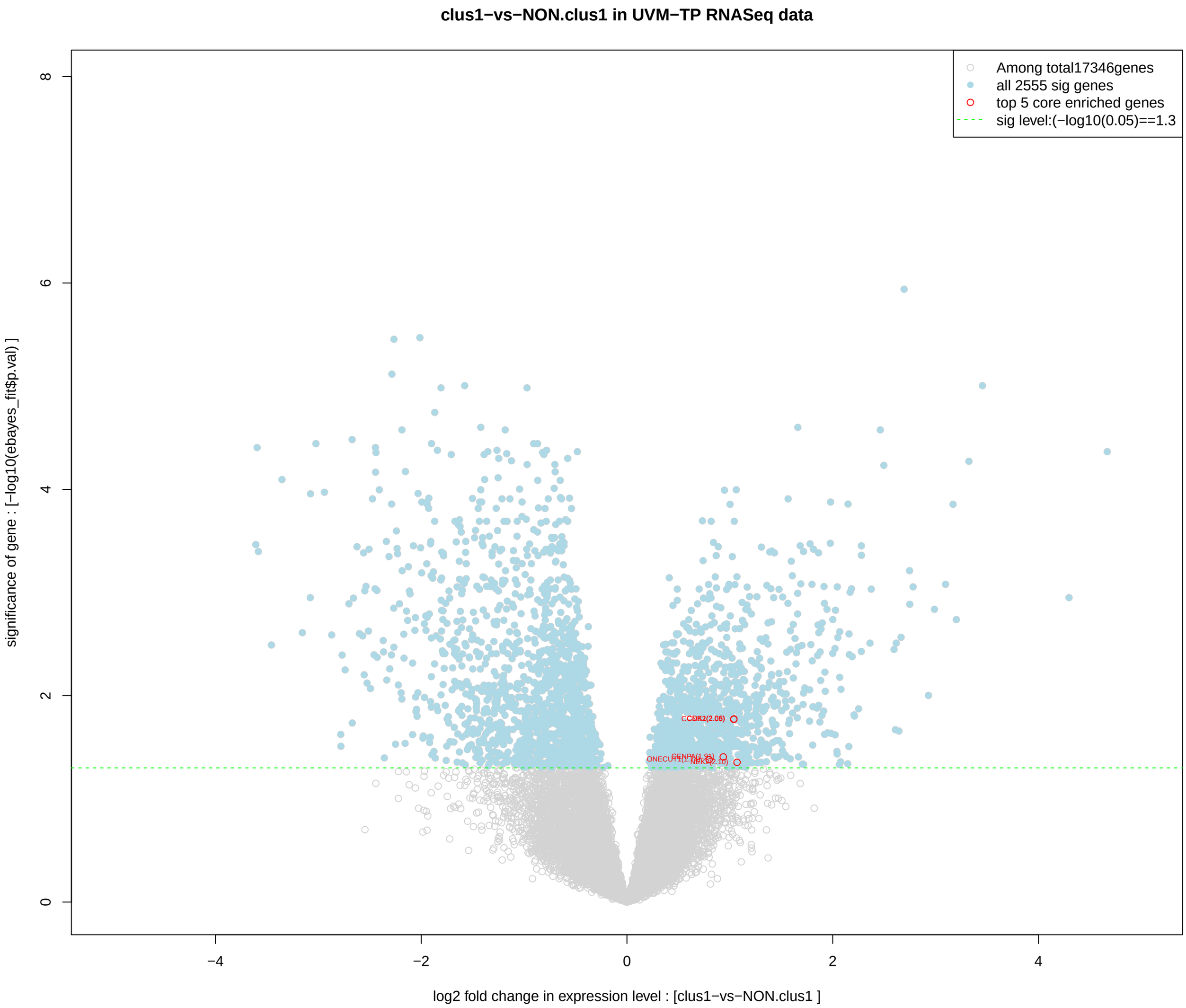
clus1−vs−NON.clus1 in UVM−TP RNASeq data
Among total17346genes
all 2555 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CCNB2(2.05)
CENPA(1.91)
ONECUT1(1.79)
NEK2(2.10)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
2
4
6
8
−4
−2
0
2
4