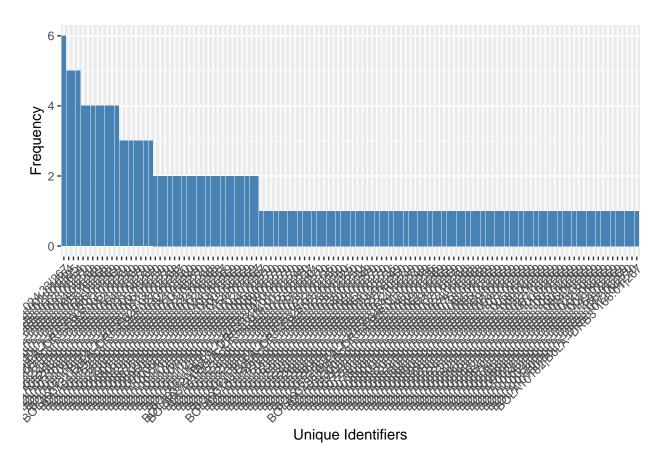
BOLA_RESULTS

KIRABO GLORIA

2023-12-20

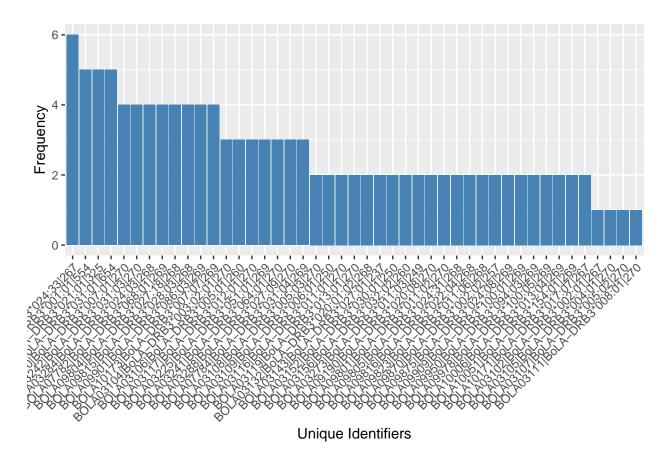
```
##Setting working directory
setwd("C:/Users/msaim/Downloads/BOLA/FASTA FILES 202")
data <- read.table("new_allele_count.txt")</pre>
dat <- read.table("sorted_alleles.txt")</pre>
head(data)
##
     V1
                                    V2
## 1 6 BOLA10181|BoLA-DRB3*024:33|267
## 2 5 BOLA03100|BoLA-DRB3*001:01|554
## 3 5 BOLA03135|BoLA-DRB3*021:01|325
## 4 5 BOLA03154|BoLA-DRB3*031:01|654
## 5 4 BOLA03110|BoLA-DRB3*007:01|270
## 6 4 BOLA03242|BoLA-DRB3*031:03|270
head(dat)
          V1
                                          ٧2
##
                                                 V3 V4
                                                               V5 V6 V7 V8
## 1 10.ab1 BOLA03100|BoLA-DRB3*001:01|554 96.552 261 1.19e-122 429 99 260
## 2 105.ab1 BOLA03100|BoLA-DRB3*001:01|554 97.414 232 1.19e-112 396 90 258
## 3 134.ab1 BOLA03100|BoLA-DRB3*001:01|554 92.562 242 1.23e-97 346 93 261
## 4 178.ab1 BOLA03100|BoLA-DRB3*001:01|554 95.935 246 1.21e-112 396 94 263
## 5 39.ab1 BOLA03100|BoLA-DRB3*001:01|554 96.063 254 1.20e-117 412 97 262
## 6 162.ab1 BOLA03102|BoLA-DRB3*002:01|267 93.902 246 1.23e-102 363 93 264
View(data)
library(ggplot2)
##Creating a dataframe
df <- data.frame(data)</pre>
# Plot using ggplot2
ggplot(df, aes(x = reorder(V2, -V1), y = V1)) +
  geom_bar(stat = "identity", fill = "steelblue") +
  labs(x = "Unique Identifiers", y = "Frequency") +
 theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
##REDUCING UNIQUE IDENTIFIERS TO 45 TO CAPTURE ALL FREQUENCIES

top_identifiers <- head(df[order(-df$V1), ], 45)

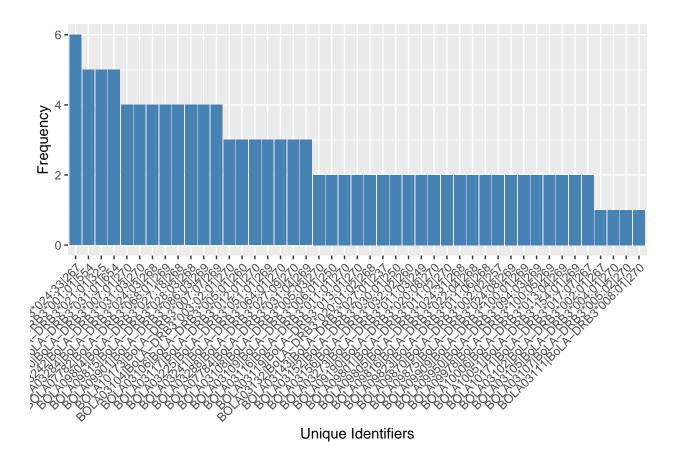
# Plot using ggplot2
ggplot(top_identifiers, aes(x = reorder(V2, -V1), y = V1)) +
   geom_bar(stat = "identity", fill = "steelblue") +
   labs(x = "Unique Identifiers", y = "Frequency") +
   theme(axis.text.x = element_text(angle = 45, hjust = 1))</pre>
```



```
##REDUCING IDENTIFIERS TO FIRST 30

top_identifier <- head(df[order(-df$V1), ], 30)

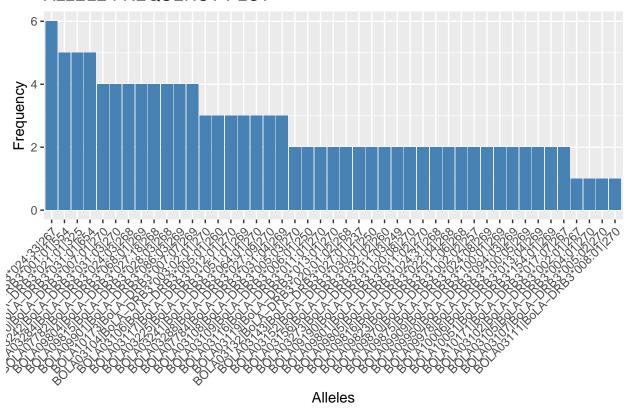
# Plot using ggplot2
ggplot(top_identifiers, aes(x = reorder(V2, -V1), y = V1)) +
   geom_bar(stat = "identity", fill = "steelblue") +
   labs(x = "Unique Identifiers", y = "Frequency") +
   theme(axis.text.x = element_text(angle = 45, hjust = 1))</pre>
```



```
##FINAL PLOT
top_identifier <- head(df[order(-df$V1), ], 28)

# Plot using ggplot2
ggplot(top_identifiers, aes(x = reorder(V2, -V1), y = V1)) +
    geom_bar(stat = "identity", fill = "steelblue") +
    labs(
        title = "ALLELE FREQUENCY PLOT",
        x = "Alleles",
        y = "Frequency"
    ) +
    theme(axis.text.x = element_text(angle = 45, hjust = 1))</pre>
```

ALLELE FREQUENCY PLOT



```
##CREATING A PIE CHART PLOT OF THE TOP 5 HITS

top_5 <- head(top_identifiers, 5)

# Extract values for plotting
values <- top_5$V1
labels <- top_5$V2

# Create a pie chart
pie(values, labels = labels, main = "Top 5 Allele Frequencies", col = rainbow(length(values)))</pre>
```

Top 5 Allele Frequencies

