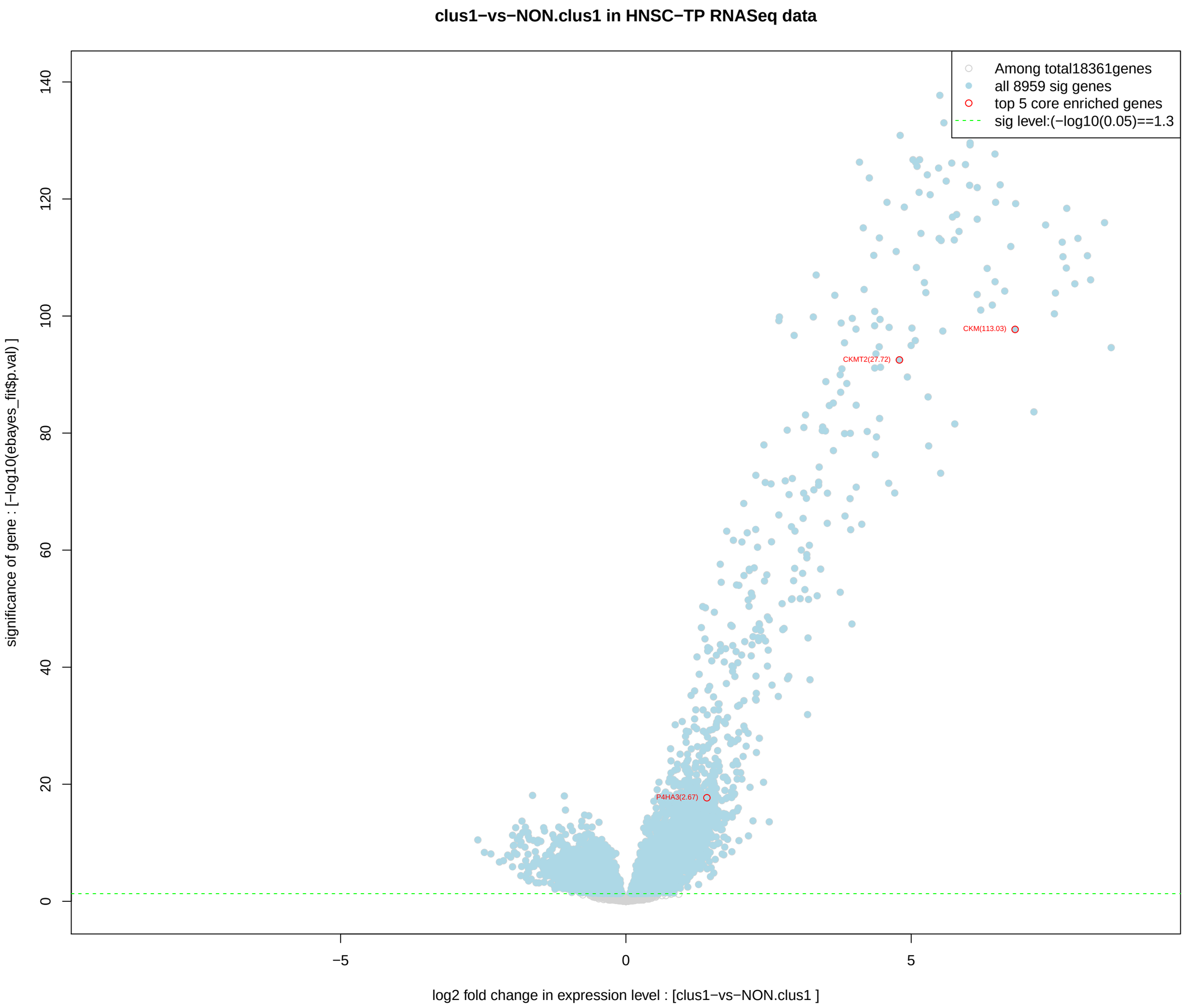
clus1−vs−NON.clus1 in HNSC−TP RNASeq data
Among total18361genes
all 8959 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CKM(113.03)
CKMT2(27.72)
P4HA3(2.67)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
20
40
60
80
100
120
140
−5
0
5