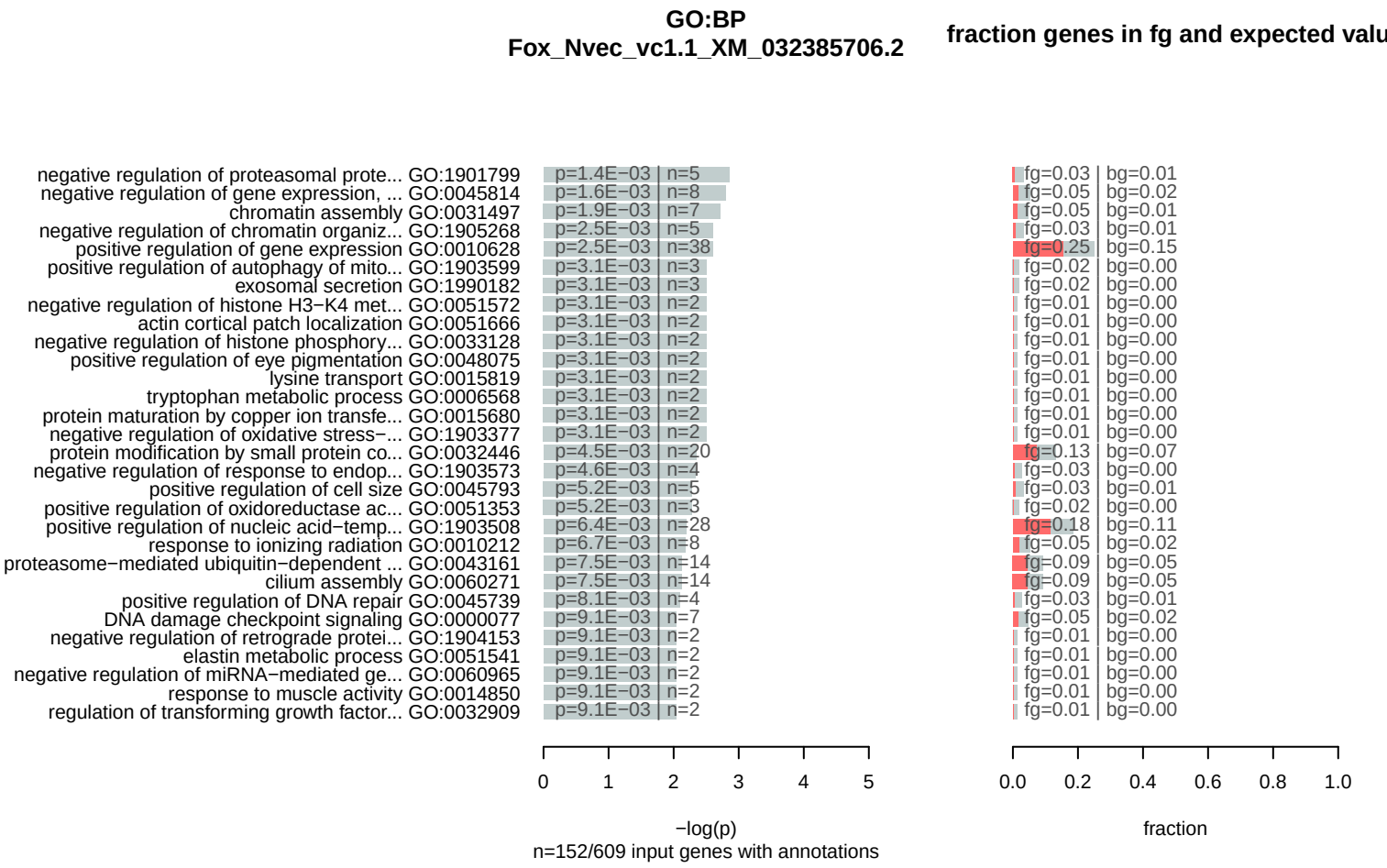
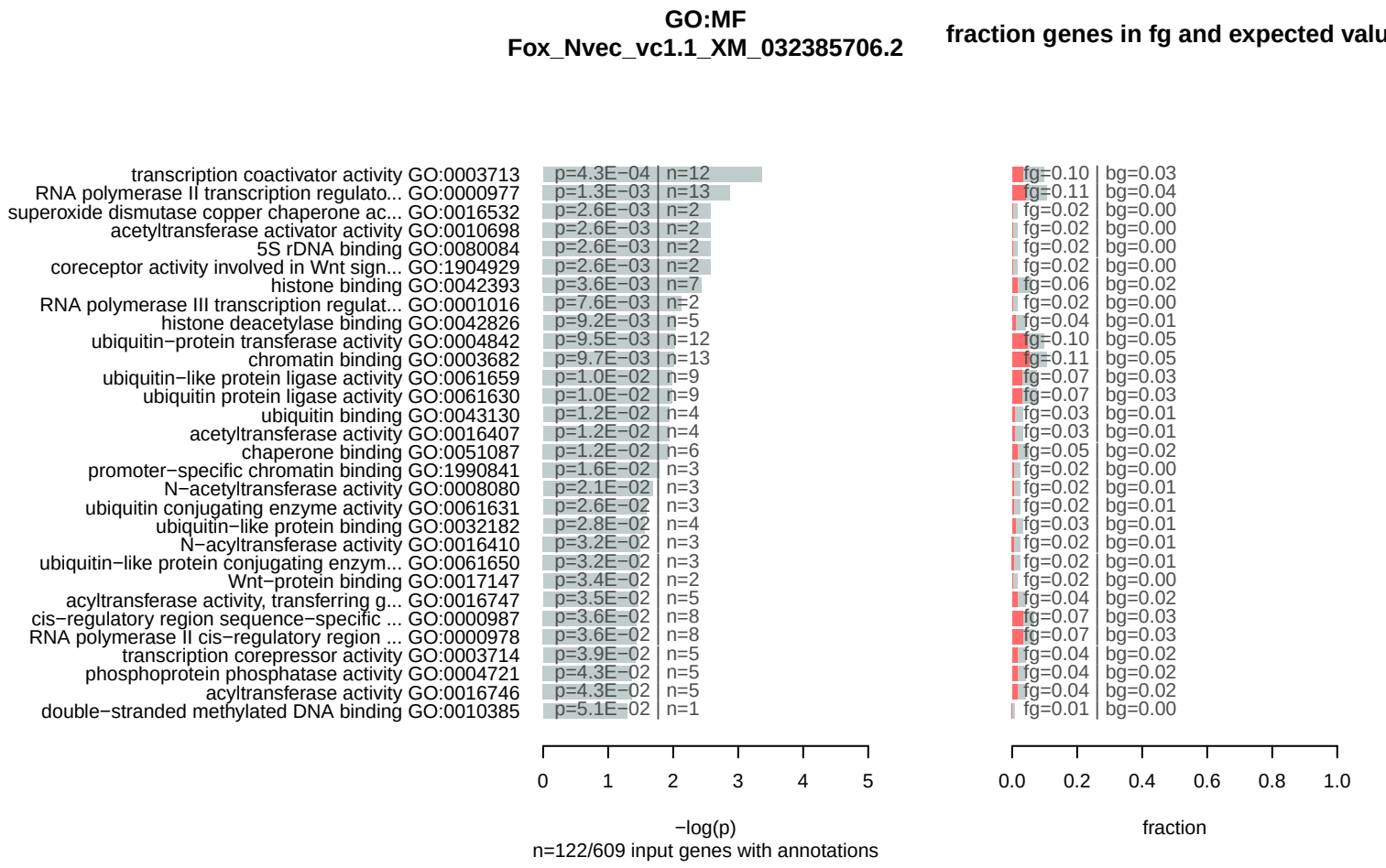

GO:BP
Fox_Nvec_vc1.1_XM_032385706.2
fraction genes in fg and expected valu
negative regulation of proteasomal prote... GO:1901799 p=1.4E−03 n=5 fg=0.03 bg=0.01
negative regulation of gene expression, ... GO:0045814 p=1.6E−03 n=8 fg=0.05 bg=0.02
chromatin assembly GO:0031497 p=1.9E−03 n=7 fg=0.05 bg=0.01
negative regulation of chromatin organiz... GO:1905268 p=2.5E−03 n=5 fg=0.03 bg=0.01
positive regulation of gene expression GO:0010628 p=2.5E−03 n=38 fg=0.25 bg=0.15
positive regulation of autophagy of mito... GO:1903599 p=3.1E−03 n=3 fg=0.02 bg=0.00
exosomal secretion GO:1990182 p=3.1E−03 n=3 fg=0.02 bg=0.00
negative regulation of histone H3−K4 met... GO:0051572 p=3.1E−03 n=2 fg=0.01 bg=0.00
actin cortical patch localization GO:0051666 p=3.1E−03 n=2 fg=0.01 bg=0.00
negative regulation of histone phosphory... GO:0033128 p=3.1E−03 n=2 fg=0.01 bg=0.00
positive regulation of eye pigmentation GO:0048075 p=3.1E−03 n=2 fg=0.01 bg=0.00
lysine transport GO:0015819 p=3.1E−03 n=2 fg=0.01 bg=0.00
tryptophan metabolic process GO:0006568 p=3.1E−03 n=2 fg=0.01 bg=0.00
protein maturation by copper ion transfe... GO:0015680 p=3.1E−03 n=2 fg=0.01 bg=0.00
negative regulation of oxidative stress−... GO:1903377 p=3.1E−03 n=2 fg=0.01 bg=0.00
protein modification by small protein co... GO:0032446 p=4.5E−03 n=20 fg=0.13 bg=0.07
