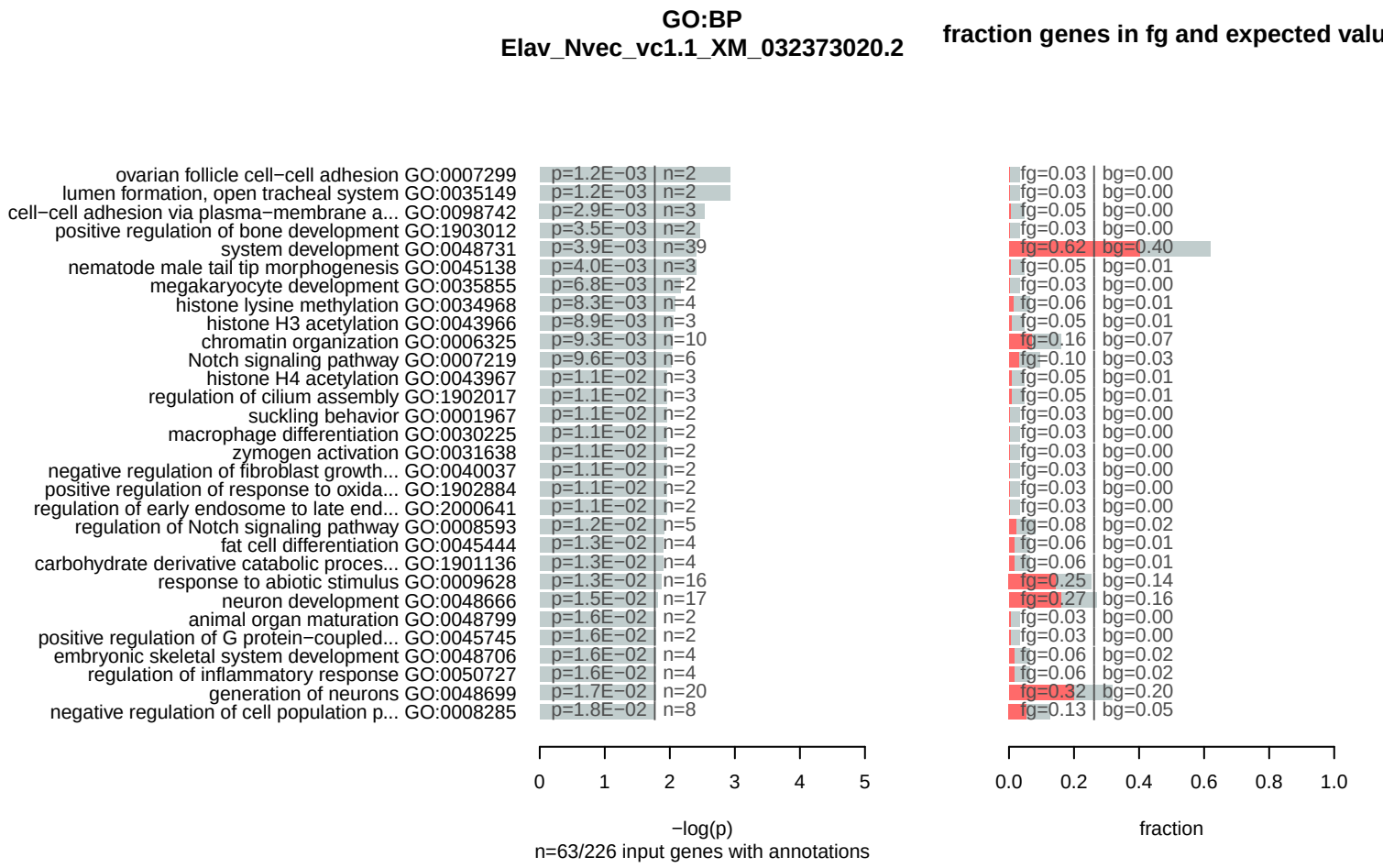
GO:BP
Elav_Nvec_vc1.1_XM_032373020.2
fraction genes in fg and expected valu
ovarian follicle cell−cell adhesion GO:0007299 p=1.2E−03 n=2 fg=0.03 bg=0.00
lumen formation, open tracheal system GO:0035149 p=1.2E−03 n=2 fg=0.03 bg=0.00
cell−cell adhesion via plasma−membrane a... GO:0098742 p=2.9E−03 n=3 fg=0.05 bg=0.00
positive regulation of bone development GO:1903012 p=3.5E−03 n=2 fg=0.03 bg=0.00
system development GO:0048731 p=3.9E−03 n=39 fg=0.62 bg=0.40
nematode male tail tip morphogenesis GO:0045138 p=4.0E−03 n=3 fg=0.05 bg=0.01
megakaryocyte development GO:0035855 p=6.8E−03 n=2 fg=0.03 bg=0.00
histone lysine methylation GO:0034968 p=8.3E−03 n=4 fg=0.06 bg=0.01
histone H3 acetylation GO:0043966 p=8.9E−03 n=3 fg=0.05 bg=0.01
chromatin organization GO:0006325 p=9.3E−03 n=10 fg=0.16 bg=0.07
Notch signaling pathway GO:0007219 p=9.6E−03 n=6 fg=0.10 bg=0.03
histone H4 acetylation GO:0043967 p=1.1E−02 n=3 fg=0.05 bg=0.01
regulation of cilium assembly GO:1902017 p=1.1E−02 n=3 fg=0.05 bg=0.01
suckling behavior GO:0001967 p=1.1E−02 n=2 fg=0.03 bg=0.00
macrophage differentiation GO:0030225 p=1.1E−02 n=2 fg=0.03 bg=0.00
zymogen activation GO:0031638 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of fibroblast growth... GO:0040037 p=1.1E−02 n=2 fg=0.03 bg=0.00
positive regulation of response to oxida... GO:1902884 p=1.1E−02 n=2 fg=0.03 bg=0.00
regulation of early endosome to late end... GO:2000641 p=1.1E−02 n=2 fg=0.03 bg=0.00
regulation of Notch signaling pathway GO:0008593 p=1.2E−02 n=5 fg=0.08 bg=0.02
fat cell differentiation GO:0045444 p=1.3E−02 n=4 fg=0.06 bg=0.01
carbohydrate derivative catabolic proces... GO:1901136 p=1.3E−02 n=4 fg=0.06 bg=0.01
response to abiotic stimulus GO:0009628 p=1.3E−02 n=16 fg=0.25 bg=0.14
neuron development GO:0048666 p=1.5E−02 n=17 fg=0.27 bg=0.16
animal organ maturation GO:0048799 p=1.6E−02 n=2 fg=0.03 bg=0.00
positive regulation of G protein−coupled... GO:0045745 p=1.6E−02 n=2 fg=0.03 bg=0.00
embryonic skeletal system development GO:0048706 p=1.6E−02 n=4 fg=0.06 bg=0.02
regulation of inflammatory response GO:0050727 p=1.6E−02 n=4 fg=0.06 bg=0.02
generation of neurons GO:0048699 p=1.7E−02 n=20 fg=0.32 bg=0.20
negative regulation of cell population p... GO:0008285 p=1.8E−02 n=8 fg=0.13 bg=0.05
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−log(p)
n=63/226 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032373020.2
fraction genes in fg and expected valu
histone acetyltransferase activity GO:0004402 p=4.2E−03 n=2 fg=0.03 bg=0.00
phosphatidylinositol−3−phosphate binding GO:0032266 p=1.3E−02 n=2 fg=0.03 bg=0.00
peptidase activator activity GO:0016504 p=2.0E−02 n=2 fg=0.03 bg=0.00
transcription coactivator activity GO:0003713 p=2.3E−02 n=6 fg=0.10 bg=0.04
hydrolase activity, hydrolyzing O−glycos... GO:0004553 p=2.5E−02 n=3 fg=0.05 bg=0.01
transcription coregulator activity GO:0003712 p=2.5E−02 n=8 fg=0.13 bg=0.06
glycosaminoglycan binding GO:0005539 p=3.5E−02 n=2 fg=0.03 bg=0.01
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=3.8E−02 n=1 fg=0.02 bg=0.00
heparan sulfate binding GO:1904399 p=3.8E−02 n=1 fg=0.02 bg=0.00
U2 snRNA binding GO:0030620 p=3.8E−02 n=1 fg=0.02 bg=0.00
U5 snRNA binding GO:0030623 p=3.8E−02 n=1 fg=0.02 bg=0.00
deubiquitinase activator activity GO:0035800 p=3.8E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=3.8E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=3.8E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=3.8E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=3.8E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=3.8E−02 n=1 fg=0.02 bg=0.00
aconitate hydratase activity GO:0003994 p=3.8E−02 n=1 fg=0.02 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=3.8E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=3.8E−02 n=1 fg=0.02 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=3.8E−02 n=1 fg=0.02 bg=0.00
chitinase activity GO:0004568 p=3.8E−02 n=1 fg=0.02 bg=0.00
DNA binding, bending GO:0008301 p=3.8E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor regulator activit... GO:0030548 p=3.8E−02 n=1 fg=0.02 bg=0.00
acetylcholine receptor activator activit... GO:0030549 p=3.8E−02 n=1 fg=0.02 bg=0.00
neurotransmitter receptor regulator acti... GO:0099602 p=3.8E−02 n=1 fg=0.02 bg=0.00
dynein light chain binding GO:0045503 p=3.8E−02 n=1 fg=0.02 bg=0.00
U6 snRNA binding GO:0017070 p=3.8E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide 1,2−alpha−manno... GO:0004571 p=3.8E−02 n=1 fg=0.02 bg=0.00
non−sequence−specific DNA binding, bendi... GO:0044378 p=3.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=61/226 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032373020.2
fraction genes in fg and expected valu
zonula adherens GO:0005915 p=1.7E−04 n=3 fg=0.05 bg=0.00
ciliary basal body GO:0036064 p=2.2E−03 n=5 fg=0.08 bg=0.01
spot adherens junction GO:0005914 p=3.7E−03 n=2 fg=0.03 bg=0.00
MLL3/4 complex GO:0044666 p=3.7E−03 n=2 fg=0.03 bg=0.00
Set1C/COMPASS complex GO:0048188 p=7.3E−03 n=2 fg=0.03 bg=0.00
cytoplasmic side of apical plasma membra... GO:0098592 p=7.3E−03 n=2 fg=0.03 bg=0.00
ficolin−1−rich granule membrane GO:0101003 p=1.7E−02 n=2 fg=0.03 bg=0.00
H4 histone acetyltransferase complex GO:1902562 p=1.7E−02 n=2 fg=0.03 bg=0.00
MLL1/2 complex GO:0044665 p=2.4E−02 n=2 fg=0.03 bg=0.00
histone acetyltransferase complex GO:0000123 p=2.5E−02 n=3 fg=0.05 bg=0.01
protein acetyltransferase complex GO:0031248 p=2.5E−02 n=3 fg=0.05 bg=0.01
acetyltransferase complex GO:1902493 p=2.5E−02 n=3 fg=0.05 bg=0.01
axonal growth cone GO:0044295 p=3.1E−02 n=2 fg=0.03 bg=0.00
lipoprotein particle GO:1990777 p=3.6E−02 n=1 fg=0.02 bg=0.00
internode region of axon GO:0033269 p=3.6E−02 n=1 fg=0.02 bg=0.00
anterior cell cortex GO:0061802 p=3.6E−02 n=1 fg=0.02 bg=0.00
Schmidt−Lanterman incisure GO:0043220 p=3.6E−02 n=1 fg=0.02 bg=0.00
dendritic microtubule GO:1901588 p=3.6E−02 n=1 fg=0.02 bg=0.00
compact myelin GO:0043218 p=3.6E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=3.6E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=3.6E−02 n=1 fg=0.02 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=3.6E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=3.6E−02 n=1 fg=0.02 bg=0.00
Swr1 complex GO:0000812 p=3.6E−02 n=1 fg=0.02 bg=0.00
plasma lipoprotein particle GO:0034358 p=3.6E−02 n=1 fg=0.02 bg=0.00
PR−DUB complex GO:0035517 p=3.6E−02 n=1 fg=0.02 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=3.6E−02 n=1 fg=0.02 bg=0.00
secretory granule membrane GO:0030667 p=4.5E−02 n=4 fg=0.06 bg=0.02
histone deacetylase complex GO:0000118 p=4.8E−02 n=2 fg=0.03 bg=0.01
somatodendritic compartment GO:0036477 p=5.2E−02 n=11 fg=0.17 bg=0.10
0 1 2 3 4 5
−log(p)
n=65/226 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction