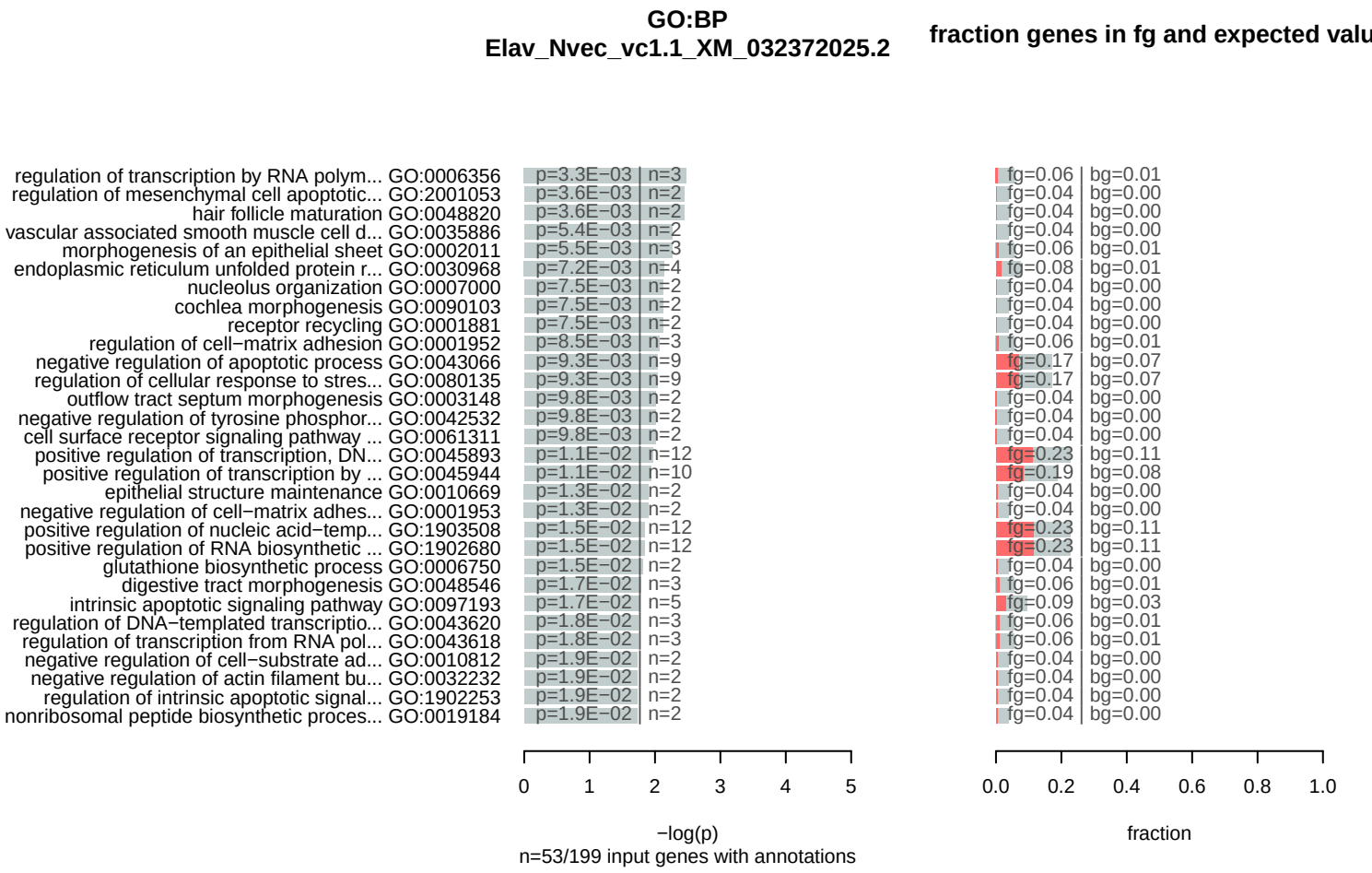
GO:BP
Elav_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
regulation of transcription by RNA polym... GO:0006356 p=3.3E−03 n=3 fg=0.06 bg=0.01
regulation of mesenchymal cell apoptotic... GO:2001053 p=3.6E−03 n=2 fg=0.04 bg=0.00
hair follicle maturation GO:0048820 p=3.6E−03 n=2 fg=0.04 bg=0.00
vascular associated smooth muscle cell d... GO:0035886 p=5.4E−03 n=2 fg=0.04 bg=0.00
morphogenesis of an epithelial sheet GO:0002011 p=5.5E−03 n=3 fg=0.06 bg=0.01
endoplasmic reticulum unfolded protein r... GO:0030968 p=7.2E−03 n=4 fg=0.08 bg=0.01
nucleolus organization GO:0007000 p=7.5E−03 n=2 fg=0.04 bg=0.00
cochlea morphogenesis GO:0090103 p=7.5E−03 n=2 fg=0.04 bg=0.00
receptor recycling GO:0001881 p=7.5E−03 n=2 fg=0.04 bg=0.00
regulation of cell−matrix adhesion GO:0001952 p=8.5E−03 n=3 fg=0.06 bg=0.01
negative regulation of apoptotic process GO:0043066 p=9.3E−03 n=9 fg=0.17 bg=0.07
regulation of cellular response to stres... GO:0080135 p=9.3E−03 n=9 fg=0.17 bg=0.07
outflow tract septum morphogenesis GO:0003148 p=9.8E−03 n=2 fg=0.04 bg=0.00
negative regulation of tyrosine phosphor... GO:0042532 p=9.8E−03 n=2 fg=0.04 bg=0.00
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positive regulation of transcription by ... GO:0045944 p=1.1E−02 n=10 fg=0.19 bg=0.08
epithelial structure maintenance GO:0010669 p=1.3E−02 n=2 fg=0.04 bg=0.00
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positive regulation of nucleic acid−temp... GO:1903508 p=1.5E−02 n=12 fg=0.23 bg=0.11
positive regulation of RNA biosynthetic ... GO:1902680 p=1.5E−02 n=12 fg=0.23 bg=0.11
glutathione biosynthetic process GO:0006750 p=1.5E−02 n=2 fg=0.04 bg=0.00
digestive tract morphogenesis GO:0048546 p=1.7E−02 n=3 fg=0.06 bg=0.01
intrinsic apoptotic signaling pathway GO:0097193 p=1.7E−02 n=5 fg=0.09 bg=0.03
regulation of DNA−templated transcriptio... GO:0043620 p=1.8E−02 n=3 fg=0.06 bg=0.01
regulation of transcription from RNA pol... GO:0043618 p=1.8E−02 n=3 fg=0.06 bg=0.01
negative regulation of cell−substrate ad... GO:0010812 p=1.9E−02 n=2 fg=0.04 bg=0.00
negative regulation of actin filament bu... GO:0032232 p=1.9E−02 n=2 fg=0.04 bg=0.00
regulation of intrinsic apoptotic signal... GO:1902253 p=1.9E−02 n=2 fg=0.04 bg=0.00
nonribosomal peptide biosynthetic proces... GO:0019184 p=1.9E−02 n=2 fg=0.04 bg=0.00
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n=53/199 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
transcription cis−regulatory region bind... GO:0000976 p=3.4E−03 n=7 fg=0.16 bg=0.05
DNA−binding transcription activator acti... GO:0001228 p=9.9E−03 n=5 fg=0.12 bg=0.03
pyrroline−5−carboxylate reductase activi... GO:0004735 p=1.8E−02 n=1 fg=0.02 bg=0.00
cytosine C−5 DNA demethylase activity GO:0051747 p=1.8E−02 n=1 fg=0.02 bg=0.00
JUN kinase kinase kinase activity GO:0004706 p=1.8E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=1.8E−02 n=1 fg=0.02 bg=0.00
methionine adenosyltransferase regulator... GO:0048270 p=1.8E−02 n=1 fg=0.02 bg=0.00
hydroxyacylglutathione hydrolase activit... GO:0004416 p=1.8E−02 n=1 fg=0.02 bg=0.00
8−oxo−7,8−dihydroguanine DNA N−glycosyla... GO:0034039 p=1.8E−02 n=1 fg=0.02 bg=0.00
RNA polymerase I general transcription i... GO:0001181 p=1.8E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide 1,2−alpha−manno... GO:0004571 p=1.8E−02 n=1 fg=0.02 bg=0.00
siRNA binding GO:0035197 p=1.8E−02 n=1 fg=0.02 bg=0.00
3'−5' exonuclease activity GO:0008408 p=2.9E−02 n=2 fg=0.05 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=3.1E−02 n=5 fg=0.12 bg=0.04
nuclease inhibitor activity GO:0140721 p=3.6E−02 n=1 fg=0.02 bg=0.00
volume−sensitive anion channel activity GO:0005225 p=3.6E−02 n=1 fg=0.02 bg=0.00
oxidized purine nucleobase lesion DNA N−... GO:0008534 p=3.6E−02 n=1 fg=0.02 bg=0.00
DNA−N1−methyladenine dioxygenase activit... GO:0043734 p=3.6E−02 n=1 fg=0.02 bg=0.00
class I DNA−(apurinic or apyrimidinic si... GO:0140078 p=3.6E−02 n=1 fg=0.02 bg=0.00
inositol monophosphate 4−phosphatase act... GO:0052833 p=3.6E−02 n=1 fg=0.02 bg=0.00
inositol monophosphate phosphatase activ... GO:0052834 p=3.6E−02 n=1 fg=0.02 bg=0.00
endoribonuclease inhibitor activity GO:0060698 p=3.6E−02 n=1 fg=0.02 bg=0.00
DNA demethylase activity GO:0035514 p=3.6E−02 n=1 fg=0.02 bg=0.00
ribonuclease inhibitor activity GO:0008428 p=3.6E−02 n=1 fg=0.02 bg=0.00
RNA polymerase I core binding GO:0001042 p=3.6E−02 n=1 fg=0.02 bg=0.00
gamma−glutamylcyclotransferase activity GO:0003839 p=3.6E−02 n=1 fg=0.02 bg=0.00
general transcription initiation factor ... GO:0140223 p=3.6E−02 n=1 fg=0.02 bg=0.00
protein kinase inhibitor activity GO:0004860 p=4.1E−02 n=2 fg=0.05 bg=0.01
kinase inhibitor activity GO:0019210 p=4.1E−02 n=2 fg=0.05 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=4.5E−02 n=4 fg=0.09 bg=0.03
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n=43/199 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
CCAAT−binding factor complex GO:0016602 p=1.9E−02 n=1 fg=0.02 bg=0.00
Dsl1/NZR complex GO:0070939 p=1.9E−02 n=1 fg=0.02 bg=0.00
DNA polymerase III, core complex GO:0044776 p=1.9E−02 n=1 fg=0.02 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=1.9E−02 n=1 fg=0.02 bg=0.00
ruffle membrane GO:0032587 p=2.1E−02 n=2 fg=0.04 bg=0.00
DNA polymerase III complex GO:0009360 p=3.8E−02 n=1 fg=0.02 bg=0.00
t−UTP complex GO:0034455 p=3.8E−02 n=1 fg=0.02 bg=0.00
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sarcoglycan complex GO:0016012 p=3.8E−02 n=1 fg=0.02 bg=0.00
Rb−E2F complex GO:0035189 p=3.8E−02 n=1 fg=0.02 bg=0.00
transcription regulator complex GO:0005667 p=4.1E−02 n=5 fg=0.10 bg=0.04
RNA polymerase II transcription regulato... GO:0090575 p=4.6E−02 n=3 fg=0.06 bg=0.02
cortical actin cytoskeleton GO:0030864 p=5.5E−02 n=2 fg=0.04 bg=0.01
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beta−catenin−TCF complex GO:1990907 p=5.7E−02 n=1 fg=0.02 bg=0.00
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cortical cytoskeleton GO:0030863 p=7.1E−02 n=2 fg=0.04 bg=0.01
cell projection membrane GO:0031253 p=7.4E−02 n=4 fg=0.08 bg=0.03
glycoprotein complex GO:0090665 p=7.5E−02 n=1 fg=0.02 bg=0.00
dystrophin−associated glycoprotein compl... GO:0016010 p=7.5E−02 n=1 fg=0.02 bg=0.00
CHD−type complex GO:0090545 p=7.5E−02 n=1 fg=0.02 bg=0.00
Cul4A−RING E3 ubiquitin ligase complex GO:0031464 p=7.5E−02 n=1 fg=0.02 bg=0.00
filamentous actin GO:0031941 p=7.5E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=7.5E−02 n=1 fg=0.02 bg=0.00
NuRD complex GO:0016581 p=7.5E−02 n=1 fg=0.02 bg=0.00
early endosome GO:0005769 p=7.6E−02 n=4 fg=0.08 bg=0.03
0 1 2 3 4 5
−log(p)
n=52/199 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction