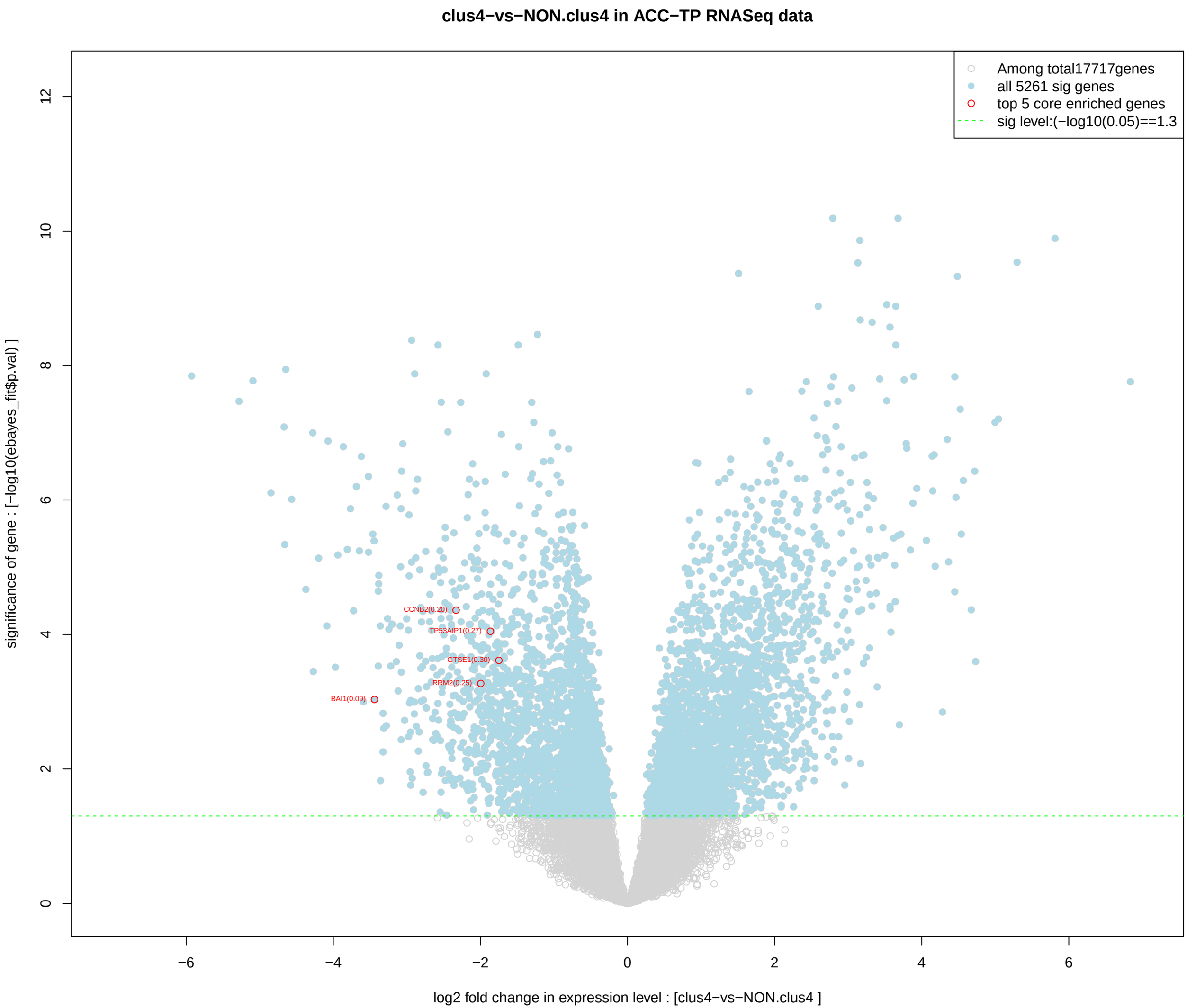
clus4−vs−NON.clus4 in ACC−TP RNASeq data
Among total17717genes
all 5261 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CCNB2(0.20)
TP53AIP1(0.27)
GTSE1(0.30)
RRM2(0.25)
BAI1(0.09)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus4−vs−NON.clus4]
0
2
4
6
8
10
12
−6
−4
−2
0
2
4
6