

Figure-2E.R

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```
# This Script Generates Figure 2E
# Script By: Eishani Kumar Sokolowski

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

# Loading libraries
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##   filter, lag
```

```
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
```

```
library(Seurat)
```

```
## Loading required package: SeuratObject
```

```
## Loading required package: sp
```

```
## 'SeuratObject' was built under R 4.4.0 but the current version is
## 4.4.1; it is recommended that you reinstall 'SeuratObject' as the ABI
## for R may have changed
```

```
##
## Attaching package: 'SeuratObject'
```

```
## The following object is masked from 'package:base':
##
##   intersect
```

```
library(ggplot2)
library(tidyverse)
```

```
## — Attaching core tidyverse packages — tidyverse 2.0.0 —
## ✓ forcats 1.0.0      ✓ stringr 1.5.1
## ✓ lubridate 1.9.3    ✓ tibble 3.2.1
## ✓ purrr 1.0.2       ✓ tidyr 1.3.1
## ✓ readr 2.1.5
```

```
## — 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(ggpubr)
```

```
# Load file
```

```
combined <- readRDS("./Combined_Islet_150_Islet_162_Islet_168_Islet_67_Islet_116_Islet_17_Cluster_All_Cell_Type_Identities_Finalized.rds")
```

```
# Keeping cell-types of interest
```

```
combined <- subset(x = combined, idents = "Acinar", invert=TRUE)
combined <- subset(x = combined, idents = "Schwann", invert=TRUE)
combined <- subset(x = combined, idents = "Immune", invert=TRUE)
combined <- subset(x = combined, idents = "Endothelial", invert=TRUE)
combined <- subset(x = combined, idents = "Activated Stellate", invert=TRUE)
combined <- subset(x = combined, idents = "Proliferating Alpha", invert=TRUE)
```

```
# Changing Idents
```

```
Idents(combined) <- "HT0_Label"
```

```
# Extracting ER stress cells
```

```
ERS <- subset(x = combined, idents = "24 Hr Cytokines", invert=TRUE)
ERS <- subset(x = ERS, idents = "24 Hr Untreated", invert=TRUE)
```

```
# Rename Treatment
```

```
ERS$HT0_Label <- gsub('24 Hr DMSO', 'DMSO', ERS$HT0_Label)
ERS$HT0_Label <- gsub('24 Hr Thapsigargin', 'Thapsigargin', ERS$HT0_Label)
```

```
# Plotting by Cell-Type
```

```
p <- DimPlot(ERS, reduction = 'umap', group.by = 'Cell_Type', cols = c('Alpha' = 'golden rod', 'Beta' = 'mediumpurple2', 'Delta' = 'lightseagreen', 'Gamma' = 'khaki4', 'Ductal' = 'deeppink3', 'Stellate' = 'darksalmon'), label=F) + theme(legend.text = element_text(size=5))
```

```
# Plotting by Treatment
```

```
q <- DimPlot(ERS, reduction = 'umap', group.by = 'HT0_Label', cols = c('Thapsigargin' = 'forestgreen', 'DMSO' = 'grey60'), label=F) + theme(legend.text = element_text(size=5))
```

```
# View
```

```
ggarrange(p, q, nrow=2, ncol=2)
```

