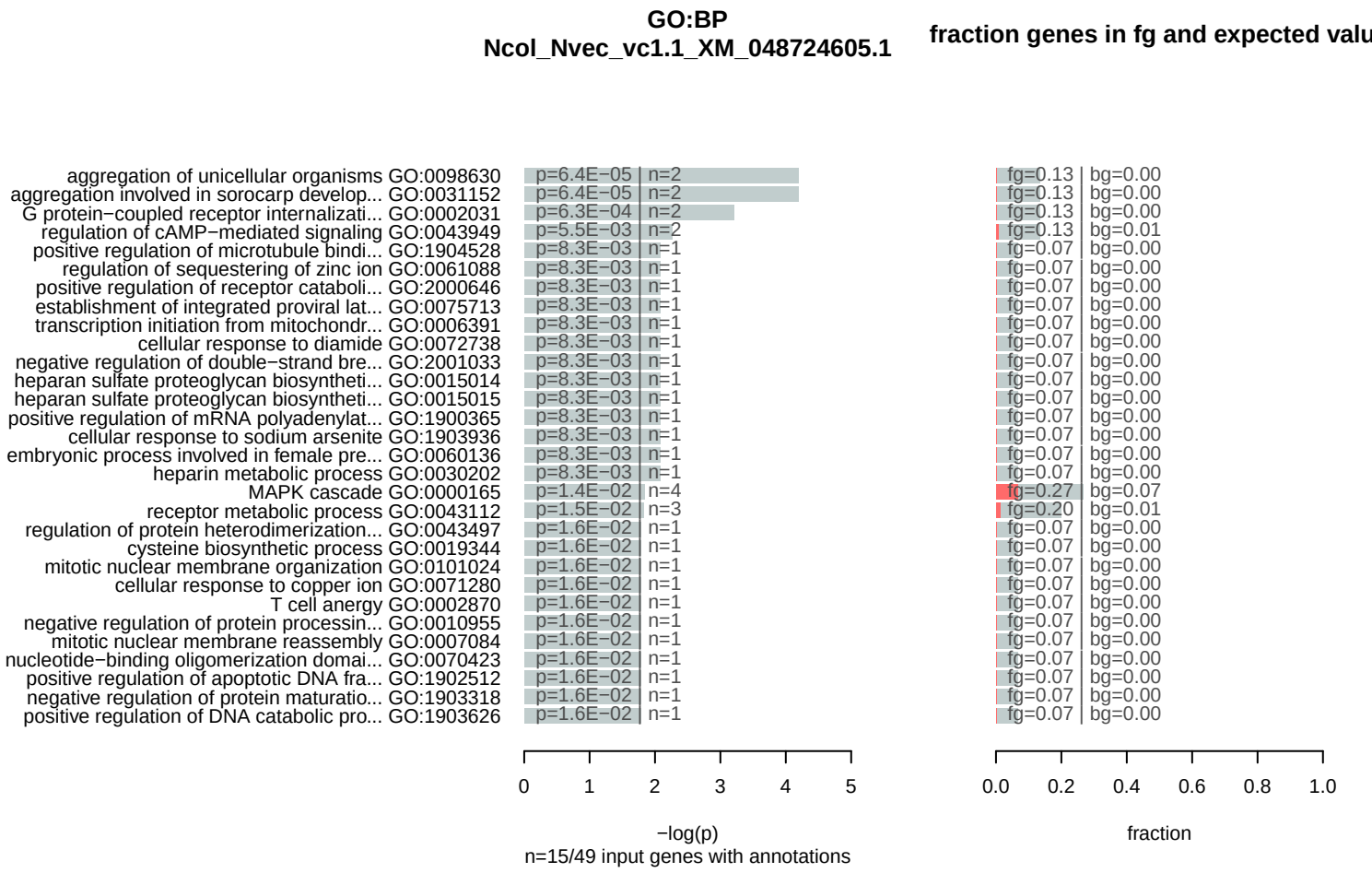
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aggregation involved in sorocarp develop... GO:0031152 p=6.4E−05 n=2 fg=0.13 bg=0.00
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receptor metabolic process GO:0043112 p=1.5E−02 n=3 fg=0.20 bg=0.01
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T cell anergy GO:0002870 p=1.6E−02 n=1 fg=0.07 bg=0.00
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nucleotide−binding oligomerization domai... GO:0070423 p=1.6E−02 n=1 fg=0.07 bg=0.00
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n=15/49 input genes with annotations
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fraction
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transferase activity, transferring alkyl... GO:0016765 p=4.1E−02 n=1 fg=0.09 bg=0.00
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transition metal ion transmembrane trans... GO:0046915 p=4.8E−02 n=1 fg=0.09 bg=0.00
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hydro−lyase activity GO:0016836 p=5.4E−02 n=1 fg=0.09 bg=0.01
promoter−specific chromatin binding GO:1990841 p=6.1E−02 n=1 fg=0.09 bg=0.01
carbon−oxygen lyase activity GO:0016835 p=6.7E−02 n=1 fg=0.09 bg=0.01
protein self−association GO:0043621 p=7.4E−02 n=1 fg=0.09 bg=0.01
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−log(p)
n=11/49 input genes with annotations
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048724605.1
fraction genes in fg and expected valu
mitochondrial DNA−directed RNA polymeras... GO:0034245 p=8.3E−03 n=1 fg=0.07 bg=0.00
condensed chromosome, centromeric region GO:0000779 p=1.2E−02 n=2 fg=0.13 bg=0.01
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contractile actin filament bundle GO:0097517 p=7.2E−02 n=1 fg=0.07 bg=0.00
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trans−Golgi network GO:0005802 p=1.0E−01 n=2 fg=0.13 bg=0.04
endopeptidase complex GO:1905369 p=1.1E−01 n=1 fg=0.07 bg=0.01
Golgi apparatus subcompartment GO:0098791 p=1.2E−01 n=3 fg=0.20 bg=0.08
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−log(p)
n=15/49 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction