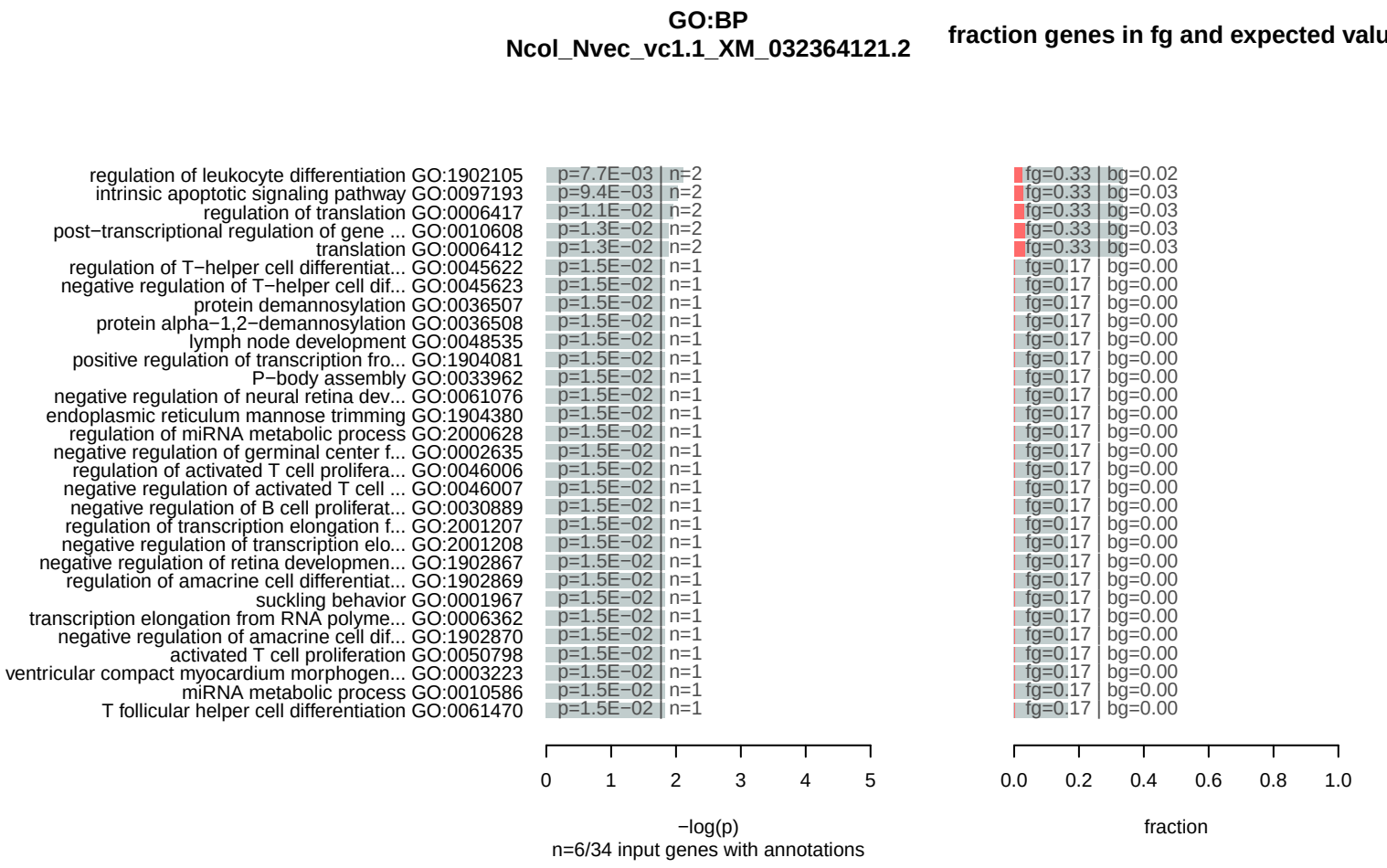
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intrinsic apoptotic signaling pathway GO:0097193 p=9.4E−03 n=2 fg=0.33 bg=0.03
regulation of translation GO:0006417 p=1.1E−02 n=2 fg=0.33 bg=0.03
post−transcriptional regulation of gene ... GO:0010608 p=1.3E−02 n=2 fg=0.33 bg=0.03
translation GO:0006412 p=1.3E−02 n=2 fg=0.33 bg=0.03
regulation of T−helper cell differentiat... GO:0045622 p=1.5E−02 n=1 fg=0.17 bg=0.00
negative regulation of T−helper cell dif... GO:0045623 p=1.5E−02 n=1 fg=0.17 bg=0.00
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positive regulation of transcription fro... GO:1904081 p=1.5E−02 n=1 fg=0.17 bg=0.00
P−body assembly GO:0033962 p=1.5E−02 n=1 fg=0.17 bg=0.00
negative regulation of neural retina dev... GO:0061076 p=1.5E−02 n=1 fg=0.17 bg=0.00
endoplasmic reticulum mannose trimming GO:1904380 p=1.5E−02 n=1 fg=0.17 bg=0.00
regulation of miRNA metabolic process GO:2000628 p=1.5E−02 n=1 fg=0.17 bg=0.00
negative regulation of germinal center f... GO:0002635 p=1.5E−02 n=1 fg=0.17 bg=0.00
regulation of activated T cell prolifera... GO:0046006 p=1.5E−02 n=1 fg=0.17 bg=0.00
negative regulation of activated T cell ... GO:0046007 p=1.5E−02 n=1 fg=0.17 bg=0.00
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regulation of transcription elongation f... GO:2001207 p=1.5E−02 n=1 fg=0.17 bg=0.00
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transcription elongation from RNA polyme... GO:0006362 p=1.5E−02 n=1 fg=0.17 bg=0.00
negative regulation of amacrine cell dif... GO:1902870 p=1.5E−02 n=1 fg=0.17 bg=0.00
activated T cell proliferation GO:0050798 p=1.5E−02 n=1 fg=0.17 bg=0.00
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T follicular helper cell differentiation GO:0061470 p=1.5E−02 n=1 fg=0.17 bg=0.00
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n=6/34 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
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zinc ion binding GO:0008270 p=1.6E−02 n=2 fg=0.29 bg=0.03
platelet−activating factor acetyltransfe... GO:0047179 p=1.9E−02 n=1 fg=0.14 bg=0.00
phospholipase A2 activity GO:0004623 p=1.9E−02 n=1 fg=0.14 bg=0.00
transition metal ion binding GO:0046914 p=3.0E−02 n=2 fg=0.29 bg=0.04
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miRNA binding GO:0035198 p=3.8E−02 n=1 fg=0.14 bg=0.01
RNA stem−loop binding GO:0035613 p=3.8E−02 n=1 fg=0.14 bg=0.01
regulatory RNA binding GO:0061980 p=3.8E−02 n=1 fg=0.14 bg=0.01
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mRNA 3'−UTR binding GO:0003730 p=7.5E−02 n=1 fg=0.14 bg=0.01
chaperone binding GO:0051087 p=7.5E−02 n=1 fg=0.14 bg=0.01
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nucleic acid binding GO:0003676 p=1.2E−01 n=3 fg=0.43 bg=0.18
metal ion binding GO:0046872 p=1.2E−01 n=2 fg=0.29 bg=0.09
transcription regulator activity GO:0140110 p=1.2E−01 n=3 fg=0.43 bg=0.18
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acyltransferase activity GO:0016746 p=1.3E−01 n=1 fg=0.14 bg=0.02
acyltransferase activity, transferring g... GO:0016747 p=1.3E−01 n=1 fg=0.14 bg=0.02
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−log(p)
n=7/34 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032364121.2
fraction genes in fg and expected valu
Hrd1p ubiquitin ligase ERAD−L complex GO:0000839 p=1.7E−02 n=1 fg=0.14 bg=0.00
P−body GO:0000932 p=3.5E−02 n=1 fg=0.14 bg=0.00
ER ubiquitin ligase complex GO:0000835 p=3.5E−02 n=1 fg=0.14 bg=0.00
Hrd1p ubiquitin ligase complex GO:0000836 p=3.5E−02 n=1 fg=0.14 bg=0.00
Derlin−1 retrotranslocation complex GO:0036513 p=3.5E−02 n=1 fg=0.14 bg=0.00
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cytoplasmic ubiquitin ligase complex GO:0000153 p=3.5E−02 n=1 fg=0.14 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=3.5E−02 n=1 fg=0.14 bg=0.00
endoplasmic reticulum protein−containing... GO:0140534 p=5.1E−02 n=1 fg=0.14 bg=0.01
ficolin−1−rich granule lumen GO:1904813 p=5.1E−02 n=1 fg=0.14 bg=0.01
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smooth endoplasmic reticulum GO:0005790 p=1.0E−01 n=1 fg=0.14 bg=0.01
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intracellular membrane−bounded organelle GO:0043231 p=1.2E−01 n=7 fg=1.00 bg=0.74
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RNA polymerase II transcription regulato... GO:0090575 p=1.3E−01 n=1 fg=0.14 bg=0.02
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vesicle lumen GO:0031983 p=1.3E−01 n=1 fg=0.14 bg=0.02
secretory granule lumen GO:0034774 p=1.3E−01 n=1 fg=0.14 bg=0.02
nuclear speck GO:0016607 p=1.3E−01 n=1 fg=0.14 bg=0.02
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organelle lumen GO:0043233 p=1.5E−01 n=4 fg=0.57 bg=0.32
membrane−enclosed lumen GO:0031974 p=1.5E−01 n=4 fg=0.57 bg=0.32
intracellular organelle GO:0043229 p=1.6E−01 n=7 fg=1.00 bg=0.77
integral component of endoplasmic reticu... GO:0030176 p=1.8E−01 n=1 fg=0.14 bg=0.03
intrinsic component of endoplasmic retic... GO:0031227 p=1.8E−01 n=1 fg=0.14 bg=0.03
organelle GO:0043226 p=1.8E−01 n=7 fg=1.00 bg=0.78
0 1 2 3 4 5
−log(p)
n=7/34 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction