BB512/BB612 - Week II

```
suppressPackageStartupMessages(library(ggpubr))
suppressPackageStartupMessages(library(Biobase))
suppressPackageStartupMessages(library(preprocessCore))
```

Data

We'll explore the `bodymap` expression dataset.

```
con <- url("http://bowtie-bio.sourceforge.net/recount/ExpressionSets/bodymap_eset.RData")
load(file=con)
close(con)

bm <- bodymap.eset

pdata <- pData(bm) # phenotype data
edata <- exprs(bm) # expression data
fdata <- fData(bm) # features data
```

Phenotype data

We'll first explore the phenotype data:

```
head(pdata, 3)
```

```
##           sample.id num.tech.reps tissue.type gender age      race
## ERS025098 ERS025098             2     adipose      F  73 caucasian
## ERS025092 ERS025092             2     adrenal      M  60 caucasian
## ERS025085 ERS025085             2       brain      F  77 caucasian
```

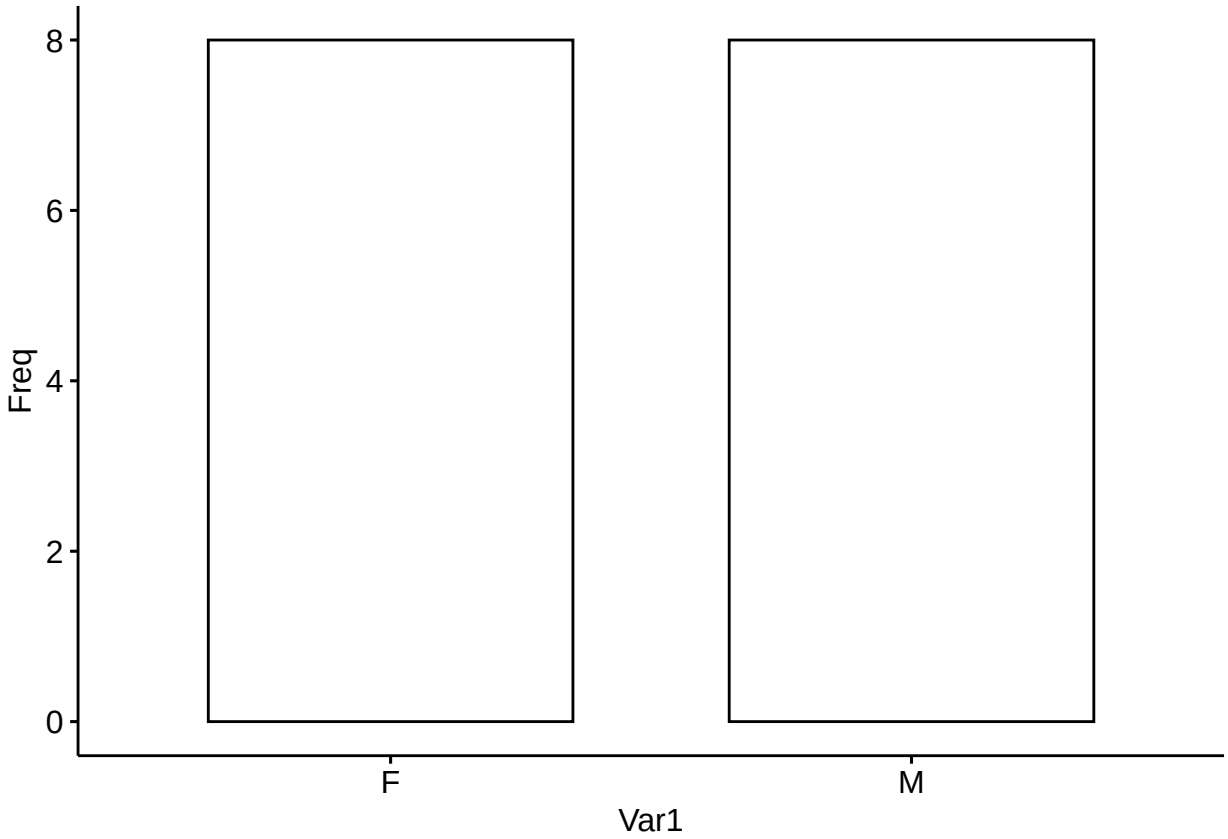
```
table(pdata$gender)
```

```
##
## F M
## 8 8
```

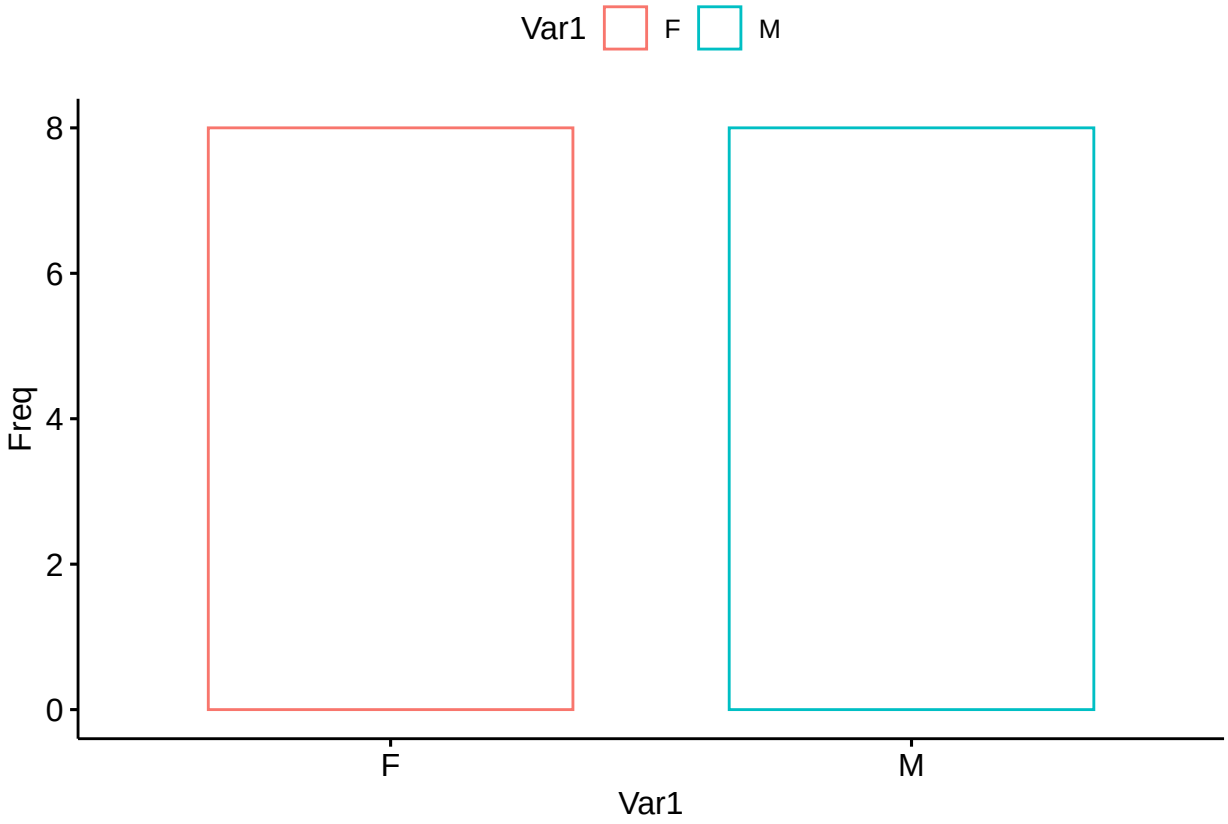
```
for_plot_df <- as.data.frame(table(pdata$gender))
head(for_plot_df)
```

```
##   Var1 Freq
## 1    F    8
## 2    M    8
```

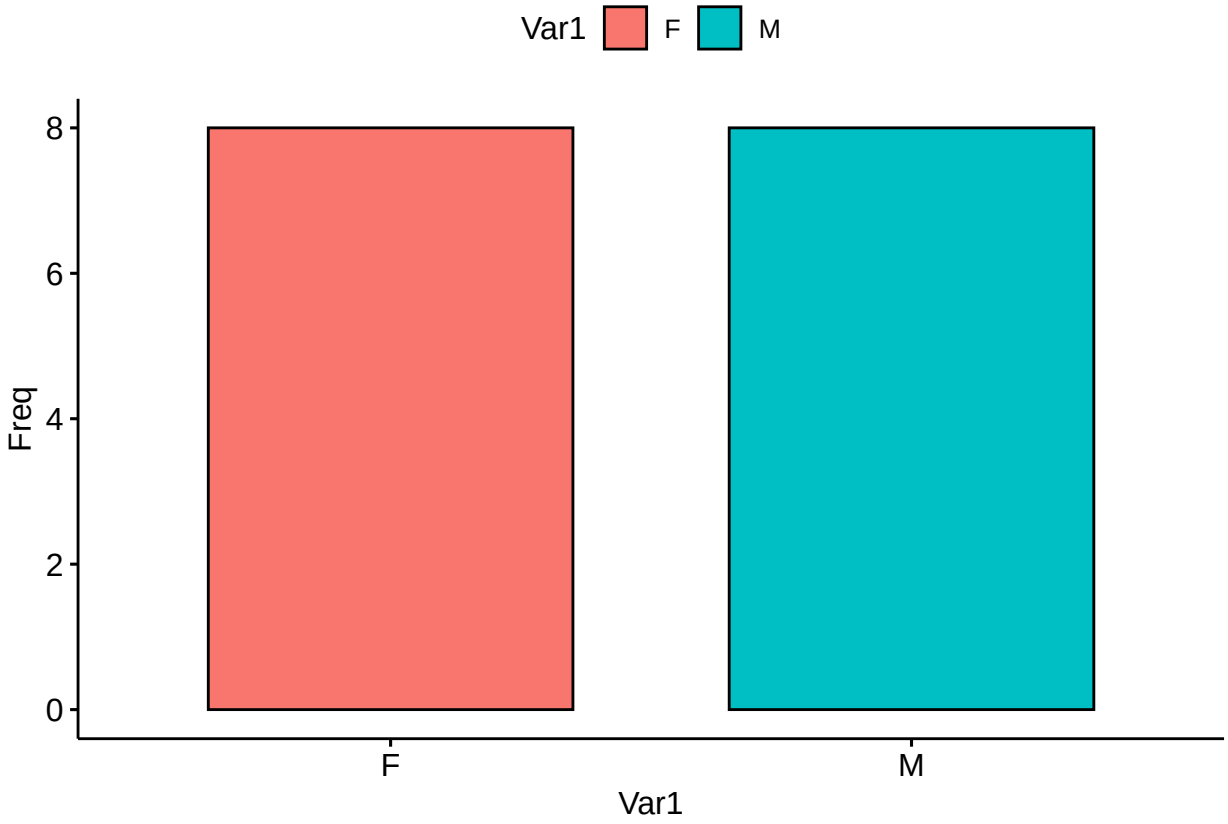
```
g <- ggbarplot(for_plot_df, x = "Var1", y = "Freq")
g
```




```
g2 <- ggbarplot(for_plot_df, x = "Var1", y = "Freq", color = "Var1")
g2
```




```
g3 <- ggbarplot(for_plot_df, x = "Var1", y = "Freq", fill = "Var1")
g3
```



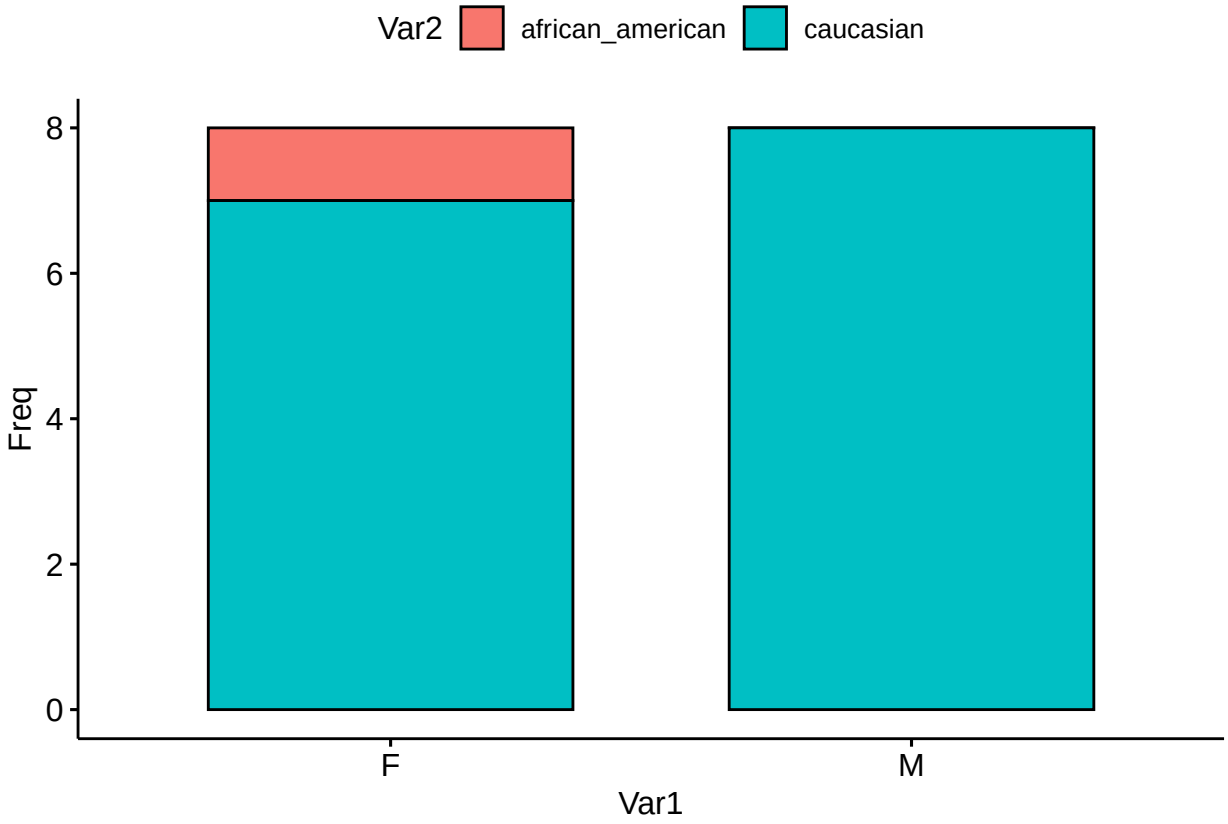

```
table(pdata$gender, pdata$race)
```

```
##
##     african_american caucasian
##   F                1         7
##   M                0         8
```

```
for_plot_df2 <- as.data.frame(table(pdata$gender, pdata$race))
head(for_plot_df2)
```

```
##   Var1            Var2 Freq
## 1    F african_american    1
## 2    M african_american    0
## 3    F        caucasian    7
## 4    M        caucasian    8
```

```
g4 <- ggbarplot(for_plot_df2, "Var1", "Freq", fill = "Var2")
g4
```

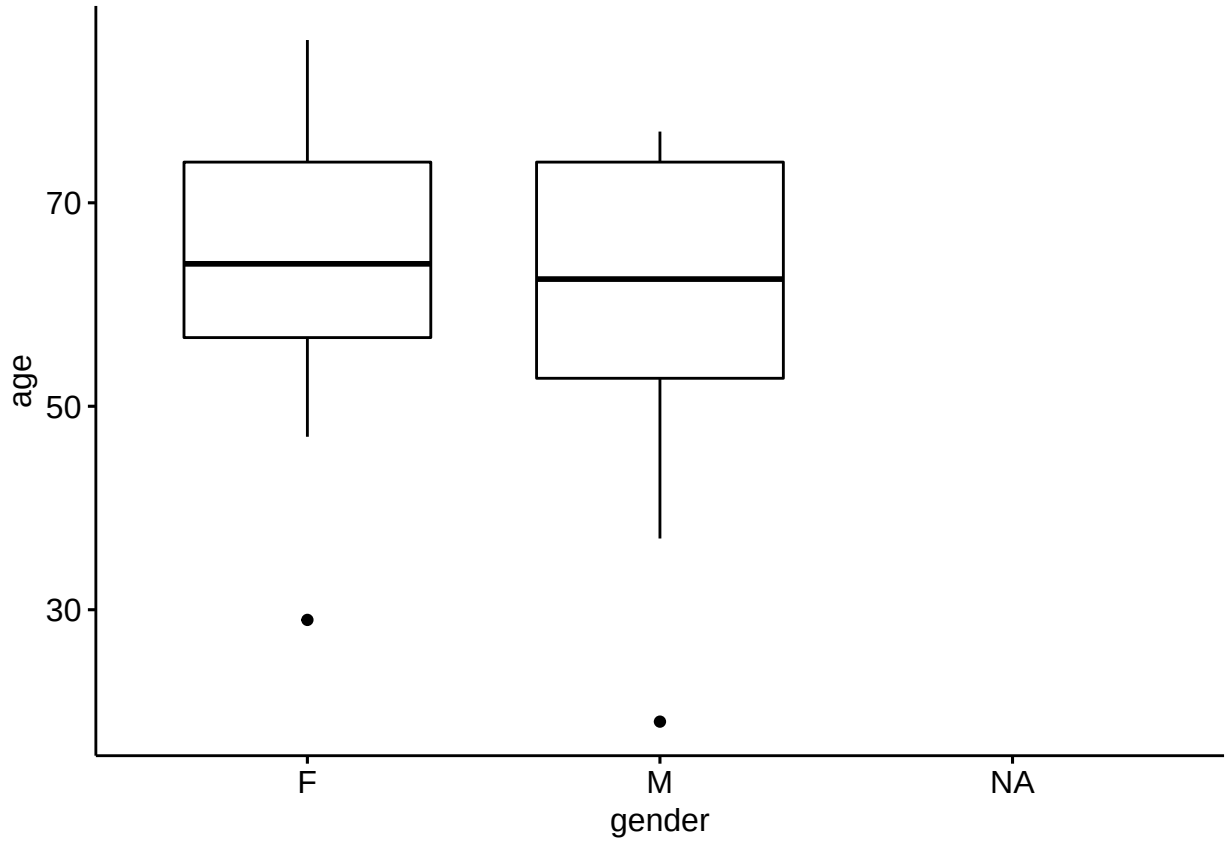



```
summary(pdata$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    19.0    55.2    62.5    60.4    74.0    86.0       3
```

```
ggboxplot(pdata, "gender", "age")
```

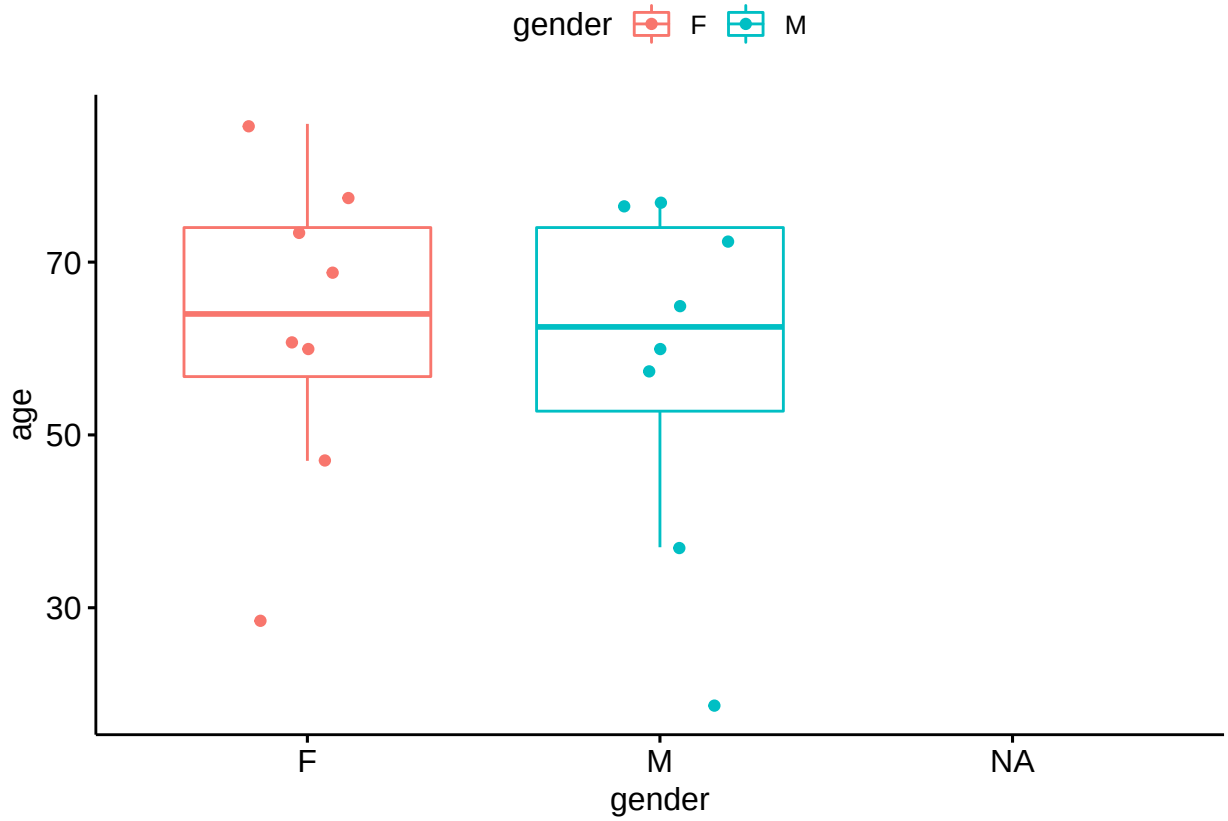
```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```




```
g5 <- ggboxplot(pdata, "gender", "age", color = "gender", add = "jitter")
g5
```

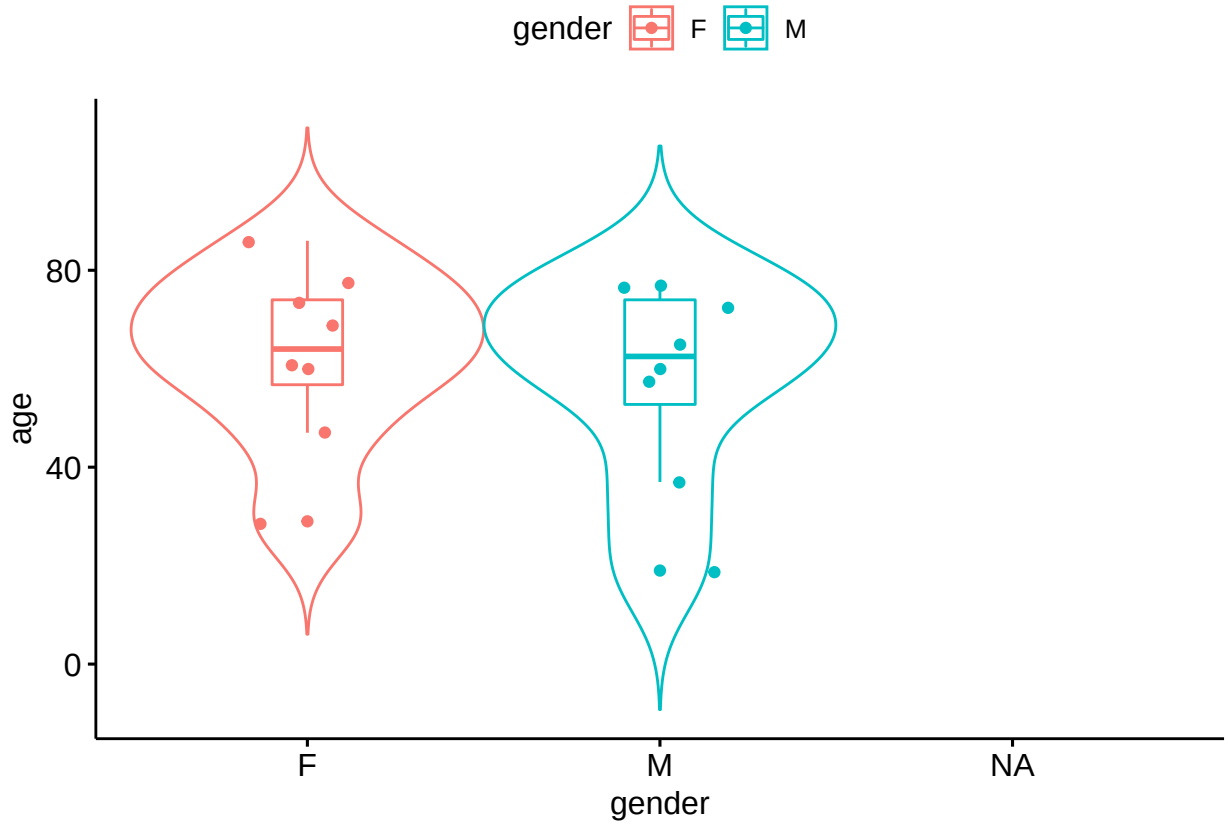
```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```




```
g6 <- ggviolin(pdata, "gender", "age", color = "gender", add = c("boxplot", "jitter"))
g6
```

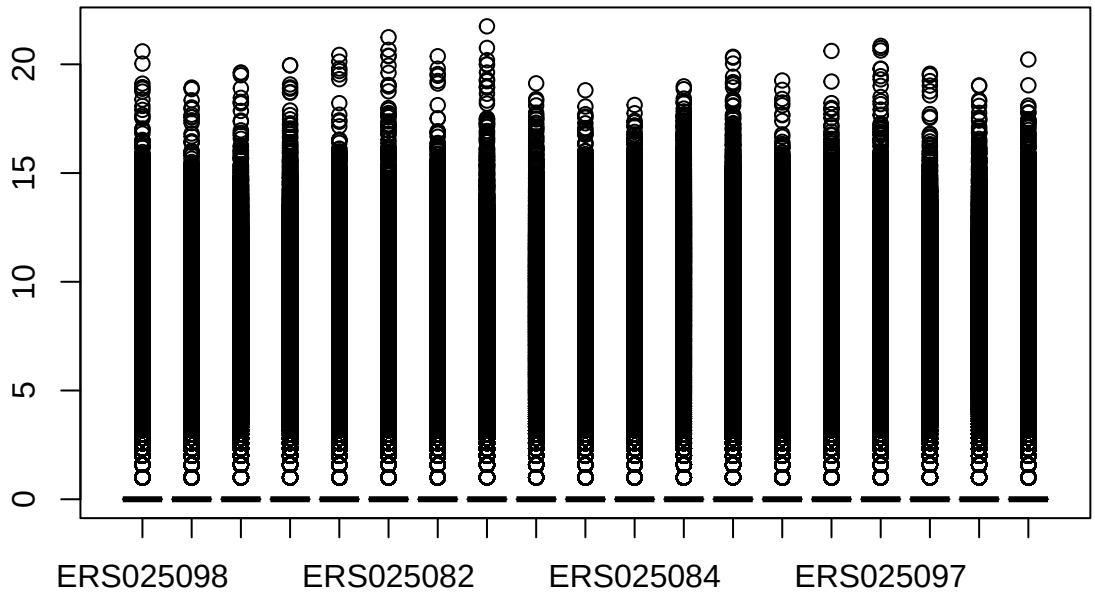
```
## Warning: Removed 3 rows containing non-finite values (stat_ydensity).
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
## Warning: Removed 3 rows containing missing values (geom_point).
```



Expression data

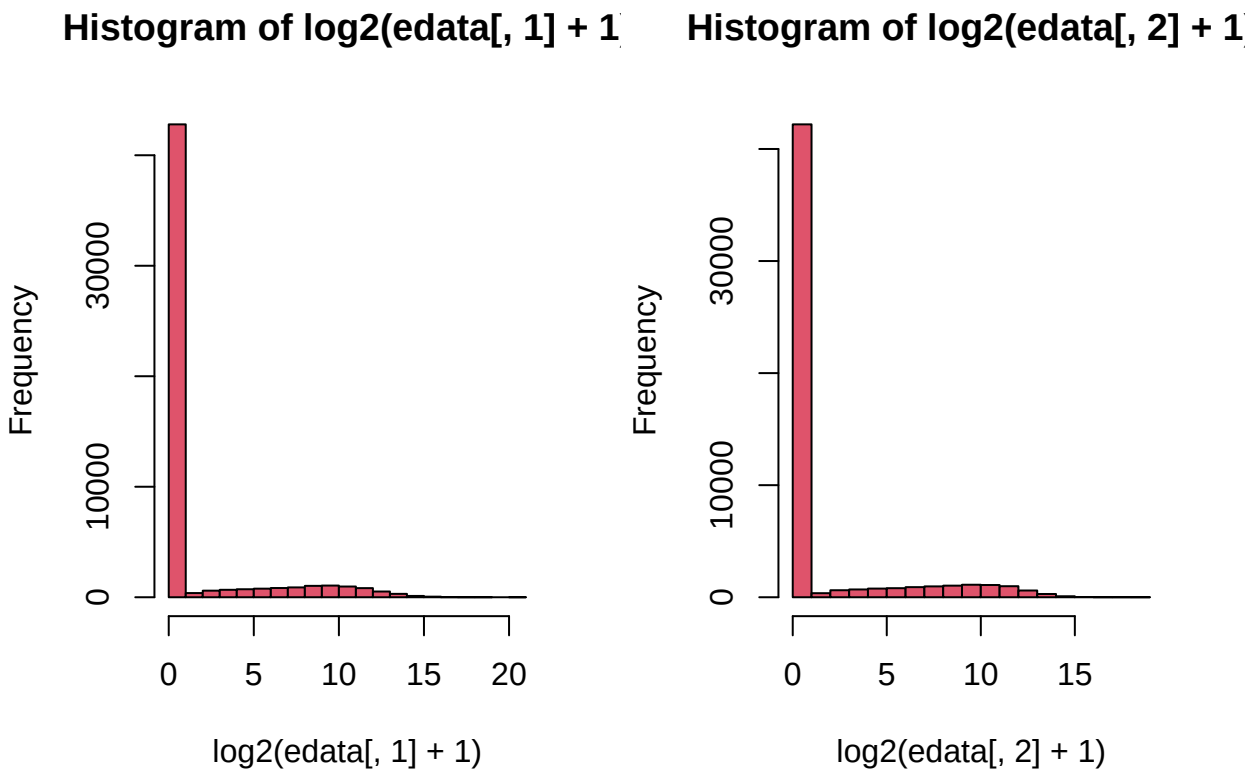
Look at overall distributions:

```
boxplot(log2(edata + 1))
```



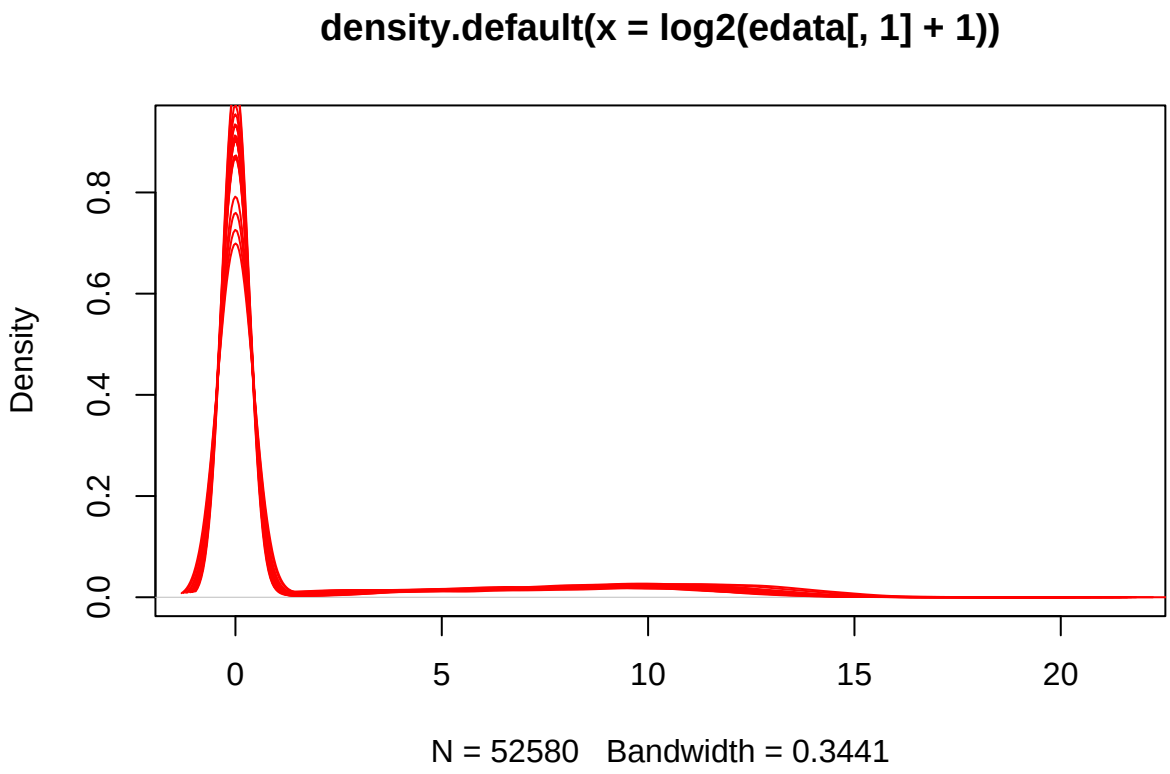
alternatives:

```
# sample by sample histograms
par(mfrow = c(1, 2))
hist(log2(edata[, 1] + 1), col = 2)
hist(log2(edata[, 2] + 1), col = 2)
```



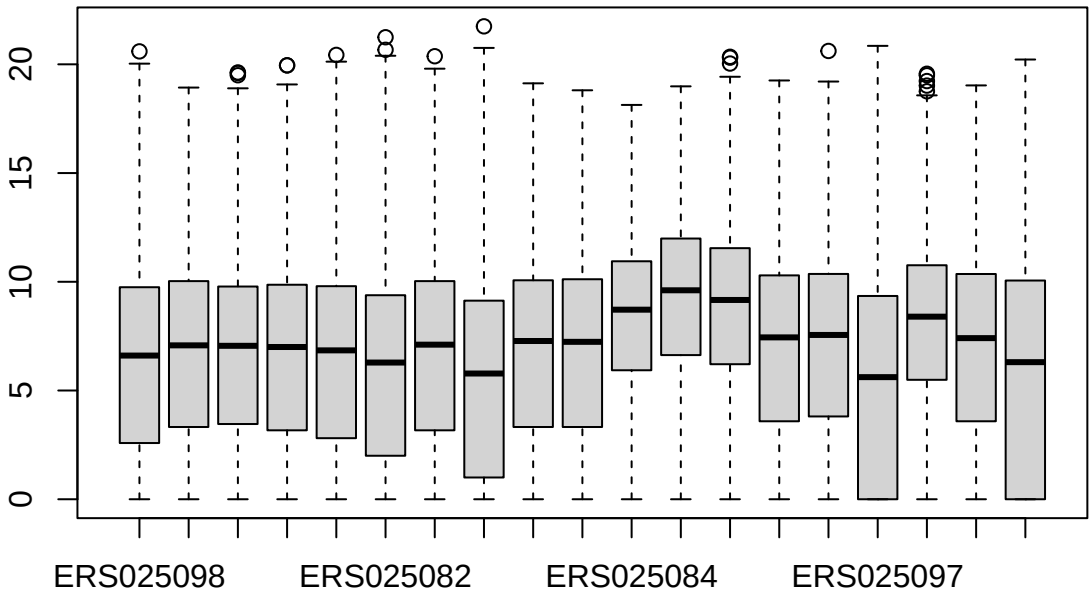

```
par(mfrow = c(1, 1))

### or with densinty plots
plot(density(log2(edata[, 1] + 1)), col = "red")
for (i in 2:ncol(edata)) {
    lines(density(log2(edata[, i] + 1)), col = "red")
}
```



