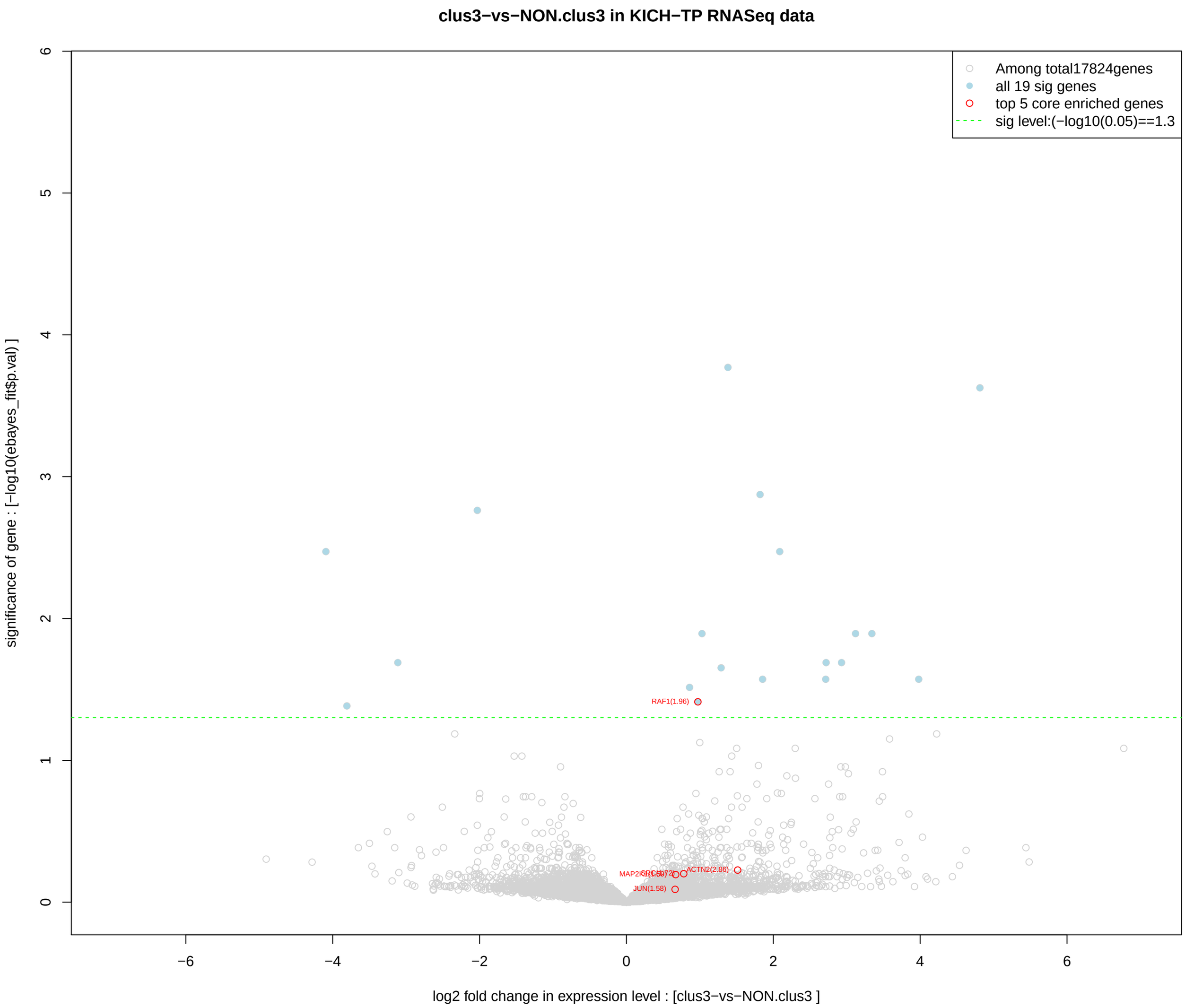
clus3−vs−NON.clus3 in KICH−TP RNASeq data
Among total17824genes
all 19 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
RAF1(1.96)
MAP2K3(1.59)
SRC(1.72)
ACTN2(2.86)
JUN(1.58)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
1
2
3
4
5
6
−6
−4
−2
0
2
4
6