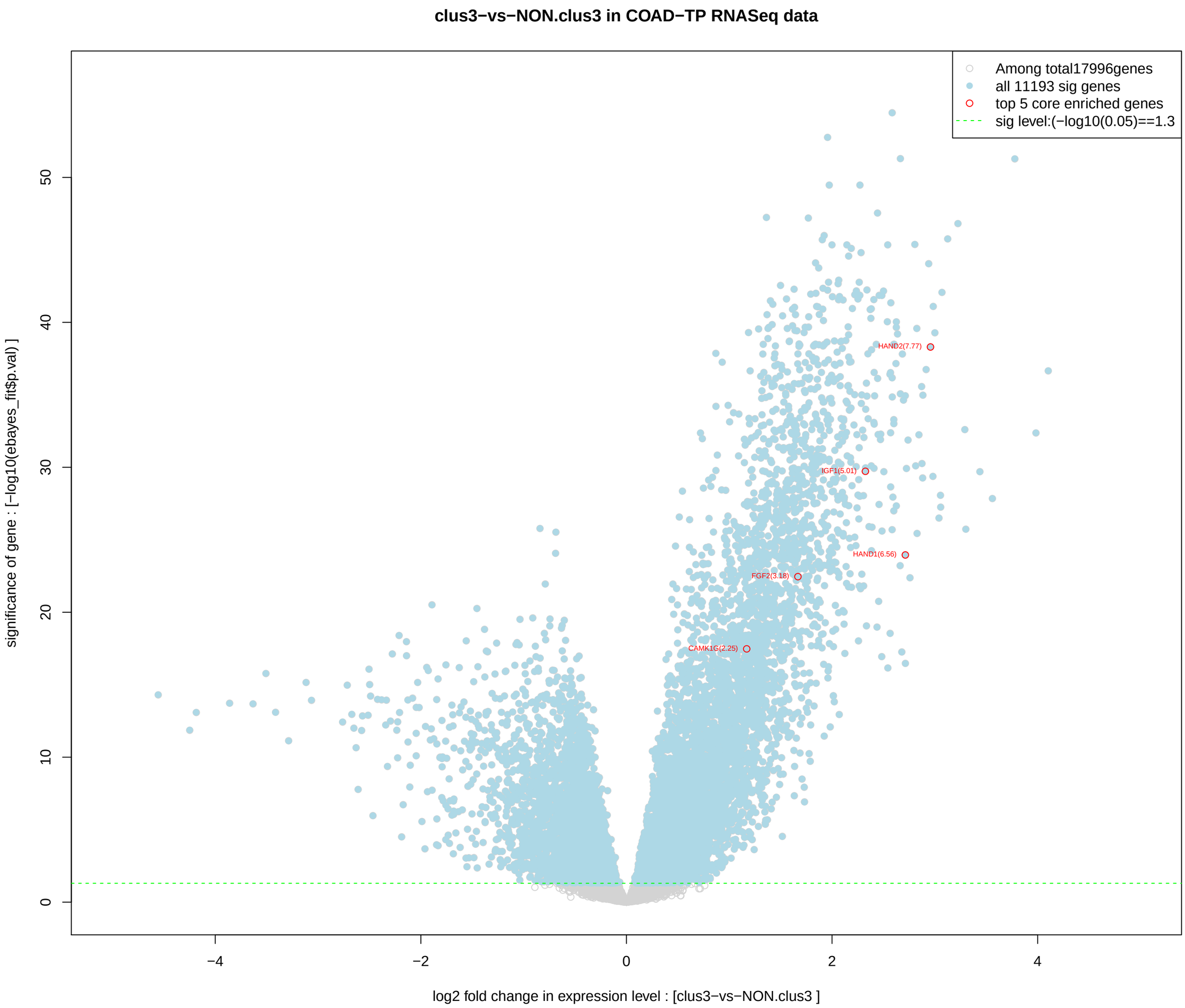
clus3−vs−NON.clus3 in COAD−TP RNASeq data
Among total17996genes
all 11193 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
HAND2(7.77)
IGF1(5.01)
HAND1(6.56)
FGF2(3.18)
CAMK1G(2.25)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
10
20
30
40
50
−4
−2
0
2
4