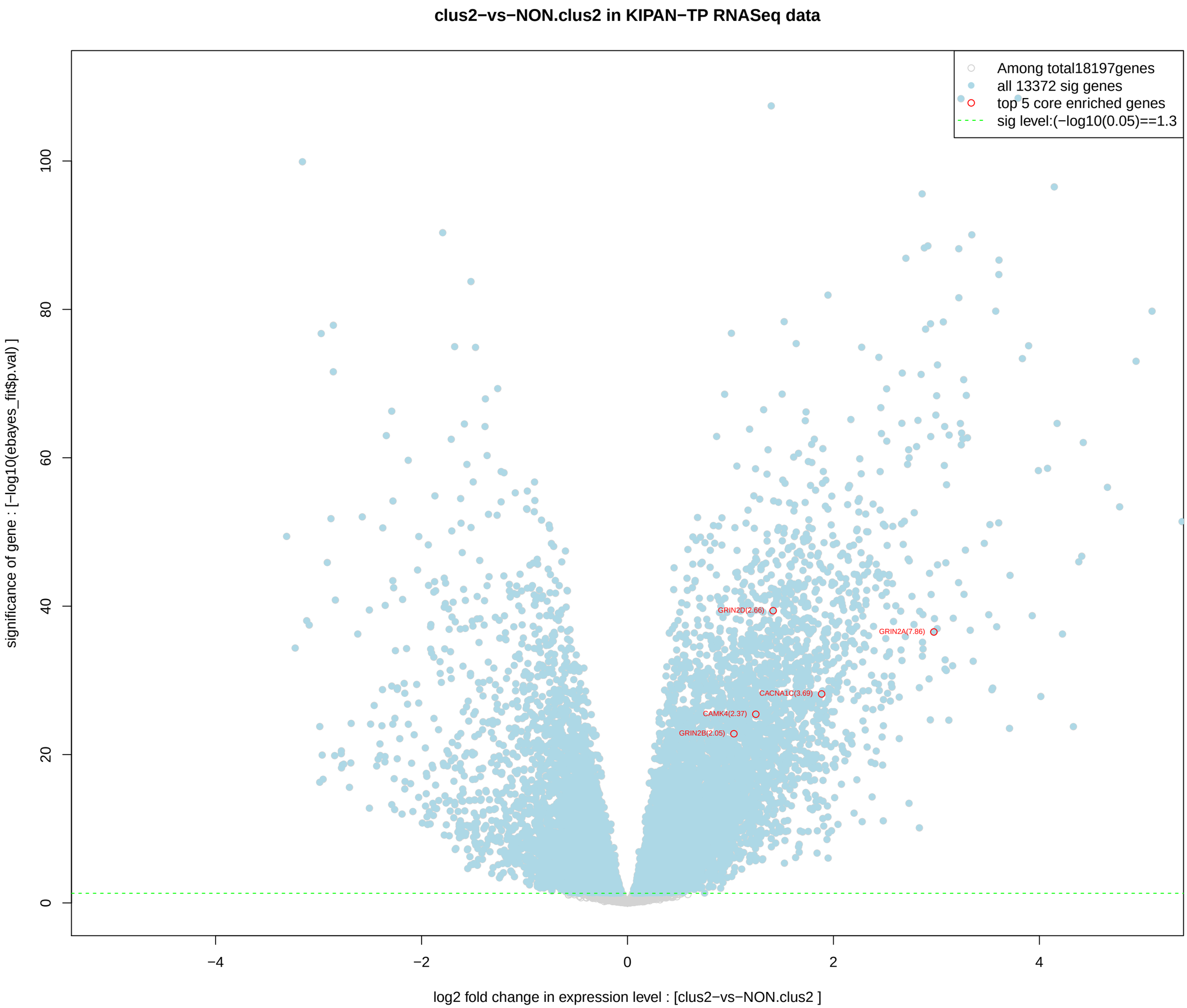
clus2−vs−NON.clus2 in KIPAN−TP RNASeq data
Among total18197genes
all 13372 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GRIN2D(2.66)
GRIN2A(7.86)
CACNA1C(3.69)
CAMK4(2.37)
GRIN2B(2.05)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
20
40
60
80
100
−4
−2
0
2
4