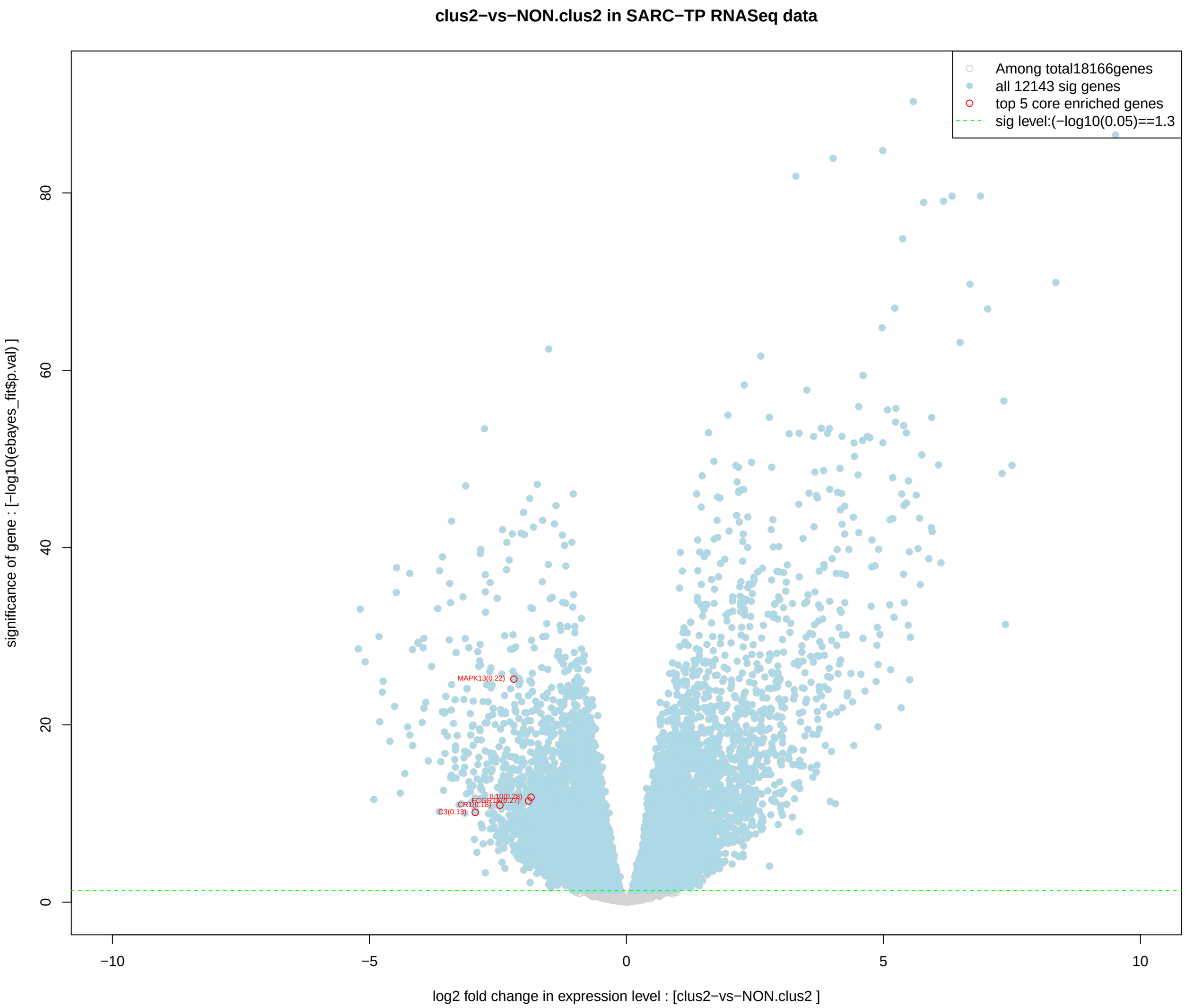
clus2−vs−NON.clus2 in SARC−TP RNASeq data
Among total18166genes
all 12143 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
MAPK13(0.22)
IL10(0.28)
FCGR1A(0.27)
CR1(0.18)
C3(0.13)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus2−vs−NON.clus2 ]
0
20
40
60
80
−10
−5
0
5
10