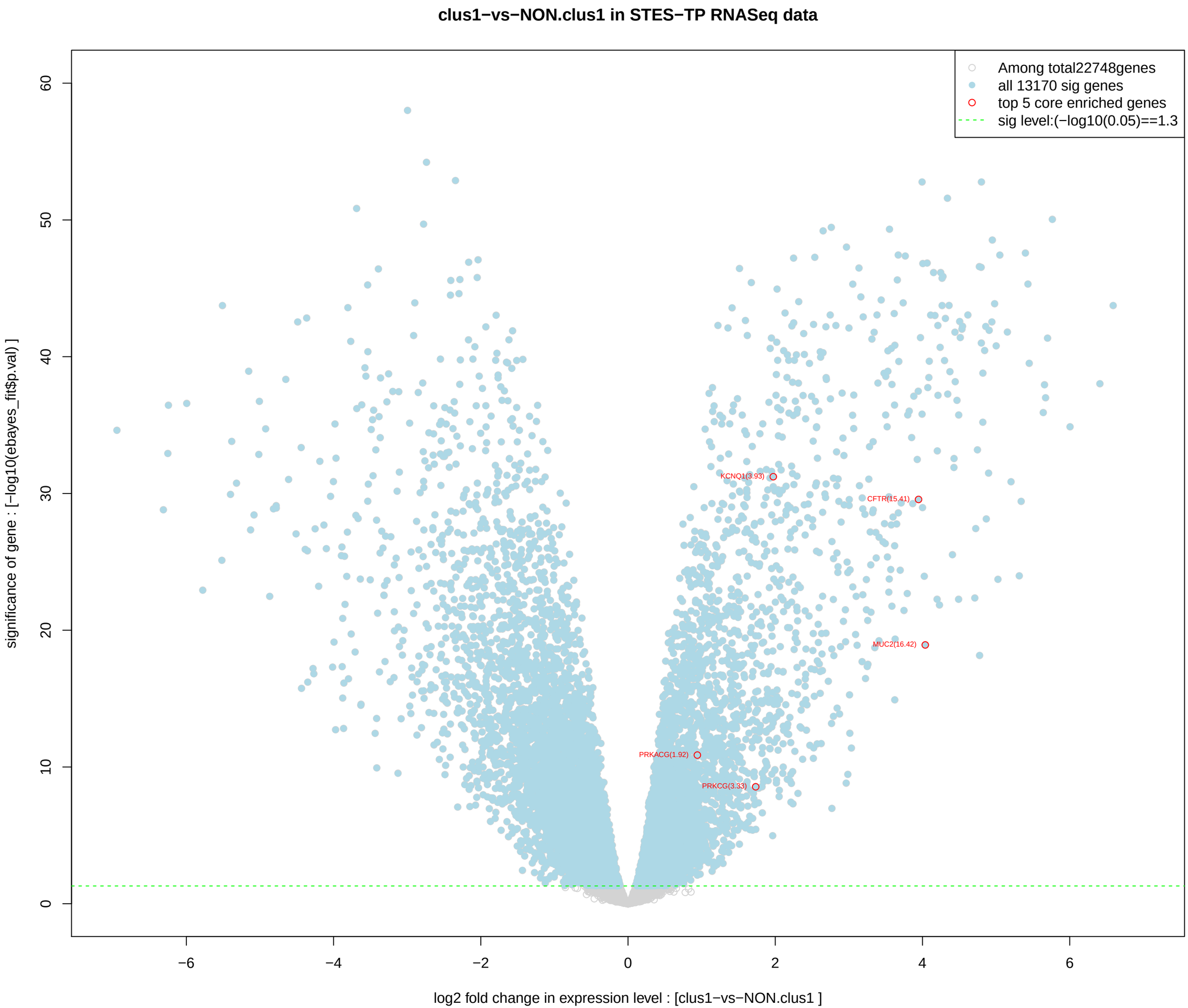
clus1−vs−NON.clus1 in STES−TP RNASeq data
Among total22748genes
all 13170 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
KCNQ1(3.93)
CFTR(15.41)
MUC2(16.42)
PRKACG(1.92)
PRKCG(3.33)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
50
60
−6
−4
−2
0
2
4
6