clus4−vs−NON.clus4 in LGG−TP RNASeq data

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

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

Legend:
- Among total18315genes
- all 13195 sig genes
- top 5 core enriched genes
- sig level:(−log10(0.05)==1.3

Labeled points:
- YWHAH(3.13)
- PRKAR1B(3.60)
- PPP2R2C(5.92)
- PRKAR2B(2.31)
- PKLR(2.09)