

# 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
## Loading required package: generics
##
## Attaching package: 'generics'
## The following objects are masked from 'package:base':
##
##   as.difftime, as.factor, as.ordered, intersect,
##   is.element, setdiff, setequal, union
##
## 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,
##   is.unsorted, lapply, mapply, match, mget, order,
##   paste, pmax, pmax.int, pmin, pmin.int, rank,
##   rbind, rownames, sapply, saveRDS, table, tapply,
##   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
## Warning: multiple methods tables found for 'union'
## Warning: multiple methods tables found for 'intersect'
## Warning: multiple methods tables found for 'setdiff'
## 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, setequal, union
## The following object is masked from 'package:generics':
##
## explain

```

```
## 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] "20241118034143"
## [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] "20241118034150"
## [1] "import BED file /tmp/Rtmp1GK8WG/Rinst14a320811e1a/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_b
## [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.
```

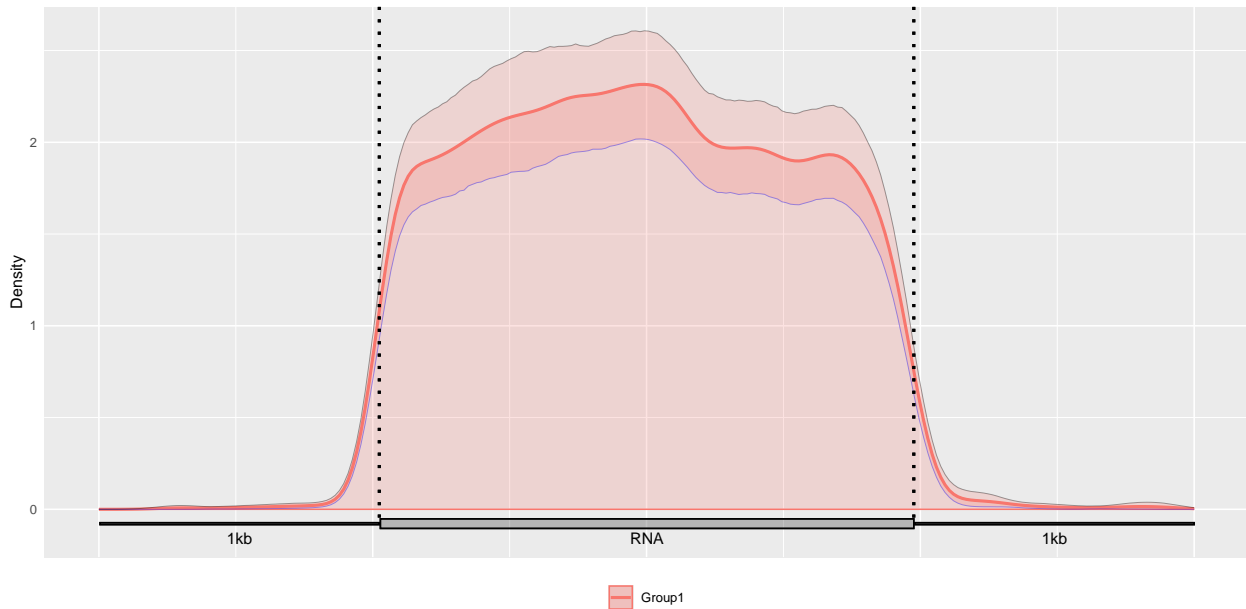
Alternatively, you may also optionally include the promoter DNA region and tail DNA region on the 5' and 3' side of a transcript in the plot with parameter `headOrtail = TRUE`.

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

## [1] "20241118034204"
## [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] "20241118034211"
## [1] "import BED file /tmp/Rtmp1GK8WG/Rinst14a320811e1a/Guitar/extdata/m6A_mm10_exomePeak_100peaks_b
## [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] "20241118034219"
## [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] "20241118034225"
## [1] "import BED file /tmp/Rtmp1GK8WG/Rinst14a320811e1a/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_b"
## [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(txdb = txdb,
           stBedFiles = stBedFiles,
```



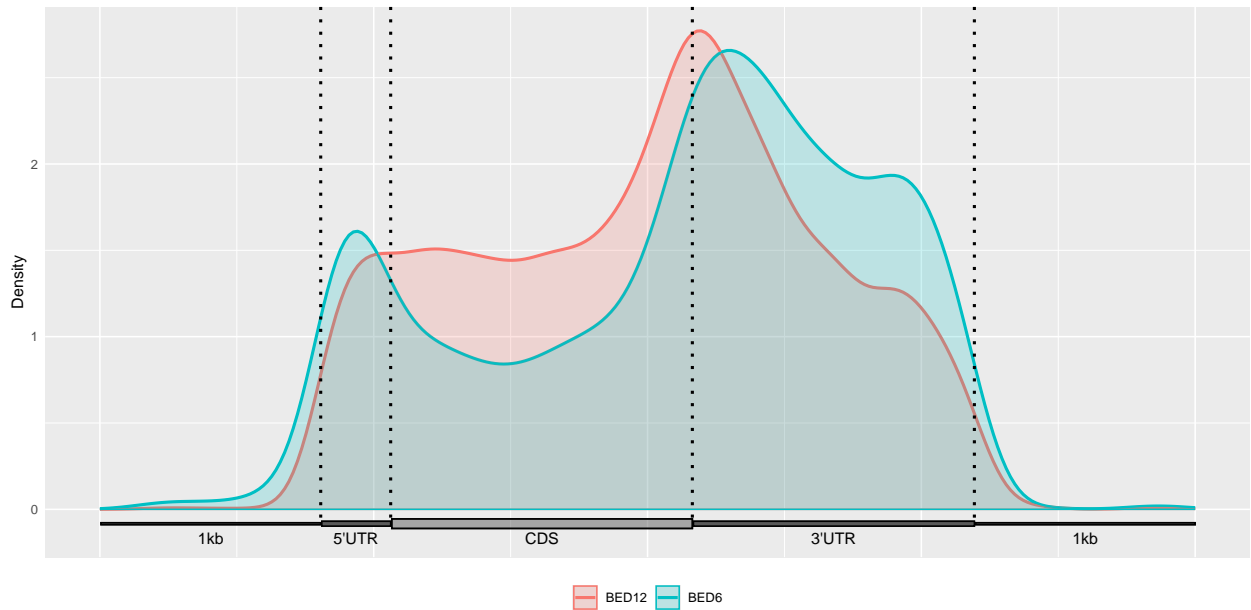
```

headOrtail = TRUE,
enableCI = FALSE,
mapFilterTranscript = TRUE,
pltTxType = c("mrna"),
stGroupName = c("BED12","BED6"))

## [1] "20241118034227"
## [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] "20241118034234"
## [1] "import BED file /tmp/Rtmp1GK8WG/Rinst14a320811e1a/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_be
## [1] "import BED file /tmp/Rtmp1GK8WG/Rinst14a320811e1a/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_be
## [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,
    stAmbiguity = 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,
                             txAmbiguity = 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.

```

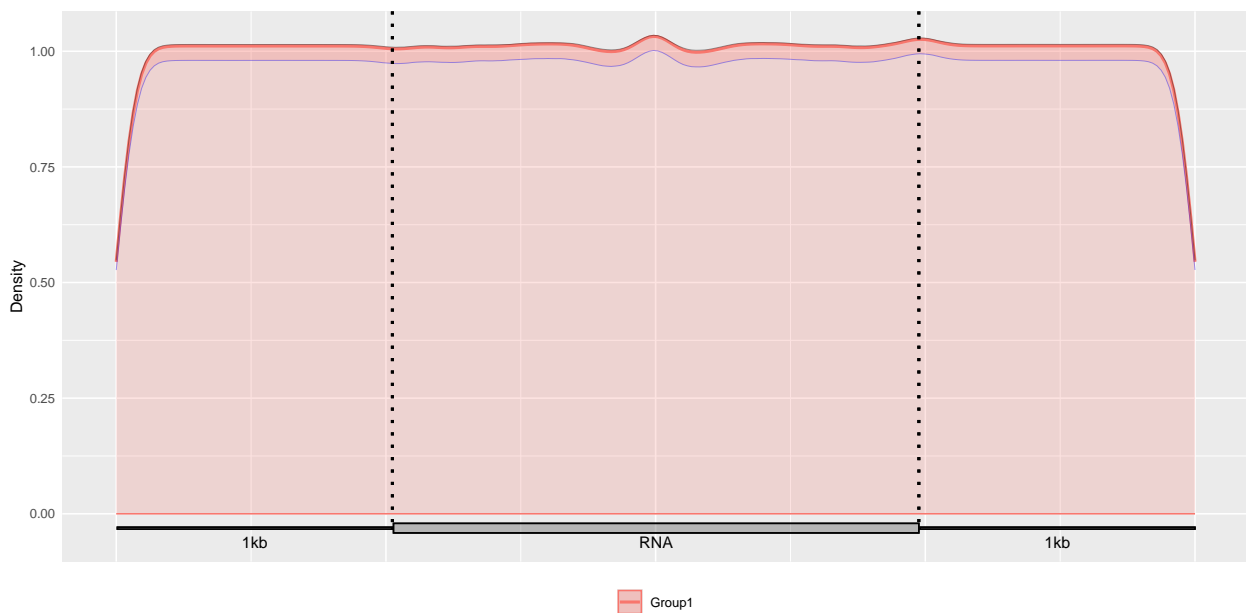
gcl <- list(guitarTxdb$tx$tx)
GuitarPlot(txTxdb = txdb,
            stGRangeLists = gcl,
            stSampleNum = 200,
            enableCI = TRUE,
            pltTxType = c("tx"),
            txPrimaryOnly = FALSE
            )

## [1] "20241118034242"
## [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] "20241118034248"
## [1] "sample 200 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, 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]]
```

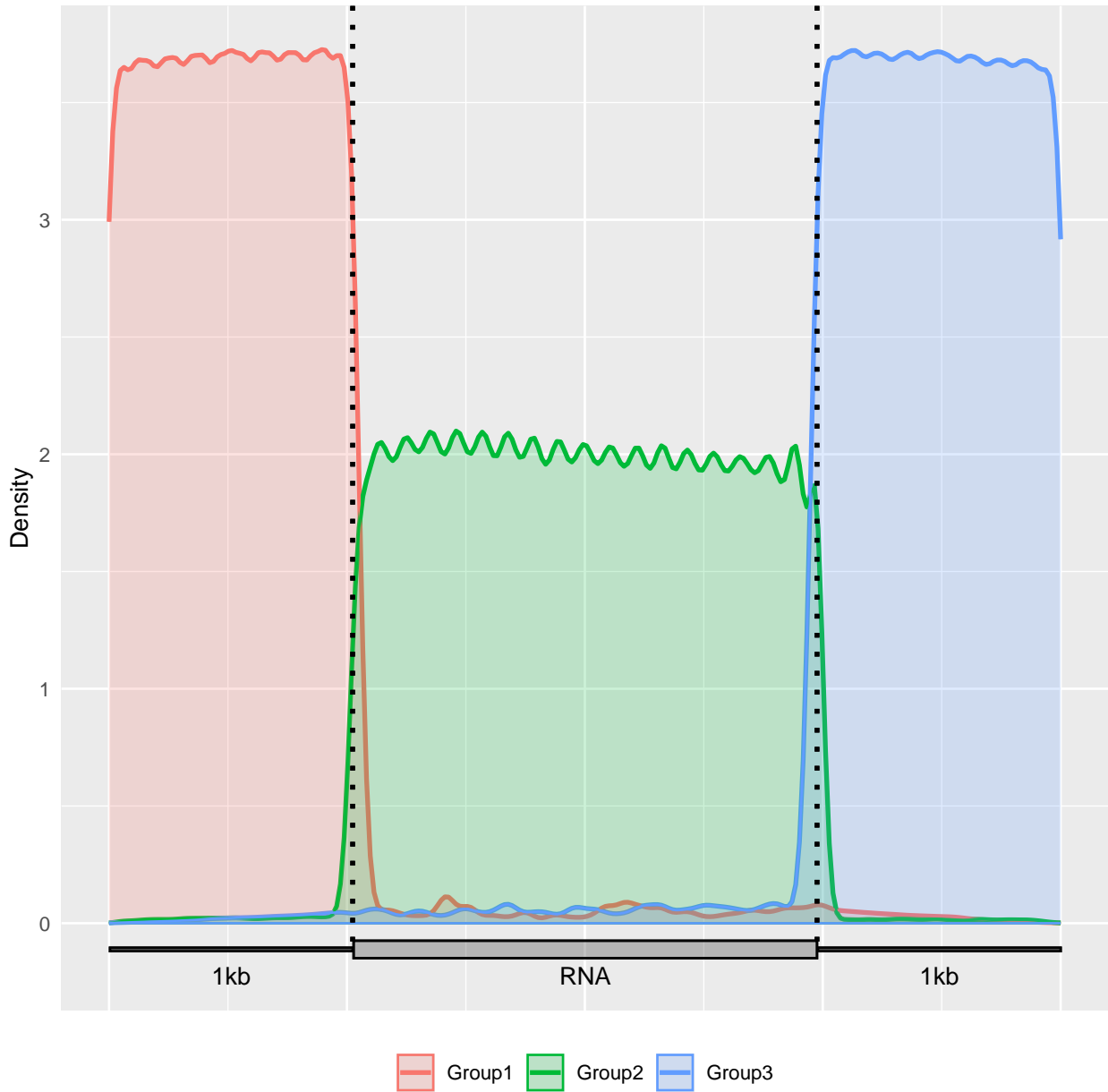
```

}
GuitarPlot(txTxdb = txdb ,
           stGRangeLists = landmark[1:3],
           pltTxType = c("tx"),
           enableCI = FALSE
)

## [1] "20241118034620"
## [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] "20241118034626"
## [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

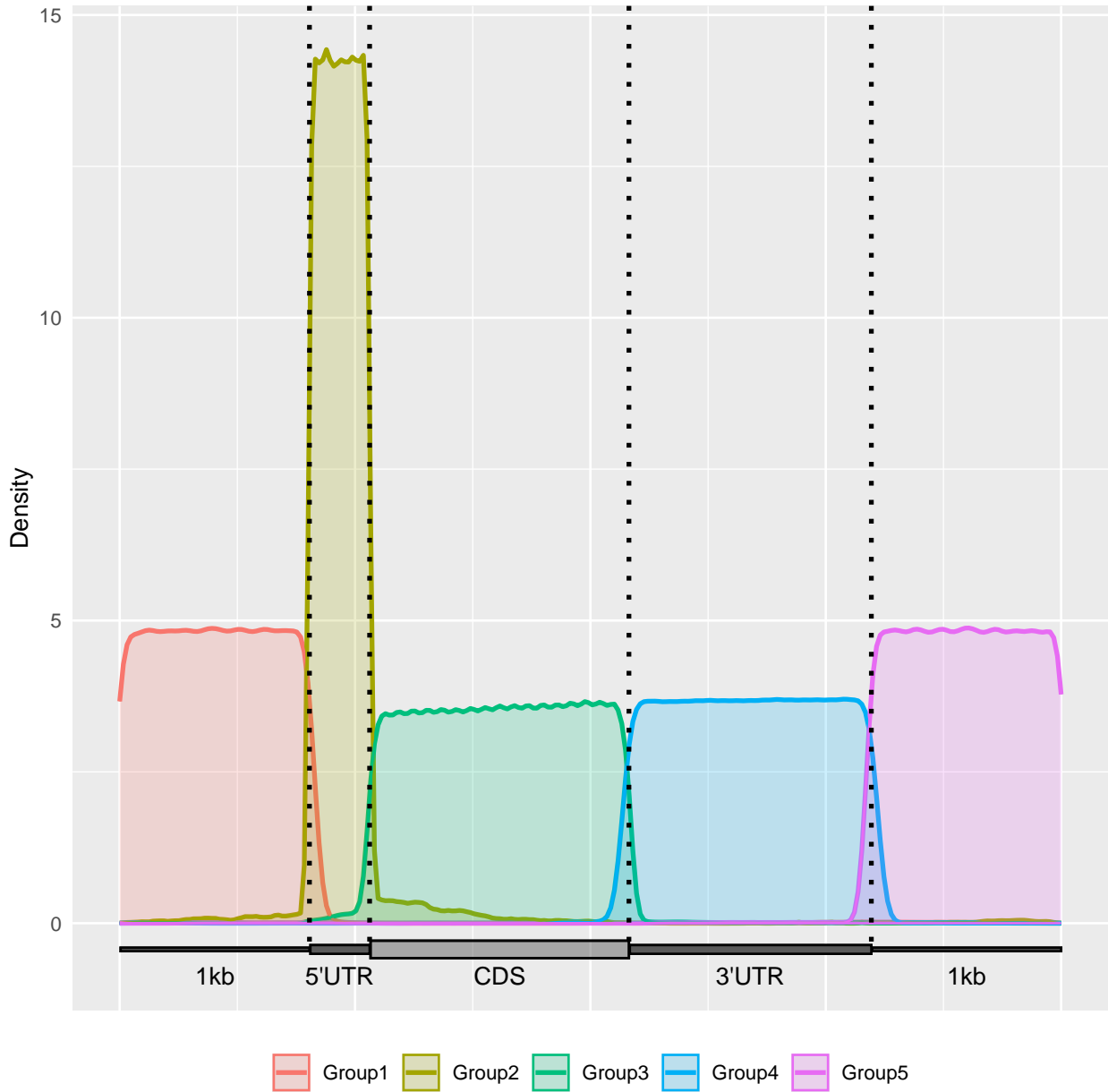
```

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

## [1] "20241118034640"
## [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 chipped transcriptome"  
## [1] "generate coverage checking ranges for mrna"  
## [1] "20241118034646"  
## [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

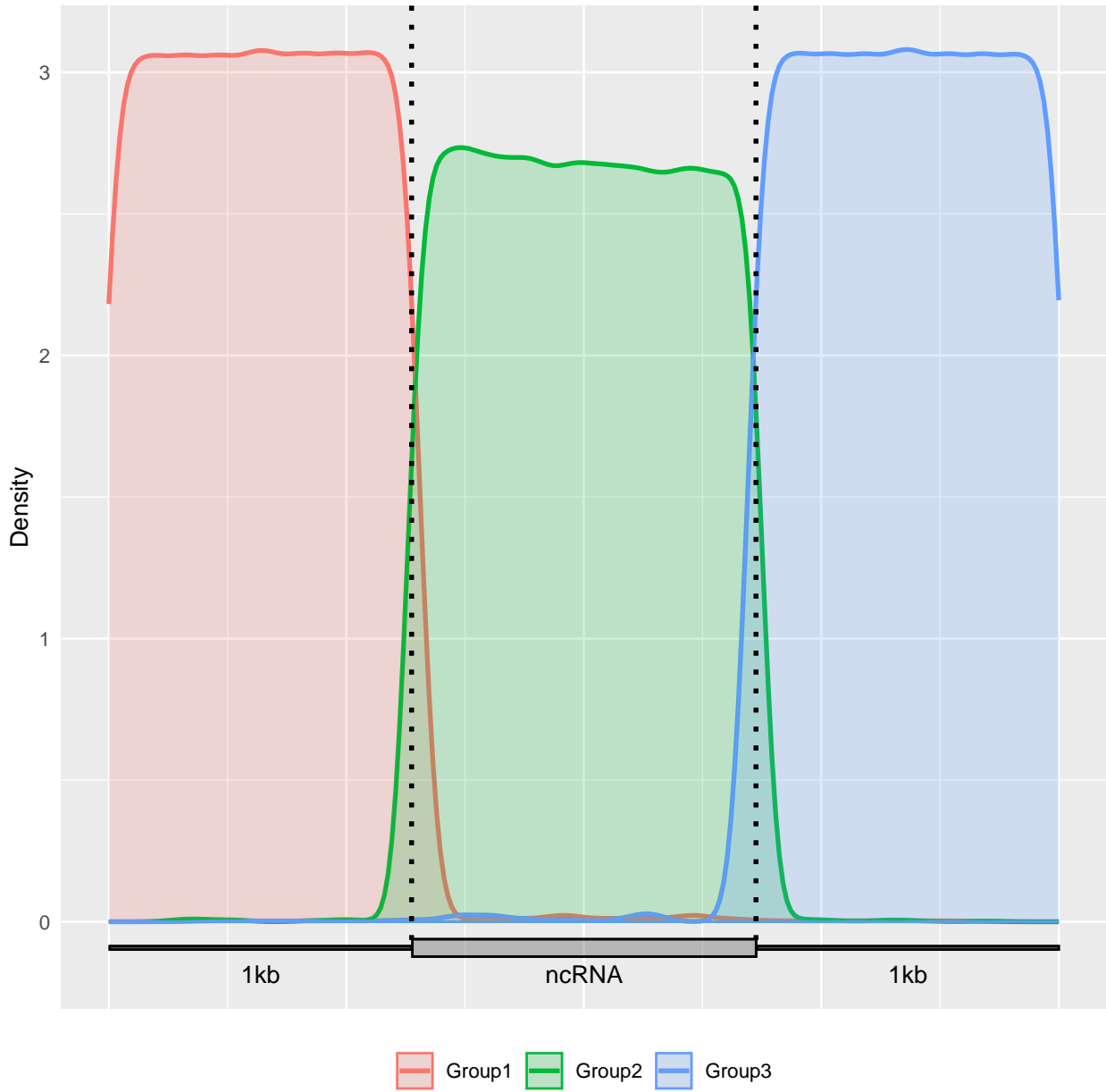
```
GuitarPlot(txTxdb = txdb ,
            stGRangeLists = landmark[9:11],
            pltTxType = c("ncrna"),
            enableCI = FALSE
)

## [1] "20241118034655"
## [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] "20241118034703"
## [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 4.4.2 (2024-10-31)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 24.04.1 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p-r0.3.26.so; LAPACK version 3.12.0

```

```

##
## locale:
## [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
## [3] LC_TIME=en_US.UTF-8       LC_COLLATE=C
## [5] LC_MONETARY=en_US.UTF-8   LC_MESSAGES=en_US.UTF-8
## [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
## [9] LC_ADDRESS=C              LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## time zone: Etc/UTC
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats4      stats      graphics  grDevices  utils
## [6] datasets   methods   base
##
## other attached packages:
## [1] Guitar_2.23.0      dplyr_1.1.4
## [3] ggplot2_3.5.1     magrittr_2.0.3
## [5] rtracklayer_1.67.0 GenomicFeatures_1.59.1
## [7] AnnotationDbi_1.69.0 Biobase_2.67.0
## [9] GenomicRanges_1.59.0 GenomeInfoDb_1.43.1
## [11] IRanges_2.41.1    S4Vectors_0.45.2
## [13] BiocGenerics_0.53.3 generics_0.1.3
## [15] knitr_1.49
##
## loaded via a namespace (and not attached):
## [1] KEGGREST_1.47.0      SummarizedExperiment_1.37.0
## [3] gtable_0.3.6        rjson_0.2.23
## [5] xfun_0.49           lattice_0.22-6
## [7] vctrs_0.6.5         tools_4.4.2
## [9] bitops_1.0-9        curl_6.0.1
## [11] parallel_4.4.2     fansi_1.0.6
## [13] tibble_3.2.1       RSQLite_2.3.8
## [15] highr_0.11         blob_1.2.4
## [17] pkgconfig_2.0.3    Matrix_1.7-1
## [19] lifecycle_1.0.4   GenomeInfoDbData_1.2.13
## [21] farver_2.1.2       compiler_4.4.2
## [23] Rsamtools_2.23.0   Biostrings_2.75.1
## [25] munsell_0.5.1     codetools_0.2-20
## [27] sys_3.4.3         buildtools_1.0.0
## [29] RCurl_1.98-1.16   yaml_2.3.10
## [31] pillar_1.9.0       crayon_1.5.3
## [33] BiocParallel_1.41.0 cachem_1.1.0
## [35] DelayedArray_0.33.2 abind_1.4-8
## [37] tidyselect_1.2.1   restfulr_0.0.15
## [39] labeling_0.4.3     maketools_1.3.1
## [41] fastmap_1.2.0      grid_4.4.2
## [43] colorspace_2.1-1  cli_3.6.3
## [45] SparseArray_1.7.2  S4Arrays_1.7.1
## [47] utf8_1.2.4        XML_3.99-0.17
## [49] withr_3.0.2       UCSC.utils_1.3.0
## [51] scales_1.3.0      bit64_4.5.2
## [53] XVector_0.47.0    httr_1.4.7

```

```
## [55] matrixStats_1.4.1      bit_4.5.0
## [57] png_0.1-8                memoise_2.0.1
## [59] evaluate_1.0.1          BiocIO_1.17.0
## [61] rlang_1.1.4             glue_1.8.0
## [63] DBI_1.2.3               jsonlite_1.8.9
## [65] R6_2.5.1                MatrixGenerics_1.19.0
## [67] GenomicAlignments_1.43.0  zlibbioc_1.52.0
```