Figure-S5C.R

sokole

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```
# This Script Generates Figure S5C
# 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)
```

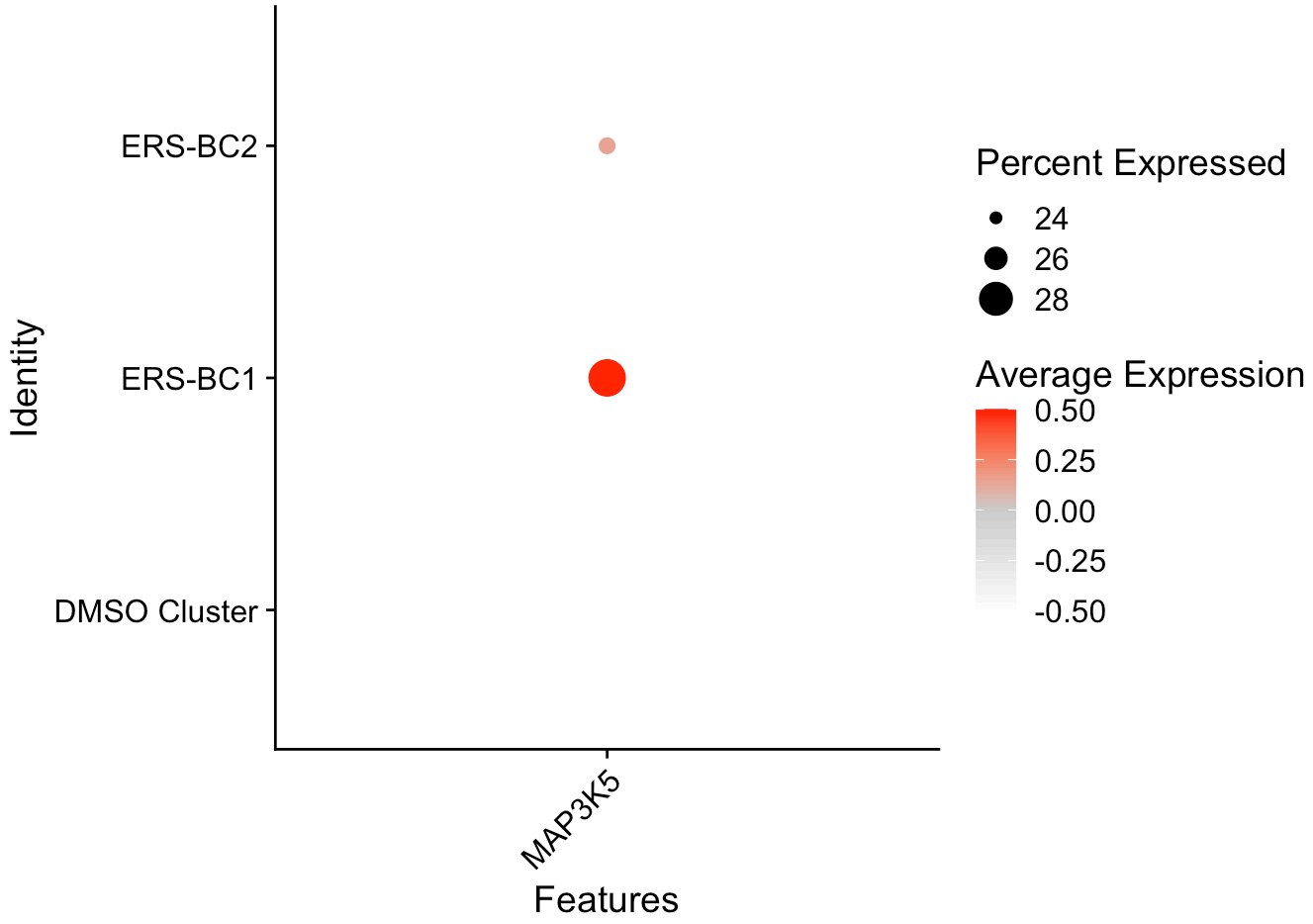
```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ forcats   1.0.0     ✔ stringr   1.5.1
## ✔ lubridate 1.9.3     ✔ tibble    3.2.1
## ✔ purrr     1.0.2     ✔ tidyr     1.3.1
## ✔ readr     2.1.5
```

```
## ── 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(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$Beta_Cluster <- factor(x = combined$Beta_Cluster, levels = c('DMSO Cluster','ER
S-BC1','ERS-BC2'))

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

# Making a dotplot
p <- DotPlot(combined, features = "MAP3K5", col.min = -0.5, col.max = 0.5) + RotatedAxis
() + scale_color_gradient2(low="white", mid = "grey80", high="red")
```

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

```
# View
ggarrange(p, ncol = 1, nrow = 1)
```


ERS-BC2
ERS-BC1
DMSO Cluster
Identity
MAP3K5
Features
Percent Expressed
24
26
28
Average Expression
0.50
0.25
0.00
-0.25
-0.50