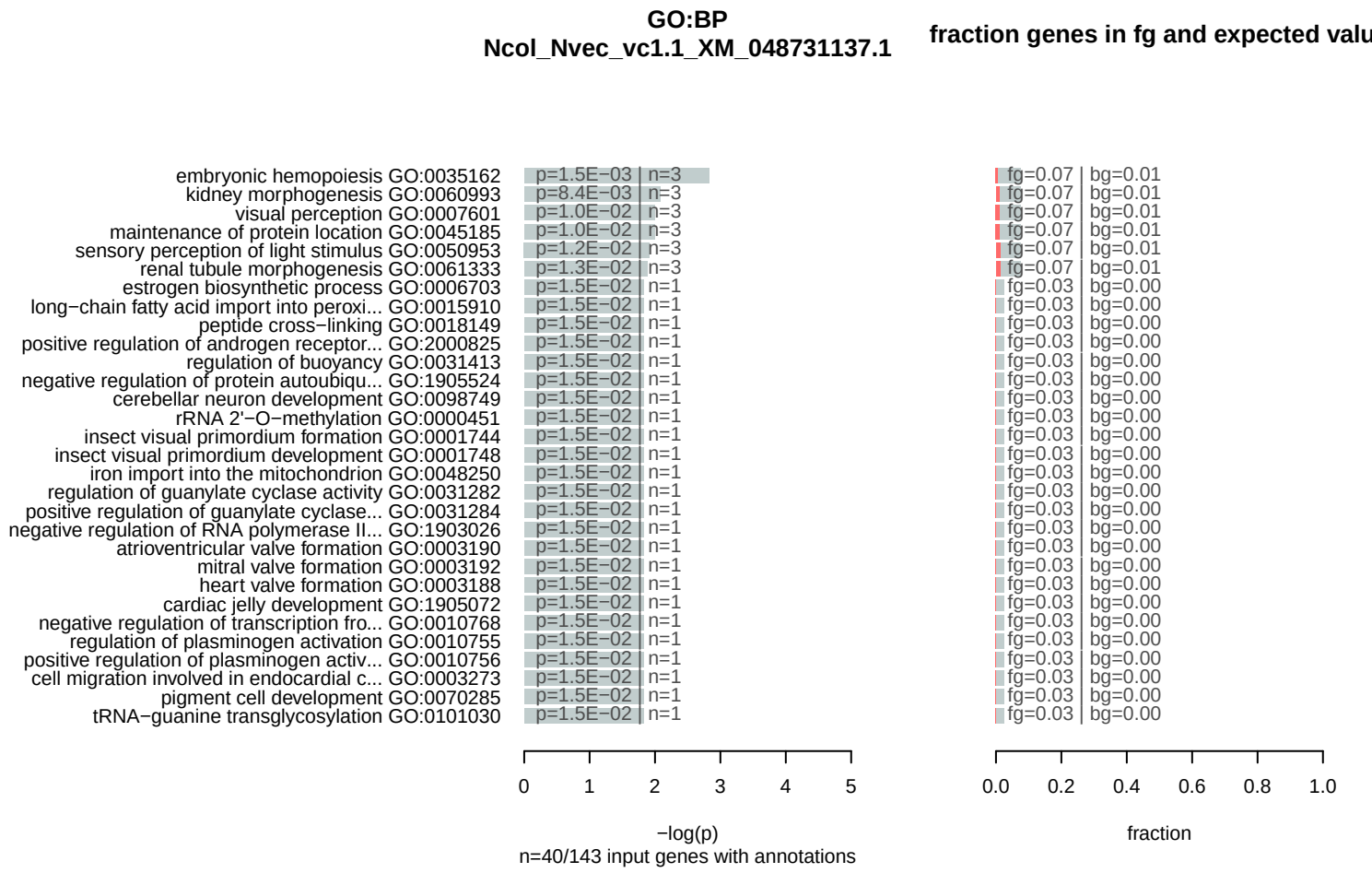
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fraction genes in fg and expected valu
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visual perception GO:0007601 p=1.0E−02 n=3 fg=0.07 bg=0.01
maintenance of protein location GO:0045185 p=1.0E−02 n=3 fg=0.07 bg=0.01
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regulation of buoyancy GO:0031413 p=1.5E−02 n=1 fg=0.03 bg=0.00
negative regulation of protein autoubiqu... GO:1905524 p=1.5E−02 n=1 fg=0.03 bg=0.00
cerebellar neuron development GO:0098749 p=1.5E−02 n=1 fg=0.03 bg=0.00
rRNA 2'−O−methylation GO:0000451 p=1.5E−02 n=1 fg=0.03 bg=0.00
insect visual primordium formation GO:0001744 p=1.5E−02 n=1 fg=0.03 bg=0.00
insect visual primordium development GO:0001748 p=1.5E−02 n=1 fg=0.03 bg=0.00
iron import into the mitochondrion GO:0048250 p=1.5E−02 n=1 fg=0.03 bg=0.00
regulation of guanylate cyclase activity GO:0031282 p=1.5E−02 n=1 fg=0.03 bg=0.00
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negative regulation of RNA polymerase II... GO:1903026 p=1.5E−02 n=1 fg=0.03 bg=0.00
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cardiac jelly development GO:1905072 p=1.5E−02 n=1 fg=0.03 bg=0.00
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regulation of plasminogen activation GO:0010755 p=1.5E−02 n=1 fg=0.03 bg=0.00
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cell migration involved in endocardial c... GO:0003273 p=1.5E−02 n=1 fg=0.03 bg=0.00
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n=40/143 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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TBP−class protein binding GO:0017025 p=9.6E−04 n=3 fg=0.09 bg=0.01
TFIID−class transcription factor complex... GO:0001094 p=2.1E−03 n=2 fg=0.06 bg=0.00
protein tyrosine/serine/threonine phosph... GO:0008138 p=4.3E−03 n=2 fg=0.06 bg=0.00
phosphatidylinositol bisphosphate phosph... GO:0034593 p=5.6E−03 n=2 fg=0.06 bg=0.00
cyclase activator activity GO:0010853 p=1.5E−02 n=1 fg=0.03 bg=0.00
long−chain fatty acid transporter activi... GO:0005324 p=1.5E−02 n=1 fg=0.03 bg=0.00
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beta−1,3−galactosyl−O−glycosyl−glycoprot... GO:0047223 p=1.5E−02 n=1 fg=0.03 bg=0.00
adenosylmethionine decarboxylase activit... GO:0004014 p=1.5E−02 n=1 fg=0.03 bg=0.00
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polyamine binding GO:0019808 p=1.5E−02 n=1 fg=0.03 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=1.5E−02 n=1 fg=0.03 bg=0.00
guanylate cyclase activator activity GO:0030250 p=1.5E−02 n=1 fg=0.03 bg=0.00
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light−activated ion channel activity GO:0010461 p=1.5E−02 n=1 fg=0.03 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=1.5E−02 n=1 fg=0.03 bg=0.00
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rRNA (guanosine−2'−O−)−methyltransferase... GO:0070039 p=1.5E−02 n=1 fg=0.03 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=1.5E−02 n=1 fg=0.03 bg=0.00
guanylate cyclase regulator activity GO:0030249 p=1.5E−02 n=1 fg=0.03 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=1.5E−02 n=1 fg=0.03 bg=0.00
ammonium ion binding GO:0070405 p=1.5E−02 n=2 fg=0.06 bg=0.01
protein tyrosine phosphatase activity GO:0004725 p=1.5E−02 n=2 fg=0.06 bg=0.01
phosphotransferase activity, alcohol gro... GO:0016773 p=1.9E−02 n=6 fg=0.17 bg=0.06
carbon−carbon lyase activity GO:0016830 p=2.2E−02 n=2 fg=0.06 bg=0.01
transferase activity, transferring phosp... GO:0016772 p=2.8E−02 n=7 fg=0.20 bg=0.09
transcription coregulator activity GO:0003712 p=2.8E−02 n=5 fg=0.14 bg=0.05
steroid dehydrogenase activity GO:0016229 p=2.9E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=35/143 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
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fraction genes in fg and expected valu
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cytoplasmic periphery of the nuclear por... GO:1990723 p=1.5E−02 n=1 fg=0.03 bg=0.00
rhabdomere microvillus GO:0035996 p=1.5E−02 n=1 fg=0.03 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=1.5E−02 n=1 fg=0.03 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=1.5E−02 n=1 fg=0.03 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=1.5E−02 n=1 fg=0.03 bg=0.00
RNA polymerase II transcription regulato... GO:0090575 p=2.3E−02 n=3 fg=0.07 bg=0.02
core mediator complex GO:0070847 p=2.9E−02 n=1 fg=0.03 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=2.9E−02 n=1 fg=0.03 bg=0.00
Lsm1−7−Pat1 complex GO:1990726 p=2.9E−02 n=1 fg=0.03 bg=0.00
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Swr1 complex GO:0000812 p=2.9E−02 n=1 fg=0.03 bg=0.00
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actin−based cell projection GO:0098858 p=3.8E−02 n=3 fg=0.07 bg=0.02
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R2TP complex GO:0097255 p=4.4E−02 n=1 fg=0.03 bg=0.00
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mRNA cap binding complex GO:0005845 p=4.4E−02 n=1 fg=0.03 bg=0.00
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membrane GO:0016020 p=5.4E−02 n=22 fg=0.55 bg=0.41
integral component of peroxisomal membra... GO:0005779 p=5.8E−02 n=1 fg=0.03 bg=0.00
brahma complex GO:0035060 p=5.8E−02 n=1 fg=0.03 bg=0.00
RNA cap binding complex GO:0034518 p=5.8E−02 n=1 fg=0.03 bg=0.00
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0 1 2 3 4 5
−log(p)
n=40/143 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction