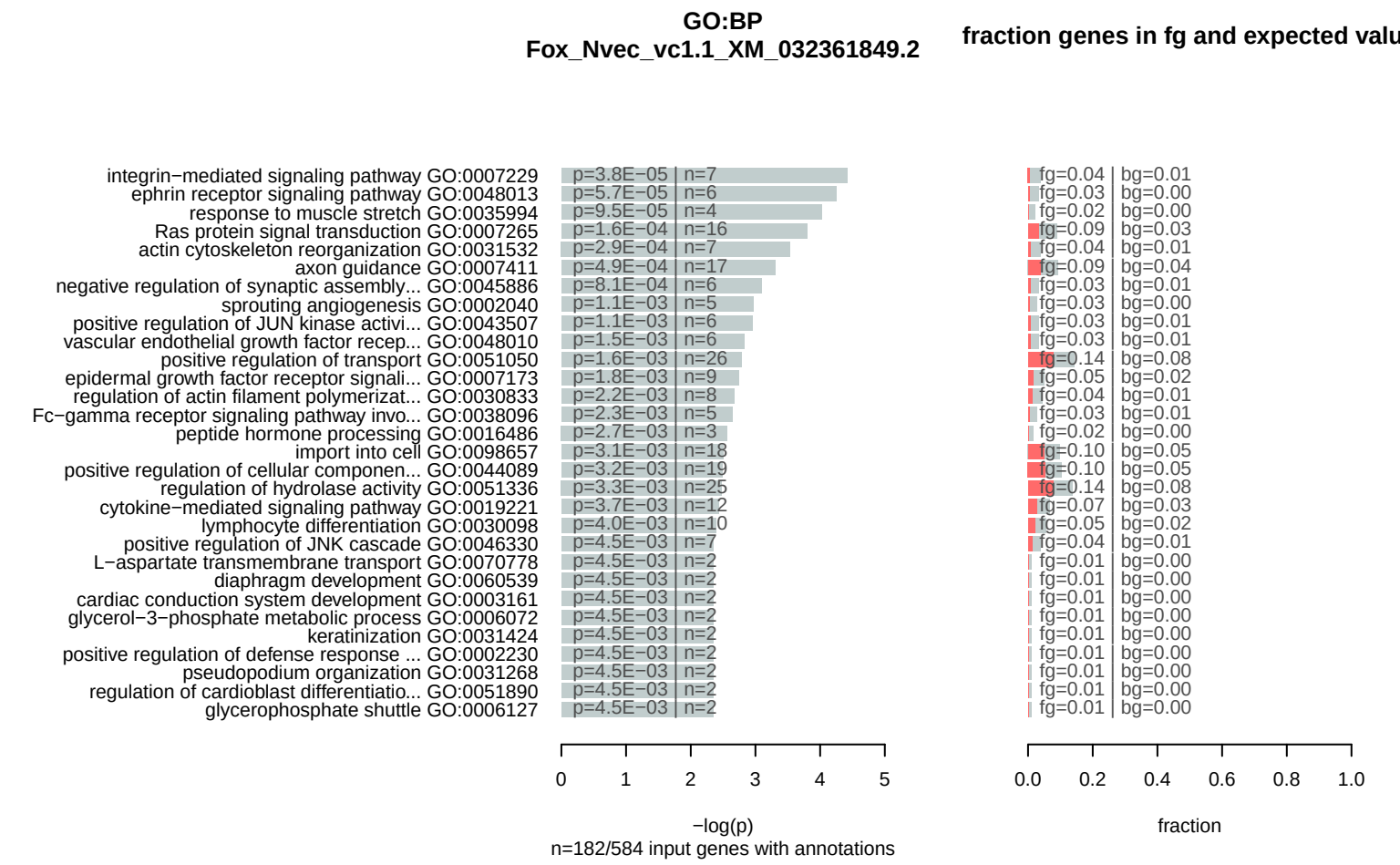
GO:BP
Fox_Nvec_vc1.1_XM_032361849.2
fraction genes in fg and expected valu
integrin−mediated signaling pathway GO:0007229 p=3.8E−05 n=7 fg=0.04 bg=0.01
ephrin receptor signaling pathway GO:0048013 p=5.7E−05 n=6 fg=0.03 bg=0.00
response to muscle stretch GO:0035994 p=9.5E−05 n=4 fg=0.02 bg=0.00
Ras protein signal transduction GO:0007265 p=1.6E−04 n=16 fg=0.09 bg=0.03
actin cytoskeleton reorganization GO:0031532 p=2.9E−04 n=7 fg=0.04 bg=0.01
axon guidance GO:0007411 p=4.9E−04 n=17 fg=0.09 bg=0.04
negative regulation of synaptic assembly... GO:0045886 p=8.1E−04 n=6 fg=0.03 bg=0.01
sprouting angiogenesis GO:0002040 p=1.1E−03 n=5 fg=0.03 bg=0.00
positive regulation of JUN kinase activi... GO:0043507 p=1.1E−03 n=6 fg=0.03 bg=0.01
vascular endothelial growth factor recep... GO:0048010 p=1.5E−03 n=6 fg=0.03 bg=0.01
positive regulation of transport GO:0051050 p=1.6E−03 n=26 fg=0.14 bg=0.08
epidermal growth factor receptor signali... GO:0007173 p=1.8E−03 n=9 fg=0.05 bg=0.02
regulation of actin filament polymerizat... GO:0030833 p=2.2E−03 n=8 fg=0.04 bg=0.01
Fc−gamma receptor signaling pathway invo... GO:0038096 p=2.3E−03 n=5 fg=0.03 bg=0.01
peptide hormone processing GO:0016486 p=2.7E−03 n=3 fg=0.02 bg=0.00
import into cell GO:0098657 p=3.1E−03 n=18 fg=0.10 bg=0.05
positive regulation of cellular componen... GO:0044089 p=3.2E−03 n=19 fg=0.10 bg=0.05
regulation of hydrolase activity GO:0051336 p=3.3E−03 n=25 fg=0.14 bg=0.08
cytokine−mediated signaling pathway GO:0019221 p=3.7E−03 n=12 fg=0.07 bg=0.03
lymphocyte differentiation GO:0030098 p=4.0E−03 n=10 fg=0.05 bg=0.02
positive regulation of JNK cascade GO:0046330 p=4.5E−03 n=7 fg=0.04 bg=0.01
L−aspartate transmembrane transport GO:0070778 p=4.5E−03 n=2 fg=0.01 bg=0.00
diaphragm development GO:0060539 p=4.5E−03 n=2 fg=0.01 bg=0.00
cardiac conduction system development GO:0003161 p=4.5E−03 n=2 fg=0.01 bg=0.00
glycerol−3−phosphate metabolic process GO:0006072 p=4.5E−03 n=2 fg=0.01 bg=0.00
keratinization GO:0031424 p=4.5E−03 n=2 fg=0.01 bg=0.00
positive regulation of defense response ... GO:0002230 p=4.5E−03 n=2 fg=0.01 bg=0.00
pseudopodium organization GO:0031268 p=4.5E−03 n=2 fg=0.01 bg=0.00
regulation of cardioblast differentiatio... GO:0051890 p=4.5E−03 n=2 fg=0.01 bg=0.00
glycerophosphate shuttle GO:0006127 p=4.5E−03 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=182/584 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032361849.2
fraction genes in fg and expected valu
signaling receptor complex adaptor activ... GO:0030159 p=2.2E−03 n=4 fg=0.02 bg=0.00
enzyme activator activity GO:0008047 p=3.4E−03 n=16 fg=0.10 bg=0.05
L−aspartate transmembrane transporter ac... GO:0015183 p=4.9E−03 n=2 fg=0.01 bg=0.00
glycerol−3−phosphate dehydrogenase [NAD+... GO:0004367 p=4.9E−03 n=2 fg=0.01 bg=0.00
glycerol−3−phosphate dehydrogenase (quin... GO:0004368 p=4.9E−03 n=2 fg=0.01 bg=0.00
L−glutamate transmembrane transporter ac... GO:0005313 p=4.9E−03 n=2 fg=0.01 bg=0.00
amide transmembrane transporter activity GO:0042887 p=7.4E−03 n=4 fg=0.02 bg=0.01
non−membrane spanning protein tyrosine k... GO:0004715 p=9.6E−03 n=3 fg=0.02 bg=0.00
protein kinase activity GO:0004672 p=1.3E−02 n=18 fg=0.11 bg=0.05
pyrimidine nucleotide−sugar transmembran... GO:0015165 p=1.4E−02 n=2 fg=0.01 bg=0.00
miRNA binding GO:0035198 p=1.4E−02 n=2 fg=0.01 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=1.4E−02 n=2 fg=0.01 bg=0.00
pre−mRNA 3'−splice site binding GO:0030628 p=1.4E−02 n=2 fg=0.01 bg=0.00
phosphotransferase activity, alcohol gro... GO:0016773 p=1.5E−02 n=20 fg=0.12 bg=0.06
protein serine/threonine kinase activity GO:0004674 p=1.7E−02 n=13 fg=0.08 bg=0.04
sodium ion transmembrane transporter act... GO:0015081 p=1.9E−02 n=5 fg=0.03 bg=0.01
binding GO:0005488 p=1.9E−02 n=137 fg=0.83 bg=0.76
signaling adaptor activity GO:0035591 p=2.0E−02 n=7 fg=0.04 bg=0.01
pre−mRNA binding GO:0036002 p=2.1E−02 n=3 fg=0.02 bg=0.00
peptide transmembrane transporter activi... GO:1904680 p=2.1E−02 n=3 fg=0.02 bg=0.00
protein tyrosine kinase binding GO:1990782 p=2.2E−02 n=4 fg=0.02 bg=0.01
regulatory RNA binding GO:0061980 p=2.7E−02 n=2 fg=0.01 bg=0.00
RNA stem−loop binding GO:0035613 p=2.7E−02 n=2 fg=0.01 bg=0.00
sequence−specific mRNA binding GO:1990825 p=2.7E−02 n=2 fg=0.01 bg=0.00
cyclase regulator activity GO:0010851 p=2.7E−02 n=2 fg=0.01 bg=0.00
translation repressor activity GO:0030371 p=2.7E−02 n=2 fg=0.01 bg=0.00
nucleotide−sugar transmembrane transport... GO:0005338 p=2.7E−02 n=2 fg=0.01 bg=0.00
