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 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)
```

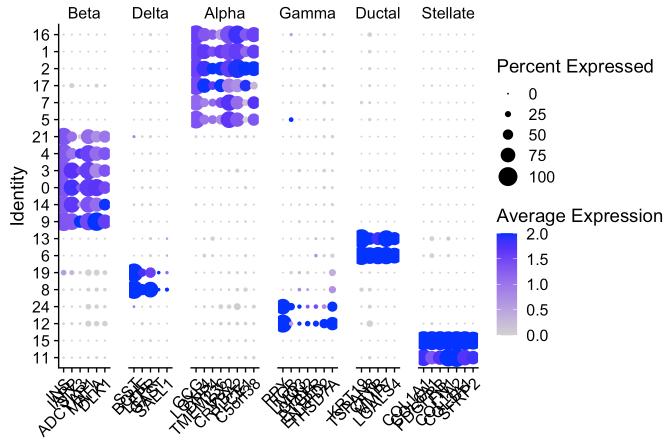
```
## — Attaching core tidyverse packages -
                                                                  - tidyverse 2.0.0 —
## ✓ forcats 1.0.0
                         ✓ stringr
                                      1.5.1
## ✓ lubridate 1.9.3
                                      3.2.1

✓ tibble

## ✓ purrr 1.0.2

✓ tidyr

                                      1.3.1
## ✓ readr
               2.1.5
                                                            - tidyverse_conflicts() —
## — Conflicts -
## * dplyr::filter() masks stats::filter()
## x 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 1
17_Cluster_All_Cell_Type_Identities_Finalized.rds")
# Changing idents
Idents(combined) <- "Cell_Type"</pre>
# Keeping cell-types of interest
combined <- subset(x = combined, idents = "Acinar", invert=TRUE)</pre>
combined <- subset(x = combined, idents = "Schwann", invert=TRUE)</pre>
combined <- subset(x = combined, idents = "Immune", invert=TRUE)</pre>
combined <- subset(x = combined, idents = "Endothelial", invert=TRUE)</pre>
combined <- subset(x = combined, idents = "Activated Stellate", invert=TRUE)</pre>
combined <- subset(x = combined, idents = "Proliferating Alpha", invert=TRUE)</pre>
# Islet markers
islet_markers <- list('Beta'=c("INS","IAPP","SIX3","ADCYAP1","MAFA","DLK1"),</pre>
                       'Delta'=c("SST", "BCHE", "LEPR", "GAST", "SALL1"),
                       'Alpha'=c("GCG","LOXL4","DPP4","TMEM236", "IRX2","CRYBA2","PLCE
1", "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","S
FRP2"))
# Changing idents
Idents(combined) <- "seurat clusters"</pre>
# Plotting
DotPlot(combined, features = islet markers, cluster.idents = T, col.min = 0, col.max =
2) + RotatedAxis()
```



Features