
clus1−vs−NON.clus1 in UCS−TP RNASeq data
Among total18646genes
all 2395 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
ENO3(30.64)
FBP2(22.30)
PYGM(13.72)
PGAM2(8.00)
PHKG1(3.88)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
5
10
15
−10
−5
0
5
10