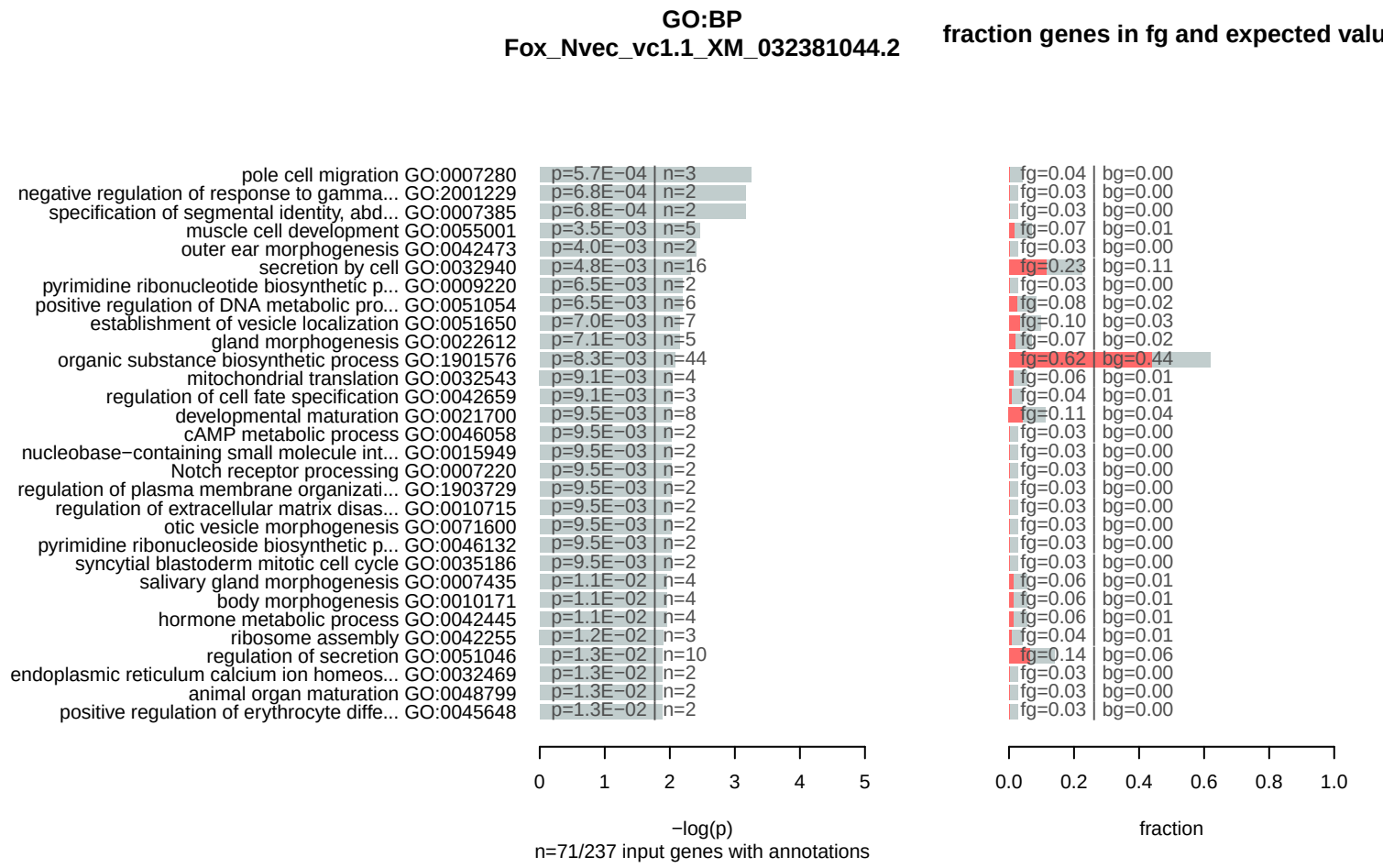
GO:BP
Fox_Nvec_vc1.1_XM_032381044.2
fraction genes in fg and expected valu
pole cell migration GO:0007280 p=5.7E−04 n=3 fg=0.04 bg=0.00
negative regulation of response to gamma... GO:2001229 p=6.8E−04 n=2 fg=0.03 bg=0.00
specification of segmental identity, abd... GO:0007385 p=6.8E−04 n=2 fg=0.03 bg=0.00
muscle cell development GO:0055001 p=3.5E−03 n=5 fg=0.07 bg=0.01
outer ear morphogenesis GO:0042473 p=4.0E−03 n=2 fg=0.03 bg=0.00
secretion by cell GO:0032940 p=4.8E−03 n=16 fg=0.23 bg=0.11
pyrimidine ribonucleotide biosynthetic p... GO:0009220 p=6.5E−03 n=2 fg=0.03 bg=0.00
positive regulation of DNA metabolic pro... GO:0051054 p=6.5E−03 n=6 fg=0.08 bg=0.02
establishment of vesicle localization GO:0051650 p=7.0E−03 n=7 fg=0.10 bg=0.03
gland morphogenesis GO:0022612 p=7.1E−03 n=5 fg=0.07 bg=0.02
organic substance biosynthetic process GO:1901576 p=8.3E−03 n=44 fg=0.62 bg=0.44
mitochondrial translation GO:0032543 p=9.1E−03 n=4 fg=0.06 bg=0.01
regulation of cell fate specification GO:0042659 p=9.1E−03 n=3 fg=0.04 bg=0.01
developmental maturation GO:0021700 p=9.5E−03 n=8 fg=0.11 bg=0.04
cAMP metabolic process GO:0046058 p=9.5E−03 n=2 fg=0.03 bg=0.00
nucleobase−containing small molecule int... GO:0015949 p=9.5E−03 n=2 fg=0.03 bg=0.00
Notch receptor processing GO:0007220 p=9.5E−03 n=2 fg=0.03 bg=0.00
regulation of plasma membrane organizati... GO:1903729 p=9.5E−03 n=2 fg=0.03 bg=0.00
regulation of extracellular matrix disas... GO:0010715 p=9.5E−03 n=2 fg=0.03 bg=0.00
otic vesicle morphogenesis GO:0071600 p=9.5E−03 n=2 fg=0.03 bg=0.00
pyrimidine ribonucleoside biosynthetic p... GO:0046132 p=9.5E−03 n=2 fg=0.03 bg=0.00
syncytial blastoderm mitotic cell cycle GO:0035186 p=9.5E−03 n=2 fg=0.03 bg=0.00
salivary gland morphogenesis GO:0007435 p=1.1E−02 n=4 fg=0.06 bg=0.01
body morphogenesis GO:0010171 p=1.1E−02 n=4 fg=0.06 bg=0.01
hormone metabolic process GO:0042445 p=1.1E−02 n=4 fg=0.06 bg=0.01
ribosome assembly GO:0042255 p=1.2E−02 n=3 fg=0.04 bg=0.01
regulation of secretion GO:0051046 p=1.3E−02 n=10 fg=0.14 bg=0.06
endoplasmic reticulum calcium ion homeos... GO:0032469 p=1.3E−02 n=2 fg=0.03 bg=0.00
animal organ maturation GO:0048799 p=1.3E−02 n=2 fg=0.03 bg=0.00
positive regulation of erythrocyte diffe... GO:0045648 p=1.3E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=71/237 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032381044.2
fraction genes in fg and expected valu
ATPase−coupled cation transmembrane tran... GO:0019829 p=6.8E−03 n=3 fg=0.05 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=8.2E−03 n=3 fg=0.05 bg=0.01
phosphoprotein phosphatase activity GO:0004721 p=1.8E−02 n=4 fg=0.06 bg=0.02
G−protein alpha−subunit binding GO:0001965 p=1.8E−02 n=2 fg=0.03 bg=0.00
Notch binding GO:0005112 p=1.8E−02 n=2 fg=0.03 bg=0.00
selenodiglutathione−disulfide reductase ... GO:0098622 p=2.7E−02 n=1 fg=0.02 bg=0.00
P−type calcium transporter activity invo... GO:0086039 p=2.7E−02 n=1 fg=0.02 bg=0.00
polypeptide N−acetylgalactosaminyltransf... GO:0004653 p=2.7E−02 n=1 fg=0.02 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=2.7E−02 n=1 fg=0.02 bg=0.00
angiostatin binding GO:0043532 p=2.7E−02 n=1 fg=0.02 bg=0.00
orotidine−5'−phosphate decarboxylase act... GO:0004590 p=2.7E−02 n=1 fg=0.02 bg=0.00
5−phosphoribosyl 1−pyrophosphate pyropho... GO:0043135 p=2.7E−02 n=1 fg=0.02 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=2.7E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=2.7E−02 n=1 fg=0.02 bg=0.00
nicotinamide−nucleotide adenylyltransfer... GO:0000309 p=2.7E−02 n=1 fg=0.02 bg=0.00
tRNA demethylase activity GO:1990984 p=2.7E−02 n=1 fg=0.02 bg=0.00
proton−transporting ATP synthase activit... GO:0046933 p=2.7E−02 n=1 fg=0.02 bg=0.00
MRF binding GO:0043426 p=2.7E−02 n=1 fg=0.02 bg=0.00
phosphomannomutase activity GO:0004615 p=2.7E−02 n=1 fg=0.02 bg=0.00
dystroglycan binding GO:0002162 p=2.7E−02 n=1 fg=0.02 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=2.7E−02 n=1 fg=0.02 bg=0.00
orotate phosphoribosyltransferase activi... GO:0004588 p=2.7E−02 n=1 fg=0.02 bg=0.00
CoA carboxylase activity GO:0016421 p=2.7E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−lysine−9 demethylase a... GO:0032454 p=2.7E−02 n=1 fg=0.02 bg=0.00
nicotinate−nucleotide adenylyltransferas... GO:0004515 p=2.7E−02 n=1 fg=0.02 bg=0.00
oxidative RNA demethylase activity GO:0035515 p=2.7E−02 n=1 fg=0.02 bg=0.00
spermine synthase activity GO:0016768 p=2.7E−02 n=1 fg=0.02 bg=0.00
proteinase activated receptor binding GO:0031871 p=2.7E−02 n=1 fg=0.02 bg=0.00
5'−deoxyribose−5−phosphate lyase activit... GO:0051575 p=2.7E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=64/237 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032381044.2
fraction genes in fg and expected valu
intercalary heterochromatin GO:0005725 p=1.9E−03 n=2 fg=0.03 bg=0.00
PRC1 complex GO:0035102 p=1.9E−03 n=2 fg=0.03 bg=0.00
transcription repressor complex GO:0017053 p=9.9E−03 n=3 fg=0.04 bg=0.01
organellar ribosome GO:0000313 p=1.1E−02 n=3 fg=0.04 bg=0.01
mitochondrial ribosome GO:0005761 p=1.1E−02 n=3 fg=0.04 bg=0.01
excitatory synapse GO:0060076 p=1.2E−02 n=2 fg=0.03 bg=0.00
DNA repair complex GO:1990391 p=1.6E−02 n=2 fg=0.03 bg=0.00
organelle subcompartment GO:0031984 p=1.9E−02 n=15 fg=0.22 bg=0.12
Golgi−associated vesicle GO:0005798 p=1.9E−02 n=4 fg=0.06 bg=0.02
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=2.0E−02 n=3 fg=0.04 bg=0.01
calcium channel complex GO:0034704 p=2.1E−02 n=2 fg=0.03 bg=0.00
Golgi cisterna membrane GO:0032580 p=2.1E−02 n=2 fg=0.03 bg=0.00
COPI−coated vesicle GO:0030137 p=2.1E−02 n=2 fg=0.03 bg=0.00
centrosome GO:0005813 p=2.5E−02 n=8 fg=0.12 bg=0.05
sarcoplasmic reticulum GO:0016529 p=2.5E−02 n=2 fg=0.03 bg=0.00
chromaffin granule GO:0042583 p=2.6E−02 n=1 fg=0.01 bg=0.00
chromaffin granule membrane GO:0042584 p=2.6E−02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0005754 p=2.6E−02 n=1 fg=0.01 bg=0.00
cortical microtubule GO:0055028 p=2.6E−02 n=1 fg=0.01 bg=0.00
centrosomal corona GO:0031592 p=2.6E−02 n=1 fg=0.01 bg=0.00
cation−transporting ATPase complex GO:0090533 p=2.6E−02 n=1 fg=0.01 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=2.6E−02 n=1 fg=0.01 bg=0.00
calcium ion−transporting ATPase complex GO:0090534 p=2.6E−02 n=1 fg=0.01 bg=0.00
cortical microtubule plus−end GO:1903754 p=2.6E−02 n=1 fg=0.01 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=2.6E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=2.6E−02 n=1 fg=0.01 bg=0.00
lumenal side of Golgi membrane GO:0098547 p=2.6E−02 n=1 fg=0.01 bg=0.00
platelet dense tubular network GO:0031094 p=2.6E−02 n=1 fg=0.01 bg=0.00
platelet dense tubular network membrane GO:0031095 p=2.6E−02 n=1 fg=0.01 bg=0.00
ribbon synapse GO:0097470 p=2.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=69/237 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction