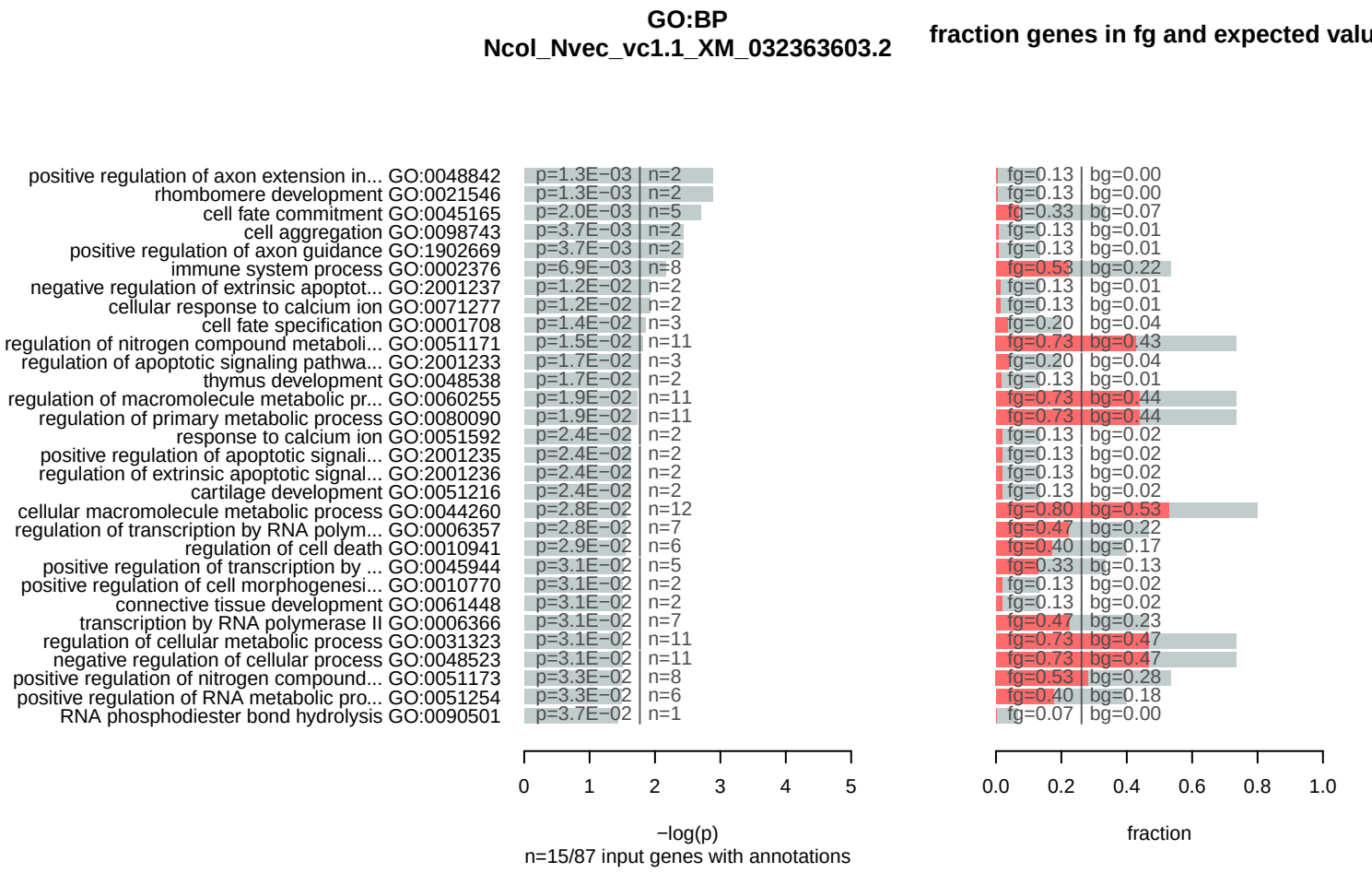
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Ncol_Nvec_vc1.1_XM_032363603.2
fraction genes in fg and expected valu
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rhombomere development GO:0021546 p=1.3E−03 n=2 fg=0.13 bg=0.00
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cell aggregation GO:0098743 p=3.7E−03 n=2 fg=0.13 bg=0.01
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immune system process GO:0002376 p=6.9E−03 n=8 fg=0.53 bg=0.22
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regulation of apoptotic signaling pathwa... GO:2001233 p=1.7E−02 n=3 fg=0.20 bg=0.04
thymus development GO:0048538 p=1.7E−02 n=2 fg=0.13 bg=0.01
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regulation of primary metabolic process GO:0080090 p=1.9E−02 n=11 fg=0.73 bg=0.44
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cartilage development GO:0051216 p=2.4E−02 n=2 fg=0.13 bg=0.02
cellular macromolecule metabolic process GO:0044260 p=2.8E−02 n=12 fg=0.80 bg=0.53
regulation of transcription by RNA polym... GO:0006357 p=2.8E−02 n=7 fg=0.47 bg=0.22
regulation of cell death GO:0010941 p=2.9E−02 n=6 fg=0.40 bg=0.17
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transcription by RNA polymerase II GO:0006366 p=3.1E−02 n=7 fg=0.47 bg=0.23
regulation of cellular metabolic process GO:0031323 p=3.1E−02 n=11 fg=0.73 bg=0.47
negative regulation of cellular process GO:0048523 p=3.1E−02 n=11 fg=0.73 bg=0.47
positive regulation of nitrogen compound... GO:0051173 p=3.3E−02 n=8 fg=0.53 bg=0.28
positive regulation of RNA metabolic pro... GO:0051254 p=3.3E−02 n=6 fg=0.40 bg=0.18
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032363603.2
fraction genes in fg and expected valu
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antigen binding GO:0003823 p=9.1E−03 n=2 fg=0.13 bg=0.01
transcription regulator activity GO:0140110 p=9.9E−03 n=7 fg=0.47 bg=0.18
hormone receptor binding GO:0051427 p=2.2E−02 n=2 fg=0.13 bg=0.02
protein transporter activity GO:0140318 p=4.1E−02 n=1 fg=0.07 bg=0.00
vascular endothelial growth factor bindi... GO:0038085 p=4.1E−02 n=1 fg=0.07 bg=0.00
exonuclease activity, active with either... GO:0016796 p=4.1E−02 n=1 fg=0.07 bg=0.00
exonuclease activity GO:0004527 p=4.1E−02 n=1 fg=0.07 bg=0.00
nuclear receptor coactivator activity GO:0030374 p=4.1E−02 n=1 fg=0.07 bg=0.00
amide transmembrane transporter activity GO:0042887 p=4.1E−02 n=1 fg=0.07 bg=0.00
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death domain binding GO:0070513 p=4.1E−02 n=1 fg=0.07 bg=0.00
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exoribonuclease activity, producing 5'−p... GO:0016896 p=4.1E−02 n=1 fg=0.07 bg=0.00
ribonuclease activity GO:0004540 p=4.1E−02 n=1 fg=0.07 bg=0.00
BH3 domain binding GO:0051434 p=4.1E−02 n=1 fg=0.07 bg=0.00
3'−5'−exoribonuclease activity GO:0000175 p=4.1E−02 n=1 fg=0.07 bg=0.00
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3'−5' exonuclease activity GO:0008408 p=4.1E−02 n=1 fg=0.07 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=4.2E−02 n=3 fg=0.20 bg=0.05
RNA polymerase II cis−regulatory region ... GO:0000978 p=4.2E−02 n=3 fg=0.20 bg=0.05
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transcription coregulator activity GO:0003712 p=7.5E−02 n=3 fg=0.20 bg=0.07
DNA−binding transcription factor activit... GO:0003700 p=7.7E−02 n=5 fg=0.33 bg=0.16
caspase binding GO:0089720 p=8.1E−02 n=1 fg=0.07 bg=0.01
molecular function activator activity GO:0140677 p=8.1E−02 n=1 fg=0.07 bg=0.01
vascular endothelial growth factor−activ... GO:0005021 p=8.1E−02 n=1 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=15/87 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032363603.2
fraction genes in fg and expected valu
Bcl−2 family protein complex GO:0097136 p=4.0E−02 n=1 fg=0.06 bg=0.00
sorting endosome GO:0097443 p=4.0E−02 n=1 fg=0.06 bg=0.00
PML body GO:0016605 p=4.0E−02 n=1 fg=0.06 bg=0.00
growth cone membrane GO:0032584 p=4.0E−02 n=1 fg=0.06 bg=0.00
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semaphorin receptor complex GO:0002116 p=4.0E−02 n=1 fg=0.06 bg=0.00
mitochondrial matrix GO:0005759 p=4.5E−02 n=2 fg=0.12 bg=0.02
intermediate filament GO:0005882 p=7.8E−02 n=1 fg=0.06 bg=0.01
neurofilament GO:0005883 p=7.8E−02 n=1 fg=0.06 bg=0.01
transcription factor AP−1 complex GO:0035976 p=7.8E−02 n=1 fg=0.06 bg=0.01
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membrane−enclosed lumen GO:0031974 p=9.3E−02 n=8 fg=0.50 bg=0.32
intracellular organelle lumen GO:0070013 p=9.3E−02 n=8 fg=0.50 bg=0.32
organelle lumen GO:0043233 p=9.3E−02 n=8 fg=0.50 bg=0.32
early endosome GO:0005769 p=1.0E−01 n=2 fg=0.12 bg=0.04
axonal growth cone GO:0044295 p=1.2E−01 n=1 fg=0.06 bg=0.01
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brush border membrane GO:0031526 p=1.5E−01 n=1 fg=0.06 bg=0.01
sperm head GO:0061827 p=1.5E−01 n=1 fg=0.06 bg=0.01
autophagosome GO:0005776 p=1.5E−01 n=1 fg=0.06 bg=0.01
cytosol GO:0005829 p=1.6E−01 n=8 fg=0.50 bg=0.35
intermediate filament cytoskeleton GO:0045111 p=1.8E−01 n=1 fg=0.06 bg=0.01
chromatin GO:0000785 p=1.9E−01 n=2 fg=0.12 bg=0.05
transcription regulator complex GO:0005667 p=2.2E−01 n=2 fg=0.12 bg=0.06
mitochondrial outer membrane GO:0005741 p=2.2E−01 n=1 fg=0.06 bg=0.01
outer membrane GO:0019867 p=2.2E−01 n=1 fg=0.06 bg=0.01
endoplasmic reticulum lumen GO:0005788 p=2.2E−01 n=1 fg=0.06 bg=0.01
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0 1 2 3 4 5
−log(p)
n=16/87 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction