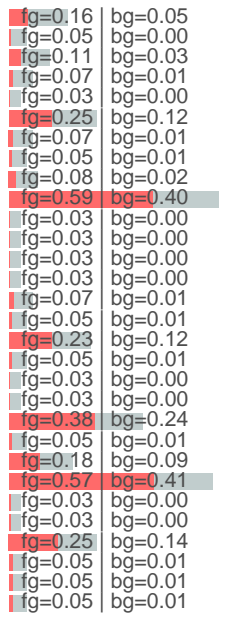
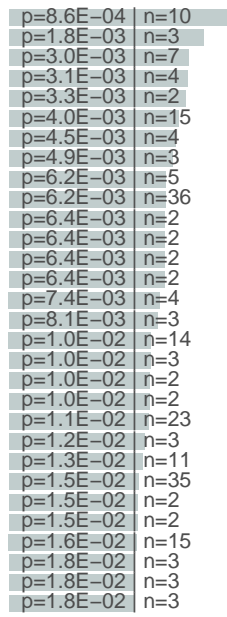


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032384172.2

fraction genes in fg and expected value

epithelial cell development GO:0002064  
glial cell proliferation GO:0014009  
epidermis development GO:0008544  
antigen processing and presentation of p... GO:0002495  
cleavage furrow ingression GO:0036090  
regulation of nervous system development GO:0051960  
neuroepithelial cell differentiation GO:0060563  
positive regulation of Notch signaling p... GO:0045747  
glial cell differentiation GO:0010001  
signaling GO:0023052  
epithelial structure maintenance GO:0010669  
response to cycloheximide GO:0046898  
adherens junction maintenance GO:0034334  
establishment of blood-brain barrier GO:0060856  
inner ear receptor cell differentiation GO:0060113  
endothelial cell differentiation GO:0045446  
positive regulation of transcription, DN... GO:0045893  
cellular response to nerve growth factor... GO:1990090  
positive regulation of cAMP-mediated sig... GO:0043950  
response to fungicide GO:0060992  
regulation of cellular component organiz... GO:0051128  
response to nerve growth factor GO:1990089  
embryonic morphogenesis GO:0048598  
cell communication GO:0007154  
spinal cord motor neuron differentiation GO:0021522  
protein localization to basolateral plas... GO:1903361  
cell-cell signaling GO:0007267  
regulation of gliogenesis GO:0014013  
response to leukemia inhibitory factor GO:1990823  
cellular response to leukemia inhibitory... GO:1990830



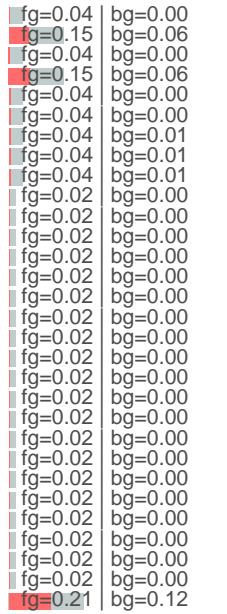
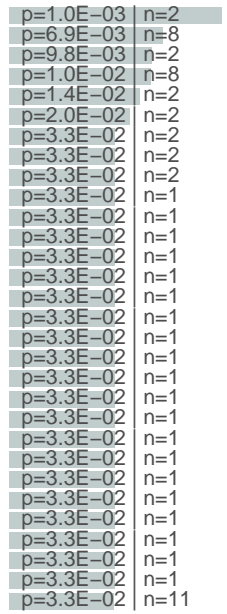
-log(p)  
n=61/207 input genes with annotations

fraction

GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032384172.2

fraction genes in fg and expected value

LIM domain binding GO:0030274  
transcription cis-regulatory region bind... GO:0000976  
arrestin family protein binding GO:1990763  
transcription coregulator activity GO:0003712  
G-protein alpha-subunit binding GO:0001965  
spectrin binding GO:0030507  
serine-type peptidase activity GO:0008236  
ion channel inhibitor activity GO:0008200  
serine-type endopeptidase activity GO:0004252  
amine N-methyltransferase activity GO:0030748  
type I transforming growth factor beta r... GO:0034713  
JUN kinase kinase kinase activity GO:0004706  
thioether S-methyltransferase activity GO:0004790  
methionine adenosyltransferase regulator... GO:0048270  
dynein light chain binding GO:0045503  
G-protein beta-subunit binding GO:0031681  
pyridine N-methyltransferase activity GO:0030760  
ATP-dependent peptidase activity GO:0004176  
dimethyl selenide methyltransferase acti... GO:0098615  
mitochondrial promoter sequence-specific... GO:0001018  
S-methyltransferase activity GO:0008172  
MHC class II protein binding GO:0042289  
single-stranded telomeric DNA binding GO:0043047  
RNA-3'-phosphate cyclase activity GO:0003963  
7SK snRNA binding GO:0097322  
calcium channel inhibitor activity GO:0019855  
dCMP deaminase activity GO:0004132  
nicotinamide N-methyltransferase activit... GO:0008112  
G-rich strand telomeric DNA binding GO:0098505  
transcription regulator activity GO:0140110



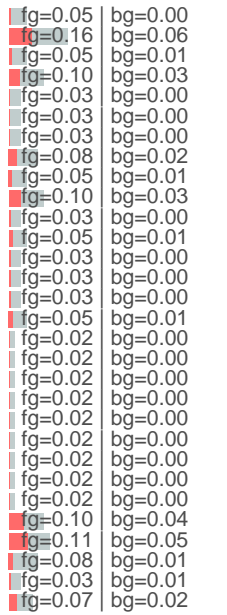
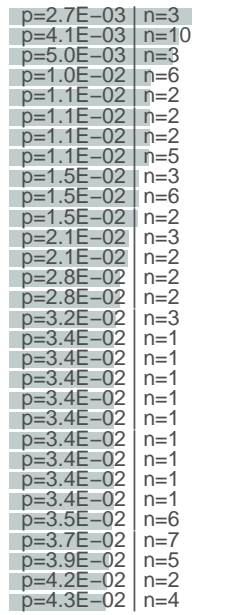
-log(p)  
n=52/207 input genes with annotations

fraction

GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032384172.2

fraction genes in fg and expected value

extrinsic component of organelle membran... GO:0031312  
nuclear body GO:0016604  
bicellular tight junction GO:0005923  
actin cytoskeleton GO:0015629  
autolysosome GO:0044754  
actin filament GO:0005884  
female germ cell nucleus GO:0001674  
polymeric cytoskeletal fiber GO:0099513  
kinetochore GO:0000776  
nuclear speck GO:0016607  
dynactin complex GO:0005869  
ruffle GO:0001726  
secondary lysosome GO:0005767  
euchromatin GO:0000791  
germ cell nucleus GO:0043073  
condensed chromosome, centromeric region GO:0000779  
extrinsic component of mitochondrial inn... GO:0031314  
methionine adenosyltransferase complex GO:0048269  
ciliary cap GO:0061822  
telomere cap complex GO:0000782  
nuclear telomere cap complex GO:0000783  
ATF4-CREB1 transcription factor complex GO:1990589  
male pronucleus GO:0001940  
chromosome, telomeric repeat region GO:0140445  
shelterin complex GO:0070187  
cell cortex GO:0005938  
cytoplasmic region GO:0099568  
apical junction complex GO:0043296  
ruffle membrane GO:0032587  
adherens junction GO:0005912



-log(p)  
n=61/207 input genes with annotations

fraction