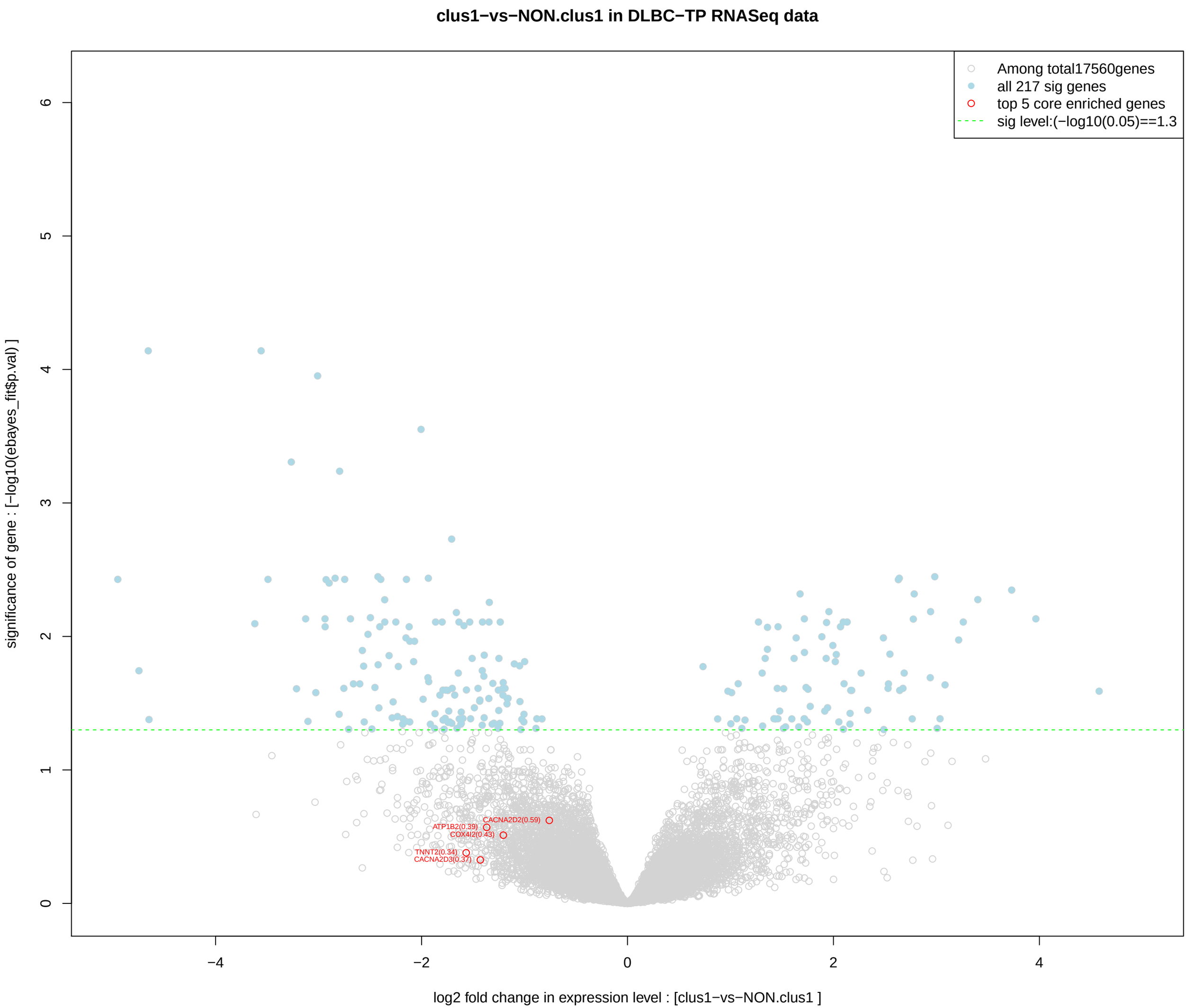
clus1−vs−NON.clus1 in DLBC−TP RNASeq data
Among total17560genes
all 217 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CACNA2D2(0.59)
ATP1B2(0.39)
COX4I2(0.43)
TNNT2(0.34)
CACNA2D3(0.37)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
1
2
3
4
5
6
−4
−2
0
2
4