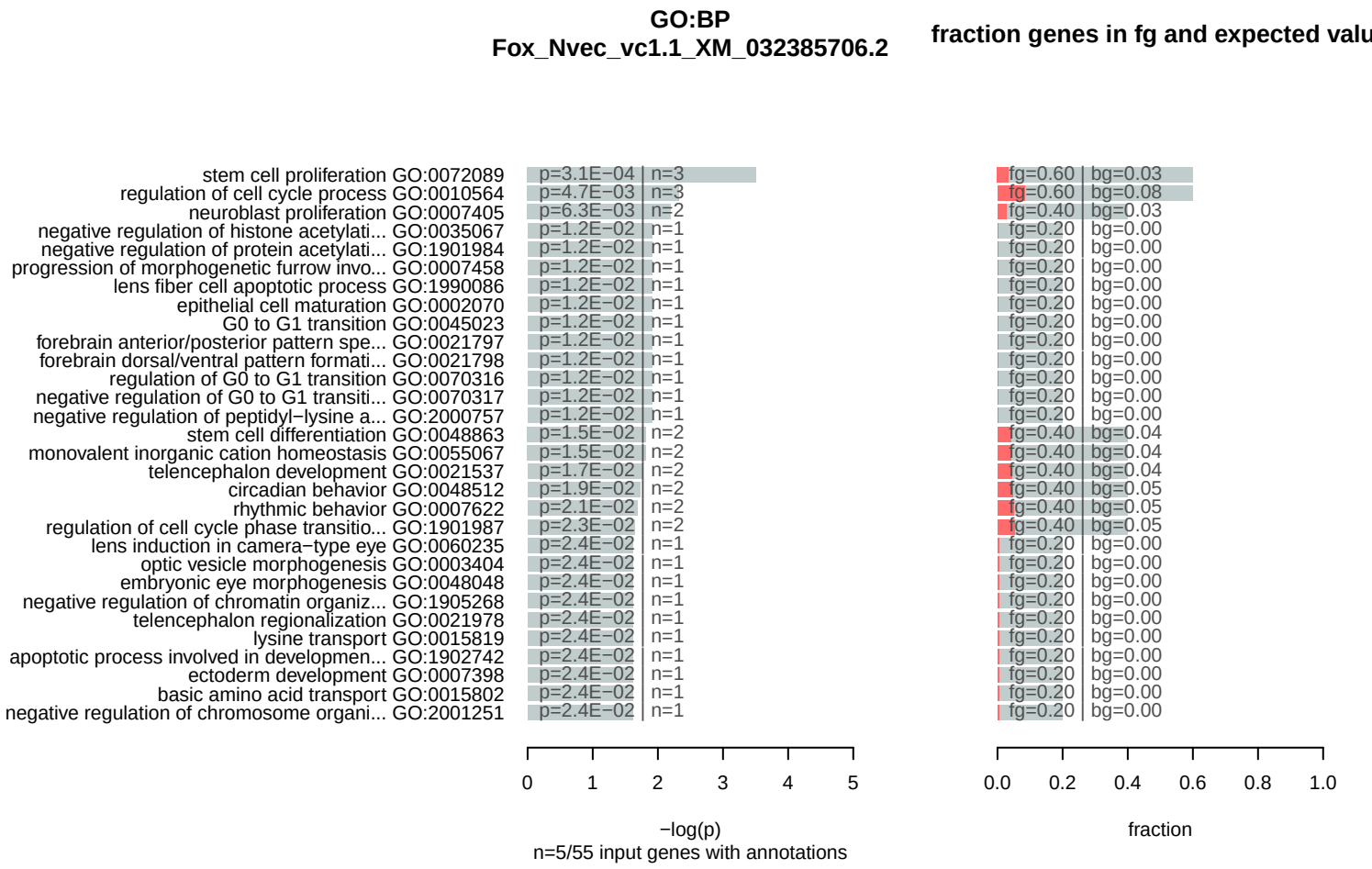
GO:BP
Fox_Nvec_vc1.1_XM_032385706.2
fraction genes in fg and expected valu
stem cell proliferation GO:0072089 p=3.1E−04 n=3 fg=0.60 bg=0.03
regulation of cell cycle process GO:0010564 p=4.7E−03 n=3 fg=0.60 bg=0.08
neuroblast proliferation GO:0007405 p=6.3E−03 n=2 fg=0.40 bg=0.03
negative regulation of histone acetylati... GO:0035067 p=1.2E−02 n=1 fg=0.20 bg=0.00
negative regulation of protein acetylati... GO:1901984 p=1.2E−02 n=1 fg=0.20 bg=0.00
progression of morphogenetic furrow invo... GO:0007458 p=1.2E−02 n=1 fg=0.20 bg=0.00
lens fiber cell apoptotic process GO:1990086 p=1.2E−02 n=1 fg=0.20 bg=0.00
epithelial cell maturation GO:0002070 p=1.2E−02 n=1 fg=0.20 bg=0.00
G0 to G1 transition GO:0045023 p=1.2E−02 n=1 fg=0.20 bg=0.00
forebrain anterior/posterior pattern spe... GO:0021797 p=1.2E−02 n=1 fg=0.20 bg=0.00
forebrain dorsal/ventral pattern formati... GO:0021798 p=1.2E−02 n=1 fg=0.20 bg=0.00
regulation of G0 to G1 transition GO:0070316 p=1.2E−02 n=1 fg=0.20 bg=0.00
negative regulation of G0 to G1 transiti... GO:0070317 p=1.2E−02 n=1 fg=0.20 bg=0.00
negative regulation of peptidyl−lysine a... GO:2000757 p=1.2E−02 n=1 fg=0.20 bg=0.00
stem cell differentiation GO:0048863 p=1.5E−02 n=2 fg=0.40 bg=0.04
monovalent inorganic cation homeostasis GO:0055067 p=1.5E−02 n=2 fg=0.40 bg=0.04
telencephalon development GO:0021537 p=1.7E−02 n=2 fg=0.40 bg=0.04
circadian behavior GO:0048512 p=1.9E−02 n=2 fg=0.40 bg=0.05
rhythmic behavior GO:0007622 p=2.1E−02 n=2 fg=0.40 bg=0.05
regulation of cell cycle phase transitio... GO:1901987 p=2.3E−02 n=2 fg=0.40 bg=0.05
lens induction in camera−type eye GO:0060235 p=2.4E−02 n=1 fg=0.20 bg=0.00
optic vesicle morphogenesis GO:0003404 p=2.4E−02 n=1 fg=0.20 bg=0.00
embryonic eye morphogenesis GO:0048048 p=2.4E−02 n=1 fg=0.20 bg=0.00
negative regulation of chromatin organiz... GO:1905268 p=2.4E−02 n=1 fg=0.20 bg=0.00
telencephalon regionalization GO:0021978 p=2.4E−02 n=1 fg=0.20 bg=0.00
lysine transport GO:0015819 p=2.4E−02 n=1 fg=0.20 bg=0.00
apoptotic process involved in developmen... GO:1902742 p=2.4E−02 n=1 fg=0.20 bg=0.00
ectoderm development GO:0007398 p=2.4E−02 n=1 fg=0.20 bg=0.00
basic amino acid transport GO:0015802 p=2.4E−02 n=1 fg=0.20 bg=0.00
negative regulation of chromosome organi... GO:2001251 p=2.4E−02 n=1 fg=0.20 bg=0.00
0 1 2 3 4 5
−log(p)
n=5/55 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032385706.2
fraction genes in fg and expected valu
transcription corepressor binding GO:0001222 p=2.2E−02 n=1 fg=0.25 bg=0.01
methylated histone binding GO:0035064 p=3.3E−02 n=1 fg=0.25 bg=0.01
methylation−dependent protein binding GO:0140034 p=3.3E−02 n=1 fg=0.25 bg=0.01
transcription coregulator binding GO:0001221 p=3.3E−02 n=1 fg=0.25 bg=0.01
promoter−specific chromatin binding GO:1990841 p=3.3E−02 n=1 fg=0.25 bg=0.01
modification−dependent protein binding GO:0140030 p=5.4E−02 n=1 fg=0.25 bg=0.01
intracellular cyclic nucleotide activate... GO:0005221 p=5.4E−02 n=1 fg=0.25 bg=0.01
voltage−gated potassium channel activity... GO:0086090 p=5.4E−02 n=1 fg=0.25 bg=0.01
cyclic nucleotide−gated ion channel acti... GO:0043855 p=5.4E−02 n=1 fg=0.25 bg=0.01
voltage−gated potassium channel activity... GO:0086008 p=5.4E−02 n=1 fg=0.25 bg=0.01
delayed rectifier potassium channel acti... GO:0005251 p=5.4E−02 n=1 fg=0.25 bg=0.01
disordered domain specific binding GO:0097718 p=5.4E−02 n=1 fg=0.25 bg=0.01
voltage−gated potassium channel activity... GO:0086087 p=5.4E−02 n=1 fg=0.25 bg=0.01
voltage−gated potassium channel activity... GO:0086089 p=5.4E−02 n=1 fg=0.25 bg=0.01
channel inhibitor activity GO:0016248 p=6.5E−02 n=1 fg=0.25 bg=0.02
molecular function inhibitor activity GO:0140678 p=6.5E−02 n=1 fg=0.25 bg=0.02
histone deacetylase binding GO:0042826 p=6.5E−02 n=1 fg=0.25 bg=0.02
alpha−actinin binding GO:0051393 p=6.5E−02 n=1 fg=0.25 bg=0.02
potassium channel inhibitor activity GO:0019870 p=6.5E−02 n=1 fg=0.25 bg=0.02
ion channel inhibitor activity GO:0008200 p=6.5E−02 n=1 fg=0.25 bg=0.02
actinin binding GO:0042805 p=6.5E−02 n=1 fg=0.25 bg=0.02
intracellular ligand−gated ion channel a... GO:0005217 p=7.5E−02 n=1 fg=0.25 bg=0.02
outward rectifier potassium channel acti... GO:0015271 p=7.5E−02 n=1 fg=0.25 bg=0.02
signaling receptor binding GO:0005102 p=8.3E−02 n=2 fg=0.50 bg=0.13
potassium channel regulator activity GO:0015459 p=9.6E−02 n=1 fg=0.25 bg=0.03
voltage−gated potassium channel activity GO:0005249 p=9.6E−02 n=1 fg=0.25 bg=0.03
ligand−gated cation channel activity GO:0099094 p=9.6E−02 n=1 fg=0.25 bg=0.03
kinesin binding GO:0019894 p=9.6E−02 n=1 fg=0.25 bg=0.03
histone binding GO:0042393 p=9.6E−02 n=1 fg=0.25 bg=0.03
mRNA binding GO:0003729 p=9.6E−02 n=1 fg=0.25 bg=0.03
0 1 2 3 4 5
−log(p)
n=4/55 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032385706.2
fraction genes in fg and expected valu
cell tip GO:0051286 p=3.0E−02 n=1 fg=0.17 bg=0.01
cell pole GO:0060187 p=3.0E−02 n=1 fg=0.17 bg=0.01
storage vacuole GO:0000322 p=4.4E−02 n=1 fg=0.17 bg=0.01
fungal−type vacuole GO:0000324 p=4.4E−02 n=1 fg=0.17 bg=0.01
fungal−type vacuole membrane GO:0000329 p=4.4E−02 n=1 fg=0.17 bg=0.01
cell division site GO:0032153 p=7.3E−02 n=1 fg=0.17 bg=0.01
juxtaparanode region of axon GO:0044224 p=7.3E−02 n=1 fg=0.17 bg=0.01
intracellular canaliculus GO:0046691 p=7.3E−02 n=1 fg=0.17 bg=0.01
PcG protein complex GO:0031519 p=8.7E−02 n=1 fg=0.17 bg=0.01
paranode region of axon GO:0033270 p=8.7E−02 n=1 fg=0.17 bg=0.01
intercalated disc GO:0014704 p=1.0E−01 n=1 fg=0.17 bg=0.02
intrinsic component of synaptic membrane GO:0099240 p=1.0E−01 n=1 fg=0.17 bg=0.02
integral component of synaptic membrane GO:0099699 p=1.0E−01 n=1 fg=0.17 bg=0.02
intrinsic component of postsynaptic memb... GO:0098936 p=1.0E−01 n=1 fg=0.17 bg=0.02
intrinsic component of presynaptic membr... GO:0098889 p=1.0E−01 n=1 fg=0.17 bg=0.02
integral component of postsynaptic membr... GO:0099055 p=1.0E−01 n=1 fg=0.17 bg=0.02
integral component of presynaptic membra... GO:0099056 p=1.0E−01 n=1 fg=0.17 bg=0.02
voltage−gated potassium channel complex GO:0008076 p=1.1E−01 n=1 fg=0.17 bg=0.02
perikaryon GO:0043204 p=1.1E−01 n=1 fg=0.17 bg=0.02
cell−cell contact zone GO:0044291 p=1.1E−01 n=1 fg=0.17 bg=0.02
potassium channel complex GO:0034705 p=1.1E−01 n=1 fg=0.17 bg=0.02
lytic vacuole membrane GO:0098852 p=1.3E−01 n=1 fg=0.17 bg=0.02
dendritic shaft GO:0043198 p=1.3E−01 n=1 fg=0.17 bg=0.02
lamellipodium GO:0030027 p=1.4E−01 n=1 fg=0.17 bg=0.02
Z disc GO:0030018 p=1.5E−01 n=1 fg=0.17 bg=0.03
intrinsic component of endoplasmic retic... GO:0031227 p=1.5E−01 n=1 fg=0.17 bg=0.03
main axon GO:0044304 p=1.5E−01 n=1 fg=0.17 bg=0.03
vacuolar membrane GO:0005774 p=1.5E−01 n=1 fg=0.17 bg=0.03
integral component of endoplasmic reticu... GO:0030176 p=1.5E−01 n=1 fg=0.17 bg=0.03
intracellular membrane−bounded organelle GO:0043231 p=1.6E−01 n=6 fg=1.00 bg=0.74
0 1 2 3 4 5
−log(p)
n=6/55 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction