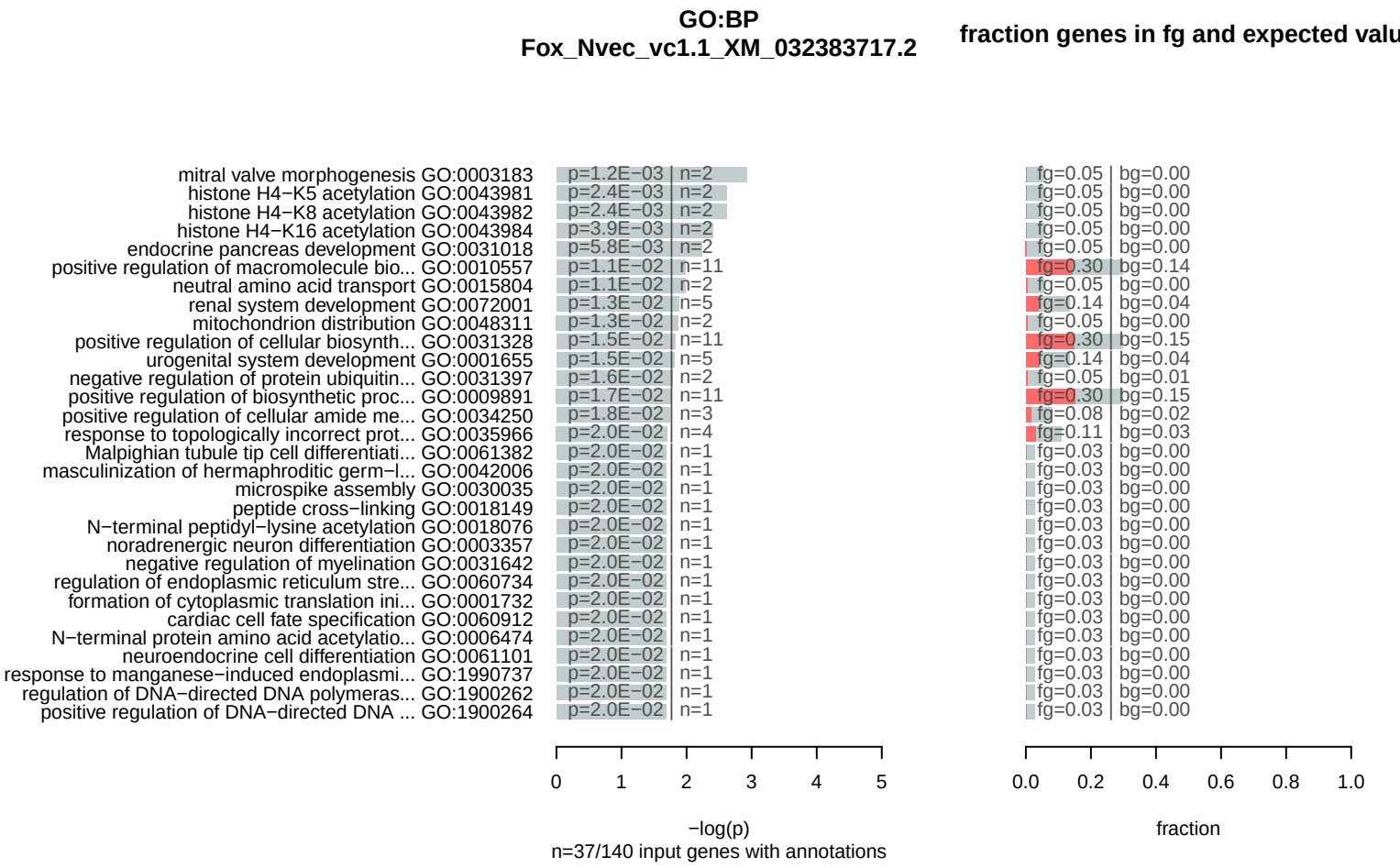
GO:BP
Fox_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
mitral valve morphogenesis GO:0003183 p=1.2E−03 n=2 fg=0.05 bg=0.00
histone H4−K5 acetylation GO:0043981 p=2.4E−03 n=2 fg=0.05 bg=0.00
histone H4−K8 acetylation GO:0043982 p=2.4E−03 n=2 fg=0.05 bg=0.00
histone H4−K16 acetylation GO:0043984 p=3.9E−03 n=2 fg=0.05 bg=0.00
endocrine pancreas development GO:0031018 p=5.8E−03 n=2 fg=0.05 bg=0.00
positive regulation of macromolecule bio... GO:0010557 p=1.1E−02 n=11 fg=0.30 bg=0.14
neutral amino acid transport GO:0015804 p=1.1E−02 n=2 fg=0.05 bg=0.00
renal system development GO:0072001 p=1.3E−02 n=5 fg=0.14 bg=0.04
mitochondrion distribution GO:0048311 p=1.3E−02 n=2 fg=0.05 bg=0.00
positive regulation of cellular biosynth... GO:0031328 p=1.5E−02 n=11 fg=0.30 bg=0.15
urogenital system development GO:0001655 p=1.5E−02 n=5 fg=0.14 bg=0.04
negative regulation of protein ubiquitin... GO:0031397 p=1.6E−02 n=2 fg=0.05 bg=0.01
positive regulation of biosynthetic proc... GO:0009891 p=1.7E−02 n=11 fg=0.30 bg=0.15
positive regulation of cellular amide me... GO:0034250 p=1.8E−02 n=3 fg=0.08 bg=0.02
response to topologically incorrect prot... GO:0035966 p=2.0E−02 n=4 fg=0.11 bg=0.03
Malpighian tubule tip cell differentiati... GO:0061382 p=2.0E−02 n=1 fg=0.03 bg=0.00
masculinization of hermaphroditic germ−l... GO:0042006 p=2.0E−02 n=1 fg=0.03 bg=0.00
microspike assembly GO:0030035 p=2.0E−02 n=1 fg=0.03 bg=0.00
peptide cross−linking GO:0018149 p=2.0E−02 n=1 fg=0.03 bg=0.00
N−terminal peptidyl−lysine acetylation GO:0018076 p=2.0E−02 n=1 fg=0.03 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=2.0E−02 n=1 fg=0.03 bg=0.00
negative regulation of myelination GO:0031642 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of endoplasmic reticulum stre... GO:0060734 p=2.0E−02 n=1 fg=0.03 bg=0.00
formation of cytoplasmic translation ini... GO:0001732 p=2.0E−02 n=1 fg=0.03 bg=0.00
cardiac cell fate specification GO:0060912 p=2.0E−02 n=1 fg=0.03 bg=0.00
N−terminal protein amino acid acetylatio... GO:0006474 p=2.0E−02 n=1 fg=0.03 bg=0.00
neuroendocrine cell differentiation GO:0061101 p=2.0E−02 n=1 fg=0.03 bg=0.00
response to manganese−induced endoplasmi... GO:1990737 p=2.0E−02 n=1 fg=0.03 bg=0.00
regulation of DNA−directed DNA polymeras... GO:1900262 p=2.0E−02 n=1 fg=0.03 bg=0.00
positive regulation of DNA−directed DNA ... GO:1900264 p=2.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=37/140 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
acetylglucosaminyltransferase activity GO:0008375 p=4.5E−03 n=2 fg=0.06 bg=0.00
neutral amino acid transmembrane transpo... GO:0015175 p=1.2E−02 n=2 fg=0.06 bg=0.01
E−box binding GO:0070888 p=1.5E−02 n=2 fg=0.06 bg=0.01
protein O−GlcNAc transferase activity GO:0097363 p=2.2E−02 n=1 fg=0.03 bg=0.00
acyl−CoA desaturase activity GO:0016215 p=2.2E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on paire... GO:0016717 p=2.2E−02 n=1 fg=0.03 bg=0.00
mRNA 5'−UTR binding GO:0048027 p=2.2E−02 n=1 fg=0.03 bg=0.00
N−acetylglucosaminyldiphosphodolichol N−... GO:0004577 p=2.2E−02 n=1 fg=0.03 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=2.2E−02 n=1 fg=0.03 bg=0.00
stearoyl−CoA 9−desaturase activity GO:0004768 p=2.2E−02 n=1 fg=0.03 bg=0.00
elongation factor−2 kinase activity GO:0004686 p=2.2E−02 n=1 fg=0.03 bg=0.00
GMP binding GO:0019002 p=2.2E−02 n=1 fg=0.03 bg=0.00
L−amino acid transmembrane transporter a... GO:0015179 p=2.3E−02 n=2 fg=0.06 bg=0.01
amino acid transmembrane transporter act... GO:0015171 p=2.7E−02 n=2 fg=0.06 bg=0.01
serine transmembrane transporter activit... GO:0022889 p=4.3E−02 n=1 fg=0.03 bg=0.00
aldo−keto reductase (NADP) activity GO:0004033 p=4.3E−02 n=1 fg=0.03 bg=0.00
eukaryotic translation initiation factor... GO:0004694 p=4.3E−02 n=1 fg=0.03 bg=0.00
GDP−dissociation inhibitor activity GO:0005092 p=4.3E−02 n=1 fg=0.03 bg=0.00
L−serine transmembrane transporter activ... GO:0015194 p=4.3E−02 n=1 fg=0.03 bg=0.00
aspartic endopeptidase activity, intrame... GO:0042500 p=4.3E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol 3−kinase regulatory... GO:0036312 p=4.3E−02 n=1 fg=0.03 bg=0.00
protein heterodimerization activity GO:0046982 p=4.7E−02 n=5 fg=0.14 bg=0.06
phosphatase binding GO:0019902 p=6.2E−02 n=3 fg=0.09 bg=0.03
cAMP response element binding GO:0035497 p=6.5E−02 n=1 fg=0.03 bg=0.00
RNA stem−loop binding GO:0035613 p=6.5E−02 n=1 fg=0.03 bg=0.00
adenyl−nucleotide exchange factor activi... GO:0000774 p=6.5E−02 n=1 fg=0.03 bg=0.00
bHLH transcription factor binding GO:0043425 p=6.5E−02 n=1 fg=0.03 bg=0.00
pyrimidine nucleotide transmembrane tran... GO:0015218 p=6.5E−02 n=1 fg=0.03 bg=0.00
eukaryotic initiation factor eIF2 bindin... GO:0071074 p=6.5E−02 n=1 fg=0.03 bg=0.00
sequence−specific mRNA binding GO:1990825 p=6.5E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/140 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
striated muscle dense body GO:0055120 p=1.1E−02 n=2 fg=0.05 bg=0.00
transcription regulator complex GO:0005667 p=2.0E−02 n=5 fg=0.13 bg=0.04
Ctf18 RFC−like complex GO:0031390 p=2.1E−02 n=1 fg=0.03 bg=0.00
Elg1 RFC−like complex GO:0031391 p=2.1E−02 n=1 fg=0.03 bg=0.00
synaptic cleft GO:0043083 p=2.1E−02 n=1 fg=0.03 bg=0.00
endocytic vesicle lumen GO:0071682 p=2.1E−02 n=1 fg=0.03 bg=0.00
eukaryotic translation initiation factor... GO:0071540 p=2.1E−02 n=1 fg=0.03 bg=0.00
eukaryotic translation initiation factor... GO:0071541 p=2.1E−02 n=1 fg=0.03 bg=0.00
DNA replication factor C complex GO:0005663 p=2.1E−02 n=1 fg=0.03 bg=0.00
transcription repressor complex GO:0017053 p=2.9E−02 n=2 fg=0.05 bg=0.01
eukaryotic translation initiation factor... GO:0005852 p=4.2E−02 n=1 fg=0.03 bg=0.00
multi−eIF complex GO:0043614 p=4.2E−02 n=1 fg=0.03 bg=0.00
NSL complex GO:0044545 p=4.2E−02 n=1 fg=0.03 bg=0.00
ATPase complex GO:1904949 p=4.8E−02 n=2 fg=0.05 bg=0.01
acetyltransferase complex GO:1902493 p=5.3E−02 n=2 fg=0.05 bg=0.01
protein acetyltransferase complex GO:0031248 p=5.3E−02 n=2 fg=0.05 bg=0.01
histone acetyltransferase complex GO:0000123 p=5.3E−02 n=2 fg=0.05 bg=0.01
CHD−type complex GO:0090545 p=6.2E−02 n=1 fg=0.03 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=6.2E−02 n=1 fg=0.03 bg=0.00
NuRD complex GO:0016581 p=6.2E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=6.6E−02 n=6 fg=0.16 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=7.0E−02 n=6 fg=0.16 bg=0.08
endoplasmic reticulum subcompartment GO:0098827 p=7.6E−02 n=6 fg=0.16 bg=0.08
integral component of lumenal side of en... GO:0071556 p=8.1E−02 n=1 fg=0.03 bg=0.00
lumenal side of endoplasmic reticulum me... GO:0098553 p=8.1E−02 n=1 fg=0.03 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=8.1E−02 n=1 fg=0.03 bg=0.00
zymogen granule GO:0042588 p=1.0E−01 n=1 fg=0.03 bg=0.00
cytoplasmic side of endoplasmic reticulu... GO:0098554 p=1.0E−01 n=1 fg=0.03 bg=0.00
septin cytoskeleton GO:0032156 p=1.0E−01 n=1 fg=0.03 bg=0.00
lumenal side of membrane GO:0098576 p=1.0E−01 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=38/140 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction