

Results Section: Public Metadata

```
library(staphopia)
library(ggplot2)
library(reshape2)
```

Aggregating Data For Public Samples

First we'll get all publicly available *S. aureus* samples.

```
ps <- get_public_samples()
```

Variation From *S. aureus* N315

In Staphopia all samples had variants (SNPs and InDels) called using *S. aureus* N315 as the reference genome. In this section we'll visualize the total number of variants each sample has. This will give us an idea of the sequenced genetic diversity with respect to N315.

Gather Variant Counts

We will use `get_variant_counts()` to get the variant counts for each sample. We will also order the counts by the total.

```
variant_counts <- get_variant_counts(ps$sample_id)
variant_counts <- variant_counts[order(total),]
```

Summary of Variant Counts

Total Variants (SNPs and InDels)

```
summary(variant_counts$total)
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	10	19457	23891	26505	37343	146962

SNPs

```
summary(variant_counts$snp_count)
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	6	18712	23162	25560	36062	141893

InDels

```
summary(variant_counts$indel_count)
```

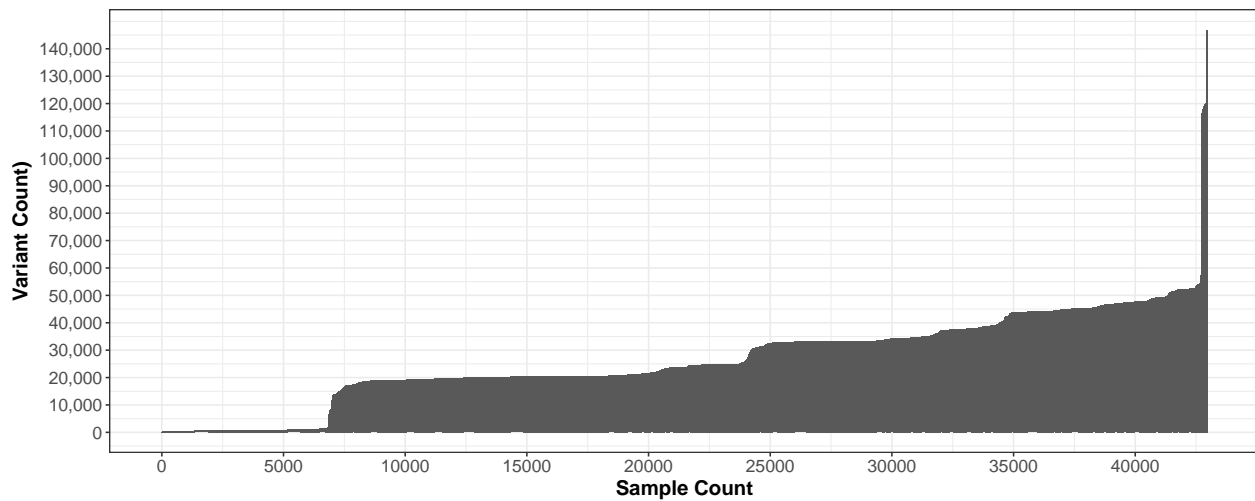
##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	1.0	709.0	901.0	944.4	1293.0	5125.0

Visualizing Variant Counts

Total Variants (SNPs and InDels)

```
p <- ggplot(data=variant_counts, aes(x=seq(1,nrow(variant_counts)), y=total)) +  
  xlab("Sample Count") +  
  ylab("Variant Count") +  
  geom_bar(stat='identity') +  
  scale_x_continuous(breaks = seq(0, nrow(variant_counts), by = 5000)) +  
  scale_y_continuous(breaks = seq(0, max(variant_counts$total), by=10000), labels = scales::comma) +  
  theme_bw() +  
  theme(axis.text=element_text(size=12),  
        axis.title=element_text(size=14,face="bold"))
```

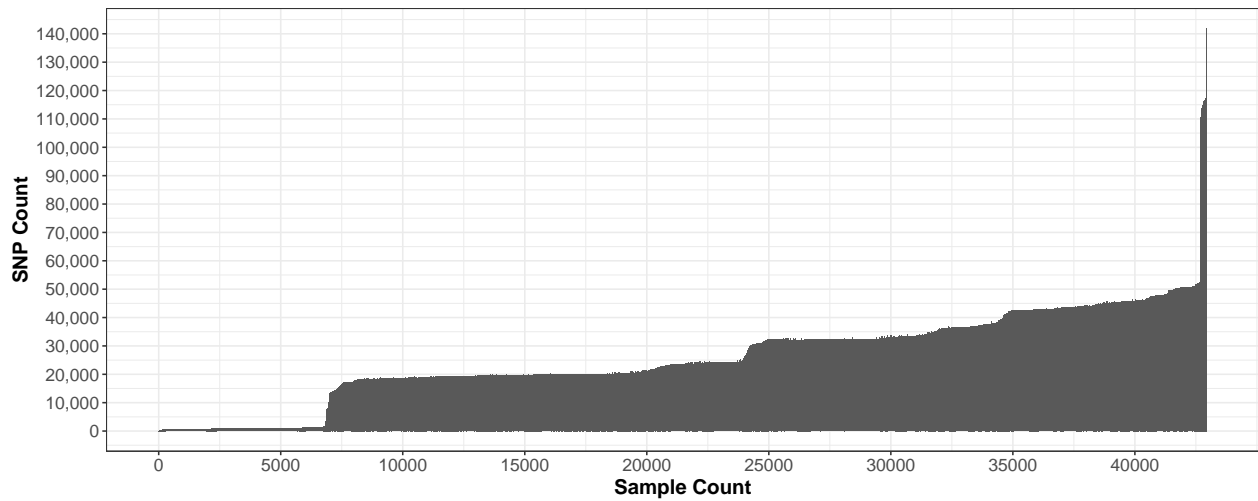
p



SNPs Only

```
p <- ggplot(data=variant_counts, aes(x=seq(1,nrow(variant_counts)), y=snp_count)) +  
  xlab("Sample Count") +  
  ylab("SNP Count") +  
  geom_bar(stat='identity') +  
  scale_x_continuous(breaks = seq(0, nrow(variant_counts), by = 5000)) +  
  scale_y_continuous(breaks = seq(0, max(variant_counts$snp_count), by=10000), labels = scales::comma) +  
  theme_bw() +  
  theme(axis.text=element_text(size=12),  
        axis.title=element_text(size=14,face="bold"))
```

p



```
# Output plot to PDF and PNG
staphopia::write_plot(p, paste0(getwd(), '/../figures/figure-09-snp-accumulation'))
```

InDels Only

```
p <- ggplot(data=variant_counts, aes(x=seq(1,nrow(variant_counts)), y=indel_count)) +
  xlab("Sample Count") +
  ylab("Indel Count") +
  geom_bar(stat='identity') +
  scale_x_continuous(breaks = seq(0, nrow(variant_counts), by = 5000)) +
  scale_y_continuous(breaks = seq(0, max(variant_counts$indel_count), by=500), labels = scales::comma) +
  theme_bw() +
  theme(axis.text=element_text(size=12),
        axis.title=element_text(size=14,face="bold"))
p
```

