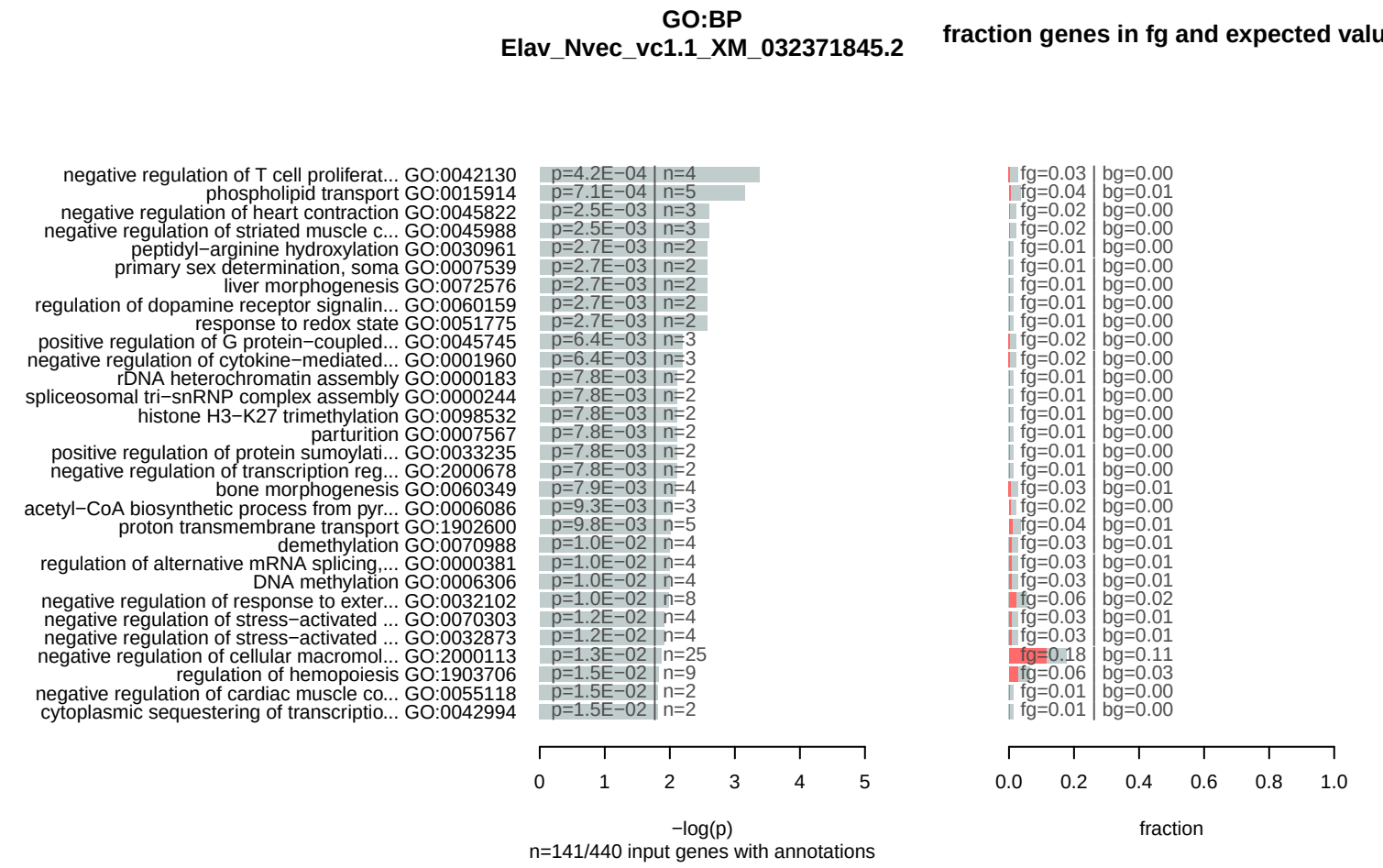
GO:BP
Elav_Nvec_vc1.1_XM_032371845.2
fraction genes in fg and expected valu
negative regulation of T cell proliferat... GO:0042130 p=4.2E−04 n=4 fg=0.03 bg=0.00
phospholipid transport GO:0015914 p=7.1E−04 n=5 fg=0.04 bg=0.01
negative regulation of heart contraction GO:0045822 p=2.5E−03 n=3 fg=0.02 bg=0.00
negative regulation of striated muscle c... GO:0045988 p=2.5E−03 n=3 fg=0.02 bg=0.00
peptidyl−arginine hydroxylation GO:0030961 p=2.7E−03 n=2 fg=0.01 bg=0.00
primary sex determination, soma GO:0007539 p=2.7E−03 n=2 fg=0.01 bg=0.00
liver morphogenesis GO:0072576 p=2.7E−03 n=2 fg=0.01 bg=0.00
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response to redox state GO:0051775 p=2.7E−03 n=2 fg=0.01 bg=0.00
positive regulation of G protein−coupled... GO:0045745 p=6.4E−03 n=3 fg=0.02 bg=0.00
negative regulation of cytokine−mediated... GO:0001960 p=6.4E−03 n=3 fg=0.02 bg=0.00
rDNA heterochromatin assembly GO:0000183 p=7.8E−03 n=2 fg=0.01 bg=0.00
spliceosomal tri−snRNP complex assembly GO:0000244 p=7.8E−03 n=2 fg=0.01 bg=0.00
histone H3−K27 trimethylation GO:0098532 p=7.8E−03 n=2 fg=0.01 bg=0.00
parturition GO:0007567 p=7.8E−03 n=2 fg=0.01 bg=0.00
positive regulation of protein sumoylati... GO:0033235 p=7.8E−03 n=2 fg=0.01 bg=0.00
negative regulation of transcription reg... GO:2000678 p=7.8E−03 n=2 fg=0.01 bg=0.00
bone morphogenesis GO:0060349 p=7.9E−03 n=4 fg=0.03 bg=0.01
acetyl−CoA biosynthetic process from pyr... GO:0006086 p=9.3E−03 n=3 fg=0.02 bg=0.00
proton transmembrane transport GO:1902600 p=9.8E−03 n=5 fg=0.04 bg=0.01
demethylation GO:0070988 p=1.0E−02 n=4 fg=0.03 bg=0.01
regulation of alternative mRNA splicing,... GO:0000381 p=1.0E−02 n=4 fg=0.03 bg=0.01
DNA methylation GO:0006306 p=1.0E−02 n=4 fg=0.03 bg=0.01
negative regulation of response to exter... GO:0032102 p=1.0E−02 n=8 fg=0.06 bg=0.02
negative regulation of stress−activated ... GO:0070303 p=1.2E−02 n=4 fg=0.03 bg=0.01
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regulation of hemopoiesis GO:1903706 p=1.5E−02 n=9 fg=0.06 bg=0.03
negative regulation of cardiac muscle co... GO:0055118 p=1.5E−02 n=2 fg=0.01 bg=0.00
cytoplasmic sequestering of transcriptio... GO:0042994 p=1.5E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=141/440 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032371845.2
