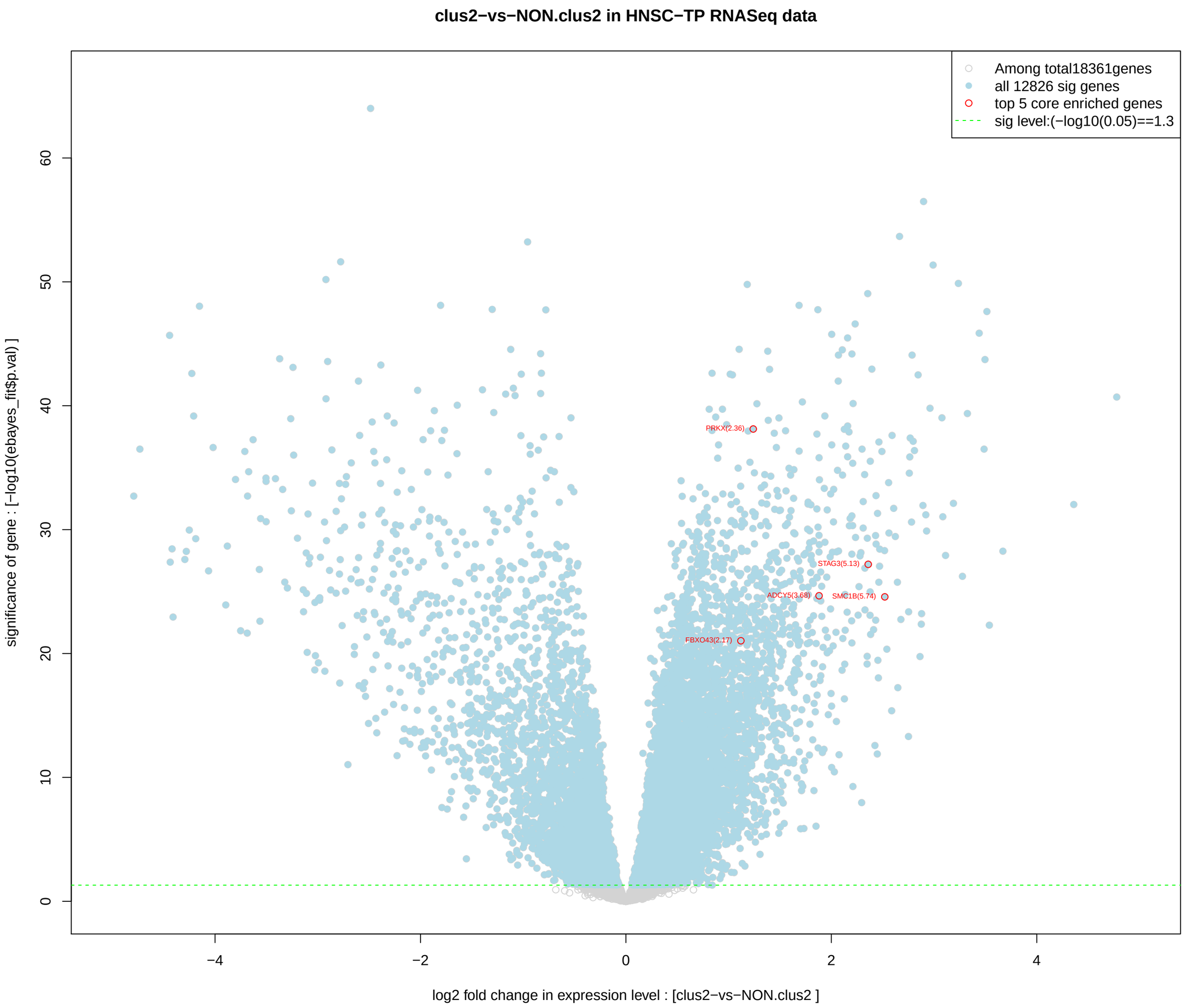
clus2−vs−NON.clus2 in HNSC−TP RNASeq data
Among total18361genes
all 12826 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PRKX(2.36)
STAG3(5.13)
ADCY5(3.68)
SMC1B(5.74)
FBXO43(2.17)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus2−vs−NON.clus2 ]
0
10
20
30
40
50
60
−4
−2
0
2
4