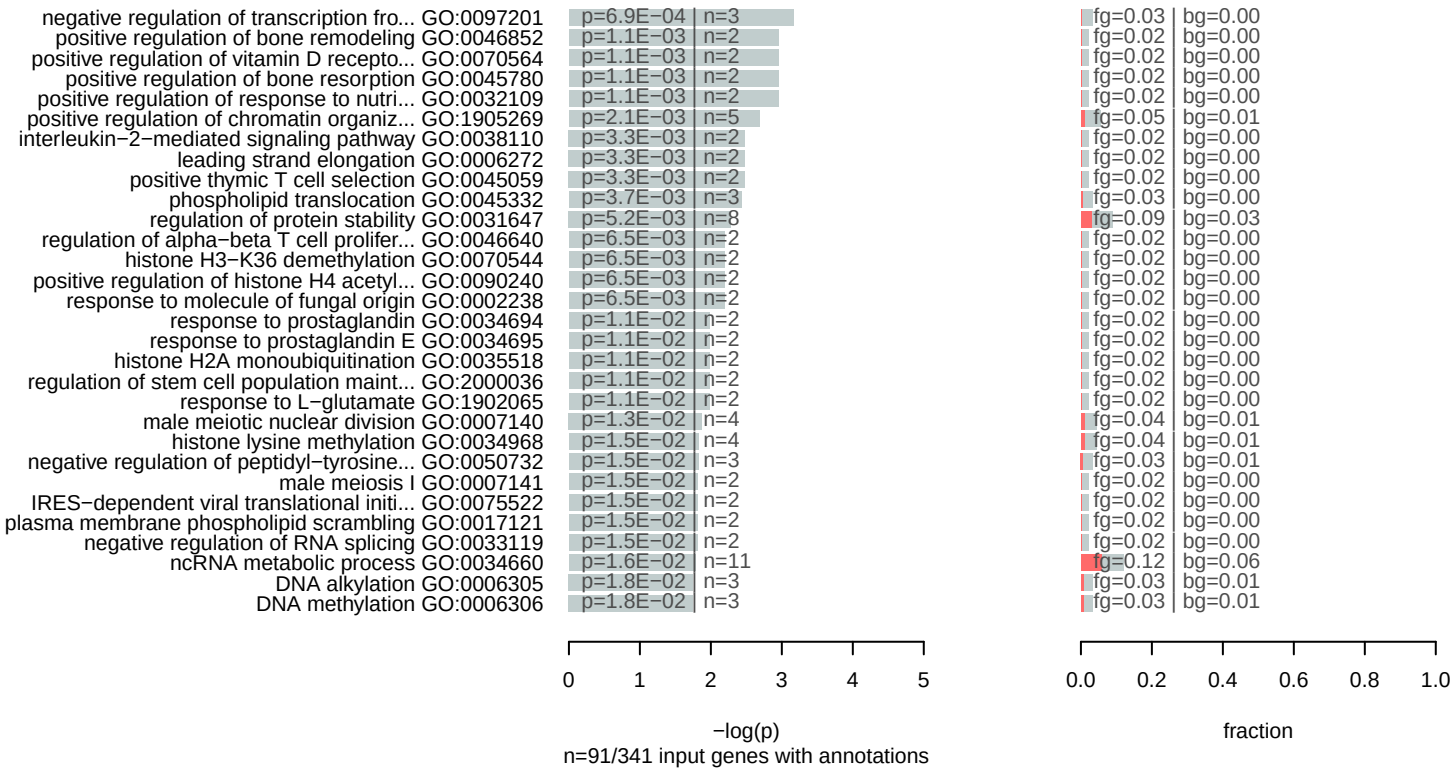
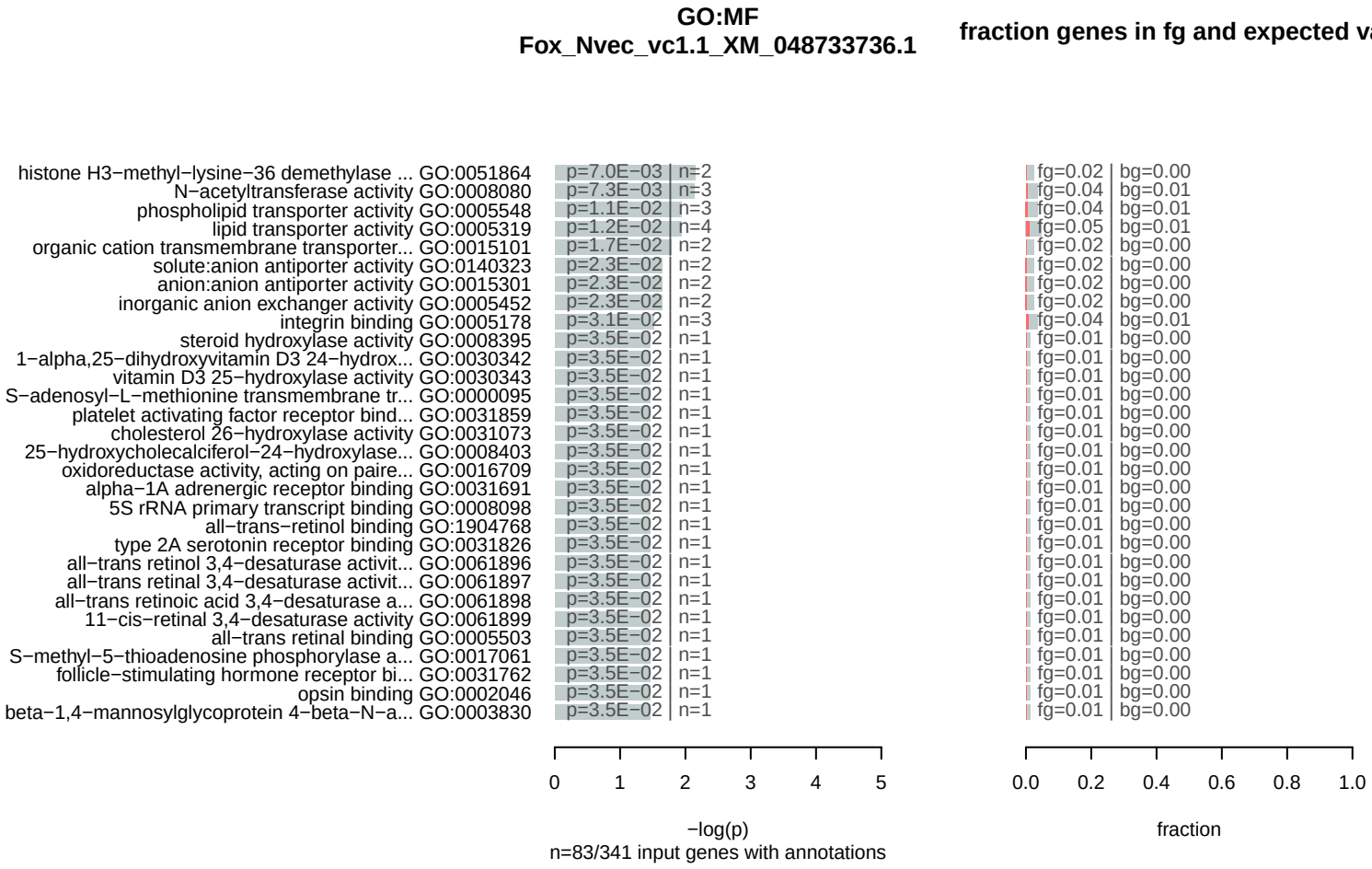
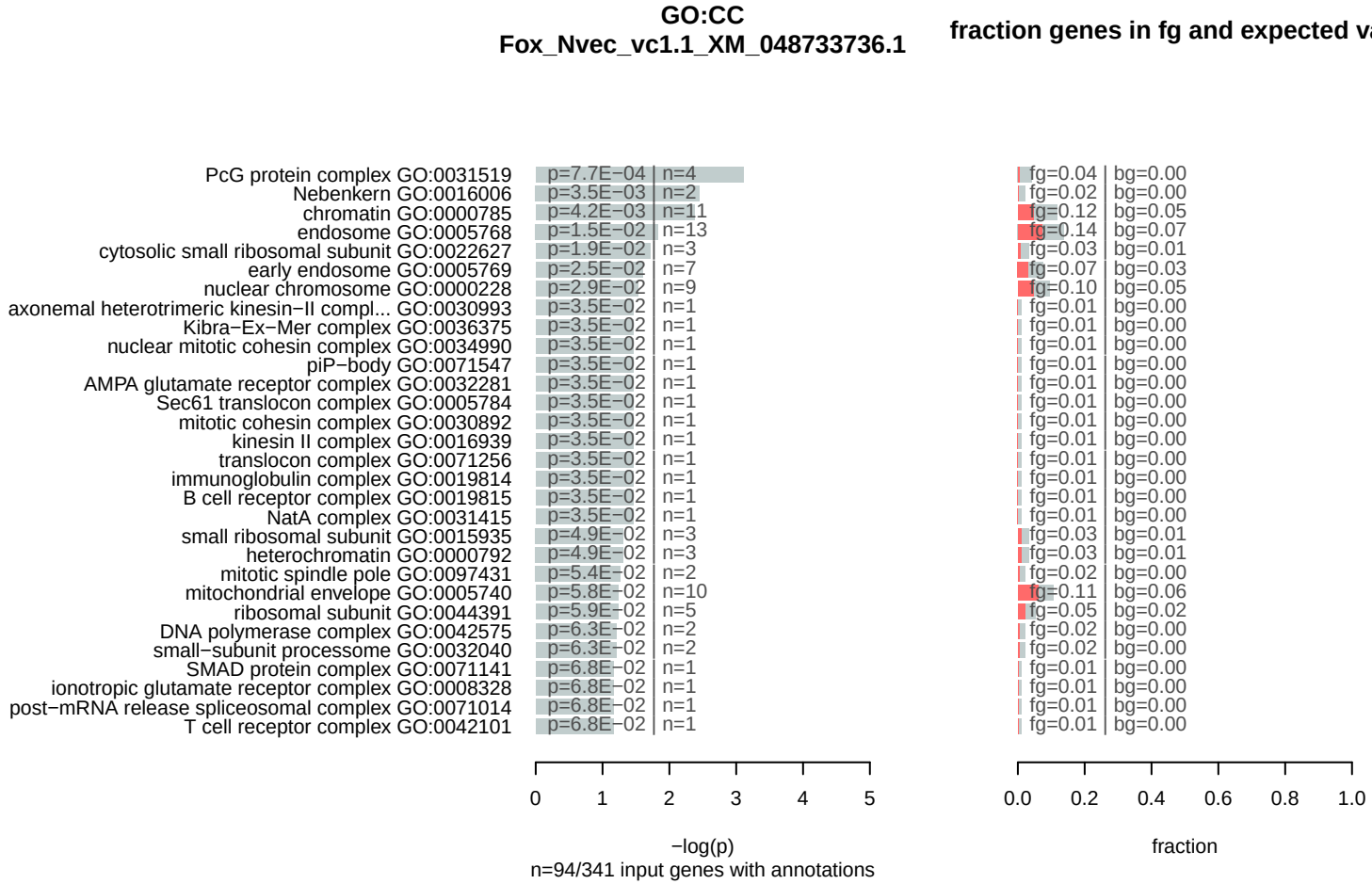

GO:BP
Fox_Nvec_vc1.1_XM_048733736.1
fraction genes in fg and expected valu
negative regulation of transcription fro... GO:0097201 p=6.9E−04 n=3 fg=0.03 bg=0.00
positive regulation of bone remodeling GO:0046852 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of vitamin D recepto... GO:0070564 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of bone resorption GO:0045780 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of response to nutri... GO:0032109 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of chromatin organiz... GO:1905269 p=2.1E−03 n=5 fg=0.05 bg=0.01
interleukin−2−mediated signaling pathway GO:0038110 p=3.3E−03 n=2 fg=0.02 bg=0.00
leading strand elongation GO:0006272 p=3.3E−03 n=2 fg=0.02 bg=0.00
positive thymic T cell selection GO:0045059 p=3.3E−03 n=2 fg=0.02 bg=0.00
phospholipid translocation GO:0045332 p=3.7E−03 n=3 fg=0.03 bg=0.00
regulation of protein stability GO:0031647 p=5.2E−03 n=8 fg=0.09 bg=0.03
regulation of alpha−beta T cell prolifer... GO:0046640 p=6.5E−03 n=2 fg=0.02 bg=0.00
histone H3−K36 demethylation GO:0070544 p=6.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of histone H4 acetyl... GO:0090240 p=6.5E−03 n=2 fg=0.02 bg=0.00
response to molecule of fungal origin GO:0002238 p=6.5E−03 n=2 fg=0.02 bg=0.00
response to prostaglandin GO:0034694 p=1.1E−02 n=2 fg=0.02 bg=0.00
response to prostaglandin E GO:0034695 p=1.1E−02 n=2 fg=0.02 bg=0.00
histone H2A monoubiquitination GO:0035518 p=1.1E−02 n=2 fg=0.02 bg=0.00
regulation of stem cell population maint... GO:2000036 p=1.1E−02 n=2 fg=0.02 bg=0.00
response to L−glutamate GO:1902065 p=1.1E−02 n=2 fg=0.02 bg=0.00
male meiotic nuclear division GO:0007140 p=1.3E−02 n=4 fg=0.04 bg=0.01
histone lysine methylation GO:0034968 p=1.5E−02 n=4 fg=0.04 bg=0.01
negative regulation of peptidyl−tyrosine... GO:0050732 p=1.5E−02 n=3 fg=0.03 bg=0.01
male meiosis I GO:0007141 p=1.5E−02 n=2 fg=0.02 bg=0.00
IRES−dependent viral translational initi... GO:0075522 p=1.5E−02 n=2 fg=0.02 bg=0.00
plasma membrane phospholipid scrambling GO:0017121 p=1.5E−02 n=2 fg=0.02 bg=0.00
negative regulation of RNA splicing GO:0033119 p=1.5E−02 n=2 fg=0.02 bg=0.00
ncRNA metabolic process GO:0034660 p=1.6E−02 n=11 fg=0.12 bg=0.06
DNA alkylation GO:0006305 p=1.8E−02 n=3 fg=0.03 bg=0.01
DNA methylation GO:0006306 p=1.8E−02 n=3 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=91/341 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Fox_Nvec_vc1.1_XM_048733736.1
fraction genes in fg and expected valu
histone H3−methyl−lysine−36 demethylase ... GO:0051864 p=7.0E−03 n=2 fg=0.02 bg=0.00
N−acetyltransferase activity GO:0008080 p=7.3E−03 n=3 fg=0.04 bg=0.01
phospholipid transporter activity GO:0005548 p=1.1E−02 n=3 fg=0.04 bg=0.01
lipid transporter activity GO:0005319 p=1.2E−02 n=4 fg=0.05 bg=0.01
organic cation transmembrane transporter... GO:0015101 p=1.7E−02 n=2 fg=0.02 bg=0.00
solute:anion antiporter activity GO:0140323 p=2.3E−02 n=2 fg=0.02 bg=0.00
anion:anion antiporter activity GO:0015301 p=2.3E−02 n=2 fg=0.02 bg=0.00
inorganic anion exchanger activity GO:0005452 p=2.3E−02 n=2 fg=0.02 bg=0.00
integrin binding GO:0005178 p=3.1E−02 n=3 fg=0.04 bg=0.01
steroid hydroxylase activity GO:0008395 p=3.5E−02 n=1 fg=0.01 bg=0.00
1−alpha,25−dihydroxyvitamin D3 24−hydrox... GO:0030342 p=3.5E−02 n=1 fg=0.01 bg=0.00
vitamin D3 25−hydroxylase activity GO:0030343 p=3.5E−02 n=1 fg=0.01 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=3.5E−02 n=1 fg=0.01 bg=0.00
platelet activating factor receptor bind... GO:0031859 p=3.5E−02 n=1 fg=0.01 bg=0.00
cholesterol 26−hydroxylase activity GO:0031073 p=3.5E−02 n=1 fg=0.01 bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403 p=3.5E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on paire... GO:0016709 p=3.5E−02 n=1 fg=0.01 bg=0.00
alpha−1A adrenergic receptor binding GO:0031691 p=3.5E−02 n=1 fg=0.01 bg=0.00
5S rRNA primary transcript binding GO:0008098 p=3.5E−02 n=1 fg=0.01 bg=0.00
all−trans−retinol binding GO:1904768 p=3.5E−02 n=1 fg=0.01 bg=0.00
type 2A serotonin receptor binding GO:0031826 p=3.5E−02 n=1 fg=0.01 bg=0.00
all−trans retinol 3,4−desaturase activit... GO:0061896 p=3.5E−02 n=1 fg=0.01 bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061897 p=3.5E−02 n=1 fg=0.01 bg=0.00
all−trans retinoic acid 3,4−desaturase a... GO:0061898 p=3.5E−02 n=1 fg=0.01 bg=0.00
11−cis−retinal 3,4−desaturase activity GO:0061899 p=3.5E−02 n=1 fg=0.01 bg=0.00
all−trans retinal binding GO:0005503 p=3.5E−02 n=1 fg=0.01 bg=0.00
S−methyl−5−thioadenosine phosphorylase a... GO:0017061 p=3.5E−02 n=1 fg=0.01 bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762 p=3.5E−02 n=1 fg=0.01 bg=0.00
opsin binding GO:0002046 p=3.5E−02 n=1 fg=0.01 bg=0.00
beta−1,4−mannosylglycoprotein 4−beta−N−a... GO:0003830 p=3.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=83/341 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Fox_Nvec_vc1.1_XM_048733736.1
fraction genes in fg and expected valu
PcG protein complex GO:0031519 p=7.7E−04 n=4 fg=0.04 bg=0.00
Nebenkern GO:0016006 p=3.5E−03 n=2 fg=0.02 bg=0.00
chromatin GO:0000785 p=4.2E−03 n=11 fg=0.12 bg=0.05
endosome GO:0005768 p=1.5E−02 n=13 fg=0.14 bg=0.07
cytosolic small ribosomal subunit GO:0022627 p=1.9E−02 n=3 fg=0.03 bg=0.01
early endosome GO:0005769 p=2.5E−02 n=7 fg=0.07 bg=0.03
nuclear chromosome GO:0000228 p=2.9E−02 n=9 fg=0.10 bg=0.05
axonemal heterotrimeric kinesin−II compl... GO:0030993 p=3.5E−02 n=1 fg=0.01 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=3.5E−02 n=1 fg=0.01 bg=0.00
nuclear mitotic cohesin complex GO:0034990 p=3.5E−02 n=1 fg=0.01 bg=0.00
piP−body GO:0071547 p=3.5E−02 n=1 fg=0.01 bg=0.00
AMPA glutamate receptor complex GO:0032281 p=3.5E−02 n=1 fg=0.01 bg=0.00
Sec61 translocon complex GO:0005784 p=3.5E−02 n=1 fg=0.01 bg=0.00
mitotic cohesin complex GO:0030892 p=3.5E−02 n=1 fg=0.01 bg=0.00
kinesin II complex GO:0016939 p=3.5E−02 n=1 fg=0.01 bg=0.00
translocon complex GO:0071256 p=3.5E−02 n=1 fg=0.01 bg=0.00
immunoglobulin complex GO:0019814 p=3.5E−02 n=1 fg=0.01 bg=0.00
B cell receptor complex GO:0019815 p=3.5E−02 n=1 fg=0.01 bg=0.00
NatA complex GO:0031415 p=3.5E−02 n=1 fg=0.01 bg=0.00
small ribosomal subunit GO:0015935 p=4.9E−02 n=3 fg=0.03 bg=0.01
heterochromatin GO:0000792 p=4.9E−02 n=3 fg=0.03 bg=0.01
mitotic spindle pole GO:0097431 p=5.4E−02 n=2 fg=0.02 bg=0.00
mitochondrial envelope GO:0005740 p=5.8E−02 n=10 fg=0.11 bg=0.06
ribosomal subunit GO:0044391 p=5.9E−02 n=5 fg=0.05 bg=0.02
DNA polymerase complex GO:0042575 p=6.3E−02 n=2 fg=0.02 bg=0.00
small−subunit processome GO:0032040 p=6.3E−02 n=2 fg=0.02 bg=0.00
SMAD protein complex GO:0071141 p=6.8E−02 n=1 fg=0.01 bg=0.00
ionotropic glutamate receptor complex GO:0008328 p=6.8E−02 n=1 fg=0.01 bg=0.00
post−mRNA release spliceosomal complex GO:0071014 p=6.8E−02 n=1 fg=0.01 bg=0.00
T cell receptor complex GO:0042101 p=6.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=94/341 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction