clus4–vs–NON.clus4 in SKCM–TM RNASeq data

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

log2 fold change in expression level : [clus4−vs−NON.clus4]

Legend:
- Among total18040genes
- all 7272 sig genes
- top 5 core enriched genes
- sig level:(−log10(0.05)==1.3

Labeled points:
- RPL7(1.59)
- DCP2(1.49)
- PRKCA(1.48)
- RPS27(1.58)
- RPL36A(1.58)