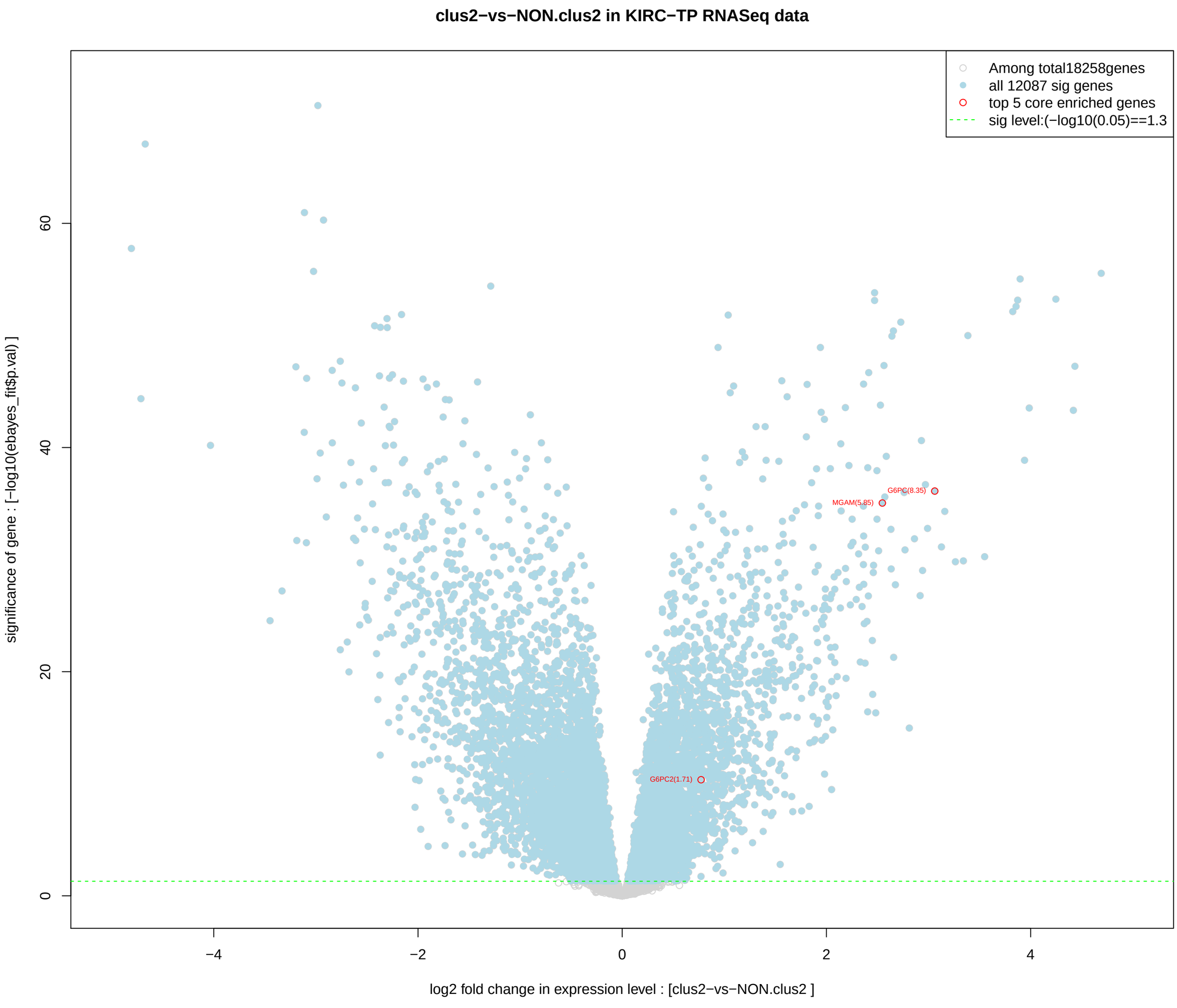
clus2−vs−NON.clus2 in KIRC−TP RNASeq data
Among total18258genes
all 12087 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
G6PC(8.35)
MGAM(5.85)
G6PC2(1.71)
significance of gene : [−log10(ebayes_fit$p.val)]
0
20
40
60
−4
−2
0
2
4
log2 fold change in expression level : [clus2−vs−NON.clus2]