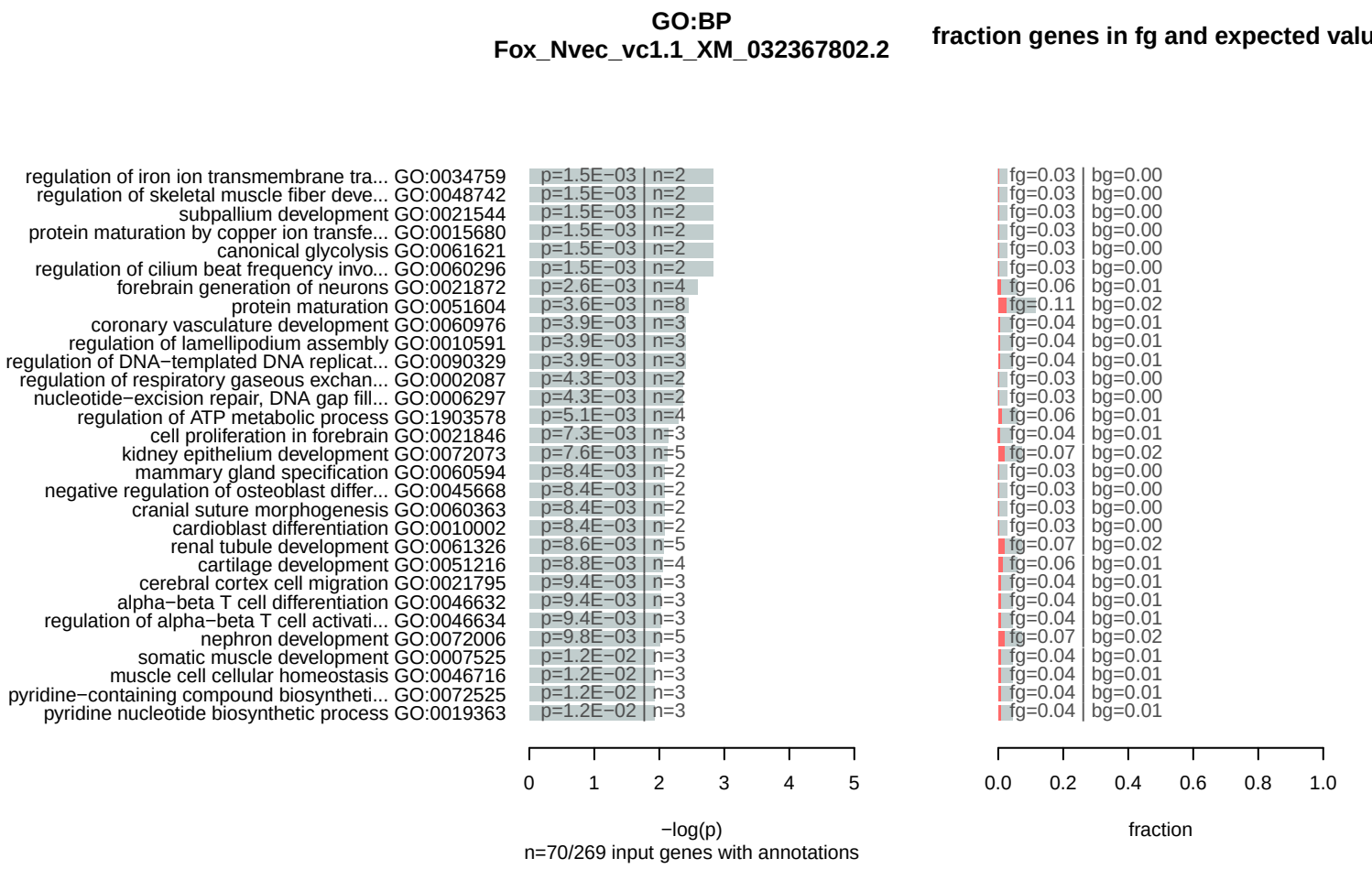
GO:BP
Fox_Nvec_vc1.1_XM_032367802.2
fraction genes in fg and expected valu
regulation of iron ion transmembrane tra... GO:0034759 p=1.5E−03 n=2 fg=0.03 bg=0.00
regulation of skeletal muscle fiber deve... GO:0048742 p=1.5E−03 n=2 fg=0.03 bg=0.00
subpallium development GO:0021544 p=1.5E−03 n=2 fg=0.03 bg=0.00
protein maturation by copper ion transfe... GO:0015680 p=1.5E−03 n=2 fg=0.03 bg=0.00
canonical glycolysis GO:0061621 p=1.5E−03 n=2 fg=0.03 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=1.5E−03 n=2 fg=0.03 bg=0.00
forebrain generation of neurons GO:0021872 p=2.6E−03 n=4 fg=0.06 bg=0.01
protein maturation GO:0051604 p=3.6E−03 n=8 fg=0.11 bg=0.02
coronary vasculature development GO:0060976 p=3.9E−03 n=3 fg=0.04 bg=0.01
regulation of lamellipodium assembly GO:0010591 p=3.9E−03 n=3 fg=0.04 bg=0.01
regulation of DNA−templated DNA replicat... GO:0090329 p=3.9E−03 n=3 fg=0.04 bg=0.01
regulation of respiratory gaseous exchan... GO:0002087 p=4.3E−03 n=2 fg=0.03 bg=0.00
nucleotide−excision repair, DNA gap fill... GO:0006297 p=4.3E−03 n=2 fg=0.03 bg=0.00
regulation of ATP metabolic process GO:1903578 p=5.1E−03 n=4 fg=0.06 bg=0.01
cell proliferation in forebrain GO:0021846 p=7.3E−03 n=3 fg=0.04 bg=0.01
kidney epithelium development GO:0072073 p=7.6E−03 n=5 fg=0.07 bg=0.02
mammary gland specification GO:0060594 p=8.4E−03 n=2 fg=0.03 bg=0.00
negative regulation of osteoblast differ... GO:0045668 p=8.4E−03 n=2 fg=0.03 bg=0.00
cranial suture morphogenesis GO:0060363 p=8.4E−03 n=2 fg=0.03 bg=0.00
cardioblast differentiation GO:0010002 p=8.4E−03 n=2 fg=0.03 bg=0.00
renal tubule development GO:0061326 p=8.6E−03 n=5 fg=0.07 bg=0.02
cartilage development GO:0051216 p=8.8E−03 n=4 fg=0.06 bg=0.01
cerebral cortex cell migration GO:0021795 p=9.4E−03 n=3 fg=0.04 bg=0.01
alpha−beta T cell differentiation GO:0046632 p=9.4E−03 n=3 fg=0.04 bg=0.01
regulation of alpha−beta T cell activati... GO:0046634 p=9.4E−03 n=3 fg=0.04 bg=0.01
nephron development GO:0072006 p=9.8E−03 n=5 fg=0.07 bg=0.02
somatic muscle development GO:0007525 p=1.2E−02 n=3 fg=0.04 bg=0.01
muscle cell cellular homeostasis GO:0046716 p=1.2E−02 n=3 fg=0.04 bg=0.01
pyridine−containing compound biosyntheti... GO:0072525 p=1.2E−02 n=3 fg=0.04 bg=0.01
