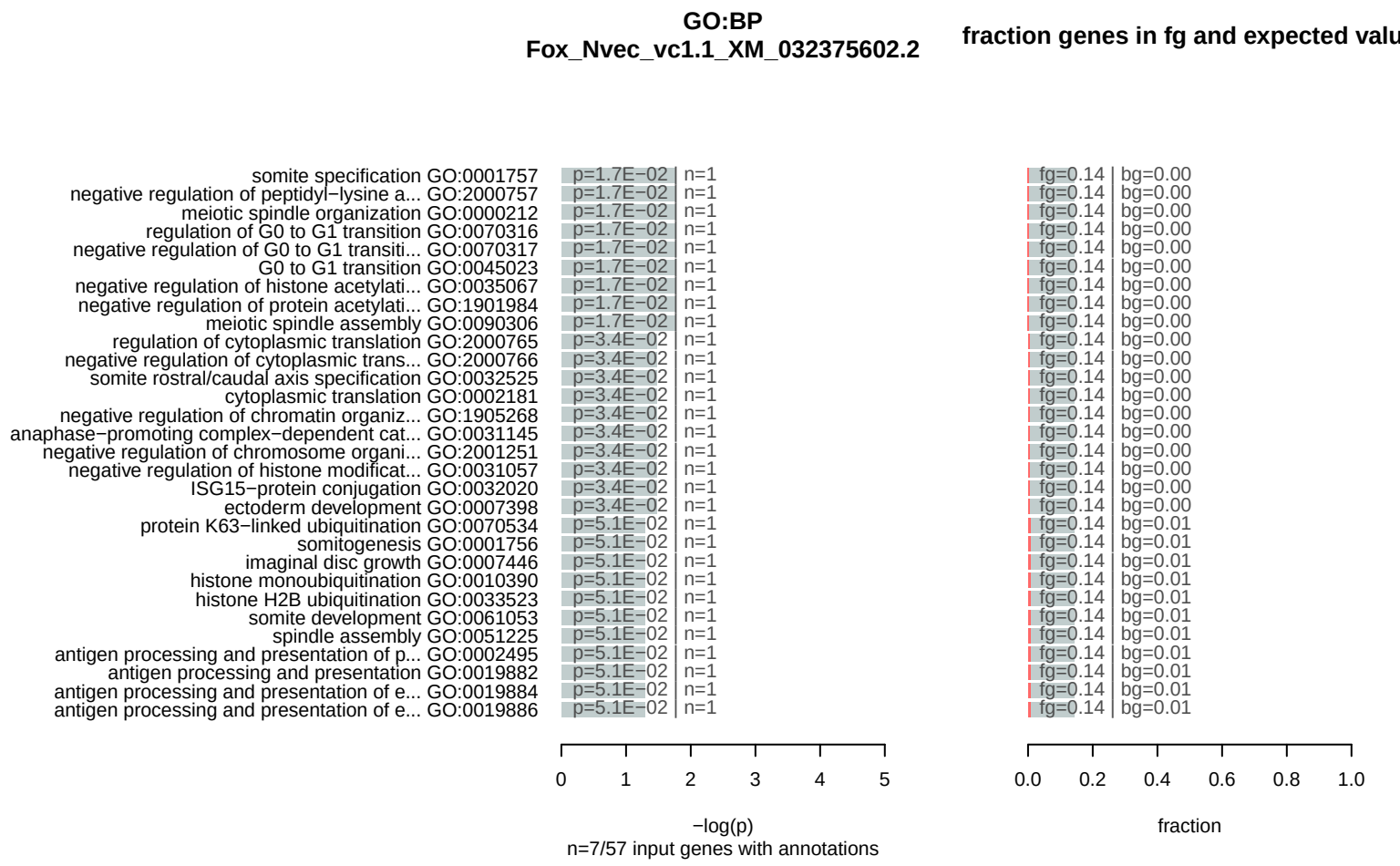
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negative regulation of peptidyl−lysine a... GO:2000757 p=1.7E−02 n=1 fg=0.14 bg=0.00
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negative regulation of histone modificat... GO:0031057 p=3.4E−02 n=1 fg=0.14 bg=0.00
ISG15−protein conjugation GO:0032020 p=3.4E−02 n=1 fg=0.14 bg=0.00
ectoderm development GO:0007398 p=3.4E−02 n=1 fg=0.14 bg=0.00
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spindle assembly GO:0051225 p=5.1E−02 n=1 fg=0.14 bg=0.01
antigen processing and presentation of p... GO:0002495 p=5.1E−02 n=1 fg=0.14 bg=0.01
antigen processing and presentation GO:0019882 p=5.1E−02 n=1 fg=0.14 bg=0.01
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−log(p)
n=7/57 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032375602.2
fraction genes in fg and expected valu
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ribosome binding GO:0043022 p=2.7E−02 n=1 fg=0.20 bg=0.01
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translation repressor activity GO:0030371 p=4.1E−02 n=1 fg=0.20 bg=0.01
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ribonucleoprotein complex binding GO:0043021 p=4.1E−02 n=1 fg=0.20 bg=0.01
translation regulator activity GO:0045182 p=4.1E−02 n=1 fg=0.20 bg=0.01
methylation−dependent protein binding GO:0140034 p=4.1E−02 n=1 fg=0.20 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=4.1E−02 n=1 fg=0.20 bg=0.01
mRNA regulatory element binding translat... GO:0000900 p=4.1E−02 n=1 fg=0.20 bg=0.01
methylated histone binding GO:0035064 p=4.1E−02 n=1 fg=0.20 bg=0.01
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mRNA 3'−UTR binding GO:0003730 p=5.4E−02 n=1 fg=0.20 bg=0.01
modification−dependent protein binding GO:0140030 p=6.7E−02 n=1 fg=0.20 bg=0.01
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cytoskeletal motor activity GO:0003774 p=6.7E−02 n=1 fg=0.20 bg=0.01
mRNA binding GO:0003729 p=1.2E−01 n=1 fg=0.20 bg=0.02
voltage−gated potassium channel activity GO:0005249 p=1.2E−01 n=1 fg=0.20 bg=0.02
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potassium ion transmembrane transporter ... GO:0015079 p=1.5E−01 n=1 fg=0.20 bg=0.03
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voltage−gated channel activity GO:0022832 p=1.9E−01 n=1 fg=0.20 bg=0.04
voltage−gated ion channel activity GO:0005244 p=1.9E−01 n=1 fg=0.20 bg=0.04
nucleic acid binding GO:0003676 p=2.2E−01 n=2 fg=0.40 bg=0.18
ubiquitin−protein transferase activity GO:0004842 p=2.3E−01 n=1 fg=0.20 bg=0.05
ATP hydrolysis activity GO:0016887 p=2.3E−01 n=1 fg=0.20 bg=0.05
ATP−dependent activity GO:0140657 p=2.4E−01 n=1 fg=0.20 bg=0.05
ubiquitin−like protein transferase activ... GO:0019787 p=2.4E−01 n=1 fg=0.20 bg=0.05
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−log(p)
n=5/57 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032375602.2
fraction genes in fg and expected valu
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protein−containing complex GO:0032991 p=4.5E−02 n=5 fg=0.71 bg=0.34
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microtubule associated complex GO:0005875 p=6.8E−02 n=1 fg=0.14 bg=0.01
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PcG protein complex GO:0031519 p=1.0E−01 n=1 fg=0.14 bg=0.01
spindle GO:0005819 p=1.2E−01 n=1 fg=0.14 bg=0.02
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ion channel complex GO:0034702 p=2.5E−01 n=1 fg=0.14 bg=0.04
transmembrane transporter complex GO:1902495 p=2.5E−01 n=1 fg=0.14 bg=0.04
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microtubule organizing center GO:0005815 p=2.8E−01 n=1 fg=0.14 bg=0.04
intracellular non−membrane−bounded organ... GO:0043232 p=2.8E−01 n=3 fg=0.43 bg=0.27
non−membrane−bounded organelle GO:0043228 p=2.8E−01 n=3 fg=0.43 bg=0.27
chromatin GO:0000785 p=3.0E−01 n=1 fg=0.14 bg=0.05
plasma membrane protein complex GO:0098797 p=3.3E−01 n=1 fg=0.14 bg=0.05
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n=7/57 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction