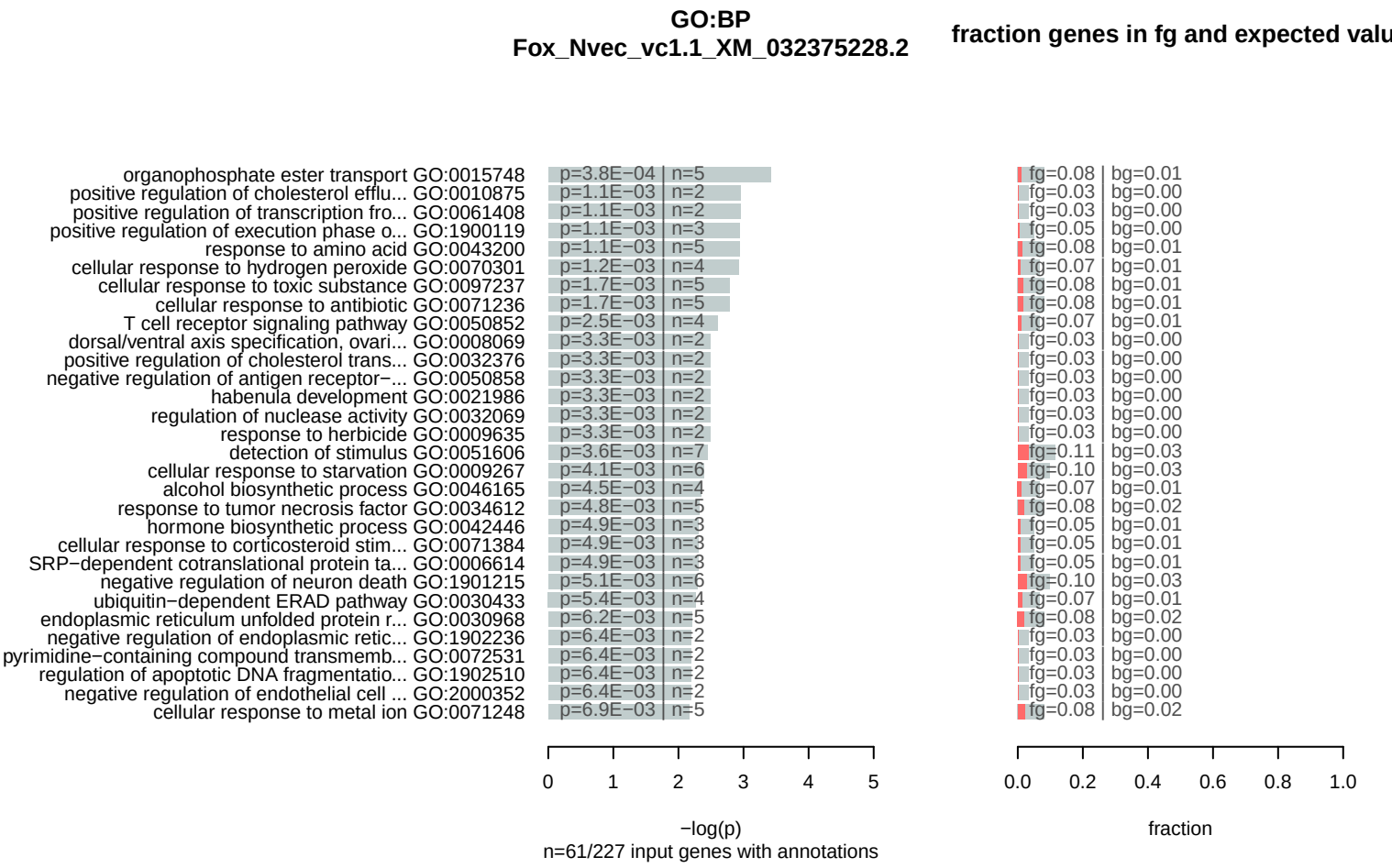
GO:BP
Fox_Nvec_vc1.1_XM_032375228.2
fraction genes in fg and expected valu
organophosphate ester transport GO:0015748 p=3.8E−04 n=5 fg=0.08 bg=0.01
positive regulation of cholesterol efflu... GO:0010875 p=1.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of transcription fro... GO:0061408 p=1.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of execution phase o... GO:1900119 p=1.1E−03 n=3 fg=0.05 bg=0.00
response to amino acid GO:0043200 p=1.1E−03 n=5 fg=0.08 bg=0.01
cellular response to hydrogen peroxide GO:0070301 p=1.2E−03 n=4 fg=0.07 bg=0.01
cellular response to toxic substance GO:0097237 p=1.7E−03 n=5 fg=0.08 bg=0.01
cellular response to antibiotic GO:0071236 p=1.7E−03 n=5 fg=0.08 bg=0.01
T cell receptor signaling pathway GO:0050852 p=2.5E−03 n=4 fg=0.07 bg=0.01
dorsal/ventral axis specification, ovari... GO:0008069 p=3.3E−03 n=2 fg=0.03 bg=0.00
positive regulation of cholesterol trans... GO:0032376 p=3.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of antigen receptor−... GO:0050858 p=3.3E−03 n=2 fg=0.03 bg=0.00
habenula development GO:0021986 p=3.3E−03 n=2 fg=0.03 bg=0.00
regulation of nuclease activity GO:0032069 p=3.3E−03 n=2 fg=0.03 bg=0.00
response to herbicide GO:0009635 p=3.3E−03 n=2 fg=0.03 bg=0.00
detection of stimulus GO:0051606 p=3.6E−03 n=7 fg=0.11 bg=0.03
cellular response to starvation GO:0009267 p=4.1E−03 n=6 fg=0.10 bg=0.03
alcohol biosynthetic process GO:0046165 p=4.5E−03 n=4 fg=0.07 bg=0.01
response to tumor necrosis factor GO:0034612 p=4.8E−03 n=5 fg=0.08 bg=0.02
hormone biosynthetic process GO:0042446 p=4.9E−03 n=3 fg=0.05 bg=0.01
cellular response to corticosteroid stim... GO:0071384 p=4.9E−03 n=3 fg=0.05 bg=0.01
SRP−dependent cotranslational protein ta... GO:0006614 p=4.9E−03 n=3 fg=0.05 bg=0.01
negative regulation of neuron death GO:1901215 p=5.1E−03 n=6 fg=0.10 bg=0.03
ubiquitin−dependent ERAD pathway GO:0030433 p=5.4E−03 n=4 fg=0.07 bg=0.01
endoplasmic reticulum unfolded protein r... GO:0030968 p=6.2E−03 n=5 fg=0.08 bg=0.02
negative regulation of endoplasmic retic... GO:1902236 p=6.4E−03 n=2 fg=0.03 bg=0.00
pyrimidine−containing compound transmemb... GO:0072531 p=6.4E−03 n=2 fg=0.03 bg=0.00
regulation of apoptotic DNA fragmentatio... GO:1902510 p=6.4E−03 n=2 fg=0.03 bg=0.00
negative regulation of endothelial cell ... GO:2000352 p=6.4E−03 n=2 fg=0.03 bg=0.00
cellular response to metal ion GO:0071248 p=6.9E−03 n=5 fg=0.08 bg=0.02
0 1 2 3 4 5
−log(p)
n=61/227 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032375228.2
fraction genes in fg and expected valu
organophosphate ester transmembrane tran... GO:0015605 p=1.4E−03 n=3 fg=0.05 bg=0.00
potassium channel activity GO:0005267 p=1.2E−02 n=3 fg=0.05 bg=0.01
cholesterol binding GO:0015485 p=1.7E−02 n=2 fg=0.04 bg=0.00
ubiquitin−specific protease binding GO:1990381 p=1.7E−02 n=2 fg=0.04 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=2.1E−02 n=3 fg=0.05 bg=0.01
outward rectifier potassium channel acti... GO:0015271 p=2.4E−02 n=2 fg=0.04 bg=0.00
sterol binding GO:0032934 p=2.4E−02 n=2 fg=0.04 bg=0.00
voltage−gated cation channel activity GO:0022843 p=2.4E−02 n=3 fg=0.05 bg=0.01
cation channel activity GO:0005261 p=2.6E−02 n=5 fg=0.09 bg=0.03
steroid binding GO:0005496 p=3.1E−02 n=2 fg=0.04 bg=0.01
choline transmembrane transporter activi... GO:0015220 p=3.6E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=3.6E−02 n=1 fg=0.02 bg=0.00
nickel cation binding GO:0016151 p=3.6E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0016649 p=3.6E−02 n=1 fg=0.02 bg=0.00
aminophospholipid flippase activity GO:0015247 p=3.6E−02 n=1 fg=0.02 bg=0.00
adenylate cyclase activator activity GO:0010856 p=3.6E−02 n=1 fg=0.02 bg=0.00
thiamine transmembrane transporter activ... GO:0015234 p=3.6E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=3.6E−02 n=1 fg=0.02 bg=0.00
NAD(P)H oxidase H2O2−forming activity GO:0016174 p=3.6E−02 n=1 fg=0.02 bg=0.00
thiamine pyrophosphate transmembrane tra... GO:0090422 p=3.6E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=3.6E−02 n=1 fg=0.02 bg=0.00
nuclease inhibitor activity GO:0140721 p=3.6E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.6E−02 n=1 fg=0.02 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=3.6E−02 n=1 fg=0.02 bg=0.00
flippase activity GO:0140327 p=3.6E−02 n=1 fg=0.02 bg=0.00
electron−transferring−flavoprotein dehyd... GO:0004174 p=3.6E−02 n=1 fg=0.02 bg=0.00
supercoiled DNA binding GO:0097100 p=3.6E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=3.6E−02 n=1 fg=0.02 bg=0.00
endoribonuclease inhibitor activity GO:0060698 p=3.6E−02 n=1 fg=0.02 bg=0.00
phosphatidylglycerol binding GO:1901611 p=3.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=57/227 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032375228.2
fraction genes in fg and expected valu
cytoskeleton GO:0005856 p=4.8E−03 n=17 fg=0.27 bg=0.14
integral component of plasma membrane GO:0005887 p=6.0E−03 n=11 fg=0.17 bg=0.08
Hrd1p ubiquitin ligase complex GO:0000836 p=6.8E−03 n=2 fg=0.03 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=6.8E−03 n=2 fg=0.03 bg=0.00
Derlin−1 retrotranslocation complex GO:0036513 p=1.6E−02 n=2 fg=0.03 bg=0.00
mitotic spindle GO:0072686 p=1.9E−02 n=3 fg=0.05 bg=0.01
ciliary plasm GO:0097014 p=2.3E−02 n=3 fg=0.05 bg=0.01
axoneme GO:0005930 p=2.3E−02 n=3 fg=0.05 bg=0.01
cation channel complex GO:0034703 p=3.4E−02 n=3 fg=0.05 bg=0.01
DNA replication factor C complex GO:0005663 p=3.5E−02 n=1 fg=0.02 bg=0.00
AP−1 adaptor complex GO:0030121 p=3.5E−02 n=1 fg=0.02 bg=0.00
actin cortical patch GO:0030479 p=3.5E−02 n=1 fg=0.02 bg=0.00
clathrin coat of trans−Golgi network ves... GO:0030130 p=3.5E−02 n=1 fg=0.02 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=3.5E−02 n=1 fg=0.02 bg=0.00
Elg1 RFC−like complex GO:0031391 p=3.5E−02 n=1 fg=0.02 bg=0.00
endocytic patch GO:0061645 p=3.5E−02 n=1 fg=0.02 bg=0.00
NF−kappaB complex GO:0071159 p=3.5E−02 n=1 fg=0.02 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=3.7E−02 n=2 fg=0.03 bg=0.00
potassium channel complex GO:0034705 p=3.7E−02 n=2 fg=0.03 bg=0.00
centrosome GO:0005813 p=3.8E−02 n=7 fg=0.11 bg=0.05
microtubule cytoskeleton GO:0015630 p=4.2E−02 n=11 fg=0.17 bg=0.10
ion channel complex GO:0034702 p=4.3E−02 n=3 fg=0.05 bg=0.01
plasma membrane bounded cell projection ... GO:0032838 p=4.8E−02 n=3 fg=0.05 bg=0.01
integral component of endoplasmic reticu... GO:0030176 p=5.2E−02 n=4 fg=0.06 bg=0.02
intrinsic component of endoplasmic retic... GO:0031227 p=5.2E−02 n=4 fg=0.06 bg=0.02
microtubule organizing center GO:0005815 p=5.3E−02 n=8 fg=0.13 bg=0.07
inner dynein arm GO:0036156 p=6.9E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=6.9E−02 n=1 fg=0.02 bg=0.00
cytoplasmic side of rough endoplasmic re... GO:0098556 p=6.9E−02 n=1 fg=0.02 bg=0.00
muscle myosin complex GO:0005859 p=6.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=63/227 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction