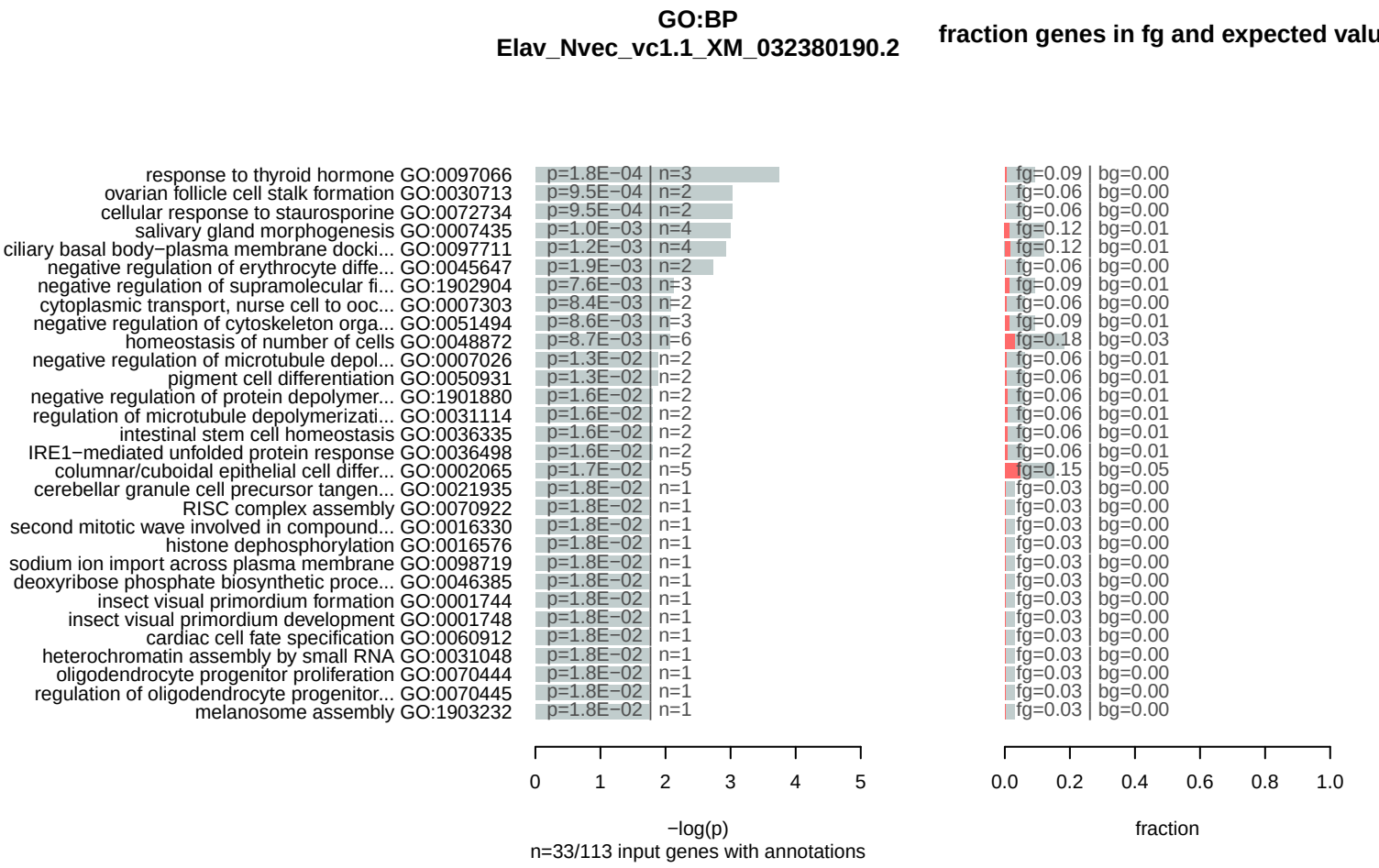
GO:BP
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fraction genes in fg and expected valu
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ovarian follicle cell stalk formation GO:0030713 p=9.5E−04 n=2 fg=0.06 bg=0.00
cellular response to staurosporine GO:0072734 p=9.5E−04 n=2 fg=0.06 bg=0.00
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ciliary basal body−plasma membrane docki... GO:0097711 p=1.2E−03 n=4 fg=0.12 bg=0.01
negative regulation of erythrocyte diffe... GO:0045647 p=1.9E−03 n=2 fg=0.06 bg=0.00
negative regulation of supramolecular fi... GO:1902904 p=7.6E−03 n=3 fg=0.09 bg=0.01
cytoplasmic transport, nurse cell to ooc... GO:0007303 p=8.4E−03 n=2 fg=0.06 bg=0.00
negative regulation of cytoskeleton orga... GO:0051494 p=8.6E−03 n=3 fg=0.09 bg=0.01
homeostasis of number of cells GO:0048872 p=8.7E−03 n=6 fg=0.18 bg=0.03
negative regulation of microtubule depol... GO:0007026 p=1.3E−02 n=2 fg=0.06 bg=0.01
pigment cell differentiation GO:0050931 p=1.3E−02 n=2 fg=0.06 bg=0.01
negative regulation of protein depolymer... GO:1901880 p=1.6E−02 n=2 fg=0.06 bg=0.01
regulation of microtubule depolymerizati... GO:0031114 p=1.6E−02 n=2 fg=0.06 bg=0.01
intestinal stem cell homeostasis GO:0036335 p=1.6E−02 n=2 fg=0.06 bg=0.01
IRE1−mediated unfolded protein response GO:0036498 p=1.6E−02 n=2 fg=0.06 bg=0.01
columnar/cuboidal epithelial cell differ... GO:0002065 p=1.7E−02 n=5 fg=0.15 bg=0.05
cerebellar granule cell precursor tangen... GO:0021935 p=1.8E−02 n=1 fg=0.03 bg=0.00
RISC complex assembly GO:0070922 p=1.8E−02 n=1 fg=0.03 bg=0.00
second mitotic wave involved in compound... GO:0016330 p=1.8E−02 n=1 fg=0.03 bg=0.00
histone dephosphorylation GO:0016576 p=1.8E−02 n=1 fg=0.03 bg=0.00
sodium ion import across plasma membrane GO:0098719 p=1.8E−02 n=1 fg=0.03 bg=0.00
deoxyribose phosphate biosynthetic proce... GO:0046385 p=1.8E−02 n=1 fg=0.03 bg=0.00
insect visual primordium formation GO:0001744 p=1.8E−02 n=1 fg=0.03 bg=0.00
insect visual primordium development GO:0001748 p=1.8E−02 n=1 fg=0.03 bg=0.00
cardiac cell fate specification GO:0060912 p=1.8E−02 n=1 fg=0.03 bg=0.00
heterochromatin assembly by small RNA GO:0031048 p=1.8E−02 n=1 fg=0.03 bg=0.00
oligodendrocyte progenitor proliferation GO:0070444 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of oligodendrocyte progenitor... GO:0070445 p=1.8E−02 n=1 fg=0.03 bg=0.00
melanosome assembly GO:1903232 p=1.8E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=33/113 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032380190.2
fraction genes in fg and expected valu
aspartic−type endopeptidase activity GO:0004190 p=4.3E−03 n=2 fg=0.07 bg=0.00
chaperone binding GO:0051087 p=8.7E−03 n=3 fg=0.11 bg=0.02
protein tyrosine phosphatase activity, m... GO:0030946 p=1.8E−02 n=1 fg=0.04 bg=0.00
dCMP deaminase activity GO:0004132 p=1.8E−02 n=1 fg=0.04 bg=0.00
JUN kinase kinase kinase activity GO:0004706 p=1.8E−02 n=1 fg=0.04 bg=0.00
BIR domain binding GO:1990525 p=1.8E−02 n=1 fg=0.04 bg=0.00
phosphate ion binding GO:0042301 p=1.8E−02 n=1 fg=0.04 bg=0.00
phosphopantothenate−−cysteine ligase act... GO:0004632 p=1.8E−02 n=1 fg=0.04 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=1.8E−02 n=1 fg=0.04 bg=0.00
protein binding GO:0005515 p=2.3E−02 n=23 fg=0.82 bg=0.60
cysteine−type endopeptidase activity inv... GO:0097153 p=3.5E−02 n=1 fg=0.04 bg=0.00
LIM domain binding GO:0030274 p=3.5E−02 n=1 fg=0.04 bg=0.00
aspartic endopeptidase activity, intrame... GO:0042500 p=3.5E−02 n=1 fg=0.04 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=3.5E−02 n=1 fg=0.04 bg=0.00
sphingolipid binding GO:0046625 p=3.5E−02 n=1 fg=0.04 bg=0.00
cysteine−type endopeptidase activity inv... GO:0097200 p=3.5E−02 n=1 fg=0.04 bg=0.00
cAMP−dependent protein kinase regulator ... GO:0008603 p=3.5E−02 n=1 fg=0.04 bg=0.00
phosphate ion transmembrane transporter ... GO:0015114 p=3.5E−02 n=1 fg=0.04 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=3.5E−02 n=1 fg=0.04 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=3.5E−02 n=1 fg=0.04 bg=0.00
acid−amino acid ligase activity GO:0016881 p=5.2E−02 n=1 fg=0.04 bg=0.00
deaminase activity GO:0019239 p=5.2E−02 n=1 fg=0.04 bg=0.00
sodium ion binding GO:0031402 p=5.2E−02 n=1 fg=0.04 bg=0.00
transcription factor binding GO:0008134 p=5.2E−02 n=5 fg=0.18 bg=0.07
hydrolase activity, acting on carbon−nit... GO:0016814 p=6.9E−02 n=1 fg=0.04 bg=0.00
microtubule plus−end binding GO:0051010 p=6.9E−02 n=1 fg=0.04 bg=0.00
tau−protein kinase activity GO:0050321 p=6.9E−02 n=1 fg=0.04 bg=0.00
cAMP binding GO:0030552 p=6.9E−02 n=1 fg=0.04 bg=0.00
nuclear thyroid hormone receptor binding GO:0046966 p=6.9E−02 n=1 fg=0.04 bg=0.00
proteasome−activating activity GO:0036402 p=6.9E−02 n=1 fg=0.04 bg=0.00
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−log(p)
n=28/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032380190.2
fraction genes in fg and expected valu
actin filament GO:0005884 p=2.9E−03 n=2 fg=0.06 bg=0.00
intermediate filament cytoskeleton GO:0045111 p=6.0E−03 n=2 fg=0.06 bg=0.00
precatalytic spliceosome GO:0071011 p=6.0E−03 n=2 fg=0.06 bg=0.00
melanosome GO:0042470 p=1.0E−02 n=2 fg=0.06 bg=0.01
pigment granule GO:0048770 p=1.3E−02 n=2 fg=0.06 bg=0.01
platelet dense granule GO:0042827 p=1.8E−02 n=1 fg=0.03 bg=0.00
BLOC−3 complex GO:0031085 p=1.8E−02 n=1 fg=0.03 bg=0.00
late endosome membrane GO:0031902 p=2.8E−02 n=2 fg=0.06 bg=0.01
microtubule cytoskeleton GO:0015630 p=3.4E−02 n=7 fg=0.22 bg=0.10
integral component of endoplasmic reticu... GO:0030176 p=3.4E−02 n=3 fg=0.09 bg=0.02
intrinsic component of endoplasmic retic... GO:0031227 p=3.4E−02 n=3 fg=0.09 bg=0.02
filamentous actin GO:0031941 p=3.5E−02 n=1 fg=0.03 bg=0.00
ficolin−1−rich granule lumen GO:1904813 p=5.2E−02 n=2 fg=0.06 bg=0.01
centriole GO:0005814 p=5.2E−02 n=2 fg=0.06 bg=0.01
Hrd1p ubiquitin ligase ERAD−L complex GO:0000839 p=5.2E−02 n=1 fg=0.03 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=5.2E−02 n=1 fg=0.03 bg=0.00
manchette GO:0002177 p=5.2E−02 n=1 fg=0.03 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=5.2E−02 n=1 fg=0.03 bg=0.00
CHD−type complex GO:0090545 p=5.2E−02 n=1 fg=0.03 bg=0.00
BLOC complex GO:0031082 p=5.2E−02 n=1 fg=0.03 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=5.2E−02 n=1 fg=0.03 bg=0.00
NuRD complex GO:0016581 p=5.2E−02 n=1 fg=0.03 bg=0.00
microtubule organizing center GO:0005815 p=5.6E−02 n=5 fg=0.16 bg=0.07
ciliary transition zone GO:0035869 p=6.1E−02 n=2 fg=0.06 bg=0.01
membrane raft GO:0045121 p=6.5E−02 n=3 fg=0.09 bg=0.03
membrane microdomain GO:0098857 p=6.5E−02 n=3 fg=0.09 bg=0.03
nucleoplasm GO:0005654 p=6.9E−02 n=13 fg=0.41 bg=0.27
ER ubiquitin ligase complex GO:0000835 p=6.9E−02 n=1 fg=0.03 bg=0.00
Hrd1p ubiquitin ligase complex GO:0000836 p=6.9E−02 n=1 fg=0.03 bg=0.00
integral component of lumenal side of en... GO:0071556 p=6.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=32/113 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction