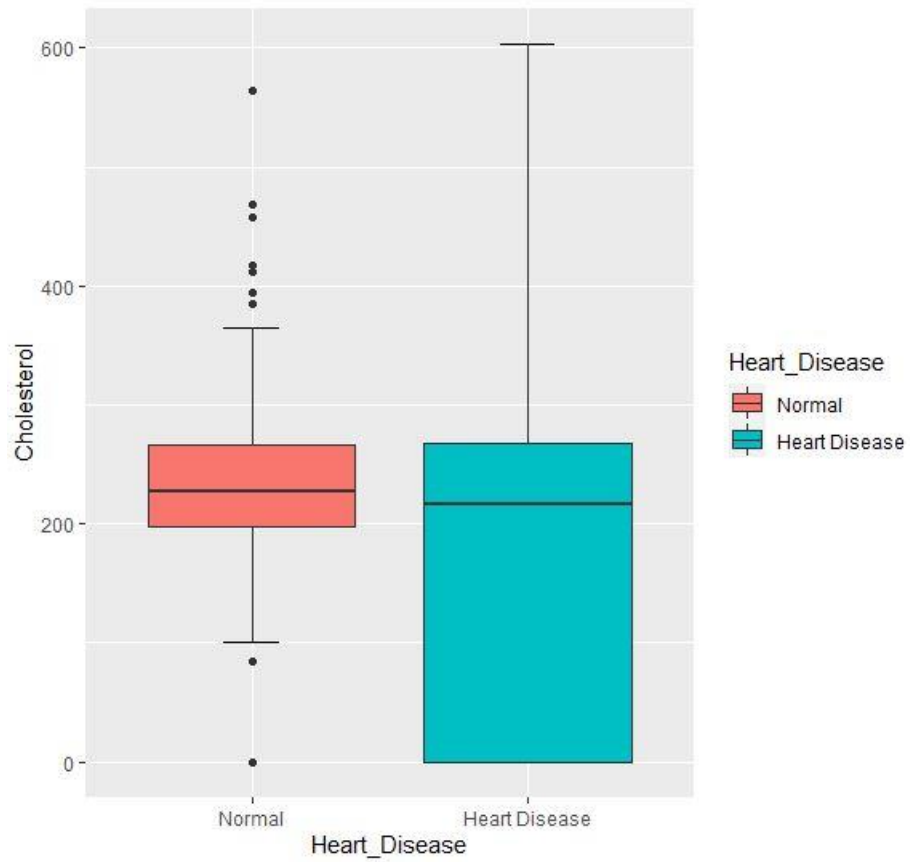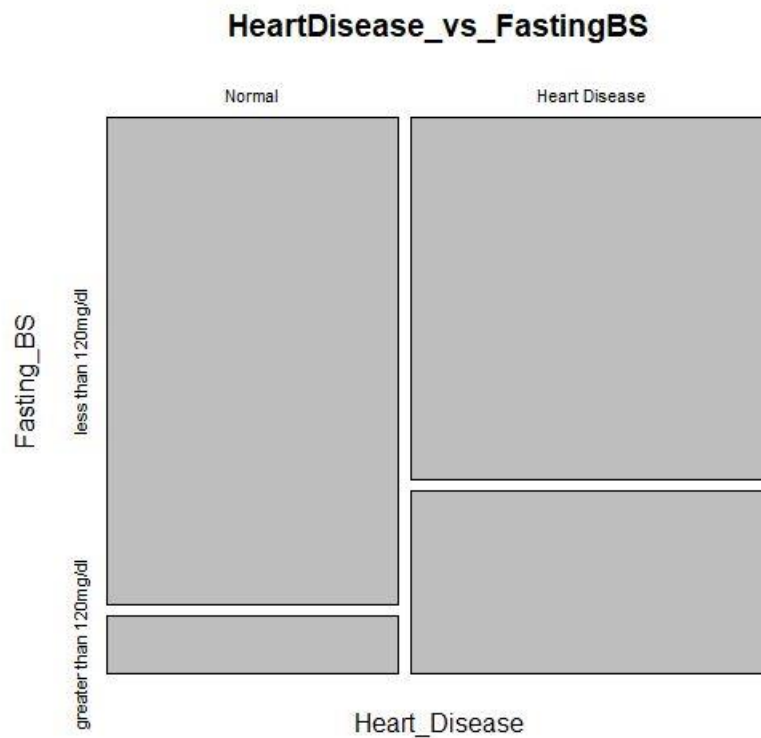The mean RestingBP for both Normal and HeartDisease is approximately equal. So, it does not seem most strongly associated with HeartDisease.

The mean Cholesterol for both Normal and HeartDisease is approximately equal. So, it does not seem most strongly associated with Heart Disease.

HeartDisease_vs_FastingBS

Most normal and heart disease cases have a fasting_BS of less than 120 mg/dl – with about 15% normal cases having fasting_BS greater than 120 mg/dl and 35% heart disease cases having fasting_BS greater than 120 mg/dl. There is an association between fasting_BS and HeartDisease in this case – however, cannot yet be determined if the association is the strongest.
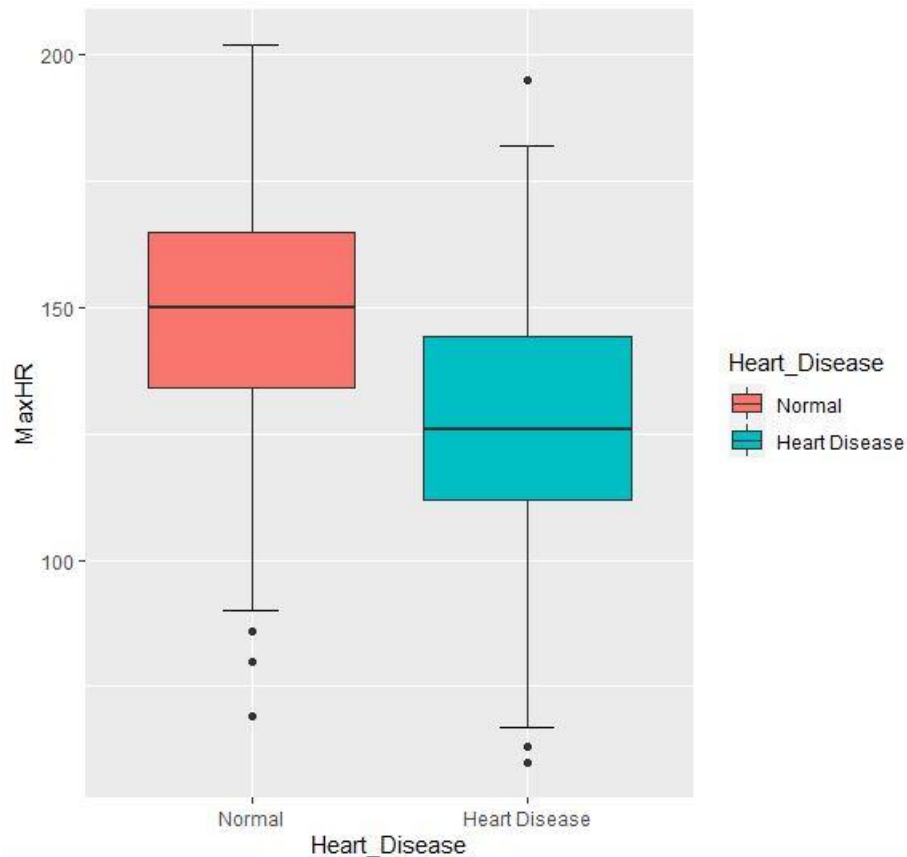
The mean MaxHR for Normal cases is much higher than that of HeartDisease cases. According to me, this has the most strong association with HeartDisease. Lower MaxHR shows signals of of HeartDisease.

Code:
```
Heart_Disease <- cut(heart_tbl$HeartDisease, breaks=c(0,0.5,1.1), labels=c("Normal", "Heart Disease"), right = FALSE)

Fasting_BS <- cut(heart_tbl$FastingBS, breaks = c(0,0.5,1.1), labels=c("less than 120mg/dl", "greater than 120mg/dl"), right = FALSE)
```

1. ggplot(heart_tbl, aes(x=Heart_Disease, y=RestingBP, fill=Heart_Disease)) + stat_boxplot(geom="errorbar", width = 0.2) + geom_boxplot()
2. ggplot(heart_tbl, aes(x=Heart_Disease, y=Cholesterol, fill=Heart_Disease)) + stat_boxplot(geom="errorbar", width = 0.2) + geom_boxplot()
3. HeartDisease_vs_FastingBS <- table(Heart_Disease, Fasting_BS)

   mosaicplot(HeartDisease_vs_FastingBS)

4. ggplot(heart_tbl, aes(x=Heart_Disease, y=Max~~HR~~, fill=Heart_Disease)) + stat_boxplot(geom="errorbar", width = 0.2) + geom_boxplot()