clus1−vs−NON.clus1 in THYM−TP RNASeq data
Among total18283genes
all 9492 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
NEIL1(2.49)
PARP3(1.57)
POLE2(1.65)
NEIL3(2.61)
FEN1(1.56)
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
35
−5
0
5