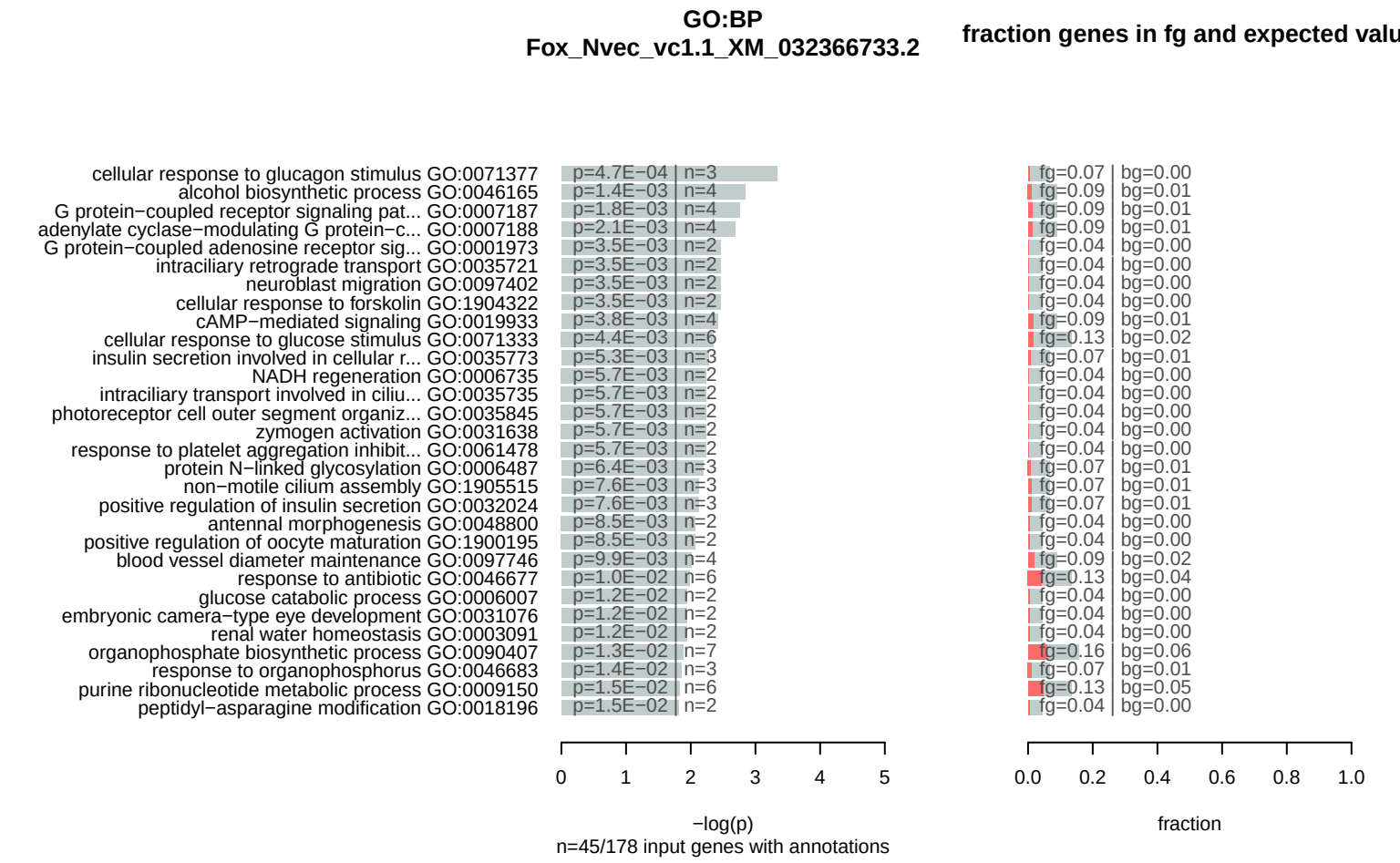
GO:BP
Fox_Nvec_vc1.1_XM_032366733.2
fraction genes in fg and expected valu
cellular response to glucagon stimulus GO:0071377 p=4.7E−04 n=3 fg=0.07 bg=0.00
alcohol biosynthetic process GO:0046165 p=1.4E−03 n=4 fg=0.09 bg=0.01
G protein−coupled receptor signaling pat... GO:0007187 p=1.8E−03 n=4 fg=0.09 bg=0.01
adenylate cyclase−modulating G protein−c... GO:0007188 p=2.1E−03 n=4 fg=0.09 bg=0.01
G protein−coupled adenosine receptor sig... GO:0001973 p=3.5E−03 n=2 fg=0.04 bg=0.00
intraciliary retrograde transport GO:0035721 p=3.5E−03 n=2 fg=0.04 bg=0.00
neuroblast migration GO:0097402 p=3.5E−03 n=2 fg=0.04 bg=0.00
cellular response to forskolin GO:1904322 p=3.5E−03 n=2 fg=0.04 bg=0.00
cAMP−mediated signaling GO:0019933 p=3.8E−03 n=4 fg=0.09 bg=0.01
cellular response to glucose stimulus GO:0071333 p=4.4E−03 n=6 fg=0.13 bg=0.02
insulin secretion involved in cellular r... GO:0035773 p=5.3E−03 n=3 fg=0.07 bg=0.01
NADH regeneration GO:0006735 p=5.7E−03 n=2 fg=0.04 bg=0.00
intraciliary transport involved in ciliu... GO:0035735 p=5.7E−03 n=2 fg=0.04 bg=0.00
photoreceptor cell outer segment organiz... GO:0035845 p=5.7E−03 n=2 fg=0.04 bg=0.00
zymogen activation GO:0031638 p=5.7E−03 n=2 fg=0.04 bg=0.00
response to platelet aggregation inhibit... GO:0061478 p=5.7E−03 n=2 fg=0.04 bg=0.00
protein N−linked glycosylation GO:0006487 p=6.4E−03 n=3 fg=0.07 bg=0.01
non−motile cilium assembly GO:1905515 p=7.6E−03 n=3 fg=0.07 bg=0.01
positive regulation of insulin secretion GO:0032024 p=7.6E−03 n=3 fg=0.07 bg=0.01
antennal morphogenesis GO:0048800 p=8.5E−03 n=2 fg=0.04 bg=0.00
positive regulation of oocyte maturation GO:1900195 p=8.5E−03 n=2 fg=0.04 bg=0.00
blood vessel diameter maintenance GO:0097746 p=9.9E−03 n=4 fg=0.09 bg=0.02
response to antibiotic GO:0046677 p=1.0E−02 n=6 fg=0.13 bg=0.04
glucose catabolic process GO:0006007 p=1.2E−02 n=2 fg=0.04 bg=0.00
embryonic camera−type eye development GO:0031076 p=1.2E−02 n=2 fg=0.04 bg=0.00
renal water homeostasis GO:0003091 p=1.2E−02 n=2 fg=0.04 bg=0.00
organophosphate biosynthetic process GO:0090407 p=1.3E−02 n=7 fg=0.16 bg=0.06
response to organophosphorus GO:0046683 p=1.4E−02 n=3 fg=0.07 bg=0.01
purine ribonucleotide metabolic process GO:0009150 p=1.5E−02 n=6 fg=0.13 bg=0.05
peptidyl−asparagine modification GO:0018196 p=1.5E−02 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=45/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032366733.2
fraction genes in fg and expected valu
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=6.8E−04 n=3 fg=0.07 bg=0.00
phospholipase C activity GO:0004629 p=4.5E−03 n=2 fg=0.04 bg=0.00
G−protein beta/gamma−subunit complex bin... GO:0031683 p=7.4E−03 n=2 fg=0.04 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0016651 p=1.7E−02 n=3 fg=0.07 bg=0.01
signaling receptor activity GO:0038023 p=1.8E−02 n=6 fg=0.13 bg=0.05
molecular transducer activity GO:0060089 p=1.9E−02 n=6 fg=0.13 bg=0.05
transcription coregulator binding GO:0001221 p=2.5E−02 n=2 fg=0.04 bg=0.01
ecdysis−triggering hormone receptor acti... GO:0042654 p=2.8E−02 n=1 fg=0.02 bg=0.00
UDP−N−acetylglucosamine−dolichyl−phospha... GO:0003975 p=2.8E−02 n=1 fg=0.02 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=2.8E−02 n=1 fg=0.02 bg=0.00
cobalt ion transmembrane transporter act... GO:0015087 p=2.8E−02 n=1 fg=0.02 bg=0.00
thioredoxin−disulfide reductase activity GO:0004791 p=2.8E−02 n=1 fg=0.02 bg=0.00
glycogen binding GO:2001069 p=2.8E−02 n=1 fg=0.02 bg=0.00
calcium− and calmodulin−responsive adeny... GO:0008294 p=2.8E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol phospholipase C act... GO:0004435 p=2.8E−02 n=1 fg=0.02 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=2.8E−02 n=1 fg=0.02 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=2.8E−02 n=1 fg=0.02 bg=0.00
manganese ion transmembrane transporter ... GO:0005384 p=2.8E−02 n=1 fg=0.02 bg=0.00
dolichyl−diphosphooligosaccharide−protei... GO:0004579 p=2.8E−02 n=1 fg=0.02 bg=0.00
selenium binding GO:0008430 p=2.8E−02 n=1 fg=0.02 bg=0.00
neurotrophin TRK receptor binding GO:0005167 p=2.8E−02 n=1 fg=0.02 bg=0.00
netrin receptor activity GO:0005042 p=2.8E−02 n=1 fg=0.02 bg=0.00
neurotrophin TRKA receptor binding GO:0005168 p=2.8E−02 n=1 fg=0.02 bg=0.00
phosphotransferase activity, carboxyl gr... GO:0016774 p=5.6E−02 n=1 fg=0.02 bg=0.00
copper ion transmembrane transporter act... GO:0005375 p=5.6E−02 n=1 fg=0.02 bg=0.00
UDP−N−acetylglucosamine−lysosomal−enzyme... GO:0003976 p=5.6E−02 n=1 fg=0.02 bg=0.00
transcription corepressor binding GO:0001222 p=5.6E−02 n=1 fg=0.02 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=5.6E−02 n=1 fg=0.02 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=5.6E−02 n=1 fg=0.02 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=5.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=45/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032366733.2
fraction genes in fg and expected valu
intraciliary transport particle A GO:0030991 p=2.1E−03 n=2 fg=0.04 bg=0.00
integral component of organelle membrane GO:0031301 p=3.6E−03 n=7 fg=0.14 bg=0.04
ciliary basal body GO:0036064 p=5.3E−03 n=4 fg=0.08 bg=0.01
non−motile cilium GO:0097730 p=9.8E−03 n=4 fg=0.08 bg=0.02
ciliary tip GO:0097542 p=1.4E−02 n=2 fg=0.04 bg=0.00
cilium GO:0005929 p=2.0E−02 n=10 fg=0.20 bg=0.06
intrinsic component of endoplasmic retic... GO:0031227 p=2.3E−02 n=4 fg=0.08 bg=0.02
integral component of endoplasmic reticu... GO:0030176 p=2.3E−02 n=4 fg=0.08 bg=0.02
DNA replication factor C complex GO:0005663 p=2.7E−02 n=1 fg=0.02 bg=0.00
plus−end kinesin complex GO:0005873 p=2.7E−02 n=1 fg=0.02 bg=0.00
synaptic cleft GO:0043083 p=2.7E−02 n=1 fg=0.02 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=2.7E−02 n=1 fg=0.02 bg=0.00
Elg1 RFC−like complex GO:0031391 p=2.7E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum protein−containing... GO:0140534 p=2.8E−02 n=3 fg=0.06 bg=0.01
cell projection membrane GO:0031253 p=3.2E−02 n=5 fg=0.10 bg=0.04
ciliary base GO:0097546 p=3.4E−02 n=2 fg=0.04 bg=0.01
integral component of synaptic vesicle m... GO:0030285 p=3.4E−02 n=2 fg=0.04 bg=0.01
photoreceptor connecting cilium GO:0032391 p=3.4E−02 n=2 fg=0.04 bg=0.01
intrinsic component of synaptic vesicle ... GO:0098563 p=4.0E−02 n=2 fg=0.04 bg=0.01
Barr body GO:0001740 p=5.3E−02 n=1 fg=0.02 bg=0.00
COP9 signalosome GO:0008180 p=5.3E−02 n=1 fg=0.02 bg=0.00
oligosaccharyltransferase complex GO:0008250 p=5.3E−02 n=1 fg=0.02 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=5.3E−02 n=1 fg=0.02 bg=0.00
terminal bouton GO:0043195 p=5.8E−02 n=3 fg=0.06 bg=0.02
early endosome membrane GO:0031901 p=6.8E−02 n=2 fg=0.04 bg=0.01
motile cilium GO:0031514 p=7.1E−02 n=3 fg=0.06 bg=0.02
endoplasmic reticulum membrane GO:0005789 p=7.7E−02 n=7 fg=0.14 bg=0.08
glycogen granule GO:0042587 p=7.9E−02 n=1 fg=0.02 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=7.9E−02 n=1 fg=0.02 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=7.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction