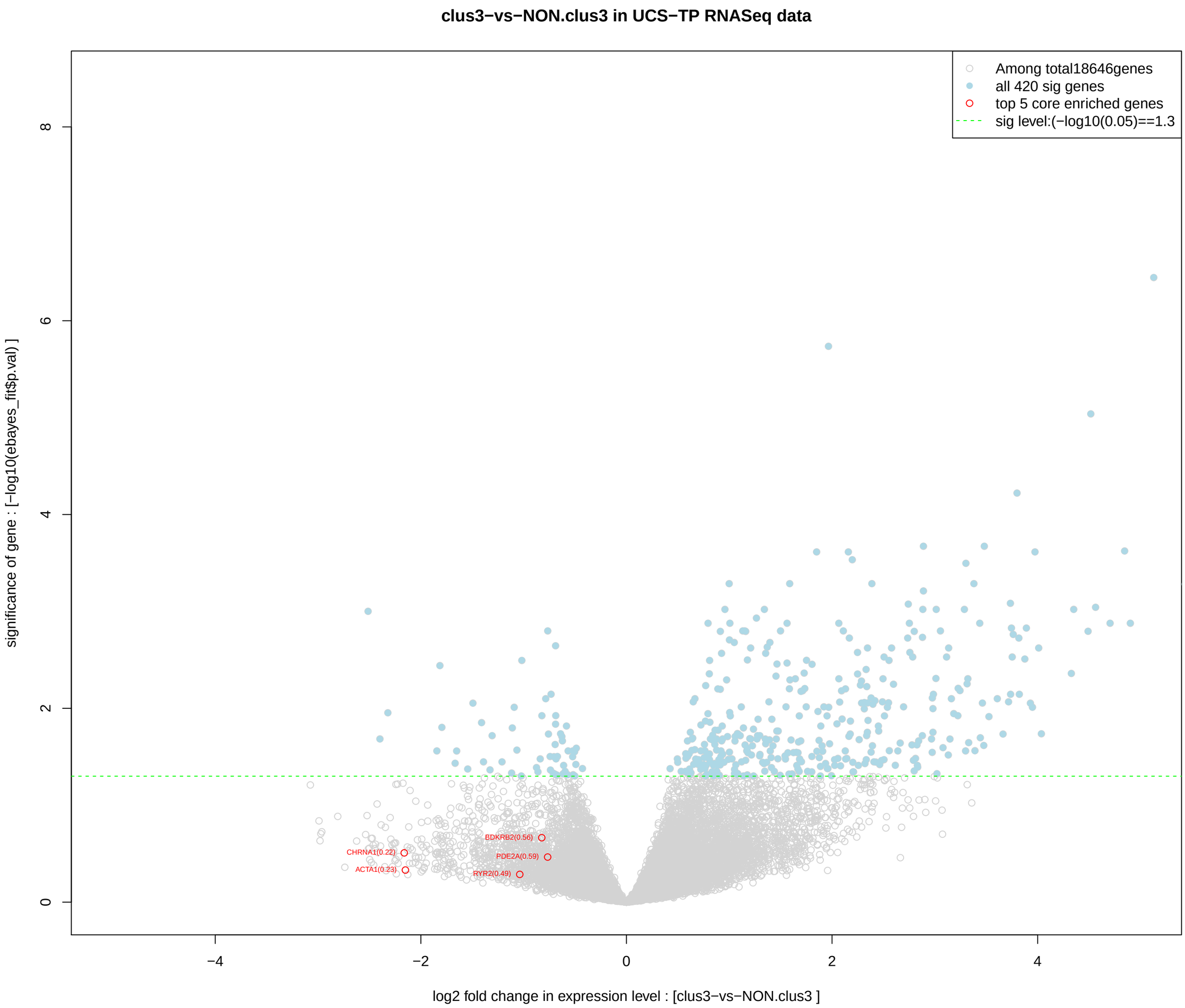
clus3−vs−NON.clus3 in UCS−TP RNASeq data
Among total18646genes
all 420 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
BDKRB2(0.56)
CHRNA1(0.22)
PDE2A(0.59)
ACTA1(0.23)
RYR2(0.49)
0
2
4
6
8
−4
−2
0
2
4