Lab 19: Galaxy

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#Section 4: Population Scale Analysis

> Q13: Read this file into R and determine the sample size for each genotype and their corresponding median expression levels for each of these genotypes.

```
hwdata <- read.table("hwfile.txt")

nrow(hwdata)
```

```
## [1] 462
```

```
summary(hwdata)
```

```
##     sample              geno                exp
##  Length:462         Length:462         Min.   : 6.675
##  Class :character   Class :character   1st Qu.:20.004
##  Mode  :character   Mode  :character   Median :25.116
##                                        Mean   :25.640
##                                        3rd Qu.:30.779
##                                        Max.   :51.518
```

```
head(hwdata)
```

```
##    sample geno      exp
## 1 HG00367  A/G 28.96038
## 2 NA20768  A/G 20.24449
## 3 HG00361  A/A 31.32628
## 4 HG00135  A/A 34.11169
## 5 NA18870  G/G 18.25141
## 6 NA11993  A/A 32.89721
```

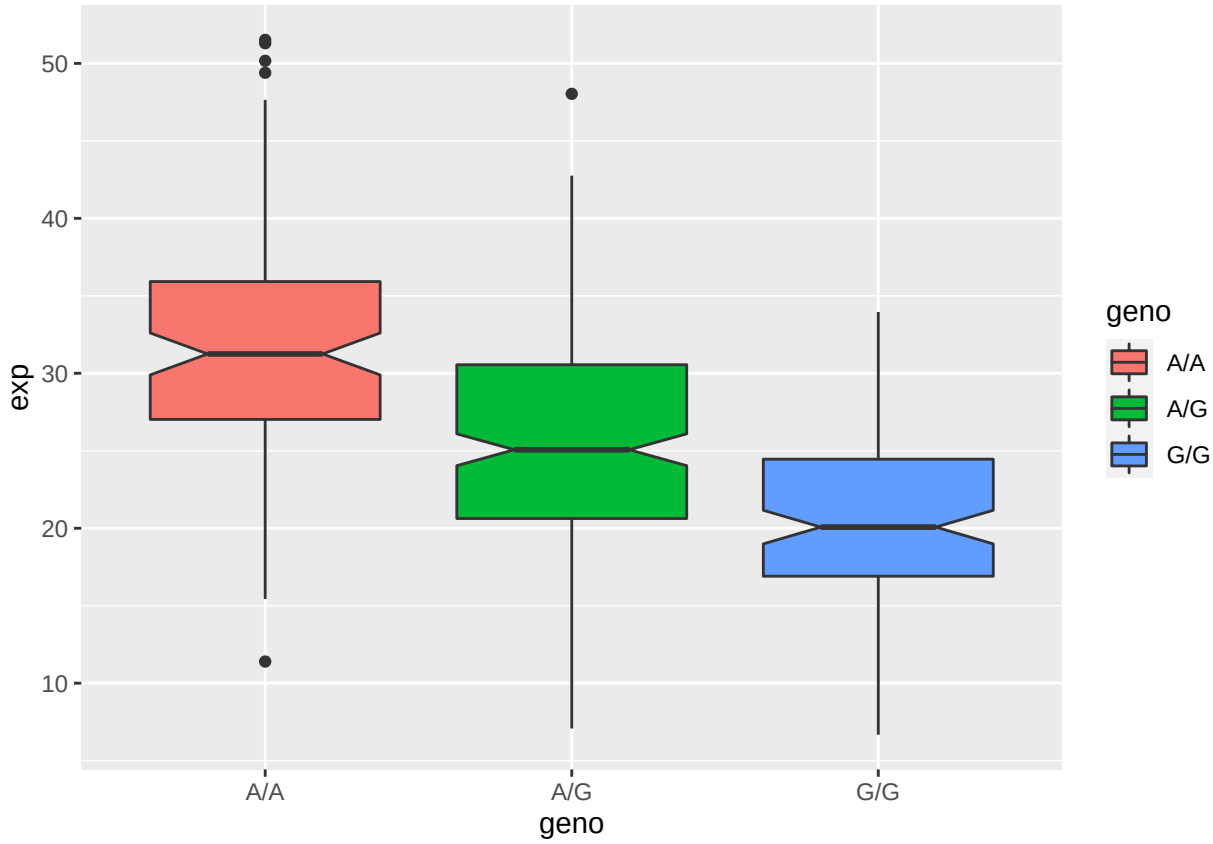
```
table(hwdata$geno)
```

```
##
## A/A A/G G/G
## 108 233 121
```

> Q14: Generate a boxplot with a box per genotype, what could you infer from the relative expression value between A/A and G/G displayed in this plot? Does the SNP effect the expression of ORMDL3?

```
library(ggplot2)

ggplot(hwdata) + aes(x = geno, y = exp, fill=geno) + geom_boxplot(notch = TRUE)
```



Here we can see that the difference is fairly statistically significant, and that having a G|G genotype correlates to having reduced expression of the gene.