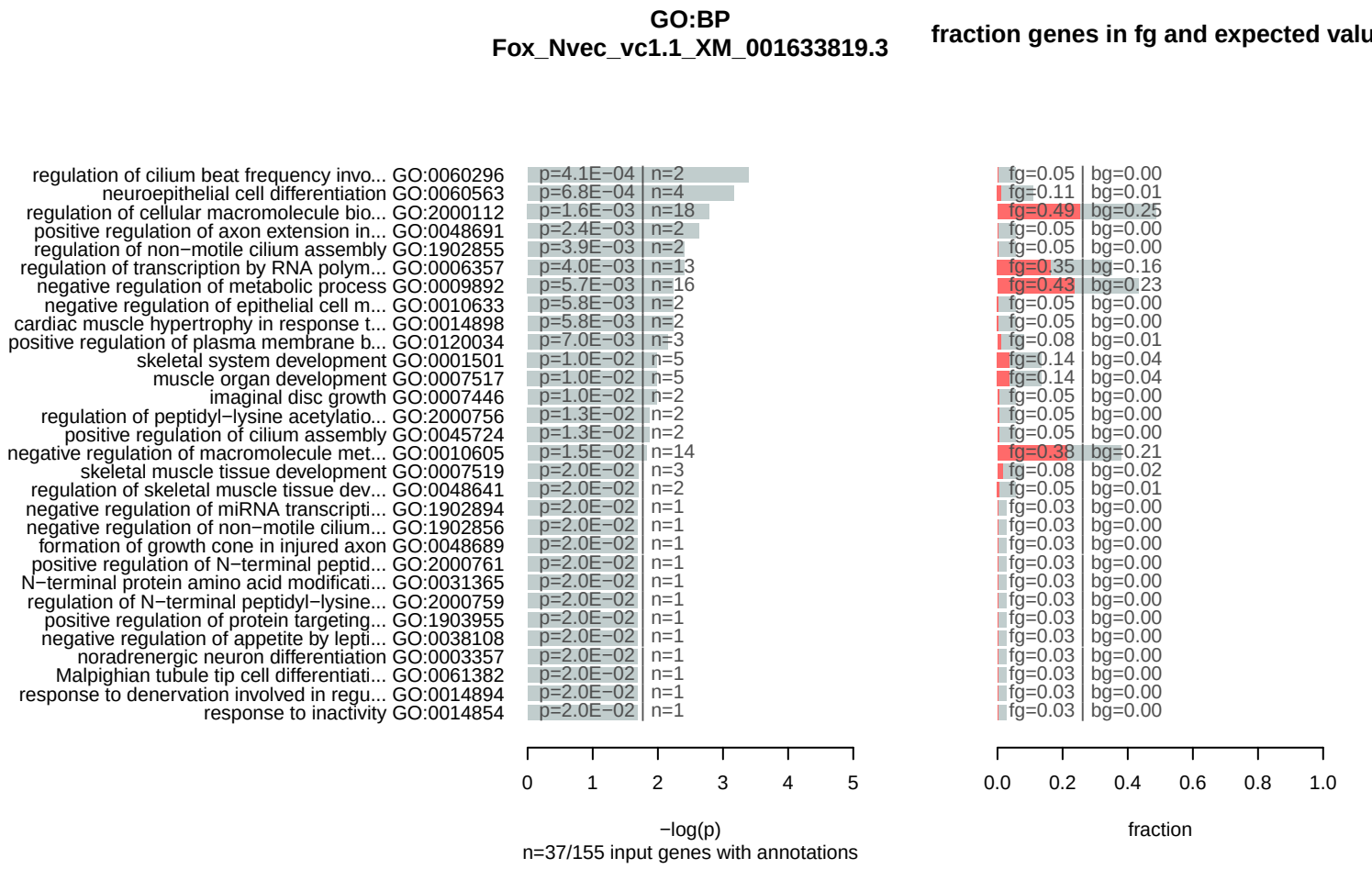
GO:BP
Fox_Nvec_vc1.1_XM_001633819.3
fraction genes in fg and expected valu
regulation of cilium beat frequency invo... GO:0060296 p=4.1E−04 n=2 fg=0.05 bg=0.00
neuroepithelial cell differentiation GO:0060563 p=6.8E−04 n=4 fg=0.11 bg=0.01
regulation of cellular macromolecule bio... GO:2000112 p=1.6E−03 n=18 fg=0.49 bg=0.25
positive regulation of axon extension in... GO:0048691 p=2.4E−03 n=2 fg=0.05 bg=0.00
regulation of non−motile cilium assembly GO:1902855 p=3.9E−03 n=2 fg=0.05 bg=0.00
regulation of transcription by RNA polym... GO:0006357 p=4.0E−03 n=13 fg=0.35 bg=0.16
negative regulation of metabolic process GO:0009892 p=5.7E−03 n=16 fg=0.43 bg=0.23
negative regulation of epithelial cell m... GO:0010633 p=5.8E−03 n=2 fg=0.05 bg=0.00
cardiac muscle hypertrophy in response t... GO:0014898 p=5.8E−03 n=2 fg=0.05 bg=0.00
positive regulation of plasma membrane b... GO:0120034 p=7.0E−03 n=3 fg=0.08 bg=0.01
skeletal system development GO:0001501 p=1.0E−02 n=5 fg=0.14 bg=0.04
muscle organ development GO:0007517 p=1.0E−02 n=5 fg=0.14 bg=0.04
imaginal disc growth GO:0007446 p=1.0E−02 n=2 fg=0.05 bg=0.00
regulation of peptidyl−lysine acetylatio... GO:2000756 p=1.3E−02 n=2 fg=0.05 bg=0.00
positive regulation of cilium assembly GO:0045724 p=1.3E−02 n=2 fg=0.05 bg=0.00
negative regulation of macromolecule met... GO:0010605 p=1.5E−02 n=14 fg=0.38 bg=0.21
skeletal muscle tissue development GO:0007519 p=2.0E−02 n=3 fg=0.08 bg=0.02
regulation of skeletal muscle tissue dev... GO:0048641 p=2.0E−02 n=2 fg=0.05 bg=0.01
negative regulation of miRNA transcripti... GO:1902894 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of non−motile cilium... GO:1902856 p=2.0E−02 n=1 fg=0.03 bg=0.00
formation of growth cone in injured axon GO:0048689 p=2.0E−02 n=1 fg=0.03 bg=0.00
positive regulation of N−terminal peptid... GO:2000761 p=2.0E−02 n=1 fg=0.03 bg=0.00
N−terminal protein amino acid modificati... GO:0031365 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of N−terminal peptidyl−lysine... GO:2000759 p=2.0E−02 n=1 fg=0.03 bg=0.00
positive regulation of protein targeting... GO:1903955 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of appetite by lepti... GO:0038108 p=2.0E−02 n=1 fg=0.03 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=2.0E−02 n=1 fg=0.03 bg=0.00
Malpighian tubule tip cell differentiati... GO:0061382 p=2.0E−02 n=1 fg=0.03 bg=0.00
response to denervation involved in regu... GO:0014894 p=2.0E−02 n=1 fg=0.03 bg=0.00
response to inactivity GO:0014854 p=2.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=37/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001633819.3
fraction genes in fg and expected valu
sequence−specific DNA binding GO:0043565 p=4.5E−03 n=7 fg=0.23 bg=0.07
DNA−binding transcription activator acti... GO:0001228 p=5.5E−03 n=5 fg=0.16 bg=0.04
microtubule motor activity GO:0003777 p=9.6E−03 n=2 fg=0.06 bg=0.01
phosphatidylinositol binding GO:0035091 p=1.1E−02 n=4 fg=0.13 bg=0.03
promoter−specific chromatin binding GO:1990841 p=1.2E−02 n=2 fg=0.06 bg=0.01
ATP hydrolysis activity GO:0016887 p=1.3E−02 n=5 fg=0.16 bg=0.05
voltage−gated potassium channel activity GO:0005249 p=1.5E−02 n=2 fg=0.06 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=1.6E−02 n=5 fg=0.16 bg=0.05
glutamate receptor binding GO:0035254 p=1.8E−02 n=2 fg=0.06 bg=0.01
transmembrane receptor protein tyrosine ... GO:0005001 p=1.9E−02 n=1 fg=0.03 bg=0.00
intracellular phosphatidylinositol−3,5−b... GO:0097682 p=1.9E−02 n=1 fg=0.03 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=1.9E−02 n=1 fg=0.03 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=1.9E−02 n=1 fg=0.03 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=1.9E−02 n=1 fg=0.03 bg=0.00
DNA/DNA annealing activity GO:1990814 p=1.9E−02 n=1 fg=0.03 bg=0.00
nucleoside−triphosphatase activity GO:0017111 p=2.1E−02 n=6 fg=0.19 bg=0.07
cis−regulatory region sequence−specific ... GO:0000987 p=2.3E−02 n=4 fg=0.13 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.3E−02 n=4 fg=0.13 bg=0.04
metal ion transmembrane transporter acti... GO:0046873 p=2.4E−02 n=4 fg=0.13 bg=0.04
hydrolase activity, acting on acid anhyd... GO:0016817 p=2.4E−02 n=6 fg=0.19 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016818 p=2.4E−02 n=6 fg=0.19 bg=0.07
pyrophosphatase activity GO:0016462 p=2.4E−02 n=6 fg=0.19 bg=0.07
transcription cis−regulatory region bind... GO:0000976 p=2.6E−02 n=5 fg=0.16 bg=0.06
potassium channel activity GO:0005267 p=2.9E−02 n=2 fg=0.06 bg=0.01
anion binding GO:0043168 p=3.3E−02 n=8 fg=0.26 bg=0.13
sequence−specific double−stranded DNA bi... GO:1990837 p=3.4E−02 n=5 fg=0.16 bg=0.06
phospholipid binding GO:0005543 p=3.6E−02 n=4 fg=0.13 bg=0.04
transcription regulatory region nucleic ... GO:0001067 p=3.8E−02 n=5 fg=0.16 bg=0.06
annealing activity GO:0140666 p=3.9E−02 n=1 fg=0.03 bg=0.00
nitric−oxide synthase regulator activity GO:0030235 p=3.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=31/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001633819.3
fraction genes in fg and expected valu
cation channel complex GO:0034703 p=8.8E−03 n=3 fg=0.08 bg=0.01
potassium channel complex GO:0034705 p=1.4E−02 n=2 fg=0.05 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=1.4E−02 n=2 fg=0.05 bg=0.01
ciliary basal body GO:0036064 p=1.8E−02 n=3 fg=0.08 bg=0.01
photoreceptor inner segment GO:0001917 p=2.1E−02 n=2 fg=0.05 bg=0.01
photoreceptor connecting cilium GO:0032391 p=2.1E−02 n=2 fg=0.05 bg=0.01
plus−end kinesin complex GO:0005873 p=2.1E−02 n=1 fg=0.03 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=2.1E−02 n=1 fg=0.03 bg=0.00
integral component of lysosomal membrane GO:1905103 p=2.1E−02 n=1 fg=0.03 bg=0.00
motile cilium GO:0031514 p=3.8E−02 n=3 fg=0.08 bg=0.02
photoreceptor outer segment GO:0001750 p=3.8E−02 n=2 fg=0.05 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=3.8E−02 n=2 fg=0.05 bg=0.01
muscle myosin complex GO:0005859 p=4.2E−02 n=1 fg=0.03 bg=0.00
myosin II complex GO:0016460 p=4.2E−02 n=1 fg=0.03 bg=0.00
BBSome GO:0034464 p=4.2E−02 n=1 fg=0.03 bg=0.00
intrinsic component of vacuolar membrane GO:0031310 p=4.2E−02 n=1 fg=0.03 bg=0.00
myosin V complex GO:0031475 p=4.2E−02 n=1 fg=0.03 bg=0.00
integral component of vacuolar membrane GO:0031166 p=4.2E−02 n=1 fg=0.03 bg=0.00
tertiary granule GO:0070820 p=5.3E−02 n=2 fg=0.05 bg=0.01
extrinsic component of membrane GO:0019898 p=5.6E−02 n=3 fg=0.08 bg=0.02
cytoplasmic side of plasma membrane GO:0009898 p=5.6E−02 n=3 fg=0.08 bg=0.02
endolysosome membrane GO:0036020 p=6.2E−02 n=1 fg=0.03 bg=0.00
exon−exon junction complex GO:0035145 p=6.2E−02 n=1 fg=0.03 bg=0.00
endolysosome GO:0036019 p=6.2E−02 n=1 fg=0.03 bg=0.00
postsynaptic specialization membrane GO:0099634 p=6.2E−02 n=1 fg=0.03 bg=0.00
dendritic spine membrane GO:0032591 p=6.2E−02 n=1 fg=0.03 bg=0.00
respiratory chain complex IV GO:0045277 p=6.2E−02 n=1 fg=0.03 bg=0.00
proximal dendrite GO:1990635 p=6.2E−02 n=1 fg=0.03 bg=0.00
postsynaptic density membrane GO:0098839 p=6.2E−02 n=1 fg=0.03 bg=0.00
mitochondrial respiratory chain complex ... GO:0005751 p=6.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=38/155 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction