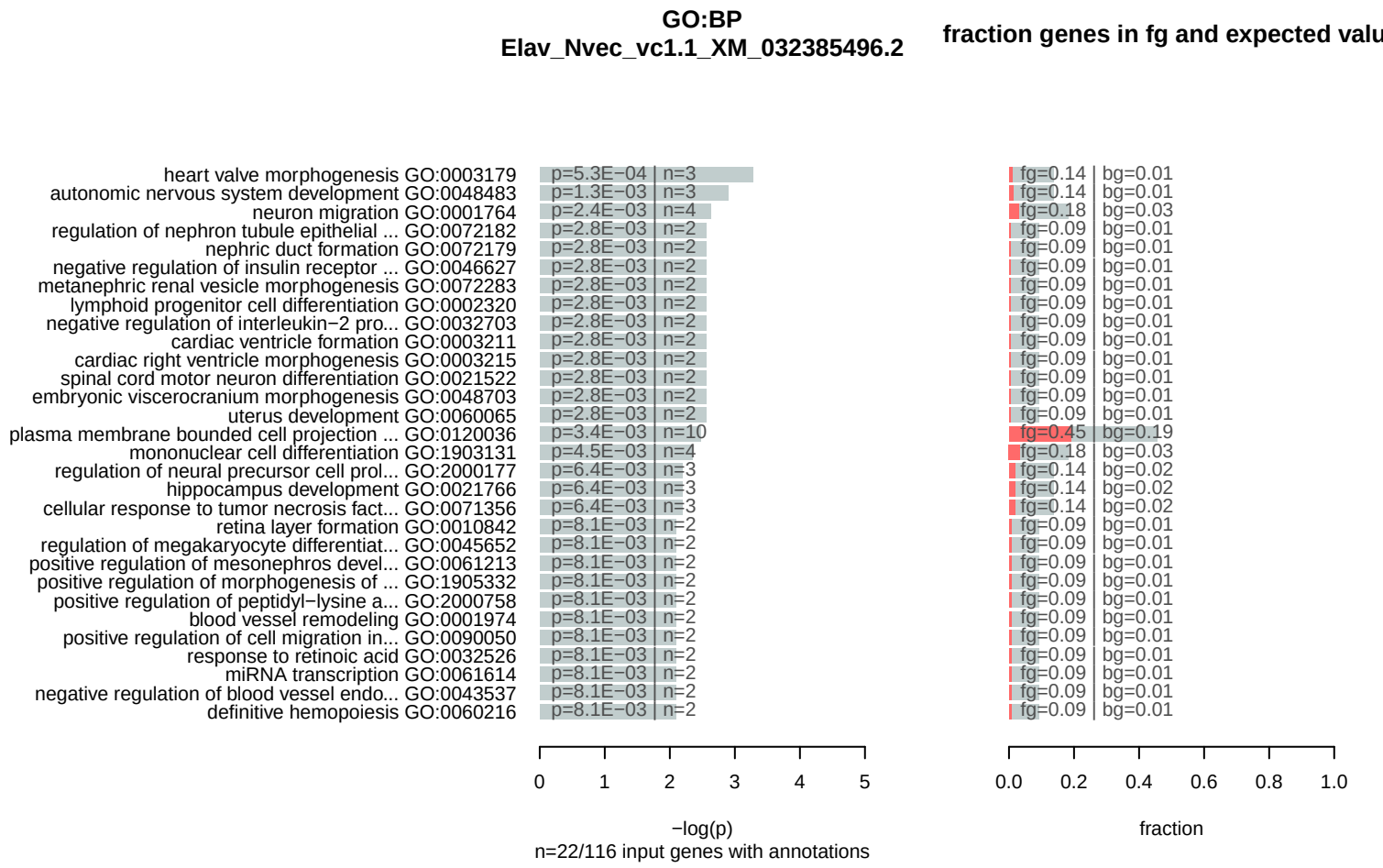
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regulation of nephron tubule epithelial ... GO:0072182 p=2.8E−03 n=2 fg=0.09 bg=0.01
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hippocampus development GO:0021766 p=6.4E−03 n=3 fg=0.14 bg=0.02
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retina layer formation GO:0010842 p=8.1E−03 n=2 fg=0.09 bg=0.01
regulation of megakaryocyte differentiat... GO:0045652 p=8.1E−03 n=2 fg=0.09 bg=0.01
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positive regulation of cell migration in... GO:0090050 p=8.1E−03 n=2 fg=0.09 bg=0.01
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fraction
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HMG box domain binding GO:0071837 p=1.6E−02 n=2 fg=0.10 bg=0.01
cytokine receptor binding GO:0005126 p=1.6E−02 n=2 fg=0.10 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=1.8E−02 n=4 fg=0.20 bg=0.06
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.8E−02 n=4 fg=0.20 bg=0.06
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histone deacetylase binding GO:0042826 p=3.8E−02 n=2 fg=0.10 bg=0.02
core promoter sequence−specific DNA bind... GO:0001046 p=3.8E−02 n=2 fg=0.10 bg=0.02
outward rectifier potassium channel acti... GO:0015271 p=5.1E−02 n=2 fg=0.10 bg=0.02
DNA−binding transcription activator acti... GO:0001228 p=5.1E−02 n=4 fg=0.20 bg=0.07
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protein serine/threonine kinase inhibito... GO:0030291 p=5.5E−02 n=1 fg=0.05 bg=0.00
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lipid phosphatase activity GO:0042577 p=5.5E−02 n=1 fg=0.05 bg=0.00
deacetylase activity GO:0019213 p=5.5E−02 n=1 fg=0.05 bg=0.00
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intronic transcription regulatory region... GO:0001161 p=5.5E−02 n=1 fg=0.05 bg=0.00
RNA polymerase II intronic transcription... GO:0001162 p=5.5E−02 n=1 fg=0.05 bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0034485 p=5.5E−02 n=1 fg=0.05 bg=0.00
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−log(p)
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032385496.2
fraction genes in fg and expected valu
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centrosome GO:0005813 p=2.9E−02 n=3 fg=0.14 bg=0.03
protein−containing complex GO:0032991 p=3.1E−02 n=12 fg=0.55 bg=0.34
sarcomere GO:0030017 p=3.5E−02 n=3 fg=0.14 bg=0.04
myofibril GO:0030016 p=4.2E−02 n=3 fg=0.14 bg=0.04
mitotic spindle pole GO:0097431 p=5.5E−02 n=1 fg=0.05 bg=0.00
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germinal vesicle GO:0042585 p=1.1E−01 n=1 fg=0.05 bg=0.01
female germ cell nucleus GO:0001674 p=1.1E−01 n=1 fg=0.05 bg=0.01
spliceosomal snRNP complex GO:0097525 p=1.1E−01 n=1 fg=0.05 bg=0.01
Sm−like protein family complex GO:0120114 p=1.1E−01 n=1 fg=0.05 bg=0.01
mitotic spindle GO:0072686 p=1.1E−01 n=1 fg=0.05 bg=0.01
catalytic step 2 spliceosome GO:0071013 p=1.1E−01 n=1 fg=0.05 bg=0.01
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−log(p)
n=22/116 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction