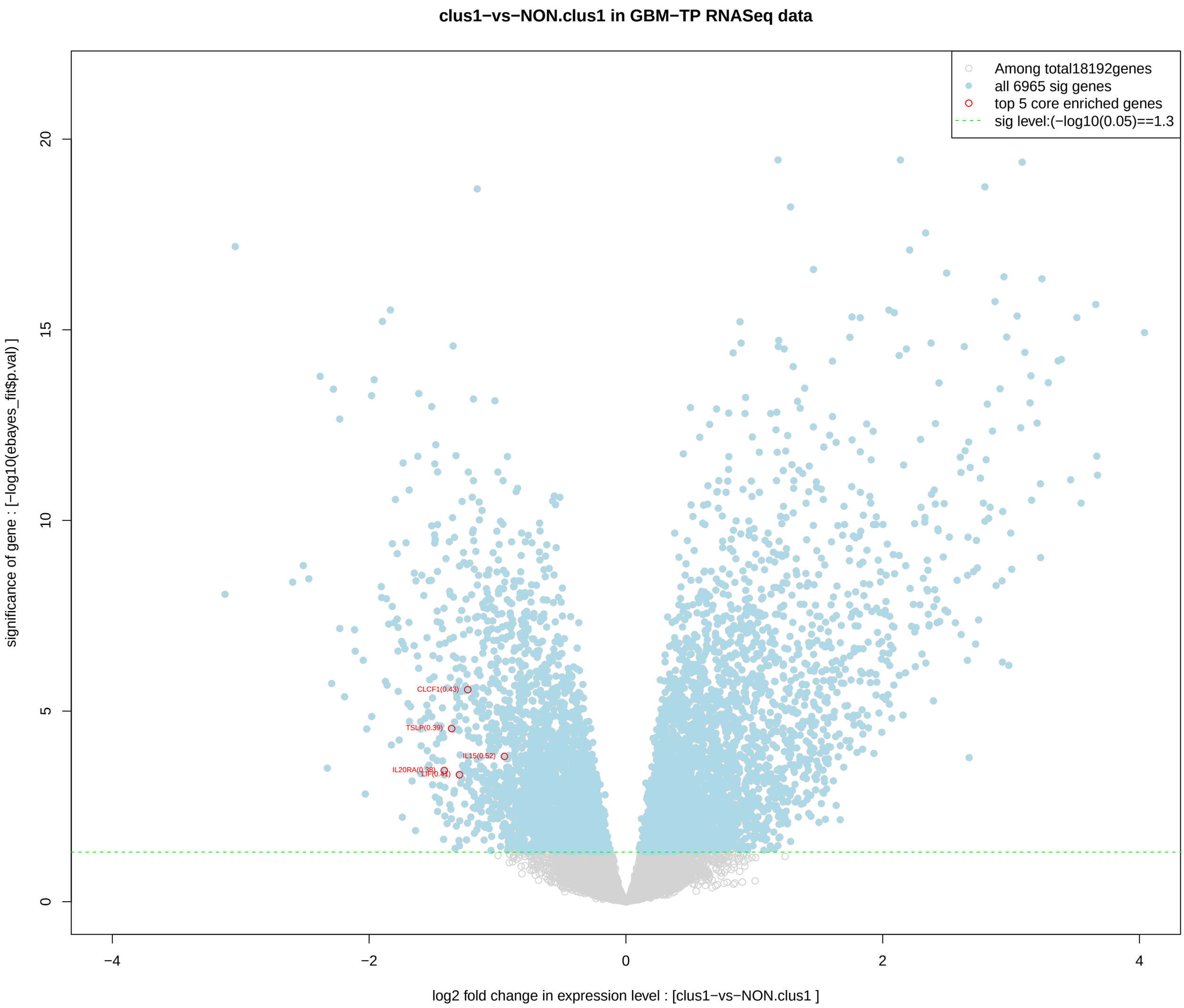
clus1−vs−NON.clus1 in GBM−TP RNASeq data
Among total18192genes
all 6965 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CLCF1(0.43)
TSLP(0.39)
IL15(0.52)
IL20RA(0.38)
LIF(0.41)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
−4
−2
0
2
4