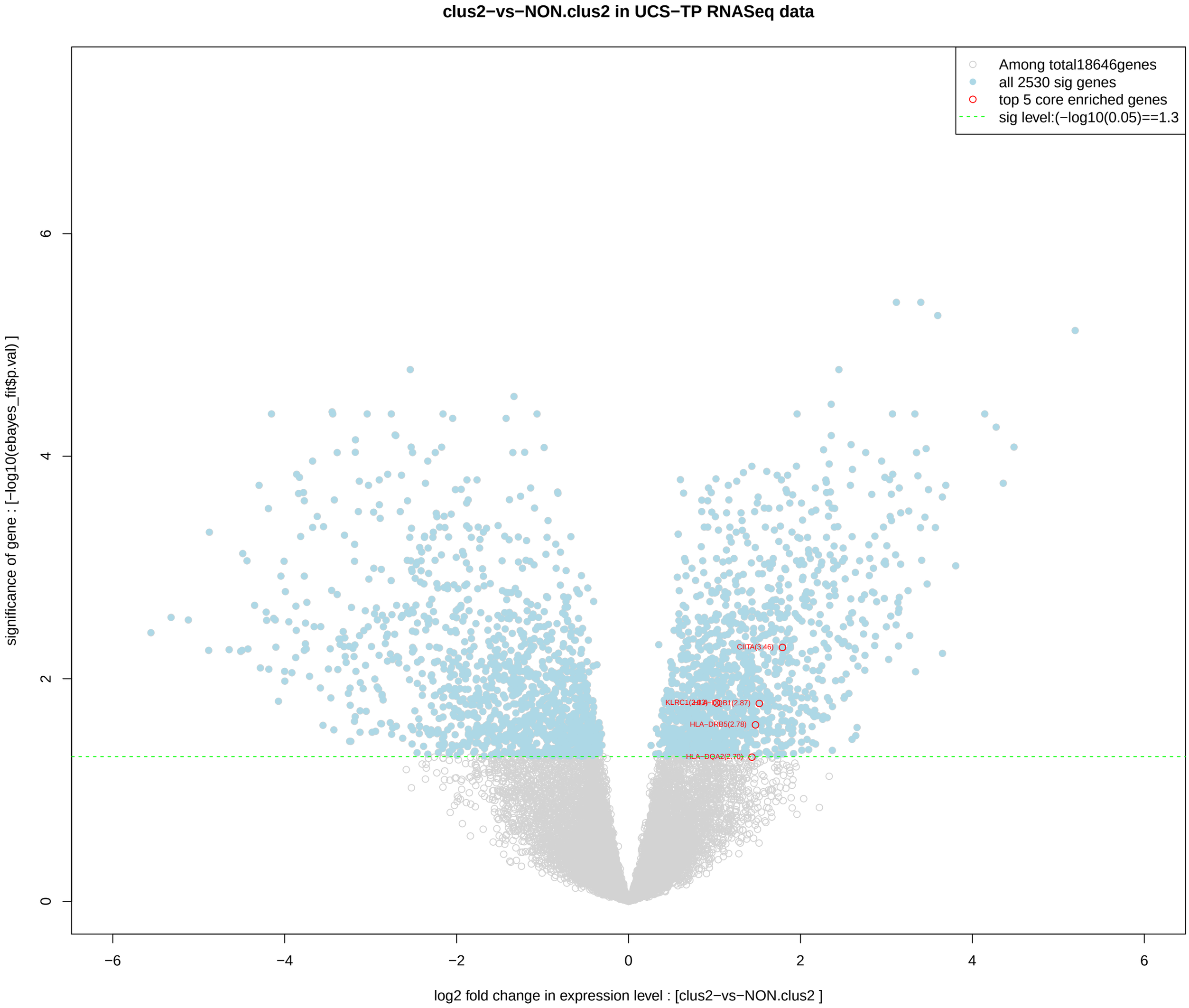

clus2−vs−NON.clus2 in UCS−TP RNASeq data
Among total18646genes
all 2530 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CIITA(3.46)
KLRC1(2.03)
HLA−DQB1(2.87)
HLA−DRB5(2.78)
HLA−DQA2(2.70)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
2
4
6
−6
−4
−2
0
2
4
6