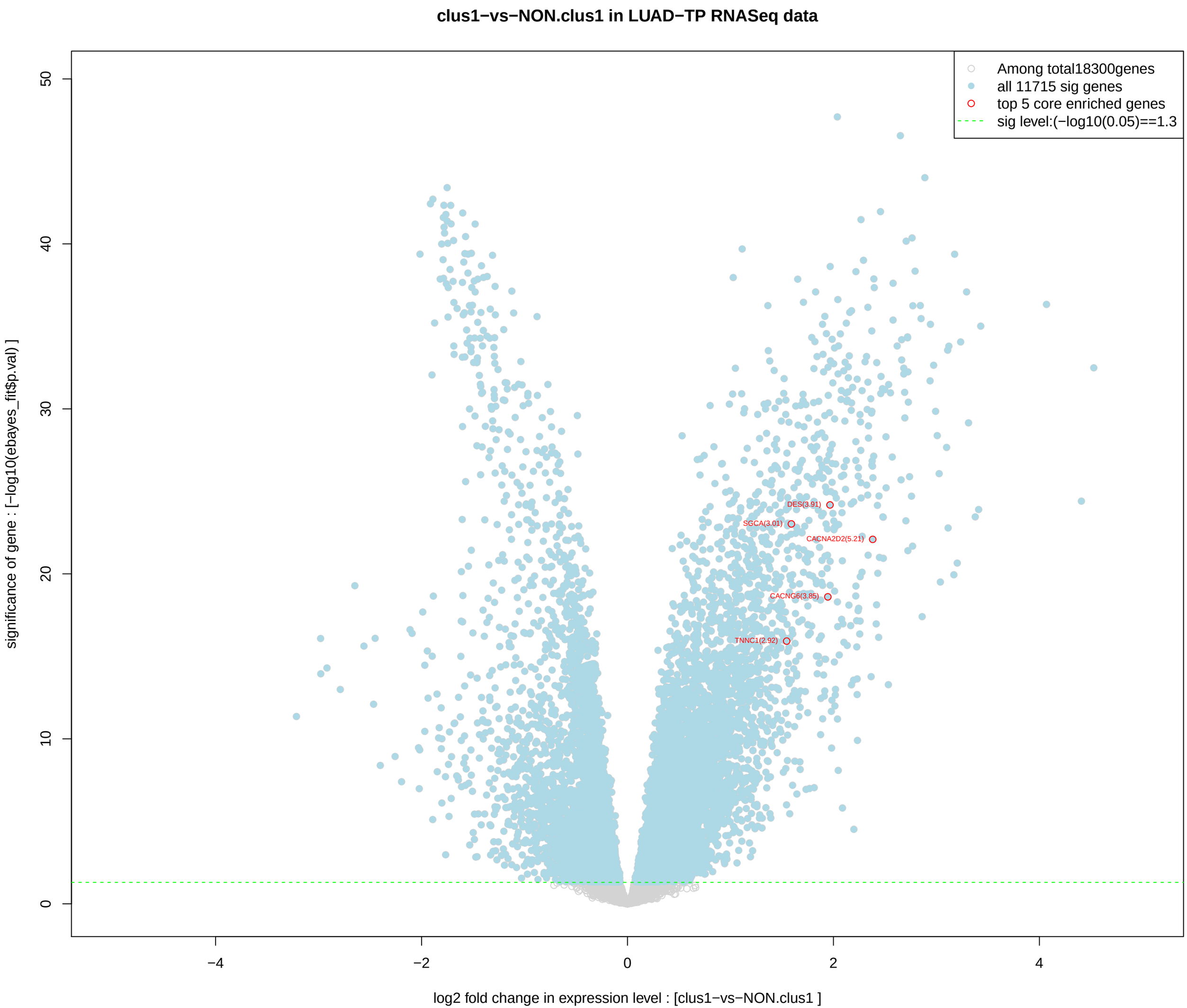
clus1−vs−NON.clus1 in LUAD−TP RNASeq data
Among total18300genes
all 11715 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
DES(3.91)
SGCA(3.01)
CACNA2D2(5.21)
CACNG6(3.85)
TNNC1(2.92)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus1−vs−NON.clus1 ]
0
10
20
30
40
50
−4
−2
0
2
4