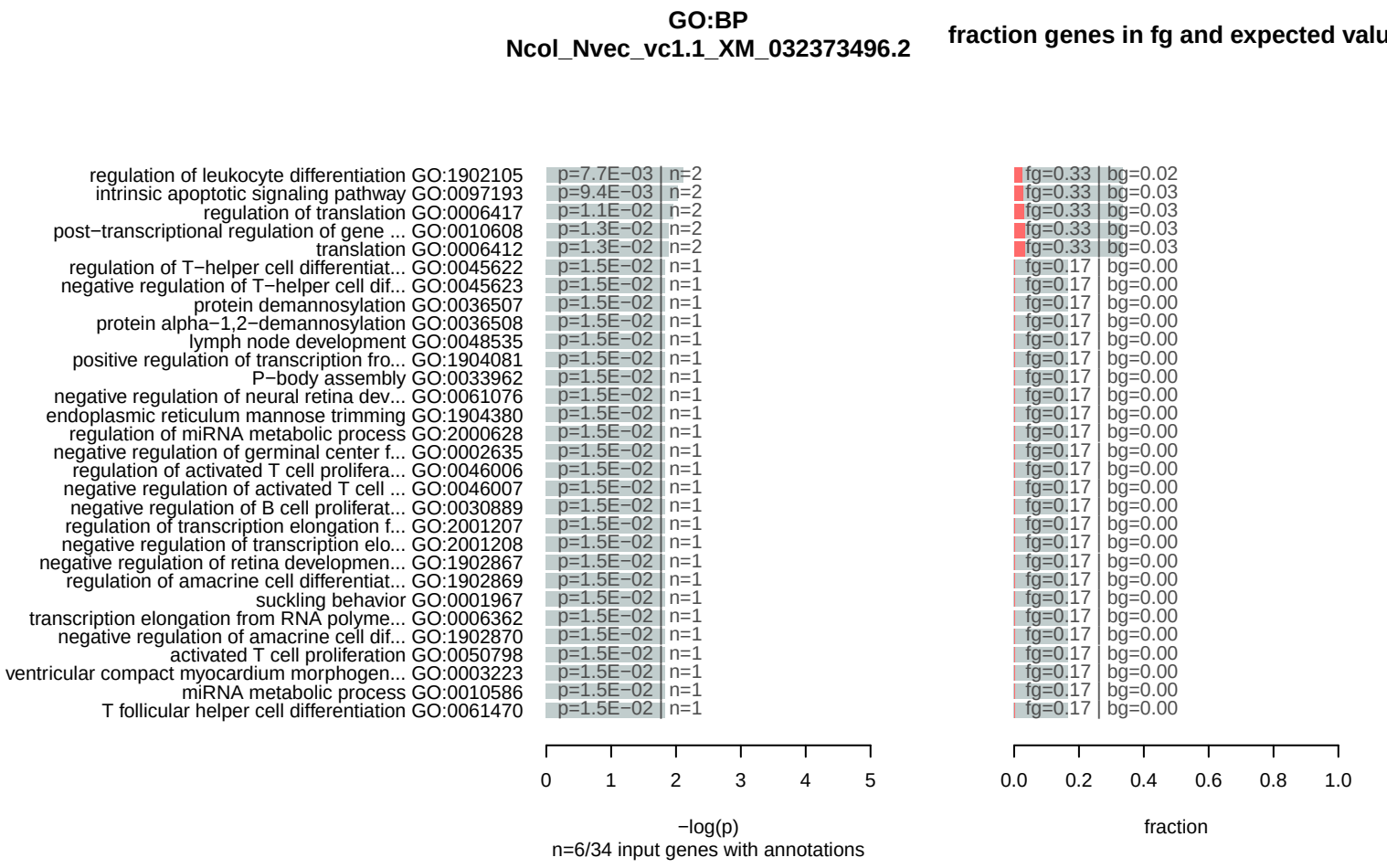
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intrinsic apoptotic signaling pathway GO:0097193 p=9.4E−03 n=2 fg=0.33 bg=0.03
regulation of translation GO:0006417 p=1.1E−02 n=2 fg=0.33 bg=0.03
post−transcriptional regulation of gene ... GO:0010608 p=1.3E−02 n=2 fg=0.33 bg=0.03
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regulation 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
protein demannosylation GO:0036507 p=1.5E−02 n=1 fg=0.17 bg=0.00
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lymph node development GO:0048535 p=1.5E−02 n=1 fg=0.17 bg=0.00
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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
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regulation of activated T cell prolifera... GO:0046006 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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n=6/34 input genes with annotations
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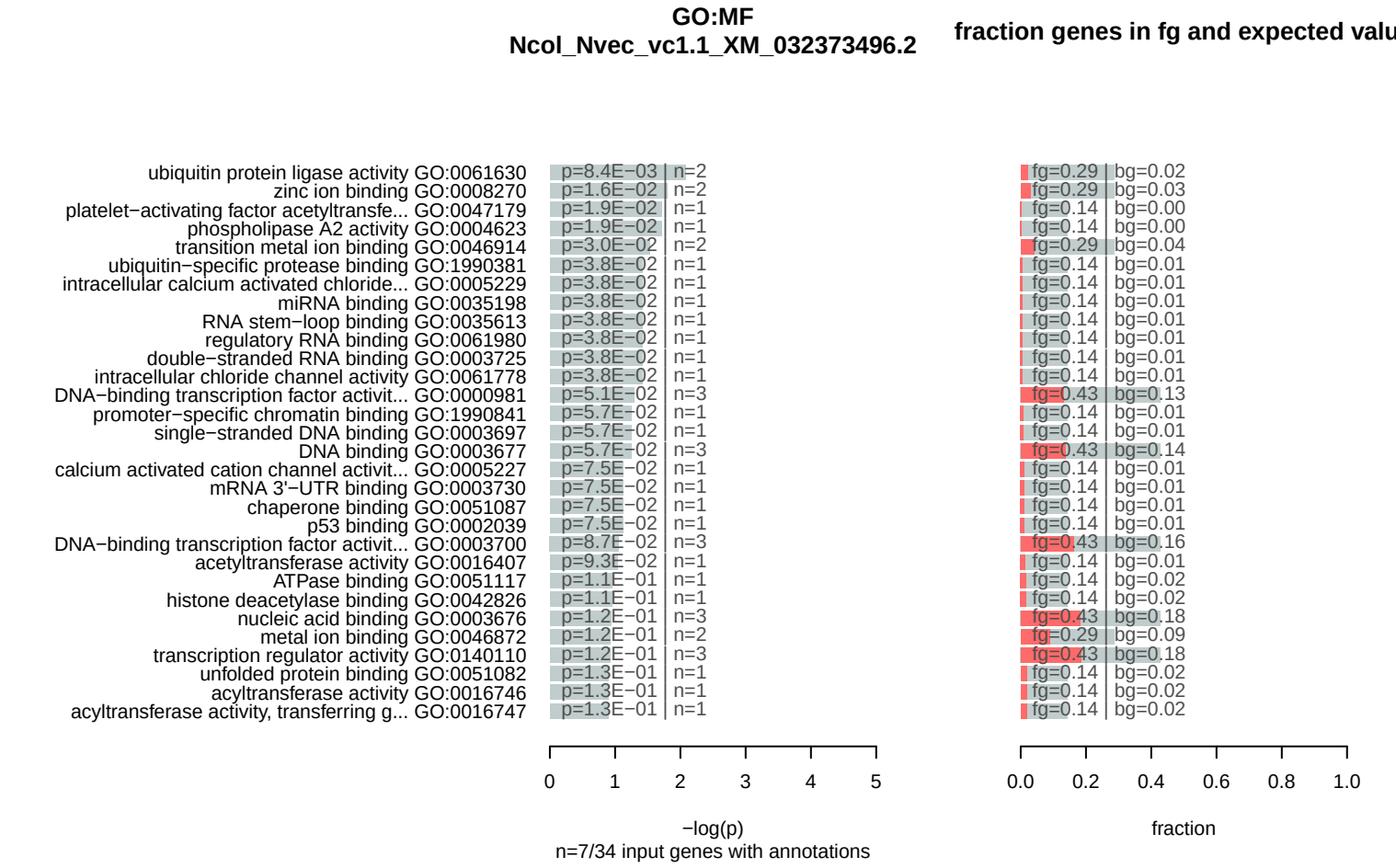
fraction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zinc ion binding GO:0008270 p=1.6E−02 n=2 fg=0.29 bg=0.03
platelet−activating factor acetyltransfe... GO:0047179 p=1.9E−02 n=1 fg=0.14 bg=0.00
phospholipase A2 activity GO:0004623 p=1.9E−02 n=1 fg=0.14 bg=0.00
transition metal ion binding GO:0046914 p=3.0E−02 n=2 fg=0.29 bg=0.04
ubiquitin−specific protease binding GO:1990381 p=3.8E−02 n=1 fg=0.14 bg=0.01
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promoter−specific chromatin binding GO:1990841 p=5.7E−02 n=1 fg=0.14 bg=0.01
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DNA−binding transcription factor activit... GO:0003700 p=8.7E−02 n=3 fg=0.43 bg=0.16
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ATPase binding GO:0051117 p=1.1E−01 n=1 fg=0.14 bg=0.02
histone deacetylase binding GO:0042826 p=1.1E−01 n=1 fg=0.14 bg=0.02
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
unfolded protein binding GO:0051082 p=1.3E−01 n=1 fg=0.14 bg=0.02
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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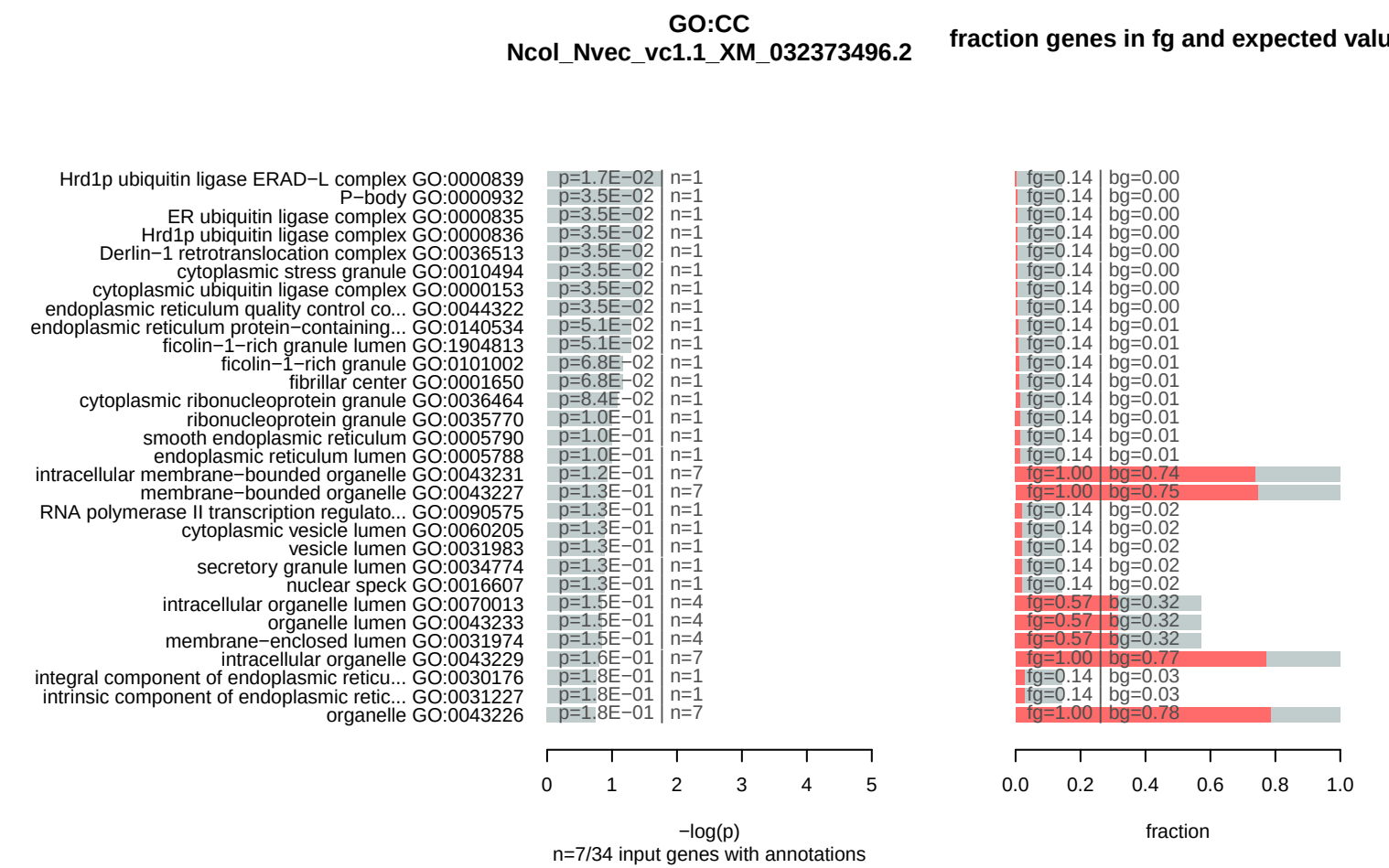
−log(p)
n=7/34 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction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Ncol_Nvec_vc1.1_XM_032373496.2
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P−body GO:0000932 p=3.5E−02 n=1 fg=0.14 bg=0.00
ER ubiquitin ligase complex GO:0000835 p=3.5E−02 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
cytoplasmic stress granule GO:0010494 p=3.5E−02 n=1 fg=0.14 bg=0.00
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endoplasmic reticulum quality control co... GO:0044322 p=3.5E−02 n=1 fg=0.14 bg=0.00
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ficolin−1−rich granule lumen GO:1904813 p=5.1E−02 n=1 fg=0.14 bg=0.01
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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
intracellular organelle lumen GO:0070013 p=1.5E−01 n=4 fg=0.57 bg=0.32
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
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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
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n=7/34 input genes with annotations
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fraction