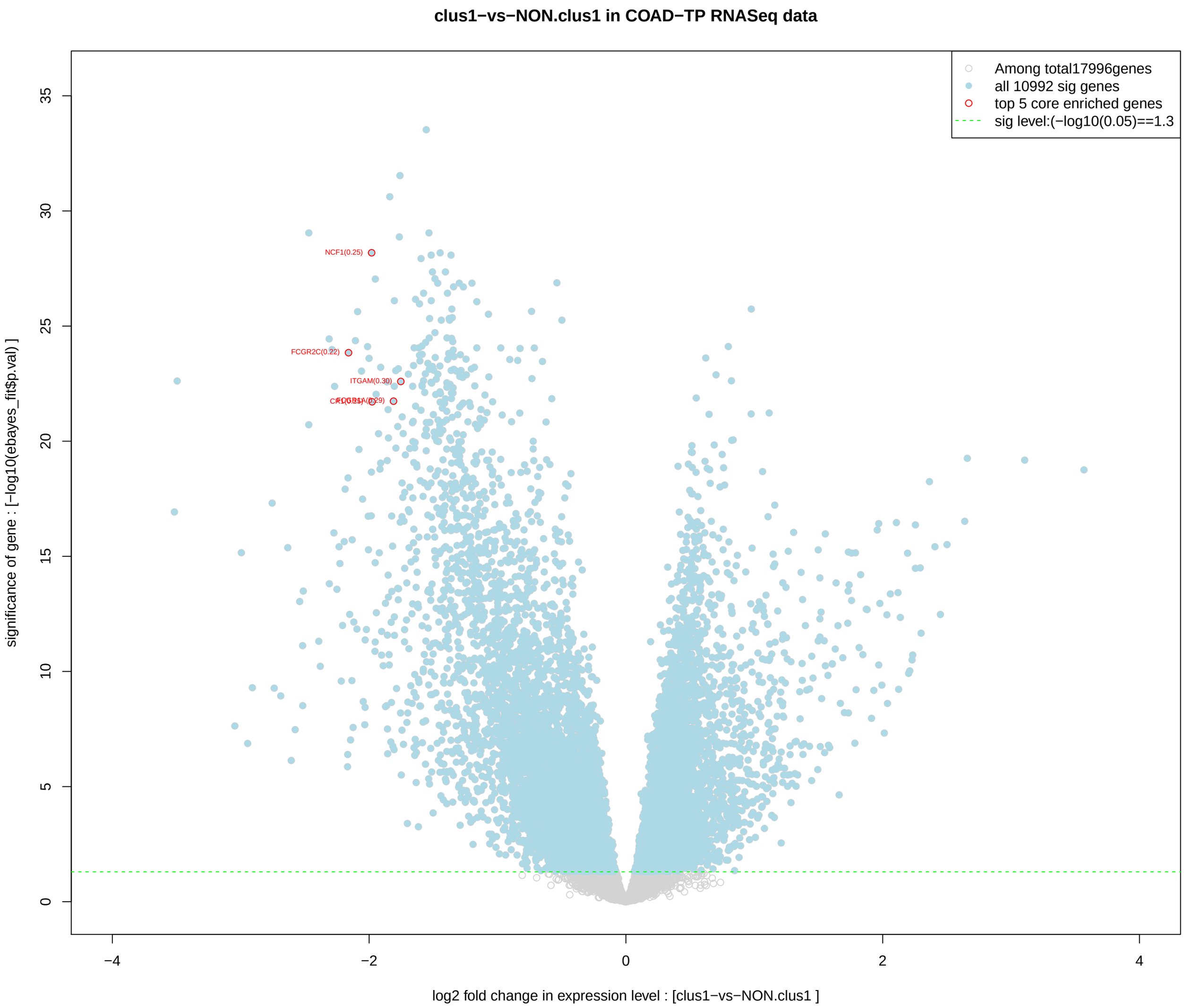
clus1−vs−NON.clus1 in COAD−TP RNASeq data
Among total17996genes
all 10992 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
NCF1(0.25)
FCGR2C(0.22)
ITGAM(0.30)
CR1(0.25)
FCGR3A(0.29)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
25
30
35
−4
−2
0
2
4