

Figure-S2B.R

sokole

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```
# This Script Generates Figure S2B
# 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
```

```
# Load file
combined <- readRDS("./Combined_Islet_150_Islet_162_Islet_168_Islet_67_Islet_116_Islet_17_Cluster_All_Cell_Type_Identities_Finalized.rds")

# Changing idents
Idents(combined) <- "Cell_Type"

# Keeping cell-types of interest
combined <- subset(x = combined, idents = "Acinar", invert=TRUE)
combined <- subset(x = combined, idents = "Schwann", invert=TRUE)
combined <- subset(x = combined, idents = "Immune", invert=TRUE)
combined <- subset(x = combined, idents = "Endothelial", invert=TRUE)
combined <- subset(x = combined, idents = "Activated Stellate", invert=TRUE)
combined <- subset(x = combined, idents = "Proliferating Alpha", invert=TRUE)

# Islet markers
islet_markers <- list('Beta'=c("INS","IAPP","SIX3","ADCYAP1","MAFA","DLK1"),
                      'Delta'=c("SST","BCHE","LEPR","GAST","SALL1"),
                      'Alpha'=c("GCG","LOXL4","DPP4","TMEM236","IRX2","CRYBA2","PLCE1",
                                "C5orf38"),
                      'Gamma'=c("PPY","FGB","LM03","CHN2","PTGFR","ENTPD2","THSD7A"),
                      'Ductal'=c("KRT19","TSPAN8","CFTR","MMP7","LGALS4"),
                      'Stellate'=c("COL1A1","COL6A1","PDGFRB","FN1","COL1A2","COL3A1","SFRP2"))

# Changing idents
Idents(combined) <- "seurat_clusters"

# Plotting
DotPlot(combined, features = islet_markers, cluster.idents = T, col.min = 0, col.max = 2) + RotatedAxis()
```

