clus2−vs−NON.clus2 in LAML−TB RNASeq data
Among total17259genes
all 9714 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
TNFRSF1B(5.15)
PRKCD(2.36)
APAF1(1.72)
LMNA(2.28)
TNF(1.99)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
5
10
15
20
25
−4
−2
0
2
4