clus3−vs−NON.clus3 in READ−TP RNASeq data

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

log2 fold change in expression level : [clus3−vs−NON.clus3]

Among total18090genes
all 4999 sig genes
top 5 core enriched genes
sig level:(−log10(0.05)==1.3

EPRS(1.36)
NARS(1.32)
DARS2(1.28)
WARS2(1.22)
SEPSECS(1.22)