

BoxPlot

Asad

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```
library(ggplot2)
library(ggpubr)
library(RColorBrewer)
library(wesanderson)

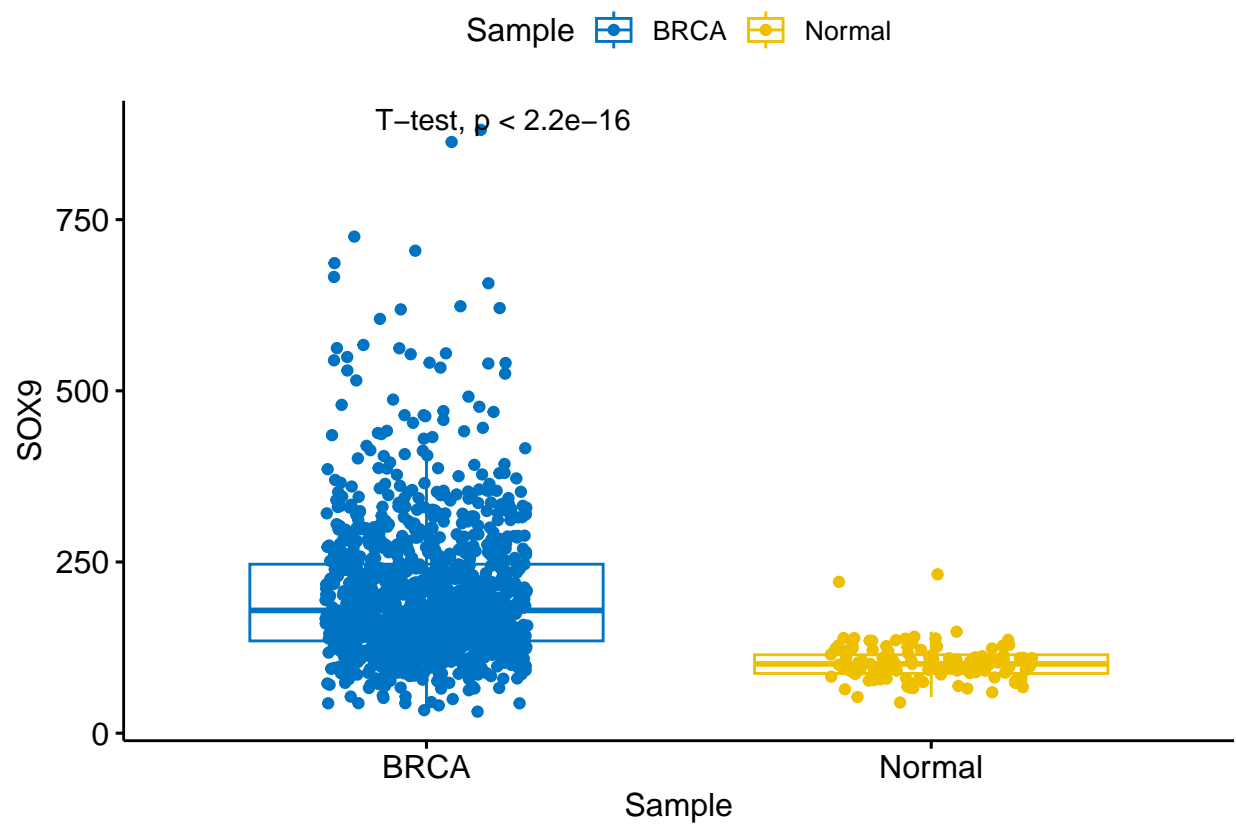
setwd('E:/R-Programming-Practices/Data Visualization/Boxplot')

data<- data.frame(read.csv('FOX1.csv'))

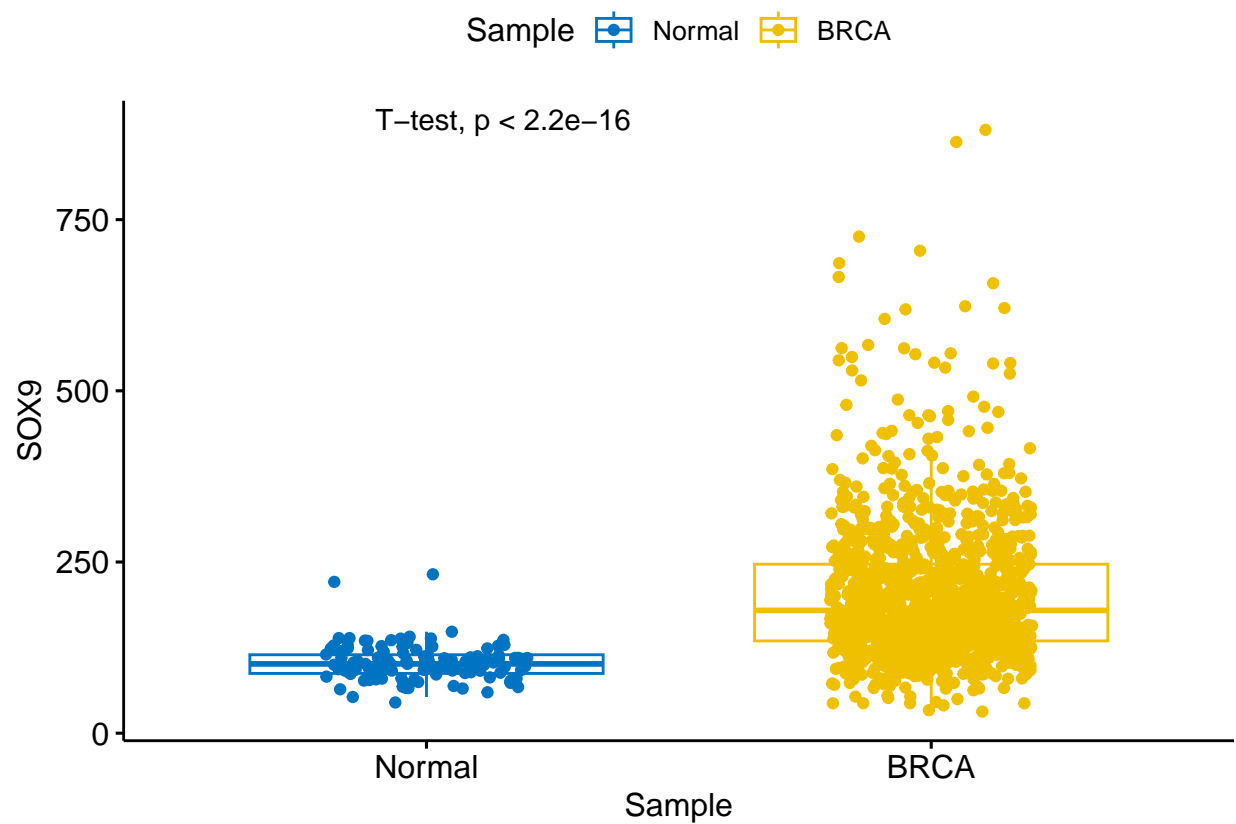
compare_means(FOX1 ~ Sample, data = data, method = 't.test', paired = F)

## # A tibble: 1 x 8
##   .y.   group1 group2      p    p.adj p.format p.signif method
##   <chr> <chr>  <chr>    <dbl>    <dbl> <chr>    <chr>    <chr>
## 1 FOX1 BRCA   Normal 8.19e-116 8.20e-116 <2e-16  ****    T-test

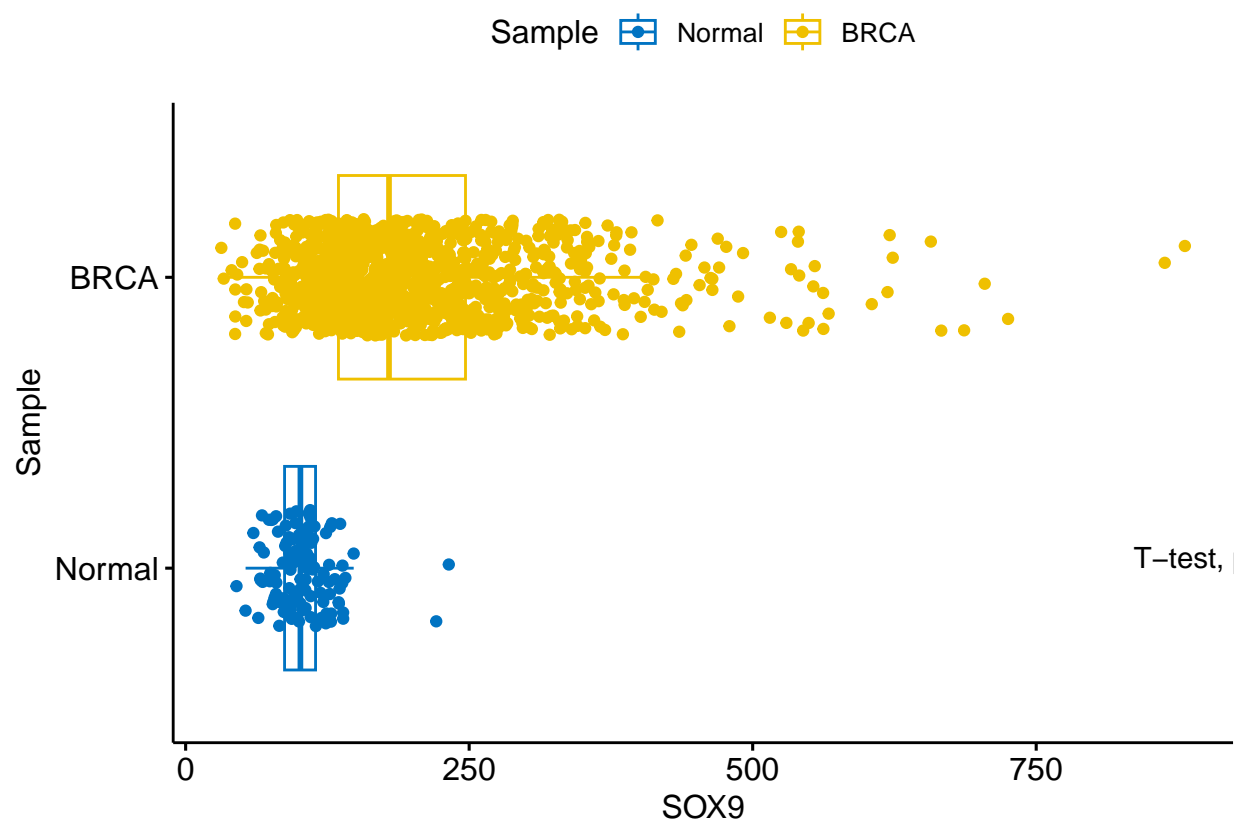
#Two Sample T Test
p <- ggboxplot(data, x = "Sample", y = "SOX9",
               color = "Sample", palette = "jco",
               add = "jitter") + stat_compare_means(method = 't.test', paired = F)
p
```



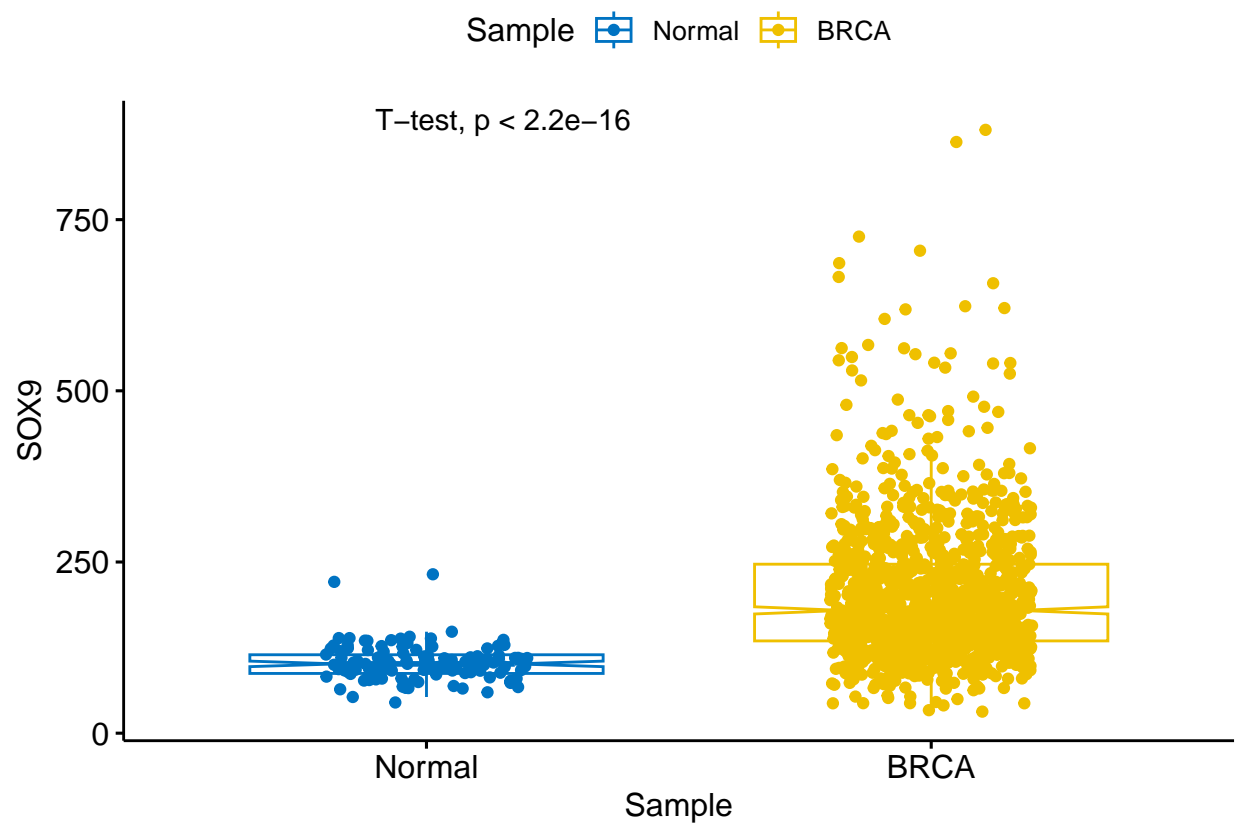
```
#Swap order
p <- ggboxplot(data, x = "Sample", y = "SOX9",
  color = "Sample", palette = "jco",
  add = "jitter", order = c("Normal", "BRCA")) +
  stat_compare_means(method = 't.test', paired = F)
p
```



```
#Change orientation
p <- ggboxplot(data, x = "Sample", y = "SOX9",
               color = "Sample", palette = "jco",
               add = "jitter", orientation = 'horizontal', order = c("Normal", "BRCA")) +
  stat_compare_means(method = 't.test', paired = F)
p
```

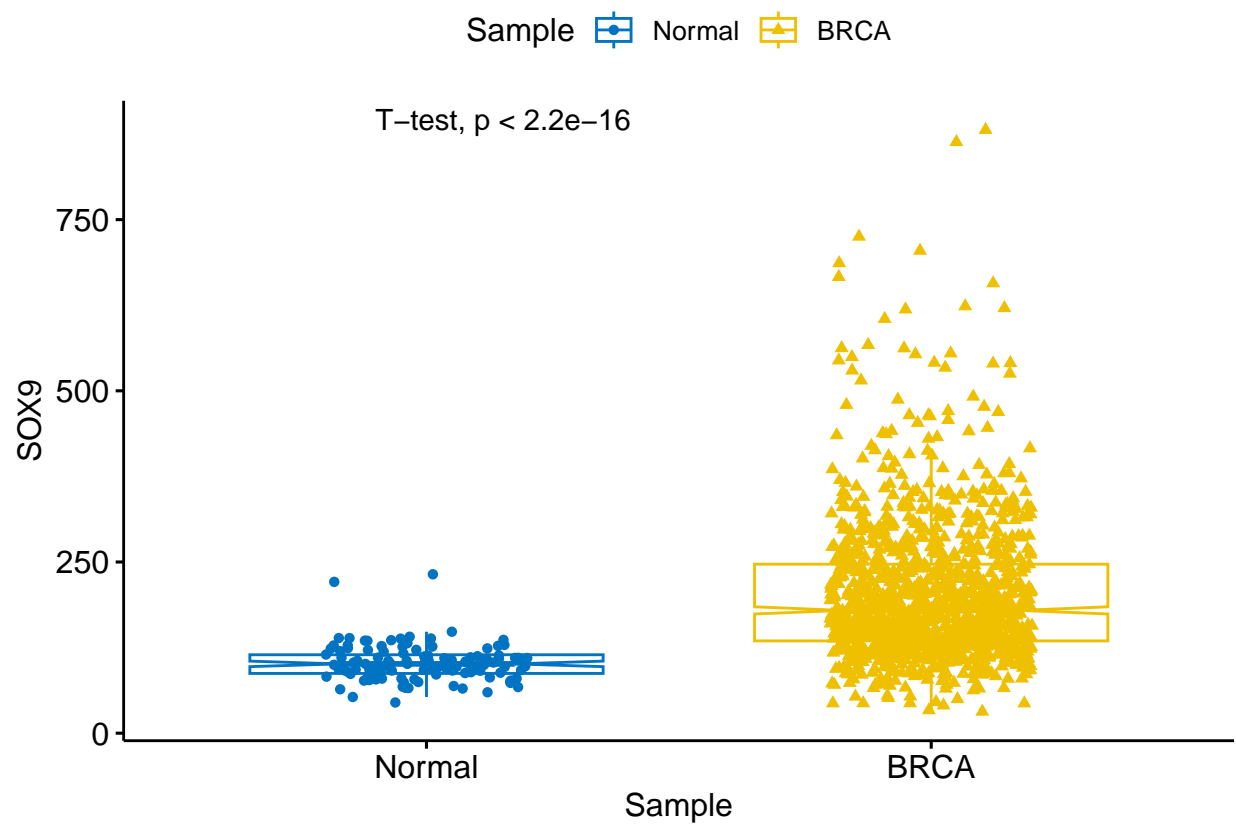


```
#Add Notch
p <- ggboxplot(data, x = "Sample", y = "SOX9",
  color = "Sample", palette = "jco",
  add = "jitter", order = c("Normal", "BRCA"), notch = T) +
  stat_compare_means(method = 't.test', paired = F)
p
```

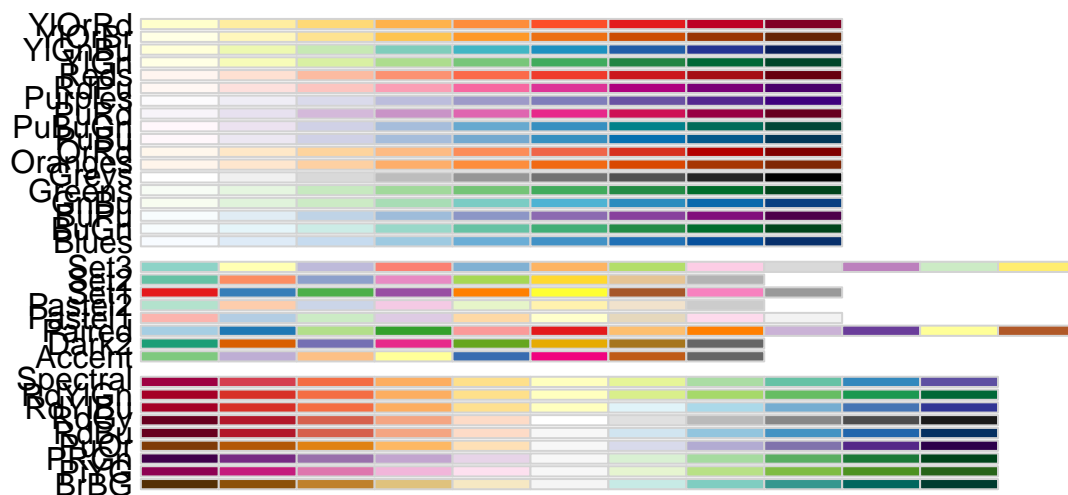


```
#Change shapes
p <- ggboxplot(data, x = "Sample", y = "SOX9",
  color = "Sample", shape='Sample', palette = "jco",
  add = "jitter", order = c("Normal", "BRCA"), notch = T) +
  stat_compare_means(method = 't.test', paired = F)
```

p



```
#Change color  
#Specify color code  
display.brewer.all()
```



```
display.brewer.pal(n = 8, name = 'RdBu')
```

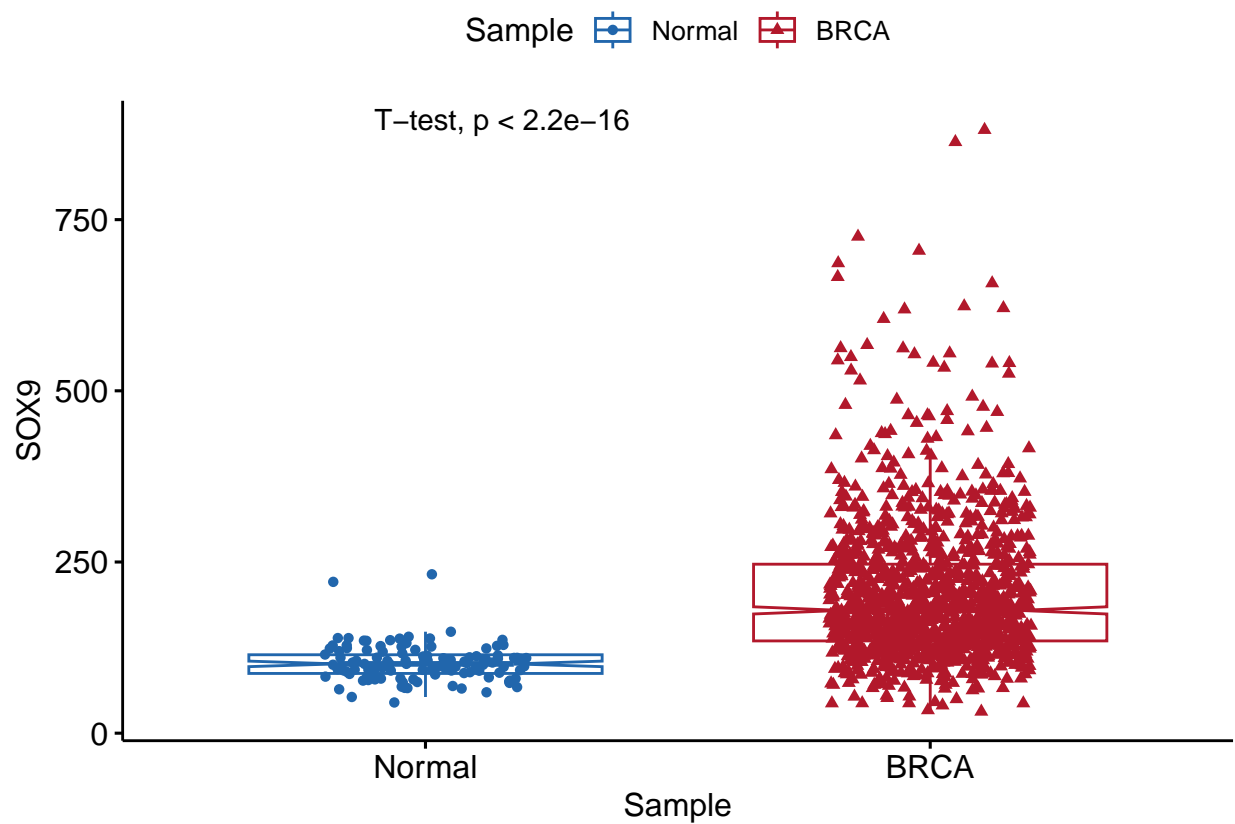


RdBu (divergent)

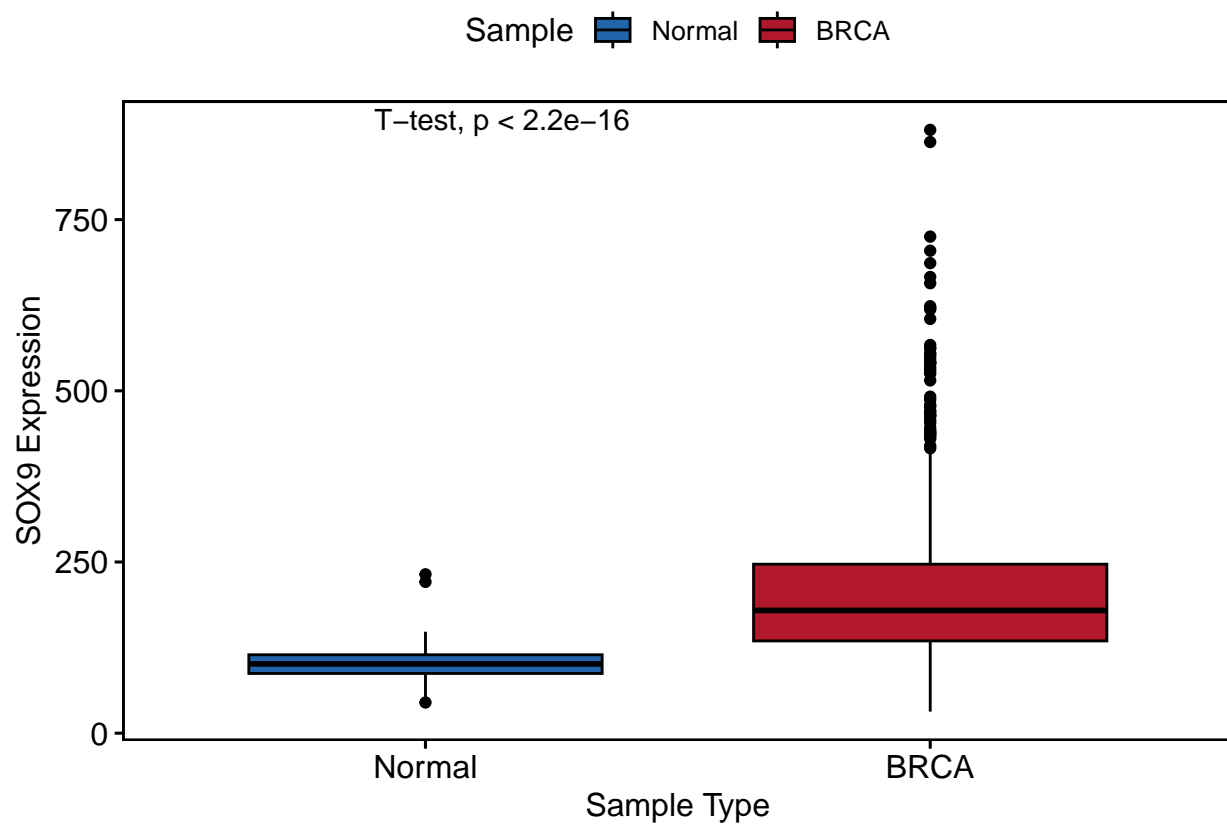
```
brewer.pal(n = 8, name = "RdBu")
```

```
## [1] "#B2182B" "#D6604D" "#F4A582" "#FDDBC7" "#D1E5F0" "#92C5DE" "#4393C3"  
## [8] "#2166AC"
```

```
p <- ggboxplot(data, x = "Sample", y = "SOX9",  
              color = "Sample", shape='Sample', palette = c("#2166AC", "#B2182B"),  
              add = "jitter", order = c("Normal", "BRCA"), notch = T) +  
  stat_compare_means(method = 't.test', paired = F)  
p
```

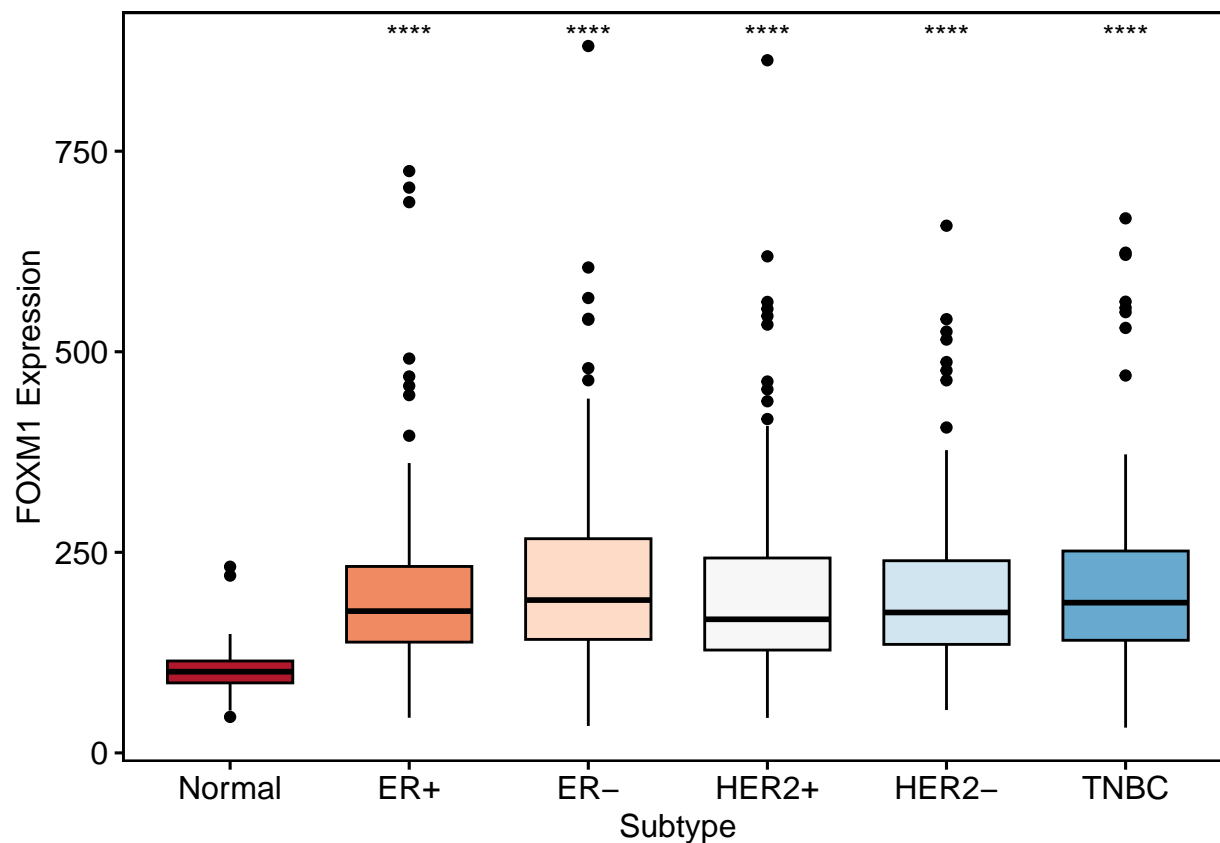
```
#Finalize
p <- ggboxplot(data, x = "Sample", y = "SOX9",
  fill = "Sample", , palette = c("#2166AC", "#B2182B"),
  order = c("Normal", "BRCA"), xlab = "Sample Type", ylab = "SOX9 Expression" ) +
  stat_compare_means(method = 't.test', paired = F) + border()
p
```



```
#Change legend position
p<- ggpar(p, legend = "bottom")

#Pairwise comparison among more than two groups
p2 <- ggboxplot(data, x = "Subtype", y = "SOX9",
  fill = "Subtype", palette = brewer.pal(n = 7, name = "RdBu"),
  xlab = "Subtype", ylab = "FOXN1 Expression", order = c("Normal", "ER+", "ER-",
    "HER2+", "HER2-", "TNBC")) + stat_compare_means(label = "p.signif", method = "t.test",
    ref.group = "Normal") + border()

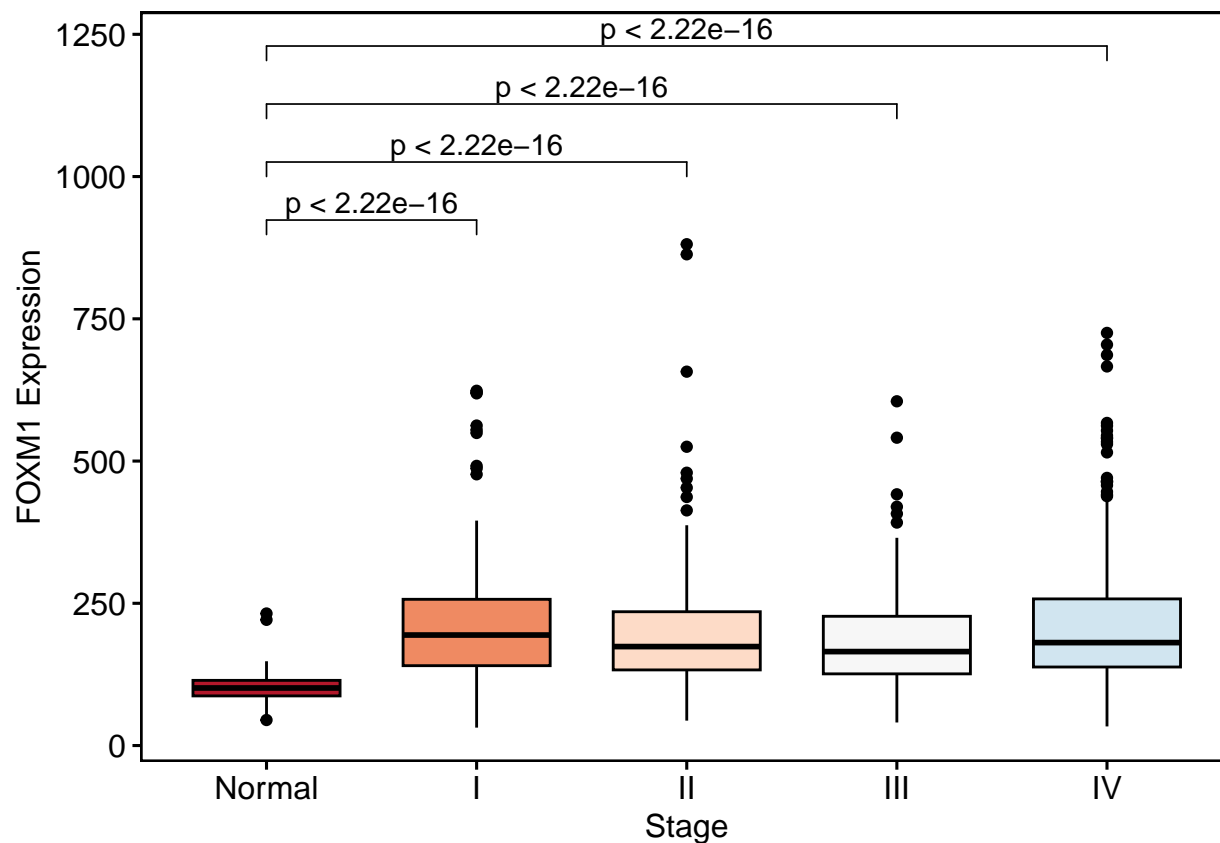
p2<- ggpar(p2, legend = 'none' )
p2
```



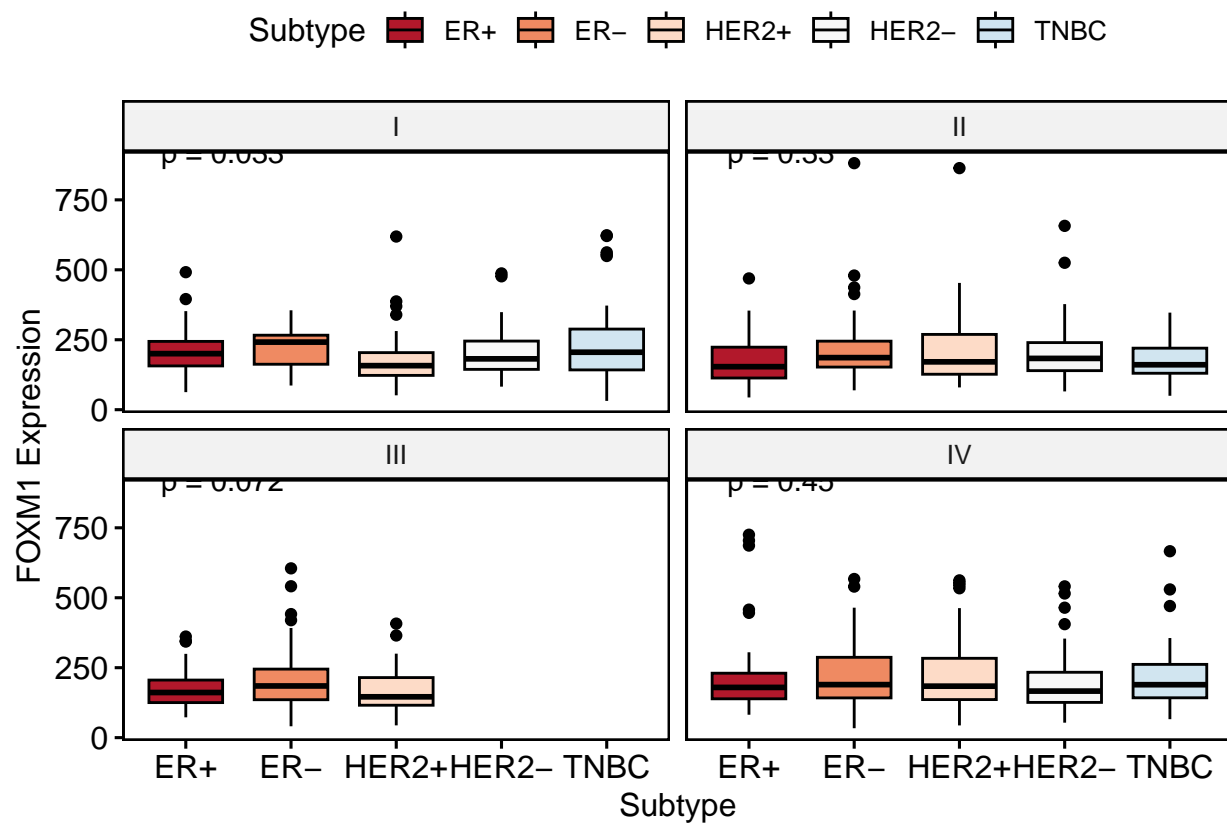
```
#Alternative pairwise comparison among more than two groups
comp<- list(c("Normal","I"), c("Normal","II"), c("Normal","III"), c("Normal","IV"))

p3 <- ggboxplot(data, x = "Stage", y = "SOX9", fill = "Stage", palette = brewer.pal(n = 7, name = "RdBu"),
               xlab = "Stage", ylab = "FOXM1 Expression", order = c("Normal", "I", "II", "III", "IV")) + stat_compare_means(method= 't.test', comparisons = comp)
               ) + border()

p3<- ggpar(p3, legend = 'none' )
p3
```



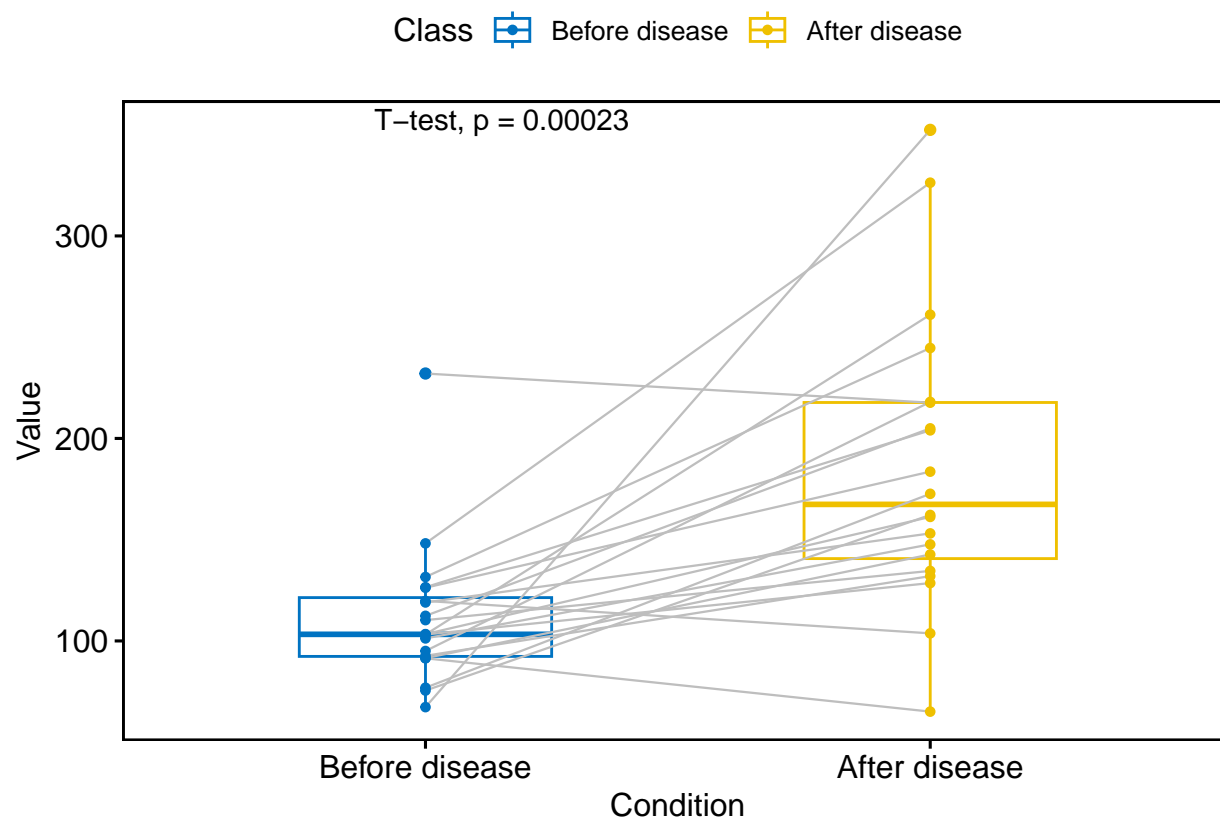
```
#Visualize with multiple panels
#Prepare data
data3<- data[1:1130,]
p4 <- ggboxplot(data3, x = "Subtype", y = "SOX9",
               fill = "Subtype", palette = brewer.pal(n = 7, name = "RdBu"),
               xlab = "Subtype", facet.by = 'Stage', ylab = "FOXM1 Expression", order = c("Normal", "E
               "HER2+", "HER2-", "TNBC")) + stat_compare_means(label = 'p.format') + border()
P4<- ggpar(p4, legend = 'none')
p4
```



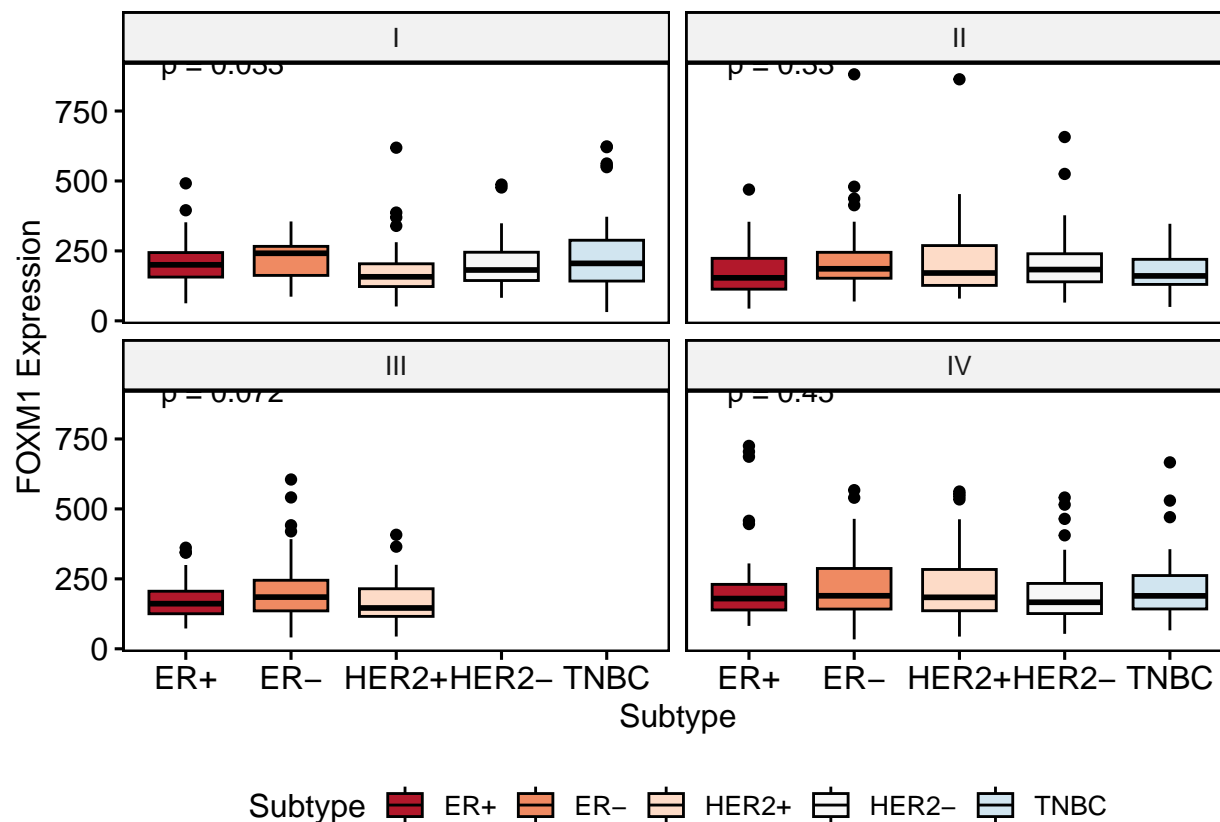
```
#Paired T Test
# Two group need to have equal variables
data2<- as.data.frame(data[1:40, 6:7])

p5 <- ggpaired(data2, x = "Class", y = "P53",
               color = "Class", palette = 'jco',
               add = "jitter", order = c("Before disease", "After disease"), line.color = "gray", line.
               stat_compare_means(method='t.test',paired = T)+border()

p5
```



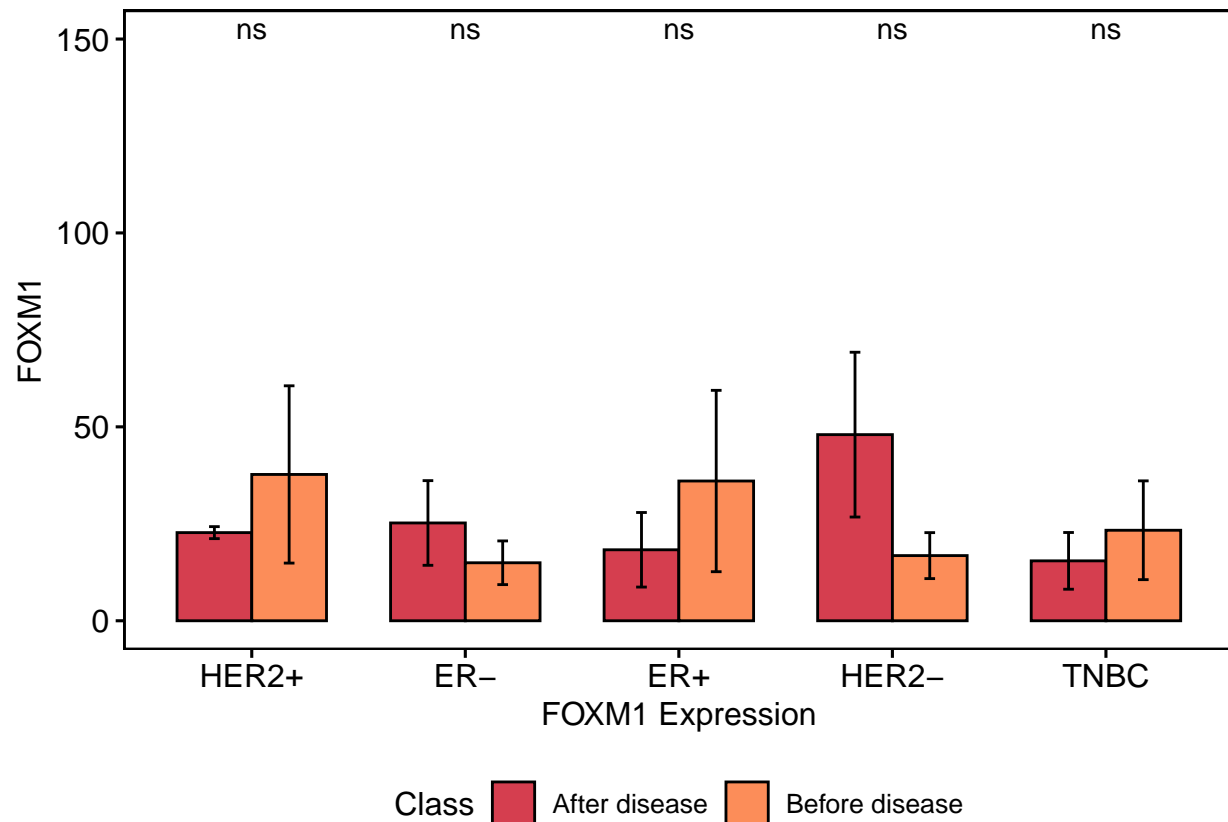
```
#### Performing ANOVA
p6<- ggboxplot(data, x = "Subtype", y = "FOXM1",
               fill = "Subtype", palette = brewer.pal(n = 7, name = "RdBu"),
               xlab = "Sample Type", ylab = "FOXM1 Expression", order = c("Normal", "ER+", "ER-",
               "HER2+", "HER2-", "TNBC")) +stat_compare_means(method = 'anova', paired = F) + border()
p6<- ggpar(p4, legend = "bottom")
p6
```



```
##Barplot
##Prepare data
data4<- data[1:40,]

p7<- ggbarplot(data4, x="Subtype", y='FOXM1', add = 'mean_se', fill = 'Class',
               palette = brewer.pal(n = 7, name = "Spectral"), position = position_dodge(0.7),
               xlab = 'FOXM1 Expression')+ stat_compare_means(aes(group = Class),
               label = "p.signif", label.y = 150) + border()

p7<- ggpar(p7, legend = 'bottom')
p7
```



```
##Line plot
p8<- ggline(data4, x="Subtype", y='FOXM1', add = 'mean_se', color = 'Class',
            palette = brewer.pal(n = 7, name = "RdBu"), xlab = 'FOXM1 Expression')+
  stat_compare_means(aes(group = Class), label = "p.signif", label.y = 70) + border()

p8<- ggpar(p8, legend = 'bottom')
p8
```