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
RRM2(2.32)
CCNE1(2.37)
GTSE1(2.12)
CCNB2(2.08)
PMAIP1(2.19)
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 ]