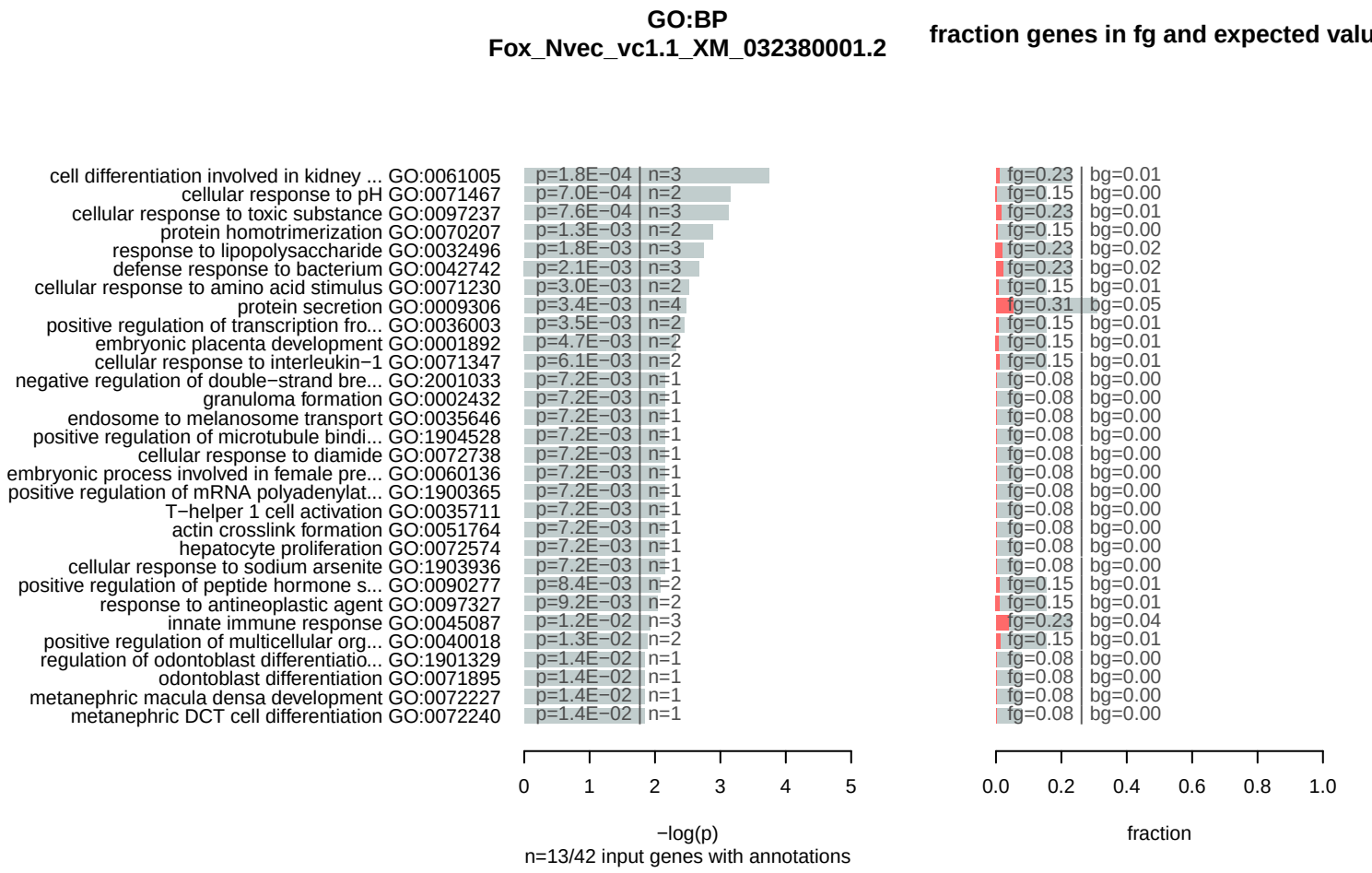
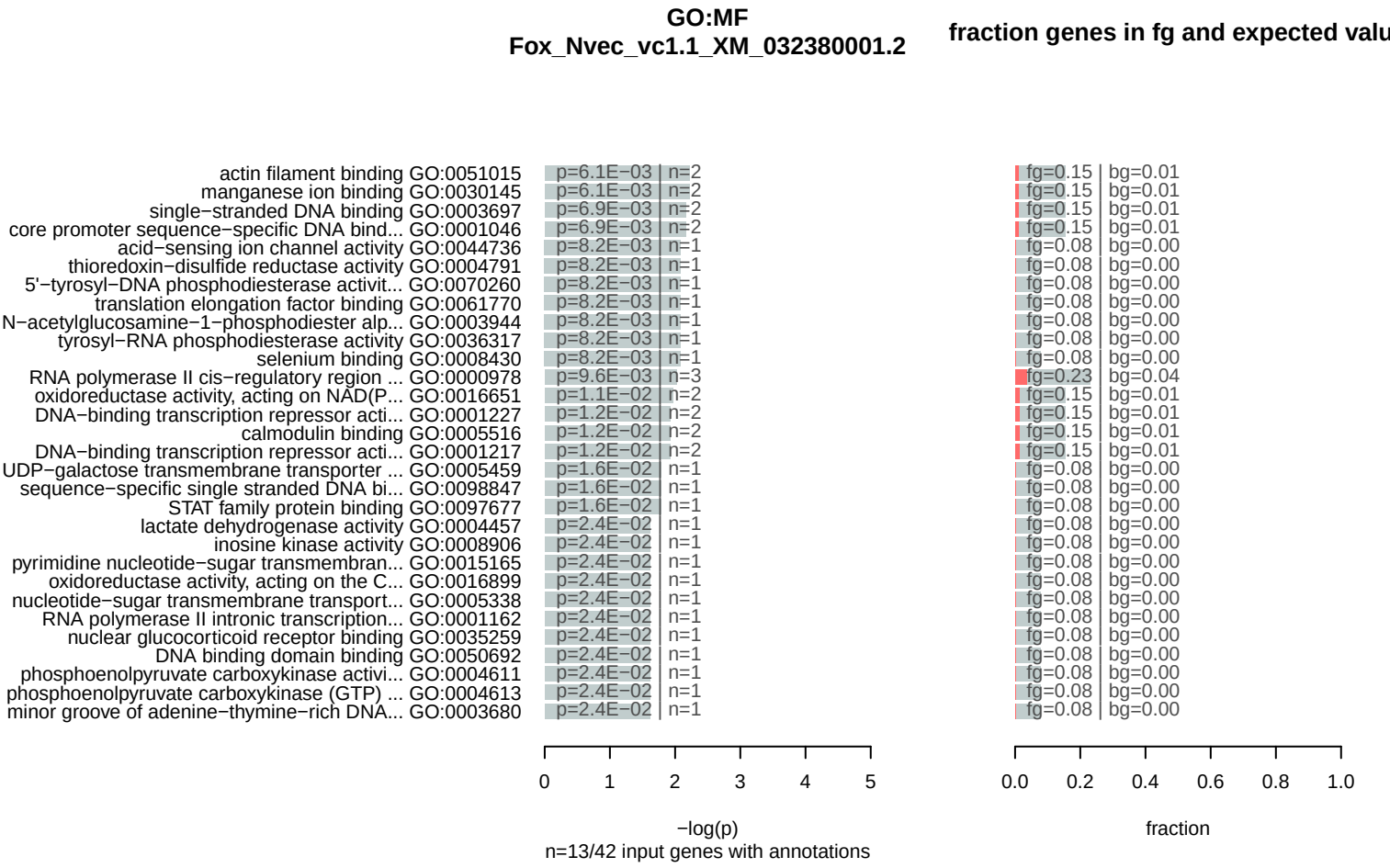
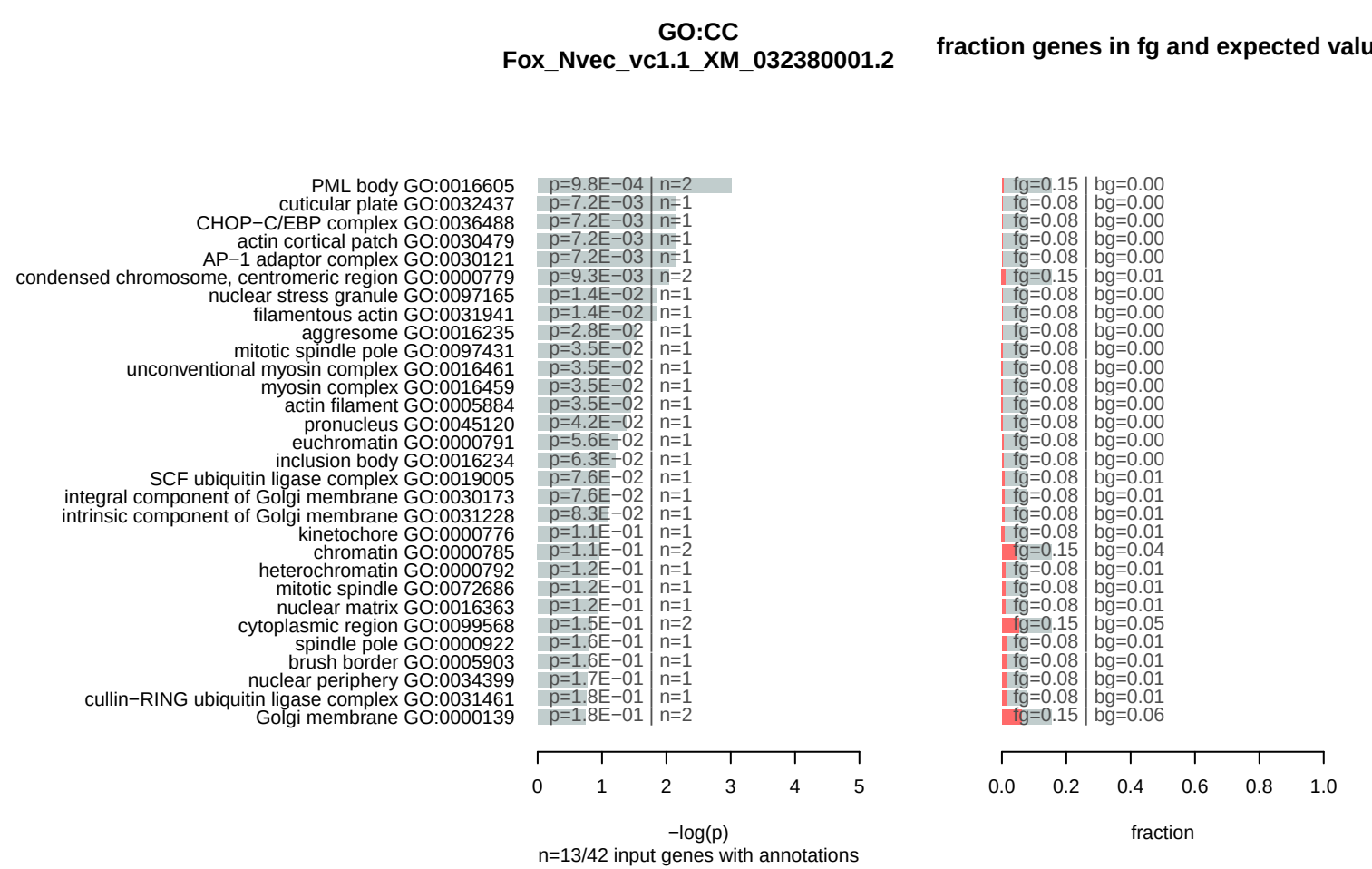

GO:BP
Fox_Nvec_vc1.1_XM_032380001.2
fraction genes in fg and expected valu
cell differentiation involved in kidney ... GO:0061005 p=1.8E−04 n=3 fg=0.23 bg=0.01
cellular response to pH GO:0071467 p=7.0E−04 n=2 fg=0.15 bg=0.00
cellular response to toxic substance GO:0097237 p=7.6E−04 n=3 fg=0.23 bg=0.01
protein homotrimerization GO:0070207 p=1.3E−03 n=2 fg=0.15 bg=0.00
response to lipopolysaccharide GO:0032496 p=1.8E−03 n=3 fg=0.23 bg=0.02
defense response to bacterium GO:0042742 p=2.1E−03 n=3 fg=0.23 bg=0.02
cellular response to amino acid stimulus GO:0071230 p=3.0E−03 n=2 fg=0.15 bg=0.01
protein secretion GO:0009306 p=3.4E−03 n=4 fg=0.31 bg=0.05
positive regulation of transcription fro... GO:0036003 p=3.5E−03 n=2 fg=0.15 bg=0.01
embryonic placenta development GO:0001892 p=4.7E−03 n=2 fg=0.15 bg=0.01
cellular response to interleukin−1 GO:0071347 p=6.1E−03 n=2 fg=0.15 bg=0.01
negative regulation of double−strand bre... GO:2001033 p=7.2E−03 n=1 fg=0.08 bg=0.00
granuloma formation GO:0002432 p=7.2E−03 n=1 fg=0.08 bg=0.00
endosome to melanosome transport GO:0035646 p=7.2E−03 n=1 fg=0.08 bg=0.00
positive regulation of microtubule bindi... GO:1904528 p=7.2E−03 n=1 fg=0.08 bg=0.00
cellular response to diamide GO:0072738 p=7.2E−03 n=1 fg=0.08 bg=0.00
embryonic process involved in female pre... GO:0060136 p=7.2E−03 n=1 fg=0.08 bg=0.00
positive regulation of mRNA polyadenylat... GO:1900365 p=7.2E−03 n=1 fg=0.08 bg=0.00
T−helper 1 cell activation GO:0035711 p=7.2E−03 n=1 fg=0.08 bg=0.00
actin crosslink formation GO:0051764 p=7.2E−03 n=1 fg=0.08 bg=0.00
hepatocyte proliferation GO:0072574 p=7.2E−03 n=1 fg=0.08 bg=0.00
cellular response to sodium arsenite GO:1903936 p=7.2E−03 n=1 fg=0.08 bg=0.00
positive regulation of peptide hormone s... GO:0090277 p=8.4E−03 n=2 fg=0.15 bg=0.01
response to antineoplastic agent GO:0097327 p=9.2E−03 n=2 fg=0.15 bg=0.01
innate immune response GO:0045087 p=1.2E−02 n=3 fg=0.23 bg=0.04
positive regulation of multicellular org... GO:0040018 p=1.3E−02 n=2 fg=0.15 bg=0.01
regulation of odontoblast differentiatio... GO:1901329 p=1.4E−02 n=1 fg=0.08 bg=0.00
odontoblast differentiation GO:0071895 p=1.4E−02 n=1 fg=0.08 bg=0.00
metanephric macula densa development GO:0072227 p=1.4E−02 n=1 fg=0.08 bg=0.00
metanephric DCT cell differentiation GO:0072240 p=1.4E−02 n=1 fg=0.08 bg=0.00
0 1 2 3 4 5
−log(p)
n=13/42 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Fox_Nvec_vc1.1_XM_032380001.2
fraction genes in fg and expected valu
actin filament binding GO:0051015 p=6.1E−03 n=2 fg=0.15 bg=0.01
manganese ion binding GO:0030145 p=6.1E−03 n=2 fg=0.15 bg=0.01
single−stranded DNA binding GO:0003697 p=6.9E−03 n=2 fg=0.15 bg=0.01
core promoter sequence−specific DNA bind... GO:0001046 p=6.9E−03 n=2 fg=0.15 bg=0.01
acid−sensing ion channel activity GO:0044736 p=8.2E−03 n=1 fg=0.08 bg=0.00
thioredoxin−disulfide reductase activity GO:0004791 p=8.2E−03 n=1 fg=0.08 bg=0.00
5'−tyrosyl−DNA phosphodiesterase activit... GO:0070260 p=8.2E−03 n=1 fg=0.08 bg=0.00
translation elongation factor binding GO:0061770 p=8.2E−03 n=1 fg=0.08 bg=0.00
N−acetylglucosamine−1−phosphodiester alp... GO:0003944 p=8.2E−03 n=1 fg=0.08 bg=0.00
tyrosyl−RNA phosphodiesterase activity GO:0036317 p=8.2E−03 n=1 fg=0.08 bg=0.00
selenium binding GO:0008430 p=8.2E−03 n=1 fg=0.08 bg=0.00
RNA polymerase II cis−regulatory region ... GO:0000978 p=9.6E−03 n=3 fg=0.23 bg=0.04
oxidoreductase activity, acting on NAD(P... GO:0016651 p=1.1E−02 n=2 fg=0.15 bg=0.01
DNA−binding transcription repressor acti... GO:0001227 p=1.2E−02 n=2 fg=0.15 bg=0.01
calmodulin binding GO:0005516 p=1.2E−02 n=2 fg=0.15 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=1.2E−02 n=2 fg=0.15 bg=0.01
UDP−galactose transmembrane transporter ... GO:0005459 p=1.6E−02 n=1 fg=0.08 bg=0.00
sequence−specific single stranded DNA bi... GO:0098847 p=1.6E−02 n=1 fg=0.08 bg=0.00
STAT family protein binding GO:0097677 p=1.6E−02 n=1 fg=0.08 bg=0.00
lactate dehydrogenase activity GO:0004457 p=2.4E−02 n=1 fg=0.08 bg=0.00
inosine kinase activity GO:0008906 p=2.4E−02 n=1 fg=0.08 bg=0.00
pyrimidine nucleotide−sugar transmembran... GO:0015165 p=2.4E−02 n=1 fg=0.08 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=2.4E−02 n=1 fg=0.08 bg=0.00
nucleotide−sugar transmembrane transport... GO:0005338 p=2.4E−02 n=1 fg=0.08 bg=0.00
RNA polymerase II intronic transcription... GO:0001162 p=2.4E−02 n=1 fg=0.08 bg=0.00
nuclear glucocorticoid receptor binding GO:0035259 p=2.4E−02 n=1 fg=0.08 bg=0.00
DNA binding domain binding GO:0050692 p=2.4E−02 n=1 fg=0.08 bg=0.00
phosphoenolpyruvate carboxykinase activi... GO:0004611 p=2.4E−02 n=1 fg=0.08 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=2.4E−02 n=1 fg=0.08 bg=0.00
minor groove of adenine−thymine−rich DNA... GO:0003680 p=2.4E−02 n=1 fg=0.08 bg=0.00
0 1 2 3 4 5
−log(p)
n=13/42 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Fox_Nvec_vc1.1_XM_032380001.2
fraction genes in fg and expected valu
PML body GO:0016605 p=9.8E−04 n=2 fg=0.15 bg=0.00
cuticular plate GO:0032437 p=7.2E−03 n=1 fg=0.08 bg=0.00
CHOP−C/EBP complex GO:0036488 p=7.2E−03 n=1 fg=0.08 bg=0.00
actin cortical patch GO:0030479 p=7.2E−03 n=1 fg=0.08 bg=0.00
AP−1 adaptor complex GO:0030121 p=7.2E−03 n=1 fg=0.08 bg=0.00
condensed chromosome, centromeric region GO:0000779 p=9.3E−03 n=2 fg=0.15 bg=0.01
nuclear stress granule GO:0097165 p=1.4E−02 n=1 fg=0.08 bg=0.00
filamentous actin GO:0031941 p=1.4E−02 n=1 fg=0.08 bg=0.00
aggresome GO:0016235 p=2.8E−02 n=1 fg=0.08 bg=0.00
mitotic spindle pole GO:0097431 p=3.5E−02 n=1 fg=0.08 bg=0.00
unconventional myosin complex GO:0016461 p=3.5E−02 n=1 fg=0.08 bg=0.00
myosin complex GO:0016459 p=3.5E−02 n=1 fg=0.08 bg=0.00
actin filament GO:0005884 p=3.5E−02 n=1 fg=0.08 bg=0.00
pronucleus GO:0045120 p=4.2E−02 n=1 fg=0.08 bg=0.00
euchromatin GO:0000791 p=5.6E−02 n=1 fg=0.08 bg=0.00
inclusion body GO:0016234 p=6.3E−02 n=1 fg=0.08 bg=0.00
SCF ubiquitin ligase complex GO:0019005 p=7.6E−02 n=1 fg=0.08 bg=0.01
integral component of Golgi membrane GO:0030173 p=7.6E−02 n=1 fg=0.08 bg=0.01
intrinsic component of Golgi membrane GO:0031228 p=8.3E−02 n=1 fg=0.08 bg=0.01
kinetochore GO:0000776 p=1.1E−01 n=1 fg=0.08 bg=0.01
chromatin GO:0000785 p=1.1E−01 n=2 fg=0.15 bg=0.04
heterochromatin GO:0000792 p=1.2E−01 n=1 fg=0.08 bg=0.01
mitotic spindle GO:0072686 p=1.2E−01 n=1 fg=0.08 bg=0.01
nuclear matrix GO:0016363 p=1.2E−01 n=1 fg=0.08 bg=0.01
cytoplasmic region GO:0099568 p=1.5E−01 n=2 fg=0.15 bg=0.05
spindle pole GO:0000922 p=1.6E−01 n=1 fg=0.08 bg=0.01
brush border GO:0005903 p=1.6E−01 n=1 fg=0.08 bg=0.01
nuclear periphery GO:0034399 p=1.7E−01 n=1 fg=0.08 bg=0.01
cullin−RING ubiquitin ligase complex GO:0031461 p=1.8E−01 n=1 fg=0.08 bg=0.01
Golgi membrane GO:0000139 p=1.8E−01 n=2 fg=0.15 bg=0.06
0 1 2 3 4 5
−log(p)
n=13/42 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction