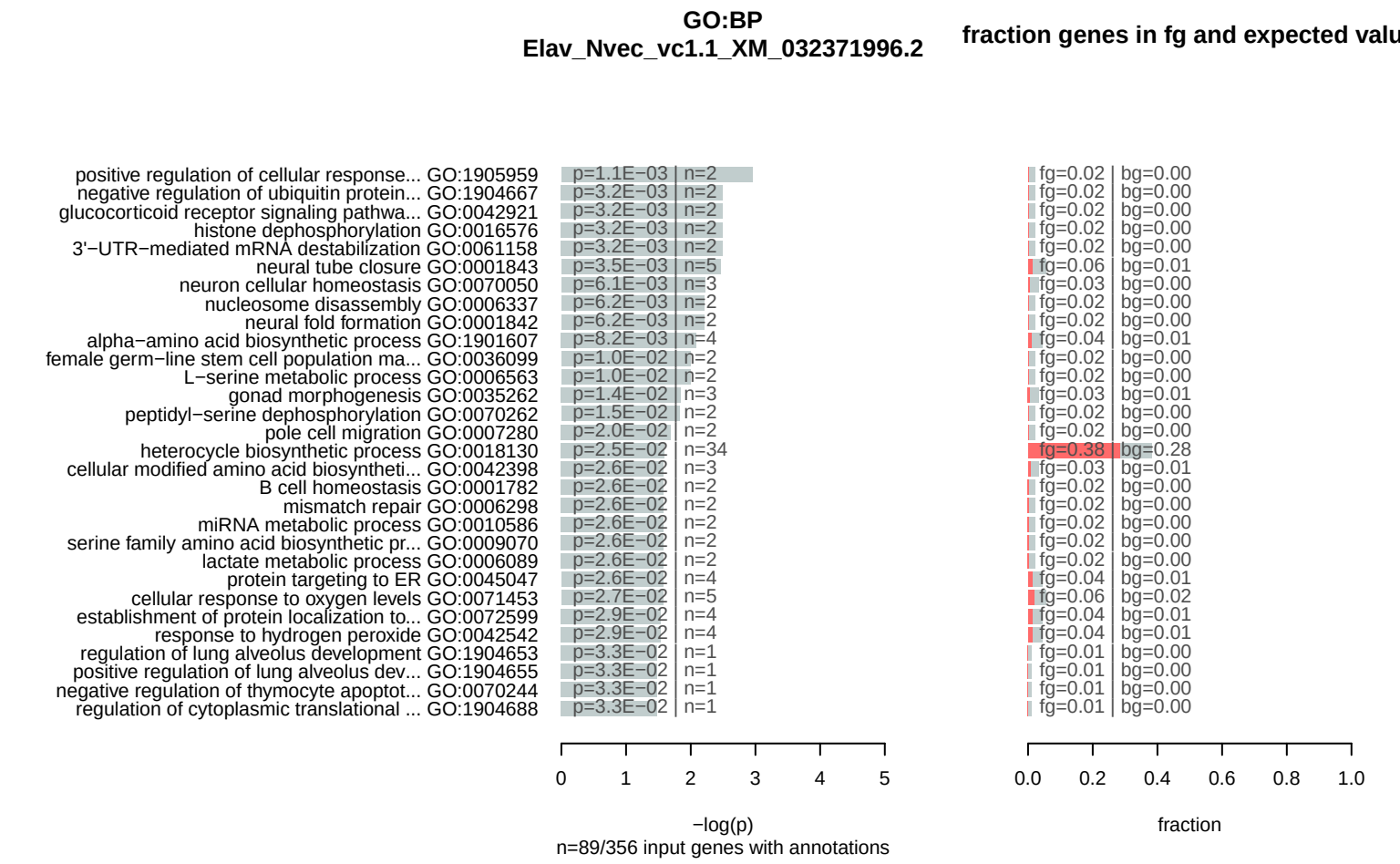
GO:BP
Elav_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
positive regulation of cellular response... GO:1905959 p=1.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of ubiquitin protein... GO:1904667 p=3.2E−03 n=2 fg=0.02 bg=0.00
glucocorticoid receptor signaling pathwa... GO:0042921 p=3.2E−03 n=2 fg=0.02 bg=0.00
histone dephosphorylation GO:0016576 p=3.2E−03 n=2 fg=0.02 bg=0.00
3'−UTR−mediated mRNA destabilization GO:0061158 p=3.2E−03 n=2 fg=0.02 bg=0.00
neural tube closure GO:0001843 p=3.5E−03 n=5 fg=0.06 bg=0.01
neuron cellular homeostasis GO:0070050 p=6.1E−03 n=3 fg=0.03 bg=0.00
nucleosome disassembly GO:0006337 p=6.2E−03 n=2 fg=0.02 bg=0.00
neural fold formation GO:0001842 p=6.2E−03 n=2 fg=0.02 bg=0.00
alpha−amino acid biosynthetic process GO:1901607 p=8.2E−03 n=4 fg=0.04 bg=0.01
female germ−line stem cell population ma... GO:0036099 p=1.0E−02 n=2 fg=0.02 bg=0.00
L−serine metabolic process GO:0006563 p=1.0E−02 n=2 fg=0.02 bg=0.00
gonad morphogenesis GO:0035262 p=1.4E−02 n=3 fg=0.03 bg=0.01
peptidyl−serine dephosphorylation GO:0070262 p=1.5E−02 n=2 fg=0.02 bg=0.00
pole cell migration GO:0007280 p=2.0E−02 n=2 fg=0.02 bg=0.00
heterocycle biosynthetic process GO:0018130 p=2.5E−02 n=34 fg=0.38 bg=0.28
cellular modified amino acid biosyntheti... GO:0042398 p=2.6E−02 n=3 fg=0.03 bg=0.01
B cell homeostasis GO:0001782 p=2.6E−02 n=2 fg=0.02 bg=0.00
mismatch repair GO:0006298 p=2.6E−02 n=2 fg=0.02 bg=0.00
miRNA metabolic process GO:0010586 p=2.6E−02 n=2 fg=0.02 bg=0.00
serine family amino acid biosynthetic pr... GO:0009070 p=2.6E−02 n=2 fg=0.02 bg=0.00
lactate metabolic process GO:0006089 p=2.6E−02 n=2 fg=0.02 bg=0.00
protein targeting to ER GO:0045047 p=2.6E−02 n=4 fg=0.04 bg=0.01
cellular response to oxygen levels GO:0071453 p=2.7E−02 n=5 fg=0.06 bg=0.02
establishment of protein localization to... GO:0072599 p=2.9E−02 n=4 fg=0.04 bg=0.01
response to hydrogen peroxide GO:0042542 p=2.9E−02 n=4 fg=0.04 bg=0.01
regulation of lung alveolus development GO:1904653 p=3.3E−02 n=1 fg=0.01 bg=0.00
positive regulation of lung alveolus dev... GO:1904655 p=3.3E−02 n=1 fg=0.01 bg=0.00
negative regulation of thymocyte apoptot... GO:0070244 p=3.3E−02 n=1 fg=0.01 bg=0.00
regulation of cytoplasmic translational ... GO:1904688 p=3.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=89/356 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
miRNA binding GO:0035198 p=3.6E−03 n=2 fg=0.02 bg=0.00
SH3 domain binding GO:0017124 p=1.1E−02 n=4 fg=0.05 bg=0.01
S−adenosyl−L−methionine binding GO:1904047 p=1.2E−02 n=2 fg=0.02 bg=0.00
cation binding GO:0043169 p=1.8E−02 n=16 fg=0.19 bg=0.11
transition metal ion binding GO:0046914 p=2.7E−02 n=10 fg=0.12 bg=0.06
oxidoreductase activity, acting on the C... GO:0016616 p=3.2E−02 n=3 fg=0.04 bg=0.01
choline binding GO:0033265 p=3.5E−02 n=1 fg=0.01 bg=0.00
U5 snRNA binding GO:0030623 p=3.5E−02 n=1 fg=0.01 bg=0.00
adiponectin binding GO:0055100 p=3.5E−02 n=1 fg=0.01 bg=0.00
NAD−retinol dehydrogenase activity GO:0004745 p=3.5E−02 n=1 fg=0.01 bg=0.00
pyrroline−5−carboxylate reductase activi... GO:0004735 p=3.5E−02 n=1 fg=0.01 bg=0.00
class II DNA−(apurinic or apyrimidinic s... GO:0052720 p=3.5E−02 n=1 fg=0.01 bg=0.00
selenocystathionine beta−synthase activi... GO:0098605 p=3.5E−02 n=1 fg=0.01 bg=0.00
phosphomannomutase activity GO:0004615 p=3.5E−02 n=1 fg=0.01 bg=0.00
phosphoglycerate dehydrogenase activity GO:0004617 p=3.5E−02 n=1 fg=0.01 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=3.5E−02 n=1 fg=0.01 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=3.5E−02 n=1 fg=0.01 bg=0.00
volume−sensitive chloride channel activi... GO:0072320 p=3.5E−02 n=1 fg=0.01 bg=0.00
DNA end binding GO:0045027 p=3.5E−02 n=1 fg=0.01 bg=0.00
cobalt ion binding GO:0050897 p=3.5E−02 n=1 fg=0.01 bg=0.00
RNA polymerase I general transcription i... GO:0001181 p=3.5E−02 n=1 fg=0.01 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=3.5E−02 n=1 fg=0.01 bg=0.00
myosin phosphatase regulator activity GO:0017020 p=3.5E−02 n=1 fg=0.01 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=3.5E−02 n=1 fg=0.01 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=3.5E−02 n=1 fg=0.01 bg=0.00
holo−[acyl−carrier−protein] synthase act... GO:0008897 p=3.5E−02 n=1 fg=0.01 bg=0.00
N−acylneuraminate−9−phosphatase activity GO:0050124 p=3.5E−02 n=1 fg=0.01 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=3.5E−02 n=1 fg=0.01 bg=0.00
uroporphyrinogen−III synthase activity GO:0004852 p=3.5E−02 n=1 fg=0.01 bg=0.00
nitrite reductase activity GO:0098809 p=3.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=84/356 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
nuclear replisome GO:0043601 p=3.1E−03 n=3 fg=0.03 bg=0.00
P−body GO:0000932 p=5.6E−03 n=4 fg=0.04 bg=0.01
vacuolar proton−transporting V−type ATPa... GO:0016471 p=2.3E−02 n=2 fg=0.02 bg=0.00
proton−transporting V−type ATPase comple... GO:0033176 p=3.0E−02 n=2 fg=0.02 bg=0.00
SWI/SNF superfamily−type complex GO:0070603 p=3.2E−02 n=3 fg=0.03 bg=0.01
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=3.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=3.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted vesicle GO:0060198 p=3.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=3.6E−02 n=1 fg=0.01 bg=0.00
FACT complex GO:0035101 p=3.6E−02 n=1 fg=0.01 bg=0.00
cyclin E1−CDK2 complex GO:0097134 p=3.6E−02 n=1 fg=0.01 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=3.6E−02 n=1 fg=0.01 bg=0.00
proton−transporting two−sector ATPase co... GO:0016469 p=4.7E−02 n=2 fg=0.02 bg=0.00
transferase complex, transferring phosph... GO:0061695 p=6.3E−02 n=6 fg=0.06 bg=0.03
type I terminal bouton GO:0061174 p=6.6E−02 n=2 fg=0.02 bg=0.00
DNA polymerase complex GO:0042575 p=6.6E−02 n=2 fg=0.02 bg=0.00
ATPase complex GO:1904949 p=6.9E−02 n=3 fg=0.03 bg=0.01
ribonucleoside−diphosphate reductase com... GO:0005971 p=7.0E−02 n=1 fg=0.01 bg=0.00
BLOC−1 complex GO:0031083 p=7.0E−02 n=1 fg=0.01 bg=0.00
axonemal central apparatus GO:1990716 p=7.0E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=7.0E−02 n=1 fg=0.01 bg=0.00
gamma−tubulin complex GO:0000930 p=7.0E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber GO:0097457 p=7.0E−02 n=1 fg=0.01 bg=0.00
ESCRT II complex GO:0000814 p=7.0E−02 n=1 fg=0.01 bg=0.00
Lewy body GO:0097413 p=7.0E−02 n=1 fg=0.01 bg=0.00
delta DNA polymerase complex GO:0043625 p=7.0E−02 n=1 fg=0.01 bg=0.00
integral component of Golgi membrane GO:0030173 p=7.6E−02 n=2 fg=0.02 bg=0.00
ESCRT complex GO:0036452 p=7.6E−02 n=2 fg=0.02 bg=0.00
nuclear DNA−directed RNA polymerase comp... GO:0055029 p=8.4E−02 n=4 fg=0.04 bg=0.02
DNA−directed RNA polymerase complex GO:0000428 p=8.9E−02 n=4 fg=0.04 bg=0.02
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−log(p)
n=96/356 input genes with annotations
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fraction