clus1−vs−NON.clus1 in LUAD−TP RNASeq data
Among total18300genes
all 11715 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CDC20(0.30)
UBE2C(0.27)
UBE2S(0.45)
BRCA1(0.53)
SKP2(0.58)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus1−vs−NON.clus1 ]
0
10
20
30
40
50
−4
−2
0
2
4