negative regulation of response to endop... GO:1903573 p=4.6E−03 n=4 fg=0.03 bg=0.00
positive regulation of cell size GO:0045793 p=5.2E−03 n=5 fg=0.03 bg=0.01
positive regulation of oxidoreductase ac... GO:0051353 p=5.2E−03 n=3 fg=0.02 bg=0.00
positive regulation of nucleic acid−temp... GO:1903508 p=6.4E−03 n=28 fg=0.18 bg=0.11
response to ionizing radiation GO:0010212 p=6.7E−03 n=8 fg=0.05 bg=0.02
proteasome−mediated ubiquitin−dependent ... GO:0043161 p=7.5E−03 n=14 fg=0.09 bg=0.05
cilium assembly GO:0060271 p=7.5E−03 n=14 fg=0.09 bg=0.05
positive regulation of DNA repair GO:0045739 p=8.1E−03 n=4 fg=0.03 bg=0.01
DNA damage checkpoint signaling GO:0000077 p=9.1E−03 n=7 fg=0.05 bg=0.02
negative regulation of retrograde protei... GO:1904153 p=9.1E−03 n=2 fg=0.01 bg=0.00
elastin metabolic process GO:0051541 p=9.1E−03 n=2 fg=0.01 bg=0.00
negative regulation of miRNA−mediated ge... GO:0060965 p=9.1E−03 n=2 fg=0.01 bg=0.00
response to muscle activity GO:0014850 p=9.1E−03 n=2 fg=0.01 bg=0.00
regulation of transforming growth factor... GO:0032909 p=9.1E−03 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=152/609 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction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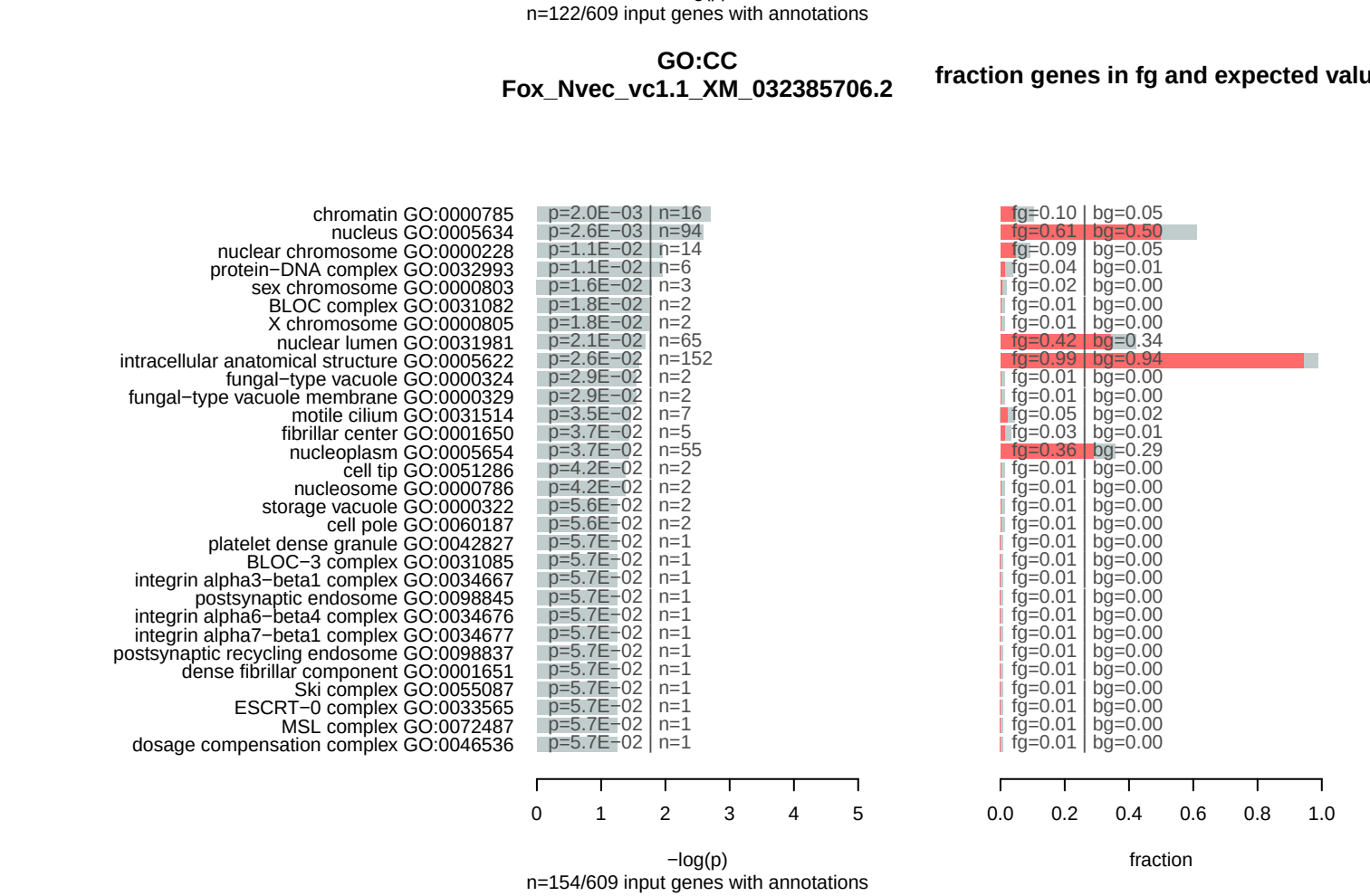
fraction genes in fg and expected valu
transcription coactivator activity GO:0003713 p=4.3E−04 n=12 fg=0.10 bg=0.03
RNA polymerase II transcription regulato... GO:0000977 p=1.3E−03 n=13 fg=0.11 bg=0.04
superoxide dismutase copper chaperone ac... GO:0016532 p=2.6E−03 n=2 fg=0.02 bg=0.00
acetyltransferase activator activity GO:0010698 p=2.6E−03 n=2 fg=0.02 bg=0.00
5S rDNA binding GO:0080084 p=2.6E−03 n=2 fg=0.02 bg=0.00
coreceptor activity involved in Wnt sign... GO:1904929 p=2.6E−03 n=2 fg=0.02 bg=0.00
histone binding GO:0042393 p=3.6E−03 n=7 fg=0.06 bg=0.02
RNA polymerase III transcription regulat... GO:0001016 p=7.6E−03 n=2 fg=0.02 bg=0.00
histone deacetylase binding GO:0042826 p=9.2E−03 n=5 fg=0.04 bg=0.01
ubiquitin−protein transferase activity GO:0004842 p=9.5E−03 n=12 fg=0.10 bg=0.05
chromatin binding GO:0003682 p=9.7E−03 n=13 fg=0.11 bg=0.05
ubiquitin−like protein ligase activity GO:0061659 p=1.0E−02 n=9 fg=0.07 bg=0.03
ubiquitin protein ligase activity GO:0061630 p=1.0E−02 n=9 fg=0.07 bg=0.03
ubiquitin binding GO:0043130 p=1.2E−02 n=4 fg=0.03 bg=0.01
acetyltransferase activity GO:0016407 p=1.2E−02 n=4 fg=0.03 bg=0.01
chaperone binding GO:0051087 p=1.2E−02 n=6 fg=0.05 bg=0.02
promoter−specific chromatin binding GO:1990841 p=1.6E−02 n=3 fg=0.02 bg=0.00
N−acetyltransferase activity GO:0008080 p=2.1E−02 n=3 fg=0.02 bg=0.01
ubiquitin conjugating enzyme activity GO:0061631 p=2.6E−02 n=3 fg=0.02 bg=0.01
ubiquitin−like protein binding GO:0032182 p=2.8E−02 n=4 fg=0.03 bg=0.01
N−acyltransferase activity GO:0016410 p=3.2E−02 n=3 fg=0.02 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0061650 p=3.2E−02 n=3 fg=0.02 bg=0.01
Wnt−protein binding GO:0017147 p=3.4E−02 n=2 fg=0.02 bg=0.00
acyltransferase activity, transferring g... GO:0016747 p=3.5E−02 n=5 fg=0.04 bg=0.02
cis−regulatory region sequence−specific ... GO:0000987 p=3.6E−02 n=8 fg=0.07 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=3.6E−02 n=8 fg=0.07 bg=0.03
transcription corepressor activity GO:0003714 p=3.9E−02 n=5 fg=0.04 bg=0.02
phosphoprotein phosphatase activity GO:0004721 p=4.3E−02 n=5 fg=0.04 bg=0.02
acyltransferase activity GO:0016746 p=4.3E−02 n=5 fg=0.04 bg=0.02
double−stranded methylated DNA binding GO:0010385 p=5.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=122/609 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Fox_Nvec_vc1.1_XM_032385706.2
fraction genes in fg and expected valu
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nucleus GO:0005634 p=2.6E−03 n=94 fg=0.61 bg=0.50
nuclear chromosome GO:0000228 p=1.1E−02 n=14 fg=0.09 bg=0.05
protein−DNA complex GO:0032993 p=1.1E−02 n=6 fg=0.04 bg=0.01
sex chromosome GO:0000803 p=1.6E−02 n=3 fg=0.02 bg=0.00
BLOC complex GO:0031082 p=1.8E−02 n=2 fg=0.01 bg=0.00
X chromosome GO:0000805 p=1.8E−02 n=2 fg=0.01 bg=0.00
nuclear lumen GO:0031981 p=2.1E−02 n=65 fg=0.42 bg=0.34
intracellular anatomical structure GO:0005622 p=2.6E−02 n=152 fg=0.99 bg=0.94
