clus2−vs−NON.clus2 in LUAD−TP RNASeq data
Among total18300genes
all 10864 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
KCNQ1(0.34)
CFTR(0.22)
ATP6V1B1(0.39)
ATP6V0A4(0.54)
ATP6V1C2(0.73)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
10
20
30
40
−4
−2
0
2
4