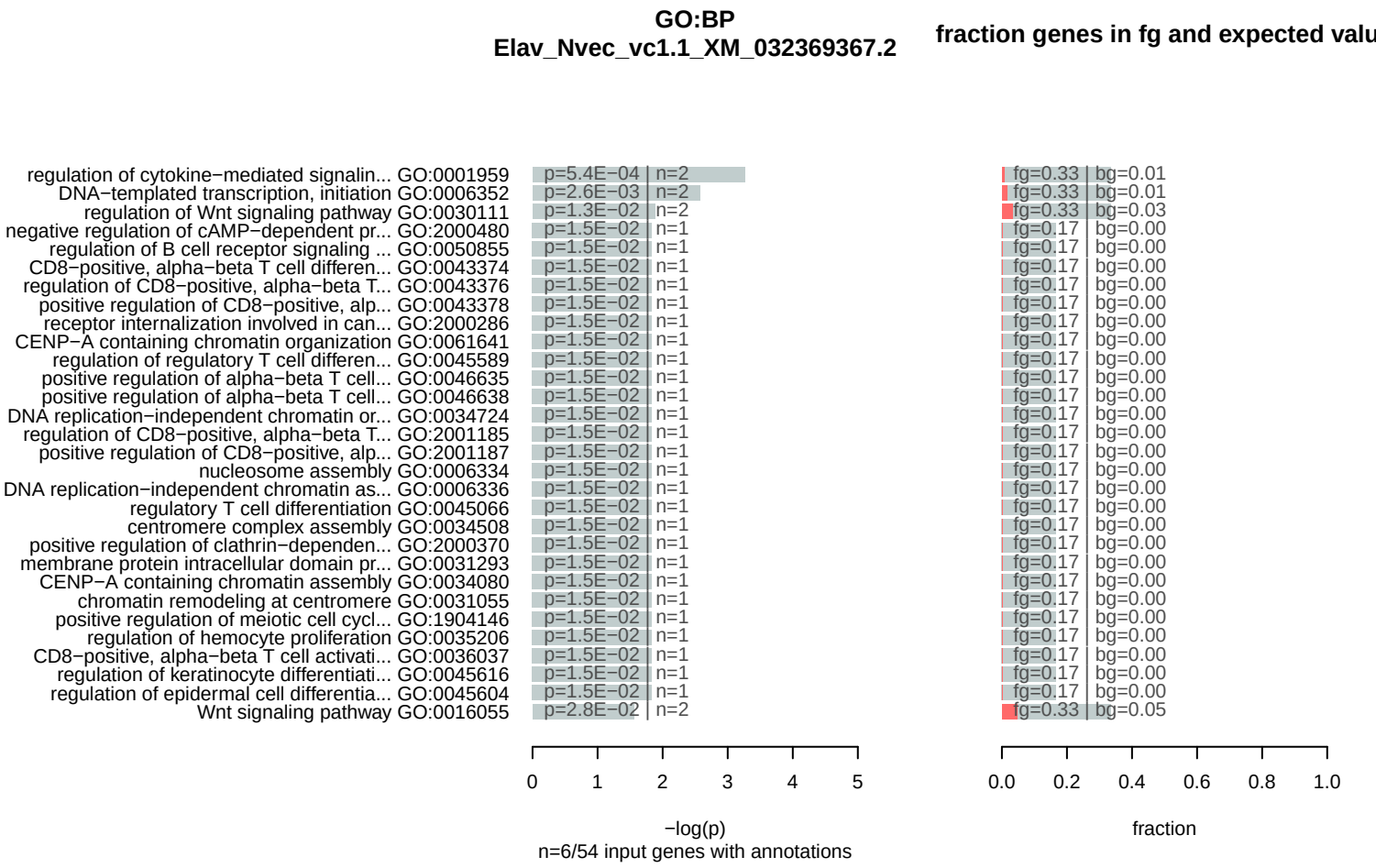
GO:BP
Elav_Nvec_vc1.1_XM_032369367.2
fraction genes in fg and expected valu
regulation of cytokine−mediated signalin... GO:0001959 p=5.4E−04 n=2 fg=0.33 bg=0.01
DNA−templated transcription, initiation GO:0006352 p=2.6E−03 n=2 fg=0.33 bg=0.01
regulation of Wnt signaling pathway GO:0030111 p=1.3E−02 n=2 fg=0.33 bg=0.03
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CD8−positive, alpha−beta T cell differen... GO:0043374 p=1.5E−02 n=1 fg=0.17 bg=0.00
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CENP−A containing chromatin organization GO:0061641 p=1.5E−02 n=1 fg=0.17 bg=0.00
regulation of regulatory T cell differen... GO:0045589 p=1.5E−02 n=1 fg=0.17 bg=0.00
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DNA replication−independent chromatin or... GO:0034724 p=1.5E−02 n=1 fg=0.17 bg=0.00
regulation of CD8−positive, alpha−beta T... GO:2001185 p=1.5E−02 n=1 fg=0.17 bg=0.00
positive regulation of CD8−positive, alp... GO:2001187 p=1.5E−02 n=1 fg=0.17 bg=0.00
nucleosome assembly GO:0006334 p=1.5E−02 n=1 fg=0.17 bg=0.00
DNA replication−independent chromatin as... GO:0006336 p=1.5E−02 n=1 fg=0.17 bg=0.00
regulatory T cell differentiation GO:0045066 p=1.5E−02 n=1 fg=0.17 bg=0.00
centromere complex assembly GO:0034508 p=1.5E−02 n=1 fg=0.17 bg=0.00
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positive regulation of meiotic cell cycl... GO:1904146 p=1.5E−02 n=1 fg=0.17 bg=0.00
regulation of hemocyte proliferation GO:0035206 p=1.5E−02 n=1 fg=0.17 bg=0.00
CD8−positive, alpha−beta T cell activati... GO:0036037 p=1.5E−02 n=1 fg=0.17 bg=0.00
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Wnt signaling pathway GO:0016055 p=2.8E−02 n=2 fg=0.33 bg=0.05
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n=6/54 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032369367.2
fraction genes in fg and expected valu
protein kinase A catalytic subunit bindi... GO:0034236 p=1.6E−02 n=1 fg=0.17 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=1.6E−02 n=1 fg=0.17 bg=0.00
translation factor activity, RNA binding GO:0008135 p=1.6E−02 n=1 fg=0.17 bg=0.00
aspartic−type peptidase activity GO:0070001 p=1.6E−02 n=1 fg=0.17 bg=0.00
aspartic endopeptidase activity, intrame... GO:0042500 p=1.6E−02 n=1 fg=0.17 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=1.6E−02 n=1 fg=0.17 bg=0.00
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protein kinase A binding GO:0051018 p=4.9E−02 n=1 fg=0.17 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=4.9E−02 n=1 fg=0.17 bg=0.01
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translation repressor activity GO:0030371 p=4.9E−02 n=1 fg=0.17 bg=0.01
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cAMP binding GO:0030552 p=4.9E−02 n=1 fg=0.17 bg=0.01
protein kinase regulator activity GO:0019887 p=6.5E−02 n=1 fg=0.17 bg=0.01
mRNA 3'−UTR binding GO:0003730 p=6.5E−02 n=1 fg=0.17 bg=0.01
cyclic nucleotide binding GO:0030551 p=6.5E−02 n=1 fg=0.17 bg=0.01
protein dimerization activity GO:0046983 p=7.0E−02 n=3 fg=0.50 bg=0.18
endopeptidase activity GO:0004175 p=8.0E−02 n=1 fg=0.17 bg=0.01
kinase regulator activity GO:0019207 p=8.0E−02 n=1 fg=0.17 bg=0.01
adrenergic receptor binding GO:0031690 p=9.6E−02 n=1 fg=0.17 bg=0.02
enzyme inhibitor activity GO:0004857 p=1.3E−01 n=1 fg=0.17 bg=0.02
histone binding GO:0042393 p=1.4E−01 n=1 fg=0.17 bg=0.02
mRNA binding GO:0003729 p=1.4E−01 n=1 fg=0.17 bg=0.02
G protein−coupled receptor binding GO:0001664 p=1.5E−01 n=1 fg=0.17 bg=0.03
0 1 2 3 4 5
−log(p)
n=6/54 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032369367.2
fraction genes in fg and expected valu
endosome membrane GO:0010008 p=1.3E−02 n=2 fg=0.33 bg=0.03
centrosome GO:0005813 p=1.3E−02 n=2 fg=0.33 bg=0.03
ISWI−type complex GO:0031010 p=1.5E−02 n=1 fg=0.17 bg=0.00
core−binding factor complex GO:0016513 p=1.5E−02 n=1 fg=0.17 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=1.5E−02 n=1 fg=0.17 bg=0.00
RSF complex GO:0031213 p=1.5E−02 n=1 fg=0.17 bg=0.00
microtubule organizing center GO:0005815 p=2.6E−02 n=2 fg=0.33 bg=0.05
late endosome membrane GO:0031902 p=3.0E−02 n=1 fg=0.17 bg=0.01
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SWI/SNF superfamily−type complex GO:0070603 p=3.0E−02 n=1 fg=0.17 bg=0.01
Golgi−associated vesicle membrane GO:0030660 p=3.0E−02 n=1 fg=0.17 bg=0.01
female germ cell nucleus GO:0001674 p=3.0E−02 n=1 fg=0.17 bg=0.01
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polytene chromosome interband GO:0005705 p=3.0E−02 n=1 fg=0.17 bg=0.01
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lumenal side of endoplasmic reticulum me... GO:0098553 p=3.0E−02 n=1 fg=0.17 bg=0.01
cytoplasmic side of endoplasmic reticulu... GO:0098554 p=3.0E−02 n=1 fg=0.17 bg=0.01
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integral component of cytoplasmic side o... GO:0071458 p=3.0E−02 n=1 fg=0.17 bg=0.01
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ciliary base GO:0097546 p=5.9E−02 n=1 fg=0.17 bg=0.01
microtubule cytoskeleton GO:0015630 p=6.3E−02 n=2 fg=0.33 bg=0.07
polytene chromosome GO:0005700 p=7.3E−02 n=1 fg=0.17 bg=0.01
nucleus GO:0005634 p=7.3E−02 n=5 fg=0.83 bg=0.46
0 1 2 3 4 5
−log(p)
n=6/54 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction