clus3−vs−NON.clus3 in STES−TP RNASeq data
Among total18748genes
all 4272 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
C2(0.33)
SERPINA1(0.17)
PROC(0.36)
F5(0.19)
C4BPB(0.16)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus3−vs−NON.clus3]
0
5
10
15
20
−5
0
5