

Figure-2G.R

sokole

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```
# This Script Generates Figure 2G
# Script By: Eishani Kumar Sokolowski

# Empty the environment & suppress warnings
rm(list = ls())
options(warn=-1)

# Loading the required 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(ggplot2)
library(ggrepel)
library(GeneOverlap)
library(Vennerable)
library(VennDiagram)
```

```
## Loading required package: grid
```

```
## Loading required package: futile.logger
```

```
#####
# Loading the genes
#####

# DEGs: ERS-BC1 vs DMS0
Bigger <- read.csv("./beta.DEGs_Bigger_Thapsi_vs_DMS0.csv")
Bigger <- Bigger[Bigger$avg_log2FC > 0,]
Bigger <- Bigger$X

# DEGs: ERS-BC2 vs DMS0
Smaller <- read.csv("./beta.DEGs_Smaller_Thapsi_vs_DMS0.csv")
Smaller <- Smaller[Smaller$avg_log2FC >= 0,]
Smaller <- Smaller$X

#####
# Venn Diagram
#####

# Making a list
Venn.Diagram <- list()
Venn.Diagram[["ERS-BC1 Upregulated DEGs"]] <- Bigger
Venn.Diagram[["ERS-BC2 Upregulated DEGs"]] <- Smaller

# Plotting the Venn diagram
Vstem <- Venn(Venn.Diagram)
plot(Vstem)
```

