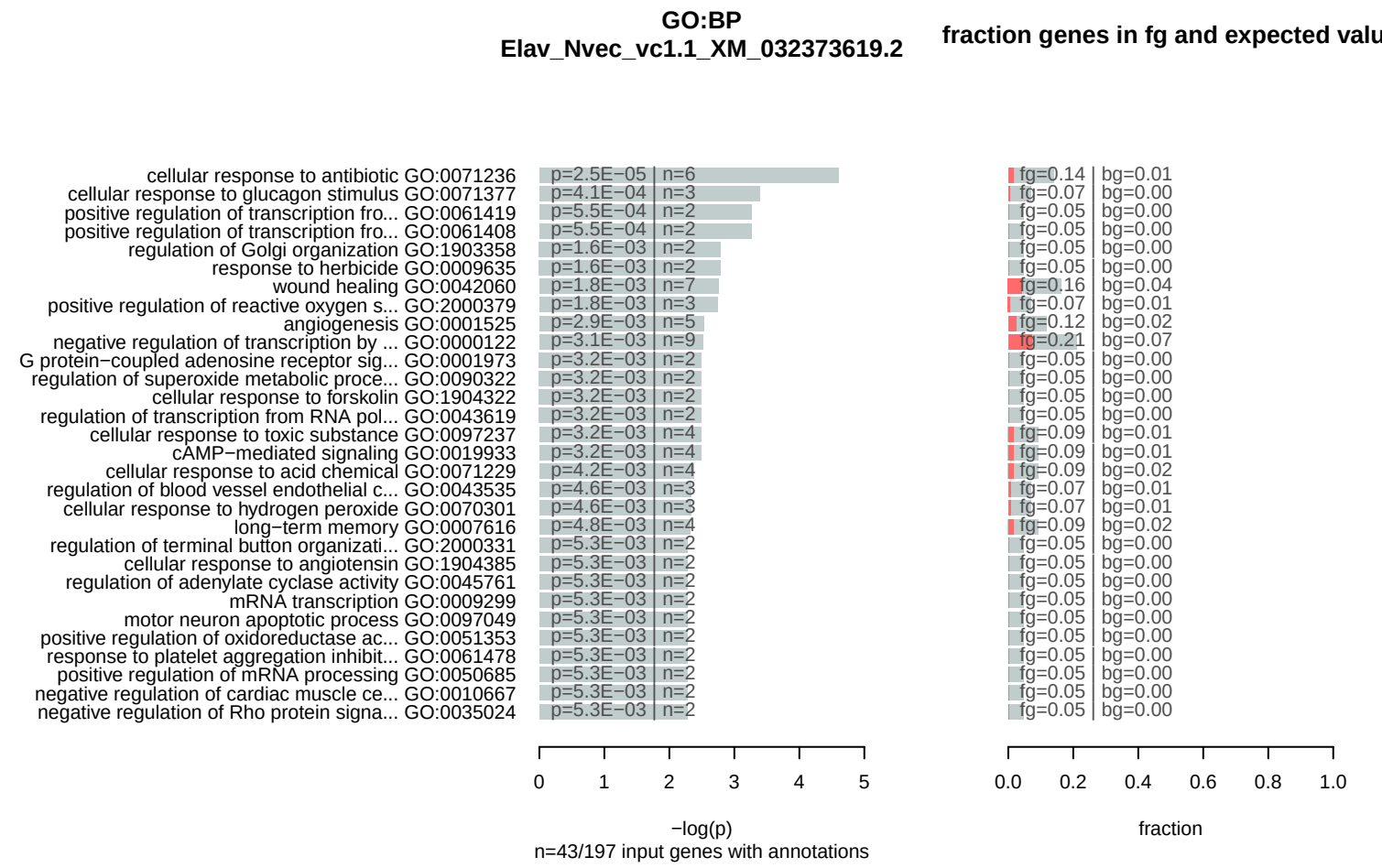
GO:BP
Elav_Nvec_vc1.1_XM_032373619.2
fraction genes in fg and expected valu
cellular response to antibiotic GO:0071236 p=2.5E−05 n=6 fg=0.14 bg=0.01
cellular response to glucagon stimulus GO:0071377 p=4.1E−04 n=3 fg=0.07 bg=0.00
positive regulation of transcription fro... GO:0061419 p=5.5E−04 n=2 fg=0.05 bg=0.00
positive regulation of transcription fro... GO:0061408 p=5.5E−04 n=2 fg=0.05 bg=0.00
regulation of Golgi organization GO:1903358 p=1.6E−03 n=2 fg=0.05 bg=0.00
response to herbicide GO:0009635 p=1.6E−03 n=2 fg=0.05 bg=0.00
wound healing GO:0042060 p=1.8E−03 n=7 fg=0.16 bg=0.04
positive regulation of reactive oxygen s... GO:2000379 p=1.8E−03 n=3 fg=0.07 bg=0.01
angiogenesis GO:0001525 p=2.9E−03 n=5 fg=0.12 bg=0.02
negative regulation of transcription by ... GO:0000122 p=3.1E−03 n=9 fg=0.21 bg=0.07
G protein−coupled adenosine receptor sig... GO:0001973 p=3.2E−03 n=2 fg=0.05 bg=0.00
regulation of superoxide metabolic proce... GO:0090322 p=3.2E−03 n=2 fg=0.05 bg=0.00
cellular response to forskolin GO:1904322 p=3.2E−03 n=2 fg=0.05 bg=0.00
regulation of transcription from RNA pol... GO:0043619 p=3.2E−03 n=2 fg=0.05 bg=0.00
cellular response to toxic substance GO:0097237 p=3.2E−03 n=4 fg=0.09 bg=0.01
cAMP−mediated signaling GO:0019933 p=3.2E−03 n=4 fg=0.09 bg=0.01
cellular response to acid chemical GO:0071229 p=4.2E−03 n=4 fg=0.09 bg=0.02
regulation of blood vessel endothelial c... GO:0043535 p=4.6E−03 n=3 fg=0.07 bg=0.01
cellular response to hydrogen peroxide GO:0070301 p=4.6E−03 n=3 fg=0.07 bg=0.01
long−term memory GO:0007616 p=4.8E−03 n=4 fg=0.09 bg=0.02
regulation of terminal button organizati... GO:2000331 p=5.3E−03 n=2 fg=0.05 bg=0.00
cellular response to angiotensin GO:1904385 p=5.3E−03 n=2 fg=0.05 bg=0.00
regulation of adenylate cyclase activity GO:0045761 p=5.3E−03 n=2 fg=0.05 bg=0.00
mRNA transcription GO:0009299 p=5.3E−03 n=2 fg=0.05 bg=0.00
motor neuron apoptotic process GO:0097049 p=5.3E−03 n=2 fg=0.05 bg=0.00
positive regulation of oxidoreductase ac... GO:0051353 p=5.3E−03 n=2 fg=0.05 bg=0.00
response to platelet aggregation inhibit... GO:0061478 p=5.3E−03 n=2 fg=0.05 bg=0.00
positive regulation of mRNA processing GO:0050685 p=5.3E−03 n=2 fg=0.05 bg=0.00
negative regulation of cardiac muscle ce... GO:0010667 p=5.3E−03 n=2 fg=0.05 bg=0.00
negative regulation of Rho protein signa... GO:0035024 p=5.3E−03 n=2 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=43/197 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032373619.2
fraction genes in fg and expected valu
protein heterodimerization activity GO:0046982 p=1.5E−03 n=8 fg=0.20 bg=0.06
protein domain specific binding GO:0019904 p=3.0E−03 n=10 fg=0.25 bg=0.09
phosphorus−oxygen lyase activity GO:0016849 p=5.9E−03 n=2 fg=0.05 bg=0.00
cholesterol binding GO:0015485 p=8.7E−03 n=2 fg=0.05 bg=0.00
cyclin−dependent protein serine/threonin... GO:0016538 p=8.7E−03 n=2 fg=0.05 bg=0.00
carboxy−lyase activity GO:0016831 p=8.7E−03 n=2 fg=0.05 bg=0.00
cyclase activity GO:0009975 p=8.7E−03 n=2 fg=0.05 bg=0.00
protein kinase A binding GO:0051018 p=1.2E−02 n=2 fg=0.05 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=1.2E−02 n=2 fg=0.05 bg=0.00
heterocyclic compound binding GO:1901363 p=2.2E−02 n=17 fg=0.42 bg=0.27
GDP binding GO:0019003 p=2.4E−02 n=2 fg=0.05 bg=0.01
cobalt ion binding GO:0050897 p=2.5E−02 n=1 fg=0.03 bg=0.00
FAD−AMP lyase (cyclizing) activity GO:0034012 p=2.5E−02 n=1 fg=0.03 bg=0.00
adenosine deaminase activity GO:0004000 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=2.5E−02 n=1 fg=0.03 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=2.5E−02 n=1 fg=0.03 bg=0.00
calcium− and calmodulin−responsive adeny... GO:0008294 p=2.5E−02 n=1 fg=0.03 bg=0.00
volume−sensitive chloride channel activi... GO:0072320 p=2.5E−02 n=1 fg=0.03 bg=0.00
glycerone kinase activity GO:0004371 p=2.5E−02 n=1 fg=0.03 bg=0.00
triokinase activity GO:0050354 p=2.5E−02 n=1 fg=0.03 bg=0.00
7SK snRNA binding GO:0097322 p=2.5E−02 n=1 fg=0.03 bg=0.00
volume−sensitive anion channel activity GO:0005225 p=2.5E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=2.5E−02 n=1 fg=0.03 bg=0.00
double−stranded RNA adenosine deaminase ... GO:0003726 p=2.5E−02 n=1 fg=0.03 bg=0.00
alpha−1,6−mannosylglycoprotein 2−beta−N−... GO:0008455 p=2.5E−02 n=1 fg=0.03 bg=0.00
nucleic acid binding GO:0003676 p=2.9E−02 n=13 fg=0.33 bg=0.19
chromatin DNA binding GO:0031490 p=4.0E−02 n=2 fg=0.05 bg=0.01
transcription corepressor activity GO:0003714 p=4.1E−02 n=3 fg=0.07 bg=0.02
RNA polymerase II transcription regulato... GO:0000977 p=4.5E−02 n=5 fg=0.12 bg=0.05
kinase inhibitor activity GO:0019210 p=4.6E−02 n=2 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=40/197 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032373619.2
fraction genes in fg and expected valu
cytosol GO:0005829 p=4.9E−03 n=25 fg=0.60 bg=0.39
germ cell nucleus GO:0043073 p=1.3E−02 n=2 fg=0.05 bg=0.00
integrin alpha9−beta1 complex GO:0034679 p=2.3E−02 n=1 fg=0.02 bg=0.00
sarcoplasmic reticulum lumen GO:0033018 p=2.3E−02 n=1 fg=0.02 bg=0.00
postsynapse GO:0098794 p=3.0E−02 n=5 fg=0.12 bg=0.04
protein kinase complex GO:1902911 p=4.0E−02 n=2 fg=0.05 bg=0.01
plasma membrane GO:0005886 p=4.1E−02 n=17 fg=0.40 bg=0.27
Golgi apparatus GO:0005794 p=4.3E−02 n=10 fg=0.24 bg=0.13
plasma membrane region GO:0098590 p=4.5E−02 n=8 fg=0.19 bg=0.10
mitochondrial crista GO:0030061 p=4.6E−02 n=1 fg=0.02 bg=0.00
integrin complex GO:0008305 p=4.6E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=4.6E−02 n=1 fg=0.02 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=4.6E−02 n=1 fg=0.02 bg=0.00
protein complex involved in cell adhesio... GO:0098636 p=4.6E−02 n=1 fg=0.02 bg=0.00
prefoldin complex GO:0016272 p=4.6E−02 n=1 fg=0.02 bg=0.00
synapse GO:0045202 p=4.9E−02 n=8 fg=0.19 bg=0.10
external side of plasma membrane GO:0009897 p=5.7E−02 n=2 fg=0.05 bg=0.01
heterochromatin GO:0000792 p=5.7E−02 n=2 fg=0.05 bg=0.01
neuron spine GO:0044309 p=6.3E−02 n=3 fg=0.07 bg=0.02
dendritic spine GO:0043197 p=6.3E−02 n=3 fg=0.07 bg=0.02
side of membrane GO:0098552 p=6.4E−02 n=4 fg=0.10 bg=0.04
mitochondrial inner membrane GO:0005743 p=6.7E−02 n=4 fg=0.10 bg=0.04
NuRD complex GO:0016581 p=6.8E−02 n=1 fg=0.02 bg=0.00
inhibitory synapse GO:0060077 p=6.8E−02 n=1 fg=0.02 bg=0.00
CHD−type complex GO:0090545 p=6.8E−02 n=1 fg=0.02 bg=0.00
male germ cell nucleus GO:0001673 p=6.8E−02 n=1 fg=0.02 bg=0.00
intercalary heterochromatin GO:0005725 p=6.8E−02 n=1 fg=0.02 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=6.8E−02 n=1 fg=0.02 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=6.8E−02 n=1 fg=0.02 bg=0.00
podosome GO:0002102 p=6.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=42/197 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction