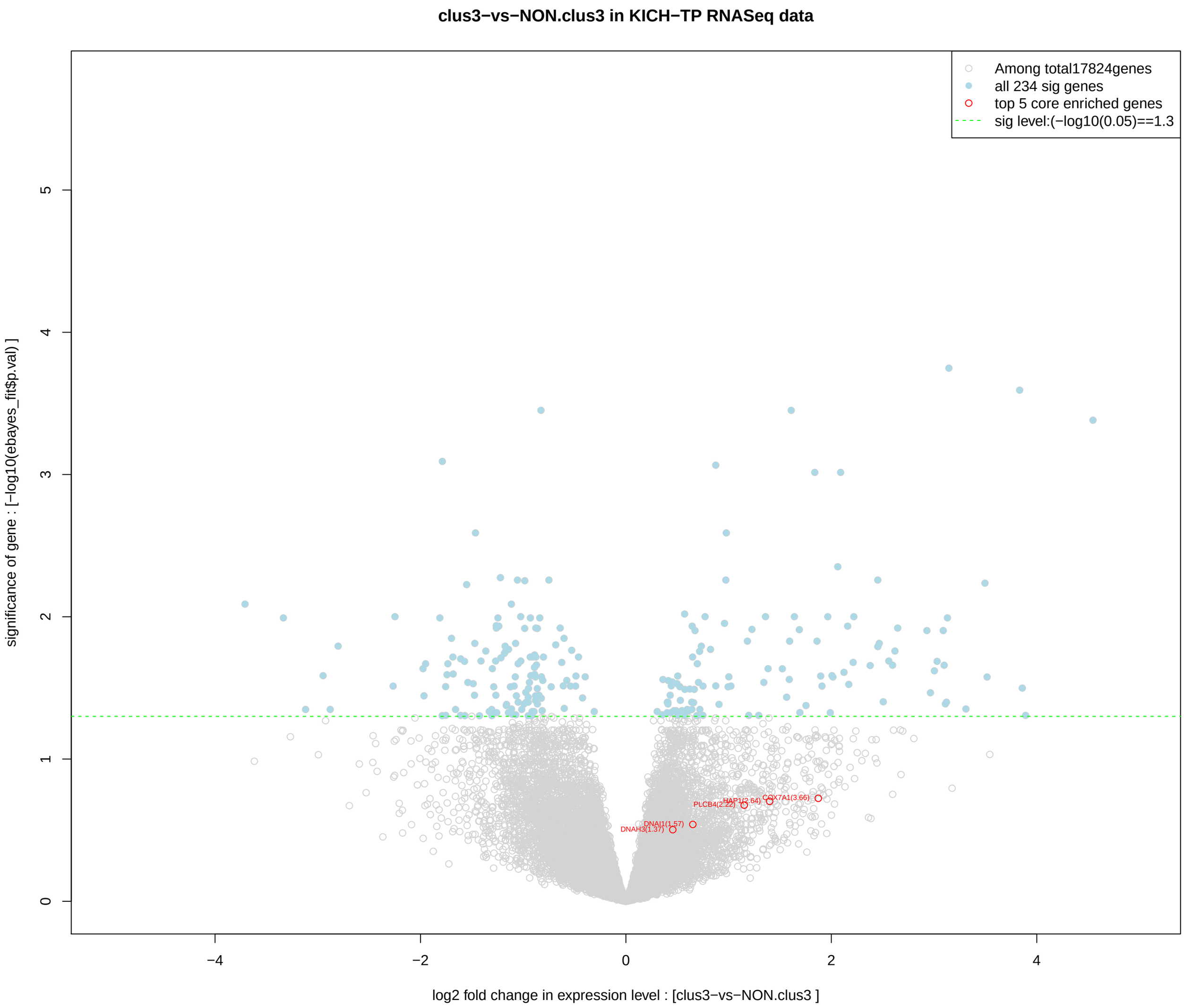
clus3−vs−NON.clus3 in KICH−TP RNASeq data
Among total17824genes
all 234 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
DNAI1(1.57)
DNAH3(1.37)
PLCB4(2.22)
HAP1(2.64)
COX7A1(3.66)
0
1
2
3
4
5
−4
−2
0
2
4