clus2−vs−NON.clus2 in UCS−TP RNASeq data
Among total18646genes
all 2530 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
F11R(3.43)
ATP6V0A4(4.65)
CXCL1(3.76)
MAPK10(2.33)
ATP6V1G3(1.51)
significance of gene : [−log10(ebayes_fit$p.val) ]
log2 fold change in expression level : [clus2−vs−NON.clus2 ]
0
2
4
6
−6
−4
−2
0
2
4
6