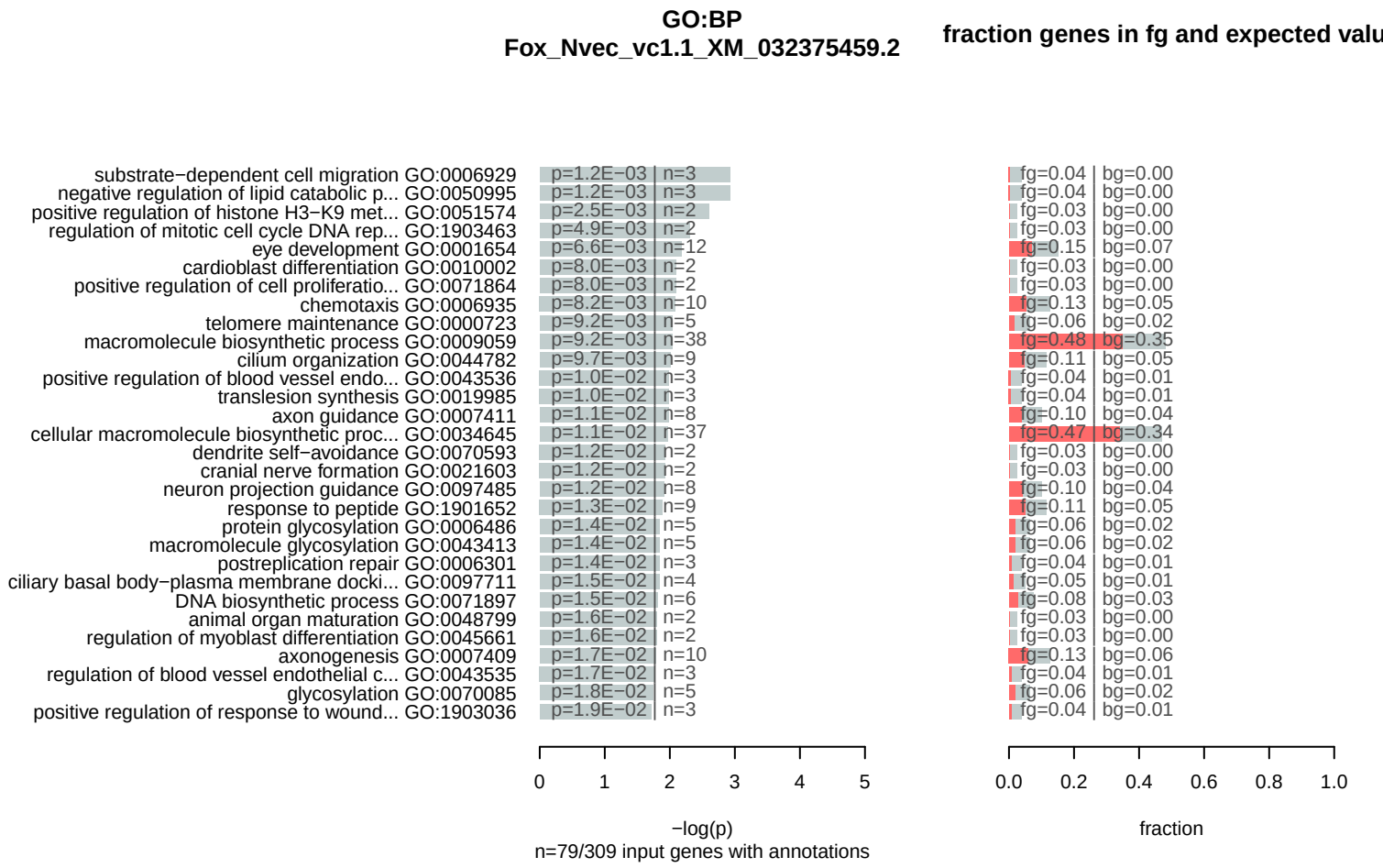
GO:BP
Fox_Nvec_vc1.1_XM_032375459.2
fraction genes in fg and expected valu
substrate−dependent cell migration GO:0006929 p=1.2E−03 n=3 fg=0.04 bg=0.00
negative regulation of lipid catabolic p... GO:0050995 p=1.2E−03 n=3 fg=0.04 bg=0.00
positive regulation of histone H3−K9 met... GO:0051574 p=2.5E−03 n=2 fg=0.03 bg=0.00
regulation of mitotic cell cycle DNA rep... GO:1903463 p=4.9E−03 n=2 fg=0.03 bg=0.00
eye development GO:0001654 p=6.6E−03 n=12 fg=0.15 bg=0.07
cardioblast differentiation GO:0010002 p=8.0E−03 n=2 fg=0.03 bg=0.00
positive regulation of cell proliferatio... GO:0071864 p=8.0E−03 n=2 fg=0.03 bg=0.00
chemotaxis GO:0006935 p=8.2E−03 n=10 fg=0.13 bg=0.05
telomere maintenance GO:0000723 p=9.2E−03 n=5 fg=0.06 bg=0.02
macromolecule biosynthetic process GO:0009059 p=9.2E−03 n=38 fg=0.48 bg=0.35
cilium organization GO:0044782 p=9.7E−03 n=9 fg=0.11 bg=0.05
positive regulation of blood vessel endo... GO:0043536 p=1.0E−02 n=3 fg=0.04 bg=0.01
translesion synthesis GO:0019985 p=1.0E−02 n=3 fg=0.04 bg=0.01
axon guidance GO:0007411 p=1.1E−02 n=8 fg=0.10 bg=0.04
cellular macromolecule biosynthetic proc... GO:0034645 p=1.1E−02 n=37 fg=0.47 bg=0.34
dendrite self−avoidance GO:0070593 p=1.2E−02 n=2 fg=0.03 bg=0.00
cranial nerve formation GO:0021603 p=1.2E−02 n=2 fg=0.03 bg=0.00
neuron projection guidance GO:0097485 p=1.2E−02 n=8 fg=0.10 bg=0.04
response to peptide GO:1901652 p=1.3E−02 n=9 fg=0.11 bg=0.05
protein glycosylation GO:0006486 p=1.4E−02 n=5 fg=0.06 bg=0.02
macromolecule glycosylation GO:0043413 p=1.4E−02 n=5 fg=0.06 bg=0.02
postreplication repair GO:0006301 p=1.4E−02 n=3 fg=0.04 bg=0.01
ciliary basal body−plasma membrane docki... GO:0097711 p=1.5E−02 n=4 fg=0.05 bg=0.01
DNA biosynthetic process GO:0071897 p=1.5E−02 n=6 fg=0.08 bg=0.03
animal organ maturation GO:0048799 p=1.6E−02 n=2 fg=0.03 bg=0.00
regulation of myoblast differentiation GO:0045661 p=1.6E−02 n=2 fg=0.03 bg=0.00
axonogenesis GO:0007409 p=1.7E−02 n=10 fg=0.13 bg=0.06
regulation of blood vessel endothelial c... GO:0043535 p=1.7E−02 n=3 fg=0.04 bg=0.01
glycosylation GO:0070085 p=1.8E−02 n=5 fg=0.06 bg=0.02
positive regulation of response to wound... GO:1903036 p=1.9E−02 n=3 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=79/309 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032375459.2
fraction genes in fg and expected valu
tau−protein kinase activity GO:0050321 p=5.1E−03 n=2 fg=0.03 bg=0.00
insulin receptor binding GO:0005158 p=1.7E−02 n=2 fg=0.03 bg=0.00
adrenergic receptor binding GO:0031690 p=1.7E−02 n=2 fg=0.03 bg=0.00
adenyl ribonucleotide binding GO:0032559 p=2.2E−02 n=8 fg=0.11 bg=0.05
protein tyrosine kinase activity GO:0004713 p=2.3E−02 n=3 fg=0.04 bg=0.01
adenyl nucleotide binding GO:0030554 p=2.5E−02 n=8 fg=0.11 bg=0.05
D−glucose transmembrane transporter acti... GO:0055056 p=3.0E−02 n=1 fg=0.01 bg=0.00
alanine−oxo−acid transaminase activity GO:0047635 p=3.0E−02 n=1 fg=0.01 bg=0.00
carbohydrate:proton symporter activity GO:0005351 p=3.0E−02 n=1 fg=0.01 bg=0.00
glucose transmembrane transporter activi... GO:0005355 p=3.0E−02 n=1 fg=0.01 bg=0.00
polypeptide N−acetylgalactosaminyltransf... GO:0004653 p=3.0E−02 n=1 fg=0.01 bg=0.00
nickel cation binding GO:0016151 p=3.0E−02 n=1 fg=0.01 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=3.0E−02 n=1 fg=0.01 bg=0.00
benzodiazepine receptor binding GO:0030156 p=3.0E−02 n=1 fg=0.01 bg=0.00
angiostatin binding GO:0043532 p=3.0E−02 n=1 fg=0.01 bg=0.00
carbohydrate:cation symporter activity GO:0005402 p=3.0E−02 n=1 fg=0.01 bg=0.00
phosphopantetheine−dependent carrier act... GO:0140414 p=3.0E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase activit... GO:0046933 p=3.0E−02 n=1 fg=0.01 bg=0.00
phosphomannomutase activity GO:0004615 p=3.0E−02 n=1 fg=0.01 bg=0.00
prosthetic group binding GO:0051192 p=3.0E−02 n=1 fg=0.01 bg=0.00
carbohydrate transmembrane transporter a... GO:0015144 p=3.0E−02 n=1 fg=0.01 bg=0.00
monosaccharide transmembrane transporter... GO:0015145 p=3.0E−02 n=1 fg=0.01 bg=0.00
hexose transmembrane transporter activit... GO:0015149 p=3.0E−02 n=1 fg=0.01 bg=0.00
phosphopantetheine binding GO:0031177 p=3.0E−02 n=1 fg=0.01 bg=0.00
phenanthrene−epoxide hydrolase activity GO:0019118 p=3.0E−02 n=1 fg=0.01 bg=0.00
phenanthrene−9,10−epoxide hydrolase acti... GO:0019119 p=3.0E−02 n=1 fg=0.01 bg=0.00
CoA carboxylase activity GO:0016421 p=3.0E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=3.0E−02 n=1 fg=0.01 bg=0.00
alpha−adrenergic receptor activity GO:0004936 p=3.0E−02 n=1 fg=0.01 bg=0.00
