Figure-S2G-Shared.R

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```
# This Script Generates Figure S2G
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# Empty the environment & suppress warnings
rm(list = ls())
options(warn=-1)

# Loading libraries
library(tidyverse)
```

```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ dplyr     1.1.4     ✔ readr     2.1.5
## ✔ forcats   1.0.0     ✔ stringr   1.5.1
## ✔ ggplot2   3.5.1     ✔ tibble    3.2.1
## ✔ lubridate 1.9.3     ✔ tidyr     1.3.1
## ✔ purrr     1.0.2
## ── 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(ggplot2)
library(ggpubr)
library(data.table)
```

```
##
## Attaching package: 'data.table'
##
## The following objects are masked from 'package:lubridate':
##
##     hour, isoweek, mday, minute, month, quarter, second, wday, week,
##     yday, year
##
## The following objects are masked from 'package:dplyr':
##
##     between, first, last
##
## The following object is masked from 'package:purrr':
##
##     transpose
```

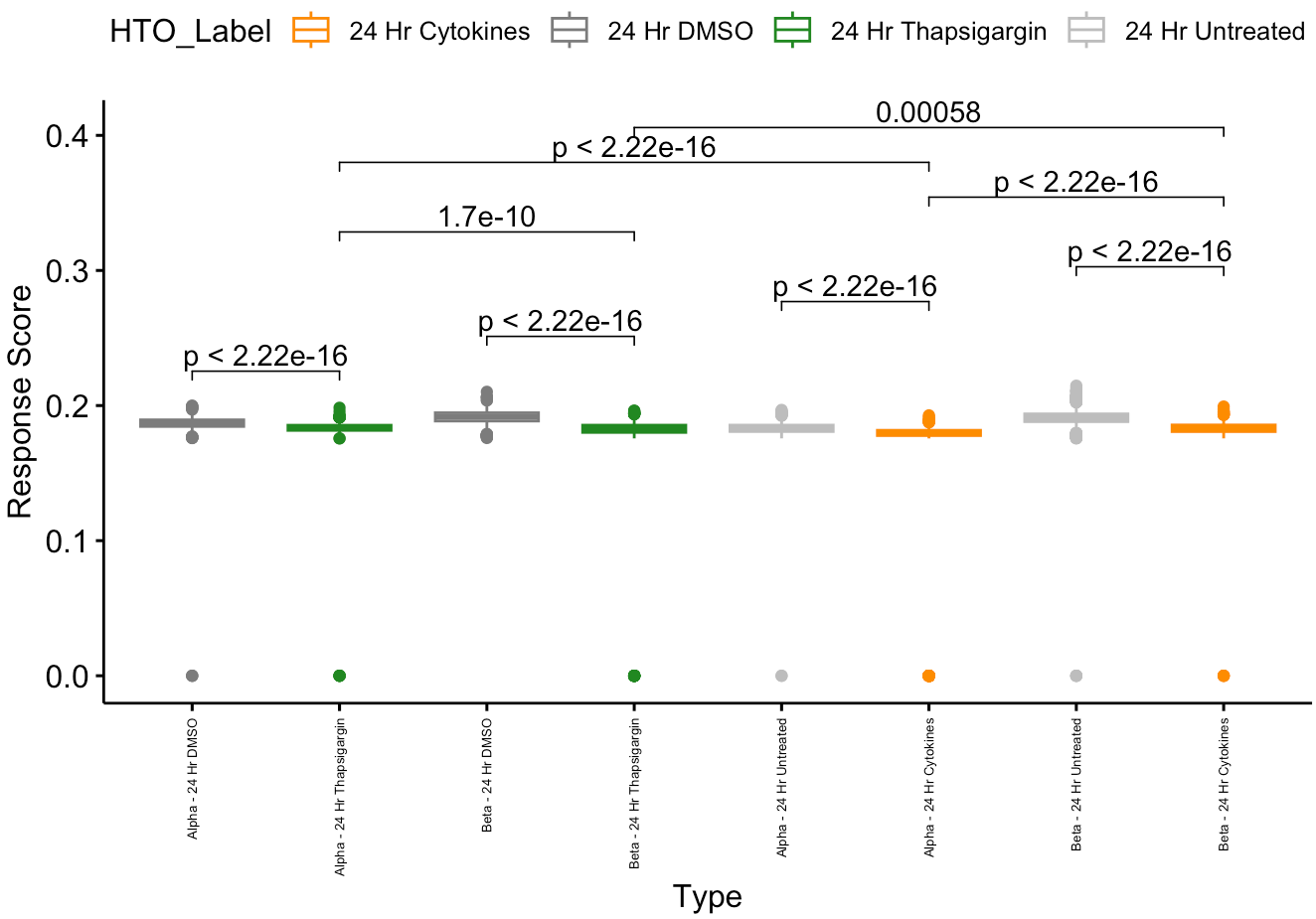
```
library(dplyr)
library(ggpubr)
library(rstatix)
```

```
##
## Attaching package: 'rstatix'
##
## The following object is masked from 'package:stats':
##
##     filter
```

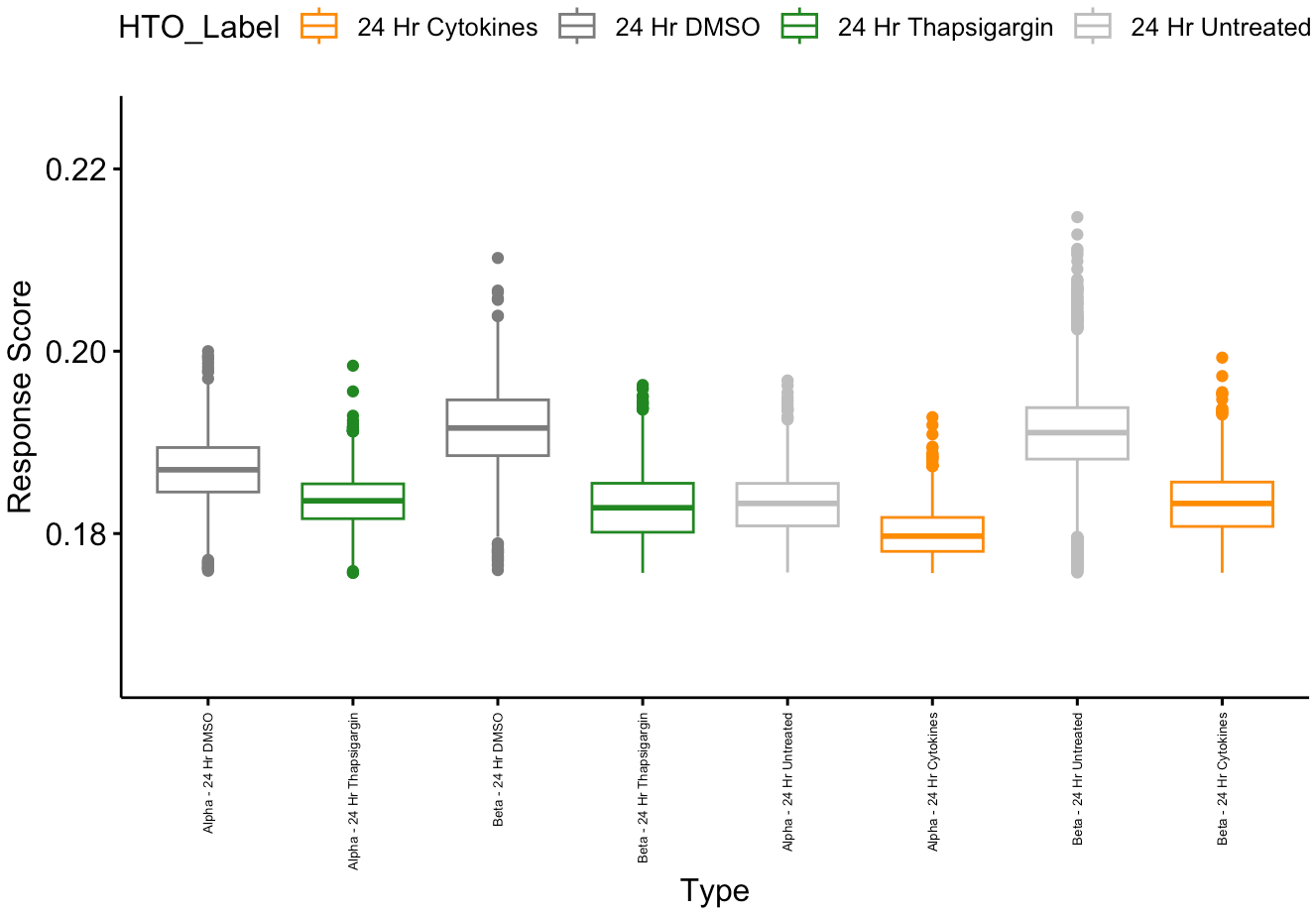
```
library(Seurat)
```

```
## 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(RColorBrewer)

# Loading the file
gene.scores <- read.csv("./Shared_Downregulated_DEGs_Gene_Score.csv")
gene.scores <- gene.scores[-c(1)]
gene.scores$Shared_Downregulated_DEGs_Gene_Score <- as.numeric(gene.scores$Shared_Downre
gulated_DEGs_Gene_Score)
gene.scores$Condition <- gene.scores$HTO_Label
gene.scores$Condition <- gsub("24 Hr Thapsigargin","ERS",gene.scores$Condition)
gene.scores$Condition <- gsub("24 Hr DMSO","ERS",gene.scores$Condition)
gene.scores$Condition <- gsub("24 Hr Cytokines","INF",gene.scores$Condition)
gene.scores$Condition <- gsub("24 Hr Untreated","INF",gene.scores$Condition)
gene.scores$Type <- paste0(gene.scores$Cell_Type," - ",gene.scores$HTO_Label)

# Create factor and levels
gene.scores$Type <- factor(gene.scores$Type,
                           levels = c('Alpha - 24 Hr DMSO','Alpha - 24 Hr Thapsigargin',
                                      'Beta - 24 Hr DMSO','Beta - 24 Hr Thapsigargin',
                                      'Alpha - 24 Hr Untreated','Alpha - 24 Hr Cytokine
s',
                                      'Beta - 24 Hr Untreated','Beta - 24 Hr Cytokine
s'))

# Visualize: Specify the comparisons you want
my_comparisons <- list( c("Alpha - 24 Hr DMSO", "Alpha - 24 Hr Thapsigargin"),
                        c("Beta - 24 Hr DMSO", "Beta - 24 Hr Thapsigargin"),
                        c("Alpha - 24 Hr Untreated", "Alpha - 24 Hr Cytokines"),
                        c("Beta - 24 Hr Untreated", "Beta - 24 Hr Cytokines"),
                        c("Alpha - 24 Hr Thapsigargin", "Beta - 24 Hr Thapsigargin"),
                        c("Alpha - 24 Hr Cytokines", "Beta - 24 Hr Cytokines"),
                        c("Alpha - 24 Hr Thapsigargin", "Alpha - 24 Hr Cytokines"),
                        c("Beta - 24 Hr Thapsigargin", "Beta - 24 Hr Cytokines"))

# Plotting with Wilcox P-value (complete y-axis)
ggboxplot(gene.scores, x = "Type", y = "Shared_Downregulated_DEGs_Gene_Score",
          color = "HTO_Label", palette = c("darkorange", "grey50", "forestgreen", "gre
y"))+
  stat_compare_means(comparisons = my_comparisons, label =  "p", method = "wilcox.test",
paired = FALSE, method.args = list(alternative = "two.sided")) +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1, size=5)) + ylab("Re
sponse Score")
```




```
# Plotting (shorter y-axis)
ggboxplot(gene.scores, x = "Type", y = "Shared_Downregulated_DEGs_Gene_Score",
          color = "HTO_Label", palette = c("darkorange", "grey50", "forestgreen", "gre
y"))+
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1, size=5)) + ylab("Re
sponse Score") + ylim(0.165,0.225)
```


HTO_Label
24 Hr Cytokines
24 Hr DMSO
24 Hr Thapsigargin
24 Hr Untreated
Response Score
0.22
0.20
0.18
Alpha - 24 Hr DMSO
Alpha - 24 Hr Thapsigargin
Beta - 24 Hr DMSO
Beta - 24 Hr Thapsigargin
Alpha - 24 Hr Untreated
Alpha - 24 Hr Cytokines
Beta - 24 Hr Untreated
Beta - 24 Hr Cytokines
Type