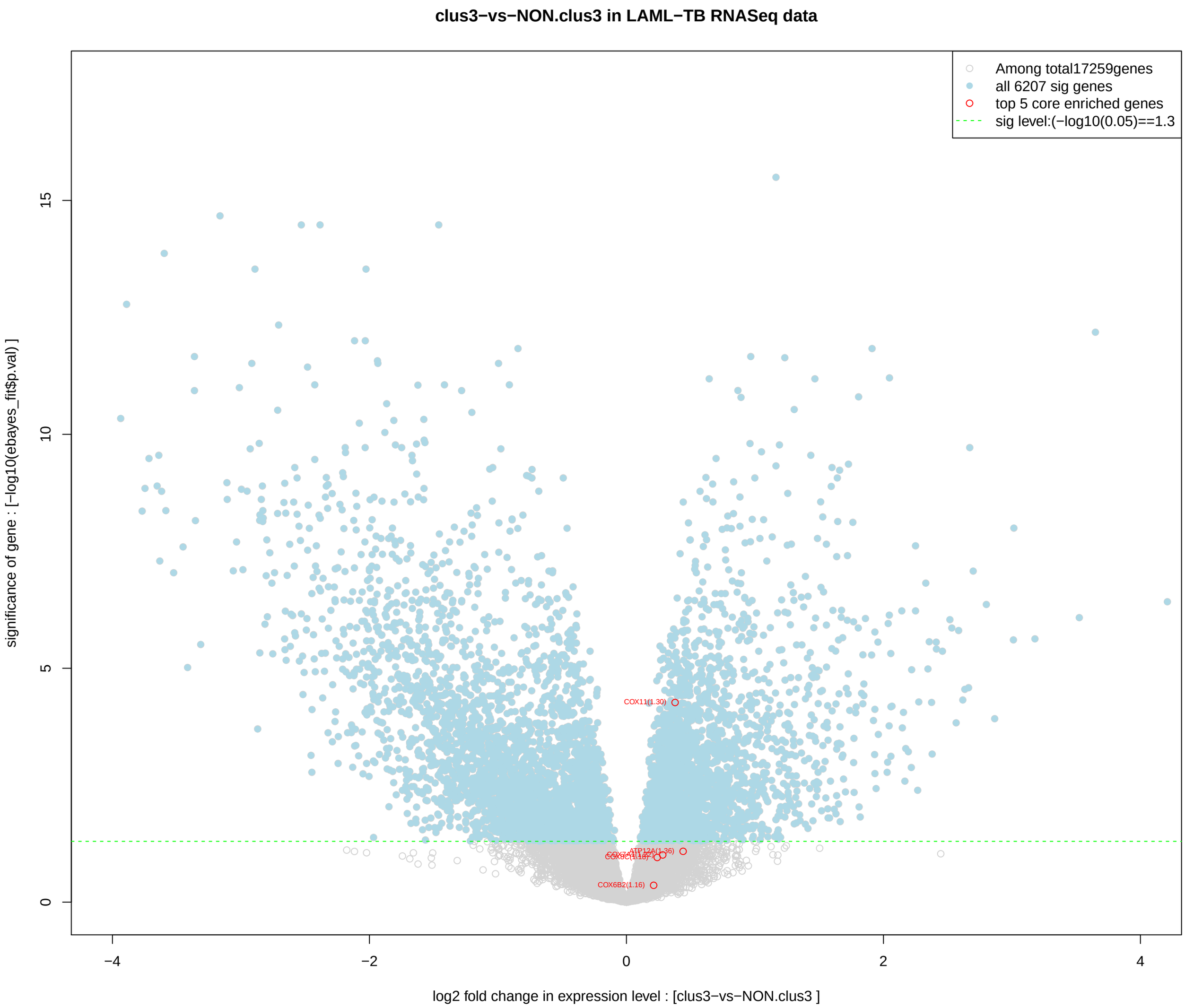
clus3−vs−NON.clus3 in LAML−TB RNASeq data
Among total17259genes
all 6207 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
COX11(1.30)
ATP12A(1.36)
COX6B2(1.16)
0
5
10
15
−4
−2
0
2
4