clus2−vs−NON.clus2 in CHOL−TP RNASeq data
Among total18113genes
all 489 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
PIK3R5(0.34)
PIK3CG(0.32)
FLT3(0.18)
RUNX1T1(0.44)
LEF1(0.50)
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