fraction genes in fg and expected valu
coreceptor activity involved in Wnt sign... GO:1904929 p=2.9E−03 n=2 fg=0.02 bg=0.00
proton transmembrane transporter activit... GO:0015078 p=4.2E−03 n=5 fg=0.04 bg=0.01
phospholipid transfer activity GO:0120014 p=8.3E−03 n=2 fg=0.02 bg=0.00
miRNA binding GO:0035198 p=8.3E−03 n=2 fg=0.02 bg=0.00
mRNA 3'−UTR binding GO:0003730 p=8.7E−03 n=4 fg=0.03 bg=0.01
iodide transmembrane transporter activit... GO:0015111 p=1.6E−02 n=2 fg=0.02 bg=0.00
temperature−gated ion channel activity GO:0097603 p=1.6E−02 n=2 fg=0.02 bg=0.00
histone H3−methyl−lysine−36 demethylase ... GO:0051864 p=1.6E−02 n=2 fg=0.02 bg=0.00
phospholipid transporter activity GO:0005548 p=1.7E−02 n=5 fg=0.04 bg=0.01
cysteine−type peptidase activity GO:0008234 p=2.3E−02 n=5 fg=0.04 bg=0.01
cysteine−type deubiquitinase activity GO:0004843 p=2.3E−02 n=3 fg=0.02 bg=0.01
demethylase activity GO:0032451 p=2.3E−02 n=3 fg=0.02 bg=0.01
phospholipid scramblase activity GO:0017128 p=2.6E−02 n=2 fg=0.02 bg=0.00
lipid transporter activity GO:0005319 p=3.0E−02 n=6 fg=0.05 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=3.5E−02 n=3 fg=0.02 bg=0.01
aryl hydrocarbon receptor binding GO:0017162 p=3.7E−02 n=2 fg=0.02 bg=0.00
intramembrane lipid transporter activity GO:0140303 p=3.7E−02 n=2 fg=0.02 bg=0.00
oxidoreductase activity, acting on the a... GO:0016903 p=3.7E−02 n=2 fg=0.02 bg=0.00
Wnt−protein binding GO:0017147 p=3.7E−02 n=2 fg=0.02 bg=0.00
intracellular calcium activated chloride... GO:0005229 p=3.7E−02 n=2 fg=0.02 bg=0.00
intracellular chloride channel activity GO:0061778 p=3.7E−02 n=2 fg=0.02 bg=0.00
palmitoyltransferase activity GO:0016409 p=3.7E−02 n=2 fg=0.02 bg=0.00
2−oxoglutarate−dependent dioxygenase act... GO:0016706 p=4.3E−02 n=3 fg=0.02 bg=0.01
voltage−gated anion channel activity GO:0008308 p=5.0E−02 n=2 fg=0.02 bg=0.00
voltage−gated chloride channel activity GO:0005247 p=5.0E−02 n=2 fg=0.02 bg=0.00
lysophospholipase activity GO:0004622 p=5.0E−02 n=2 fg=0.02 bg=0.00
methylcytosine dioxygenase activity GO:0070579 p=5.4E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=5.4E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=5.4E−02 n=1 fg=0.01 bg=0.00
oxidative RNA demethylase activity GO:0035515 p=5.4E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=127/440 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032371845.2
fraction genes in fg and expected valu
pyruvate dehydrogenase complex GO:0045254 p=5.5E−04 n=3 fg=0.02 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=8.0E−03 n=2 fg=0.01 bg=0.00
CCR4−NOT complex GO:0030014 p=8.0E−03 n=2 fg=0.01 bg=0.00
Cul5−RING ubiquitin ligase complex GO:0031466 p=8.0E−03 n=2 fg=0.01 bg=0.00
cytoplasmic ribonucleoprotein granule GO:0036464 p=1.1E−02 n=8 fg=0.06 bg=0.02
intracellular anatomical structure GO:0005622 p=1.3E−02 n=140 fg=0.99 bg=0.94
ribonucleoprotein granule GO:0035770 p=1.5E−02 n=8 fg=0.06 bg=0.02
cytoplasmic stress granule GO:0010494 p=2.2E−02 n=3 fg=0.02 bg=0.00
MLL3/4 complex GO:0044666 p=2.5E−02 n=2 fg=0.01 bg=0.00
cluster of actin−based cell projections GO:0098862 p=2.6E−02 n=6 fg=0.04 bg=0.02
organelle GO:0043226 p=2.6E−02 n=129 fg=0.91 bg=0.85
intracellular organelle GO:0043229 p=2.9E−02 n=127 fg=0.89 bg=0.83
brush border GO:0005903 p=3.4E−02 n=5 fg=0.04 bg=0.01
lipid droplet GO:0005811 p=3.4E−02 n=4 fg=0.03 bg=0.01
plasma membrane proton−transporting V−ty... GO:0033181 p=3.6E−02 n=2 fg=0.01 bg=0.00
nucleus GO:0005634 p=4.6E−02 n=81 fg=0.57 bg=0.50
P granule GO:0043186 p=4.8E−02 n=3 fg=0.02 bg=0.01
Cul2−RING ubiquitin ligase complex GO:0031462 p=4.8E−02 n=2 fg=0.01 bg=0.00
intracellular membrane−bounded organelle GO:0043231 p=5.1E−02 n=118 fg=0.83 bg=0.77
host cell nucleus GO:0042025 p=5.3E−02 n=1 fg=0.01 bg=0.00
acrosomal matrix GO:0043159 p=5.3E−02 n=1 fg=0.01 bg=0.00
RCAF complex GO:0035059 p=5.3E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=5.3E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=5.3E−02 n=1 fg=0.01 bg=0.00
WASH complex GO:0071203 p=5.3E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=5.3E−02 n=1 fg=0.01 bg=0.00
podocyte foot GO:0098846 p=5.3E−02 n=1 fg=0.01 bg=0.00
catalytic step 1 spliceosome GO:0071012 p=5.3E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=5.3E−02 n=1 fg=0.01 bg=0.00
TIM22 mitochondrial import inner membran... GO:0042721 p=5.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=142/440 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction