clus1−vs−NON.clus1 in COAD−TP RNASeq data
Among total17996genes
all 10992 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CTSE(0.09)
SLC11A1(0.36)
CTSW(0.32)
HYAL1(0.30)
CTSG(0.33)
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
−4
−2
0
2
4