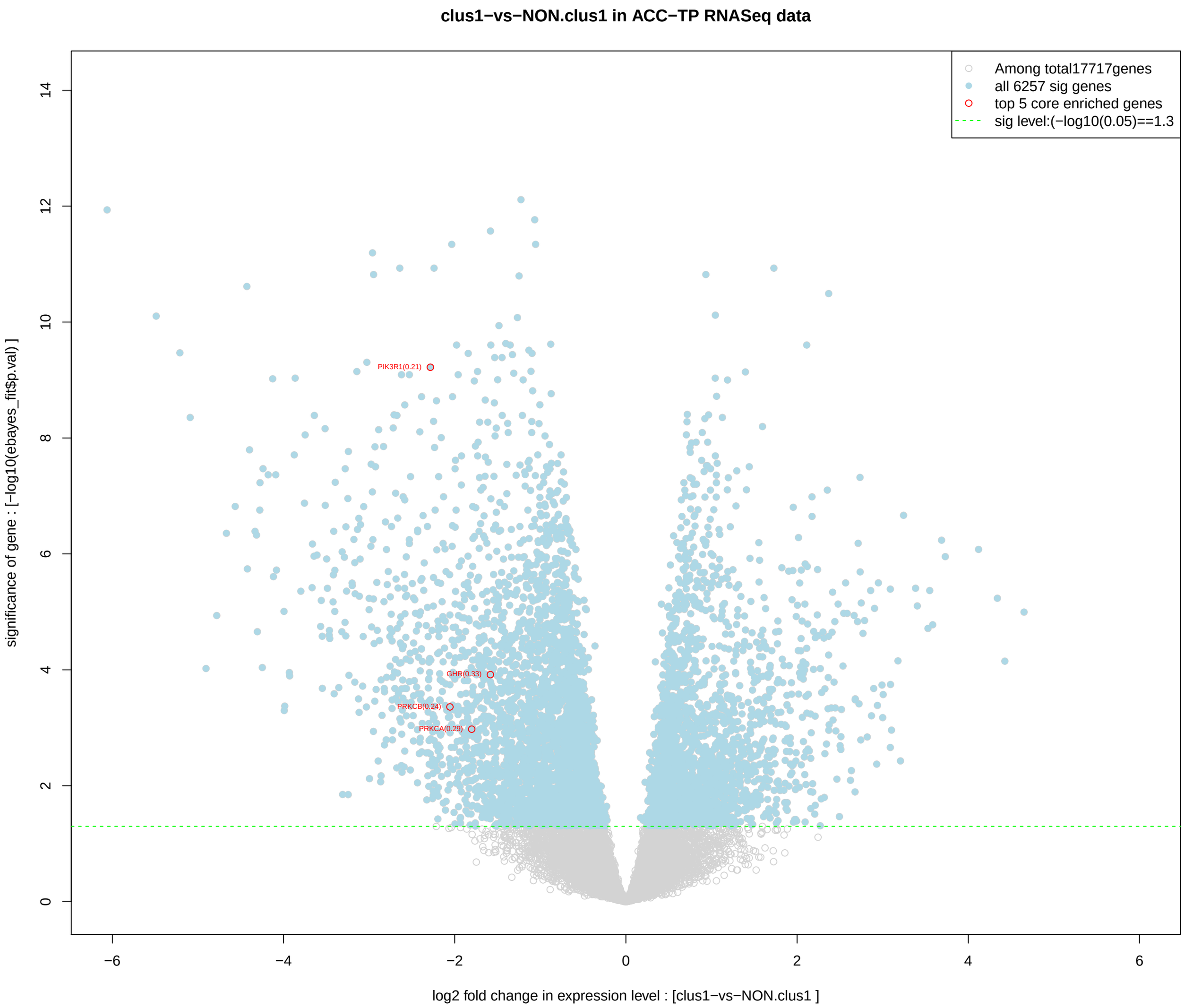
clus1−vs−NON.clus1 in ACC−TP RNASeq data
Among total17717genes
all 6257 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PIK3R1(0.21)
GHR(0.33)
PRKCB(0.24)
PRKCA(0.29)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
2
4
6
8
10
12
14
−6
−4
−2
0
2
4
6