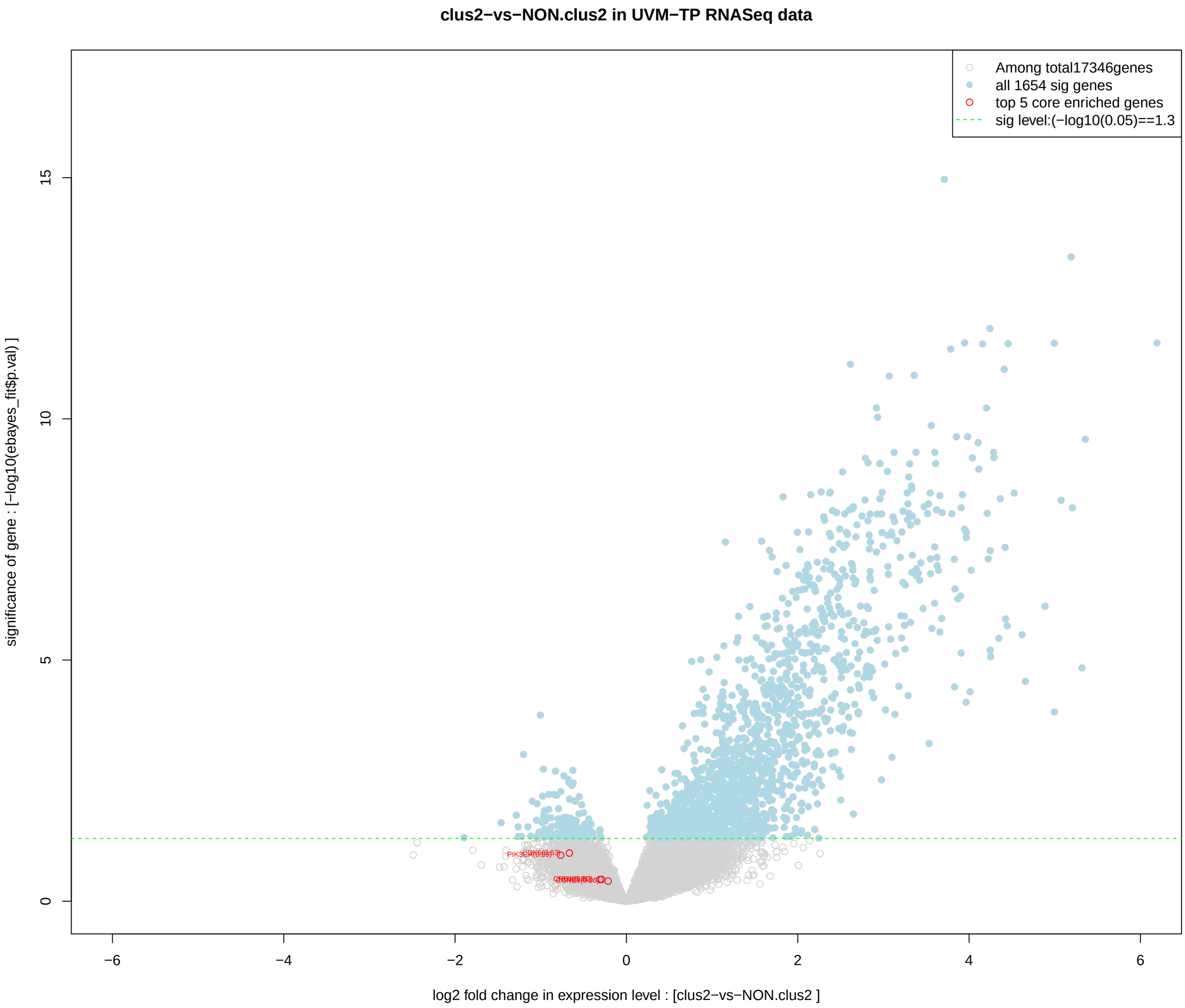
clus2−vs−NON.clus2 in UVM−TP RNASeq data
Among total17346genes
all 1654 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
5
10
15
−6
−4
−2
0
2
4
6