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

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

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

- ○ Among total18748genes
- ● all 10615 sig genes
- ○ top 5 core enriched genes
- --- sig level:(−log10(0.05)==1.3

HSPA2(2.89)
PRPF40B(1.61)
THOC3(1.60)
HSPA1A(1.69)
HSPA6(1.89)