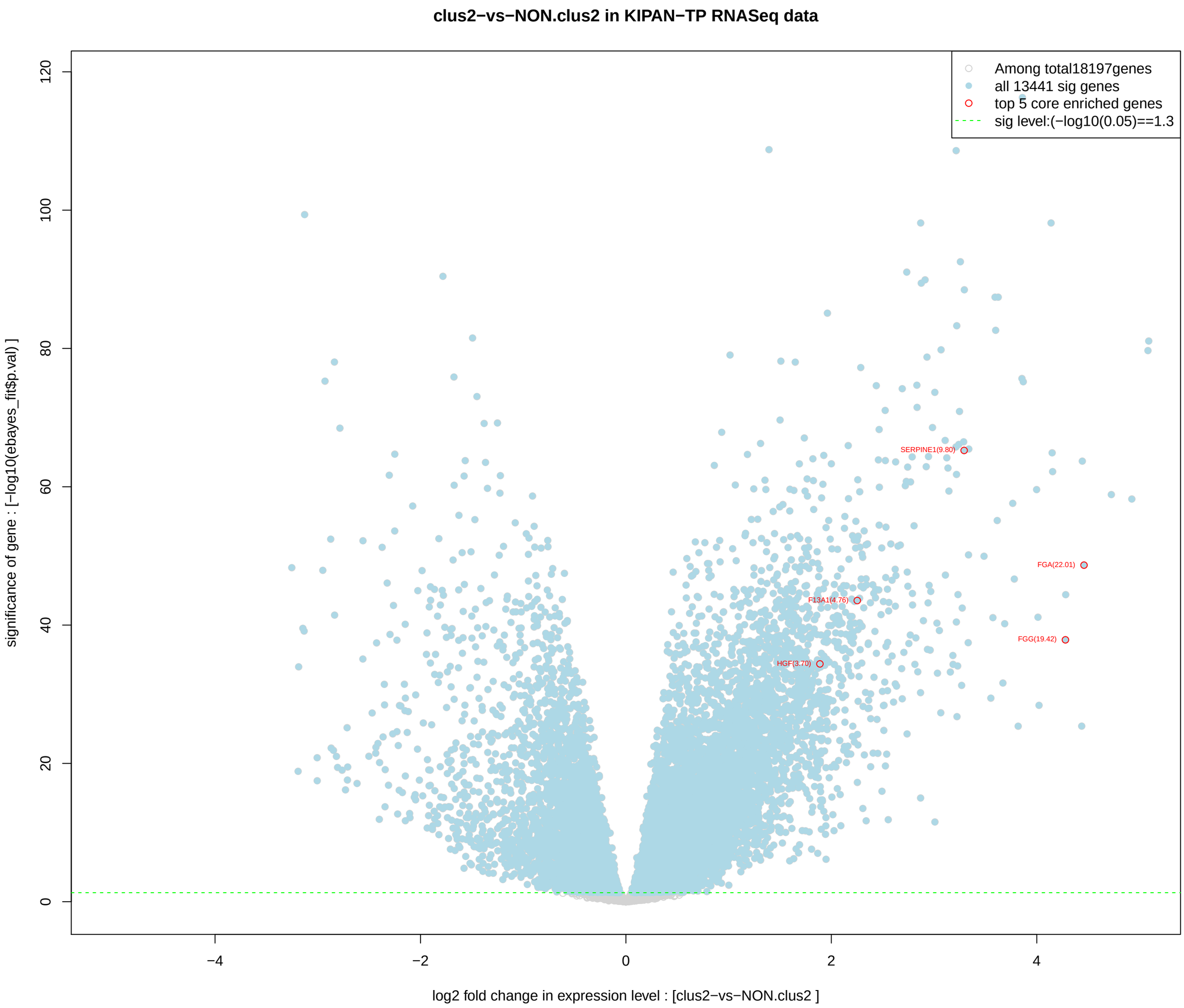
clus2−vs−NON.clus2 in KIPAN−TP RNASeq data
Among total18197genes
all 13441 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
SERPINE1(9.80)
FGA(22.01)
F13A1(4.76)
FGG(19.42)
HGF(3.70)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
20
40
60
80
100
120
−4
−2
0
2
4