pyridine nucleotide biosynthetic process GO:0019363 p=1.2E−02 n=3 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=70/269 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032367802.2
fraction genes in fg and expected valu
superoxide dismutase copper chaperone ac... GO:0016532 p=1.4E−03 n=2 fg=0.03 bg=0.00
ribonucleoprotein complex binding GO:0043021 p=2.1E−03 n=5 fg=0.08 bg=0.02
carbohydrate derivative binding GO:0097367 p=7.1E−03 n=11 fg=0.18 bg=0.08
adenyl ribonucleotide binding GO:0032559 p=1.0E−02 n=8 fg=0.13 bg=0.05
adenyl nucleotide binding GO:0030554 p=1.2E−02 n=8 fg=0.13 bg=0.05
ATP binding GO:0005524 p=1.3E−02 n=7 fg=0.11 bg=0.04
ribonucleotide binding GO:0032553 p=1.8E−02 n=9 fg=0.15 bg=0.07
purine ribonucleotide binding GO:0032555 p=1.8E−02 n=9 fg=0.15 bg=0.07
hydrolase activity, acting on carbon−nit... GO:0016811 p=2.1E−02 n=3 fg=0.05 bg=0.01
purine nucleotide binding GO:0017076 p=2.1E−02 n=9 fg=0.15 bg=0.07
purine ribonucleoside triphosphate bindi... GO:0035639 p=2.3E−02 n=8 fg=0.13 bg=0.06
histone deacetylase activity GO:0004407 p=2.7E−02 n=2 fg=0.03 bg=0.00
protein lysine deacetylase activity GO:0033558 p=2.7E−02 n=2 fg=0.03 bg=0.00
phosphoric diester hydrolase activity GO:0008081 p=2.9E−02 n=3 fg=0.05 bg=0.01
anion binding GO:0043168 p=3.5E−02 n=13 fg=0.21 bg=0.13
microtubule motor activity GO:0003777 p=3.5E−02 n=2 fg=0.03 bg=0.01
deacetylase activity GO:0019213 p=3.5E−02 n=2 fg=0.03 bg=0.01
glyceraldehyde−3−phosphate dehydrogenase... GO:0043891 p=3.8E−02 n=1 fg=0.02 bg=0.00
cuprous ion binding GO:1903136 p=3.8E−02 n=1 fg=0.02 bg=0.00
U12 snRNA binding GO:0030626 p=3.8E−02 n=1 fg=0.02 bg=0.00
RNA strand annealing activity GO:0033592 p=3.8E−02 n=1 fg=0.02 bg=0.00
CXCR chemokine receptor binding GO:0045236 p=3.8E−02 n=1 fg=0.02 bg=0.00
ribokinase activity GO:0004747 p=3.8E−02 n=1 fg=0.02 bg=0.00
aminophospholipid flippase activity GO:0015247 p=3.8E−02 n=1 fg=0.02 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=3.8E−02 n=1 fg=0.02 bg=0.00
beta−galactosidase activity GO:0004565 p=3.8E−02 n=1 fg=0.02 bg=0.00
DNA binding, bending GO:0008301 p=3.8E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.8E−02 n=1 fg=0.02 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=3.8E−02 n=1 fg=0.02 bg=0.00
flippase activity GO:0140327 p=3.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=61/269 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032367802.2
fraction genes in fg and expected valu
lipid droplet GO:0005811 p=5.7E−03 n=4 fg=0.06 bg=0.01
cilium GO:0005929 p=1.3E−02 n=10 fg=0.14 bg=0.06
A band GO:0031672 p=1.3E−02 n=3 fg=0.04 bg=0.01
sperm fibrous sheath GO:0035686 p=1.5E−02 n=2 fg=0.03 bg=0.00
tertiary granule membrane GO:0070821 p=2.1E−02 n=2 fg=0.03 bg=0.00
acrosomal vesicle GO:0001669 p=2.1E−02 n=2 fg=0.03 bg=0.00
intracellular vesicle GO:0097708 p=2.5E−02 n=20 fg=0.28 bg=0.18
cytoplasmic vesicle GO:0031410 p=2.5E−02 n=20 fg=0.28 bg=0.18
tertiary granule GO:0070820 p=3.2E−02 n=3 fg=0.04 bg=0.01
dihydrolipoyl dehydrogenase complex GO:0045240 p=4.0E−02 n=1 fg=0.01 bg=0.00
DNA replication factor C complex GO:0005663 p=4.0E−02 n=1 fg=0.01 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=4.0E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=4.0E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=4.0E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=4.0E−02 n=1 fg=0.01 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=4.0E−02 n=1 fg=0.01 bg=0.00
ciliary transition fiber GO:0097539 p=4.0E−02 n=1 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0016281 p=4.0E−02 n=1 fg=0.01 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=4.0E−02 n=1 fg=0.01 bg=0.00
Elg1 RFC−like complex GO:0031391 p=4.0E−02 n=1 fg=0.01 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=4.0E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber GO:0097457 p=4.0E−02 n=1 fg=0.01 bg=0.00
desmosome GO:0030057 p=4.0E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=4.0E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=4.0E−02 n=1 fg=0.01 bg=0.00
vesicle GO:0031982 p=4.2E−02 n=20 fg=0.28 bg=0.19
sperm flagellum GO:0036126 p=4.2E−02 n=3 fg=0.04 bg=0.01
phagocytic vesicle membrane GO:0030670 p=4.7E−02 n=2 fg=0.03 bg=0.01
cell projection membrane GO:0031253 p=4.7E−02 n=6 fg=0.08 bg=0.04
trans−Golgi network GO:0005802 p=4.7E−02 n=6 fg=0.08 bg=0.04
0 1 2 3 4 5
−log(p)
n=72/269 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction