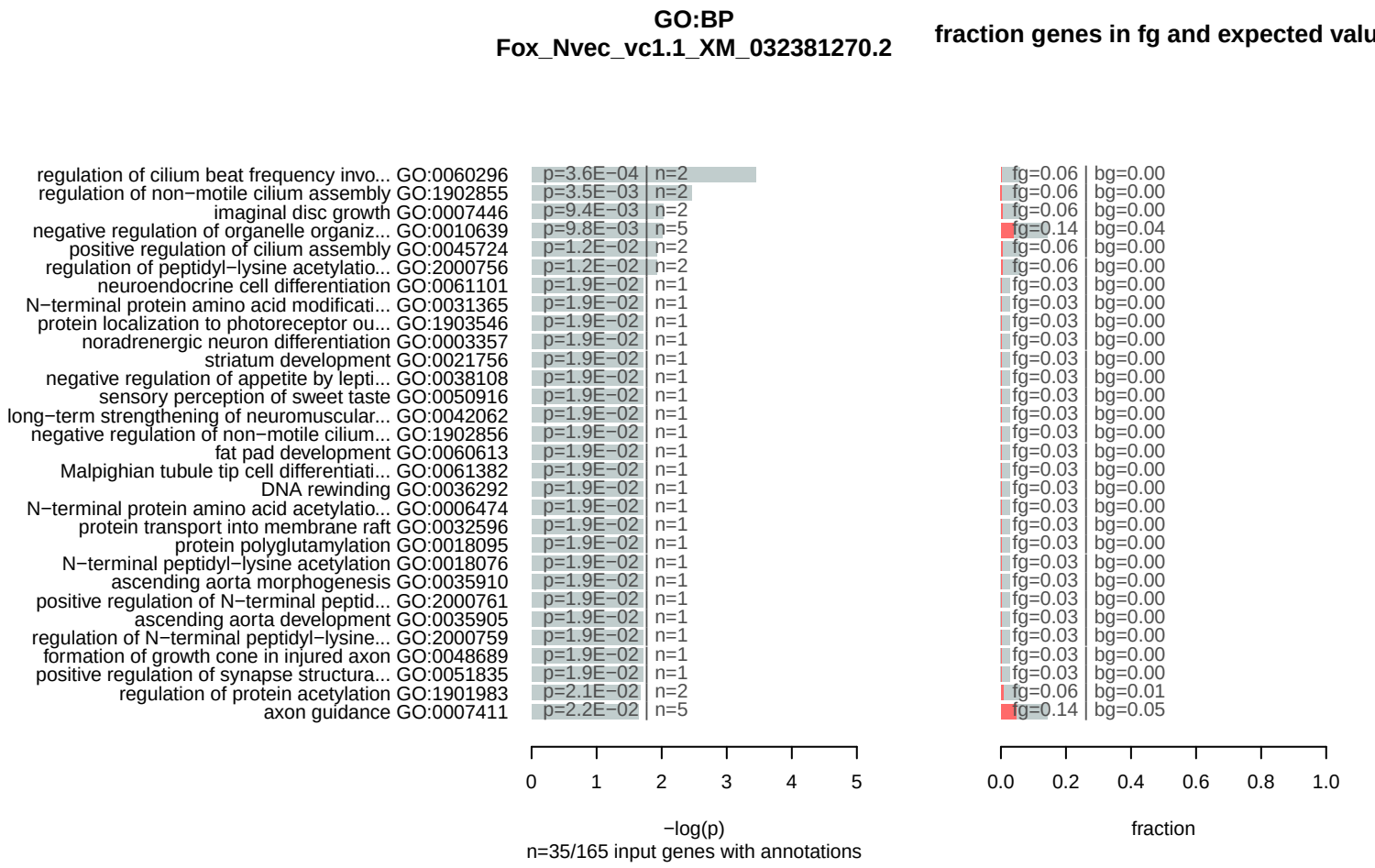
GO:BP
Fox_Nvec_vc1.1_XM_032381270.2
fraction genes in fg and expected valu
regulation of cilium beat frequency invo... GO:0060296 p=3.6E−04 n=2 fg=0.06 bg=0.00
regulation of non−motile cilium assembly GO:1902855 p=3.5E−03 n=2 fg=0.06 bg=0.00
imaginal disc growth GO:0007446 p=9.4E−03 n=2 fg=0.06 bg=0.00
negative regulation of organelle organiz... GO:0010639 p=9.8E−03 n=5 fg=0.14 bg=0.04
positive regulation of cilium assembly GO:0045724 p=1.2E−02 n=2 fg=0.06 bg=0.00
regulation of peptidyl−lysine acetylatio... GO:2000756 p=1.2E−02 n=2 fg=0.06 bg=0.00
neuroendocrine cell differentiation GO:0061101 p=1.9E−02 n=1 fg=0.03 bg=0.00
N−terminal protein amino acid modificati... GO:0031365 p=1.9E−02 n=1 fg=0.03 bg=0.00
protein localization to photoreceptor ou... GO:1903546 p=1.9E−02 n=1 fg=0.03 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=1.9E−02 n=1 fg=0.03 bg=0.00
striatum development GO:0021756 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of appetite by lepti... GO:0038108 p=1.9E−02 n=1 fg=0.03 bg=0.00
sensory perception of sweet taste GO:0050916 p=1.9E−02 n=1 fg=0.03 bg=0.00
long−term strengthening of neuromuscular... GO:0042062 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of non−motile cilium... GO:1902856 p=1.9E−02 n=1 fg=0.03 bg=0.00
fat pad development GO:0060613 p=1.9E−02 n=1 fg=0.03 bg=0.00
Malpighian tubule tip cell differentiati... GO:0061382 p=1.9E−02 n=1 fg=0.03 bg=0.00
DNA rewinding GO:0036292 p=1.9E−02 n=1 fg=0.03 bg=0.00
N−terminal protein amino acid acetylatio... GO:0006474 p=1.9E−02 n=1 fg=0.03 bg=0.00
protein transport into membrane raft GO:0032596 p=1.9E−02 n=1 fg=0.03 bg=0.00
protein polyglutamylation GO:0018095 p=1.9E−02 n=1 fg=0.03 bg=0.00
N−terminal peptidyl−lysine acetylation GO:0018076 p=1.9E−02 n=1 fg=0.03 bg=0.00
ascending aorta morphogenesis GO:0035910 p=1.9E−02 n=1 fg=0.03 bg=0.00
positive regulation of N−terminal peptid... GO:2000761 p=1.9E−02 n=1 fg=0.03 bg=0.00
ascending aorta development GO:0035905 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of N−terminal peptidyl−lysine... GO:2000759 p=1.9E−02 n=1 fg=0.03 bg=0.00
formation of growth cone in injured axon GO:0048689 p=1.9E−02 n=1 fg=0.03 bg=0.00
positive regulation of synapse structura... GO:0051835 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of protein acetylation GO:1901983 p=2.1E−02 n=2 fg=0.06 bg=0.01
axon guidance GO:0007411 p=2.2E−02 n=5 fg=0.14 bg=0.05
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−log(p)
n=35/165 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032381270.2
fraction genes in fg and expected valu
microtubule motor activity GO:0003777 p=9.6E−03 n=2 fg=0.06 bg=0.01
mRNA binding GO:0003729 p=1.3E−02 n=4 fg=0.13 bg=0.03
voltage−gated potassium channel activity GO:0005249 p=1.5E−02 n=2 fg=0.06 bg=0.01
DNA/DNA annealing activity GO:1990814 p=1.9E−02 n=1 fg=0.03 bg=0.00
taste receptor binding GO:0031883 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
ATP−dependent DNA/DNA annealing activity GO:0036310 p=1.9E−02 n=1 fg=0.03 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=2.8E−02 n=4 fg=0.13 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=2.8E−02 n=4 fg=0.13 bg=0.04
potassium channel activity GO:0005267 p=2.9E−02 n=2 fg=0.06 bg=0.01
phosphatidylinositol−4,5−bisphosphate bi... GO:0005546 p=3.7E−02 n=2 fg=0.06 bg=0.01
ISG15 transferase activity GO:0042296 p=3.9E−02 n=1 fg=0.03 bg=0.00
telomeric D−loop binding GO:0061821 p=3.9E−02 n=1 fg=0.03 bg=0.00
four−way junction helicase activity GO:0009378 p=3.9E−02 n=1 fg=0.03 bg=0.00
annealing activity GO:0140666 p=3.9E−02 n=1 fg=0.03 bg=0.00
dipeptidase activity GO:0016805 p=3.9E−02 n=1 fg=0.03 bg=0.00
D−loop DNA binding GO:0062037 p=3.9E−02 n=1 fg=0.03 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=4.2E−02 n=2 fg=0.06 bg=0.01
voltage−gated cation channel activity GO:0022843 p=4.6E−02 n=2 fg=0.06 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=5.2E−02 n=5 fg=0.16 bg=0.07
nucleic acid binding GO:0003676 p=5.5E−02 n=10 fg=0.32 bg=0.19
phosphatidylinositol bisphosphate bindin... GO:1902936 p=5.6E−02 n=2 fg=0.06 bg=0.01
cAMP response element binding GO:0035497 p=5.7E−02 n=1 fg=0.03 bg=0.00
3'−5' DNA helicase activity GO:0043138 p=5.7E−02 n=1 fg=0.03 bg=0.00
ankyrin binding GO:0030506 p=5.7E−02 n=1 fg=0.03 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=5.7E−02 n=1 fg=0.03 bg=0.00
bHLH transcription factor binding GO:0043425 p=5.7E−02 n=1 fg=0.03 bg=0.00
bubble DNA binding GO:0000405 p=5.7E−02 n=1 fg=0.03 bg=0.00
calcium−activated potassium channel acti... GO:0015269 p=5.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol binding GO:0035091 p=5.8E−02 n=3 fg=0.10 bg=0.03
0 1 2 3 4 5
−log(p)
n=31/165 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032381270.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=1.4E−02 n=2 fg=0.05 bg=0.01
potassium channel complex GO:0034705 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
lateral plasma membrane GO:0016328 p=2.1E−02 n=2 fg=0.05 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
spectrin GO:0008091 p=2.1E−02 n=1 fg=0.03 bg=0.00
spectrosome GO:0045170 p=2.1E−02 n=1 fg=0.03 bg=0.00
photoreceptor outer segment GO:0001750 p=3.8E−02 n=2 fg=0.05 bg=0.01
BBSome GO:0034464 p=4.2E−02 n=1 fg=0.03 bg=0.00
transmembrane transporter complex GO:1902495 p=4.4E−02 n=3 fg=0.08 bg=0.02
transporter complex GO:1990351 p=5.0E−02 n=3 fg=0.08 bg=0.02
tertiary granule GO:0070820 p=5.3E−02 n=2 fg=0.05 bg=0.01
exon−exon junction complex GO:0035145 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
mitochondrial respiratory chain complex ... GO:0005751 p=6.2E−02 n=1 fg=0.03 bg=0.00
cation channel complex GO:0034703 p=7.0E−02 n=2 fg=0.05 bg=0.01
centriole GO:0005814 p=7.0E−02 n=2 fg=0.05 bg=0.01
9+0 non−motile cilium GO:0097731 p=7.6E−02 n=2 fg=0.05 bg=0.01
photoreceptor cell cilium GO:0097733 p=7.6E−02 n=2 fg=0.05 bg=0.01
pericentriolar material GO:0000242 p=8.1E−02 n=1 fg=0.03 bg=0.00
extrinsic component of endosome membrane GO:0031313 p=8.1E−02 n=1 fg=0.03 bg=0.00
ciliary transition zone GO:0035869 p=8.2E−02 n=2 fg=0.05 bg=0.01
ion channel complex GO:0034702 p=8.2E−02 n=2 fg=0.05 bg=0.01
cytochrome complex GO:0070069 p=1.0E−01 n=1 fg=0.03 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=1.0E−01 n=1 fg=0.03 bg=0.00
microtubule organizing center GO:0005815 p=1.0E−01 n=5 fg=0.13 bg=0.07
tertiary granule lumen GO:1904724 p=1.2E−01 n=1 fg=0.03 bg=0.00
centriolar satellite GO:0034451 p=1.2E−01 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=38/165 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction