

# Figure-5G.R

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2024-07-28

```
# This Script Generates Figure 5G
# 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 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$Cell_Type_HT0_Label <- paste0(combined$Cell_Type,"_",combined$HT0_Label)
```

```
# Making factors
```

```
combined$Cell_Type_HT0_Label <- factor(combined$Cell_Type_HT0_Label, levels=c("Beta_24 H  
r DMSO",  
r Thapsigargin",  
r Untreated",  
r Cytokines",  
Hr DMSO",  
Hr Thapsigargin",  
Hr Untreated",  
Hr Cytokines"))
```

```
# Assigning Idents
```

```
Idents(combined) <- "Cell_Type_HT0_Label"
```

```
# Making the dot plot
```

```
p <- DotPlot(object = combined, features = "MAP3K5", col.min = -1, col.max = 1.5) +  
  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)
```

