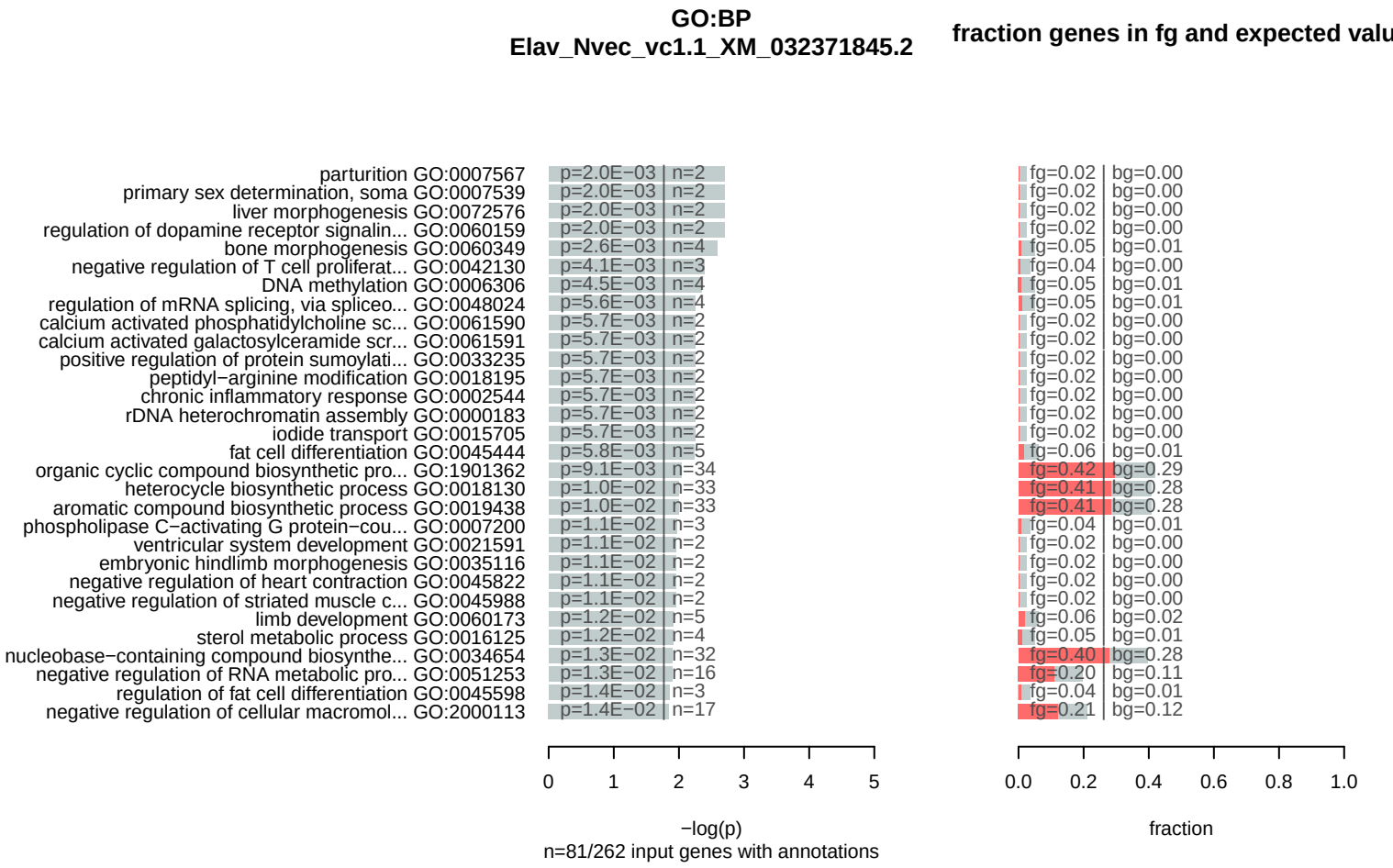
GO:BP
Elav_Nvec_vc1.1_XM_032371845.2
fraction genes in fg and expected valu
parturition GO:0007567 p=2.0E−03 n=2 fg=0.02 bg=0.00
primary sex determination, soma GO:0007539 p=2.0E−03 n=2 fg=0.02 bg=0.00
liver morphogenesis GO:0072576 p=2.0E−03 n=2 fg=0.02 bg=0.00
regulation of dopamine receptor signalin... GO:0060159 p=2.0E−03 n=2 fg=0.02 bg=0.00
bone morphogenesis GO:0060349 p=2.6E−03 n=4 fg=0.05 bg=0.01
negative regulation of T cell proliferat... GO:0042130 p=4.1E−03 n=3 fg=0.04 bg=0.00
DNA methylation GO:0006306 p=4.5E−03 n=4 fg=0.05 bg=0.01
regulation of mRNA splicing, via spliceo... GO:0048024 p=5.6E−03 n=4 fg=0.05 bg=0.01
calcium activated phosphatidylcholine sc... GO:0061590 p=5.7E−03 n=2 fg=0.02 bg=0.00
calcium activated galactosylceramide scr... GO:0061591 p=5.7E−03 n=2 fg=0.02 bg=0.00
positive regulation of protein sumoylati... GO:0033235 p=5.7E−03 n=2 fg=0.02 bg=0.00
peptidyl−arginine modification GO:0018195 p=5.7E−03 n=2 fg=0.02 bg=0.00
chronic inflammatory response GO:0002544 p=5.7E−03 n=2 fg=0.02 bg=0.00
rDNA heterochromatin assembly GO:0000183 p=5.7E−03 n=2 fg=0.02 bg=0.00
iodide transport GO:0015705 p=5.7E−03 n=2 fg=0.02 bg=0.00
fat cell differentiation GO:0045444 p=5.8E−03 n=5 fg=0.06 bg=0.01
organic cyclic compound biosynthetic pro... GO:1901362 p=9.1E−03 n=34 fg=0.42 bg=0.29
heterocycle biosynthetic process GO:0018130 p=1.0E−02 n=33 fg=0.41 bg=0.28
aromatic compound biosynthetic process GO:0019438 p=1.0E−02 n=33 fg=0.41 bg=0.28
phospholipase C−activating G protein−cou... GO:0007200 p=1.1E−02 n=3 fg=0.04 bg=0.01
ventricular system development GO:0021591 p=1.1E−02 n=2 fg=0.02 bg=0.00
embryonic hindlimb morphogenesis GO:0035116 p=1.1E−02 n=2 fg=0.02 bg=0.00
negative regulation of heart contraction GO:0045822 p=1.1E−02 n=2 fg=0.02 bg=0.00
negative regulation of striated muscle c... GO:0045988 p=1.1E−02 n=2 fg=0.02 bg=0.00
limb development GO:0060173 p=1.2E−02 n=5 fg=0.06 bg=0.02
sterol metabolic process GO:0016125 p=1.2E−02 n=4 fg=0.05 bg=0.01
nucleobase−containing compound biosynthe... GO:0034654 p=1.3E−02 n=32 fg=0.40 bg=0.28
negative regulation of RNA metabolic pro... GO:0051253 p=1.3E−02 n=16 fg=0.20 bg=0.11
regulation of fat cell differentiation GO:0045598 p=1.4E−02 n=3 fg=0.04 bg=0.01
negative regulation of cellular macromol... GO:2000113 p=1.4E−02 n=17 fg=0.21 bg=0.12
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n=81/262 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
nucleic acid binding GO:0003676 p=6.1E−04 n=25 fg=0.36 bg=0.19
phospholipid transporter activity GO:0005548 p=1.8E−03 n=4 fg=0.06 bg=0.01
coreceptor activity involved in Wnt sign... GO:1904929 p=1.9E−03 n=2 fg=0.03 bg=0.00
temperature−gated ion channel activity GO:0097603 p=5.6E−03 n=2 fg=0.03 bg=0.00
iodide transmembrane transporter activit... GO:0015111 p=5.6E−03 n=2 fg=0.03 bg=0.00
phospholipid scramblase activity GO:0017128 p=1.1E−02 n=2 fg=0.03 bg=0.00
intracellular calcium activated chloride... GO:0005229 p=1.1E−02 n=2 fg=0.03 bg=0.00
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Wnt−protein binding GO:0017147 p=1.7E−02 n=2 fg=0.03 bg=0.00
intramembrane lipid transporter activity GO:0140303 p=1.7E−02 n=2 fg=0.03 bg=0.00
sequence−specific DNA binding GO:0043565 p=2.2E−02 n=10 fg=0.14 bg=0.07
aryl hydrocarbon receptor binding GO:0017162 p=2.5E−02 n=2 fg=0.03 bg=0.00
lipoprotein particle receptor binding GO:0070325 p=2.5E−02 n=2 fg=0.03 bg=0.00
voltage−gated anion channel activity GO:0008308 p=2.5E−02 n=2 fg=0.03 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=2.5E−02 n=2 fg=0.03 bg=0.00
voltage−gated chloride channel activity GO:0005247 p=2.5E−02 n=2 fg=0.03 bg=0.00
low−density lipoprotein particle recepto... GO:0050750 p=2.5E−02 n=2 fg=0.03 bg=0.00
DNA binding GO:0003677 p=2.6E−02 n=14 fg=0.20 bg=0.12
calcium activated cation channel activit... GO:0005227 p=3.5E−02 n=2 fg=0.03 bg=0.00
p53 binding GO:0002039 p=3.6E−02 n=3 fg=0.04 bg=0.01
proton transmembrane transporter activit... GO:0015078 p=3.6E−02 n=3 fg=0.04 bg=0.01
arginine N−methyltransferase activity GO:0016273 p=4.4E−02 n=1 fg=0.01 bg=0.00
protein−arginine N−methyltransferase act... GO:0016274 p=4.4E−02 n=1 fg=0.01 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=4.4E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on the a... GO:0016624 p=4.4E−02 n=1 fg=0.01 bg=0.00
CXCR chemokine receptor binding GO:0045236 p=4.4E−02 n=1 fg=0.01 bg=0.00
pyruvate dehydrogenase (acetyl−transferr... GO:0004740 p=4.4E−02 n=1 fg=0.01 bg=0.00
ribokinase activity GO:0004747 p=4.4E−02 n=1 fg=0.01 bg=0.00
rhodopsin kinase activity GO:0050254 p=4.4E−02 n=1 fg=0.01 bg=0.00
pyruvate dehydrogenase activity GO:0004738 p=4.4E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=70/262 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−03 n=2 fg=0.03 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=5.5E−03 n=2 fg=0.03 bg=0.00
nucleus GO:0005634 p=5.8E−03 n=49 fg=0.62 bg=0.48
cytoplasmic ribonucleoprotein granule GO:0036464 p=1.1E−02 n=6 fg=0.08 bg=0.02
ribonucleoprotein granule GO:0035770 p=1.5E−02 n=6 fg=0.08 bg=0.03
plasma membrane proton−transporting V−ty... GO:0033181 p=2.5E−02 n=2 fg=0.03 bg=0.00
tertiary granule lumen GO:1904724 p=2.5E−02 n=2 fg=0.03 bg=0.00
ciliary membrane GO:0060170 p=3.0E−02 n=3 fg=0.04 bg=0.01
intracellular anatomical structure GO:0005622 p=3.1E−02 n=79 fg=1.00 bg=0.94
external side of plasma membrane GO:0009897 p=3.5E−02 n=3 fg=0.04 bg=0.01
neuronal ribonucleoprotein granule GO:0071598 p=4.4E−02 n=1 fg=0.01 bg=0.00
PET complex GO:1990923 p=4.4E−02 n=1 fg=0.01 bg=0.00
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CHOP−C/EBP complex GO:0036488 p=4.4E−02 n=1 fg=0.01 bg=0.00
mitochondrial DNA−directed RNA polymeras... GO:0034245 p=4.4E−02 n=1 fg=0.01 bg=0.00
podocyte foot GO:0098846 p=4.4E−02 n=1 fg=0.01 bg=0.00
mitochondrial pyruvate dehydrogenase com... GO:0005967 p=4.4E−02 n=1 fg=0.01 bg=0.00
extrinsic component of mitochondrial inn... GO:0031314 p=4.4E−02 n=1 fg=0.01 bg=0.00
methylosome GO:0034709 p=4.4E−02 n=1 fg=0.01 bg=0.00
non−motile cilium GO:0097730 p=4.8E−02 n=4 fg=0.05 bg=0.02
melanosome GO:0042470 p=5.6E−02 n=2 fg=0.03 bg=0.00
nuclear body GO:0016604 p=5.9E−02 n=9 fg=0.11 bg=0.06
organelle GO:0043226 p=6.4E−02 n=75 fg=0.95 bg=0.85
cytoplasmic stress granule GO:0010494 p=6.8E−02 n=2 fg=0.03 bg=0.01
ESCRT complex GO:0036452 p=6.8E−02 n=2 fg=0.03 bg=0.01
pigment granule GO:0048770 p=6.8E−02 n=2 fg=0.03 bg=0.01
intracellular organelle GO:0043229 p=8.1E−02 n=74 fg=0.94 bg=0.84
U2AF complex GO:0089701 p=8.6E−02 n=1 fg=0.01 bg=0.00
cell body fiber GO:0070852 p=8.6E−02 n=1 fg=0.01 bg=0.00
HULC complex GO:0033503 p=8.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=79/262 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction