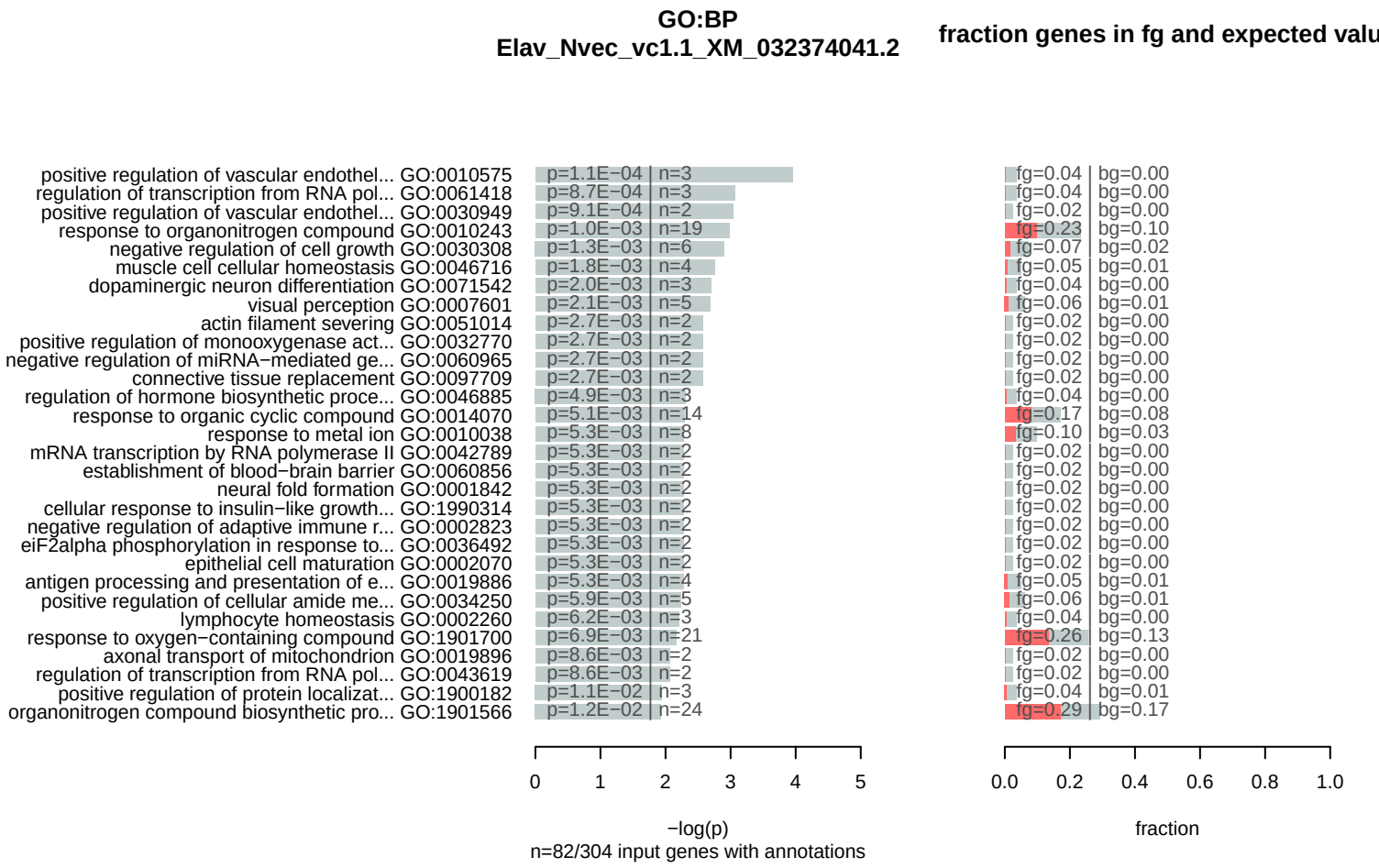
GO:BP
Elav_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
positive regulation of vascular endothel... GO:0010575 p=1.1E−04 n=3 fg=0.04 bg=0.00
regulation of transcription from RNA pol... GO:0061418 p=8.7E−04 n=3 fg=0.04 bg=0.00
positive regulation of vascular endothel... GO:0030949 p=9.1E−04 n=2 fg=0.02 bg=0.00
response to organonitrogen compound GO:0010243 p=1.0E−03 n=19 fg=0.23 bg=0.10
negative regulation of cell growth GO:0030308 p=1.3E−03 n=6 fg=0.07 bg=0.02
muscle cell cellular homeostasis GO:0046716 p=1.8E−03 n=4 fg=0.05 bg=0.01
dopaminergic neuron differentiation GO:0071542 p=2.0E−03 n=3 fg=0.04 bg=0.00
visual perception GO:0007601 p=2.1E−03 n=5 fg=0.06 bg=0.01
actin filament severing GO:0051014 p=2.7E−03 n=2 fg=0.02 bg=0.00
positive regulation of monooxygenase act... GO:0032770 p=2.7E−03 n=2 fg=0.02 bg=0.00
negative regulation of miRNA−mediated ge... GO:0060965 p=2.7E−03 n=2 fg=0.02 bg=0.00
connective tissue replacement GO:0097709 p=2.7E−03 n=2 fg=0.02 bg=0.00
regulation of hormone biosynthetic proce... GO:0046885 p=4.9E−03 n=3 fg=0.04 bg=0.00
response to organic cyclic compound GO:0014070 p=5.1E−03 n=14 fg=0.17 bg=0.08
response to metal ion GO:0010038 p=5.3E−03 n=8 fg=0.10 bg=0.03
mRNA transcription by RNA polymerase II GO:0042789 p=5.3E−03 n=2 fg=0.02 bg=0.00
establishment of blood−brain barrier GO:0060856 p=5.3E−03 n=2 fg=0.02 bg=0.00
neural fold formation GO:0001842 p=5.3E−03 n=2 fg=0.02 bg=0.00
cellular response to insulin−like growth... GO:1990314 p=5.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of adaptive immune r... GO:0002823 p=5.3E−03 n=2 fg=0.02 bg=0.00
eiF2alpha phosphorylation in response to... GO:0036492 p=5.3E−03 n=2 fg=0.02 bg=0.00
epithelial cell maturation GO:0002070 p=5.3E−03 n=2 fg=0.02 bg=0.00
antigen processing and presentation of e... GO:0019886 p=5.3E−03 n=4 fg=0.05 bg=0.01
positive regulation of cellular amide me... GO:0034250 p=5.9E−03 n=5 fg=0.06 bg=0.01
lymphocyte homeostasis GO:0002260 p=6.2E−03 n=3 fg=0.04 bg=0.00
response to oxygen−containing compound GO:1901700 p=6.9E−03 n=21 fg=0.26 bg=0.13
axonal transport of mitochondrion GO:0019896 p=8.6E−03 n=2 fg=0.02 bg=0.00
regulation of transcription from RNA pol... GO:0043619 p=8.6E−03 n=2 fg=0.02 bg=0.00
positive regulation of protein localizat... GO:1900182 p=1.1E−02 n=3 fg=0.04 bg=0.01
organonitrogen compound biosynthetic pro... GO:1901566 p=1.2E−02 n=24 fg=0.29 bg=0.17
0 1 2 3 4 5
−log(p)
n=82/304 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
miRNA binding GO:0035198 p=3.0E−03 n=2 fg=0.03 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=3.0E−03 n=2 fg=0.03 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=3.2E−03 n=3 fg=0.04 bg=0.00
protein−cysteine S−palmitoyltransferase ... GO:0019706 p=5.8E−03 n=2 fg=0.03 bg=0.00
tau−protein kinase activity GO:0050321 p=5.8E−03 n=2 fg=0.03 bg=0.00
eukaryotic initiation factor eIF2 bindin... GO:0071074 p=9.5E−03 n=2 fg=0.03 bg=0.00
ligase activity GO:0016874 p=1.2E−02 n=5 fg=0.07 bg=0.02
ion binding GO:0043167 p=1.2E−02 n=24 fg=0.32 bg=0.20
mRNA 3'−UTR binding GO:0003730 p=1.3E−02 n=3 fg=0.04 bg=0.01
gamma−tubulin binding GO:0043015 p=1.4E−02 n=2 fg=0.03 bg=0.00
insulin receptor binding GO:0005158 p=1.9E−02 n=2 fg=0.03 bg=0.00
poly(U) RNA binding GO:0008266 p=3.2E−02 n=2 fg=0.03 bg=0.00
alpha−tubulin binding GO:0043014 p=3.2E−02 n=2 fg=0.03 bg=0.00
neurotransmitter transmembrane transport... GO:0005326 p=3.2E−02 n=2 fg=0.03 bg=0.00
signal sequence binding GO:0005048 p=3.2E−02 n=2 fg=0.03 bg=0.00
protein−containing complex binding GO:0044877 p=3.2E−02 n=14 fg=0.18 bg=0.11
steroid hydroxylase activity GO:0008395 p=3.2E−02 n=1 fg=0.01 bg=0.00
CoA carboxylase activity GO:0016421 p=3.2E−02 n=1 fg=0.01 bg=0.00
alkanesulfonate transmembrane transporte... GO:0042959 p=3.2E−02 n=1 fg=0.01 bg=0.00
1−alpha,25−dihydroxyvitamin D3 24−hydrox... GO:0030342 p=3.2E−02 n=1 fg=0.01 bg=0.00
vitamin D3 25−hydroxylase activity GO:0030343 p=3.2E−02 n=1 fg=0.01 bg=0.00
amino acid:sodium symporter activity GO:0005283 p=3.2E−02 n=1 fg=0.01 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=3.2E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=3.2E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=3.2E−02 n=1 fg=0.01 bg=0.00
glutaminase activity GO:0004359 p=3.2E−02 n=1 fg=0.01 bg=0.00
cholesterol 26−hydroxylase activity GO:0031073 p=3.2E−02 n=1 fg=0.01 bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403 p=3.2E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on paire... GO:0016709 p=3.2E−02 n=1 fg=0.01 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=3.2E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/304 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
manchette GO:0002177 p=5.3E−03 n=2 fg=0.02 bg=0.00
dendrite cytoplasm GO:0032839 p=8.6E−03 n=2 fg=0.02 bg=0.00
integral component of organelle membrane GO:0031301 p=8.8E−03 n=8 fg=0.10 bg=0.04
SNARE complex GO:0031201 p=1.1E−02 n=3 fg=0.04 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=1.4E−02 n=12 fg=0.15 bg=0.07
endoplasmic reticulum GO:0005783 p=1.6E−02 n=18 fg=0.22 bg=0.13
nuclear outer membrane−endoplasmic retic... GO:0042175 p=1.7E−02 n=12 fg=0.15 bg=0.07
endoplasmic reticulum subcompartment GO:0098827 p=1.7E−02 n=12 fg=0.15 bg=0.07
cytoplasmic ubiquitin ligase complex GO:0000153 p=1.7E−02 n=2 fg=0.02 bg=0.00
dendritic spine GO:0043197 p=1.9E−02 n=5 fg=0.06 bg=0.02
neuron spine GO:0044309 p=1.9E−02 n=5 fg=0.06 bg=0.02
cell junction GO:0030054 p=2.0E−02 n=16 fg=0.20 bg=0.11
cytoplasm GO:0005737 p=2.1E−02 n=73 fg=0.89 bg=0.80
integral component of endoplasmic reticu... GO:0030176 p=2.2E−02 n=5 fg=0.06 bg=0.02
supramolecular complex GO:0099080 p=2.8E−02 n=12 fg=0.15 bg=0.08
intrinsic component of endoplasmic retic... GO:0031227 p=2.8E−02 n=5 fg=0.06 bg=0.02
melanosome GO:0042470 p=2.9E−02 n=2 fg=0.02 bg=0.00
ER to Golgi transport vesicle membrane GO:0012507 p=2.9E−02 n=2 fg=0.02 bg=0.00
postsynapse GO:0098794 p=3.0E−02 n=7 fg=0.09 bg=0.04
actin rod GO:0031002 p=3.0E−02 n=1 fg=0.01 bg=0.00
plasmodesma GO:0009506 p=3.0E−02 n=1 fg=0.01 bg=0.00
chloroplast GO:0009507 p=3.0E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=3.0E−02 n=1 fg=0.01 bg=0.00
symplast GO:0055044 p=3.0E−02 n=1 fg=0.01 bg=0.00
centralspindlin complex GO:0097149 p=3.0E−02 n=1 fg=0.01 bg=0.00
desmosome GO:0030057 p=3.0E−02 n=1 fg=0.01 bg=0.00
apoplast GO:0048046 p=3.0E−02 n=1 fg=0.01 bg=0.00
syntrophin complex GO:0016013 p=3.0E−02 n=1 fg=0.01 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=3.0E−02 n=1 fg=0.01 bg=0.00
stereocilia ankle link GO:0002141 p=3.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=82/304 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction