Supplemental Code. R script for normalization read counts to FPKM.

```
# [readCount.txt] is the input file of read counts produced by featureCount, and [fpkm.csv] is the output file of FPKM
readCount = read.table('readCount.txt', header = T)
for (i in c(7:12)){
   readCount[,i] = readCount[,i] * 1000000 / sum(readCount[,i])
   readCount[,i] = readCount[,i] * 1000 / readCount$Length
}
fpkm = readCount[,-2:-6]
colnames(fpkm) = c('geneID', 'Control_1', 'Control_2', 'Control_3', 'NPV_1', 'NPV_2', 'NPV_3')
fpkm$Control = rowMeans(data.frame(fpkm$Control_1, fpkm$Control_2, fpkm$Control_3))
fpkm$NPV = rowMeans(data.frame(fpkm$NPV_1, fpkm$NPV_2, fpkm$NPV_3))
write.csv(fpkm, 'fpkm.csv', row.names = F)
```