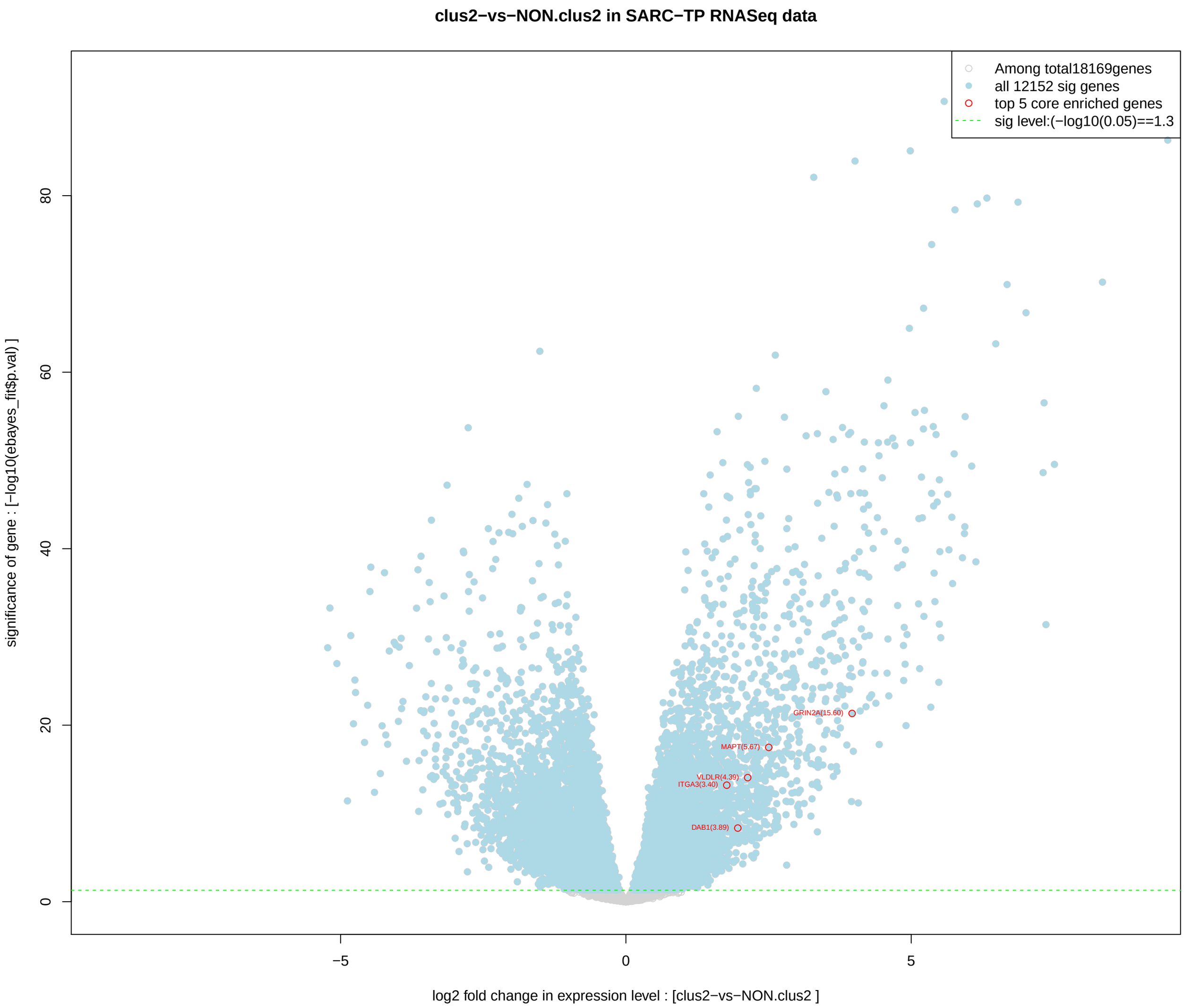
clus2−vs−NON.clus2 in SARC−TP RNASeq data
Among total18169genes
all 12152 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GRIN2A(15.60)
MAPT(5.67)
VLDLR(4.39)
ITGA3(3.40)
DAB1(3.89)
significance of gene : [−log10(ebayes_fit$p.val)]
0
20
40
60
80
−5
0
5
log2 fold change in expression level : [clus2−vs−NON.clus2]