Figure-3A.R

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```r
# This Script Generates Figure 3A
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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
```

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

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

```r
library(dplyr)

# Loading files
my.data.1 <- read.csv("./ERS_Specific_Proximal_Opening_DAPs_CPM_Normalized_Counts.csv")
my.data.2 <- read.csv("./ERS_Specific_Distal_Opening_DAPs_CPM_Normalized_Counts.csv")
my.data.3 <- read.csv("./INF_Specific_Proximal_Opening_DAPs_CPM_Normalized_Counts.csv")
my.data.4 <- read.csv("./INF_Specific_Distal_Opening_DAPs_CPM_Normalized_Counts.csv")
my.data.5 <- read.csv("./Shared_Proximal_Opening_DAPs_CPM_Normalized_Counts.csv")
my.data.6 <- read.csv("./Shared_Distal_Opening_DAPs_CPM_Normalized_Counts.csv")

# Combine
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_24huntreated_25K",
 "Islet_125_24_hr",
 "Islet_151_24h_untreated",
 "Islet_152_24h_untreated",
 "Islet_153_24h_untreated",
 "Islet_99_24hr_Untreated",
 "Islet_106_24hcytokine",
 "Islet_125_24_hr_IL1B",
 "Islet_151_24h_cyto",
 "Islet_152_24h_cyto" ,
 "Islet_153_24h_cyto",
 "Islet_99_24hr_Cytokines")

# Ordering
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,
```

```
cluster_cols = F,
fontsize_row = 0.01,
fontsize_col = 11,
annotation_colors = ann_colors,
color=bluered(1000))
```