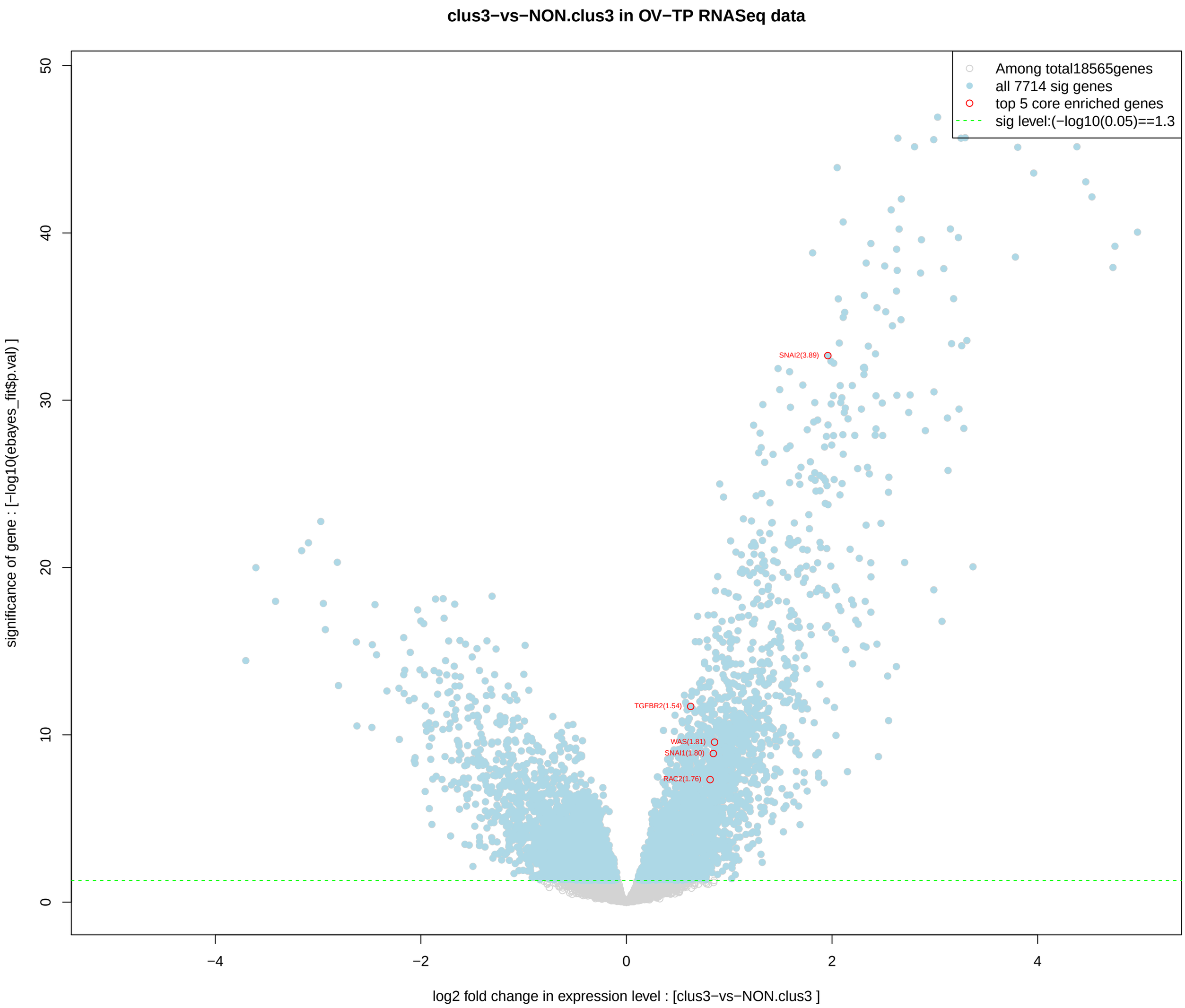
clus3−vs−NON.clus3 in OV−TP RNASeq data
Among total18565genes
all 7714 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
SNAI2(3.89)
TGFBR2(1.54)
WAS(1.81)
SNAI1(1.80)
RAC2(1.76)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
10
20
30
40
50
−4
−2
0
2
4