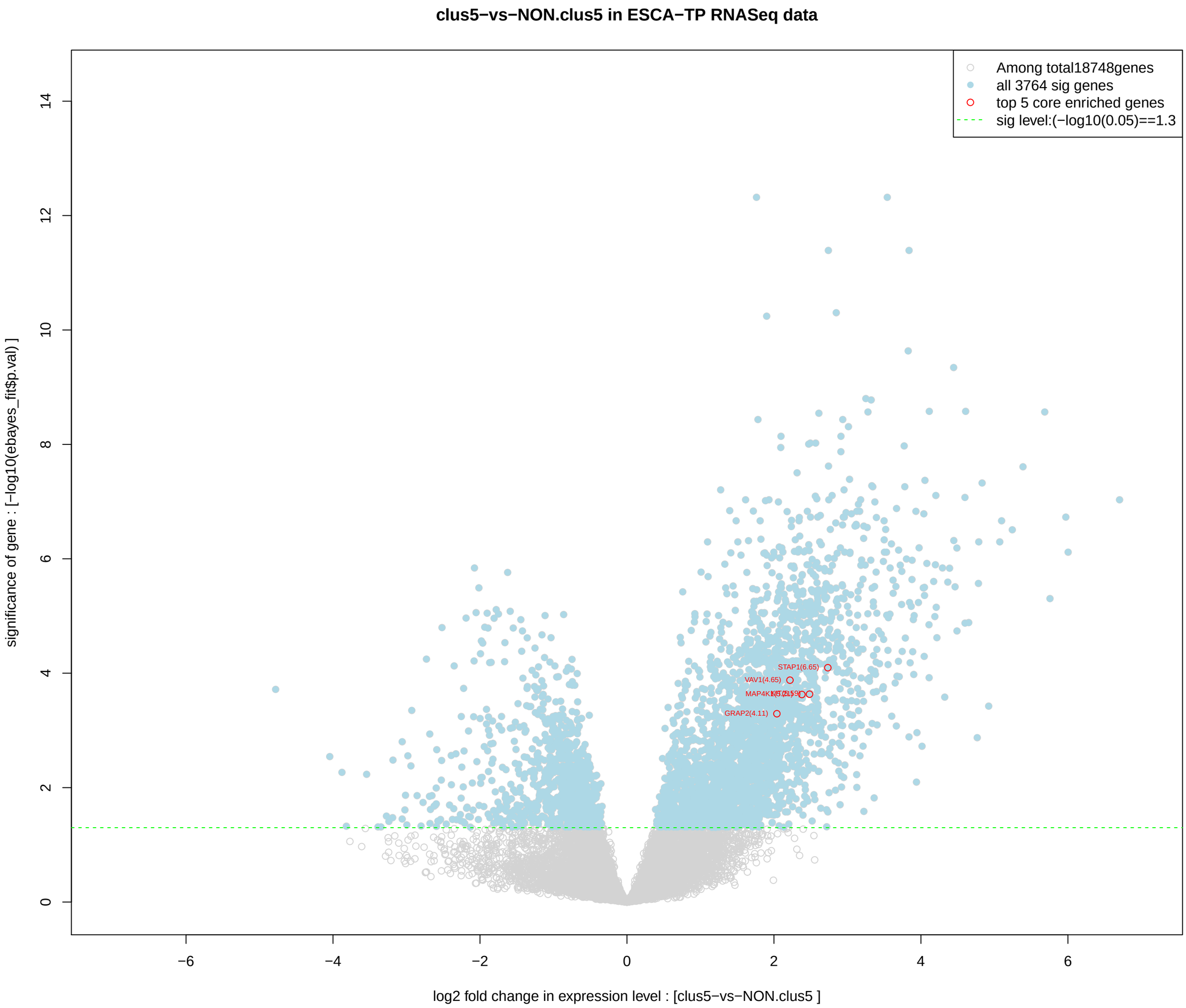
clus5−vs−NON.clus5 in ESCA−TP RNASeq data
Among total18748genes
all 3764 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
STAP1(6.65)
VAV1(4.65)
GRAP2(4.11)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus5−vs−NON.clus5]
0
2
4
6
8
10
12
14
−6
−4
−2
0
2
4
6