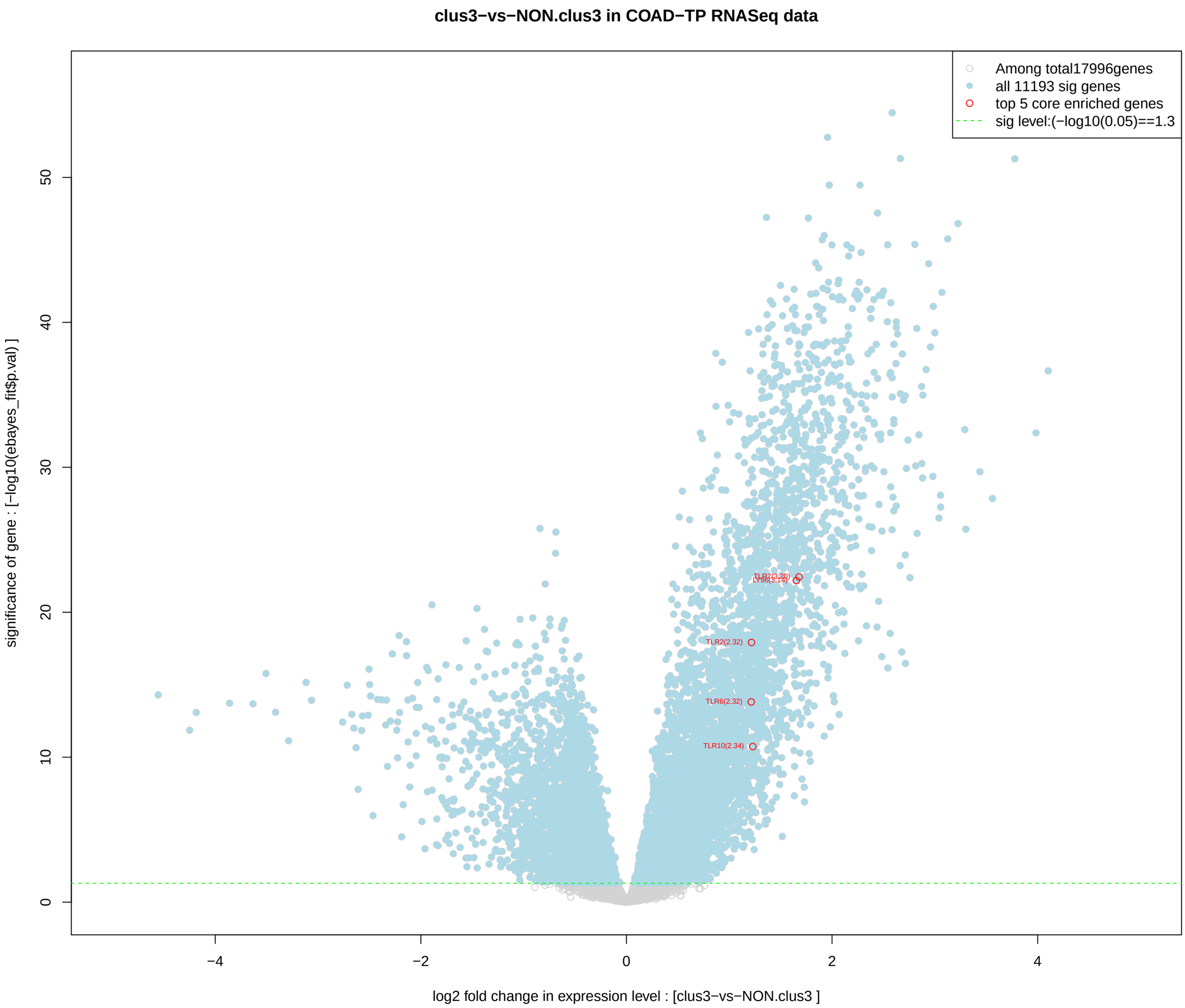
clus3−vs−NON.clus3 in COAD−TP RNASeq data
Among total17996genes
all 11193 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
TLR7(3.20)
LY96(3.14)
TLR2(2.32)
TLR6(2.32)
TLR10(2.34)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus3−vs−NON.clus3 ]
0
10
20
30
40
50
−4
−2
0
2
4