

lab17.0

Ilyas Darif

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```
library(tximport)

# setup the folder and filenames to read
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

```
colSums(txi.kallisto$counts)
```

```
SRR2156848 SRR2156849 SRR2156850 SRR2156851
      2563611      2600800      2372309      2111474
```

```
sum(rowSums(txi.kallisto$counts)>0)
```

```
[1] 94561
```

```
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,]
```

Principle Component Analysis

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

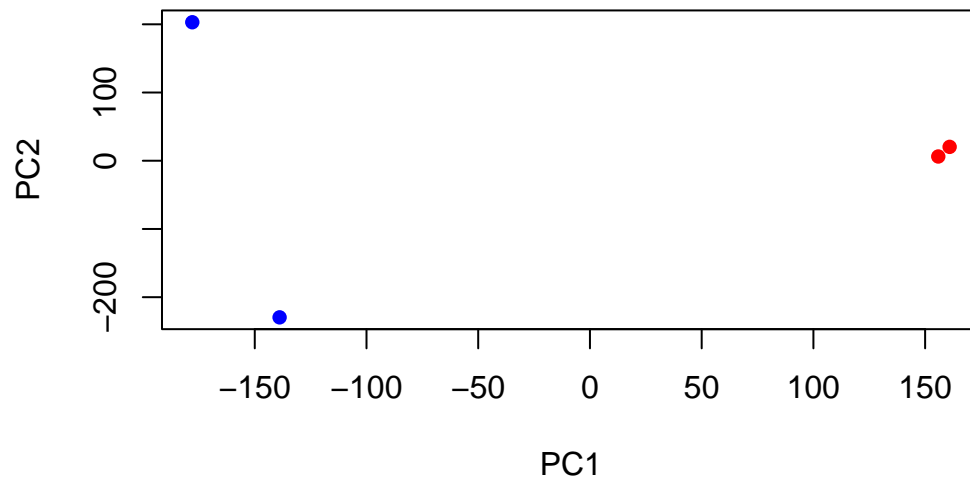
```
summary(pca)
```

Importance of components:

	PC1	PC2	PC3	PC4
Standard deviation	183.6353	177.3561	171.3005	4.877e-11
Proportion of Variance	0.3568	0.3328	0.3105	0.000e+00
Cumulative Proportion	0.3568	0.6895	1.0000	1.000e+00

Now we can use the first two principal components as a co-ordinate system for visualizing the summarized transcriptomic profiles of each sample:

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

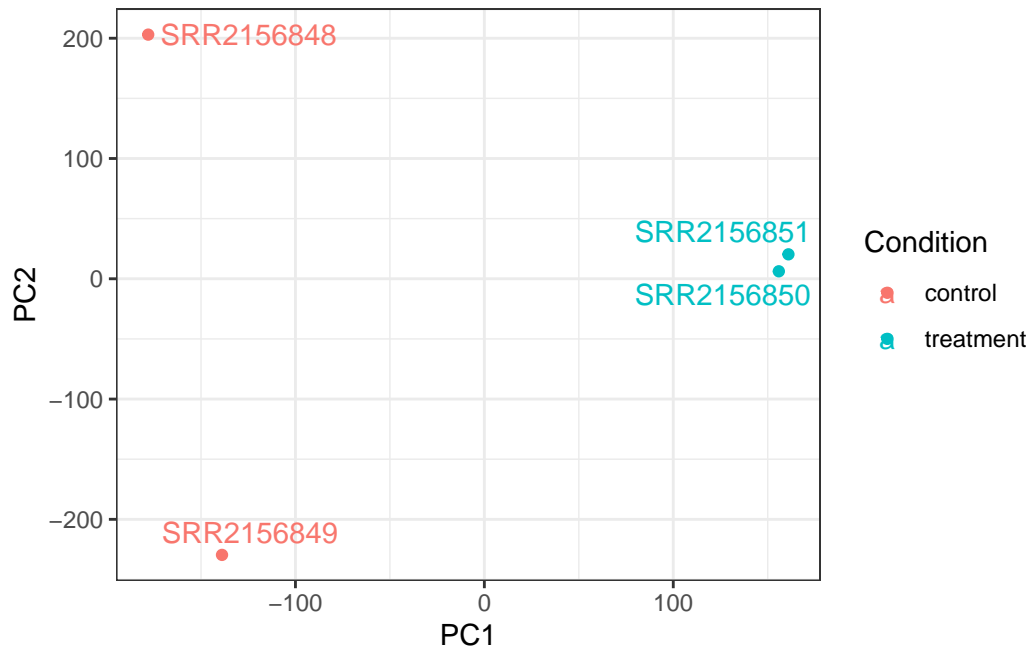


```
library(ggplot2)
library(ggrepel)

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

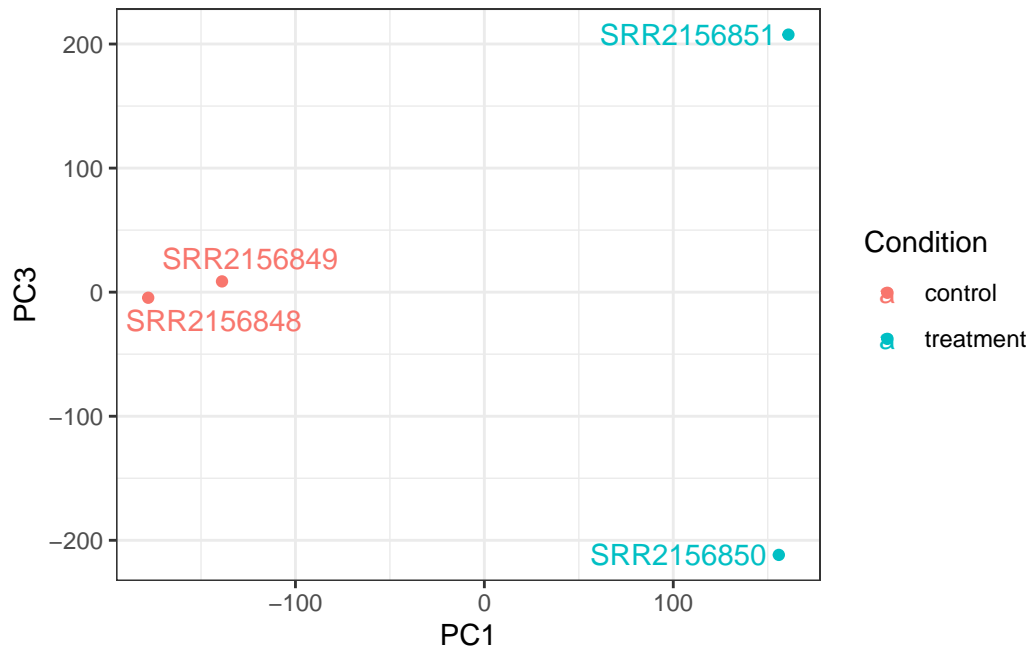


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ggplot(y) +
  aes(PC1, PC3, col=Condition) +
  geom_point() +
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```



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rownames(colData) <- colnames(tri.kallisto$counts)

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

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

