# class17

Tin

```
# Load required library
# install.packages("BiocManager")
# BiocManager::install("tximport")
library(tximport)

# Automatically find all *_quant folders in the current directory
folders <- list.dirs(path = ".", full.names = FALSE, recursive = FALSE)
folders <- folders[grepl("^SRR21568.*_quant$", folders)]

# Extract sample names (e.g., "SRR2156848" from "SRR2156848_quant")
samples <- sub("_quant$", "", folders)

# Create full paths to abundance.h5 files
files <- file.path(folders, "abundance.h5")
names(files) <- samples

# Import transcript-level counts
txi.kallisto <- tximport(files, type = "kallisto", txOut = TRUE)</pre>
```

### 1 2 3 4

```
# Optional: quick preview
head(txi.kallisto$counts)
```

#### SRR2156848 SRR2156849 SRR2156850 SRR2156851 ENST00000539570 0.00000 ENST00000576455 0 2.62037 0 ENST00000510508 0 0.00000 0 0 ENST00000474471 1 1.00000 0 ENST00000381700 0 0.00000 0 0.00000 ENST00000445946 0

### head(txi.kallisto\$counts)

```
SRR2156848 SRR2156849 SRR2156850 SRR2156851
ENST00000539570
                                      0.00000
ENST00000576455
                       0
                                      2.62037
                                                       0
ENST00000510508
                       0
                                 0.00000
                                                      0
                                 1 1.00000
                       0
ENST00000474471
                                                      0
ENST00000381700
                       0
                                 0.00000
                                                      0
ENST00000445946
                                      0.00000
                       0
                                                       0
```

## colSums(txi.kallisto\$counts)

SRR2156848 SRR2156849 SRR2156850 SRR2156851 2563611 2600800 2372309 2111474

```
to.keep <- rowSums(txi.kallisto$counts) > 0
kset.nonzero <- txi.kallisto$counts[to.keep,]</pre>
```

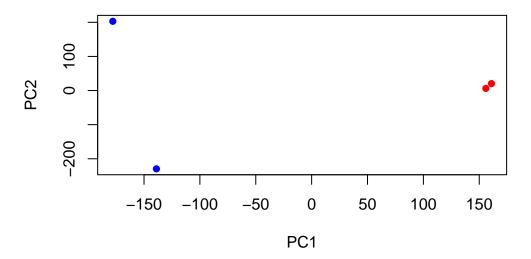
```
keep2 <- apply(kset.nonzero,1,sd)>0
x <- kset.nonzero[keep2,]</pre>
```

```
pca <- prcomp(t(x), scale=TRUE)</pre>
```

```
summary(pca)
```

Importance of components:

PC1 PC2 PC3 PC4
Standard deviation 183.6379 177.3605 171.3020 1e+00
Proportion of Variance 0.3568 0.3328 0.3104 1e-05
Cumulative Proportion 0.3568 0.6895 1.0000 1e+00



```
library(ggplot2)
library(ggrepel)

# Make metadata object for the samples
colData <- data.frame(condition = factor(rep(c("control", "treatment"), each = 2)))
rownames(colData) <- colnames(txi.kallisto$counts)

# Make the data.frame for ggplot
y <- as.data.frame(pca$x)
y$Condition <- as.factor(colData$condition)

ggplot(y) +
   aes(PC1, PC2, col=Condition) +
   geom_point() +
   geom_text_repel(label=rownames(y)) +
   theme_bw()</pre>
```

