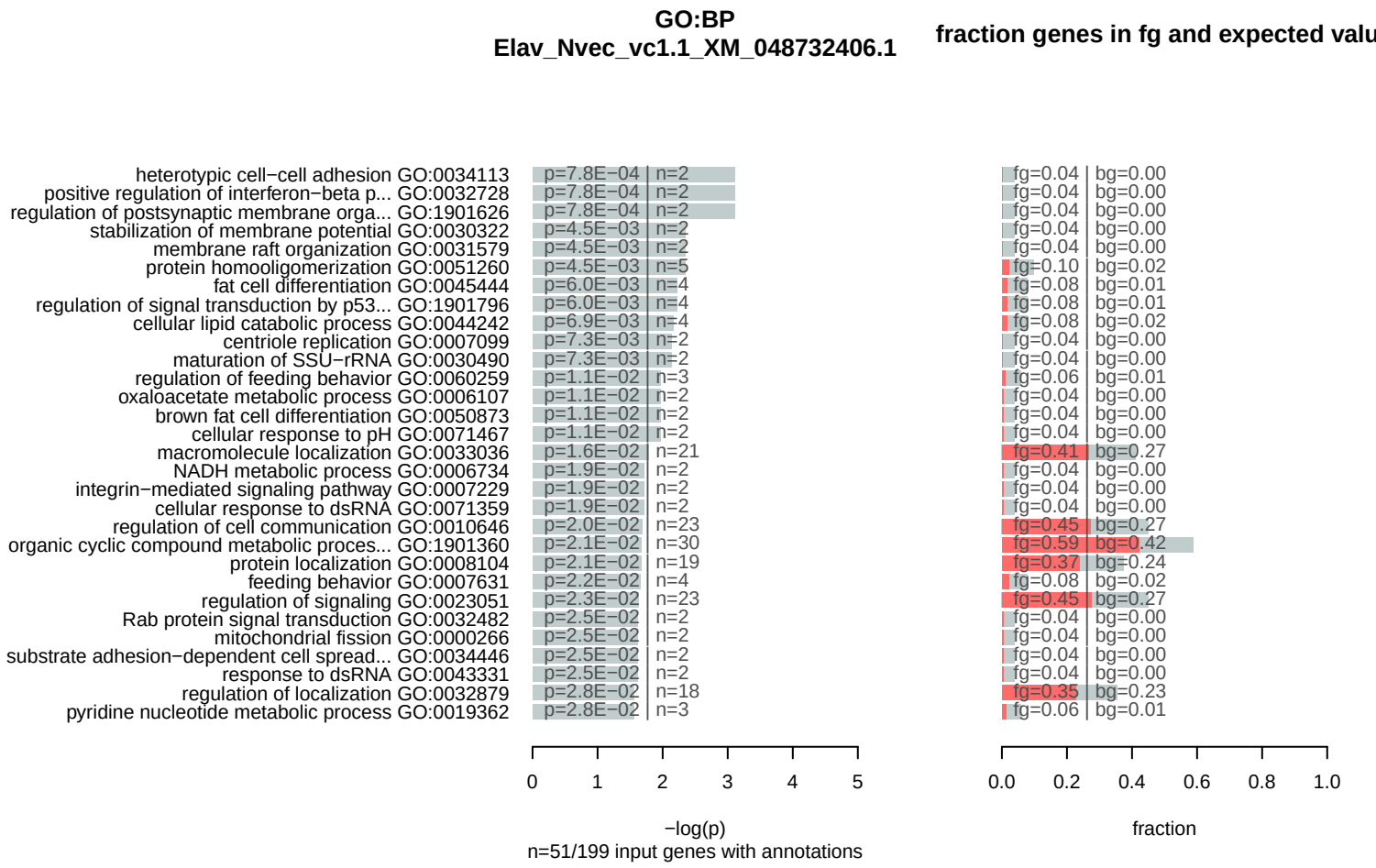
GO:BP
Elav_Nvec_vc1.1_XM_048732406.1
fraction genes in fg and expected valu
heterotypic cell−cell adhesion GO:0034113 p=7.8E−04 n=2 fg=0.04 bg=0.00
positive regulation of interferon−beta p... GO:0032728 p=7.8E−04 n=2 fg=0.04 bg=0.00
regulation of postsynaptic membrane orga... GO:1901626 p=7.8E−04 n=2 fg=0.04 bg=0.00
stabilization of membrane potential GO:0030322 p=4.5E−03 n=2 fg=0.04 bg=0.00
membrane raft organization GO:0031579 p=4.5E−03 n=2 fg=0.04 bg=0.00
protein homooligomerization GO:0051260 p=4.5E−03 n=5 fg=0.10 bg=0.02
fat cell differentiation GO:0045444 p=6.0E−03 n=4 fg=0.08 bg=0.01
regulation of signal transduction by p53... GO:1901796 p=6.0E−03 n=4 fg=0.08 bg=0.01
cellular lipid catabolic process GO:0044242 p=6.9E−03 n=4 fg=0.08 bg=0.02
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maturation of SSU−rRNA GO:0030490 p=7.3E−03 n=2 fg=0.04 bg=0.00
regulation of feeding behavior GO:0060259 p=1.1E−02 n=3 fg=0.06 bg=0.01
oxaloacetate metabolic process GO:0006107 p=1.1E−02 n=2 fg=0.04 bg=0.00
brown fat cell differentiation GO:0050873 p=1.1E−02 n=2 fg=0.04 bg=0.00
cellular response to pH GO:0071467 p=1.1E−02 n=2 fg=0.04 bg=0.00
macromolecule localization GO:0033036 p=1.6E−02 n=21 fg=0.41 bg=0.27
NADH metabolic process GO:0006734 p=1.9E−02 n=2 fg=0.04 bg=0.00
integrin−mediated signaling pathway GO:0007229 p=1.9E−02 n=2 fg=0.04 bg=0.00
cellular response to dsRNA GO:0071359 p=1.9E−02 n=2 fg=0.04 bg=0.00
regulation of cell communication GO:0010646 p=2.0E−02 n=23 fg=0.45 bg=0.27
organic cyclic compound metabolic proces... GO:1901360 p=2.1E−02 n=30 fg=0.59 bg=0.42
protein localization GO:0008104 p=2.1E−02 n=19 fg=0.37 bg=0.24
feeding behavior GO:0007631 p=2.2E−02 n=4 fg=0.08 bg=0.02
regulation of signaling GO:0023051 p=2.3E−02 n=23 fg=0.45 bg=0.27
Rab protein signal transduction GO:0032482 p=2.5E−02 n=2 fg=0.04 bg=0.00
mitochondrial fission GO:0000266 p=2.5E−02 n=2 fg=0.04 bg=0.00
substrate adhesion−dependent cell spread... GO:0034446 p=2.5E−02 n=2 fg=0.04 bg=0.00
response to dsRNA GO:0043331 p=2.5E−02 n=2 fg=0.04 bg=0.00
regulation of localization GO:0032879 p=2.8E−02 n=18 fg=0.35 bg=0.23
pyridine nucleotide metabolic process GO:0019362 p=2.8E−02 n=3 fg=0.06 bg=0.01
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−log(p)
n=51/199 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_048732406.1
fraction genes in fg and expected valu
NF−kappaB binding GO:0051059 p=2.4E−03 n=2 fg=0.04 bg=0.00
phosphatidic acid binding GO:0070300 p=4.7E−03 n=2 fg=0.04 bg=0.00
potassium ion leak channel activity GO:0022841 p=7.7E−03 n=2 fg=0.04 bg=0.00
phosphatidylinositol binding GO:0035091 p=9.1E−03 n=5 fg=0.11 bg=0.03
protease binding GO:0002020 p=1.4E−02 n=3 fg=0.07 bg=0.01
GTPase activating protein binding GO:0032794 p=2.1E−02 n=2 fg=0.04 bg=0.01
phosphatidylinositol−4−phosphate binding GO:0070273 p=2.1E−02 n=2 fg=0.04 bg=0.01
protein−disulfide reductase activity GO:0015035 p=2.6E−02 n=2 fg=0.04 bg=0.01
G−protein gamma−subunit binding GO:0031682 p=2.9E−02 n=1 fg=0.02 bg=0.00
alpha−methylacyl−CoA racemase activity GO:0008111 p=2.9E−02 n=1 fg=0.02 bg=0.00
phospholipase A1 activity GO:0008970 p=2.9E−02 n=1 fg=0.02 bg=0.00
phosphopantothenate−−cysteine ligase act... GO:0004632 p=2.9E−02 n=1 fg=0.02 bg=0.00
fibronectin binding GO:0001968 p=2.9E−02 n=1 fg=0.02 bg=0.00
BH4 domain binding GO:0051435 p=2.9E−02 n=1 fg=0.02 bg=0.00
neuregulin binding GO:0038132 p=2.9E−02 n=1 fg=0.02 bg=0.00
ribokinase activity GO:0004747 p=2.9E−02 n=1 fg=0.02 bg=0.00
insulin−like growth factor I binding GO:0031994 p=2.9E−02 n=1 fg=0.02 bg=0.00
ATP−dependent peptidase activity GO:0004176 p=2.9E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=2.9E−02 n=1 fg=0.02 bg=0.00
L−malate dehydrogenase activity GO:0030060 p=2.9E−02 n=1 fg=0.02 bg=0.00
8−oxo−dGDP phosphatase activity GO:0044715 p=2.9E−02 n=1 fg=0.02 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=2.9E−02 n=1 fg=0.02 bg=0.00
GMP binding GO:0019002 p=2.9E−02 n=1 fg=0.02 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=2.9E−02 n=1 fg=0.02 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=2.9E−02 n=1 fg=0.02 bg=0.00
C−methyltransferase activity GO:0008169 p=2.9E−02 n=1 fg=0.02 bg=0.00
neuropilin binding GO:0038191 p=2.9E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=2.9E−02 n=1 fg=0.02 bg=0.00
Roundabout binding GO:0048495 p=2.9E−02 n=1 fg=0.02 bg=0.00
mitochondrial promoter sequence−specific... GO:0001018 p=2.9E−02 n=1 fg=0.02 bg=0.00
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n=46/199 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_048732406.1
fraction genes in fg and expected valu
filopodium membrane GO:0031527 p=7.4E−03 n=2 fg=0.04 bg=0.00
intrinsic component of plasma membrane GO:0031226 p=1.8E−02 n=9 fg=0.18 bg=0.08
preribosome GO:0030684 p=2.0E−02 n=2 fg=0.04 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=2.8E−02 n=1 fg=0.02 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=2.8E−02 n=1 fg=0.02 bg=0.00
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cell trailing edge GO:0031254 p=2.8E−02 n=1 fg=0.02 bg=0.00
integral component of lysosomal membrane GO:1905103 p=2.8E−02 n=1 fg=0.02 bg=0.00
uropod GO:0001931 p=2.8E−02 n=1 fg=0.02 bg=0.00
piP−body GO:0071547 p=2.8E−02 n=1 fg=0.02 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=2.8E−02 n=1 fg=0.02 bg=0.00
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nucleolus GO:0005730 p=3.0E−02 n=8 fg=0.16 bg=0.07
integral component of plasma membrane GO:0005887 p=3.3E−02 n=8 fg=0.16 bg=0.08
NSL complex GO:0044545 p=5.6E−02 n=1 fg=0.02 bg=0.00
integral component of vacuolar membrane GO:0031166 p=5.6E−02 n=1 fg=0.02 bg=0.00
flotillin complex GO:0016600 p=5.6E−02 n=1 fg=0.02 bg=0.00
NELF complex GO:0032021 p=5.6E−02 n=1 fg=0.02 bg=0.00
integrin complex GO:0008305 p=5.6E−02 n=1 fg=0.02 bg=0.00
preribosome, small subunit precursor GO:0030688 p=5.6E−02 n=1 fg=0.02 bg=0.00
protein complex involved in cell adhesio... GO:0098636 p=5.6E−02 n=1 fg=0.02 bg=0.00
intrinsic component of vacuolar membrane GO:0031310 p=5.6E−02 n=1 fg=0.02 bg=0.00
focal adhesion GO:0005925 p=6.5E−02 n=2 fg=0.04 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=6.5E−02 n=2 fg=0.04 bg=0.01
non−membrane−bounded organelle GO:0043228 p=6.5E−02 n=21 fg=0.41 bg=0.30
intracellular non−membrane−bounded organ... GO:0043232 p=6.5E−02 n=21 fg=0.41 bg=0.30
cell−cell contact zone GO:0044291 p=7.3E−02 n=2 fg=0.04 bg=0.01
lamellipodium GO:0030027 p=7.3E−02 n=3 fg=0.06 bg=0.02
mitochondrion GO:0005739 p=7.4E−02 n=11 fg=0.22 bg=0.14
endolysosome membrane GO:0036020 p=8.2E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=51/199 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction