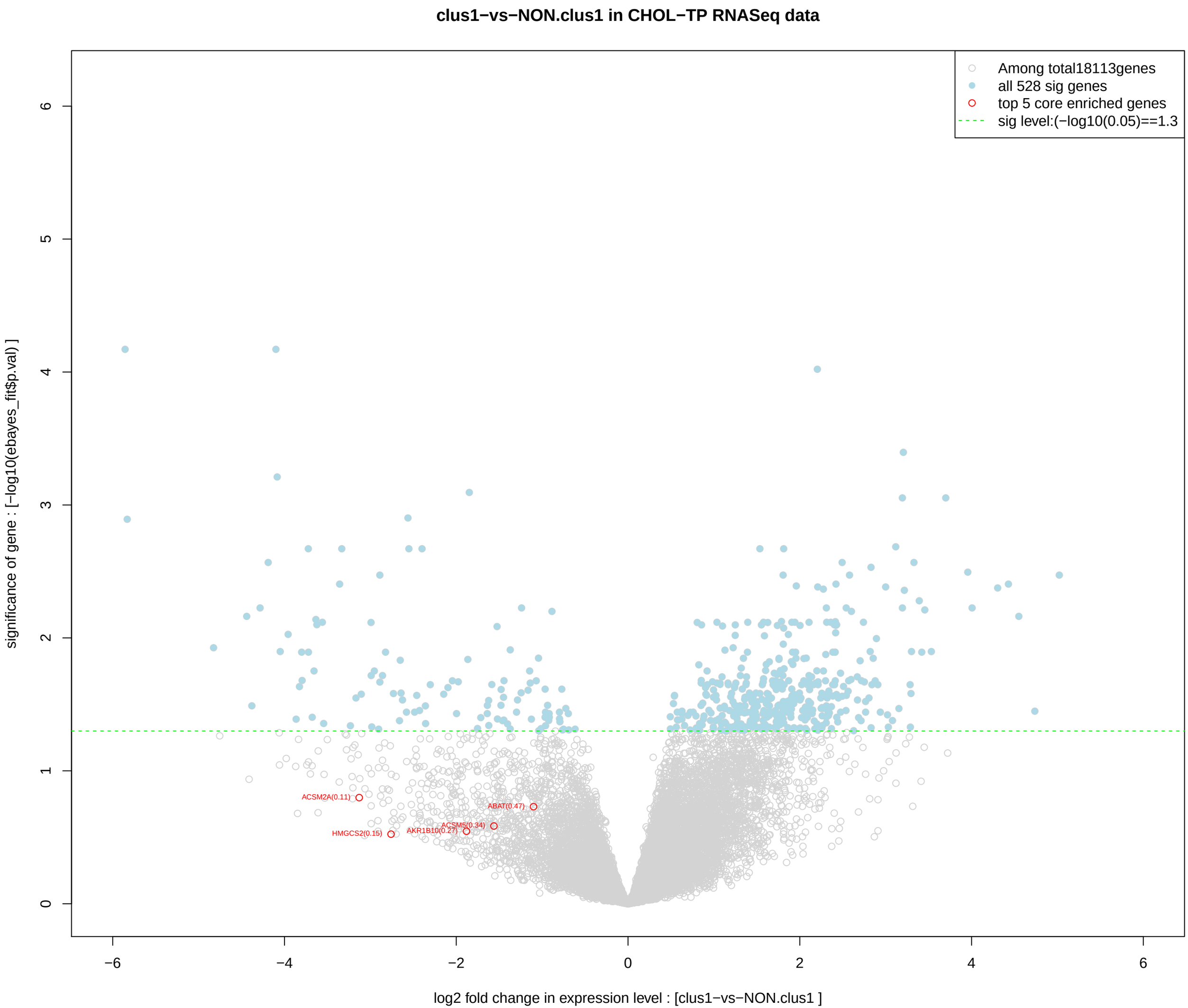
clus1−vs−NON.clus1 in CHOL−TP RNASeq data
Among total18113genes
all 528 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
ACSM2A(0.11)
HMGCS2(0.15)
AKR1B10(0.27)
ACSM5(0.34)
ABAT(0.47)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
−6
−4
−2
0
2
4
6
0
1
2
3
4
5
6