Figure-1A.R

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```
# This Script Generates Figure 1A
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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
```

```
# Load metadata
metadata <- read.csv("./Metadata_Heatmap.csv")
rownames(metadata) <- metadata$Islet_Number

# Load normalized expression matrices
my.data.1 <- read.csv("./normalized.with.ERCC.counts.for.heatmap.ER.Stress.csv")
my.data.2 <- read.csv("./normalized.with.ERCC.counts.for.heatmap.Inflammation.csv")
my.data <- merge(my.data.1,my.data.2, by="X")
rownames(my.data) <- my.data[,1]
my.data <- my.data[-c(1)]

# Load DEGs
ERS.specific <- read.csv("./Upregulated_only_in_ER_Stress_DEGs.csv")
ERS.specific <- ERS.specific[-c(2:7)]
ERS.specific$Regulation <- c("Upregulated_ERS_specific")

INF.specific <- read.csv("./Upregulated_only_in_Inflammation_DEGs.csv")
INF.specific <- INF.specific[-c(2:7)]
INF.specific$Regulation <- c("Upregulated_INF_specific")

Shared <- read.csv("./Upregulated_common_between_ER_Stress_Inflammation_DEGs.csv")
Shared <- Shared[-c(2:7)]
Shared$Regulation <- c("Upregulated_ERS_and_INF_Shared")

# Making annotation dataframes
metadata.annotation <- metadata
metadata.annotation <- metadata.annotation[order(metadata.annotation$Treatment),]
metadata.annotation <- metadata.annotation[-c(1:7)]
metadata.annotation.names <- rownames(metadata.annotation)
matrix.annotation <- rbind(ERS.specific,INF.specific,Shared)
rownames(matrix.annotation) <- matrix.annotation$X
matrix.annotation <- matrix.annotation[-c(1)]

# Making the heatmap matrix
genes.list <- rownames(matrix.annotation)
matrix <- my.data[(genes.list),]
matrix.ordered <- matrix %>% select(metadata.annotation.names)
matrix.ordered <- as.matrix.data.frame(matrix.ordered)
matrix.ordered <- na.omit(matrix.ordered)
matrix.ordered[is.na(matrix.ordered)] <- 0

# Specify colors
ann_colors = list(
  Treatment = c(A_DMSO="gray", B_Thapsigargin="forestgreen",C_Untreated="grey50",D_Cytok
ines="darkorange"),
  Regulation = c(Upregulated_ERS_specific = "forestgreen",
                 Upregulated_INF_specific="darkorange",
                 Upregulated_ERS_and_INF_Shared = "coral4")
)

# Make heatmap
pheatmap(matrix.ordered,
```

```
        scale = "row",
        clustering_distance_rows = "correlation",
        treeheight_row = 0,
        treeheight_col = 0,
        annotation_row = matrix.annotation,
        annotation_col = metadata.annotation,
        cluster_row = F,
        cluster_cols = F,
        fontsize_row = 0.01,
        fontsize_col = 0.01,
        annotation_colors = ann_colors,
        color=bluered(1000))
```