

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.

```
# Read the tab-delimited file
data <- read.table("rs8067378_ENSG00000172057.6.txt", header = TRUE)

# Check the first few rows
head(data)
```

```
##   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
```

```
str(data)
```

```
## 'data.frame': 462 obs. of 3 variables:
## $ sample: chr "HG00367" "NA20768" "HG00361" "HG00135" ...
## $ geno  : chr "A/G" "A/G" "A/A" "A/A" ...
## $ exp   : num 29 20.2 31.3 34.1 18.3 ...
```

```
summary(data)
```

```
##      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
```

```
table(data$geno)
```

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

```
tapply(data$exp, data$geno, median)
```

```
##      A/A      A/G      G/G
## 31.24847 25.06486 20.07363
```

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':  
##  
##     filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
##     intersect, setdiff, setequal, union
```

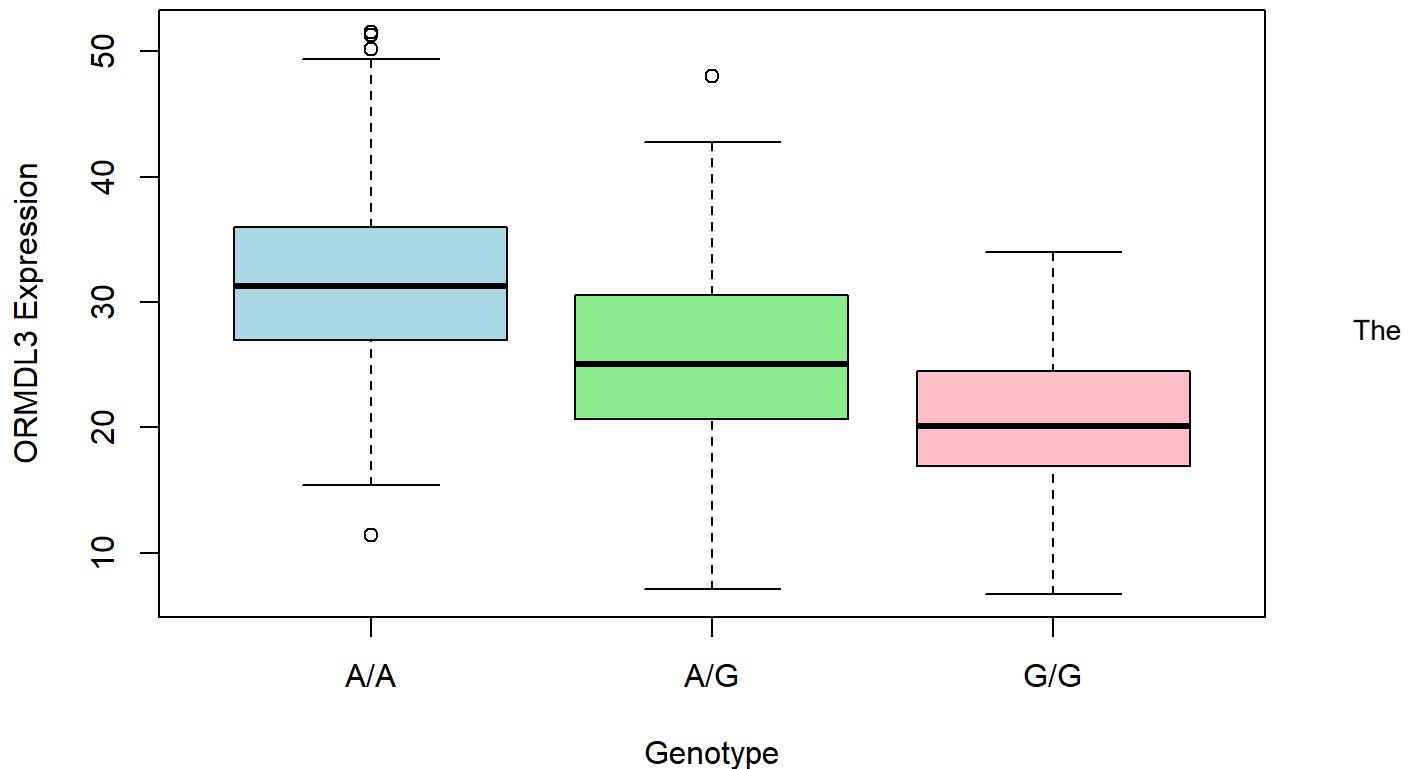
```
data %>%  
  group_by(geno) %>%  
  summarise(  
    n = n(),  
    median_expression = median(exp)  
)
```

```
## # A tibble: 3 × 3  
##   geno      n median_expression  
##   <chr> <int>          <dbl>  
## 1 A/A     108            31.2  
## 2 A/G     233            25.1  
## 3 G/G     121            20.1
```

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?

```
boxplot(exp ~ geno, data = data,  
       main = "ORMDL3 Expression by rs8067378 Genotype",  
       xlab = "Genotype",  
       ylab = "ORMDL3 Expression",  
       col = c("lightblue", "lightgreen", "pink"))
```

ORMDL3 Expression by rs8067378 Genotype



boxplot shows that median ORMDL3 expression varies among genotypes. The G/G genotype exhibits higher median expression compared to the A/A genotype, indicating that the rs8067378 SNP is associated with differences in ORMDL3 expression, with the G allele linked to increased expression.