alpha2−adrenergic receptor activity GO:0004938 p=3.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=71/309 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032375459.2
fraction genes in fg and expected valu
presynaptic active zone GO:0048786 p=4.3E−03 n=4 fg=0.05 bg=0.01
voltage−gated calcium channel complex GO:0005891 p=1.2E−02 n=2 fg=0.02 bg=0.00
excitatory synapse GO:0060076 p=1.7E−02 n=2 fg=0.02 bg=0.00
vesicle coat GO:0030120 p=2.2E−02 n=2 fg=0.02 bg=0.00
COPI−coated vesicle GO:0030137 p=2.8E−02 n=2 fg=0.02 bg=0.00
calcium channel complex GO:0034704 p=2.8E−02 n=2 fg=0.02 bg=0.00
polytene chromosome band GO:0005704 p=3.0E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=3.0E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=3.0E−02 n=1 fg=0.01 bg=0.00
chromaffin granule GO:0042583 p=3.0E−02 n=1 fg=0.01 bg=0.00
chromaffin granule membrane GO:0042584 p=3.0E−02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005754 p=3.0E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase, cataly... GO:0045267 p=3.0E−02 n=1 fg=0.01 bg=0.00
ACF complex GO:0016590 p=3.0E−02 n=1 fg=0.01 bg=0.00
membrane−bounded organelle GO:0043227 p=4.6E−02 n=71 fg=0.88 bg=0.80
T−tubule GO:0030315 p=5.6E+02 n=2 fg=0.02 bg=0.00
transport vesicle GO:0030133 p=5.8E+02 n=6 fg=0.07 bg=0.03
intracellular organelle GO:0043229 p=5.9E+02 n=73 fg=0.90 bg=0.83
box H/ACA telomerase RNP complex GO:0090661 p=5.9E+02 n=1 fg=0.01 bg=0.00
COPII vesicle coat GO:0030127 p=5.9E+02 n=1 fg=0.01 bg=0.00
gut granule GO:0044840 p=5.9E+02 n=1 fg=0.01 bg=0.00
gut granule membrane GO:0044841 p=5.9E+02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005753 p=5.9E+02 n=1 fg=0.01 bg=0.00
RSF complex GO:0031213 p=5.9E+02 n=1 fg=0.01 bg=0.00
activating signal cointegrator 1 complex GO:0099053 p=5.9E+02 n=1 fg=0.01 bg=0.00
box H/ACA snoRNP complex GO:0031429 p=5.9E+02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase complex... GO:0045261 p=5.9E+02 n=1 fg=0.01 bg=0.00
delta DNA polymerase complex GO:0043625 p=5.9E+02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0000275 p=5.9E+02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase complex GO:0045259 p=5.9E+02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=81/309 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction