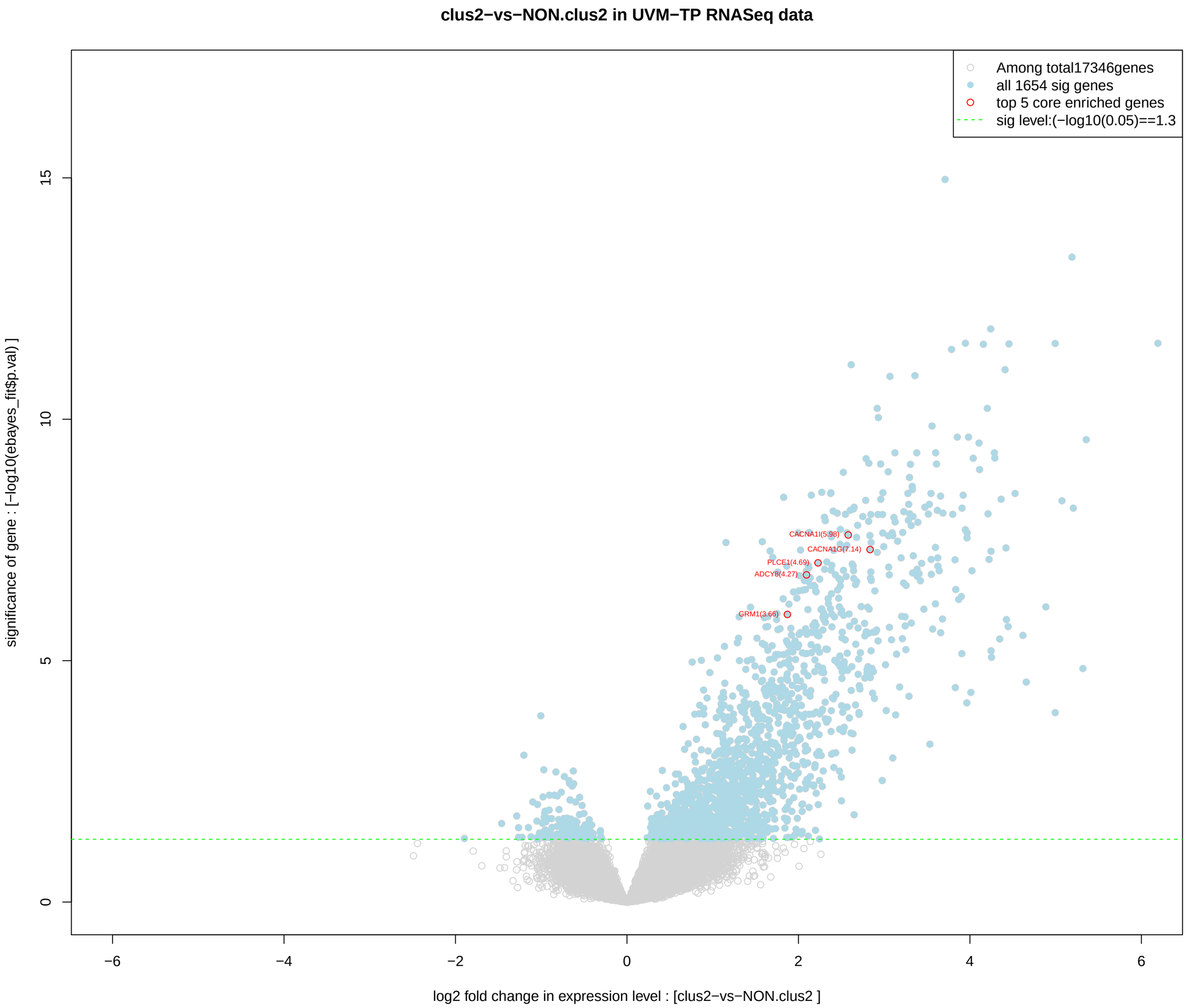
clus2−vs−NON.clus2 in UVM−TP RNASeq data
Among total17346genes
all 1654 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CACNA1I(5.98)
CACNA1G(7.14)
PLCE1(4.69)
ADCY8(4.27)
GRM1(3.66)
significance of gene : [−log10(ebayes_fit$p.val) ]
0
5
10
15
−6
−4
−2
0
2
4
6
log2 fold change in expression level : [clus2−vs−NON.clus2 ]