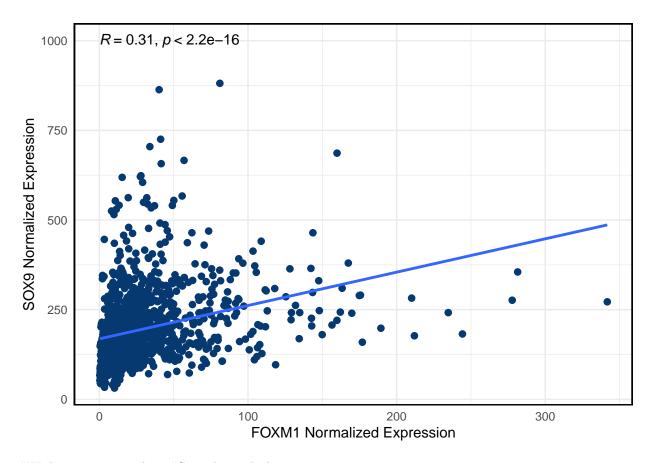
```
#Call libraries
library(ggplot2)
library(ggpubr)
library(ggExtra)
#Set directory and read data
setwd("E:/R-Programming-Practices/Data Visualization/Scatter Plot")
data<- data.frame(read.csv("FOXM1 and SOX9.csv", header = T))</pre>
#Select color
col=c('#063970')
#Plot a basic scatterplot
sc_plot<- ggplot(data, aes(x=F0XM1, y=S0X9))+</pre>
     geom_point(color=col, size=2)+ labs(x= "FOXM1 Normalized Expression", y="SOX9 Normalized Expression")
    geom_smooth(method = lm, se=F)+stat_cor(method = "pearson", label.x = 0, label.y = 1000)+theme_mini
     theme(panel.border = element_rect(color = 'black', fill = NA, size = 1))
## Warning: The 'size' argument of 'element_rect()' is deprecated as of ggplot2 3.4.0.
## i Please use the 'linewidth' argument instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
sc_plot
## 'geom_smooth()' using formula = 'y ~ x'
```

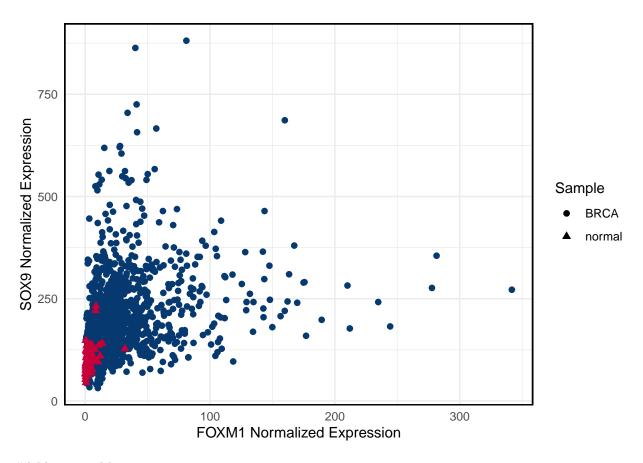


#Without regression line #Set color and plot

```
data2<- data
data2$Color<- ifelse(data2$Sample=="BRCA", "#063970", '#C70039')

sc_plot2<- ggplot(data, aes(x=F0XM1, y=S0X9, shape=Sample))+
  geom_point(color=data2$Color, size=2) +theme_minimal()+ #Can change to spearman
  theme(panel.border = element_rect(color = 'black', fill = NA, size = 1))+
  labs(x= "F0XM1 Normalized Expression", y="S0X9 Normalized Expression")

sc_plot2</pre>
```



# Add marginal histogram

```
sc_plot3<- sc_plot2+theme(legend.position = 'bottom')
sc_plot3<- ggMarginal(sc_plot3, type = 'histogram', groupColour = TRUE, groupFill = TRUE)
sc_plot3</pre>
```

