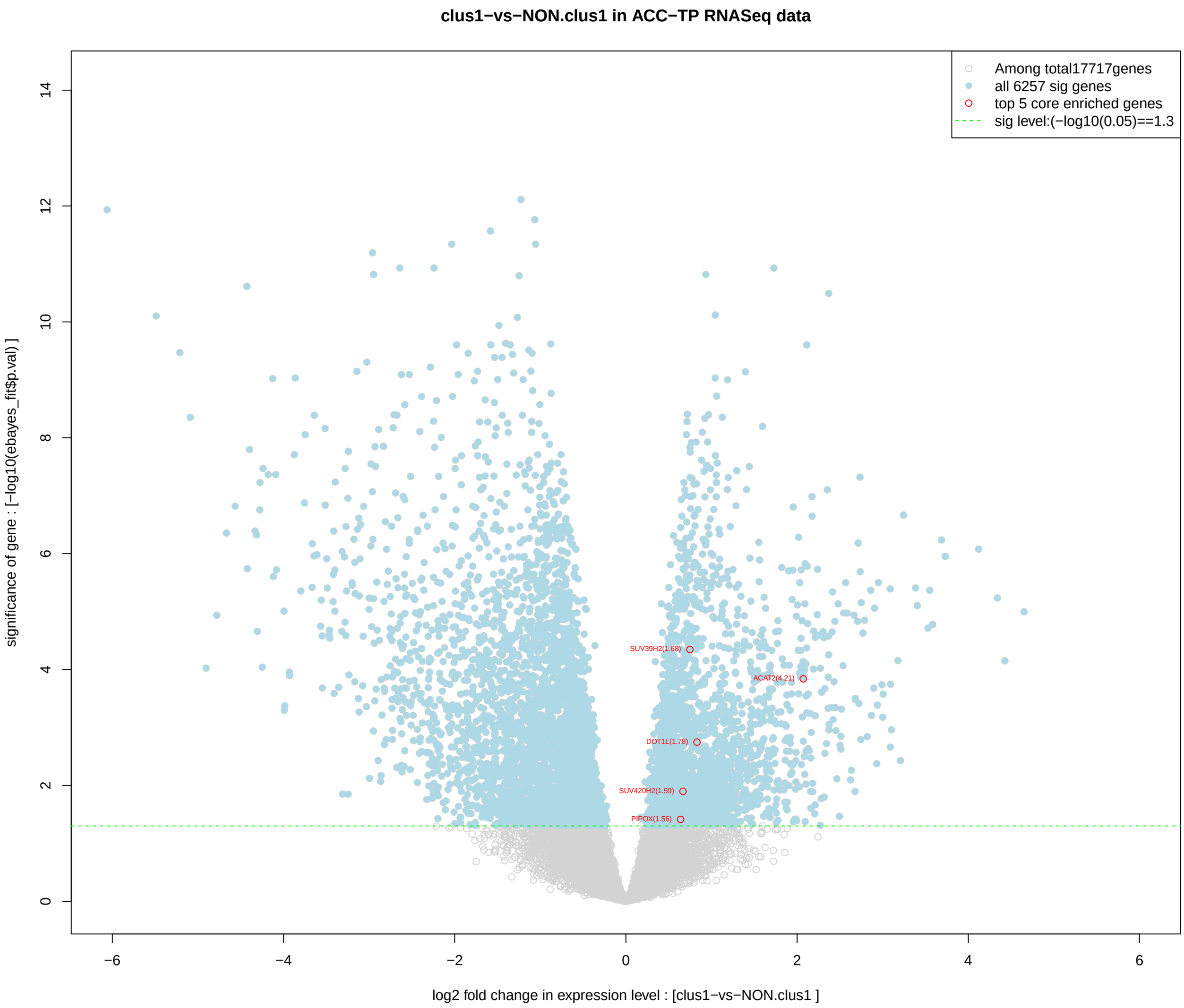
clus1−vs−NON.clus1 in ACC−TP RNASeq data
Among total17717genes
all 6257 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
SUV39H2(1.68)
ACAT2(4.21)
DOT1L(1.78)
SUV420H2(1.59)
PIPOX(1.56)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
2
4
6
8
10
12
14
−6
−4
−2
0
2
4
6