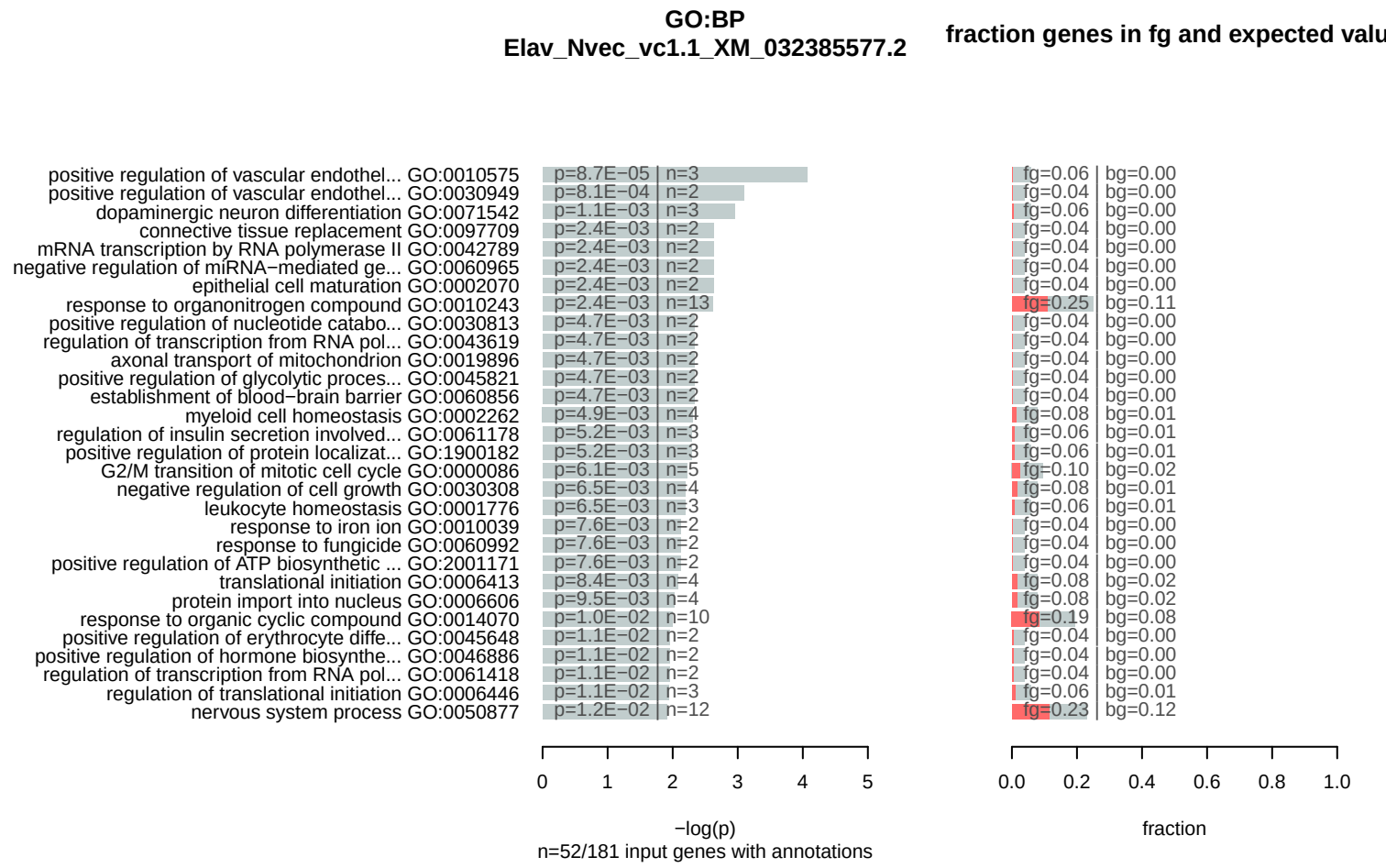
GO:BP
Elav_Nvec_vc1.1_XM_032385577.2
fraction genes in fg and expected valu
positive regulation of vascular endothel... GO:0010575 p=8.7E−05 n=3 fg=0.06 bg=0.00
positive regulation of vascular endothel... GO:0030949 p=8.1E−04 n=2 fg=0.04 bg=0.00
dopaminergic neuron differentiation GO:0071542 p=1.1E−03 n=3 fg=0.06 bg=0.00
connective tissue replacement GO:0097709 p=2.4E−03 n=2 fg=0.04 bg=0.00
mRNA transcription by RNA polymerase II GO:0042789 p=2.4E−03 n=2 fg=0.04 bg=0.00
negative regulation of miRNA−mediated ge... GO:0060965 p=2.4E−03 n=2 fg=0.04 bg=0.00
epithelial cell maturation GO:0002070 p=2.4E−03 n=2 fg=0.04 bg=0.00
response to organonitrogen compound GO:0010243 p=2.4E−03 n=13 fg=0.25 bg=0.11
positive regulation of nucleotide catabo... GO:0030813 p=4.7E−03 n=2 fg=0.04 bg=0.00
regulation of transcription from RNA pol... GO:0043619 p=4.7E−03 n=2 fg=0.04 bg=0.00
axonal transport of mitochondrion GO:0019896 p=4.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of glycolytic proces... GO:0045821 p=4.7E−03 n=2 fg=0.04 bg=0.00
establishment of blood−brain barrier GO:0060856 p=4.7E−03 n=2 fg=0.04 bg=0.00
myeloid cell homeostasis GO:0002262 p=4.9E−03 n=4 fg=0.08 bg=0.01
regulation of insulin secretion involved... GO:0061178 p=5.2E−03 n=3 fg=0.06 bg=0.01
positive regulation of protein localizat... GO:1900182 p=5.2E−03 n=3 fg=0.06 bg=0.01
G2/M transition of mitotic cell cycle GO:0000086 p=6.1E−03 n=5 fg=0.10 bg=0.02
negative regulation of cell growth GO:0030308 p=6.5E−03 n=4 fg=0.08 bg=0.01
leukocyte homeostasis GO:0001776 p=6.5E−03 n=3 fg=0.06 bg=0.01
response to iron ion GO:0010039 p=7.6E−03 n=2 fg=0.04 bg=0.00
response to fungicide GO:0060992 p=7.6E−03 n=2 fg=0.04 bg=0.00
positive regulation of ATP biosynthetic ... GO:2001171 p=7.6E−03 n=2 fg=0.04 bg=0.00
translational initiation GO:0006413 p=8.4E−03 n=4 fg=0.08 bg=0.02
protein import into nucleus GO:0006606 p=9.5E−03 n=4 fg=0.08 bg=0.02
response to organic cyclic compound GO:0014070 p=1.0E−02 n=10 fg=0.19 bg=0.08
positive regulation of erythrocyte diffe... GO:0045648 p=1.1E−02 n=2 fg=0.04 bg=0.00
positive regulation of hormone biosynthe... GO:0046886 p=1.1E−02 n=2 fg=0.04 bg=0.00
regulation of transcription from RNA pol... GO:0061418 p=1.1E−02 n=2 fg=0.04 bg=0.00
regulation of translational initiation GO:0006446 p=1.1E−02 n=3 fg=0.06 bg=0.01
nervous system process GO:0050877 p=1.2E−02 n=12 fg=0.23 bg=0.12
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−log(p)
n=52/181 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032385577.2
fraction genes in fg and expected valu
mRNA regulatory element binding translat... GO:0000900 p=2.5E−03 n=2 fg=0.04 bg=0.00
tau−protein kinase activity GO:0050321 p=4.9E−03 n=2 fg=0.04 bg=0.00
transcription coactivator activity GO:0003713 p=6.6E−03 n=6 fg=0.13 bg=0.04
ligase activity GO:0016874 p=7.1E−03 n=4 fg=0.09 bg=0.02
poly(U) RNA binding GO:0008266 p=8.1E−03 n=2 fg=0.04 bg=0.00
translation factor activity, RNA binding GO:0008135 p=1.0E−02 n=3 fg=0.06 bg=0.01
histone deacetylase binding GO:0042826 p=1.4E−02 n=3 fg=0.06 bg=0.01
translation regulator activity GO:0045182 p=1.5E−02 n=5 fg=0.11 bg=0.01
signal sequence binding GO:0005048 p=2.1E−02 n=2 fg=0.04 bg=0.01
ligase activity, forming carbon−nitrogen... GO:0016879 p=2.1E−02 n=2 fg=0.04 bg=0.01
translation initiation factor binding GO:0031369 p=2.7E−02 n=2 fg=0.04 bg=0.01
poly−pyrimidine tract binding GO:0008187 p=2.8E−02 n=3 fg=0.06 bg=0.00
leptin receptor binding GO:1990460 p=2.9E−02 n=1 fg=0.02 bg=0.00
cobalt ion binding GO:0050897 p=2.9E−02 n=1 fg=0.02 bg=0.00
cyclohydrolase activity GO:0019238 p=2.9E−02 n=1 fg=0.02 bg=0.00
transferrin receptor binding GO:1990459 p=2.9E−02 n=1 fg=0.02 bg=0.00
calmodulin−dependent protein phosphatase... GO:0033192 p=2.9E−02 n=1 fg=0.02 bg=0.00
L−alanine:2−oxoglutarate aminotransferas... GO:0004021 p=2.9E−02 n=1 fg=0.02 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=2.9E−02 n=1 fg=0.02 bg=0.00
glutaminase activity GO:0004359 p=2.9E−02 n=1 fg=0.02 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004486 p=2.9E−02 n=1 fg=0.02 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=2.9E−02 n=1 fg=0.02 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004487 p=2.9E−02 n=1 fg=0.02 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004488 p=2.9E−02 n=1 fg=0.02 bg=0.00
NAD+ synthase activity GO:0008795 p=2.9E−02 n=1 fg=0.02 bg=0.00
methenyltetrahydrofolate cyclohydrolase ... GO:0004477 p=2.9E−02 n=1 fg=0.02 bg=0.00
formate−tetrahydrofolate ligase activity GO:0004329 p=2.9E−02 n=1 fg=0.02 bg=0.00
UFM1 activating enzyme activity GO:0071566 p=2.9E−02 n=1 fg=0.02 bg=0.00
glucose−6−phosphate dehydrogenase activi... GO:0004345 p=2.9E−02 n=1 fg=0.02 bg=0.00
nickel cation binding GO:0016151 p=2.9E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=47/181 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032385577.2
fraction genes in fg and expected valu
dendrite cytoplasm GO:0032839 p=4.9E−03 n=2 fg=0.04 bg=0.00
ER to Golgi transport vesicle membrane GO:0012507 p=1.6E−02 n=2 fg=0.04 bg=0.00
PML body GO:0016605 p=1.6E−02 n=2 fg=0.04 bg=0.00
nuclear body GO:0016604 p=1.7E−02 n=8 fg=0.15 bg=0.06
supramolecular complex GO:0099080 p=1.8E−02 n=9 fg=0.17 bg=0.08
integral component of organelle membrane GO:0031301 p=2.1E−02 n=6 fg=0.11 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=2.4E−02 n=6 fg=0.11 bg=0.04
melanosome GO:0042470 p=2.7E−02 n=2 fg=0.04 bg=0.00
tubulin folding cofactor complex GO:1990727 p=2.9E−02 n=1 fg=0.02 bg=0.00
keratin filament GO:0045095 p=2.9E−02 n=1 fg=0.02 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=2.9E−02 n=1 fg=0.02 bg=0.00
ciliary transition fiber GO:0097539 p=2.9E−02 n=1 fg=0.02 bg=0.00
desmosome GO:0030057 p=2.9E−02 n=1 fg=0.02 bg=0.00
molybdopterin synthase complex GO:0019008 p=2.9E−02 n=1 fg=0.02 bg=0.00
calcineurin complex GO:0005955 p=2.9E−02 n=1 fg=0.02 bg=0.00
nuclear speck GO:0016607 p=3.1E−02 n=5 fg=0.09 bg=0.03
T−tubule GO:0030315 p=3.3E−02 n=2 fg=0.04 bg=0.01
pigment granule GO:0048770 p=3.3E−02 n=2 fg=0.04 bg=0.01
endosome membrane GO:0010008 p=3.5E−02 n=5 fg=0.09 bg=0.03
cytoplasmic ribonucleoprotein granule GO:0036464 p=3.7E−02 n=4 fg=0.08 bg=0.02
membrane−bounded organelle GO:0043227 p=3.8E−02 n=48 fg=0.91 bg=0.81
nuclear periphery GO:0034399 p=3.8E−02 n=3 fg=0.06 bg=0.01
integral component of Golgi membrane GO:0030173 p=3.9E−02 n=2 fg=0.04 bg=0.01
ficolin−1−rich granule GO:0101002 p=4.2E−02 n=3 fg=0.06 bg=0.01
intrinsic component of Golgi membrane GO:0031228 p=4.6E−02 n=2 fg=0.04 bg=0.01
ribonucleoprotein granule GO:0035770 p=4.6E−02 n=4 fg=0.08 bg=0.03
COPII−coated ER to Golgi transport vesic... GO:0030134 p=5.3E−02 n=2 fg=0.04 bg=0.01
U2AF complex GO:0089701 p=5.8E−02 n=1 fg=0.02 bg=0.00
pleated septate junction GO:0005919 p=5.8E−02 n=1 fg=0.02 bg=0.00
COPII vesicle coat GO:0030127 p=5.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=53/181 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction