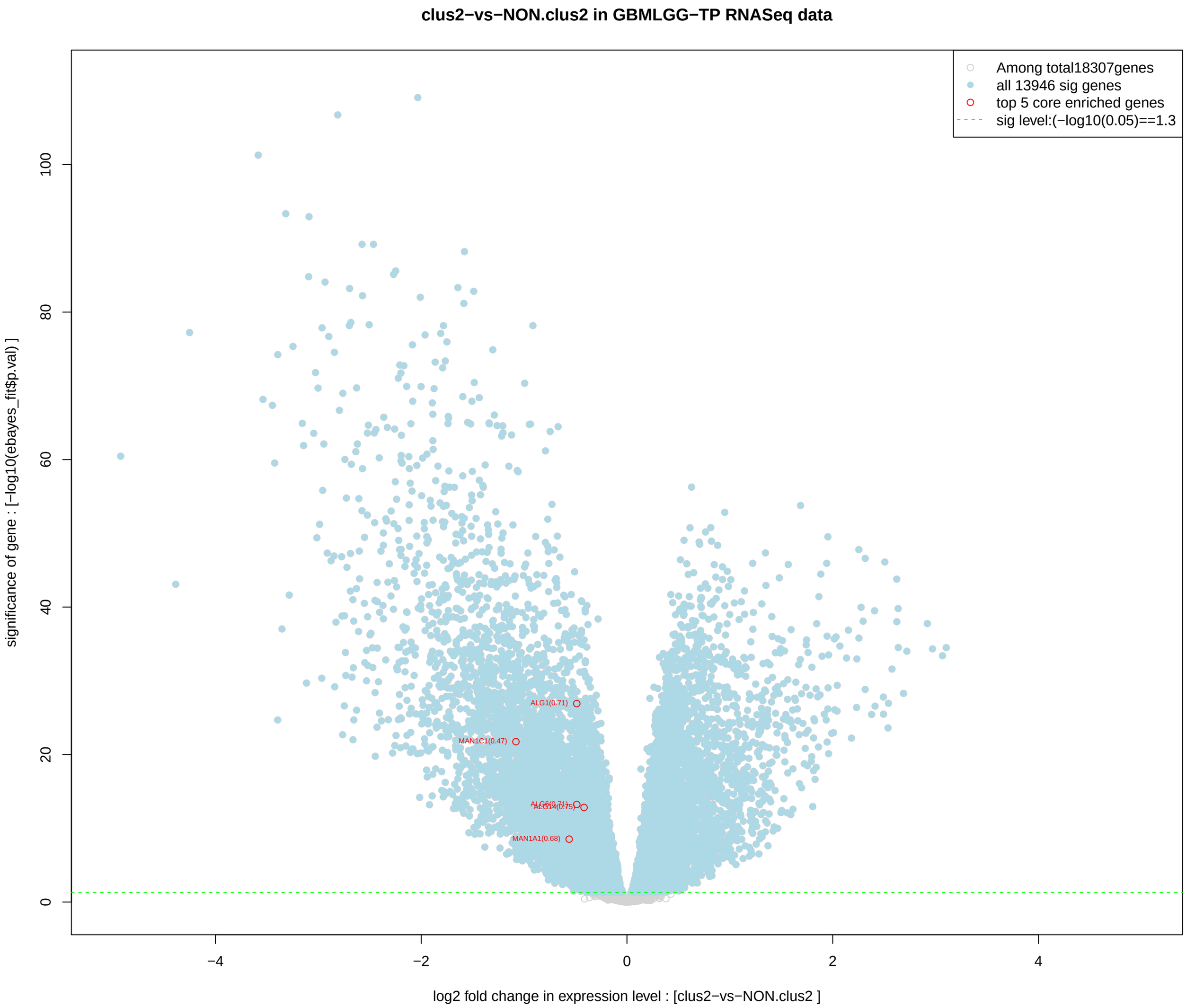
clus2−vs−NON.clus2 in GBMLGG−TP RNASeq data
Among total18307genes
all 13946 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
ALG1(0.71)
MAN1C1(0.47)
ALG6(0.71)
ALG14(0.75)
MAN1A1(0.68)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
20
40
60
80
100
−4
−2
0
2
4