clus1−vs−NON.clus1 in LIHC−TP RNASeq data
Among total17728genes
all 9079 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
RFC4(1.89)
MCM2(2.24)
PRIM1(1.80)
POLE2(1.92)
DNA2(1.50)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
20
25
30
−4
−2
0
2
4