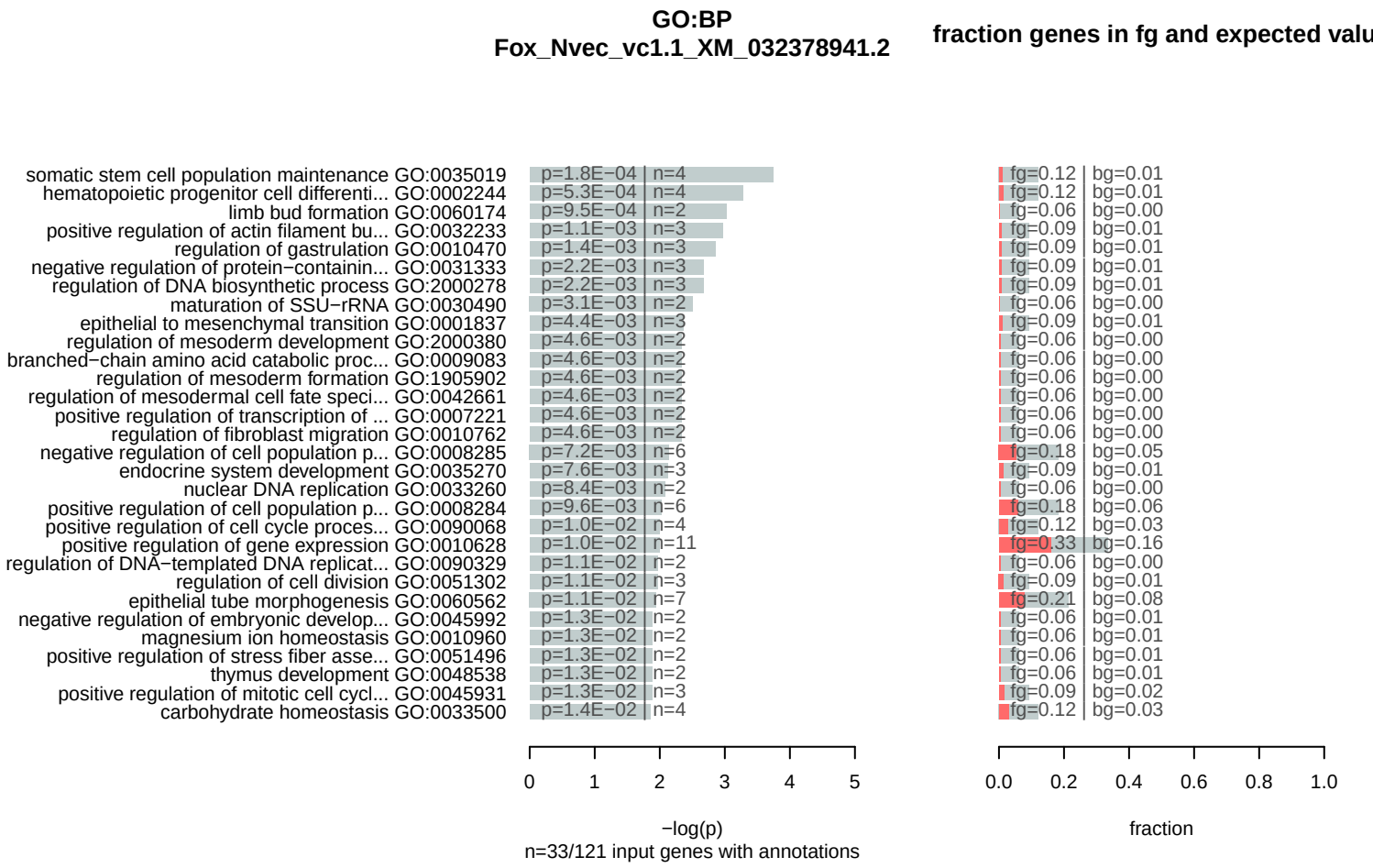
GO:BP
Fox_Nvec_vc1.1_XM_032378941.2
fraction genes in fg and expected valu
somatic stem cell population maintenance GO:0035019 p=1.8E−04 n=4 fg=0.12 bg=0.01
hematopoietic progenitor cell differenti... GO:0002244 p=5.3E−04 n=4 fg=0.12 bg=0.01
limb bud formation GO:0060174 p=9.5E−04 n=2 fg=0.06 bg=0.00
positive regulation of actin filament bu... GO:0032233 p=1.1E−03 n=3 fg=0.09 bg=0.01
regulation of gastrulation GO:0010470 p=1.4E−03 n=3 fg=0.09 bg=0.01
negative regulation of protein−containin... GO:0031333 p=2.2E−03 n=3 fg=0.09 bg=0.01
regulation of DNA biosynthetic process GO:2000278 p=2.2E−03 n=3 fg=0.09 bg=0.01
maturation of SSU−rRNA GO:0030490 p=3.1E−03 n=2 fg=0.06 bg=0.00
epithelial to mesenchymal transition GO:0001837 p=4.4E−03 n=3 fg=0.09 bg=0.01
regulation of mesoderm development GO:2000380 p=4.6E−03 n=2 fg=0.06 bg=0.00
branched−chain amino acid catabolic proc... GO:0009083 p=4.6E−03 n=2 fg=0.06 bg=0.00
regulation of mesoderm formation GO:1905902 p=4.6E−03 n=2 fg=0.06 bg=0.00
regulation of mesodermal cell fate speci... GO:0042661 p=4.6E−03 n=2 fg=0.06 bg=0.00
positive regulation of transcription of ... GO:0007221 p=4.6E−03 n=2 fg=0.06 bg=0.00
regulation of fibroblast migration GO:0010762 p=4.6E−03 n=2 fg=0.06 bg=0.00
negative regulation of cell population p... GO:0008285 p=7.2E−03 n=6 fg=0.18 bg=0.05
endocrine system development GO:0035270 p=7.6E−03 n=3 fg=0.09 bg=0.01
nuclear DNA replication GO:0033260 p=8.4E−03 n=2 fg=0.06 bg=0.00
positive regulation of cell population p... GO:0008284 p=9.6E−03 n=6 fg=0.18 bg=0.06
positive regulation of cell cycle proces... GO:0090068 p=1.0E−02 n=4 fg=0.12 bg=0.03
positive regulation of gene expression GO:0010628 p=1.0E−02 n=11 fg=0.33 bg=0.16
regulation of DNA−templated DNA replicat... GO:0090329 p=1.1E−02 n=2 fg=0.06 bg=0.00
regulation of cell division GO:0051302 p=1.1E−02 n=3 fg=0.09 bg=0.01
epithelial tube morphogenesis GO:0060562 p=1.1E−02 n=7 fg=0.21 bg=0.08
negative regulation of embryonic develop... GO:0045992 p=1.3E−02 n=2 fg=0.06 bg=0.01
magnesium ion homeostasis GO:0010960 p=1.3E−02 n=2 fg=0.06 bg=0.01
positive regulation of stress fiber asse... GO:0051496 p=1.3E−02 n=2 fg=0.06 bg=0.01
thymus development GO:0048538 p=1.3E−02 n=2 fg=0.06 bg=0.01
positive regulation of mitotic cell cycl... GO:0045931 p=1.3E−02 n=3 fg=0.09 bg=0.02
carbohydrate homeostasis GO:0033500 p=1.4E−02 n=4 fg=0.12 bg=0.03
0 1 2 3 4 5
−log(p)
n=33/121 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032378941.2
fraction genes in fg and expected valu
RNA polymerase II cis−regulatory region ... GO:0000978 p=4.7E−03 n=5 fg=0.16 bg=0.04
transferase activity, transferring phosp... GO:0016772 p=1.2E−02 n=7 fg=0.22 bg=0.08
phosphotransferase activity, alcohol gro... GO:0016773 p=1.3E−02 n=6 fg=0.19 bg=0.06
kinase activity GO:0016301 p=1.9E−02 n=6 fg=0.19 bg=0.07
acid−sensing ion channel activity GO:0044736 p=2.0E−02 n=1 fg=0.03 bg=0.00
adenylate cyclase activator activity GO:0010856 p=2.0E−02 n=1 fg=0.03 bg=0.00
ribokinase activity GO:0004747 p=2.0E−02 n=1 fg=0.03 bg=0.00
short−branched−chain−acyl−CoA dehydrogen... GO:0016937 p=2.0E−02 n=1 fg=0.03 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=2.0E−02 n=1 fg=0.03 bg=0.00
SMC family protein binding GO:0043221 p=2.0E−02 n=1 fg=0.03 bg=0.00
protein kinase activity GO:0004672 p=2.3E−02 n=5 fg=0.16 bg=0.05
DNA−binding transcription activator acti... GO:0001228 p=3.1E−02 n=4 fg=0.12 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=3.1E−02 n=4 fg=0.12 bg=0.04
ligand−gated cation channel activity GO:0099094 p=3.5E−02 n=2 fg=0.06 bg=0.01
protein serine/threonine kinase activity GO:0004674 p=3.8E−02 n=4 fg=0.12 bg=0.04
co−SMAD binding GO:0070410 p=4.0E−02 n=1 fg=0.03 bg=0.00
telomerase RNA binding GO:0070034 p=4.0E−02 n=1 fg=0.03 bg=0.00
ligand−gated sodium channel activity GO:0015280 p=4.0E−02 n=1 fg=0.03 bg=0.00
caspase binding GO:0089720 p=4.0E−02 n=1 fg=0.03 bg=0.00
acyl−CoA dehydrogenase activity GO:0003995 p=4.0E−02 n=1 fg=0.03 bg=0.00
alpha−(1−>3)−fucosyltransferase activity GO:0046920 p=5.9E−02 n=1 fg=0.03 bg=0.00
fucosyltransferase activity GO:0008417 p=5.9E−02 n=1 fg=0.03 bg=0.00
cyclase regulator activity GO:0010851 p=5.9E−02 n=1 fg=0.03 bg=0.00
beta−glucuronidase activity GO:0004566 p=5.9E−02 n=1 fg=0.03 bg=0.00
fibroblast growth factor−activated recep... GO:0005007 p=5.9E−02 n=1 fg=0.03 bg=0.00
receptor−receptor interaction GO:0090722 p=5.9E−02 n=1 fg=0.03 bg=0.00
DNA−binding transcription repressor acti... GO:0001227 p=6.5E−02 n=2 fg=0.06 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=6.5E−02 n=2 fg=0.06 bg=0.01
ligand−gated ion channel activity GO:0015276 p=7.6E−02 n=2 fg=0.06 bg=0.01
ligand−gated channel activity GO:0022834 p=7.6E−02 n=2 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=32/121 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032378941.2
fraction genes in fg and expected valu
preribosome, small subunit precursor GO:0030688 p=3.4E−04 n=2 fg=0.06 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=1.9E−02 n=1 fg=0.03 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=1.9E−02 n=1 fg=0.03 bg=0.00
Elg1 RFC−like complex GO:0031391 p=1.9E−02 n=1 fg=0.03 bg=0.00
bleb GO:0032059 p=1.9E−02 n=1 fg=0.03 bg=0.00
DNA replication factor C complex GO:0005663 p=1.9E−02 n=1 fg=0.03 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=1.9E−02 n=1 fg=0.03 bg=0.00
intercalated disc GO:0014704 p=2.4E−02 n=2 fg=0.06 bg=0.01
cell−cell contact zone GO:0044291 p=3.5E−02 n=2 fg=0.06 bg=0.01
striated muscle thin filament GO:0005865 p=3.7E−02 n=1 fg=0.03 bg=0.00
AP−2 adaptor complex GO:0030122 p=3.7E−02 n=1 fg=0.03 bg=0.00
oligosaccharyltransferase complex GO:0008250 p=3.7E−02 n=1 fg=0.03 bg=0.00
clathrin coat of endocytic vesicle GO:0030128 p=3.7E−02 n=1 fg=0.03 bg=0.00
TRAMP complex GO:0031499 p=3.7E−02 n=1 fg=0.03 bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=3.7E−02 n=1 fg=0.03 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=3.7E−02 n=1 fg=0.03 bg=0.00
myofilament GO:0036379 p=3.7E−02 n=1 fg=0.03 bg=0.00
signal peptidase complex GO:0005787 p=3.7E−02 n=1 fg=0.03 bg=0.00
transcription regulator complex GO:0005667 p=5.3E−02 n=4 fg=0.12 bg=0.04
clathrin vesicle coat GO:0030125 p=5.5E−02 n=1 fg=0.03 bg=0.00
pseudopodium GO:0031143 p=5.5E−02 n=1 fg=0.03 bg=0.00
clathrin adaptor complex GO:0030131 p=5.5E−02 n=1 fg=0.03 bg=0.00
endocytic vesicle GO:0030139 p=5.6E−02 n=3 fg=0.09 bg=0.03
endocytic vesicle membrane GO:0030666 p=5.8E−02 n=2 fg=0.06 bg=0.01
clathrin coat of coated pit GO:0030132 p=7.3E−02 n=1 fg=0.03 bg=0.00
XY body GO:0001741 p=7.3E−02 n=1 fg=0.03 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=7.3E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum protein−containing... GO:0140534 p=7.9E−02 n=2 fg=0.06 bg=0.01
Z disc GO:0030018 p=7.9E−02 n=2 fg=0.06 bg=0.01
I band GO:0031674 p=8.4E−02 n=2 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=34/121 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction