

PolyATails Lengths

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2025-03-19

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

```
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
)

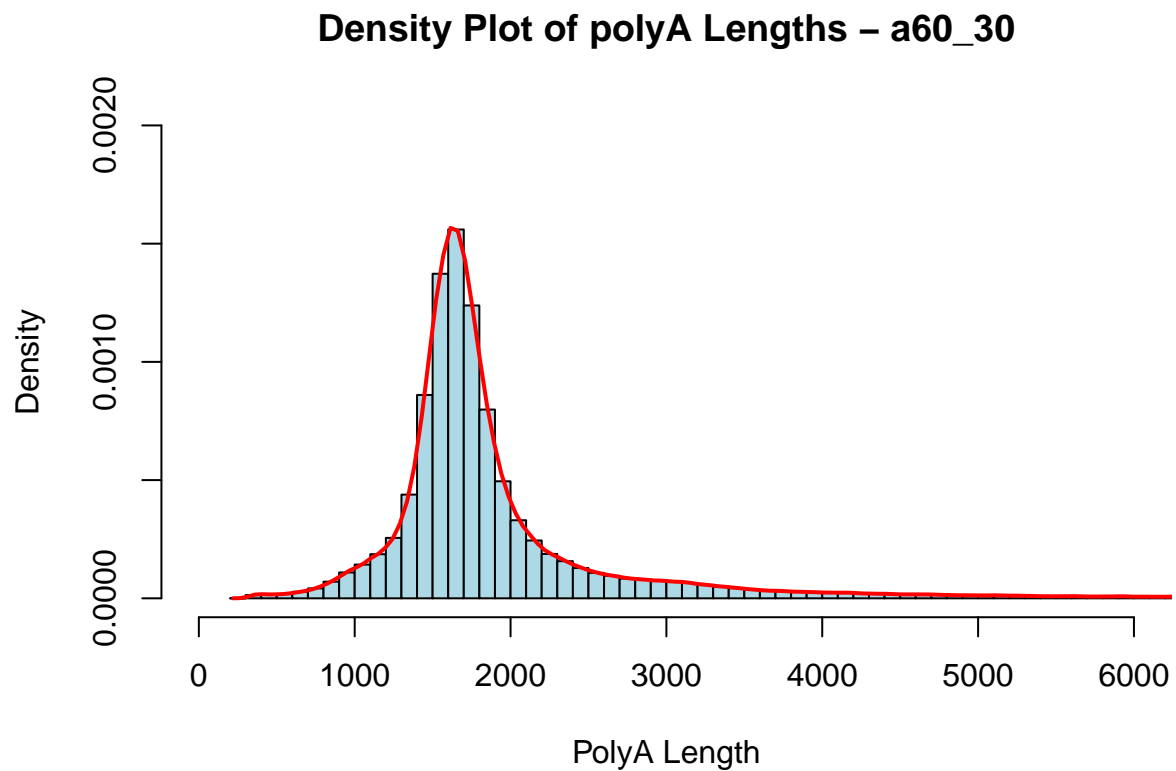
for (name in names(datasets)) {
  polyA_length <- datasets[[name]]$polyA_length
}
```

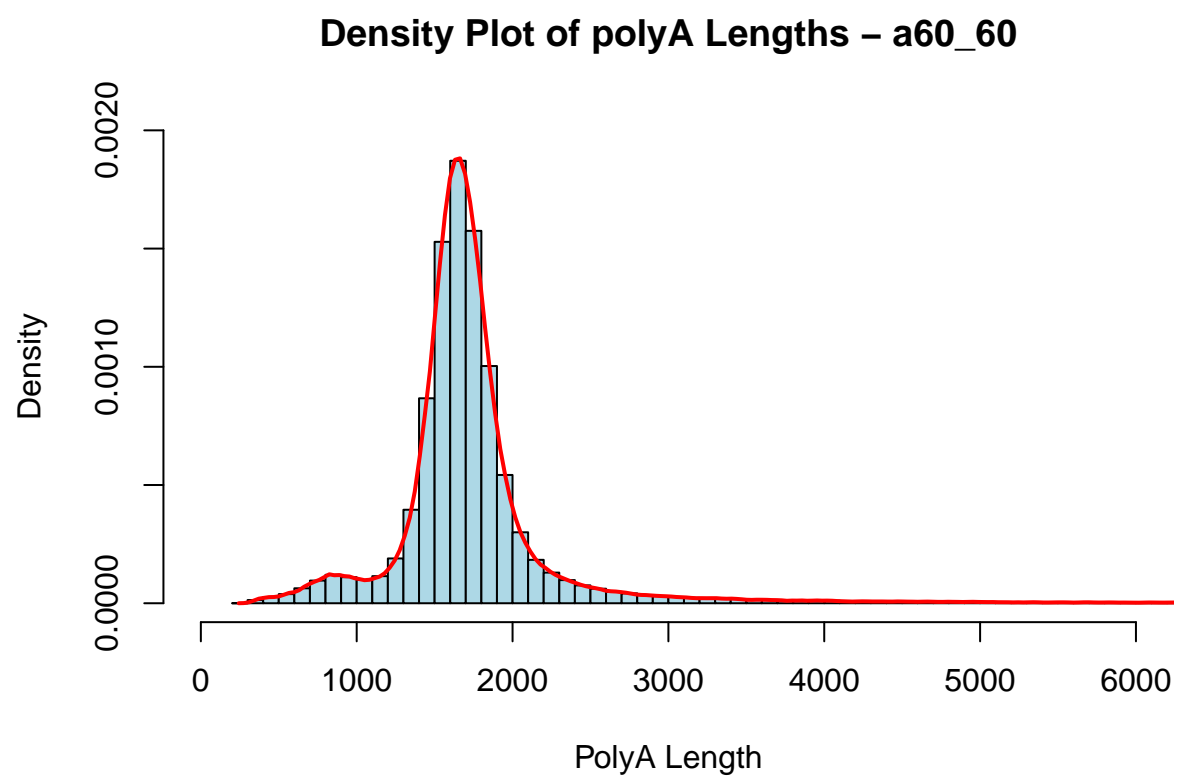
```

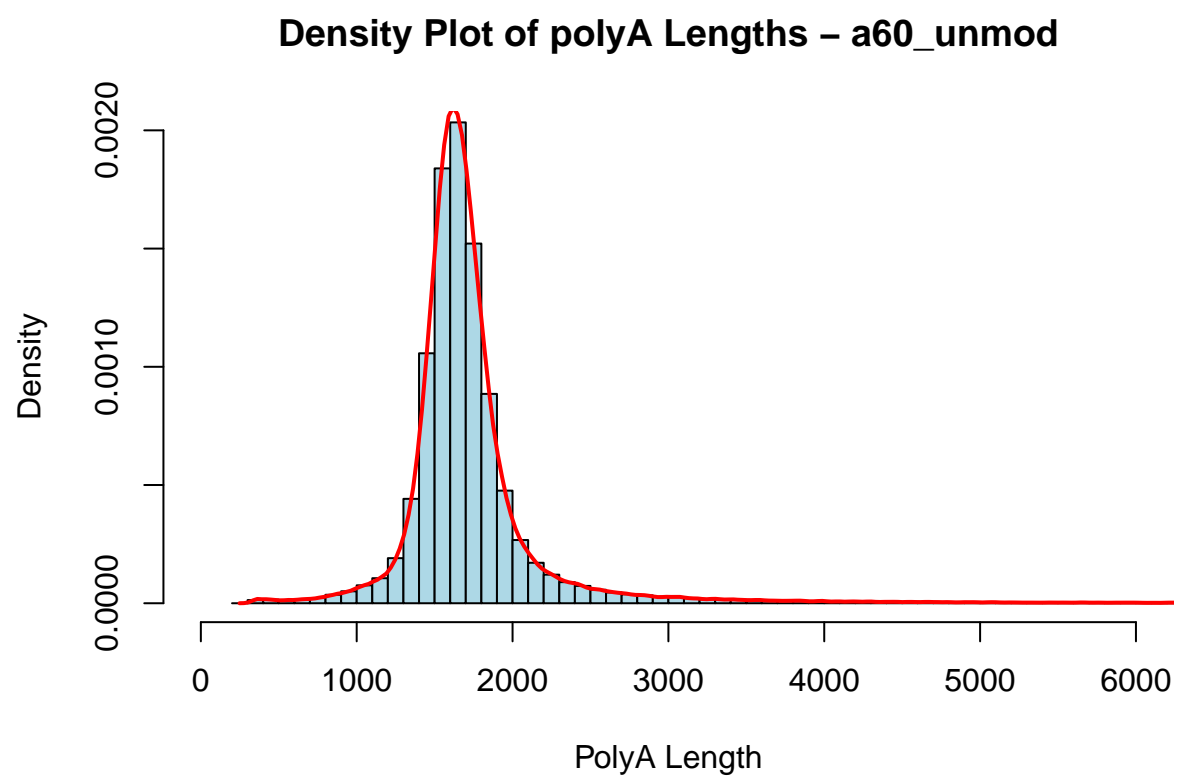
hist(polyA_length,
     probability = TRUE,
     main = paste("Density Plot of polyA Lengths -", name),
     xlab = "PolyA Length",
     ylab = "Density",
     xlim = c(0, 6000),
     ylim = c(0, 0.0020),
     border = "black",
     col = "lightblue",
     breaks = 200)

lines(density(polyA_length), col = "red", lwd = 2)
}

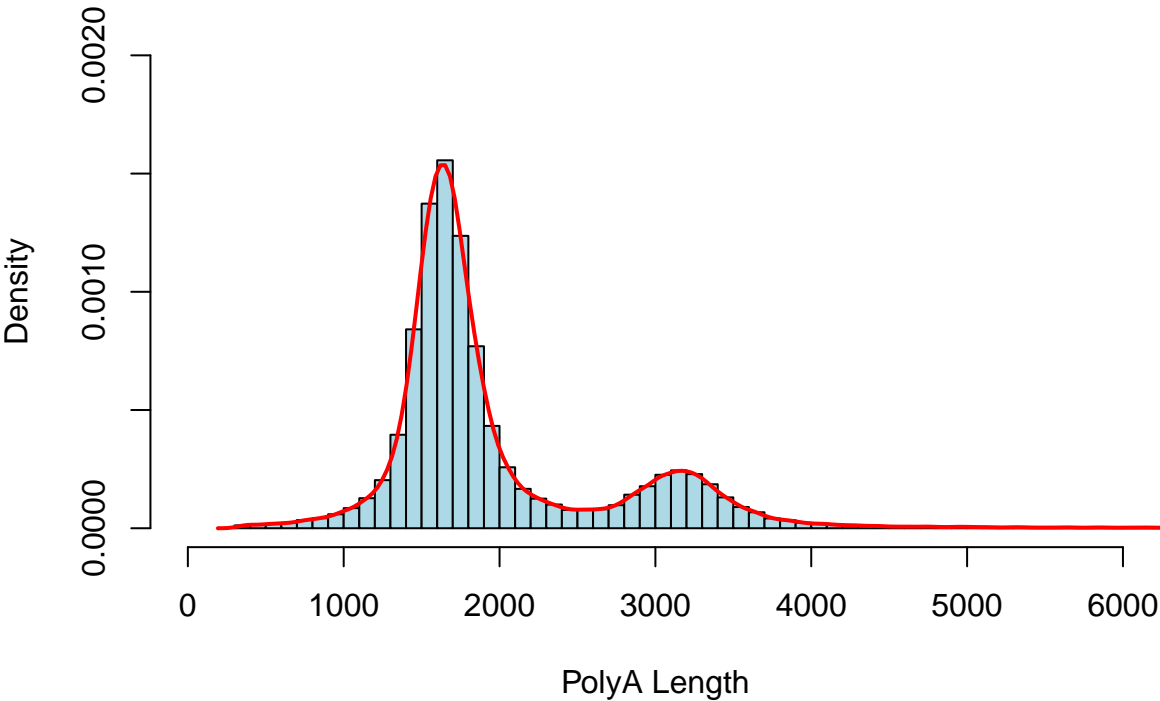
```



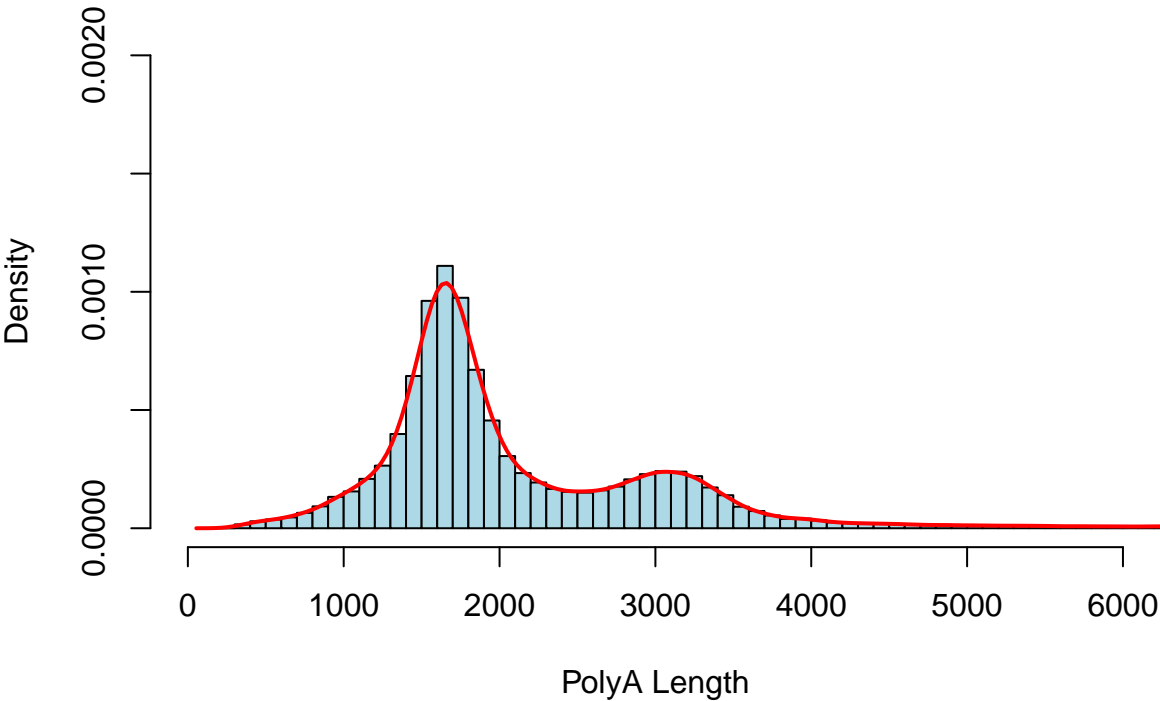




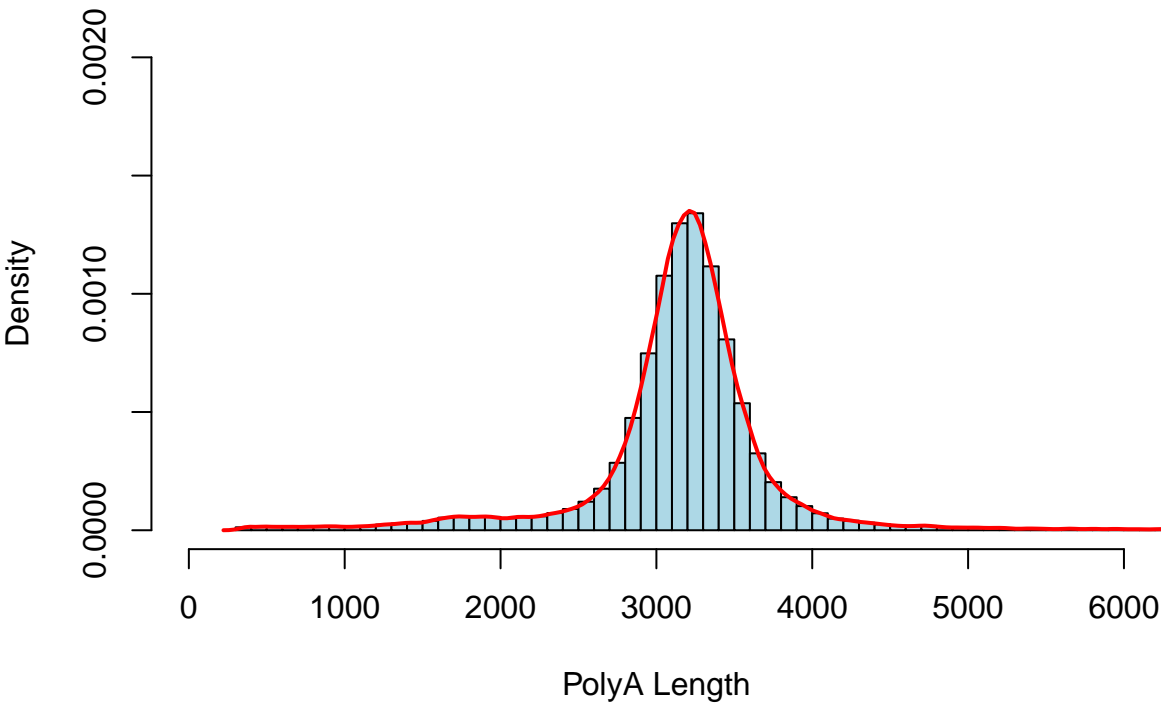
Density Plot of polyA Lengths – a120_1mod

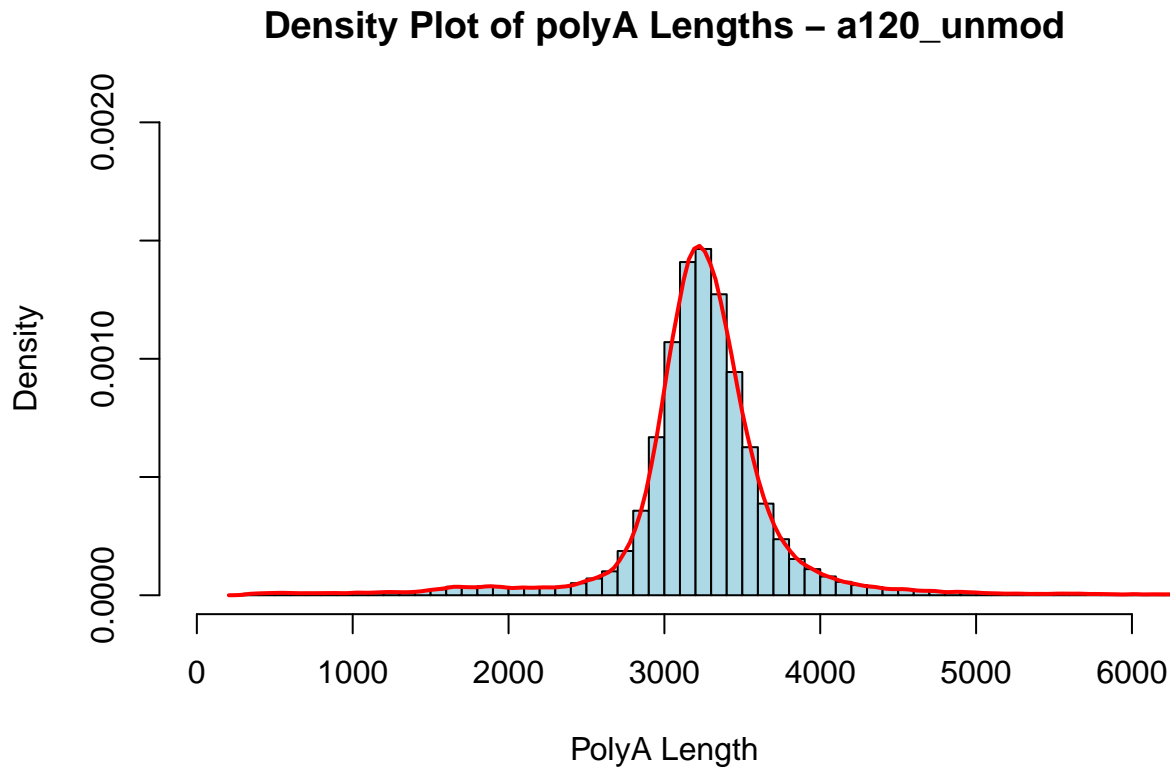


Density Plot of polyA Lengths – a120_2mod



Density Plot of polyA Lengths – a120_4mod





Histograms of all the data with log transformation

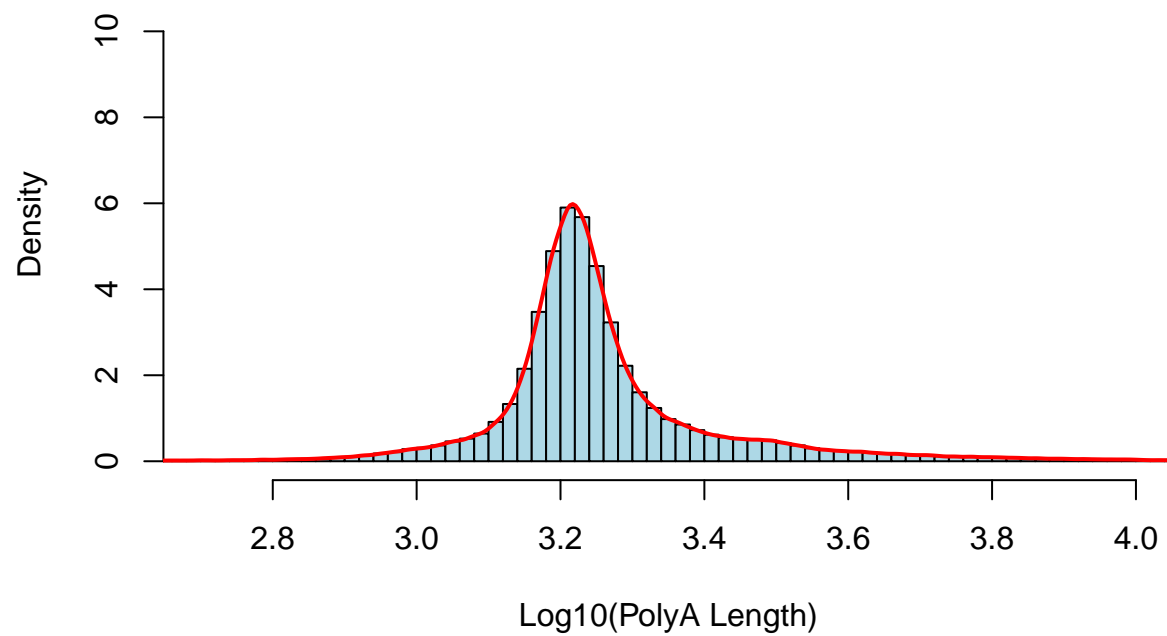
```
for (name in names(datasets)) {
  polyA_length <- datasets[[name]]$polyA_length

  log_polyA_length <- log10(polyA_length)

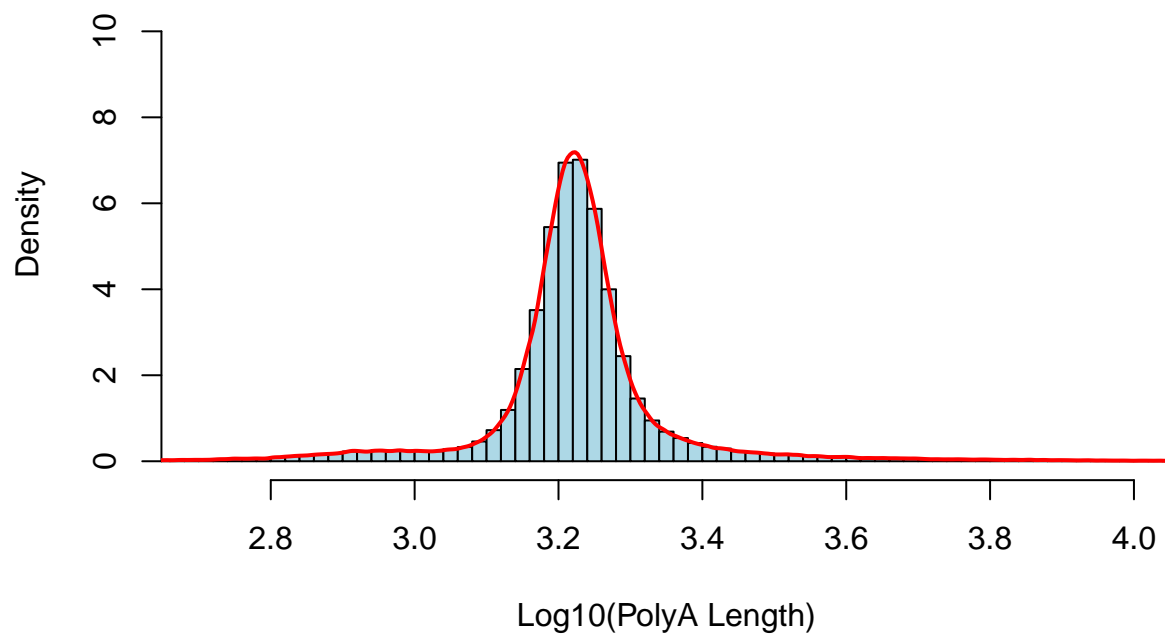
  hist(log_polyA_length,
       probability = TRUE,
       main = paste("Density Plot of log-transformed polyA Lengths -", name),
       xlab = "Log10(PolyA Length)",
       ylab = "Density",
       border = "black",
       col = "lightblue",
       xlim = c(2.7,4),
       ylim = c(0,11),
       breaks = 100)

  lines(density(log_polyA_length), col = "red", lwd = 2)
}
```

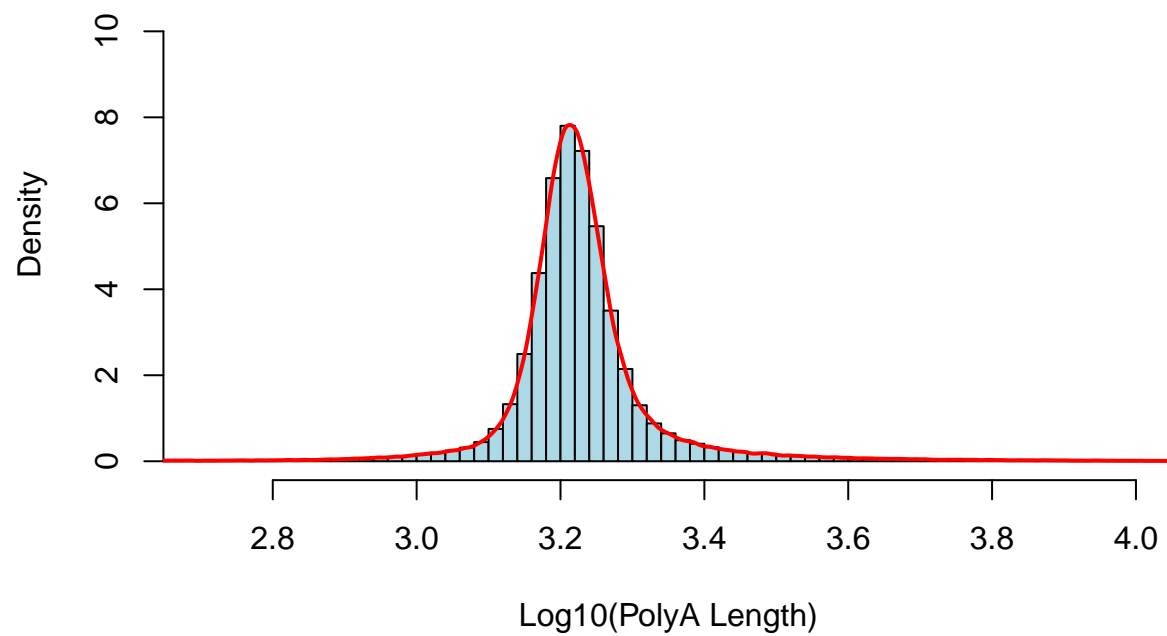

Density Plot of log-transformed polyA Lengths – a60_30



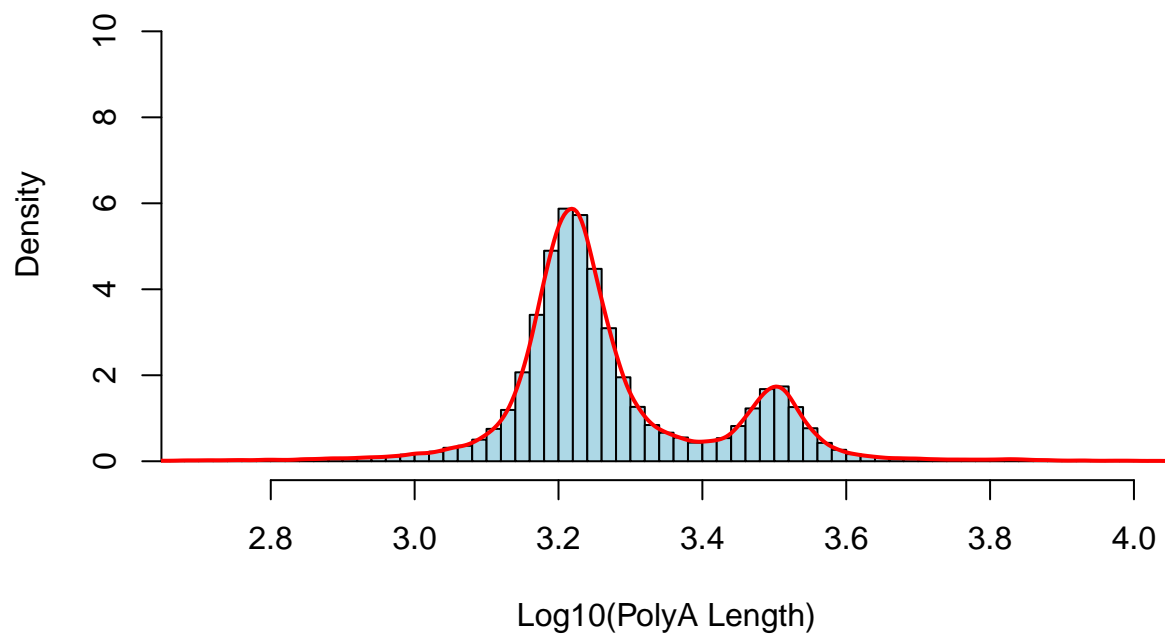
Density Plot of log-transformed polyA Lengths – a60_60



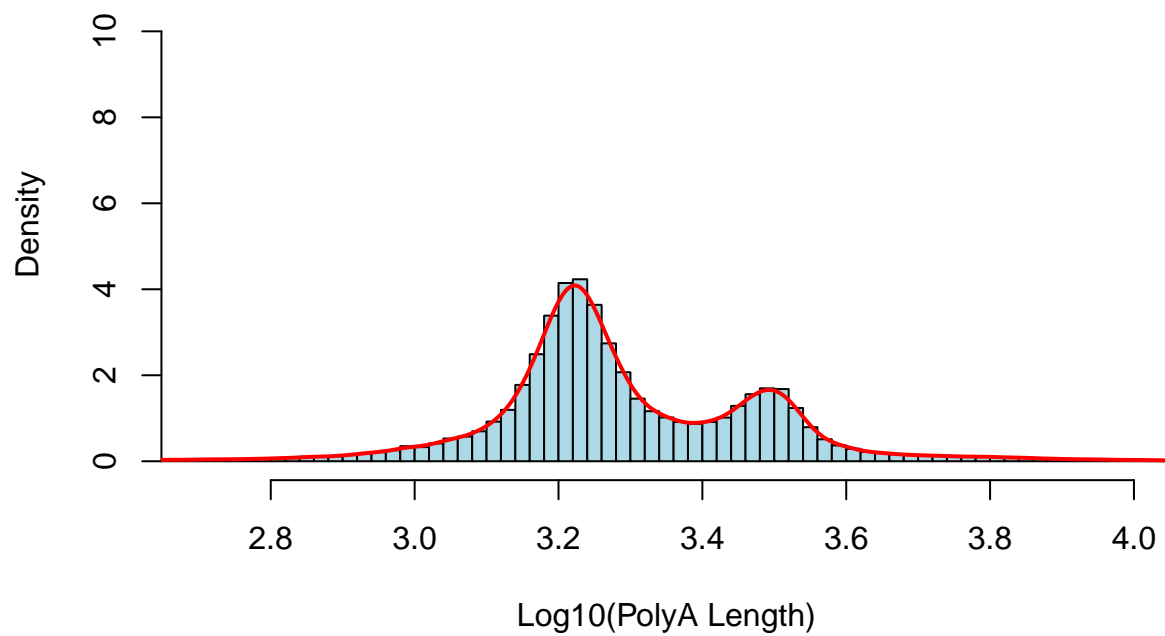
Density Plot of log-transformed polyA Lengths – a60_unmod



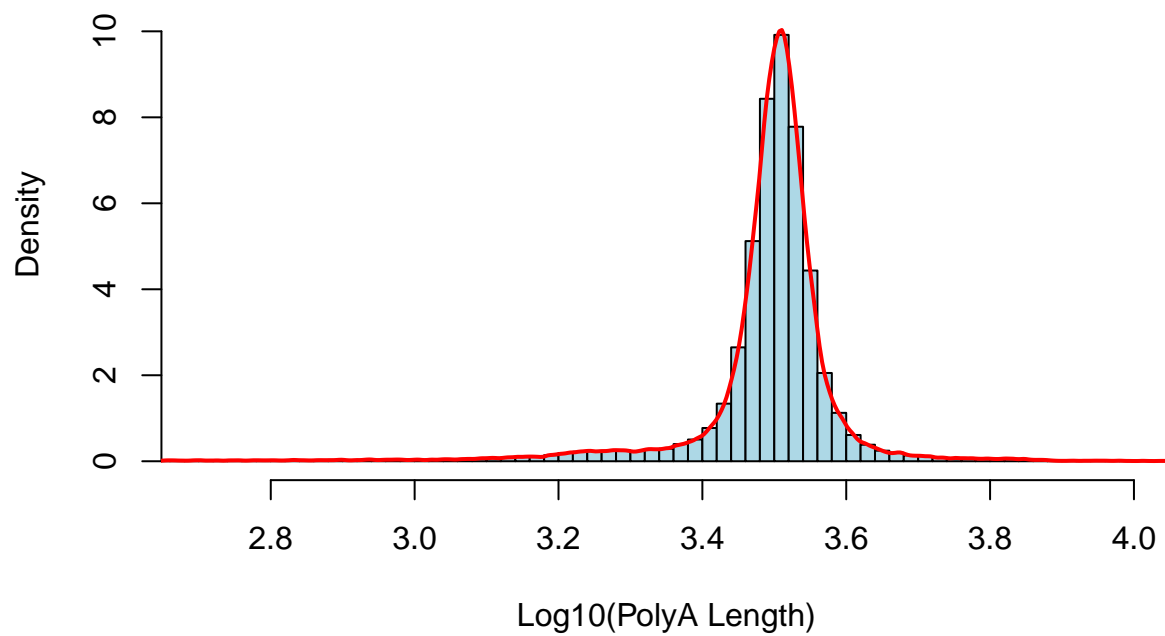
Density Plot of log-transformed polyA Lengths – a120_1mod



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

