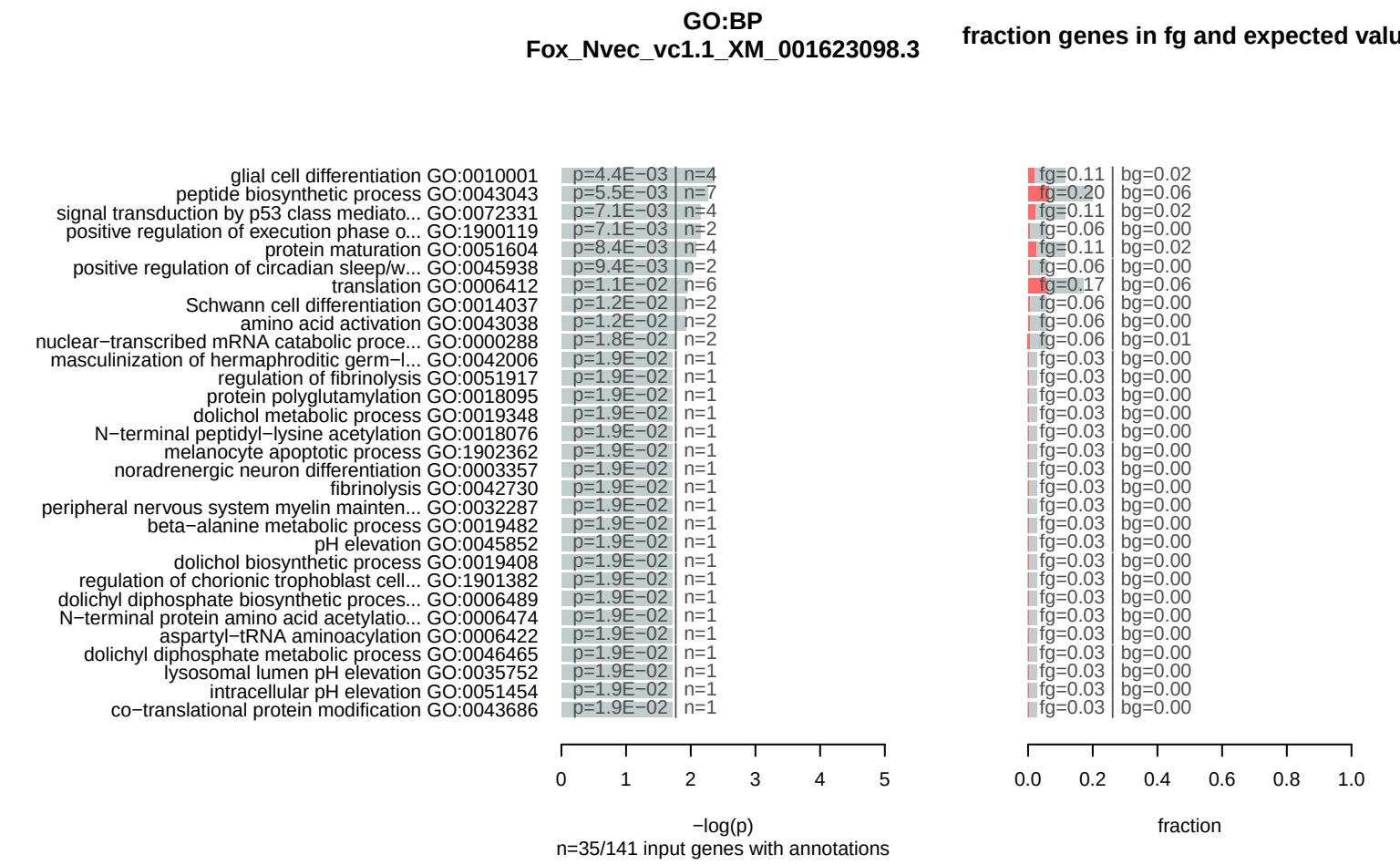
GO:BP
Fox_Nvec_vc1.1_XM_001623098.3
fraction genes in fg and expected valu
glial cell differentiation GO:0010001 p=4.4E−03 n=4 fg=0.11 bg=0.02
peptide biosynthetic process GO:0043043 p=5.5E−03 n=7 fg=0.20 bg=0.06
signal transduction by p53 class mediato... GO:0072331 p=7.1E−03 n=4 fg=0.11 bg=0.02
positive regulation of execution phase o... GO:1900119 p=7.1E−03 n=2 fg=0.06 bg=0.00
protein maturation GO:0051604 p=8.4E−03 n=4 fg=0.11 bg=0.02
positive regulation of circadian sleep/w... GO:0045938 p=9.4E−03 n=2 fg=0.06 bg=0.00
translation GO:0006412 p=1.1E−02 n=6 fg=0.17 bg=0.06
Schwann cell differentiation GO:0014037 p=1.2E−02 n=2 fg=0.06 bg=0.00
amino acid activation GO:0043038 p=1.2E−02 n=2 fg=0.06 bg=0.00
nuclear−transcribed mRNA catabolic proce... GO:0000288 p=1.8E−02 n=2 fg=0.06 bg=0.01
masculinization of hermaphroditic germ−l... GO:0042006 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of fibrinolysis GO:0051917 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
dolichol metabolic process GO:0019348 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
melanocyte apoptotic process GO:1902362 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
fibrinolysis GO:0042730 p=1.9E−02 n=1 fg=0.03 bg=0.00
peripheral nervous system myelin mainten... GO:0032287 p=1.9E−02 n=1 fg=0.03 bg=0.00
beta−alanine metabolic process GO:0019482 p=1.9E−02 n=1 fg=0.03 bg=0.00
pH elevation GO:0045852 p=1.9E−02 n=1 fg=0.03 bg=0.00
dolichol biosynthetic process GO:0019408 p=1.9E−02 n=1 fg=0.03 bg=0.00
regulation of chorionic trophoblast cell... GO:1901382 p=1.9E−02 n=1 fg=0.03 bg=0.00
dolichyl diphosphate biosynthetic proces... GO:0006489 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
aspartyl−tRNA aminoacylation GO:0006422 p=1.9E−02 n=1 fg=0.03 bg=0.00
dolichyl diphosphate metabolic process GO:0046465 p=1.9E−02 n=1 fg=0.03 bg=0.00
lysosomal lumen pH elevation GO:0035752 p=1.9E−02 n=1 fg=0.03 bg=0.00
intracellular pH elevation GO:0051454 p=1.9E−02 n=1 fg=0.03 bg=0.00
co−translational protein modification GO:0043686 p=1.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/141 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001623098.3
fraction genes in fg and expected valu
hydrolase activity, acting on carbon−nit... GO:0016810 p=9.1E−03 n=3 fg=0.09 bg=0.01
aspartate−tRNA ligase activity GO:0004815 p=2.1E−02 n=1 fg=0.03 bg=0.00
UDP−N−acetylglucosamine−dolichyl−phospha... GO:0003975 p=2.1E−02 n=1 fg=0.03 bg=0.00
non−sequence−specific DNA binding, bendi... GO:0044378 p=2.1E−02 n=1 fg=0.03 bg=0.00
DNA binding, bending GO:0008301 p=2.1E−02 n=1 fg=0.03 bg=0.00
interferon binding GO:0019961 p=2.1E−02 n=1 fg=0.03 bg=0.00
interferon−gamma binding GO:0019964 p=2.1E−02 n=1 fg=0.03 bg=0.00
glycogen binding GO:2001069 p=2.1E−02 n=1 fg=0.03 bg=0.00
aminoacylase activity GO:0004046 p=2.1E−02 n=1 fg=0.03 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.1E−02 n=1 fg=0.03 bg=0.00
AMP deaminase activity GO:0003876 p=2.1E−02 n=1 fg=0.03 bg=0.00
beta−galactosidase activity GO:0004565 p=2.1E−02 n=1 fg=0.03 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=2.1E−02 n=1 fg=0.03 bg=0.00
dolichyl−diphosphooligosaccharide−protei... GO:0004579 p=2.1E−02 n=1 fg=0.03 bg=0.00
cell adhesion molecule binding GO:0050839 p=2.2E−02 n=3 fg=0.09 bg=0.02
integrin binding GO:0005178 p=2.6E−02 n=2 fg=0.06 bg=0.01
UDP−N−acetylglucosamine−lysosomal−enzyme... GO:0003976 p=4.2E−02 n=1 fg=0.03 bg=0.00
dipeptidyl−peptidase activity GO:0008239 p=4.2E−02 n=1 fg=0.03 bg=0.00
galactosidase activity GO:0015925 p=4.2E−02 n=1 fg=0.03 bg=0.00
metallochaperone activity GO:0016530 p=4.2E−02 n=1 fg=0.03 bg=0.00
copper chaperone activity GO:0016531 p=4.2E−02 n=1 fg=0.03 bg=0.00
superoxide dismutase copper chaperone ac... GO:0016532 p=4.2E−02 n=1 fg=0.03 bg=0.00
heparan−alpha−glucosaminide N−acetyltran... GO:0015019 p=4.2E−02 n=1 fg=0.03 bg=0.00
virus receptor activity GO:0001618 p=4.2E−02 n=1 fg=0.03 bg=0.00
retinal binding GO:0016918 p=4.2E−02 n=1 fg=0.03 bg=0.00
exogenous protein binding GO:0140272 p=4.2E−02 n=1 fg=0.03 bg=0.00
phosphotransferase activity, for other s... GO:0016780 p=4.2E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−5−phosphate binding GO:0010314 p=4.2E−02 n=1 fg=0.03 bg=0.00
11−cis retinal binding GO:0005502 p=4.2E−02 n=1 fg=0.03 bg=0.00
oligosaccharyl transferase activity GO:0004576 p=4.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=34/141 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001623098.3
fraction genes in fg and expected valu
recycling endosome membrane GO:0055038 p=1.3E−02 n=2 fg=0.06 bg=0.01
Ski complex GO:0055087 p=2.0E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum subcompartment GO:0098827 p=2.1E−02 n=7 fg=0.19 bg=0.08
anchoring junction GO:0070161 p=2.1E−02 n=5 fg=0.14 bg=0.05
cell−cell junction GO:0005911 p=2.1E−02 n=5 fg=0.14 bg=0.05
cis−Golgi network membrane GO:0033106 p=3.9E−02 n=1 fg=0.03 bg=0.00
signal peptidase complex GO:0005787 p=3.9E−02 n=1 fg=0.03 bg=0.00
RNA polymerase II, core complex GO:0005665 p=3.9E−02 n=1 fg=0.03 bg=0.00
aminoacyl−tRNA synthetase multienzyme co... GO:0017101 p=3.9E−02 n=1 fg=0.03 bg=0.00
oligosaccharyltransferase complex GO:0008250 p=3.9E−02 n=1 fg=0.03 bg=0.00
adherens junction GO:0005912 p=4.3E−02 n=3 fg=0.08 bg=0.02
early endosome GO:0005769 p=4.6E−02 n=4 fg=0.11 bg=0.04
endoplasmic reticulum membrane GO:0005789 p=5.3E−02 n=6 fg=0.17 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=5.6E−02 n=6 fg=0.17 bg=0.08
glycogen granule GO:0042587 p=5.9E−02 n=1 fg=0.03 bg=0.00
inaD signaling complex GO:0016027 p=5.9E−02 n=1 fg=0.03 bg=0.00
subrhabdomeral cisterna GO:0016029 p=5.9E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum cisternal network GO:0071781 p=5.9E−02 n=1 fg=0.03 bg=0.00
smooth endoplasmic reticulum cisterna GO:0120082 p=5.9E−02 n=1 fg=0.03 bg=0.00
photoreceptor disc membrane GO:0097381 p=5.9E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum GO:0005783 p=6.5E−02 n=9 fg=0.25 bg=0.14
intracellular membrane−bounded organelle GO:0043231 p=7.4E−02 n=32 fg=0.89 bg=0.78
intercellular canaliculus GO:0046581 p=7.7E−02 n=1 fg=0.03 bg=0.00
microvillus membrane GO:0031528 p=7.7E−02 n=1 fg=0.03 bg=0.00
presynaptic membrane GO:0042734 p=8.7E−02 n=2 fg=0.06 bg=0.01
endoplasmic reticulum protein−containing... GO:0140534 p=8.7E−02 n=2 fg=0.06 bg=0.01
protein phosphatase type 1 complex GO:0000164 p=9.6E−02 n=1 fg=0.03 bg=0.00
septin cytoskeleton GO:0032156 p=9.6E−02 n=1 fg=0.03 bg=0.00
juxtaparanode region of axon GO:0044224 p=9.6E−02 n=1 fg=0.03 bg=0.00
presynaptic active zone membrane GO:0048787 p=9.6E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/141 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction