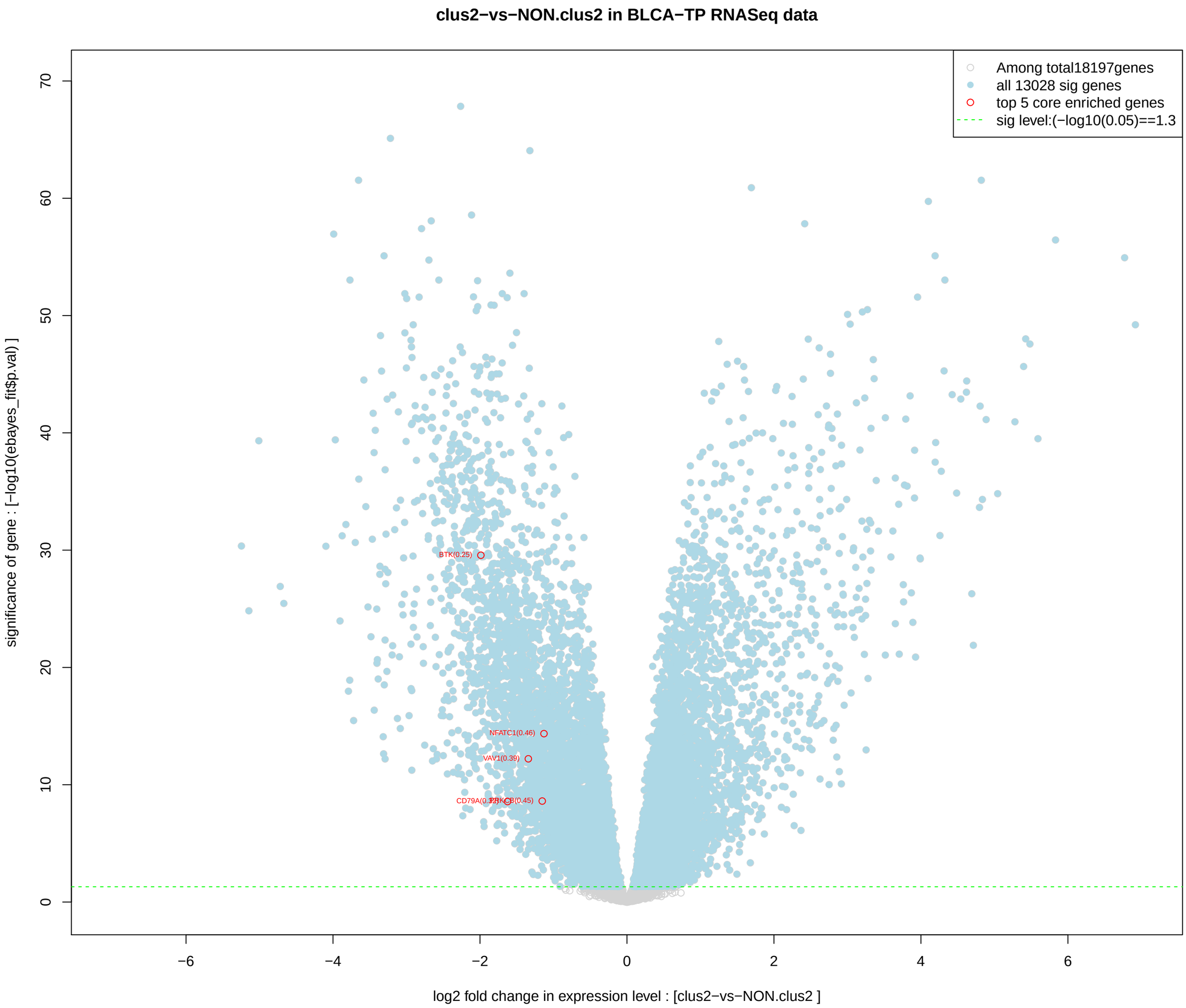
clus2−vs−NON.clus2 in BLCA−TP RNASeq data
Among total18197genes
all 13028 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
BTK(0.25)
NFATC1(0.46)
VAV1(0.39)
CD79A(0.32)
PRKCB(0.45)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
10
20
30
40
50
60
70
−6
−4
−2
0
2
4
6