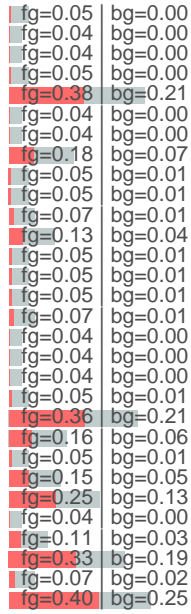
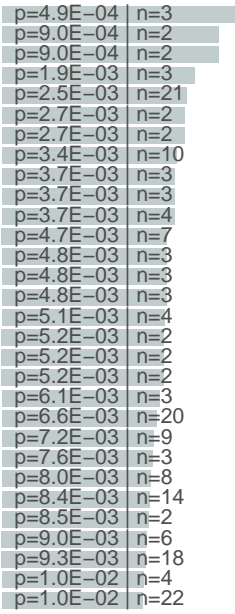


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001634845.3

fraction genes in fg and expected value

cardiac muscle hypertrophy in response t... GO:0014898  
negative regulation of sprouting angioge... GO:1903671  
negative regulation of cell migration in... GO:0090051  
positive regulation of protein dephospho... GO:0035307  
regulation of transcription, DNA-templat... GO:0006355  
negative regulation of adenylate cyclase... GO:0140199  
pyrimidine deoxyribonucleotide metabolic... GO:0009219  
cellular response to hormone stimulus GO:0032870  
acute inflammatory response GO:0002526  
histone deacetylation GO:0016575  
regulation of intracellular pH GO:0051453  
nematode larval development GO:0002119  
response to vitamin GO:0033273  
regulation of fat cell differentiation GO:0045598  
negative regulation of small molecule me... GO:0062014  
excretion GO:0007588  
G protein-coupled adenosine receptor sig... GO:0001973  
G protein-coupled acetylcholine receptor... GO:0007213  
regulation of pathway-restricted SMAD pr... GO:0060393  
pharyngeal pumping GO:0043050  
negative regulation of macromolecule met... GO:0010605  
cellular response to organonitrogen comp... GO:0071417  
endothelium development GO:0003158  
negative regulation of cell population p... GO:0008285  
negative regulation of cellular biosynth... GO:0031327  
bicarbonate transport GO:0015701  
response to acid chemical GO:0001101  
negative regulation of nitrogen compound... GO:0051172  
regulation of reactive oxygen species me... GO:2000377  
regulation of cellular macromolecule bio... GO:2000112



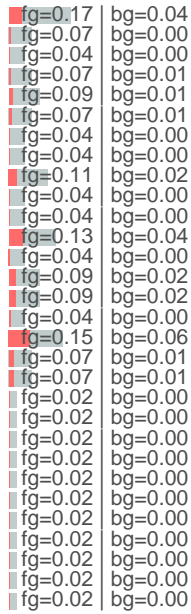
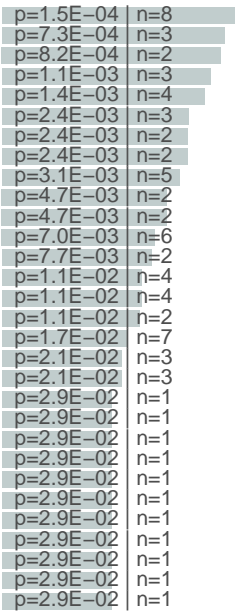
-log(p)  
n=55/185 input genes with annotations

fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001634845.3

fraction genes in fg and expected value

RNA polymerase II cis-regulatory region ... GO:0000978  
histone deacetylase activity GO:0004407  
vinculin binding GO:0017166  
GTPase activating protein binding GO:0032794  
histone deacetylase binding GO:0042826  
GDP binding GO:0019003  
bicarbonate transmembrane transporter ac... GO:0015106  
nuclear glucocorticoid receptor binding GO:0035259  
GTPase activity GO:0003924  
anion:anion antiporter activity GO:0015301  
inorganic anion exchanger activity GO:0005452  
DNA-binding transcription activator acti... GO:0001228  
G-protein beta/gamma-subunit complex bin... GO:0031683  
nucleoside binding GO:0001882  
purine nucleoside binding GO:0001883  
HMG box domain binding GO:0071837  
transcription coregulator activity GO:0003712  
DNA-binding transcription repressor acti... GO:0001227  
DNA-binding transcription repressor acti... GO:0001217  
L-alanine:2-oxoglutarate aminotransferas... GO:0004021  
G-protein gamma-subunit binding GO:0031682  
methionine adenosyltransferase regulator... GO:0048270  
oxidoreductase activity, acting on the a... GO:0016624  
sulfate transmembrane transporter activi... GO:0015116  
BH4 domain binding GO:0051435  
8-oxo-7,8-dihydroguanine DNA N-glycosyla... GO:0034039  
leucine binding GO:0070728  
pyruvate dehydrogenase activity GO:0004738  
pyruvate dehydrogenase (acetyl-transferr... GO:0004739  
alanine-oxo-acid transaminase activity GO:0047635



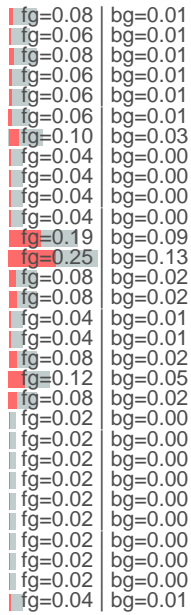
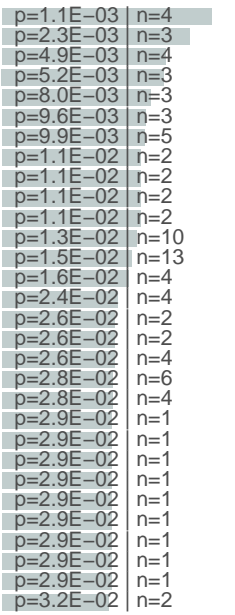
-log(p)  
n=46/185 input genes with annotations

fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001634845.3

fraction genes in fg and expected value

nuclear matrix GO:0016363  
histone deacetylase complex GO:0000118  
leading edge membrane GO:0031256  
transcription repressor complex GO:0017053  
focal adhesion GO:0005925  
caveola GO:0005901  
basolateral plasma membrane GO:0016323  
GTPase complex GO:1905360  
sarcoplasm GO:0016528  
sarcoplasmic reticulum GO:0016529  
heterotrimeric G-protein complex GO:0005834  
endosome GO:0005768  
Golgi apparatus GO:0005794  
sarcomere GO:0030017  
recycling endosome GO:0055037  
melanosome GO:0042470  
clathrin-coated endocytic vesicle GO:0045334  
adherens junction GO:0005912  
cell-cell junction GO:0005911  
myofibril GO:0030016  
neuronal ribonucleoprotein granule GO:0071598  
lamellipodium membrane GO:0031258  
RNA polymerase II transcription represso... GO:0090571  
CHOP-C/EBP complex GO:0036488  
trans-synaptic protein complex GO:0098820  
anchored component of synaptic vesicle m... GO:0098993  
CA3 pyramidal cell dendrite GO:0097442  
GTPase activator complex GO:1902773  
methionine adenosyltransferase complex GO:0048269  
pigment granule GO:0048770



-log(p)  
n=52/185 input genes with annotations

fraction