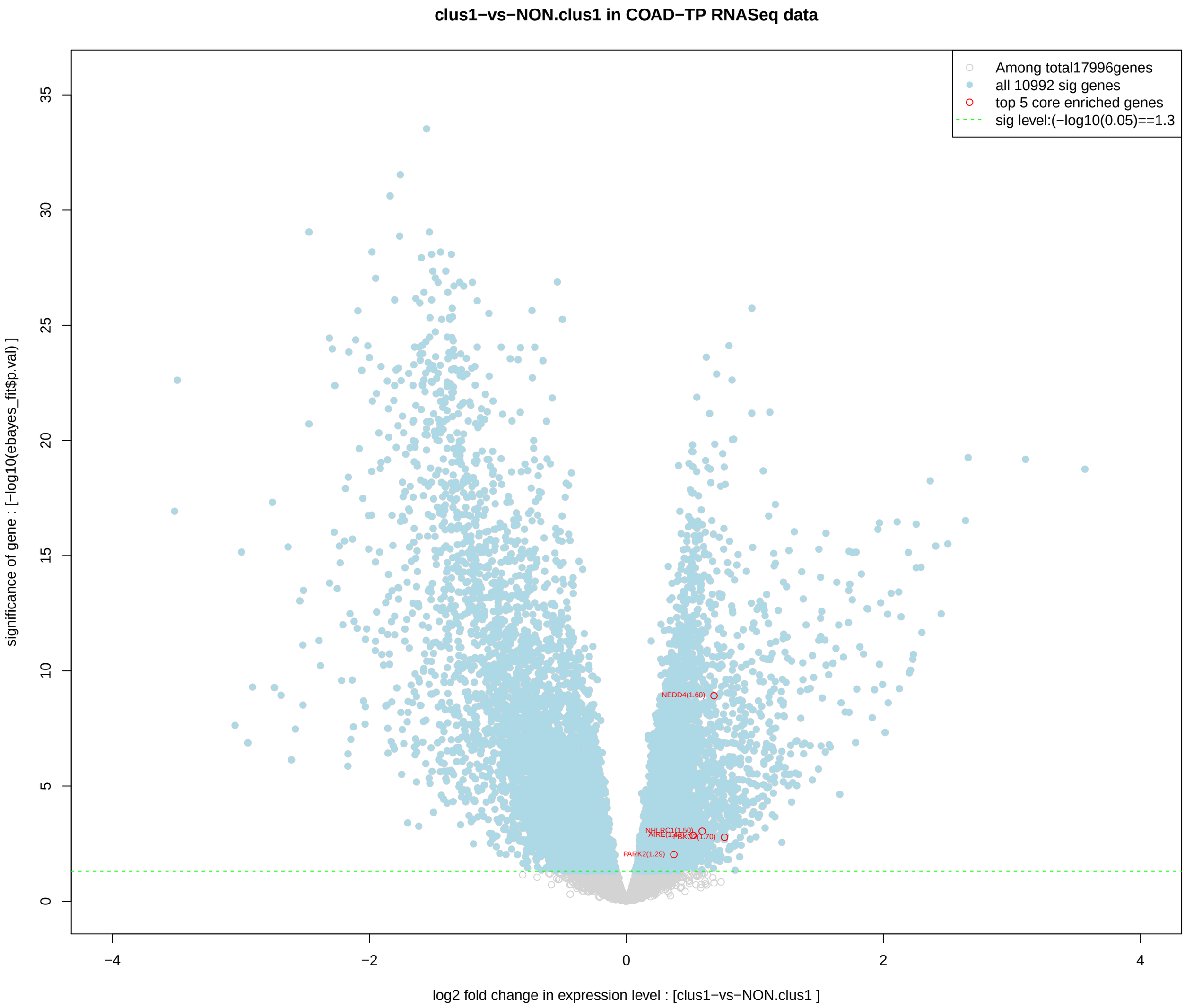
clus1−vs−NON.clus1 in COAD−TP RNASeq data
Among total17996genes
all 10992 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
NEDD4(1.60)
NHLRC1(1.50)
AIRE(1.44)
PBX2(1.70)
PARK2(1.29)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
25
30
35
−4
−2
0
2
4