fungal−type vacuole GO:0000324 p=2.9E−02 n=2 fg=0.01 bg=0.00
fungal−type vacuole membrane GO:0000329 p=2.9E−02 n=2 fg=0.01 bg=0.00
motile cilium GO:0031514 p=3.5E−02 n=7 fg=0.05 bg=0.02
fibrillar center GO:0001650 p=3.7E−02 n=5 fg=0.03 bg=0.01
nucleoplasm GO:0005654 p=3.7E−02 n=55 fg=0.36 bg=0.29
cell tip GO:0051286 p=4.2E−02 n=2 fg=0.01 bg=0.00
nucleosome GO:0000786 p=4.2E−02 n=2 fg=0.01 bg=0.00
storage vacuole GO:0000322 p=5.6E−02 n=2 fg=0.01 bg=0.00
cell pole GO:0060187 p=5.6E−02 n=2 fg=0.01 bg=0.00
platelet dense granule GO:0042827 p=5.7E−02 n=1 fg=0.01 bg=0.00
BLOC−3 complex GO:0031085 p=5.7E−02 n=1 fg=0.01 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=5.7E−02 n=1 fg=0.01 bg=0.00
postsynaptic endosome GO:0098845 p=5.7E−02 n=1 fg=0.01 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=5.7E−02 n=1 fg=0.01 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=5.7E−02 n=1 fg=0.01 bg=0.00
postsynaptic recycling endosome GO:0098837 p=5.7E−02 n=1 fg=0.01 bg=0.00
dense fibrillar component GO:0001651 p=5.7E−02 n=1 fg=0.01 bg=0.00
Ski complex GO:0055087 p=5.7E−02 n=1 fg=0.01 bg=0.00
ESCRT−0 complex GO:0033565 p=5.7E−02 n=1 fg=0.01 bg=0.00
MSL complex GO:0072487 p=5.7E−02 n=1 fg=0.01 bg=0.00
dosage compensation complex GO:0046536 p=5.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=154/609 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction