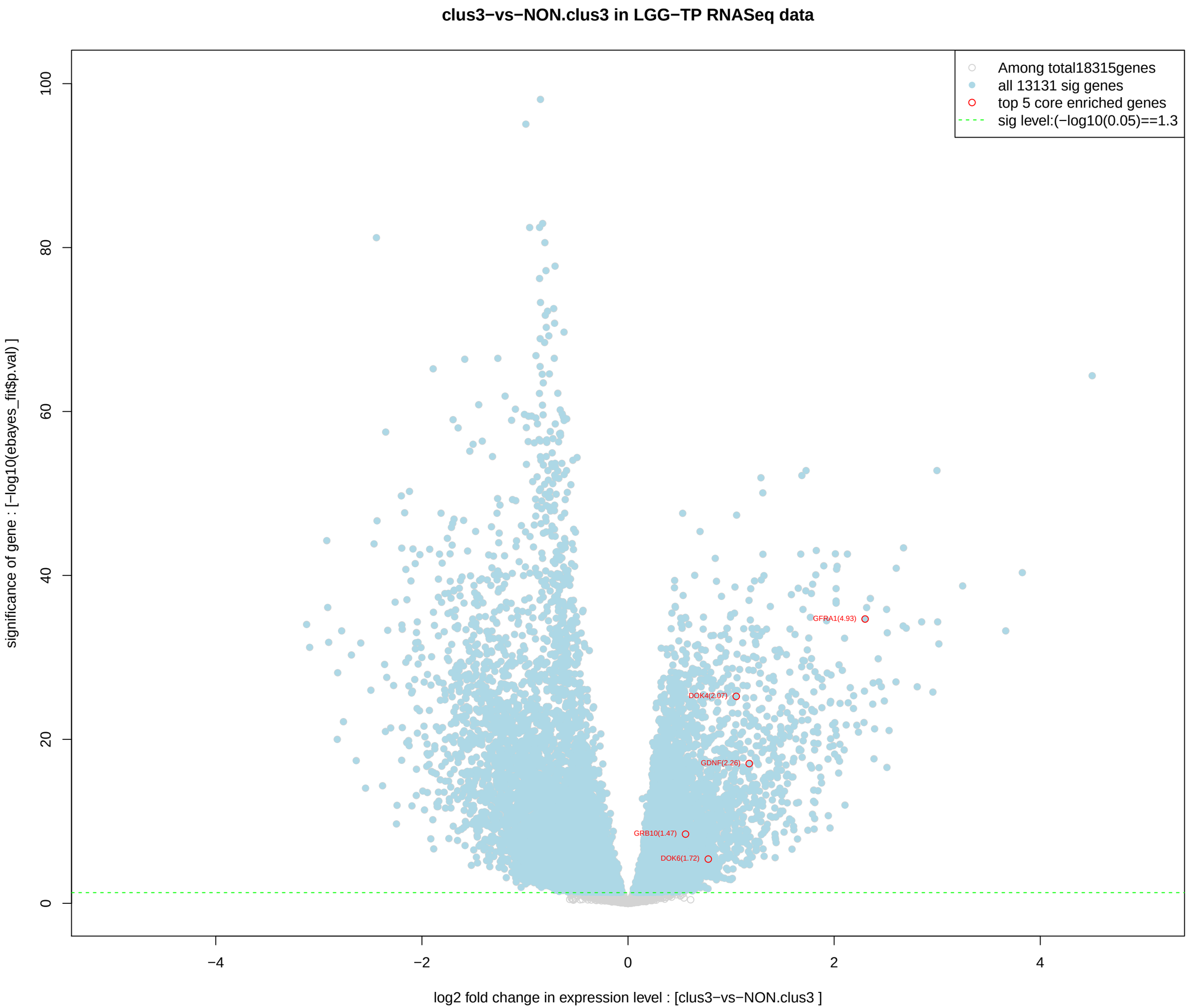
clus3−vs−NON.clus3 in LGG−TP RNASeq data
Among total18315genes
all 13131 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GFRA1(4.93)
DOK4(2.07)
GDNF(2.26)
GRB10(1.47)
DOK6(1.72)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
20
40
60
80
100
−4
−2
0
2
4