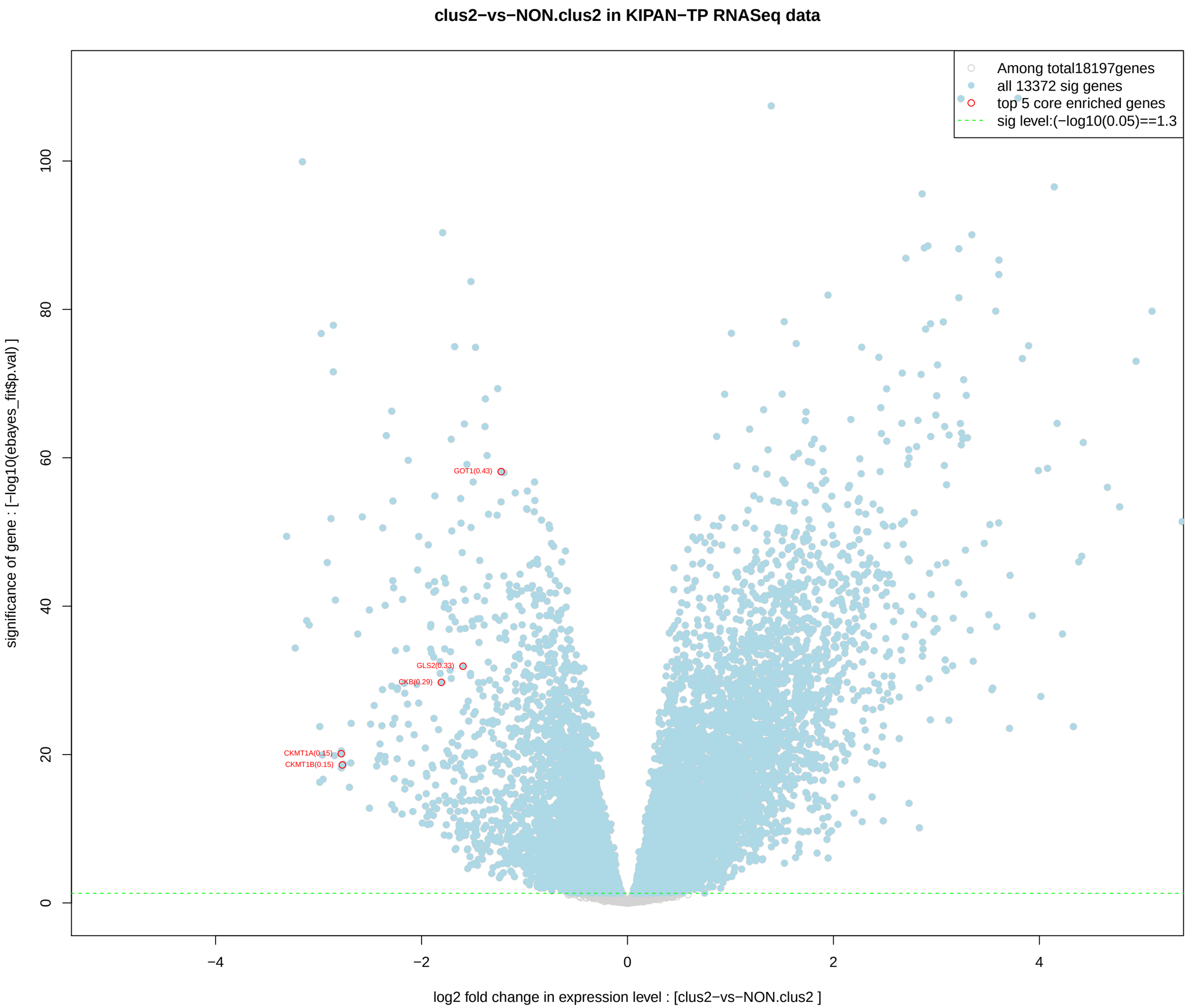
clus2−vs−NON.clus2 in KIPAN−TP RNASeq data
Among total18197genes
all 13372 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GOT1(0.43)
GLS2(0.33)
CKB(0.29)
CKMT1A(0.15)
CKMT1B(0.15)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus2−vs−NON.clus2 ]
0
20
40
60
80
100
−4
−2
0
2
4