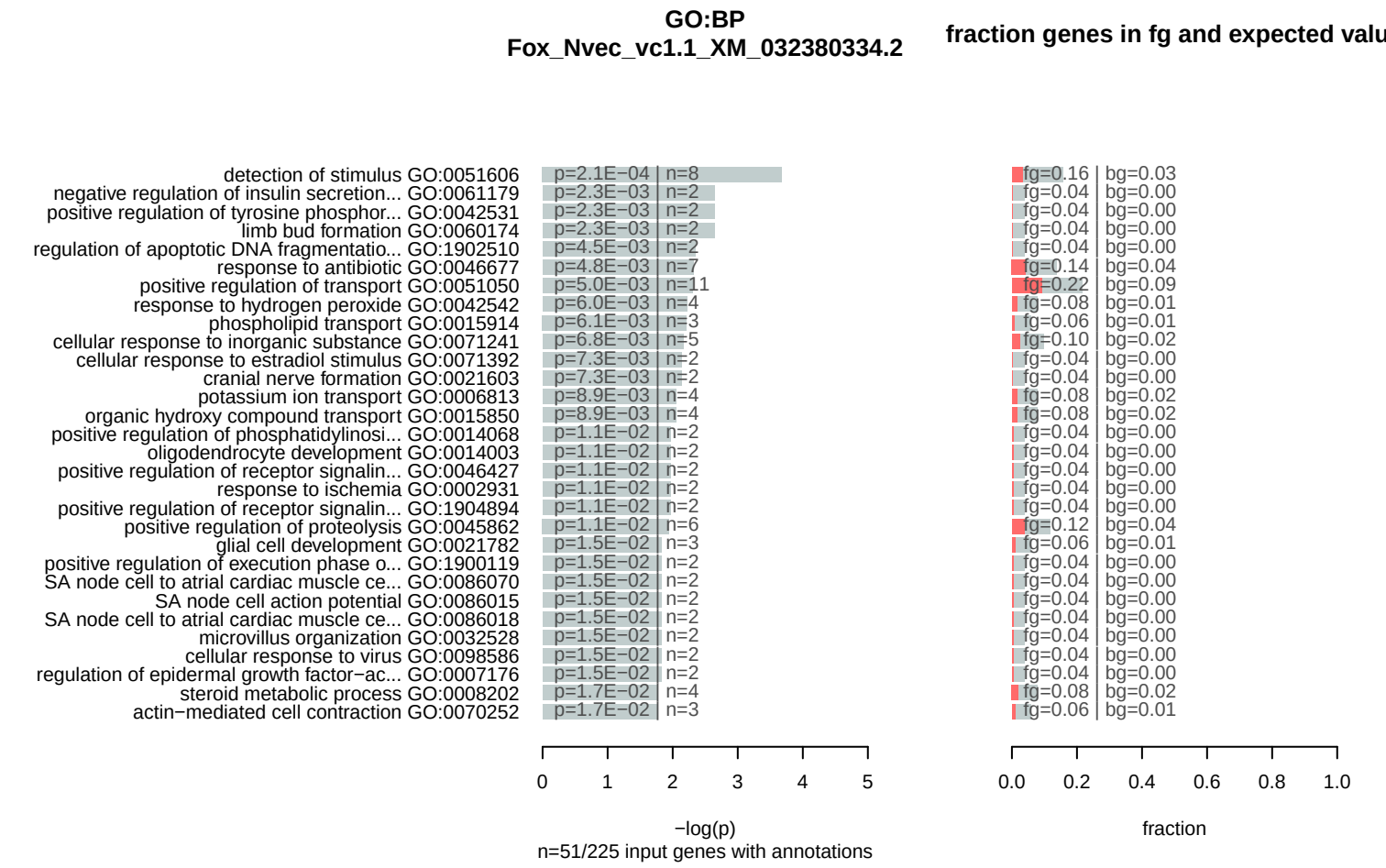
GO:BP
Fox_Nvec_vc1.1_XM_032380334.2
fraction genes in fg and expected valu
detection of stimulus GO:0051606 p=2.1E−04 n=8 fg=0.16 bg=0.03
negative regulation of insulin secretion... GO:0061179 p=2.3E−03 n=2 fg=0.04 bg=0.00
positive regulation of tyrosine phosphor... GO:0042531 p=2.3E−03 n=2 fg=0.04 bg=0.00
limb bud formation GO:0060174 p=2.3E−03 n=2 fg=0.04 bg=0.00
regulation of apoptotic DNA fragmentatio... GO:1902510 p=4.5E−03 n=2 fg=0.04 bg=0.00
response to antibiotic GO:0046677 p=4.8E−03 n=7 fg=0.14 bg=0.04
positive regulation of transport GO:0051050 p=5.0E−03 n=11 fg=0.22 bg=0.09
response to hydrogen peroxide GO:0042542 p=6.0E−03 n=4 fg=0.08 bg=0.01
phospholipid transport GO:0015914 p=6.1E−03 n=3 fg=0.06 bg=0.01
cellular response to inorganic substance GO:0071241 p=6.8E−03 n=5 fg=0.10 bg=0.02
cellular response to estradiol stimulus GO:0071392 p=7.3E−03 n=2 fg=0.04 bg=0.00
cranial nerve formation GO:0021603 p=7.3E−03 n=2 fg=0.04 bg=0.00
potassium ion transport GO:0006813 p=8.9E−03 n=4 fg=0.08 bg=0.02
organic hydroxy compound transport GO:0015850 p=8.9E−03 n=4 fg=0.08 bg=0.02
positive regulation of phosphatidylinosi... GO:0014068 p=1.1E−02 n=2 fg=0.04 bg=0.00
oligodendrocyte development GO:0014003 p=1.1E−02 n=2 fg=0.04 bg=0.00
positive regulation of receptor signalin... GO:0046427 p=1.1E−02 n=2 fg=0.04 bg=0.00
response to ischemia GO:0002931 p=1.1E−02 n=2 fg=0.04 bg=0.00
positive regulation of receptor signalin... GO:1904894 p=1.1E−02 n=2 fg=0.04 bg=0.00
positive regulation of proteolysis GO:0045862 p=1.1E−02 n=6 fg=0.12 bg=0.04
glial cell development GO:0021782 p=1.5E−02 n=3 fg=0.06 bg=0.01
positive regulation of execution phase o... GO:1900119 p=1.5E−02 n=2 fg=0.04 bg=0.00
SA node cell to atrial cardiac muscle ce... GO:0086070 p=1.5E−02 n=2 fg=0.04 bg=0.00
SA node cell action potential GO:0086015 p=1.5E−02 n=2 fg=0.04 bg=0.00
SA node cell to atrial cardiac muscle ce... GO:0086018 p=1.5E−02 n=2 fg=0.04 bg=0.00
microvillus organization GO:0032528 p=1.5E−02 n=2 fg=0.04 bg=0.00
cellular response to virus GO:0098586 p=1.5E−02 n=2 fg=0.04 bg=0.00
regulation of epidermal growth factor−ac... GO:0007176 p=1.5E−02 n=2 fg=0.04 bg=0.00
