

Figure-2F-ERS-BC2-vs-DMSO.R

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```
# This Script Generates Figure 2F
# 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()
## ⓘ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(Scillum)
```

```
# Load the seurat object
```

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

```
# Loading the DEGs
```

```
Genes <- read.csv("./beta.DEGs_Smaller_Thapsi_vs_DMSO.csv")
```

```
Genes <- Genes[order(-Genes$avg_log2FC),]
```

```
Genes <- Genes$X
```

```
# Scaling
```

```
combined <- ScaleData(object = combined, features = rownames(combined))
```

```
## Centering and scaling data matrix
```

```
# Making HTO as ident
```

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

```
# Plotting heatmap
```

```
plot_heatmap(dataset = combined,
              hm_limit = c(-2, 0, 2),
              markers = Genes,
              row_font_size = 0,
              sort_var = c("HTO_Label"),
              anno_var = c("HTO_Label"),
              anno_colors = list(c("grey", "forestgreen")),
              hm_colors = c("blue", "white", "red"))
```

```
## `use_raster` is automatically set to TRUE for a matrix with more than  
## 2000 columns You can control `use_raster` argument by explicitly  
## setting TRUE/FALSE to it.  
##  
## Set `ht_opt$message = FALSE` to turn off this message.
```

