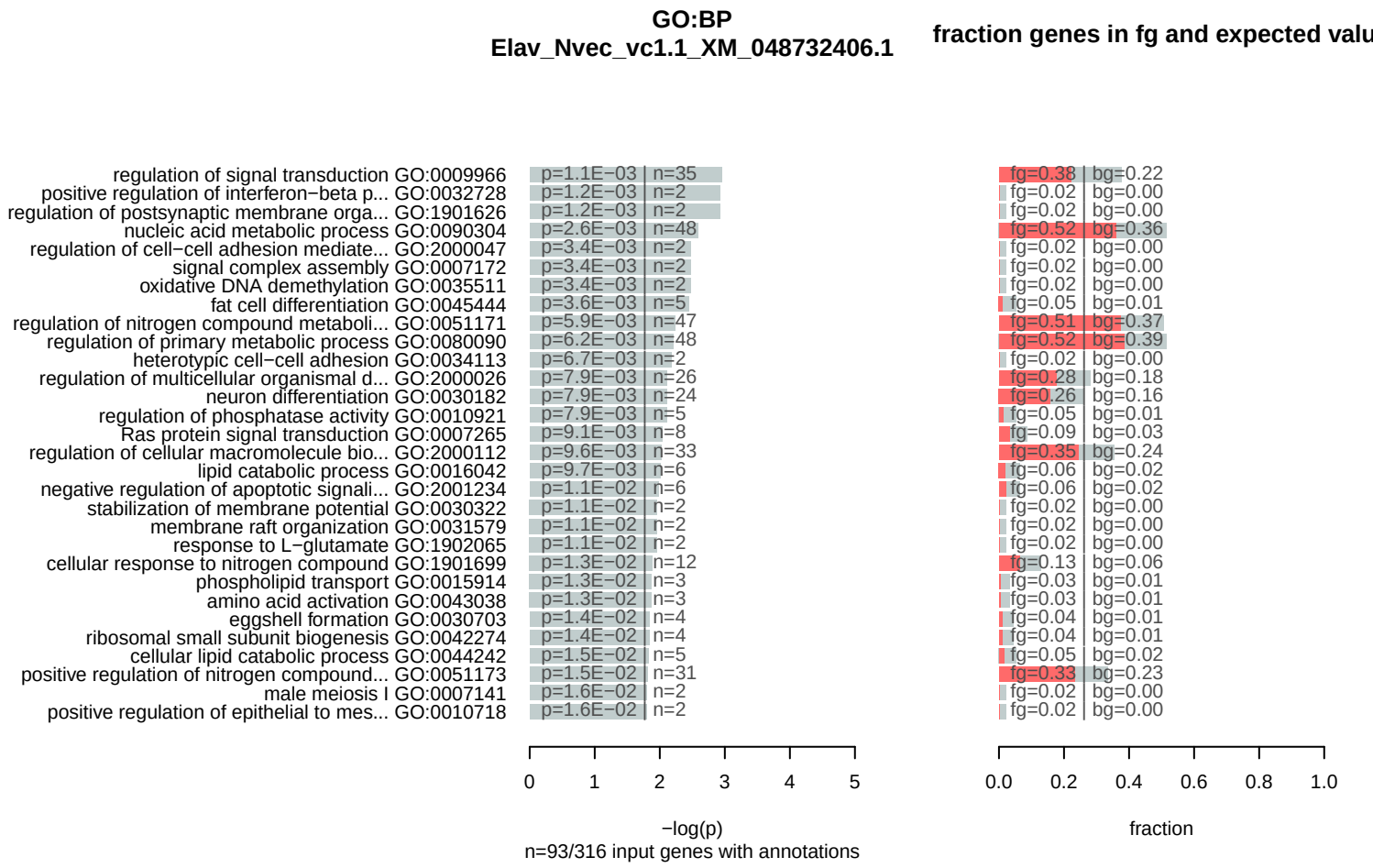
GO:BP
Elav_Nvec_vc1.1_XM_048732406.1
fraction genes in fg and expected valu
regulation of signal transduction GO:0009966 p=1.1E−03 n=35 fg=0.38 bg=0.22
positive regulation of interferon−beta p... GO:0032728 p=1.2E−03 n=2 fg=0.02 bg=0.00
regulation of postsynaptic membrane orga... GO:1901626 p=1.2E−03 n=2 fg=0.02 bg=0.00
nucleic acid metabolic process GO:0090304 p=2.6E−03 n=48 fg=0.52 bg=0.36
regulation of cell−cell adhesion mediate... GO:2000047 p=3.4E−03 n=2 fg=0.02 bg=0.00
signal complex assembly GO:0007172 p=3.4E−03 n=2 fg=0.02 bg=0.00
oxidative DNA demethylation GO:0035511 p=3.4E−03 n=2 fg=0.02 bg=0.00
fat cell differentiation GO:0045444 p=3.6E−03 n=5 fg=0.05 bg=0.01
regulation of nitrogen compound metaboli... GO:0051171 p=5.9E−03 n=47 fg=0.51 bg=0.37
regulation of primary metabolic process GO:0080090 p=6.2E−03 n=48 fg=0.52 bg=0.39
heterotypic cell−cell adhesion GO:0034113 p=6.7E−03 n=2 fg=0.02 bg=0.00
regulation of multicellular organismal d... GO:2000026 p=7.9E−03 n=26 fg=0.28 bg=0.18
neuron differentiation GO:0030182 p=7.9E−03 n=24 fg=0.26 bg=0.16
regulation of phosphatase activity GO:0010921 p=7.9E−03 n=5 fg=0.05 bg=0.01
Ras protein signal transduction GO:0007265 p=9.1E−03 n=8 fg=0.09 bg=0.03
regulation of cellular macromolecule bio... GO:2000112 p=9.6E−03 n=33 fg=0.35 bg=0.24
lipid catabolic process GO:0016042 p=9.7E−03 n=6 fg=0.06 bg=0.02
negative regulation of apoptotic signali... GO:2001234 p=1.1E−02 n=6 fg=0.06 bg=0.02
stabilization of membrane potential GO:0030322 p=1.1E−02 n=2 fg=0.02 bg=0.00
membrane raft organization GO:0031579 p=1.1E−02 n=2 fg=0.02 bg=0.00
response to L−glutamate GO:1902065 p=1.1E−02 n=2 fg=0.02 bg=0.00
cellular response to nitrogen compound GO:1901699 p=1.3E−02 n=12 fg=0.13 bg=0.06
phospholipid transport GO:0015914 p=1.3E−02 n=3 fg=0.03 bg=0.01
amino acid activation GO:0043038 p=1.3E−02 n=3 fg=0.03 bg=0.01
eggshell formation GO:0030703 p=1.4E−02 n=4 fg=0.04 bg=0.01
ribosomal small subunit biogenesis GO:0042274 p=1.4E−02 n=4 fg=0.04 bg=0.01
cellular lipid catabolic process GO:0044242 p=1.5E−02 n=5 fg=0.05 bg=0.02
positive regulation of nitrogen compound... GO:0051173 p=1.5E−02 n=31 fg=0.33 bg=0.23
male meiosis I GO:0007141 p=1.6E−02 n=2 fg=0.02 bg=0.00
positive regulation of epithelial to mes... GO:0010718 p=1.6E−02 n=2 fg=0.02 bg=0.00
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n=93/316 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
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methyl−CpG binding GO:0008327 p=7.6E−03 n=2 fg=0.02 bg=0.00
phosphatidylinositol−4−phosphate binding GO:0070273 p=8.3E−03 n=3 fg=0.03 bg=0.01
phosphatidylinositol−5−phosphate binding GO:0010314 p=1.2E−02 n=2 fg=0.02 bg=0.00
NF−kappaB binding GO:0051059 p=1.2E−02 n=2 fg=0.02 bg=0.00
leak channel activity GO:0022840 p=1.2E−02 n=2 fg=0.02 bg=0.00
potassium ion leak channel activity GO:0022841 p=1.2E−02 n=2 fg=0.02 bg=0.00
narrow pore channel activity GO:0022842 p=1.2E−02 n=2 fg=0.02 bg=0.00
DNA polymerase binding GO:0070182 p=1.8E−02 n=2 fg=0.02 bg=0.00
SMAD binding GO:0046332 p=1.9E−02 n=3 fg=0.03 bg=0.01
ligase activity GO:0016874 p=2.1E−02 n=5 fg=0.06 bg=0.02
phosphatidic acid binding GO:0070300 p=2.5E−02 n=2 fg=0.02 bg=0.00
potassium channel activity GO:0005267 p=2.6E−02 n=3 fg=0.03 bg=0.01
catalytic activity, acting on a tRNA GO:0140101 p=2.8E−02 n=4 fg=0.05 bg=0.01
catalytic activity, acting on RNA GO:0140098 p=2.8E−02 n=8 fg=0.09 bg=0.04
oxidoreductase activity, acting on paire... GO:0016705 p=3.0E−02 n=3 fg=0.03 bg=0.01
catalytic activity, acting on a nucleic ... GO:0140640 p=3.1E−02 n=11 fg=0.13 bg=0.07
vitamin D 24−hydroxylase activity GO:0070576 p=3.7E−02 n=1 fg=0.01 bg=0.00
neuregulin binding GO:0038132 p=3.7E−02 n=1 fg=0.01 bg=0.00
methylcytosine dioxygenase activity GO:0070579 p=3.7E−02 n=1 fg=0.01 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=3.7E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=3.7E−02 n=1 fg=0.01 bg=0.00
oxidative RNA demethylase activity GO:0035515 p=3.7E−02 n=1 fg=0.01 bg=0.00
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oxidoreductase activity, acting on paire... GO:0016709 p=3.7E−02 n=1 fg=0.01 bg=0.00
tRNA demethylase activity GO:1990984 p=3.7E−02 n=1 fg=0.01 bg=0.00
alpha−L−fucosidase activity GO:0004560 p=3.7E−02 n=1 fg=0.01 bg=0.00
insulin−like growth factor I binding GO:0031994 p=3.7E−02 n=1 fg=0.01 bg=0.00
ATP−dependent peptidase activity GO:0004176 p=3.7E−02 n=1 fg=0.01 bg=0.00
all−trans retinal binding GO:0005503 p=3.7E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=87/316 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048732406.1
fraction genes in fg and expected valu
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mitochondrion GO:0005739 p=1.7E−02 n=21 fg=0.22 bg=0.14
aminoacyl−tRNA synthetase multienzyme co... GO:0017101 p=2.2E−02 n=2 fg=0.02 bg=0.00
intrinsic component of plasma membrane GO:0031226 p=2.6E−02 n=12 fg=0.13 bg=0.07
fibrillar center GO:0001650 p=2.6E−02 n=4 fg=0.04 bg=0.01
plasma membrane signaling receptor compl... GO:0098802 p=3.5E−02 n=3 fg=0.03 bg=0.01
piP−body GO:0071547 p=3.5E−02 n=1 fg=0.01 bg=0.00
kinocilium GO:0060091 p=3.5E−02 n=1 fg=0.01 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=3.5E−02 n=1 fg=0.01 bg=0.00
GTPase activator complex GO:1902773 p=3.5E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=3.5E−02 n=1 fg=0.01 bg=0.00
acrosomal membrane GO:0002080 p=3.5E−02 n=1 fg=0.01 bg=0.00
outer acrosomal membrane GO:0002081 p=3.5E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=3.5E−02 n=1 fg=0.01 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=3.5E−02 n=1 fg=0.01 bg=0.00
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TIM22 mitochondrial import inner membran... GO:0042721 p=3.5E−02 n=1 fg=0.01 bg=0.00
cyclin A1−CDK2 complex GO:0097123 p=3.5E−02 n=1 fg=0.01 bg=0.00
cyclin A2−CDK2 complex GO:0097124 p=3.5E−02 n=1 fg=0.01 bg=0.00
anchored component of the cytoplasmic si... GO:0098753 p=3.5E−02 n=1 fg=0.01 bg=0.00
fungal biofilm matrix GO:0062040 p=3.5E−02 n=1 fg=0.01 bg=0.00
biofilm matrix GO:0062039 p=3.5E−02 n=1 fg=0.01 bg=0.00
9+2 non−motile cilium GO:0097732 p=3.5E−02 n=1 fg=0.01 bg=0.00
meiotic cohesin complex GO:0030893 p=3.5E−02 n=1 fg=0.01 bg=0.00
AMPA glutamate receptor complex GO:0032281 p=3.5E−02 n=1 fg=0.01 bg=0.00
cytoophidium GO:0097268 p=3.5E−02 n=1 fg=0.01 bg=0.00
nuclear meiotic cohesin complex GO:0034991 p=3.5E−02 n=1 fg=0.01 bg=0.00
mitochondrial nucleoid GO:0042645 p=3.7E−02 n=2 fg=0.02 bg=0.00
H4 histone acetyltransferase complex GO:1902562 p=3.7E−02 n=2 fg=0.02 bg=0.00
nucleoid GO:0009295 p=3.7E−02 n=2 fg=0.02 bg=0.00
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−log(p)
n=94/316 input genes with annotations
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fraction