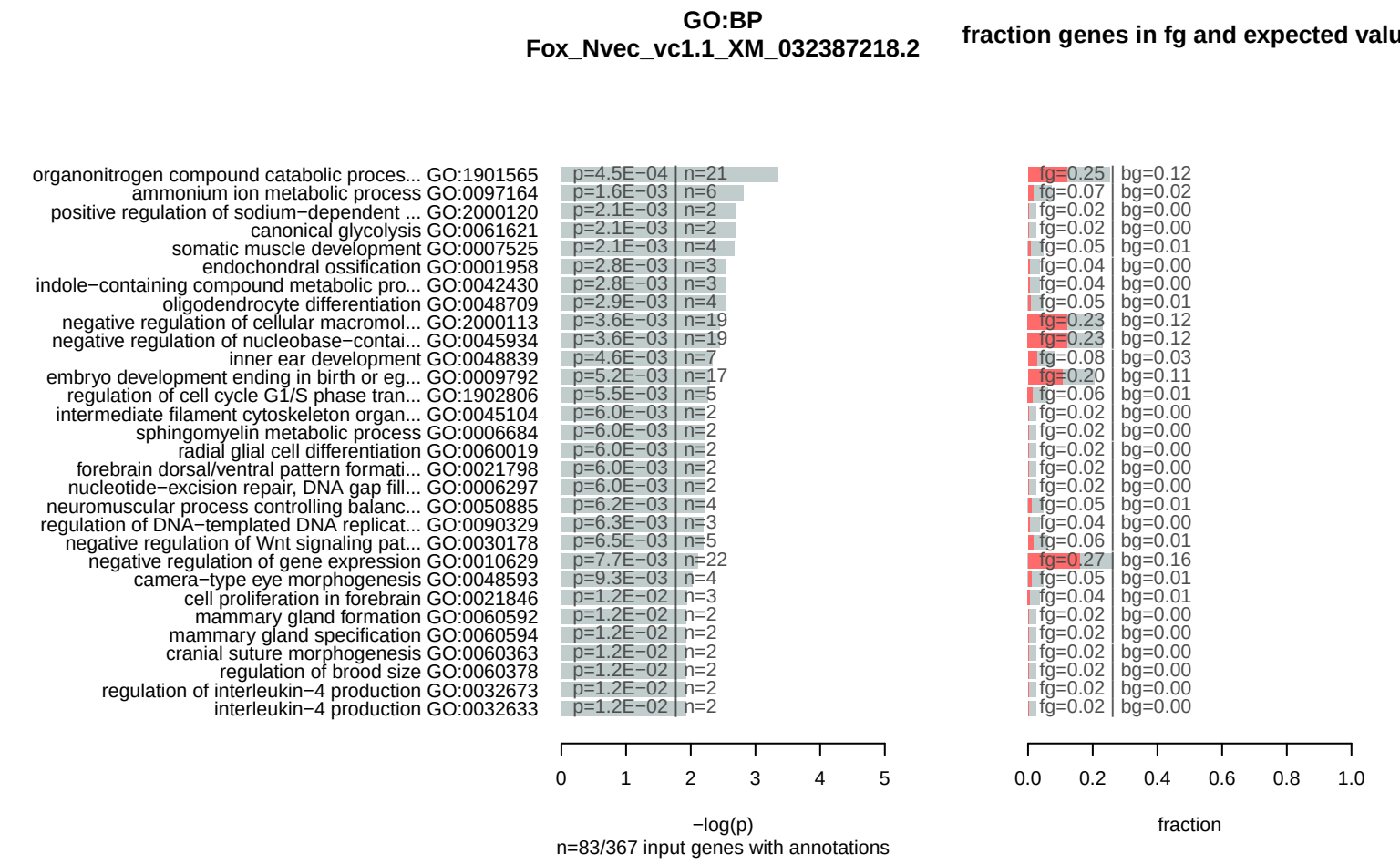
GO:BP
Fox_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
organonitrogen compound catabolic proces... GO:1901565 p=4.5E−04 n=21 fg=0.25 bg=0.12
ammonium ion metabolic process GO:0097164 p=1.6E−03 n=6 fg=0.07 bg=0.02
positive regulation of sodium−dependent ... GO:2000120 p=2.1E−03 n=2 fg=0.02 bg=0.00
canonical glycolysis GO:0061621 p=2.1E−03 n=2 fg=0.02 bg=0.00
somatic muscle development GO:0007525 p=2.1E−03 n=4 fg=0.05 bg=0.01
endochondral ossification GO:0001958 p=2.8E−03 n=3 fg=0.04 bg=0.00
indole−containing compound metabolic pro... GO:0042430 p=2.8E−03 n=3 fg=0.04 bg=0.00
oligodendrocyte differentiation GO:0048709 p=2.9E−03 n=4 fg=0.05 bg=0.01
negative regulation of cellular macromol... GO:2000113 p=3.6E−03 n=19 fg=0.23 bg=0.12
negative regulation of nucleobase−contai... GO:0045934 p=3.6E−03 n=19 fg=0.23 bg=0.12
inner ear development GO:0048839 p=4.6E−03 n=7 fg=0.08 bg=0.03
embryo development ending in birth or eg... GO:0009792 p=5.2E−03 n=17 fg=0.20 bg=0.11
regulation of cell cycle G1/S phase tran... GO:1902806 p=5.5E−03 n=5 fg=0.06 bg=0.01
intermediate filament cytoskeleton organ... GO:0045104 p=6.0E−03 n=2 fg=0.02 bg=0.00
sphingomyelin metabolic process GO:0006684 p=6.0E−03 n=2 fg=0.02 bg=0.00
radial glial cell differentiation GO:0060019 p=6.0E−03 n=2 fg=0.02 bg=0.00
forebrain dorsal/ventral pattern formati... GO:0021798 p=6.0E−03 n=2 fg=0.02 bg=0.00
nucleotide−excision repair, DNA gap fill... GO:0006297 p=6.0E−03 n=2 fg=0.02 bg=0.00
neuromuscular process controlling balanc... GO:0050885 p=6.2E−03 n=4 fg=0.05 bg=0.01
regulation of DNA−templated DNA replicat... GO:0090329 p=6.3E−03 n=3 fg=0.04 bg=0.00
negative regulation of Wnt signaling pat... GO:0030178 p=6.5E−03 n=5 fg=0.06 bg=0.01
negative regulation of gene expression GO:0010629 p=7.7E−03 n=22 fg=0.27 bg=0.16
camera−type eye morphogenesis GO:0048593 p=9.3E−03 n=4 fg=0.05 bg=0.01
cell proliferation in forebrain GO:0021846 p=1.2E−02 n=3 fg=0.04 bg=0.01
mammary gland formation GO:0060592 p=1.2E−02 n=2 fg=0.02 bg=0.00
mammary gland specification GO:0060594 p=1.2E−02 n=2 fg=0.02 bg=0.00
cranial suture morphogenesis GO:0060363 p=1.2E−02 n=2 fg=0.02 bg=0.00
regulation of brood size GO:0060378 p=1.2E−02 n=2 fg=0.02 bg=0.00
regulation of interleukin−4 production GO:0032673 p=1.2E−02 n=2 fg=0.02 bg=0.00
interleukin−4 production GO:0032633 p=1.2E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=83/367 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
heparan−alpha−glucosaminide N−acetyltran... GO:0015019 p=2.4E−03 n=2 fg=0.03 bg=0.00
phospholipase activity GO:0004620 p=6.5E−03 n=4 fg=0.05 bg=0.01
phosphoric diester hydrolase activity GO:0008081 p=1.0E−02 n=4 fg=0.05 bg=0.01
cyclin−dependent protein serine/threonin... GO:0004693 p=1.4E−02 n=2 fg=0.03 bg=0.00
cyclin−dependent protein kinase activity GO:0097472 p=1.4E−02 n=2 fg=0.03 bg=0.00
ubiquitin conjugating enzyme activity GO:0061631 p=1.5E−02 n=3 fg=0.04 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0061650 p=1.9E−02 n=3 fg=0.04 bg=0.01
ATPase−coupled cation transmembrane tran... GO:0019829 p=1.9E−02 n=3 fg=0.04 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=2.4E−02 n=3 fg=0.04 bg=0.01
hydrolase activity, acting on carbon−nit... GO:0016811 p=4.1E−02 n=3 fg=0.04 bg=0.01
RNA polymerase II core promoter sequence... GO:0000979 p=4.3E−02 n=2 fg=0.03 bg=0.00
carboxylic ester hydrolase activity GO:0052689 p=4.8E−02 n=3 fg=0.04 bg=0.01
glyceraldehyde−3−phosphate dehydrogenase... GO:0043891 p=5.0E−02 n=1 fg=0.01 bg=0.00
sphingomyelin phosphodiesterase D activi... GO:0050290 p=5.0E−02 n=1 fg=0.01 bg=0.00
lysophosphatidic acid binding GO:0035727 p=5.0E−02 n=1 fg=0.01 bg=0.00
RNA strand annealing activity GO:0033592 p=5.0E−02 n=1 fg=0.01 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=5.0E−02 n=1 fg=0.01 bg=0.00
ubiquitin−protein transferase inhibitor ... GO:0055105 p=5.0E−02 n=1 fg=0.01 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=5.0E−02 n=1 fg=0.01 bg=0.00
aminophospholipid flippase activity GO:0015247 p=5.0E−02 n=1 fg=0.01 bg=0.00
mono−olein transacylation activity GO:0051264 p=5.0E−02 n=1 fg=0.01 bg=0.00
diolein transacylation activity GO:0051265 p=5.0E−02 n=1 fg=0.01 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=5.0E−02 n=1 fg=0.01 bg=0.00
beta−galactosidase activity GO:0004565 p=5.0E−02 n=1 fg=0.01 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=5.0E−02 n=1 fg=0.01 bg=0.00
DNA binding, bending GO:0008301 p=5.0E−02 n=1 fg=0.01 bg=0.00
leptin receptor binding GO:1990460 p=5.0E−02 n=1 fg=0.01 bg=0.00
ubiquitin ligase inhibitor activity GO:1990948 p=5.0E−02 n=1 fg=0.01 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=5.0E−02 n=1 fg=0.01 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=5.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=79/367 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
tertiary granule membrane GO:0070821 p=1.6E−03 n=3 fg=0.04 bg=0.00
specific granule membrane GO:0035579 p=2.8E−03 n=4 fg=0.05 bg=0.01
lysosomal membrane GO:0005765 p=1.1E−02 n=6 fg=0.07 bg=0.02
microvillus membrane GO:0031528 p=1.1E−02 n=2 fg=0.02 bg=0.00
9+2 motile cilium GO:0097729 p=1.3E−02 n=4 fg=0.05 bg=0.01
polysome GO:0005844 p=1.5E−02 n=3 fg=0.04 bg=0.01
lytic vacuole membrane GO:0098852 p=1.7E−02 n=6 fg=0.07 bg=0.03
brush border membrane GO:0031526 p=1.8E−02 n=3 fg=0.04 bg=0.01
sperm principal piece GO:0097228 p=1.9E−02 n=2 fg=0.02 bg=0.00
sperm fibrous sheath GO:0035686 p=1.9E−02 n=2 fg=0.02 bg=0.00
nuclear membrane GO:0031965 p=2.4E−02 n=5 fg=0.06 bg=0.02
lysosome GO:0005764 p=2.7E−02 n=9 fg=0.11 bg=0.05
acrosomal vesicle GO:0001669 p=2.7E−02 n=2 fg=0.02 bg=0.00
nuclear chromosome GO:0000228 p=2.9E−02 n=7 fg=0.09 bg=0.04
trans−Golgi network GO:0005802 p=2.9E−02 n=7 fg=0.09 bg=0.04
early endosome membrane GO:0031901 p=3.3E−02 n=3 fg=0.04 bg=0.01
lytic vacuole GO:0000323 p=3.4E−02 n=9 fg=0.11 bg=0.06
dynein complex GO:0030286 p=3.7E−02 n=2 fg=0.02 bg=0.00
ATPase complex GO:1904949 p=3.9E−02 n=3 fg=0.04 bg=0.01
cell−substrate junction GO:0030055 p=4.5E−02 n=3 fg=0.04 bg=0.01
eukaryotic translation initiation factor... GO:0016281 p=4.5E−02 n=1 fg=0.01 bg=0.00
molybdopterin synthase complex GO:0019008 p=4.5E−02 n=1 fg=0.01 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=4.5E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=4.5E−02 n=1 fg=0.01 bg=0.00
synaptic cleft GO:0043083 p=4.5E−02 n=1 fg=0.01 bg=0.00
DNA replication factor C complex GO:0005663 p=4.5E−02 n=1 fg=0.01 bg=0.00
Swi5−Swi2 complex GO:0034974 p=4.5E−02 n=1 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=4.5E−02 n=1 fg=0.01 bg=0.00
DNA recombinase mediator complex GO:0033061 p=4.5E−02 n=1 fg=0.01 bg=0.00
Swi5−Sfr1 complex GO:0032798 p=4.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=82/367 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction