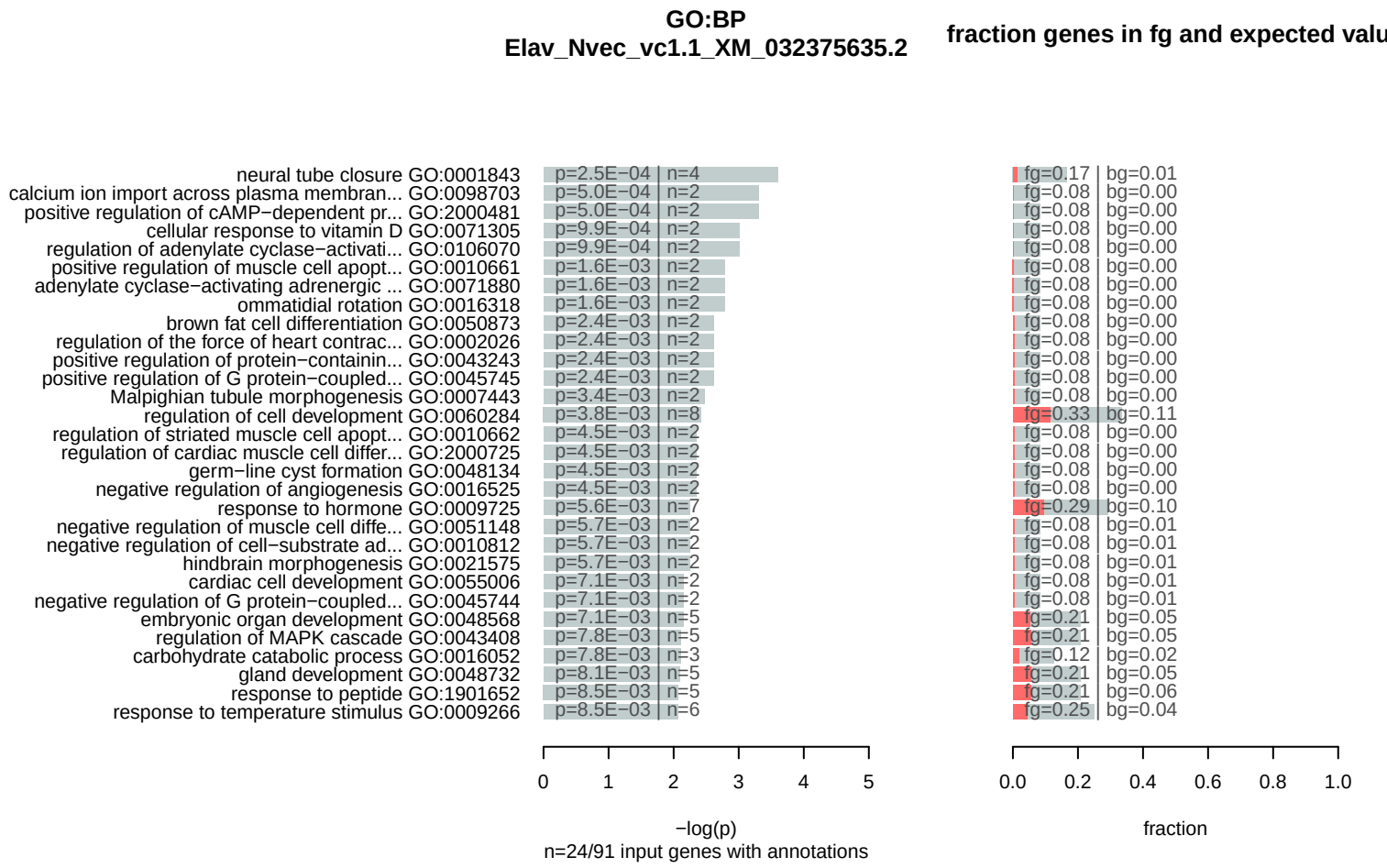
GO:BP
Elav_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
neural tube closure GO:0001843 p=2.5E−04 n=4 fg=0.17 bg=0.01
calcium ion import across plasma membran... GO:0098703 p=5.0E−04 n=2 fg=0.08 bg=0.00
positive regulation of cAMP−dependent pr... GO:2000481 p=5.0E−04 n=2 fg=0.08 bg=0.00
cellular response to vitamin D GO:0071305 p=9.9E−04 n=2 fg=0.08 bg=0.00
regulation of adenylate cyclase−activati... GO:0106070 p=9.9E−04 n=2 fg=0.08 bg=0.00
positive regulation of muscle cell apopt... GO:0010661 p=1.6E−03 n=2 fg=0.08 bg=0.00
adenylate cyclase−activating adrenergic ... GO:0071880 p=1.6E−03 n=2 fg=0.08 bg=0.00
ommatidial rotation GO:0016318 p=1.6E−03 n=2 fg=0.08 bg=0.00
brown fat cell differentiation GO:0050873 p=2.4E−03 n=2 fg=0.08 bg=0.00
regulation of the force of heart contrac... GO:0002026 p=2.4E−03 n=2 fg=0.08 bg=0.00
positive regulation of protein−containin... GO:0043243 p=2.4E−03 n=2 fg=0.08 bg=0.00
positive regulation of G protein−coupled... GO:0045745 p=2.4E−03 n=2 fg=0.08 bg=0.00
Malpighian tubule morphogenesis GO:0007443 p=3.4E−03 n=2 fg=0.08 bg=0.00
regulation of cell development GO:0060284 p=3.8E−03 n=8 fg=0.33 bg=0.11
regulation of striated muscle cell apopt... GO:0010662 p=4.5E−03 n=2 fg=0.08 bg=0.00
regulation of cardiac muscle cell differ... GO:2000725 p=4.5E−03 n=2 fg=0.08 bg=0.00
germ−line cyst formation GO:0048134 p=4.5E−03 n=2 fg=0.08 bg=0.00
negative regulation of angiogenesis GO:0016525 p=4.5E−03 n=2 fg=0.08 bg=0.00
response to hormone GO:0009725 p=5.6E−03 n=7 fg=0.29 bg=0.10
negative regulation of muscle cell diffe... GO:0051148 p=5.7E−03 n=2 fg=0.08 bg=0.01
negative regulation of cell−substrate ad... GO:0010812 p=5.7E−03 n=2 fg=0.08 bg=0.01
hindbrain morphogenesis GO:0021575 p=5.7E−03 n=2 fg=0.08 bg=0.01
cardiac cell development GO:0055006 p=7.1E−03 n=2 fg=0.08 bg=0.01
negative regulation of G protein−coupled... GO:0045744 p=7.1E−03 n=2 fg=0.08 bg=0.01
embryonic organ development GO:0048568 p=7.1E−03 n=5 fg=0.21 bg=0.05
regulation of MAPK cascade GO:0043408 p=7.8E−03 n=5 fg=0.21 bg=0.05
carbohydrate catabolic process GO:0016052 p=7.8E−03 n=3 fg=0.12 bg=0.02
gland development GO:0048732 p=8.1E−03 n=5 fg=0.21 bg=0.05
response to peptide GO:1901652 p=8.5E−03 n=5 fg=0.21 bg=0.06
response to temperature stimulus GO:0009266 p=8.5E−03 n=6 fg=0.25 bg=0.04
0 1 2 3 4 5
−log(p)
n=24/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
G protein−coupled amine receptor activit... GO:0008227 p=1.9E−03 n=2 fg=0.09 bg=0.00
adenyl ribonucleotide binding GO:0032559 p=4.9E−03 n=5 fg=0.22 bg=0.05
PDZ domain binding GO:0030165 p=6.8E−03 n=3 fg=0.13 bg=0.02
glutamate receptor binding GO:0035254 p=1.0E−02 n=2 fg=0.09 bg=0.01
oxidoreductase activity, acting on NAD(P... GO:0016652 p=1.4E−02 n=1 fg=0.04 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=1.4E−02 n=1 fg=0.04 bg=0.00
beta1−adrenergic receptor activity GO:0004940 p=1.4E−02 n=1 fg=0.04 bg=0.00
beta2−adrenergic receptor activity GO:0004941 p=1.4E−02 n=1 fg=0.04 bg=0.00
formate−tetrahydrofolate ligase activity GO:0004329 p=1.4E−02 n=1 fg=0.04 bg=0.00
beta−adrenergic receptor activity GO:0004939 p=1.4E−02 n=1 fg=0.04 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004486 p=1.4E−02 n=1 fg=0.04 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004487 p=1.4E−02 n=1 fg=0.04 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004488 p=1.4E−02 n=1 fg=0.04 bg=0.00
methenyltetrahydrofolate cyclohydrolase ... GO:0004477 p=1.4E−02 n=1 fg=0.04 bg=0.00
dopamine binding GO:0035240 p=1.4E−02 n=1 fg=0.04 bg=0.00
cyclohydrolase activity GO:0019238 p=1.4E−02 n=1 fg=0.04 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=1.4E−02 n=1 fg=0.04 bg=0.00
alpha−galactosidase activity GO:0004557 p=1.4E−02 n=1 fg=0.04 bg=0.00
alpha−N−acetylgalactosaminidase activity GO:0008456 p=1.4E−02 n=1 fg=0.04 bg=0.00
U2 snRNP binding GO:1990447 p=1.4E−02 n=1 fg=0.04 bg=0.00
bradykinin receptor binding GO:0031711 p=1.4E−02 n=1 fg=0.04 bg=0.00
B2 bradykinin receptor binding GO:0031713 p=1.4E−02 n=1 fg=0.04 bg=0.00
ATP binding GO:0005524 p=1.5E−02 n=4 fg=0.17 bg=0.04
adenyl nucleotide binding GO:0030554 p=2.4E−02 n=6 fg=0.26 bg=0.05
nitric−oxide synthase inhibitor activity GO:0036487 p=2.9E−02 n=1 fg=0.04 bg=0.00
copper−dependent protein binding GO:0032767 p=2.9E−02 n=1 fg=0.04 bg=0.00
alpha−2A adrenergic receptor binding GO:0031694 p=2.9E−02 n=1 fg=0.04 bg=0.00
vinculin binding GO:0017166 p=2.9E−02 n=1 fg=0.04 bg=0.00
adrenergic receptor activity GO:0004935 p=2.9E−02 n=1 fg=0.04 bg=0.00
LIM domain binding GO:0030274 p=2.9E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=23/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
caveola GO:0005901 p=1.0E−03 n=3 fg=0.12 bg=0.01
neuronal cell body membrane GO:0032809 p=1.4E−02 n=2 fg=0.08 bg=0.01
cell body membrane GO:0044298 p=1.6E−02 n=2 fg=0.08 bg=0.01
clathrin−coated vesicle membrane GO:0030665 p=1.6E−02 n=2 fg=0.08 bg=0.01
cell−substrate junction GO:0030055 p=2.3E−02 n=2 fg=0.08 bg=0.01
Wnt signalosome GO:1990909 p=2.6E−02 n=1 fg=0.04 bg=0.00
integral component of plasma membrane GO:0005887 p=3.0E−02 n=5 fg=0.21 bg=0.07
sarcolemma GO:0042383 p=3.0E−02 n=2 fg=0.08 bg=0.01
plasma membrane bounded cell projection GO:0120025 p=3.1E−02 n=9 fg=0.38 bg=0.20
cell projection GO:0042995 p=3.2E−02 n=9 fg=0.38 bg=0.20
apical part of cell GO:0045177 p=3.6E−02 n=4 fg=0.17 bg=0.05
intrinsic component of plasma membrane GO:0031226 p=3.9E−02 n=5 fg=0.21 bg=0.08
coated vesicle membrane GO:0030662 p=3.9E−02 n=2 fg=0.08 bg=0.01
dendritic spine membrane GO:0032591 p=3.9E−02 n=1 fg=0.04 bg=0.00
postsynaptic specialization membrane GO:0099634 p=3.9E−02 n=1 fg=0.04 bg=0.00
intrinsic component of mitochondrial out... GO:0031306 p=3.9E−02 n=1 fg=0.04 bg=0.00
integral component of mitochondrial oute... GO:0031307 p=3.9E−02 n=1 fg=0.04 bg=0.00
inaD signaling complex GO:0016027 p=3.9E−02 n=1 fg=0.04 bg=0.00
U2 snRNP GO:0005686 p=3.9E−02 n=1 fg=0.04 bg=0.00
postsynaptic density membrane GO:0098839 p=3.9E−02 n=1 fg=0.04 bg=0.00
neuron projection GO:0043005 p=3.9E−02 n=7 fg=0.29 bg=0.14
Z disc GO:0030018 p=4.2E−02 n=2 fg=0.08 bg=0.01
leading edge membrane GO:0031256 p=4.2E−02 n=2 fg=0.08 bg=0.01
I band GO:0031674 p=4.5E−02 n=2 fg=0.08 bg=0.01
eukaryotic translation initiation factor... GO:0005851 p=5.2E−02 n=1 fg=0.04 bg=0.00
zonula adherens GO:0005915 p=5.2E−02 n=1 fg=0.04 bg=0.00
sperm principal piece GO:0097228 p=6.5E−02 n=1 fg=0.04 bg=0.00
clathrin−coated vesicle GO:0030136 p=6.6E−02 n=2 fg=0.08 bg=0.02
apical plasma membrane GO:0016324 p=6.7E−02 n=3 fg=0.12 bg=0.04
cell cortex GO:0005938 p=7.2E−02 n=3 fg=0.12 bg=0.04
0 1 2 3 4 5
−log(p)
n=24/91 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction