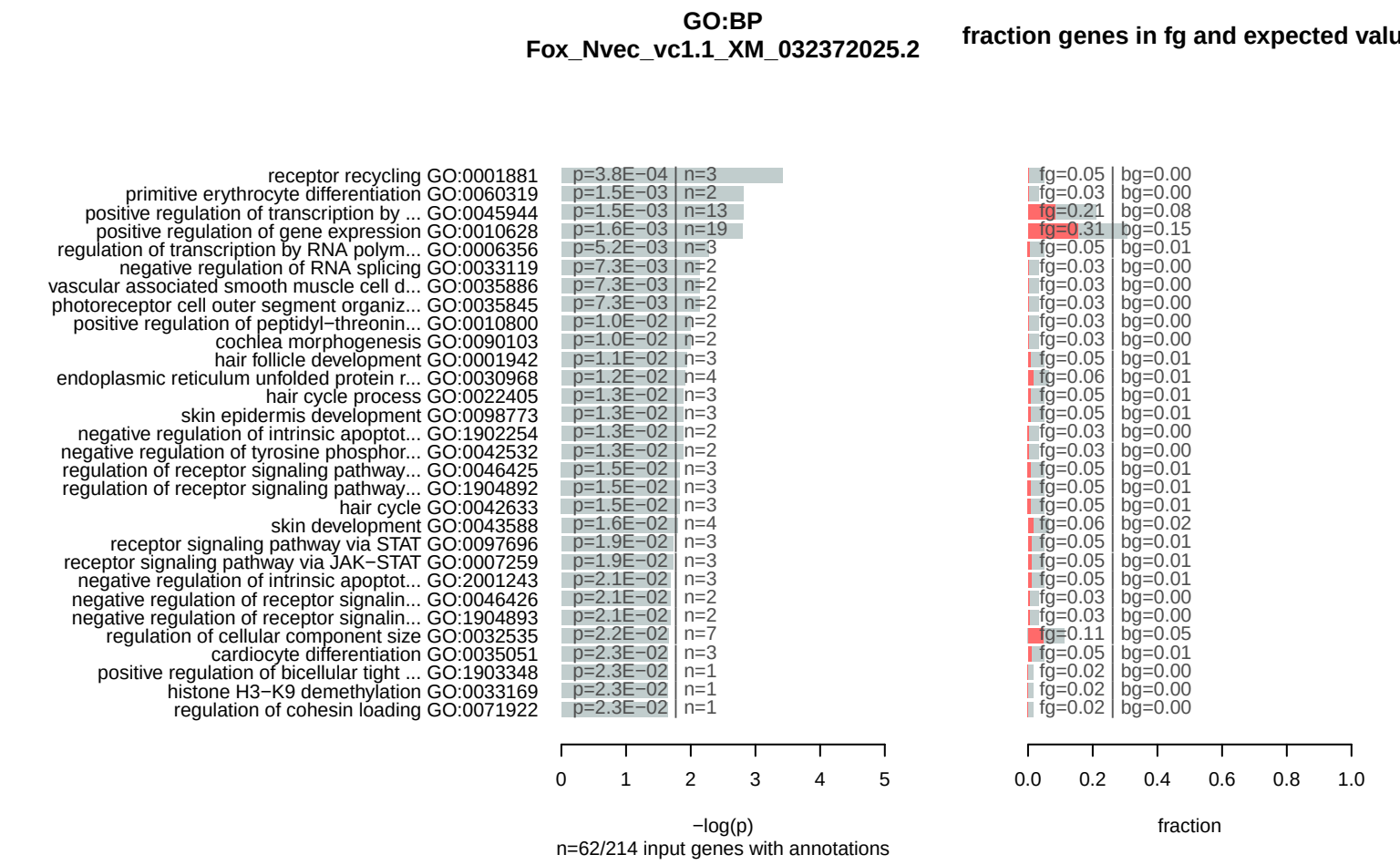
GO:BP
Fox_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
receptor recycling GO:0001881 p=3.8E−04 n=3 fg=0.05 bg=0.00
primitive erythrocyte differentiation GO:0060319 p=1.5E−03 n=2 fg=0.03 bg=0.00
positive regulation of transcription by ... GO:0045944 p=1.5E−03 n=13 fg=0.21 bg=0.08
positive regulation of gene expression GO:0010628 p=1.6E−03 n=19 fg=0.31 bg=0.15
regulation of transcription by RNA polym... GO:0006356 p=5.2E−03 n=3 fg=0.05 bg=0.01
negative regulation of RNA splicing GO:0033119 p=7.3E−03 n=2 fg=0.03 bg=0.00
vascular associated smooth muscle cell d... GO:0035886 p=7.3E−03 n=2 fg=0.03 bg=0.00
photoreceptor cell outer segment organiz... GO:0035845 p=7.3E−03 n=2 fg=0.03 bg=0.00
positive regulation of peptidyl−threonin... GO:0010800 p=1.0E−02 n=2 fg=0.03 bg=0.00
cochlea morphogenesis GO:0090103 p=1.0E−02 n=2 fg=0.03 bg=0.00
hair follicle development GO:0001942 p=1.1E−02 n=3 fg=0.05 bg=0.01
endoplasmic reticulum unfolded protein r... GO:0030968 p=1.2E−02 n=4 fg=0.06 bg=0.01
hair cycle process GO:0022405 p=1.3E−02 n=3 fg=0.05 bg=0.01
skin epidermis development GO:0098773 p=1.3E−02 n=3 fg=0.05 bg=0.01
negative regulation of intrinsic apoptot... GO:1902254 p=1.3E−02 n=2 fg=0.03 bg=0.00
negative regulation of tyrosine phosphor... GO:0042532 p=1.3E−02 n=2 fg=0.03 bg=0.00
regulation of receptor signaling pathway... GO:0046425 p=1.5E−02 n=3 fg=0.05 bg=0.01
regulation of receptor signaling pathway... GO:1904892 p=1.5E−02 n=3 fg=0.05 bg=0.01
hair cycle GO:0042633 p=1.5E−02 n=3 fg=0.05 bg=0.01
skin development GO:0043588 p=1.6E−02 n=4 fg=0.06 bg=0.02
receptor signaling pathway via STAT GO:0097696 p=1.9E−02 n=3 fg=0.05 bg=0.01
receptor signaling pathway via JAK−STAT GO:0007259 p=1.9E−02 n=3 fg=0.05 bg=0.01
negative regulation of intrinsic apoptot... GO:2001243 p=2.1E−02 n=3 fg=0.05 bg=0.01
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regulation of cellular component size GO:0032535 p=2.2E−02 n=7 fg=0.11 bg=0.05
cardiocyte differentiation GO:0035051 p=2.3E−02 n=3 fg=0.05 bg=0.01
positive regulation of bicellular tight ... GO:1903348 p=2.3E−02 n=1 fg=0.02 bg=0.00
histone H3−K9 demethylation GO:0033169 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of cohesin loading GO:0071922 p=2.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=62/214 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
RNA polymerase II transcription regulato... GO:0000977 p=5.1E−03 n=7 fg=0.13 bg=0.04
protein kinase inhibitor activity GO:0004860 p=6.5E−03 n=3 fg=0.06 bg=0.01
DNA−binding transcription factor activit... GO:0003700 p=9.1E−03 n=9 fg=0.17 bg=0.07
HMG box domain binding GO:0071837 p=9.2E−03 n=2 fg=0.04 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=2.1E−02 n=5 fg=0.10 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=2.1E−02 n=5 fg=0.10 bg=0.03
AMP−activated protein kinase activity GO:0004679 p=2.2E−02 n=1 fg=0.02 bg=0.00
pyrroline−5−carboxylate reductase activi... GO:0004735 p=2.2E−02 n=1 fg=0.02 bg=0.00
cytosine C−5 DNA demethylase activity GO:0051747 p=2.2E−02 n=1 fg=0.02 bg=0.00
telomeric repeat−containing RNA binding GO:0061752 p=2.2E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−lysine−9 demethylase a... GO:0032454 p=2.2E−02 n=1 fg=0.02 bg=0.00
JUN kinase kinase kinase activity GO:0004706 p=2.2E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=2.2E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=2.2E−02 n=1 fg=0.02 bg=0.00
methionine adenosyltransferase regulator... GO:0048270 p=2.2E−02 n=1 fg=0.02 bg=0.00
N2−acetyl−L−ornithine:2−oxoglutarate 5−a... GO:0003992 p=2.2E−02 n=1 fg=0.02 bg=0.00
hydroxyacylglutathione hydrolase activit... GO:0004416 p=2.2E−02 n=1 fg=0.02 bg=0.00
ornithine−oxo−acid transaminase activity GO:0004587 p=2.2E−02 n=1 fg=0.02 bg=0.00
RNA polymerase I general transcription i... GO:0001181 p=2.2E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide 1,2−alpha−manno... GO:0004571 p=2.2E−02 n=1 fg=0.02 bg=0.00
MRF binding GO:0043426 p=2.2E−02 n=1 fg=0.02 bg=0.00
transcription regulatory region nucleic ... GO:0001067 p=2.2E−02 n=10 fg=0.19 bg=0.05
cis−regulatory region sequence−specific ... GO:0000987 p=2.3E−02 n=5 fg=0.10 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.3E−02 n=5 fg=0.10 bg=0.03
transcription cis−regulatory region bind... GO:0000976 p=2.6E−02 n=9 fg=0.17 bg=0.05
demethylase activity GO:0032451 p=2.7E−02 n=2 fg=0.04 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=3.0E−02 n=7 fg=0.13 bg=0.06
nuclease inhibitor activity GO:0140721 p=4.3E−02 n=1 fg=0.02 bg=0.00
U1 snRNA binding GO:0030619 p=4.3E−02 n=1 fg=0.02 bg=0.00
volume−sensitive anion channel activity GO:0005225 p=4.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=52/214 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
transcription regulator complex GO:0005667 p=7.1E−03 n=7 fg=0.11 bg=0.04
DNA polymerase III, core complex GO:0044776 p=2.3E−02 n=1 fg=0.02 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=2.3E−02 n=1 fg=0.02 bg=0.00
CCAAT−binding factor complex GO:0016602 p=2.3E−02 n=1 fg=0.02 bg=0.00
Dsl1/NZR complex GO:0070939 p=2.3E−02 n=1 fg=0.02 bg=0.00
bicellular tight junction GO:0005923 p=2.9E−02 n=2 fg=0.03 bg=0.00
Rb−E2F complex GO:0035189 p=4.5E−02 n=1 fg=0.02 bg=0.00
dystroglycan complex GO:0016011 p=4.5E−02 n=1 fg=0.02 bg=0.00
sarcoglycan complex GO:0016012 p=4.5E−02 n=1 fg=0.02 bg=0.00
t−UTP complex GO:0034455 p=4.5E−02 n=1 fg=0.02 bg=0.00
DNA polymerase III complex GO:0009360 p=4.5E−02 n=1 fg=0.02 bg=0.00
tight junction GO:0070160 p=5.1E−02 n=2 fg=0.03 bg=0.01
transcription repressor complex GO:0017053 p=6.3E−02 n=2 fg=0.03 bg=0.01
methionine adenosyltransferase complex GO:0048269 p=6.7E−02 n=1 fg=0.02 bg=0.00
DNA replication factor C complex GO:0005663 p=6.7E−02 n=1 fg=0.02 bg=0.00
beta−catenin−TCF complex GO:1990907 p=6.7E−02 n=1 fg=0.02 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=6.7E−02 n=1 fg=0.02 bg=0.00
Nebenkern GO:0016006 p=6.7E−02 n=1 fg=0.02 bg=0.00
mitochondrial derivative GO:0016007 p=6.7E−02 n=1 fg=0.02 bg=0.00
RNA polymerase II transcription regulato... GO:0090575 p=7.0E−02 n=3 fg=0.05 bg=0.02
neuromuscular junction GO:0031594 p=7.4E−02 n=3 fg=0.05 bg=0.02
glycoprotein complex GO:0090665 p=8.9E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=8.9E−02 n=1 fg=0.02 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=8.9E−02 n=1 fg=0.02 bg=0.00
dystrophin−associated glycoprotein compl... GO:0016010 p=8.9E−02 n=1 fg=0.02 bg=0.00
Cul4A−RING E3 ubiquitin ligase complex GO:0031464 p=8.9E−02 n=1 fg=0.02 bg=0.00
filamentous actin GO:0031941 p=8.9E−02 n=1 fg=0.02 bg=0.00
recycling endosome GO:0055037 p=9.2E−02 n=3 fg=0.05 bg=0.02
apical junction complex GO:0043296 p=1.0E−01 n=2 fg=0.03 bg=0.01
nucleolus GO:0005730 p=1.1E−01 n=9 fg=0.15 bg=0.09
0 1 2 3 4 5
−log(p)
n=62/214 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction