# Figure-5D-NFIL3-Dot-Plot.R

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```
# This Script Generates Figure 5D
# 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 the seurat object
combined <- readRDS("./Combined_Islet_150_Islet_162_Islet_168_Islet_67_Islet_116_Islet_1
17_Cluster_All_Cell_Type_Identities_Finalized.rds")

# Assigning Idents
Idents(combined) <- "Cell_Type"

# Keeping only alpha and beta cells
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)
combined <- subset(x = combined, idents = "Ductal", invert=TRUE)
combined <- subset(x = combined, idents = "Stellate", invert=TRUE)
combined <- subset(x = combined, idents = "Delta", invert=TRUE)
combined <- subset(x = combined, idents = "Gamma", invert=TRUE)

# Making a new column
combined$Cell_Type_HTO_Label <- paste0(combined$Cell_Type,"_",combined$HTO_Label)

# Making factors
combined$Cell_Type_HTO_Label <- factor(combined$Cell_Type_HTO_Label, levels=c("Beta_24 H
r DMSO",
                                                                               "Beta_24 H
r Thapsigargin",
                                                                               "Beta_24 H
r Untreated",
                                                                               "Beta_24 H
r Cytokines",
                                                                               "Alpha_24
Hr DMSO",
                                                                               "Alpha_24
Hr Thapsigargin",
                                                                               "Alpha_24
Hr Untreated",
                                                                               "Alpha_24
Hr Cytokines"))

# Assigning Idents
Idents(combined) <- "Cell_Type_HTO_Label"

# Making the dot plot
p <- DotPlot(object = combined, features = "NFIL3", col.min = -1.5, col.max = 1) +
  theme(axis.text.x = element_text(angle=90)) +
  scale_color_gradient2(low="white", mid = "grey80", high="red") + coord_flip()
```

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

```
# View
ggarrange(p, ncol = 1, nrow = 1)
```