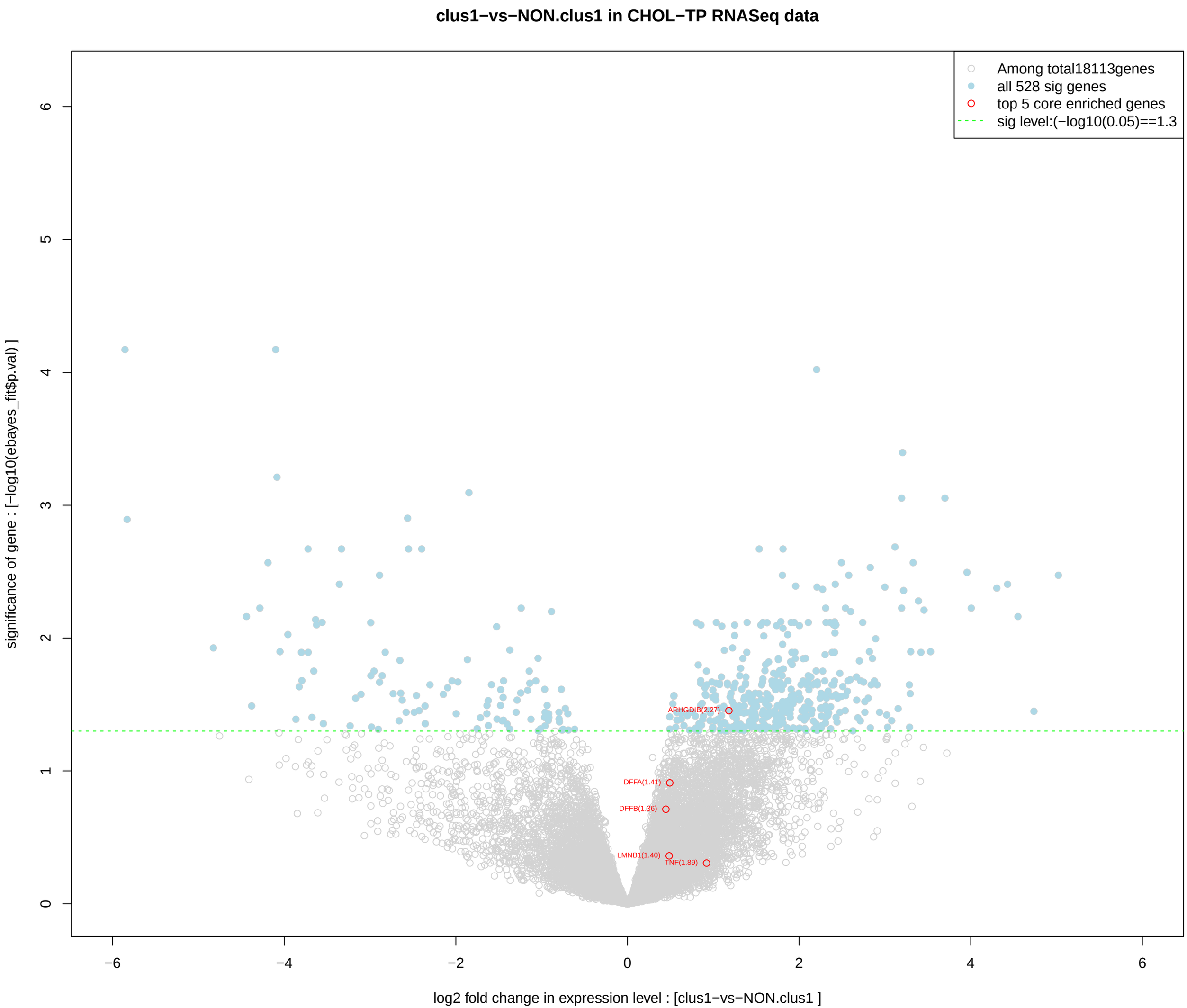
clus1−vs−NON.clus1 in CHOL−TP RNASeq data
Among total18113genes
all 528 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
ARHGDIB(2.27)
DFFA(1.41)
DFFB(1.36)
LMNB1(1.40)
TNF(1.89)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
1
2
3
4
5
6
−6
−4
−2
0
2
4
6