

CYTO DE

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Report Outline:

This report is on Differential Expression (DE) between S2 and WT samples in the Treated (CYTO) samples.

Stringtie to DESeq2 object:

```
library(DESeq2)

## Loading required package: S4Vectors
## Loading required package: stats4
## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:parallel':
##       clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##       clusterExport, clusterMap, parApply, parCapply, parLapply,
##       parLapplyLB, parRapply, parSapply, parSapplyLB
## The following objects are masked from 'package:stats':
##       IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##       anyDuplicated, append, as.data.frame, basename, cbind,
##       colMeans, colnames, colSums, dirname, do.call, duplicated,
##       eval, evalq, Filter, Find, get, grep, grepl, intersect,
##       is.unsorted, lapply, lengths, Map, mapply, match, mget, order,
##       paste, pmax, pmax.int, pmin, pmin.int, Position, rank, rbind,
##       Reduce, rowMeans, rownames, rowSums, sapply, setdiff, sort,
##       table, tapply, union, unique, unsplit, which, which.max,
##       which.min
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:base':
##       expand.grid
## Loading required package: IRanges
## Loading required package: GenomicRanges
## Loading required package: GenomeInfoDb
## Loading required package: SummarizedExperiment
```

```

## Loading required package: Biobase
## Welcome to Bioconductor
##
##      Vignettes contain introductory material; view with
##      'browseVignettes()'. To cite Bioconductor, see
##      'citation("Biobase")', and for packages 'citation("pkgname")'.
## Loading required package: DelayedArray
## Loading required package: matrixStats
##
## Attaching package: 'matrixStats'
## The following objects are masked from 'package:Biobase':
## 
##     anyMissing, rowMedians
## Loading required package: BiocParallel
##
## Attaching package: 'DelayedArray'
## The following objects are masked from 'package:matrixStats':
## 
##     colMaxs, colMins, colRanges, rowMaxs, rowMins, rowRanges
## The following objects are masked from 'package:base':
## 
##     aperm, apply
library(tximport)

directory <- "/Users/barrydigby/Desktop/read_tables/"

data <- c("/Users/barrydigby/Desktop/read_tables/H84S2CYTO_S10/t_data.ctab",
         "/Users/barrydigby/Desktop/read_tables/H84WTCYTO_S4/t_data.ctab",
         "/Users/barrydigby/Desktop/read_tables/H85S2CYTO_S11/t_data.ctab",
         "/Users/barrydigby/Desktop/read_tables/H85WTCYTO_S5/t_data.ctab",
         "/Users/barrydigby/Desktop/read_tables/H86S2CYTO_S12/t_data.ctab",
         "/Users/barrydigby/Desktop/read_tables/H86WTCYTO_S6/t_data.ctab")

tmp <- read.table(data[1], header = TRUE)
names(data) <- c("S2CYTO_10", "WTCYTO_4", "S2CYTO_11", "WTCYTO_5", "S2CYTO_12", "WTCYTO_6")
tx2gene <- tmp[, c("t_name", "gene_name")]
txi <- tximport(data, type = "stringtie", tx2gene = tx2gene)

## reading in files with read_tsv
## 1 2 3 4 5 6
## summarizing abundance
## summarizing counts
## summarizing length

sampleNames <- c("S2CYTO_10", "WTCYTO_4", "S2CYTO_11", "WTCYTO_5", "S2CYTO_12", "WTCYTO_6")
sampleGroup <- c("S2", "WT", "S2", "WT", "S2", "WT")
sampleTable <- data.frame(sampleName = sampleNames, type = sampleGroup)

```

```

rownames(sampleTable) <- colnames(txr$counts)
ddsTxr <- DESeqDataSetFromTximport(txr, sampleTable, design = ~ type)

## using counts and average transcript lengths from tximport
dds <- DESeq(ddsTxr)

## estimating size factors
## using 'avgTxLength' from assays(dds), correcting for library size
## estimating dispersions
## gene-wise dispersion estimates
## mean-dispersion relationship
## final dispersion estimates
## fitting model and testing
res <- results(dds)
counts <- counts(dds)

```

Data Quality Assessment

Transformation & Visualization

The majority of genes have zero or very low counts, thus we apply a log2-transformation on counts before visualization. The distribution of log2 transformed counts are shown as a boxplot and a density plot:

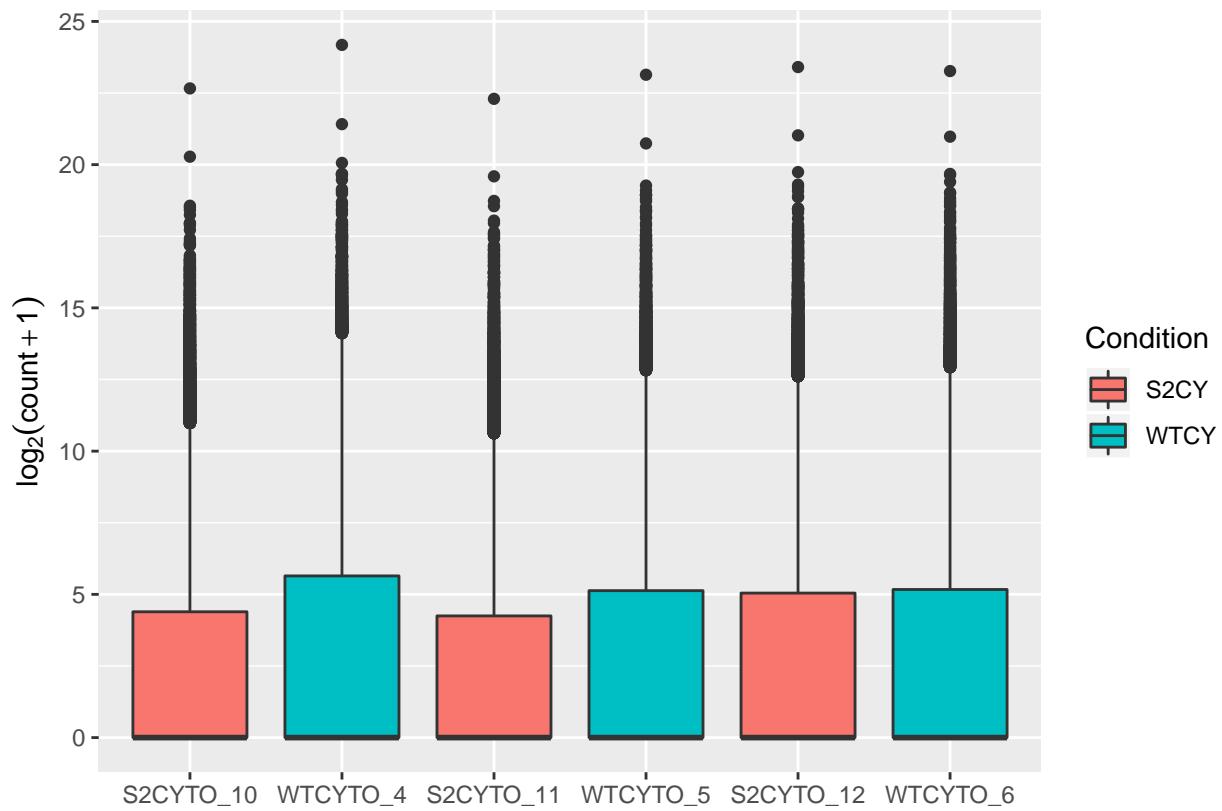
```

pseudoCount = log2(counts + 1)

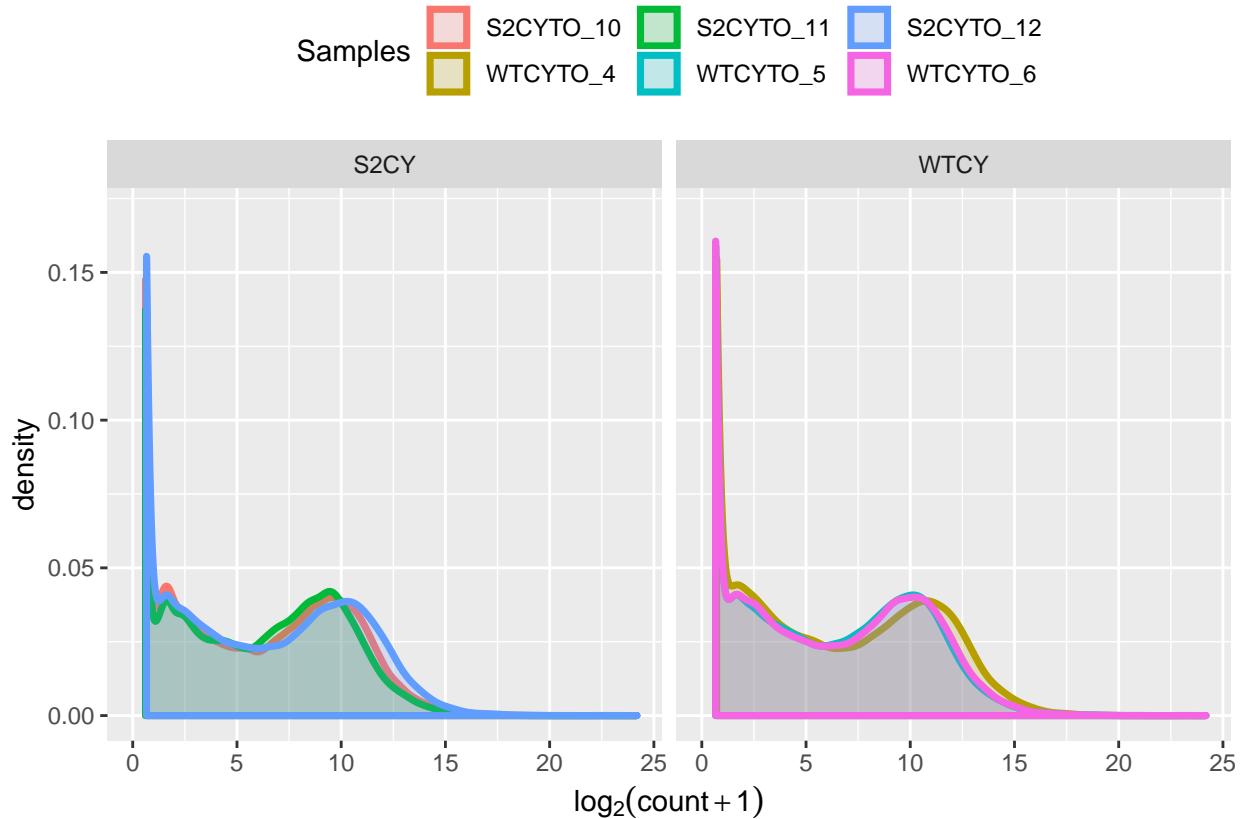
library(reshape2)
library(ggplot2)
pseudoCount = as.data.frame(pseudoCount)
df = melt(pseudoCount, variable.name = "Samples", value.name = "count") # reshape the matrix

## No id variables; using all as measure variables
df = data.frame(df, Condition = substr(df$Samples, 1, 4))
ggplot(df, aes(x = df$Samples, y = count, fill = Condition)) + geom_boxplot() + xlab("") +
  ylab(expression(log[2](count + 1)))

```

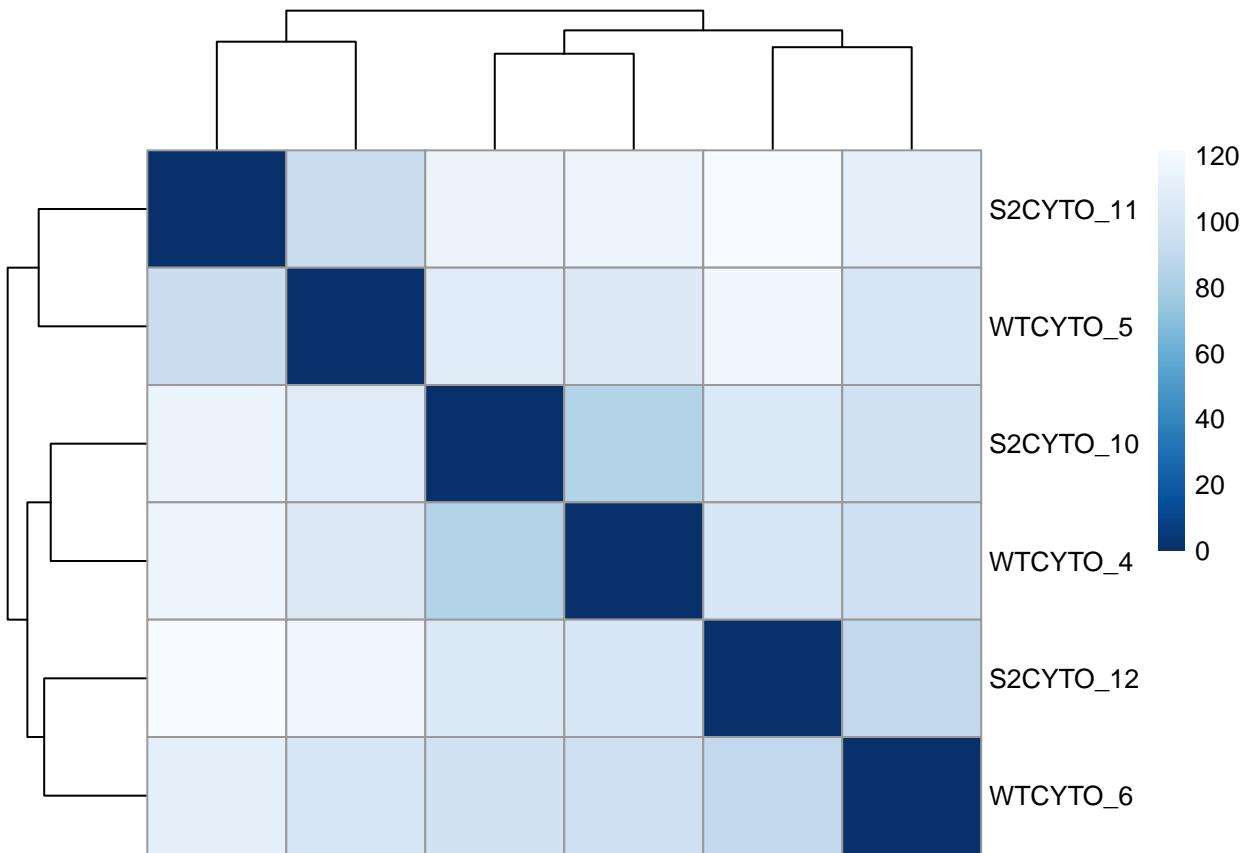


```
ggplot(df, aes(x = count, colour = Samples, fill = Samples)) + ylim(c(0, 0.17)) +
  geom_density(alpha = 0.2, size = 1.25) + facet_wrap(~ Condition) +
  theme(legend.position = "top") + xlab(expression(log[2](count + 1)))
```



Sample to Sample Distances

```
sampleDists <- dist(t(assay(vsd)))
library("pheatmap")
library("RColorBrewer")
sampleDistMatrix <- as.matrix(sampleDists)
rownames(sampleDistMatrix) <- vsd$sampleName
colnames(sampleDistMatrix) <- NULL
colors <- colorRampPalette( rev(brewer.pal(9, "Blues")) )(255)
pheatmap(sampleDistMatrix,
         clustering_distance_rows=sampleDists,
         clustering_distance_cols=sampleDists,
         col=colors)
```



```

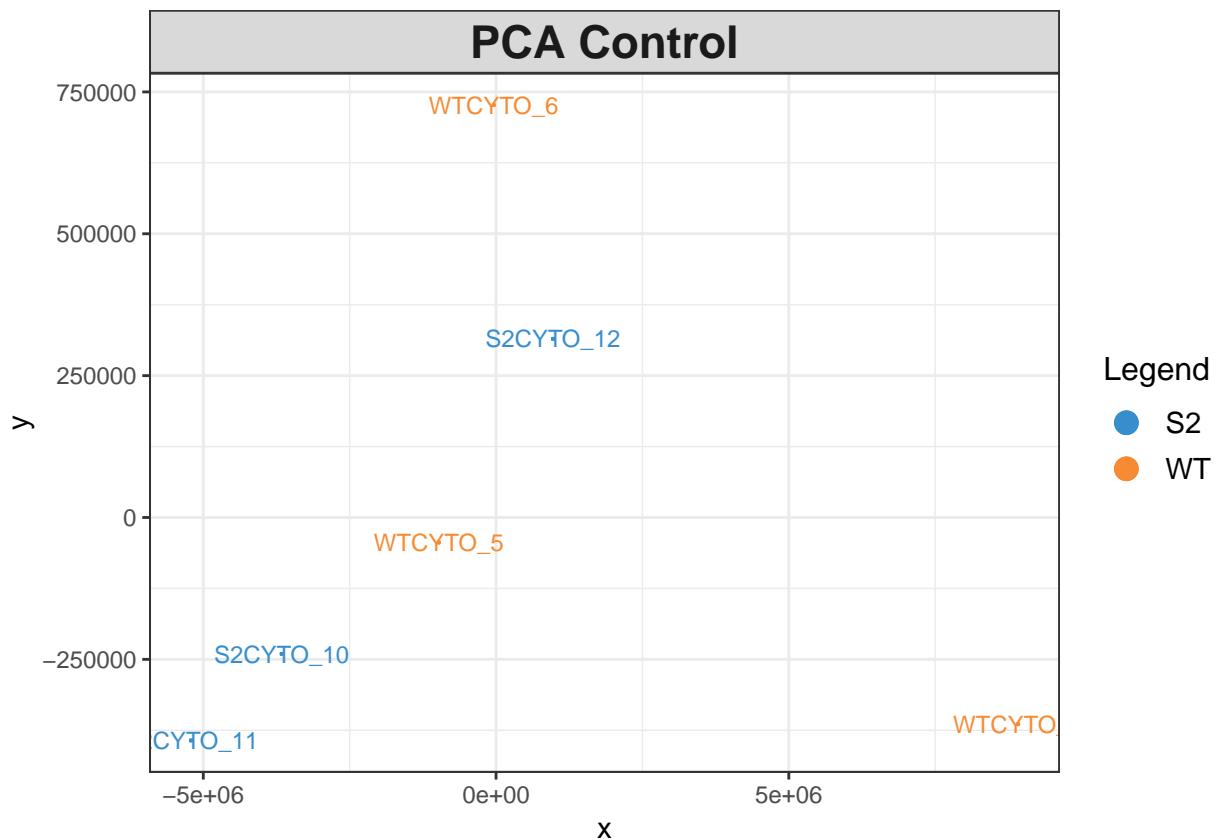
# PCA plots
library(mixOmics)

## Loading required package: MASS
## Loading required package: lattice
##
## Loaded mixOmics 6.6.0
##
## Thank you for using mixOmics! Learn how to apply our methods with our tutorials on www.mixOmics.org,
## Questions: email us at mixomics[at]math.univ-toulouse.fr
## Bugs, Issues? https://github.com/mixOmicsTeam/mixOmics/issues
## Cite us: citation('mixOmics')

counts.t <- t(counts(dds))
outcome <- as.factor(dds$type)

pca = pca(counts.t, ncomp = 6)
plotIndiv(pca, group = outcome, ind.names = TRUE, legend = TRUE, title = 'PCA Control')

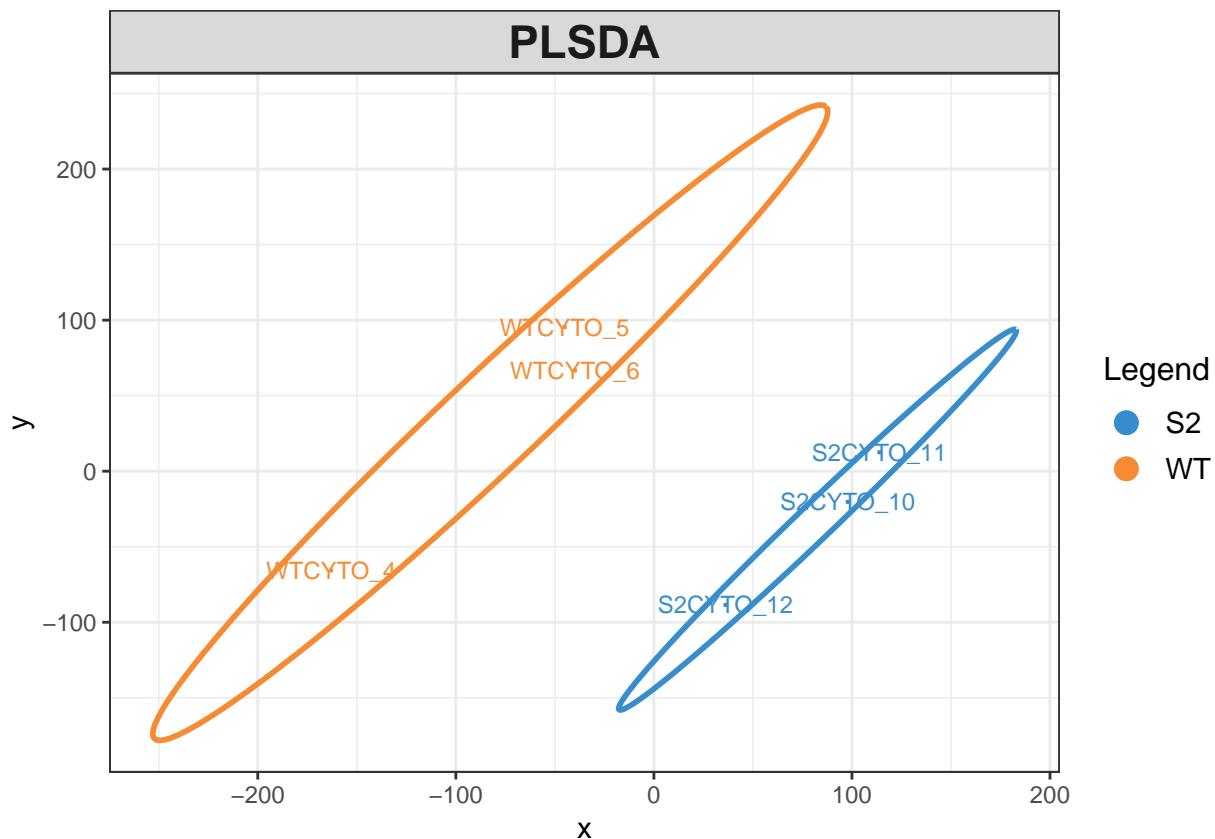
```



```
plsda_ <- plsda(counts.t, outcome, ncomp = 5)
```

```
## Warning in cor(A[[k]], variates.A[[k]]): the standard deviation is zero
```

```
plotIndiv(plsda_, comp = 1:2, group = outcome, ind.names = TRUE, ellipse = TRUE, legend = TRUE, title =
```

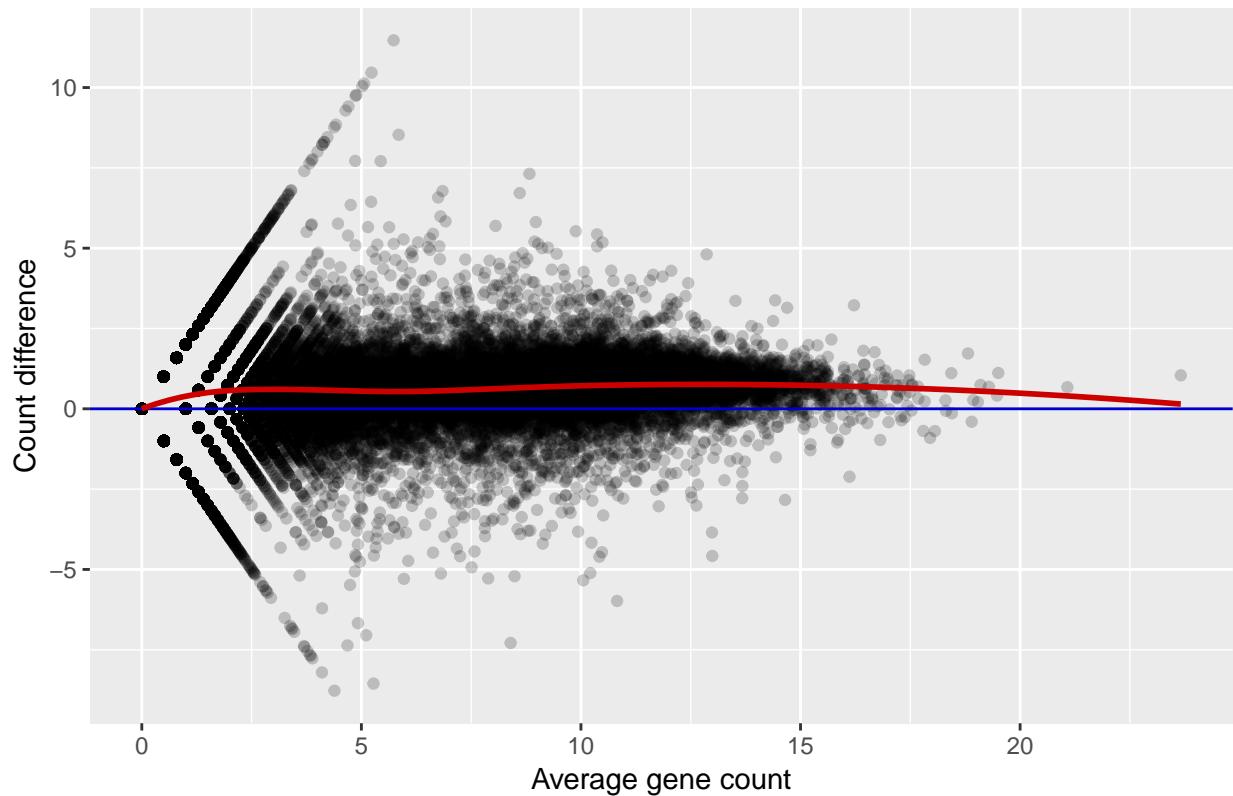


Systematic biases

Plot

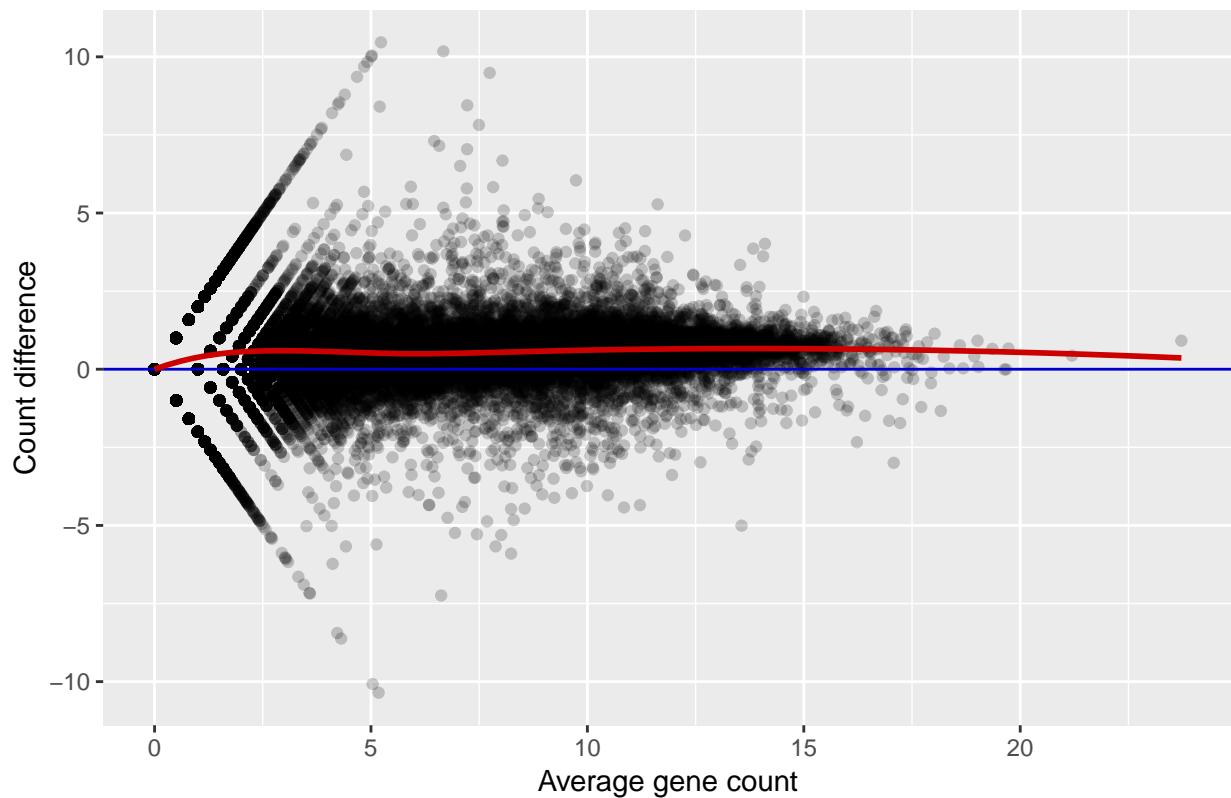
```
x = pseudoCount[, 2] #
y = pseudoCount[, 4]
M = x - y # M-values (differences between samples)
A = (x + y)/2 # A-values (averages)
df = data.frame(A, M)
ggplot(df, aes(x = A, y = M)) + geom_point(size = 1.5, alpha = 1/5) +
  geom_hline(aes(yintercept = 0), color = "blue3") + stat_smooth(se =
  FALSE, method = "loess", color = "red3") +
  xlab("Average gene count") +
  ylab("Count difference") +
  ggtitle("WTCYT04 vs. WTCYT05")
```

WTCYTO4 vs. WTCYTO5



```
x = pseudoCount[, 2] #
y = pseudoCount[, 6] #
M = x - y # M-values (differences between samples)
A = (x + y)/2 # A-values (averages)
df = data.frame(A, M)
ggplot(df, aes(x = A, y = M)) + geom_point(size = 1.5, alpha = 1/5) +
  geom_hline(aes(yintercept = 0), color = "blue3") + stat_smooth(se =
  FALSE, method = "loess", color = "red3") +
  xlab("Average gene count") +
  ylab("Count difference") +
  ggtitle("WTCYTO4 vs. WTCYTO5")
```

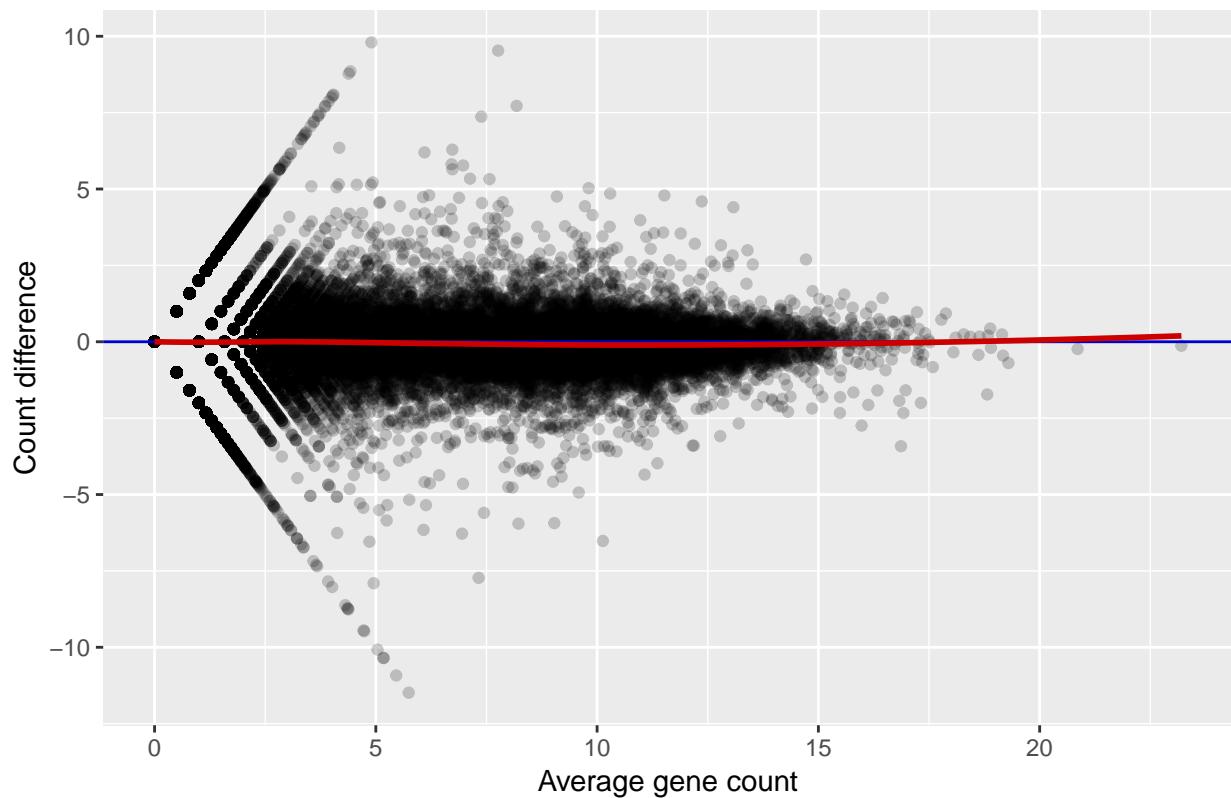
WTCYTO4 vs. WTCYTO6



```

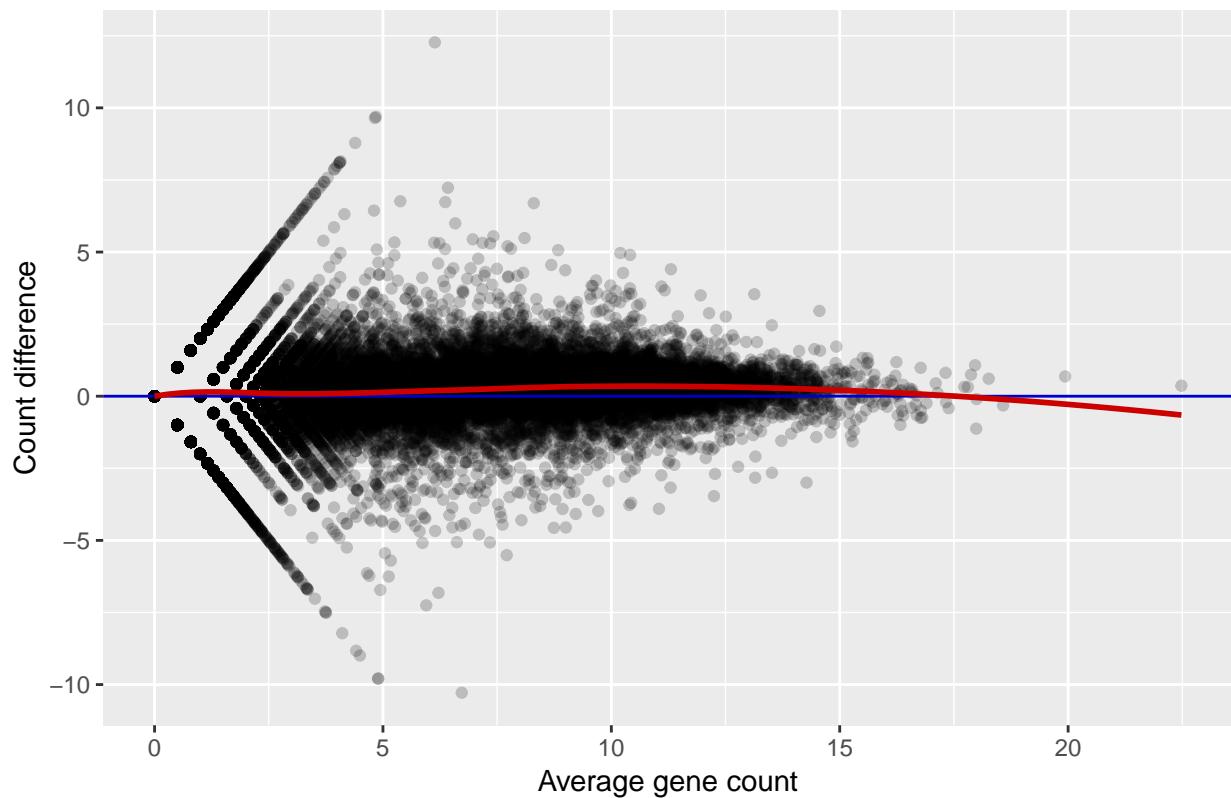
x = pseudoCount[, 4]
y = pseudoCount[, 6]
M = x - y # M-values (differences between samples)
A = (x + y)/2 # A-values (averages)
df = data.frame(A, M)
ggplot(df, aes(x = A, y = M)) + geom_point(size = 1.5, alpha = 1/5) +
  geom_hline(aes(yintercept = 0), color = "blue3") + stat_smooth(se =
  FALSE, method = "loess", color = "red3") +
  xlab("Average gene count") +
  ylab("Count difference") +
  ggtitle("WTCYTO5 vs. WTCYTO6")
  
```

WTCYTO5 vs. WTCYTO6



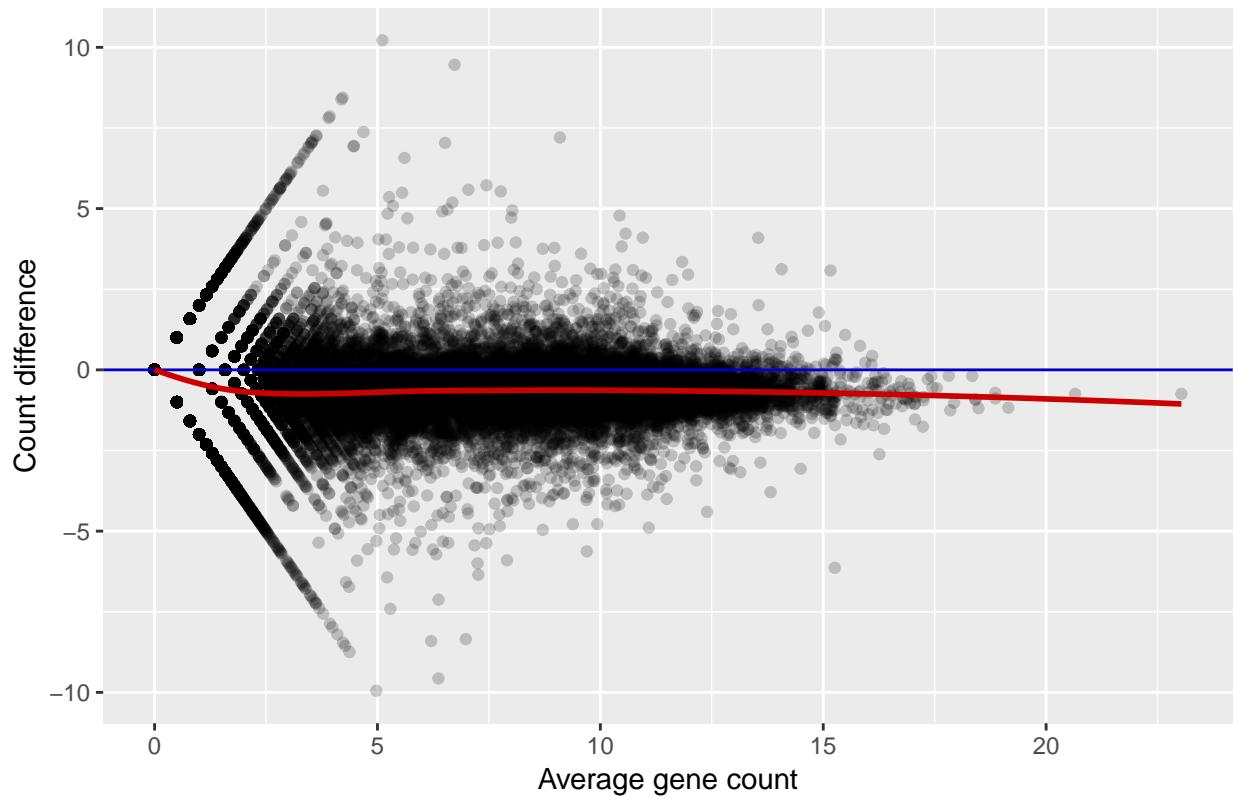
```
x = pseudoCount[, 1]
y = pseudoCount[, 3]
M = x - y # M-values (differences between samples)
A = (x + y)/2 # A-values (averages)
df = data.frame(A, M)
ggplot(df, aes(x = A, y = M)) + geom_point(size = 1.5, alpha = 1/5) +
  geom_hline(aes(yintercept = 0), color = "blue3") + stat_smooth(se =
  FALSE, method = "loess", color = "red3") +
  xlab("Average gene count") +
  ylab("Count difference") +
  ggtitle("S2CYT010 vs. S2CYT011")
```

S2CYTO10 vs. S2CYTO11



```
x = pseudoCount[, 1]
y = pseudoCount[, 5]
M = x - y # M-values (differences between samples)
A = (x + y)/2 # A-values (averages)
df = data.frame(A, M)
ggplot(df, aes(x = A, y = M)) + geom_point(size = 1.5, alpha = 1/5) +
  geom_hline(aes(yintercept = 0), color = "blue3") + stat_smooth(se =
  FALSE, method = "loess", color = "red3") +
  xlab("Average gene count") +
  ylab("Count difference") +
  ggtitle("S2CYT010 vs. S2CYT012")
```

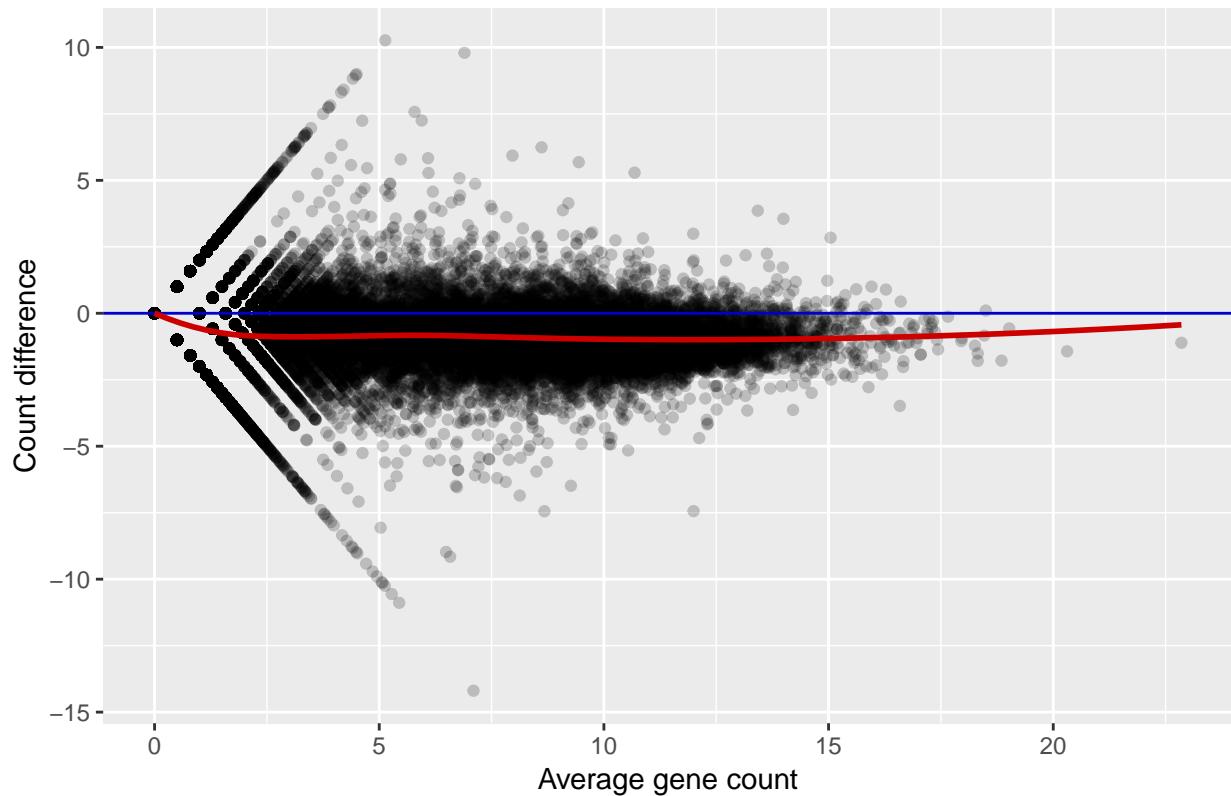
S2CYTO10 vs. S2CYTO12



```

x = pseudoCount[, 3]
y = pseudoCount[, 5]
M = x - y # M-values (differences between samples)
A = (x + y)/2 # A-values (averages)
df = data.frame(A, M)
ggplot(df, aes(x = A, y = M)) + geom_point(size = 1.5, alpha = 1/5) +
  geom_hline(aes(yintercept = 0), color = "blue3") + stat_smooth(se =
  FALSE, method = "loess", color = "red3") +
  xlab("Average gene count") +
  ylab("Count difference") +
  ggtitle("S2CYT011 vs. S2CYT012")
  
```

S2CYTO11 vs. S2CYTO12



Differential expression analysis

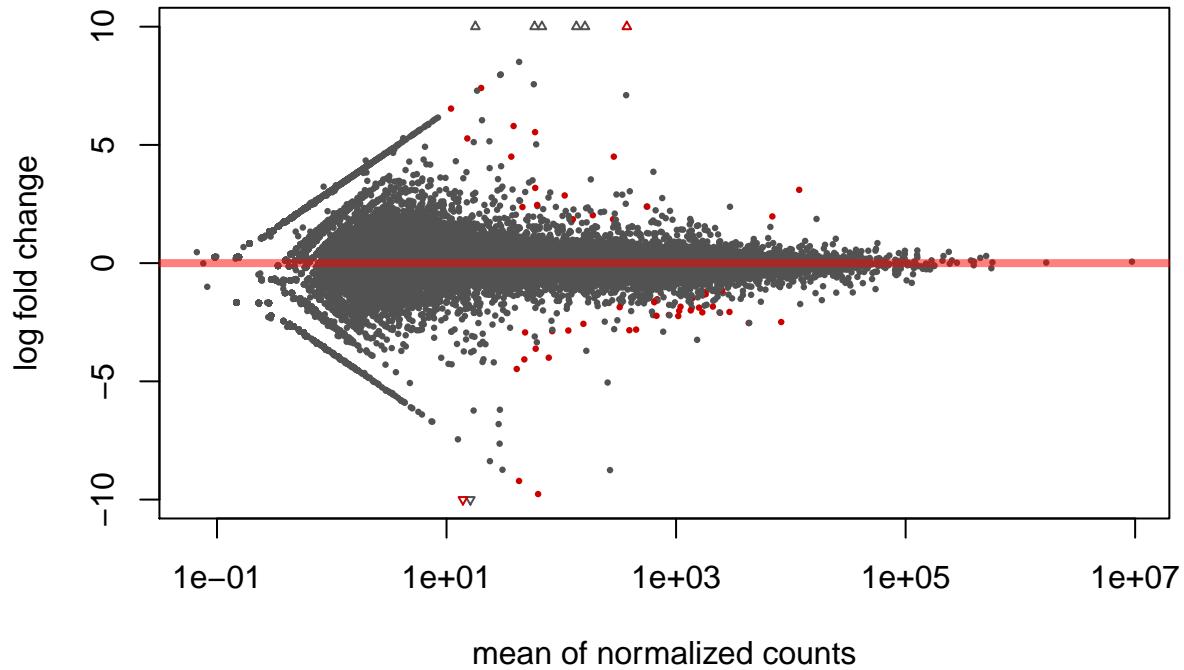
```
summary(res)

##
## out of 28605 with nonzero total read count
## adjusted p-value < 0.1
## LFC > 0 (up)      : 18, 0.063%
## LFC < 0 (down)    : 34, 0.12%
## outliers [1]       : 89, 0.31%
## low counts [2]     : 11034, 39%
## (mean count < 7)
## [1] see 'cooksCutoff' argument of ?results
## [2] see 'independentFiltering' argument of ?results
```

MA Plot

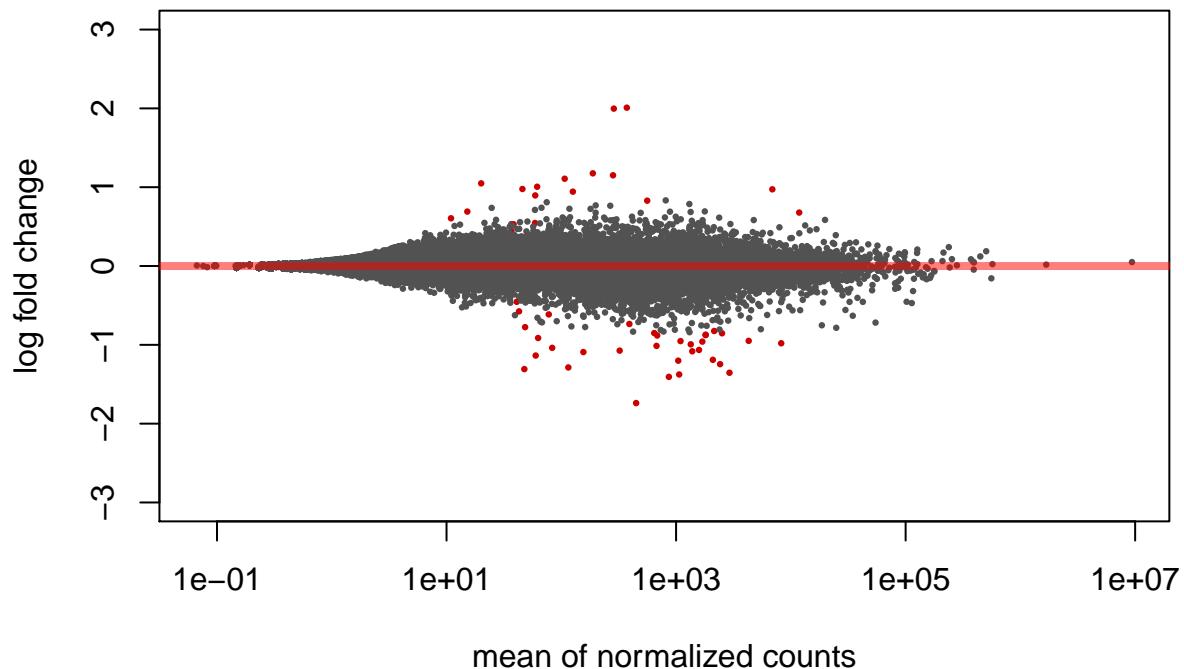
Red points have adjusted p value < 0.1. We can see a lot of noise, using a shrunken log2 fold change reduces the noise.

```
plotMA(res, ylim=c(-10,10))
```



```
resShrink = lfcShrink(dds, coef=2)

## using 'normal' for LFC shrinkage, the Normal prior from Love et al (2014).
## additional priors are available via the 'type' argument, see ?lfcShrink for details
plotMA(resShrink, ylim=c(-3,3))
```



Extract Significant genes:

P value = 0.05 = 599 genes \ Adj P value = 0.1 = 53 genes \ Both write to csv ..

```

resOrdered <- res[order(res$pvalue),]

pvalue <- subset(resOrdered, pvalue < 0.05)

write.csv(pvalue, file="Control_0.05_Pvalue.csv")

padj <- subset(resOrdered, padj < 0.1)

write.csv(padj, file="Control_0.1_Padj.csv")

```

Heatmaps

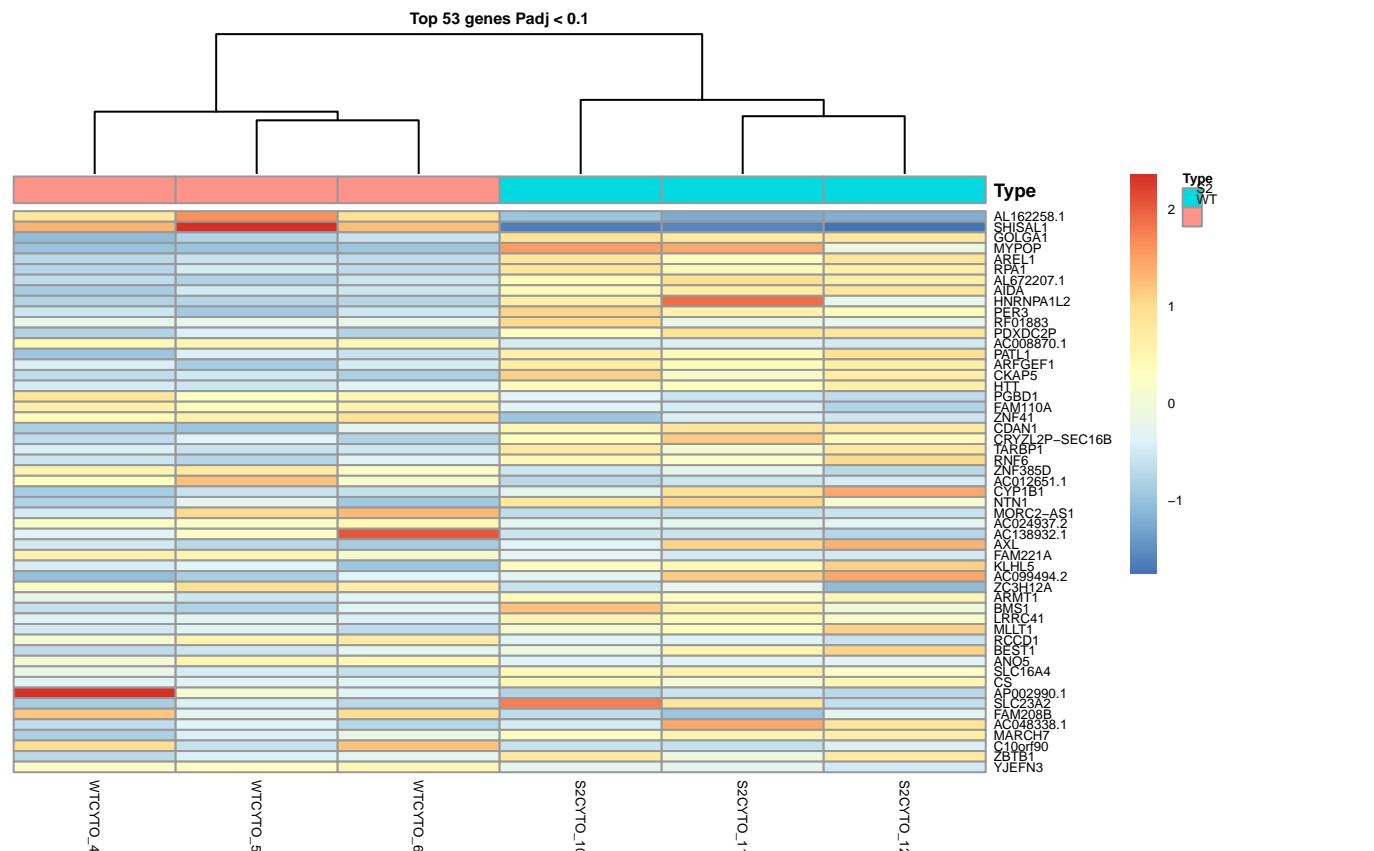
Here I have plotted the top Genes by Pvalue, and Adjusted P value. The rows will correspond to the csv files created in the last step, helping visualize DE across samples. Row orders will not directly correspond to the csv files when clustering = TRUE for rows.

I apologise for the scale, it had to be shrunk to fit in.

```

library("pheatmap")
mat = assay(rld)[ head(order(res$padj),53), ]
mat = mat - rowMeans(mat)
df = as.data.frame(colData(rld)[,c("type")])
colnames(df) = "Type"
rownames(df) = colnames(mat)
pheatmap(mat, annotation_col=df, cluster_rows = FALSE, cex=0.7, main = "Top 53 genes Padj < 0.1")

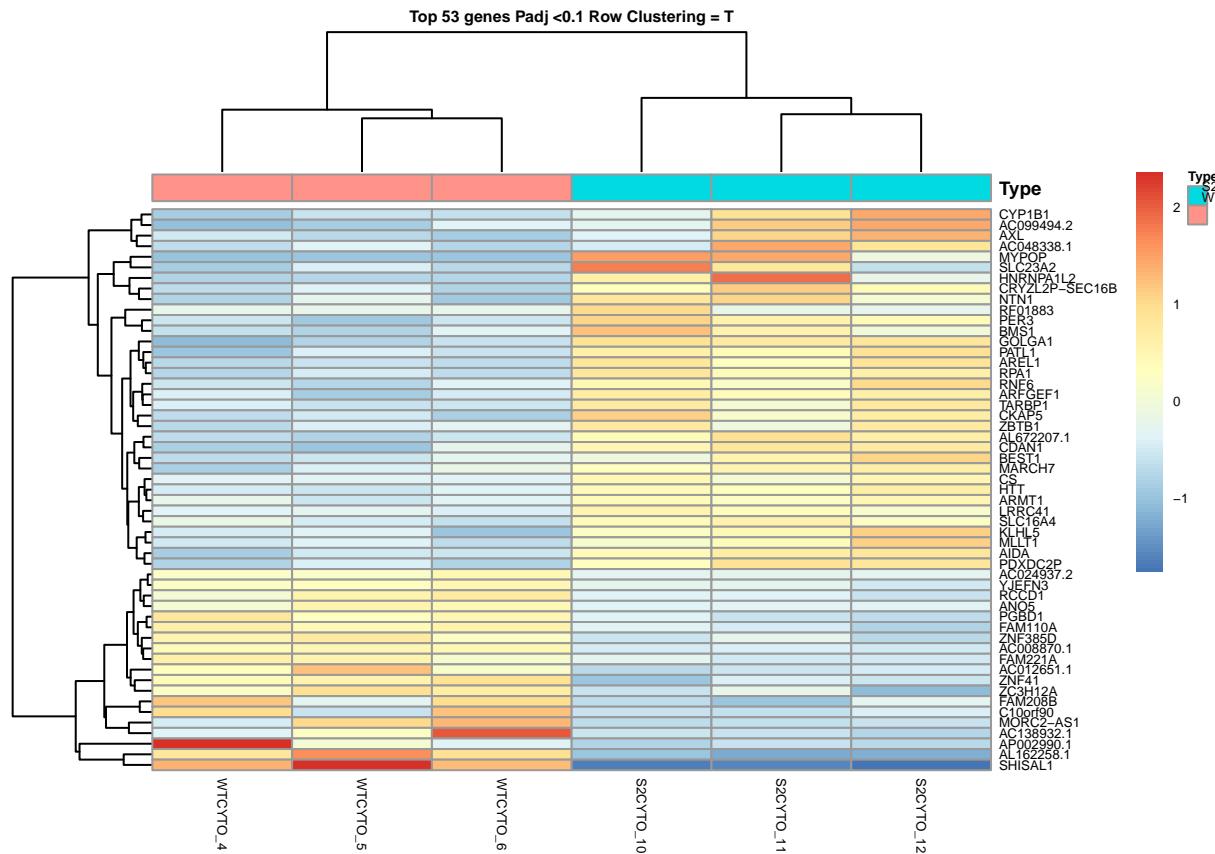
```



```

mat = assay(rld)[ head(order(res$padj),53), ]
mat = mat - rowMeans(mat)
df = as.data.frame(colData(rld)[,c("type")])
colnames(df) = "Type"
rownames(df) = colnames(mat)
pheatmap(mat, annotation_col=df, cluster_rows = TRUE, cex=0.7, main = "Top 53 genes Padj <0.1 Row Clust")

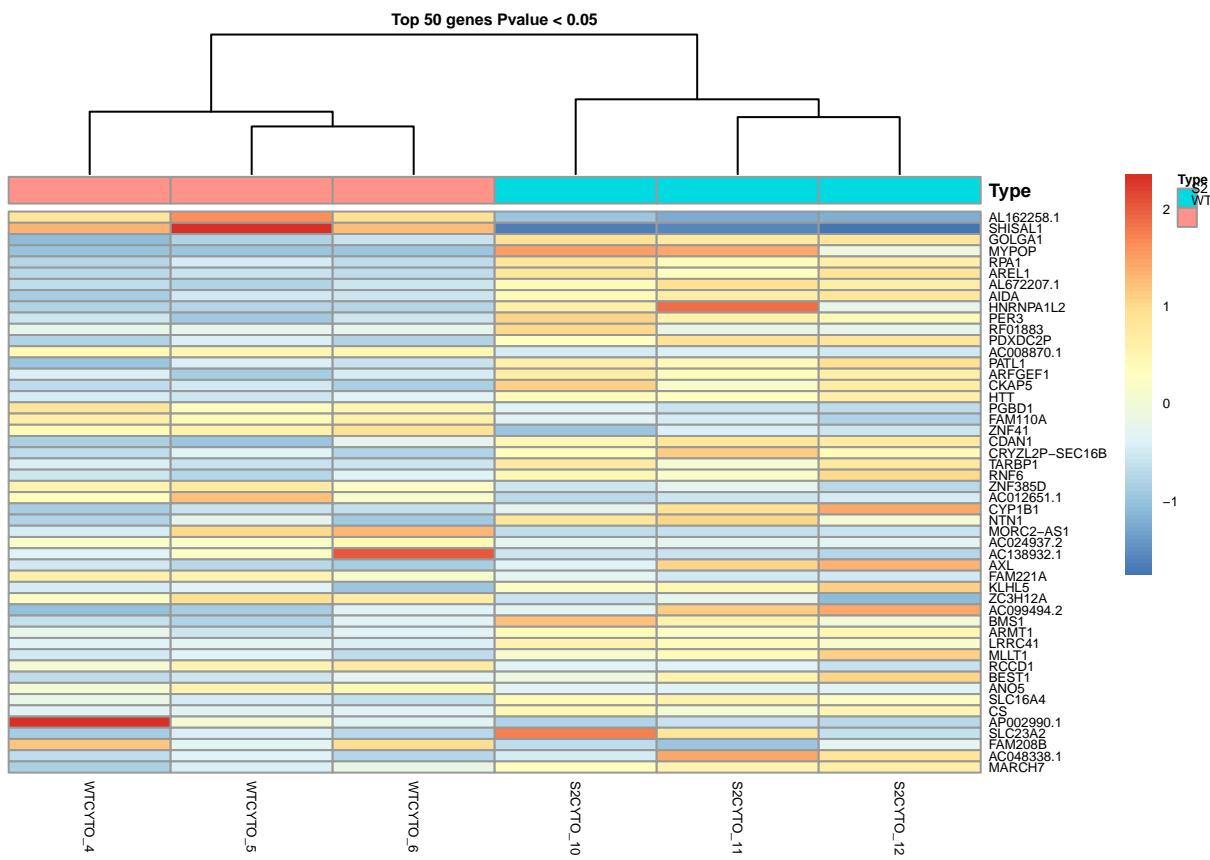
```



```

library("pheatmap")
mat = assay(rld)[ head(order(res$pvalue),50), ]
mat = mat - rowMeans(mat)
df = as.data.frame(colData(rld)[,c("type")])
colnames(df) = "Type"
rownames(df) = colnames(mat)
pheatmap(mat, annotation_col=df, cluster_rows = FALSE, cex=0.7, main = "Top 50 genes Pvalue < 0.05")

```



```
mat = assay(rld)[ head(order(res$pvalue),50), ]
mat = mat - rowMeans(mat)
df = as.data.frame(colData(rld)[,c("type")])
colnames(df) = "Type"
rownames(df) = colnames(mat)
pheatmap(mat, annotation_col=df, cluster_rows = TRUE, cex=0.7, main = "Top 50 genes Pvalue <0.05 Row Clust")
```

