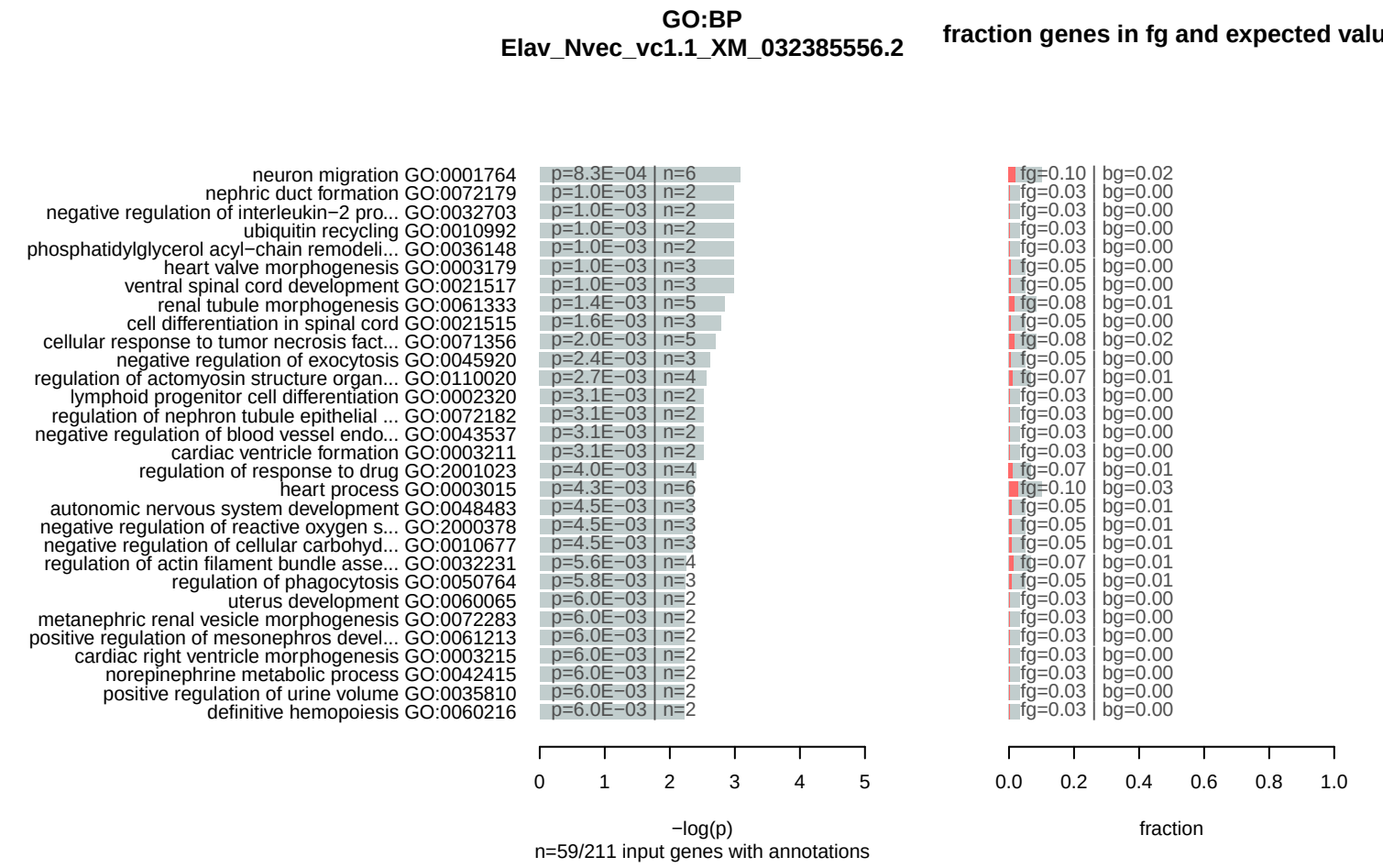
GO:BP
Elav_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
neuron migration GO:0001764 p=8.3E−04 n=6 fg=0.10 bg=0.02
nephric duct formation GO:0072179 p=1.0E−03 n=2 fg=0.03 bg=0.00
negative regulation of interleukin−2 pro... GO:0032703 p=1.0E−03 n=2 fg=0.03 bg=0.00
ubiquitin recycling GO:0010992 p=1.0E−03 n=2 fg=0.03 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=1.0E−03 n=2 fg=0.03 bg=0.00
heart valve morphogenesis GO:0003179 p=1.0E−03 n=3 fg=0.05 bg=0.00
ventral spinal cord development GO:0021517 p=1.0E−03 n=3 fg=0.05 bg=0.00
renal tubule morphogenesis GO:0061333 p=1.4E−03 n=5 fg=0.08 bg=0.01
cell differentiation in spinal cord GO:0021515 p=1.6E−03 n=3 fg=0.05 bg=0.00
cellular response to tumor necrosis fact... GO:0071356 p=2.0E−03 n=5 fg=0.08 bg=0.02
negative regulation of exocytosis GO:0045920 p=2.4E−03 n=3 fg=0.05 bg=0.00
regulation of actomyosin structure organ... GO:0110020 p=2.7E−03 n=4 fg=0.07 bg=0.01
lymphoid progenitor cell differentiation GO:0002320 p=3.1E−03 n=2 fg=0.03 bg=0.00
regulation of nephron tubule epithelial ... GO:0072182 p=3.1E−03 n=2 fg=0.03 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=3.1E−03 n=2 fg=0.03 bg=0.00
cardiac ventricle formation GO:0003211 p=3.1E−03 n=2 fg=0.03 bg=0.00
regulation of response to drug GO:2001023 p=4.0E−03 n=4 fg=0.07 bg=0.01
heart process GO:0003015 p=4.3E−03 n=6 fg=0.10 bg=0.03
autonomic nervous system development GO:0048483 p=4.5E−03 n=3 fg=0.05 bg=0.01
negative regulation of reactive oxygen s... GO:2000378 p=4.5E−03 n=3 fg=0.05 bg=0.01
negative regulation of cellular carbohyd... GO:0010677 p=4.5E−03 n=3 fg=0.05 bg=0.01
regulation of actin filament bundle asse... GO:0032231 p=5.6E−03 n=4 fg=0.07 bg=0.01
regulation of phagocytosis GO:0050764 p=5.8E−03 n=3 fg=0.05 bg=0.01
uterus development GO:0060065 p=6.0E−03 n=2 fg=0.03 bg=0.00
metanephric renal vesicle morphogenesis GO:0072283 p=6.0E−03 n=2 fg=0.03 bg=0.00
positive regulation of mesonephros devel... GO:0061213 p=6.0E−03 n=2 fg=0.03 bg=0.00
cardiac right ventricle morphogenesis GO:0003215 p=6.0E−03 n=2 fg=0.03 bg=0.00
norepinephrine metabolic process GO:0042415 p=6.0E−03 n=2 fg=0.03 bg=0.00
positive regulation of urine volume GO:0035810 p=6.0E−03 n=2 fg=0.03 bg=0.00
definitive hemopoiesis GO:0060216 p=6.0E−03 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=59/211 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
tumor necrosis factor receptor binding GO:0005164 p=2.6E−03 n=2 fg=0.04 bg=0.00
protein kinase binding GO:0019901 p=7.9E−03 n=9 fg=0.19 bg=0.08
HMG box domain binding GO:0071837 p=1.2E−02 n=2 fg=0.04 bg=0.00
beta−catenin binding GO:0008013 p=1.2E−02 n=2 fg=0.04 bg=0.00
DNA−binding transcription factor activit... GO:0003700 p=1.3E−02 n=9 fg=0.19 bg=0.08
transcription cis−regulatory region bind... GO:0000976 p=1.5E−02 n=7 fg=0.15 bg=0.06
voltage−gated cation channel activity GO:0022843 p=1.5E−02 n=3 fg=0.06 bg=0.01
histone deacetylase binding GO:0042826 p=1.5E−02 n=3 fg=0.06 bg=0.01
outward rectifier potassium channel acti... GO:0015271 p=1.7E−02 n=2 fg=0.04 bg=0.00
neurotransmitter binding GO:0042165 p=1.7E−02 n=2 fg=0.04 bg=0.00
sequence−specific double−stranded DNA bi... GO:1990837 p=2.1E−02 n=7 fg=0.15 bg=0.06
microtubule motor activity GO:0003777 p=2.2E−02 n=2 fg=0.04 bg=0.01
transcription regulatory region nucleic ... GO:0001067 p=2.5E−02 n=7 fg=0.15 bg=0.06
cis−regulatory region sequence−specific ... GO:0000987 p=2.6E−02 n=5 fg=0.10 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.6E−02 n=5 fg=0.10 bg=0.04
RNA polymerase II transcription regulato... GO:0000977 p=2.9E−02 n=6 fg=0.12 bg=0.05
type I transforming growth factor beta r... GO:0034713 p=3.0E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.0E−02 n=1 fg=0.02 bg=0.00
Roundabout binding GO:0048495 p=3.0E−02 n=1 fg=0.02 bg=0.00
BH4 domain binding GO:0051435 p=3.0E−02 n=1 fg=0.02 bg=0.00
neuropilin binding GO:0038191 p=3.0E−02 n=1 fg=0.02 bg=0.00
beta−endorphin binding GO:0031626 p=3.0E−02 n=1 fg=0.02 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=3.0E−02 n=1 fg=0.02 bg=0.00
chitinase activity GO:0004568 p=3.0E−02 n=1 fg=0.02 bg=0.00
small molecule sensor activity GO:0140299 p=3.0E−02 n=1 fg=0.02 bg=0.00
phorbol ester receptor activity GO:0001565 p=3.0E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.0E−02 n=1 fg=0.02 bg=0.00
oxygen sensor activity GO:0019826 p=3.0E−02 n=1 fg=0.02 bg=0.00
chitin binding GO:0008061 p=3.0E−02 n=1 fg=0.02 bg=0.00
F−box domain binding GO:1990444 p=3.0E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=48/211 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032385556.2
fraction genes in fg and expected valu
Lewy body GO:0097413 p=1.1E−03 n=2 fg=0.03 bg=0.00
secretory granule membrane GO:0030667 p=7.3E−03 n=5 fg=0.08 bg=0.02
A band GO:0031672 p=7.8E−03 n=3 fg=0.05 bg=0.01
cell periphery GO:0071944 p=1.1E−02 n=26 fg=0.43 bg=0.29
plasma membrane GO:0005886 p=2.0E−02 n=24 fg=0.40 bg=0.27
precatalytic spliceosome GO:0071011 p=2.0E−02 n=2 fg=0.03 bg=0.00
lipid droplet GO:0005811 p=2.3E−02 n=3 fg=0.05 bg=0.01
cation channel complex GO:0034703 p=3.0E−02 n=3 fg=0.05 bg=0.01
interphase microtubule organizing center GO:0031021 p=3.3E−02 n=1 fg=0.02 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=3.3E−02 n=1 fg=0.02 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=3.3E−02 n=1 fg=0.02 bg=0.00
male pronucleus GO:0001940 p=3.3E−02 n=1 fg=0.02 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=3.3E−02 n=1 fg=0.02 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=3.4E−02 n=2 fg=0.03 bg=0.01
potassium channel complex GO:0034705 p=3.4E−02 n=2 fg=0.03 bg=0.01
ion channel complex GO:0034702 p=3.8E−02 n=3 fg=0.05 bg=0.01
M band GO:0031430 p=4.1E−02 n=2 fg=0.03 bg=0.01
Z disc GO:0030018 p=4.8E−02 n=3 fg=0.05 bg=0.01
nuclear speck GO:0016607 p=4.9E−02 n=5 fg=0.08 bg=0.03
photoreceptor inner segment GO:0001917 p=4.9E−02 n=2 fg=0.03 bg=0.01
plasma membrane protein complex GO:0098797 p=5.2E−02 n=5 fg=0.08 bg=0.03
I band GO:0031674 p=5.2E−02 n=3 fg=0.05 bg=0.01
catalytic step 2 spliceosome GO:0071013 p=5.8E−02 n=2 fg=0.03 bg=0.01
Parkin−FBXW7−Cul1 ubiquitin ligase compl... GO:1990452 p=6.5E−02 n=1 fg=0.02 bg=0.00
U5 snRNP GO:0005682 p=6.5E−02 n=1 fg=0.02 bg=0.00
BBSome GO:0034464 p=6.5E−02 n=1 fg=0.02 bg=0.00
actomyosin GO:0042641 p=6.7E−02 n=2 fg=0.03 bg=0.01
specific granule membrane GO:0035579 p=7.6E−02 n=2 fg=0.03 bg=0.01
nuclear body GO:0016604 p=8.2E−02 n=7 fg=0.12 bg=0.06
Golgi apparatus GO:0005794 p=9.0E−02 n=12 fg=0.20 bg=0.13
0 1 2 3 4 5
−log(p)
n=60/211 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction