Figure-2A.R

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```r
# This Script Generates Figure 2A
# 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
```

```r
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 recomended 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_1
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)

# Plotting by Cell Type
p <- DimPlot(object = combined, reduction = 'umap', group.by = 'Cell_Type', cols = c('Al
pha' = 'goldenrod', 'Beta' = 'mediumpurple2', 'Delta' = 'lightseagreen', 'Gamma' = 'khak
i4', 'Ductal' = 'deeppink3', 'Stellate' = 'darksalmon'), label=F) + theme(legend.text =
element_text(size=5))

# Plotting by Treatment
q <- DimPlot(combined, group.by = "HTO_Label", cols = c('24 Hr Thapsigargin' = 'forestgr
een', '24 Hr DMSO' = 'grey60', '24 Hr Cytokines' = 'darkorange', '24 Hr Untreated' = 'gr
ey80'), order = F) + theme(legend.text = element_text(size=5))

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

Cell_Type

- Alpha
- Beta
- Delta
- Ductal
- Gamma
- Stellate

HTO_Label

- 24 Hr Cytokines
- 24 Hr DMSO
- 24 Hr Thapsigargin
- 24 Hr Untreated