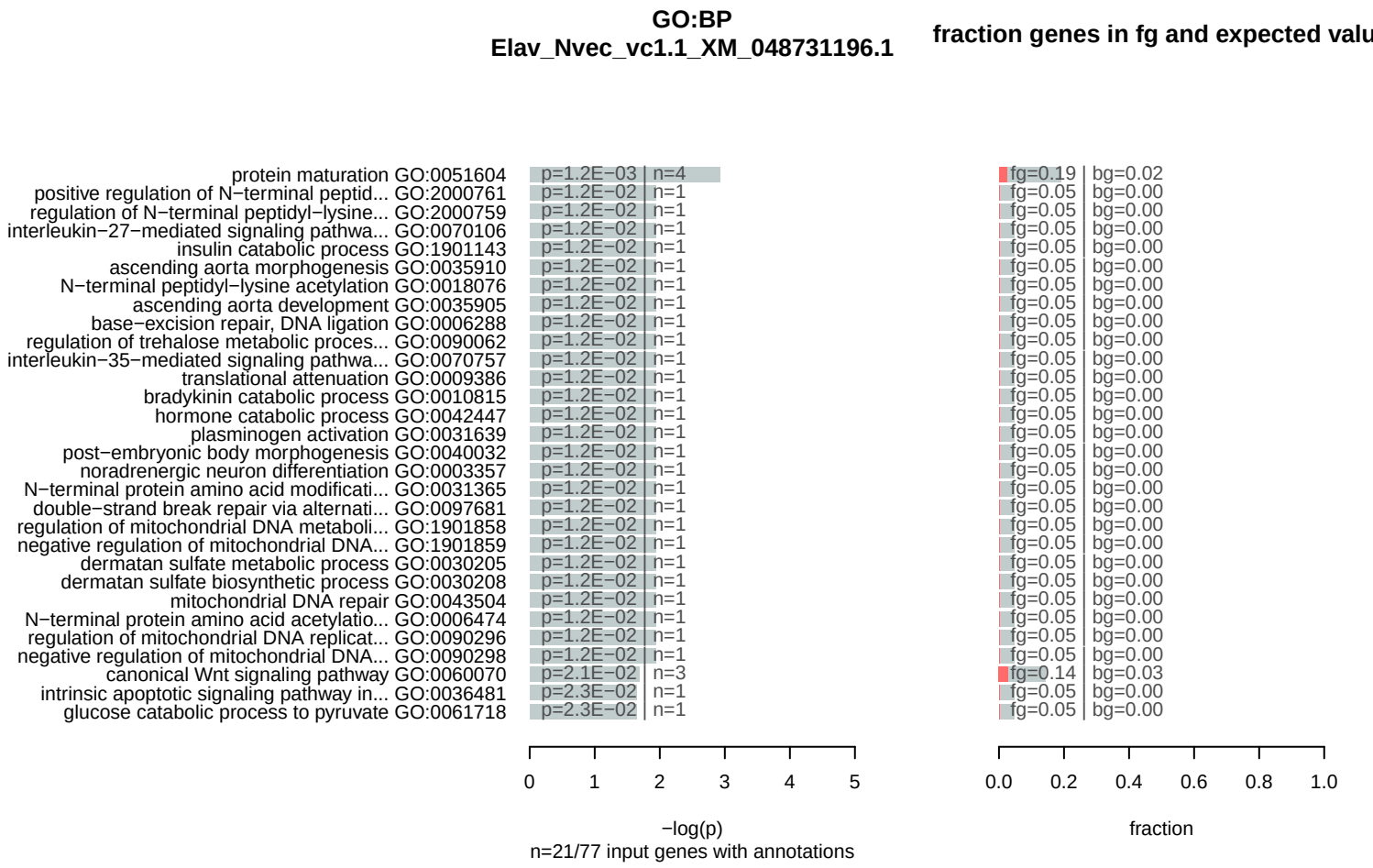
GO:BP
Elav_Nvec_vc1.1_XM_048731196.1
fraction genes in fg and expected valu
protein maturation GO:0051604 p=1.2E−03 n=4 fg=0.19 bg=0.02
positive regulation of N−terminal peptid... GO:2000761 p=1.2E−02 n=1 fg=0.05 bg=0.00
regulation of N−terminal peptidyl−lysine... GO:2000759 p=1.2E−02 n=1 fg=0.05 bg=0.00
interleukin−27−mediated signaling pathwa... GO:0070106 p=1.2E−02 n=1 fg=0.05 bg=0.00
insulin catabolic process GO:1901143 p=1.2E−02 n=1 fg=0.05 bg=0.00
ascending aorta morphogenesis GO:0035910 p=1.2E−02 n=1 fg=0.05 bg=0.00
N−terminal peptidyl−lysine acetylation GO:0018076 p=1.2E−02 n=1 fg=0.05 bg=0.00
ascending aorta development GO:0035905 p=1.2E−02 n=1 fg=0.05 bg=0.00
base−excision repair, DNA ligation GO:0006288 p=1.2E−02 n=1 fg=0.05 bg=0.00
regulation of trehalose metabolic proces... GO:0090062 p=1.2E−02 n=1 fg=0.05 bg=0.00
interleukin−35−mediated signaling pathwa... GO:0070757 p=1.2E−02 n=1 fg=0.05 bg=0.00
translational attenuation GO:0009386 p=1.2E−02 n=1 fg=0.05 bg=0.00
bradykinin catabolic process GO:0010815 p=1.2E−02 n=1 fg=0.05 bg=0.00
hormone catabolic process GO:0042447 p=1.2E−02 n=1 fg=0.05 bg=0.00
plasminogen activation GO:0031639 p=1.2E−02 n=1 fg=0.05 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=1.2E−02 n=1 fg=0.05 bg=0.00
noradrenergic neuron differentiation GO:0003357 p=1.2E−02 n=1 fg=0.05 bg=0.00
N−terminal protein amino acid modificati... GO:0031365 p=1.2E−02 n=1 fg=0.05 bg=0.00
double−strand break repair via alternati... GO:0097681 p=1.2E−02 n=1 fg=0.05 bg=0.00
regulation of mitochondrial DNA metaboli... GO:1901858 p=1.2E−02 n=1 fg=0.05 bg=0.00
negative regulation of mitochondrial DNA... GO:1901859 p=1.2E−02 n=1 fg=0.05 bg=0.00
dermatan sulfate metabolic process GO:0030205 p=1.2E−02 n=1 fg=0.05 bg=0.00
dermatan sulfate biosynthetic process GO:0030208 p=1.2E−02 n=1 fg=0.05 bg=0.00
mitochondrial DNA repair GO:0043504 p=1.2E−02 n=1 fg=0.05 bg=0.00
N−terminal protein amino acid acetylatio... GO:0006474 p=1.2E−02 n=1 fg=0.05 bg=0.00
regulation of mitochondrial DNA replicat... GO:0090296 p=1.2E−02 n=1 fg=0.05 bg=0.00
negative regulation of mitochondrial DNA... GO:0090298 p=1.2E−02 n=1 fg=0.05 bg=0.00
canonical Wnt signaling pathway GO:0060070 p=2.1E−02 n=3 fg=0.14 bg=0.03
intrinsic apoptotic signaling pathway in... GO:0036481 p=2.3E−02 n=1 fg=0.05 bg=0.00
glucose catabolic process to pyruvate GO:0061718 p=2.3E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=21/77 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048731196.1
fraction genes in fg and expected valu
protein heterodimerization activity GO:0046982 p=2.1E−03 n=5 fg=0.29 bg=0.06
neurotransmitter binding GO:0042165 p=2.2E−03 n=2 fg=0.12 bg=0.00
neurotrophin p75 receptor binding GO:0005166 p=1.1E−02 n=1 fg=0.06 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=1.1E−02 n=1 fg=0.06 bg=0.00
beta−endorphin binding GO:0031626 p=1.1E−02 n=1 fg=0.06 bg=0.00
N−acetylglucosamine−1−phosphodiester alp... GO:0003944 p=1.1E−02 n=1 fg=0.06 bg=0.00
poly(G) binding GO:0034046 p=1.1E−02 n=1 fg=0.06 bg=0.00
insulin binding GO:0043559 p=1.1E−02 n=1 fg=0.06 bg=0.00
small molecule sensor activity GO:0140299 p=1.1E−02 n=1 fg=0.06 bg=0.00
tumor necrosis factor−activated receptor... GO:0005031 p=1.1E−02 n=1 fg=0.06 bg=0.00
death receptor activity GO:0005035 p=1.1E−02 n=1 fg=0.06 bg=0.00
oxygen sensor activity GO:0019826 p=1.1E−02 n=1 fg=0.06 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=1.1E−02 n=1 fg=0.06 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=1.1E−02 n=1 fg=0.06 bg=0.00
cytokine receptor binding GO:0005126 p=1.2E−02 n=2 fg=0.12 bg=0.01
lipase activity GO:0016298 p=1.7E−02 n=2 fg=0.12 bg=0.01
neurotrophin receptor binding GO:0005165 p=2.1E−02 n=1 fg=0.06 bg=0.00
DNA ligase (ATP) activity GO:0003910 p=2.1E−02 n=1 fg=0.06 bg=0.00
apolipoprotein binding GO:0034185 p=2.1E−02 n=1 fg=0.06 bg=0.00
phosphotransferase activity, carboxyl gr... GO:0016774 p=2.1E−02 n=1 fg=0.06 bg=0.00
N4−(beta−N−acetylglucosaminyl)−L−asparag... GO:0003948 p=2.1E−02 n=1 fg=0.06 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=2.1E−02 n=1 fg=0.06 bg=0.00
ubiquitination−like modification−depende... GO:0140035 p=2.1E−02 n=1 fg=0.06 bg=0.00
ubiquitin−dependent protein binding GO:0140036 p=2.1E−02 n=1 fg=0.06 bg=0.00
DNA ligase activity GO:0003909 p=2.1E−02 n=1 fg=0.06 bg=0.00
racemase and epimerase activity GO:0016854 p=2.1E−02 n=1 fg=0.06 bg=0.00
oxygen binding GO:0019825 p=2.1E−02 n=1 fg=0.06 bg=0.00
carbon monoxide binding GO:0070025 p=2.1E−02 n=1 fg=0.06 bg=0.00
nitric oxide binding GO:0070026 p=2.1E−02 n=1 fg=0.06 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=2.5E−02 n=3 fg=0.18 bg=0.04
0 1 2 3 4 5
−log(p)
n=17/77 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048731196.1
fraction genes in fg and expected valu
extracellular space GO:0005615 p=4.4E−03 n=4 fg=0.17 bg=0.03
DNA ligase III−XRCC1 complex GO:0070421 p=1.3E−02 n=1 fg=0.04 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.3E−02 n=1 fg=0.04 bg=0.00
lipid droplet GO:0005811 p=2.3E−02 n=2 fg=0.09 bg=0.01
organelle envelope lumen GO:0031970 p=2.6E−02 n=2 fg=0.09 bg=0.01
mitochondria−associated endoplasmic reti... GO:0044233 p=3.8E−02 n=1 fg=0.04 bg=0.00
perinuclear endoplasmic reticulum GO:0097038 p=3.8E−02 n=1 fg=0.04 bg=0.00
peroxisomal matrix GO:0005782 p=5.0E−02 n=1 fg=0.04 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=5.0E−02 n=1 fg=0.04 bg=0.00
dendrite cytoplasm GO:0032839 p=5.0E−02 n=1 fg=0.04 bg=0.00
lumenal side of endoplasmic reticulum me... GO:0098553 p=5.0E−02 n=1 fg=0.04 bg=0.00
microbody lumen GO:0031907 p=5.0E−02 n=1 fg=0.04 bg=0.00
guanylate cyclase complex, soluble GO:0008074 p=5.0E−02 n=1 fg=0.04 bg=0.00
integral component of lumenal side of en... GO:0071556 p=5.0E−02 n=1 fg=0.04 bg=0.00
nuclear envelope GO:0005635 p=6.0E−02 n=3 fg=0.13 bg=0.04
sperm fibrous sheath GO:0035686 p=6.2E−02 n=1 fg=0.04 bg=0.00
synaptonemal complex GO:0000795 p=6.2E−02 n=1 fg=0.04 bg=0.00
lumenal side of membrane GO:0098576 p=6.2E−02 n=1 fg=0.04 bg=0.00
synaptonemal structure GO:0099086 p=6.2E−02 n=1 fg=0.04 bg=0.00
organelle lumen GO:0043233 p=6.8E−02 n=13 fg=0.57 bg=0.39
membrane−enclosed lumen GO:0031974 p=6.8E−02 n=13 fg=0.57 bg=0.39
intracellular organelle lumen GO:0070013 p=6.8E−02 n=13 fg=0.57 bg=0.39
organelle membrane contact site GO:0044232 p=7.4E−02 n=1 fg=0.04 bg=0.00
cytosolic proteasome complex GO:0031597 p=7.4E−02 n=1 fg=0.04 bg=0.00
nuclear envelope lumen GO:0005641 p=7.4E−02 n=1 fg=0.04 bg=0.00
secretory granule lumen GO:0034774 p=7.5E−02 n=2 fg=0.09 bg=0.02
mitochondrion GO:0005739 p=8.0E−02 n=6 fg=0.26 bg=0.14
cytoplasmic vesicle lumen GO:0060205 p=8.2E−02 n=2 fg=0.09 bg=0.02
vesicle lumen GO:0031983 p=8.2E−02 n=2 fg=0.09 bg=0.02
collagen−containing extracellular matrix GO:0062023 p=8.6E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=23/77 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction