# plot_genome_size

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### 1/28/2021

```r
knitr::opts_chunk$set(echo = TRUE)

##Barplot of the size of the genomes in Mpb that was converted from the estimation with flow cytometry##
##Load libraries
library(ggplot2)
library(RColorBrewer)
##Convert of Picograms to Mpb##
picograms <- c("Atexcac"=0.37, "Carmen"=0.41, "Preciosa"=0.25, "Quechulac"=0.33, "Alchichica"=0.4)

picograms_to_Mpb <- function(picograms) {
  ## converts picograms value to Mpb (million base pairs)
  ## Arguments:
  # Mpb: value of Mpb converted to be pg
  Mpb <- ((picograms*978)) ## 1pg = 978 Mpb
  return(Mpb)
}

picograms_to_Mpb(picograms)
```

```
##    Atexcac     Carmen   Preciosa  Quechulac Alchichica
##     361.86     400.98     244.50     322.74     391.20
```

```r
##create dataframe with the genome size by populations##
genome_size <- data.frame(Population= c("Atx ", "Car", "Pre", "Que", "Alch"),
                          Mpb= c(361.86, 400.98, 244.50, 322.74, 391.20))

##Generate plot
graph_size <- ggplot(data = genome_size, aes(x=Population, y=Mpb, fill=Population)) +
  geom_bar(stat = "identity") +
  scale_fill_manual(values=c("orange", "blue", "red", "green", "purple"))+
  geom_text(aes(label=Mpb), vjust=4, color="black", size=3)+
  labs(title="Genome sizes")+
  theme_minimal()

graph_size
```

Genome sizes