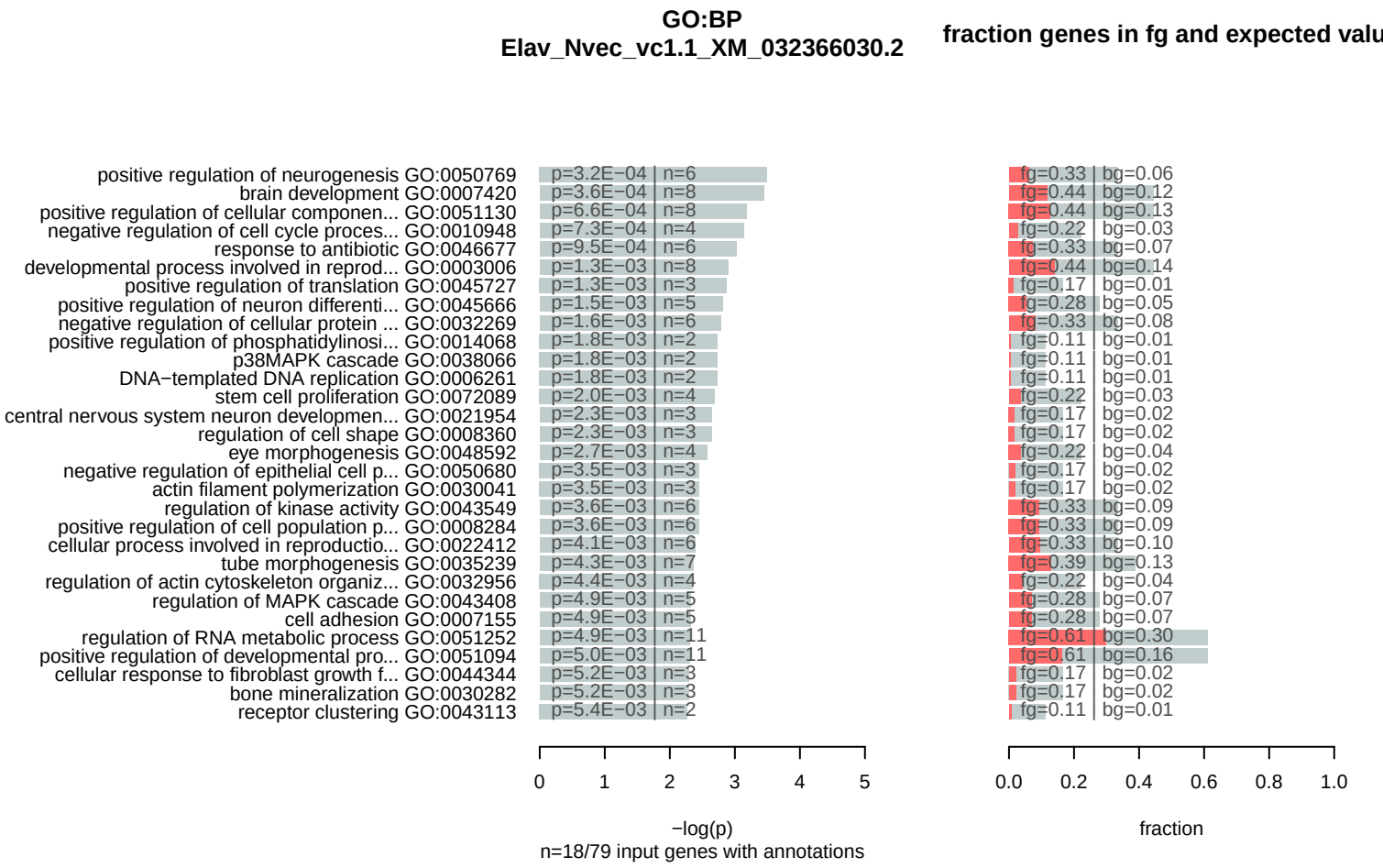
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actin filament polymerization GO:0030041 p=3.5E−03 n=3 fg=0.17 bg=0.02
regulation of kinase activity GO:0043549 p=3.6E−03 n=6 fg=0.33 bg=0.09
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regulation of RNA metabolic process GO:0051252 p=4.9E−03 n=11 fg=0.61 bg=0.30
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cellular response to fibroblast growth f... GO:0044344 p=5.2E−03 n=3 fg=0.17 bg=0.02
bone mineralization GO:0030282 p=5.2E−03 n=3 fg=0.17 bg=0.02
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n=18/79 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032366030.2
fraction genes in fg and expected valu
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growth factor receptor binding GO:0070851 p=7.5E−03 n=2 fg=0.11 bg=0.01
mRNA regulatory element binding translat... GO:0000900 p=7.5E−03 n=2 fg=0.11 bg=0.01
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poly−pyrimidine tract binding GO:0008187 p=5.2E−02 n=1 fg=0.05 bg=0.00
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phosphotransferase activity, phosphate g... GO:0016776 p=5.2E−02 n=1 fg=0.05 bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 p=5.2E−02 n=1 fg=0.05 bg=0.00
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0 1 2 3 4 5
−log(p)
n=19/79 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032366030.2
fraction genes in fg and expected valu
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intrinsic component of the cytoplasmic s... GO:0031235 p=1.9E−03 n=2 fg=0.11 bg=0.01
cytoskeleton GO:0005856 p=2.6E−03 n=7 fg=0.39 bg=0.12
cytoplasmic side of plasma membrane GO:0009898 p=3.8E−03 n=5 fg=0.28 bg=0.03
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microvillus GO:0005902 p=5.5E−03 n=2 fg=0.11 bg=0.01
filopodium GO:0030175 p=5.5E−03 n=2 fg=0.11 bg=0.01
adherens junction GO:0005912 p=7.5E−03 n=3 fg=0.17 bg=0.03
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polysomal ribosome GO:0042788 p=4.5E−02 n=1 fg=0.06 bg=0.00
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node of Ranvier GO:0033268 p=4.5E−02 n=1 fg=0.06 bg=0.00
myelin sheath abaxonal region GO:0035748 p=4.5E−02 n=1 fg=0.06 bg=0.00
bicellular tight junction GO:0005923 p=4.5E−02 n=1 fg=0.06 bg=0.00
0 1 2 3 4 5
−log(p)
n=18/79 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction