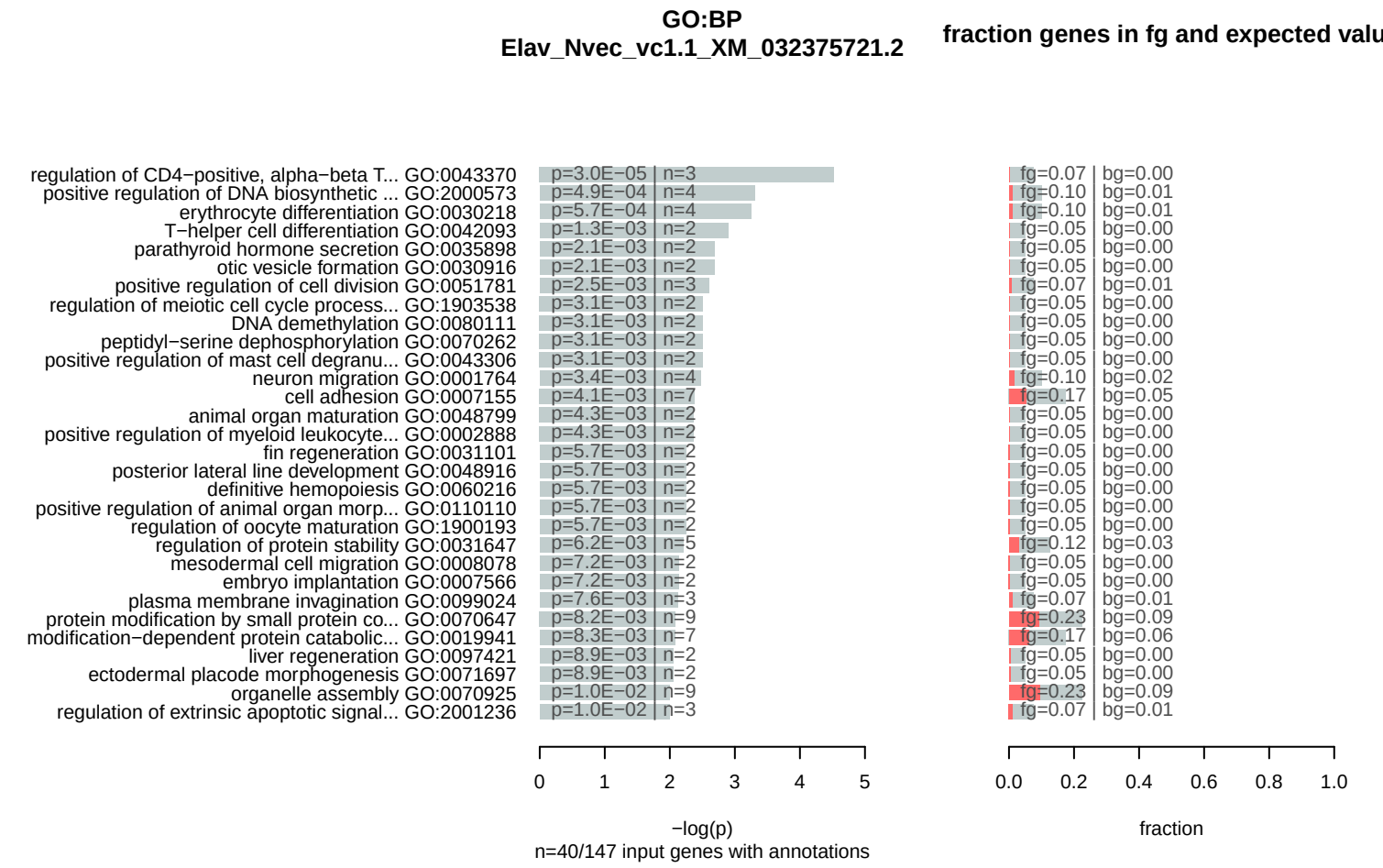
GO:BP
Elav_Nvec_vc1.1_XM_032375721.2
fraction genes in fg and expected valu
regulation of CD4−positive, alpha−beta T... GO:0043370 p=3.0E−05 n=3 fg=0.07 bg=0.00
positive regulation of DNA biosynthetic ... GO:2000573 p=4.9E−04 n=4 fg=0.10 bg=0.01
erythrocyte differentiation GO:0030218 p=5.7E−04 n=4 fg=0.10 bg=0.01
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parathyroid hormone secretion GO:0035898 p=2.1E−03 n=2 fg=0.05 bg=0.00
otic vesicle formation GO:0030916 p=2.1E−03 n=2 fg=0.05 bg=0.00
positive regulation of cell division GO:0051781 p=2.5E−03 n=3 fg=0.07 bg=0.01
regulation of meiotic cell cycle process... GO:1903538 p=3.1E−03 n=2 fg=0.05 bg=0.00
DNA demethylation GO:0080111 p=3.1E−03 n=2 fg=0.05 bg=0.00
peptidyl−serine dephosphorylation GO:0070262 p=3.1E−03 n=2 fg=0.05 bg=0.00
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neuron migration GO:0001764 p=3.4E−03 n=4 fg=0.10 bg=0.02
cell adhesion GO:0007155 p=4.1E−03 n=7 fg=0.17 bg=0.05
animal organ maturation GO:0048799 p=4.3E−03 n=2 fg=0.05 bg=0.00
positive regulation of myeloid leukocyte... GO:0002888 p=4.3E−03 n=2 fg=0.05 bg=0.00
fin regeneration GO:0031101 p=5.7E−03 n=2 fg=0.05 bg=0.00
posterior lateral line development GO:0048916 p=5.7E−03 n=2 fg=0.05 bg=0.00
definitive hemopoiesis GO:0060216 p=5.7E−03 n=2 fg=0.05 bg=0.00
positive regulation of animal organ morp... GO:0110110 p=5.7E−03 n=2 fg=0.05 bg=0.00
regulation of oocyte maturation GO:1900193 p=5.7E−03 n=2 fg=0.05 bg=0.00
regulation of protein stability GO:0031647 p=6.2E−03 n=5 fg=0.12 bg=0.03
mesodermal cell migration GO:0008078 p=7.2E−03 n=2 fg=0.05 bg=0.00
embryo implantation GO:0007566 p=7.2E−03 n=2 fg=0.05 bg=0.00
plasma membrane invagination GO:0099024 p=7.6E−03 n=3 fg=0.07 bg=0.01
protein modification by small protein co... GO:0070647 p=8.2E−03 n=9 fg=0.23 bg=0.09
modification−dependent protein catabolic... GO:0019941 p=8.3E−03 n=7 fg=0.17 bg=0.06
liver regeneration GO:0097421 p=8.9E−03 n=2 fg=0.05 bg=0.00
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organelle assembly GO:0070925 p=1.0E−02 n=9 fg=0.23 bg=0.09
regulation of extrinsic apoptotic signal... GO:2001236 p=1.0E−02 n=3 fg=0.07 bg=0.01
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n=40/147 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032375721.2
fraction genes in fg and expected valu
transferrin receptor binding GO:1990459 p=6.3E−04 n=2 fg=0.06 bg=0.00
mRNA 3'−UTR binding GO:0003730 p=1.4E−03 n=3 fg=0.09 bg=0.01
ubiquitin protein ligase activity GO:0061630 p=3.6E−03 n=5 fg=0.14 bg=0.03
sequence−specific double−stranded DNA bi... GO:1990837 p=7.5E−03 n=6 fg=0.17 bg=0.05
transcription regulatory region nucleic ... GO:0001067 p=1.1E−02 n=6 fg=0.17 bg=0.05
arylformamidase activity GO:0004061 p=1.5E−02 n=1 fg=0.03 bg=0.00
pyrimidine nucleotide binding GO:0019103 p=1.5E−02 n=1 fg=0.03 bg=0.00
ubiquitin−like protein−specific endopept... GO:0070137 p=1.5E−02 n=1 fg=0.03 bg=0.00
SUMO−specific endopeptidase activity GO:0070139 p=1.5E−02 n=1 fg=0.03 bg=0.00
histone serine kinase activity GO:0035174 p=1.5E−02 n=1 fg=0.03 bg=0.00
histone kinase activity (H3−S10 specific... GO:0035175 p=1.5E−02 n=1 fg=0.03 bg=0.00
interleukin−2 receptor binding GO:0005134 p=1.5E−02 n=1 fg=0.03 bg=0.00
glycogenin glucosyltransferase activity GO:0008466 p=1.5E−02 n=1 fg=0.03 bg=0.00
mannose−6−phosphate isomerase activity GO:0004476 p=1.5E−02 n=1 fg=0.03 bg=0.00
ATP−dependent peptidase activity GO:0004176 p=1.5E−02 n=1 fg=0.03 bg=0.00
mitochondrial promoter sequence−specific... GO:0001018 p=1.5E−02 n=1 fg=0.03 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=1.5E−02 n=1 fg=0.03 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016861 p=1.5E−02 n=1 fg=0.03 bg=0.00
protein phosphatase regulator activity GO:0019888 p=2.0E−02 n=2 fg=0.06 bg=0.01
growth factor receptor binding GO:0070851 p=2.2E−02 n=2 fg=0.06 bg=0.01
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isopeptidase activity GO:0070122 p=2.9E−02 n=1 fg=0.03 bg=0.00
leptin receptor binding GO:1990460 p=2.9E−02 n=1 fg=0.03 bg=0.00
phosphatidate phosphatase activity GO:0008195 p=2.9E−02 n=1 fg=0.03 bg=0.00
deSUMOylase activity GO:0016929 p=2.9E−02 n=1 fg=0.03 bg=0.00
DNA demethylase activity GO:0035514 p=2.9E−02 n=1 fg=0.03 bg=0.00
angiotensin receptor binding GO:0031701 p=2.9E−02 n=1 fg=0.03 bg=0.00
type 1 angiotensin receptor binding GO:0031702 p=2.9E−02 n=1 fg=0.03 bg=0.00
ferrous iron transmembrane transporter a... GO:0015093 p=2.9E−02 n=1 fg=0.03 bg=0.00
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032375721.2
fraction genes in fg and expected valu
protein phosphatase type 2A complex GO:0000159 p=2.2E−03 n=2 fg=0.05 bg=0.00
excitatory synapse GO:0060076 p=4.5E−03 n=2 fg=0.05 bg=0.00
contractile ring GO:0070938 p=5.9E−03 n=2 fg=0.05 bg=0.00
chromocenter GO:0010369 p=7.6E−03 n=2 fg=0.05 bg=0.00
centriole GO:0005814 p=1.1E−02 n=3 fg=0.07 bg=0.01
chromaffin granule GO:0042583 p=1.5E−02 n=1 fg=0.02 bg=0.00
chromaffin granule membrane GO:0042584 p=1.5E−02 n=1 fg=0.02 bg=0.00
meiotic spindle midzone GO:1990385 p=1.5E−02 n=1 fg=0.02 bg=0.00
axon hillock GO:0043203 p=1.5E−02 n=1 fg=0.02 bg=0.00
chromosome passenger complex GO:0032133 p=1.5E−02 n=1 fg=0.02 bg=0.00
cytoplasm GO:0005737 p=2.0E−02 n=38 fg=0.93 bg=0.80
P granule GO:0043186 p=2.4E−02 n=2 fg=0.05 bg=0.01
receptor complex GO:0043235 p=2.6E−02 n=3 fg=0.07 bg=0.02
pole plasm GO:0045495 p=2.6E−02 n=2 fg=0.05 bg=0.01
germ plasm GO:0060293 p=2.6E−02 n=2 fg=0.05 bg=0.01
cytosolic region GO:0099522 p=3.0E−02 n=1 fg=0.02 bg=0.00
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zona pellucida receptor complex GO:0002199 p=4.5E−02 n=1 fg=0.02 bg=0.00
lamellipodium GO:0030027 p=4.5E−02 n=3 fg=0.07 bg=0.02
cytoplasmic ribonucleoprotein granule GO:0036464 p=5.9E−02 n=3 fg=0.07 bg=0.02
pi−body GO:0071546 p=5.9E−02 n=1 fg=0.02 bg=0.00
chromatoid body GO:0033391 p=5.9E−02 n=1 fg=0.02 bg=0.00
alpha DNA polymerase:primase complex GO:0005658 p=5.9E−02 n=1 fg=0.02 bg=0.00
sperm head GO:0061827 p=5.9E−02 n=1 fg=0.02 bg=0.00
growth cone membrane GO:0032584 p=5.9E−02 n=1 fg=0.02 bg=0.00
ribonucleoprotein complex GO:1990904 p=6.6E−02 n=7 fg=0.17 bg=0.09
ribonucleoprotein granule GO:0035770 p=6.6E−02 n=3 fg=0.07 bg=0.02
nuclear proteasome complex GO:0031595 p=7.4E−02 n=1 fg=0.02 bg=0.00
anchored component of plasma membrane GO:0046658 p=7.4E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=41/147 input genes with annotations
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fraction