

lab12

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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.

```
res <- read.table("https://bioboot.github.io/bimm143_F24/class-material/rs8067378_ENSG0000001
```

```
nrow(res)
```

```
[1] 462
```

```
table(res$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(res) + aes(geno, exp, fill = geno) +  
  geom_boxplot(notch = T)
```

