

QAA

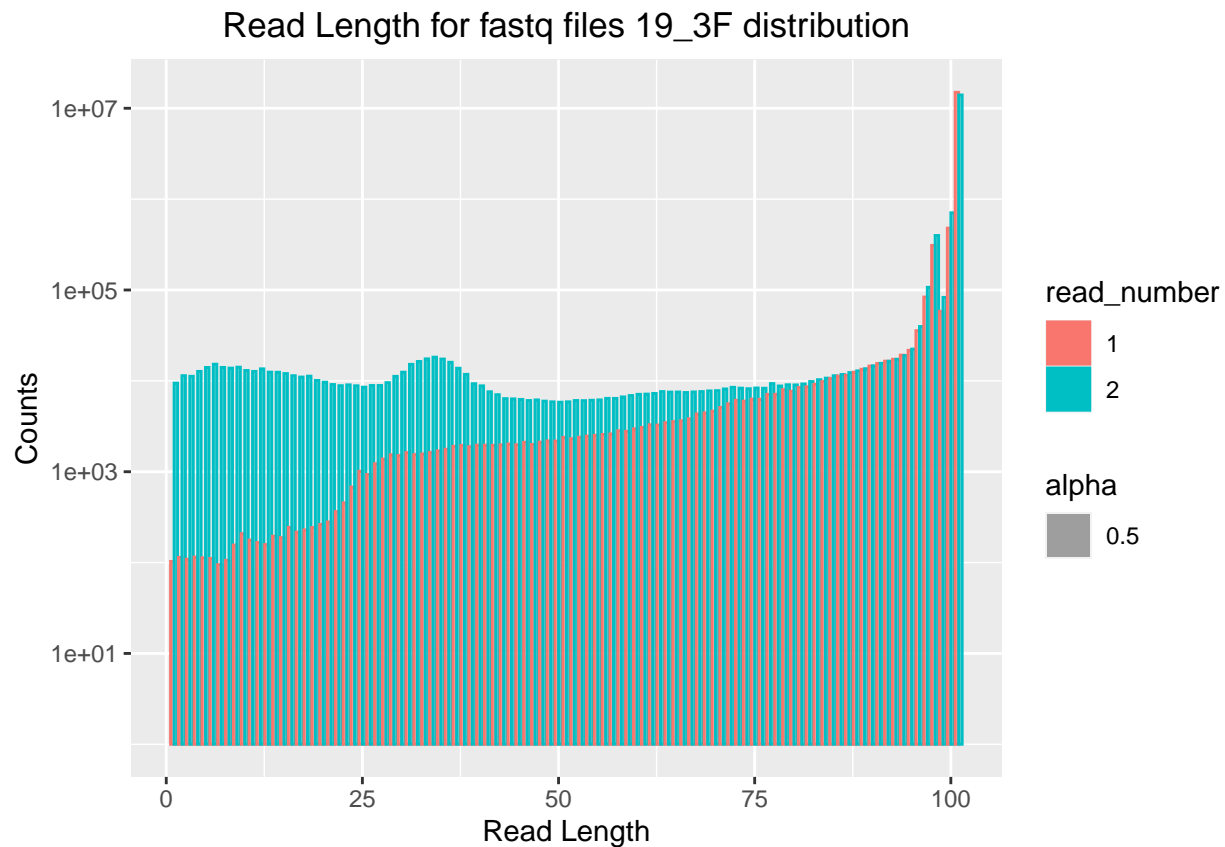
```
read1_2B = read.table('/Users/andrewpowers/bioinformatics/Bi623/ps-qaa/ps3-QAA/trimmed_tsv_files/size_2B.tsv',
                      header = F)
read2_2B = read.table('/Users/andrewpowers/bioinformatics/Bi623/ps-qaa/ps3-QAA/trimmed_tsv_files/size_2B.tsv',
                      header = F)
read1_19 = read.table('/Users/andrewpowers/bioinformatics/Bi623/ps-qaa/ps3-QAA/trimmed_tsv_files/size_19_3F.tsv',
                      header = F)
read2_19 = read.table('/Users/andrewpowers/bioinformatics/Bi623/ps-qaa/ps3-QAA/trimmed_tsv_files/size_19_3F.tsv',
                      header = F)
```

```
read1_19$read_number = rep(1, nrow(read1_19))
read2_19$read_number = rep(2, nrow(read2_19))
read1_2B$read_number = rep(1, nrow(read1_2B))
read2_2B$read_number = rep(2, nrow(read2_2B))
```

```
total_2B = rbind(read1_2B, read2_2B)
total_19 = rbind(read1_19, read2_19)
```

```
total_2B = total_2B %>% group_by(`V2`) %>% dplyr::count(V2, read_number) %>% mutate(read_number = as.character(read_number))
total_19 = total_19 %>% group_by(`V2`) %>% dplyr::count(V2, read_number) %>% mutate(read_number = as.character(read_number))
```

```
ggplot(data = total_19) +
  geom_bar(aes(x=`V2`, y=`n`, color=`read_number`, fill=`read_number`, alpha=0.5),
           stat='identity', position='dodge') +
  scale_y_log10() +
  labs(x='Read Length', y='Counts', title='Read Length for fastq files 19_3F distribution') +
  theme(plot.title = element_text(hjust=0.5))
```



```
ggplot(data = total_2B) +
  geom_bar(aes(x=`V2`, y=`n`, color=`read_number`, fill=`read_number`, alpha=0.5),
    stat='identity', position='dodge') +
  scale_y_log10() +
  labs(x='Read Length', y='Counts', title='Read Length for fastq files 2_2B distribution') +
  theme(plot.title = element_text(hjust=0.5))
```

