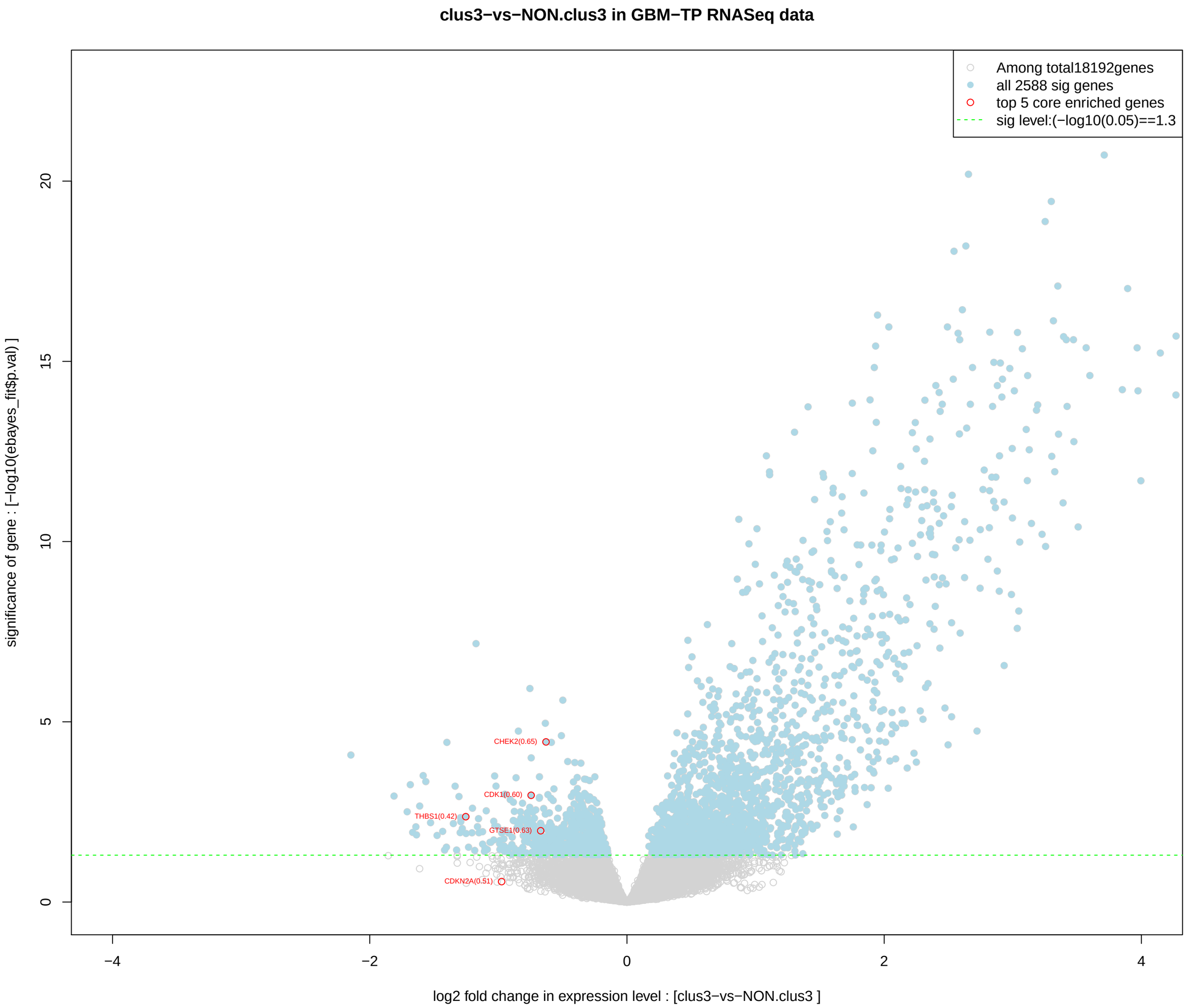
clus3−vs−NON.clus3 in GBM−TP RNASeq data
Among total18192genes
all 2588 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CHEK2(0.65)
CDK1(0.60)
THBS1(0.42)
GTSE1(0.63)
CDKN2A(0.51)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
5
10
15
20
−4
−2
0
2
4