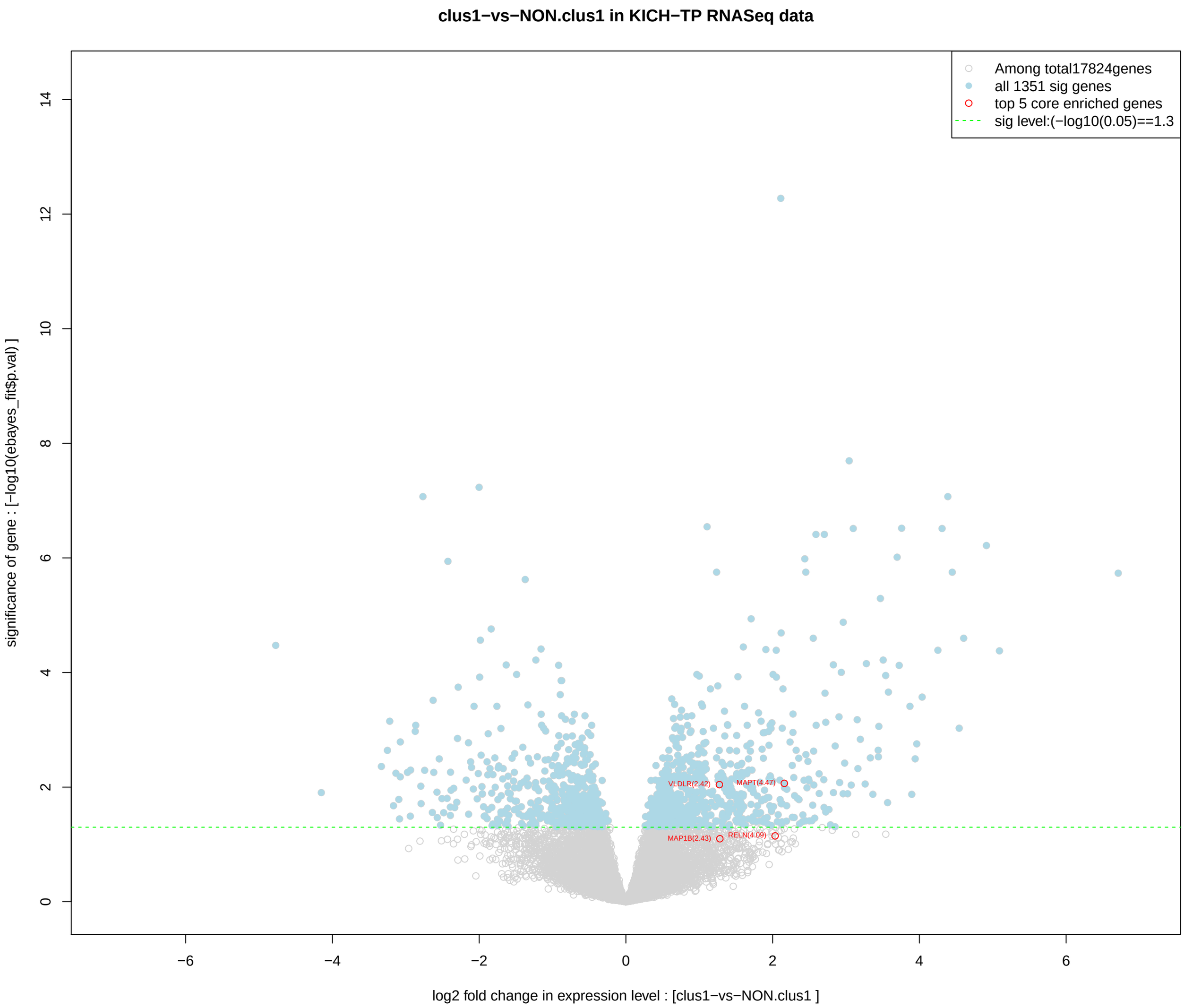
clus1−vs−NON.clus1 in KICH−TP RNASeq data
Among total17824genes
all 1351 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
VLDLR(2.42)
MAPT(4.47)
MAP1B(2.43)
RELN(4.09)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
2
4
6
8
10
12
14
−6
−4
−2
0
2
4
6