

# Figure-S3A.R

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```
# This Script Generates Figure S3A
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```

```
# Empty the environment & suppress warnings
rm(list = ls())
options(warn=-1)
```

```
# Loading the required libraries
library(tidyverse)
```

```
## — Attaching core tidyverse packages — tidyverse 2.0.0 —
## ✓ dplyr      1.1.4      ✓ readr      2.1.5
## ✓ forcats    1.0.0      ✓ stringr    1.5.1
## ✓ ggplot2     3.5.1      ✓ tibble     3.2.1
## ✓ lubridate  1.9.3      ✓ tidyr      1.3.1
## ✓ purrr      1.0.2
## — Conflicts — tidyverse_conflicts() —
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts
to become errors
```

```
library(pheatmap)
library(Vennerable)
library(gplots)
```

```
##
## Attaching package: 'gplots'
##
## The following object is masked from 'package:stats':
##
##     lowess
```

```
library(dplyr)
```

```
# Loading files
```

```
my.data.1 <- read.csv("./ERS_Specific_Proximal_Closing_DAPs_CPM_Normalized_Counts.csv")  
my.data.2 <- read.csv("./ERS_Specific_Distal_Closing_DAPs_CPM_Normalized_Counts.csv")  
my.data.3 <- read.csv("./INF_Specific_Proximal_Closing_DAPs_CPM_Normalized_Counts.csv")  
my.data.4 <- read.csv("./INF_Specific_Distal_Closing_DAPs_CPM_Normalized_Counts.csv")  
my.data.5 <- read.csv("./Shared_Proximal_Closing_DAPs_CPM_Normalized_Counts.csv")  
my.data.6 <- read.csv("./Shared_Distal_Closing_DAPs_CPM_Normalized_Counts.csv")
```

```
# Combining into a single dataframe
```

```
my.data <- unique(rbind(my.data.1,my.data.2,my.data.3,  
  my.data.4,my.data.5,my.data.6))  
rownames(my.data) <- my.data$X  
my.data <- my.data[-c(1,2)]
```

```
# Making a vector
```

```
order <- c("Islet_144_24h_DMSO",  
"Islet_146_24h_DMSO",  
"Islet_147_24h_DMSO",  
"Islet_148_24h_DMSO",  
"Islet_151_24h_DMSO",  
"Islet_153_24h_DMSO",  
"Islet_144_24h_Thapsi",  
"Islet_146_24h_Thapsi",  
"Islet_147_24h_Thapsi",  
"Islet_148_24h_Thapsi",  
"Islet_151_24h_Thapsi",  
"Islet_153_24h_Thapsi",  
"Islet_106_24h_untreated_25K",  
"Islet_125_24_hr",  
"Islet_151_24h_untreated",  
"Islet_152_24h_untreated",  
"Islet_153_24h_untreated",  
"Islet_99_24hr_Untreated",  
"Islet_106_24h_cytokine",  
"Islet_125_24_hr_IL1B",  
"Islet_151_24h_cyto",  
"Islet_152_24h_cyto",  
"Islet_153_24h_cyto",  
"Islet_99_24hr_Cytokines")
```

```
# Ordering by vector
```

```
my.data.ordered <- my.data[order]
```

```
# Making a heatmap
```

```
pheatmap(my.data.ordered,  
scale = "row",  
clustering_distance_rows = "correlation",  
treeheight_row = 0,  
treeheight_col = 0,  
cluster_row = F, # Manually clustered by Peaks
```

```

cluster_cols = F, # Manually clustered by Treatment
fontsize_row = 0.01,
fontsize_col = 11,
annotation_colors = ann_colors,
color=bluered(1000)) # high number of n to make it a gradient

```

