

# Figure-S3F-MAFA.R

sokole

2024-07-26

```
# This Script Generates Figure S3F
# 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(pheatmap)
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
```

```

# Load the gene of interest
DEG.of.interest <- c("MAFA")

#####
# Loading the normalized expression matrix
#####

normalized.counts.ERS <- read.csv("./normalized.with.ERCC.counts.for.heatmap.ER.Stress.csv")
normalized.counts.INF <- read.csv("./normalized.with.ERCC.counts.for.heatmap.Inflammation.csv")

final.df <- merge(normalized.counts.ERS,normalized.counts.INF,by="Genes", all = TRUE)
final.df <- final.df[final.df$Genes %in% DEG.of.interest,]

rownames(final.df) <- final.df$Genes
final.df <- final.df[-c(1)]

#####
# ER stress
#####

normalized.counts.ERS.Thaps <- final.df[ , grep("Thaps", colnames(final.df))]
normalized.counts.ERS.DMSO <- final.df[ , grep("DMSO", colnames(final.df))]

#####
# Thapsigargin expression
#####

normalized.counts.ERS.Thaps.Islet_144_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,1])
normalized.counts.ERS.Thaps.Islet_146_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,2])
normalized.counts.ERS.Thaps.Islet_147_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,3])
normalized.counts.ERS.Thaps.Islet_148_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,4])
normalized.counts.ERS.Thaps.Islet_149_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,5])
normalized.counts.ERS.Thaps.Islet_75_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,6])
normalized.counts.ERS.Thaps.Islet_78_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,7])
normalized.counts.ERS.Thaps.Islet_81_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,8])
normalized.counts.ERS.Thaps.Islet_82_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,9])
normalized.counts.ERS.Thaps.Islet_86_Thapsigargin<- as.data.frame(normalized.counts.ERS.Thaps[,10])

colnames(normalized.counts.ERS.Thaps.Islet_144_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_146_Thapsigargin) <- c("Expression")

```

```

colnames(normalized.counts.ERS.Thaps.Islet_147_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_148_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_149_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_75_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_78_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_81_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_82_Thapsigargin) <- c("Expression")
colnames(normalized.counts.ERS.Thaps.Islet_86_Thapsigargin) <- c("Expression")

normalized.counts.ERS.Thaps.Islet_144_Thapsigargin$Islet<- c(colnames(normalized.counts.
ERS.Thaps)[1])
normalized.counts.ERS.Thaps.Islet_146_Thapsigargin$Islet<- c(colnames(normalized.counts.
ERS.Thaps)[2])
normalized.counts.ERS.Thaps.Islet_147_Thapsigargin$Islet<- c(colnames(normalized.counts.
ERS.Thaps)[3])
normalized.counts.ERS.Thaps.Islet_148_Thapsigargin$Islet<- c(colnames(normalized.counts.
ERS.Thaps)[4])
normalized.counts.ERS.Thaps.Islet_149_Thapsigargin$Islet<- c(colnames(normalized.counts.
ERS.Thaps)[5])
normalized.counts.ERS.Thaps.Islet_75_Thapsigargin$Islet<- c(colnames(normalized.counts.E
RS.Thaps)[6])
normalized.counts.ERS.Thaps.Islet_78_Thapsigargin$Islet<- c(colnames(normalized.counts.E
RS.Thaps)[7])
normalized.counts.ERS.Thaps.Islet_81_Thapsigargin$Islet<- c(colnames(normalized.counts.E
RS.Thaps)[8])
normalized.counts.ERS.Thaps.Islet_82_Thapsigargin$Islet<- c(colnames(normalized.counts.E
RS.Thaps)[9])
normalized.counts.ERS.Thaps.Islet_86_Thapsigargin$Islet<- c(colnames(normalized.counts.E
RS.Thaps)[10])

normalized.counts.ERS.Thaps.Islet_144_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_146_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_147_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_148_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_149_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_75_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_78_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_81_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_82_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)
normalized.counts.ERS.Thaps.Islet_86_Thapsigargin$Genes<- rownames(normalized.counts.ER
S.Thaps)

final.df.Thaps <- rbind(normalized.counts.ERS.Thaps.Islet_144_Thapsigargin,

```

```
normalized.counts.ERS.Thaps.Islet_146_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_147_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_148_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_149_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_75_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_78_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_81_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_82_Thapsigargin,  
normalized.counts.ERS.Thaps.Islet_86_Thapsigargin)
```

```
final.df.Thaps$Treatment <- c("B_Thapsigargin")
```

```
#####  
# DMSO expression  
#####
```

```
normalized.counts.ERS.DMS0.Islet_144_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
1])  
normalized.counts.ERS.DMS0.Islet_146_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
2])  
normalized.counts.ERS.DMS0.Islet_147_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
3])  
normalized.counts.ERS.DMS0.Islet_148_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
4])  
normalized.counts.ERS.DMS0.Islet_149_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
5])  
normalized.counts.ERS.DMS0.Islet_75_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
6])  
normalized.counts.ERS.DMS0.Islet_78_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
7])  
normalized.counts.ERS.DMS0.Islet_81_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
8])  
normalized.counts.ERS.DMS0.Islet_82_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,  
9])  
normalized.counts.ERS.DMS0.Islet_86_DMS0<- as.data.frame(normalized.counts.ERS.DMS0[,1  
0])
```

```
colnames(normalized.counts.ERS.DMS0.Islet_144_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_146_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_147_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_148_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_149_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_75_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_78_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_81_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_82_DMS0) <- c("Expression")  
colnames(normalized.counts.ERS.DMS0.Islet_86_DMS0) <- c("Expression")
```

```
normalized.counts.ERS.DMS0.Islet_144_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)  
[1])  
normalized.counts.ERS.DMS0.Islet_146_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)  
[2])
```

```

normalized.counts.ERS.DMS0.Islet_147_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[3])
normalized.counts.ERS.DMS0.Islet_148_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[4])
normalized.counts.ERS.DMS0.Islet_149_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[5])
normalized.counts.ERS.DMS0.Islet_75_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[6])
normalized.counts.ERS.DMS0.Islet_78_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[7])
normalized.counts.ERS.DMS0.Islet_81_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[8])
normalized.counts.ERS.DMS0.Islet_82_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[9])
normalized.counts.ERS.DMS0.Islet_86_DMS0$Islet<- c(colnames(normalized.counts.ERS.DMS0)
[10])

normalized.counts.ERS.DMS0.Islet_144_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_146_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_147_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_148_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_149_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_75_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_78_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_81_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_82_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)
normalized.counts.ERS.DMS0.Islet_86_DMS0$Genes<- rownames(normalized.counts.ERS.DMS0)

final.df.DMS0 <- rbind(normalized.counts.ERS.DMS0.Islet_144_DMS0,
                        normalized.counts.ERS.DMS0.Islet_146_DMS0,
                        normalized.counts.ERS.DMS0.Islet_147_DMS0,
                        normalized.counts.ERS.DMS0.Islet_148_DMS0,
                        normalized.counts.ERS.DMS0.Islet_149_DMS0,
                        normalized.counts.ERS.DMS0.Islet_75_DMS0,
                        normalized.counts.ERS.DMS0.Islet_78_DMS0,
                        normalized.counts.ERS.DMS0.Islet_81_DMS0,
                        normalized.counts.ERS.DMS0.Islet_82_DMS0,
                        normalized.counts.ERS.DMS0.Islet_86_DMS0)

final.df.DMS0$Treatment <- c("A_DMS0")

final.df.ERS <- rbind(final.df.DMS0,final.df.Thaps)

#####
# Cytokine-induced inflammation
#####

normalized.counts.Cytokines <- final.df[ , grep("Cytokines", colnames(final.df))]
normalized.counts.Untreated <- final.df[ , grep("Untreated", colnames(final.df))]

#####
# Cytokines expression

```

#####

```
normalized.counts.Cytokines.Islet_100_Cytokines<- as.data.frame(normalized.counts.Cytokines[,1])
normalized.counts.Cytokines.Islet_103_Cytokines<- as.data.frame(normalized.counts.Cytokines[,2])
normalized.counts.Cytokines.Islet_144_Cytokines<- as.data.frame(normalized.counts.Cytokines[,3])
normalized.counts.Cytokines.Islet_146_Cytokines<- as.data.frame(normalized.counts.Cytokines[,4])
normalized.counts.Cytokines.Islet_147_Cytokines<- as.data.frame(normalized.counts.Cytokines[,5])
normalized.counts.Cytokines.Islet_148_Cytokines<- as.data.frame(normalized.counts.Cytokines[,6])
normalized.counts.Cytokines.Islet_149_Cytokines<- as.data.frame(normalized.counts.Cytokines[,7])
normalized.counts.Cytokines.Islet_75_Cytokines<- as.data.frame(normalized.counts.Cytokines[,8])
normalized.counts.Cytokines.Islet_78_Cytokines<- as.data.frame(normalized.counts.Cytokines[,9])
normalized.counts.Cytokines.Islet_81_Cytokines<- as.data.frame(normalized.counts.Cytokines[,10])
normalized.counts.Cytokines.Islet_82_Cytokines<- as.data.frame(normalized.counts.Cytokines[,11])
normalized.counts.Cytokines.Islet_86_Cytokines<- as.data.frame(normalized.counts.Cytokines[,12])
normalized.counts.Cytokines.Islet_92_Cytokines<- as.data.frame(normalized.counts.Cytokines[,13])
normalized.counts.Cytokines.Islet_93_Cytokines<- as.data.frame(normalized.counts.Cytokines[,14])
normalized.counts.Cytokines.Islet_94_Cytokines<- as.data.frame(normalized.counts.Cytokines[,15])
normalized.counts.Cytokines.Islet_95_Cytokines<- as.data.frame(normalized.counts.Cytokines[,16])
normalized.counts.Cytokines.Islet_96_Cytokines<- as.data.frame(normalized.counts.Cytokines[,17])
normalized.counts.Cytokines.Islet_97_Cytokines<- as.data.frame(normalized.counts.Cytokines[,18])
normalized.counts.Cytokines.Islet_99_Cytokines<- as.data.frame(normalized.counts.Cytokines[,19])
```

```
colnames(normalized.counts.Cytokines.Islet_100_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_103_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_144_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_146_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_147_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_148_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_149_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_75_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_78_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_81_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_82_Cytokines) <- c("Expression")
```

```

colnames(normalized.counts.Cytokines.Islet_86_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_92_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_93_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_94_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_95_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_96_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_97_Cytokines) <- c("Expression")
colnames(normalized.counts.Cytokines.Islet_99_Cytokines) <- c("Expression")

normalized.counts.Cytokines.Islet_100_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[1])
normalized.counts.Cytokines.Islet_103_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[2])
normalized.counts.Cytokines.Islet_144_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[3])
normalized.counts.Cytokines.Islet_146_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[4])
normalized.counts.Cytokines.Islet_147_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[5])
normalized.counts.Cytokines.Islet_148_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[6])
normalized.counts.Cytokines.Islet_149_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[7])
normalized.counts.Cytokines.Islet_75_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[8])
normalized.counts.Cytokines.Islet_78_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[9])
normalized.counts.Cytokines.Islet_81_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[10])
normalized.counts.Cytokines.Islet_82_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[11])
normalized.counts.Cytokines.Islet_86_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[12])
normalized.counts.Cytokines.Islet_92_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[13])
normalized.counts.Cytokines.Islet_93_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[14])
normalized.counts.Cytokines.Islet_94_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[15])
normalized.counts.Cytokines.Islet_95_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[16])
normalized.counts.Cytokines.Islet_96_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[17])
normalized.counts.Cytokines.Islet_97_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[18])
normalized.counts.Cytokines.Islet_99_Cytokines$Islet<- c(colnames(normalized.counts.Cytokines)[19])

normalized.counts.Cytokines.Islet_100_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_103_Cytokines$Genes<- rownames(normalized.counts.Cytokines)

```



```

normalized.counts.Cytokines.Islet_144_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_146_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_147_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_148_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_149_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_75_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_78_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_81_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_82_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_86_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_92_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_93_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_94_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_95_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_96_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_97_Cytokines$Genes<- rownames(normalized.counts.Cytokines)
normalized.counts.Cytokines.Islet_99_Cytokines$Genes<- rownames(normalized.counts.Cytokines)

final.df.Cytokines <- rbind(normalized.counts.Cytokines.Islet_100_Cytokines,
                             normalized.counts.Cytokines.Islet_103_Cytokines,
                             normalized.counts.Cytokines.Islet_144_Cytokines,
                             normalized.counts.Cytokines.Islet_146_Cytokines,
                             normalized.counts.Cytokines.Islet_147_Cytokines,
                             normalized.counts.Cytokines.Islet_148_Cytokines,
                             normalized.counts.Cytokines.Islet_149_Cytokines,
                             normalized.counts.Cytokines.Islet_75_Cytokines,
                             normalized.counts.Cytokines.Islet_78_Cytokines,
                             normalized.counts.Cytokines.Islet_81_Cytokines,
                             normalized.counts.Cytokines.Islet_82_Cytokines,
                             normalized.counts.Cytokines.Islet_86_Cytokines,
                             normalized.counts.Cytokines.Islet_92_Cytokines,
                             normalized.counts.Cytokines.Islet_93_Cytokines,
                             normalized.counts.Cytokines.Islet_94_Cytokines,
                             normalized.counts.Cytokines.Islet_95_Cytokines,
                             normalized.counts.Cytokines.Islet_96_Cytokines,

```

```
normalized.counts.Cytokines.Islet_97_Cytokines,  
normalized.counts.Cytokines.Islet_99_Cytokines)
```

```
final.df.Cytokines$Treatment <- c("D_Cytokines")
```

```
#####  
# Untreated expression  
#####
```

```
normalized.counts.Untreated.Islet_100_Untreated<- as.data.frame(normalized.counts.Untre  
ated[,1])  
normalized.counts.Untreated.Islet_103_Untreated<- as.data.frame(normalized.counts.Untre  
ated[,2])  
normalized.counts.Untreated.Islet_144_Untreated<- as.data.frame(normalized.counts.Untre  
ated[,3])  
normalized.counts.Untreated.Islet_146_Untreated<- as.data.frame(normalized.counts.Untre  
ated[,4])  
normalized.counts.Untreated.Islet_147_Untreated<- as.data.frame(normalized.counts.Untre  
ated[,5])  
normalized.counts.Untreated.Islet_148_Untreated<- as.data.frame(normalized.counts.Untre  
ated[,6])  
normalized.counts.Untreated.Islet_149_Untreated<- as.data.frame(normalized.counts.Untre  
ated[,7])  
normalized.counts.Untreated.Islet_75_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,8])  
normalized.counts.Untreated.Islet_78_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,9])  
normalized.counts.Untreated.Islet_81_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,10])  
normalized.counts.Untreated.Islet_82_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,11])  
normalized.counts.Untreated.Islet_86_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,12])  
normalized.counts.Untreated.Islet_92_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,13])  
normalized.counts.Untreated.Islet_93_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,14])  
normalized.counts.Untreated.Islet_94_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,15])  
normalized.counts.Untreated.Islet_95_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,16])  
normalized.counts.Untreated.Islet_96_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,17])  
normalized.counts.Untreated.Islet_97_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,18])  
normalized.counts.Untreated.Islet_99_Untreated<- as.data.frame(normalized.counts.Untrea  
ted[,19])
```

```
colnames(normalized.counts.Untreated.Islet_100_Untreated) <- c("Expression")  
colnames(normalized.counts.Untreated.Islet_103_Untreated) <- c("Expression")  
colnames(normalized.counts.Untreated.Islet_144_Untreated) <- c("Expression")  
colnames(normalized.counts.Untreated.Islet_146_Untreated) <- c("Expression")
```

[illegible]

```
normalized.counts.Untreated.Islet_99_Untreated$Islet<- c(colnames(normalized.counts.Untreated)[19])
```

```
normalized.counts.Untreated.Islet_100_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_103_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_144_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_146_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_147_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_148_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_149_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_75_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_78_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_81_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_82_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_86_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_92_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_93_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_94_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_95_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_96_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_97_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
normalized.counts.Untreated.Islet_99_Untreated$Genes<- rownames(normalized.counts.Untreated)
```

```
final.df.Untreated <- rbind(normalized.counts.Untreated.Islet_100_Untreated,  
                             normalized.counts.Untreated.Islet_103_Untreated,  
                             normalized.counts.Untreated.Islet_144_Untreated,  
                             normalized.counts.Untreated.Islet_146_Untreated,  
                             normalized.counts.Untreated.Islet_147_Untreated,  
                             normalized.counts.Untreated.Islet_148_Untreated,  
                             normalized.counts.Untreated.Islet_149_Untreated,  
                             normalized.counts.Untreated.Islet_75_Untreated,  
                             normalized.counts.Untreated.Islet_78_Untreated,  
                             normalized.counts.Untreated.Islet_81_Untreated,
```

```
normalized.counts.Untreated.Islet_82_Untreated,  
normalized.counts.Untreated.Islet_86_Untreated,  
normalized.counts.Untreated.Islet_92_Untreated,  
normalized.counts.Untreated.Islet_93_Untreated,  
normalized.counts.Untreated.Islet_94_Untreated,  
normalized.counts.Untreated.Islet_95_Untreated,  
normalized.counts.Untreated.Islet_96_Untreated,  
normalized.counts.Untreated.Islet_97_Untreated,  
normalized.counts.Untreated.Islet_99_Untreated)
```

```
final.df.Untreated$Treatment <- c("C_Untreated")
```

```
final.df.INF <- rbind(final.df.Untreated,final.df.Cytokines)
```

```
#####  
# Generating dot-and-boxplot  
#####
```

```
final.df.ERS$Type <- c("ERS")
```

```
final.df.INF$Type <- c("INF")
```

```
final.df <- rbind(final.df.ERS,final.df.INF)  
final.df$Expression <- log(final.df$Expression)
```

```
p <- ggboxplot(  
  final.df, x = "Type", y = "Expression", color = "Treatment",  
  palette = c("grey45", "forestgreen", "grey45","darkorange"), facet.by = "Genes", add =  
  "jitter", size=0.5,  
  ) + ylab("Normalized Expression") + ylim(5.5,10.3)
```

```
ggarrange(p, nrow=1, ncol=2)
```

A\_DMSO B\_Thapsigargin C\_Untreated D\_Cytokines

