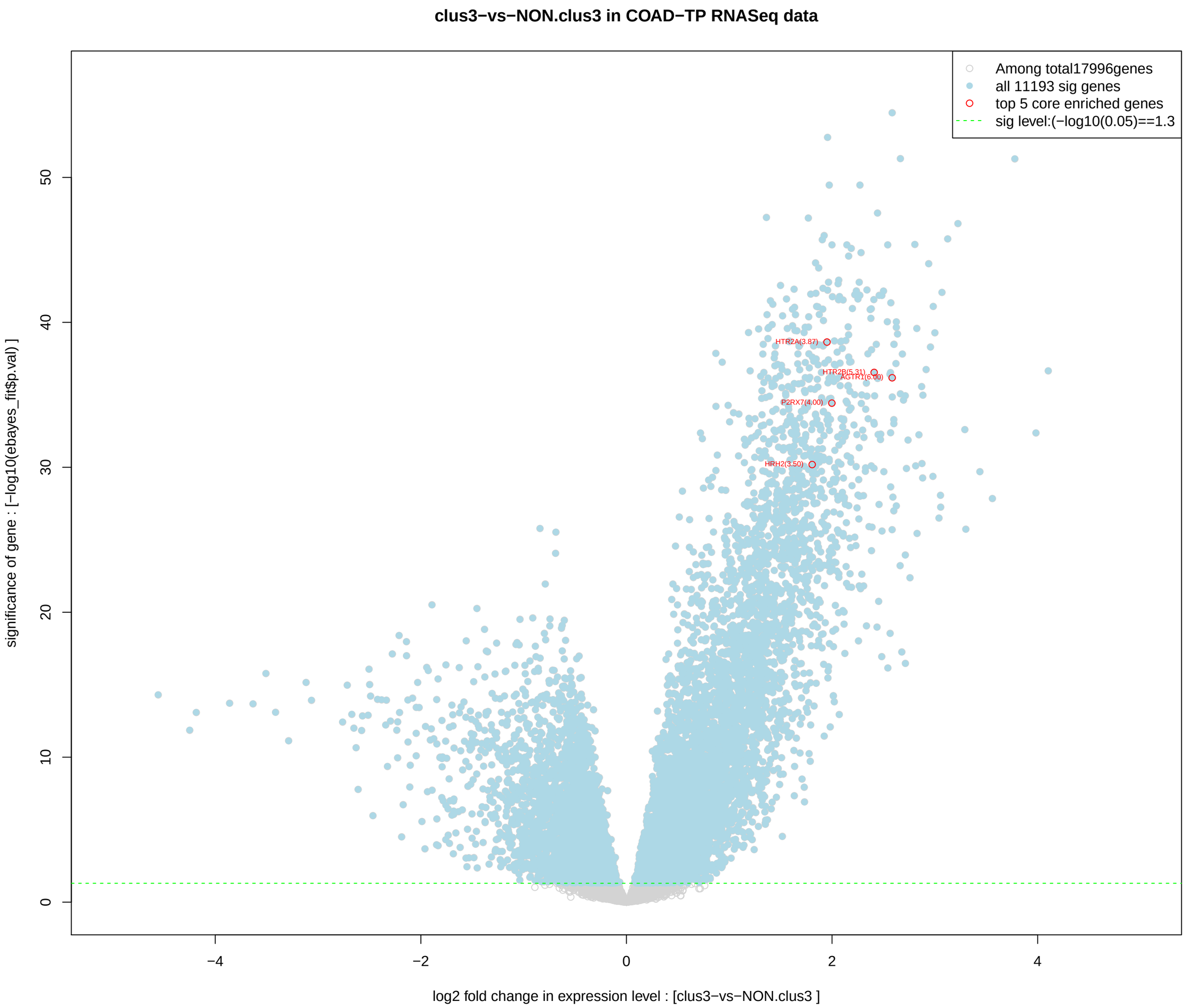
clus3−vs−NON.clus3 in COAD−TP RNASeq data
Among total17996genes
all 11193 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
HTR2A(3.87)
HTR2B(5.31)
AGTR1(6.00)
P2RX7(4.00)
HRH2(3.50)
significance of gene : [−log10(ebayes_fit$p.val)]
0
10
20
30
40
50
−4
−2
0
2
4
log2 fold change in expression level : [clus3−vs−NON.clus3]