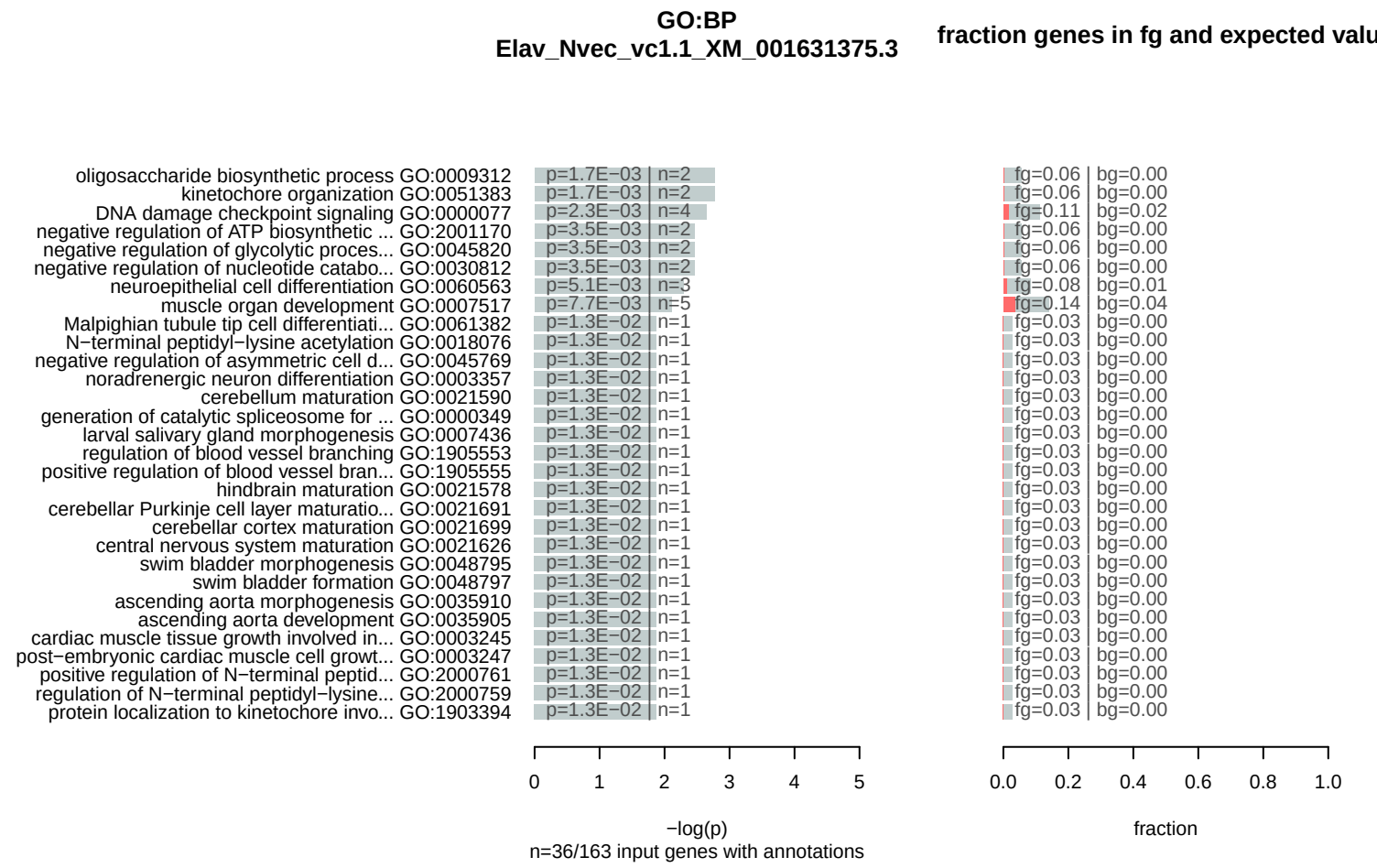
GO:BP
Elav_Nvec_vc1.1_XM_001631375.3
fraction genes in fg and expected valu
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kinetochore organization GO:0051383 p=1.7E−03 n=2 fg=0.06 bg=0.00
DNA damage checkpoint signaling GO:0000077 p=2.3E−03 n=4 fg=0.11 bg=0.02
negative regulation of ATP biosynthetic ... GO:2001170 p=3.5E−03 n=2 fg=0.06 bg=0.00
negative regulation of glycolytic proces... GO:0045820 p=3.5E−03 n=2 fg=0.06 bg=0.00
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neuroepithelial cell differentiation GO:0060563 p=5.1E−03 n=3 fg=0.08 bg=0.01
muscle organ development GO:0007517 p=7.7E−03 n=5 fg=0.14 bg=0.04
Malpighian tubule tip cell differentiati... GO:0061382 p=1.3E−02 n=1 fg=0.03 bg=0.00
N−terminal peptidyl−lysine acetylation GO:0018076 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of asymmetric cell d... GO:0045769 p=1.3E−02 n=1 fg=0.03 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=1.3E−02 n=1 fg=0.03 bg=0.00
cerebellum maturation GO:0021590 p=1.3E−02 n=1 fg=0.03 bg=0.00
generation of catalytic spliceosome for ... GO:0000349 p=1.3E−02 n=1 fg=0.03 bg=0.00
larval salivary gland morphogenesis GO:0007436 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of blood vessel branching GO:1905553 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of blood vessel bran... GO:1905555 p=1.3E−02 n=1 fg=0.03 bg=0.00
hindbrain maturation GO:0021578 p=1.3E−02 n=1 fg=0.03 bg=0.00
cerebellar Purkinje cell layer maturatio... GO:0021691 p=1.3E−02 n=1 fg=0.03 bg=0.00
cerebellar cortex maturation GO:0021699 p=1.3E−02 n=1 fg=0.03 bg=0.00
central nervous system maturation GO:0021626 p=1.3E−02 n=1 fg=0.03 bg=0.00
swim bladder morphogenesis GO:0048795 p=1.3E−02 n=1 fg=0.03 bg=0.00
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ascending aorta morphogenesis GO:0035910 p=1.3E−02 n=1 fg=0.03 bg=0.00
ascending aorta development GO:0035905 p=1.3E−02 n=1 fg=0.03 bg=0.00
cardiac muscle tissue growth involved in... GO:0003245 p=1.3E−02 n=1 fg=0.03 bg=0.00
post−embryonic cardiac muscle cell growt... GO:0003247 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of N−terminal peptid... GO:2000761 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of N−terminal peptidyl−lysine... GO:2000759 p=1.3E−02 n=1 fg=0.03 bg=0.00
protein localization to kinetochore invo... GO:1903394 p=1.3E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=36/163 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001631375.3
fraction genes in fg and expected valu
DNA−binding transcription factor activit... GO:0000981 p=3.6E−04 n=8 fg=0.25 bg=0.06
alpha−tubulin binding GO:0043014 p=6.0E−03 n=2 fg=0.06 bg=0.00
beta−tubulin binding GO:0048487 p=7.4E−03 n=2 fg=0.06 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=9.4E−03 n=5 fg=0.16 bg=0.04
polyubiquitin modification−dependent pro... GO:0031593 p=1.1E−02 n=2 fg=0.06 bg=0.01
intracellular sodium activated potassium... GO:0005228 p=1.4E−02 n=1 fg=0.03 bg=0.00
NAD−dependent histone deacetylase activi... GO:0017136 p=1.4E−02 n=1 fg=0.03 bg=0.00
NAD−dependent histone deacetylase activi... GO:0046969 p=1.4E−02 n=1 fg=0.03 bg=0.00
histone deacetylase activity (H3−K9 spec... GO:0032129 p=1.4E−02 n=1 fg=0.03 bg=0.00
hedgehog receptor activity GO:0008158 p=1.4E−02 n=1 fg=0.03 bg=0.00
isocitrate dehydrogenase (NAD+) activity GO:0004449 p=1.4E−02 n=1 fg=0.03 bg=0.00
E−box binding GO:0070888 p=1.5E−02 n=2 fg=0.06 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=1.6E−02 n=4 fg=0.12 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=1.6E−02 n=4 fg=0.12 bg=0.03
cis−regulatory region sequence−specific ... GO:0000987 p=1.7E−02 n=4 fg=0.12 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.7E−02 n=4 fg=0.12 bg=0.03
second spliceosomal transesterification ... GO:0000386 p=2.7E−02 n=1 fg=0.03 bg=0.00
NAD+ binding GO:0070403 p=2.7E−02 n=1 fg=0.03 bg=0.00
NAD−dependent protein deacetylase activi... GO:0034979 p=2.7E−02 n=1 fg=0.03 bg=0.00
3'−5'−exodeoxyribonuclease activity GO:0008296 p=2.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol 3−kinase regulatory... GO:0036312 p=2.7E−02 n=1 fg=0.03 bg=0.00
6−phosphofructo−2−kinase activity GO:0003873 p=2.7E−02 n=1 fg=0.03 bg=0.00
K48−linked polyubiquitin modification−de... GO:0036435 p=2.7E−02 n=1 fg=0.03 bg=0.00
isocitrate dehydrogenase activity GO:0004448 p=2.7E−02 n=1 fg=0.03 bg=0.00
mismatch repair complex binding GO:0032404 p=2.7E−02 n=1 fg=0.03 bg=0.00
MutLalpha complex binding GO:0032405 p=2.7E−02 n=1 fg=0.03 bg=0.00
MutSalpha complex binding GO:0032407 p=2.7E−02 n=1 fg=0.03 bg=0.00
Hsp90 protein binding GO:0051879 p=2.9E−02 n=2 fg=0.06 bg=0.01
pre−mRNA 3'−splice site binding GO:0030628 p=4.0E−02 n=1 fg=0.03 bg=0.00
formate transmembrane transporter activi... GO:0015499 p=4.0E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=32/163 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001631375.3
fraction genes in fg and expected valu
U2−type catalytic step 1 spliceosome GO:0071006 p=1.3E−02 n=1 fg=0.03 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=1.3E−02 n=1 fg=0.03 bg=0.00
isocitrate dehydrogenase complex (NAD+) GO:0045242 p=1.3E−02 n=1 fg=0.03 bg=0.00
catalytic step 1 spliceosome GO:0071012 p=1.3E−02 n=1 fg=0.03 bg=0.00
ciliary basal body GO:0036064 p=1.8E−02 n=3 fg=0.08 bg=0.02
nuclear body GO:0016604 p=1.9E−02 n=6 fg=0.17 bg=0.06
nuclear speck GO:0016607 p=2.4E−02 n=4 fg=0.11 bg=0.03
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=2.6E−02 n=1 fg=0.03 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=2.6E−02 n=1 fg=0.03 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=2.6E−02 n=1 fg=0.03 bg=0.00
microtubule minus−end GO:0036449 p=2.6E−02 n=1 fg=0.03 bg=0.00
TORC2 complex GO:0031932 p=2.6E−02 n=1 fg=0.03 bg=0.00
spermatoproteasome complex GO:1990111 p=2.6E−02 n=1 fg=0.03 bg=0.00
COPI vesicle coat GO:0030126 p=3.9E−02 n=1 fg=0.03 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=3.9E−02 n=1 fg=0.03 bg=0.00
proteasome core complex, alpha−subunit c... GO:0019773 p=3.9E−02 n=1 fg=0.03 bg=0.00
TOR complex GO:0038201 p=3.9E−02 n=1 fg=0.03 bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=3.9E−02 n=1 fg=0.03 bg=0.00
TORC1 complex GO:0031931 p=3.9E−02 n=1 fg=0.03 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=3.9E−02 n=1 fg=0.03 bg=0.00
ciliary rootlet GO:0035253 p=3.9E−02 n=1 fg=0.03 bg=0.00
catalytic step 2 spliceosome GO:0071013 p=4.0E−02 n=2 fg=0.06 bg=0.01
inner dynein arm GO:0036156 p=5.2E−02 n=1 fg=0.03 bg=0.00
COPI−coated vesicle membrane GO:0030663 p=5.2E−02 n=1 fg=0.03 bg=0.00
proteasome core complex GO:0005839 p=5.2E−02 n=1 fg=0.03 bg=0.00
ciliary transition zone GO:0035869 p=5.6E−02 n=2 fg=0.06 bg=0.01
nucleus GO:0005634 p=6.2E−02 n=23 fg=0.64 bg=0.50
Prp19 complex GO:0000974 p=6.5E−02 n=1 fg=0.03 bg=0.00
microtubule end GO:1990752 p=6.5E−02 n=1 fg=0.03 bg=0.00
cilium GO:0005929 p=6.9E−02 n=5 fg=0.14 bg=0.06
0 1 2 3 4 5
−log(p)
n=36/163 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction