

An Introduction to *Guitar* Package

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1 Quick Start with Guitar

This is a manual for Guitar package. The Guitar package is aimed for RNA landmark-guided transcriptomic analysis of RNA-related genomic features.

The Guitar package enables the comparison of multiple genomic features, which need to be stored in a name list. Please see the following example, which reads 1000 RNA m6A methylation sites into R for detection. Of course, in actual data analysis, features may come from multiple sets of resources.

```
library(Guitar)

## Loading required package: GenomicFeatures
## Loading required package: BiocGenerics
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:stats':
##
##   IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##   Filter, Find, Map, Position, Reduce,
##   anyDuplicated, aperm, append, as.data.frame,
##   basename, cbind, colnames, dirname, do.call,
##   duplicated, eval, evalq, get, grep, grepl,
##   intersect, is.unsorted, lapply, mapply, match,
##   mget, order, paste, pmax, pmax.int, pmin,
##   pmin.int, rank, rbind, rownames, sapply, setdiff,
##   sort, table, tapply, union, unique, unsplit,
##   which.max, which.min
## Loading required package: S4Vectors
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:utils':
##
##   findMatches
## The following objects are masked from 'package:base':
##
##   I, expand.grid, unname
## Loading required package: IRanges
## Loading required package: GenomeInfoDb
## Loading required package: GenomicRanges
## Loading required package: AnnotationDbi
```

```

## Loading required package: Biobase
## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view
##     with 'browseVignettes()'. To cite Bioconductor,
##     see 'citation("Biobase)", and for packages
##     'citation("pkgname)".
## Loading required package: rtracklayer
## Loading required package: magrittr
##
## Attaching package: 'magrittr'
## The following object is masked from 'package:GenomicRanges':
##
##     subtract
## Loading required package: ggplot2
## Loading required package: dplyr
##
## Attaching package: 'dplyr'
## The following object is masked from 'package:AnnotationDbi':
##
##     select
## The following object is masked from 'package:Biobase':
##
##     combine
## The following objects are masked from 'package:GenomicRanges':
##
##     intersect, setdiff, union
## The following object is masked from 'package:GenomeInfoDb':
##
##     intersect
## The following objects are masked from 'package:IRanges':
##
##     collapse, desc, intersect, setdiff, slice, union
## The following objects are masked from 'package:S4Vectors':
##
##     first, intersect, rename, setdiff, setequal,
##     union
## The following objects are masked from 'package:BiocGenerics':
##
##     combine, intersect, setdiff, union
## The following objects are masked from 'package:stats':
##
##     filter, lag
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
##
## Attaching package: 'Guitar'
## The following object is masked from 'package:BiocGenerics':
##
##     normalize

# genomic features imported into named list
stBedFiles <- list(system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed12.bed",

```

```
package="Guitar"))
```

With the following script, we may generate the transcriptomic distribution of genomic features to be tested, and the result will be automatically saved into a PDF file under the working directory with prefix "example". With the `GuitarPlot` function, the gene annotation can be downloaded from internet automatically with a genome assembly number provided; however, this feature requires working internet and might take a longer time. The toy Guitar coordinates generated internally should never be re-used in other real data analysis.

```
count <- GuitarPlot(txGenomeVer = "mm10",
                    stBedFiles = stBedFiles,
                    miscOutFilePrefix = NA)
```

In a more efficient protocol, in order to re-use the gene annotation and *Guitar coordinates*, you will have to build Guitar Coordinates from a *txdb* object in a separate step. The *transcriptDb* contains the gene annotation information and can be obtained in a number of ways, .e.g, download the complete gene annotation of species from UCSC automatically, which might takes a few minutes. In the following analysis, we load the *Txdb* object from a toy dataset provided with the Guitar package. Please note that this is only a very small part of the complete hg19 transcriptome, and the *Txdb* object provided with *Guitar* package should not be used in real data analysis. With a *Txdb* object that contains gene annotation information, we in the next build *Guitar coordinates*, which is essentially a bridge connects the transcriptomic landmarks and genomic coordinates.

```
txdb_file <- system.file("extdata", "mm10_toy.sqlite",
                        package="Guitar")
txdb <- loadDb(txdb_file)
guitarTxdb <- makeGuitarTxdb(txdb = txdb, txPrimaryOnly = FALSE)

## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for all tx"
## [1] "generate components for mRNA"
## [1] "generate components for lncRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "generate coverage checking ranges for mrna"
## [1] "generate coverage checking ranges for ncRNA"

# Or use gff. file to generate guitarTxdb
# Or use getTxdb() to download TxDb from internet:
# txdb <- getTxdb(txGenomeVer="hg19")
# guitarTxdb <- makeGuitarTxdb(txdb)
```

You may now generate the Guitar plot from the named list of genome-based features.

```
GuitarPlot(txTxdb = txdb,
           stBedFiles = stBedFiles,
           miscOutFilePrefix = "example")

## [1] "20231024172415"
```

```

## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for all tx"
## [1] "generate components for mRNA"
## [1] "generate components for lncRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "generate coverage checking ranges for mrna"
## [1] "generate coverage checking ranges for ncrna"
## [1] "20231024172427"
## [1] "import BED file /private/tmp/Rtmp5aNRV6/Rinst102c5177bd1dd/Guitar/extdata/m6A_mm10_exomePeak_100
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.

## [1] "start figure plotting for mrna ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.

```

```
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.

## [1] "start figure plotting for ncrna ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.
```

Alternatively, you may also optionally include the promoter DNA region and tail DNA region on the 5' and 3' side of a transcript in the plot with parameter `headOrtail = TRUE`.

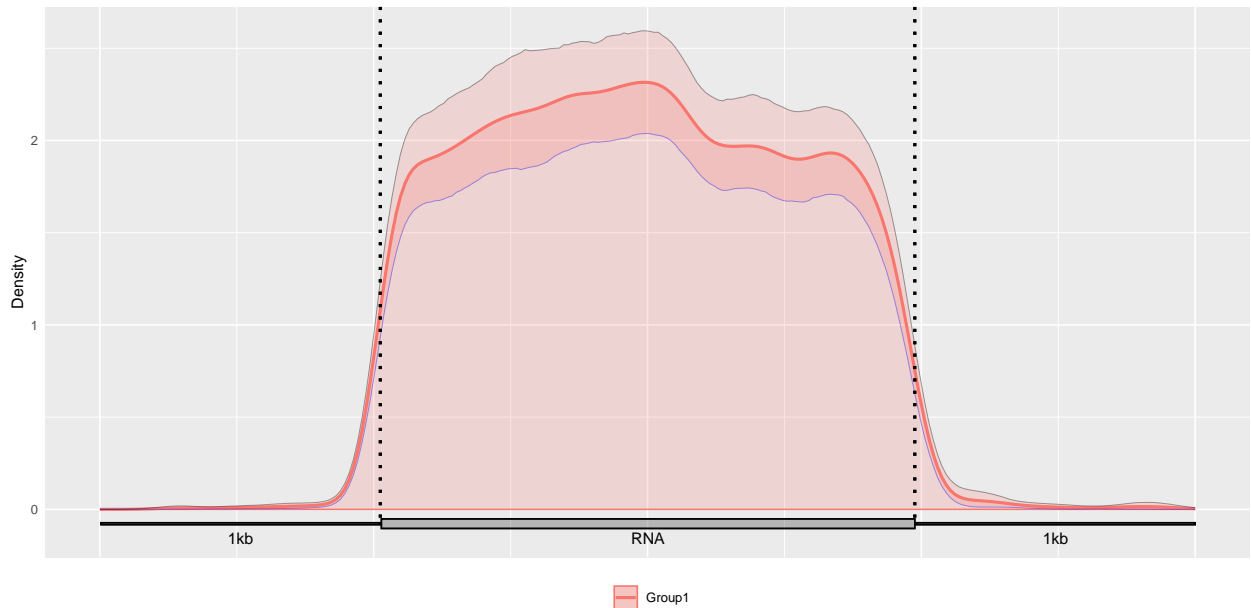
```
GuitarPlot(txTxdb = txdb,
            stBedFiles = stBedFiles,
            headOrtail = TRUE)
```

```

## [1] "20231024172455"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for all tx"
## [1] "generate components for mRNA"
## [1] "generate components for lncRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "generate coverage checking ranges for mrna"
## [1] "generate coverage checking ranges for ncrna"
## [1] "20231024172510"
## [1] "import BED file /private/tmp/Rtmp5aNRV6/Rinst102c5177bdidd/Guitar/extdata/m6A_mm10_exomePeak_100
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.

```



Alternatively, you may also optionally include the Confidence Interval for guitar plot with parameter `enableCI = FALSE`.

```
GuitarPlot(txTxdb = txdb,
           stBedFiles = stBedFiles,
           headOrtail = TRUE,
           enableCI = FALSE)

## [1] "20231024172528"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for all tx"
## [1] "generate components for mRNA"
## [1] "generate components for lncRNA"
## [1] "generate chipped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "generate coverage checking ranges for mrna"
## [1] "generate coverage checking ranges for ncrna"
## [1] "20231024172541"
## [1] "import BED file /private/tmp/Rtmp5aNRV6/Rinst102c5177bd1dd/Guitar/extdata/m6A_mm10_exomePeak_100"
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
```

```
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.
```



2 Supported Data Format

Besides BED file, Guitar package also supports GRangesList and GRanges data structures. Please see the following examples.

```
# import different data formats into a named list object.
# These genomic features are using mm10 genome assembly
stBedFiles <- list(system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed12.bed",
                             package="Guitar"),
                  system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed6.bed",
                             package="Guitar"))

# Build Guitar Coordinates
txdb_file <- system.file("extdata", "mm10_toy.sqlite",
                        package="Guitar")
txdb <- loadDb(txdb_file)

# Guitar Plot
GuitarPlot(txTxdb = txdb,
           stBedFiles = stBedFiles,
           headOrtail = TRUE,
           enableCI = FALSE,
           mapFilterTranscript = TRUE,
           pltTxType = c("mrna"),
```



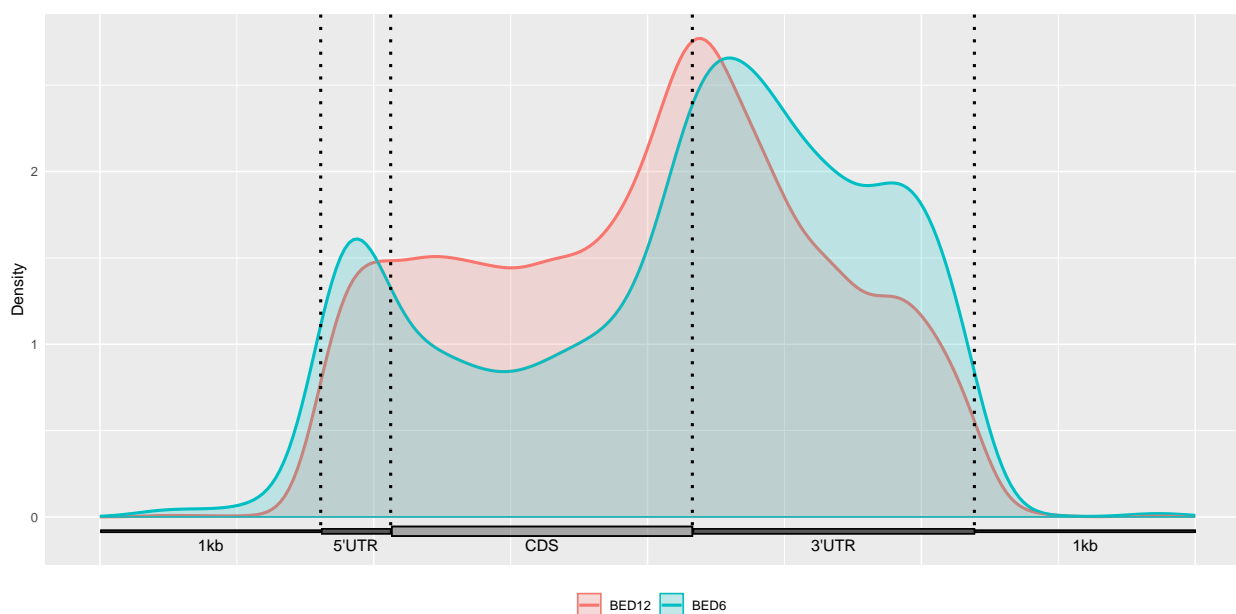
```

stGroupName = c("BED12", "BED6"))

## [1] "20231024172544"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for mRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for mrna"
## [1] "20231024172556"
## [1] "import BED file /private/tmp/Rtmp5aNRV6/Rinst102c5177bd1dd/Guitar/extdata/m6A_mm10_exomePeak_100
## [1] "import BED file /private/tmp/Rtmp5aNRV6/Rinst102c5177bd1dd/Guitar/extdata/m6A_mm10_exomePeak_100
## [1] "sample 10 points for BED12"
## [1] "sample 10 points for BED6"
## [1] "start figure plotting for mrna ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.

```



3 Processing of sampling sites information

We can select parameters for site sampling.

```
stGRangeLists = vector("list", length(stBedFiles))
sitesPoints <- list()
for (i in seq_len(length(stBedFiles))) {
  stGRangeLists[[i]] <- blocks(import(stBedFiles[[i]]))
}
for (i in seq_len(length(stGRangeLists))) {
  sitesPoints[[i]] <- samplePoints(stGRangeLists[i],
                                   stSampleNum = 10,
                                   stAmblguity = 5,
                                   pltTxType = c("mrna"),
                                   stSampleModle = "Equidistance",
                                   mapFilterTranscript = FALSE,
                                   guitarTxdb = guitarTxdb)
}
```

4 Guitar Coordinates - Transcriptomic Landmarks Projected on Genome

The guitarTxdb object contains the genome-projected transcriptome coordinates, which can be valuable for evaluating transcriptomic information related applications, such as checking the quality of MeRIP-Seq data. The Guitar coordinates are essentially the genomic projection of standardized transcript-based coordinates, making a viable bridge between the landmarks on transcript and genome-based coordinates.

It is based on the *txdb* object input, extracts the transcript information in *txdb*, selects the transcripts that match the parameters according to the component parameters set by the user, and saves according to the transcript type (tx, mrna, ncRNA).

```
guitarTxdb <- makeGuitarTxdb(txdb = txdb,
                             txAmblguity = 5,
                             txMrnaComponentProp = c(0.1,0.15,0.6,0.05,0.1),
                             txLncrnaComponentProp = c(0.2,0.6,0.2),
                             pltTxType = c("tx","mrna","ncrna"),
                             txPrimaryOnly = FALSE)

## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for all tx"
## [1] "generate components for mRNA"
## [1] "generate components for lncRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "generate coverage checking ranges for mrna"
## [1] "generate coverage checking ranges for ncRNA"
```

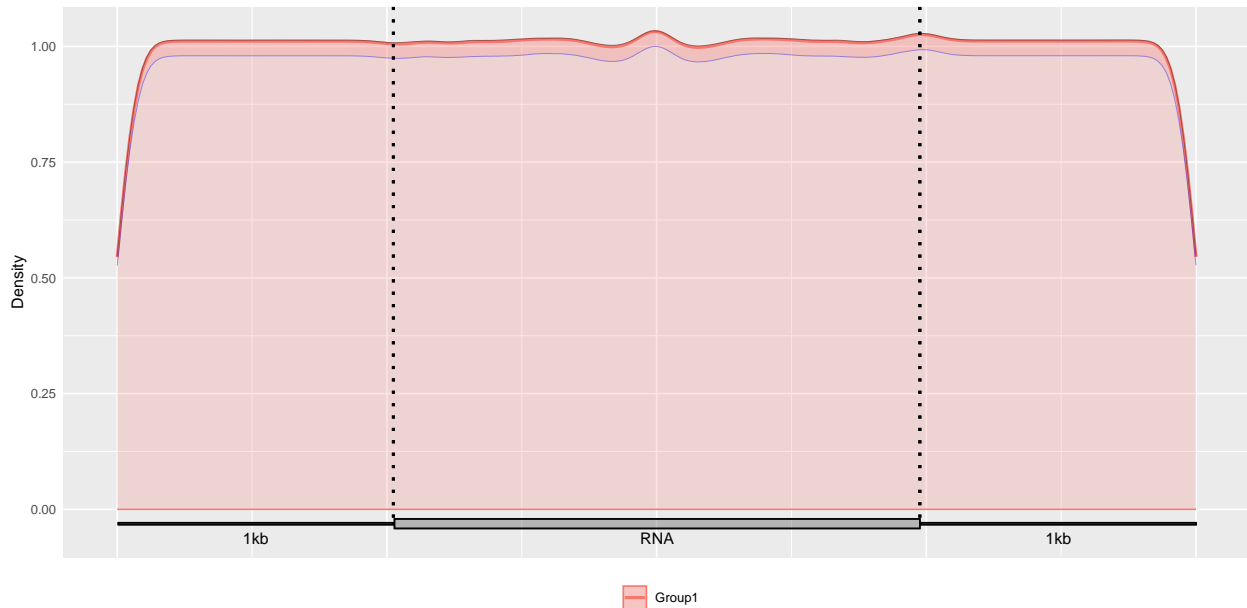
5 Check the Overlapping between Different Components

We can also check the distribution of the Guitar coordinates built.

```
gcl <- list(guitarTxdb$tx$tx)
GuitarPlot(txTxdb = txdb,
           stGRangeLists = gcl,
           stSampleNum = 200,
           enableCI = TRUE,
           pltTxType = c("tx"),
           txPrimaryOnly = FALSE
           )

## [1] "20231024172614"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for all tx"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "20231024172628"
## [1] "sample 200 points for Group1"
## [1] "start figure plotting for tx ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$confidenceDown' is discouraged.
## i Use 'confidenceDown' instead.
## Warning: Use of 'densityCI$confidenceUp' is discouraged.
## i Use 'confidenceUp' instead.
## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.
```



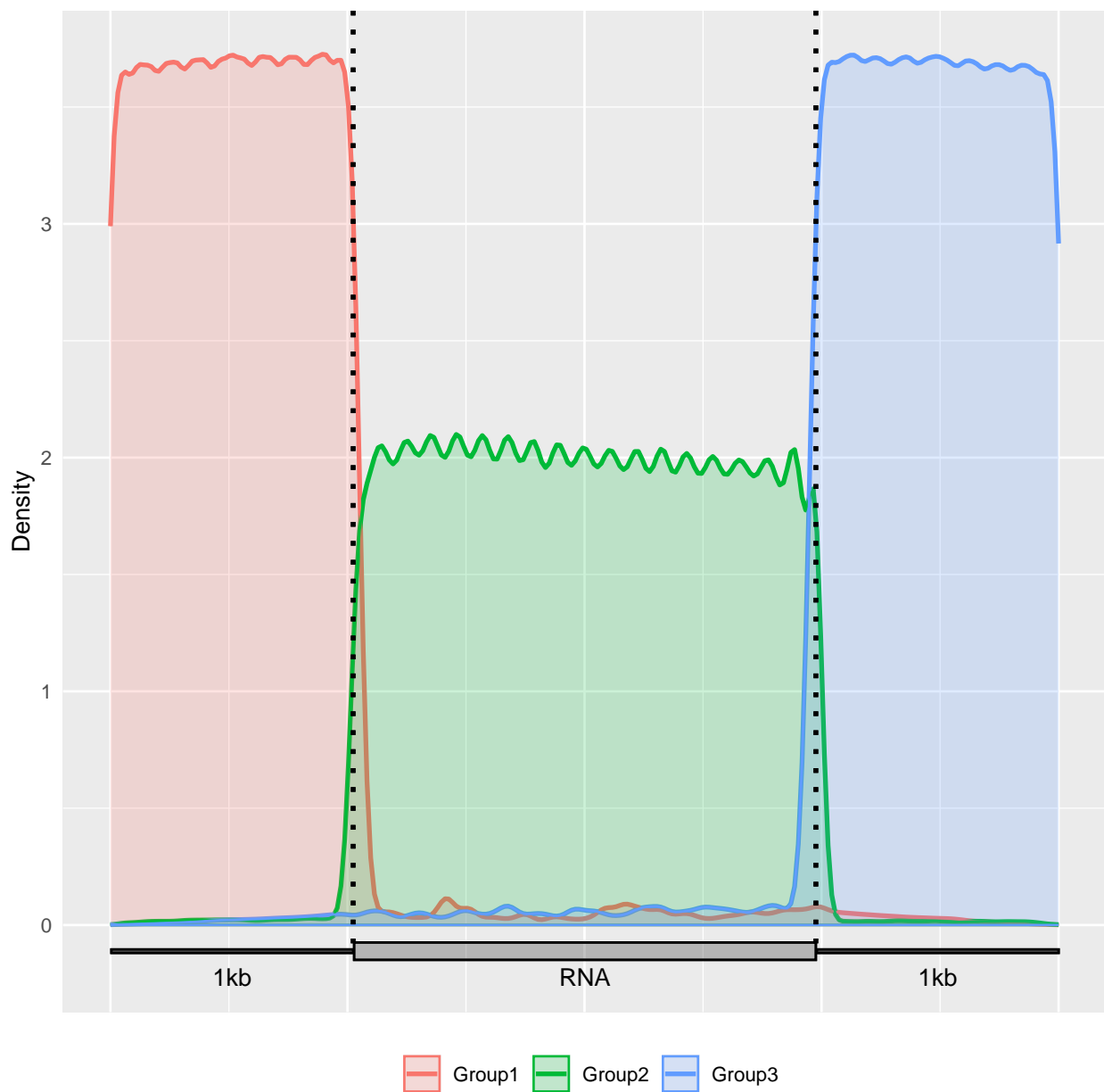
Alternatively, we can extract the RNA components, check the distribution of tx components in the transcriptome

```
GuitarCoords <- guitarTxdb$tx$txComponentGRange
type <- paste(mcols(GuitarCoords)$componentType, mcols(GuitarCoords)$txType)
key <- unique(type)
landmark <- list(1,2,3,4,5,6,7,8,9,10,11)
names(landmark) <- key
for (i in 1:length(key)) {
  landmark[[i]] <- GuitarCoords[type==key[i]]
}
GuitarPlot(txTxdb = txdb ,
            stGRangeLists = landmark[1:3],
            pltTxType = c("tx"),
            enableCI = FALSE
)
```

```
## [1] "20231024173327"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for all tx"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "20231024173341"
## [1] "sample 10 points for Group1"
## [1] "sample 10 points for Group2"
## [1] "sample 10 points for Group3"
## [1] "start figure plotting for tx ..."
```

```
## Warning: Use of 'densityCI$x' is discouraged.
```

```
## i Use 'x' instead.
## Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.
```



Check the distribution of mRNA components in the transcriptome

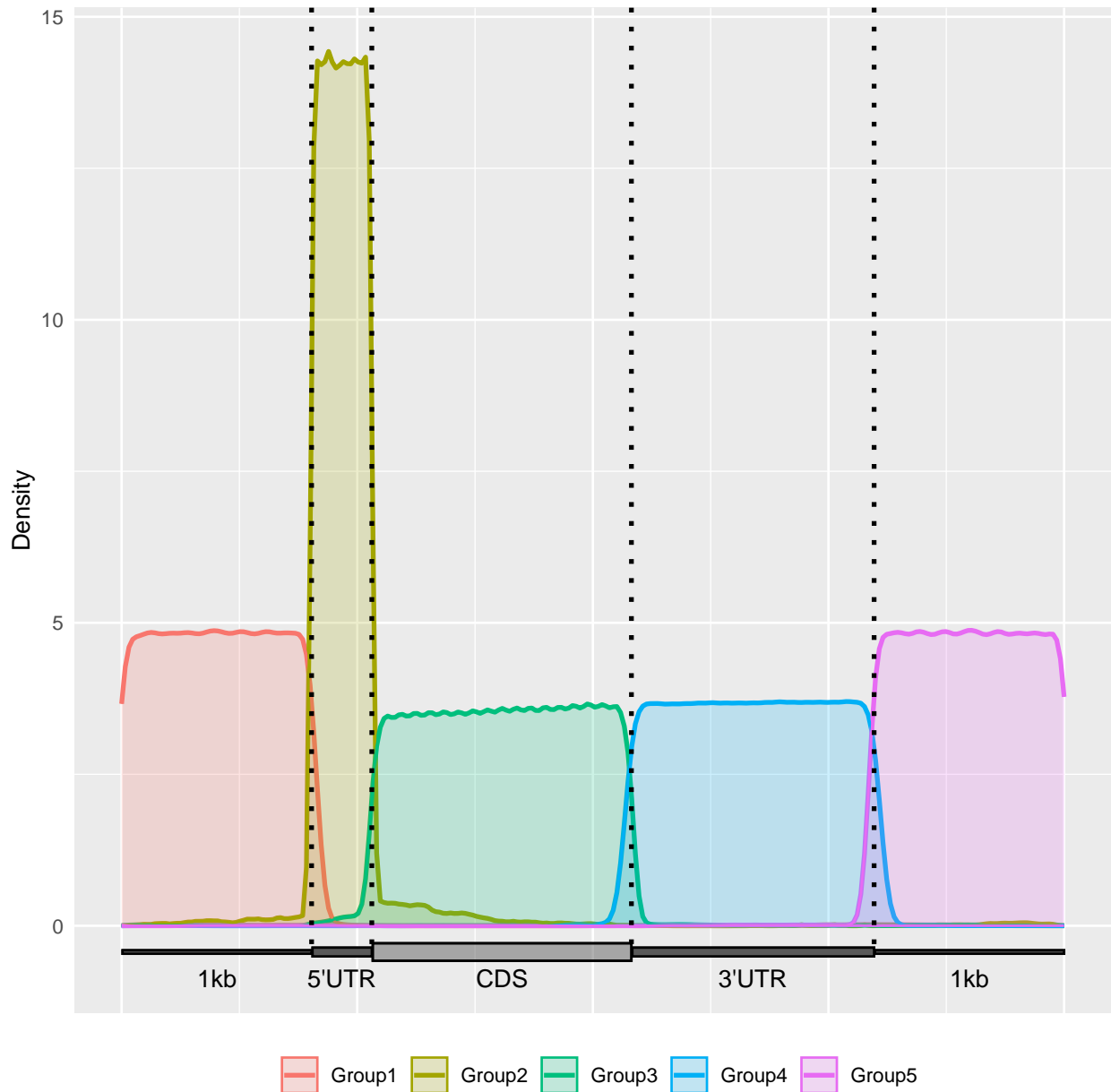
```

GuitarPlot(txTxdb = txdb ,
            stGRangeLists = landmark[4:8],
            pltTxType = c("mrna"),
            enableCI = FALSE
)

## [1] "20231024173404"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
## [1] "generate components for mRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for mrna"
## [1] "20231024173421"
## [1] "sample 10 points for Group1"
## [1] "sample 10 points for Group2"
## [1] "sample 10 points for Group3"
## [1] "sample 10 points for Group4"
## [1] "sample 10 points for Group5"
## [1] "start figure plotting for mrna ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.

```



Check the distribution of lncRNA components in the transcriptome

```
GuitarPlot(txTxdb = txdb ,
            stGRangeLists = landmark[9:11],
            pltTxType = c("ncrna"),
            enableCI = FALSE
)

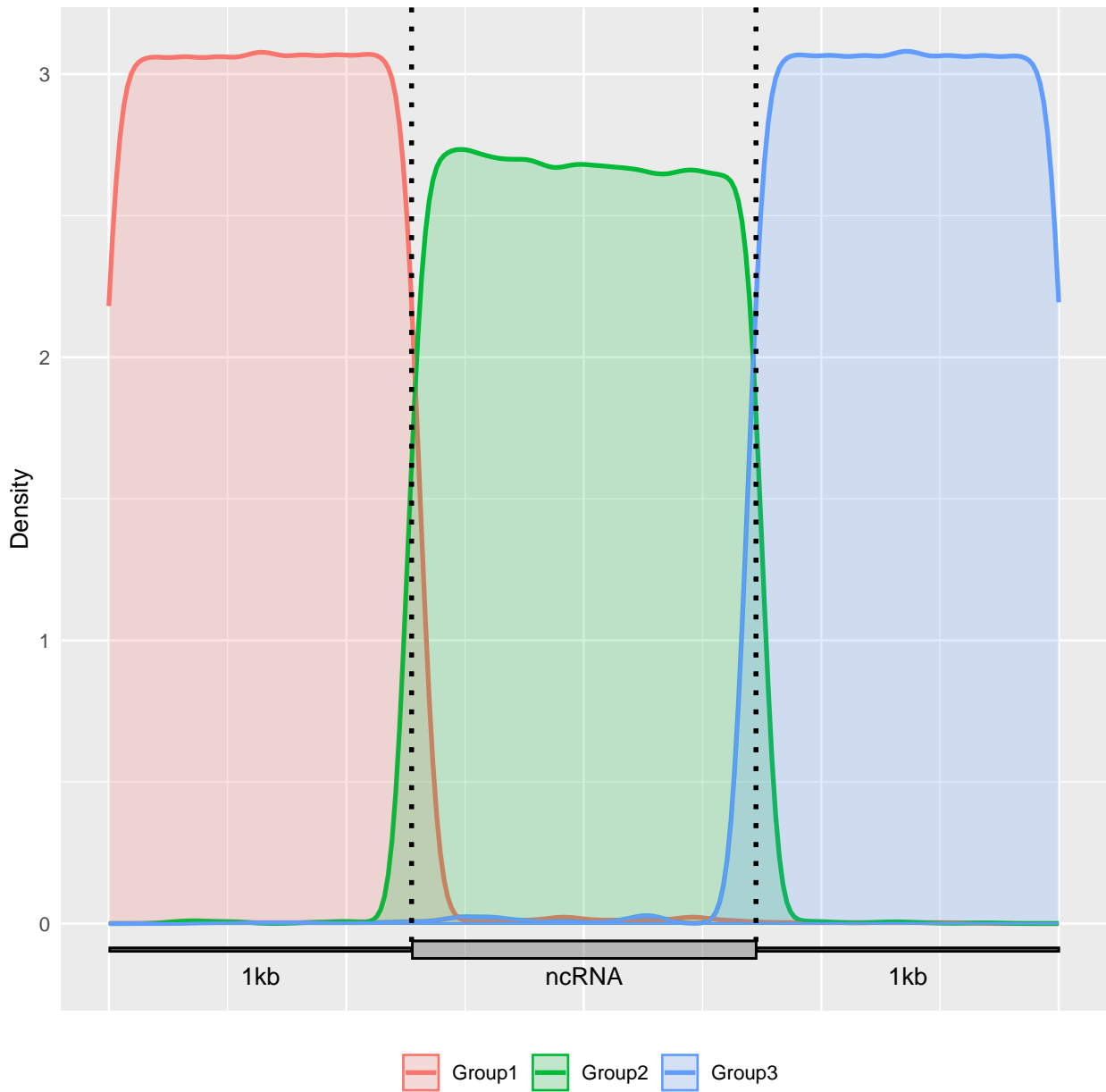
## [1] "20231024173436"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left after component length filter ..."
## [1] "total 307 ncRNAs left after ncRNA length filter ..."
```

```

## [1] "generate components for lncRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for ncrna"
## [1] "20231024173451"
## [1] "sample 10 points for Group1"
## [1] "sample 10 points for Group2"
## [1] "sample 10 points for Group3"
## [1] "start figure plotting for ncrna ..."

## Warning: Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Use of 'densityCI$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged.
## i Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged.
## i Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged.
## i Use 'y2' instead.

```

6 Session Information

```
sessionInfo()
```

```
## R version 4.3.1 Patched (2023-06-17 r84564)
```

```
## Platform: x86_64-apple-darwin20 (64-bit)
```

```
## Running under: macOS Monterey 12.6.5
```

```
##
```

```
## Matrix products: default
```

```
## BLAS: /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRblas.0.dylib
```

```
## LAPACK: /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRlapack.dylib; LAPACK v
```

```

##
## locale:
## [1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats4      stats      graphics  grDevices  utils
## [6] datasets    methods    base
##
## other attached packages:
## [1] Guitar_2.18.0      dplyr_1.1.3
## [3] ggplot2_3.4.4      magrittr_2.0.3
## [5] rtracklayer_1.62.0 GenomicFeatures_1.54.0
## [7] AnnotationDbi_1.64.0 Biobase_2.62.0
## [9] GenomicRanges_1.54.0 GenomeInfoDb_1.38.0
## [11] IRanges_2.36.0      S4Vectors_0.40.0
## [13] BiocGenerics_0.48.0 knitr_1.44
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.2.0      farver_2.1.1
## [3] blob_1.2.4            filelock_1.0.2
## [5] Biostrings_2.70.0     bitops_1.0-7
## [7] fastmap_1.1.1         RCurl_1.98-1.12
## [9] BiocFileCache_2.10.0  GenomicAlignments_1.38.0
## [11] XML_3.99-0.14         digest_0.6.33
## [13] lifecycle_1.0.3      KEGGREST_1.42.0
## [15] RSQLite_2.3.1         compiler_4.3.1
## [17] rlang_1.1.1           progress_1.2.2
## [19] tools_4.3.1           utf8_1.2.4
## [21] yaml_2.3.7            prettyunits_1.2.0
## [23] S4Arrays_1.2.0        labeling_0.4.3
## [25] bit_4.0.5             curl_5.1.0
## [27] DelayedArray_0.28.0   xml2_1.3.5
## [29] abind_1.4-5           BiocParallel_1.36.0
## [31] withr_2.5.1           grid_4.3.1
## [33] fansi_1.0.5           colorspace_2.1-0
## [35] scales_1.2.1          biomaRt_2.58.0
## [37] SummarizedExperiment_1.32.0 cli_3.6.1
## [39] crayon_1.5.2          ragg_1.2.6
## [41] generics_0.1.3        httr_1.4.7
## [43] rjson_0.2.21          DBI_1.1.3
## [45] cachem_1.0.8          stringr_1.5.0
## [47] zlibbioc_1.48.0       parallel_4.3.1
## [49] XVector_0.42.0        restfulr_0.0.15
## [51] matrixStats_1.0.0     vctrs_0.6.4
## [53] Matrix_1.6-1.1        hms_1.1.3
## [55] bit64_4.0.5           systemfonts_1.0.5
## [57] glue_1.6.2            codetools_0.2-19
## [59] stringi_1.7.12        gtable_0.3.4
## [61] BiocIO_1.12.0         munsell_0.5.0
## [63] tibble_3.2.1          pillar_1.9.0
## [65] rappdirs_0.3.3        GenomeInfoDbData_1.2.11

```

```
## [67] R6_2.5.1          dbplyr_2.3.4
## [69] textshaping_0.3.7 evaluate_0.22
## [71] lattice_0.22-5    highr_0.10
## [73] png_0.1-8         Rsamtools_2.18.0
## [75] memoise_2.0.1     SparseArray_1.2.0
## [77] xfun_0.40         MatrixGenerics_1.14.0
## [79] pkgconfig_2.0.3
```