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
MCM2(1.91)
RFC4(1.75)
RNASEH2A(1.60)
POLE2(1.91)
PRIM1(1.53)
significance of gene : [−log10(ebayes_fit$p.val)]
0
10
20
30
40
−4
−2
0
2
4
log2 fold change in expression level : [clus2−vs−NON.clus2]