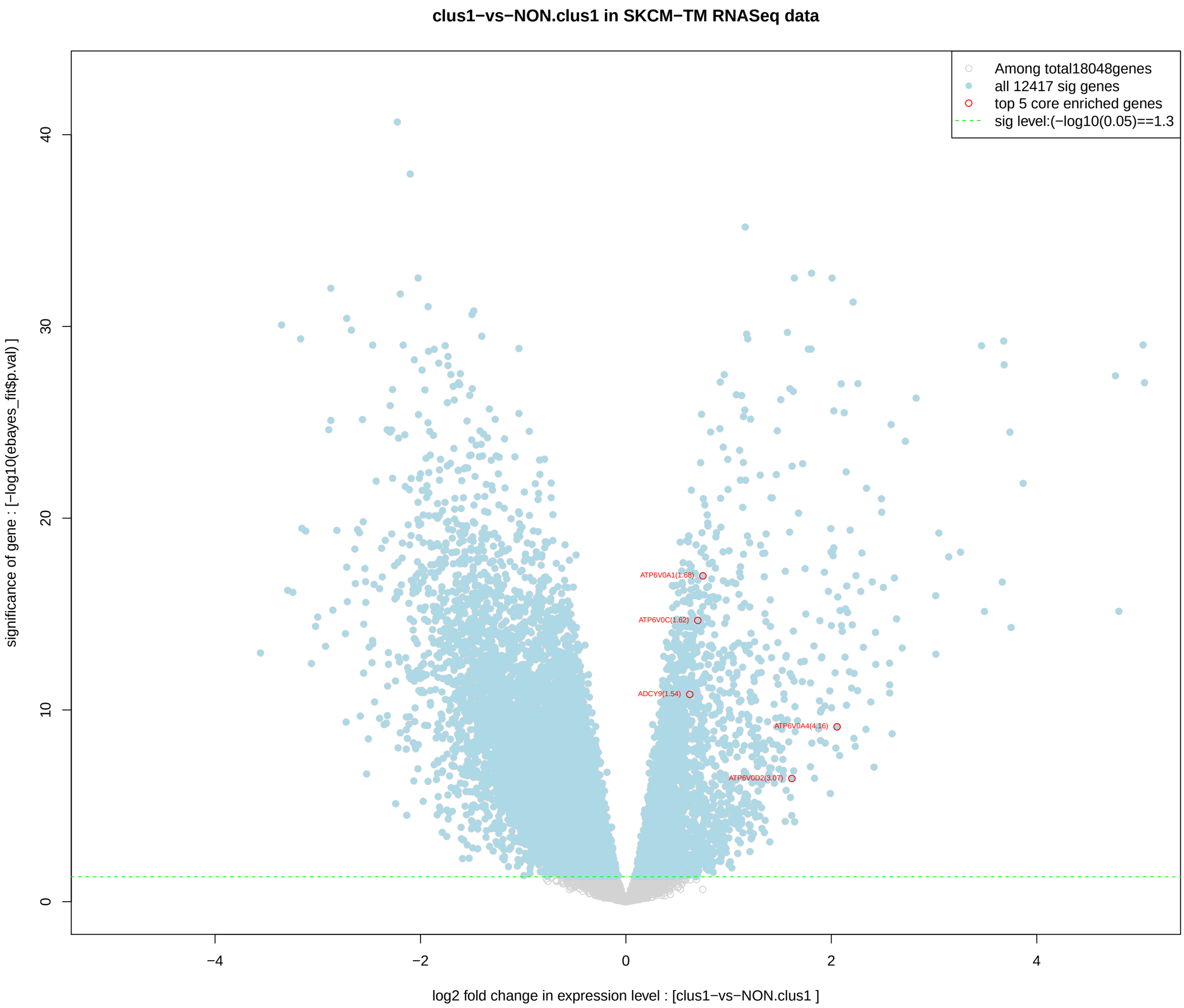
clus1−vs−NON.clus1 in SKCM−TM RNASeq data
Among total18048genes
all 12417 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
ATP6V0A1(1.68)
ATP6V0C(1.62)
ADCY9(1.54)
ATP6V0A4(4.16)
ATP6V0D2(3.07)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
−4
−2
0
2
4