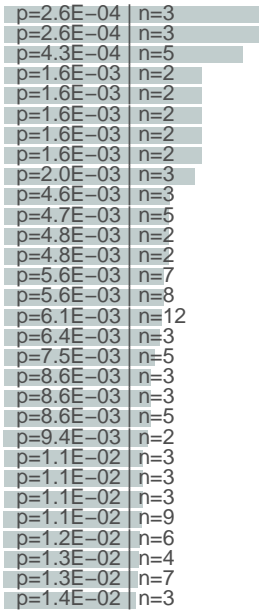


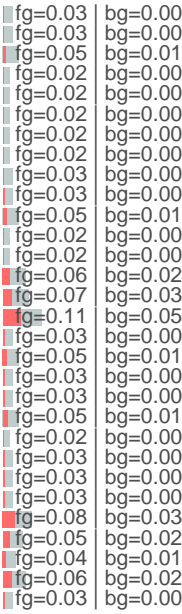
GO:BP
Elav_Nvec_vc1.1_XM_032386992.2

fraction genes in fg and expected value

purine nucleobase biosynthetic process	GO:0009113
de novo IMP biosynthetic process	GO:0006189
negative regulation of smoothened signal...	GO:0045879
actin cortical patch localization	GO:0051666
negative regulation of type 2 immune res...	GO:0002829
negative regulation of fibroblast apopto...	GO:2000270
negative regulation of myfibroblast dif...	GO:1904761
lysine transport	GO:0015819
regulation of release of sequestered cal...	GO:0010880
regulation of synaptic activity	GO:0060025
regulation of intracellular pH	GO:0051453
cell communication by electrical couplin...	GO:0086064
haltere development	GO:0007482
cellular response to topologically incor...	GO:0035967
cellular response to insulin stimulus	GO:0032869
autophagy	GO:0006914
glutamine metabolic process	GO:0006541
potassium ion transmembrane transport	GO:0071805
negative regulation of vasculature devel...	GO:1901343
startle response	GO:0001964
neural tube closure	GO:0001843
establishment of blood–brain barrier	GO:0060856
NADH metabolic process	GO:0006734
imaginal disc–derived wing vein morphoge...	GO:0008586
segment specification	GO:0007379
regulation of autophagy	GO:0010506
cellular response to unfolded protein	GO:0034620
pigment biosynthetic process	GO:0046148
heart morphogenesis	GO:0003007
larval locomotory behavior	GO:0008345



–log(p)
n=110/365 input genes with annotations

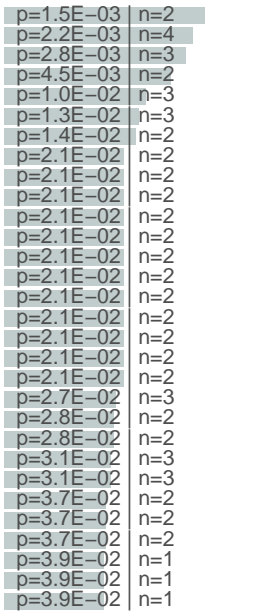


fraction

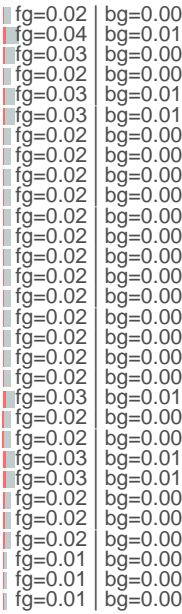
GO:MF
Elav_Nvec_vc1.1_XM_032386992.2

fraction genes in fg and expected value

phosphotransferase activity, carboxyl gr...	GO:0016774
ligase activity, forming carbon–nitrogen...	GO:0016879
outward rectifier potassium channel acti...	GO:0015271
mRNA 3'–UTR AU–rich region binding	GO:0035925
ion channel inhibitor activity	GO:0008200
potassium channel regulator activity	GO:0015459
calcium–activated potassium channel acti...	GO:0015269
proton–transporting ATPase activity, rot...	GO:0046961
delayed rectifier potassium channel acti...	GO:0005251
voltage–gated potassium channel activity...	GO:0086087
voltage–gated potassium channel activity...	GO:0086089
intracellular cyclic nucleotide activate...	GO:0005221
aspartic–type endopeptidase activity	GO:0004190
ATPase activity, coupled to transmembran...	GO:0044769
voltage–gated potassium channel activity...	GO:0086008
aspartic–type peptidase activity	GO:0070001
pyrophosphate hydrolysis–driven proton t...	GO:0009678
cyclic nucleotide–gated ion channel acti...	GO:0043855
voltage–gated potassium channel activity...	GO:0086090
kinesin binding	GO:0019894
phosphatase inhibitor activity	GO:0019212
potassium channel inhibitor activity	GO:0019870
phosphatase regulator activity	GO:0019208
transmembrane transporter binding	GO:0044325
acid–amino acid ligase activity	GO:0016881
ubiquitin–ubiquitin ligase activity	GO:0034450
carboxy–lyase activity	GO:0016831
CoA carboxylase activity	GO:0016421
glutamate–5–semialdehyde dehydrogenase a...	GO:0004350
phosphatidylinositol 3–kinase catalytic ...	GO:0036313



–log(p)
n=93/365 input genes with annotations

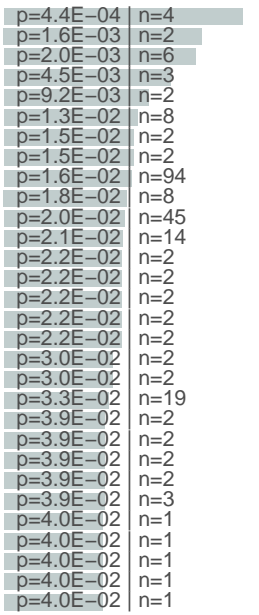


fraction

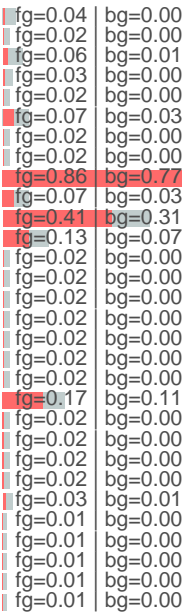
GO:CC
Elav_Nvec_vc1.1_XM_032386992.2

fraction genes in fg and expected value

voltage–gated potassium channel complex	GO:0008076
vacuolar proton–transporting V–type ATPa...	GO:0000220
Z disc	GO:0030018
integral component of presynaptic membra...	GO:0099056
integral component of luminal side of en...	GO:0071556
endosome membrane	GO:0010008
fungal–type vacuole	GO:0000324
fungal–type vacuole membrane	GO:0000329
intracellular membrane–bounded organelle	GO:0043231
early endosome	GO:0005769
endomembrane system	GO:0012505
endosome	GO:0005768
intracellular canaliculus	GO:0046691
extrinsic component of endosome membrane	GO:0031313
plasma membrane proton–transporting V–ty...	GO:0033181
cell tip	GO:0051286
juxtaparanode region of axon	GO:0044224
storage vacuole	GO:0000322
cell pole	GO:0060187
Golgi apparatus	GO:0005794
integral component of postsynaptic membr...	GO:0099055
magnesium–dependent protein serine/threo...	GO:0005963
intrinsic component of postsynaptic memb...	GO:0098936
paranode region of axon	GO:0033270
main axon	GO:0044304
Shu complex	GO:0097196
sarcoplasmic reticulum lumen	GO:0033018
apical cytoplasm	GO:0090651
synaptobrevin 2–SNAP–25–syntaxin–1a–comp...	GO:0070032
synaptobrevin 2–SNAP–25–syntaxin–1a–comp...	GO:0070033



–log(p)
n=109/365 input genes with annotations



fraction