clus2−vs−NON.clus2 in LUSC−TP RNASeq data

significance of gene : [−log10(ebayes_fit$p.val)]

log2 fold change in expression level : [clus2−vs−NON.clus2]

○ Among total18496genes
● all 12351 sig genes
○ top 5 core enriched genes
--- sig level:(−log10(0.05)==1.3

UGT1A7(97.73)

UGT1A9(11.67)

UGT1A1(6.07)

UGT1A5(2.11) UGT1A3(3.48)