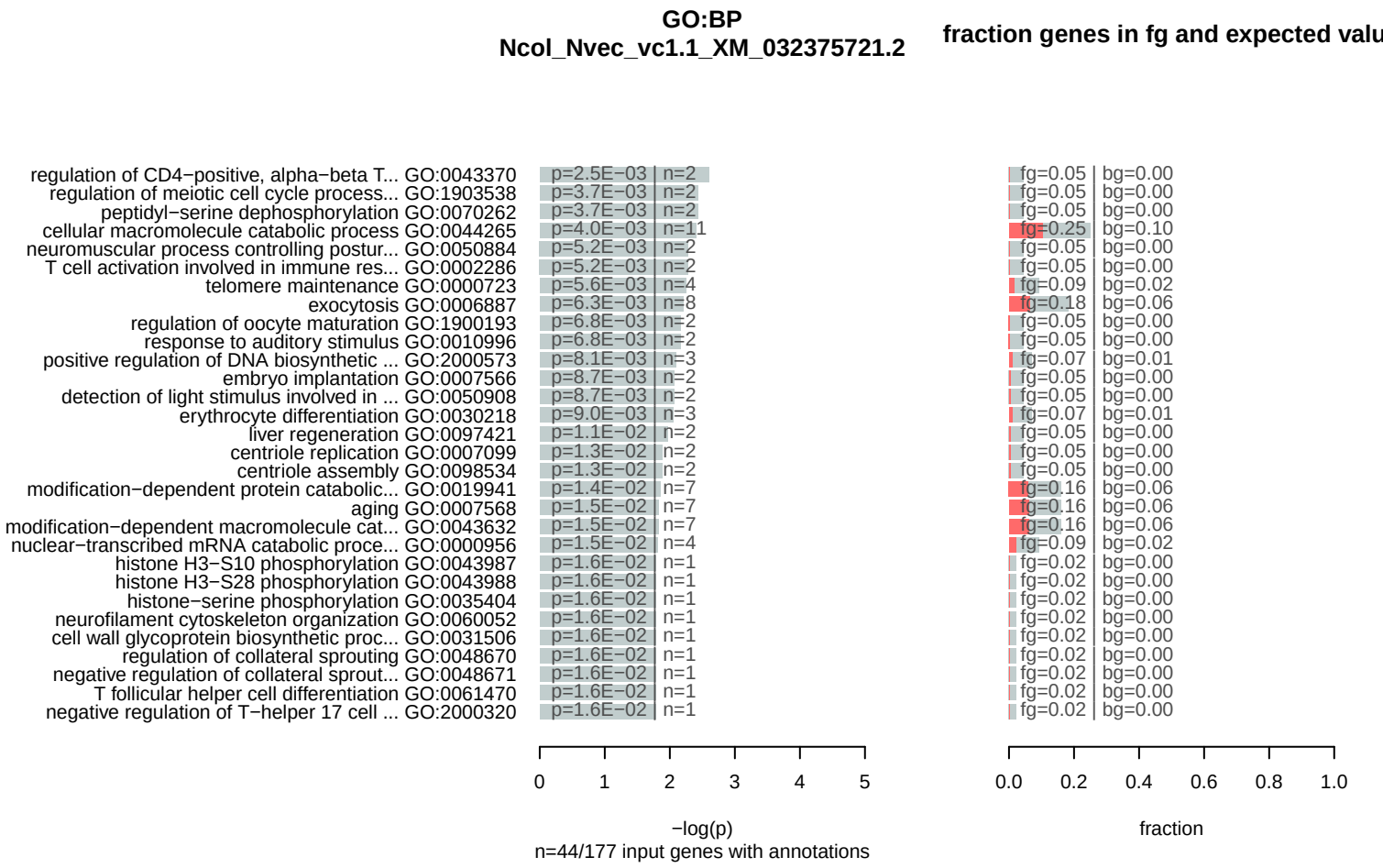
GO:BP
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fraction genes in fg and expected valu
regulation of CD4−positive, alpha−beta T... GO:0043370 p=2.5E−03 n=2 fg=0.05 bg=0.00
regulation of meiotic cell cycle process... GO:1903538 p=3.7E−03 n=2 fg=0.05 bg=0.00
peptidyl−serine dephosphorylation GO:0070262 p=3.7E−03 n=2 fg=0.05 bg=0.00
cellular macromolecule catabolic process GO:0044265 p=4.0E−03 n=11 fg=0.25 bg=0.10
neuromuscular process controlling postur... GO:0050884 p=5.2E−03 n=2 fg=0.05 bg=0.00
T cell activation involved in immune res... GO:0002286 p=5.2E−03 n=2 fg=0.05 bg=0.00
telomere maintenance GO:0000723 p=5.6E−03 n=4 fg=0.09 bg=0.02
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positive regulation of DNA biosynthetic ... GO:2000573 p=8.1E−03 n=3 fg=0.07 bg=0.01
embryo implantation GO:0007566 p=8.7E−03 n=2 fg=0.05 bg=0.00
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erythrocyte differentiation GO:0030218 p=9.0E−03 n=3 fg=0.07 bg=0.01
liver regeneration GO:0097421 p=1.1E−02 n=2 fg=0.05 bg=0.00
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centriole assembly GO:0098534 p=1.3E−02 n=2 fg=0.05 bg=0.00
modification−dependent protein catabolic... GO:0019941 p=1.4E−02 n=7 fg=0.16 bg=0.06
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nuclear−transcribed mRNA catabolic proce... GO:0000956 p=1.5E−02 n=4 fg=0.09 bg=0.02
histone H3−S10 phosphorylation GO:0043987 p=1.6E−02 n=1 fg=0.02 bg=0.00
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histone−serine phosphorylation GO:0035404 p=1.6E−02 n=1 fg=0.02 bg=0.00
neurofilament cytoskeleton organization GO:0060052 p=1.6E−02 n=1 fg=0.02 bg=0.00
cell wall glycoprotein biosynthetic proc... GO:0031506 p=1.6E−02 n=1 fg=0.02 bg=0.00
regulation of collateral sprouting GO:0048670 p=1.6E−02 n=1 fg=0.02 bg=0.00
negative regulation of collateral sprout... GO:0048671 p=1.6E−02 n=1 fg=0.02 bg=0.00
T follicular helper cell differentiation GO:0061470 p=1.6E−02 n=1 fg=0.02 bg=0.00
negative regulation of T−helper 17 cell ... GO:2000320 p=1.6E−02 n=1 fg=0.02 bg=0.00
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n=44/177 input genes with annotations
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fraction
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double−stranded DNA binding GO:0003690 p=5.6E−03 n=7 fg=0.18 bg=0.06
sequence−specific double−stranded DNA bi... GO:1990837 p=1.1E−02 n=6 fg=0.16 bg=0.05
DNA−binding transcription factor activit... GO:0003700 p=1.5E−02 n=7 fg=0.18 bg=0.07
transcription regulatory region nucleic ... GO:0001067 p=1.6E−02 n=6 fg=0.16 bg=0.05
light−activated ion channel activity GO:0010461 p=1.6E−02 n=1 fg=0.03 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=1.6E−02 n=1 fg=0.03 bg=0.00
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intramolecular oxidoreductase activity, ... GO:0016861 p=1.6E−02 n=1 fg=0.03 bg=0.00
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mitochondrial promoter sequence−specific... GO:0001018 p=1.6E−02 n=1 fg=0.03 bg=0.00
ATP−dependent peptidase activity GO:0004176 p=1.6E−02 n=1 fg=0.03 bg=0.00
glycogenin glucosyltransferase activity GO:0008466 p=1.6E−02 n=1 fg=0.03 bg=0.00
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protein heterodimerization activity GO:0046982 p=1.9E−02 n=6 fg=0.16 bg=0.06
cysteine−type endopeptidase activity GO:0004197 p=2.0E−02 n=2 fg=0.05 bg=0.01
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protein phosphatase regulator activity GO:0019888 p=2.3E−02 n=2 fg=0.05 bg=0.01
mRNA 3'−UTR binding GO:0003730 p=2.6E−02 n=2 fg=0.05 bg=0.01
transcription cis−regulatory region bind... GO:0000976 p=3.1E−02 n=5 fg=0.13 bg=0.05
choline kinase activity GO:0004103 p=3.2E−02 n=1 fg=0.03 bg=0.00
DNA demethylase activity GO:0035514 p=3.2E−02 n=1 fg=0.03 bg=0.00
deSUMOylase activity GO:0016929 p=3.2E−02 n=1 fg=0.03 bg=0.00
isopeptidase activity GO:0070122 p=3.2E−02 n=1 fg=0.03 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=3.2E−02 n=1 fg=0.03 bg=0.00
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n=38/177 input genes with annotations
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032375721.2
fraction genes in fg and expected valu
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contractile ring GO:0070938 p=6.8E−03 n=2 fg=0.05 bg=0.00
chromocenter GO:0010369 p=8.7E−03 n=2 fg=0.05 bg=0.00
centriole GO:0005814 p=1.3E−02 n=3 fg=0.07 bg=0.01
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meiotic spindle midzone GO:1990385 p=1.6E−02 n=1 fg=0.02 bg=0.00
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TORC2 complex GO:0031932 p=3.2E−02 n=1 fg=0.02 bg=0.00
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lamellipodium GO:0030027 p=5.4E−02 n=3 fg=0.07 bg=0.02
condensed nuclear chromosome GO:0000794 p=6.1E−02 n=2 fg=0.05 bg=0.01
pi−body GO:0071546 p=6.4E−02 n=1 fg=0.02 bg=0.00
chromatoid body GO:0033391 p=6.4E−02 n=1 fg=0.02 bg=0.00
outer dense fiber GO:0001520 p=6.4E−02 n=1 fg=0.02 bg=0.00
alpha DNA polymerase:primase complex GO:0005658 p=6.4E−02 n=1 fg=0.02 bg=0.00
inaD signaling complex GO:0016027 p=6.4E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=44/177 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction