clus1−vs−NON.clus1 in KIRC−TP RNASeq data
Among total18258genes
all 10265 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
LAMA2(3.98)
CACNA2D2(1.97)
TNNC1(2.79)
ACTC1(3.62)
DES(5.19)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
−4
−2
0
2
4