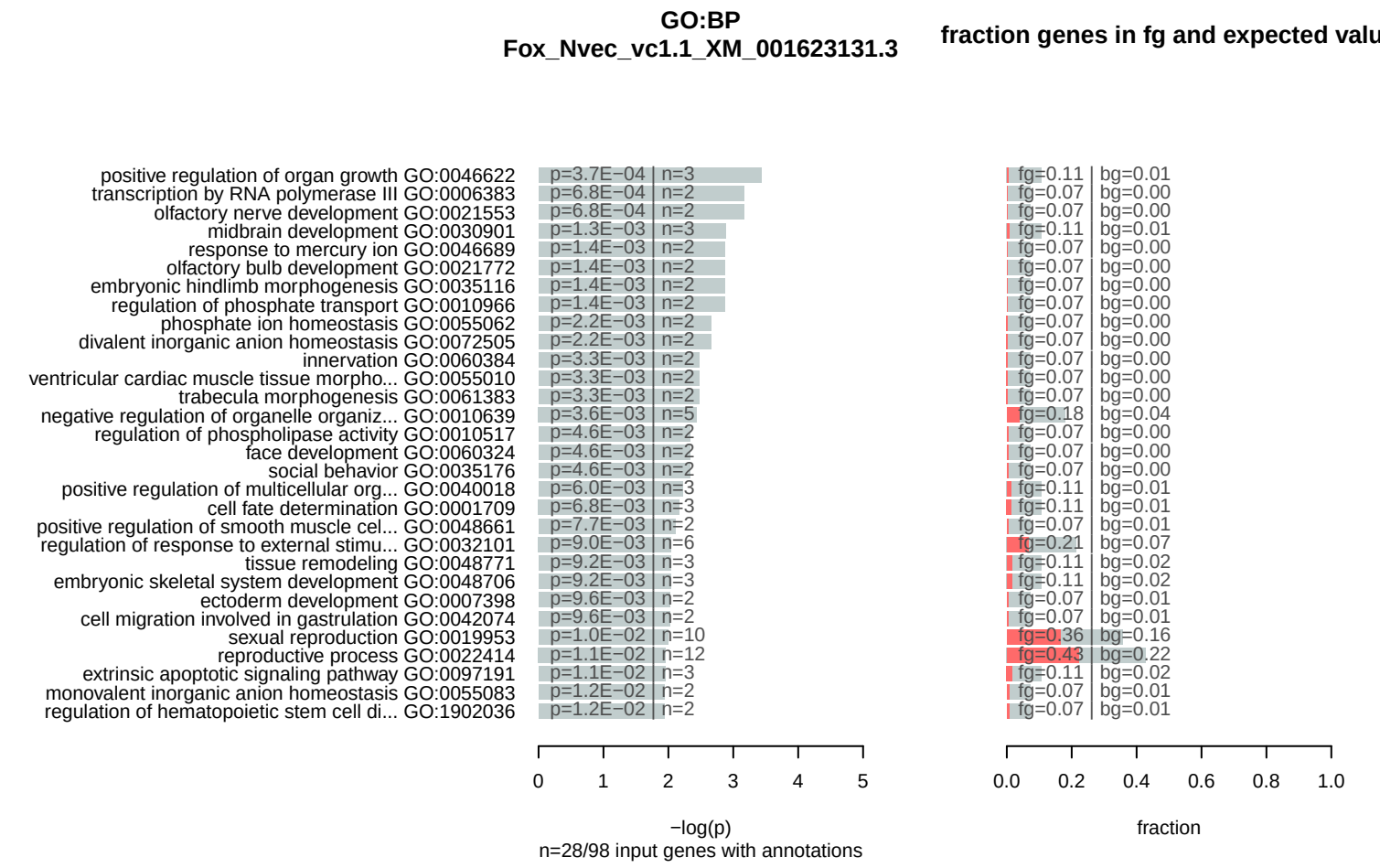
GO:BP
Fox_Nvec_vc1.1_XM_001623131.3
fraction genes in fg and expected valu
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transcription by RNA polymerase III GO:0006383 p=6.8E−04 n=2 fg=0.07 bg=0.00
olfactory nerve development GO:0021553 p=6.8E−04 n=2 fg=0.07 bg=0.00
midbrain development GO:0030901 p=1.3E−03 n=3 fg=0.11 bg=0.01
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olfactory bulb development GO:0021772 p=1.4E−03 n=2 fg=0.07 bg=0.00
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regulation of phosphate transport GO:0010966 p=1.4E−03 n=2 fg=0.07 bg=0.00
phosphate ion homeostasis GO:0055062 p=2.2E−03 n=2 fg=0.07 bg=0.00
divalent inorganic anion homeostasis GO:0072505 p=2.2E−03 n=2 fg=0.07 bg=0.00
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trabecula morphogenesis GO:0061383 p=3.3E−03 n=2 fg=0.07 bg=0.00
negative regulation of organelle organiz... GO:0010639 p=3.6E−03 n=5 fg=0.18 bg=0.04
regulation of phospholipase activity GO:0010517 p=4.6E−03 n=2 fg=0.07 bg=0.00
face development GO:0060324 p=4.6E−03 n=2 fg=0.07 bg=0.00
social behavior GO:0035176 p=4.6E−03 n=2 fg=0.07 bg=0.00
positive regulation of multicellular org... GO:0040018 p=6.0E−03 n=3 fg=0.11 bg=0.01
cell fate determination GO:0001709 p=6.8E−03 n=3 fg=0.11 bg=0.01
positive regulation of smooth muscle cel... GO:0048661 p=7.7E−03 n=2 fg=0.07 bg=0.01
regulation of response to external stimu... GO:0032101 p=9.0E−03 n=6 fg=0.21 bg=0.07
tissue remodeling GO:0048771 p=9.2E−03 n=3 fg=0.11 bg=0.02
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ectoderm development GO:0007398 p=9.6E−03 n=2 fg=0.07 bg=0.01
cell migration involved in gastrulation GO:0042074 p=9.6E−03 n=2 fg=0.07 bg=0.01
sexual reproduction GO:0019953 p=1.0E−02 n=10 fg=0.36 bg=0.16
reproductive process GO:0022414 p=1.1E−02 n=12 fg=0.43 bg=0.22
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monovalent inorganic anion homeostasis GO:0055083 p=1.2E−02 n=2 fg=0.07 bg=0.01
regulation of hematopoietic stem cell di... GO:1902036 p=1.2E−02 n=2 fg=0.07 bg=0.01
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−log(p)
n=28/98 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_001623131.3
fraction genes in fg and expected valu
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adenyl nucleotide binding GO:0030554 p=7.9E−03 n=5 fg=0.20 bg=0.05
protein kinase activity GO:0004672 p=7.9E−03 n=5 fg=0.20 bg=0.05
promoter−specific chromatin binding GO:1990841 p=8.0E−03 n=2 fg=0.08 bg=0.01
ubiquitin conjugating enzyme activity GO:0061631 p=1.2E−02 n=2 fg=0.08 bg=0.01
ubiquitin−protein transferase activity GO:0004842 p=1.2E−02 n=5 fg=0.20 bg=0.06
ubiquitin−like protein transferase activ... GO:0019787 p=1.4E−02 n=5 fg=0.20 bg=0.06
ubiquitin−like protein conjugating enzym... GO:0061650 p=1.4E−02 n=2 fg=0.08 bg=0.01
phosphate ion binding GO:0042301 p=1.6E−02 n=1 fg=0.04 bg=0.00
formate−tetrahydrofolate ligase activity GO:0004329 p=1.6E−02 n=1 fg=0.04 bg=0.00
aminoacyltransferase activity GO:0016755 p=1.6E−02 n=1 fg=0.04 bg=0.00
glutathione gamma−glutamylcysteinyltrans... GO:0016756 p=1.6E−02 n=1 fg=0.04 bg=0.00
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ribosomal protein S6 kinase activity GO:0004711 p=1.6E−02 n=1 fg=0.04 bg=0.00
methenyltetrahydrofolate cyclohydrolase ... GO:0004477 p=1.6E−02 n=1 fg=0.04 bg=0.00
cyclohydrolase activity GO:0019238 p=1.6E−02 n=1 fg=0.04 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=1.6E−02 n=1 fg=0.04 bg=0.00
D5 dopamine receptor binding GO:0031752 p=1.6E−02 n=1 fg=0.04 bg=0.00
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myosin VI heavy chain binding GO:0070854 p=1.6E−02 n=1 fg=0.04 bg=0.00
protein serine/threonine kinase activity GO:0004674 p=1.7E−02 n=4 fg=0.16 bg=0.04
ATP binding GO:0005524 p=1.9E−02 n=4 fg=0.16 bg=0.04
p53 binding GO:0002039 p=2.8E−02 n=2 fg=0.08 bg=0.01
lysine−acetylated histone binding GO:0070577 p=3.1E−02 n=1 fg=0.04 bg=0.00
phosphate ion transmembrane transporter ... GO:0015114 p=3.1E−02 n=1 fg=0.04 bg=0.00
acetylation−dependent protein binding GO:0140033 p=3.1E−02 n=1 fg=0.04 bg=0.00
armadillo repeat domain binding GO:0070016 p=3.1E−02 n=1 fg=0.04 bg=0.00
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−log(p)
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fraction
GO:CC
Fox_Nvec_vc1.1_XM_001623131.3
fraction genes in fg and expected valu
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intracellular organelle GO:0043229 p=8.8E−03 n=28 fg=1.00 bg=0.84
RNA polymerase III transcription regulat... GO:0090576 p=1.5E−02 n=1 fg=0.04 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=1.5E−02 n=1 fg=0.04 bg=0.00
dendritic microtubule GO:1901588 p=1.5E−02 n=1 fg=0.04 bg=0.00
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motile cilium GO:0031514 p=1.7E−02 n=3 fg=0.11 bg=0.02
nucleus GO:0005634 p=2.0E−02 n=20 fg=0.71 bg=0.48
non−membrane−bounded organelle GO:0043228 p=2.3E−02 n=14 fg=0.50 bg=0.30
intracellular non−membrane−bounded organ... GO:0043232 p=2.3E−02 n=14 fg=0.50 bg=0.30
BBSome GO:0034464 p=3.1E−02 n=1 fg=0.04 bg=0.00
microtubule plus−end GO:0035371 p=4.6E−02 n=1 fg=0.04 bg=0.00
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brush border GO:0005903 p=5.2E−02 n=2 fg=0.07 bg=0.01
microvillus membrane GO:0031528 p=6.0E−02 n=1 fg=0.04 bg=0.00
pericentriolar material GO:0000242 p=6.0E−02 n=1 fg=0.04 bg=0.00
chromatoid body GO:0033391 p=6.0E−02 n=1 fg=0.04 bg=0.00
pi−body GO:0071546 p=6.0E−02 n=1 fg=0.04 bg=0.00
nucleoplasm GO:0005654 p=6.6E−02 n=13 fg=0.46 bg=0.27
cluster of actin−based cell projections GO:0098862 p=6.8E−02 n=2 fg=0.07 bg=0.02
microtubule end GO:1990752 p=7.5E−02 n=1 fg=0.04 bg=0.00
plasma membrane bounded cell projection GO:0120025 p=8.0E−02 n=9 fg=0.32 bg=0.20
cell projection GO:0042995 p=8.1E−02 n=9 fg=0.32 bg=0.20
cell projection membrane GO:0031253 p=8.2E−02 n=3 fg=0.11 bg=0.04
cell surface GO:0009986 p=8.2E−02 n=3 fg=0.11 bg=0.04
membrane−enclosed lumen GO:0031974 p=8.8E−02 n=16 fg=0.57 bg=0.39
intracellular organelle lumen GO:0070013 p=8.8E−02 n=16 fg=0.57 bg=0.39
organelle lumen GO:0043233 p=8.8E−02 n=16 fg=0.57 bg=0.39
0 1 2 3 4 5
−log(p)
n=28/98 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction