clus1−vs−NON.clus1 in BLCA−TP RNASeq data
Among total18197genes
all 10015 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
JAM3(3.37)
JAM2(4.33)
CCL5(3.38)
ATP6V1G2(1.74)
ATP6V0D2(1.88)
significance of gene : [−log10(ebayes_fit$p.val)]
log2 fold change in expression level : [clus1−vs−NON.clus1]
0
10
20
30
40
50
−4
−2
0
2
4