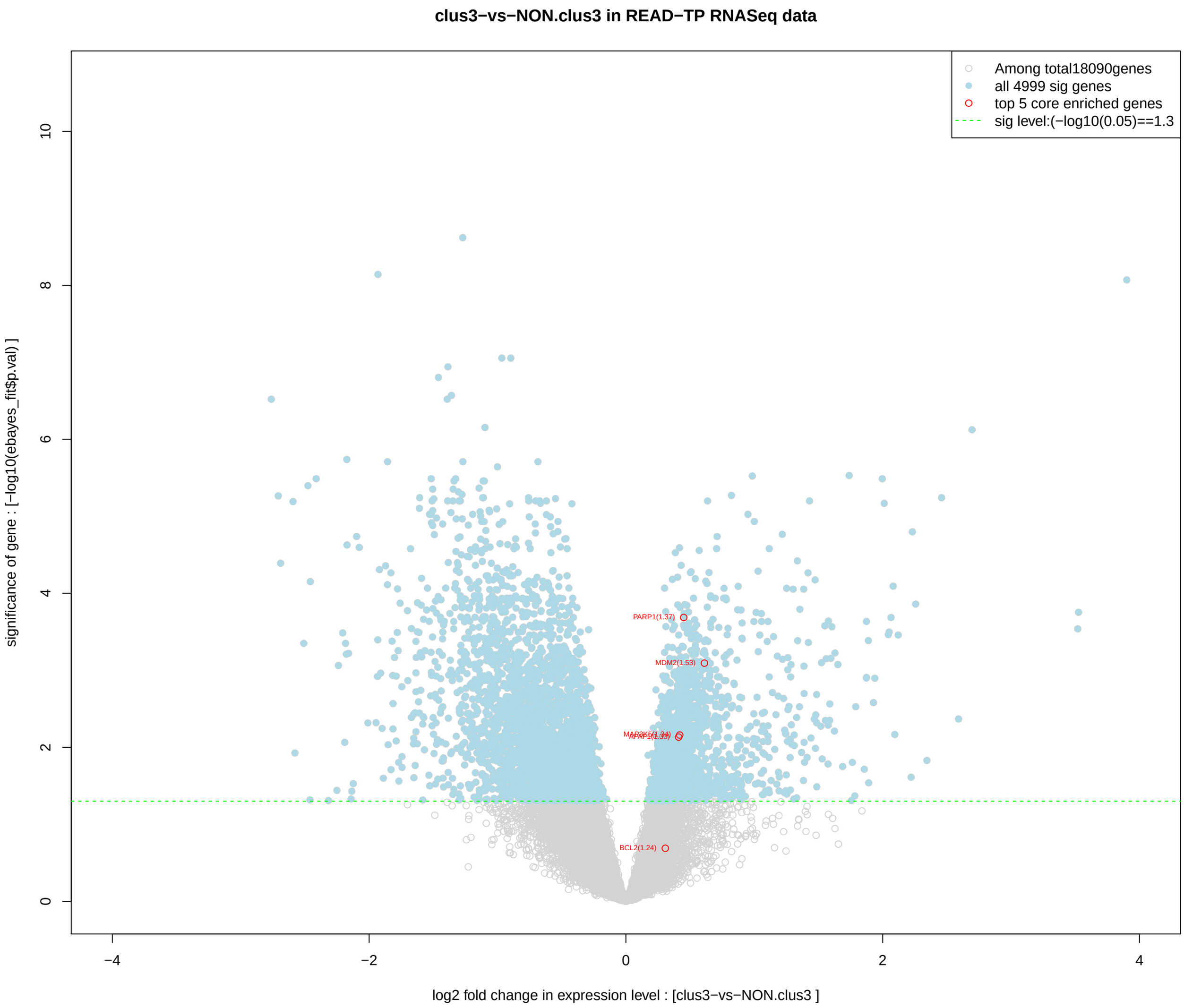
clus3−vs−NON.clus3 in READ−TP RNASeq data
Among total18090genes
all 4999 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PARP1(1.37)
MDM2(1.53)
MAP2K5(1.34)
APAF1(1.55)
BCL2(1.24)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
2
4
6
8
10
−4
−2
0
2
4