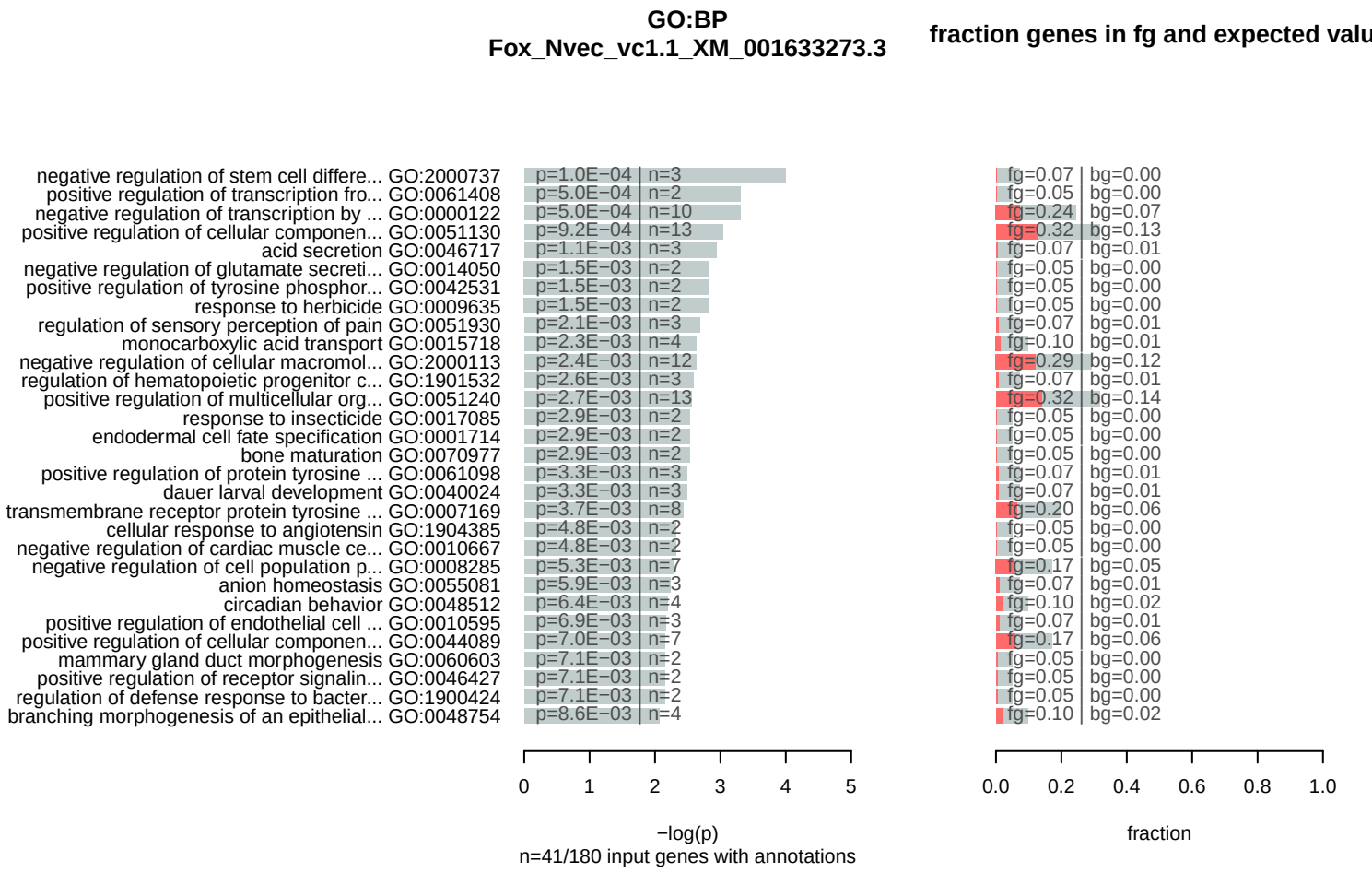
GO:BP
Fox_Nvec_vc1.1_XM_001633273.3
fraction genes in fg and expected valu
negative regulation of stem cell differe... GO:2000737 p=1.0E−04 n=3 fg=0.07 bg=0.00
positive regulation of transcription fro... GO:0061408 p=5.0E−04 n=2 fg=0.05 bg=0.00
negative regulation of transcription by ... GO:0000122 p=5.0E−04 n=10 fg=0.24 bg=0.07
positive regulation of cellular componen... GO:0051130 p=9.2E−04 n=13 fg=0.32 bg=0.13
acid secretion GO:0046717 p=1.1E−03 n=3 fg=0.07 bg=0.01
negative regulation of glutamate secreti... GO:0014050 p=1.5E−03 n=2 fg=0.05 bg=0.00
positive regulation of tyrosine phosphor... GO:0042531 p=1.5E−03 n=2 fg=0.05 bg=0.00
response to herbicide GO:0009635 p=1.5E−03 n=2 fg=0.05 bg=0.00
regulation of sensory perception of pain GO:0051930 p=2.1E−03 n=3 fg=0.07 bg=0.01
monocarboxylic acid transport GO:0015718 p=2.3E−03 n=4 fg=0.10 bg=0.01
negative regulation of cellular macromol... GO:2000113 p=2.4E−03 n=12 fg=0.29 bg=0.12
regulation of hematopoietic progenitor c... GO:1901532 p=2.6E−03 n=3 fg=0.07 bg=0.01
positive regulation of multicellular org... GO:0051240 p=2.7E−03 n=13 fg=0.32 bg=0.14
response to insecticide GO:0017085 p=2.9E−03 n=2 fg=0.05 bg=0.00
endodermal cell fate specification GO:0001714 p=2.9E−03 n=2 fg=0.05 bg=0.00
bone maturation GO:0070977 p=2.9E−03 n=2 fg=0.05 bg=0.00
positive regulation of protein tyrosine ... GO:0061098 p=3.3E−03 n=3 fg=0.07 bg=0.01
dauer larval development GO:0040024 p=3.3E−03 n=3 fg=0.07 bg=0.01
transmembrane receptor protein tyrosine ... GO:0007169 p=3.7E−03 n=8 fg=0.20 bg=0.06
cellular response to angiotensin GO:1904385 p=4.8E−03 n=2 fg=0.05 bg=0.00
negative regulation of cardiac muscle ce... GO:0010667 p=4.8E−03 n=2 fg=0.05 bg=0.00
negative regulation of cell population p... GO:0008285 p=5.3E−03 n=7 fg=0.17 bg=0.05
anion homeostasis GO:0055081 p=5.9E−03 n=3 fg=0.07 bg=0.01
circadian behavior GO:0048512 p=6.4E−03 n=4 fg=0.10 bg=0.02
positive regulation of endothelial cell ... GO:0010595 p=6.9E−03 n=3 fg=0.07 bg=0.01
positive regulation of cellular componen... GO:0044089 p=7.0E−03 n=7 fg=0.17 bg=0.06
mammary gland duct morphogenesis GO:0060603 p=7.1E−03 n=2 fg=0.05 bg=0.00
positive regulation of receptor signalin... GO:0046427 p=7.1E−03 n=2 fg=0.05 bg=0.00
regulation of defense response to bacter... GO:1900424 p=7.1E−03 n=2 fg=0.05 bg=0.00
branching morphogenesis of an epithelial... GO:0048754 p=8.6E−03 n=4 fg=0.10 bg=0.02
0 1 2 3 4 5
−log(p)
n=41/180 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001633273.3
fraction genes in fg and expected valu
chromatin DNA binding GO:0031490 p=2.8E−03 n=3 fg=0.08 bg=0.01
protein−macromolecule adaptor activity GO:0030674 p=4.7E−03 n=5 fg=0.14 bg=0.03
transcription factor binding GO:0008134 p=4.7E−03 n=8 fg=0.22 bg=0.07
protein tyrosine kinase activator activi... GO:0030296 p=5.0E−03 n=2 fg=0.05 bg=0.00
protein dimerization activity GO:0046983 p=5.2E−03 n=11 fg=0.30 bg=0.13
heat shock protein binding GO:0031072 p=6.2E−03 n=4 fg=0.11 bg=0.02
cholesterol binding GO:0015485 p=7.4E−03 n=2 fg=0.05 bg=0.00
heparin binding GO:0008201 p=1.0E−02 n=2 fg=0.05 bg=0.00
DNA−binding transcription repressor acti... GO:0001227 p=1.1E−02 n=3 fg=0.08 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=1.1E−02 n=3 fg=0.08 bg=0.01
glycosaminoglycan binding GO:0005539 p=1.3E−02 n=2 fg=0.05 bg=0.01
oxidoreductase activity, acting on paire... GO:0016705 p=1.7E−02 n=2 fg=0.05 bg=0.01
amino acid binding GO:0016597 p=2.1E−02 n=2 fg=0.05 bg=0.01
A2A adenosine receptor binding GO:0031687 p=2.3E−02 n=1 fg=0.03 bg=0.00
G protein−coupled glutamate receptor act... GO:0098988 p=2.3E−02 n=1 fg=0.03 bg=0.00
PLC activating G protein−coupled glutama... GO:0001639 p=2.3E−02 n=1 fg=0.03 bg=0.00
stearoyl−CoA 9−desaturase activity GO:0004768 p=2.3E−02 n=1 fg=0.03 bg=0.00
G protein−coupled receptor activity invo... GO:0099530 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=2.3E−02 n=1 fg=0.03 bg=0.00
glutamate receptor activity GO:0008066 p=2.3E−02 n=1 fg=0.03 bg=0.00
histone H3−tri/di/monomethyl−lysine−4 de... GO:0034647 p=2.3E−02 n=1 fg=0.03 bg=0.00
4−hydroxyglutamate transaminase activity GO:0047578 p=2.3E−02 n=1 fg=0.03 bg=0.00
acetyltransferase activator activity GO:0010698 p=2.3E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on paire... GO:0016717 p=2.3E−02 n=1 fg=0.03 bg=0.00
protein O−GlcNAc transferase activity GO:0097363 p=2.3E−02 n=1 fg=0.03 bg=0.00
acyl−CoA desaturase activity GO:0016215 p=2.3E−02 n=1 fg=0.03 bg=0.00
mRNA 5'−UTR binding GO:0048027 p=2.3E−02 n=1 fg=0.03 bg=0.00
L−aspartate:2−oxoglutarate aminotransfer... GO:0004069 p=2.3E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.3E−02 n=1 fg=0.03 bg=0.00
neurotransmitter receptor activity invol... GO:0099583 p=2.3E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=37/180 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001633273.3
fraction genes in fg and expected valu
euchromatin GO:0000791 p=5.6E−04 n=3 fg=0.07 bg=0.00
intercellular canaliculus GO:0046581 p=2.9E−03 n=2 fg=0.05 bg=0.00
actin−based cell projection GO:0098858 p=8.7E−03 n=4 fg=0.10 bg=0.02
endoplasmic reticulum GO:0005783 p=1.0E−02 n=12 fg=0.29 bg=0.14
endoplasmic reticulum subcompartment GO:0098827 p=1.3E−02 n=8 fg=0.20 bg=0.08
histone deacetylase complex GO:0000118 p=2.0E−02 n=2 fg=0.05 bg=0.01
G protein−coupled receptor complex GO:0097648 p=2.3E−02 n=1 fg=0.02 bg=0.00
new growing cell tip GO:0035841 p=2.3E−02 n=1 fg=0.02 bg=0.00
growing cell tip GO:0035838 p=2.3E−02 n=1 fg=0.02 bg=0.00
G protein−coupled receptor dimeric compl... GO:0038037 p=2.3E−02 n=1 fg=0.02 bg=0.00
G protein−coupled receptor homodimeric c... GO:0038038 p=2.3E−02 n=1 fg=0.02 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=2.3E−02 n=1 fg=0.02 bg=0.00
polytene chromosome GO:0005700 p=3.1E−02 n=3 fg=0.07 bg=0.02
nuclear lumen GO:0031981 p=3.2E−02 n=19 fg=0.46 bg=0.32
transcription repressor complex GO:0017053 p=3.3E−02 n=2 fg=0.05 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=3.3E−02 n=7 fg=0.17 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=3.6E−02 n=7 fg=0.17 bg=0.08
intrinsic component of membrane GO:0031224 p=3.8E−02 n=12 fg=0.29 bg=0.17
Golgi−associated vesicle membrane GO:0030660 p=3.8E−02 n=2 fg=0.05 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=4.2E−02 n=7 fg=0.17 bg=0.08
TORC1 complex GO:0031931 p=4.5E−02 n=1 fg=0.02 bg=0.00
RNA polymerase II, core complex GO:0005665 p=4.5E−02 n=1 fg=0.02 bg=0.00
TOR complex GO:0038201 p=4.5E−02 n=1 fg=0.02 bg=0.00
gut granule GO:0044840 p=4.5E−02 n=1 fg=0.02 bg=0.00
gut granule membrane GO:0044841 p=4.5E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=4.5E−02 n=1 fg=0.02 bg=0.00
protein−DNA complex GO:0032993 p=4.9E−02 n=2 fg=0.05 bg=0.01
filopodium GO:0030175 p=4.9E−02 n=2 fg=0.05 bg=0.01
rough endoplasmic reticulum GO:0005791 p=5.5E−02 n=2 fg=0.05 bg=0.01
cell leading edge GO:0031252 p=5.7E−02 n=4 fg=0.10 bg=0.04
0 1 2 3 4 5
−log(p)
n=41/180 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction