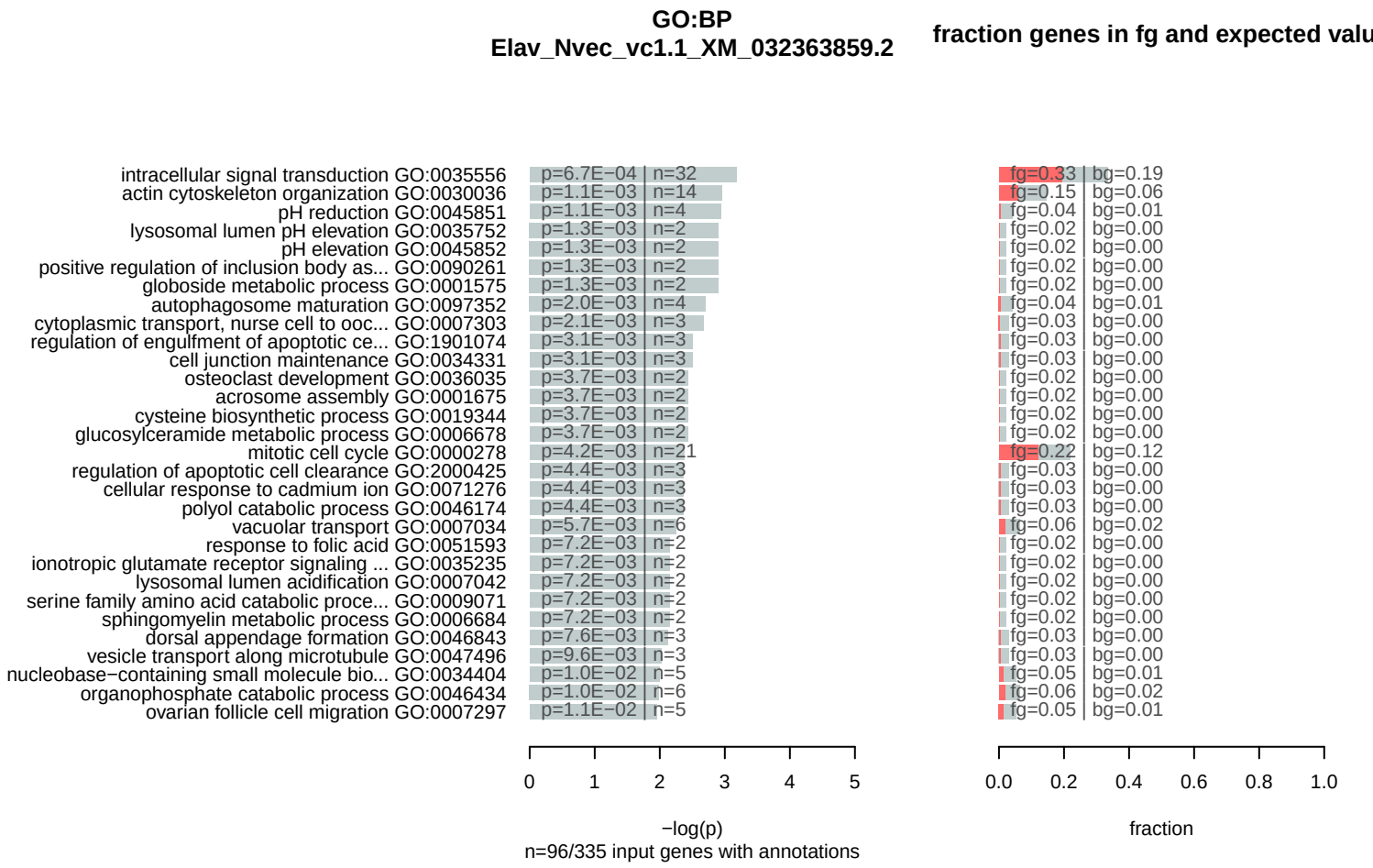
GO:BP
Elav_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
intracellular signal transduction GO:0035556 p=6.7E−04 n=32 fg=0.33 bg=0.19
actin cytoskeleton organization GO:0030036 p=1.1E−03 n=14 fg=0.15 bg=0.06
pH reduction GO:0045851 p=1.1E−03 n=4 fg=0.04 bg=0.01
lysosomal lumen pH elevation GO:0035752 p=1.3E−03 n=2 fg=0.02 bg=0.00
pH elevation GO:0045852 p=1.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of inclusion body as... GO:0090261 p=1.3E−03 n=2 fg=0.02 bg=0.00
globoside metabolic process GO:0001575 p=1.3E−03 n=2 fg=0.02 bg=0.00
autophagosome maturation GO:0097352 p=2.0E−03 n=4 fg=0.04 bg=0.01
cytoplasmic transport, nurse cell to ooc... GO:0007303 p=2.1E−03 n=3 fg=0.03 bg=0.00
regulation of engulfment of apoptotic ce... GO:1901074 p=3.1E−03 n=3 fg=0.03 bg=0.00
cell junction maintenance GO:0034331 p=3.1E−03 n=3 fg=0.03 bg=0.00
osteoclast development GO:0036035 p=3.7E−03 n=2 fg=0.02 bg=0.00
acrosome assembly GO:0001675 p=3.7E−03 n=2 fg=0.02 bg=0.00
cysteine biosynthetic process GO:0019344 p=3.7E−03 n=2 fg=0.02 bg=0.00
glucosylceramide metabolic process GO:0006678 p=3.7E−03 n=2 fg=0.02 bg=0.00
mitotic cell cycle GO:0000278 p=4.2E−03 n=21 fg=0.22 bg=0.12
regulation of apoptotic cell clearance GO:2000425 p=4.4E−03 n=3 fg=0.03 bg=0.00
cellular response to cadmium ion GO:0071276 p=4.4E−03 n=3 fg=0.03 bg=0.00
polyol catabolic process GO:0046174 p=4.4E−03 n=3 fg=0.03 bg=0.00
vacuolar transport GO:0007034 p=5.7E−03 n=6 fg=0.06 bg=0.02
response to folic acid GO:0051593 p=7.2E−03 n=2 fg=0.02 bg=0.00
ionotropic glutamate receptor signaling ... GO:0035235 p=7.2E−03 n=2 fg=0.02 bg=0.00
lysosomal lumen acidification GO:0007042 p=7.2E−03 n=2 fg=0.02 bg=0.00
serine family amino acid catabolic proce... GO:0009071 p=7.2E−03 n=2 fg=0.02 bg=0.00
sphingomyelin metabolic process GO:0006684 p=7.2E−03 n=2 fg=0.02 bg=0.00
dorsal appendage formation GO:0046843 p=7.6E−03 n=3 fg=0.03 bg=0.00
vesicle transport along microtubule GO:0047496 p=9.6E−03 n=3 fg=0.03 bg=0.00
nucleobase−containing small molecule bio... GO:0034404 p=1.0E−02 n=5 fg=0.05 bg=0.01
organophosphate catabolic process GO:0046434 p=1.0E−02 n=6 fg=0.06 bg=0.02
ovarian follicle cell migration GO:0007297 p=1.1E−02 n=5 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=96/335 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
1−phosphatidylinositol binding GO:0005545 p=1.3E−03 n=2 fg=0.02 bg=0.00
carbon monoxide binding GO:0070025 p=1.3E−03 n=2 fg=0.02 bg=0.00
nitric oxide binding GO:0070026 p=1.3E−03 n=2 fg=0.02 bg=0.00
cystathionine beta−synthase activity GO:0004122 p=1.3E−03 n=2 fg=0.02 bg=0.00
cysteine synthase activity GO:0004124 p=1.3E−03 n=2 fg=0.02 bg=0.00
RNA 7−methylguanosine cap binding GO:0000340 p=3.9E−03 n=2 fg=0.02 bg=0.00
oxygen binding GO:0019825 p=3.9E−03 n=2 fg=0.02 bg=0.00
heme binding GO:0020037 p=4.8E−03 n=3 fg=0.03 bg=0.00
damaged DNA binding GO:0003684 p=2.2E−02 n=3 fg=0.03 bg=0.01
calcium−release channel activity GO:0015278 p=2.5E−02 n=2 fg=0.02 bg=0.00
aminopeptidase activity GO:0004177 p=2.5E−02 n=2 fg=0.02 bg=0.00
protein tyrosine/serine/threonine phosph... GO:0008138 p=2.5E−02 n=2 fg=0.02 bg=0.00
rRNA methyltransferase activity GO:0008649 p=2.5E−02 n=2 fg=0.02 bg=0.00
catalytic activity, acting on a rRNA GO:0140102 p=2.5E−02 n=2 fg=0.02 bg=0.00
metallopeptidase activity GO:0008237 p=3.0E−02 n=3 fg=0.03 bg=0.01
methyltransferase activity GO:0008168 p=3.2E−02 n=5 fg=0.06 bg=0.02
pyridoxal phosphate binding GO:0030170 p=3.2E−02 n=2 fg=0.02 bg=0.00
dynein complex binding GO:0070840 p=3.2E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol bisphosphate phosph... GO:0034593 p=3.2E−02 n=2 fg=0.02 bg=0.00
vitamin B6 binding GO:0070279 p=3.2E−02 n=2 fg=0.02 bg=0.00
nitrite reductase (NO−forming) activity GO:0050421 p=3.7E−02 n=1 fg=0.01 bg=0.00
heteroduplex DNA loop binding GO:0000404 p=3.7E−02 n=1 fg=0.01 bg=0.00
double−strand/single−strand DNA junction... GO:0000406 p=3.7E−02 n=1 fg=0.01 bg=0.00
phosphatidylinositol 3−kinase catalytic ... GO:0036313 p=3.7E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=3.7E−02 n=1 fg=0.01 bg=0.00
volume−sensitive chloride channel activi... GO:0072320 p=3.7E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=3.7E−02 n=1 fg=0.01 bg=0.00
8−oxo−7,8−dihydroguanine DNA N−glycosyla... GO:0034039 p=3.7E−02 n=1 fg=0.01 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=3.7E−02 n=1 fg=0.01 bg=0.00
adenylylsulfatase activity GO:0047627 p=3.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=87/335 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032363859.2
fraction genes in fg and expected valu
late endosome GO:0005770 p=4.2E−03 n=7 fg=0.07 bg=0.02
ruffle membrane GO:0032587 p=7.8E−03 n=3 fg=0.03 bg=0.00
actin−based cell projection GO:0098858 p=9.0E−03 n=6 fg=0.06 bg=0.02
synaptic vesicle GO:0008021 p=1.4E−02 n=6 fg=0.06 bg=0.02
MCM complex GO:0042555 p=1.7E−02 n=2 fg=0.02 bg=0.00
cell cortex GO:0005938 p=1.8E−02 n=8 fg=0.08 bg=0.03
microvillus membrane GO:0031528 p=2.4E−02 n=2 fg=0.02 bg=0.00
dynactin complex GO:0005869 p=2.4E−02 n=2 fg=0.02 bg=0.00
exocytic vesicle GO:0070382 p=2.4E−02 n=6 fg=0.06 bg=0.02
early endosome GO:0005769 p=2.9E−02 n=7 fg=0.07 bg=0.03
protein phosphatase 4 complex GO:0030289 p=3.6E−02 n=1 fg=0.01 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=3.6E−02 n=1 fg=0.01 bg=0.00
steroid hormone aporeceptor complex GO:0005831 p=3.6E−02 n=1 fg=0.01 bg=0.00
MutSbeta complex GO:0032302 p=3.6E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=3.6E−02 n=1 fg=0.01 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=3.6E−02 n=1 fg=0.01 bg=0.00
retromer, cargo−selective complex GO:0030906 p=3.6E−02 n=1 fg=0.01 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=3.6E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=3.6E−02 n=1 fg=0.01 bg=0.00
cell cortex region GO:0099738 p=3.7E−02 n=3 fg=0.03 bg=0.01
late endosome membrane GO:0031902 p=3.7E−02 n=3 fg=0.03 bg=0.01
nuclear replisome GO:0043601 p=3.9E−02 n=2 fg=0.02 bg=0.00
replisome GO:0030894 p=3.9E−02 n=2 fg=0.02 bg=0.00
filopodium GO:0030175 p=4.2E−02 n=3 fg=0.03 bg=0.01
integral component of endoplasmic reticu... GO:0030176 p=4.3E−02 n=5 fg=0.05 bg=0.02
intrinsic component of endoplasmic retic... GO:0031227 p=5.2E−02 n=5 fg=0.05 bg=0.02
pronucleus GO:0045120 p=5.7E−02 n=2 fg=0.02 bg=0.00
endosome membrane GO:0010008 p=6.2E−02 n=6 fg=0.06 bg=0.03
DNA polymerase complex GO:0042575 p=6.7E−02 n=2 fg=0.02 bg=0.00
nuclear body GO:0016604 p=6.7E−02 n=10 fg=0.10 bg=0.06
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−log(p)
n=97/335 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction