

Class 12: Differential Expression Analysis

Marcos

2. Import countData and colData

```
counts <- read.csv('airway_scaledcounts.csv', row.names = 1)
metadata <- read.csv('airway_metadata.csv')
```

Q1. How many genes are in this dataset?

In this dataset there are 38694 genes.

Q2. How many control cell lines do we have?

We have 4 control cell lines.