

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
## 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 take 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] "20211026173750"
## [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 ncra"
## [1] "20211026173800"
## [1] "import BED file /tmp/Rtmp5FY3Wg/Rinst1023d651ea577d/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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

## 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.

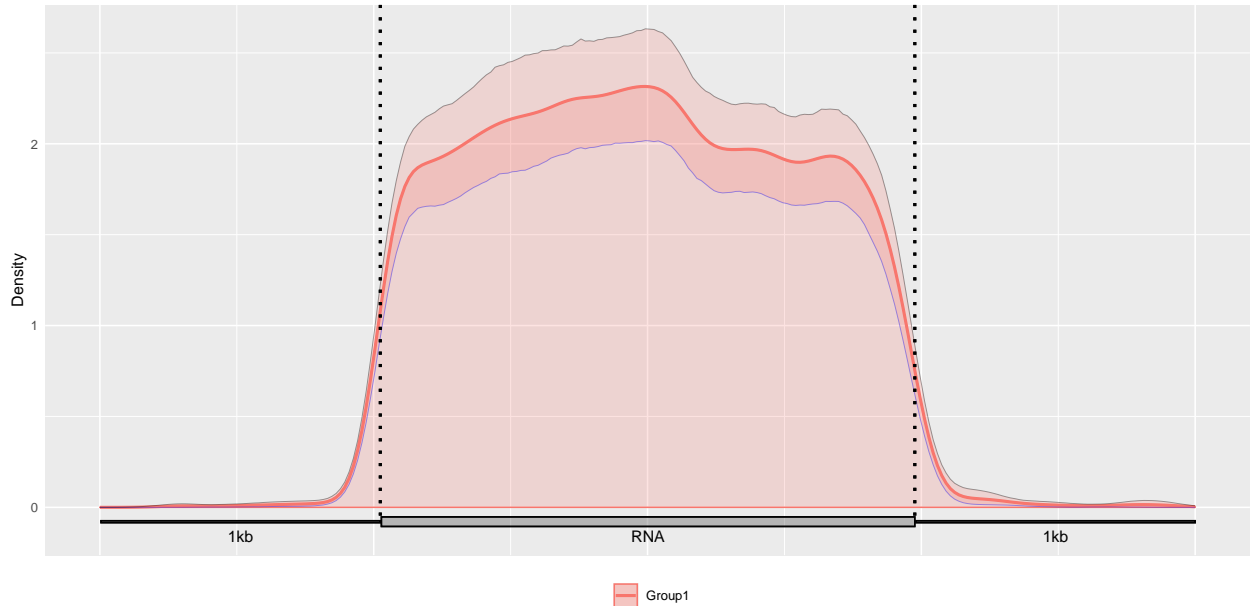
```

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] "20211026173827"
## [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] "20211026173838"
## [1] "import BED file /tmp/Rtmp5FY3Wg/Rinst1023d651ea577d/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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

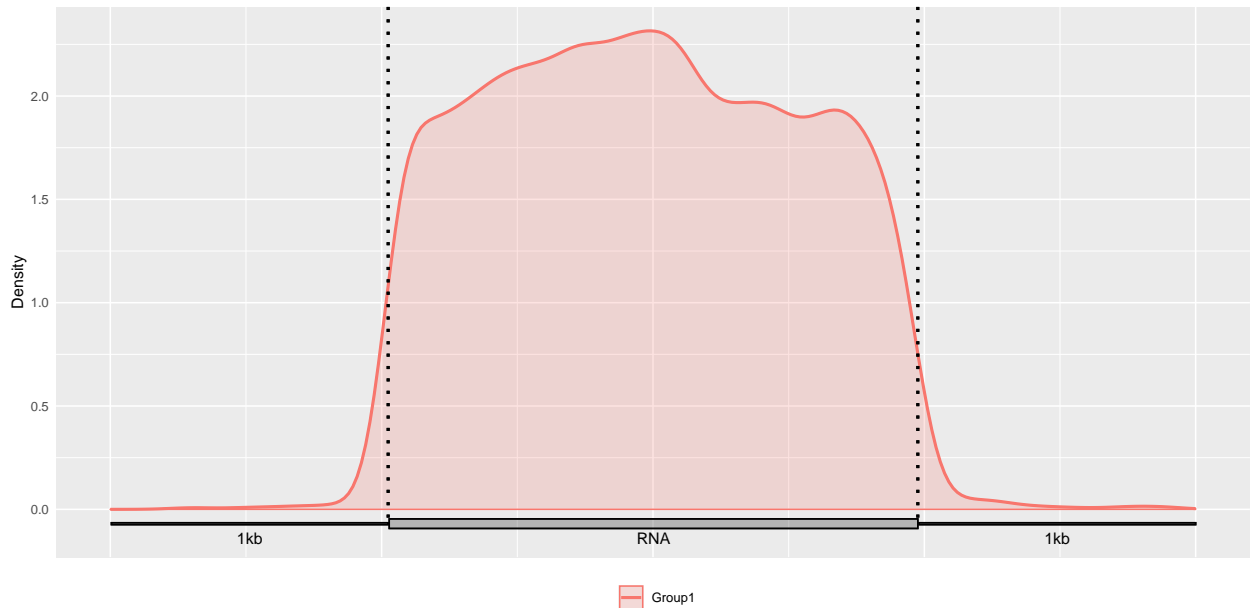


Alternatively, you may also optionally include the Confidence Interval for guitar plot with parameter `enableCI = FALSE`.

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

## [1] "20211026173859"
## [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] "20211026173909"
## [1] "import BED file /tmp/Rtmp5FY3Wg/Rinst1023d651ea577d/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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

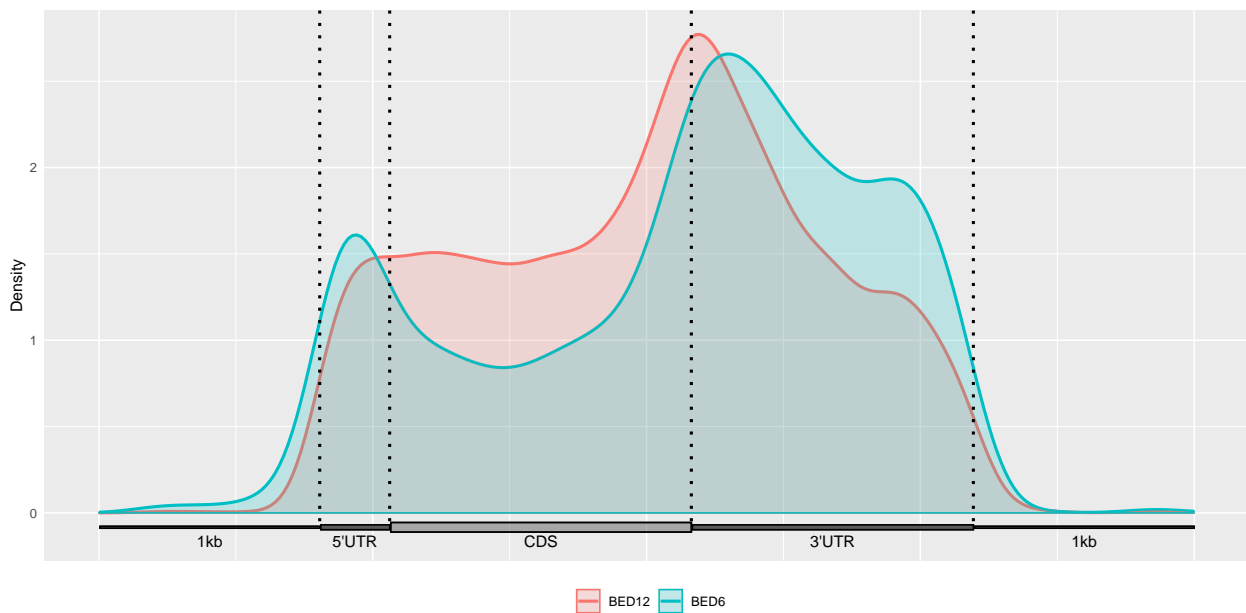
```
# import different data formats into a named list object.
# These genomic features are using mm10 genome assembly
stBedFiles <- list(system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed12.bed",
                             package="Guitar"),
                  system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed6.bed",
                             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] "20211026173912"
## [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] "20211026173922"
## [1] "import BED file /tmp/Rtmp5FY3Wg/Rinst1023d651ea577d/Guitar/extdata/m6A_mm10_exomePeak_1000peaks"
## [1] "import BED file /tmp/Rtmp5FY3Wg/Rinst1023d651ea577d/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$x' is discouraged. Use 'x' instead.
## Warning: Use of 'densityCI$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.

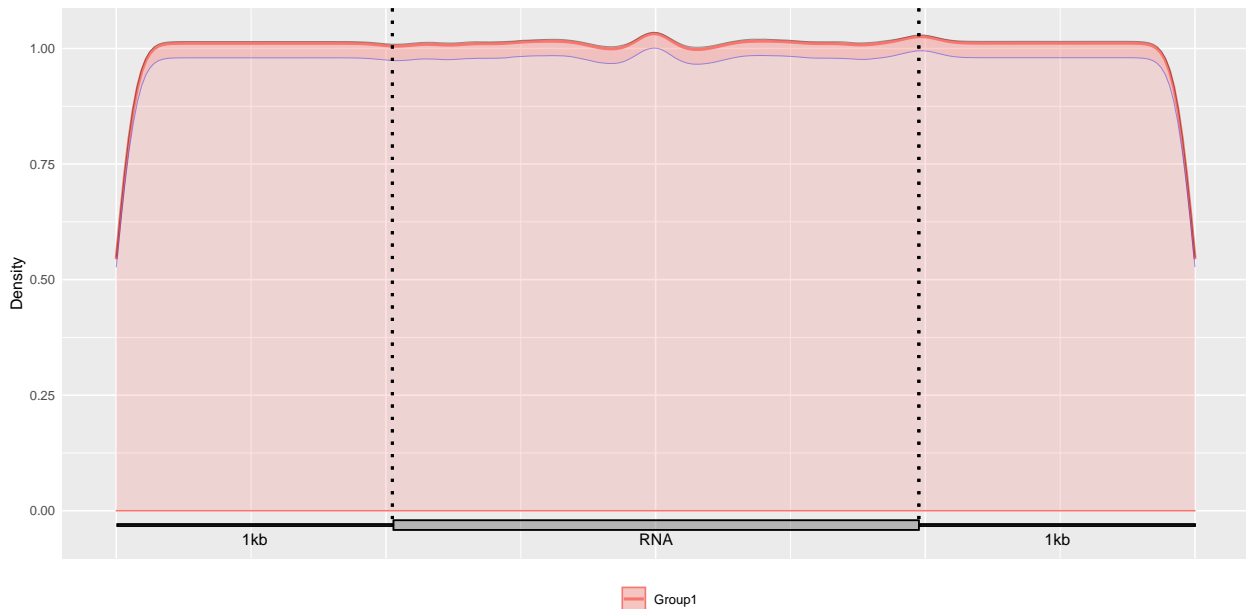
```

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

```

```
## [1] "20211026173937"
## [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] "20211026173948"
## [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)
```

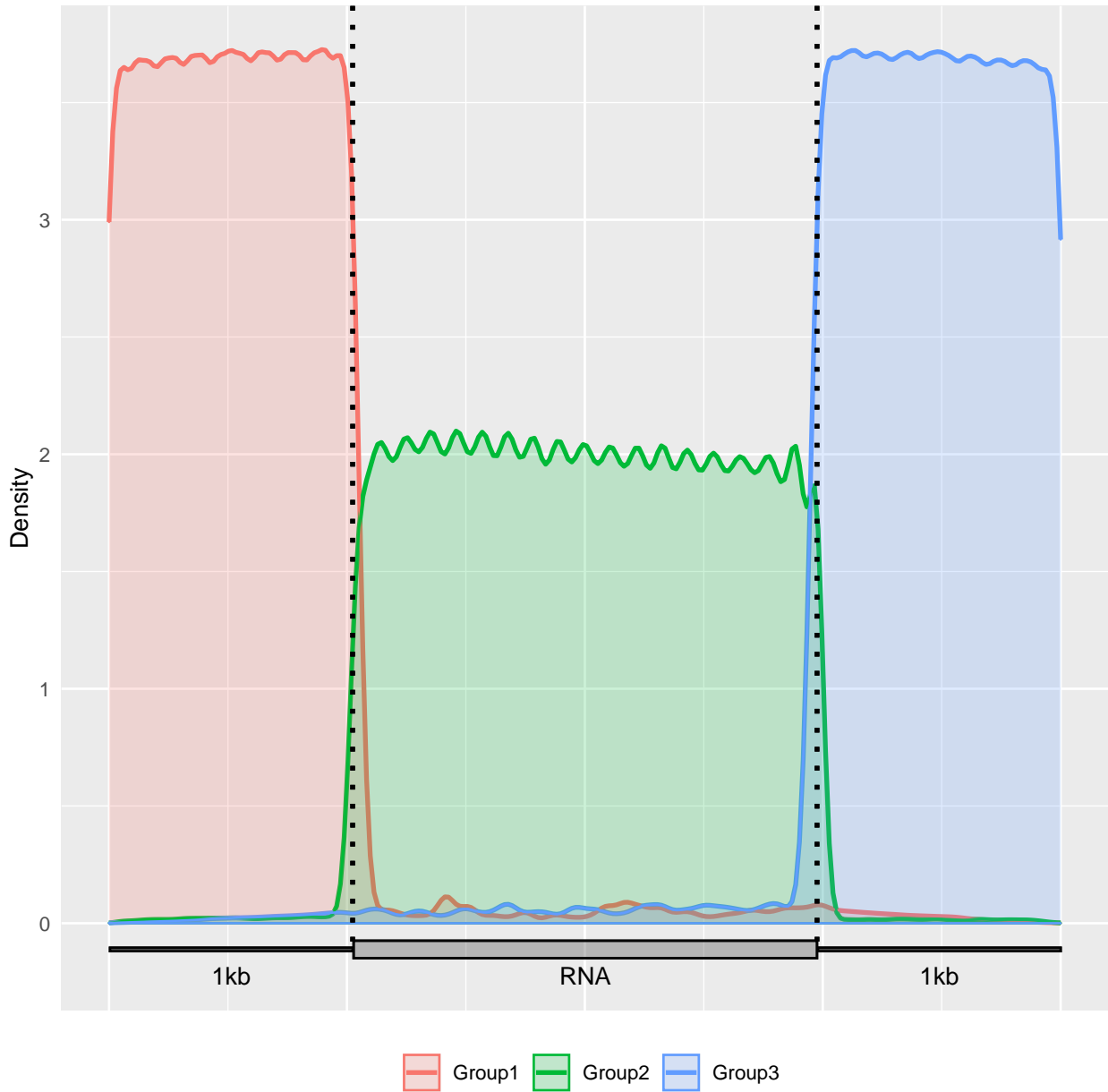
```

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] "20211026174710"
## [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] "20211026174720"
## [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.

```

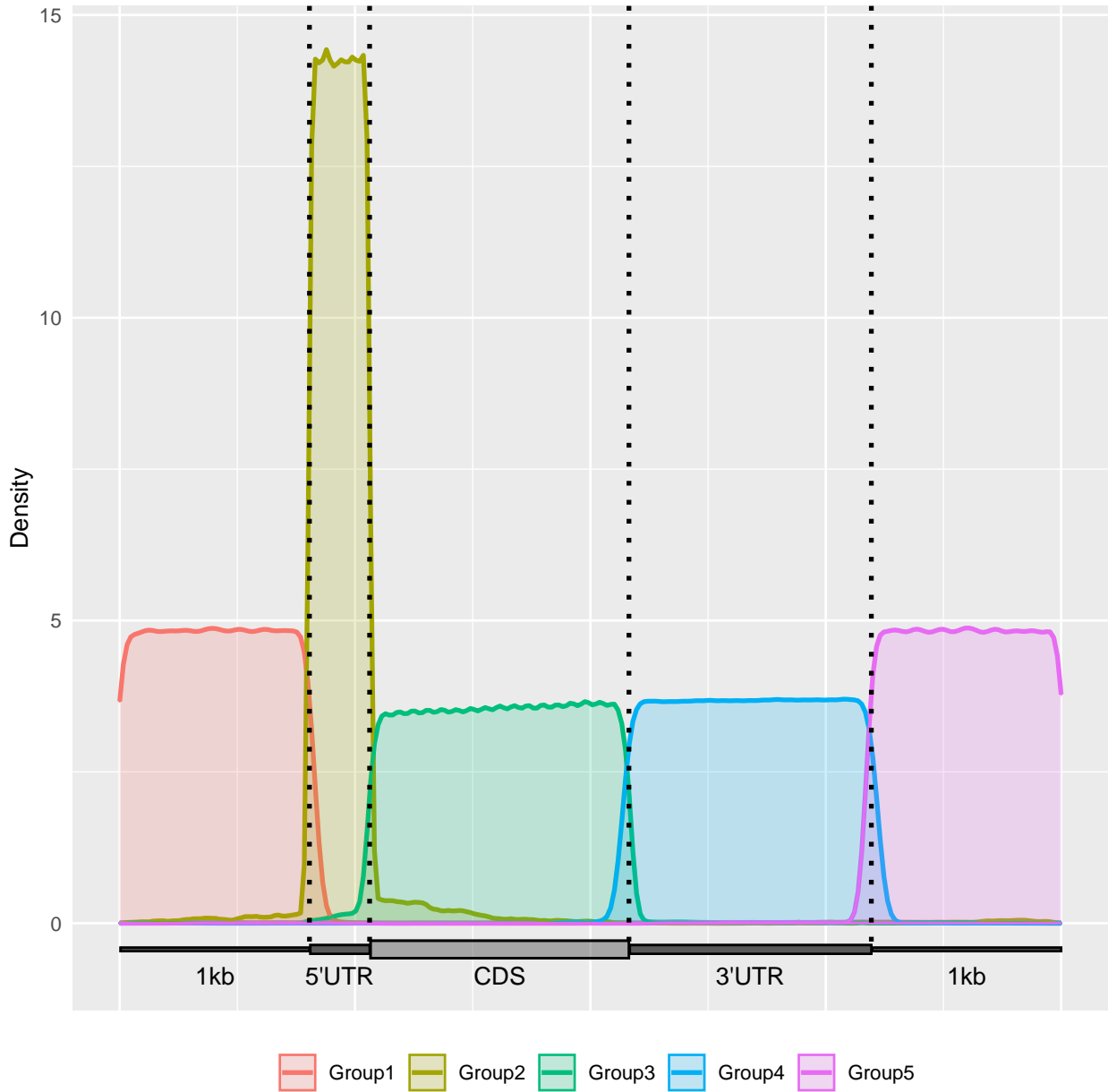


Check the distribution of mRNA components in the transcriptome

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

## [1] "20211026174740"
## [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] "20211026174750"  
## [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.
```



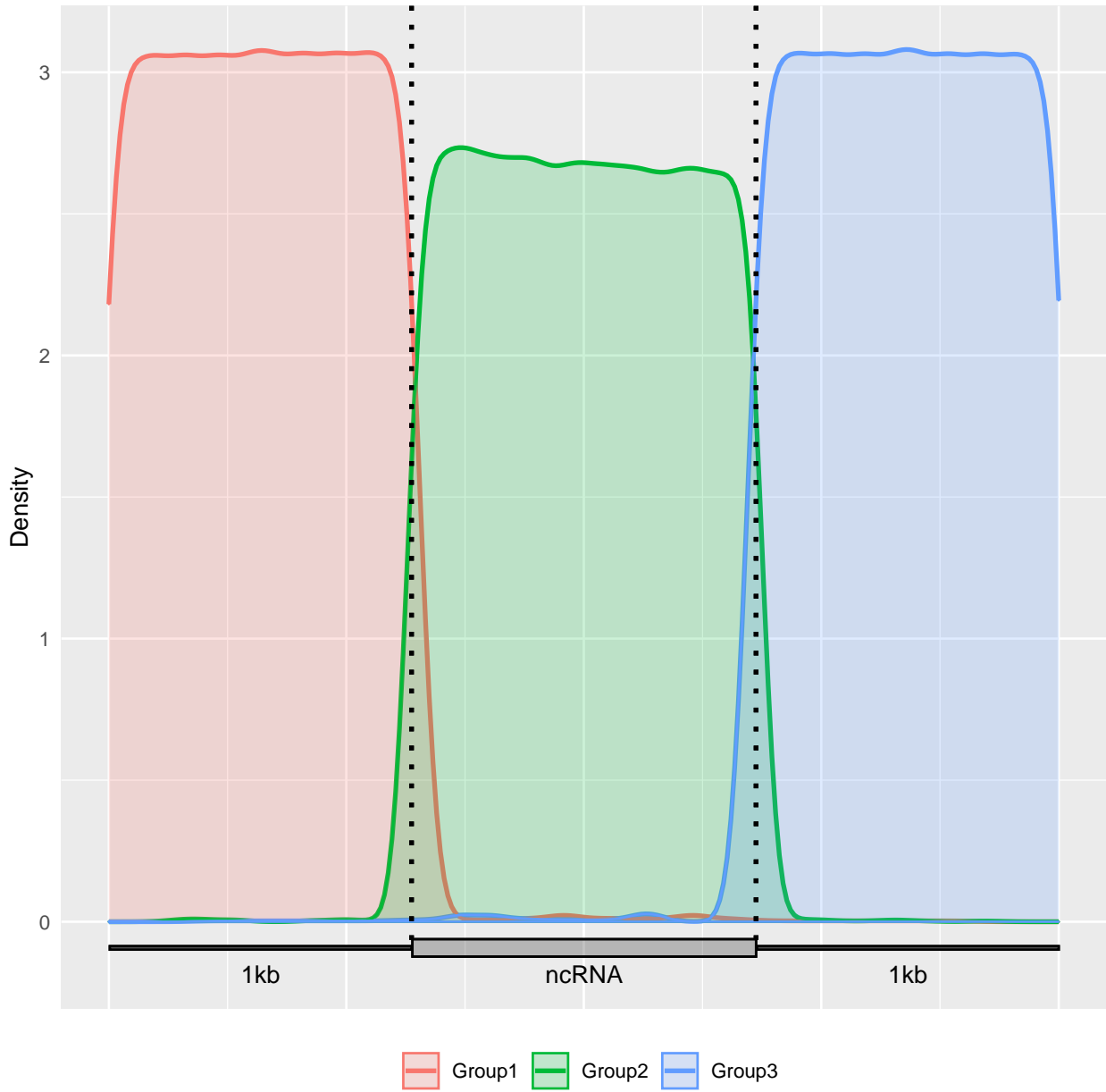
Check the distribution of lncRNA components in the transcriptome

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

## [1] "20211026174803"
## [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] "20211026174815"
## [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 4.1.1 (2021-08-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.3 LTS
##
## Matrix products: default
## BLAS: /home/biocbuild/bbs-3.14-bioc/R/lib/libRblas.so
## LAPACK: /home/biocbuild/bbs-3.14-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_2.10.0      dplyr_1.0.7
## [3] ggplot2_3.3.5      magrittr_2.0.1
## [5] rtracklayer_1.54.0 GenomicFeatures_1.46.0
## [7] AnnotationDbi_1.56.0 Biobase_2.54.0
## [9] GenomicRanges_1.46.0 GenomeInfoDb_1.30.0
## [11] IRanges_2.28.0     S4Vectors_0.32.0
## [13] BiocGenerics_0.40.0 knitr_1.36
##
## loaded via a namespace (and not attached):
## [1] MatrixGenerics_1.6.0      httr_1.4.2
## [3] bit64_4.0.5               assertthat_0.2.1
## [5] highr_0.9                 BiocFileCache_2.2.0
## [7] blob_1.2.2                GenomeInfoDbData_1.2.7
## [9] Rsamtools_2.10.0         yaml_2.2.1
## [11] progress_1.2.2           pillar_1.6.4
## [13] RSQLite_2.2.8            lattice_0.20-45
## [15] glue_1.4.2                digest_0.6.28
## [17] XVector_0.34.0           colorspace_2.0-2
## [19] Matrix_1.3-4             XML_3.99-0.8
## [21] pkgconfig_2.0.3          biomaRt_2.50.0
## [23] zlibbioc_1.40.0          purrr_0.3.4
## [25] scales_1.1.1             BiocParallel_1.28.0
## [27] tibble_3.1.5             KEGGREST_1.34.0
## [29] farver_2.1.0             generics_0.1.1
## [31] ellipsis_0.3.2          withr_2.4.2
## [33] cachem_1.0.6            SummarizedExperiment_1.24.0
## [35] crayon_1.4.1            memoise_2.0.0
## [37] evaluate_0.14           fansi_0.5.0
## [39] xml2_1.3.2              textshaping_0.3.6
## [41] tools_4.1.1             prettyunits_1.1.1
## [43] hms_1.1.1               BiocIO_1.4.0
## [45] lifecycle_1.0.1         matrixStats_0.61.0
## [47] stringr_1.4.0           munsell_0.5.0
## [49] DelayedArray_0.20.0     Biostrings_2.62.0
## [51] compiler_4.1.1          systemfonts_1.0.3
## [53] rlang_0.4.12            grid_4.1.1
## [55] RCurl_1.98-1.5          rjson_0.2.20
## [57] rappdirs_0.3.3         labeling_0.4.2
## [59] bitops_1.0-7            restfulr_0.0.13
## [61] gtable_0.3.0           DBI_1.1.1

```

```
## [63] curl_4.3.2          R6_2.5.1
## [65] GenomicAlignments_1.30.0 fastmap_1.1.0
## [67] bit_4.0.4             utf8_1.2.2
## [69] filelock_1.0.2       ragg_1.1.3
## [71] stringi_1.7.5        parallel_4.1.1
## [73] Rcpp_1.0.7           vctrs_0.3.8
## [75] png_0.1-7            dbplyr_2.1.1
## [77] tidyselect_1.1.1     xfun_0.27
```