

Figure-2C-Shared.R

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

```
# 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 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(RColorBrewer)
```

```
# Loading the file
```

```
gene.scores <- read.csv("./Shared_Upregulated_DEGs_Gene_Score.csv")  
gene.scores <- gene.scores[-c(1)]  
gene.scores$Shared_Upregulated_DEGs_Gene_Score <- as.numeric(gene.scores$Shared_Upregulated_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
```

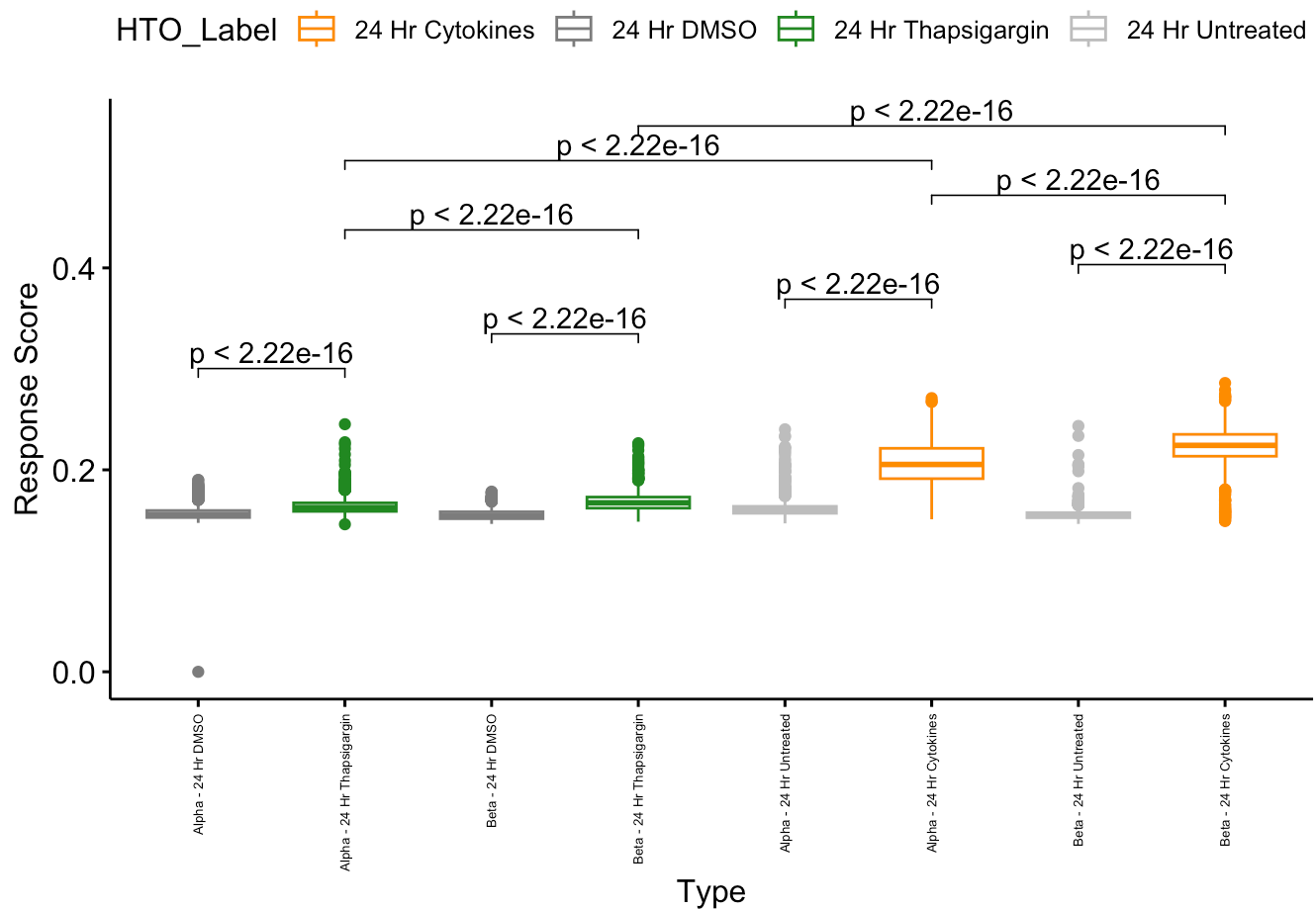
```
gene.scores$Type <- factor(gene.scores$Type,  
                           levels = c('Alpha - 24 Hr DMSO','Alpha - 24 Hr Thapsigargin',  
                                       'Beta - 24 Hr DMSO','Beta - 24 Hr Thapsigargin',  
                                       'Alpha - 24 Hr Untreated','Alpha - 24 Hr Cytokines',  
                                       'Beta - 24 Hr Untreated','Beta - 24 Hr Cytokines'))
```

```
# 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_Upregulated_DEGs_Gene_Score",  
           color = "HTO_Label", palette = c("darkorange", "grey50", "forestgreen", "grey"))+  
  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("Response Score")
```



```
# Plotting (shorter y-axis)
ggboxplot(gene.scores, x = "Type", y = "Shared_Upregulated_DEGs_Gene_Score",
          color = "HTO_Label", palette = c("darkorange", "grey50", "forestgreen", "grey50"))+
  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("Response Score") + ylim(0.13,0.30)
```

HTO_Label 24 Hr Cytokines 24 Hr DMSO 24 Hr Thapsigargin 24 Hr Untreated

