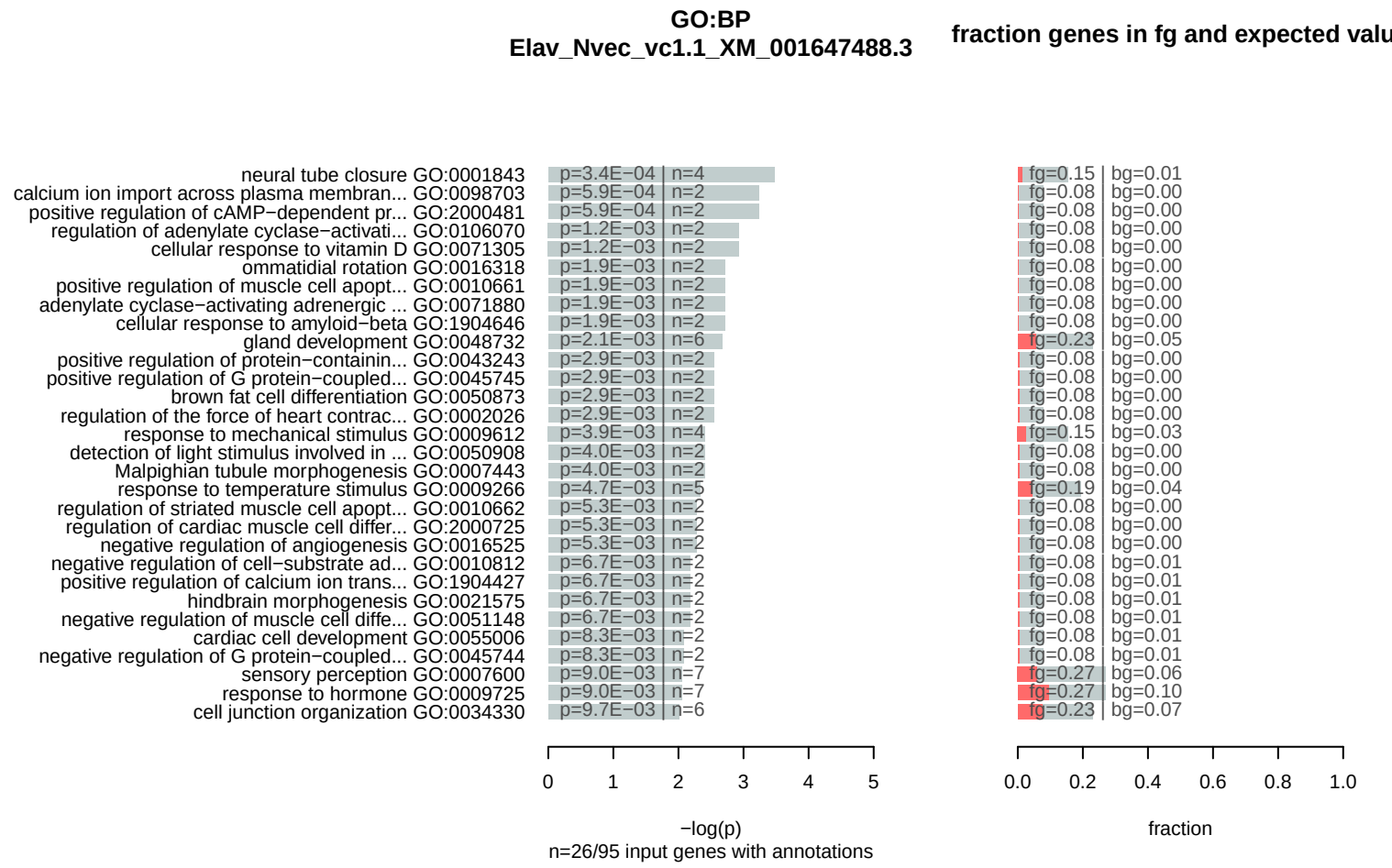
GO:BP
Elav_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
neural tube closure GO:0001843 p=3.4E−04 n=4 fg=0.15 bg=0.01
calcium ion import across plasma membran... GO:0098703 p=5.9E−04 n=2 fg=0.08 bg=0.00
positive regulation of cAMP−dependent pr... GO:2000481 p=5.9E−04 n=2 fg=0.08 bg=0.00
regulation of adenylate cyclase−activati... GO:0106070 p=1.2E−03 n=2 fg=0.08 bg=0.00
cellular response to vitamin D GO:0071305 p=1.2E−03 n=2 fg=0.08 bg=0.00
ommatidial rotation GO:0016318 p=1.9E−03 n=2 fg=0.08 bg=0.00
positive regulation of muscle cell apopt... GO:0010661 p=1.9E−03 n=2 fg=0.08 bg=0.00
adenylate cyclase−activating adrenergic ... GO:0071880 p=1.9E−03 n=2 fg=0.08 bg=0.00
cellular response to amyloid−beta GO:1904646 p=1.9E−03 n=2 fg=0.08 bg=0.00
gland development GO:0048732 p=2.1E−03 n=6 fg=0.23 bg=0.05
positive regulation of protein−containin... GO:0043243 p=2.9E−03 n=2 fg=0.08 bg=0.00
positive regulation of G protein−coupled... GO:0045745 p=2.9E−03 n=2 fg=0.08 bg=0.00
brown fat cell differentiation GO:0050873 p=2.9E−03 n=2 fg=0.08 bg=0.00
regulation of the force of heart contrac... GO:0002026 p=2.9E−03 n=2 fg=0.08 bg=0.00
response to mechanical stimulus GO:0009612 p=3.9E−03 n=4 fg=0.15 bg=0.03
detection of light stimulus involved in ... GO:0050908 p=4.0E−03 n=2 fg=0.08 bg=0.00
Malpighian tubule morphogenesis GO:0007443 p=4.0E−03 n=2 fg=0.08 bg=0.00
response to temperature stimulus GO:0009266 p=4.7E−03 n=5 fg=0.19 bg=0.04
regulation of striated muscle cell apopt... GO:0010662 p=5.3E−03 n=2 fg=0.08 bg=0.00
regulation of cardiac muscle cell differ... GO:2000725 p=5.3E−03 n=2 fg=0.08 bg=0.00
negative regulation of angiogenesis GO:0016525 p=5.3E−03 n=2 fg=0.08 bg=0.00
negative regulation of cell−substrate ad... GO:0010812 p=6.7E−03 n=2 fg=0.08 bg=0.01
positive regulation of calcium ion trans... GO:1904427 p=6.7E−03 n=2 fg=0.08 bg=0.01
hindbrain morphogenesis GO:0021575 p=6.7E−03 n=2 fg=0.08 bg=0.01
negative regulation of muscle cell diffe... GO:0051148 p=6.7E−03 n=2 fg=0.08 bg=0.01
cardiac cell development GO:0055006 p=8.3E−03 n=2 fg=0.08 bg=0.01
negative regulation of G protein−coupled... GO:0045744 p=8.3E−03 n=2 fg=0.08 bg=0.01
sensory perception GO:0007600 p=9.0E−03 n=7 fg=0.27 bg=0.06
response to hormone GO:0009725 p=9.0E−03 n=7 fg=0.27 bg=0.10
cell junction organization GO:0034330 p=9.7E−03 n=6 fg=0.23 bg=0.07
0 1 2 3 4 5
−log(p)
n=26/95 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
P−type calcium transporter activity GO:0005388 p=6.5E−04 n=2 fg=0.08 bg=0.00
ATP binding GO:0005524 p=2.8E−03 n=5 fg=0.21 bg=0.04
voltage−gated calcium channel activity GO:0005245 p=5.8E−03 n=2 fg=0.08 bg=0.01
PDZ domain binding GO:0030165 p=7.7E−03 n=3 fg=0.12 bg=0.02
glutamate receptor binding GO:0035254 p=1.1E−02 n=2 fg=0.08 bg=0.01
oxidoreductase activity, acting on the C... GO:0016616 p=1.1E−02 n=2 fg=0.08 bg=0.01
ammonium ion binding GO:0070405 p=1.3E−02 n=2 fg=0.08 bg=0.01
steroid dehydrogenase activity GO:0016229 p=1.5E−02 n=1 fg=0.04 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=1.5E−02 n=1 fg=0.04 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0016652 p=1.5E−02 n=1 fg=0.04 bg=0.00
cyclohydrolase activity GO:0019238 p=1.5E−02 n=1 fg=0.04 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=1.5E−02 n=1 fg=0.04 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=1.5E−02 n=1 fg=0.04 bg=0.00
beta1−adrenergic receptor activity GO:0004940 p=1.5E−02 n=1 fg=0.04 bg=0.00
beta2−adrenergic receptor activity GO:0004941 p=1.5E−02 n=1 fg=0.04 bg=0.00
bradykinin receptor binding GO:0031711 p=1.5E−02 n=1 fg=0.04 bg=0.00
B2 bradykinin receptor binding GO:0031713 p=1.5E−02 n=1 fg=0.04 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004486 p=1.5E−02 n=1 fg=0.04 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004487 p=1.5E−02 n=1 fg=0.04 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004488 p=1.5E−02 n=1 fg=0.04 bg=0.00
U2 snRNP binding GO:1990447 p=1.5E−02 n=1 fg=0.04 bg=0.00
beta−adrenergic receptor activity GO:0004939 p=1.5E−02 n=1 fg=0.04 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=1.5E−02 n=1 fg=0.04 bg=0.00
methenyltetrahydrofolate cyclohydrolase ... GO:0004477 p=1.5E−02 n=1 fg=0.04 bg=0.00
formate−tetrahydrofolate ligase activity GO:0004329 p=1.5E−02 n=1 fg=0.04 bg=0.00
alpha−N−acetylgalactosaminidase activity GO:0008456 p=1.5E−02 n=1 fg=0.04 bg=0.00
dopamine binding GO:0035240 p=1.5E−02 n=1 fg=0.04 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=1.5E−02 n=1 fg=0.04 bg=0.00
alpha−galactosidase activity GO:0004557 p=1.5E−02 n=1 fg=0.04 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=1.5E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=24/95 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
caveola GO:0005901 p=1.2E−03 n=3 fg=0.12 bg=0.01
rhabdomere GO:0016028 p=4.9E−03 n=2 fg=0.08 bg=0.00
T−tubule GO:0030315 p=7.7E−03 n=2 fg=0.08 bg=0.01
integral component of plasma membrane GO:0005887 p=8.7E−03 n=6 fg=0.24 bg=0.08
L−type voltage−gated calcium channel com... GO:1990454 p=1.4E−02 n=1 fg=0.04 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=1.4E−02 n=1 fg=0.04 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=1.4E−02 n=1 fg=0.04 bg=0.00
neuronal cell body membrane GO:0032809 p=1.5E−02 n=2 fg=0.08 bg=0.01
cell body membrane GO:0044298 p=1.7E−02 n=2 fg=0.08 bg=0.01
clathrin−coated vesicle membrane GO:0030665 p=1.7E−02 n=2 fg=0.08 bg=0.01
cell−substrate junction GO:0030055 p=2.5E−02 n=2 fg=0.08 bg=0.01
Wnt signalosome GO:1990909 p=2.8E−02 n=1 fg=0.04 bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=2.8E−02 n=1 fg=0.04 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=2.8E−02 n=1 fg=0.04 bg=0.00
dendritic spine membrane GO:0032591 p=4.1E−02 n=1 fg=0.04 bg=0.00
postsynaptic specialization membrane GO:0099634 p=4.1E−02 n=1 fg=0.04 bg=0.00
endoplasmic reticulum cisternal network GO:0071781 p=4.1E−02 n=1 fg=0.04 bg=0.00
intrinsic component of mitochondrial out... GO:0031306 p=4.1E−02 n=1 fg=0.04 bg=0.00
integral component of mitochondrial oute... GO:0031307 p=4.1E−02 n=1 fg=0.04 bg=0.00
inaD signaling complex GO:0016027 p=4.1E−02 n=1 fg=0.04 bg=0.00
subrhabdomeral cisterna GO:0016029 p=4.1E−02 n=1 fg=0.04 bg=0.00
smooth endoplasmic reticulum cisterna GO:0120082 p=4.1E−02 n=1 fg=0.04 bg=0.00
U2 snRNP GO:0005686 p=4.1E−02 n=1 fg=0.04 bg=0.00
postsynaptic density membrane GO:0098839 p=4.1E−02 n=1 fg=0.04 bg=0.00
apical part of cell GO:0045177 p=4.1E−02 n=4 fg=0.16 bg=0.05
cell junction GO:0030054 p=4.2E−02 n=7 fg=0.28 bg=0.13
coated vesicle membrane GO:0030662 p=4.2E−02 n=2 fg=0.08 bg=0.01
Z disc GO:0030018 p=4.5E−02 n=2 fg=0.08 bg=0.01
leading edge membrane GO:0031256 p=4.5E−02 n=2 fg=0.08 bg=0.01
neuron projection GO:0043005 p=4.9E−02 n=7 fg=0.28 bg=0.14
0 1 2 3 4 5
−log(p)
n=25/95 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction