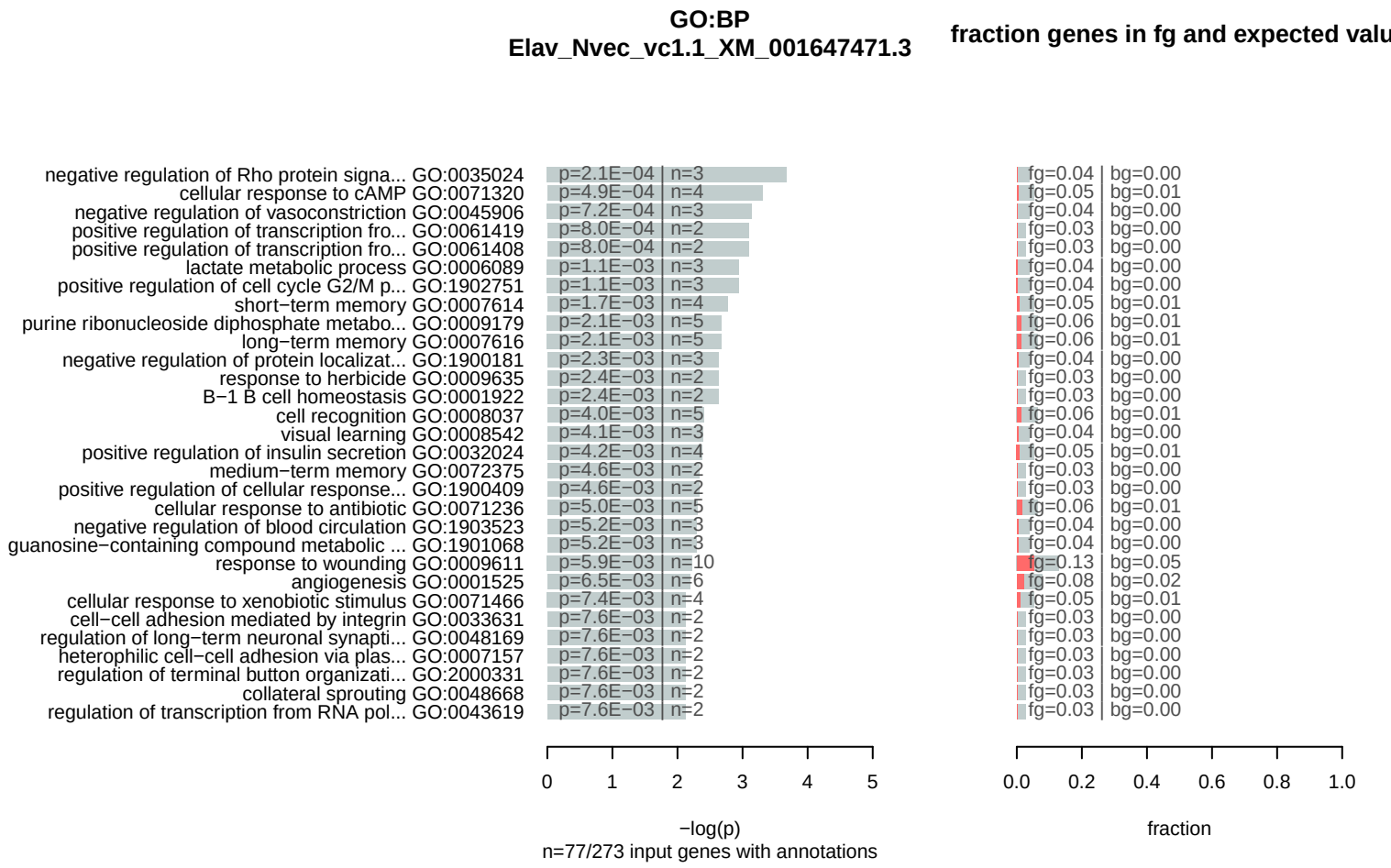
GO:BP
Elav_Nvec_vc1.1_XM_001647471.3
fraction genes in fg and expected valu
negative regulation of Rho protein signa... GO:0035024 p=2.1E−04 n=3 fg=0.04 bg=0.00
cellular response to cAMP GO:0071320 p=4.9E−04 n=4 fg=0.05 bg=0.01
negative regulation of vasoconstriction GO:0045906 p=7.2E−04 n=3 fg=0.04 bg=0.00
positive regulation of transcription fro... GO:0061419 p=8.0E−04 n=2 fg=0.03 bg=0.00
positive regulation of transcription fro... GO:0061408 p=8.0E−04 n=2 fg=0.03 bg=0.00
lactate metabolic process GO:0006089 p=1.1E−03 n=3 fg=0.04 bg=0.00
positive regulation of cell cycle G2/M p... GO:1902751 p=1.1E−03 n=3 fg=0.04 bg=0.00
short−term memory GO:0007614 p=1.7E−03 n=4 fg=0.05 bg=0.01
purine ribonucleoside diphosphate metabo... GO:0009179 p=2.1E−03 n=5 fg=0.06 bg=0.01
long−term memory GO:0007616 p=2.1E−03 n=5 fg=0.06 bg=0.01
negative regulation of protein localizat... GO:1900181 p=2.3E−03 n=3 fg=0.04 bg=0.00
response to herbicide GO:0009635 p=2.4E−03 n=2 fg=0.03 bg=0.00
B−1 B cell homeostasis GO:0001922 p=2.4E−03 n=2 fg=0.03 bg=0.00
cell recognition GO:0008037 p=4.0E−03 n=5 fg=0.06 bg=0.01
visual learning GO:0008542 p=4.1E−03 n=3 fg=0.04 bg=0.00
positive regulation of insulin secretion GO:0032024 p=4.2E−03 n=4 fg=0.05 bg=0.01
medium−term memory GO:0072375 p=4.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of cellular response... GO:1900409 p=4.6E−03 n=2 fg=0.03 bg=0.00
cellular response to antibiotic GO:0071236 p=5.0E−03 n=5 fg=0.06 bg=0.01
negative regulation of blood circulation GO:1903523 p=5.2E−03 n=3 fg=0.04 bg=0.00
guanosine−containing compound metabolic ... GO:1901068 p=5.2E−03 n=3 fg=0.04 bg=0.00
response to wounding GO:0009611 p=5.9E−03 n=10 fg=0.13 bg=0.05
angiogenesis GO:0001525 p=6.5E−03 n=6 fg=0.08 bg=0.02
cellular response to xenobiotic stimulus GO:0071466 p=7.4E−03 n=4 fg=0.05 bg=0.01
cell−cell adhesion mediated by integrin GO:0033631 p=7.6E−03 n=2 fg=0.03 bg=0.00
regulation of long−term neuronal synapti... GO:0048169 p=7.6E−03 n=2 fg=0.03 bg=0.00
heterophilic cell−cell adhesion via plas... GO:0007157 p=7.6E−03 n=2 fg=0.03 bg=0.00
regulation of terminal button organizati... GO:2000331 p=7.6E−03 n=2 fg=0.03 bg=0.00
collateral sprouting GO:0048668 p=7.6E−03 n=2 fg=0.03 bg=0.00
regulation of transcription from RNA pol... GO:0043619 p=7.6E−03 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=77/273 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001647471.3
fraction genes in fg and expected valu
tRNA (cytosine−5−)−methyltransferase act... GO:0016428 p=8.1E−04 n=2 fg=0.03 bg=0.00
collagen binding GO:0005518 p=1.1E−03 n=3 fg=0.04 bg=0.00
integrin binding GO:0005178 p=2.1E−03 n=4 fg=0.06 bg=0.01
laminin binding GO:0043236 p=7.7E−03 n=2 fg=0.03 bg=0.00
protein domain specific binding GO:0019904 p=8.5E−03 n=12 fg=0.18 bg=0.08
proteoglycan binding GO:0043394 p=1.1E−02 n=2 fg=0.03 bg=0.00
MAP kinase kinase kinase activity GO:0004709 p=1.6E−02 n=2 fg=0.03 bg=0.00
aminopeptidase activity GO:0004177 p=1.6E−02 n=2 fg=0.03 bg=0.00
Hsp90 protein binding GO:0051879 p=1.8E−02 n=3 fg=0.04 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=2.2E−02 n=7 fg=0.10 bg=0.04
quaternary ammonium group binding GO:0050997 p=2.6E−02 n=2 fg=0.03 bg=0.00
transcription coregulator binding GO:0001221 p=2.6E−02 n=2 fg=0.03 bg=0.00
heparan sulfate binding GO:1904399 p=2.9E−02 n=1 fg=0.01 bg=0.00
calcitonin family binding GO:0097644 p=2.9E−02 n=1 fg=0.01 bg=0.00
amylin binding GO:0097645 p=2.9E−02 n=1 fg=0.01 bg=0.00
insulin−like growth factor I binding GO:0031994 p=2.9E−02 n=1 fg=0.01 bg=0.00
class II DNA−(apurinic or apyrimidinic s... GO:0052720 p=2.9E−02 n=1 fg=0.01 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=2.9E−02 n=1 fg=0.01 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=2.9E−02 n=1 fg=0.01 bg=0.00
NAD+ synthase (glutamine−hydrolyzing) ac... GO:0003952 p=2.9E−02 n=1 fg=0.01 bg=0.00
succinate transmembrane transporter acti... GO:0015141 p=2.9E−02 n=1 fg=0.01 bg=0.00
acetylcholine receptor regulator activit... GO:0030548 p=2.9E−02 n=1 fg=0.01 bg=0.00
acetylcholine receptor activator activit... GO:0030549 p=2.9E−02 n=1 fg=0.01 bg=0.00
neurotransmitter receptor regulator acti... GO:0099602 p=2.9E−02 n=1 fg=0.01 bg=0.00
cobalt ion binding GO:0050897 p=2.9E−02 n=1 fg=0.01 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=2.9E−02 n=1 fg=0.01 bg=0.00
neuregulin binding GO:0038132 p=2.9E−02 n=1 fg=0.01 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=2.9E−02 n=1 fg=0.01 bg=0.00
AMP deaminase activity GO:0003876 p=2.9E−02 n=1 fg=0.01 bg=0.00
translation elongation factor binding GO:0061770 p=2.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=68/273 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001647471.3
fraction genes in fg and expected valu
integrin complex GO:0008305 p=4.4E−03 n=2 fg=0.03 bg=0.00
terminal bouton GO:0043195 p=5.0E−03 n=5 fg=0.07 bg=0.02
external side of plasma membrane GO:0009897 p=5.9E−03 n=4 fg=0.05 bg=0.01
microtubule GO:0005874 p=1.1E−02 n=5 fg=0.07 bg=0.02
anchoring junction GO:0070161 p=1.1E−02 n=8 fg=0.11 bg=0.04
cell−cell junction GO:0005911 p=1.1E−02 n=8 fg=0.11 bg=0.04
centrosome GO:0005813 p=1.4E−02 n=9 fg=0.12 bg=0.05
basement membrane GO:0005604 p=1.5E−02 n=2 fg=0.03 bg=0.00
plasma membrane region GO:0098590 p=1.8E−02 n=12 fg=0.16 bg=0.08
Golgi lumen GO:0005796 p=2.4E−02 n=2 fg=0.03 bg=0.00
cell body GO:0044297 p=2.5E−02 n=10 fg=0.13 bg=0.07
polar microtubule GO:0005827 p=2.8E−02 n=1 fg=0.01 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=2.8E−02 n=1 fg=0.01 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=2.8E−02 n=1 fg=0.01 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=2.8E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=2.8E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=2.8E−02 n=1 fg=0.01 bg=0.00
gamma−tubulin small complex GO:0008275 p=2.8E−02 n=1 fg=0.01 bg=0.00
equatorial microtubule organizing center GO:0000923 p=2.8E−02 n=1 fg=0.01 bg=0.00
DNA polymerase III, core complex GO:0044776 p=2.8E−02 n=1 fg=0.01 bg=0.00
podocyte foot GO:0098846 p=2.8E−02 n=1 fg=0.01 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=2.8E−02 n=1 fg=0.01 bg=0.00
high−density lipoprotein particle GO:0034364 p=2.8E−02 n=1 fg=0.01 bg=0.00
plasma lipoprotein particle GO:0034358 p=2.8E−02 n=1 fg=0.01 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=2.8E−02 n=1 fg=0.01 bg=0.00
lipoprotein particle GO:1990777 p=2.8E−02 n=1 fg=0.01 bg=0.00
neuromuscular junction GO:0031594 p=3.0E−02 n=4 fg=0.05 bg=0.02
neuronal cell body GO:0043025 p=3.2E−02 n=9 fg=0.12 bg=0.06
mitotic spindle pole GO:0097431 p=3.6E−02 n=2 fg=0.03 bg=0.00
microtubule cytoskeleton GO:0015630 p=3.9E−02 n=13 fg=0.17 bg=0.10
0 1 2 3 4 5
−log(p)
n=75/273 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction