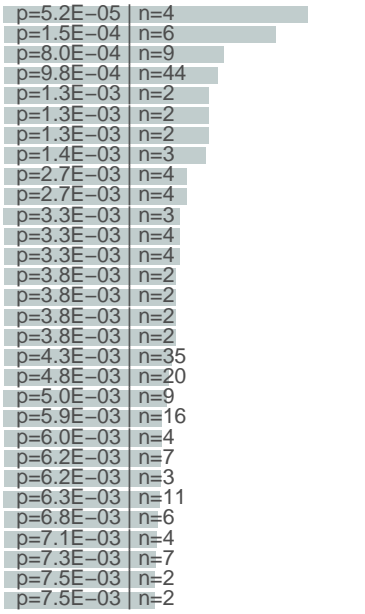


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032373099.2

fraction genes in fg and expected value

germarium-derived oocyte differentiation	GO:0030706
potassium ion transmembrane transport	GO:0071805
regulation of membrane potential	GO:0042391
positive regulation of cellular process	GO:0048522
male courtship behavior, veined wing gen...	GO:0045433
semi-lunar valve development	GO:1905314
membrane bending	GO:0097753
oocyte fate determination	GO:0030716
somatic stem cell population maintenance	GO:0035019
cell differentiation involved in kidney ...	GO:0061005
lymphocyte migration	GO:0072676
regulation of cell maturation	GO:1903429
regulation of meiotic cell cycle	GO:0051445
lymphoid progenitor cell differentiation	GO:0002320
histamine transport	GO:0051608
ovarian follicle cell stalk formation	GO:0030713
mitral valve morphogenesis	GO:0003183
signal transduction	GO:0007165
multi-organism reproductive process	GO:0044703
regulation of system process	GO:0044057
positive regulation of transport	GO:0051050
kidney morphogenesis	GO:0060993
regulation of mitotic cell cycle phase t...	GO:1901990
ventricular septum morphogenesis	GO:0060412
ion homeostasis	GO:0050801
positive regulation of cell cycle proces...	GO:0090068
regulation of neurotransmitter secretion	GO:0046928
positive regulation of secretion by cell	GO:1903532
female germ-line stem cell asymmetric di...	GO:0048132
commissural neuron axon guidance	GO:0071679



–log(p)  
n=66/246 input genes with annotations

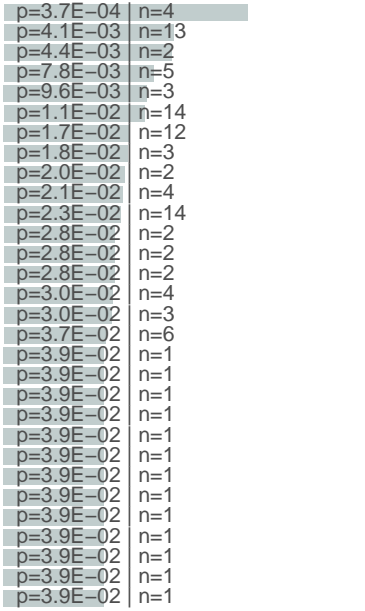
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fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032373099.2

fraction genes in fg and expected value

voltage-gated potassium channel activity	GO:0005249
protein domain specific binding	GO:0019904
calcium-activated potassium channel acti...	GO:0015269
actin binding	GO:0003779
growth factor receptor binding	GO:0070851
molecular function regulator activity	GO:0098772
enzyme regulator activity	GO:0030234
actin filament binding	GO:0051015
HMG box domain binding	GO:0071837
protein kinase regulator activity	GO:0019887
protein dimerization activity	GO:0046983
outward rectifier potassium channel acti...	GO:0015271
DEAD/H-box RNA helicase binding	GO:0017151
adrenergic receptor binding	GO:0031690
kinase regulator activity	GO:0019207
SH3 domain binding	GO:0017124
protein serine/threonine kinase activity	GO:0004674
fibroblast growth factor receptor bindin...	GO:0005104
ABC-type 3',5'-cyclic GMP transmembrane ...	GO:1905948
sodium:phosphate symporter activity	GO:0005436
guanine nucleotide transmembrane transpo...	GO:0001409
purine nucleobase transmembrane transpor...	GO:0005345
nucleobase transmembrane transporter act...	GO:0015205
guanine transmembrane transporter activi...	GO:0015208
large conductance calcium-activated pota...	GO:0060072
amine transmembrane transporter activity	GO:0005275
leptin receptor binding	GO:1990460
phosphopantothenate--cysteine ligase act...	GO:0004632
ubiquitin-like modifier activating enzym...	GO:0008641
intracellular sodium activated potassium...	GO:0005228



–log(p)  
n=62/246 input genes with annotations

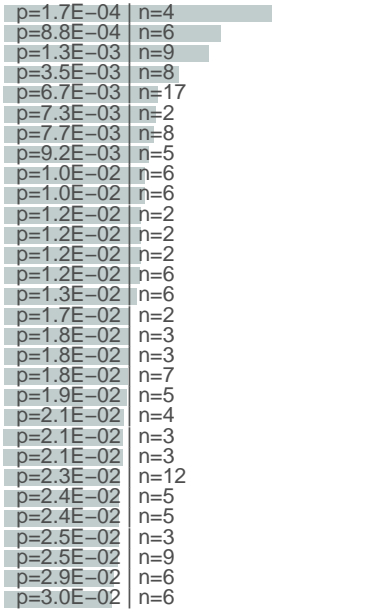
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fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032373099.2

fraction genes in fg and expected value

voltage-gated potassium channel complex	GO:0008076
neuromuscular junction	GO:0031594
postsynapse	GO:0098794
apical plasma membrane	GO:0016324
cytoskeleton	GO:0005856
presynaptic periaxial zone	GO:0036062
cell-cell junction	GO:0005911
actin-based cell projection	GO:0098858
membrane raft	GO:0045121
membrane microdomain	GO:0098857
cell pole	GO:0060187
postsynapse of neuromuscular junction	GO:0098975
female germ cell nucleus	GO:0001674
basal part of cell	GO:0045178
actin cytoskeleton	GO:0015629
acrosomal vesicle	GO:0001669
filopodium	GO:0030175
main axon	GO:0044304
transcription regulator complex	GO:0005667
neuron to neuron synapse	GO:0098984
postsynaptic membrane	GO:0045211
mitotic spindle	GO:0072686
external side of plasma membrane	GO:0009897
microtubule cytoskeleton	GO:0015630
basal plasma membrane	GO:0009925
basolateral plasma membrane	GO:0016323
presynaptic active zone	GO:0048786
microtubule organizing center	GO:0005815
side of membrane	GO:0098552
cell surface	GO:0009986



–log(p)  
n=65/246 input genes with annotations

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fraction