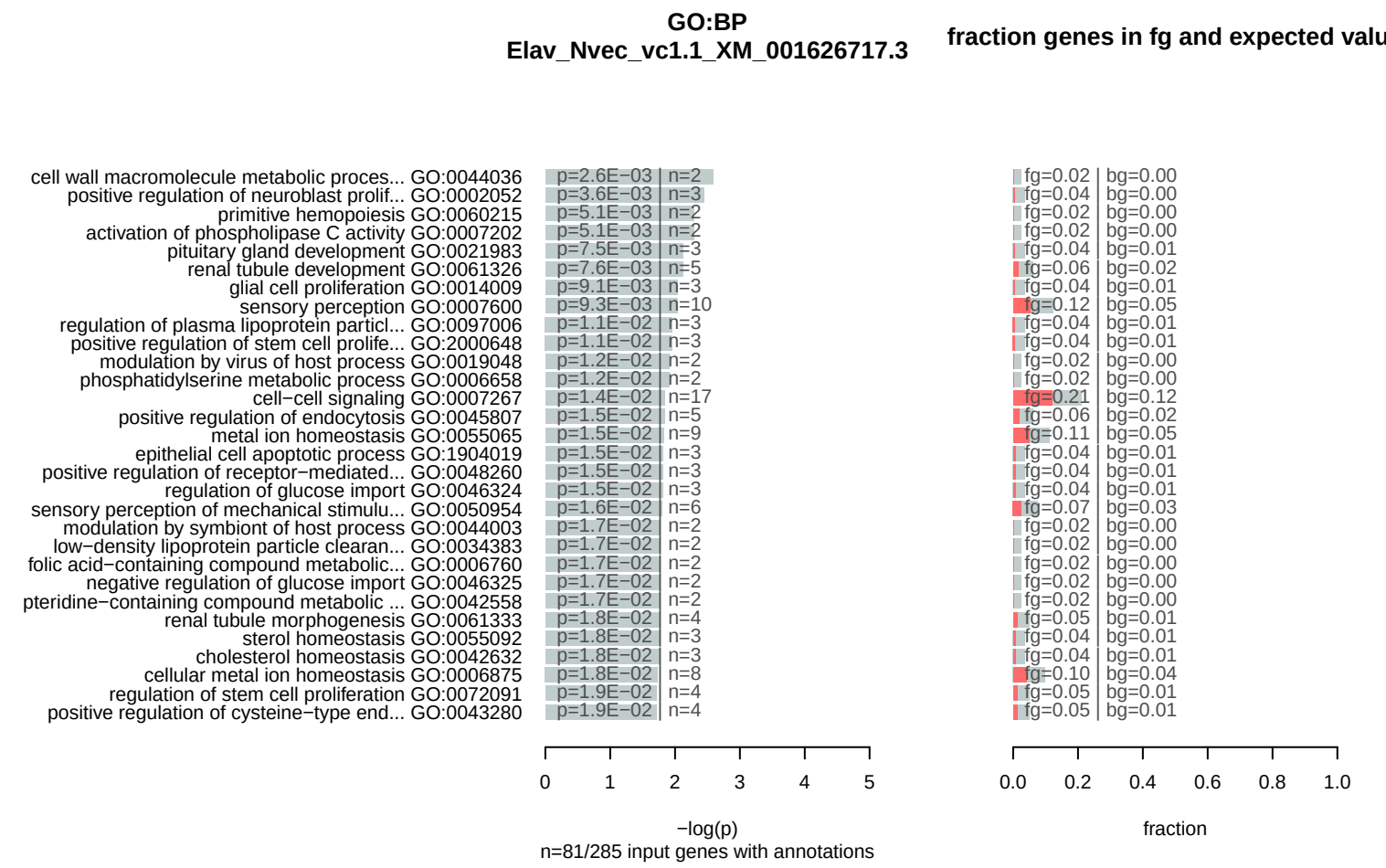
GO:BP
Elav_Nvec_vc1.1_XM_001626717.3
fraction genes in fg and expected valu
cell wall macromolecule metabolic proces... GO:0044036 p=2.6E−03 n=2 fg=0.02 bg=0.00
positive regulation of neuroblast prolif... GO:0002052 p=3.6E−03 n=3 fg=0.04 bg=0.00
primitive hemopoiesis GO:0060215 p=5.1E−03 n=2 fg=0.02 bg=0.00
activation of phospholipase C activity GO:0007202 p=5.1E−03 n=2 fg=0.02 bg=0.00
pituitary gland development GO:0021983 p=7.5E−03 n=3 fg=0.04 bg=0.01
renal tubule development GO:0061326 p=7.6E−03 n=5 fg=0.06 bg=0.02
glial cell proliferation GO:0014009 p=9.1E−03 n=3 fg=0.04 bg=0.01
sensory perception GO:0007600 p=9.3E−03 n=10 fg=0.12 bg=0.05
regulation of plasma lipoprotein particl... GO:0097006 p=1.1E−02 n=3 fg=0.04 bg=0.01
positive regulation of stem cell prolife... GO:2000648 p=1.1E−02 n=3 fg=0.04 bg=0.01
modulation by virus of host process GO:0019048 p=1.2E−02 n=2 fg=0.02 bg=0.00
phosphatidylserine metabolic process GO:0006658 p=1.2E−02 n=2 fg=0.02 bg=0.00
cell−cell signaling GO:0007267 p=1.4E−02 n=17 fg=0.21 bg=0.12
positive regulation of endocytosis GO:0045807 p=1.5E−02 n=5 fg=0.06 bg=0.02
metal ion homeostasis GO:0055065 p=1.5E−02 n=9 fg=0.11 bg=0.05
epithelial cell apoptotic process GO:1904019 p=1.5E−02 n=3 fg=0.04 bg=0.01
positive regulation of receptor−mediated... GO:0048260 p=1.5E−02 n=3 fg=0.04 bg=0.01
regulation of glucose import GO:0046324 p=1.5E−02 n=3 fg=0.04 bg=0.01
sensory perception of mechanical stimulu... GO:0050954 p=1.6E−02 n=6 fg=0.07 bg=0.03
modulation by symbiont of host process GO:0044003 p=1.7E−02 n=2 fg=0.02 bg=0.00
low−density lipoprotein particle clearan... GO:0034383 p=1.7E−02 n=2 fg=0.02 bg=0.00
folic acid−containing compound metabolic... GO:0006760 p=1.7E−02 n=2 fg=0.02 bg=0.00
negative regulation of glucose import GO:0046325 p=1.7E−02 n=2 fg=0.02 bg=0.00
pteridine−containing compound metabolic ... GO:0042558 p=1.7E−02 n=2 fg=0.02 bg=0.00
renal tubule morphogenesis GO:0061333 p=1.8E−02 n=4 fg=0.05 bg=0.01
sterol homeostasis GO:0055092 p=1.8E−02 n=3 fg=0.04 bg=0.01
cholesterol homeostasis GO:0042632 p=1.8E−02 n=3 fg=0.04 bg=0.01
cellular metal ion homeostasis GO:0006875 p=1.8E−02 n=8 fg=0.10 bg=0.04
regulation of stem cell proliferation GO:0072091 p=1.9E−02 n=4 fg=0.05 bg=0.01
positive regulation of cysteine−type end... GO:0043280 p=1.9E−02 n=4 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=81/285 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001626717.3
fraction genes in fg and expected valu
fatty acid transmembrane transporter act... GO:0015245 p=2.6E−03 n=2 fg=0.03 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=3.6E−03 n=3 fg=0.04 bg=0.00
bHLH transcription factor binding GO:0043425 p=5.1E−03 n=2 fg=0.03 bg=0.00
actin monomer binding GO:0003785 p=8.4E−03 n=2 fg=0.03 bg=0.00
myosin light chain binding GO:0032027 p=8.4E−03 n=2 fg=0.03 bg=0.00
carbohydrate kinase activity GO:0019200 p=1.7E−02 n=2 fg=0.03 bg=0.00
phosphoprotein binding GO:0051219 p=2.0E−02 n=3 fg=0.04 bg=0.01
phosphotyrosine residue binding GO:0001784 p=2.2E−02 n=2 fg=0.03 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=2.2E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate bi... GO:0005546 p=2.6E−02 n=3 fg=0.04 bg=0.01
vitamin transmembrane transporter activi... GO:0090482 p=2.8E−02 n=2 fg=0.03 bg=0.00
ribokinase activity GO:0004747 p=3.0E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.0E−02 n=1 fg=0.01 bg=0.00
MRF binding GO:0043426 p=3.0E−02 n=1 fg=0.01 bg=0.00
very long−chain fatty acid−CoA ligase ac... GO:0031957 p=3.0E−02 n=1 fg=0.01 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016861 p=3.0E−02 n=1 fg=0.01 bg=0.00
BIR domain binding GO:1990525 p=3.0E−02 n=1 fg=0.01 bg=0.00
phosphoribosylaminoimidazolecarboxamide ... GO:0004643 p=3.0E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.0E−02 n=1 fg=0.01 bg=0.00
neurotrophin TRK receptor binding GO:0005167 p=3.0E−02 n=1 fg=0.01 bg=0.00
neurotrophin TRKA receptor binding GO:0005168 p=3.0E−02 n=1 fg=0.01 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=3.0E−02 n=1 fg=0.01 bg=0.00
histone H3−methyl−lysine−9 demethylase a... GO:0032454 p=3.0E−02 n=1 fg=0.01 bg=0.00
long−chain fatty acid−CoA ligase activit... GO:0004467 p=3.0E−02 n=1 fg=0.01 bg=0.00
methotrexate transmembrane transporter a... GO:0015350 p=3.0E−02 n=1 fg=0.01 bg=0.00
IMP cyclohydrolase activity GO:0003937 p=3.0E−02 n=1 fg=0.01 bg=0.00
telomeric repeat−containing RNA binding GO:0061752 p=3.0E−02 n=1 fg=0.01 bg=0.00
mannose−6−phosphate isomerase activity GO:0004476 p=3.0E−02 n=1 fg=0.01 bg=0.00
glycine−tRNA ligase activity GO:0004820 p=3.0E−02 n=1 fg=0.01 bg=0.00
hydroxymethyl−, formyl− and related tran... GO:0016742 p=3.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=71/285 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001626717.3
fraction genes in fg and expected valu
plasma membrane bounded cell projection GO:0120025 p=1.6E−04 n=28 fg=0.35 bg=0.18
transporter complex GO:1990351 p=4.6E−03 n=6 fg=0.07 bg=0.02
brush border membrane GO:0031526 p=1.5E−02 n=3 fg=0.04 bg=0.01
transmembrane transporter complex GO:1902495 p=1.5E−02 n=5 fg=0.06 bg=0.02
DNA repair complex GO:1990391 p=2.2E−02 n=2 fg=0.03 bg=0.00
caveola GO:0005901 p=2.9E−02 n=3 fg=0.04 bg=0.01
female germline ring canal outer rim GO:0035182 p=3.0E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=3.0E−02 n=1 fg=0.01 bg=0.00
XPC complex GO:0071942 p=3.0E−02 n=1 fg=0.01 bg=0.00
nucleotide−excision repair complex GO:0000109 p=3.0E−02 n=1 fg=0.01 bg=0.00
micropyle GO:0070825 p=3.0E−02 n=1 fg=0.01 bg=0.00
sperm connecting piece GO:0097224 p=3.0E−02 n=1 fg=0.01 bg=0.00
egg chorion GO:0042600 p=3.0E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber expansion GO:1990026 p=3.0E−02 n=1 fg=0.01 bg=0.00
varicosity GO:0043196 p=3.0E−02 n=1 fg=0.01 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=3.3E−02 n=2 fg=0.03 bg=0.00
potassium channel complex GO:0034705 p=3.3E−02 n=2 fg=0.03 bg=0.00
cation channel complex GO:0034703 p=4.0E−02 n=3 fg=0.04 bg=0.01
cell−cell junction GO:0005911 p=4.4E−02 n=7 fg=0.09 bg=0.04
anchoring junction GO:0070161 p=4.4E−02 n=7 fg=0.09 bg=0.04
neuron projection GO:0043005 p=4.5E−02 n=15 fg=0.19 bg=0.12
cytoplasmic region GO:0099568 p=4.6E−02 n=8 fg=0.10 bg=0.05
Golgi trans cisterna GO:0000138 p=4.7E−02 n=2 fg=0.03 bg=0.00
ruffle GO:0001726 p=5.3E−02 n=3 fg=0.04 bg=0.01
basal part of cell GO:0045178 p=5.7E−02 n=5 fg=0.06 bg=0.03
plasma membrane raft GO:0044853 p=5.7E−02 n=3 fg=0.04 bg=0.01
ion channel complex GO:0034702 p=5.7E−02 n=3 fg=0.04 bg=0.01
ribonucleoside−diphosphate reductase com... GO:0005971 p=5.8E−02 n=1 fg=0.01 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=5.8E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=5.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=80/285 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction