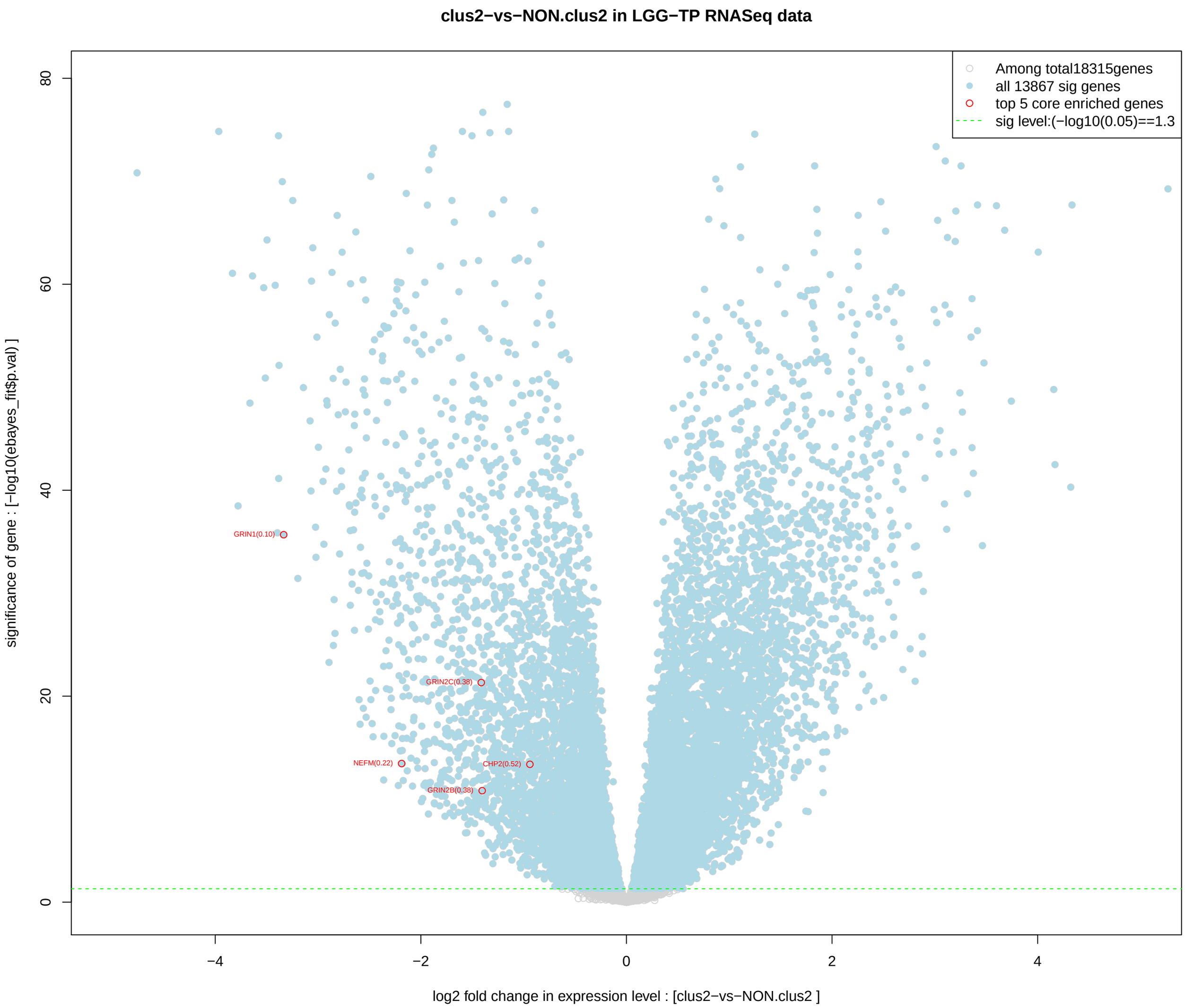
clus2−vs−NON.clus2 in LGG−TP RNASeq data
Among total18315genes
all 13867 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GRIN1(0.10)
GRIN2C(0.38)
NEFM(0.22)
CHP2(0.52)
GRIN2B(0.38)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
20
40
60
80
−4
−2
0
2
4