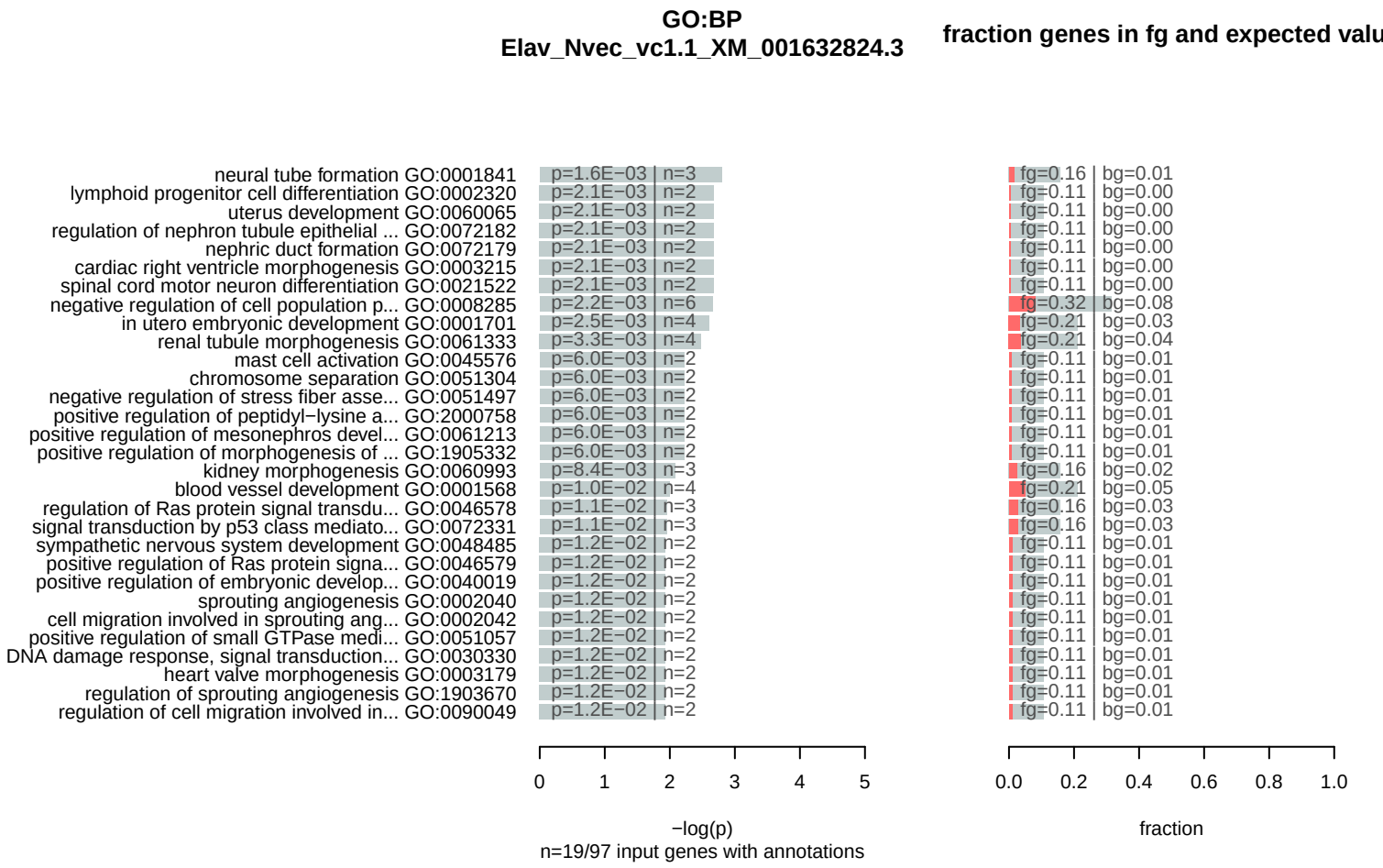
GO:BP
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fraction genes in fg and expected valu
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lymphoid progenitor cell differentiation GO:0002320 p=2.1E−03 n=2 fg=0.11 bg=0.00
uterus development GO:0060065 p=2.1E−03 n=2 fg=0.11 bg=0.00
regulation of nephron tubule epithelial ... GO:0072182 p=2.1E−03 n=2 fg=0.11 bg=0.00
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cardiac right ventricle morphogenesis GO:0003215 p=2.1E−03 n=2 fg=0.11 bg=0.00
spinal cord motor neuron differentiation GO:0021522 p=2.1E−03 n=2 fg=0.11 bg=0.00
negative regulation of cell population p... GO:0008285 p=2.2E−03 n=6 fg=0.32 bg=0.08
in utero embryonic development GO:0001701 p=2.5E−03 n=4 fg=0.21 bg=0.03
renal tubule morphogenesis GO:0061333 p=3.3E−03 n=4 fg=0.21 bg=0.04
mast cell activation GO:0045576 p=6.0E−03 n=2 fg=0.11 bg=0.01
chromosome separation GO:0051304 p=6.0E−03 n=2 fg=0.11 bg=0.01
negative regulation of stress fiber asse... GO:0051497 p=6.0E−03 n=2 fg=0.11 bg=0.01
positive regulation of peptidyl−lysine a... GO:2000758 p=6.0E−03 n=2 fg=0.11 bg=0.01
positive regulation of mesonephros devel... GO:0061213 p=6.0E−03 n=2 fg=0.11 bg=0.01
positive regulation of morphogenesis of ... GO:1905332 p=6.0E−03 n=2 fg=0.11 bg=0.01
kidney morphogenesis GO:0060993 p=8.4E−03 n=3 fg=0.16 bg=0.02
blood vessel development GO:0001568 p=1.0E−02 n=4 fg=0.21 bg=0.05
regulation of Ras protein signal transdu... GO:0046578 p=1.1E−02 n=3 fg=0.16 bg=0.03
signal transduction by p53 class mediato... GO:0072331 p=1.1E−02 n=3 fg=0.16 bg=0.03
sympathetic nervous system development GO:0048485 p=1.2E−02 n=2 fg=0.11 bg=0.01
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sprouting angiogenesis GO:0002040 p=1.2E−02 n=2 fg=0.11 bg=0.01
cell migration involved in sprouting ang... GO:0002042 p=1.2E−02 n=2 fg=0.11 bg=0.01
positive regulation of small GTPase medi... GO:0051057 p=1.2E−02 n=2 fg=0.11 bg=0.01
DNA damage response, signal transduction... GO:0030330 p=1.2E−02 n=2 fg=0.11 bg=0.01
heart valve morphogenesis GO:0003179 p=1.2E−02 n=2 fg=0.11 bg=0.01
regulation of sprouting angiogenesis GO:1903670 p=1.2E−02 n=2 fg=0.11 bg=0.01
regulation of cell migration involved in... GO:0090049 p=1.2E−02 n=2 fg=0.11 bg=0.01
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n=19/97 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
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transcription coregulator activity GO:0003712 p=2.8E−02 n=4 fg=0.22 bg=0.07
core promoter sequence−specific DNA bind... GO:0001046 p=3.1E−02 n=2 fg=0.11 bg=0.02
oxidoreductase activity, acting on the C... GO:0016616 p=4.9E−02 n=1 fg=0.06 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=4.9E−02 n=1 fg=0.06 bg=0.00
electron transfer activity GO:0009055 p=4.9E−02 n=1 fg=0.06 bg=0.00
phospholipase binding GO:0043274 p=4.9E−02 n=1 fg=0.06 bg=0.00
inositol−1,4,5−trisphosphate 5−phosphata... GO:0052658 p=4.9E−02 n=1 fg=0.06 bg=0.00
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lipid phosphatase activity GO:0042577 p=4.9E−02 n=1 fg=0.06 bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0034485 p=4.9E−02 n=1 fg=0.06 bg=0.00
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NAD binding GO:0051287 p=4.9E−02 n=1 fg=0.06 bg=0.00
nuclear receptor coactivator activity GO:0030374 p=4.9E−02 n=1 fg=0.06 bg=0.00
SH2 domain binding GO:0042169 p=4.9E−02 n=1 fg=0.06 bg=0.00
vinculin binding GO:0017166 p=4.9E−02 n=1 fg=0.06 bg=0.00
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phosphatidylinositol−4,5−bisphosphate ph... GO:0106019 p=4.9E−02 n=1 fg=0.06 bg=0.00
glycolipid transfer activity GO:0017089 p=4.9E−02 n=1 fg=0.06 bg=0.00
NADP binding GO:0050661 p=4.9E−02 n=1 fg=0.06 bg=0.00
malic enzyme activity GO:0004470 p=4.9E−02 n=1 fg=0.06 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=4.9E−02 n=1 fg=0.06 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004473 p=4.9E−02 n=1 fg=0.06 bg=0.00
glycolipid binding GO:0051861 p=4.9E−02 n=1 fg=0.06 bg=0.00
interleukin−2 receptor binding GO:0005134 p=4.9E−02 n=1 fg=0.06 bg=0.00
intronic transcription regulatory region... GO:0001161 p=4.9E−02 n=1 fg=0.06 bg=0.00
RNA polymerase II intronic transcription... GO:0001162 p=4.9E−02 n=1 fg=0.06 bg=0.00
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−log(p)
n=18/97 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_001632824.3
fraction genes in fg and expected valu
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adherens junction GO:0005912 p=1.0E−02 n=3 fg=0.15 bg=0.03
ruffle membrane GO:0032587 p=1.3E−02 n=2 fg=0.10 bg=0.01
nucleus GO:0005634 p=2.2E−02 n=14 fg=0.70 bg=0.46
NuRD complex GO:0016581 p=5.0E−02 n=1 fg=0.05 bg=0.00
presynaptic active zone membrane GO:0048787 p=5.0E−02 n=1 fg=0.05 bg=0.00
PML body GO:0016605 p=5.0E−02 n=1 fg=0.05 bg=0.00
CHD−type complex GO:0090545 p=5.0E−02 n=1 fg=0.05 bg=0.00
intracellular anatomical structure GO:0005622 p=7.4E−02 n=20 fg=1.00 bg=0.88
cytoskeleton GO:0005856 p=7.6E−02 n=5 fg=0.25 bg=0.12
cell−cell junction GO:0005911 p=7.9E−02 n=3 fg=0.15 bg=0.05
anchoring junction GO:0070161 p=7.9E−02 n=3 fg=0.15 bg=0.05
transcription regulator complex GO:0005667 p=8.8E−02 n=3 fg=0.15 bg=0.05
centriole GO:0005814 p=9.7E−02 n=1 fg=0.05 bg=0.01
SWI/SNF superfamily−type complex GO:0070603 p=9.7E−02 n=1 fg=0.05 bg=0.01
intrinsic component of the cytoplasmic s... GO:0031235 p=9.7E−02 n=1 fg=0.05 bg=0.01
ATPase complex GO:1904949 p=9.7E−02 n=1 fg=0.05 bg=0.01
dendrite terminus GO:0044292 p=9.7E−02 n=1 fg=0.05 bg=0.01
cortical actin cytoskeleton GO:0030864 p=9.7E−02 n=1 fg=0.05 bg=0.01
extrinsic component of membrane GO:0019898 p=9.9E−02 n=2 fg=0.10 bg=0.03
intracellular organelle GO:0043229 p=1.2E−01 n=18 fg=0.90 bg=0.77
non−membrane−bounded organelle GO:0043228 p=1.4E−01 n=8 fg=0.40 bg=0.27
intracellular non−membrane−bounded organ... GO:0043232 p=1.4E−01 n=8 fg=0.40 bg=0.27
recycling endosome membrane GO:0055038 p=1.4E−01 n=1 fg=0.05 bg=0.01
filopodium GO:0030175 p=1.4E−01 n=1 fg=0.05 bg=0.01
histone deacetylase complex GO:0000118 p=1.4E−01 n=1 fg=0.05 bg=0.01
cortical cytoskeleton GO:0030863 p=1.4E−01 n=1 fg=0.05 bg=0.01
leading edge membrane GO:0031256 p=1.5E−01 n=2 fg=0.10 bg=0.03
actin cytoskeleton GO:0015629 p=1.5E−01 n=2 fg=0.10 bg=0.03
organelle GO:0043226 p=1.5E−01 n=18 fg=0.90 bg=0.78
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n=20/97 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction