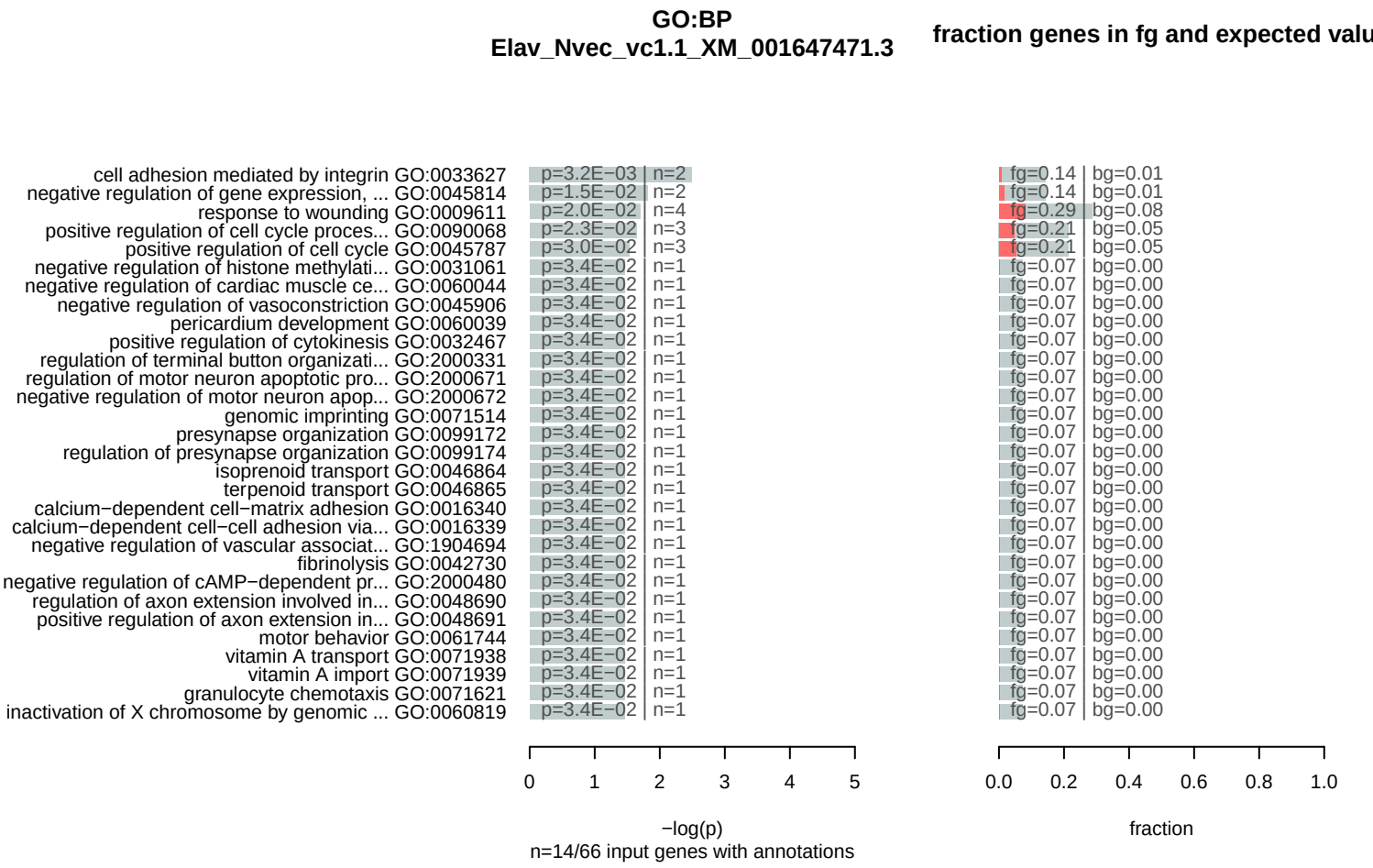
GO:BP
Elav_Nvec_vc1.1_XM_001647471.3
fraction genes in fg and expected valu
cell adhesion mediated by integrin GO:0033627 p=3.2E−03 n=2 fg=0.14 bg=0.01
negative regulation of gene expression, ... GO:0045814 p=1.5E−02 n=2 fg=0.14 bg=0.01
response to wounding GO:0009611 p=2.0E−02 n=4 fg=0.29 bg=0.08
positive regulation of cell cycle proces... GO:0090068 p=2.3E−02 n=3 fg=0.21 bg=0.05
positive regulation of cell cycle GO:0045787 p=3.0E−02 n=3 fg=0.21 bg=0.05
negative regulation of histone methylati... GO:0031061 p=3.4E−02 n=1 fg=0.07 bg=0.00
negative regulation of cardiac muscle ce... GO:0060044 p=3.4E−02 n=1 fg=0.07 bg=0.00
negative regulation of vasoconstriction GO:0045906 p=3.4E−02 n=1 fg=0.07 bg=0.00
pericardium development GO:0060039 p=3.4E−02 n=1 fg=0.07 bg=0.00
positive regulation of cytokinesis GO:0032467 p=3.4E−02 n=1 fg=0.07 bg=0.00
regulation of terminal button organizati... GO:2000331 p=3.4E−02 n=1 fg=0.07 bg=0.00
regulation of motor neuron apoptotic pro... GO:2000671 p=3.4E−02 n=1 fg=0.07 bg=0.00
negative regulation of motor neuron apop... GO:2000672 p=3.4E−02 n=1 fg=0.07 bg=0.00
genomic imprinting GO:0071514 p=3.4E−02 n=1 fg=0.07 bg=0.00
presynapse organization GO:0099172 p=3.4E−02 n=1 fg=0.07 bg=0.00
regulation of presynapse organization GO:0099174 p=3.4E−02 n=1 fg=0.07 bg=0.00
isoprenoid transport GO:0046864 p=3.4E−02 n=1 fg=0.07 bg=0.00
terpenoid transport GO:0046865 p=3.4E−02 n=1 fg=0.07 bg=0.00
calcium−dependent cell−matrix adhesion GO:0016340 p=3.4E−02 n=1 fg=0.07 bg=0.00
calcium−dependent cell−cell adhesion via... GO:0016339 p=3.4E−02 n=1 fg=0.07 bg=0.00
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fibrinolysis GO:0042730 p=3.4E−02 n=1 fg=0.07 bg=0.00
negative regulation of cAMP−dependent pr... GO:2000480 p=3.4E−02 n=1 fg=0.07 bg=0.00
regulation of axon extension involved in... GO:0048690 p=3.4E−02 n=1 fg=0.07 bg=0.00
positive regulation of axon extension in... GO:0048691 p=3.4E−02 n=1 fg=0.07 bg=0.00
motor behavior GO:0061744 p=3.4E−02 n=1 fg=0.07 bg=0.00
vitamin A transport GO:0071938 p=3.4E−02 n=1 fg=0.07 bg=0.00
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granulocyte chemotaxis GO:0071621 p=3.4E−02 n=1 fg=0.07 bg=0.00
inactivation of X chromosome by genomic ... GO:0060819 p=3.4E−02 n=1 fg=0.07 bg=0.00
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−log(p)
n=14/66 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
collagen binding GO:0005518 p=2.9E−03 n=2 fg=0.17 bg=0.01
mRNA binding GO:0003729 p=3.2E−02 n=2 fg=0.17 bg=0.02
aminopeptidase activity GO:0004177 p=3.3E−02 n=1 fg=0.08 bg=0.00
exogenous protein binding GO:0140272 p=3.3E−02 n=1 fg=0.08 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=3.3E−02 n=1 fg=0.08 bg=0.00
serine−type endopeptidase activity GO:0004252 p=3.3E−02 n=1 fg=0.08 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=3.3E−02 n=1 fg=0.08 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=3.3E−02 n=1 fg=0.08 bg=0.00
serine−type peptidase activity GO:0008236 p=3.3E−02 n=1 fg=0.08 bg=0.00
extracellular matrix binding GO:0050840 p=3.3E−02 n=1 fg=0.08 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=3.3E−02 n=1 fg=0.08 bg=0.00
cAMP−dependent protein kinase regulator ... GO:0008603 p=3.3E−02 n=1 fg=0.08 bg=0.00
dipeptidyl−peptidase activity GO:0008239 p=3.3E−02 n=1 fg=0.08 bg=0.00
laminin binding GO:0043236 p=3.3E−02 n=1 fg=0.08 bg=0.00
translation factor activity, RNA binding GO:0008135 p=3.3E−02 n=1 fg=0.08 bg=0.00
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virus receptor activity GO:0001618 p=3.3E−02 n=1 fg=0.08 bg=0.00
ubiquitin−like protein ligase binding GO:0044389 p=6.4E−02 n=2 fg=0.17 bg=0.04
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ribosome binding GO:0043022 p=6.5E−02 n=1 fg=0.08 bg=0.01
serine hydrolase activity GO:0017171 p=6.5E−02 n=1 fg=0.08 bg=0.01
cAMP binding GO:0030552 p=9.6E−02 n=1 fg=0.08 bg=0.01
kinase inhibitor activity GO:0019210 p=9.6E−02 n=1 fg=0.08 bg=0.01
mRNA regulatory element binding translat... GO:0000900 p=9.6E−02 n=1 fg=0.08 bg=0.01
ribonucleoprotein complex binding GO:0043021 p=9.6E−02 n=1 fg=0.08 bg=0.01
protein kinase inhibitor activity GO:0004860 p=9.6E−02 n=1 fg=0.08 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=9.6E−02 n=1 fg=0.08 bg=0.01
metallopeptidase activity GO:0008237 p=9.6E−02 n=1 fg=0.08 bg=0.01
exopeptidase activity GO:0008238 p=9.6E−02 n=1 fg=0.08 bg=0.01
translation repressor activity GO:0030371 p=9.6E−02 n=1 fg=0.08 bg=0.01
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−log(p)
n=12/66 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
PcG protein complex GO:0031519 p=1.3E−02 n=2 fg=0.15 bg=0.01
ESC/E(Z) complex GO:0035098 p=3.2E−02 n=1 fg=0.08 bg=0.00
integrin alpha9−beta1 complex GO:0034679 p=3.2E−02 n=1 fg=0.08 bg=0.00
integrin complex GO:0008305 p=3.2E−02 n=1 fg=0.08 bg=0.00
protein complex involved in cell adhesio... GO:0098636 p=3.2E−02 n=1 fg=0.08 bg=0.00
costamere GO:0043034 p=3.2E−02 n=1 fg=0.08 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=3.2E−02 n=1 fg=0.08 bg=0.00
microtubule minus−end GO:0036449 p=3.2E−02 n=1 fg=0.08 bg=0.00
microtubule cytoskeleton GO:0015630 p=5.9E−02 n=3 fg=0.23 bg=0.07
centrosome GO:0005813 p=6.2E−02 n=2 fg=0.15 bg=0.03
euchromatin GO:0000791 p=6.4E−02 n=1 fg=0.08 bg=0.00
intercellular canaliculus GO:0046581 p=6.4E−02 n=1 fg=0.08 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=6.4E−02 n=1 fg=0.08 bg=0.00
female germ cell nucleus GO:0001674 p=6.4E−02 n=1 fg=0.08 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=6.4E−02 n=1 fg=0.08 bg=0.00
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microtubule end GO:1990752 p=6.4E−02 n=1 fg=0.08 bg=0.00
germ cell nucleus GO:0043073 p=9.4E−02 n=1 fg=0.08 bg=0.01
cleavage furrow GO:0032154 p=9.4E−02 n=1 fg=0.08 bg=0.01
plasma membrane signaling receptor compl... GO:0098802 p=9.4E−02 n=1 fg=0.08 bg=0.01
protein kinase complex GO:1902911 p=9.4E−02 n=1 fg=0.08 bg=0.01
plasma membrane region GO:0098590 p=1.1E−01 n=4 fg=0.31 bg=0.15
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histone methyltransferase complex GO:0035097 p=1.2E−01 n=1 fg=0.08 bg=0.01
ruffle membrane GO:0032587 p=1.2E−01 n=1 fg=0.08 bg=0.01
T−tubule GO:0030315 p=1.2E−01 n=1 fg=0.08 bg=0.01
methyltransferase complex GO:0034708 p=1.2E−01 n=1 fg=0.08 bg=0.01
ciliary base GO:0097546 p=1.2E−01 n=1 fg=0.08 bg=0.01
basal part of cell GO:0045178 p=1.3E−01 n=2 fg=0.15 bg=0.05
cell−cell junction GO:0005911 p=1.4E−01 n=2 fg=0.15 bg=0.05
0 1 2 3 4 5
−log(p)
n=13/66 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction