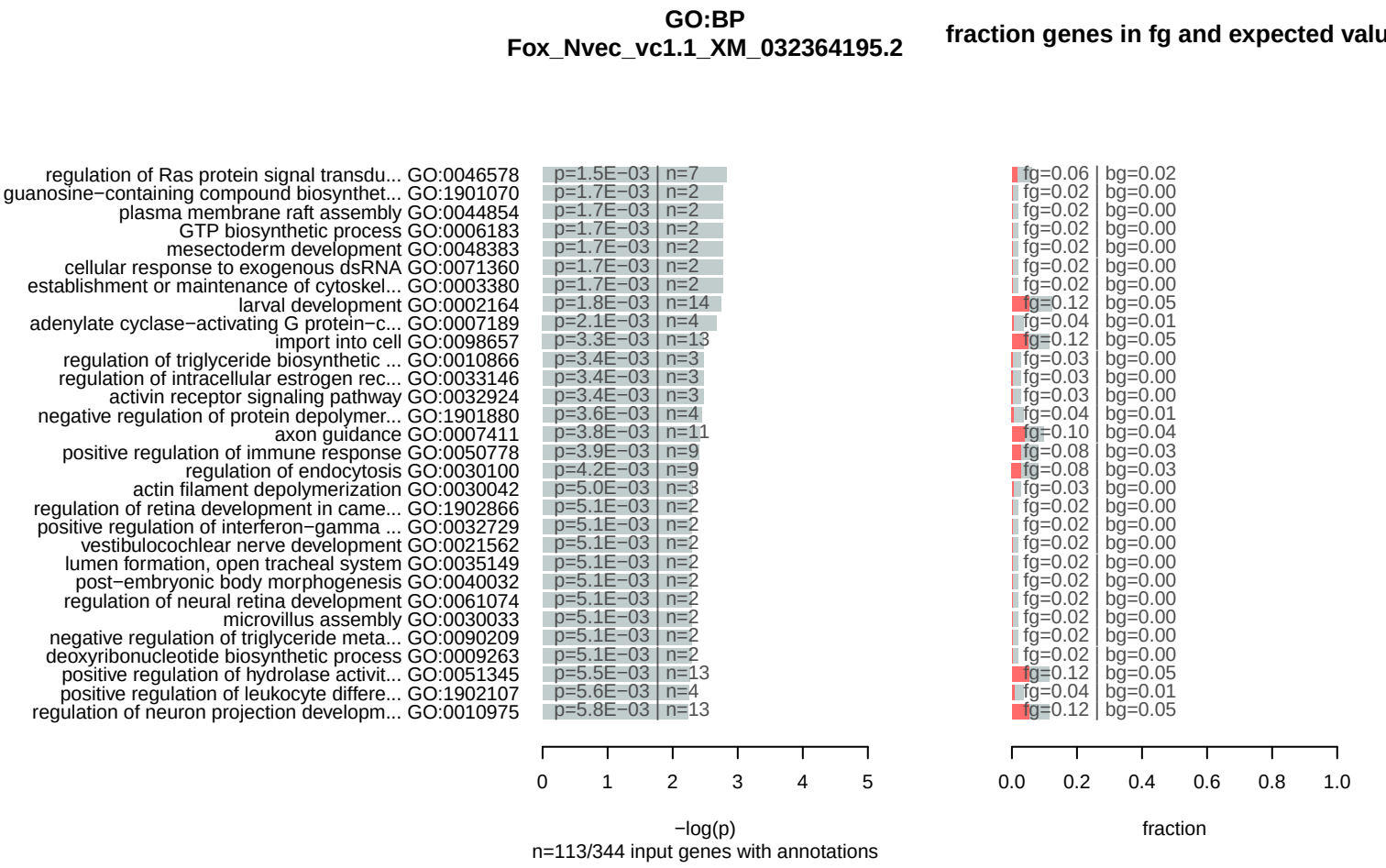
GO:BP
Fox_Nvec_vc1.1_XM_032364195.2
fraction genes in fg and expected valu
regulation of Ras protein signal transdu... GO:0046578 p=1.5E−03 n=7 fg=0.06 bg=0.02
guanosine−containing compound biosynthet... GO:1901070 p=1.7E−03 n=2 fg=0.02 bg=0.00
plasma membrane raft assembly GO:0044854 p=1.7E−03 n=2 fg=0.02 bg=0.00
GTP biosynthetic process GO:0006183 p=1.7E−03 n=2 fg=0.02 bg=0.00
mesectoderm development GO:0048383 p=1.7E−03 n=2 fg=0.02 bg=0.00
cellular response to exogenous dsRNA GO:0071360 p=1.7E−03 n=2 fg=0.02 bg=0.00
establishment or maintenance of cytoskel... GO:0003380 p=1.7E−03 n=2 fg=0.02 bg=0.00
larval development GO:0002164 p=1.8E−03 n=14 fg=0.12 bg=0.05
adenylate cyclase−activating G protein−c... GO:0007189 p=2.1E−03 n=4 fg=0.04 bg=0.01
import into cell GO:0098657 p=3.3E−03 n=13 fg=0.12 bg=0.05
regulation of triglyceride biosynthetic ... GO:0010866 p=3.4E−03 n=3 fg=0.03 bg=0.00
regulation of intracellular estrogen rec... GO:0033146 p=3.4E−03 n=3 fg=0.03 bg=0.00
activin receptor signaling pathway GO:0032924 p=3.4E−03 n=3 fg=0.03 bg=0.00
negative regulation of protein depolymer... GO:1901880 p=3.6E−03 n=4 fg=0.04 bg=0.01
axon guidance GO:0007411 p=3.8E−03 n=11 fg=0.10 bg=0.04
positive regulation of immune response GO:0050778 p=3.9E−03 n=9 fg=0.08 bg=0.03
regulation of endocytosis GO:0030100 p=4.2E−03 n=9 fg=0.08 bg=0.03
actin filament depolymerization GO:0030042 p=5.0E−03 n=3 fg=0.03 bg=0.00
regulation of retina development in came... GO:1902866 p=5.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of interferon−gamma ... GO:0032729 p=5.1E−03 n=2 fg=0.02 bg=0.00
vestibulocochlear nerve development GO:0021562 p=5.1E−03 n=2 fg=0.02 bg=0.00
lumen formation, open tracheal system GO:0035149 p=5.1E−03 n=2 fg=0.02 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=5.1E−03 n=2 fg=0.02 bg=0.00
regulation of neural retina development GO:0061074 p=5.1E−03 n=2 fg=0.02 bg=0.00
microvillus assembly GO:0030033 p=5.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of triglyceride meta... GO:0090209 p=5.1E−03 n=2 fg=0.02 bg=0.00
deoxyribonucleotide biosynthetic process GO:0009263 p=5.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of hydrolase activit... GO:0051345 p=5.5E−03 n=13 fg=0.12 bg=0.05
positive regulation of leukocyte differe... GO:1902107 p=5.6E−03 n=4 fg=0.04 bg=0.01
regulation of neuron projection developm... GO:0010975 p=5.8E−03 n=13 fg=0.12 bg=0.05
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−log(p)
n=113/344 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
phosphatidylcholine binding GO:0031210 p=2.4E−03 n=3 fg=0.03 bg=0.00
ligase activity, forming phosphoric este... GO:0016886 p=5.4E−03 n=2 fg=0.02 bg=0.00
actin binding GO:0003779 p=6.7E−03 n=7 fg=0.07 bg=0.02
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phosphatidylethanolamine binding GO:0008429 p=1.0E−02 n=2 fg=0.02 bg=0.00
microtubule binding GO:0008017 p=1.2E−02 n=7 fg=0.07 bg=0.02
ammonium ion binding GO:0070405 p=1.6E−02 n=3 fg=0.03 bg=0.01
glucosyltransferase activity GO:0046527 p=1.7E−02 n=2 fg=0.02 bg=0.00
signaling receptor binding GO:0005102 p=2.0E−02 n=17 fg=0.17 bg=0.10
actin filament binding GO:0051015 p=2.3E−02 n=4 fg=0.04 bg=0.01
intramembrane lipid transporter activity GO:0140303 p=2.5E−02 n=2 fg=0.02 bg=0.00
BH domain binding GO:0051400 p=2.5E−02 n=2 fg=0.02 bg=0.00
non−membrane spanning protein tyrosine k... GO:0004715 p=3.4E−02 n=2 fg=0.02 bg=0.00
spectrin binding GO:0030507 p=3.4E−02 n=2 fg=0.02 bg=0.00
neuregulin binding GO:0038132 p=4.3E−02 n=1 fg=0.01 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=4.3E−02 n=1 fg=0.01 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=4.3E−02 n=1 fg=0.01 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=4.3E−02 n=1 fg=0.01 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=4.3E−02 n=1 fg=0.01 bg=0.00
interleukin−6 receptor binding GO:0005138 p=4.3E−02 n=1 fg=0.01 bg=0.00
sodium:dicarboxylate symporter activity GO:0017153 p=4.3E−02 n=1 fg=0.01 bg=0.00
MHC protein complex binding GO:0023023 p=4.3E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein complex binding GO:0023025 p=4.3E−02 n=1 fg=0.01 bg=0.00
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glutaminase activity GO:0004359 p=4.3E−02 n=1 fg=0.01 bg=0.00
aminophospholipid flippase activity GO:0015247 p=4.3E−02 n=1 fg=0.01 bg=0.00
alcohol dehydrogenase (NADP+) activity GO:0008106 p=4.3E−02 n=1 fg=0.01 bg=0.00
GABA receptor binding GO:0050811 p=4.3E−02 n=1 fg=0.01 bg=0.00
IMP dehydrogenase activity GO:0003938 p=4.3E−02 n=1 fg=0.01 bg=0.00
MHC class Ib protein binding, via antige... GO:0023030 p=4.3E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=102/344 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032364195.2
fraction genes in fg and expected valu
cell projection membrane GO:0031253 p=1.3E−03 n=12 fg=0.11 bg=0.03
extrinsic component of cytoplasmic side ... GO:0031234 p=1.3E−03 n=5 fg=0.05 bg=0.01
cell leading edge GO:0031252 p=1.6E−03 n=11 fg=0.10 bg=0.04
photoreceptor outer segment membrane GO:0042622 p=1.7E−03 n=2 fg=0.02 bg=0.00
uropod GO:0001931 p=1.7E−03 n=2 fg=0.02 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.7E−03 n=2 fg=0.02 bg=0.00
external side of plasma membrane GO:0009897 p=4.2E−03 n=5 fg=0.05 bg=0.01
clathrin−coated pit GO:0005905 p=4.7E−03 n=3 fg=0.03 bg=0.00
plasma membrane raft GO:0044853 p=6.7E−03 n=5 fg=0.05 bg=0.01
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filamentous actin GO:0031941 p=9.5E−03 n=2 fg=0.02 bg=0.00
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brush border GO:0005903 p=1.3E−02 n=5 fg=0.05 bg=0.01
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sensory dendrite GO:0071683 p=1.5E−02 n=2 fg=0.02 bg=0.00
apical part of cell GO:0045177 p=1.6E−02 n=11 fg=0.10 bg=0.05
mitochondrial outer membrane GO:0005741 p=1.8E−02 n=5 fg=0.05 bg=0.01
lamellipodium GO:0030027 p=2.0E−02 n=6 fg=0.05 bg=0.02
organelle outer membrane GO:0031968 p=2.0E−02 n=5 fg=0.05 bg=0.01
outer membrane GO:0019867 p=2.0E−02 n=5 fg=0.05 bg=0.01
heterotrimeric G−protein complex GO:0005834 p=2.2E−02 n=2 fg=0.02 bg=0.00
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filopodium membrane GO:0031527 p=2.2E−02 n=2 fg=0.02 bg=0.00
sarcolemma GO:0042383 p=2.3E−02 n=4 fg=0.04 bg=0.01
neuron projection GO:0043005 p=2.7E−02 n=22 fg=0.20 bg=0.12
cytoplasmic vesicle GO:0031410 p=2.9E−02 n=25 fg=0.23 bg=0.15
intracellular vesicle GO:0097708 p=2.9E−02 n=25 fg=0.23 bg=0.15
axon GO:0030424 p=3.0E−02 n=13 fg=0.12 bg=0.07
synaptic membrane GO:0097060 p=3.0E−02 n=6 fg=0.05 bg=0.02
0 1 2 3 4 5
−log(p)
n=111/344 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction