

Lab 11

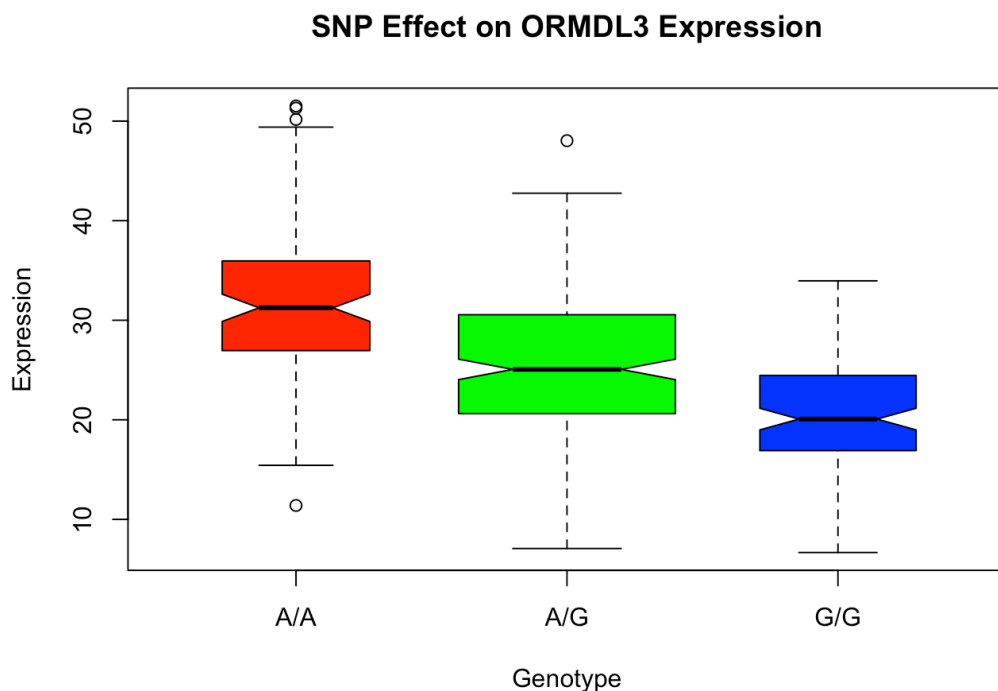
AUTHOR

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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?

```
data11 <- read.table("data11.txt")
```

```
boxplot11 <- boxplot(exp~geno, data= data11, xlab="Genotype", y
```



A/A is more highly expressed than G/G. The SNP does affect the expression of ORMDL3.

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.

```
summary(boxplot11)
```

```
      Length Class  Mode
stats 15      -none- numeric
n       3      -none- numeric
conf   6      -none- numeric
out    5      -none- numeric
group  5      -none- numeric
names  3      -none- character
```

```
boxplot11
```

```
$stats
```

```
      [,1]      [,2]      [,3]
[1,] 15.42908  7.07505  6.67482
[2,] 26.95022 20.62572 16.90256
[3,] 31.24847 25.06486 20.07363
[4,] 35.95503 30.55183 24.45672
[5,] 49.39612 42.75662 33.95602
```

```
$n
```

```
[1] 108 233 121
```

```
$conf
```

```
      [,1]      [,2]      [,3]
[1,] 29.87942 24.03742 18.98858
[2,] 32.61753 26.09230 21.15868
```

```
$out
```

```
[1] 51.51787 50.16704 51.30170 11.39643 48.03410
```

```
$group
```

```
[1] 1 1 1 1 2
```

```
$names
```

```
[1] "A/A" "A/G" "G/G"
```

```
#subset(data11, geno%in% c("A/A"))
```

```
#subset(data11, geno%in% c("A/G"))
```

```
#subset(data11, geno%in% c("G/G"))
```

The median expression level for genotype A/A is 31.25, for A/G is 25.06, and for G/G is 20.07. The sample sizes are 108 for A/A, 233 for A/G, and 121 for G/G.

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