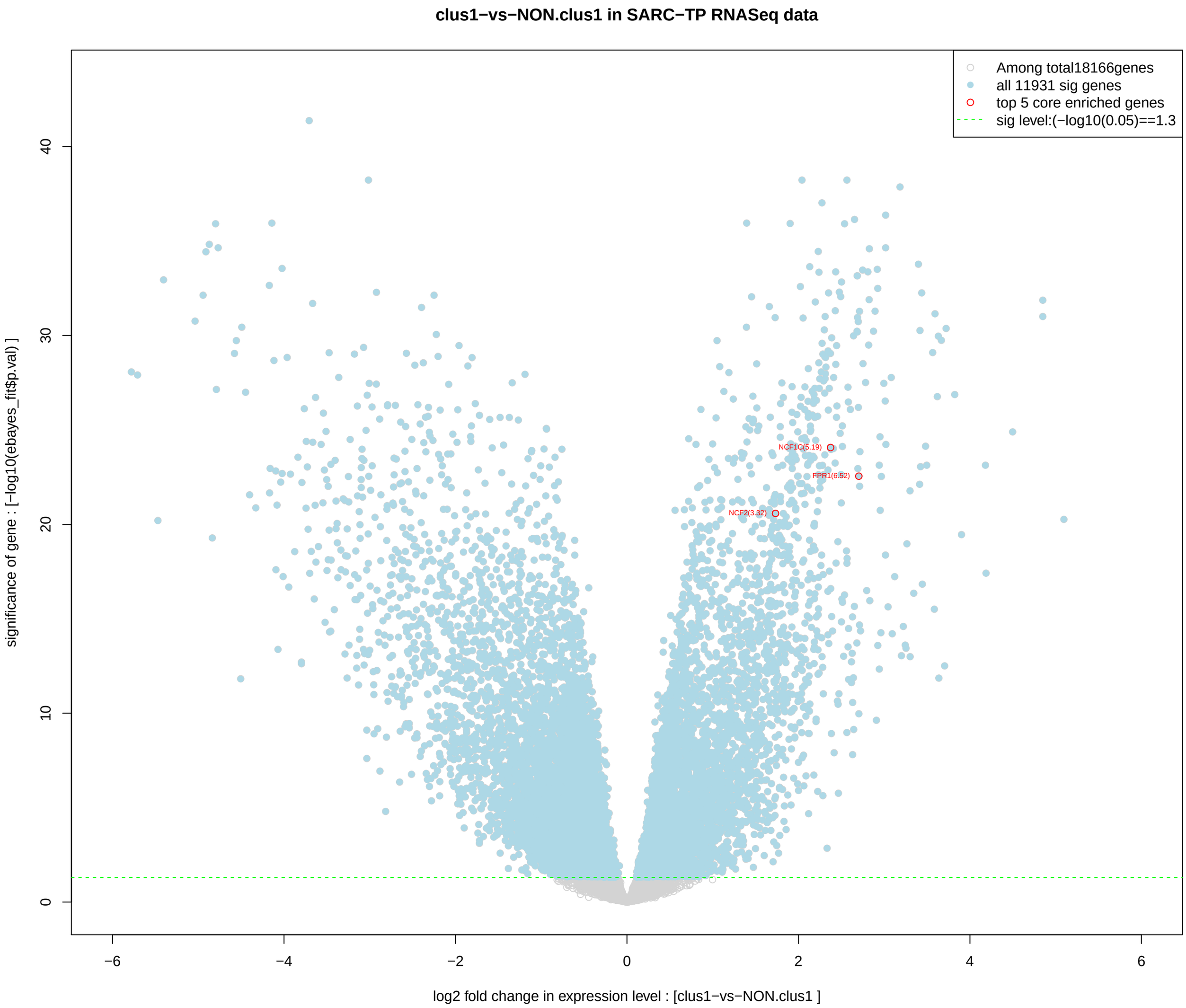
clus1−vs−NON.clus1 in SARC−TP RNASeq data
Among total18166genes
all 11931 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
NCF1C(5.19)
FPR1(6.52)
NCF2(3.32)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
−6
−4
−2
0
2
4
6