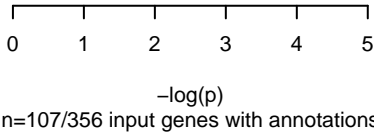
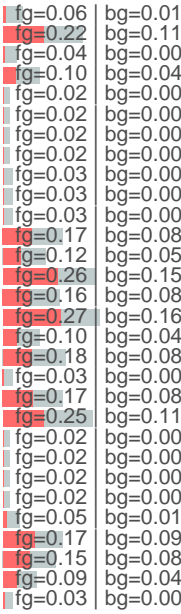
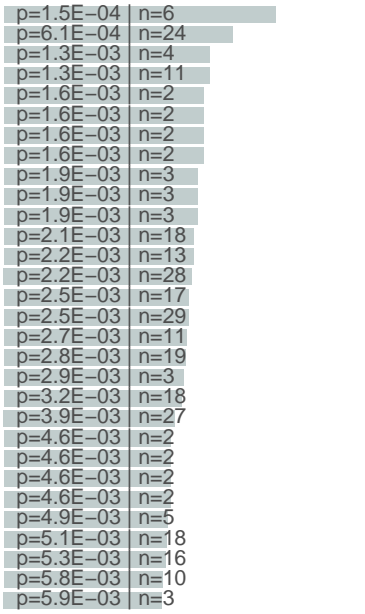


GO:BP
Elav_Nvec_vc1.1_XM_032366030.2

fraction genes in fg and expected value

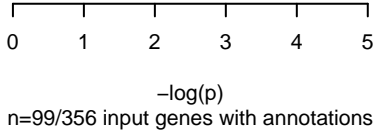
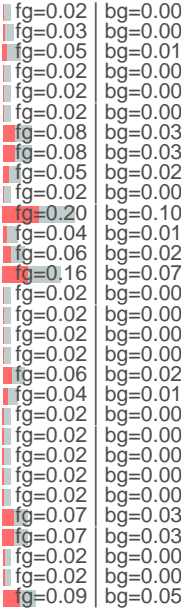
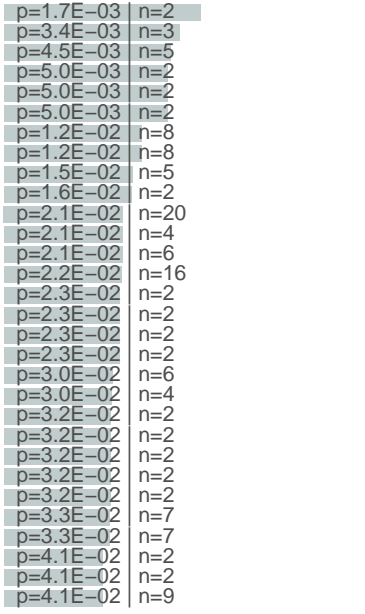
regulation of mitochondrial membrane pot... GO:0051881
negative regulation of cellular macromol... GO:2000113
eye-antennal disc morphogenesis GO:0007455
establishment or maintenance of cell pol... GO:0007163
liver morphogenesis GO:0072576
Golgi to transport vesicle transport GO:0055108
negative regulation by host of viral gen... GO:0044828
negative regulation of imaginal disc gro... GO:0045571
negative regulation of cell fate specifi... GO:0009996
pole cell migration GO:0007280
regulation of R7 cell differentiation GO:0045676
negative regulation of cellular protein ... GO:0032269
positive regulation of neurogenesis GO:0050769
negative regulation of gene expression GO:0010629
oogenesis GO:0048477
multi-organism reproductive process GO:0044703
positive regulation of neuron differenti... GO:0045666
regulation of anatomical structure morph... GO:0022603
negative regulation of T cell proliferat... GO:0042130
neuron projection morphogenesis GO:0048812
positive regulation of developmental pro... GO:0051094
phosphatidylglycerol acyl-chain remodeli... GO:0036148
modulation by virus of host cellular pro... GO:0019054
deoxynucleotide transport GO:0030302
pyrimidine nucleotide import into mitoch... GO:1990519
embryonic skeletal system morphogenesis GO:0048704
negative regulation of multicellular org... GO:0051241
brain development GO:0007420
anatomical structure maturation GO:0071695
response to gravity GO:0009629



GO:MF
Elav_Nvec_vc1.1_XM_032366030.2

fraction genes in fg and expected value

DNA replication origin binding GO:0003688
phosphotyrosine residue binding GO:0001784
DNA-binding transcription repressor acti... GO:0001227
pyrimidine nucleotide transmembrane tran... GO:0015218
mRNA 3'-UTR AU-rich region binding GO:0035925
mRNA regulatory element binding translat... GO:0000900
cis-regulatory region sequence-specific ... GO:0000987
RNA polymerase II cis-regulatory region ... GO:0000978
channel regulator activity GO:0016247
nucleoside monophosphate kinase activity GO:0050145
transcription regulator activity GO:0140110
myosin binding GO:0017022
RNA polymerase II-specific DNA-binding t... GO:0061629
DNA-binding transcription factor activit... GO:0003700
mRNA 5'-UTR binding GO:0048027
1-acylglycerol-3-phosphate O-acyltransfe... GO:0003841
aryl hydrocarbon receptor binding GO:0017162
cyclase activity GO:0009975
DNA-binding transcription factor binding GO:0140297
single-stranded DNA binding GO:0003697
acylglycerol O-acyltransferase activity GO:0016411
nuclear receptor activity GO:0004879
adenylate cyclase binding GO:0008179
ubiquitin-specific protease binding GO:1990381
ligand-activated transcription factor ac... GO:0098531
DNA-binding transcription activator acti... GO:0001228
DNA-binding transcription activator acti... GO:0001216
lysophosphatidic acid acyltransferase ac... GO:0042171
lysophospholipid acyltransferase activit... GO:0071617
transcription cis-regulatory region bind... GO:0000976



GO:CC
Elav_Nvec_vc1.1_XM_032366030.2

fraction genes in fg and expected value

Lewy body GO:0097413
lysosomal membrane GO:0005765
postsynaptic density GO:0014069
supramolecular complex GO:0099080
dendrite GO:0030425
myelin sheath abaxonal region GO:0035748
intracellular organelle GO:0043229
microvillus GO:0005902
cytoplasmic stress granule GO:0010494
intrinsic component of the cytoplasmic s... GO:0031235
contractile fiber GO:0043292
cytoplasmic side of plasma membrane GO:0009898
cytoplasmic ribonucleoprotein granule GO:0036464
excitatory synapse GO:0060076
azurophil granule GO:0042582
primary lysosome GO:0005766
ribonucleoprotein granule GO:0035770
cytoplasmic side of membrane GO:0098562
membrane-bounded organelle GO:0043227
nucleus GO:0005634
chromosome, centromeric region GO:0000775
immunological synapse GO:0001772
microvesicle GO:1990742
sperm connecting piece GO:0097224
sperm mitochondrial sheath GO:0097226
Ndc80 complex GO:0031262
XPC complex GO:0071942
apicomedial cortex GO:0106037
Sec61 translocon complex GO:0005784
alpha-heterochromatin GO:0005723

