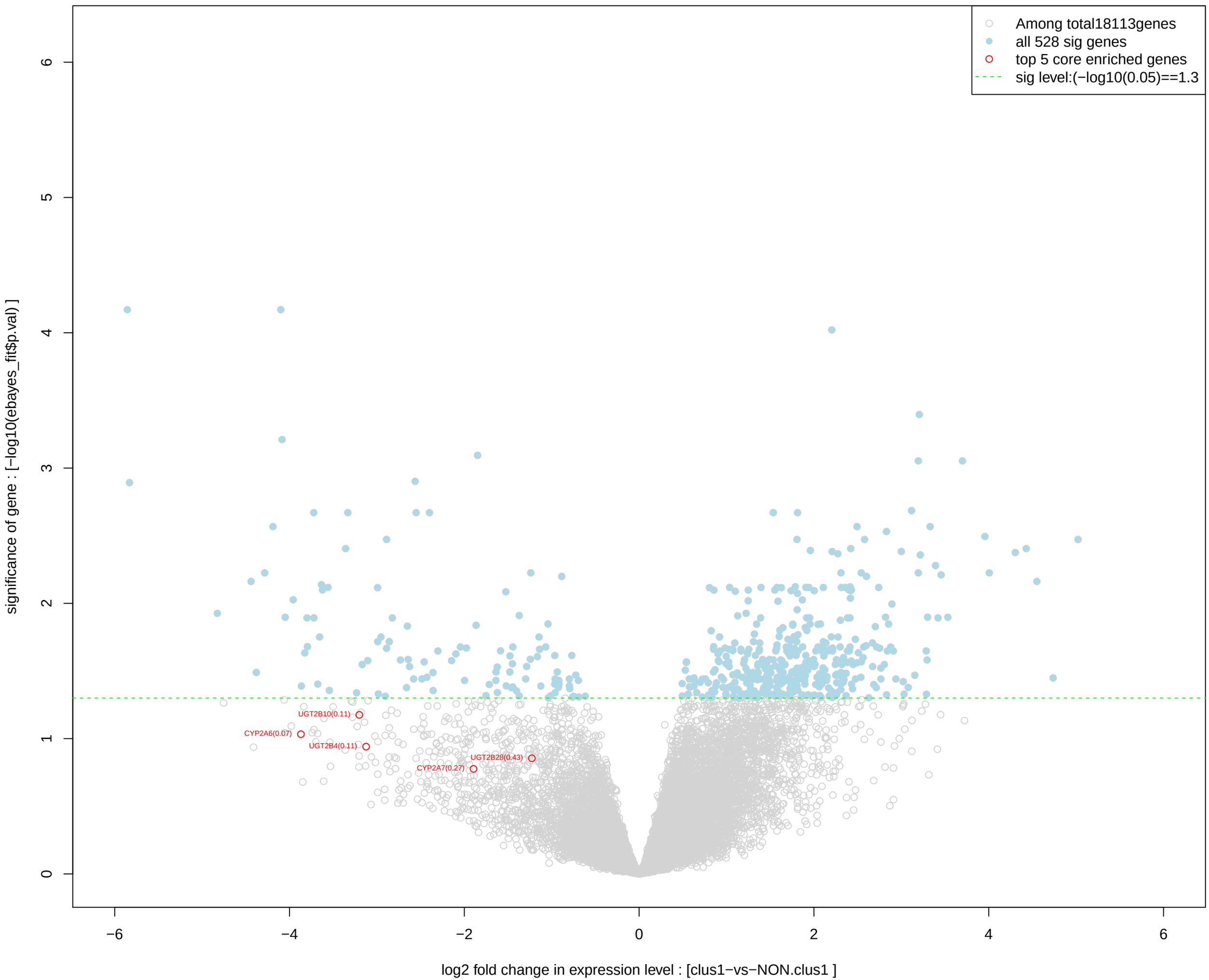
clus1−vs−NON.clus1 in CHOL−TP RNASeq data
Among total18113genes
all 528 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
UGT2B10(0.11)
CYP2A6(0.07)
UGT2B4(0.11)
UGT2B28(0.43)
CYP2A7(0.27)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
−6
−4
−2
0
2
4
6
0
1
2
3
4
5
6