ion channel regulator activity GO:0099106 p=2.8E−02 n=6 fg=0.04 bg=0.01
calmodulin−dependent protein kinase acti... GO:0004683 p=2.8E−02 n=3 fg=0.02 bg=0.00
transferase activity, transferring phosp... GO:0016772 p=2.9E−02 n=24 fg=0.14 bg=0.09
0 1 2 3 4 5
−log(p)
n=166/584 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032361849.2
fraction genes in fg and expected valu
axon terminus GO:0043679 p=9.1E−04 n=11 fg=0.06 bg=0.02
septin cytoskeleton GO:0032156 p=2.5E−03 n=3 fg=0.02 bg=0.00
podosome GO:0002102 p=2.5E−03 n=3 fg=0.02 bg=0.00
stress fiber GO:0001725 p=2.7E−03 n=4 fg=0.02 bg=0.00
focal adhesion GO:0005925 p=2.9E−03 n=6 fg=0.03 bg=0.01
Arp2/3 protein complex GO:0005885 p=4.3E−03 n=2 fg=0.01 bg=0.00
U2AF complex GO:0089701 p=4.3E−03 n=2 fg=0.01 bg=0.00
glycerol−3−phosphate dehydrogenase compl... GO:0009331 p=4.3E−03 n=2 fg=0.01 bg=0.00
peripheral region of growth cone GO:0090725 p=4.3E−03 n=2 fg=0.01 bg=0.00
cell cortex GO:0005938 p=7.3E−03 n=13 fg=0.07 bg=0.03
axolemma GO:0030673 p=8.0E−03 n=3 fg=0.02 bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234 p=9.8E−03 n=5 fg=0.03 bg=0.01
cleavage furrow GO:0032154 p=1.1E−02 n=4 fg=0.02 bg=0.01
cell body GO:0044297 p=1.2E−02 n=20 fg=0.11 bg=0.07
specific granule lumen GO:0035580 p=1.2E−02 n=3 fg=0.02 bg=0.00
septin ring GO:0005940 p=1.2E−02 n=2 fg=0.01 bg=0.00
sperm annulus GO:0097227 p=1.2E−02 n=2 fg=0.01 bg=0.00
septin complex GO:0031105 p=1.2E−02 n=2 fg=0.01 bg=0.00
type Ib terminal bouton GO:0061176 p=1.2E−02 n=2 fg=0.01 bg=0.00
type Is terminal bouton GO:0061177 p=1.2E−02 n=2 fg=0.01 bg=0.00
cytoplasmic ribonucleoprotein granule GO:0036464 p=1.3E−02 n=9 fg=0.05 bg=0.02
Golgi−associated vesicle GO:0005798 p=1.6E−02 n=7 fg=0.04 bg=0.02
terminal bouton GO:0043195 p=1.6E−02 n=7 fg=0.04 bg=0.02
neuronal cell body GO:0043025 p=1.6E−02 n=18 fg=0.10 bg=0.06
site of polarized growth GO:0030427 p=1.7E−02 n=10 fg=0.06 bg=0.02
trans−Golgi network GO:0005802 p=1.7E−02 n=10 fg=0.06 bg=0.03
ribonucleoprotein granule GO:0035770 p=1.8E−02 n=9 fg=0.05 bg=0.02
neuron spine GO:0044309 p=1.8E−02 n=8 fg=0.05 bg=0.02
dendritic spine GO:0043197 p=1.8E−02 n=8 fg=0.05 bg=0.02
dendrite GO:0030425 p=1.9E−02 n=18 fg=0.10 bg=0.06
0 1 2 3 4 5
−log(p)
n=177/584 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction