Figure-1C-MT1F.R

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```r
# This Script Generates Figure 1C
# 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
```

```r
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
```

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

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

```r
# Load the gene of interest
DEG.of.interest <- c("MT1F")


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

normalized.counts.ERS <- read.csv("./normalized.with.ERCC.counts.for.heatmap.ER.Stress.c
sv")
normalized.counts.INF <- read.csv("./normalized.with.ERCC.counts.for.heatmap.Inflammatio
n.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.ER
S.Thaps[,1])
normalized.counts.ERS.Thaps.Islet_146_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,2])
normalized.counts.ERS.Thaps.Islet_147_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,3])
normalized.counts.ERS.Thaps.Islet_148_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,4])
normalized.counts.ERS.Thaps.Islet_149_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,5])
normalized.counts.ERS.Thaps.Islet_75_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,6])
normalized.counts.ERS.Thaps.Islet_78_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,7])
normalized.counts.ERS.Thaps.Islet_81_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,8])
normalized.counts.ERS.Thaps.Islet_82_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.Thaps[,9])
normalized.counts.ERS.Thaps.Islet_86_Thapsigargin<-  as.data.frame(normalized.counts.ER
S.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.DMSO.Islet_144_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
1])
normalized.counts.ERS.DMSO.Islet_146_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
2])
normalized.counts.ERS.DMSO.Islet_147_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
3])
normalized.counts.ERS.DMSO.Islet_148_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
4])
normalized.counts.ERS.DMSO.Islet_149_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
5])
normalized.counts.ERS.DMSO.Islet_75_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
6])
normalized.counts.ERS.DMSO.Islet_78_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
7])
normalized.counts.ERS.DMSO.Islet_81_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
8])
normalized.counts.ERS.DMSO.Islet_82_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,
9])
normalized.counts.ERS.DMSO.Islet_86_DMSO<- as.data.frame(normalized.counts.ERS.DMSO[,1
0])

colnames(normalized.counts.ERS.DMSO.Islet_144_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_146_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_147_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_148_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_149_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_75_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_78_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_81_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_82_DMSO) <- c("Expression")
colnames(normalized.counts.ERS.DMSO.Islet_86_DMSO) <- c("Expression")

normalized.counts.ERS.DMSO.Islet_144_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[1])
normalized.counts.ERS.DMSO.Islet_146_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[2])
```

```r
normalized.counts.ERS.DMSO.Islet_147_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[3])
normalized.counts.ERS.DMSO.Islet_148_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[4])
normalized.counts.ERS.DMSO.Islet_149_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[5])
normalized.counts.ERS.DMSO.Islet_75_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[6])
normalized.counts.ERS.DMSO.Islet_78_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[7])
normalized.counts.ERS.DMSO.Islet_81_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[8])
normalized.counts.ERS.DMSO.Islet_82_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[9])
normalized.counts.ERS.DMSO.Islet_86_DMSO$Islet<- c(colnames(normalized.counts.ERS.DMSO)
[10])

normalized.counts.ERS.DMSO.Islet_144_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_146_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_147_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_148_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_149_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_75_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_78_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_81_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_82_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)
normalized.counts.ERS.DMSO.Islet_86_DMSO$Genes<- rownames(normalized.counts.ERS.DMSO)

final.df.DMSO <- rbind(normalized.counts.ERS.DMSO.Islet_144_DMSO,
                       normalized.counts.ERS.DMSO.Islet_146_DMSO,
                       normalized.counts.ERS.DMSO.Islet_147_DMSO,
                       normalized.counts.ERS.DMSO.Islet_148_DMSO,
                       normalized.counts.ERS.DMSO.Islet_149_DMSO,
                       normalized.counts.ERS.DMSO.Islet_75_DMSO,
                       normalized.counts.ERS.DMSO.Islet_78_DMSO,
                       normalized.counts.ERS.DMSO.Islet_81_DMSO,
                       normalized.counts.ERS.DMSO.Islet_82_DMSO,
                       normalized.counts.ERS.DMSO.Islet_86_DMSO)

final.df.DMSO$Treatment <- c("A_DMSO")

final.df.ERS <- rbind(final.df.DMSO,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.Cytok
ines[,1])
normalized.counts.Cytokines.Islet_103_Cytokines<- as.data.frame(normalized.counts.Cytok
ines[,2])
normalized.counts.Cytokines.Islet_144_Cytokines<- as.data.frame(normalized.counts.Cytok
ines[,3])
normalized.counts.Cytokines.Islet_146_Cytokines<- as.data.frame(normalized.counts.Cytok
ines[,4])
normalized.counts.Cytokines.Islet_147_Cytokines<- as.data.frame(normalized.counts.Cytok
ines[,5])
normalized.counts.Cytokines.Islet_148_Cytokines<- as.data.frame(normalized.counts.Cytok
ines[,6])
normalized.counts.Cytokines.Islet_149_Cytokines<- as.data.frame(normalized.counts.Cytok
ines[,7])
normalized.counts.Cytokines.Islet_75_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,8])
normalized.counts.Cytokines.Islet_78_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,9])
normalized.counts.Cytokines.Islet_81_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,10])
normalized.counts.Cytokines.Islet_82_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,11])
normalized.counts.Cytokines.Islet_86_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,12])
normalized.counts.Cytokines.Islet_92_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,13])
normalized.counts.Cytokines.Islet_93_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,14])
normalized.counts.Cytokines.Islet_94_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,15])
normalized.counts.Cytokines.Islet_95_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,16])
normalized.counts.Cytokines.Islet_96_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,17])
normalized.counts.Cytokines.Islet_97_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,18])
normalized.counts.Cytokines.Islet_99_Cytokines<- as.data.frame(normalized.counts.Cytoki
nes[,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$Islet<- c(colnames(normalized.counts.Cyt
okines)[1])
normalized.counts.Cytokines.Islet_103_Cytokines$Islet<- c(colnames(normalized.counts.Cyt
okines)[2])
normalized.counts.Cytokines.Islet_144_Cytokines$Islet<- c(colnames(normalized.counts.Cyt
okines)[3])
normalized.counts.Cytokines.Islet_146_Cytokines$Islet<- c(colnames(normalized.counts.Cyt
okines)[4])
normalized.counts.Cytokines.Islet_147_Cytokines$Islet<- c(colnames(normalized.counts.Cyt
okines)[5])
normalized.counts.Cytokines.Islet_148_Cytokines$Islet<- c(colnames(normalized.counts.Cyt
okines)[6])
normalized.counts.Cytokines.Islet_149_Cytokines$Islet<- c(colnames(normalized.counts.Cyt
okines)[7])
normalized.counts.Cytokines.Islet_75_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[8])
normalized.counts.Cytokines.Islet_78_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[9])
normalized.counts.Cytokines.Islet_81_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[10])
normalized.counts.Cytokines.Islet_82_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[11])
normalized.counts.Cytokines.Islet_86_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[12])
normalized.counts.Cytokines.Islet_92_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[13])
normalized.counts.Cytokines.Islet_93_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[14])
normalized.counts.Cytokines.Islet_94_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[15])
normalized.counts.Cytokines.Islet_95_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[16])
normalized.counts.Cytokines.Islet_96_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[17])
normalized.counts.Cytokines.Islet_97_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[18])
normalized.counts.Cytokines.Islet_99_Cytokines$Islet<- c(colnames(normalized.counts.Cyto
kines)[19])

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

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

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")
```

```
colnames(normalized.counts.Untreated.Islet_147_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_148_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_149_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_75_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_78_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_81_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_82_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_86_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_92_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_93_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_94_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_95_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_96_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_97_Untreated) <- c("Expression")
colnames(normalized.counts.Untreated.Islet_99_Untreated) <- c("Expression")

normalized.counts.Untreated.Islet_100_Untreated$Islet<- c(colnames(normalized.counts.Unt
reated)[1])
normalized.counts.Untreated.Islet_103_Untreated$Islet<- c(colnames(normalized.counts.Unt
reated)[2])
normalized.counts.Untreated.Islet_144_Untreated$Islet<- c(colnames(normalized.counts.Unt
reated)[3])
normalized.counts.Untreated.Islet_146_Untreated$Islet<- c(colnames(normalized.counts.Unt
reated)[4])
normalized.counts.Untreated.Islet_147_Untreated$Islet<- c(colnames(normalized.counts.Unt
reated)[5])
normalized.counts.Untreated.Islet_148_Untreated$Islet<- c(colnames(normalized.counts.Unt
reated)[6])
normalized.counts.Untreated.Islet_149_Untreated$Islet<- c(colnames(normalized.counts.Unt
reated)[7])
normalized.counts.Untreated.Islet_75_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[8])
normalized.counts.Untreated.Islet_78_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[9])
normalized.counts.Untreated.Islet_81_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[10])
normalized.counts.Untreated.Islet_82_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[11])
normalized.counts.Untreated.Islet_86_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[12])
normalized.counts.Untreated.Islet_92_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[13])
normalized.counts.Untreated.Islet_93_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[14])
normalized.counts.Untreated.Islet_94_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[15])
normalized.counts.Untreated.Islet_95_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[16])
normalized.counts.Untreated.Islet_96_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[17])
normalized.counts.Untreated.Islet_97_Untreated$Islet<- c(colnames(normalized.counts.Untr
eated)[18])
```

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

normalized.counts.Untreated.Islet_100_Untreated$Genes<- rownames(normalized.counts.Untre
ated)
normalized.counts.Untreated.Islet_103_Untreated$Genes<- rownames(normalized.counts.Untre
ated)
normalized.counts.Untreated.Islet_144_Untreated$Genes<- rownames(normalized.counts.Untre
ated)
normalized.counts.Untreated.Islet_146_Untreated$Genes<- rownames(normalized.counts.Untre
ated)
normalized.counts.Untreated.Islet_147_Untreated$Genes<- rownames(normalized.counts.Untre
ated)
normalized.counts.Untreated.Islet_148_Untreated$Genes<- rownames(normalized.counts.Untre
ated)
normalized.counts.Untreated.Islet_149_Untreated$Genes<- rownames(normalized.counts.Untre
ated)
normalized.counts.Untreated.Islet_75_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_78_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_81_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_82_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_86_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_92_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_93_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_94_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_95_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_96_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_97_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)
normalized.counts.Untreated.Islet_99_Untreated$Genes<- rownames(normalized.counts.Untrea
ted)

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(5.5,8.5)

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