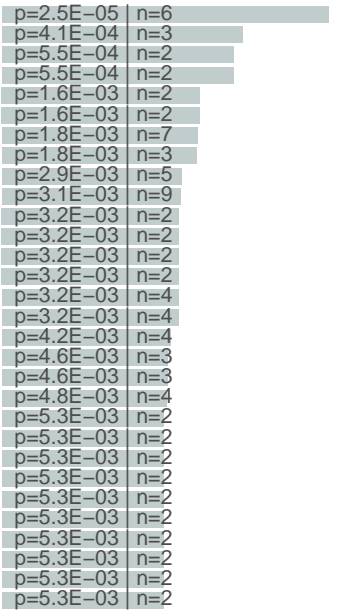


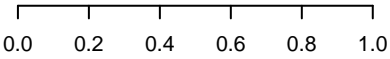
GO:BP
Elav_Nvec_vc1.1_XM_032362379.2

fraction genes in fg and expected value

cellular response to antibiotic	GO:0071236
cellular response to glucagon stimulus	GO:0071377
positive regulation of transcription fro...	GO:0061419
positive regulation of transcription fro...	GO:0061408
regulation of Golgi organization	GO:1903358
response to herbicide	GO:0009635
wound healing	GO:0042060
positive regulation of reactive oxygen s...	GO:2000379
angiogenesis	GO:0001525
negative regulation of transcription by ...	GO:0000122
G protein-coupled adenosine receptor sig...	GO:0001973
regulation of superoxide metabolic proce...	GO:0090322
cellular response to forskolin	GO:1904322
regulation of transcription from RNA pol...	GO:0043619
cellular response to toxic substance	GO:0097237
cAMP-mediated signaling	GO:0019933
cellular response to acid chemical	GO:0071229
regulation of blood vessel endothelial c...	GO:0043535
cellular response to hydrogen peroxide	GO:0070301
long-term memory	GO:0007616
regulation of terminal button organizati...	GO:2000331
cellular response to angiotensin	GO:1904385
regulation of adenylate cyclase activity	GO:0045761
mRNA transcription	GO:0009299
motor neuron apoptotic process	GO:0097049
positive regulation of oxidoreductase ac...	GO:0051353
response to platelet aggregation inhibit...	GO:0061478
positive regulation of mRNA processing	GO:0050685
negative regulation of cardiac muscle ce...	GO:0010667
negative regulation of Rho protein signa...	GO:0035024



fg=0.14	bg=0.01
fg=0.07	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.16	bg=0.04
fg=0.07	bg=0.01
fg=0.12	bg=0.02
fg=0.21	bg=0.07
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.09	bg=0.01
fg=0.09	bg=0.01
fg=0.09	bg=0.02
fg=0.07	bg=0.01
fg=0.07	bg=0.01
fg=0.09	bg=0.02
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00



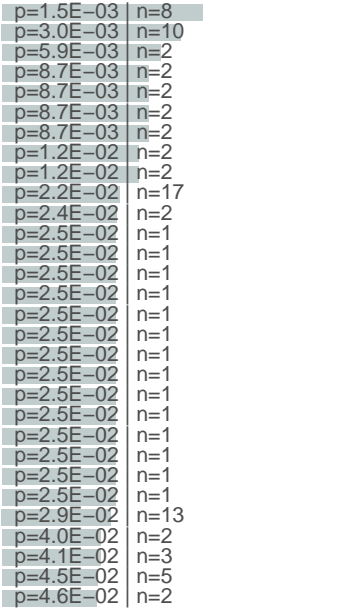
-log(p)
n=43/197 input genes with annotations

fraction

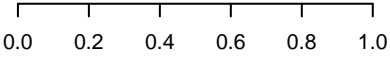
GO:MF
Elav_Nvec_vc1.1_XM_032362379.2

fraction genes in fg and expected value

protein heterodimerization activity	GO:0046982
protein domain specific binding	GO:0019904
phosphorus-oxygen lyase activity	GO:0016849
cholesterol binding	GO:0015485
cyclin-dependent protein serine/threonin...	GO:0016538
carboxy-lyase activity	GO:0016831
cyclase activity	GO:0009975
protein kinase A binding	GO:0051018
protein serine/threonine kinase inhibito...	GO:0030291
heterocyclic compound binding	GO:1901363
GDP binding	GO:0019003
cobalt ion binding	GO:0050897
FAD-AMP lyase (cyclizing) activity	GO:0034012
adenosine deaminase activity	GO:0004000
phosphatidylserine decarboxylase activit...	GO:0004609
ABC-type sterol transporter activity	GO:0034041
calcium- and calmodulin-responsive adeny...	GO:0008294
volume-sensitive chloride channel activi...	GO:0072320
glycerone kinase activity	GO:0004371
triokinase activity	GO:0050354
7SK snRNA binding	GO:0097322
volume-sensitive anion channel activity	GO:0005225
translation elongation factor binding	GO:0061770
double-stranded RNA adenosine deaminase ...	GO:0003726
alpha-1,6-mannosylglycoprotein 2-beta-N-...	GO:0008455
nucleic acid binding	GO:0003676
chromatin DNA binding	GO:0031490
transcription corepressor activity	GO:0003714
RNA polymerase II transcription regulato...	GO:0000977
kinase inhibitor activity	GO:0019210



fg=0.20	bg=0.06
fg=0.25	bg=0.09
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.05	bg=0.00
fg=0.42	bg=0.27
fg=0.05	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.33	bg=0.19
fg=0.05	bg=0.01
fg=0.07	bg=0.02
fg=0.12	bg=0.05
fg=0.05	bg=0.01



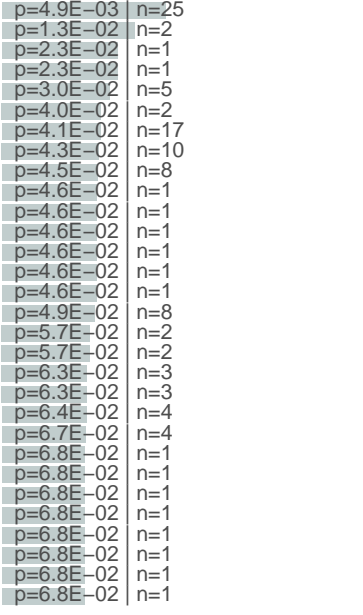
-log(p)
n=40/197 input genes with annotations

fraction

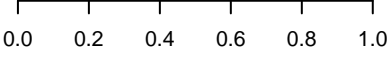
GO:CC
Elav_Nvec_vc1.1_XM_032362379.2

fraction genes in fg and expected value

cytosol	GO:0005829
germ cell nucleus	GO:0043073
integrin alpha9-beta1 complex	GO:0034679
sarcoplasmic reticulum lumen	GO:0033018
postsynapse	GO:0098794
protein kinase complex	GO:1902911
plasma membrane	GO:0005886
Golgi apparatus	GO:0005794
plasma membrane region	GO:0098590
mitochondrial crista	GO:0030061
integrin complex	GO:0008305
nuclear stress granule	GO:0097165
cytoplasmic cyclin-dependent protein kin...	GO:0000308
protein complex involved in cell adhesio...	GO:0098636
prefoldin complex	GO:0016272
synapse	GO:0045202
external side of plasma membrane	GO:0009897
heterochromatin	GO:0000792
neuron spine	GO:0044309
dendritic spine	GO:0043197
side of membrane	GO:0098552
mitochondrial inner membrane	GO:0005743
NuRD complex	GO:0016581
inhibitory synapse	GO:0060077
CHD-type complex	GO:0090545
male germ cell nucleus	GO:0001673
intercalary heterochromatin	GO:0005725
nucleotide-activated protein kinase comp...	GO:0031588
cAMP-dependent protein kinase complex	GO:0005952
podosome	GO:0002102



fg=0.60	bg=0.39
fg=0.05	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.12	bg=0.04
fg=0.05	bg=0.01
fg=0.40	bg=0.27
fg=0.24	bg=0.13
fg=0.19	bg=0.10
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.19	bg=0.10
fg=0.05	bg=0.01
fg=0.05	bg=0.01
fg=0.07	bg=0.02
fg=0.07	bg=0.02
fg=0.10	bg=0.04
fg=0.10	bg=0.04
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00



-log(p)
n=42/197 input genes with annotations

fraction