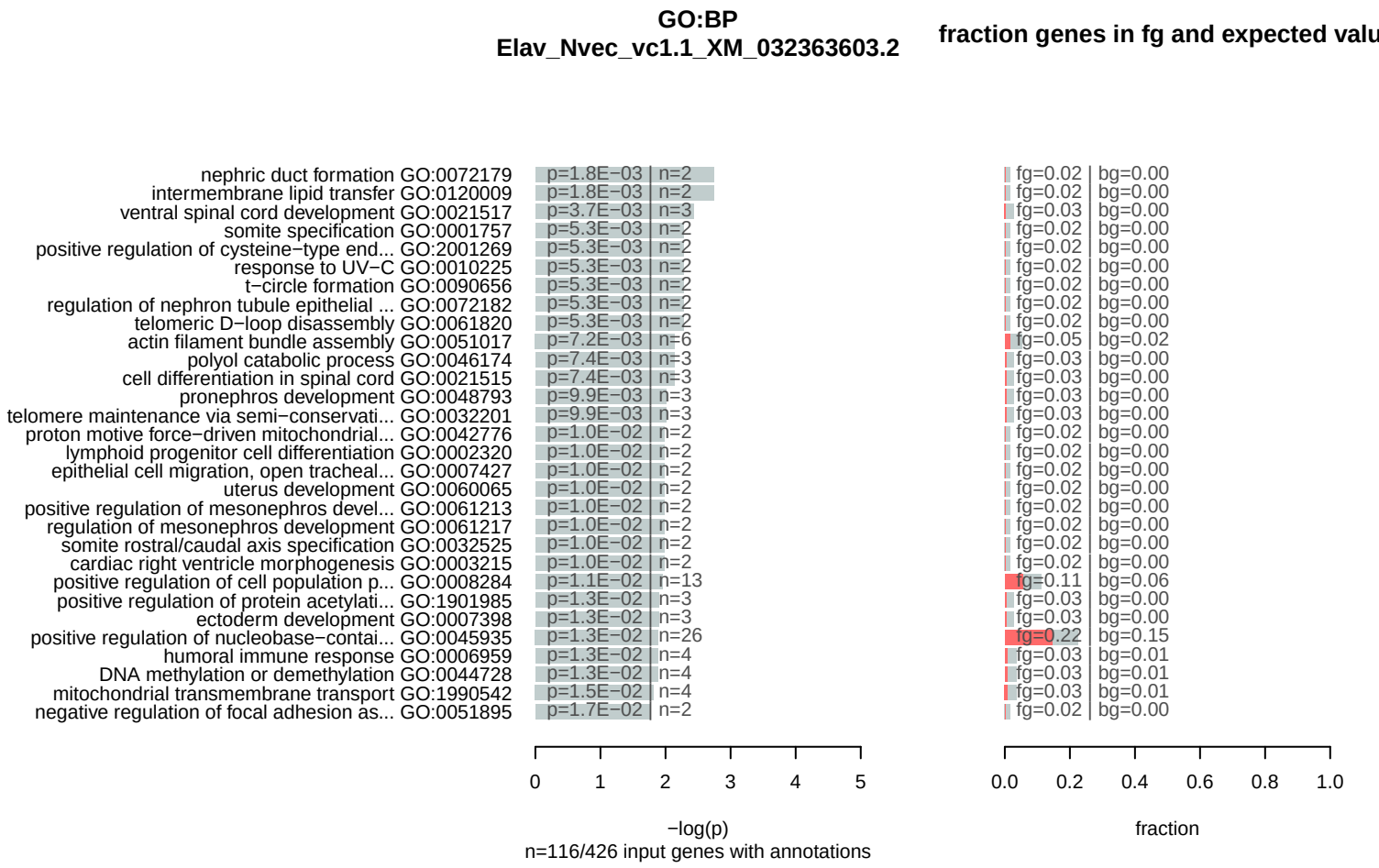
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ventral spinal cord development GO:0021517 p=3.7E−03 n=3 fg=0.03 bg=0.00
somite specification GO:0001757 p=5.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of cysteine−type end... GO:2001269 p=5.3E−03 n=2 fg=0.02 bg=0.00
response to UV−C GO:0010225 p=5.3E−03 n=2 fg=0.02 bg=0.00
t−circle formation GO:0090656 p=5.3E−03 n=2 fg=0.02 bg=0.00
regulation of nephron tubule epithelial ... GO:0072182 p=5.3E−03 n=2 fg=0.02 bg=0.00
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actin filament bundle assembly GO:0051017 p=7.2E−03 n=6 fg=0.05 bg=0.02
polyol catabolic process GO:0046174 p=7.4E−03 n=3 fg=0.03 bg=0.00
cell differentiation in spinal cord GO:0021515 p=7.4E−03 n=3 fg=0.03 bg=0.00
pronephros development GO:0048793 p=9.9E−03 n=3 fg=0.03 bg=0.00
telomere maintenance via semi−conservati... GO:0032201 p=9.9E−03 n=3 fg=0.03 bg=0.00
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lymphoid progenitor cell differentiation GO:0002320 p=1.0E−02 n=2 fg=0.02 bg=0.00
epithelial cell migration, open tracheal... GO:0007427 p=1.0E−02 n=2 fg=0.02 bg=0.00
uterus development GO:0060065 p=1.0E−02 n=2 fg=0.02 bg=0.00
positive regulation of mesonephros devel... GO:0061213 p=1.0E−02 n=2 fg=0.02 bg=0.00
regulation of mesonephros development GO:0061217 p=1.0E−02 n=2 fg=0.02 bg=0.00
somite rostral/caudal axis specification GO:0032525 p=1.0E−02 n=2 fg=0.02 bg=0.00
cardiac right ventricle morphogenesis GO:0003215 p=1.0E−02 n=2 fg=0.02 bg=0.00
positive regulation of cell population p... GO:0008284 p=1.1E−02 n=13 fg=0.11 bg=0.06
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ectoderm development GO:0007398 p=1.3E−02 n=3 fg=0.03 bg=0.00
positive regulation of nucleobase−contai... GO:0045935 p=1.3E−02 n=26 fg=0.22 bg=0.15
humoral immune response GO:0006959 p=1.3E−02 n=4 fg=0.03 bg=0.01
DNA methylation or demethylation GO:0044728 p=1.3E−02 n=4 fg=0.03 bg=0.01
mitochondrial transmembrane transport GO:1990542 p=1.5E−02 n=4 fg=0.03 bg=0.01
negative regulation of focal adhesion as... GO:0051895 p=1.7E−02 n=2 fg=0.02 bg=0.00
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fraction
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Elav_Nvec_vc1.1_XM_032363603.2
fraction genes in fg and expected valu
inositol bisphosphate phosphatase activi... GO:0016312 p=1.8E−03 n=2 fg=0.02 bg=0.00
transcription coregulator activity GO:0003712 p=1.1E−02 n=11 fg=0.11 bg=0.05
nuclear receptor coactivator activity GO:0030374 p=1.3E−02 n=3 fg=0.03 bg=0.01
mRNA binding GO:0003729 p=1.3E−02 n=8 fg=0.08 bg=0.03
transcription coactivator activity GO:0003713 p=1.5E−02 n=8 fg=0.08 bg=0.03
actin monomer binding GO:0003785 p=1.7E−02 n=2 fg=0.02 bg=0.00
E−box binding GO:0070888 p=1.9E−02 n=3 fg=0.03 bg=0.01
nucleotidyltransferase activity GO:0016779 p=2.3E−02 n=5 fg=0.05 bg=0.02
lipid transfer activity GO:0120013 p=2.4E−02 n=2 fg=0.02 bg=0.00
protein tyrosine/serine/threonine phosph... GO:0008138 p=3.3E−02 n=2 fg=0.02 bg=0.00
HMG box domain binding GO:0071837 p=3.3E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol bisphosphate phosph... GO:0034593 p=4.3E−02 n=2 fg=0.02 bg=0.00
carboxy−lyase activity GO:0016831 p=4.3E−02 n=2 fg=0.02 bg=0.00
sphingolipid transfer activity GO:0120016 p=4.3E−02 n=1 fg=0.01 bg=0.00
ceramide transfer activity GO:0120017 p=4.3E−02 n=1 fg=0.01 bg=0.00
3'−flap−structured DNA binding GO:0070337 p=4.3E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=4.3E−02 n=1 fg=0.01 bg=0.00
interleukin−2 receptor binding GO:0005134 p=4.3E−02 n=1 fg=0.01 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=4.3E−02 n=1 fg=0.01 bg=0.00
sphingolipid transporter activity GO:0046624 p=4.3E−02 n=1 fg=0.01 bg=0.00
telomeric G−quadruplex DNA binding GO:0061849 p=4.3E−02 n=1 fg=0.01 bg=0.00
BIR domain binding GO:1990525 p=4.3E−02 n=1 fg=0.01 bg=0.00
UDP−glucose:hexose−1−phosphate uridylylt... GO:0008108 p=4.3E−02 n=1 fg=0.01 bg=0.00
galactose binding GO:0005534 p=4.3E−02 n=1 fg=0.01 bg=0.00
FAD transmembrane transporter activity GO:0015230 p=4.3E−02 n=1 fg=0.01 bg=0.00
D5 dopamine receptor binding GO:0031752 p=4.3E−02 n=1 fg=0.01 bg=0.00
molybdopterin cofactor binding GO:0043546 p=4.3E−02 n=1 fg=0.01 bg=0.00
polynucleotide phosphatase activity GO:0098518 p=4.3E−02 n=1 fg=0.01 bg=0.00
8−hydroxy−2'−deoxyguanosine DNA binding GO:1905773 p=4.3E−02 n=1 fg=0.01 bg=0.00
sulfite oxidase activity GO:0008482 p=4.3E−02 n=1 fg=0.01 bg=0.00
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n=101/426 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032363603.2
fraction genes in fg and expected valu
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NuRD complex GO:0016581 p=1.0E−02 n=2 fg=0.02 bg=0.00
exon−exon junction complex GO:0035145 p=1.0E−02 n=2 fg=0.02 bg=0.00
ruffle membrane GO:0032587 p=1.2E−02 n=3 fg=0.03 bg=0.00
chromosome, telomeric region GO:0000781 p=2.4E−02 n=3 fg=0.03 bg=0.01
Derlin−1 retrotranslocation complex GO:0036513 p=2.4E−02 n=2 fg=0.02 bg=0.00
ruffle GO:0001726 p=3.3E−02 n=4 fg=0.03 bg=0.01
chaperone complex GO:0101031 p=3.3E−02 n=2 fg=0.02 bg=0.00
myelin sheath GO:0043209 p=3.7E−02 n=5 fg=0.04 bg=0.02
mitochondrial proton−transporting ATP sy... GO:0005756 p=4.3E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=4.3E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=4.3E−02 n=1 fg=0.01 bg=0.00
SAM complex GO:0001401 p=4.3E−02 n=1 fg=0.01 bg=0.00
mitochondrial proton−transporting ATP sy... GO:0000276 p=4.3E−02 n=1 fg=0.01 bg=0.00
signal recognition particle GO:0048500 p=4.3E−02 n=1 fg=0.01 bg=0.00
serine−type endopeptidase complex GO:1905370 p=4.3E−02 n=1 fg=0.01 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=4.3E−02 n=1 fg=0.01 bg=0.00
serine−type peptidase complex GO:1905286 p=4.3E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase complex... GO:0045263 p=4.3E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase, centra... GO:0045269 p=4.3E−02 n=1 fg=0.01 bg=0.00
replication fork GO:0005657 p=4.4E−02 n=3 fg=0.03 bg=0.01
membrane−bounded organelle GO:0043227 p=5.3E−02 n=99 fg=0.86 bg=0.80
nucleus GO:0005634 p=5.9E−02 n=66 fg=0.57 bg=0.50
transcription regulator complex GO:0005667 p=6.0E−02 n=8 fg=0.07 bg=0.04
nuclear speck GO:0016607 p=6.4E−02 n=7 fg=0.06 bg=0.03
striated muscle dense body GO:0055120 p=6.5E−02 n=2 fg=0.02 bg=0.00
caveola GO:0005901 p=7.2E−02 n=3 fg=0.03 bg=0.01
recycling endosome membrane GO:0055038 p=7.7E−02 n=2 fg=0.02 bg=0.00
lipid droplet GO:0005811 p=8.0E−02 n=3 fg=0.03 bg=0.01
origin recognition complex GO:0000808 p=8.3E−02 n=1 fg=0.01 bg=0.00
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n=115/426 input genes with annotations
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fraction