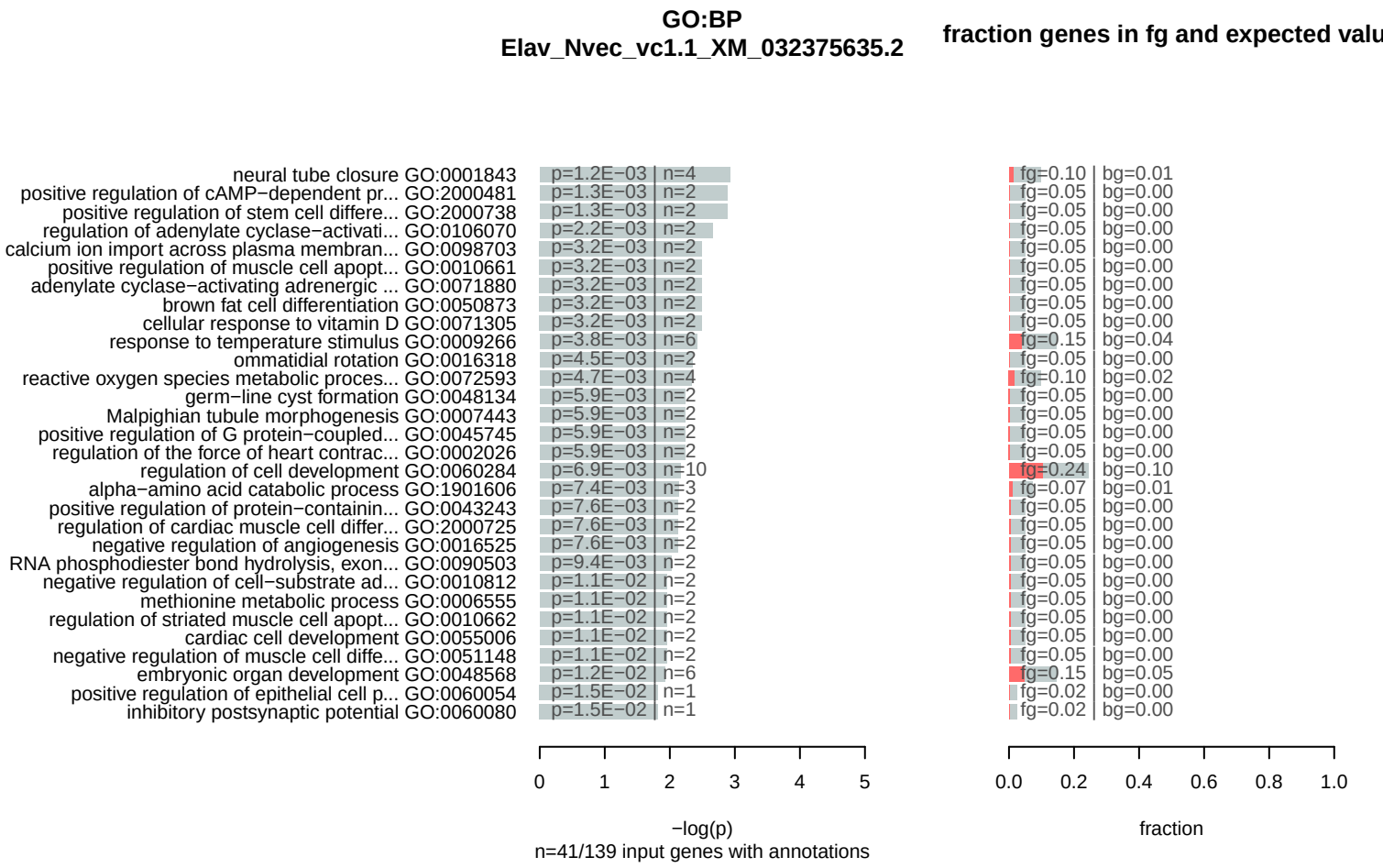
GO:BP
Elav_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
neural tube closure GO:0001843 p=1.2E−03 n=4 fg=0.10 bg=0.01
positive regulation of cAMP−dependent pr... GO:2000481 p=1.3E−03 n=2 fg=0.05 bg=0.00
positive regulation of stem cell differe... GO:2000738 p=1.3E−03 n=2 fg=0.05 bg=0.00
regulation of adenylate cyclase−activati... GO:0106070 p=2.2E−03 n=2 fg=0.05 bg=0.00
calcium ion import across plasma membran... GO:0098703 p=3.2E−03 n=2 fg=0.05 bg=0.00
positive regulation of muscle cell apopt... GO:0010661 p=3.2E−03 n=2 fg=0.05 bg=0.00
adenylate cyclase−activating adrenergic ... GO:0071880 p=3.2E−03 n=2 fg=0.05 bg=0.00
brown fat cell differentiation GO:0050873 p=3.2E−03 n=2 fg=0.05 bg=0.00
cellular response to vitamin D GO:0071305 p=3.2E−03 n=2 fg=0.05 bg=0.00
response to temperature stimulus GO:0009266 p=3.8E−03 n=6 fg=0.15 bg=0.04
ommatidial rotation GO:0016318 p=4.5E−03 n=2 fg=0.05 bg=0.00
reactive oxygen species metabolic proces... GO:0072593 p=4.7E−03 n=4 fg=0.10 bg=0.02
germ−line cyst formation GO:0048134 p=5.9E−03 n=2 fg=0.05 bg=0.00
Malpighian tubule morphogenesis GO:0007443 p=5.9E−03 n=2 fg=0.05 bg=0.00
positive regulation of G protein−coupled... GO:0045745 p=5.9E−03 n=2 fg=0.05 bg=0.00
regulation of the force of heart contrac... GO:0002026 p=5.9E−03 n=2 fg=0.05 bg=0.00
regulation of cell development GO:0060284 p=6.9E−03 n=10 fg=0.24 bg=0.10
alpha−amino acid catabolic process GO:1901606 p=7.4E−03 n=3 fg=0.07 bg=0.01
positive regulation of protein−containin... GO:0043243 p=7.6E−03 n=2 fg=0.05 bg=0.00
regulation of cardiac muscle cell differ... GO:2000725 p=7.6E−03 n=2 fg=0.05 bg=0.00
negative regulation of angiogenesis GO:0016525 p=7.6E−03 n=2 fg=0.05 bg=0.00
RNA phosphodiester bond hydrolysis, exon... GO:0090503 p=9.4E−03 n=2 fg=0.05 bg=0.00
negative regulation of cell−substrate ad... GO:0010812 p=1.1E−02 n=2 fg=0.05 bg=0.00
methionine metabolic process GO:0006555 p=1.1E−02 n=2 fg=0.05 bg=0.00
regulation of striated muscle cell apopt... GO:0010662 p=1.1E−02 n=2 fg=0.05 bg=0.00
cardiac cell development GO:0055006 p=1.1E−02 n=2 fg=0.05 bg=0.00
negative regulation of muscle cell diffe... GO:0051148 p=1.1E−02 n=2 fg=0.05 bg=0.00
embryonic organ development GO:0048568 p=1.2E−02 n=6 fg=0.15 bg=0.05
positive regulation of epithelial cell p... GO:0060054 p=1.5E−02 n=1 fg=0.02 bg=0.00
inhibitory postsynaptic potential GO:0060080 p=1.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=41/139 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
NAD(P)+ transhydrogenase activity GO:0008746 p=2.2E−04 n=2 fg=0.06 bg=0.00
G protein−coupled amine receptor activit... GO:0008227 p=2.2E−03 n=2 fg=0.06 bg=0.00
adenyl ribonucleotide binding GO:0032559 p=7.4E−03 n=6 fg=0.17 bg=0.05
3'−5'−exoribonuclease activity GO:0000175 p=7.6E−03 n=2 fg=0.06 bg=0.00
PDZ domain binding GO:0030165 p=1.3E−02 n=3 fg=0.08 bg=0.01
aminomethyltransferase activity GO:0004047 p=1.5E−02 n=1 fg=0.03 bg=0.00
dopamine binding GO:0035240 p=1.5E−02 n=1 fg=0.03 bg=0.00
NAD(P)+ transhydrogenase (B−specific) ac... GO:0003957 p=1.5E−02 n=1 fg=0.03 bg=0.00
histone pre−mRNA stem−loop binding GO:0071207 p=1.5E−02 n=1 fg=0.03 bg=0.00
bradykinin receptor binding GO:0031711 p=1.5E−02 n=1 fg=0.03 bg=0.00
B2 bradykinin receptor binding GO:0031713 p=1.5E−02 n=1 fg=0.03 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004486 p=1.5E−02 n=1 fg=0.03 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004487 p=1.5E−02 n=1 fg=0.03 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004488 p=1.5E−02 n=1 fg=0.03 bg=0.00
methenyltetrahydrofolate cyclohydrolase ... GO:0004477 p=1.5E−02 n=1 fg=0.03 bg=0.00
NAD(P)+ transhydrogenase (AB−specific) a... GO:0008750 p=1.5E−02 n=1 fg=0.03 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=1.5E−02 n=1 fg=0.03 bg=0.00
formate−tetrahydrofolate ligase activity GO:0004329 p=1.5E−02 n=1 fg=0.03 bg=0.00
beta1−adrenergic receptor activity GO:0004940 p=1.5E−02 n=1 fg=0.03 bg=0.00
beta2−adrenergic receptor activity GO:0004941 p=1.5E−02 n=1 fg=0.03 bg=0.00
beta−adrenergic receptor activity GO:0004939 p=1.5E−02 n=1 fg=0.03 bg=0.00
glutamate receptor binding GO:0035254 p=1.6E−02 n=2 fg=0.06 bg=0.01
ATP binding GO:0005524 p=1.7E−02 n=5 fg=0.14 bg=0.04
G protein−coupled receptor binding GO:0001664 p=2.3E−02 n=3 fg=0.08 bg=0.02
norepinephrine binding GO:0051380 p=3.0E−02 n=1 fg=0.03 bg=0.00
U2 snRNP binding GO:1990447 p=3.0E−02 n=1 fg=0.03 bg=0.00
methionine adenosyltransferase activity GO:0004478 p=3.0E−02 n=1 fg=0.03 bg=0.00
copper−dependent protein binding GO:0032767 p=3.0E−02 n=1 fg=0.03 bg=0.00
octopamine receptor activity GO:0004989 p=3.0E−02 n=1 fg=0.03 bg=0.00
alpha−2A adrenergic receptor binding GO:0031694 p=3.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/139 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=5.0E−03 n=3 fg=0.07 bg=0.01
histone pre−mRNA 3'end processing comple... GO:0071204 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell part GO:0033643 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular part GO:0033646 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular organelle GO:0033647 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular region GO:0043656 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell GO:0043657 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell nuclear part GO:0044094 p=1.6E−02 n=1 fg=0.02 bg=0.00
other organism part GO:0044217 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell nucleus GO:0042025 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cellular component GO:0018995 p=1.6E−02 n=1 fg=0.02 bg=0.00
paraspeckles GO:0042382 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell PML body GO:0075341 p=1.6E−02 n=1 fg=0.02 bg=0.00
NLS−dependent protein nuclear import com... GO:0042564 p=1.6E−02 n=1 fg=0.02 bg=0.00
neuronal cell body membrane GO:0032809 p=2.8E−02 n=2 fg=0.05 bg=0.01
clathrin−coated vesicle membrane GO:0030665 p=2.8E−02 n=2 fg=0.05 bg=0.01
CCR4−NOT core complex GO:0030015 p=3.1E−02 n=1 fg=0.02 bg=0.00
Wnt signalosome GO:1990909 p=3.1E−02 n=1 fg=0.02 bg=0.00
glycine cleavage complex GO:0005960 p=3.1E−02 n=1 fg=0.02 bg=0.00
nucleocytoplasmic transport complex GO:0031074 p=3.1E−02 n=1 fg=0.02 bg=0.00
cell body membrane GO:0044298 p=3.1E−02 n=2 fg=0.05 bg=0.01
RSC−type complex GO:0016586 p=4.6E−02 n=1 fg=0.02 bg=0.00
methionine adenosyltransferase complex GO:0048269 p=4.6E−02 n=1 fg=0.02 bg=0.00
CCR4−NOT complex GO:0030014 p=4.6E−02 n=1 fg=0.02 bg=0.00
astral microtubule GO:0000235 p=4.6E−02 n=1 fg=0.02 bg=0.00
motile cilium GO:0031514 p=5.2E−02 n=3 fg=0.07 bg=0.02
dendritic spine membrane GO:0032591 p=6.1E−02 n=1 fg=0.02 bg=0.00
intrinsic component of mitochondrial out... GO:0031306 p=6.1E−02 n=1 fg=0.02 bg=0.00
integral component of mitochondrial oute... GO:0031307 p=6.1E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=42/139 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction