

Figure-S2C.R

sokole

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```
# This Script Generates Figure S2C
# 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(dittoSeq)
```

```
# Load file
```

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

```
# Specifying idents
```

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

```
# Rename Cell-Types for Plot Order
```

```
combined$Cell_Type_New <- combined$Cell_Type
```

```
combined$Cell_Type_New <- gsub("Proliferating Alpha","J_Proliferating Alpha",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Activated Stellate","K_Activated Stellate",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Alpha","A_Alpha",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Beta","B_Beta",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Delta","C_Delta",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Gamma","D_Gamma",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Ductal","E_Ductal",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Stellate","F_Stellate",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Acinar","G_Acinar",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Endothelial","H_Endothelial",combined$Cell_Type_New)
```

```
combined$Cell_Type_New <- gsub("Immune","I_Immune",combined$Cell_Type_New)
```

```
# Plotting: Number of Cells - Treatment
```

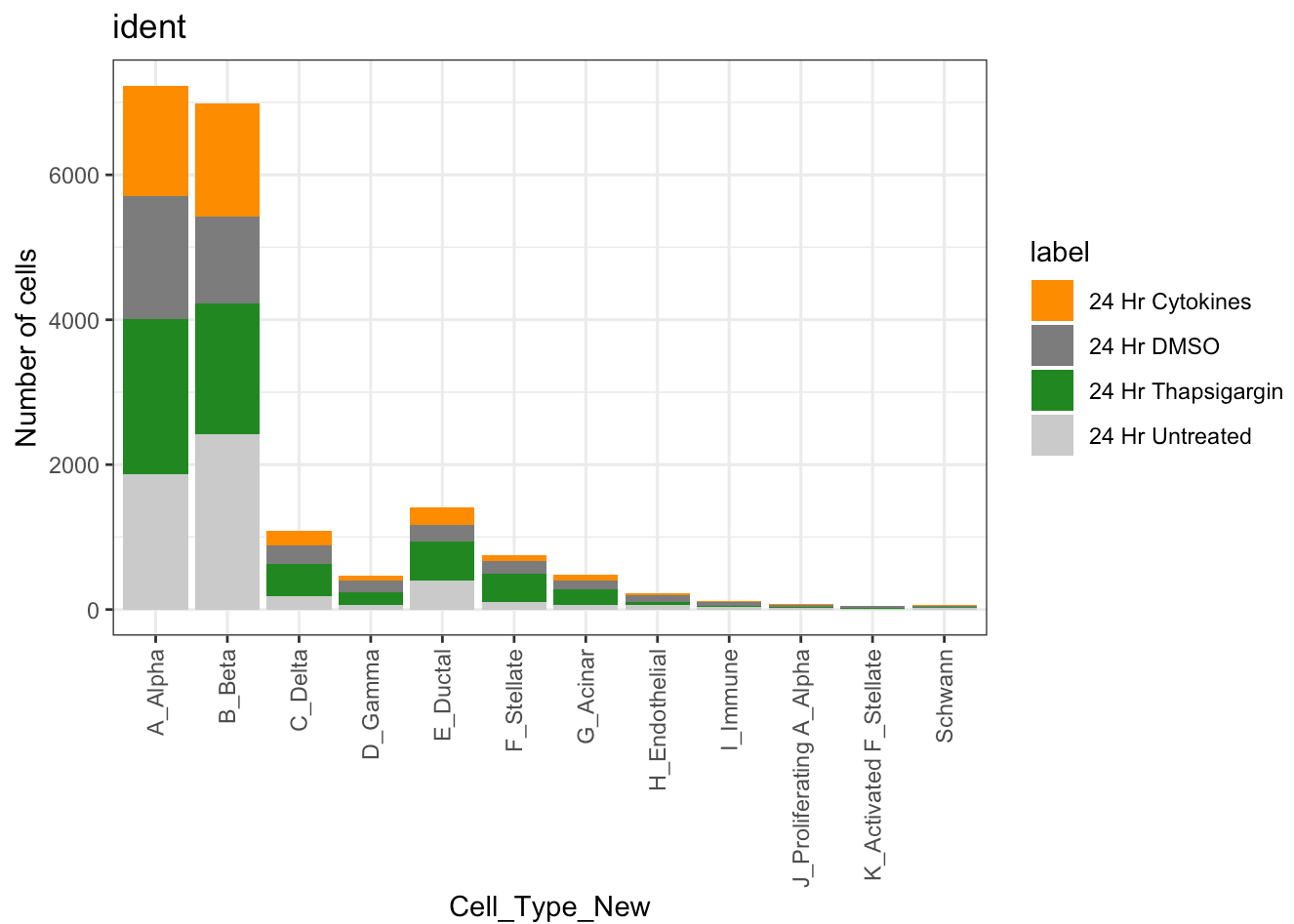
```
Idents(combined) <- "HT0_Label"
```

```
dittoBarPlot(combined, "ident", group.by = "Cell_Type_New", scale = "count")+  
  scale_fill_manual(values = c("darkorange","grey50","forestgreen","grey80")) + theme_bw
```

```
( ) + theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```

```
## Scale for fill is already present.
```

```
## Adding another scale for fill, which will replace the existing scale.
```



```
# Plotting: Percent of Cells by Donor
Idents(combined) <- "Islet_Number"
dittoBarPlot(combined, "ident", group.by = "Cell_Type_New", scale = "percent")+
  scale_fill_brewer(palette = "Accent") + theme_bw() + theme(axis.text.x = element_text
(angle = 90, vjust = 0.5, hjust=1))
```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```

