Figure-S2I.R

sokole

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```
# This Script Generates Figure S2I
# 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 recomended that you reinstall 'SeuratObject' as the ABI
## for R may have changed
```

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

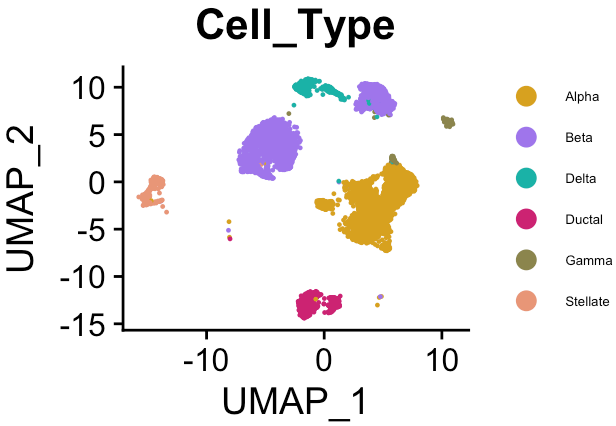
```
## The following object is masked from 'package:base':
##
##     intersect
```

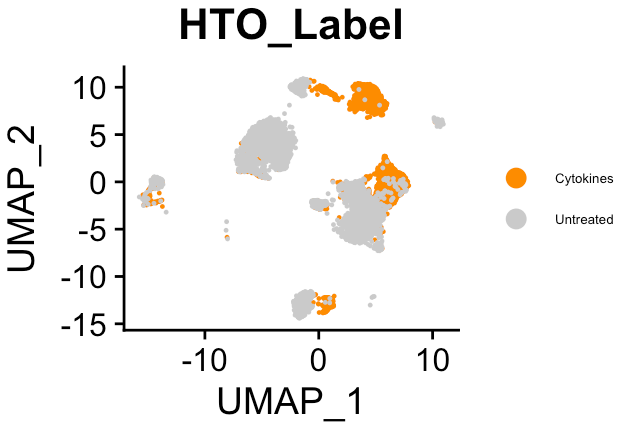
```
library(ggplot2)
library(tidyverse)
```

```
## ── 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)

# Changing Idents
Idents(combined) <- "HTO_Label"

# Extracting inflammation cells
INF <- subset(x = combined, idents = "24 Hr Thapsigargin", invert=TRUE)
INF <- subset(x = INF, idents = "24 Hr DMSO", invert=TRUE)

# Rename Treatment
INF$HTO_Label <- gsub('24 Hr Untreated', 'Untreated', INF$HTO_Label)
INF$HTO_Label <- gsub('24 Hr Cytokines', 'Cytokines', INF$HTO_Label)

# Plotting by Cell-Type
p <- DimPlot(INF, 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(s
ize=5))

# Plotting by Treatment
q <- DimPlot(INF, reduction = 'umap', group.by = 'HTO_Label', cols = c('Cytokines' = 'da
rkorange', 'Untreated' = 'grey80'), label=F, order = T) + theme(legend.text = element_te
xt(size=5))

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


Cell_Type
UMAP_2
UMAP_1
10
5
0
-5
-10
-15
-10
0
10
Alpha
Beta
Delta
Ductal
Gamma
Stellate


HTO_Label
UMAP_2
UMAP_1
10
5
0
-5
-10
-15
-10
0
10
Cytokines
Untreated