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

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

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

Legend:
- ○ Among total18258genes
- ● all 11907 sig genes
- ○ top 5 core enriched genes
- --- sig level:(−log10(0.05)==1.3

Labeled points:
- AMDHD1(3.57)
- DDC(5.75)
- ASPA(2.68)
- FTCD(5.50)
- ABP1(3.28)