0.10 bg=0.01
post−translational protein modification GO:0043687 p=2.2E−03 n=6 fg=0.15 bg=0.03
cellular response to toxic substance GO:0097237 p=2.7E−03 n=4 fg=0.10 bg=0.01
cellular response to antibiotic GO:0071236 p=2.7E−03 n=4 fg=0.10 bg=0.01
response to cycloheximide GO:0046898 p=2.9E−03 n=2 fg=0.05 bg=0.00
antibiotic catabolic process GO:0017001 p=2.9E−03 n=2 fg=0.05 bg=0.00
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−log(p)
n=41/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
GTP binding GO:0005525 p=5.2E−04 n=5 fg=0.13 bg=0.02
purine ribonucleoside binding GO:0032550 p=5.2E−04 n=5 fg=0.13 bg=0.02
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=1.7E−03 n=2 fg=0.05 bg=0.00
DNA binding domain binding GO:0050692 p=1.7E−03 n=2 fg=0.05 bg=0.00
lactate dehydrogenase activity GO:0004457 p=1.7E−03 n=2 fg=0.05 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=1.7E−03 n=2 fg=0.05 bg=0.00
inosine kinase activity GO:0008906 p=1.7E−03 n=2 fg=0.05 bg=0.00
nucleoside diphosphate kinase activity GO:0004550 p=3.4E−03 n=2 fg=0.05 bg=0.00
epinephrine binding GO:0051379 p=5.6E−03 n=2 fg=0.05 bg=0.00
heat shock protein binding GO:0031072 p=7.6E−03 n=4 fg=0.10 bg=0.02
oxidoreductase activity, acting on a sul... GO:0016668 p=1.1E−02 n=2 fg=0.05 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=1.1E−02 n=2 fg=0.05 bg=0.00
calmodulin binding GO:0005516 p=1.3E−02 n=3 fg=0.08 bg=0.01
protein−disulfide reductase activity GO:0015035 p=1.9E−02 n=2 fg=0.05 bg=0.01
GDP binding GO:0019003 p=2.3E−02 n=2 fg=0.05 bg=0.01
ribokinase activity GO:0004747 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−malate dehydrogenase activity GO:0030060 p=2.5E−02 n=1 fg=0.03 bg=0.00
cobalt ion binding GO:0050897 p=2.5E−02 n=1 fg=0.03 bg=0.00
ATP−gated ion channel activity GO:0035381 p=2.5E−02 n=1 fg=0.03 bg=0.00
interferon binding GO:0019961 p=2.5E−02 n=1 fg=0.03 bg=0.00
interferon−gamma binding GO:0019964 p=2.5E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.5E−02 n=1 fg=0.03 bg=0.00
extracellularly ATP−gated cation channel... GO:0004931 p=2.5E−02 n=1 fg=0.03 bg=0.00
purinergic nucleotide receptor activity GO:0001614 p=2.5E−02 n=1 fg=0.03 bg=0.00
alkylglycerophosphoethanolamine phosphod... GO:0047391 p=2.5E−02 n=1 fg=0.03 bg=0.00
nucleotide receptor activity GO:0016502 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphatidyl−N−methylethanolamine N−meth... GO:0000773 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphatidyl−N−dimethylethanolamine N−me... GO:0080101 p=2.5E−02 n=1 fg=0.03 bg=0.00
GMP binding GO:0019002 p=2.5E−02 n=1 fg=0.03 bg=0.00
ATPase regulator activity GO:0060590 p=2.8E−02 n=2 fg=0.05 bg=0.01
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−log(p)
n=39/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
transcription repressor complex GO:0017053 p=2.5E−03 n=3 fg=0.07 bg=0.01
specific granule membrane GO:0035579 p=3.1E−03 n=3 fg=0.07 bg=0.01
ficolin−1−rich granule membrane GO:0101003 p=6.8E−03 n=2 fg=0.05 bg=0.00
PML body GO:0016605 p=9.3E−03 n=2 fg=0.05 bg=0.00
azurophil granule membrane GO:0035577 p=1.2E−02 n=2 fg=0.05 bg=0.00
azurophil granule GO:0042582 p=1.5E−02 n=3 fg=0.07 bg=0.01
primary lysosome GO:0005766 p=1.5E−02 n=3 fg=0.07 bg=0.01
multivesicular body GO:0005771 p=1.6E−02 n=2 fg=0.05 bg=0.01
melanosome GO:0042470 p=1.6E−02 n=2 fg=0.05 bg=0.01
pigment granule GO:0048770 p=1.9E−02 n=2 fg=0.05 bg=0.01
presynapse GO:0098793 p=1.9E−02 n=6 fg=0.15 bg=0.05
phagolysosome membrane GO:0061474 p=2.2E−02 n=1 fg=0.03 bg=0.00
phagolysosome GO:0032010 p=2.2E−02 n=1 fg=0.03 bg=0.00
alveolar lamellar body GO:0097208 p=2.2E−02 n=1 fg=0.03 bg=0.00
SMC loading complex GO:0032116 p=2.2E−02 n=1 fg=0.03 bg=0.00
Scc2−Scc4 cohesin loading complex GO:0090694 p=2.2E−02 n=1 fg=0.03 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=2.3E−02 n=7 fg=0.17 bg=0.07
cytosol GO:0005829 p=2.7E−02 n=22 fg=0.55 bg=0.39
exocytic vesicle GO:0070382 p=3.1E−02 n=4 fg=0.10 bg=0.03
synapse GO:0045202 p=3.8E−02 n=8 fg=0.20 bg=0.10
cytosolic region GO:0099522 p=4.4E−02 n=1 fg=0.03 bg=0.00
postsynaptic cytosol GO:0099524 p=4.4E−02 n=1 fg=0.03 bg=0.00
NELF complex GO:0032021 p=4.4E−02 n=1 fg=0.03 bg=0.00
photoreceptor outer segment membrane GO:0042622 p=4.4E−02 n=1 fg=0.03 bg=0.00
intrinsic component of nuclear inner mem... GO:0031229 p=4.4E−02 n=1 fg=0.03 bg=0.00
phagophore assembly site membrane GO:0034045 p=4.4E−02 n=1 fg=0.03 bg=0.00
oligosaccharyltransferase complex GO:0008250 p=4.4E−02 n=1 fg=0.03 bg=0.00
nuclear stress granule GO:0097165 p=4.4E−02 n=1 fg=0.03 bg=0.00
integral component of nuclear inner memb... GO:0005639 p=4.4E−02 n=1 fg=0.03 bg=0.00
postsynaptic density GO:0014069 p=5.0E−02 n=3 fg=0.07 bg=0.02
0 1 2 3 4 5
−log(p)
n=40/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction