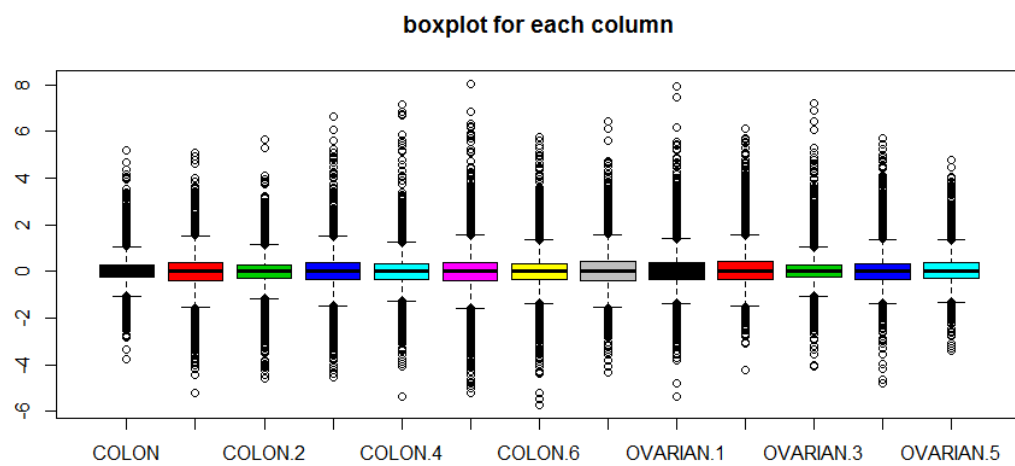
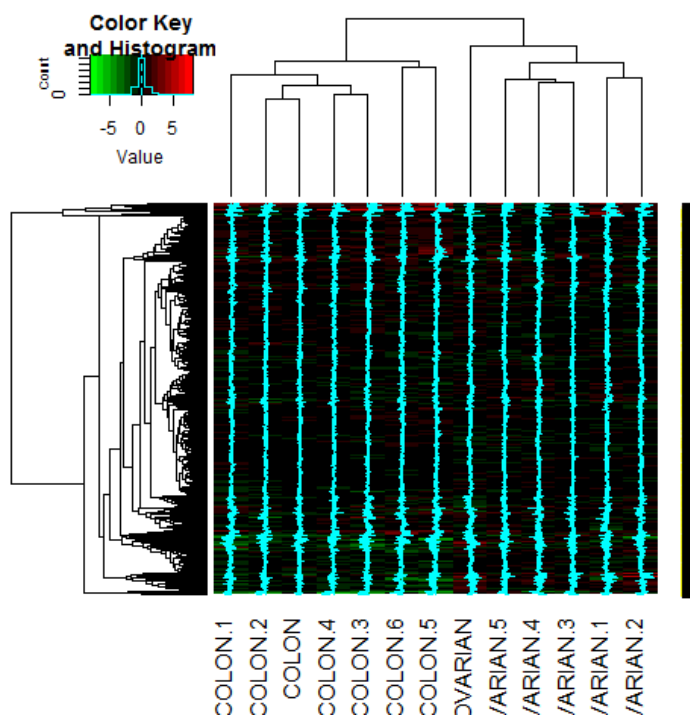


1. Side by side boxplot.



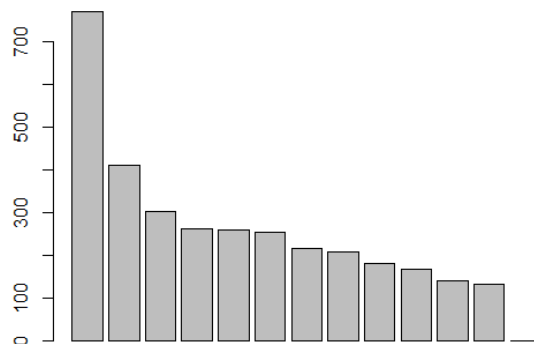
2. Plot a heatmap for the data


```
> install.packages("gplots")
> library(gplots)
> heatmap.2(m, col=greenred)
```



3. Plot the barplot of the eigenvalues.

```
> barplot(microarray.pca$sdev^2)
```



4. Find the three genes that contribute most to the first principal component positively, and three genes that contribute most to the first principal components negatively.

```
> pca1 <- microarray.pca$rotation[,1]
> order(pca1, decreasing = TRUE)[1:3]
[1] 6554 5948 5955
> order(pca1)[1:3]
[1] 229 224 231
```

5. Plot the projection of the data set on the first two principal components, and color the two classes (COLON and OVARIAN) into two different colors.

```
> plot(microarray.pca$x[, 1:2], type = "n")
> points(microarray.pca$x[1:7,1:2],pch="c",col="blue")
> points(microarray.pca$x[8:13,1:2],pch="o",col="red")
```

