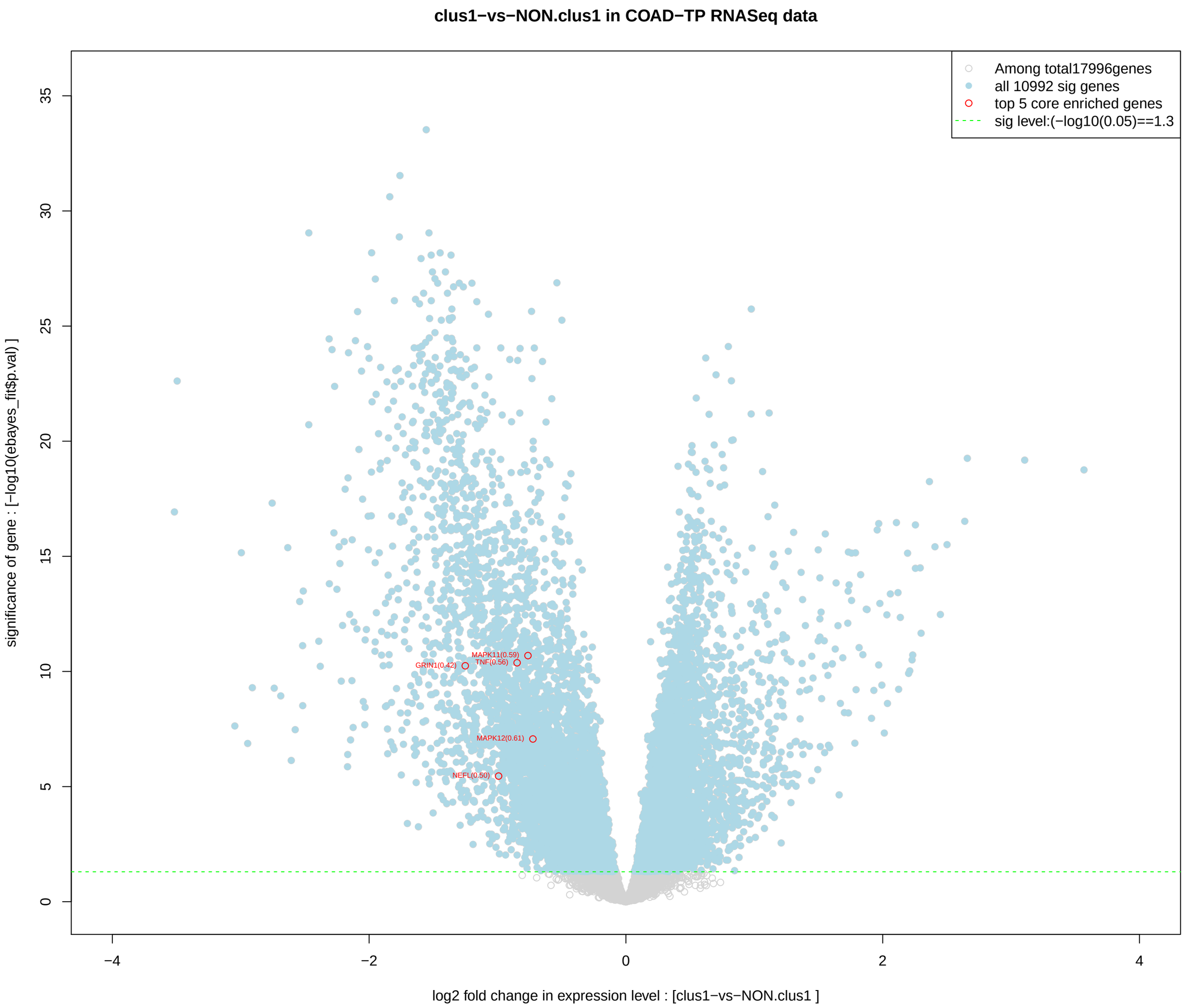
clus1−vs−NON.clus1 in COAD−TP RNASeq data
Among total17996genes
all 10992 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
MAPK11(0.59)
TNF(0.56)
GRIN1(0.42)
MAPK12(0.61)
NEFL(0.50)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
25
30
35
−4
−2
0
2
4