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

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

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

Legend:
- ○ Among total17996genes
- ● all 9769 sig genes
- ○ top 5 core enriched genes
- --- sig level:(−log10(0.05)==1.3

Labeled points: DMD(0.37), DES(0.27), CACNA2D1(0.45), MYL3(0.51), SGCA(0.42)