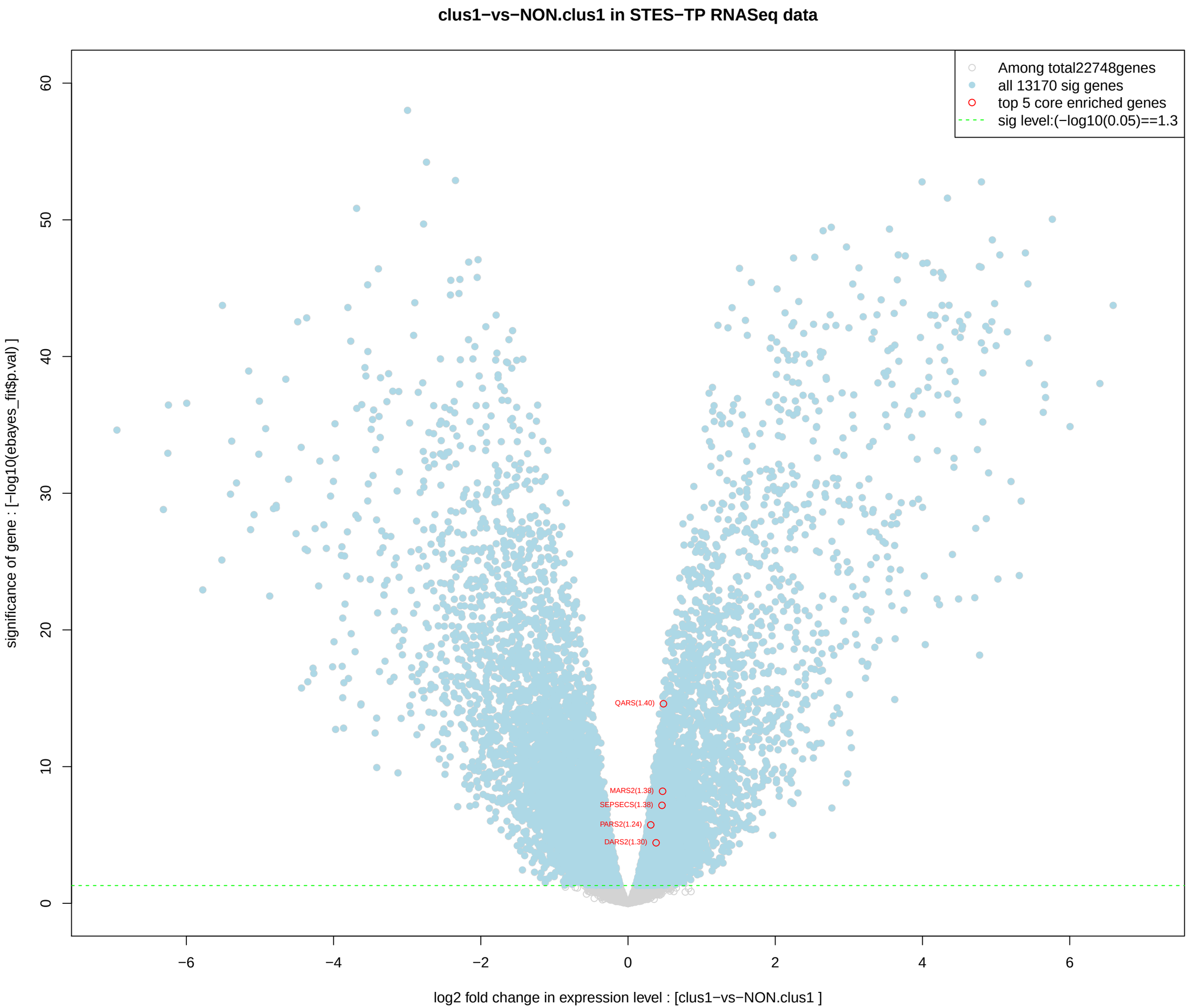
clus1−vs−NON.clus1 in STES−TP RNASeq data
Among total22748genes
all 13170 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
QARS(1.40)
MARS2(1.38)
SEPSECS(1.38)
PARS2(1.24)
DARS2(1.30)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
50
60
−6
−4
−2
0
2
4
6