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
TK1(2.35)
RRM2(2.32)
POLE2(1.91)
CDA(2.53)
POLR3G(1.49)
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