

# Figure-2H-UPR.R

sokole

2024-07-23

```
# This Script Generates Figure 2H
# 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(Scillum)
library(ggpubr)

# 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")

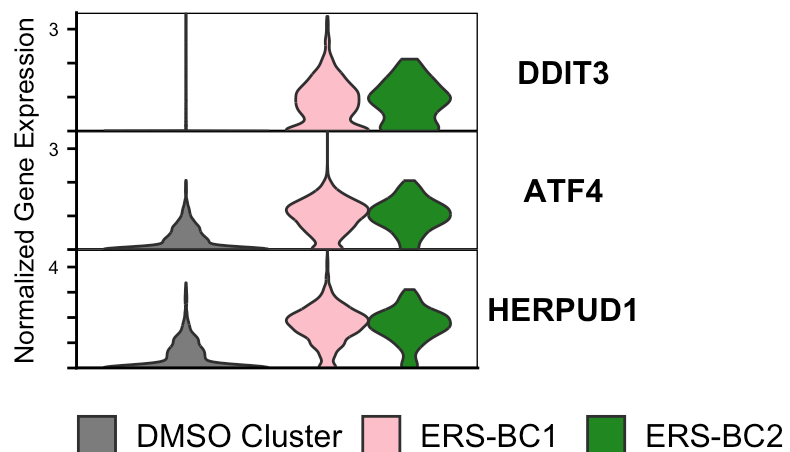
# Ordering
combined$HT0_Label <- factor(x = combined$HT0_Label, levels = c('24 Hr DMS0', '24 Hr Thalpsigargin'))

# Changing Idents
Idents(combined) <- "HT0_Label"

# Plotting Violin Plot with different colors
p <- VlnPlot(combined, c("DDIT3","ATF4","HERPUD1"), split.by = "Beta_Cluster", stack = TRUE, sort = FALSE, flip = TRUE) +
  ylab("Normalized Gene Expression") +
  scale_fill_manual(values = c('grey50', 'pink','forestgreen')) + theme(legend.position = "bottom",
axis.title.y=element_text(size=10),
axis.title.x = element_blank(),
axis.ticks.x=element_blank(),
axis.text.x = element_blank())
```

```
## The default behaviour of split.by has changed.  
## Separate violin plots are now plotted side-by-side.  
## To restore the old behaviour of a single split violin,  
## set split.plot = TRUE.  
##  
## This message will be shown once per session.  
## Scale for fill is already present.  
## Adding another scale for fill, which will replace the existing scale.
```

```
# View  
ggarrange(p, ncol = 2, nrow = 2)
```



```
# Plotting Violin Plot with final colors
p <- VlnPlot(combined, c("DDIT3","ATF4","HERPUD1"), split.by = "Beta_Cluster", stack = TRUE, sort = FALSE, flip = TRUE) +
  ylab("Normalized Gene Expression") +
  scale_fill_manual(values = c('grey50', 'forestgreen','forestgreen')) + theme(legend.position="bottom",
axis.title.y=element_text(size=10),
axis.title.x = element_blank(),
axis.ticks.x=element_blank(),
axis.text.x = element_blank())
```

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

```
# View
ggarrange(p, ncol = 2, nrow = 2)
```

