class12: population scale analysis

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```
expr <- read.table("rs8067378_ENSG00000172057.6.txt")
head(expr)
```

```
   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
```

```
nrow(expr)
```

```
[1] 462
```

```
table(expr$geno)
```

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

```
median(31.32628+34.11169+32.89721)
```

```
[1] 98.33518
```

```
median(28.96038+20.24449)
```

```
[1] 49.20487
```

```
median(18.25141)
```

```
[1] 18.25141
```

```
summary(expr)
```

```
   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  
```

```
library(ggplot2)
```

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