

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, 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 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 chipped 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] "20220501164050"
## [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] "20220501164100"
## [1] "import BED file /tmp/RtmpV9qX2k/Rinst2583337ecac019/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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

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

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

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

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

```

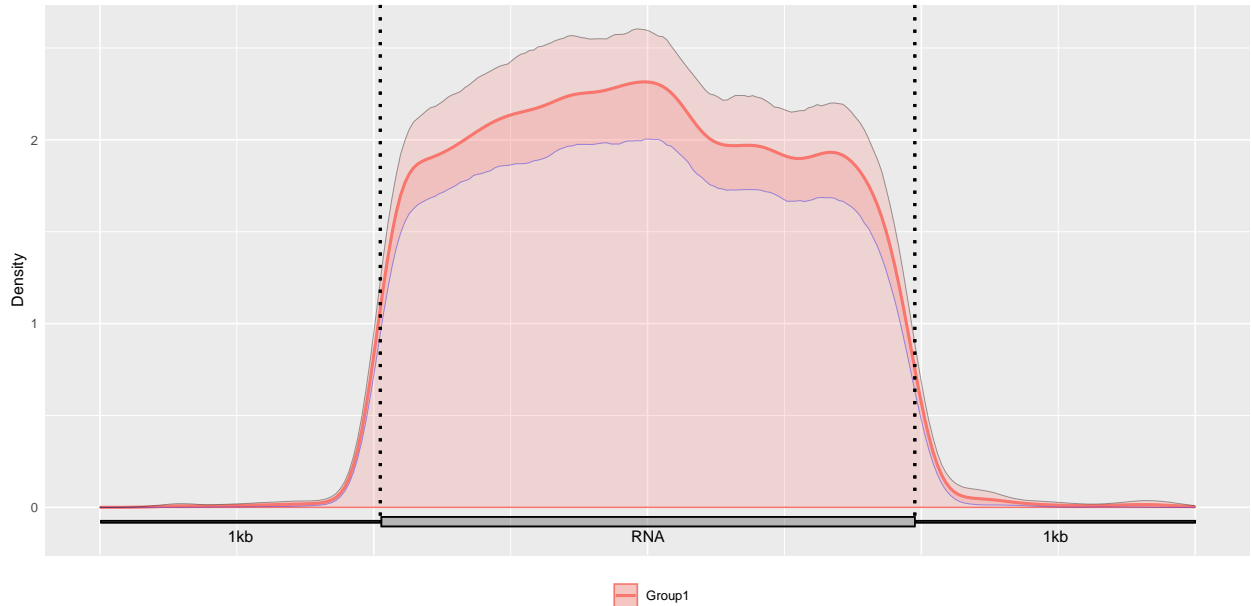
```
## Warning: Use of 'vline_pos$x1' is discouraged. Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged. Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged. Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged. Use 'y2' instead.
```

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] "20220501164127"
## [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] "20220501164137"
## [1] "import BED file /tmp/RtmpV9qX2k/Rinst2583337ecac019/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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

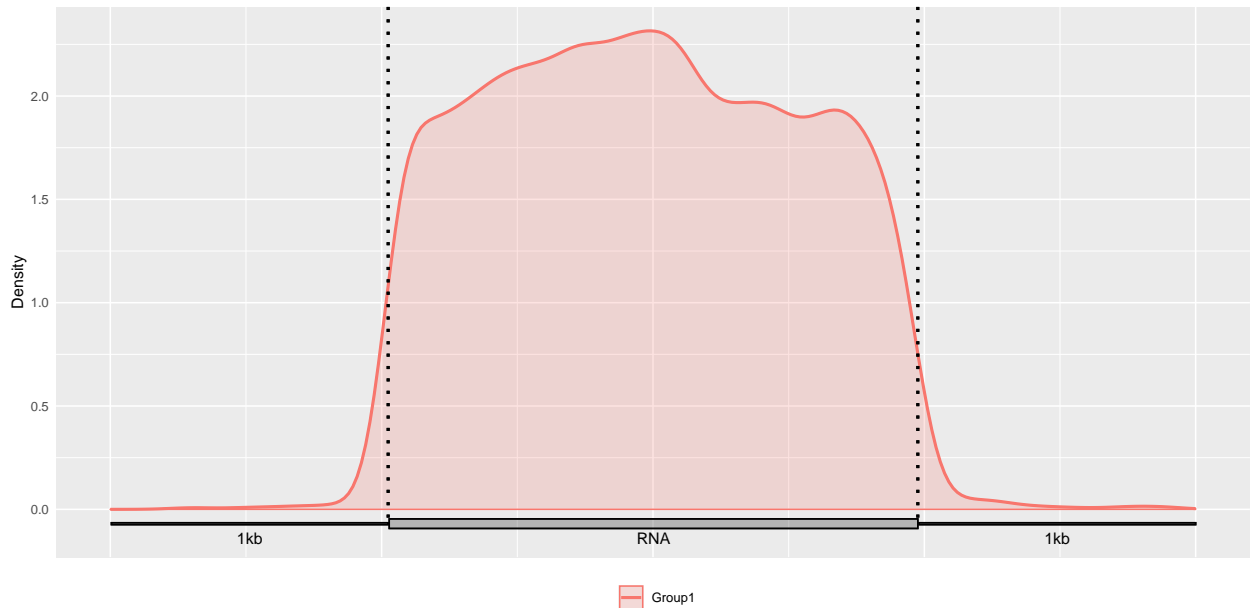


Alternatively, you may also optionally include the Confidence Interval for guitar plot with parameter `enableCI = FALSE`.

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

## [1] "20220501164157"
## [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] "20220501164208"
## [1] "import BED file /tmp/RtmpV9qX2k/Rinst2583337ecac019/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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



2 Supported Data Format

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

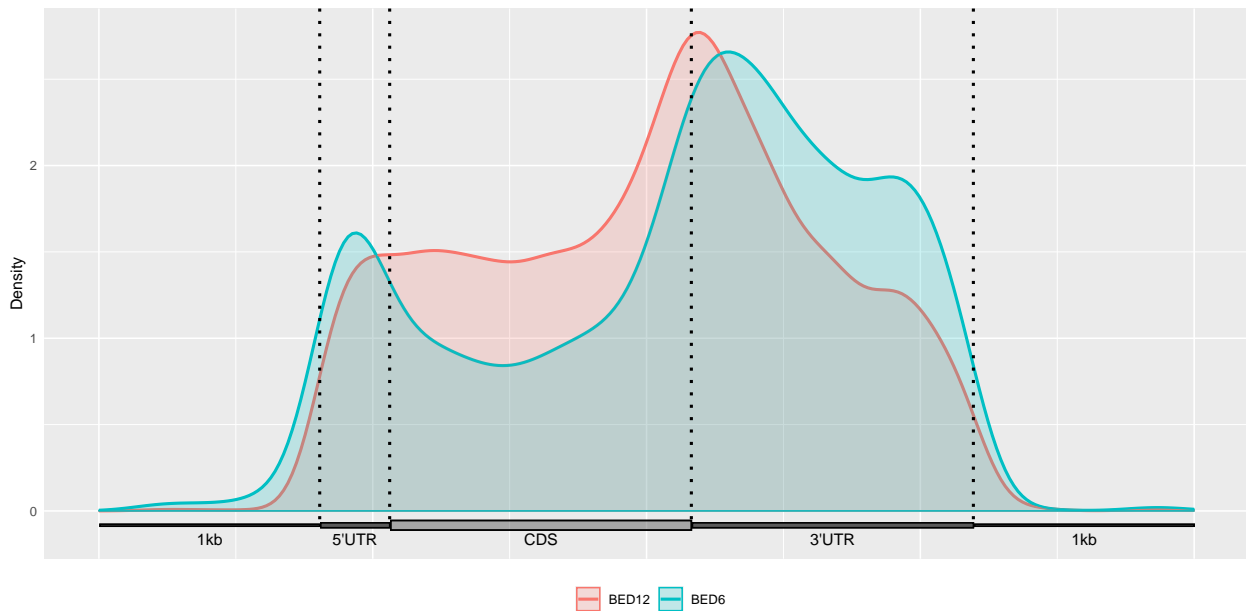
```
# import different data formats into a named list object.
# These genomic features are using mm10 genome assembly
stBedFiles <- list(system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed12.bed",
                             package="Guitar"),
                  system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed6.bed",
                             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] "20220501164210"
## [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] "20220501164220"
## [1] "import BED file /tmp/RtmpV9qX2k/Rinst2583337ecac019/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "import BED file /tmp/RtmpV9qX2k/Rinst2583337ecac019/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "sample 10 points for BED12"
## [1] "sample 10 points for BED6"
## [1] "start figure plotting for mrna ..."

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

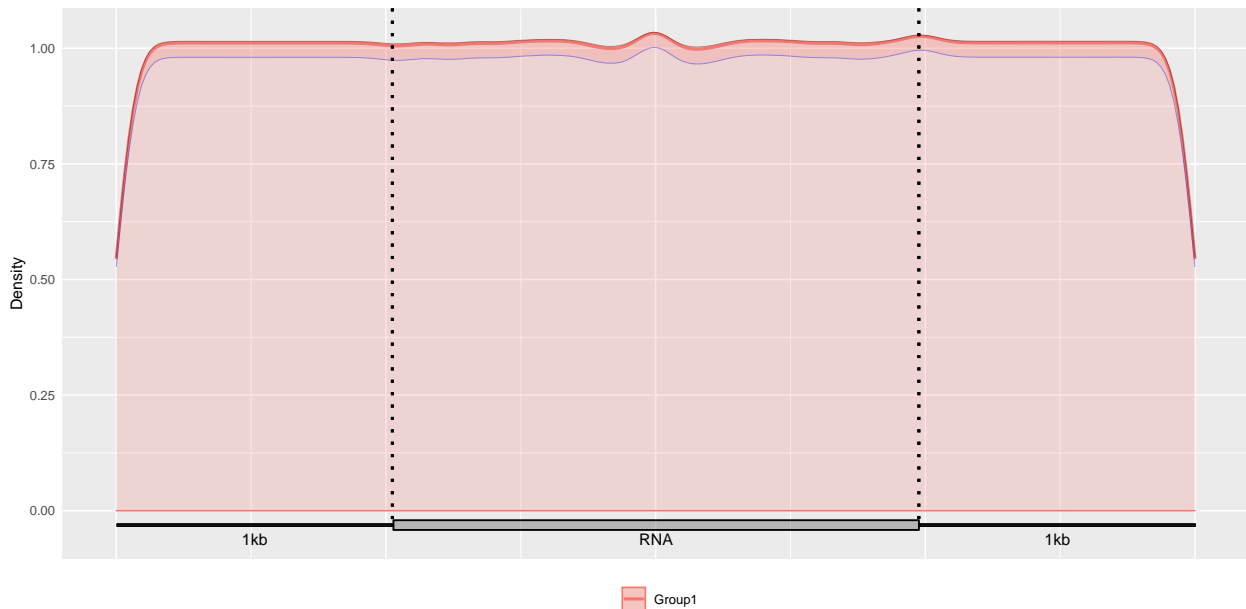
```

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

```

```
## [1] "20220501164235"
## [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 chipped transcriptome"
## [1] "generate coverage checking ranges for tx"
## [1] "20220501164245"
## [1] "sample 200 points for Group1"
## [1] "start figure plotting for tx ..."

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

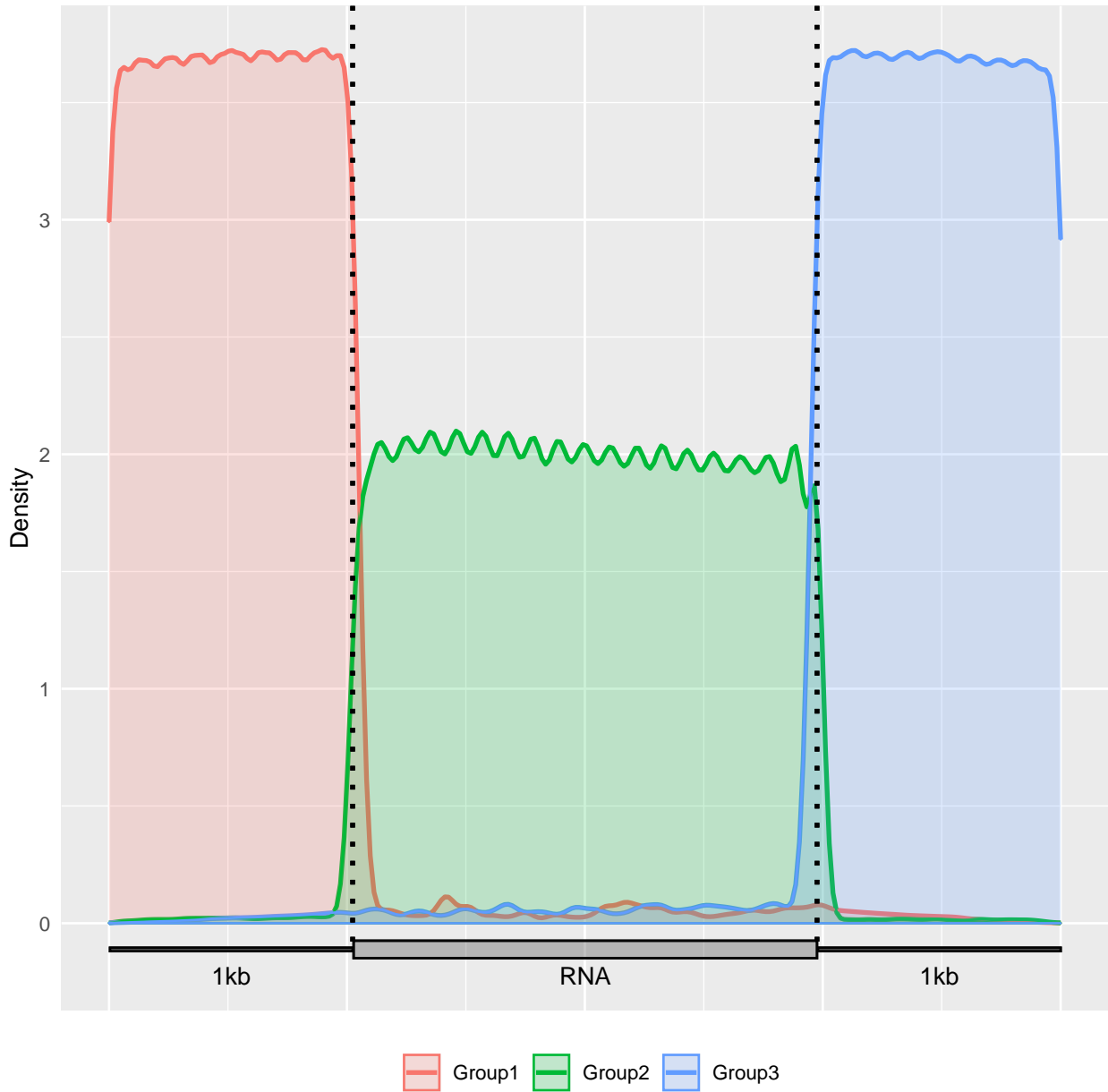
```

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] "20220501165007"
## [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] "20220501165016"
## [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$x' is discouraged. Use 'x' instead.
## Use of 'densityCI$x' is discouraged. Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged. Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged. Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged. Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged. Use 'y2' instead.

```

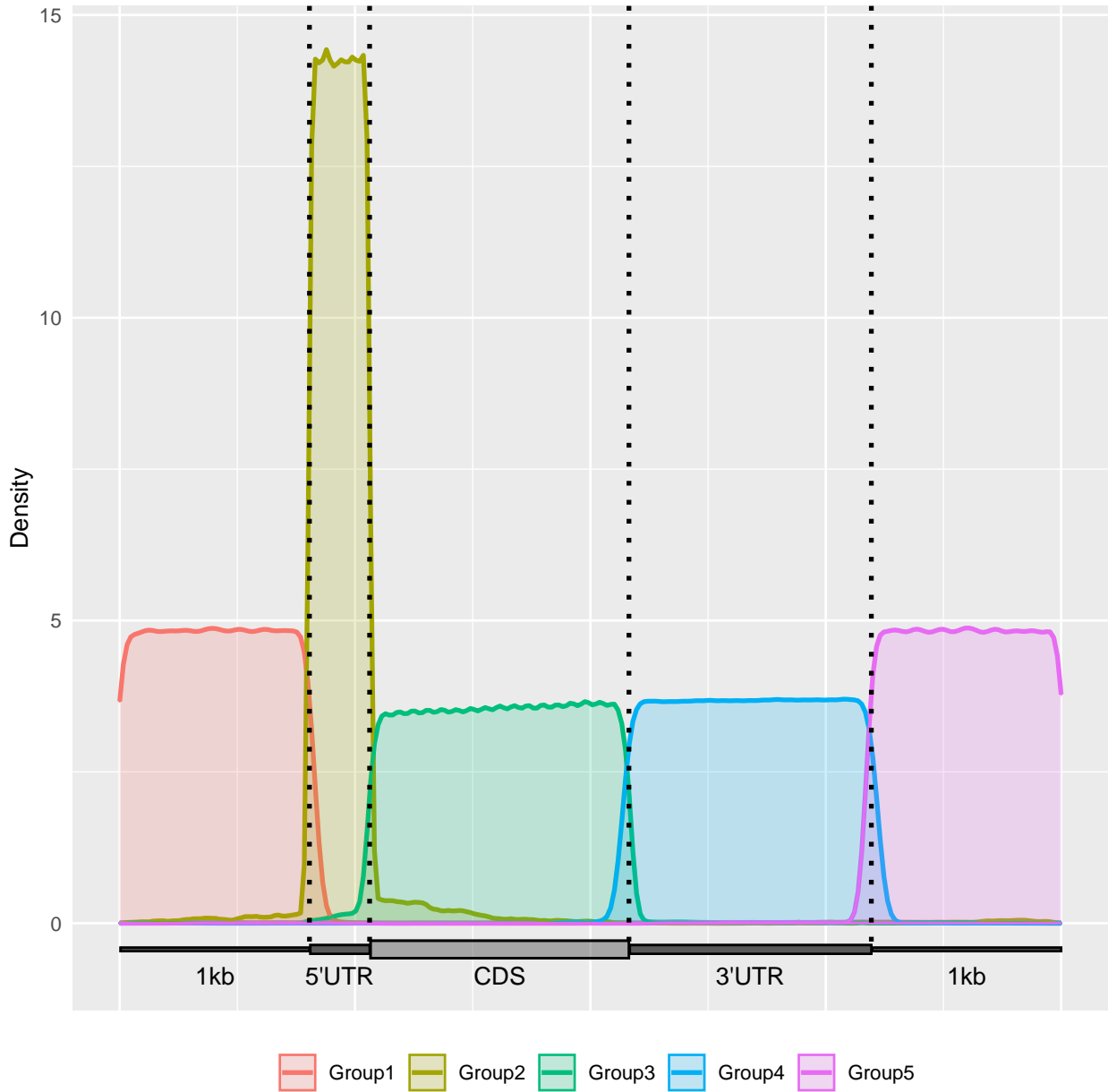


Check the distribution of mRNA components in the transcriptome

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

## [1] "20220501165036"
## [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] "20220501165045"  
## [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$x' is discouraged. Use 'x' instead.  
## Use of 'densityCI$x' is discouraged. Use 'x' instead.  
## Warning: Use of 'vline_pos$x1' is discouraged. Use 'x1' instead.  
## Warning: Use of 'vline_pos$y1' is discouraged. Use 'y1' instead.  
## Warning: Use of 'vline_pos$x2' is discouraged. Use 'x2' instead.  
## Warning: Use of 'vline_pos$y2' is discouraged. Use 'y2' instead.
```



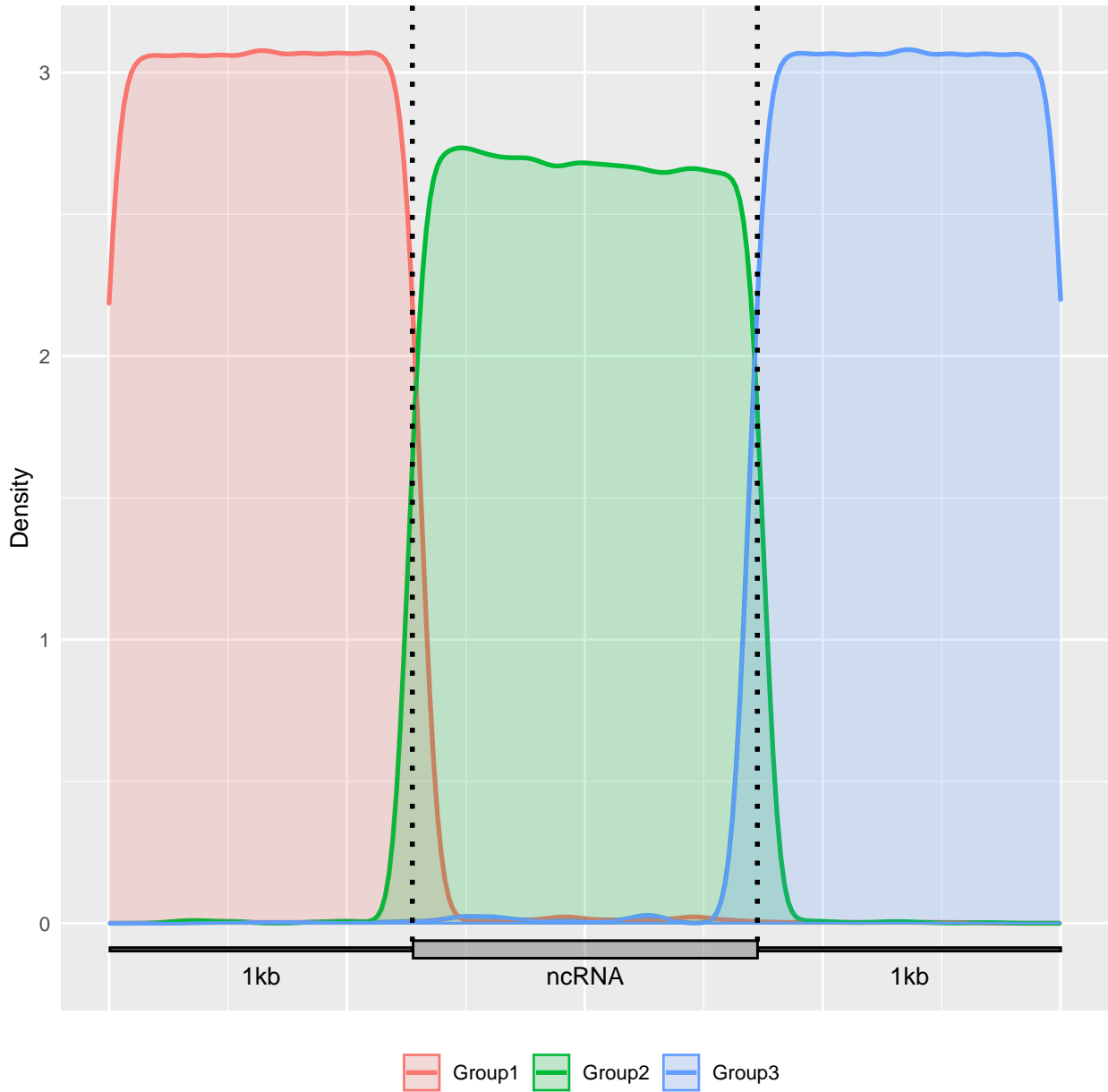
Check the distribution of lncRNA components in the transcriptome

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

## [1] "20220501165058"
## [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] "20220501165108"
## [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$x' is discouraged. Use 'x' instead.
## Use of 'densityCI$x' is discouraged. Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged. Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged. Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged. Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' is discouraged. Use 'y2' instead.
```



6 Session Information

```

sessionInfo()

## R version 4.2.0 RC (2022-04-21 r82226)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.4 LTS
##
## Matrix products: default
## BLAS: /home/biocbuild/bbs-3.16-bioc/R/lib/libRblas.so
## LAPACK: /home/biocbuild/bbs-3.16-bioc/R/lib/libRlapack.so

```



```

##
## locale:
## [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
## [3] LC_TIME=en_GB             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
##
## attached base packages:
## [1] stats4      stats      graphics  grDevices  utils
## [6] datasets    methods    base
##
## other attached packages:
## [1] Guitar_2.13.0      dplyr_1.0.9
## [3] ggplot2_3.3.5      magrittr_2.0.3
## [5] rtracklayer_1.57.0 GenomicFeatures_1.49.1
## [7] AnnotationDbi_1.59.0 Biobase_2.57.0
## [9] GenomicRanges_1.49.0 GenomeInfoDb_1.33.1
## [11] IRanges_2.31.0     S4Vectors_0.35.0
## [13] BiocGenerics_0.43.0 knitr_1.39
##
## loaded via a namespace (and not attached):
## [1] MatrixGenerics_1.9.0      httr_1.4.2
## [3] bit64_4.0.5              assertthat_0.2.1
## [5] highr_0.9                 BiocFileCache_2.5.0
## [7] blob_1.2.3               GenomeInfoDbData_1.2.8
## [9] Rsamtools_2.13.0         yaml_2.3.5
## [11] progress_1.2.2           pillar_1.7.0
## [13] RSQLite_2.2.13          lattice_0.20-45
## [15] glue_1.6.2              digest_0.6.29
## [17] XVector_0.37.0          colorspace_2.0-3
## [19] Matrix_1.4-1            XML_3.99-0.9
## [21] pkgconfig_2.0.3         biomaRt_2.53.0
## [23] zlibbioc_1.43.0         purrr_0.3.4
## [25] scales_1.2.0            BiocParallel_1.31.0
## [27] tibble_3.1.6            KEGGREST_1.37.0
## [29] farver_2.1.0            generics_0.1.2
## [31] ellipsis_0.3.2         withr_2.5.0
## [33] cachem_1.0.6           SummarizedExperiment_1.27.1
## [35] cli_3.3.0              crayon_1.5.1
## [37] memoise_2.0.1          evaluate_0.15
## [39] fansi_1.0.3            xml2_1.3.3
## [41] textshaping_0.3.6     tools_4.2.0
## [43] prettyunits_1.1.1      hms_1.1.1
## [45] BiocIO_1.7.0           lifecycle_1.0.1
## [47] matrixStats_0.62.0     stringr_1.4.0
## [49] munsell_0.5.0          DelayedArray_0.23.0
## [51] Biostrings_2.65.0      compiler_4.2.0
## [53] systemfonts_1.0.4     rlang_1.0.2
## [55] grid_4.2.0            RCurl_1.98-1.6
## [57] rjson_0.2.21          rappdirs_0.3.3
## [59] labeling_0.4.2        bitops_1.0-7
## [61] restfulr_0.0.13       gtable_0.3.0

```

```
## [63] DBI_1.1.2          curl_4.3.2
## [65] R6_2.5.1             GenomicAlignments_1.33.0
## [67] fastmap_1.1.0       bit_4.0.4
## [69] utf8_1.2.2          filelock_1.0.2
## [71] ragg_1.2.2           stringi_1.7.6
## [73] parallel_4.2.0      Rcpp_1.0.8.3
## [75] vctrs_0.4.1         png_0.1-7
## [77] dbplyr_2.1.1        tidyselect_1.1.2
## [79] xfun_0.30
```