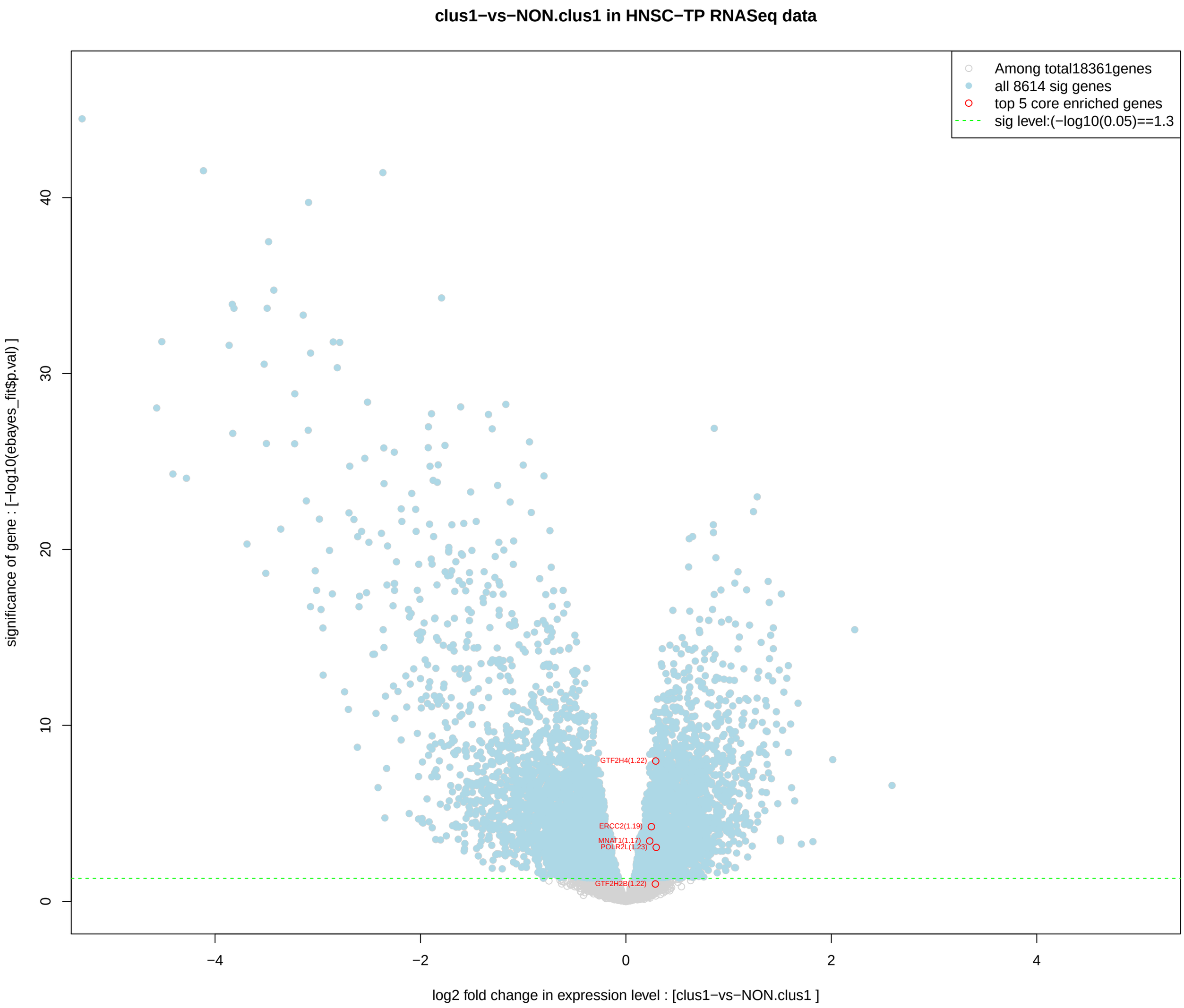
clus1−vs−NON.clus1 in HNSC−TP RNASeq data
Among total18361genes
all 8614 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GTF2H4(1.22)
ERCC2(1.19)
MNAT1(1.17)
POLR2L(1.23)
GTF2H2B(1.22)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
−4
−2
0
2
4