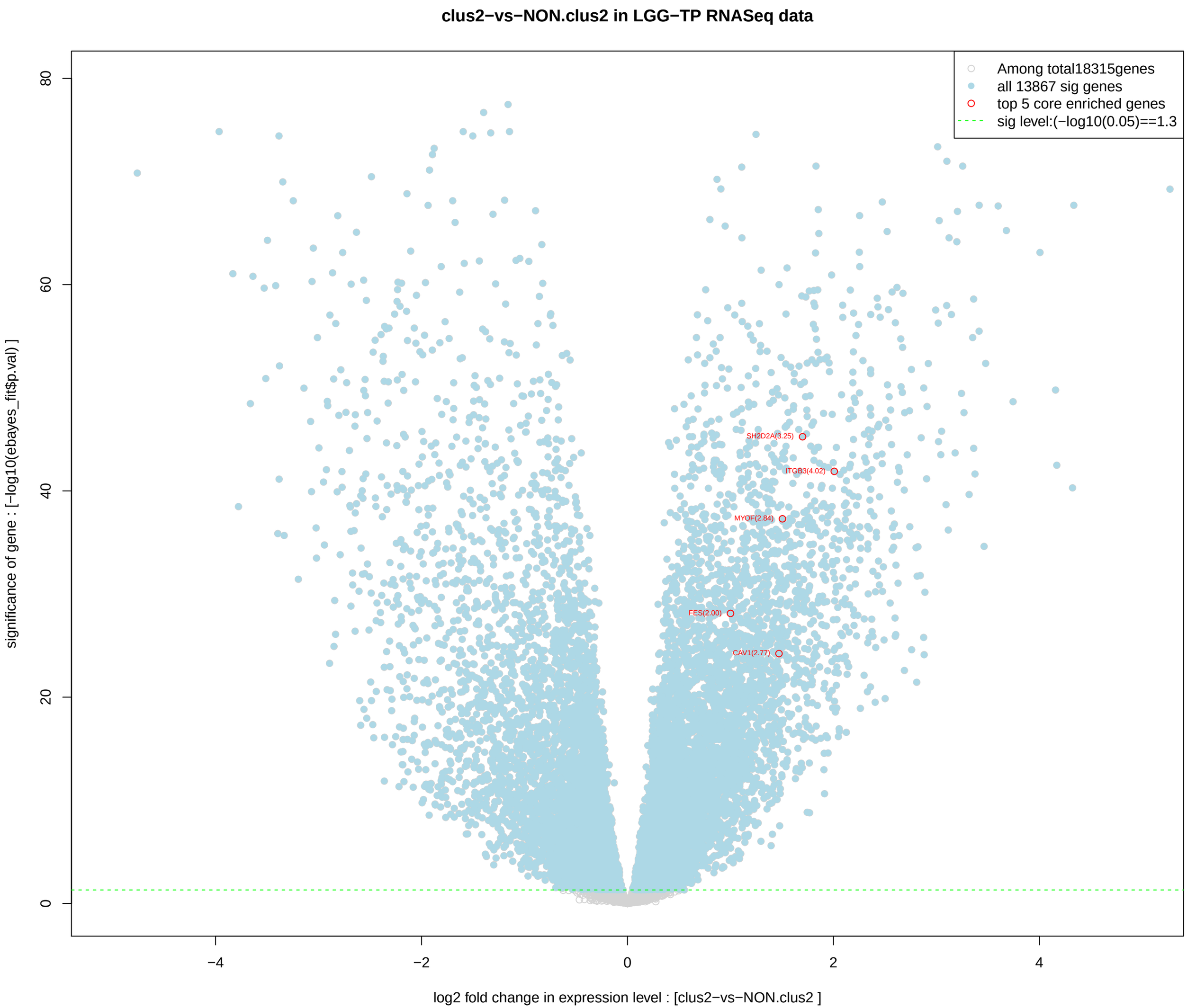
clus2−vs−NON.clus2 in LGG−TP RNASeq data
Among total18315genes
all 13867 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
SH2D2A(3.25)
ITGB3(4.02)
MYOF(2.84)
FES(2.00)
CAV1(2.77)
significance of gene : [−log10(ebayes_fit$p.val)]
0
20
40
60
80
−4
−2
0
2
4
log2 fold change in expression level : [clus2−vs−NON.clus2]