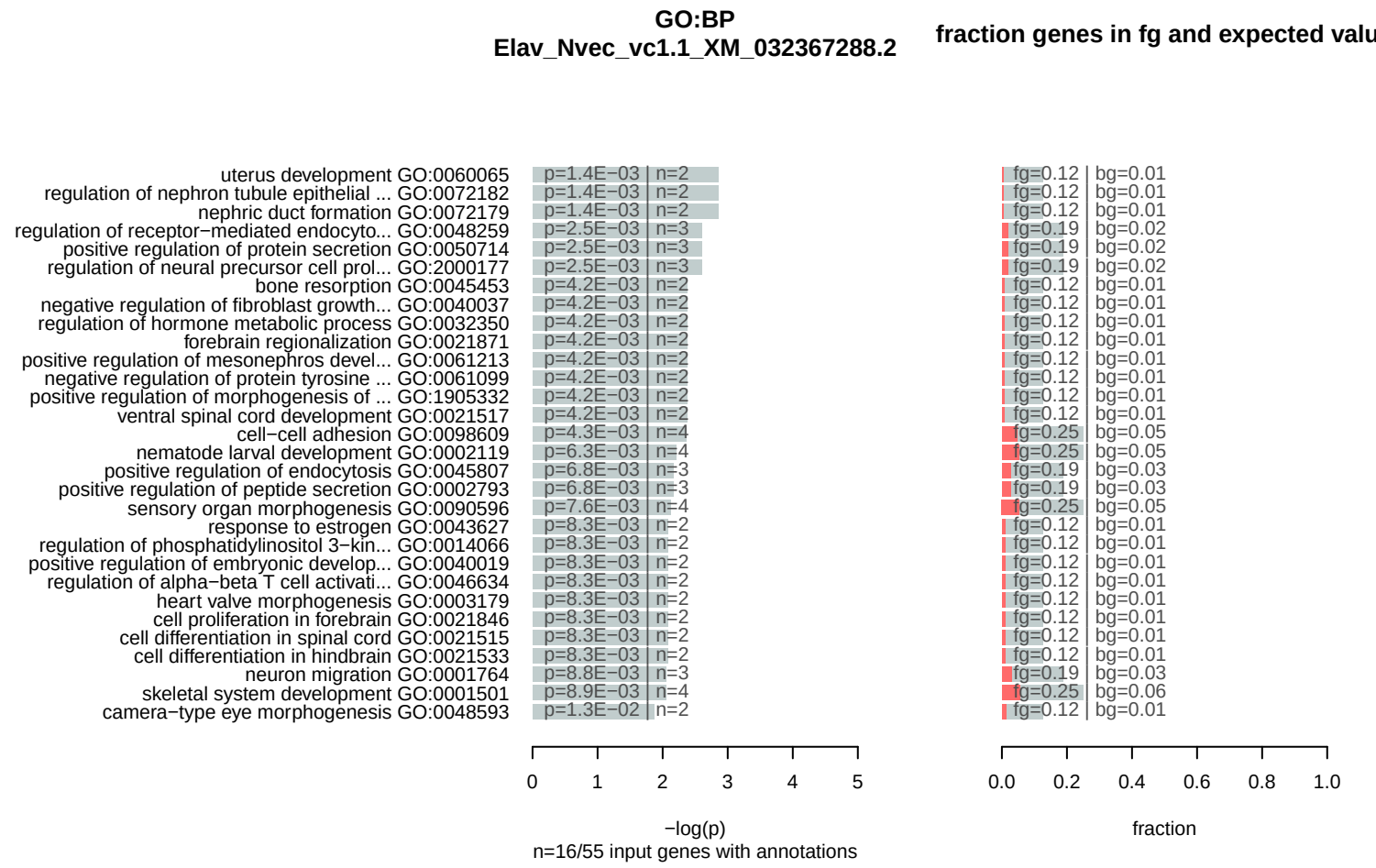
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positive regulation of protein secretion GO:0050714 p=2.5E−03 n=3 fg=0.19 bg=0.02
regulation of neural precursor cell prol... GO:2000177 p=2.5E−03 n=3 fg=0.19 bg=0.02
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response to estrogen GO:0043627 p=8.3E−03 n=2 fg=0.12 bg=0.01
regulation of phosphatidylinositol 3−kin... GO:0014066 p=8.3E−03 n=2 fg=0.12 bg=0.01
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heart valve morphogenesis GO:0003179 p=8.3E−03 n=2 fg=0.12 bg=0.01
cell proliferation in forebrain GO:0021846 p=8.3E−03 n=2 fg=0.12 bg=0.01
cell differentiation in spinal cord GO:0021515 p=8.3E−03 n=2 fg=0.12 bg=0.01
cell differentiation in hindbrain GO:0021533 p=8.3E−03 n=2 fg=0.12 bg=0.01
neuron migration GO:0001764 p=8.8E−03 n=3 fg=0.19 bg=0.03
skeletal system development GO:0001501 p=8.9E−03 n=4 fg=0.25 bg=0.06
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fraction
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beta1−adrenergic receptor activity GO:0004940 p=4.1E−02 n=1 fg=0.07 bg=0.00
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C2H2 zinc finger domain binding GO:0070742 p=4.1E−02 n=1 fg=0.07 bg=0.00
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RNA polymerase II intronic transcription... GO:0001162 p=4.1E−02 n=1 fg=0.07 bg=0.00
retromer complex binding GO:1905394 p=4.1E−02 n=1 fg=0.07 bg=0.00
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1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=4.1E−02 n=1 fg=0.07 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=4.1E−02 n=1 fg=0.07 bg=0.00
epidermal growth factor receptor binding GO:0005154 p=4.1E−02 n=1 fg=0.07 bg=0.00
dopamine binding GO:0035240 p=4.1E−02 n=1 fg=0.07 bg=0.00
protein phosphatase 2A binding GO:0051721 p=4.1E−02 n=1 fg=0.07 bg=0.00
non−tyrosine kinase fibroblast growth fa... GO:0001571 p=4.1E−02 n=1 fg=0.07 bg=0.00
GTPase regulator activity GO:0030695 p=4.8E−02 n=3 fg=0.20 bg=0.06
peptide binding GO:0042277 p=5.9E−02 n=2 fg=0.13 bg=0.03
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−log(p)
n=15/55 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032367288.2
fraction genes in fg and expected valu
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endosome membrane GO:0010008 p=9.0E−02 n=2 fg=0.12 bg=0.03
axon GO:0030424 p=9.7E−02 n=4 fg=0.25 bg=0.11
early endosome GO:0005769 p=1.0E−01 n=2 fg=0.12 bg=0.04
site of polarized growth GO:0030427 p=1.0E−01 n=2 fg=0.12 bg=0.04
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dendritic spine GO:0043197 p=1.9E−01 n=2 fg=0.12 bg=0.05
neuron spine GO:0044309 p=1.9E−01 n=2 fg=0.12 bg=0.05
integral component of plasma membrane GO:0005887 p=2.0E−01 n=4 fg=0.25 bg=0.15
anchoring junction GO:0070161 p=2.0E−01 n=2 fg=0.12 bg=0.05
cell−cell junction GO:0005911 p=2.0E−01 n=2 fg=0.12 bg=0.05
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nuclear lumen GO:0031981 p=2.3E−01 n=6 fg=0.38 bg=0.27
intrinsic component of plasma membrane GO:0031226 p=2.4E−01 n=4 fg=0.25 bg=0.16
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caveola GO:0005901 p=2.5E−01 n=1 fg=0.06 bg=0.02
focal adhesion GO:0005925 p=2.5E−01 n=1 fg=0.06 bg=0.02
protein−containing complex GO:0032991 p=2.7E−01 n=7 fg=0.44 bg=0.34
distal axon GO:0150034 p=2.8E−01 n=2 fg=0.12 bg=0.06
voltage−gated potassium channel complex GO:0008076 p=2.8E−01 n=1 fg=0.06 bg=0.02
0 1 2 3 4 5
−log(p)
n=16/55 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction