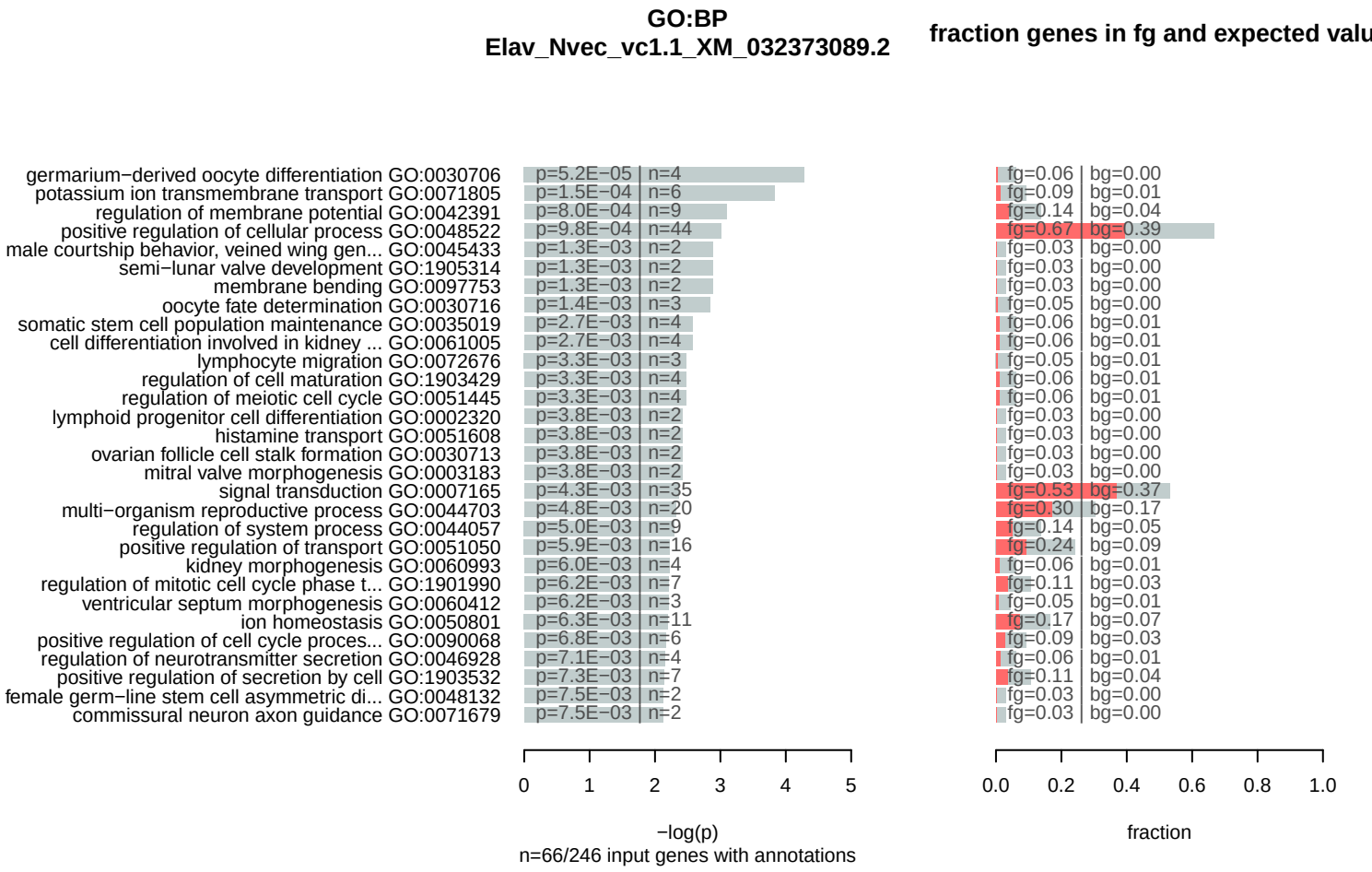
GO:BP
Elav_Nvec_vc1.1_XM_032373089.2
fraction genes in fg and expected valu
germarium−derived oocyte differentiation GO:0030706 p=5.2E−05 n=4 fg=0.06 bg=0.00
potassium ion transmembrane transport GO:0071805 p=1.5E−04 n=6 fg=0.09 bg=0.01
regulation of membrane potential GO:0042391 p=8.0E−04 n=9 fg=0.14 bg=0.04
positive regulation of cellular process GO:0048522 p=9.8E−04 n=44 fg=0.67 bg=0.39
male courtship behavior, veined wing gen... GO:0045433 p=1.3E−03 n=2 fg=0.03 bg=0.00
semi−lunar valve development GO:1905314 p=1.3E−03 n=2 fg=0.03 bg=0.00
membrane bending GO:0097753 p=1.3E−03 n=2 fg=0.03 bg=0.00
oocyte fate determination GO:0030716 p=1.4E−03 n=3 fg=0.05 bg=0.00
somatic stem cell population maintenance GO:0035019 p=2.7E−03 n=4 fg=0.06 bg=0.01
cell differentiation involved in kidney ... GO:0061005 p=2.7E−03 n=4 fg=0.06 bg=0.01
lymphocyte migration GO:0072676 p=3.3E−03 n=3 fg=0.05 bg=0.01
regulation of cell maturation GO:1903429 p=3.3E−03 n=4 fg=0.06 bg=0.01
regulation of meiotic cell cycle GO:0051445 p=3.3E−03 n=4 fg=0.06 bg=0.01
lymphoid progenitor cell differentiation GO:0002320 p=3.8E−03 n=2 fg=0.03 bg=0.00
histamine transport GO:0051608 p=3.8E−03 n=2 fg=0.03 bg=0.00
ovarian follicle cell stalk formation GO:0030713 p=3.8E−03 n=2 fg=0.03 bg=0.00
mitral valve morphogenesis GO:0003183 p=3.8E−03 n=2 fg=0.03 bg=0.00
signal transduction GO:0007165 p=4.3E−03 n=35 fg=0.53 bg=0.37
multi−organism reproductive process GO:0044703 p=4.8E−03 n=20 fg=0.30 bg=0.17
regulation of system process GO:0044057 p=5.0E−03 n=9 fg=0.14 bg=0.05
positive regulation of transport GO:0051050 p=5.9E−03 n=16 fg=0.24 bg=0.09
kidney morphogenesis GO:0060993 p=6.0E−03 n=4 fg=0.06 bg=0.01
regulation of mitotic cell cycle phase t... GO:1901990 p=6.2E−03 n=7 fg=0.11 bg=0.03
ventricular septum morphogenesis GO:0060412 p=6.2E−03 n=3 fg=0.05 bg=0.01
ion homeostasis GO:0050801 p=6.3E−03 n=11 fg=0.17 bg=0.07
positive regulation of cell cycle proces... GO:0090068 p=6.8E−03 n=6 fg=0.09 bg=0.03
regulation of neurotransmitter secretion GO:0046928 p=7.1E−03 n=4 fg=0.06 bg=0.01
positive regulation of secretion by cell GO:1903532 p=7.3E−03 n=7 fg=0.11 bg=0.04
female germ−line stem cell asymmetric di... GO:0048132 p=7.5E−03 n=2 fg=0.03 bg=0.00
commissural neuron axon guidance GO:0071679 p=7.5E−03 n=2 fg=0.03 bg=0.00
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−log(p)
n=66/246 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032373089.2
fraction genes in fg and expected valu
voltage−gated potassium channel activity GO:0005249 p=3.7E−04 n=4 fg=0.06 bg=0.01
protein domain specific binding GO:0019904 p=4.1E−03 n=13 fg=0.21 bg=0.09
calcium−activated potassium channel acti... GO:0015269 p=4.4E−03 n=2 fg=0.03 bg=0.00
actin binding GO:0003779 p=7.8E−03 n=5 fg=0.08 bg=0.02
growth factor receptor binding GO:0070851 p=9.6E−03 n=3 fg=0.05 bg=0.01
molecular function regulator activity GO:0098772 p=1.1E−02 n=14 fg=0.23 bg=0.12
enzyme regulator activity GO:0030234 p=1.7E−02 n=12 fg=0.19 bg=0.10
actin filament binding GO:0051015 p=1.8E−02 n=3 fg=0.05 bg=0.01
HMG box domain binding GO:0071837 p=2.0E−02 n=2 fg=0.03 bg=0.00
protein kinase regulator activity GO:0019887 p=2.1E−02 n=4 fg=0.06 bg=0.02
protein dimerization activity GO:0046983 p=2.3E−02 n=14 fg=0.23 bg=0.13
outward rectifier potassium channel acti... GO:0015271 p=2.8E−02 n=2 fg=0.03 bg=0.00
DEAD/H−box RNA helicase binding GO:0017151 p=2.8E−02 n=2 fg=0.03 bg=0.00
adrenergic receptor binding GO:0031690 p=2.8E−02 n=2 fg=0.03 bg=0.00
kinase regulator activity GO:0019207 p=3.0E−02 n=4 fg=0.06 bg=0.02
SH3 domain binding GO:0017124 p=3.0E−02 n=3 fg=0.05 bg=0.01
protein serine/threonine kinase activity GO:0004674 p=3.7E−02 n=6 fg=0.10 bg=0.04
fibroblast growth factor receptor bindin... GO:0005104 p=3.9E−02 n=1 fg=0.02 bg=0.00
ABC−type 3',5'−cyclic GMP transmembrane ... GO:1905948 p=3.9E−02 n=1 fg=0.02 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=3.9E−02 n=1 fg=0.02 bg=0.00
guanine nucleotide transmembrane transpo... GO:0001409 p=3.9E−02 n=1 fg=0.02 bg=0.00
purine nucleobase transmembrane transpor... GO:0005345 p=3.9E−02 n=1 fg=0.02 bg=0.00
nucleobase transmembrane transporter act... GO:0015205 p=3.9E−02 n=1 fg=0.02 bg=0.00
guanine transmembrane transporter activi... GO:0015208 p=3.9E−02 n=1 fg=0.02 bg=0.00
large conductance calcium−activated pota... GO:0060072 p=3.9E−02 n=1 fg=0.02 bg=0.00
amine transmembrane transporter activity GO:0005275 p=3.9E−02 n=1 fg=0.02 bg=0.00
leptin receptor binding GO:1990460 p=3.9E−02 n=1 fg=0.02 bg=0.00
phosphopantothenate−−cysteine ligase act... GO:0004632 p=3.9E−02 n=1 fg=0.02 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=3.9E−02 n=1 fg=0.02 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.9E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=62/246 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032373089.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=1.7E−04 n=4 fg=0.06 bg=0.00
neuromuscular junction GO:0031594 p=8.8E−04 n=6 fg=0.09 bg=0.02
postsynapse GO:0098794 p=1.3E−03 n=9 fg=0.14 bg=0.04
apical plasma membrane GO:0016324 p=3.5E−03 n=8 fg=0.12 bg=0.04
cytoskeleton GO:0005856 p=6.7E−03 n=17 fg=0.26 bg=0.14
presynaptic periactive zone GO:0036062 p=7.3E−03 n=2 fg=0.03 bg=0.00
cell−cell junction GO:0005911 p=7.7E−03 n=8 fg=0.12 bg=0.05
actin−based cell projection GO:0098858 p=9.2E−03 n=5 fg=0.08 bg=0.02
membrane raft GO:0045121 p=1.0E−02 n=6 fg=0.09 bg=0.03
membrane microdomain GO:0098857 p=1.0E−02 n=6 fg=0.09 bg=0.03
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postsynapse of neuromuscular junction GO:0098975 p=1.2E−02 n=2 fg=0.03 bg=0.00
female germ cell nucleus GO:0001674 p=1.2E−02 n=2 fg=0.03 bg=0.00
basal part of cell GO:0045178 p=1.2E−02 n=6 fg=0.09 bg=0.03
actin cytoskeleton GO:0015629 p=1.3E−02 n=6 fg=0.09 bg=0.03
acrosomal vesicle GO:0001669 p=1.7E−02 n=2 fg=0.03 bg=0.00
filopodium GO:0030175 p=1.8E−02 n=3 fg=0.05 bg=0.01
main axon GO:0044304 p=1.8E−02 n=3 fg=0.05 bg=0.01
transcription regulator complex GO:0005667 p=1.8E−02 n=7 fg=0.11 bg=0.04
neuron to neuron synapse GO:0098984 p=1.9E−02 n=5 fg=0.08 bg=0.02
postsynaptic membrane GO:0045211 p=2.1E−02 n=4 fg=0.06 bg=0.02
mitotic spindle GO:0072686 p=2.1E−02 n=3 fg=0.05 bg=0.01
external side of plasma membrane GO:0009897 p=2.1E−02 n=3 fg=0.05 bg=0.01
microtubule cytoskeleton GO:0015630 p=2.3E−02 n=12 fg=0.18 bg=0.10
basal plasma membrane GO:0009925 p=2.4E−02 n=5 fg=0.08 bg=0.03
basolateral plasma membrane GO:0016323 p=2.4E−02 n=5 fg=0.08 bg=0.03
presynaptic active zone GO:0048786 p=2.5E−02 n=3 fg=0.05 bg=0.01
microtubule organizing center GO:0005815 p=2.5E−02 n=9 fg=0.14 bg=0.07
side of membrane GO:0098552 p=2.9E−02 n=6 fg=0.09 bg=0.04
cell surface GO:0009986 p=3.0E−02 n=6 fg=0.09 bg=0.04
0 1 2 3 4 5
−log(p)
n=65/246 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction