Figure-S2K.R

sokole

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```
# This Script Generates Figure S2K
# 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)
```

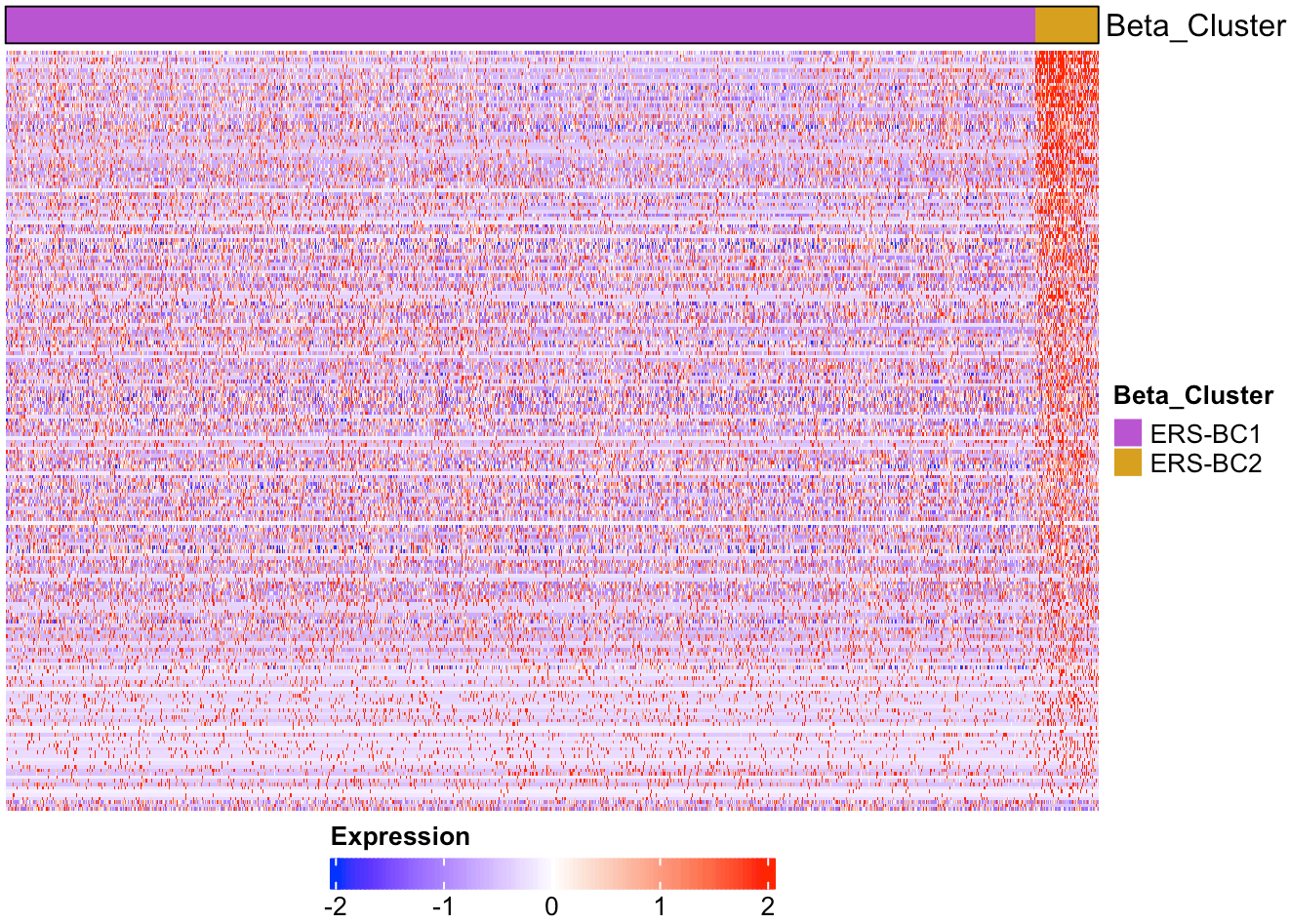
```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ forcats   1.0.0     ✔ stringr   1.5.1
## ✔ lubridate 1.9.3     ✔ tibble    3.2.1
## ✔ purrr     1.0.2     ✔ tidyr     1.3.1
## ✔ readr     2.1.5
```

```
## ── 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(Scillus)
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 - Beta - ERS.rds")

# Loading the DEGs
Genes <- read.csv("./beta.DEGs_Smaller_vs_Bigger_Thapsi_Clusters.csv")
Genes <- Genes[order(-Genes$avg_log2FC),]
Genes <- Genes$X

# Making HTO as ident
Idents(combined) <- "Beta_Cluster"

# Extract ERS-BC1 and ERS-BC2 clusters
combined <- subset(x = combined, idents = "DMSO Cluster", invert = T)

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

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

```
# Plotting heatmap
plot_heatmap(dataset = combined,
             hm_limit = c(-2, 0, 2),
             markers = Genes,
             row_font_size = 0,
             sort_var = c("Beta_Cluster"),
             anno_var = c("Beta_Cluster"),
             anno_colors = list(c("mediumorchid","goldenrod")),
             hm_colors = c("blue","white","red"))
```


Beta_Cluster
Beta_Cluster
ERS-BC1
ERS-BC2
Expression
-2
-1
0
1
2