clus2−vs−NON.clus2 in LUAD−TP RNASeq data
Among total18300genes
all 10864 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3
GSTA1(0.11)
ADH1B(0.17)
ADH1A(0.36)
GSTA2(0.19)
UGT2B4(0.32)
significance of gene : [−log10(ebayes_fit$p.val)]
0
10
20
30
40
−4
−2
0
2
4
log2 fold change in expression level : [clus2−vs−NON.clus2]