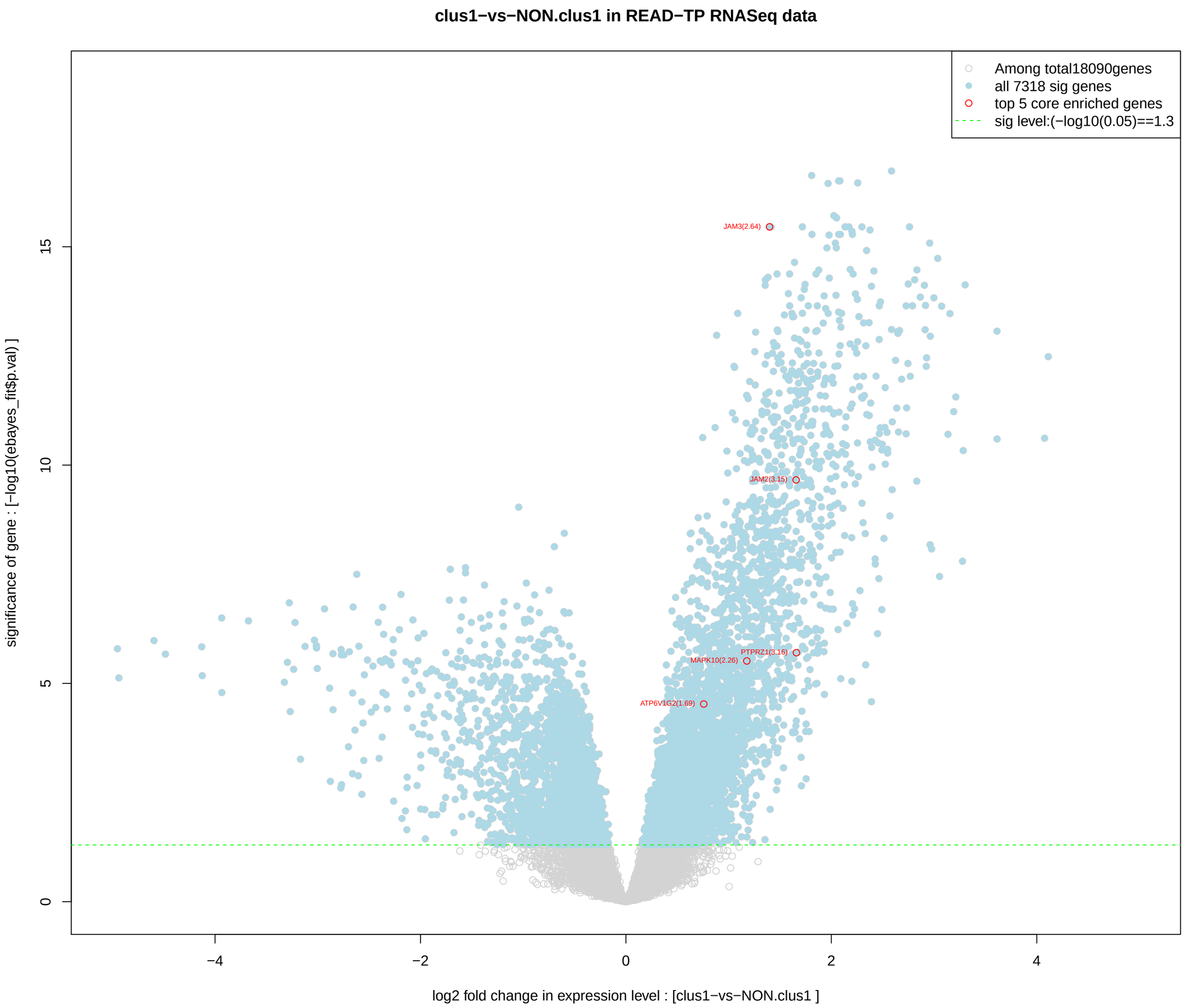
clus1−vs−NON.clus1 in READ−TP RNASeq data
Among total18090genes
all 7318 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
JAM3(2.64)
JAM2(3.15)
PTPRZ1(3.16)
MAPK10(2.26)
ATP6V1G2(1.69)
significance of gene : [−log10(ebayes_fit$p.val)]
0
5
10
15
−4
−2
0
2
4
log2 fold change in expression level : [clus1−vs−NON.clus1]