steroid metabolic process GO:0008202 p=1.7E−02 n=4 fg=0.08 bg=0.02
actin−mediated cell contraction GO:0070252 p=1.7E−02 n=3 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=51/225 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032380334.2
fraction genes in fg and expected valu
potassium channel activity GO:0005267 p=7.9E−03 n=3 fg=0.06 bg=0.01
voltage−gated cation channel activity GO:0022843 p=1.6E−02 n=3 fg=0.06 bg=0.01
guanyl−nucleotide exchange factor activi... GO:0005085 p=1.7E−02 n=4 fg=0.08 bg=0.02
outward rectifier potassium channel acti... GO:0015271 p=1.8E−02 n=2 fg=0.04 bg=0.00
organophosphate ester transmembrane tran... GO:0015605 p=1.8E−02 n=2 fg=0.04 bg=0.00
5S rDNA binding GO:0080084 p=3.1E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=3.1E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=3.1E−02 n=1 fg=0.02 bg=0.00
ATPase−coupled inorganic anion transmemb... GO:0043225 p=3.1E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=3.1E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0016649 p=3.1E−02 n=1 fg=0.02 bg=0.00
aminophospholipid flippase activity GO:0015247 p=3.1E−02 n=1 fg=0.02 bg=0.00
phosphatidylglycerol binding GO:1901611 p=3.1E−02 n=1 fg=0.02 bg=0.00
cardiolipin binding GO:1901612 p=3.1E−02 n=1 fg=0.02 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=3.1E−02 n=1 fg=0.02 bg=0.00
palmitoleyl hydrolase activity GO:1990699 p=3.1E−02 n=1 fg=0.02 bg=0.00
ribokinase activity GO:0004747 p=3.1E−02 n=1 fg=0.02 bg=0.00
nickel cation binding GO:0016151 p=3.1E−02 n=1 fg=0.02 bg=0.00
electron−transferring−flavoprotein dehyd... GO:0004174 p=3.1E−02 n=1 fg=0.02 bg=0.00
GABA receptor binding GO:0050811 p=3.1E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=3.1E−02 n=1 fg=0.02 bg=0.00
NAD(P)H oxidase H2O2−forming activity GO:0016174 p=3.1E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=3.1E−02 n=1 fg=0.02 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=3.1E−02 n=1 fg=0.02 bg=0.00
flippase activity GO:0140327 p=3.1E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=3.1E−02 n=1 fg=0.02 bg=0.00
alpha−2C adrenergic receptor binding GO:0031696 p=3.1E−02 n=1 fg=0.02 bg=0.00
RNA polymerase III core binding GO:0000994 p=3.1E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.1E−02 n=1 fg=0.02 bg=0.00
translation elongation factor binding GO:0061770 p=3.1E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/225 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032380334.2
fraction genes in fg and expected valu
inner dynein arm GO:0036156 p=9.4E−04 n=2 fg=0.04 bg=0.00
integral component of plasma membrane GO:0005887 p=2.3E−03 n=11 fg=0.20 bg=0.08
perinuclear region of cytoplasm GO:0048471 p=1.8E−02 n=9 fg=0.16 bg=0.07
cation channel complex GO:0034703 p=2.5E−02 n=3 fg=0.05 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=2.9E−02 n=2 fg=0.04 bg=0.01
potassium channel complex GO:0034705 p=2.9E−02 n=2 fg=0.04 bg=0.01
DNA replication factor C complex GO:0005663 p=3.1E−02 n=1 fg=0.02 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=3.1E−02 n=1 fg=0.02 bg=0.00
Elg1 RFC−like complex GO:0031391 p=3.1E−02 n=1 fg=0.02 bg=0.00
postsynaptic endosome GO:0098845 p=3.1E−02 n=1 fg=0.02 bg=0.00
postsynaptic recycling endosome GO:0098837 p=3.1E−02 n=1 fg=0.02 bg=0.00
ion channel complex GO:0034702 p=3.2E−02 n=3 fg=0.05 bg=0.01
nuclear stress granule GO:0097165 p=6.1E−02 n=1 fg=0.02 bg=0.00
muscle myosin complex GO:0005859 p=6.1E−02 n=1 fg=0.02 bg=0.00
myosin II complex GO:0016460 p=6.1E−02 n=1 fg=0.02 bg=0.00
TOR complex GO:0038201 p=6.1E−02 n=1 fg=0.02 bg=0.00
myosin V complex GO:0031475 p=6.1E−02 n=1 fg=0.02 bg=0.00
TORC1 complex GO:0031931 p=6.1E−02 n=1 fg=0.02 bg=0.00
ciliary plasm GO:0097014 p=8.1E−02 n=4 fg=0.07 bg=0.01
axoneme GO:0005930 p=8.1E−02 n=4 fg=0.07 bg=0.01
filopodium GO:0030175 p=8.6E−02 n=2 fg=0.04 bg=0.01
inhibitory synapse GO:0060077 p=9.0E−02 n=1 fg=0.02 bg=0.00
myosin VI complex GO:0031476 p=9.0E−02 n=1 fg=0.02 bg=0.00
myosin VII complex GO:0031477 p=9.0E−02 n=1 fg=0.02 bg=0.00
manchette GO:0002177 p=9.0E−02 n=1 fg=0.02 bg=0.00
mitotic spindle GO:0072686 p=9.5E−02 n=2 fg=0.04 bg=0.01
motile cilium GO:0031514 p=9.8E−02 n=3 fg=0.05 bg=0.02
transport vesicle GO:0030133 p=1.0E−01 n=5 fg=0.09 bg=0.04
actin−based cell projection GO:0098858 p=1.0E−01 n=3 fg=0.05 bg=0.02
transmembrane transporter complex GO:1902495 p=1.1E−01 n=3 fg=0.05 bg=0.02
0 1 2 3 4 5
−log(p)
n=56/225 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction