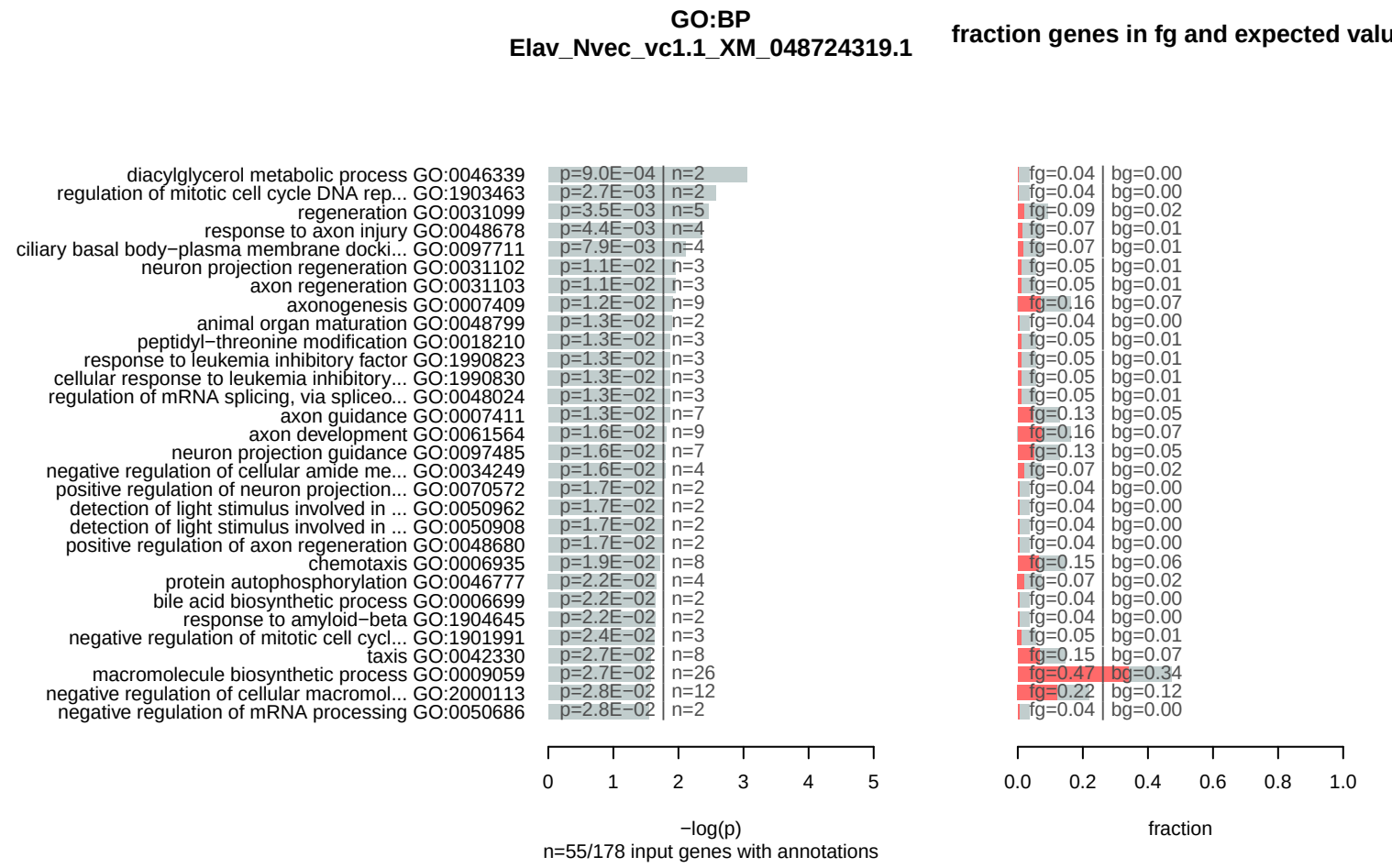
GO:BP
Elav_Nvec_vc1.1_XM_048724319.1
fraction genes in fg and expected valu
diacylglycerol metabolic process GO:0046339 p=9.0E−04 n=2 fg=0.04 bg=0.00
regulation of mitotic cell cycle DNA rep... GO:1903463 p=2.7E−03 n=2 fg=0.04 bg=0.00
regeneration GO:0031099 p=3.5E−03 n=5 fg=0.09 bg=0.02
response to axon injury GO:0048678 p=4.4E−03 n=4 fg=0.07 bg=0.01
ciliary basal body−plasma membrane docki... GO:0097711 p=7.9E−03 n=4 fg=0.07 bg=0.01
neuron projection regeneration GO:0031102 p=1.1E−02 n=3 fg=0.05 bg=0.01
axon regeneration GO:0031103 p=1.1E−02 n=3 fg=0.05 bg=0.01
axonogenesis GO:0007409 p=1.2E−02 n=9 fg=0.16 bg=0.07
animal organ maturation GO:0048799 p=1.3E−02 n=2 fg=0.04 bg=0.00
peptidyl−threonine modification GO:0018210 p=1.3E−02 n=3 fg=0.05 bg=0.01
response to leukemia inhibitory factor GO:1990823 p=1.3E−02 n=3 fg=0.05 bg=0.01
cellular response to leukemia inhibitory... GO:1990830 p=1.3E−02 n=3 fg=0.05 bg=0.01
regulation of mRNA splicing, via spliceo... GO:0048024 p=1.3E−02 n=3 fg=0.05 bg=0.01
axon guidance GO:0007411 p=1.3E−02 n=7 fg=0.13 bg=0.05
axon development GO:0061564 p=1.6E−02 n=9 fg=0.16 bg=0.07
neuron projection guidance GO:0097485 p=1.6E−02 n=7 fg=0.13 bg=0.05
negative regulation of cellular amide me... GO:0034249 p=1.6E−02 n=4 fg=0.07 bg=0.02
positive regulation of neuron projection... GO:0070572 p=1.7E−02 n=2 fg=0.04 bg=0.00
detection of light stimulus involved in ... GO:0050962 p=1.7E−02 n=2 fg=0.04 bg=0.00
detection of light stimulus involved in ... GO:0050908 p=1.7E−02 n=2 fg=0.04 bg=0.00
positive regulation of axon regeneration GO:0048680 p=1.7E−02 n=2 fg=0.04 bg=0.00
chemotaxis GO:0006935 p=1.9E−02 n=8 fg=0.15 bg=0.06
protein autophosphorylation GO:0046777 p=2.2E−02 n=4 fg=0.07 bg=0.02
bile acid biosynthetic process GO:0006699 p=2.2E−02 n=2 fg=0.04 bg=0.00
response to amyloid−beta GO:1904645 p=2.2E−02 n=2 fg=0.04 bg=0.00
negative regulation of mitotic cell cycl... GO:1901991 p=2.4E−02 n=3 fg=0.05 bg=0.01
taxis GO:0042330 p=2.7E−02 n=8 fg=0.15 bg=0.07
macromolecule biosynthetic process GO:0009059 p=2.7E−02 n=26 fg=0.47 bg=0.34
negative regulation of cellular macromol... GO:2000113 p=2.8E−02 n=12 fg=0.22 bg=0.12
negative regulation of mRNA processing GO:0050686 p=2.8E−02 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=55/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048724319.1
fraction genes in fg and expected valu
mRNA regulatory element binding translat... GO:0000900 p=2.7E−03 n=2 fg=0.04 bg=0.00
tau−protein kinase activity GO:0050321 p=5.4E−03 n=2 fg=0.04 bg=0.00
poly(U) RNA binding GO:0008266 p=8.7E−03 n=2 fg=0.04 bg=0.00
protein tyrosine kinase activity GO:0004713 p=1.4E−02 n=3 fg=0.06 bg=0.01
guanyl−nucleotide exchange factor activi... GO:0005085 p=1.7E−02 n=4 fg=0.08 bg=0.02
ubiquitin−like protein ligase binding GO:0044389 p=1.8E−02 n=6 fg=0.12 bg=0.04
voltage−gated calcium channel activity GO:0005245 p=2.3E−02 n=2 fg=0.04 bg=0.01
transcription coregulator activity GO:0003712 p=2.4E−02 n=7 fg=0.14 bg=0.06
calcium channel regulator activity GO:0005246 p=2.9E−02 n=2 fg=0.04 bg=0.01
D−glucose transmembrane transporter acti... GO:0055056 p=3.1E−02 n=1 fg=0.02 bg=0.00
L−alanine:2−oxoglutarate aminotransferas... GO:0004021 p=3.1E−02 n=1 fg=0.02 bg=0.00
rRNA primary transcript binding GO:0042134 p=3.1E−02 n=1 fg=0.02 bg=0.00
leptin receptor binding GO:1990460 p=3.1E−02 n=1 fg=0.02 bg=0.00
sugar transmembrane transporter activity GO:0051119 p=3.1E−02 n=1 fg=0.02 bg=0.00
transferrin receptor binding GO:1990459 p=3.1E−02 n=1 fg=0.02 bg=0.00
carbohydrate:cation symporter activity GO:0005402 p=3.1E−02 n=1 fg=0.02 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=3.1E−02 n=1 fg=0.02 bg=0.00
carbohydrate transmembrane transporter a... GO:0015144 p=3.1E−02 n=1 fg=0.02 bg=0.00
monosaccharide transmembrane transporter... GO:0015145 p=3.1E−02 n=1 fg=0.02 bg=0.00
hexose transmembrane transporter activit... GO:0015149 p=3.1E−02 n=1 fg=0.02 bg=0.00
nickel cation binding GO:0016151 p=3.1E−02 n=1 fg=0.02 bg=0.00
alanine−oxo−acid transaminase activity GO:0047635 p=3.1E−02 n=1 fg=0.02 bg=0.00
polypeptide N−acetylgalactosaminyltransf... GO:0004653 p=3.1E−02 n=1 fg=0.02 bg=0.00
SUMO binding GO:0032183 p=3.1E−02 n=1 fg=0.02 bg=0.00
carbohydrate:proton symporter activity GO:0005351 p=3.1E−02 n=1 fg=0.02 bg=0.00
glucose transmembrane transporter activi... GO:0005355 p=3.1E−02 n=1 fg=0.02 bg=0.00
riboflavin transmembrane transporter act... GO:0032217 p=3.1E−02 n=1 fg=0.02 bg=0.00
transcription coactivator activity GO:0003713 p=3.2E−02 n=5 fg=0.10 bg=0.04
ribonucleoprotein complex binding GO:0043021 p=3.9E−02 n=3 fg=0.06 bg=0.02
nucleoside−triphosphatase regulator acti... GO:0060589 p=4.3E−02 n=6 fg=0.12 bg=0.05
0 1 2 3 4 5
−log(p)
n=49/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048724319.1
fraction genes in fg and expected valu
presynaptic active zone GO:0048786 p=1.7E−03 n=4 fg=0.07 bg=0.01
nuclear body GO:0016604 p=6.6E−03 n=9 fg=0.16 bg=0.06
voltage−gated calcium channel complex GO:0005891 p=8.6E−03 n=2 fg=0.04 bg=0.00
transcription factor TFTC complex GO:0033276 p=8.6E−03 n=2 fg=0.04 bg=0.00
excitatory synapse GO:0060076 p=1.3E−02 n=2 fg=0.04 bg=0.00
vesicle coat GO:0030120 p=1.7E−02 n=2 fg=0.04 bg=0.00
COPI−coated vesicle GO:0030137 p=1.7E−02 n=2 fg=0.04 bg=0.00
membrane−bounded organelle GO:0043227 p=2.8E−02 n=51 fg=0.93 bg=0.81
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=3.0E−02 n=1 fg=0.02 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=3.0E−02 n=1 fg=0.02 bg=0.00
chromaffin granule GO:0042583 p=3.0E−02 n=1 fg=0.02 bg=0.00
chromaffin granule membrane GO:0042584 p=3.0E−02 n=1 fg=0.02 bg=0.00
CHRAC GO:0008623 p=3.0E−02 n=1 fg=0.02 bg=0.00
ACF complex GO:0016590 p=3.0E−02 n=1 fg=0.02 bg=0.00
T−tubule GO:0030315 p=3.5E−02 n=2 fg=0.04 bg=0.01
nuclear speck GO:0016607 p=3.5E−02 n=5 fg=0.09 bg=0.03
NURF complex GO:0016589 p=6.0E+02 n=1 fg=0.02 bg=0.00
RNA polymerase II, core complex GO:0005665 p=6.0E+02 n=1 fg=0.02 bg=0.00
COPI vesicle coat GO:0030126 p=6.0E+02 n=1 fg=0.02 bg=0.00
COPII vesicle coat GO:0030127 p=6.0E+02 n=1 fg=0.02 bg=0.00
gut granule GO:0044840 p=6.0E+02 n=1 fg=0.02 bg=0.00
gut granule membrane GO:0044841 p=6.0E+02 n=1 fg=0.02 bg=0.00
COPI−coated vesicle membrane GO:0030663 p=6.0E+02 n=1 fg=0.02 bg=0.00
RSF complex GO:0031213 p=6.0E+02 n=1 fg=0.02 bg=0.00
activating signal cointegrator 1 complex GO:0099053 p=6.0E+02 n=1 fg=0.02 bg=0.00
coated vesicle GO:0030135 p=6.3E+02 n=4 fg=0.07 bg=0.03
Golgi−associated vesicle membrane GO:0030660 p=6.5E−02 n=2 fg=0.04 bg=0.01
intracellular membrane−bounded organelle GO:0043231 p=6.6E−02 n=49 fg=0.89 bg=0.78
commitment complex GO:0000243 p=8.8E−02 n=1 fg=0.02 bg=0.00
podosome GO:0002102 p=8.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=55/178 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction