

# An Introduction to *Guitar* Package

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## 1 Quick Start with Guitar

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

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

```
library(Guitar)

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

```

## The following objects are masked from 'package:base':
##
##   I, expand.grid, unname
## Loading required package: IRanges
## Loading required package: Seqinfo
## 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:Seqinfo':
##
##   intersect
## The following objects are masked from 'package:IRanges':
##
##   collapse, desc, intersect, setdiff, slice, union
## The following objects are masked from 'package:S4Vectors':
##
##   first, intersect, rename, setdiff, setequal,
##   union
## The following objects are masked from 'package:BiocGenerics':
##
##   combine, intersect, setdiff, setequal, union
## The following object is masked from 'package:generics':
##
##   explain
## The following objects are masked from 'package:stats':
##
##   filter, lag

```

```
## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union
##
## Attaching package: 'Guitar'
## The following object is masked from 'package:BiocGenerics':
##
##      normalize

# genomic features imported into named list
stBedFiles <- list(system.file("extdata", "m6A_mm10_exomePeak_1000peaks_bed12.bed",
                             package="Guitar"))
```

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

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

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

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

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

# Or use gff. file to generate guitarTxdb
# Or use getTxdb() to download TxDb from internet:
```

```
# txdb <- getTxdb(txGenomeVer="hg19")
# guitarTxdb <- makeGuitarTxdb(txdb)
```

You may now generate the Guitar plot from the named list of genome-based features.

```
GuitarPlot(txTxdb = txdb,
           stBedFiles = stBedFiles,
           miscOutFilePrefix = "example")

## [1] "20260428190327"
## [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] "20260428190337"
## [1] "import BED file /tmp/Rtmp9ld8x1/Rinst1ef60ee024ff2/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_b
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2
## 3.4.0.
## i Please use 'linewidth' instead.
## i The deprecated feature was likely used in the Guitar
## package.
## Please report the issue to the authors.
## This warning is displayed once per session.
## Call 'lifecycle::last_lifecycle_warnings()' to see where
## this warning was generated.
## 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.
```

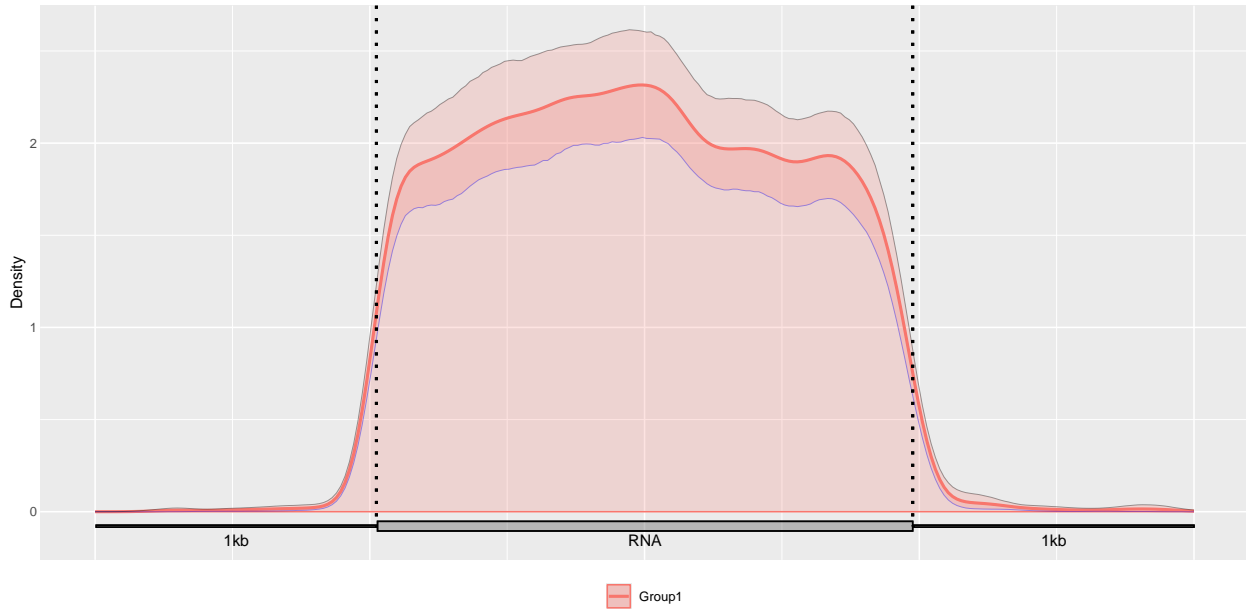
Alternatively, you may also optionally include the promoter DNA region and tail DNA region on the 5' and 3' side of a transcript in the plot with parameter `headOrtail = TRUE`.

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

## [1] "20260428190444"
## [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] "20260428190456"
## [1] "import BED file /tmp/Rtmp9ld8x1/Rinst1ef60ee024ff2/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.
```



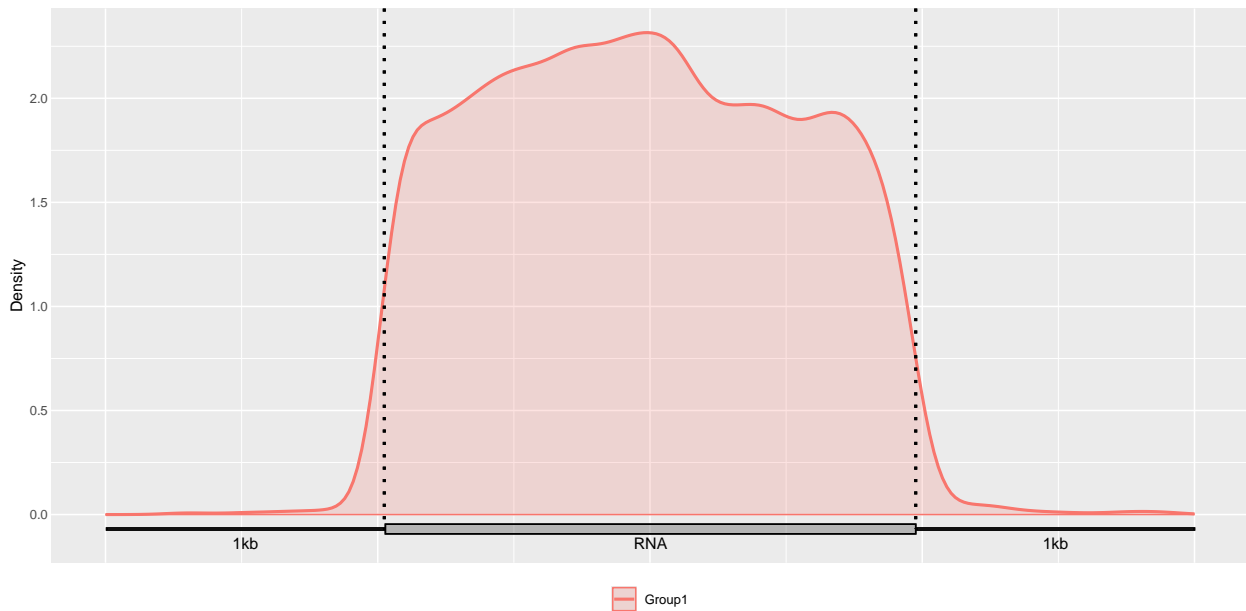
Alternatively, you may also optionally include the Confidence Interval for guitar plot with parameter `enableCI = FALSE`.

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

## [1] "20260428190533"
## [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] "20260428190544"
## [1] "import BED file /tmp/Rtmp9ld8x1/Rinst1ef60ee024ff2/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_b
## [1] "sample 10 points for Group1"
## [1] "start figure plotting for tx ..."

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



## 2 Supported Data Format

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

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

# Build Guitar Coordinates
txdb_file <- system.file("extdata", "mm10_toy.sqlite",
```



```

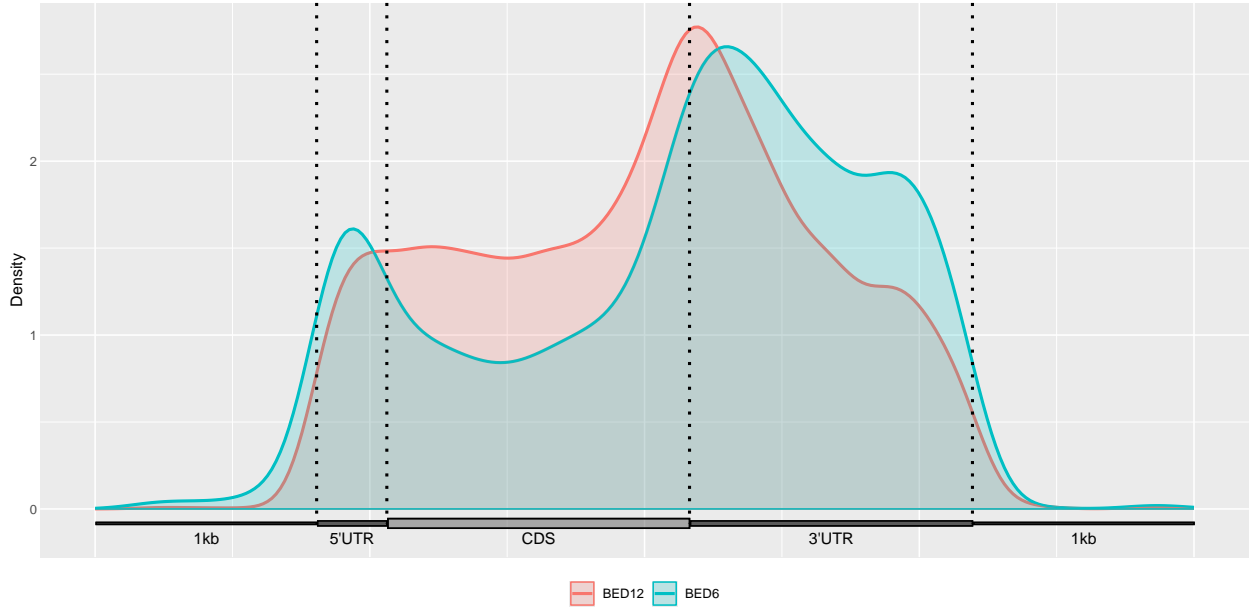
                                package="Guitar")
txdb <- loadDb(txdb_file)

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

## [1] "20260428190546"
## [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] "20260428190557"
## [1] "import BED file /tmp/Rtmp9ld8x1/Rinst1ef60ee024ff2/Guitar/extdata/m6A_mm10_exomePeak_1000peaks_b
## [1] "import BED file /tmp/Rtmp9ld8x1/Rinst1ef60ee024ff2/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$x' is discouraged.
## i Use 'x' instead.
## Warning: Use of 'densityCI$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.

```



### 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.

```

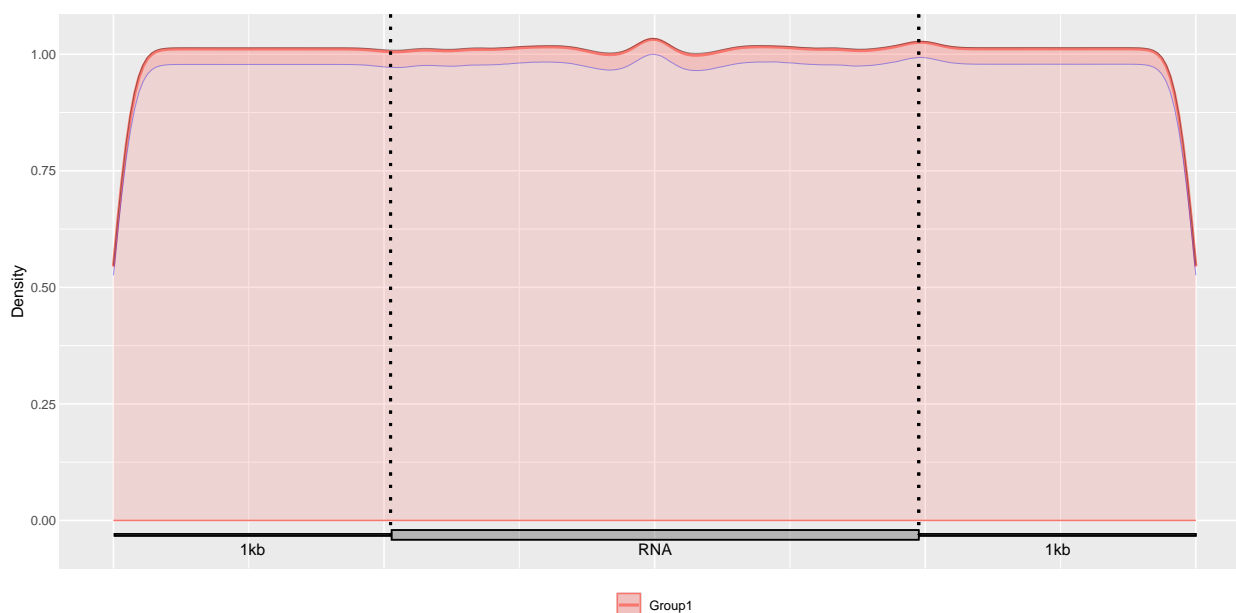
gcl <- list(guitarTxdb$tx$tx)
GuitarPlot(txTxdb = txdb,
            stGRangeLists = gcl,
            stSampleNum = 200,
            enableCI = TRUE,
            pltTxType = c("tx"),
            txPrimaryOnly = FALSE
)

## [1] "20260428190611"
## [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] "20260428190621"
## [1] "sample 200 points for Group1"
## [1] "start figure plotting for tx ..."

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

```

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



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

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

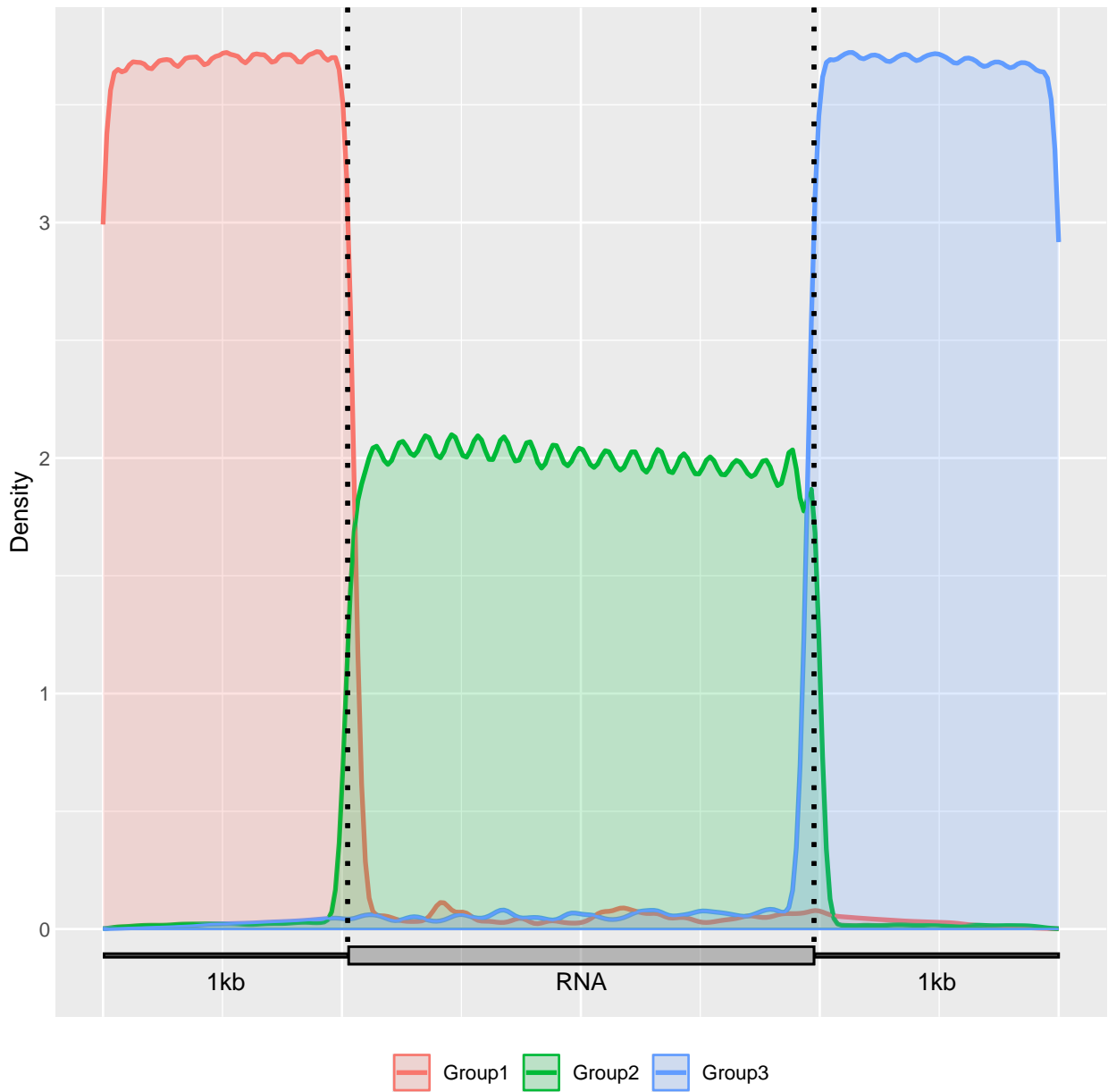
```

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

## [1] "20260428192559"
## [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] "20260428192609"
## [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
)

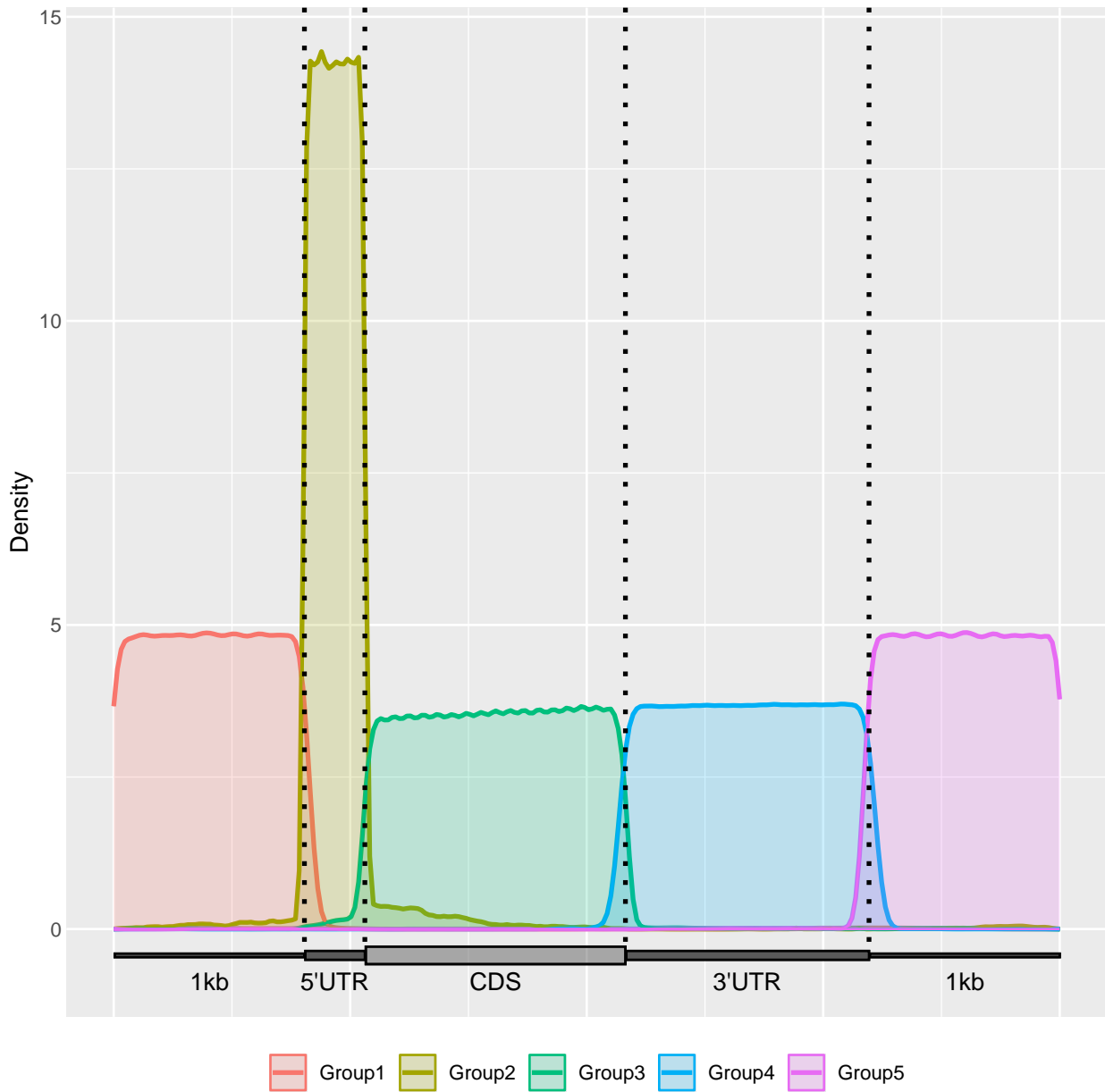
## [1] "20260428192628"
## [1] "There are 2946 transcripts of 2946 genes in the genome."
## [1] "total 2946 transcripts extracted ..."
## [1] "total 2719 transcripts left after ambiguity filter ..."
## [1] "total 2719 transcripts left after check chromosome validity ..."
## [1] "total 1342 mRNAs left 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] "20260428192640"
## [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] "20260428192654"
## [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 ..."
```

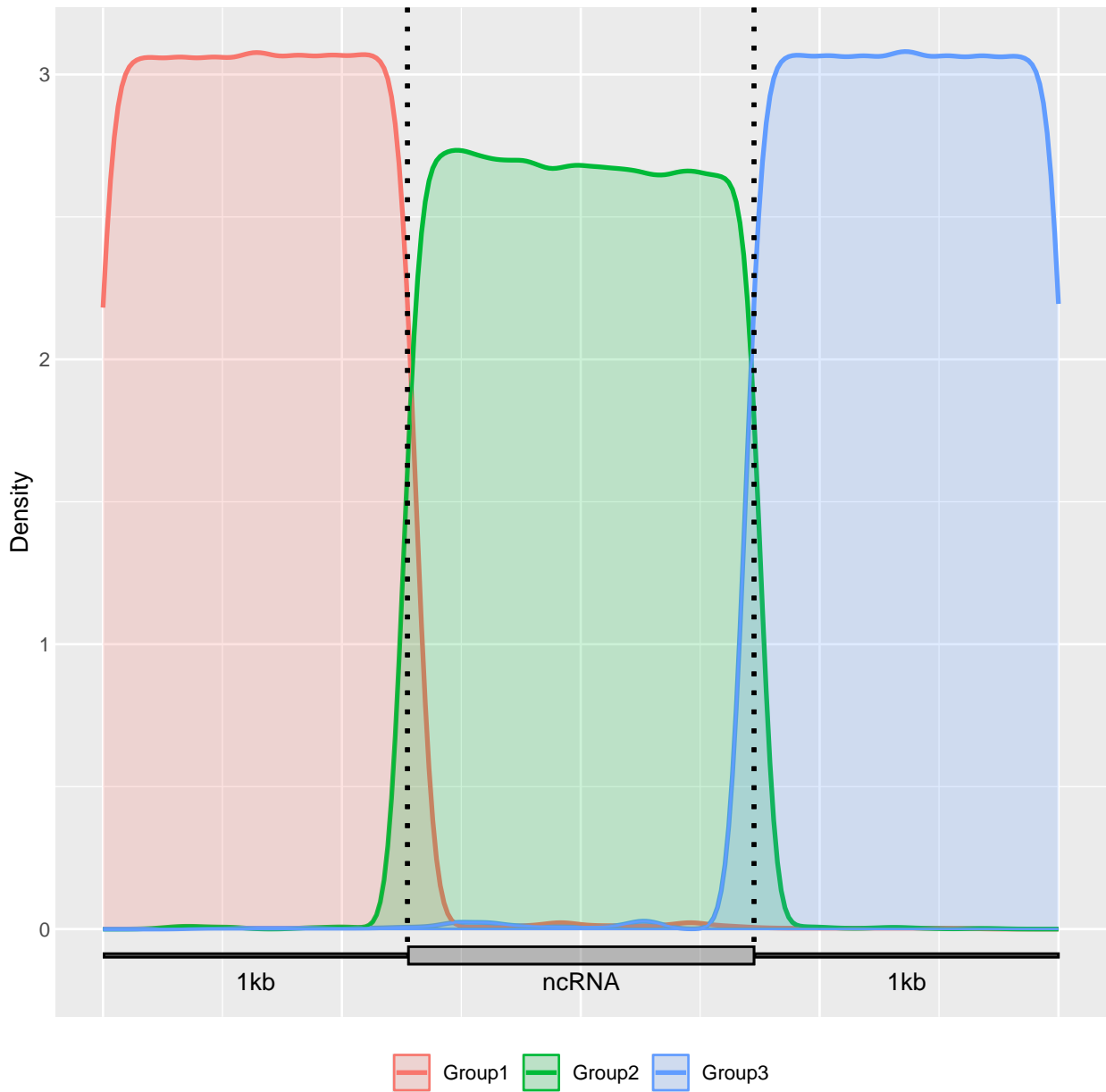


```

## [1] "generate components for lncRNA"
## [1] "generate chiped transcriptome"
## [1] "generate coverage checking ranges for ncrna"
## [1] "20260428192704"
## [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 4.6.0 RC (2026-04-17 r89917)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 24.04.4 LTS
##
## Matrix products: default
## BLAS: /home/biocbuild/bbs-3.24-bioc/R/lib/libRblas.so
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.12.0 LAPACK version 3.12.0
```

```

##
## 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
##
## time zone: America/New_York
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats4      stats      graphics  grDevices utils
## [6] datasets    methods    base
##
## other attached packages:
## [1] Guitar_2.29.0      dplyr_1.2.1
## [3] ggplot2_4.0.3      magrittr_2.0.5
## [5] rtracklayer_1.73.0 GenomicFeatures_1.65.0
## [7] AnnotationDbi_1.75.0 Biobase_2.73.0
## [9] GenomicRanges_1.65.0 Seqinfo_1.3.0
## [11] IRanges_2.47.0      S4Vectors_0.51.0
## [13] BiocGenerics_0.59.0 generics_0.1.4
## [15] knitr_1.51
##
## loaded via a namespace (and not attached):
## [1] KEGGREST_1.53.0      SummarizedExperiment_1.43.0
## [3] gtable_0.3.6         rjson_0.2.23
## [5] xfun_0.57            lattice_0.22-9
## [7] vctrs_0.7.3          tools_4.6.0
## [9] bitops_1.0-9         curl_7.1.0
## [11] parallel_4.6.0       tibble_3.3.1
## [13] RSQLite_2.4.6         highr_0.12
## [15] blob_1.3.0           pkgconfig_2.0.3
## [17] Matrix_1.7-5         RColorBrewer_1.1-3
## [19] S7_0.2.2             cigarillo_1.3.0
## [21] lifecycle_1.0.5      compiler_4.6.0
## [23] farver_2.1.2         textshaping_1.0.5
## [25] Rsamtools_2.29.0     Biostrings_2.81.0
## [27] codetools_0.2-20     RCurl_1.98-1.18
## [29] yaml_2.3.12          pillar_1.11.1
## [31] crayon_1.5.3         BiocParallel_1.47.0
## [33] DelayedArray_0.39.0  cachem_1.1.0
## [35] abind_1.4-8          tidyselect_1.2.1
## [37] restfulr_0.0.16      labeling_0.4.3
## [39] fastmap_1.2.0        grid_4.6.0
## [41] cli_3.6.6            SparseArray_1.13.0
## [43] S4Arrays_1.13.0      dichromat_2.0-0.1
## [45] XML_3.99-0.23        withr_3.0.2
## [47] scales_1.4.0         bit64_4.8.0
## [49] XVector_0.53.0       httr_1.4.8
## [51] matrixStats_1.5.0    bit_4.6.0
## [53] otel_0.2.0           ragg_1.5.2

```

```
## [55] png_0.1-9          memoise_2.0.1
## [57] evaluate_1.0.5      BiocIO_1.23.0
## [59] rlang_1.2.0         glue_1.8.1
## [61] DBI_1.3.0           R6_2.6.1
## [63] systemfonts_1.3.2   MatrixGenerics_1.25.0
## [65] GenomicAlignments_1.49.0
```