

Exploring Differential Expression (DE) in common between *tf2* and wt of the same regions

Question

Are there similar up/down-regulated genes in the same region between the two genotypes.

Approach:

1. Read in the results from the DE analysis between mbr_other in each genotype.
2. The results of this analysis is all significant DE genes. Subset the up-regulated and down-regulated by a fold change of 1 (-1 for down-regulated).
3. Compare up-regulated in *tf2* to up-regulated in WT. 1.) visualize with venn diagram and 2.) print out list of similar vs dissimilar genes.
4. Repeat for each region A, B, C.

Script

To run script and create a report at the end, run `rmarkdown` code below.

```
library(rmarkdown)
render("vennDiagram.wtVStf2.Rmd", "pdf_document")
```

Read in required libraries.

```
library(VennDiagram)
```

Upload annotation data for table outputs

```
annotation1<- read.delim("../requisiteData/ITAG2.3_all_Arabidopsis_ITAG_annotations.tsv", header=FALSE)
colnames(annotation1) <- c("ITAG", "SGN_annotation")
annotation2<- read.delim("../requisiteData/ITAG2.3_all_Arabidopsis_annotated.tsv")
annotation <- merge(annotation1,annotation2, by = "ITAG")
```

A region (tip)

```
#Read in Data
aRegionWt <- read.table("../DE/wtambr_wtaother/wtambr_wtaother_DE_sig.txt", sep=" ", header = TRUE, fill=NA)
aRegionTf2 <- read.table("../DE/tf2ambr_tf2aother/tf2ambr_tf2aother_DE_sig.txt", header = TRUE, fill=NA)

#Force numeric
aRegionWt$logFC <- as.numeric(as.character(aRegionWt$logFC))
```

```
aRegionTf2$logFC <- as.numeric(as.character(aRegionTf2$logFC))
```

```
#Subset based on Log Fold Change (logFC)
```

```
#tf2
```

```
aRegionTf2Up <- subset(aRegionTf2, logFC > 0)
```

```
aRegionTf2Down <- subset(aRegionTf2, logFC < 0)
```

```
#wt
```

```
aRegionWtUp <- subset(aRegionWt, logFC > 0)
```

```
aRegionWtDown <- subset(aRegionWt, logFC < 0)
```

ALL GENES

This takes all significant gene regardless of up-regulated or down-regulated.

```
dir.create("aRegion/all") #Creates directory to put all out tables.
```

```
## Warning: 'aRegion/all' already exists
```

```
#all
```

```
aRegionAll <- matrix(intersect(aRegionWt$ITAG, aRegionTf2$ITAG))
```

```
colnames(aRegionAll) <- c("ITAG")
```

```
aRegionAll.annotated <- merge(aRegionAll, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with annotation
```

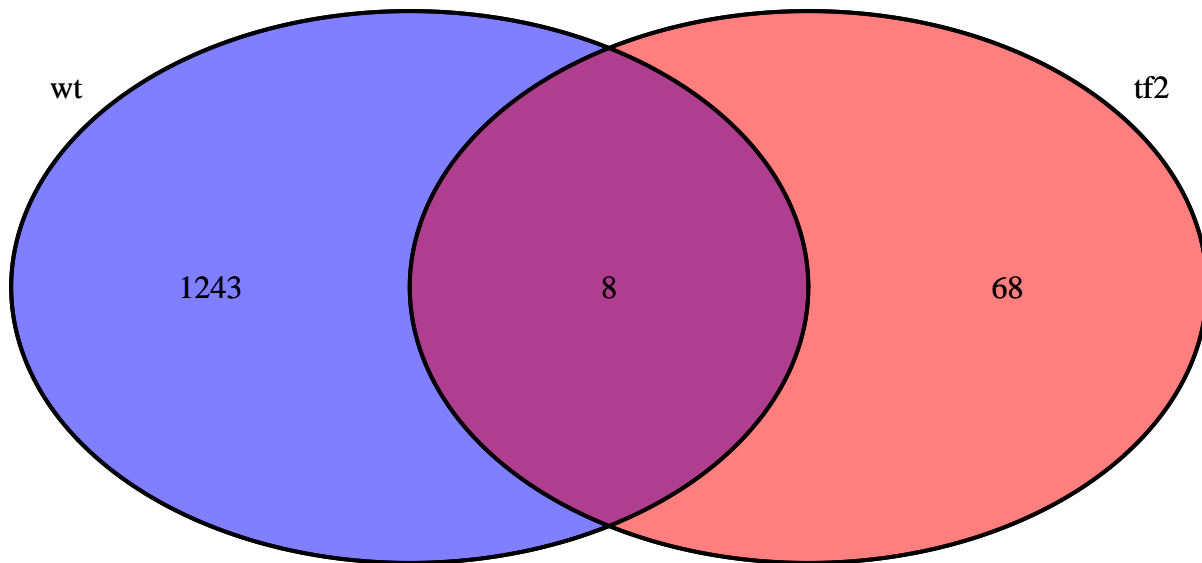
```
write.csv(aRegionAll.annotated, file = "aRegion/all/aRegionAll.annotated.csv") #write .csv file
```

```
#Makes the grid
```

```
grid.newpage()
```

```
venn.plot <- draw.pairwise.venn(area1 = length(aRegionWt$ITAG),  
                                area2 = length(aRegionTf2$ITAG),  
                                cross.area = length(aRegionAll),  
                                scaled = FALSE,  
                                category = c("wt", "tf2"),  
                                fill = c("blue", "red"),  
                                alpha = 0.3)
```

```
grid.draw(venn.plot)
```



```
#Get only genes specific to wt
aRegionWtOnly <- matrix(setdiff(aRegionWt$ITAG, aRegionTf2$ITAG))
aRegionTf2Only <- matrix(setdiff(aRegionTf2$ITAG, aRegionWt$ITAG))

colnames(aRegionWtOnly) <- c("ITAG")
colnames(aRegionTf2Only) <- c("ITAG")

aRegionWtOnly.annotated <- merge(aRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with annotation
aRegionTf2Only.annotated <- merge(aRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with annotation

write.csv(aRegionTf2Only.annotated, file = "aRegion/all/aRegionTf2Only.annotated.csv") #write .csv file
write.csv(aRegionWtOnly.annotated, file = "aRegion/all/aRegionWtOnly.annotated.csv") #write .csv file
```

UP Regulation Genes

This takes up significant gene up-regulated.

```
dir.create("aRegion/up") #Creates directory to put up out tables.
```

```
## Warning: 'aRegion/up' already exists
```

```
#up
aRegionup <- matrix(intersect(aRegionWtUp$ITAG, aRegionTf2Up$ITAG))
colnames(aRegionup) <- c("ITAG")
aRegionup.annotated <- merge(aRegionup, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with annotation
write.csv(aRegionup.annotated, file = "aRegion/up/aRegionup.annotated.csv") #write .csv file

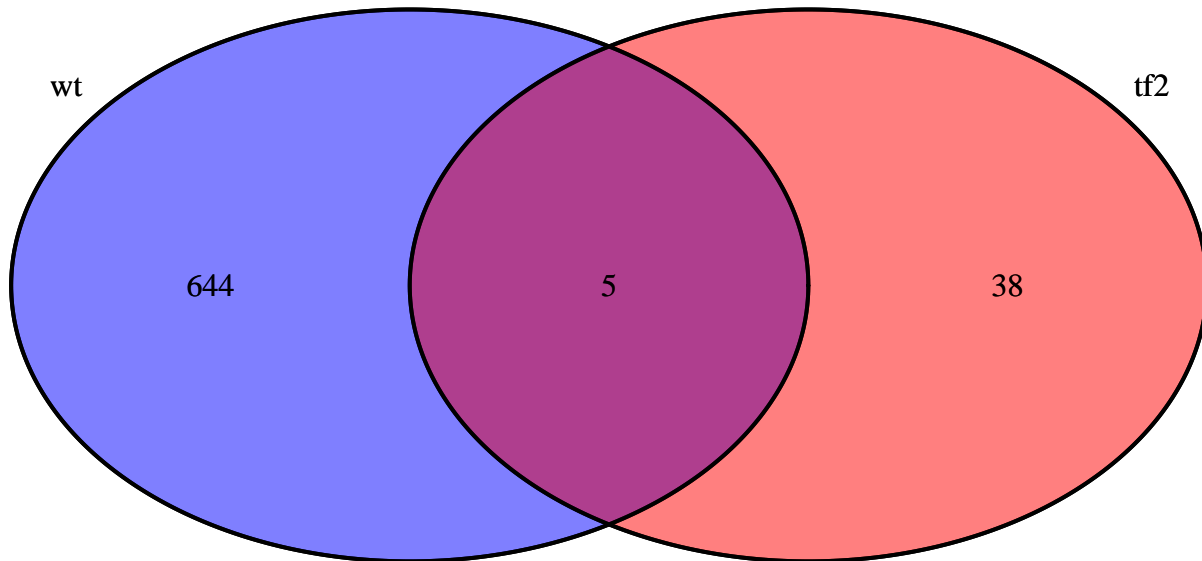
#Makes the grid
grid.newpage()
venn.plot <- draw.pairwise.venn(area1 = length(aRegionWtUp$ITAG),
                                area2 = length(aRegionTf2Up$ITAG),
                                cross.area = length(aRegionup),
                                scaled = FALSE,
```

```

category = c("wt", "tf2"),
fill      = c("blue", "red"),
alpha     = 0.3)

grid.draw(venn.plot)

```



```

#Get only genes specific to wt
aRegionWtOnly <- matrix(setdiff(aRegionWtUp$ITAG, aRegionTf2Up$ITAG))
aRegionTf2Only <- matrix(setdiff(aRegionTf2Up$ITAG, aRegionWtUp$ITAG))

colnames(aRegionWtOnly) <- c("ITAG")
colnames(aRegionTf2Only) <- c("ITAG")

aRegionWtOnly.annotated <- merge(aRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
aRegionTf2Only.annotated <- merge(aRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(aRegionTf2Only.annotated, file = "aRegion/up/aRegionTf2Only.annotated.csv") #write .csv file
write.csv(aRegionWtOnly.annotated, file = "aRegion/up/aRegionWtOnly.annotated.csv") #write .csv file

```

Down Regulated Genes

Down regulated genes means significantly down regulated.

```

dir.create("aRegion/down") #Creates directory to put Down out tables.

```

```

## Warning: 'aRegion/down' already exists

```

```

#Down
aRegionDown <- matrix(intersect(aRegionWtDown$ITAG, aRegionTf2Down$ITAG))
colnames(aRegionDown) <- c("ITAG")
aRegionDown.annotated <- merge(aRegionDown, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
write.csv(aRegionDown.annotated, file = "aRegion/down/aRegionDown.annotated.csv") #write .csv file

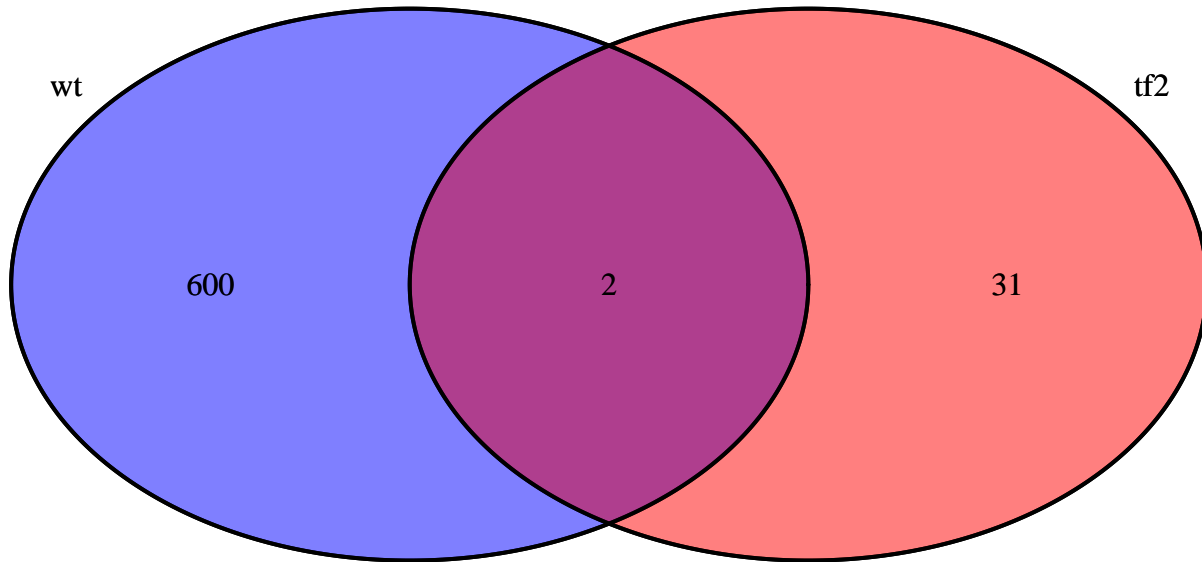
```

```

#Makes the grid
grid.newpage()
venn.plot <- draw.pairwise.venn(area1 = length(aRegionWtDown$ITAG),
                                area2 = length(aRegionTf2Down$ITAG),
                                cross.area = length(aRegionDown),
                                scaled = FALSE,
                                category = c("wt", "tf2"),
                                fill = c("blue", "red"),
                                alpha = 0.3)

grid.draw(venn.plot)

```



```

#Get only genes specific to wt

aRegionWtOnly <- matrix(setdiff(aRegionWtDown$ITAG, aRegionTf2Down$ITAG))
aRegionTf2Only <- matrix(setdiff(aRegionTf2Down$ITAG, aRegionWtDown$ITAG))

colnames(aRegionWtOnly) <- c("ITAG")
colnames(aRegionTf2Only) <- c("ITAG")

aRegionWtOnly.annotated <- merge(aRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
aRegionTf2Only.annotated <- merge(aRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(aRegionTf2Only.annotated, file = "aRegion/down/aRegionTf2Only.annotated.csv") #write .csv file
write.csv(aRegionWtOnly.annotated, file = "aRegion/down/aRegionWtOnly.annotated.csv") #write .csv file

```

B region (middle)

```

#Read in Data
bRegionWt <- read.table("../DE/wtbmbr_wtbother/wtbmbr_wtbother_DE_sig.txt", sep=" ", header = TRUE, fill = NA)
bRegionTf2 <- read.table("../DE/tf2bmbr_tf2bother/tf2bmbr_tf2bother_DE_sig.txt", header = TRUE, fill = NA)

#Force numeric
bRegionWt$logFC <- as.numeric(as.character(bRegionWt$logFC))

```

```
## Warning: NAs introduced by coercion
```

```
bRegionTf2$logFC <- as.numeric(as.character(bRegionTf2$logFC))
```

```
#Subset based on Log Fold Change (logFC)
```

```
#tf2
```

```
bRegionTf2Up <- subset(bRegionTf2, logFC > 0)
```

```
bRegionTf2Down <- subset(bRegionTf2, logFC < 0)
```

```
#wt
```

```
bRegionWtUp <- subset(bRegionWt, logFC > 0)
```

```
bRegionWtDown <- subset(bRegionWt, logFC < 0)
```

ALL GENES

This takes all significant gene regardless of up-regulated or down-regulated.

```
dir.create("bRegion/all") #Creates directory to put all out tables.
```

```
## Warning: 'bRegion/all' already exists
```

```
#all
```

```
bRegionAll <- matrix(intersect(bRegionWt$ITAG, bRegionTf2$ITAG))
```

```
colnames(bRegionAll) <- c("ITAG")
```

```
bRegionAll.annotated <- merge(bRegionAll, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with annotation
```

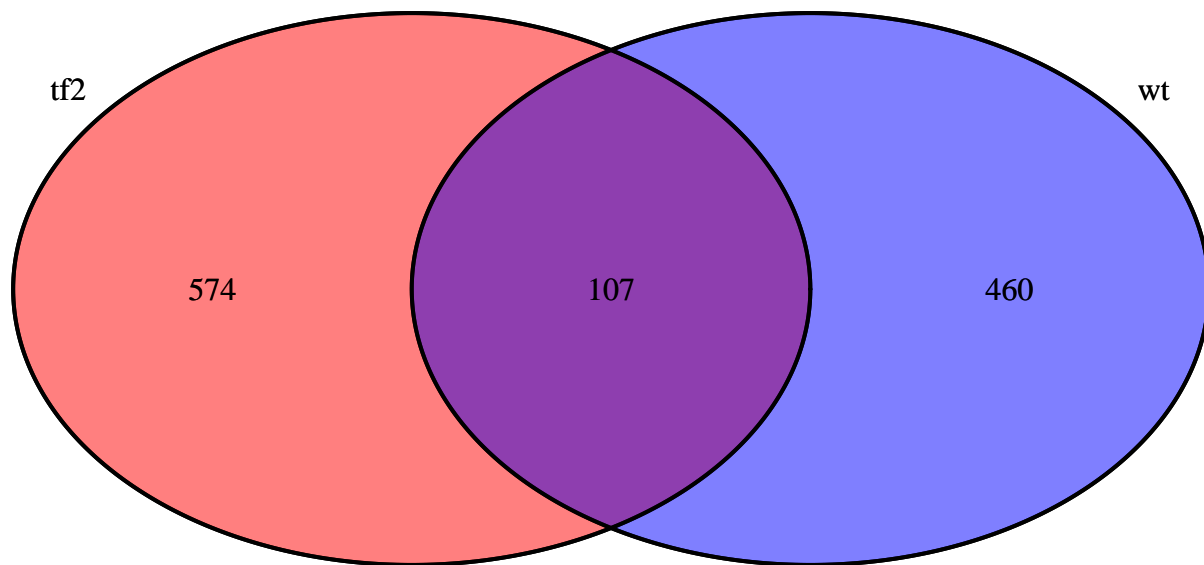
```
write.csv(bRegionAll.annotated, file = "bRegion/all/bRegionAll.annotated.csv") #write .csv file
```

```
#Makes the grid
```

```
grid.newpage()
```

```
venn.plot <- draw.pairwise.venn(area1 = length(bRegionWt$ITAG),  
                                area2 = length(bRegionTf2$ITAG),  
                                cross.area = length(bRegionAll),  
                                scaled = FALSE,  
                                category = c("wt", "tf2"),  
                                fill = c("blue", "red"),  
                                alpha = 0.3)
```

```
grid.draw(venn.plot)
```



```
#Get only genes specific to wt
bRegionWtOnly <- matrix(setdiff(bRegionWt$ITAG, bRegionTf2$ITAG))
bRegionTf2Only <- matrix(setdiff(bRegionTf2$ITAG, bRegionWt$ITAG))

colnames(bRegionWtOnly) <- c("ITAG")
colnames(bRegionTf2Only) <- c("ITAG")

bRegionWtOnly.annotated <- merge(bRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
bRegionTf2Only.annotated <- merge(bRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(bRegionTf2Only.annotated, file = "bRegion/all/bRegionTf2Only.annotated.csv") #write .csv file
write.csv(bRegionWtOnly.annotated, file = "bRegion/all/bRegionWtOnly.annotated.csv") #write .csv file
```

UP Regulation Genes

This takes up significant gene up-regulated.

```
dir.create("bRegion/up") #Creates directory to put up out tables.
```

```
## Warning: 'bRegion/up' already exists
```

```
#up
bRegionup <- matrix(intersect(bRegionWtUp$ITAG, bRegionTf2Up$ITAG))
colnames(bRegionup) <- c("ITAG")
bRegionup.annotated <- merge(bRegionup, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with
write.csv(bRegionup.annotated, file = "bRegion/up/bRegionup.annotated.csv") #write .csv file

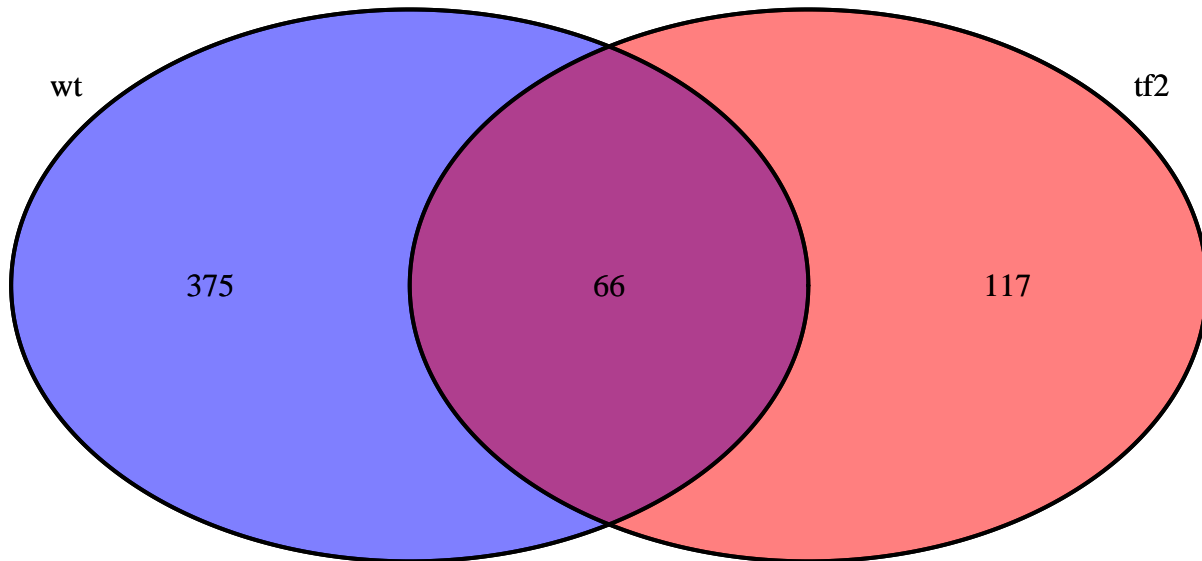
#Makes the grid
grid.newpage()
venn.plot <- draw.pairwise.venn(area1 = length(bRegionWtUp$ITAG),
                                area2 = length(bRegionTf2Up$ITAG),
                                cross.area = length(bRegionup),
                                scaled = FALSE,
```

```

category = c("wt", "tf2"),
fill      = c("blue", "red"),
alpha     = 0.3)

grid.draw(venn.plot)

```



```

#Get only genes specific to wt
bRegionWtOnly <- matrix(setdiff(bRegionWtUp$ITAG, bRegionTf2Up$ITAG))
bRegionTf2Only <- matrix(setdiff(bRegionTf2Up$ITAG, bRegionWtUp$ITAG))

colnames(bRegionWtOnly) <- c("ITAG")
colnames(bRegionTf2Only) <- c("ITAG")

bRegionWtOnly.annotated <- merge(bRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
bRegionTf2Only.annotated <- merge(bRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(bRegionTf2Only.annotated, file = "bRegion/up/bRegionTf2Only.annotated.csv") #write .csv file
write.csv(bRegionWtOnly.annotated, file = "bRegion/up/bRegionWtOnly.annotated.csv") #write .csv file

```

Down Regulated Genes

Down regulated genes means significantly down regulated.

```

dir.create("bRegion/down") #Creates directory to put Down out tables.

```

```

## Warning: 'bRegion/down' already exists

```

```

#Down
bRegionDown <- matrix(intersect(bRegionWtDown$ITAG, bRegionTf2Down$ITAG))
colnames(bRegionDown) <- c("ITAG")
bRegionDown.annotated <- merge(bRegionDown, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
write.csv(bRegionDown.annotated, file = "bRegion/down/bRegionDown.annotated.csv") #write .csv file

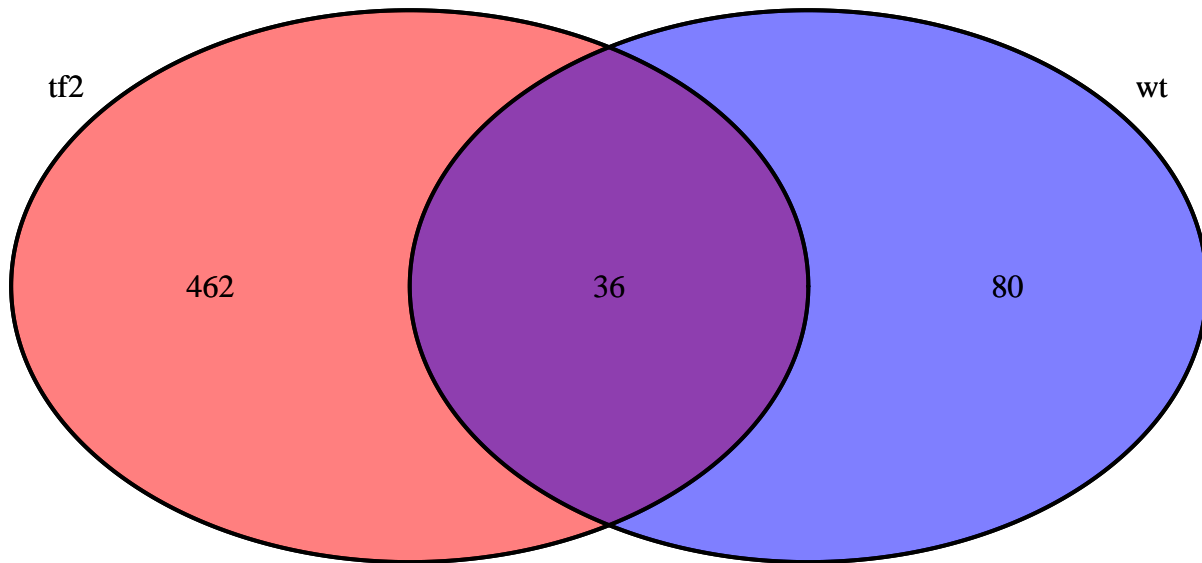
```



```

#Makes the grid
grid.newpage()
venn.plot <- draw.pairwise.venn(area1 = length(bRegionWtDown$ITAG),
                                area2 = length(bRegionTf2Down$ITAG),
                                cross.area = length(bRegionDown),
                                scaled = FALSE,
                                category = c("wt", "tf2"),
                                fill = c("blue", "red"),
                                alpha = 0.3)
grid.draw(venn.plot)

```



```

#Get only genes specific to wt

bRegionWtOnly <- matrix(setdiff(bRegionWtDown$ITAG, bRegionTf2Down$ITAG))
bRegionTf2Only <- matrix(setdiff(bRegionTf2Down$ITAG, bRegionWtDown$ITAG))

colnames(bRegionWtOnly) <- c("ITAG")
colnames(bRegionTf2Only) <- c("ITAG")

bRegionWtOnly.annotated <- merge(bRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
bRegionTf2Only.annotated <- merge(bRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(bRegionTf2Only.annotated, file = "bRegion/down/bRegionTf2Only.annotated.csv") #write .csv file
write.csv(bRegionWtOnly.annotated, file = "bRegion/down/bRegionWtOnly.annotated.csv") #write .csv file

```

C region (tip)

```

#Read in Data
bRegionWt <- read.table("../DE/wtcmbr_wtcother/wtcmbr_wtcother_DE_sig.txt", sep=" ", header = TRUE, fill = NA)
bRegionTf2 <- read.table("../DE/tf2cmbr_tf2cother/tf2cmbr_tf2cother_DE_sig.txt", header = TRUE, fill = NA)

#Force numeric

```

```
cRegionWt$logFC <- as.numeric(as.character(cRegionWt$logFC))
cRegionTf2$logFC <- as.numeric(as.character(cRegionTf2$logFC))
```

```
#Subset based on Log Fold Change (logFC)
```

```
#tf2
```

```
cRegionTf2Up <- subset(cRegionTf2, logFC > 0)
cRegionTf2Down <- subset(cRegionTf2, logFC < 0)
```

```
#wt
```

```
cRegionWtUp <- subset(cRegionWt, logFC > 0)
cRegionWtDown <- subset(cRegionWt, logFC < 0)
```

ALL GENES

This takes all significant gene regardless of up-regulated or down-regulated.

```
dir.create("cRegion/all") #Creates directory to put all out tables.
```

```
## Warning: 'cRegion/all' already exists
```

```
#all
```

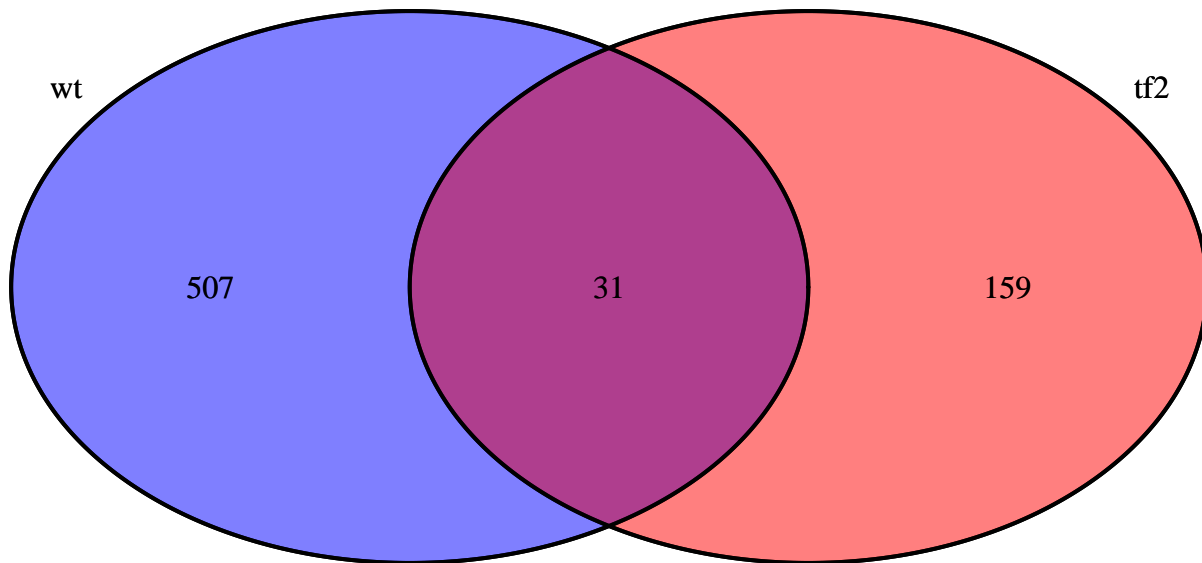
```
cRegionAll <- matrix(intersect(cRegionWt$ITAG, cRegionTf2$ITAG))
colnames(cRegionAll) <- c("ITAG")
```

```
cRegionAll.annotated <- merge(cRegionAll, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with annotation
write.csv(cRegionAll.annotated, file = "cRegion/all/cRegionAll.annotated.csv") #write .csv file
```

```
#Makes the grid
```

```
grid.newpage()
venn.plot <- draw.pairwise.venn(area1 = length(cRegionWt$ITAG),
                                area2 = length(cRegionTf2$ITAG),
                                cross.area = length(cRegionAll),
                                scaled = FALSE,
                                category = c("wt", "tf2"),
                                fill = c("blue", "red"),
                                alpha = 0.3)
```

```
grid.draw(venn.plot)
```



```
#Get only genes specific to wt
cRegionWtOnly <- matrix(setdiff(cRegionWt$ITAG, cRegionTf2$ITAG))
cRegionTf2Only <- matrix(setdiff(cRegionTf2$ITAG, cRegionWt$ITAG))

colnames(cRegionWtOnly) <- c("ITAG")
colnames(cRegionTf2Only) <- c("ITAG")

cRegionWtOnly.annotated <- merge(cRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
cRegionTf2Only.annotated <- merge(cRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(cRegionTf2Only.annotated, file = "cRegion/all/cRegionTf2Only.annotated.csv") #write .csv file
write.csv(cRegionWtOnly.annotated, file = "cRegion/all/cRegionWtOnly.annotated.csv") #write .csv file
```

UP Regulation Genes

This takes up significant gene up-regulated.

```
dir.create("cRegion/up") #Creates directory to put up out tables.
```

```
## Warning: 'cRegion/up' already exists
```

```
#up
cRegionup <- matrix(intersect(cRegionWtUp$ITAG, cRegionTf2Up$ITAG))
colnames(cRegionup) <- c("ITAG")
cRegionup.annotated <- merge(cRegionup, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge with
write.csv(cRegionup.annotated, file = "cRegion/up/cRegionup.annotated.csv") #write .csv file

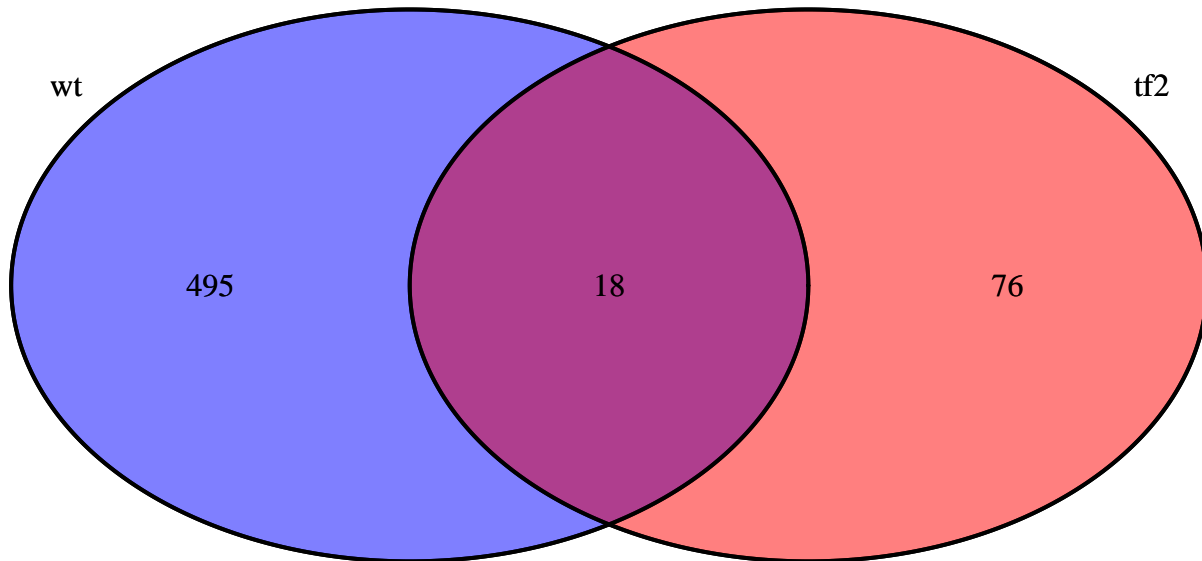
#Makes the grid
grid.newpage()
venn.plot <- draw.pairwise.venn(area1 = length(cRegionWtUp$ITAG),
                                area2 = length(cRegionTf2Up$ITAG),
                                cross.area = length(cRegionup),
                                scaled = FALSE,
```

```

category = c("wt", "tf2"),
fill      = c("blue", "red"),
alpha     = 0.3)

grid.draw(venn.plot)

```



```

#Get only genes specific to wt
cRegionWtOnly <- matrix(setdiff(cRegionWtUp$ITAG, cRegionTf2Up$ITAG))
cRegionTf2Only <- matrix(setdiff(cRegionTf2Up$ITAG, cRegionWtUp$ITAG))

colnames(cRegionWtOnly) <- c("ITAG")
colnames(cRegionTf2Only) <- c("ITAG")

cRegionWtOnly.annotated <- merge(cRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
cRegionTf2Only.annotated <- merge(cRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(cRegionTf2Only.annotated, file = "cRegion/up/cRegionTf2Only.annotated.csv") #write .csv file
write.csv(cRegionWtOnly.annotated, file = "cRegion/up/cRegionWtOnly.annotated.csv") #write .csv file

```

Down Regulated Genes

Down regulated genes means significantly down regulated.

```

dir.create("bRegion/down") #Creates directory to put Down out tables.

```

```

## Warning: 'bRegion/down' already exists

```

```

#Down
bRegionDown <- matrix(intersect(bRegionWtDown$ITAG, bRegionTf2Down$ITAG))
colnames(bRegionDown) <- c("ITAG")
bRegionDown.annotated <- merge(bRegionDown, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
write.csv(bRegionDown.annotated, file = "bRegion/down/bRegionDown.annotated.csv") #write .csv file

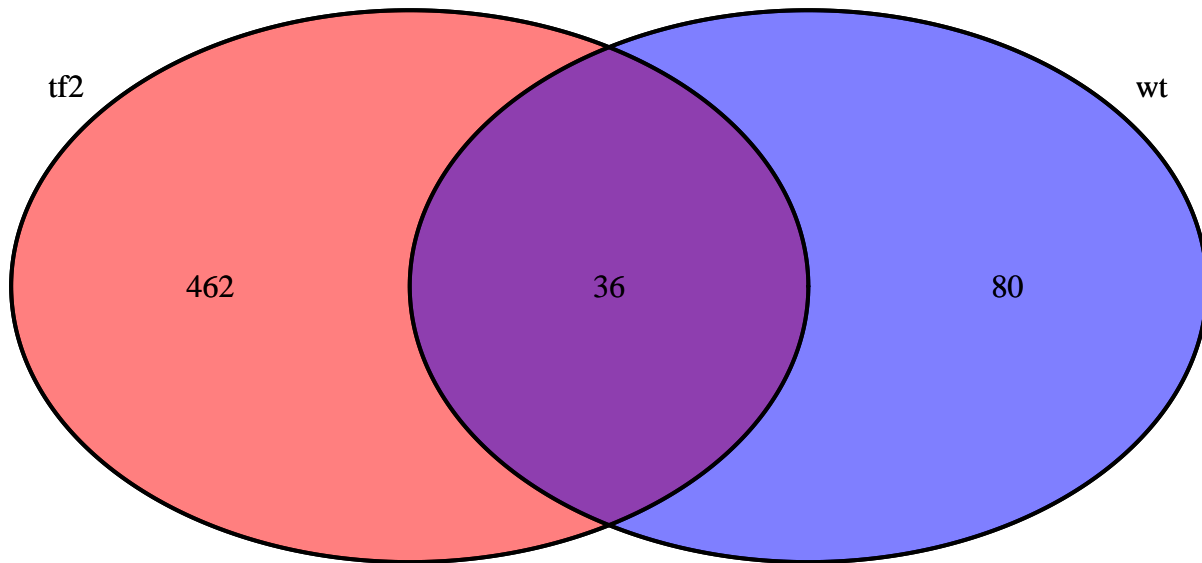
```

```

#Makes the grid
grid.newpage()
venn.plot <- draw.pairwise.venn(area1 = length(bRegionWtDown$ITAG),
                                area2 = length(bRegionTf2Down$ITAG),
                                cross.area = length(bRegionDown),
                                scaled = FALSE,
                                category = c("wt", "tf2"),
                                fill = c("blue", "red"),
                                alpha = 0.3)

grid.draw(venn.plot)

```



```

#Get only genes specific to wt

bRegionWtOnly <- matrix(setdiff(bRegionWtDown$ITAG, bRegionTf2Down$ITAG))
bRegionTf2Only <- matrix(setdiff(bRegionTf2Down$ITAG, bRegionWtDown$ITAG))

colnames(bRegionWtOnly) <- c("ITAG")
colnames(bRegionTf2Only) <- c("ITAG")

bRegionWtOnly.annotated <- merge(bRegionWtOnly, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge
bRegionTf2Only.annotated <- merge(bRegionTf2Only, annotation, by = "ITAG", by.x = TRUE, all.x = TRUE) #Merge

write.csv(bRegionTf2Only.annotated, file = "bRegion/down/bRegionTf2Only.annotated.csv") #write .csv file
write.csv(bRegionWtOnly.annotated, file = "bRegion/down/bRegionWtOnly.annotated.csv") #write .csv file

```