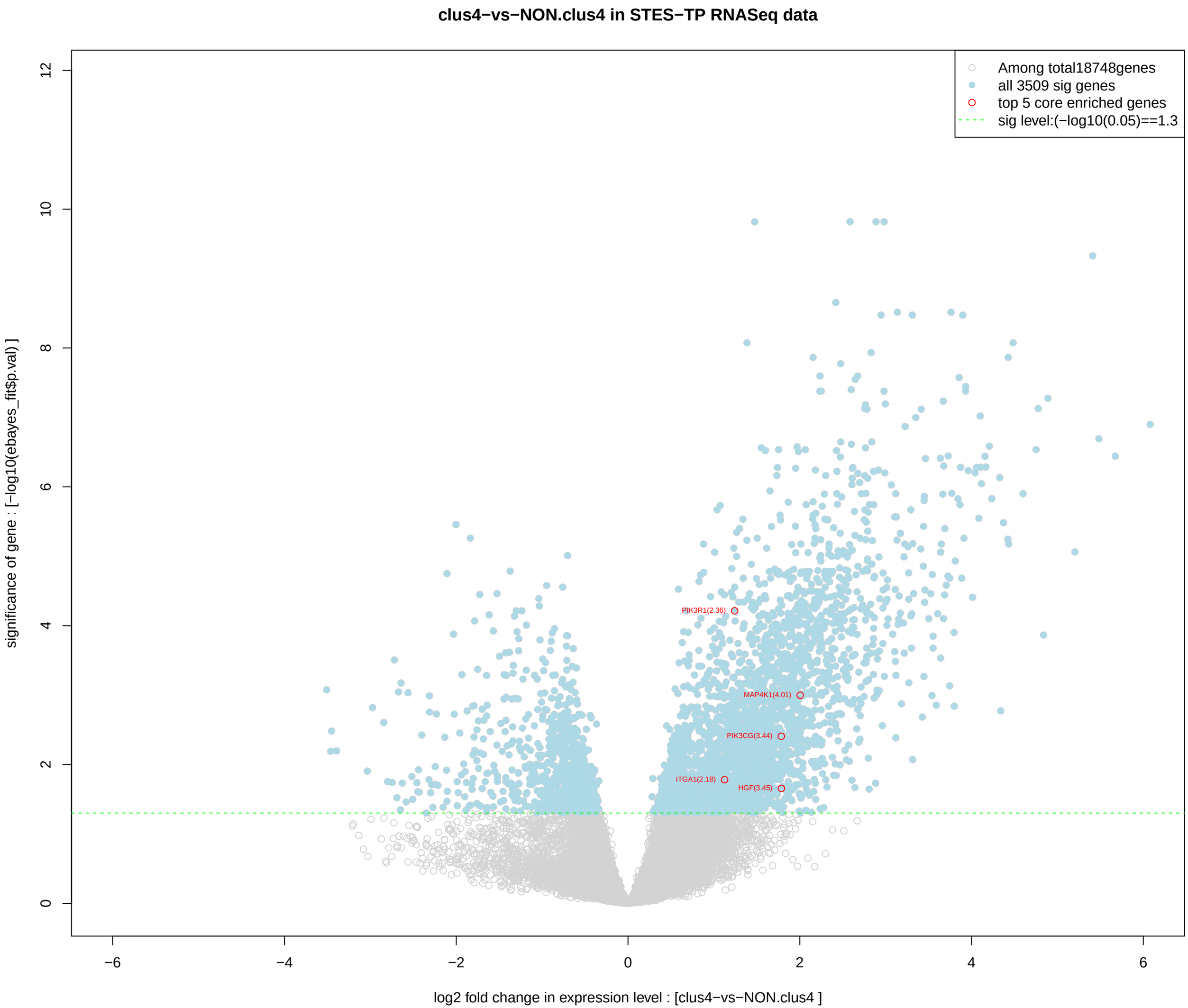
clus4−vs−NON.clus4 in STES−TP RNASeq data
Among total18748genes
all 3509 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PIK3R1(2.36)
MAP4K1(4.01)
PIK3CG(3.44)
ITGA1(2.18)
HGF(3.45)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus4−vs−NON.clus4]
0
2
4
6
8
10
12
−6
−4
−2
0
2
4
6