> library(cummeRbund)

> cuff\_data <- readCufflinks('diff\_out')

> csDensity(genes(cuff\_data))

> csVolcano(genes(cuff\_data), 'C1', 'C2'

> mygene<- getGene(cuff\_data,'regucalcin')> expressionBarplot(mygene)

> expressionBarplot(isoforms(mygene))