

# MitoGraph\_simplified\_width\_filtered.R

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2022-05-26

```
#  
# Summarize MitoGraph Metrics using Box Plots  
#  
  
# First set working directory to source file location  
# Run with command + option + R  
  
library(tidyverse)  
  
## -- Attaching packages ----- tidyverse 1.3.1 --  
  
## v ggplot2 3.3.5      v purrr  0.3.4  
## v tibble  3.1.6      v dplyr  1.0.7  
## v tidyr   1.2.0      v stringr 1.4.0  
## v readr   2.1.2      v forcats 0.5.1  
  
## -- Conflicts ----- tidyverse_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()    masks stats::lag()  
  
library(reshape2)  
  
##  
## Attaching package: 'reshape2'  
  
## The following object is masked from 'package:tidyr':  
##  
## smiths  
  
library(stringr)  
library(formattable)  
library(igraph)  
  
##  
## Attaching package: 'igraph'  
  
## The following object is masked from 'package:formattable':  
##  
## normalize
```

```
## The following objects are masked from 'package:dplyr':
##
##   as_data_frame, groups, union

## The following objects are masked from 'package:purrr':
##
##   compose, simplify

## The following object is masked from 'package:tidyr':
##
##   crossing

## The following object is masked from 'package:tibble':
##
##   as_data_frame

## The following objects are masked from 'package:stats':
##
##   decompose, spectrum

## The following object is masked from 'package:base':
##
##   union
```

```
# Import data from log files (*.txt)
```

```
datafolder1 <- "~/mount/home110/mcharwig/20210903_Ntermtrun_repeat4/reto_TBC_stable_settings/channel2-T"
```

```
# Import data
```

```
# with read_csv command below
```

```
data <- read_csv(file = "output-summary_filtered.csv")
```

```
## Rows: 265 Columns: 19
```

```
## -- Column specification -----
```

```
## Delimiter: ","
```

```
## chr (4): file, job, isoform, treatment
```

```
## dbl (15): Total_Nodes, Total_Edges, Total_Length_um, Total_Connected_Compone...
```

```
##
```

```
## i Use 'spec()' to retrieve the full column specification for this data.
```

```
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
data2 <- data %>%
```

```
  mutate(job = factor(job, levels = c("WT_RPE_TBC15_pcDNA",
                                       "Fis1_RPE_TBC15_pcDNA",
                                       "Fis1_RPE_TBC15_hFis1_WT",
                                       "Fis1_RPE_TBC15_hFis1_dN8"), ordered = T)) #RENAME with your sample order
```

```
data3 <- data2 %>%
```

```
  mutate(treatment = factor(treatment, levels = c("pcDNA",
                                                    "hFis1_WT",
                                                    "hFis1_dN8"), ordered = T)) #RENAME with your sample order
```

```
data3
```

```
## # A tibble: 265 x 19
##   file          job  isoform treatment Total_Nodes Total_Edges Total_Length_um
##   <chr>         <ord> <chr>   <ord>         <dbl>         <dbl>         <dbl>
## 1 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           576           527           749.
## 2 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           453           453           622.
## 3 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           254           248           301.
## 4 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           497           477           626.
## 5 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           371           358           524.
## 6 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           472           485           625.
## 7 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           461           491           681.
## 8 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           359           374           543.
## 9 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           341           354           462.
## 10 /Users/mclel~ Fis1~ Fis1_R~ pcDNA           364           354           491.
## # ... with 255 more rows, and 12 more variables:
## #   Total_Connected_Components <dbl>, PHI <dbl>, Avg_Edge_Length_um <dbl>,
## #   Total_Edge_Norm_to_Length_um <dbl>, Total_Node_Norm_to_Length_um <dbl>,
## #   Total_Connected_Components_Norm_to_Length_um <dbl>, Free_Ends <dbl>,
## #   three_way_junction <dbl>, four_way_junction <dbl>, Avg_Degree <dbl>,
## #   MitoGraph_Connectivity_Score <dbl>, Average_width_um <dbl>
```

*# Here is a loop that creates 11 graphs where the X and Y variable are listed accordingly.*

```
PlotsToBeMade <- c("job",
  "treatment",
  "PHI",
  "Avg_Edge_Length_um",
  "Total_Node_Norm_to_Length_um",
  "Total_Connected_Components_Norm_to_Length_um",
  "Free_Ends",
  "three_way_junction",
  "four_way_junction",
  "Avg_Degree",
  "MitoGraph_Connectivity_Score",
  "Average_width_um")
```

```
AxisLabels <- c("job",
  "treatment",
  "PHI",
  "Avg Edge Length um",
  "Total Node Norm to Length um",
  "Total Connected Components Norm to Length um",
  "Free Ends",
  "three way junction",
  "four way junction",
  "Avg Degree",
  "MitoGraph Connectivity Score",
  "Average width um")
```

```
Titles <- c("job",
  "treatment",
  "PHI",
  "Avg Edge Length um",
  "Total Node Norm to Length um",
  "Total Connected Components Norm to Length um",
  "Free Ends",
```

```

    "Three way junction",
    "Four way junction",
    "Avg Degree",
    "MitoGraph Connectivity Score",
    "Average width um")

# Uncomment to modify specific axis settings
yAxisMinimum <- c(0,
                  0,
                  0,
                  0,
                  0,
                  0,
                  0,
                  0,
                  0,
                  0,
                  0,
                  0)

#
# yAxisMaximum <- c(1,
#                   150,
#                   150,
#                   150,
#                   150,
#                   150,
#                   1.5,
#                   10000,
#                   20000,
#                   10000,
#                   20000)

for (p in seq(3,length(PlotsToBeMade))) {

  yaxis <- PlotsToBeMade[p]
  xaxis <- PlotsToBeMade[1]
  fill <- PlotsToBeMade[1]

  # Adjust to modify error bar width
  # error <- c(0.03,0.05,
  #            0.03,0.025,
  #            0.02,0.05,
  #            8,0.005)

  plot(ggplot(data=data3,aes_string(x=xaxis, y=yaxis, fill=fill)) +
        geom_boxplot(outlier.size = 0, colour = "grey10", position = position_dodge (width = 1), size = 0.25) +
        stat_boxplot(geom="errorbar", position = position_dodge (width = 1), width = 0.5, size = 0.25) +
        scale_fill_manual(values = c("#707070","#BBBBBB","#4F9ACB","#E02A26")) +
        geom_point(data=data3,aes_string(colour = fill, x=xaxis, y=yaxis), pch=20, size=0.01, position = position_dodge (width = 1)) +
        scale_colour_manual(values=c("#4e4e4e","#828282","#376b8e","#9c1d1a")) +
        labs(title = Titles[p],

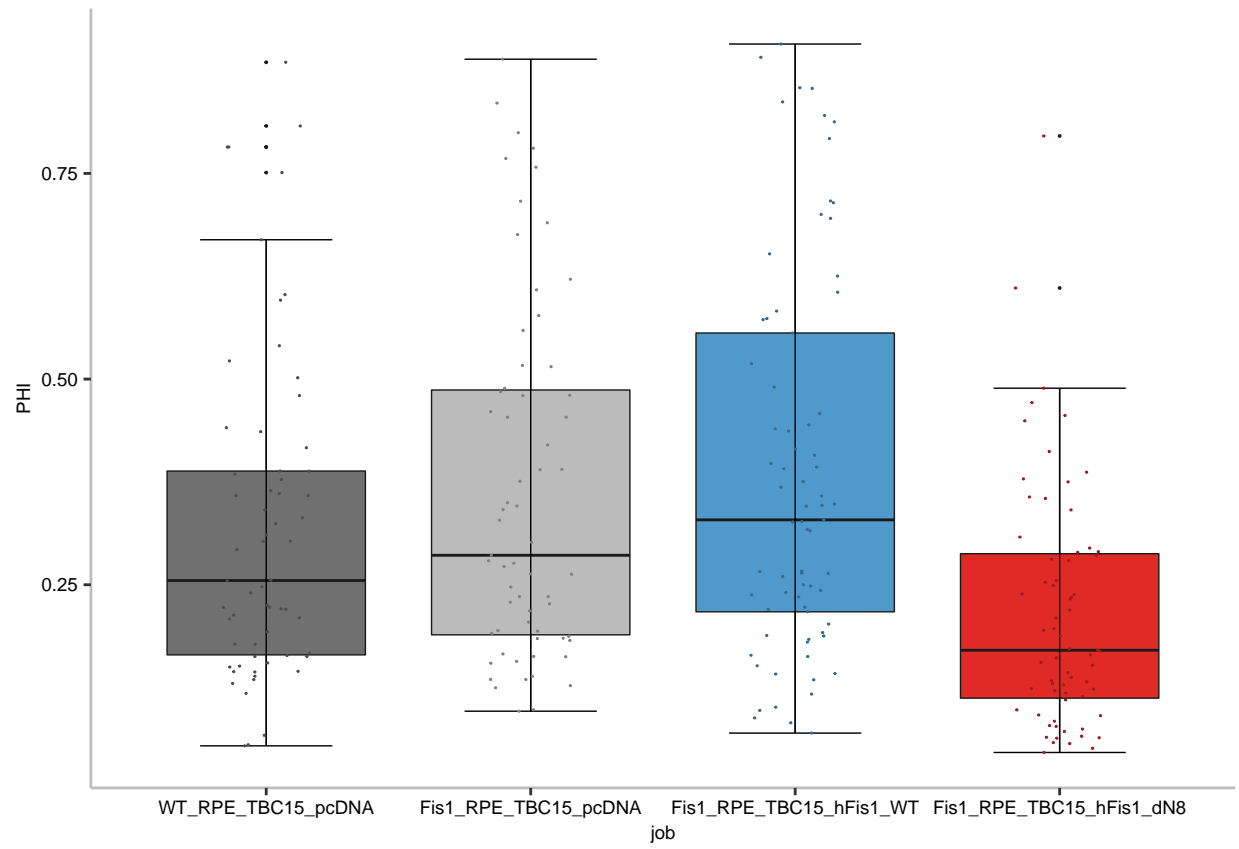
```

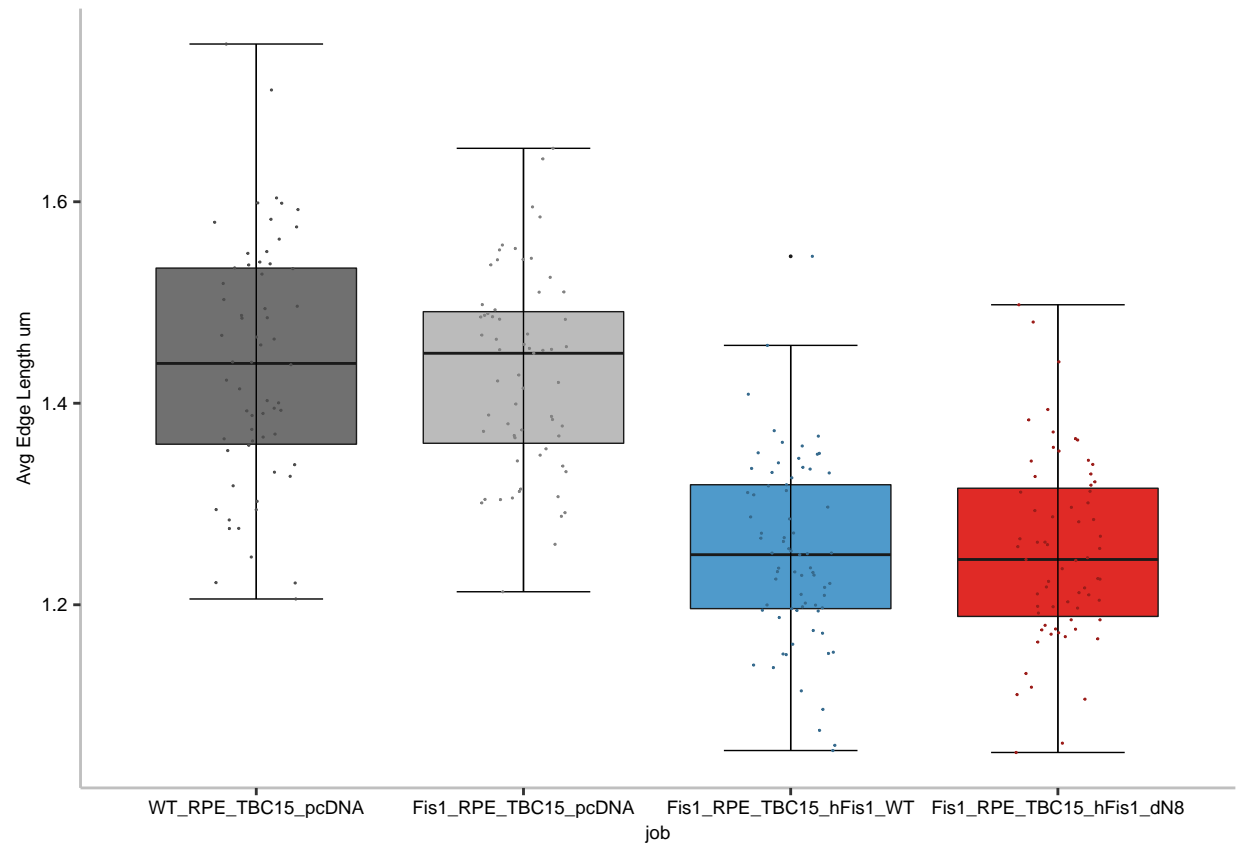
```

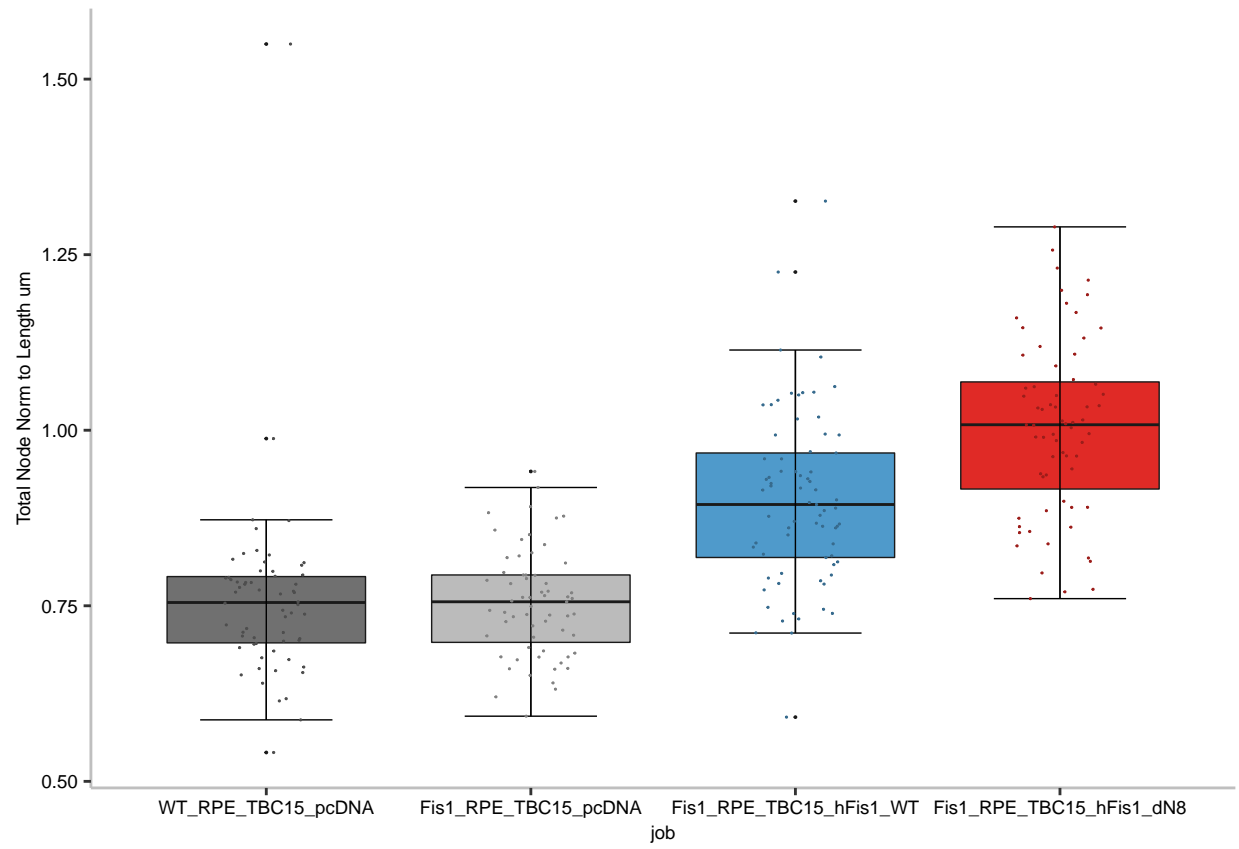
        x = xaxis,
        y = AxisLabels[p]) +
#ylab(AxisLabels[p]) +
theme_bw() +
theme(axis.text.x = element_text(size = 7, color = "black"),
      axis.title.x = element_text(size = 7, color = "black"),
      axis.text.y = element_text(size = 7, color = "black"),
      axis.title.y = element_text(size = 7, color = "black"),
      plot.title = element_blank(),
      #plot.title = element_text(size = 8, color = "black", hjust = 0.5, face = "bold"),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      panel.border = element_blank(),
      panel.background = element_blank(),
      axis.line.x = element_line(color = "grey75", size = 0.5, linetype = 1),
      axis.line.y = element_line(color = "grey75", size = 0.5, linetype = 1),
      legend.position = "none"
      #legend.title = element_blank(),
      #legend.justification = c(0, 1),
      #legend.position = "right",
      #legend.text = element_text(size = 6, color = "black")
    )
# Add a "+" above and uncomment the below 2 lines to add custom axis scales.
#ylim(yAxisMinimum[p], yAxisMaximum[p])
)

ggsave(paste(datafolder1,"Plot-filtered", yaxis,".eps",sep=""), width = 5.8, height = 8, units = "cm"
}

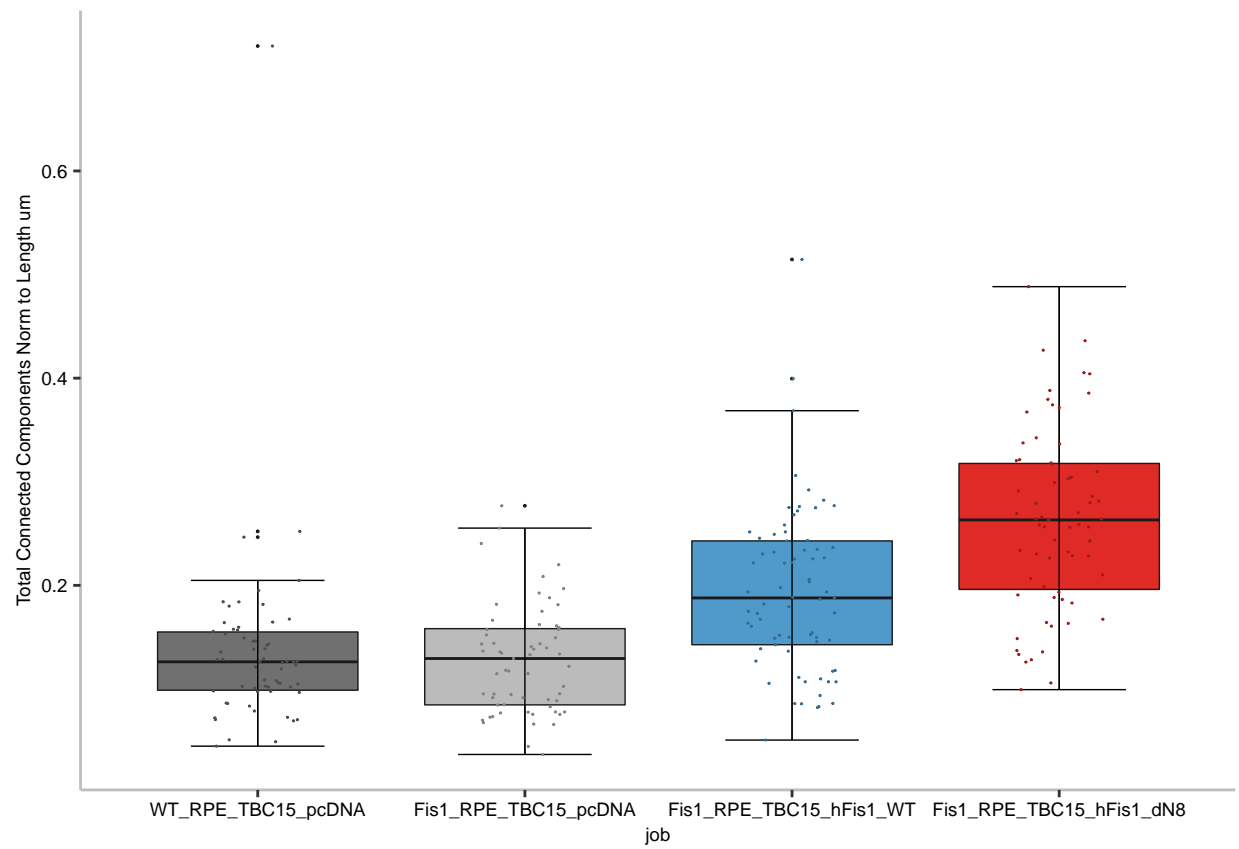
```

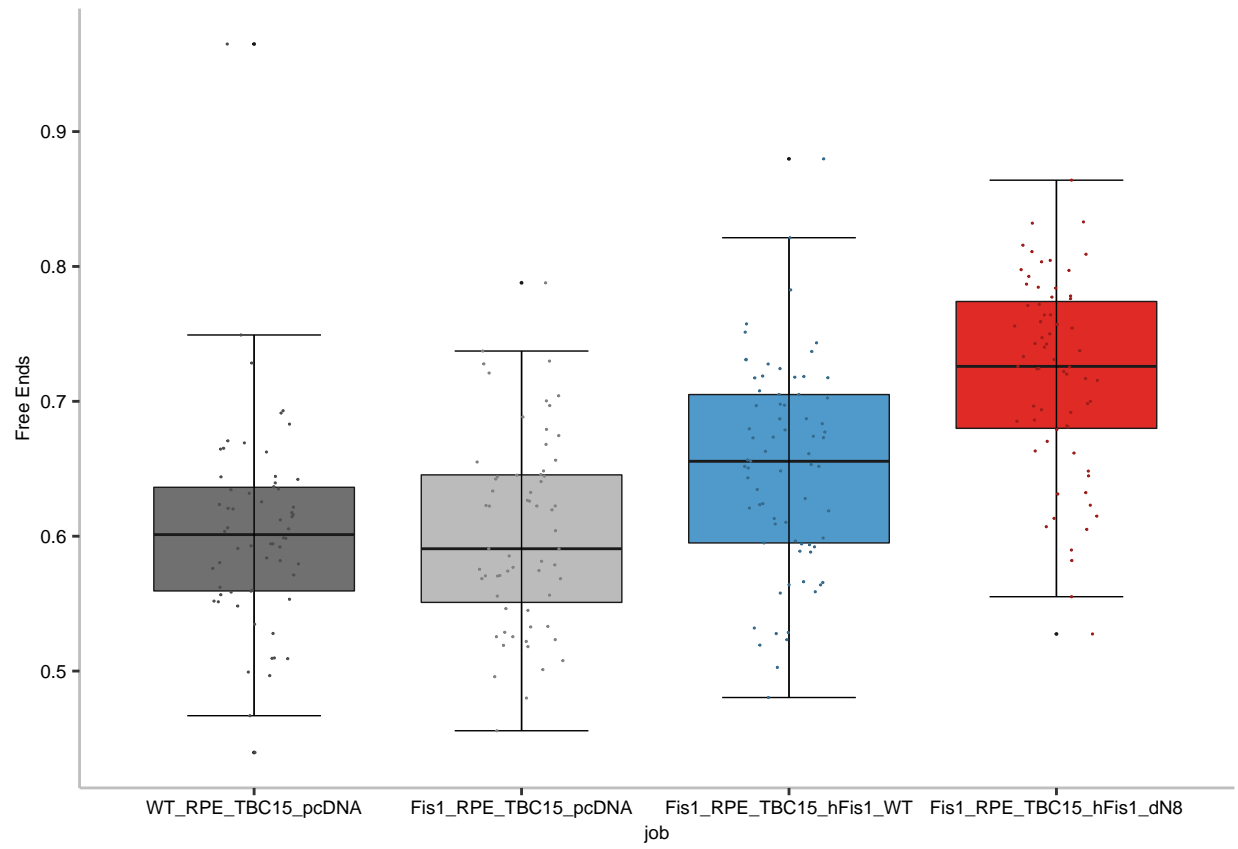


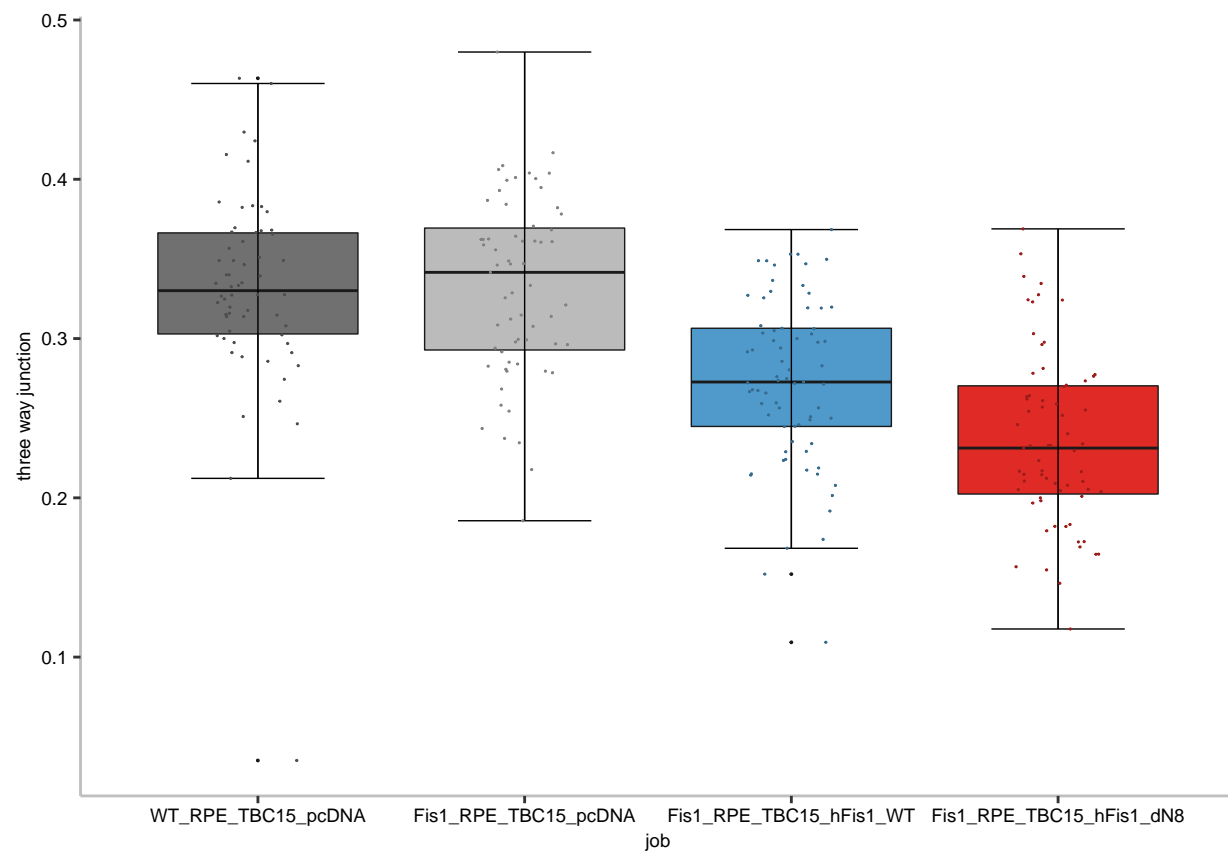


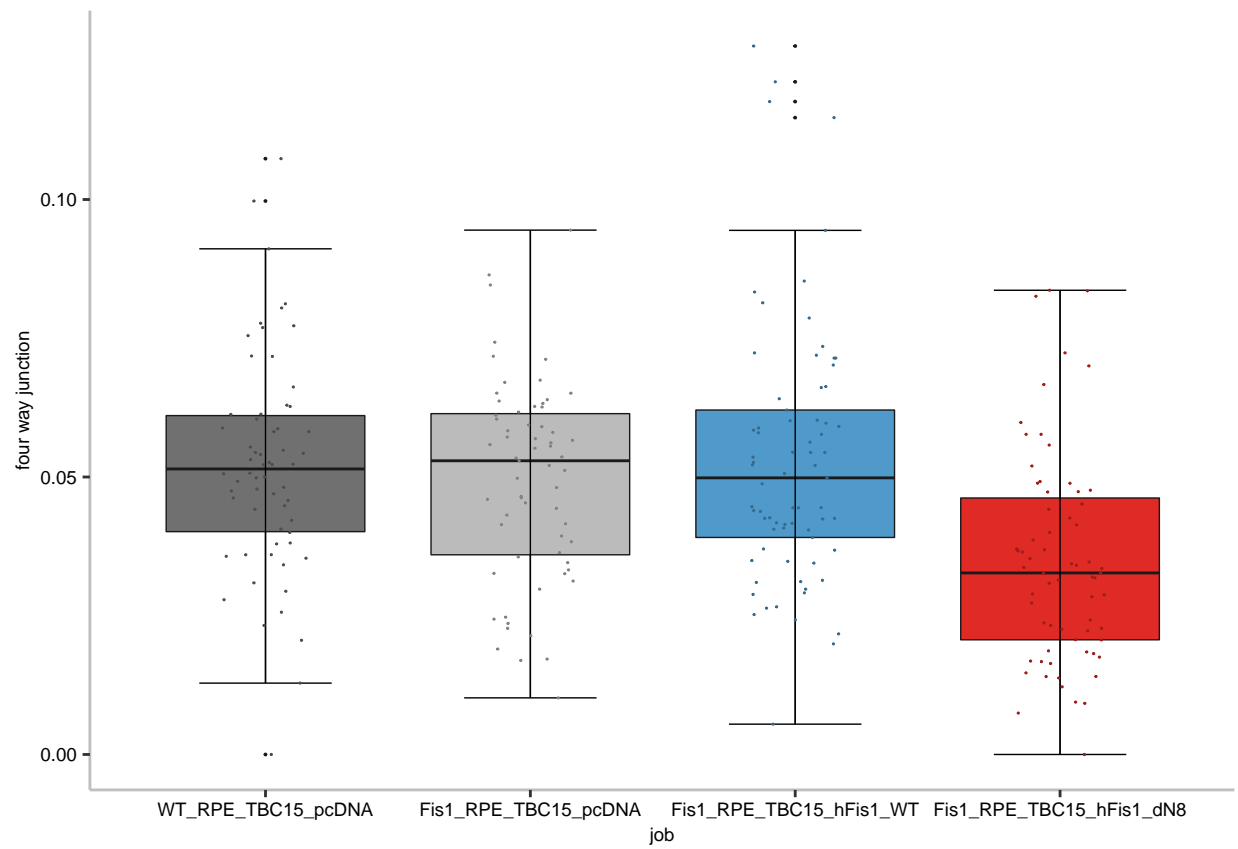


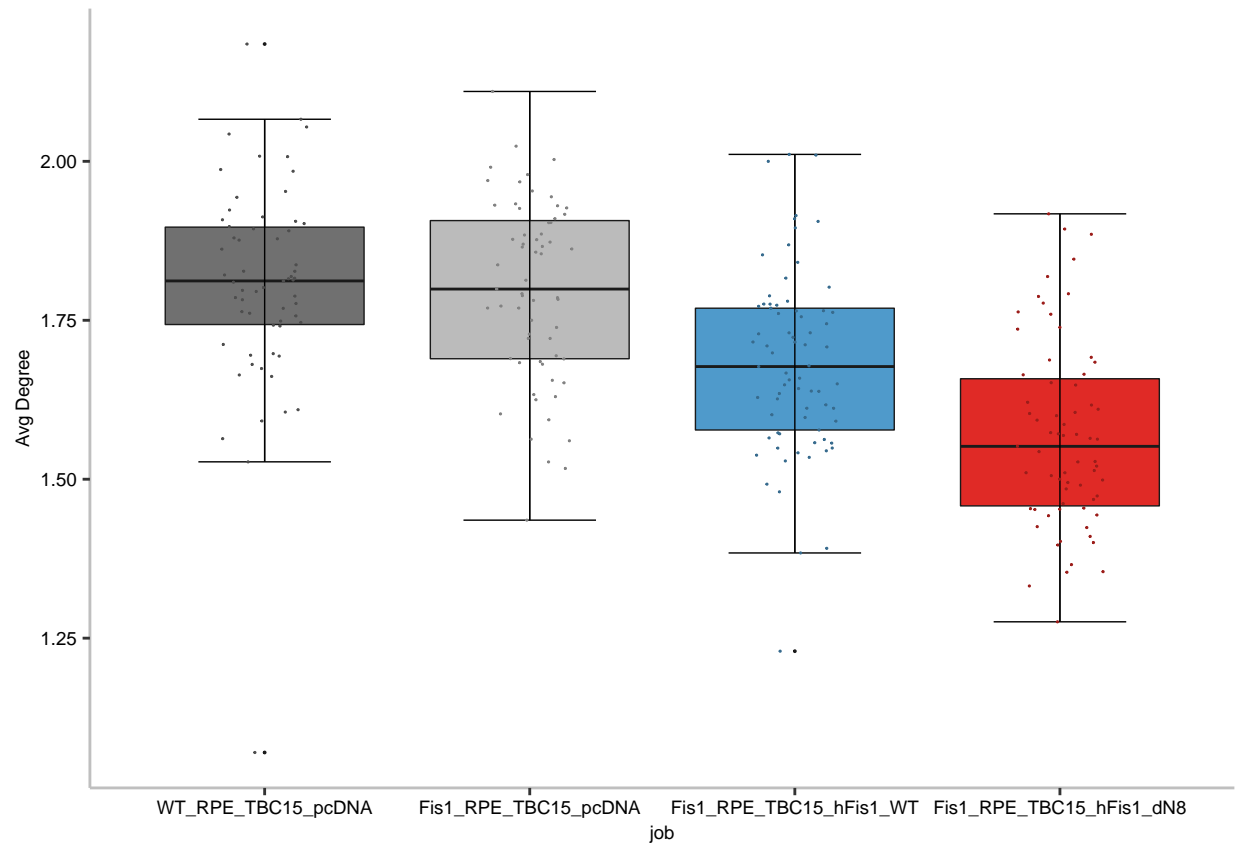


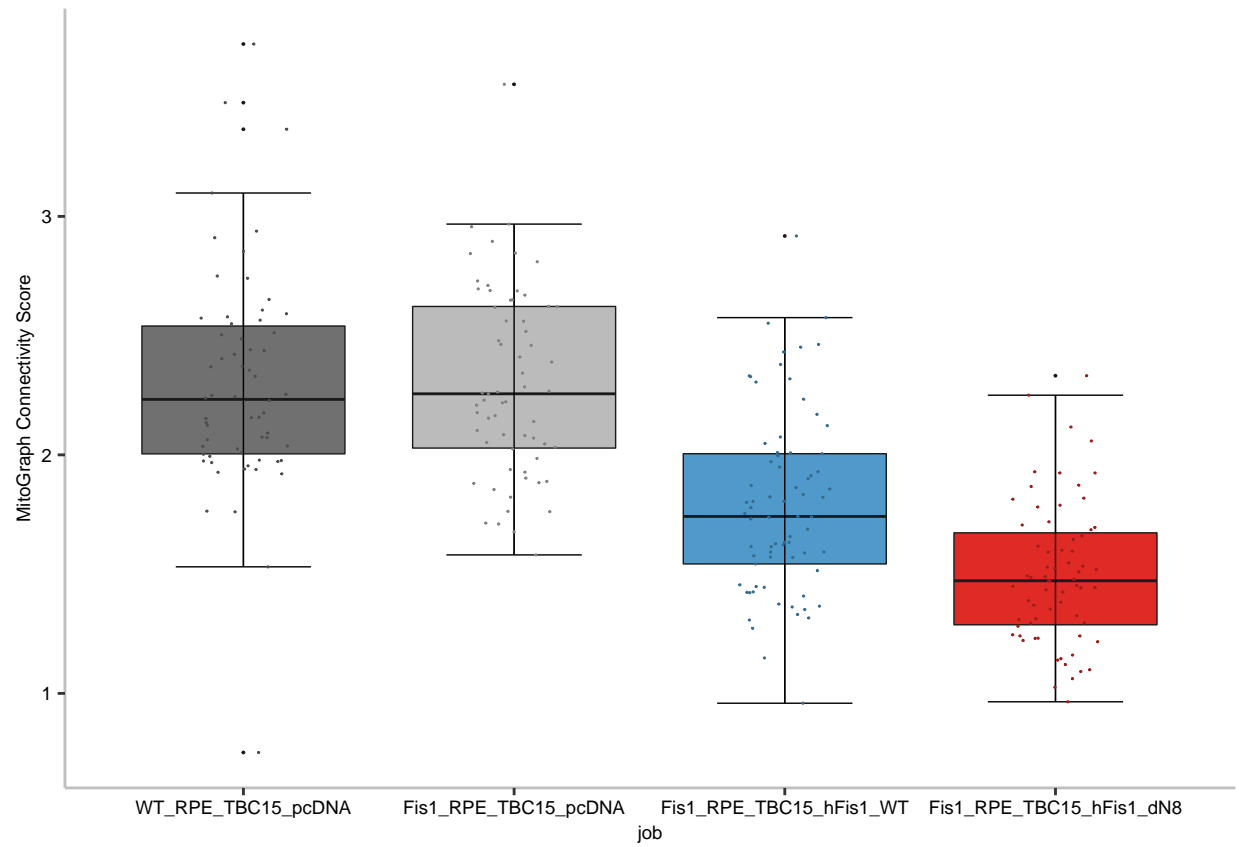


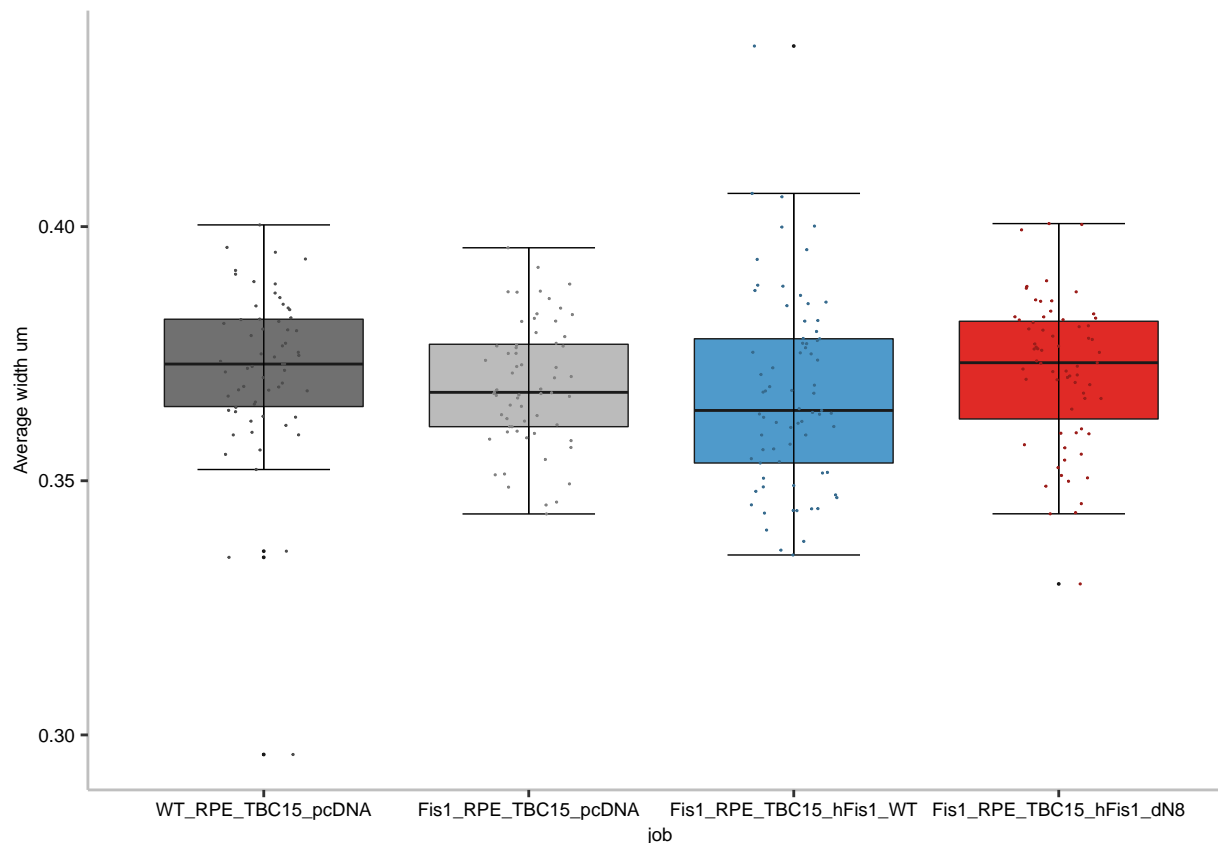












```
#test
```

```
data4 <- read_csv(file = "output-summary_filtered.csv")
```

```
## Rows: 265 Columns: 19
## -- Column specification -----
## Delimiter: ","
## chr (4): file, job, isoform, treatment
## dbl (15): Total_Nodes, Total_Edges, Total_Length_um, Total_Connected_Componen...
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
data5 <- data4 %>%
  mutate(job = factor(job, levels = c("WT_RPE_TBC15_pcDNA",
    "Fis1_RPE_TBC15_pcDNA",
    "Fis1_RPE_TBC15_hFis1_WT",
    "Fis1_RPE_TBC15_hFis1_dN8"), ordered = T)) #RENAME with your samp

data5_long <- reshape2::melt(data = data5, id.vars = "job", measure.vars = c("PHI",
  "Total_Edge_Norm_to_Length",
  "Avg_Edge_Length_um",
  "Total_Node_Norm_to_Length",
  "three_way_junction",
  "Total_Connected_Component"))
```

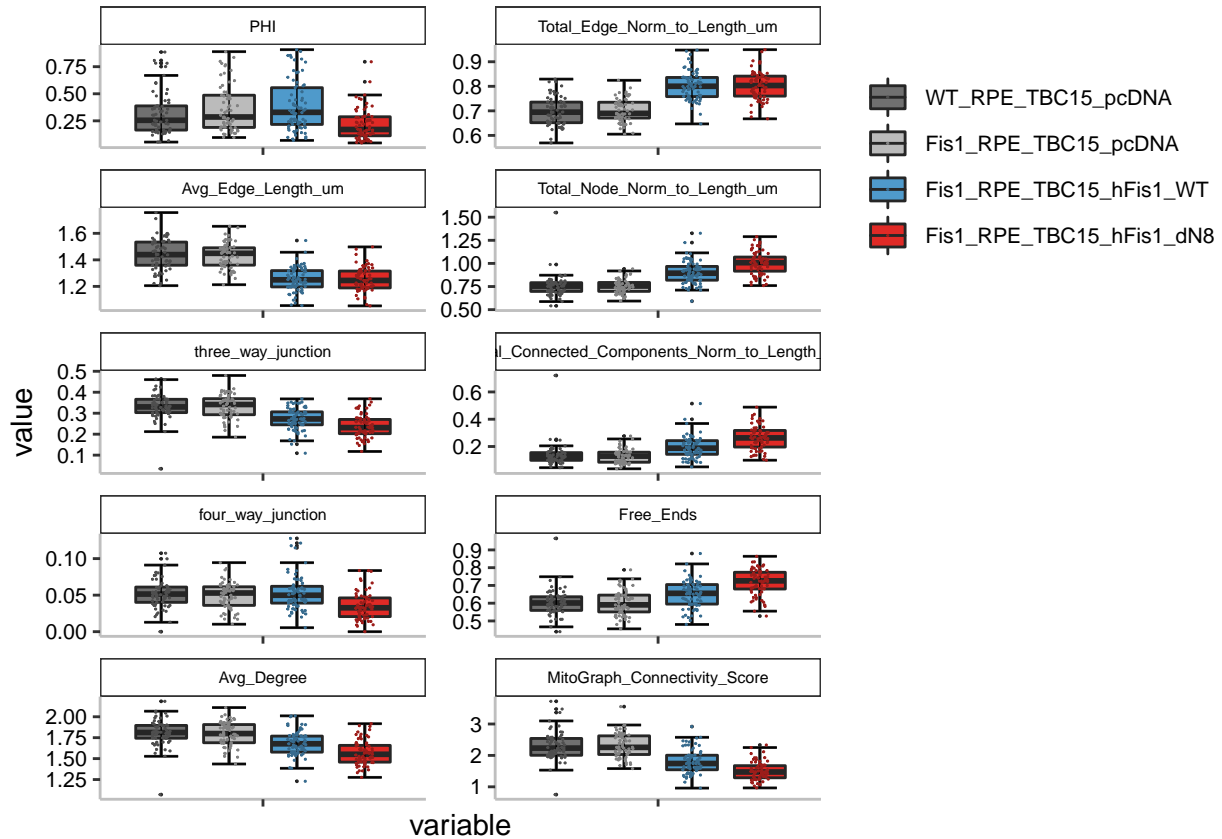
```

"four_way_junction",
"Free_Ends",
"Avg_Degree",
"MitoGraph_Connectivity_Sc

ggplot(data5_long, aes(fill=job, x=variable, y=value)) +
  stat_boxplot(geom = "errorbar", colour = "grey15", width = 0.5, position = position_dodge (width = 1)) +
  geom_boxplot (outlier.size = 0, colour = "grey15", position = position_dodge (width = 1)) +
  stat_boxplot(geom="errorbar", position = position_dodge (width = 1), width = 0.5, size = 0.25) +
  scale_fill_manual(values = c( "#707070", "#BBBBBB", "#4F9ACB", "#E02A26")) +
  facet_wrap(~variable, scales = "free", ncol = 2)+
  geom_point (aes(colour = job, x=variable, y=value), pch=20, position=position_jitterdodge(jitter.width=
  scale_colour_manual(values=c("#4e4e4e", "#828282", "#376b8e", "#9c1d1a")) +
  theme_bw() +
  theme(axis.text.x = element_blank(),
        axis.text.y = element_text(size = 8, color = "black"),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.border = element_blank(),
        panel.background = element_blank(),
        axis.line.x = element_line(color = "grey75", size = 0.5, linetype = 1),
        axis.line.y = element_line(color = "grey75", size = 0.5, linetype = 1),
        #legend.position = "none",
        legend.title = element_blank(),
        legend.justification = c(0, 1),
        legend.position = "right",
        legend.text = element_text(size = 8, color = "black"),
        strip.background = element_rect(fill = "white"),
        strip.text.x = element_text(size = 6, colour = "black")
  )

```





```

ggsave(paste("All_metrics-filtered.eps",sep=""), width = 9, height = 13, units = "cm", dpi = 300)
ggsave(paste("All_metrics-filtered.png",sep=""), width = 9, height = 13, units = "cm", dpi = 300)

#AOV_STATS (ANOVA and TUKEY Post Hoc analysis)

AOV_STATS <- TukeyHSD(aov(data=data, MitoGraph_Connectivity_Score~job))

AOV_Table <- (AOV_STATS)

AOV_Table_summary <- as.data.frame(AOV_Table[1:1])

write.csv(AOV_Table_summary, paste("MitoGraph_CS_AOV_stats.csv",sep=""))

formattable(AOV_Table_summary, Condition.p.adj=formatter("span", style = x~style(color=ifelse(x < 0.05
job.diff
job.lwr
job.upr
job.p.adj
Fis1_RPE_TBC15_hFis1_WT-Fis1_RPE_TBC15_hFis1_dN8
0.292795986
0.1239292

```

0.4616627  
6.483388e-05  
Fis1\_RPE\_TBC15\_pcDNA-Fis1\_RPE\_TBC15\_hFis1\_dN8  
0.802930346  
0.6277671  
0.9780936  
6.750156e-14  
WT\_RPE\_TBC15\_pcDNA-Fis1\_RPE\_TBC15\_hFis1\_dN8  
0.798844853  
0.6229551  
0.9747346  
6.883383e-14  
Fis1\_RPE\_TBC15\_pcDNA-Fis1\_RPE\_TBC15\_hFis1\_WT  
0.510134360  
0.3384951  
0.6817737  
1.961431e-12  
WT\_RPE\_TBC15\_pcDNA-Fis1\_RPE\_TBC15\_hFis1\_WT  
0.506048867  
0.3336682  
0.6784295  
3.486766e-12  
WT\_RPE\_TBC15\_pcDNA-Fis1\_RPE\_TBC15\_pcDNA  
-0.004085493  
-0.1826388  
0.1744678  
9.999255e-01