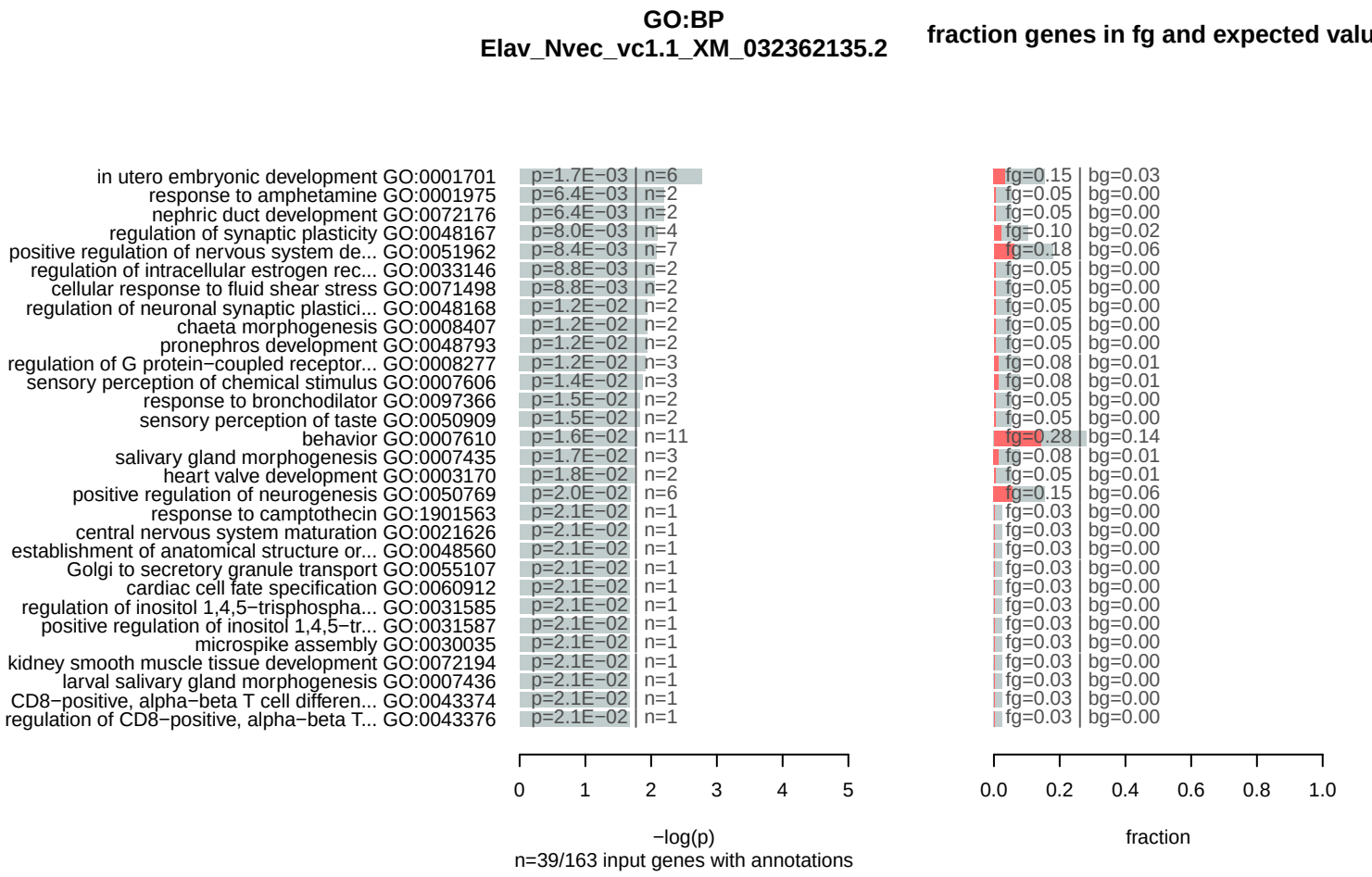
GO:BP
Elav_Nvec_vc1.1_XM_032362135.2
fraction genes in fg and expected valu
in utero embryonic development GO:0001701 p=1.7E−03 n=6 fg=0.15 bg=0.03
response to amphetamine GO:0001975 p=6.4E−03 n=2 fg=0.05 bg=0.00
nephric duct development GO:0072176 p=6.4E−03 n=2 fg=0.05 bg=0.00
regulation of synaptic plasticity GO:0048167 p=8.0E−03 n=4 fg=0.10 bg=0.02
positive regulation of nervous system de... GO:0051962 p=8.4E−03 n=7 fg=0.18 bg=0.06
regulation of intracellular estrogen rec... GO:0033146 p=8.8E−03 n=2 fg=0.05 bg=0.00
cellular response to fluid shear stress GO:0071498 p=8.8E−03 n=2 fg=0.05 bg=0.00
regulation of neuronal synaptic plastici... GO:0048168 p=1.2E−02 n=2 fg=0.05 bg=0.00
chaeta morphogenesis GO:0008407 p=1.2E−02 n=2 fg=0.05 bg=0.00
pronephros development GO:0048793 p=1.2E−02 n=2 fg=0.05 bg=0.00
regulation of G protein−coupled receptor... GO:0008277 p=1.2E−02 n=3 fg=0.08 bg=0.01
sensory perception of chemical stimulus GO:0007606 p=1.4E−02 n=3 fg=0.08 bg=0.01
response to bronchodilator GO:0097366 p=1.5E−02 n=2 fg=0.05 bg=0.00
sensory perception of taste GO:0050909 p=1.5E−02 n=2 fg=0.05 bg=0.00
behavior GO:0007610 p=1.6E−02 n=11 fg=0.28 bg=0.14
salivary gland morphogenesis GO:0007435 p=1.7E−02 n=3 fg=0.08 bg=0.01
heart valve development GO:0003170 p=1.8E−02 n=2 fg=0.05 bg=0.01
positive regulation of neurogenesis GO:0050769 p=2.0E−02 n=6 fg=0.15 bg=0.06
response to camptothecin GO:1901563 p=2.1E−02 n=1 fg=0.03 bg=0.00
central nervous system maturation GO:0021626 p=2.1E−02 n=1 fg=0.03 bg=0.00
establishment of anatomical structure or... GO:0048560 p=2.1E−02 n=1 fg=0.03 bg=0.00
Golgi to secretory granule transport GO:0055107 p=2.1E−02 n=1 fg=0.03 bg=0.00
cardiac cell fate specification GO:0060912 p=2.1E−02 n=1 fg=0.03 bg=0.00
regulation of inositol 1,4,5−trisphospha... GO:0031585 p=2.1E−02 n=1 fg=0.03 bg=0.00
positive regulation of inositol 1,4,5−tr... GO:0031587 p=2.1E−02 n=1 fg=0.03 bg=0.00
microspike assembly GO:0030035 p=2.1E−02 n=1 fg=0.03 bg=0.00
kidney smooth muscle tissue development GO:0072194 p=2.1E−02 n=1 fg=0.03 bg=0.00
larval salivary gland morphogenesis GO:0007436 p=2.1E−02 n=1 fg=0.03 bg=0.00
CD8−positive, alpha−beta T cell differen... GO:0043374 p=2.1E−02 n=1 fg=0.03 bg=0.00
regulation of CD8−positive, alpha−beta T... GO:0043376 p=2.1E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=39/163 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032362135.2
fraction genes in fg and expected valu
P−type ion transporter activity GO:0015662 p=4.2E−04 n=3 fg=0.09 bg=0.01
ATPase−coupled cation transmembrane tran... GO:0019829 p=1.6E−03 n=3 fg=0.09 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=2.0E−03 n=3 fg=0.09 bg=0.01
lipid transfer activity GO:0120013 p=4.0E−03 n=2 fg=0.06 bg=0.00
ubiquitin conjugating enzyme binding GO:0031624 p=1.7E−02 n=2 fg=0.06 bg=0.01
glutamate receptor binding GO:0035254 p=2.0E−02 n=2 fg=0.06 bg=0.01
ceramide binding GO:0097001 p=2.1E−02 n=1 fg=0.03 bg=0.00
type I transforming growth factor beta r... GO:0034713 p=2.1E−02 n=1 fg=0.03 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=2.1E−02 n=1 fg=0.03 bg=0.00
transmembrane receptor protein tyrosine ... GO:0005001 p=2.1E−02 n=1 fg=0.03 bg=0.00
non−tyrosine kinase fibroblast growth fa... GO:0001571 p=2.1E−02 n=1 fg=0.03 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=2.1E−02 n=1 fg=0.03 bg=0.00
sphingolipid transporter activity GO:0046624 p=2.1E−02 n=1 fg=0.03 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=2.1E−02 n=1 fg=0.03 bg=0.00
HLH domain binding GO:0043398 p=2.1E−02 n=1 fg=0.03 bg=0.00
alpha−N−acetylgalactosaminidase activity GO:0008456 p=2.1E−02 n=1 fg=0.03 bg=0.00
UFM1 activating enzyme activity GO:0071566 p=2.1E−02 n=1 fg=0.03 bg=0.00
muscle alpha−actinin binding GO:0051371 p=2.1E−02 n=1 fg=0.03 bg=0.00
inositol trisphosphate kinase activity GO:0051766 p=2.1E−02 n=1 fg=0.03 bg=0.00
alpha−galactosidase activity GO:0004557 p=2.1E−02 n=1 fg=0.03 bg=0.00
sphingolipid transfer activity GO:0120016 p=2.1E−02 n=1 fg=0.03 bg=0.00
ceramide transfer activity GO:0120017 p=2.1E−02 n=1 fg=0.03 bg=0.00
inositol−1,4,5−trisphosphate 3−kinase ac... GO:0008440 p=2.1E−02 n=1 fg=0.03 bg=0.00
receptor tyrosine kinase binding GO:0030971 p=2.4E−02 n=2 fg=0.06 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0044390 p=2.4E−02 n=2 fg=0.06 bg=0.01
protein tyrosine kinase binding GO:1990782 p=3.2E−02 n=2 fg=0.06 bg=0.01
transmembrane signaling receptor activit... GO:0004888 p=3.7E−02 n=4 fg=0.12 bg=0.04
sodium ion transmembrane transporter act... GO:0015081 p=3.7E−02 n=2 fg=0.06 bg=0.01
phosphatidylinositol transfer activity GO:0008526 p=4.1E−02 n=1 fg=0.03 bg=0.00
calcium−induced calcium release activity GO:0048763 p=4.1E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=33/163 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032362135.2
fraction genes in fg and expected valu
axon GO:0030424 p=1.9E−03 n=9 fg=0.24 bg=0.08
cell body GO:0044297 p=6.1E−03 n=8 fg=0.21 bg=0.08
endoplasmic reticulum subcompartment GO:0098827 p=8.3E−03 n=8 fg=0.21 bg=0.08
somatodendritic compartment GO:0036477 p=9.9E−03 n=9 fg=0.24 bg=0.10
chromaffin granule GO:0042583 p=2.1E−02 n=1 fg=0.03 bg=0.00
chromaffin granule membrane GO:0042584 p=2.1E−02 n=1 fg=0.03 bg=0.00
core−binding factor complex GO:0016513 p=2.1E−02 n=1 fg=0.03 bg=0.00
polycystin complex GO:0002133 p=2.1E−02 n=1 fg=0.03 bg=0.00
molybdopterin synthase complex GO:0019008 p=2.1E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=2.3E−02 n=7 fg=0.18 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=2.4E−02 n=7 fg=0.18 bg=0.08
cell junction GO:0030054 p=2.5E−02 n=10 fg=0.26 bg=0.14
transport vesicle GO:0030133 p=2.5E−02 n=5 fg=0.13 bg=0.04
intrinsic component of plasma membrane GO:0031226 p=2.9E−02 n=7 fg=0.18 bg=0.08
gut granule GO:0044840 p=4.2E−02 n=1 fg=0.03 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=4.2E−02 n=1 fg=0.03 bg=0.00
gut granule membrane GO:0044841 p=4.2E−02 n=1 fg=0.03 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=4.2E−02 n=1 fg=0.03 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=4.2E−02 n=1 fg=0.03 bg=0.00
COPI vesicle coat GO:0030126 p=4.2E−02 n=1 fg=0.03 bg=0.00
COPI−coated vesicle membrane GO:0030663 p=4.2E−02 n=1 fg=0.03 bg=0.00
neuronal cell body GO:0043025 p=4.6E−02 n=6 fg=0.16 bg=0.07
dendritic tree GO:0097447 p=5.0E−02 n=6 fg=0.16 bg=0.07
dendrite GO:0030425 p=5.0E−02 n=6 fg=0.16 bg=0.07
integral component of plasma membrane GO:0005887 p=6.0E−02 n=6 fg=0.16 bg=0.08
proximal dendrite GO:1990635 p=6.2E−02 n=1 fg=0.03 bg=0.00
NuRD complex GO:0016581 p=6.2E−02 n=1 fg=0.03 bg=0.00
mitochondrial respiratory chain complex ... GO:0005751 p=6.2E−02 n=1 fg=0.03 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=6.2E−02 n=1 fg=0.03 bg=0.00
CHD−type complex GO:0090545 p=6.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=38/163 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction