

# An Introduction to *Guitar* Package

Xiao Du

Modified: 26 April, 2019. Compiled: May 19, 2021

## 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: parallel
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall,
##   clusterEvalQ, clusterExport, clusterMap,
##   parApply, parCapply, parLapply, parLapplyLB,
##   parRapply, parSapply, parSapplyLB
## 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
## 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] "20210519200150"
## [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] "20210519200220"
## [1] "import BED file /private/tmp/RtmpCJMrla/Rinst4d647316355/Guitar/extdata/m6A_mm10_exomePeak_1000p
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

## 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 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.

```

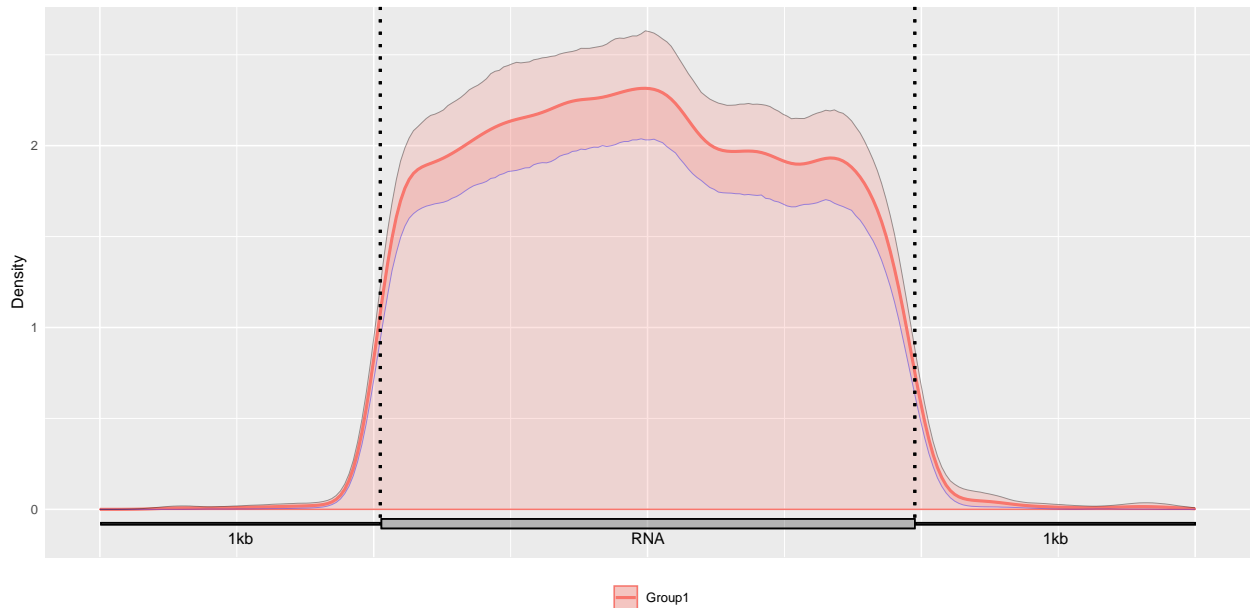
```
## Warning: Use of 'densityCI$x' is discouraged. Use 'x' instead.
## Warning: Use of 'vline_pos$x1' is discouraged. Use 'x1' instead.
## Warning: Use of 'vline_pos$y1' is discouraged. Use 'y1' instead.
## Warning: Use of 'vline_pos$x2' is discouraged. Use 'x2' instead.
## Warning: Use of 'vline_pos$y2' 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] "20210519200258"
## [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] "20210519200336"
## [1] "import BED file /private/tmp/RtmpCJMrla/Rinst4d647316355/Guitar/extdata/m6A_mm10_exomePeak_1000p
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

## 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.
```

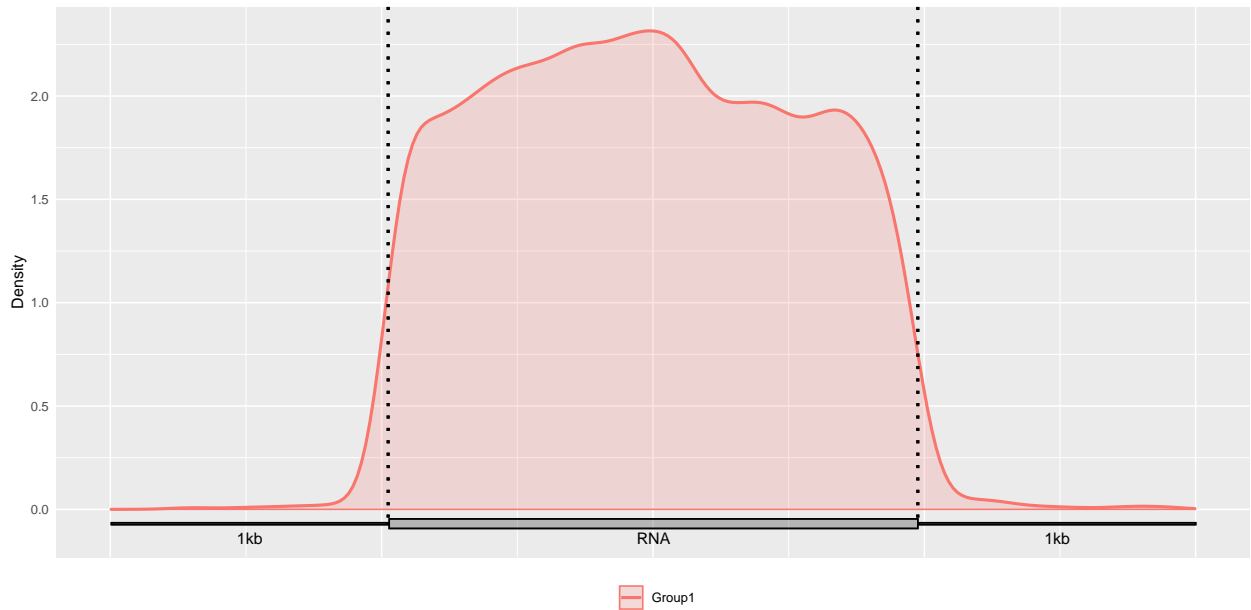


Alternatively, you may also optionally include the Confidence Interval for guitar plot with parameter `enableCI = FALSE`.

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

## [1] "20210519200358"
## [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] "20210519200429"
## [1] "import BED file /private/tmp/RtmpCJMrla/Rinst4d647316355/Guitar/extdata/m6A_mm10_exomePeak_1000p
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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



## 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"))

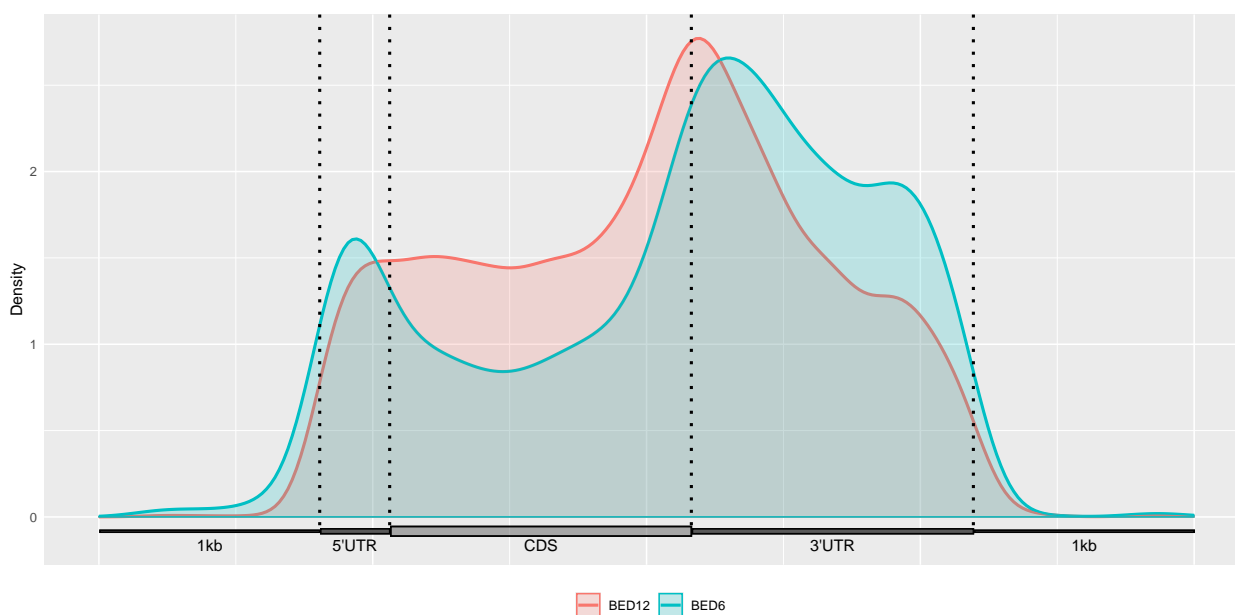
# Build Guitar Coordinates
txdb_file <- system.file("extdata", "mm10_toy.sqlite",
                        package="Guitar")
txdb <- loadDb(txdb_file)

# Guitar Plot
GuitarPlot(txTxdb = txdb,
           stBedFiles = stBedFiles,
           headOrtail = TRUE,
           enableCI = FALSE,
           mapFilterTranscript = TRUE,
           pltTxType = c("mrna"),
           stGroupName = c("BED12", "BED6"))

## [1] "20210519200432"
## [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] "20210519200504"
## [1] "import BED file /private/tmp/RtmpCJMrla/Rinst4d647316355/Guitar/extdata/m6A_mm10_exomePeak_1000p"
## [1] "import BED file /private/tmp/RtmpCJMrla/Rinst4d647316355/Guitar/extdata/m6A_mm10_exomePeak_1000p"
## [1] "sample 10 points for BED12"
## [1] "sample 10 points for BED6"
## [1] "start figure plotting for mrna ..."

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



### 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.

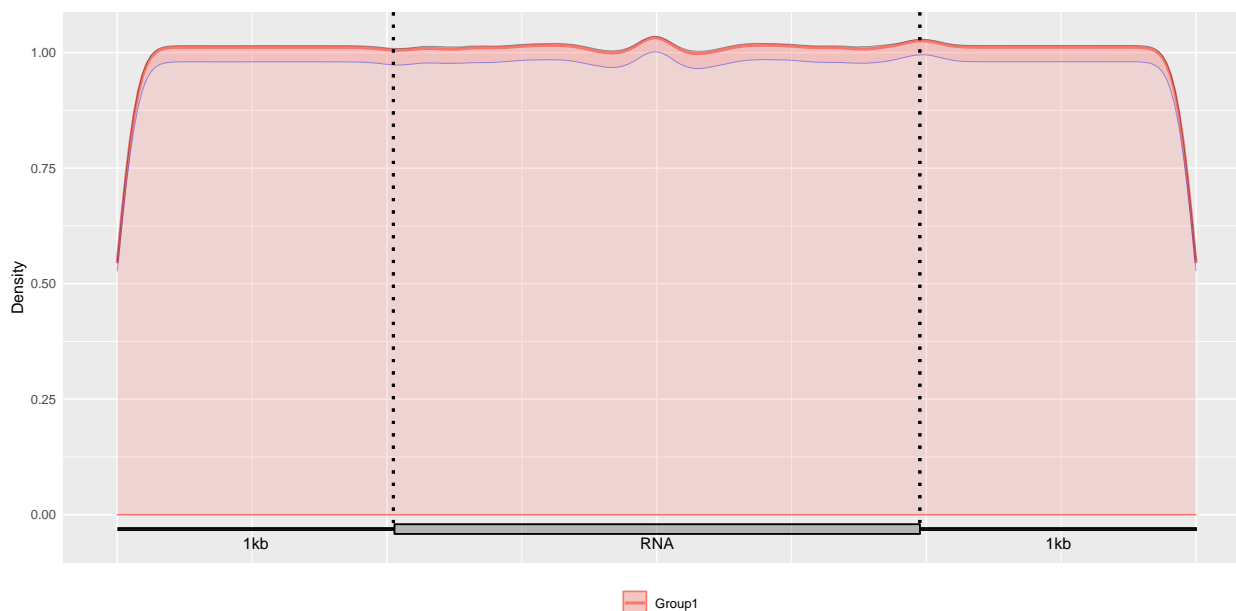
```

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

```

```
## [1] "20210519200541"
## [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] "20210519200612"
## [1] "sample 200 points for Group1"
## [1] "start figure plotting for tx ..."

## 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, 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)
```

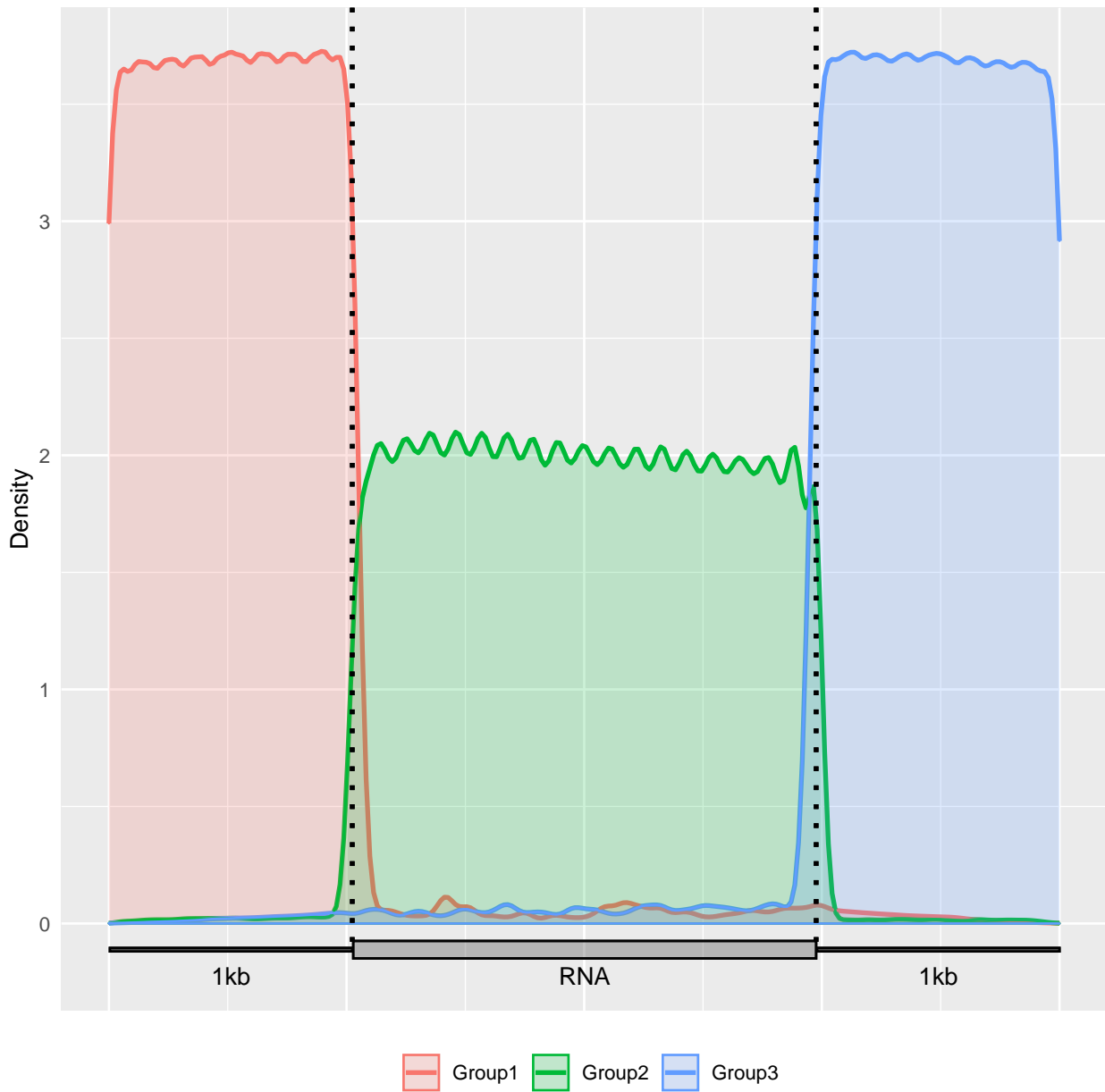
```

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] "20210519201522"
## [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] "20210519201543"
## [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$x' is discouraged. Use 'x' instead.
## Warning: Use of 'densityCI$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.

```



Check the distribution of mRNA components in the transcriptome

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

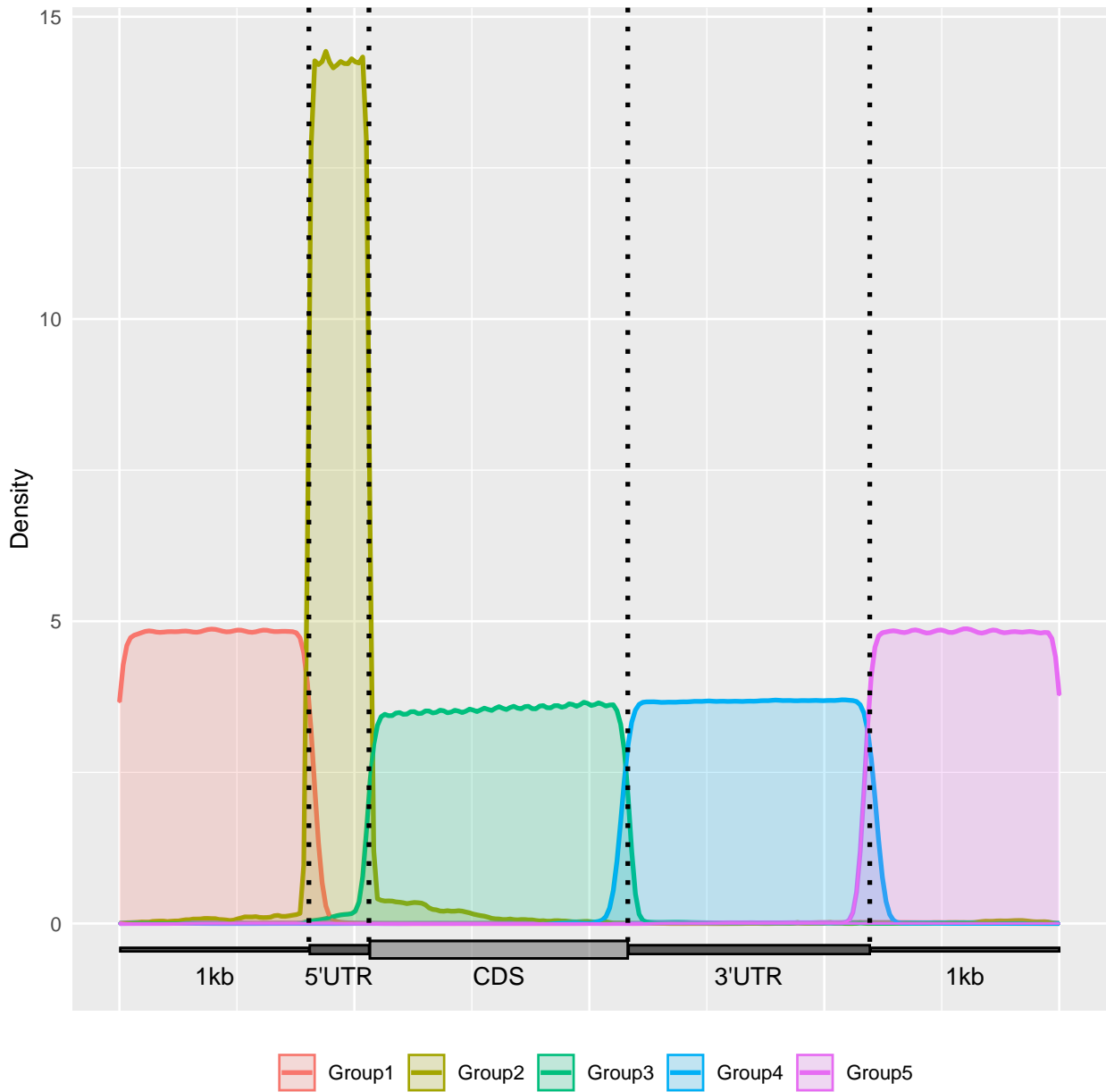
## [1] "20210519201606"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left 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] "20210519201630"
## [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$x' is discouraged. Use 'x' instead.
## Warning: Use of 'densityCI$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.

```



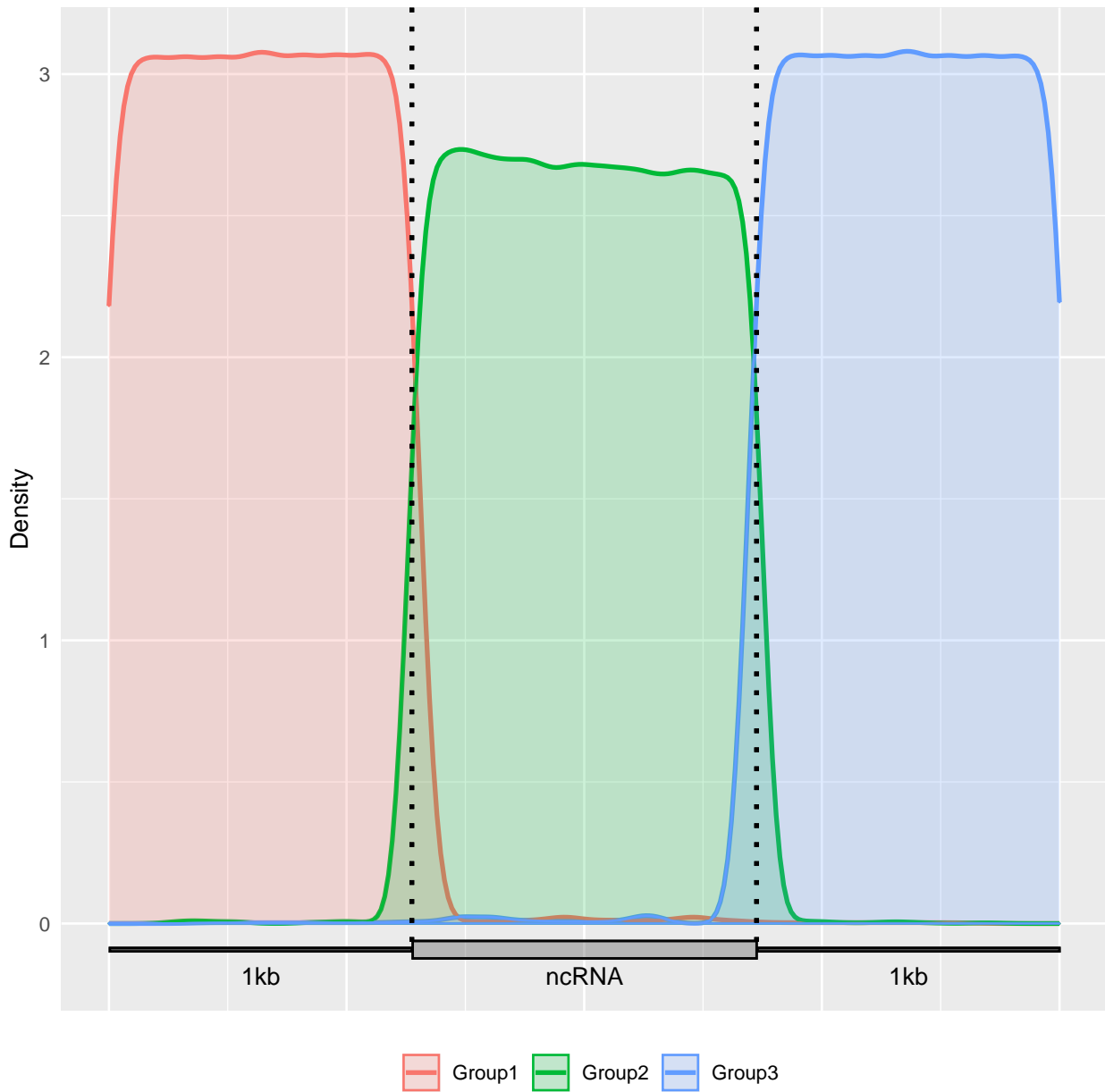
Check the distribution of lncRNA components in the transcriptome

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

## [1] "20210519201649"
## [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] "20210519201711"
## [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$x' is discouraged. Use 'x' instead.
## Warning: Use of 'densityCI$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.
```



## 6 Session Information

```
sessionInfo()

## R version 4.1.0 RC (2021-05-16 r80304)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Mojave 10.14.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
```



```

##
## locale:
## [1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4      parallel  stats      graphics  grDevices
## [6] utils       datasets  methods    base
##
## other attached packages:
## [1] Guitar_2.9.0          dplyr_1.0.6
## [3] ggplot2_3.3.3         magrittr_2.0.1
## [5] rtracklayer_1.53.0    GenomicFeatures_1.45.0
## [7] AnnotationDbi_1.55.0  Biobase_2.53.0
## [9] GenomicRanges_1.45.0  GenomeInfoDb_1.29.0
## [11] IRanges_2.27.0        S4Vectors_0.31.0
## [13] BiocGenerics_0.39.0   knitr_1.33
##
## loaded via a namespace (and not attached):
## [1] MatrixGenerics_1.5.0    httr_1.4.2
## [3] bit64_4.0.5             assertthat_0.2.1
## [5] highr_0.9               BiocFileCache_2.1.0
## [7] blob_1.2.1              GenomeInfoDbData_1.2.6
## [9] Rsamtools_2.9.0         yaml_2.2.1
## [11] progress_1.2.2          pillar_1.6.1
## [13] RSQLite_2.2.7           lattice_0.20-44
## [15] glue_1.4.2              digest_0.6.27
## [17] XVector_0.33.0          colorspace_2.0-1
## [19] Matrix_1.3-3            XML_3.99-0.6
## [21] pkgconfig_2.0.3         biomaRt_2.49.0
## [23] zlibbioc_1.39.0         purrr_0.3.4
## [25] scales_1.1.1            BiocParallel_1.27.0
## [27] tibble_3.1.2            KEGGREST_1.33.0
## [29] farver_2.1.0            generics_0.1.0
## [31] ellipsis_0.3.2          cachem_1.0.5
## [33] withr_2.4.2             SummarizedExperiment_1.23.0
## [35] crayon_1.4.1            memoise_2.0.0
## [37] evaluate_0.14           fansi_0.4.2
## [39] tools_4.1.0             prettyunits_1.1.1
## [41] hms_1.1.0               BiocIO_1.3.0
## [43] lifecycle_1.0.0         matrixStats_0.58.0
## [45] stringr_1.4.0           munsell_0.5.0
## [47] DelayedArray_0.19.0     Biostrings_2.61.0
## [49] compiler_4.1.0          rlang_0.4.11
## [51] grid_4.1.0              RCurl_1.98-1.3
## [53] rjson_0.2.20            rappdirs_0.3.3
## [55] labeling_0.4.2          bitops_1.0-7
## [57] restfulr_0.0.13         gtable_0.3.0
## [59] DBI_1.1.1               curl_4.3.1
## [61] R6_2.5.0                GenomicAlignments_1.29.0
## [63] fastmap_1.1.0           bit_4.0.4
## [65] utf8_1.2.1             filelock_1.0.2
## [67] stringi_1.6.2           Rcpp_1.0.6
## [69] vctrs_0.3.8             png_0.1-7
## [71] dbplyr_2.1.1            tidyselect_1.1.1

```

```
## [73] xfun_0.23
```