Figure-2H-Apoptosis.R

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```r
# 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
```

```r
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")

# Ordering
combined$HTO_Label <- factor(x = combined$HTO_Label, levels = c('24 Hr DMSO', '24 Hr Tha
psigargin'))

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

# Plotting Violin Plot with different colors
p <- VlnPlot(combined, c("PSMB8","PSMB10","PSMB9"), split.by = "Beta_Cluster", stack = T
RUE, sort = FALSE, flip = TRUE) +
  ylab("Normalized Gene Expression") +
  scale_fill_manual(values = c('grey50', 'pink','forestgreen')) + theme(legend.position
="bottom",
                                                                        axis.title.y=ele
ment_text(size=10),
                                                                        axis.title.x = e
lement_blank(),
                                                                        axis.ticks.x=ele
ment_blank(),
                                                                        axis.text.x = el
ement_blank())
```
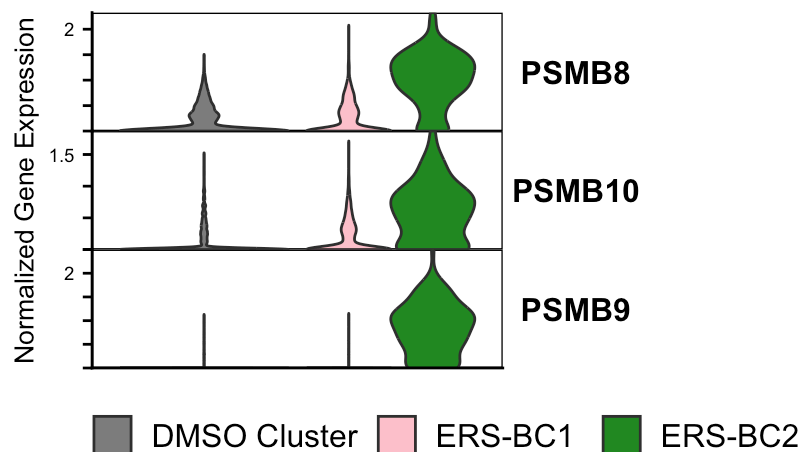
```
## The default behaviour of split.by has changed.
## Separate violin plots are now plotted side-by-side.
## To restore the old behaviour of a single split violin,
## set split.plot = TRUE.
##
## This message will be shown once per session.
## Scale for fill is already present.
## Adding another scale 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("PSMB8","PSMB10","PSMB9"), split.by = "Beta_Cluster", stack = T
RUE, sort = FALSE, flip = TRUE) +
  ylab("Normalized Gene Expression") +
  scale_fill_manual(values = c('grey50', 'forestgreen','forestgreen')) + theme(legend.po
sition="bottom",
                                                                axis.title.y=ele
ment_text(size=10),
                                                                axis.title.x = e
lement_blank(),
                                                                axis.ticks.x=ele
ment_blank(),
                                                                axis.text.x = el
ement_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)
```