

# Class16

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```
library(tximport)
folders <- dir(pattern="SRR21568*")
samples <- sub("_quant", "", folders)
files <- file.path( folders, "abundance.tsv" )
names(files) <- samples

txi.kallisto <- tximport(files, type = "kallisto", txOut = TRUE)
```

Note: importing `abundance.h5` is typically faster than `abundance.tsv`

reading in files with `read_tsv`

1 2 3 4

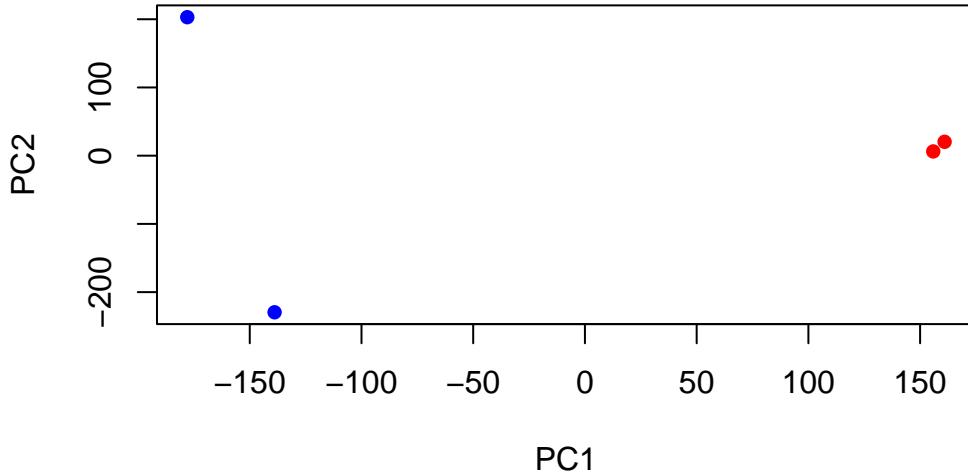
```
to.keep <- rowSums(txi.kallisto$counts) > 0
kset.nonzero <- txi.kallisto$counts[to.keep,]
keep2 <- apply(kset.nonzero, 1, sd) > 0
x <- kset.nonzero[keep2,]
```

```
pca <- prcomp(t(x), scale=TRUE)
summary(pca)
```

Importance of components:

	PC1	PC2	PC3	PC4
Standard deviation	183.6353	177.3561	171.3005	4.91e-11
Proportion of Variance	0.3568	0.3328	0.3105	0.00e+00
Cumulative Proportion	0.3568	0.6895	1.0000	1.00e+00

```
plot(pca$x[,1], pca$x[,2],
      col=c("blue","blue","red","red"),
      xlab="PC1", ylab="PC2", pch=16)
```

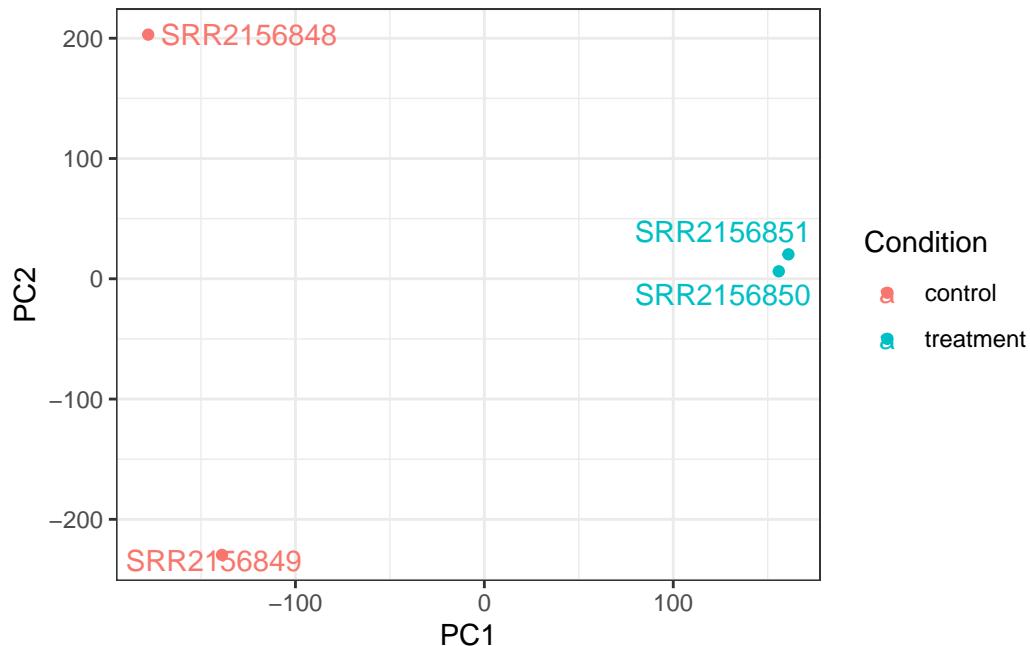


```
library(ggplot2)
library(ggrepel)

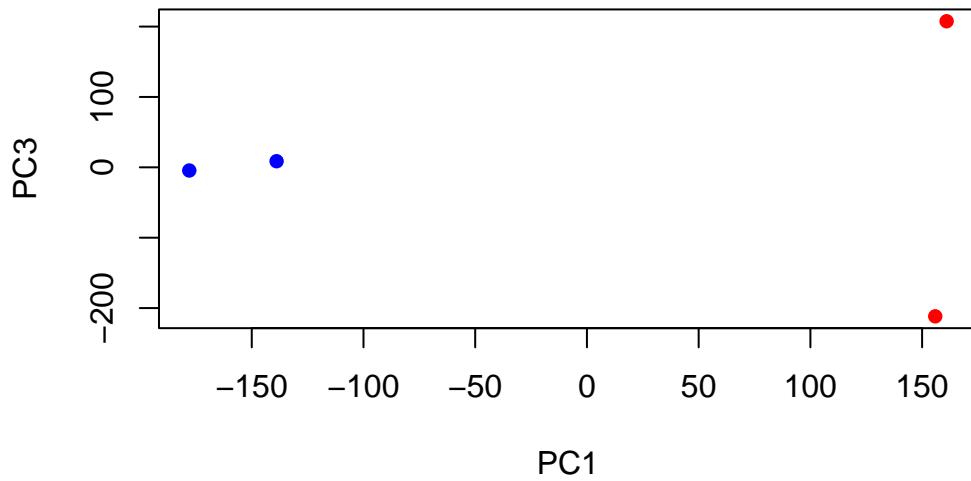
# Make metadata object for the samples
colData <- data.frame(condition = factor(rep(c("control", "treatment"), each = 2)))
rownames(colData) <- colnames(tx1.kallisto$counts)

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

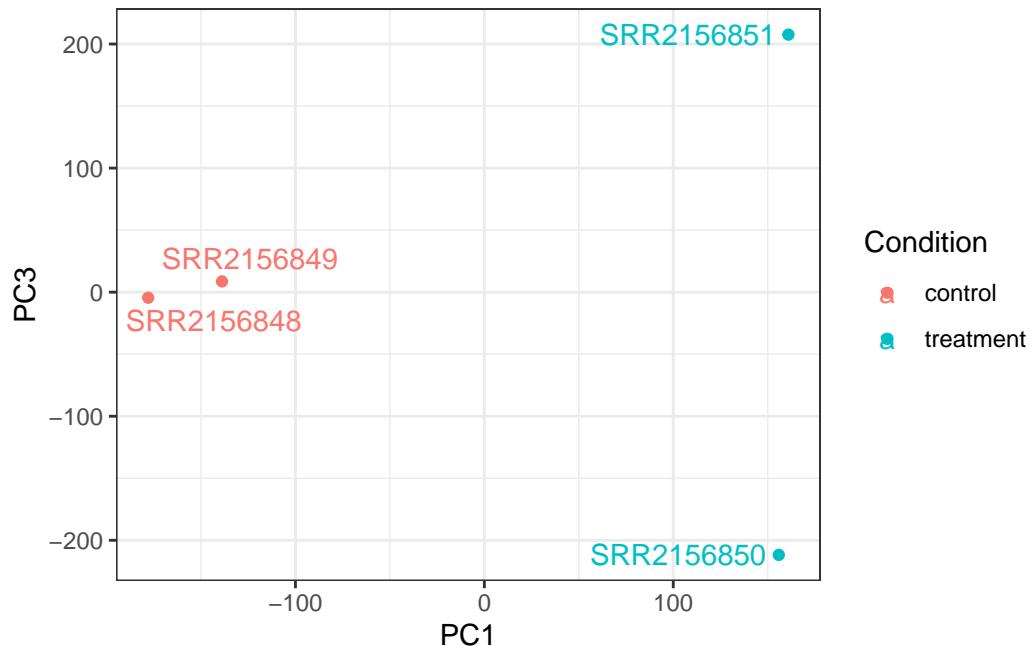
ggplot(y) +
  aes(PC1, PC2, col=Condition) +
  geom_point() +
  geom_text_repel(label=rownames(y)) +
  theme_bw()
```



```
pca <- prcomp(t(x), scale=TRUE)
plot(pca$x[,1], pca$x[,3],
      col=c("blue","blue","red","red"),
      xlab="PC1", ylab="PC3", pch=16)
```



```
ggplot(y) +  
  aes(PC1, PC3, col=Condition) +  
  geom_point() +  
  geom_text_repel(label=rownames(y)) +  
  theme_bw()
```

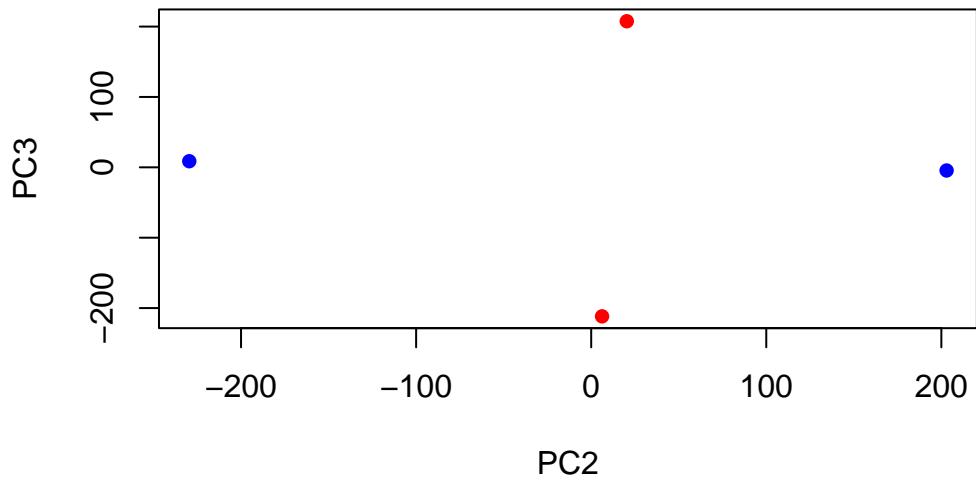


```
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```
plot(pca$x[,2], pca$x[,3],
     col=c("blue","blue","red","red"),
     xlab="PC2", ylab="PC3", pch=16)
```



```
ggplot(y) +
  aes(PC2, PC3, col=Condition) +
  geom_point() +
  geom_text_repel(label=rownames(y)) +
  theme_bw()
```

