clus2−vs−NON.clus2 in DLBC−TP RNASeq data
Among total17560genes
all 217 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PRKCB(2.14)
MAP3K1(1.73)
NFATC1(1.79)
ZAP70(1.84)
PRKCA(1.91)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
1
2
3
4
5
6
−4
−2
0
2
4