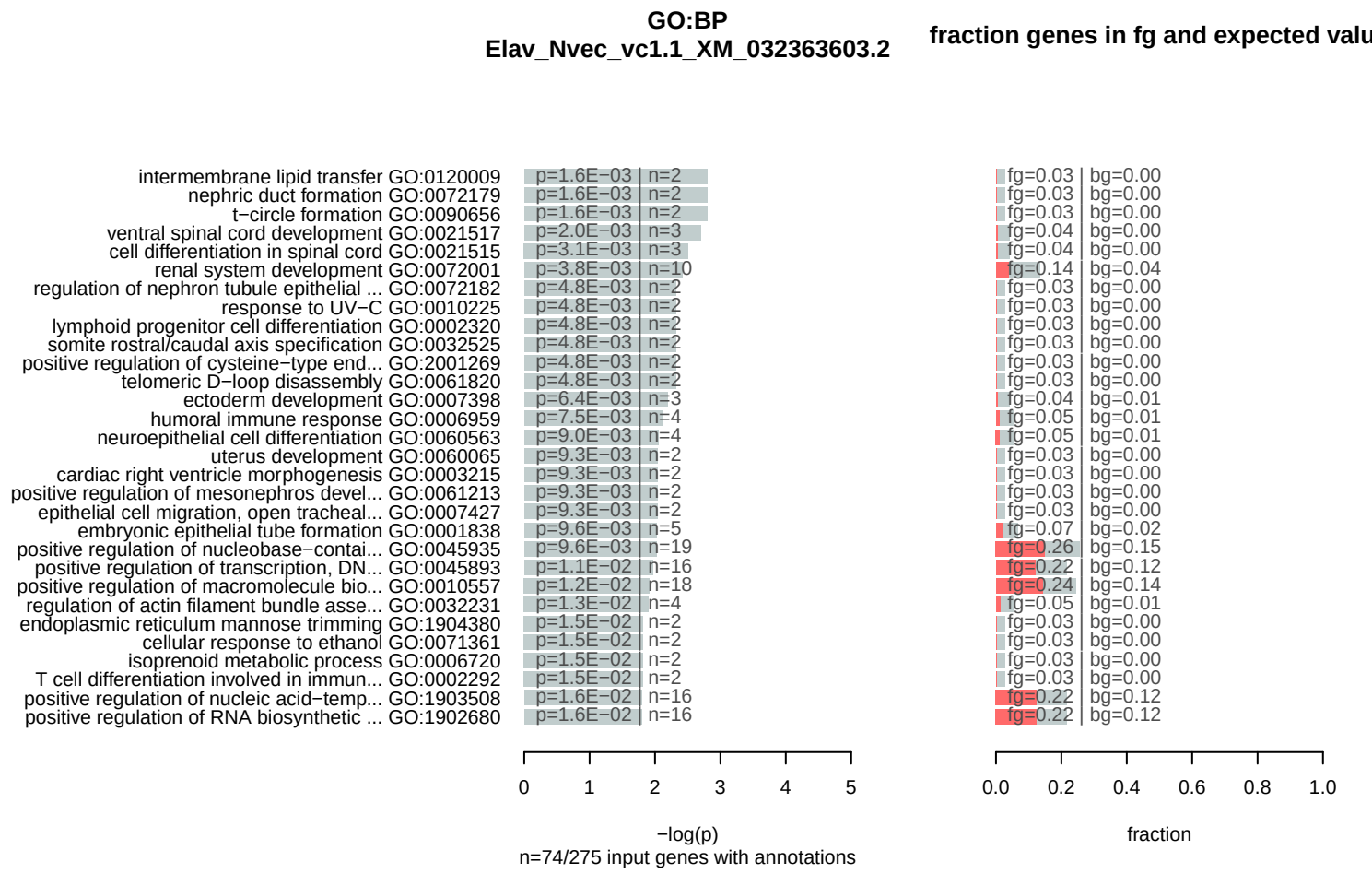
GO:BP
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fraction genes in fg and expected valu
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nephric duct formation GO:0072179 p=1.6E−03 n=2 fg=0.03 bg=0.00
t−circle formation GO:0090656 p=1.6E−03 n=2 fg=0.03 bg=0.00
ventral spinal cord development GO:0021517 p=2.0E−03 n=3 fg=0.04 bg=0.00
cell differentiation in spinal cord GO:0021515 p=3.1E−03 n=3 fg=0.04 bg=0.00
renal system development GO:0072001 p=3.8E−03 n=10 fg=0.14 bg=0.04
regulation of nephron tubule epithelial ... GO:0072182 p=4.8E−03 n=2 fg=0.03 bg=0.00
response to UV−C GO:0010225 p=4.8E−03 n=2 fg=0.03 bg=0.00
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somite rostral/caudal axis specification GO:0032525 p=4.8E−03 n=2 fg=0.03 bg=0.00
positive regulation of cysteine−type end... GO:2001269 p=4.8E−03 n=2 fg=0.03 bg=0.00
telomeric D−loop disassembly GO:0061820 p=4.8E−03 n=2 fg=0.03 bg=0.00
ectoderm development GO:0007398 p=6.4E−03 n=3 fg=0.04 bg=0.01
humoral immune response GO:0006959 p=7.5E−03 n=4 fg=0.05 bg=0.01
neuroepithelial cell differentiation GO:0060563 p=9.0E−03 n=4 fg=0.05 bg=0.01
uterus development GO:0060065 p=9.3E−03 n=2 fg=0.03 bg=0.00
cardiac right ventricle morphogenesis GO:0003215 p=9.3E−03 n=2 fg=0.03 bg=0.00
positive regulation of mesonephros devel... GO:0061213 p=9.3E−03 n=2 fg=0.03 bg=0.00
epithelial cell migration, open tracheal... GO:0007427 p=9.3E−03 n=2 fg=0.03 bg=0.00
embryonic epithelial tube formation GO:0001838 p=9.6E−03 n=5 fg=0.07 bg=0.02
positive regulation of nucleobase−contai... GO:0045935 p=9.6E−03 n=19 fg=0.26 bg=0.15
positive regulation of transcription, DN... GO:0045893 p=1.1E−02 n=16 fg=0.22 bg=0.12
positive regulation of macromolecule bio... GO:0010557 p=1.2E−02 n=18 fg=0.24 bg=0.14
regulation of actin filament bundle asse... GO:0032231 p=1.3E−02 n=4 fg=0.05 bg=0.01
endoplasmic reticulum mannose trimming GO:1904380 p=1.5E−02 n=2 fg=0.03 bg=0.00
cellular response to ethanol GO:0071361 p=1.5E−02 n=2 fg=0.03 bg=0.00
isoprenoid metabolic process GO:0006720 p=1.5E−02 n=2 fg=0.03 bg=0.00
T cell differentiation involved in immun... GO:0002292 p=1.5E−02 n=2 fg=0.03 bg=0.00
positive regulation of nucleic acid−temp... GO:1903508 p=1.6E−02 n=16 fg=0.22 bg=0.12
positive regulation of RNA biosynthetic ... GO:1902680 p=1.6E−02 n=16 fg=0.22 bg=0.12
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n=74/275 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032363603.2
fraction genes in fg and expected valu
E−box binding GO:0070888 p=4.2E−03 n=3 fg=0.05 bg=0.01
nuclear receptor coactivator activity GO:0030374 p=4.2E−03 n=3 fg=0.05 bg=0.01
lipid transfer activity GO:0120013 p=1.4E−02 n=2 fg=0.03 bg=0.00
structural constituent of nuclear pore GO:0017056 p=1.4E−02 n=2 fg=0.03 bg=0.00
telomeric DNA binding GO:0042162 p=1.4E−02 n=2 fg=0.03 bg=0.00
manganese ion binding GO:0030145 p=1.9E−02 n=3 fg=0.05 bg=0.01
HMG box domain binding GO:0071837 p=2.1E−02 n=2 fg=0.03 bg=0.00
carboxy−lyase activity GO:0016831 p=2.1E−02 n=2 fg=0.03 bg=0.00
DNA−binding transcription factor activit... GO:0000981 p=2.2E−02 n=9 fg=0.14 bg=0.07
damaged DNA binding GO:0003684 p=3.7E−02 n=2 fg=0.03 bg=0.01
transcription coactivator activity GO:0003713 p=3.8E−02 n=8 fg=0.13 bg=0.04
four−way junction DNA binding GO:0000400 p=4.0E−02 n=1 fg=0.02 bg=0.00
forked DNA−dependent helicase activity GO:0061749 p=4.0E−02 n=1 fg=0.02 bg=0.00
fibroblast growth factor receptor bindin... GO:0005104 p=4.0E−02 n=1 fg=0.02 bg=0.00
sphingomyelin phosphodiesterase D activi... GO:0050290 p=4.0E−02 n=1 fg=0.02 bg=0.00
sphingolipid transfer activity GO:0120016 p=4.0E−02 n=1 fg=0.02 bg=0.00
ceramide transfer activity GO:0120017 p=4.0E−02 n=1 fg=0.02 bg=0.00
signal recognition particle binding GO:0005047 p=4.0E−02 n=1 fg=0.02 bg=0.00
heparanase activity GO:0030305 p=4.0E−02 n=1 fg=0.02 bg=0.00
G−protein beta−subunit binding GO:0031681 p=4.0E−02 n=1 fg=0.02 bg=0.00
polynucleotide 5'−phosphatase activity GO:0004651 p=4.0E−02 n=1 fg=0.02 bg=0.00
molybdopterin cofactor binding GO:0043546 p=4.0E−02 n=1 fg=0.02 bg=0.00
7S RNA binding GO:0008312 p=4.0E−02 n=1 fg=0.02 bg=0.00
polynucleotide phosphatase activity GO:0098518 p=4.0E−02 n=1 fg=0.02 bg=0.00
BIR domain binding GO:1990525 p=4.0E−02 n=1 fg=0.02 bg=0.00
8−hydroxy−2'−deoxyguanosine DNA binding GO:1905773 p=4.0E−02 n=1 fg=0.02 bg=0.00
glycolipid transfer activity GO:0017089 p=4.0E−02 n=1 fg=0.02 bg=0.00
mevalonate kinase activity GO:0004496 p=4.0E−02 n=1 fg=0.02 bg=0.00
flap−structured DNA binding GO:0070336 p=4.0E−02 n=1 fg=0.02 bg=0.00
3'−flap−structured DNA binding GO:0070337 p=4.0E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=63/275 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032363603.2
fraction genes in fg and expected valu
NuRD complex GO:0016581 p=4.7E−03 n=2 fg=0.03 bg=0.00
intracellular membrane−bounded organelle GO:0043231 p=5.3E−03 n=66 fg=0.90 bg=0.78
ruffle membrane GO:0032587 p=6.2E−03 n=3 fg=0.04 bg=0.01
nucleus GO:0005634 p=1.6E−02 n=45 fg=0.62 bg=0.48
Derlin−1 retrotranslocation complex GO:0036513 p=2.2E−02 n=2 fg=0.03 bg=0.00
nuclear speck GO:0016607 p=3.4E−02 n=6 fg=0.08 bg=0.03
lipid droplet GO:0005811 p=3.8E−02 n=3 fg=0.04 bg=0.01
chromosome, telomeric region GO:0000781 p=3.8E−02 n=2 fg=0.03 bg=0.00
signal recognition particle GO:0048500 p=4.0E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=4.0E−02 n=1 fg=0.01 bg=0.00
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mitochondrial outer membrane translocase... GO:0005742 p=4.0E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=4.0E−02 n=1 fg=0.01 bg=0.00
serine−type endopeptidase complex GO:1905370 p=4.0E−02 n=1 fg=0.01 bg=0.00
serine−type peptidase complex GO:1905286 p=4.0E−02 n=1 fg=0.01 bg=0.00
outer mitochondrial membrane protein com... GO:0098799 p=4.0E−02 n=1 fg=0.01 bg=0.00
recycling endosome membrane GO:0055038 p=4.8E−02 n=2 fg=0.03 bg=0.00
type I terminal bouton GO:0061174 p=5.9E−02 n=2 fg=0.03 bg=0.01
mitochondrion GO:0005739 p=5.9E−02 n=15 fg=0.21 bg=0.14
transcription regulator complex GO:0005667 p=6.7E−02 n=8 fg=0.11 bg=0.04
endoplasmic reticulum protein−containing... GO:0140534 p=7.7E−02 n=3 fg=0.04 bg=0.01
glycosylphosphatidylinositol−N−acetylglu... GO:0000506 p=7.9E−02 n=1 fg=0.01 bg=0.00
Nebenkern GO:0016006 p=7.9E−02 n=1 fg=0.01 bg=0.00
mitochondrial derivative GO:0016007 p=7.9E−02 n=1 fg=0.01 bg=0.00
extrinsic component of membrane GO:0019898 p=8.6E−02 n=4 fg=0.05 bg=0.02
nuclear body GO:0016604 p=8.7E−02 n=8 fg=0.11 bg=0.06
transcription repressor complex GO:0017053 p=9.4E−02 n=2 fg=0.03 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=1.0E−01 n=9 fg=0.12 bg=0.08
mitochondrial intermembrane space GO:0005758 p=1.1E−01 n=2 fg=0.03 bg=0.01
extracellular matrix GO:0031012 p=1.1E−01 n=2 fg=0.03 bg=0.01
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−log(p)
n=73/275 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction