

# An Introduction to *Guitar* Package

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## 1 Quick Start with Guitar

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

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

```
library(Guitar)

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

```

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

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

```

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

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

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

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

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

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

# 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] "20240713050523"
```

```

## [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] "20240713050530"
## [1] "import BED file /tmp/RtmpIOdZ0l/Rinst15e33560ce81/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 '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`.

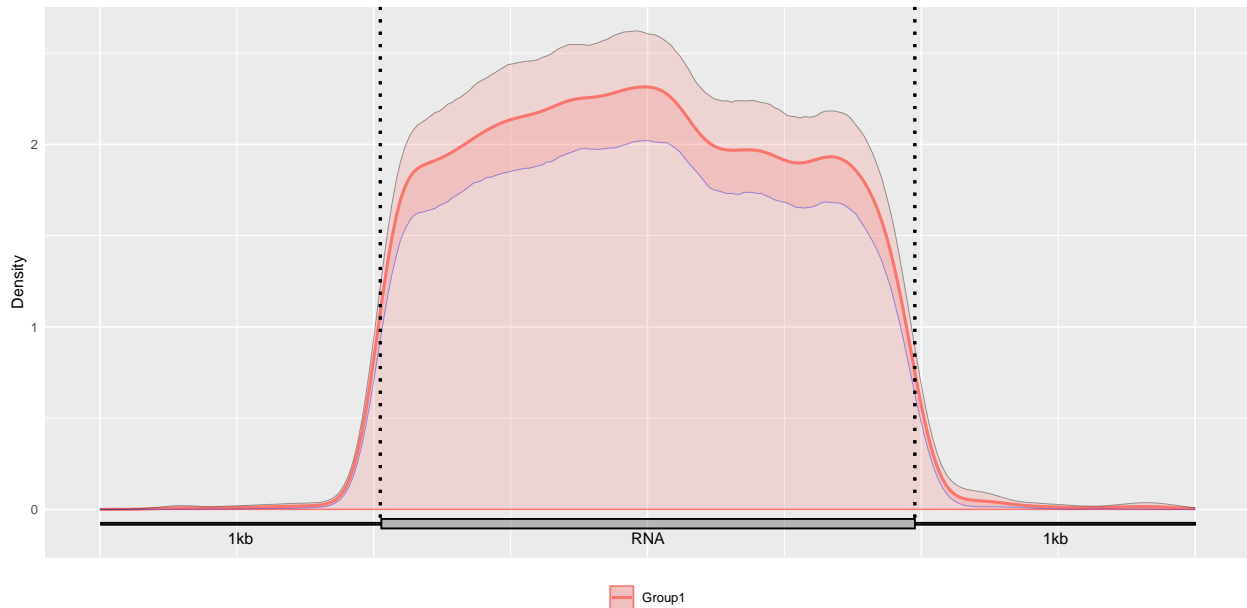
```
GuitarPlot(txTxdb = txdb,
            stBedFiles = stBedFiles,
            headOrtail = TRUE)
```

```

## [1] "20240713050544"
## [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] "20240713050551"
## [1] "import BED file /tmp/RtmpIOdZ0l/Rinst15e33560ce81/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.

```



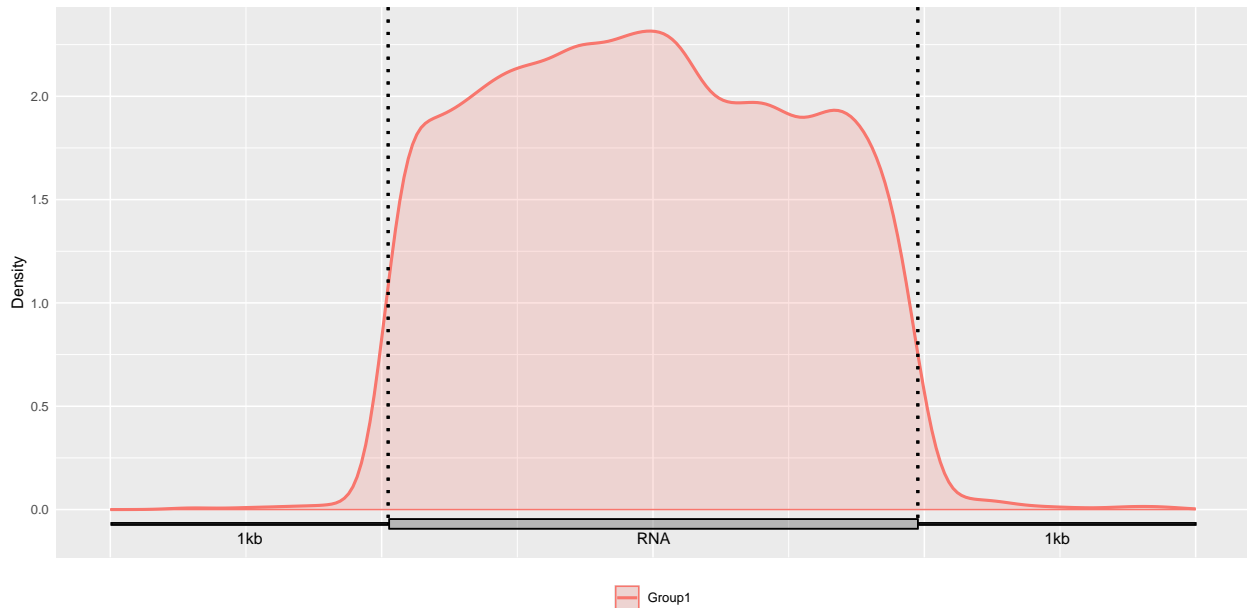
Alternatively, you may also optionally include the Confidence Interval for guitar plot with parameter `enableCI = FALSE`.

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

## [1] "20240713050559"
## [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] "20240713050605"
## [1] "import BED file /tmp/RtmpI0dZ0l/Rinst15e33560ce81/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 'vline_pos$x1' is discouraged.
## i Use 'x1' instead.
```

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



## 2 Supported Data Format

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

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

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

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



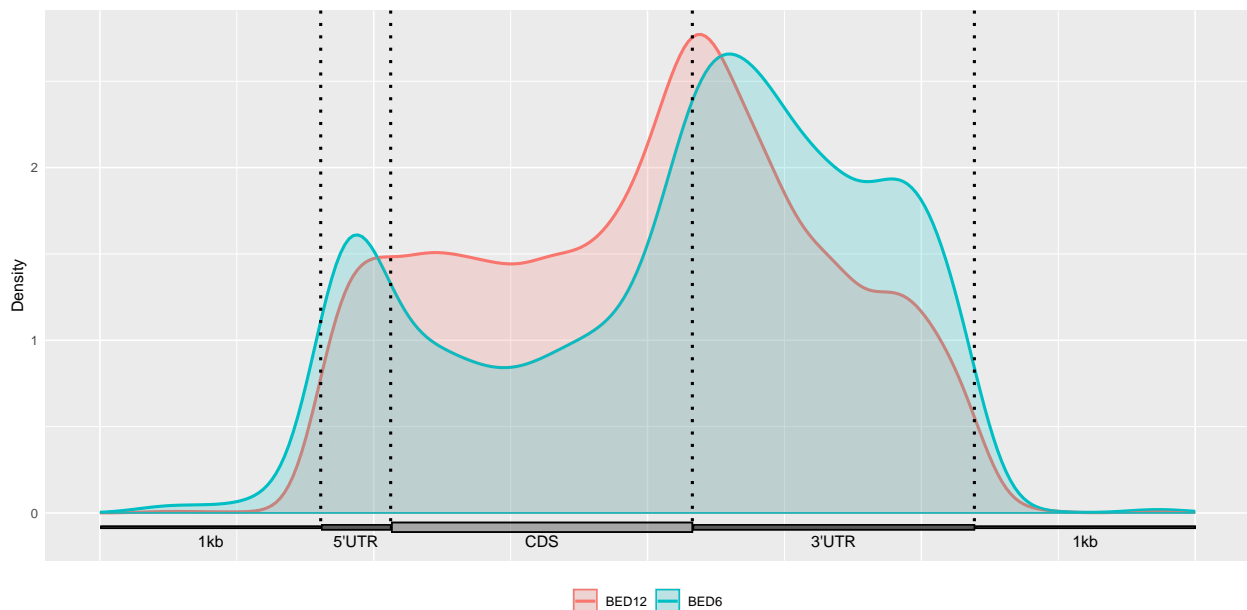
```

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

## [1] "20240713050607"
## [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] "20240713050613"
## [1] "import BED file /tmp/RtmpI0dZ0l/Rinst15e33560ce81/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_b
## [1] "import BED file /tmp/RtmpI0dZ0l/Rinst15e33560ce81/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_b
## [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"
```

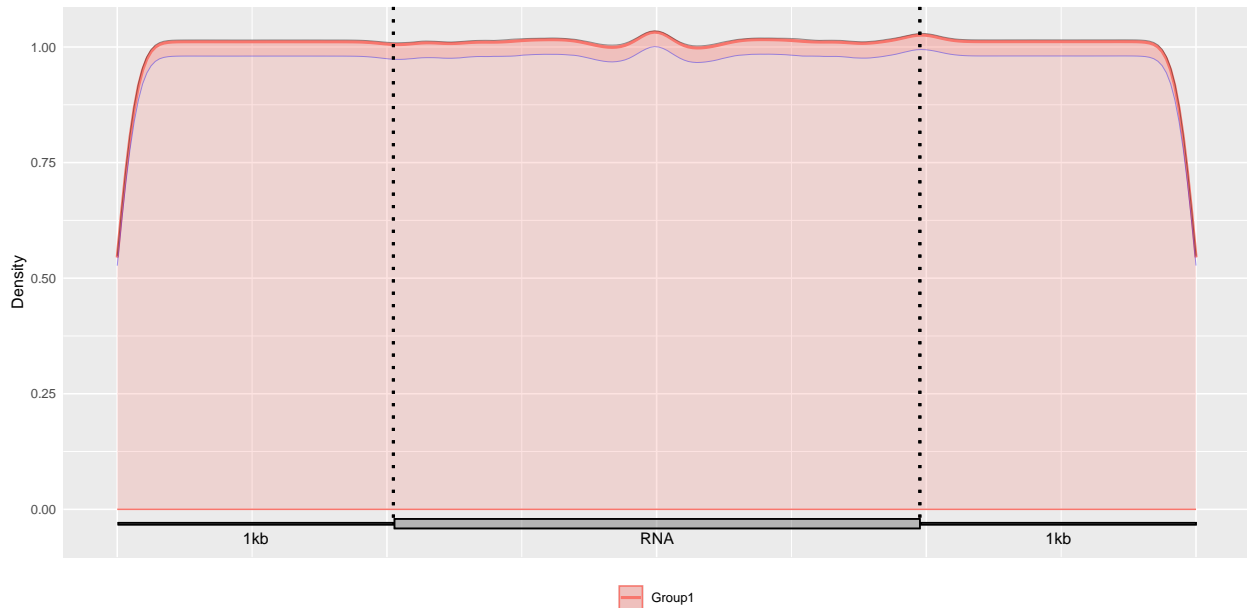
## 5 Check the Overlapping between Different Components

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] "20240713050622"
## [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] "20240713050628"
## [1] "sample 200 points for Group1"
## [1] "start figure plotting for tx ..."

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



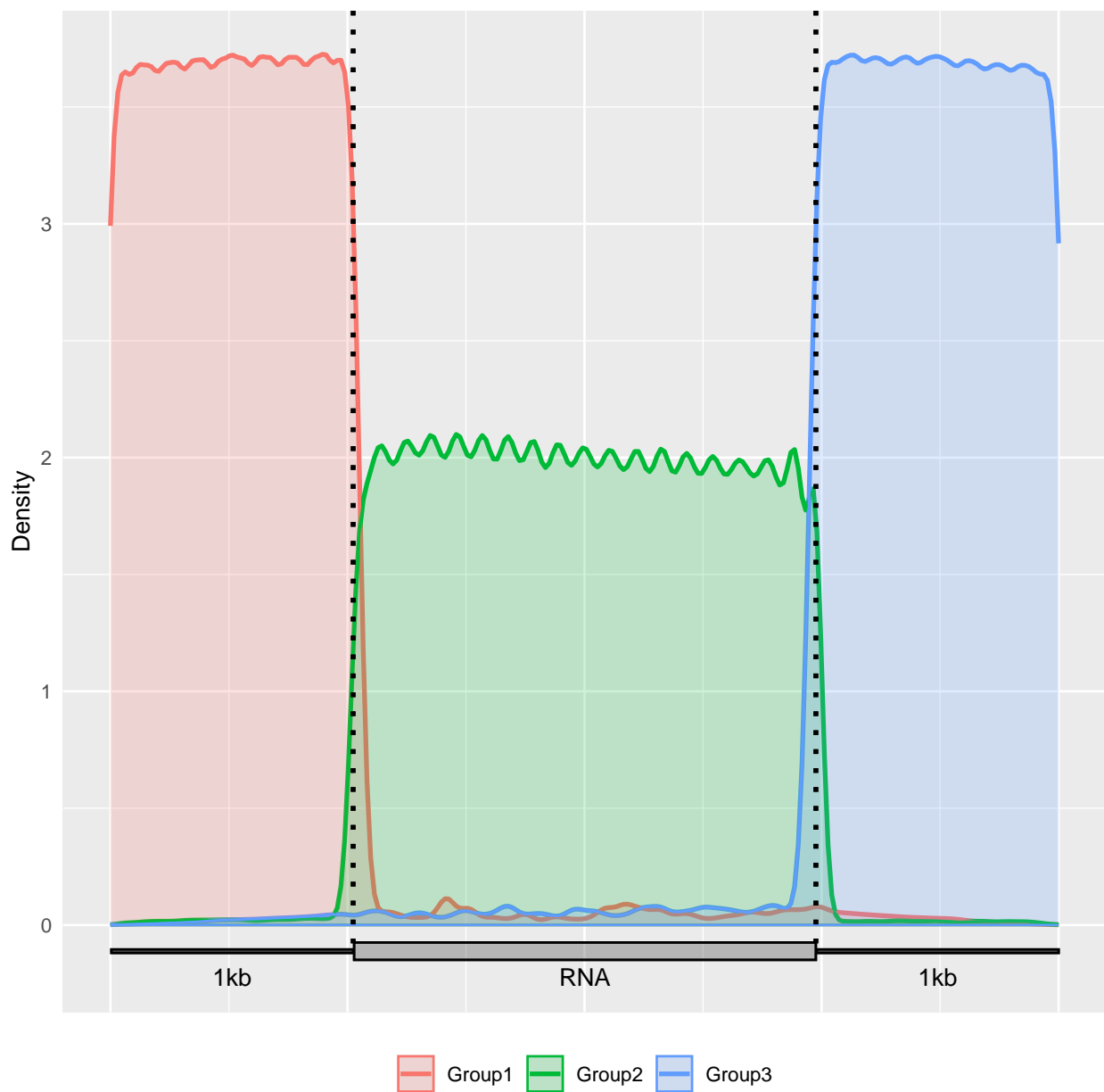
Alternatively, we can extract the RNA components, check the distribution of tx components in the transcriptome

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

## [1] "20240713050942"
## [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] "20240713050949"
## [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

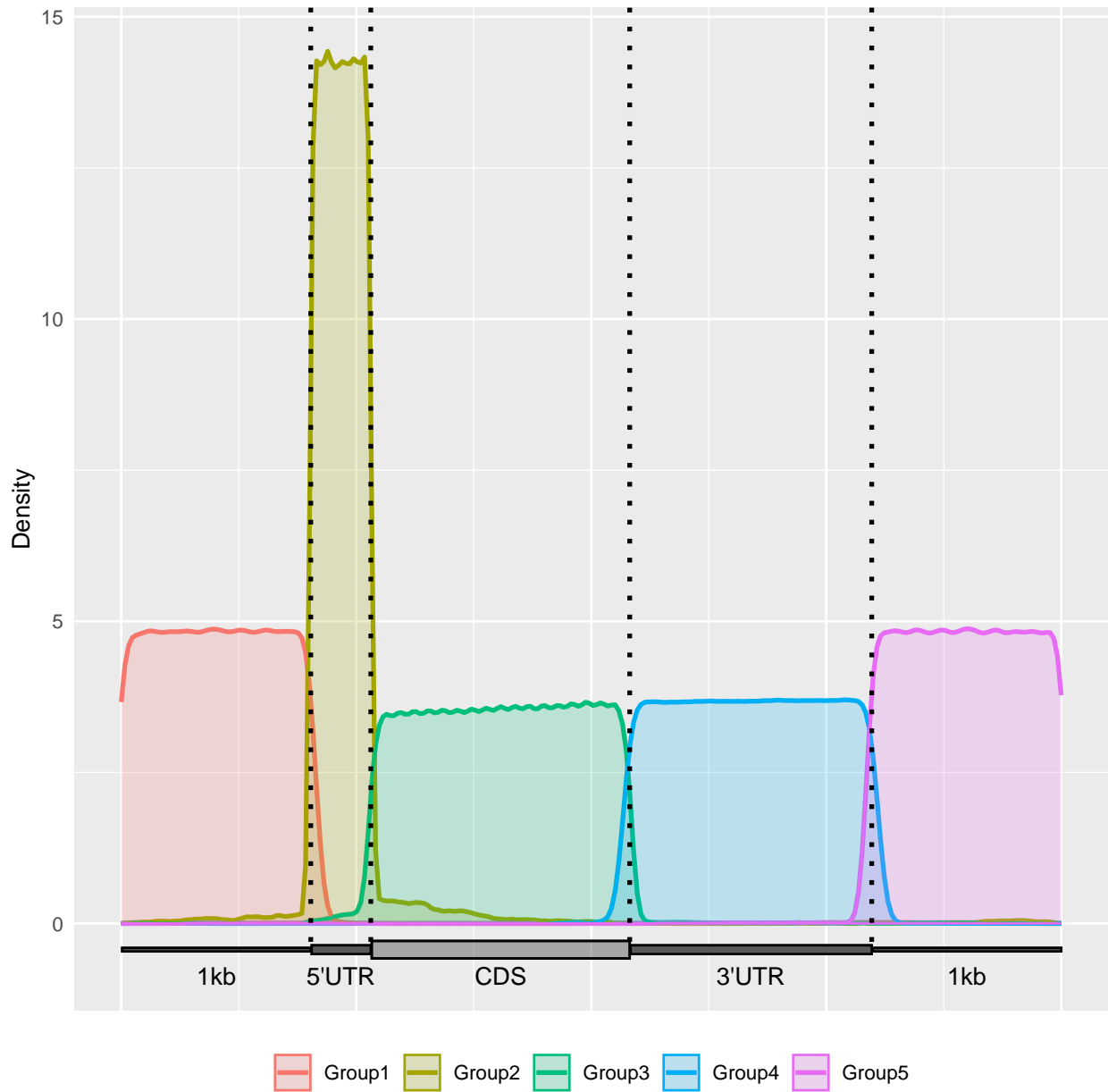
```

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

## [1] "20240713051001"
## [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] "20240713051008"
## [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

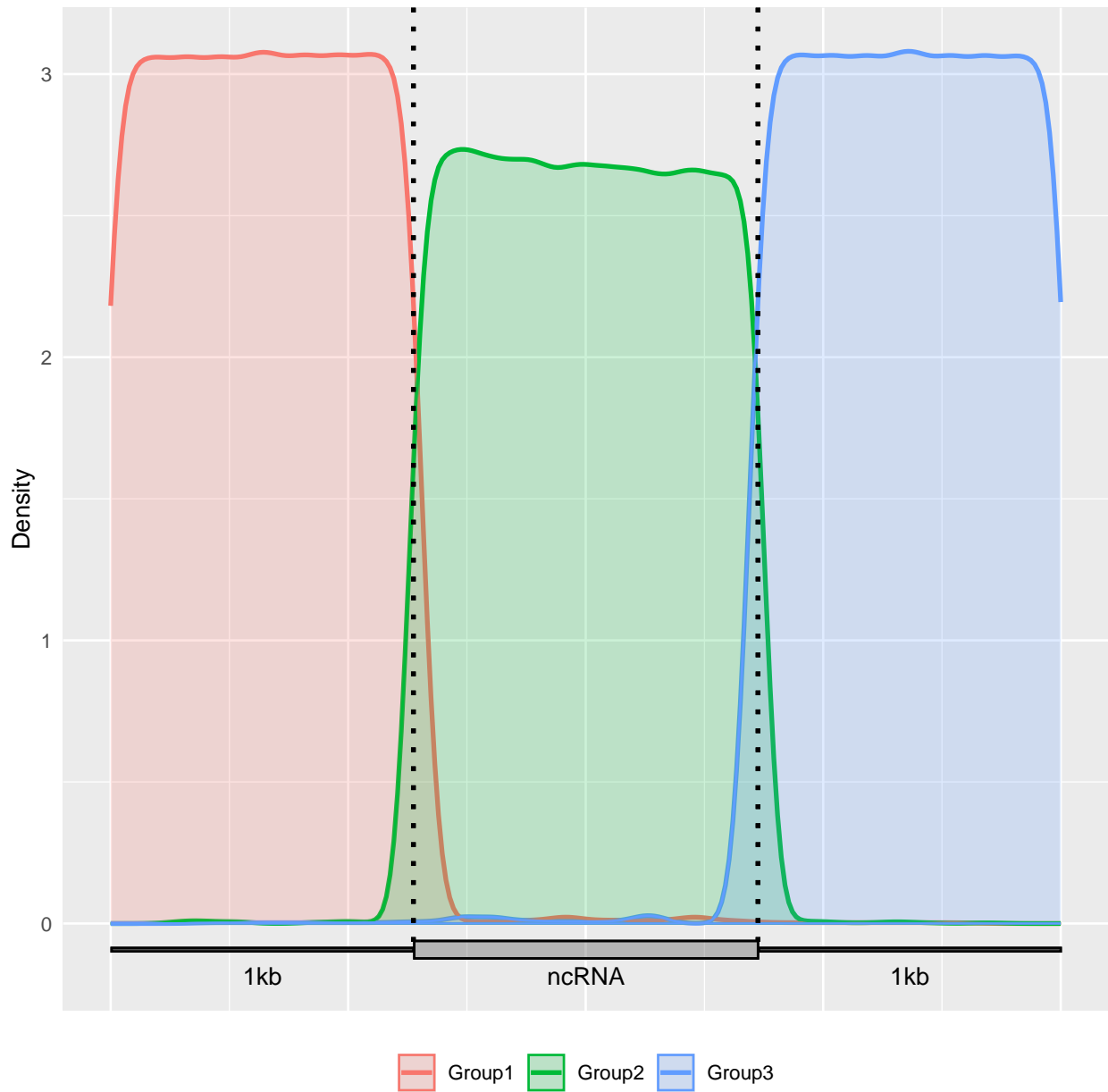
```
GuitarPlot(txTxdb = txdb ,
            stGRangeLists = landmark[9:11],
            pltTxType = c("ncrna"),
            enableCI = FALSE
)

## [1] "20240713051016"
## [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] "20240713051022"
## [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 4.4.1 (2024-06-14)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 24.04 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_2.21.0      dplyr_1.1.4
## [3] ggplot2_3.5.1      magrittr_2.0.3
## [5] rtracklayer_1.65.0 GenomicFeatures_1.57.0
## [7] AnnotationDbi_1.67.0 Biobase_2.65.0
## [9] GenomicRanges_1.57.1 GenomeInfoDb_1.41.1
## [11] IRanges_2.39.1     S4Vectors_0.43.1
## [13] BiocGenerics_0.51.0 knitr_1.48
##
## loaded via a namespace (and not attached):
## [1] KEGGREST_1.45.1      SummarizedExperiment_1.35.1
## [3] gtable_0.3.5         rjson_0.2.21
## [5] xfun_0.45            lattice_0.22-6
## [7] generics_0.1.3       vctrs_0.6.5
## [9] tools_4.4.1          bitops_1.0-7
## [11] curl_5.2.1           parallel_4.4.1
## [13] fansi_1.0.6          tibble_3.2.1
## [15] RSQLite_2.3.7        highr_0.11
## [17] blob_1.2.4           pkgconfig_2.0.3
## [19] Matrix_1.7-0         lifecycle_1.0.4
## [21] GenomeInfoDbData_1.2.12 farver_2.1.2
## [23] compiler_4.4.1       Rsamtools_2.21.0
## [25] Biostrings_2.73.1    munsell_0.5.1
## [27] codetools_0.2-20     sys_3.4.2
## [29] buildtools_1.0.0     RCurl_1.98-1.16
## [31] yaml_2.3.9           pillar_1.9.0
## [33] crayon_1.5.3         BiocParallel_1.39.0
## [35] cachem_1.1.0         DelayedArray_0.31.7
## [37] abind_1.4-5          tidyselect_1.2.1
## [39] restfulr_0.0.15      labeling_0.4.3
## [41] maketools_1.3.0      fastmap_1.2.0
## [43] grid_4.4.1           colorspace_2.1-0
## [45] cli_3.6.3            SparseArray_1.5.18
## [47] S4Arrays_1.5.4       utf8_1.2.4
## [49] XML_3.99-0.17        withr_3.0.0
## [51] UCSC.utils_1.1.0     scales_1.3.0
## [53] bit64_4.0.5          XVector_0.45.0
## [55] httr_1.4.7           matrixStats_1.3.0

```

```
## [57] bit_4.0.5          png_0.1-8
## [59] memoise_2.0.1      evaluate_0.24.0
## [61] BiocIO_1.15.0      rlang_1.1.4
## [63] glue_1.7.0         DBI_1.2.3
## [65] jsonlite_1.8.8     R6_2.5.1
## [67] MatrixGenerics_1.17.0 GenomicAlignments_1.41.0
## [69] zlibbioc_1.51.1
```