clus1−vs−NON.clus1 in COAD−TP RNASeq data

Legend:
- ○ Among total17996genes
- ● all 10999 sig genes
- ○ top 5 core enriched genes
- - - sig level:(−log10(0.05)==1.3

Labeled genes: SETDB2(1.47), PIPOX(3.09), TMLHE(1.27), SETMAR(1.28), OGDHL(2.50)

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

x-axis: log2 fold change in expression level : [clus1−vs−NON.clus1]