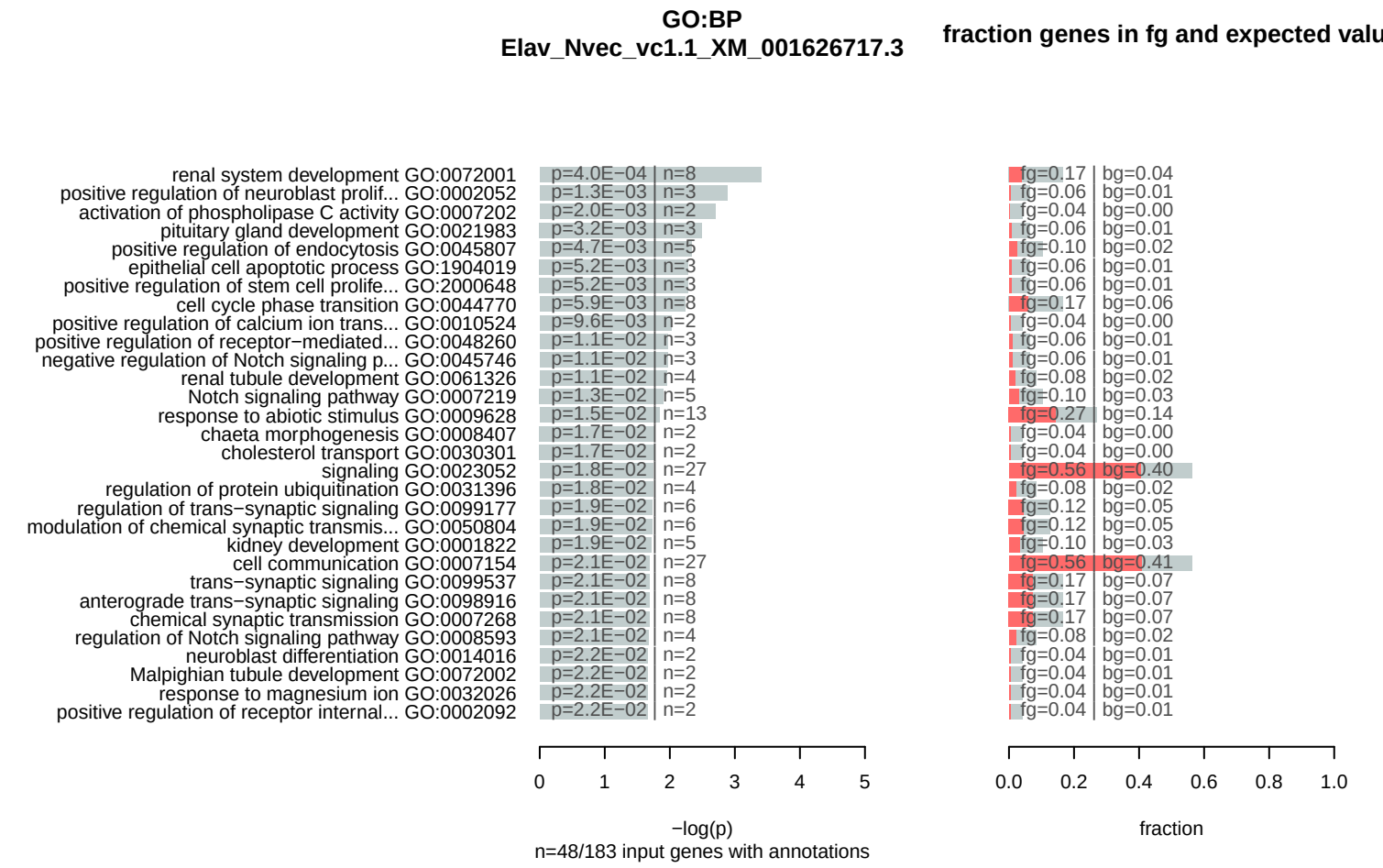
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fraction genes in fg and expected valu
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positive regulation of neuroblast prolif... GO:0002052 p=1.3E−03 n=3 fg=0.06 bg=0.01
activation of phospholipase C activity GO:0007202 p=2.0E−03 n=2 fg=0.04 bg=0.00
pituitary gland development GO:0021983 p=3.2E−03 n=3 fg=0.06 bg=0.01
positive regulation of endocytosis GO:0045807 p=4.7E−03 n=5 fg=0.10 bg=0.02
epithelial cell apoptotic process GO:1904019 p=5.2E−03 n=3 fg=0.06 bg=0.01
positive regulation of stem cell prolife... GO:2000648 p=5.2E−03 n=3 fg=0.06 bg=0.01
cell cycle phase transition GO:0044770 p=5.9E−03 n=8 fg=0.17 bg=0.06
positive regulation of calcium ion trans... GO:0010524 p=9.6E−03 n=2 fg=0.04 bg=0.00
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negative regulation of Notch signaling p... GO:0045746 p=1.1E−02 n=3 fg=0.06 bg=0.01
renal tubule development GO:0061326 p=1.1E−02 n=4 fg=0.08 bg=0.02
Notch signaling pathway GO:0007219 p=1.3E−02 n=5 fg=0.10 bg=0.03
response to abiotic stimulus GO:0009628 p=1.5E−02 n=13 fg=0.27 bg=0.14
chaeta morphogenesis GO:0008407 p=1.7E−02 n=2 fg=0.04 bg=0.00
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signaling GO:0023052 p=1.8E−02 n=27 fg=0.56 bg=0.40
regulation of protein ubiquitination GO:0031396 p=1.8E−02 n=4 fg=0.08 bg=0.02
regulation of trans−synaptic signaling GO:0099177 p=1.9E−02 n=6 fg=0.12 bg=0.05
modulation of chemical synaptic transmis... GO:0050804 p=1.9E−02 n=6 fg=0.12 bg=0.05
kidney development GO:0001822 p=1.9E−02 n=5 fg=0.10 bg=0.03
cell communication GO:0007154 p=2.1E−02 n=27 fg=0.56 bg=0.41
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regulation of Notch signaling pathway GO:0008593 p=2.1E−02 n=4 fg=0.08 bg=0.02
neuroblast differentiation GO:0014016 p=2.2E−02 n=2 fg=0.04 bg=0.01
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response to magnesium ion GO:0032026 p=2.2E−02 n=2 fg=0.04 bg=0.01
positive regulation of receptor internal... GO:0002092 p=2.2E−02 n=2 fg=0.04 bg=0.01
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001626717.3
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voltage−gated potassium channel activity GO:0005249 p=1.7E−03 n=3 fg=0.07 bg=0.01
bHLH transcription factor binding GO:0043425 p=1.9E−03 n=2 fg=0.05 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=1.3E−02 n=2 fg=0.05 bg=0.00
phosphotyrosine residue binding GO:0001784 p=1.6E−02 n=2 fg=0.05 bg=0.01
cysteine−type peptidase activity GO:0008234 p=1.7E−02 n=3 fg=0.07 bg=0.01
ion gated channel activity GO:0022839 p=2.1E−02 n=4 fg=0.10 bg=0.03
protein phosphorylated amino acid bindin... GO:0045309 p=2.6E−02 n=2 fg=0.05 bg=0.01
ribokinase activity GO:0004747 p=2.6E−02 n=1 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=2.6E−02 n=1 fg=0.02 bg=0.00
choline dehydrogenase activity GO:0008812 p=2.6E−02 n=1 fg=0.02 bg=0.00
telomeric repeat−containing RNA binding GO:0061752 p=2.6E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−lysine−9 demethylase a... GO:0032454 p=2.6E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=2.6E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=2.6E−02 n=1 fg=0.02 bg=0.00
mannose−6−phosphate isomerase activity GO:0004476 p=2.6E−02 n=1 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=2.6E−02 n=1 fg=0.02 bg=0.00
BIR domain binding GO:1990525 p=2.6E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol phospholipase C act... GO:0004435 p=2.6E−02 n=1 fg=0.02 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016861 p=2.6E−02 n=1 fg=0.02 bg=0.00
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MRF binding GO:0043426 p=2.6E−02 n=1 fg=0.02 bg=0.00
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cadherin binding GO:0045296 p=3.1E−02 n=2 fg=0.05 bg=0.01
amyloid−beta binding GO:0001540 p=3.1E−02 n=2 fg=0.05 bg=0.01
deubiquitinase activity GO:0101005 p=3.6E−02 n=2 fg=0.05 bg=0.01
cell adhesion molecule binding GO:0050839 p=3.6E−02 n=3 fg=0.07 bg=0.02
ubiquitin−like protein peptidase activit... GO:0019783 p=4.2E−02 n=2 fg=0.05 bg=0.01
phosphatidylinositol phosphate binding GO:1901981 p=4.3E−02 n=3 fg=0.07 bg=0.02
myosin light chain binding GO:0032027 p=5.1E−02 n=1 fg=0.02 bg=0.00
transcription corepressor binding GO:0001222 p=5.1E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=41/183 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_001626717.3
fraction genes in fg and expected valu
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transmembrane transporter complex GO:1902495 p=1.7E−02 n=4 fg=0.08 bg=0.02
cation channel complex GO:0034703 p=1.7E−02 n=3 fg=0.06 bg=0.01
anchoring junction GO:0070161 p=1.9E−02 n=6 fg=0.12 bg=0.05
cell−cell junction GO:0005911 p=1.9E−02 n=6 fg=0.12 bg=0.05
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ion channel complex GO:0034702 p=2.1E−02 n=3 fg=0.06 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=2.2E−02 n=2 fg=0.04 bg=0.01
potassium channel complex GO:0034705 p=2.2E−02 n=2 fg=0.04 bg=0.01
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=2.7E−02 n=1 fg=0.02 bg=0.00
female germline ring canal outer rim GO:0035182 p=2.7E−02 n=1 fg=0.02 bg=0.00
micropyle GO:0070825 p=2.7E−02 n=1 fg=0.02 bg=0.00
egg chorion GO:0042600 p=2.7E−02 n=1 fg=0.02 bg=0.00
Golgi trans cisterna GO:0000138 p=3.3E−02 n=2 fg=0.04 bg=0.01
plasma membrane bounded cell projection GO:0120025 p=3.6E−02 n=15 fg=0.31 bg=0.20
cell projection GO:0042995 p=3.6E−02 n=15 fg=0.31 bg=0.20
catalytic step 2 spliceosome GO:0071013 p=3.8E−02 n=2 fg=0.04 bg=0.01
apical cortex GO:0045179 p=3.8E−02 n=2 fg=0.04 bg=0.01
cell junction GO:0030054 p=4.9E−02 n=11 fg=0.23 bg=0.13
clathrin−coated vesicle GO:0030136 p=5.1E−02 n=3 fg=0.06 bg=0.02
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postsynaptic cytosol GO:0099524 p=5.2E−02 n=1 fg=0.02 bg=0.00
female germline ring canal GO:0035324 p=5.2E−02 n=1 fg=0.02 bg=0.00
neurofilament GO:0005883 p=5.2E−02 n=1 fg=0.02 bg=0.00
extrinsic component of Golgi membrane GO:0090498 p=5.2E−02 n=1 fg=0.02 bg=0.00
COP9 signalosome GO:0008180 p=5.2E−02 n=1 fg=0.02 bg=0.00
TRAMP complex GO:0031499 p=5.2E−02 n=1 fg=0.02 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=5.2E−02 n=1 fg=0.02 bg=0.00
basal part of cell GO:0045178 p=5.5E−02 n=4 fg=0.08 bg=0.03
myosin VI complex GO:0031476 p=7.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=48/183 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction