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

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

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

- ○ Among total18457genes
- ● all 1688 sig genes
- ○ top 5 core enriched genes
- -- sig level:(−log10(0.05)==1.3

ERBB4(3.48)
EGF(6.86)
FGFR3(2.77)
FGFR2(2.26)
FGFR4(2.16)