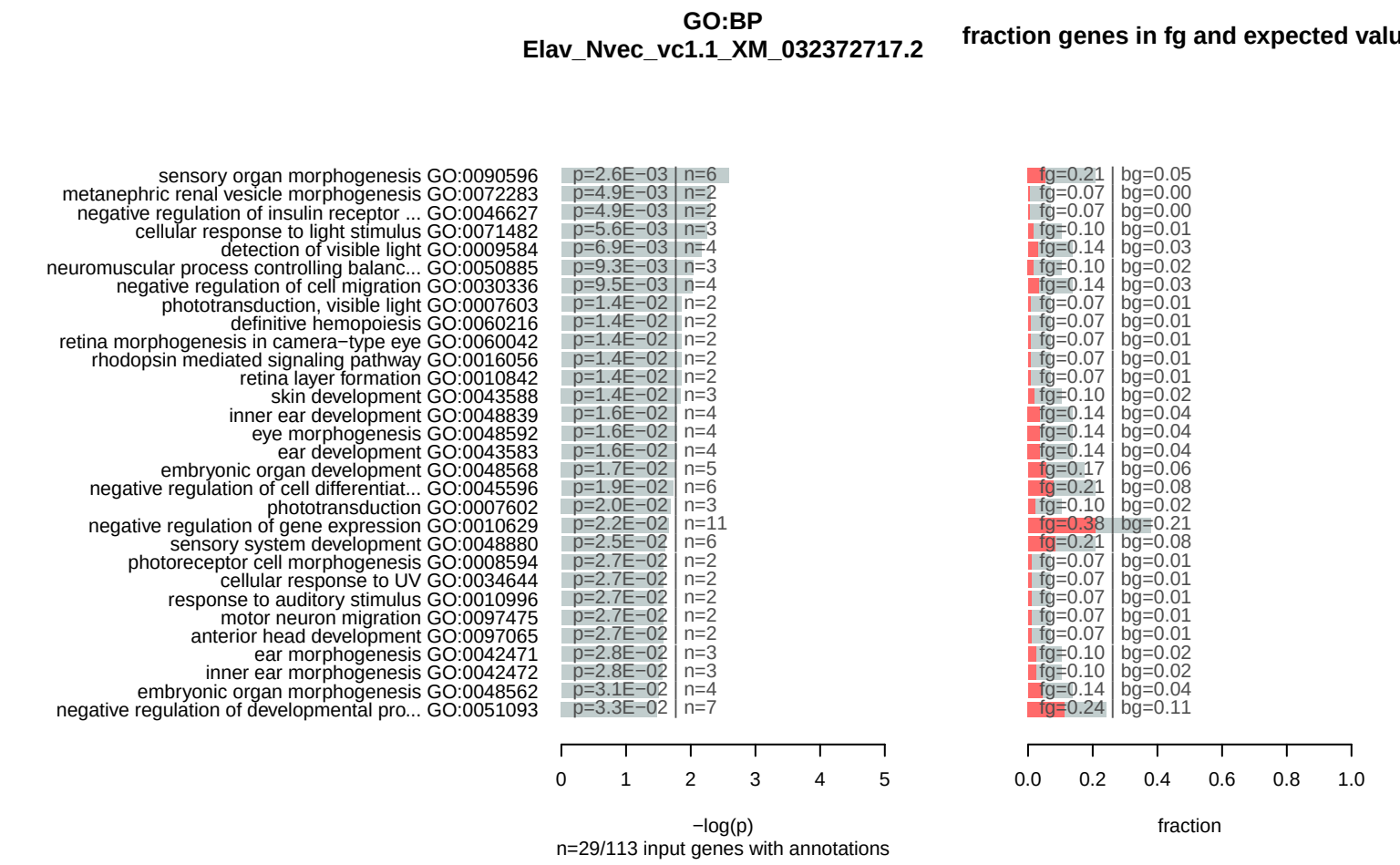
GO:BP
Elav_Nvec_vc1.1_XM_032372717.2
fraction genes in fg and expected valu
sensory organ morphogenesis GO:0090596 p=2.6E−03 n=6 fg=0.21 bg=0.05
metanephric renal vesicle morphogenesis GO:0072283 p=4.9E−03 n=2 fg=0.07 bg=0.00
negative regulation of insulin receptor ... GO:0046627 p=4.9E−03 n=2 fg=0.07 bg=0.00
cellular response to light stimulus GO:0071482 p=5.6E−03 n=3 fg=0.10 bg=0.01
detection of visible light GO:0009584 p=6.9E−03 n=4 fg=0.14 bg=0.03
neuromuscular process controlling balanc... GO:0050885 p=9.3E−03 n=3 fg=0.10 bg=0.02
negative regulation of cell migration GO:0030336 p=9.5E−03 n=4 fg=0.14 bg=0.03
phototransduction, visible light GO:0007603 p=1.4E−02 n=2 fg=0.07 bg=0.01
definitive hemopoiesis GO:0060216 p=1.4E−02 n=2 fg=0.07 bg=0.01
retina morphogenesis in camera−type eye GO:0060042 p=1.4E−02 n=2 fg=0.07 bg=0.01
rhodopsin mediated signaling pathway GO:0016056 p=1.4E−02 n=2 fg=0.07 bg=0.01
retina layer formation GO:0010842 p=1.4E−02 n=2 fg=0.07 bg=0.01
skin development GO:0043588 p=1.4E−02 n=3 fg=0.10 bg=0.02
inner ear development GO:0048839 p=1.6E−02 n=4 fg=0.14 bg=0.04
eye morphogenesis GO:0048592 p=1.6E−02 n=4 fg=0.14 bg=0.04
ear development GO:0043583 p=1.6E−02 n=4 fg=0.14 bg=0.04
embryonic organ development GO:0048568 p=1.7E−02 n=5 fg=0.17 bg=0.06
negative regulation of cell differentiat... GO:0045596 p=1.9E−02 n=6 fg=0.21 bg=0.08
phototransduction GO:0007602 p=2.0E−02 n=3 fg=0.10 bg=0.02
negative regulation of gene expression GO:0010629 p=2.2E−02 n=11 fg=0.38 bg=0.21
sensory system development GO:0048880 p=2.5E−02 n=6 fg=0.21 bg=0.08
photoreceptor cell morphogenesis GO:0008594 p=2.7E−02 n=2 fg=0.07 bg=0.01
cellular response to UV GO:0034644 p=2.7E−02 n=2 fg=0.07 bg=0.01
response to auditory stimulus GO:0010996 p=2.7E−02 n=2 fg=0.07 bg=0.01
motor neuron migration GO:0097475 p=2.7E−02 n=2 fg=0.07 bg=0.01
anterior head development GO:0097065 p=2.7E−02 n=2 fg=0.07 bg=0.01
ear morphogenesis GO:0042471 p=2.8E−02 n=3 fg=0.10 bg=0.02
inner ear morphogenesis GO:0042472 p=2.8E−02 n=3 fg=0.10 bg=0.02
embryonic organ morphogenesis GO:0048562 p=3.1E−02 n=4 fg=0.14 bg=0.04
negative regulation of developmental pro... GO:0051093 p=3.3E−02 n=7 fg=0.24 bg=0.11
0 1 2 3 4 5
−log(p)
n=29/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032372717.2
fraction genes in fg and expected valu
ATPase−coupled cation transmembrane tran... GO:0019829 p=5.6E−03 n=3 fg=0.12 bg=0.02
ATPase−coupled ion transmembrane transpo... GO:0042625 p=5.6E−03 n=3 fg=0.12 bg=0.02
ATP hydrolysis activity GO:0016887 p=3.2E−02 n=4 fg=0.15 bg=0.05
deacetylase activity GO:0019213 p=7.1E−02 n=1 fg=0.04 bg=0.00
dioxygenase activity GO:0051213 p=7.1E−02 n=1 fg=0.04 bg=0.00
histone deacetylase activity GO:0004407 p=7.1E−02 n=1 fg=0.04 bg=0.00
translation factor activity, RNA binding GO:0008135 p=7.1E−02 n=1 fg=0.04 bg=0.00
amidinotransferase activity GO:0015067 p=7.1E−02 n=1 fg=0.04 bg=0.00
glycine amidinotransferase activity GO:0015068 p=7.1E−02 n=1 fg=0.04 bg=0.00
lipid phosphatase activity GO:0042577 p=7.1E−02 n=1 fg=0.04 bg=0.00
potassium ion binding GO:0030955 p=7.1E−02 n=1 fg=0.04 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=7.1E−02 n=1 fg=0.04 bg=0.00
alkali metal ion binding GO:0031420 p=7.1E−02 n=1 fg=0.04 bg=0.00
phosphatidylinositol transfer activity GO:0008526 p=7.1E−02 n=1 fg=0.04 bg=0.00
cytosine C−5 DNA demethylase activity GO:0051747 p=7.1E−02 n=1 fg=0.04 bg=0.00
demethylase activity GO:0032451 p=7.1E−02 n=1 fg=0.04 bg=0.00
isoprenoid binding GO:0019840 p=7.1E−02 n=1 fg=0.04 bg=0.00
inositol−1,4,5−trisphosphate 5−phosphata... GO:0052658 p=7.1E−02 n=1 fg=0.04 bg=0.00
inositol−1,3,4,5−tetrakisphosphate 5−pho... GO:0052659 p=7.1E−02 n=1 fg=0.04 bg=0.00
phosphatidic acid binding GO:0070300 p=7.1E−02 n=1 fg=0.04 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=7.1E−02 n=1 fg=0.04 bg=0.00
inositol tetrakisphosphate phosphatase a... GO:0052743 p=7.1E−02 n=1 fg=0.04 bg=0.00
DNA−N1−methyladenine dioxygenase activit... GO:0043734 p=7.1E−02 n=1 fg=0.04 bg=0.00
ferrous iron binding GO:0008198 p=7.1E−02 n=1 fg=0.04 bg=0.00
G protein−coupled photoreceptor activity GO:0008020 p=7.1E−02 n=1 fg=0.04 bg=0.00
oxidoreductase activity, acting on paire... GO:0016705 p=7.1E−02 n=1 fg=0.04 bg=0.00
photoreceptor activity GO:0009881 p=7.1E−02 n=1 fg=0.04 bg=0.00
2−oxoglutarate−dependent dioxygenase act... GO:0016706 p=7.1E−02 n=1 fg=0.04 bg=0.00
nuclear receptor coactivator activity GO:0030374 p=7.1E−02 n=1 fg=0.04 bg=0.00
retinal binding GO:0016918 p=7.1E−02 n=1 fg=0.04 bg=0.00
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−log(p)
n=26/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032372717.2
fraction genes in fg and expected valu
subrhabdomeral cisterna GO:0016029 p=4.7E−03 n=2 fg=0.07 bg=0.01
vacuole GO:0005773 p=1.9E−02 n=5 fg=0.18 bg=0.06
vacuolar membrane GO:0005774 p=3.4E−02 n=3 fg=0.11 bg=0.03
secretory granule membrane GO:0030667 p=4.1E−02 n=2 fg=0.07 bg=0.01
microtubule cytoskeleton GO:0015630 p=4.1E−02 n=5 fg=0.18 bg=0.07
plasma membrane protein complex GO:0098797 p=5.8E−02 n=4 fg=0.14 bg=0.05
integral component of membrane GO:0016021 p=5.9E−02 n=11 fg=0.39 bg=0.25
multivesicular body GO:0005771 p=7.0E−02 n=1 fg=0.04 bg=0.00
core−binding factor complex GO:0016513 p=7.0E−02 n=1 fg=0.04 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=7.0E−02 n=1 fg=0.04 bg=0.00
photoreceptor disc membrane GO:0097381 p=7.0E−02 n=1 fg=0.04 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=7.0E−02 n=1 fg=0.04 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=7.0E−02 n=1 fg=0.04 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=7.0E−02 n=1 fg=0.04 bg=0.00
presynaptic active zone membrane GO:0048787 p=7.0E−02 n=1 fg=0.04 bg=0.00
inaD signaling complex GO:0016027 p=7.0E−02 n=1 fg=0.04 bg=0.00
PML body GO:0016605 p=7.0E−02 n=1 fg=0.04 bg=0.00
secondary lysosome GO:0005767 p=7.0E−02 n=1 fg=0.04 bg=0.00
mitochondrial intermembrane space GO:0005758 p=7.0E−02 n=1 fg=0.04 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=7.0E−02 n=1 fg=0.04 bg=0.00
intrinsic component of membrane GO:0031224 p=8.1E−02 n=11 fg=0.39 bg=0.26
potassium channel complex GO:0034705 p=1.0E−01 n=2 fg=0.07 bg=0.02
voltage−gated potassium channel complex GO:0008076 p=1.0E−01 n=2 fg=0.07 bg=0.02
protein−containing complex GO:0032991 p=1.0E−01 n=13 fg=0.46 bg=0.34
cytoskeleton GO:0005856 p=1.0E−01 n=6 fg=0.21 bg=0.12
bounding membrane of organelle GO:0098588 p=1.2E−01 n=7 fg=0.25 bg=0.15
dendritic shaft GO:0043198 p=1.2E−01 n=2 fg=0.07 bg=0.02
lytic vacuole membrane GO:0098852 p=1.2E−01 n=2 fg=0.07 bg=0.02
membrane protein complex GO:0098796 p=1.3E−01 n=4 fg=0.14 bg=0.07
specific granule GO:0042581 p=1.3E−01 n=1 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=28/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction