#df <- read.csv("input\_file.csv", header=T)

### TO keep the original/default order of the X-axis

df$Sample <- factor(df$Sample, levels = unique(df$Sample))

require(ggplot2)

library(RColorBrewer)

## Color palatte to define the color of the different bars

cbPalette <- c("#9933FF", "#FF9900", "#FFFF00", "#006699", "#FF0000", "#009933", "#993300")

## Barplot

ggplot(df, aes(x=Sample, y=Mutation\_number)) +geom\_bar(stat="identity", aes(fill=Variant\_type)) + theme(axis.text.x = element\_text(angle=90, vjust=1, hjust=1, size=12, face = "bold"))+ theme(title = element\_text(face = "bold", size = 28))+ xlab("")+ ylab("Frequency")

### For classic background in the Barplot, i.e. plain background and customized color palatte

ggplot(df, aes(x=Sample, y=Mutation\_number)) +geom\_bar(stat="identity", aes(fill=Variant\_type)) + theme(axis.text.x = element\_text(angle=90, vjust=1, hjust=1, size=12, face = "bold"))+ theme(title = element\_text(face = "bold", size = 12))+ xlab("")+ ylab("Number of mutations")+ scale\_fill\_manual(values=cbPalette)+ theme\_classic()