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
UGT2A3(0.17)
UGT1A9(0.16)
UGT1A3(0.31)
UGT1A8(0.32)
UGT1A5(0.60)
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