clus2−vs−NON.clus2 in KICH−TP RNASeq data
Among total17824genes
all 2612 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
CAMKK1(1.89)
NFKBIE(2.02)
RXRG(3.01)
ACSL5(2.07)
TNF(1.63)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus2−vs−NON.clus2]
0
2
4
6
8
10
−4
−2
0
2
4