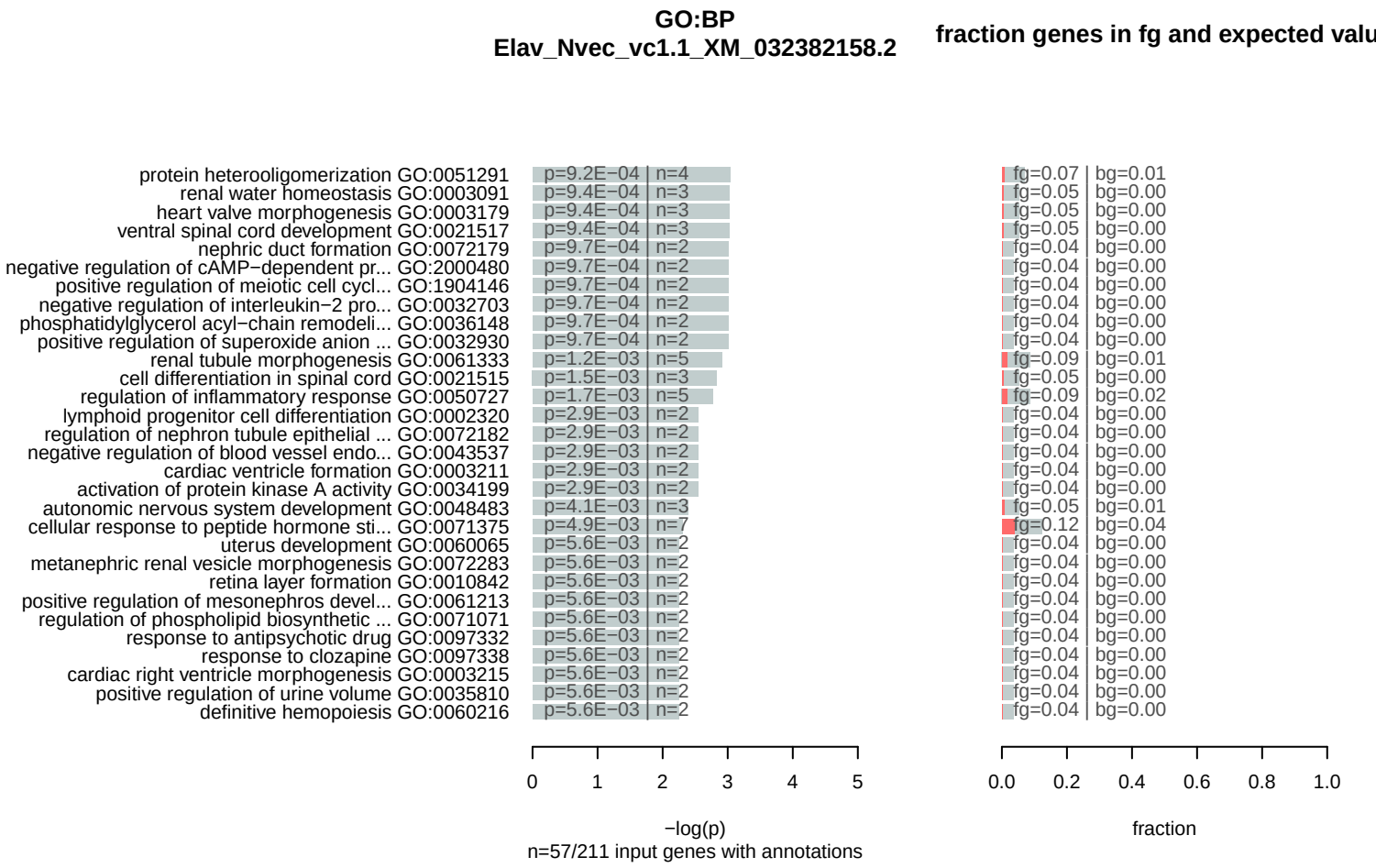
GO:BP
Elav_Nvec_vc1.1_XM_032382158.2
fraction genes in fg and expected valu
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renal water homeostasis GO:0003091 p=9.4E−04 n=3 fg=0.05 bg=0.00
heart valve morphogenesis GO:0003179 p=9.4E−04 n=3 fg=0.05 bg=0.00
ventral spinal cord development GO:0021517 p=9.4E−04 n=3 fg=0.05 bg=0.00
nephric duct formation GO:0072179 p=9.7E−04 n=2 fg=0.04 bg=0.00
negative regulation of cAMP−dependent pr... GO:2000480 p=9.7E−04 n=2 fg=0.04 bg=0.00
positive regulation of meiotic cell cycl... GO:1904146 p=9.7E−04 n=2 fg=0.04 bg=0.00
negative regulation of interleukin−2 pro... GO:0032703 p=9.7E−04 n=2 fg=0.04 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=9.7E−04 n=2 fg=0.04 bg=0.00
positive regulation of superoxide anion ... GO:0032930 p=9.7E−04 n=2 fg=0.04 bg=0.00
renal tubule morphogenesis GO:0061333 p=1.2E−03 n=5 fg=0.09 bg=0.01
cell differentiation in spinal cord GO:0021515 p=1.5E−03 n=3 fg=0.05 bg=0.00
regulation of inflammatory response GO:0050727 p=1.7E−03 n=5 fg=0.09 bg=0.02
lymphoid progenitor cell differentiation GO:0002320 p=2.9E−03 n=2 fg=0.04 bg=0.00
regulation of nephron tubule epithelial ... GO:0072182 p=2.9E−03 n=2 fg=0.04 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=2.9E−03 n=2 fg=0.04 bg=0.00
cardiac ventricle formation GO:0003211 p=2.9E−03 n=2 fg=0.04 bg=0.00
activation of protein kinase A activity GO:0034199 p=2.9E−03 n=2 fg=0.04 bg=0.00
autonomic nervous system development GO:0048483 p=4.1E−03 n=3 fg=0.05 bg=0.01
cellular response to peptide hormone sti... GO:0071375 p=4.9E−03 n=7 fg=0.12 bg=0.04
uterus development GO:0060065 p=5.6E−03 n=2 fg=0.04 bg=0.00
metanephric renal vesicle morphogenesis GO:0072283 p=5.6E−03 n=2 fg=0.04 bg=0.00
retina layer formation GO:0010842 p=5.6E−03 n=2 fg=0.04 bg=0.00
positive regulation of mesonephros devel... GO:0061213 p=5.6E−03 n=2 fg=0.04 bg=0.00
regulation of phospholipid biosynthetic ... GO:0071071 p=5.6E−03 n=2 fg=0.04 bg=0.00
response to antipsychotic drug GO:0097332 p=5.6E−03 n=2 fg=0.04 bg=0.00
response to clozapine GO:0097338 p=5.6E−03 n=2 fg=0.04 bg=0.00
cardiac right ventricle morphogenesis GO:0003215 p=5.6E−03 n=2 fg=0.04 bg=0.00
positive regulation of urine volume GO:0035810 p=5.6E−03 n=2 fg=0.04 bg=0.00
definitive hemopoiesis GO:0060216 p=5.6E−03 n=2 fg=0.04 bg=0.00
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−log(p)
n=57/211 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032382158.2
fraction genes in fg and expected valu
protein kinase A catalytic subunit bindi... GO:0034236 p=8.5E−04 n=2 fg=0.04 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=8.5E−04 n=2 fg=0.04 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=8.5E−04 n=2 fg=0.04 bg=0.00
peptide hormone binding GO:0017046 p=2.5E−03 n=2 fg=0.04 bg=0.00
cAMP binding GO:0030552 p=4.9E−03 n=2 fg=0.04 bg=0.00
ephrin receptor binding GO:0046875 p=8.1E−03 n=2 fg=0.04 bg=0.00
cytokine receptor binding GO:0005126 p=1.0E−02 n=3 fg=0.06 bg=0.01
HMG box domain binding GO:0071837 p=1.2E−02 n=2 fg=0.04 bg=0.00
voltage−gated cation channel activity GO:0022843 p=1.4E−02 n=3 fg=0.06 bg=0.01
outward rectifier potassium channel acti... GO:0015271 p=1.6E−02 n=2 fg=0.04 bg=0.00
purine ribonucleoside triphosphate bindi... GO:0035639 p=1.7E−02 n=7 fg=0.15 bg=0.06
carbohydrate derivative binding GO:0097367 p=1.9E−02 n=10 fg=0.21 bg=0.08
metalloendopeptidase activity GO:0004222 p=2.1E−02 n=2 fg=0.04 bg=0.01
ribonucleotide binding GO:0032553 p=2.3E−02 n=9 fg=0.19 bg=0.07
purine ribonucleotide binding GO:0032555 p=2.3E−02 n=9 fg=0.19 bg=0.07
purine nucleotide binding GO:0017076 p=2.7E−02 n=9 fg=0.19 bg=0.07
protein domain specific binding GO:0019904 p=2.9E−02 n=9 fg=0.19 bg=0.09
type I transforming growth factor beta r... GO:0034713 p=3.0E−02 n=1 fg=0.02 bg=0.00
heparan sulfate binding GO:1904399 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
tRNA (uracil) methyltransferase activity GO:0016300 p=3.0E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=3.0E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 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
acetylcholine receptor regulator activit... GO:0030548 p=3.0E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor activator activit... GO:0030549 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
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−log(p)
n=47/211 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032382158.2
fraction genes in fg and expected valu
germinal vesicle GO:0042585 p=1.1E−04 n=3 fg=0.05 bg=0.00
dendritic shaft GO:0043198 p=1.5E−04 n=5 fg=0.09 bg=0.01
nucleotide−activated protein kinase comp... GO:0031588 p=2.8E−03 n=2 fg=0.04 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=2.8E−03 n=2 fg=0.04 bg=0.00
T−tubule GO:0030315 p=2.9E−03 n=3 fg=0.05 bg=0.01
actomyosin GO:0042641 p=6.5E−03 n=3 fg=0.05 bg=0.01
dendritic spine GO:0043197 p=6.8E−03 n=5 fg=0.09 bg=0.02
precatalytic spliceosome GO:0071011 p=1.8E−02 n=2 fg=0.04 bg=0.00
sarcomere GO:0030017 p=2.1E−02 n=4 fg=0.07 bg=0.02
membrane raft GO:0045121 p=2.2E−02 n=5 fg=0.09 bg=0.03
membrane microdomain GO:0098857 p=2.2E−02 n=5 fg=0.09 bg=0.03
azurophil granule membrane GO:0035577 p=2.3E−02 n=2 fg=0.04 bg=0.00
cation channel complex GO:0034703 p=2.5E−02 n=3 fg=0.05 bg=0.01
secretory granule membrane GO:0030667 p=2.8E−02 n=4 fg=0.07 bg=0.02
cell periphery GO:0071944 p=2.8E−02 n=25 fg=0.45 bg=0.29
stress fiber GO:0001725 p=2.9E−02 n=2 fg=0.04 bg=0.01
contractile actin filament bundle GO:0097517 p=2.9E−02 n=2 fg=0.04 bg=0.01
actin filament bundle GO:0032432 p=2.9E−02 n=2 fg=0.04 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=2.9E−02 n=2 fg=0.04 bg=0.01
potassium channel complex GO:0034705 p=2.9E−02 n=2 fg=0.04 bg=0.01
lipoprotein particle GO:1990777 p=3.1E−02 n=1 fg=0.02 bg=0.00
interphase microtubule organizing center GO:0031021 p=3.1E−02 n=1 fg=0.02 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=3.1E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=3.1E−02 n=1 fg=0.02 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=3.1E−02 n=1 fg=0.02 bg=0.00
male pronucleus GO:0001940 p=3.1E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=3.1E−02 n=1 fg=0.02 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=3.1E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=3.1E−02 n=1 fg=0.02 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=3.1E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=56/211 input genes with annotations
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fraction