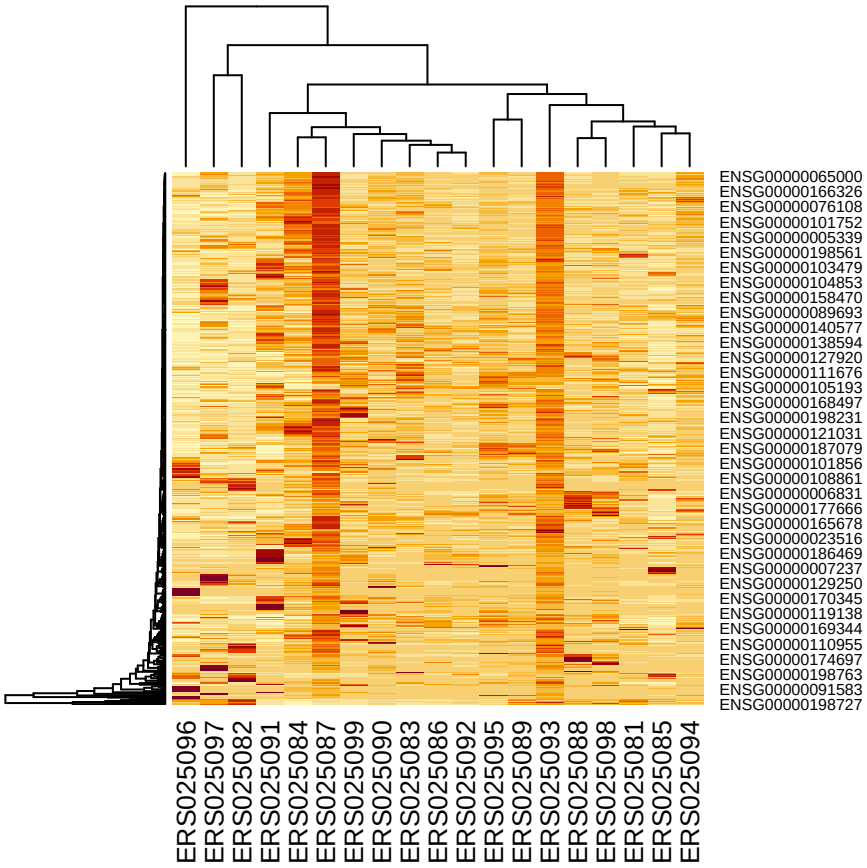
We can remove rows that are mostly zero and notice any differences in the distributions across samples.

```
filt_edata <- edata[rowMeans(edata) > 1, ]
boxplot(log2(filt_edata + 1))
```



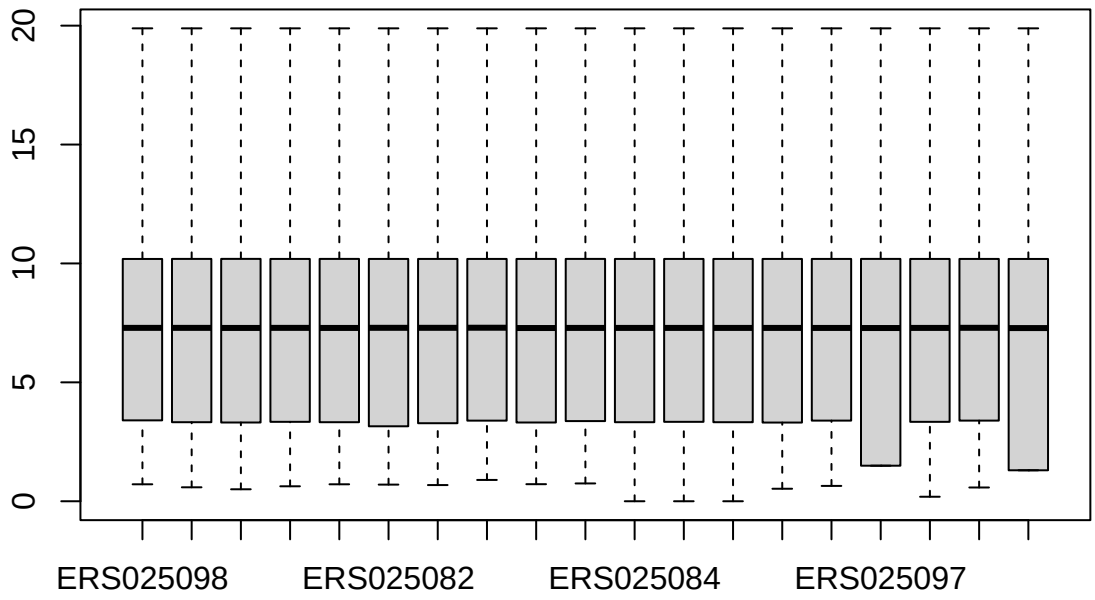
A common type of plot for genomics data is a heatmap. They are usually used for visualizing matrices. For example we can look at all genes with an average number of counts greater than 10000:

```
ematrix <- as.matrix(filt_edata)[rowMeans(filt_edata) > 10000, ]
heatmap(ematrix)
```



Quantile normalization:

```
lt_filt_edata <- log2(filt_edata + 1)
norm_edata <- normalize.quantiles(lt_filt_edata)
colnames(norm_edata) <- colnames(lt_filt_edata)
rownames(norm_edata) <- rownames(lt_filt_edata)
boxplot(norm_edata)
```


20
15
10
5
0
ERS025098
ERS025082
ERS025084
ERS025097