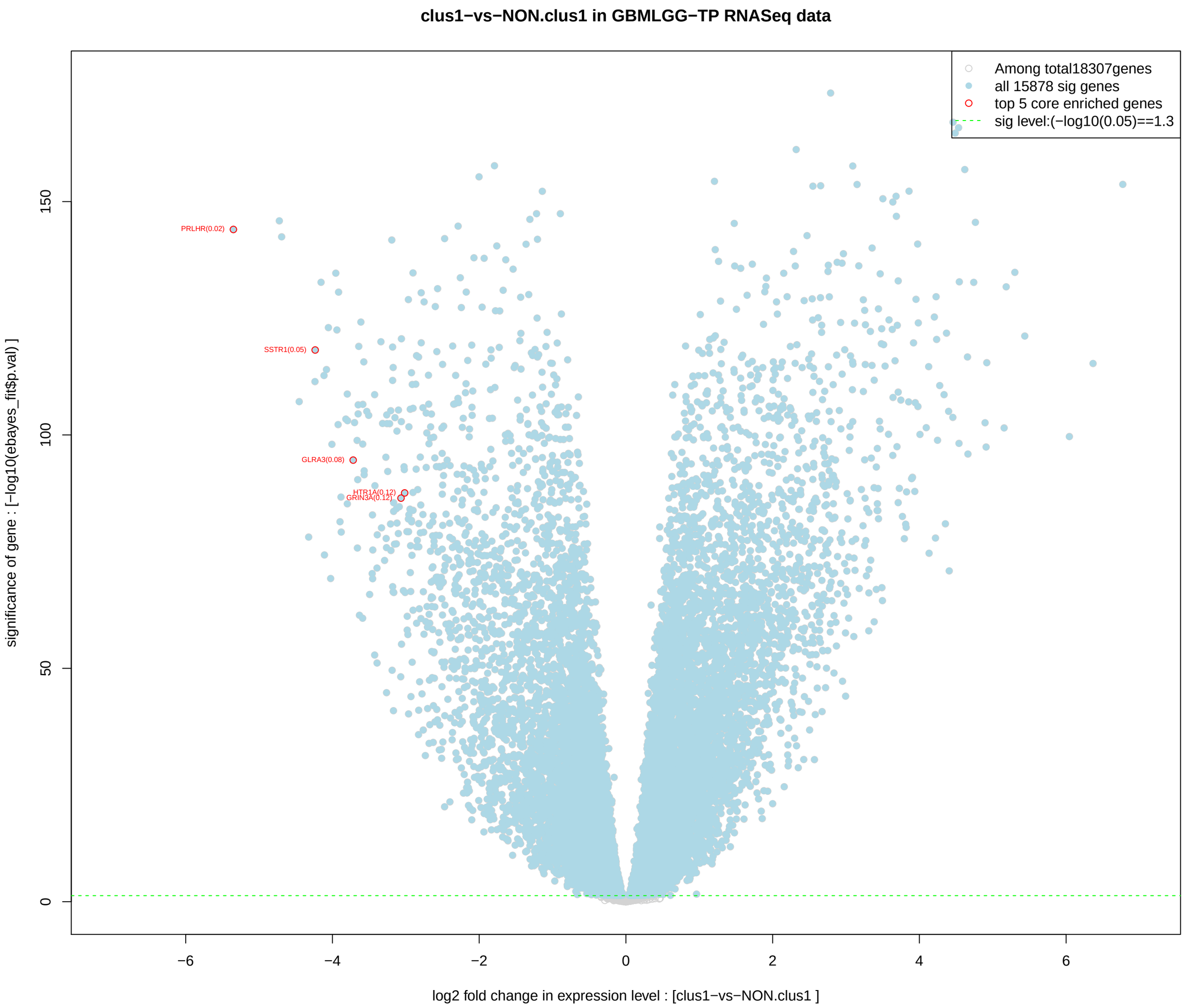
clus1−vs−NON.clus1 in GBMLGG−TP RNASeq data
Among total18307genes
all 15878 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PRLHR(0.02)
SSTR1(0.05)
GLRA3(0.08)
HTR1A(0.12)
GRIN3A(0.12)
significance of gene : [−log10(ebayes_fit$p.val)]
0
50
100
150
−6
−4
−2
0
2
4
6
log2 fold change in expression level : [clus1−vs−NON.clus1]