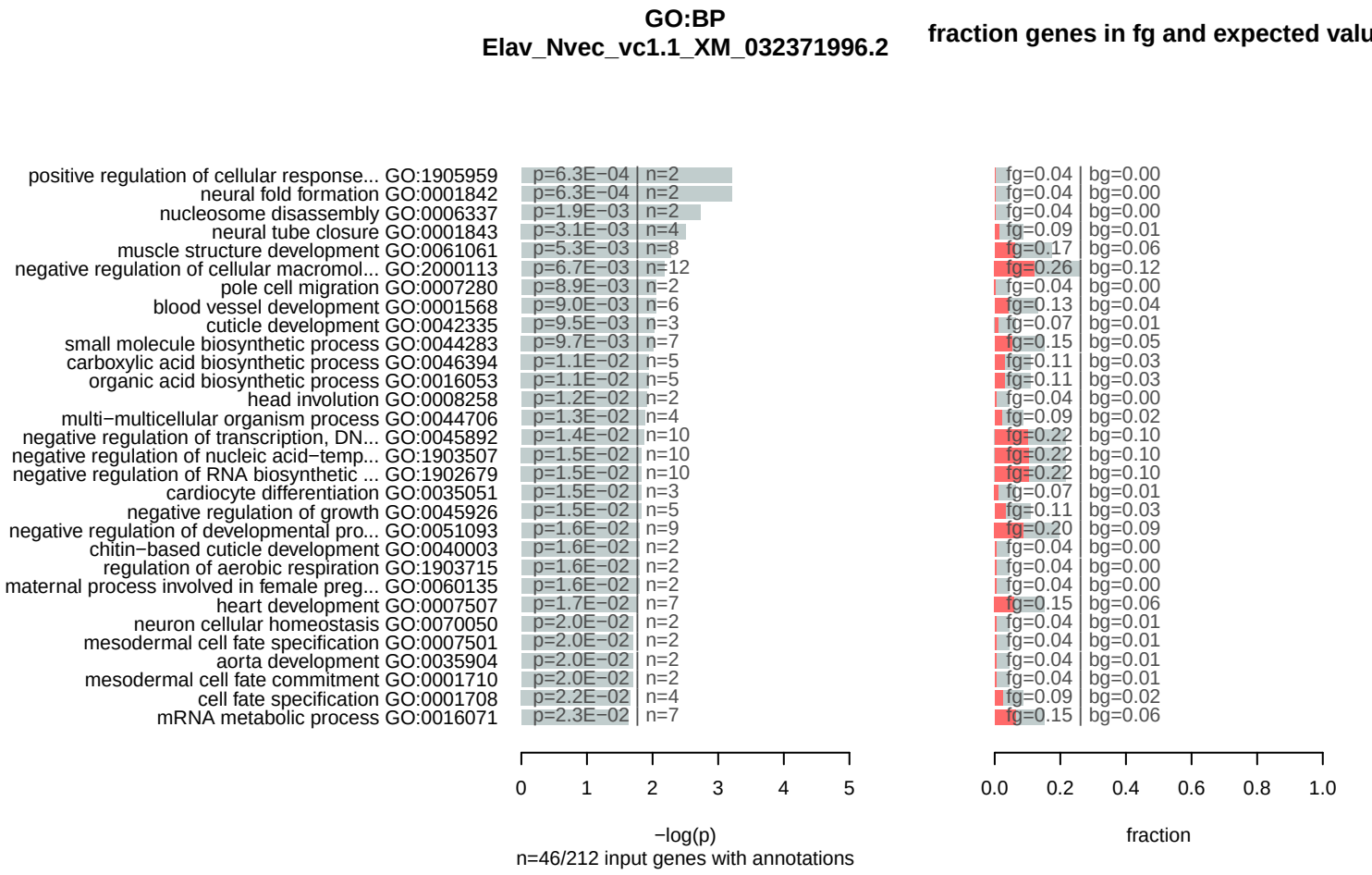
GO:BP
Elav_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
positive regulation of cellular response... GO:1905959 p=6.3E−04 n=2 fg=0.04 bg=0.00
neural fold formation GO:0001842 p=6.3E−04 n=2 fg=0.04 bg=0.00
nucleosome disassembly GO:0006337 p=1.9E−03 n=2 fg=0.04 bg=0.00
neural tube closure GO:0001843 p=3.1E−03 n=4 fg=0.09 bg=0.01
muscle structure development GO:0061061 p=5.3E−03 n=8 fg=0.17 bg=0.06
negative regulation of cellular macromol... GO:2000113 p=6.7E−03 n=12 fg=0.26 bg=0.12
pole cell migration GO:0007280 p=8.9E−03 n=2 fg=0.04 bg=0.00
blood vessel development GO:0001568 p=9.0E−03 n=6 fg=0.13 bg=0.04
cuticle development GO:0042335 p=9.5E−03 n=3 fg=0.07 bg=0.01
small molecule biosynthetic process GO:0044283 p=9.7E−03 n=7 fg=0.15 bg=0.05
carboxylic acid biosynthetic process GO:0046394 p=1.1E−02 n=5 fg=0.11 bg=0.03
organic acid biosynthetic process GO:0016053 p=1.1E−02 n=5 fg=0.11 bg=0.03
head involution GO:0008258 p=1.2E−02 n=2 fg=0.04 bg=0.00
multi−multicellular organism process GO:0044706 p=1.3E−02 n=4 fg=0.09 bg=0.02
negative regulation of transcription, DN... GO:0045892 p=1.4E−02 n=10 fg=0.22 bg=0.10
negative regulation of nucleic acid−temp... GO:1903507 p=1.5E−02 n=10 fg=0.22 bg=0.10
negative regulation of RNA biosynthetic ... GO:1902679 p=1.5E−02 n=10 fg=0.22 bg=0.10
cardiocyte differentiation GO:0035051 p=1.5E−02 n=3 fg=0.07 bg=0.01
negative regulation of growth GO:0045926 p=1.5E−02 n=5 fg=0.11 bg=0.03
negative regulation of developmental pro... GO:0051093 p=1.6E−02 n=9 fg=0.20 bg=0.09
chitin−based cuticle development GO:0040003 p=1.6E−02 n=2 fg=0.04 bg=0.00
regulation of aerobic respiration GO:1903715 p=1.6E−02 n=2 fg=0.04 bg=0.00
maternal process involved in female preg... GO:0060135 p=1.6E−02 n=2 fg=0.04 bg=0.00
heart development GO:0007507 p=1.7E−02 n=7 fg=0.15 bg=0.06
neuron cellular homeostasis GO:0070050 p=2.0E−02 n=2 fg=0.04 bg=0.01
mesodermal cell fate specification GO:0007501 p=2.0E−02 n=2 fg=0.04 bg=0.01
aorta development GO:0035904 p=2.0E−02 n=2 fg=0.04 bg=0.01
mesodermal cell fate commitment GO:0001710 p=2.0E−02 n=2 fg=0.04 bg=0.01
cell fate specification GO:0001708 p=2.2E−02 n=4 fg=0.09 bg=0.02
mRNA metabolic process GO:0016071 p=2.3E−02 n=7 fg=0.15 bg=0.06
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−log(p)
n=46/212 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
SH3 domain binding GO:0017124 p=1.2E−03 n=4 fg=0.09 bg=0.01
modified amino acid binding GO:0072341 p=2.1E−03 n=3 fg=0.07 bg=0.01
phosphatidylinositol−3−phosphate binding GO:0032266 p=7.1E−03 n=2 fg=0.05 bg=0.00
hydro−lyase activity GO:0016836 p=1.9E−02 n=2 fg=0.05 bg=0.01
oxidoreductase activity, acting on other... GO:0016661 p=2.8E−02 n=1 fg=0.02 bg=0.00
selenocystathionine beta−synthase activi... GO:0098605 p=2.8E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on other... GO:0016662 p=2.8E−02 n=1 fg=0.02 bg=0.00
adipokinetic hormone receptor activity GO:0097003 p=2.8E−02 n=1 fg=0.02 bg=0.00
pyrroline−5−carboxylate reductase activi... GO:0004735 p=2.8E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0016652 p=2.8E−02 n=1 fg=0.02 bg=0.00
ATP−dependent protein binding GO:0043008 p=2.8E−02 n=1 fg=0.02 bg=0.00
U2 snRNA binding GO:0030620 p=2.8E−02 n=1 fg=0.02 bg=0.00
U5 snRNA binding GO:0030623 p=2.8E−02 n=1 fg=0.02 bg=0.00
cobalt ion binding GO:0050897 p=2.8E−02 n=1 fg=0.02 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=2.8E−02 n=1 fg=0.02 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=2.8E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=2.8E−02 n=1 fg=0.02 bg=0.00
nitrite reductase (NO−forming) activity GO:0050421 p=2.8E−02 n=1 fg=0.02 bg=0.00
volume−sensitive anion channel activity GO:0005225 p=2.8E−02 n=1 fg=0.02 bg=0.00
adiponectin binding GO:0055100 p=2.8E−02 n=1 fg=0.02 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=2.8E−02 n=1 fg=0.02 bg=0.00
volume−sensitive chloride channel activi... GO:0072320 p=2.8E−02 n=1 fg=0.02 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=2.8E−02 n=1 fg=0.02 bg=0.00
U6 snRNA binding GO:0017070 p=2.8E−02 n=1 fg=0.02 bg=0.00
uroporphyrinogen−III synthase activity GO:0004852 p=2.8E−02 n=1 fg=0.02 bg=0.00
K48−linked polyubiquitin modification−de... GO:0036435 p=2.8E−02 n=1 fg=0.02 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=2.8E−02 n=1 fg=0.02 bg=0.00
nitrite reductase activity GO:0098809 p=2.8E−02 n=1 fg=0.02 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=2.8E−02 n=1 fg=0.02 bg=0.00
NAD−retinol dehydrogenase activity GO:0004745 p=2.8E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=44/212 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032371996.2
fraction genes in fg and expected valu
vacuolar proton−transporting V−type ATPa... GO:0016471 p=1.4E−02 n=2 fg=0.04 bg=0.00
proton−transporting two−sector ATPase co... GO:0016469 p=1.8E−02 n=2 fg=0.04 bg=0.00
proton−transporting V−type ATPase comple... GO:0033176 p=1.8E−02 n=2 fg=0.04 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=2.7E−02 n=1 fg=0.02 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=2.7E−02 n=1 fg=0.02 bg=0.00
clathrin−sculpted vesicle GO:0060198 p=2.7E−02 n=1 fg=0.02 bg=0.00
FACT complex GO:0035101 p=2.7E−02 n=1 fg=0.02 bg=0.00
hippocampal mossy fiber GO:0097457 p=2.7E−02 n=1 fg=0.02 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=2.7E−02 n=1 fg=0.02 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=2.7E−02 n=1 fg=0.02 bg=0.00
type I terminal bouton GO:0061174 p=2.8E−02 n=2 fg=0.04 bg=0.01
SWI/SNF superfamily−type complex GO:0070603 p=4.0E−02 n=2 fg=0.04 bg=0.01
transcription repressor complex GO:0017053 p=4.6E−02 n=2 fg=0.04 bg=0.01
SWI/SNF complex GO:0016514 p=5.3E−02 n=1 fg=0.02 bg=0.00
brahma complex GO:0035060 p=5.3E−02 n=1 fg=0.02 bg=0.00
extrinsic component of endoplasmic retic... GO:0042406 p=5.3E−02 n=1 fg=0.02 bg=0.00
type Ib terminal bouton GO:0061176 p=5.3E−02 n=1 fg=0.02 bg=0.00
type Is terminal bouton GO:0061177 p=5.3E−02 n=1 fg=0.02 bg=0.00
U5 snRNP GO:0005682 p=5.3E−02 n=1 fg=0.02 bg=0.00
Lewy body GO:0097413 p=5.3E−02 n=1 fg=0.02 bg=0.00
npBAF complex GO:0071564 p=5.3E−02 n=1 fg=0.02 bg=0.00
nBAF complex GO:0071565 p=5.3E−02 n=1 fg=0.02 bg=0.00
transcription regulator complex GO:0005667 p=5.4E−02 n=5 fg=0.10 bg=0.04
nuclear protein−containing complex GO:0140513 p=7.5E−02 n=9 fg=0.18 bg=0.11
P−body GO:0000932 p=7.5E−02 n=2 fg=0.04 bg=0.01
ATPase complex GO:1904949 p=7.5E−02 n=2 fg=0.04 bg=0.01
exon−exon junction complex GO:0035145 p=7.9E−02 n=1 fg=0.02 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=7.9E−02 n=1 fg=0.02 bg=0.00
proton−transporting V−type ATPase, V1 do... GO:0033180 p=7.9E−02 n=1 fg=0.02 bg=0.00
proton−transporting two−sector ATPase co... GO:0033178 p=7.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/212 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction