

# PolyATails Lengths

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## Load all data

```
a60_30 <- read.table(file = 'a60_30_polyA_position.tsv', sep = '\t', header = TRUE)
a60_60 <- read.table(file = 'a60_60_polyA_position.tsv', sep = '\t', header = TRUE)
a60_unmod <- read.table(file = 'a60_unmod_polyA_position.tsv', sep = '\t', header = TRUE)

a120_1mod <- read.table(file = 'a120_1mod_polyA_position.tsv', sep = '\t', header = TRUE)
a120_2mod <- read.table(file = 'a120_2mod_polyA_position.tsv', sep = '\t', header = TRUE)
a120_4mod <- read.table(file = 'a120_4mod_polyA_position.tsv', sep = '\t', header = TRUE)
a120_unmod <- read.table(file = 'a120_unmod_polyA_position.tsv', sep = '\t', header = TRUE)
```

## Define lengths of polyATail

```
a60_30['polyA_length'] <- a60_30$end - a60_30$start
a60_60['polyA_length'] <- a60_60$end - a60_60$start
a60_unmod['polyA_length'] <- a60_unmod$end - a60_unmod$start

a120_1mod['polyA_length'] <- a120_1mod$end - a120_1mod$start
a120_2mod['polyA_length'] <- a120_2mod$end - a120_2mod$start
a120_4mod['polyA_length'] <- a120_4mod$end - a120_4mod$start
a120_unmod['polyA_length'] <- a120_unmod$end - a120_unmod$start
```

## Histograms of all the data

```
# List of loaded datasets and their corresponding names
datasets <- list(
  a60_30 = a60_30,
  a60_60 = a60_60,
  a60_unmod = a60_unmod,
  a120_1mod = a120_1mod,
  a120_2mod = a120_2mod,
  a120_4mod = a120_4mod,
  a120_unmod = a120_unmod
)

for (name in names(datasets)) {
```

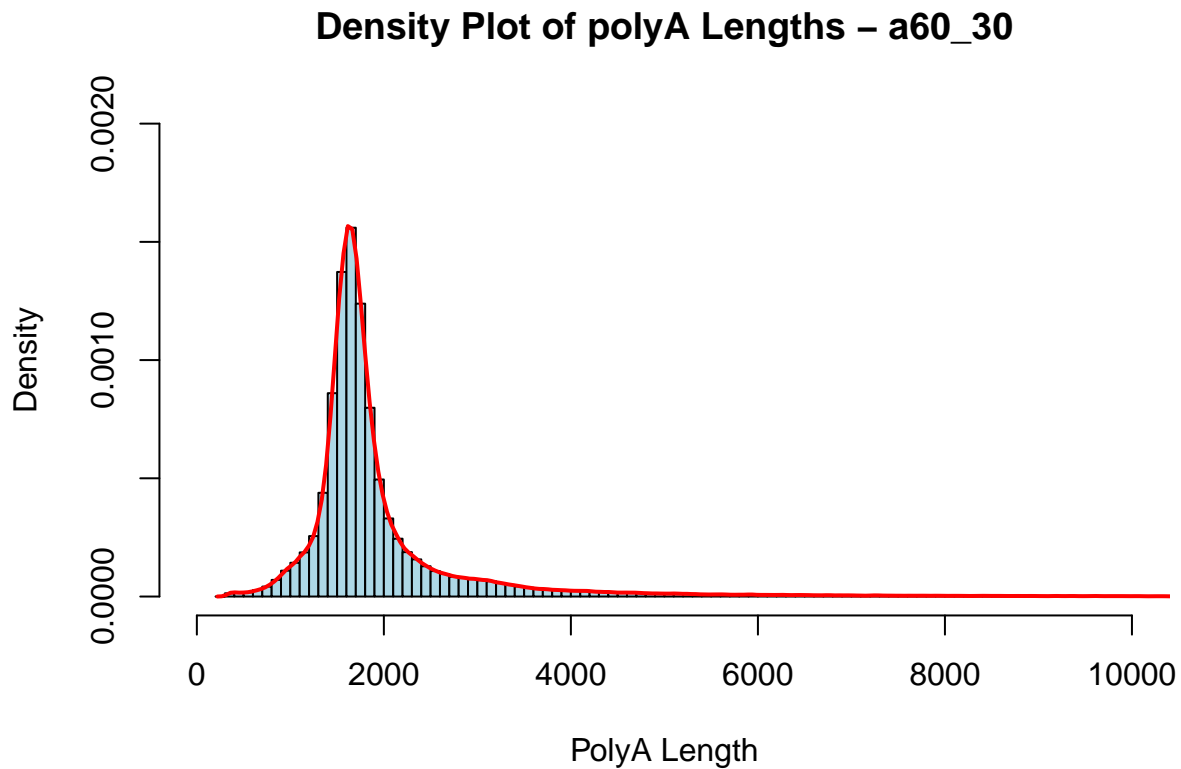
```

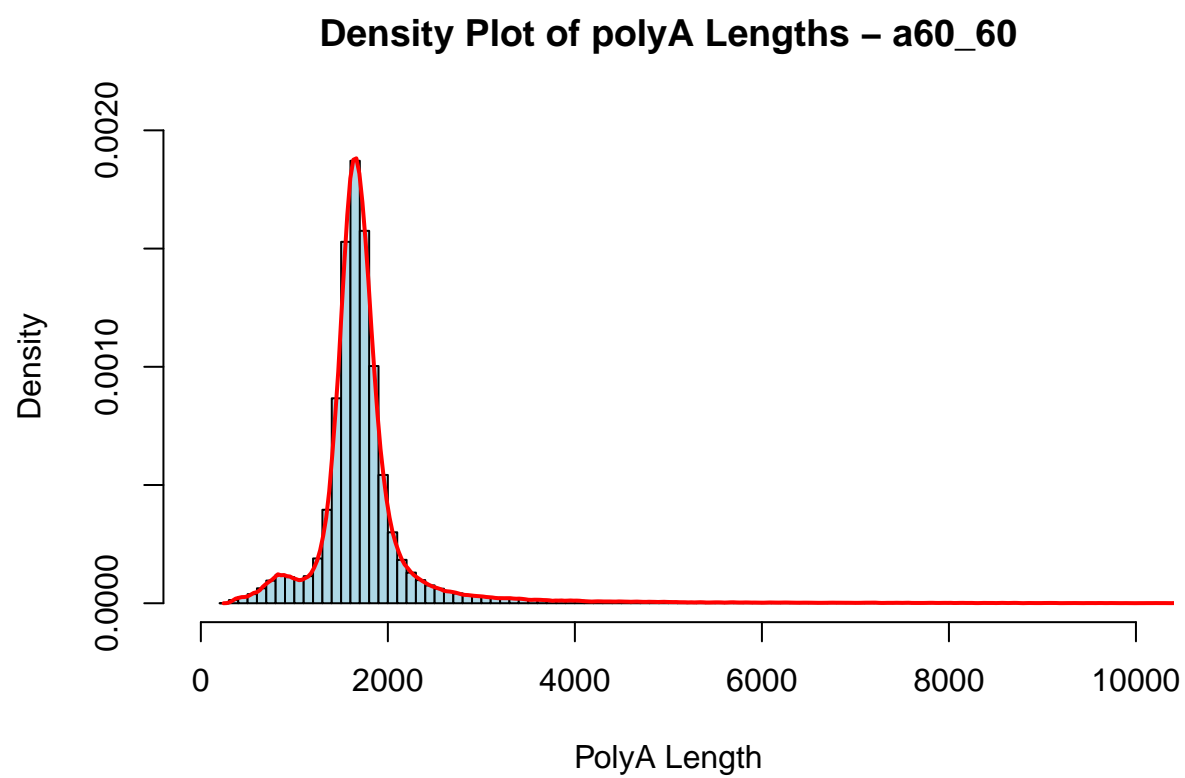
polyA_length <- datasets[[name]]$polyA_length

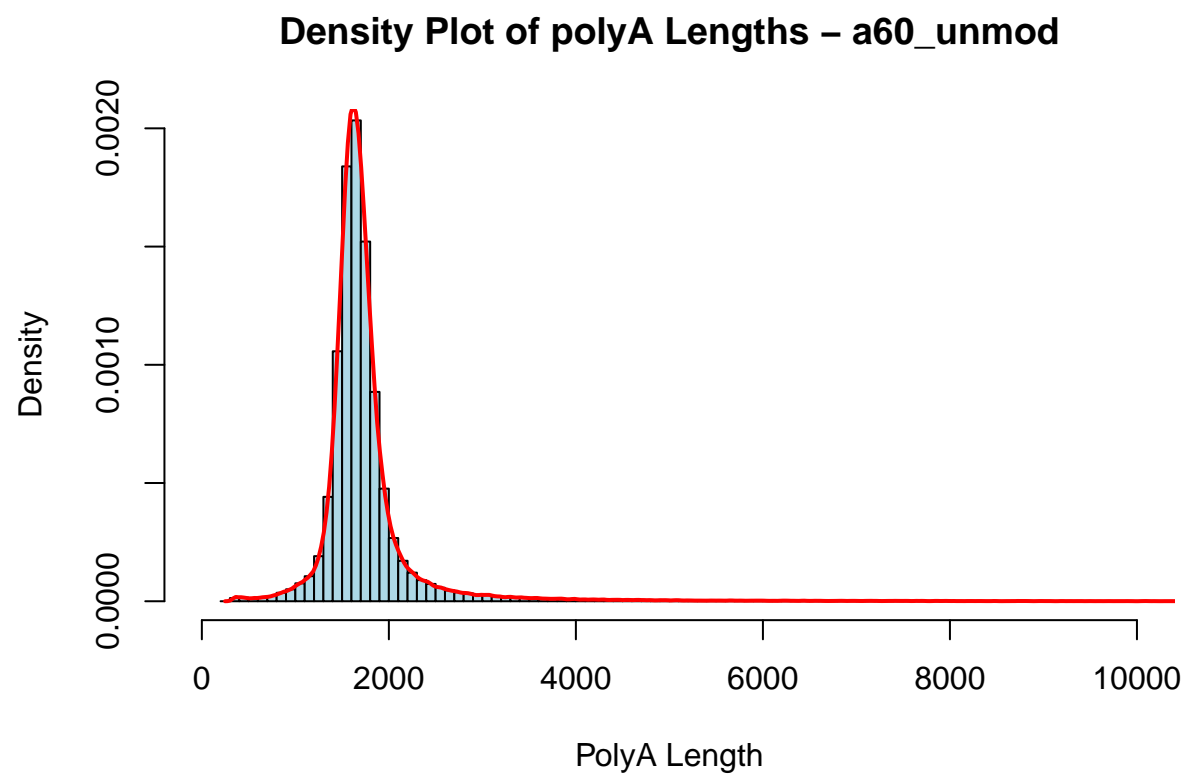
hist(polyA_length,
      probability = TRUE,
      main = paste("Density Plot of polyA Lengths -", name),
      xlab = "PolyA Length",
      ylab = "Density",
      xlim = c(0, 10000),
      ylim = c(0, 0.0020),
      border = "black",
      col = "lightblue",
      breaks = 200)

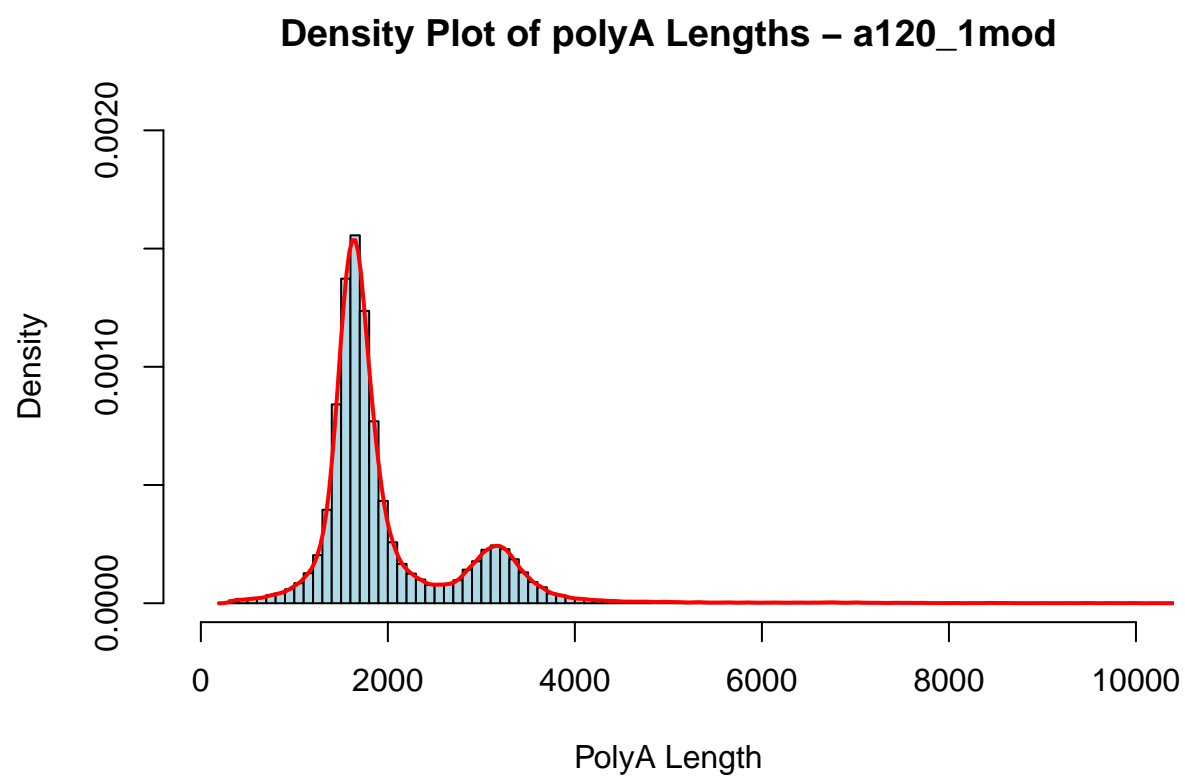
# Add the density line in red
lines(density(polyA_length), col = "red", lwd = 2)
}

```

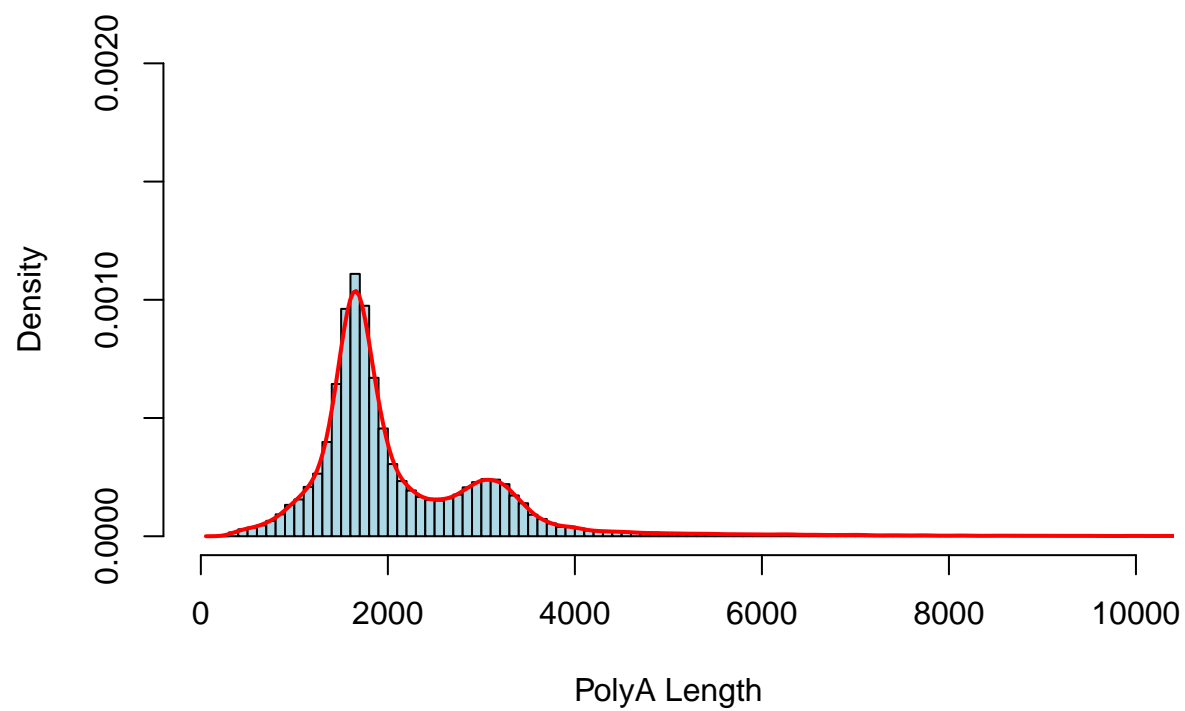




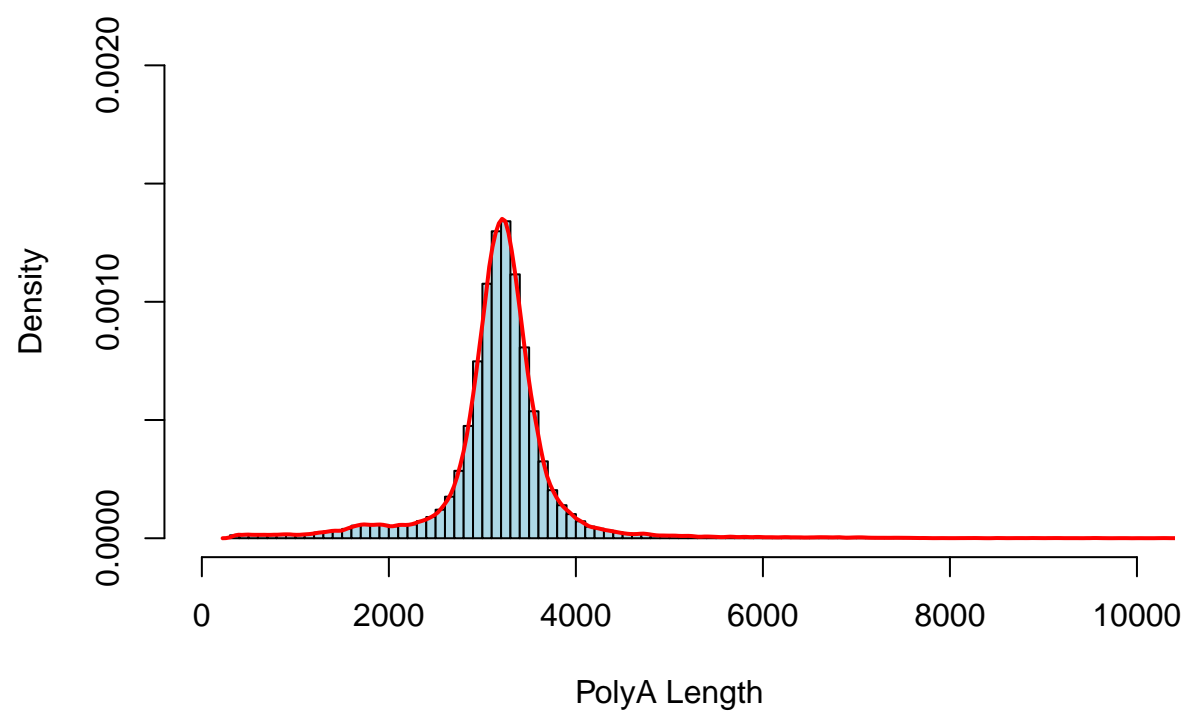


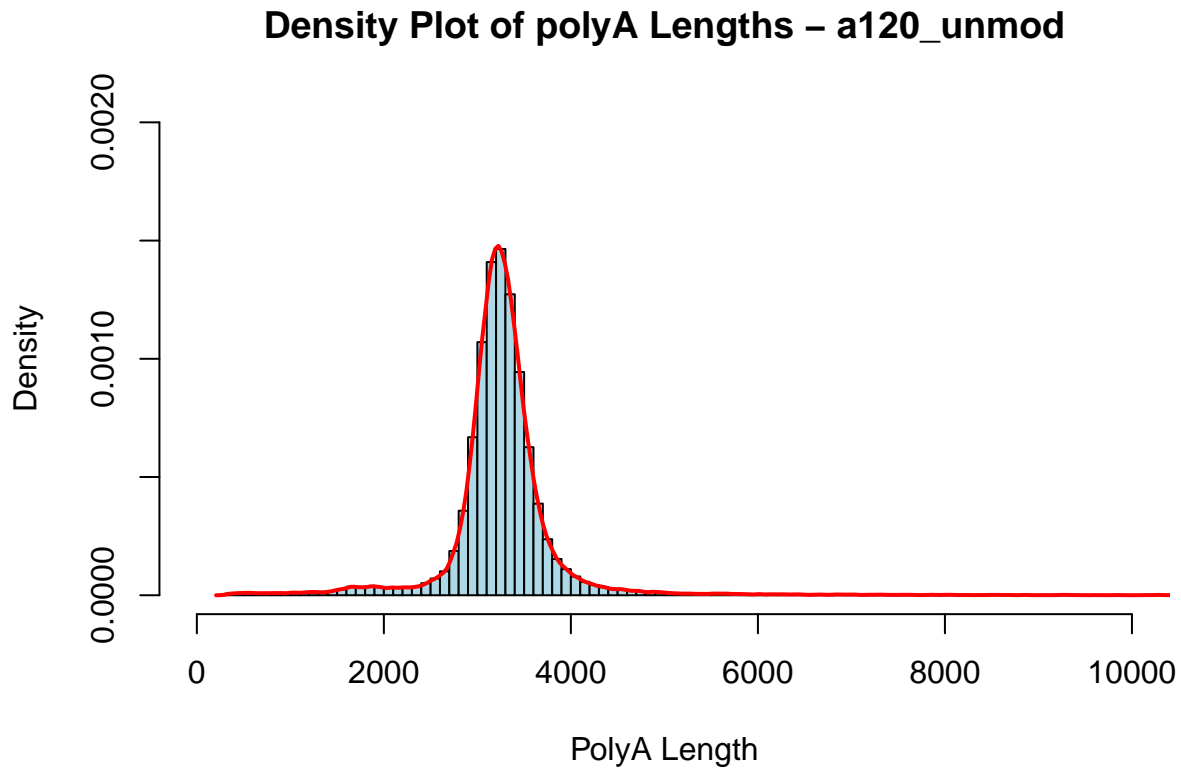


**Density Plot of polyA Lengths – a120\_2mod**



Density Plot of polyA Lengths – a120\_4mod



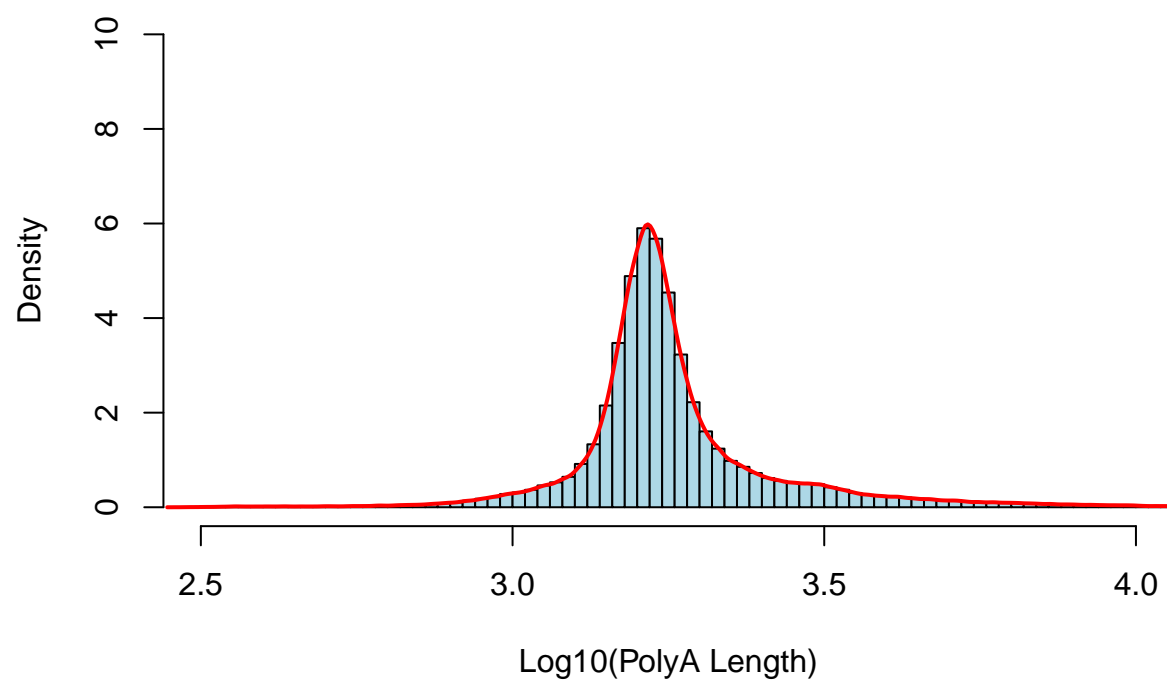


Histograms of all the data with log transformation

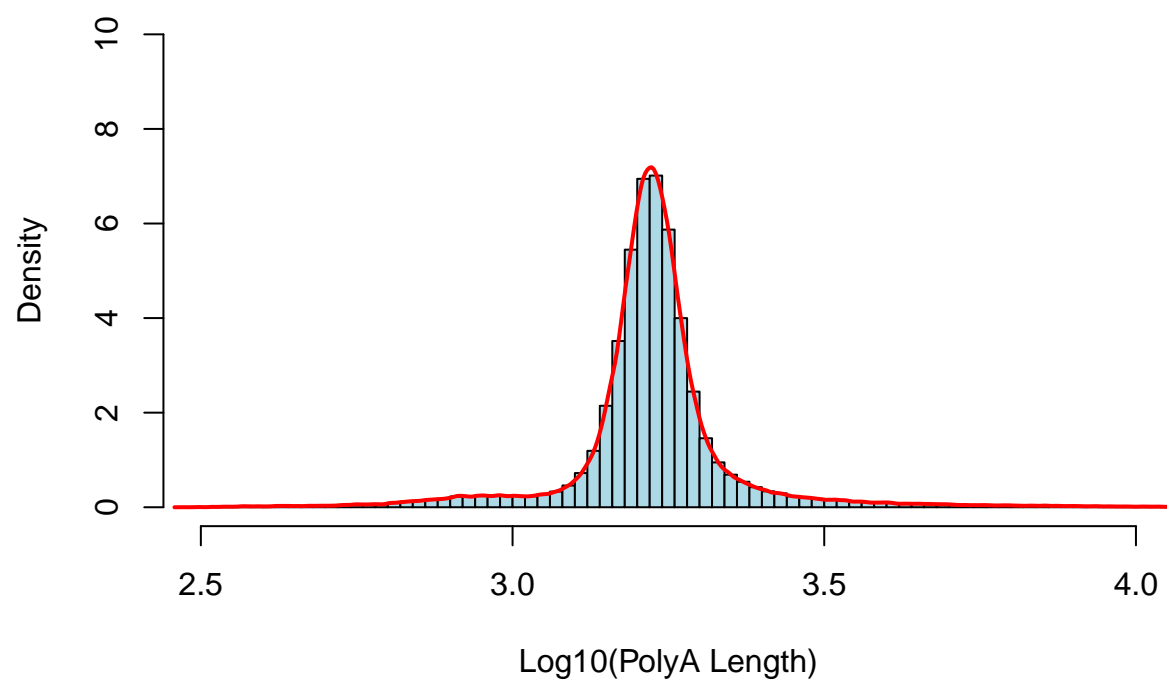
```
for (name in names(datasets)) {  
  polyA_length <- datasets[[name]]$polyA_length  
  
  log_polyA_length <- log10(polyA_length)  
  
  hist(log_polyA_length,  
        probability = TRUE,  
        main = paste("Density Plot of log-transformed polyA Lengths -", name),  
        xlab = "Log10(PolyA Length)",  
        ylab = "Density",  
        border = "black",  
        col = "lightblue",  
        xlim = c(2.5,4.0),  
        ylim = c(0,10),  
        breaks = 100)  
  
  lines(density(log_polyA_length), col = "red", lwd = 2)  
}
```



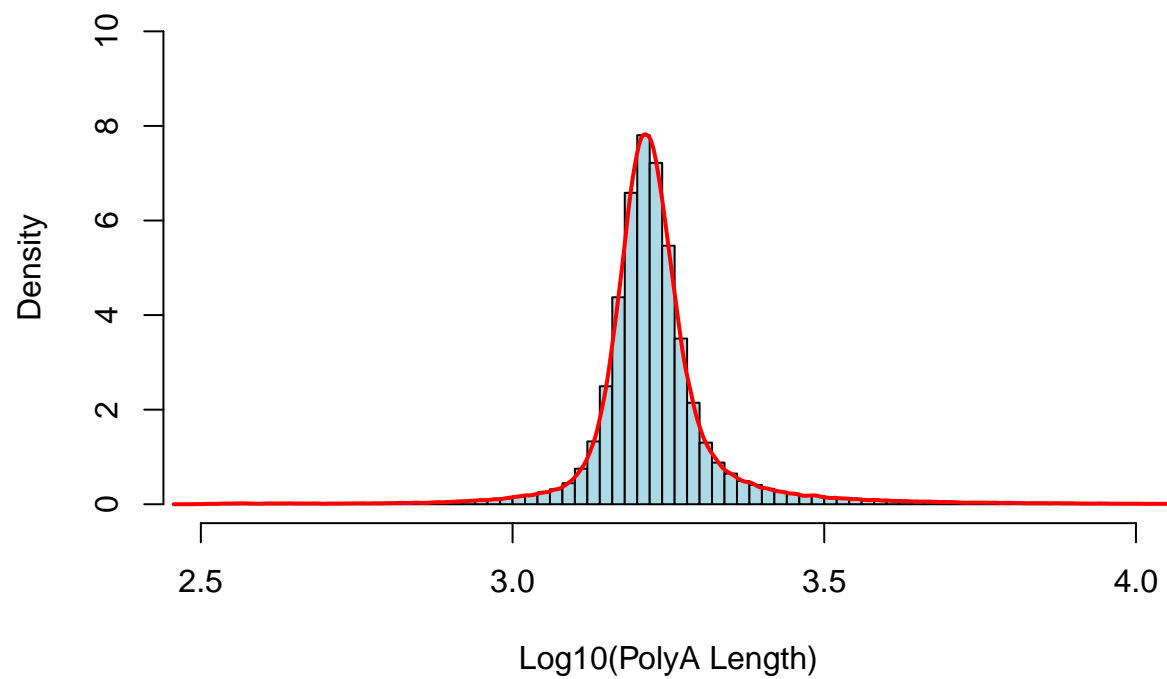
**Density Plot of log-transformed polyA Lengths – a60\_30**



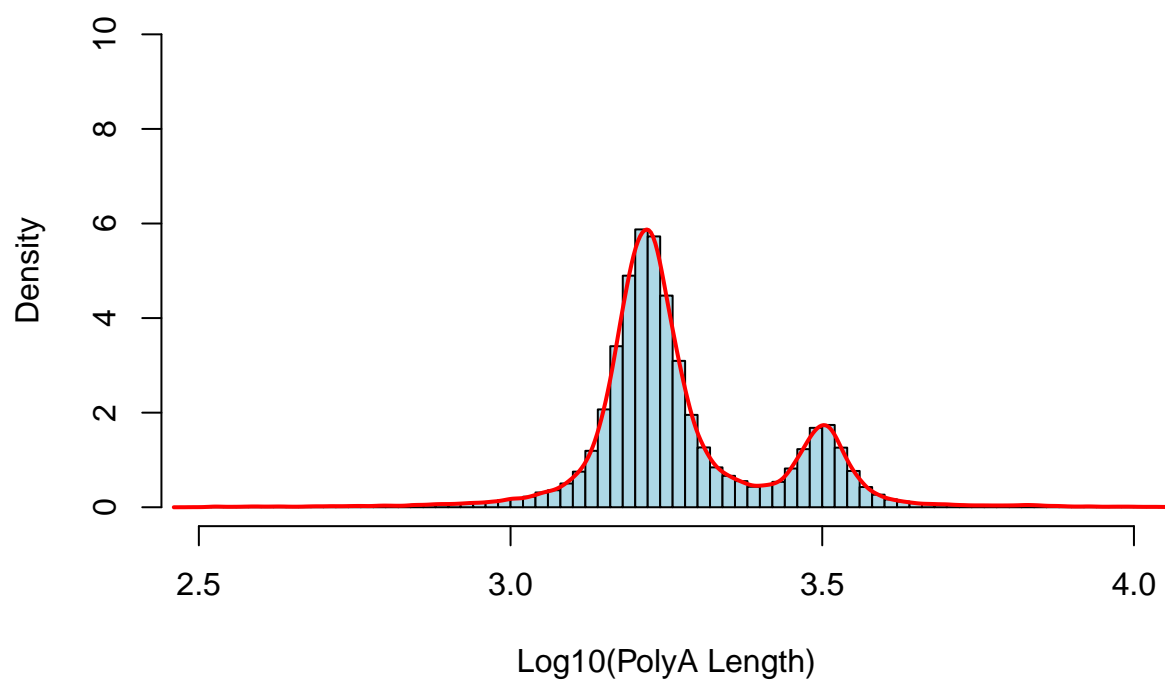
**Density Plot of log-transformed polyA Lengths – a60\_60**



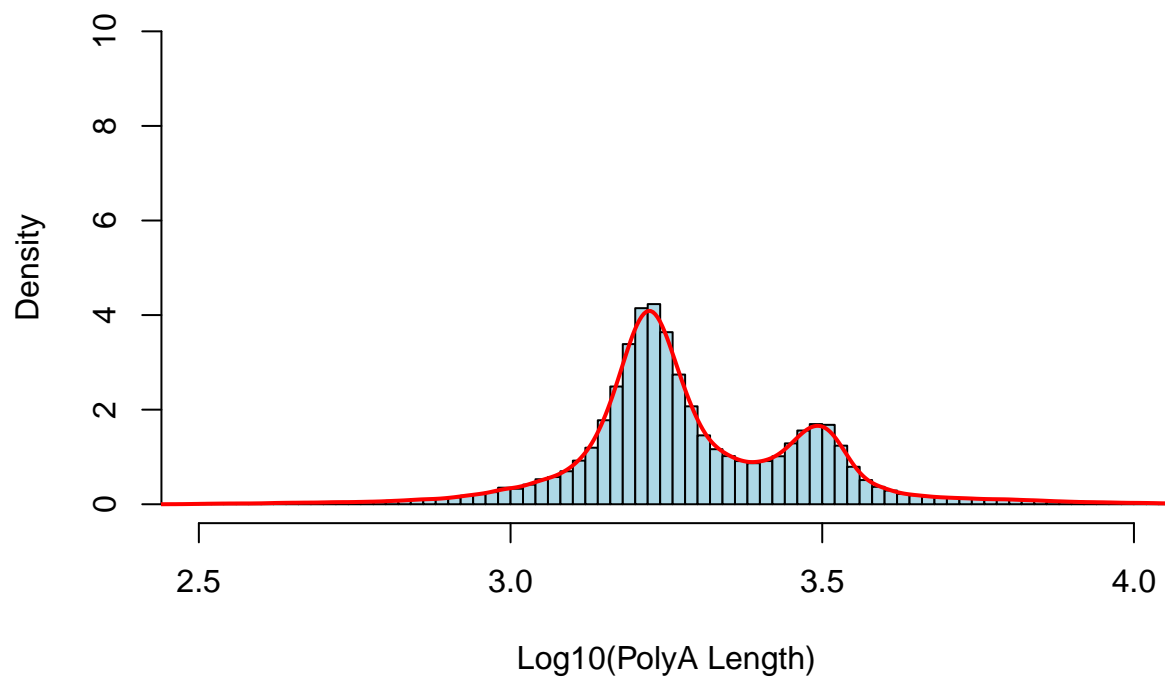
**Density Plot of log-transformed polyA Lengths – a60\_unmod**



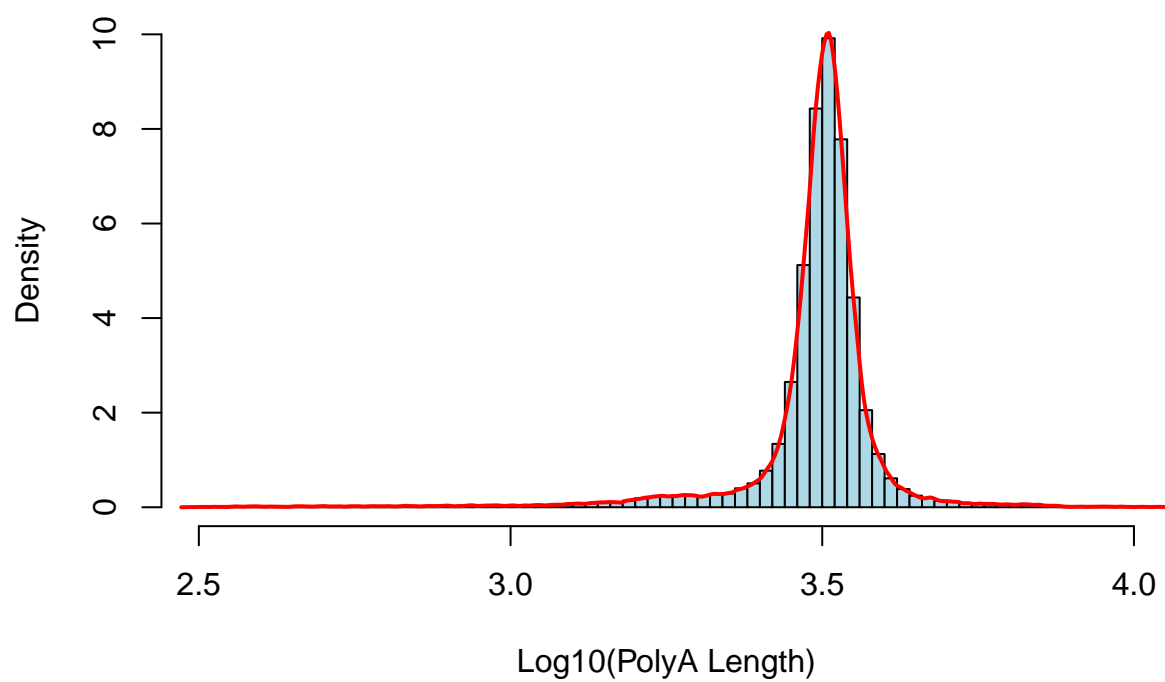
**Density Plot of log-transformed polyA Lengths – a120\_1mod**



**Density Plot of log-transformed polyA Lengths – a120\_2mod**



**Density Plot of log-transformed polyA Lengths – a120\_4mod**



**Density Plot of log-transformed polyA Lengths – a120\_unmod**

