

# Package ‘RCircos’

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**Type** Package

**Title** Circos 2D Track Plot

**Version** 1.1.0

**Date** 2013-05-09

**Author** Hongen Zhang

**Maintainer** Hongen Zhang <hzhang@mail.nih.gov>

**Description** RCircos package provides a simple and flexible way to generate Circos 2D track plot images for genomic data visualization. The types of plots include: heatmap, histogram, lines, scatterplot, tiles and plot items for further decorations include connector, links, and text (gene) label. All functions require only R graphics package that comes with R base installation.

**License** GPL (>=2)

**Depends** R (>= 2.10)

**URL** <http://bitbucket.org/henryhzhang/rcircos>

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---

RCircos-package

*Circos-like Plot of Genomic Data*


---

## Description

This is the R implement of basic Circos plots of genomic data.

## Details

Package: RCircos  
 Type: Package  
 Version: 1.1.0  
 Date: 2013-05-09  
 License: GPL (>=2)

RCircos package provides a simple and flexible way to make Circos 2D track plots with R and could be easily integrated into other R data processing and graphic manipulation pipelines for presenting large-scale multi-sample genomic research data. It can also serve as a base tool to generate complex Circos images. Currently, RCircos supports genomic data plot for three species: human, mouse, and rat. Data plots include chromosome ideogram with cytoband, heatmap, histogram, lines, scatterplot, and tiles. Plot items for further decorations have connectors, links, and text (gene) labels. Each plot is implemented with a specific function and input data for all functions are data frames which can be objects read from text files or generated with other R pipelines.

Hongen Zhang  
Maintainer: Hongen Zhang <hzhang@mail.nih.gov>

Hongen Zhang, Paul Meltzer, and Sean Davis. RCircos: an R package for Circos 2D track plots. To be published soon.

```
# Load RCircos library
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);


# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);


# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);
```

```
# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();
```

---

RCircos.Data.Point *Convert a Genomic Position to an Index of Circos Plot Position*

---

### Description

Calculate the index of Circos plot positions (a set of x- and y-coordinates for a circular line) for a genomic position (chromosome name and start position). This function is for internal use only.

### Usage

```
RCircos.Data.Point(chromosome, start)
```

### Arguments

chromosome	Character vector, a chromosome name with prefix of "chr", e.g., "chr1".
start	Integer, start position of a genomic interval (e.g, a gene or a band) on the chromosome.

### Value

An integer representing the index of RCircos plot positions.

### Author(s)

Hongen Zhang

---

RCircos.Gene.Connector.Plot  
*Draw Connectors between Chromosome Ideogram and Gene Names*

---

### Description

Draw a set of connectors (three lines for each connector) between chromosome ideogram and gene names. RCircos core components and graphics device must be initialized before drawing.

### Usage

```
RCircos.Gene.Connector.Plot(genomic.data, track.num, side)
```

## Arguments

<code>genomic.data</code>	A data frame with the first four columns for chromosome names, start positions, end positions, and gene names.
<code>track.num</code>	Integer, representing the ordinal number of the plot track where the connectors are plotted.
<code>side</code>	Character vector, either "in" or "out" representing the position related to chromosome ideogram.

**Author(s)**

Hongen Zhang

## Examples

[illegible]

```
RCircos.Gene.Connector.Plot(RCircos.Gene.Label.Data, 1, "in");
```

---

```
RCircos.Gene.Label.Data
```

*Sample Data for Gene Labels*

---

## Description

RCircos.Gene.Label.Data contains genomic position information for 192 genes. Each row of the data contains genomic position and gene name for one gene in the order of chromosome name, start position, end position, and gene name.

## Usage

```
data(RCircos.Gene.Label.Data)
```

## Format

A data frame with 192 observations on the following 4 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8  
chr9 chrX

chromStart a numeric vector

chromEnd a numeric vector

Gene a factor with levels ABL1 ACN9 ACVR1B AKT1 ALK APC ARHGEF2 ARID1A ASXL1 ATM  
ATRX BAG3 BAI3 BAP1 BCAN BCL2 BRAF BRCA1 BRCA2 CA12 CA9 CALU CARD11 CBL  
CCND1 CD34 CDC73 CDH1 CDK4 CDKN2A CDX2 CEACAM7 CEBPA CES3 CRLF2 CSF1R  
CSF3 CTNNA1 CTNNB1 CUL2 CYLD CYP1A1 DAXX DCC DES DIRAS1 DIRC2 DKK3  
DLD DMBT1 DNMT3A DPYD EGF EGFR EGR3 EIF4G2 EML4 ENO1 ENO2 ERBB2 ERBB3  
ERBB4 ERG EZH2 F10 FAM123B FBXW7 FGFR1 FGFR2 FGFR3 FH FHIT FLCN FLT3  
FOXL2 FZR1 GATA1 GATA2 GATA3 GFAP GNA11 GNAQ GNAS GRP GSTM1 HIVEP3  
HNF1A HRAS IDH1 IDH2 IFNA1 IL2 ITGB5 JAK1 JAK2 JAK3 KDR KIT KRAS KRT20  
MAGI1 MAP2K4 MEN1 MET MGMT MIB1 MKI67 MLH1 MPL MSH2 MSH6 MUC1 MUC17  
MUC2 MUTYH MVP MYC MYD88 NAT1 NAT2 NES NF1 NF2 NOTCH1 NOTCH2 NPM1 NRAS  
PBRM1 PCNA PDGFRA PDZD4 PGR PHOX2B PIK3CA PMS2 PPP2R1A PRCC PRKAR1A  
PTCH1 PTEN PTGS2 PTPN11 RB1 REEP5 RET RNF139 RNF2 RPS15 RUNX1 SDHA  
SDHAF1 SDHAF2 SDHB SDHC SDHD SELT SETD2 SLC38A1 SLC6A2 SLTM SMAD4  
SMARCA4 SMARCB1 SMO SMOX SMUG1 SOCS1 SRC SST STC1 STK11 SUFU SYP TCF7L2  
TET2 TFE3 TFEB TMEM97 TNFAIP3 TNFSF13 TP53 TPD52L2 TPM4 TSC1 TSC2  
TSHR TYK2 VHL VIM WT1 XRCC1 ZNF135

## Source

Unpublished data.

---

RCircos.Gene.Name.Plot

*Draw Gene Names on a Data Track*


---

## Description

Label gene names along chromosome ideogram or a data track. RCircos core components and graphic device must be initialized before drawing.

## Usage

```
RCircos.Gene.Name.Plot(gene.data, name.col, track.num, side)
```

## Arguments

gene.data	A data frame. The first three columns should be chromosome name, start position, end position.
name.col	Integer, representing the ordinal number of the column in input data that contains gene names.
track.num	Integer, representing the ordinal number of the plot track where the gene names are plotted.
side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

## Author(s)

Hongen Zhang

## Examples

```
# Load RCircos library
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
```

```

RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);

# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();

# Load gene label data and plot gene names
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Gene.Label.Data);
name.col <- 4;
track.num <- 2;
side <- "in";
RCircos.Gene.Name.Plot(RCircos.Gene.Label.Data,
                       name.col, track.num, side);

```

---

```
RCircos.Get.Gene.Label.Locations
```

*Calculate New Position for Gene Labels*

---

## Description

This function calculates new plot position from genomic positions for gene labeling. In case there are too many genes in a genomic interval, the labels may become overlapped so that correct numbers and new plot positions are often needed to make the labels readable. This function will remove extra label data points if they cannot fit in the given genomic interval.

This function is for internal use only.

## Usage

```
RCircos.Get.Gene.Label.Locations(genomic.data)
```

## Arguments

`genomic.data` A data frame. The first three columns should be chromosome name, start position, end position.

## Value

A data frame containing same contents as the input `genomic.data` plus one column with RCircos plot positions.

## Author(s)

Hongen Zhang



---

RCircos.Get.Plot.Data

*Convert Genomic Data to RCircos Plot Data*


---

### Description

This function calculates the RCircos plot positions for genomic positions of the dataset. RCircos plot position is the row index of matrix that contains x- and y-coordinates of a circular line. A new column for RCircos plot positions is appended to the input genomic.data and returned.

This function is for internal use.

### Usage

```
RCircos.Get.Plot.Data(genomic.data, plot.type)
```

### Arguments

`genomic.data` A data frame with the first three columns as chromosome name, start and end position followed by data values for one or more samples.

`plot.type` Character vector, either "plot" or "link".

### Value

Updated genomic data (with a new column for RCircos plot positions)

### Author(s)

Hongen Zhang

---

RCircos.Get.Plot.Ideogram

*Get Chromosome Ideogram Object*


---

### Description

Get the chromosome ideogram object used during current RCircos session. RCircos core components must be initialized first. This function is mainly for internal use.

### Usage

```
RCircos.Get.Plot.Ideogram()
```

### Value

A data frame containing all information for chromosome ideogram plot. The first five column are original cytoband data and following are chromosome highlight colors, and plot colors, length, number of chromosome unit, and relative location on the circular layout of each band.

### Author(s)

Hongen Zhang

---

```
RCircos.Get.Plot.Parameters
```

*Get All RCircos Plot Parameters*

---

## Description

Get all parameters used during current RCircos session in order to check and reset plot parameters. RCircos core components must be initialized first.

## Usage

```
RCircos.Get.Plot.Parameters()
```

## Value

A list of all parameters used for RCircos plot.

## Author(s)

Hongen Zhang

## Examples

```
# Load RCircos library
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);

# Get RCircos plot parameters
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

params <- RCircos.Get.Plot.Parameters();
params
```

### Get RCircos Plot Position Object

Get the data frame of base plot positions which are used to derive all other positions of RCircos plot. RCircos core components must be initialized first. This function is mainly for internal use.

```
RCircos.Get.Plot.Positions()
```

Hongen Zhang

[illegible]

```
positions <- RCircos.Get.Plot.Positions();
head(positions)
```

---

```
RCircos.Heatmap.Data
```

*Sample Data for RCircos Heatmap Plot*

---

## Description

A dataset with the first three columns as chromosome names, start position, and end position followed by a column of gene names then columns of gene expression values.

## Usage

```
data(RCircos.Heatmap.Data)
```

## Format

A data frame with 6660 observations on the following 10 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8  
chr9 chrX chrY

chromStart a numeric vector

chromEnd a numeric vector

GeneName a character vector

X786.O a numeric vector

A498 a numeric vector

A549.ATCC a numeric vector

ACHN a numeric vector

BT.549 a numeric vector

CAKI.1 a numeric vector

## Source

Modified from NCBI GEO dataset: GSE32474.

---

RCircos.Heatmap.Plot

*Circos-like Heatmap Plot*


---

## Description

Draw one track of heatmap. RCircos core components and graphic device must be initialized before drawing.

## Usage

```
RCircos.Heatmap.Plot(heatmap.data, data.col, track.num, side)
```

## Arguments

heatmap.data	A data frame with the first three columns as chromosome names, start position and end position of each data point followed by data values for one or more samples.
data.col	Integer, representing the ordinal number of the column in input data set that contains the data to be plotted.
track.num	Integer, representing the ordinal number of the plot track where the heatmap will be plotted.
side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

## Author(s)

Hongen Zhang

## Examples

```
# Load RCircos library
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);

# Set RCircso core components
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
```

```

num.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);

# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();

# Load heatmap label data and plot one heatmap track
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Heatmap.Data);
data.col <- 5
track.num <- 4;
side <- "in";
RCircos.Heatmap.Plot(RCircos.Heatmap.Data, data.col,
                     track.num, side);

```

---

RCircos.Histogram.Data

*Sample Data for Circos Histogram Plot*

---

## Description

A dataset with the first three columns as chromosome names, start position, and end position followed by a column of histogram data.

## Usage

```
data(RCircos.Histogram.Data)
```

## Format

A data frame with 324 observations on the following 4 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8  
chr9 chrX chrY

chromStart a numeric vector

chromEnd a numeric vector

Data a numeric vector

## Source

Unpublished data.

---

RCircos.Histogram.Plot

*Circos-like Histogram Plot*


---

## Description

Draw one track of histogram. RCircos core components and graphic device must be initialized before drawing.

## Usage

```
RCircos.Histogram.Plot(hist.data, data.col, track.num, side)
```

## Arguments

hist.data	A data frame with the first three columns as chromosome names, start position and end position of each data point followed by data values for one or more samples.
data.col	Integer, representing the ordinal number of the column in input data that contains the data to be plotted.
track.num	Integer, representing the ordinal number of the plot track where the histogram will be plotted.
side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

## Author(s)

Hongen Zhang

## Examples

```
# Load RCircos library
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);

# Set RCircso core components
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
```

```

num.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);

# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();

# Load histogram data and plot one histogram track
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Histogram.Data);
data.col <- 4;
track.num <- 5;
side <- "in";
RCircos.Histogram.Plot(RCircos.Histogram.Data,
                       data.col, track.num, side);

```

---

```
RCircos.Initialize.Parameters
```

*Initialize RCircos Plot Parameters*

---

## Description

Setup default values for RCircos plot. All parameters are held in one list. This function is for internal use.

## Usage

```
RCircos.Initialize.Parameters(tracks.inside, tracks.outside)
```

## Arguments

`tracks.inside`

Integer, how many tracks will be put inside of chromosome ideogram.

`tracks.outside`

Integer, how many tracks will be put outside of chromosome ideogram.

## Author(s)

Hongen Zhang



---

RCircos.Line.Data    *Sample Data for Circos Line Plot*


---

**Description**

A data frame with the first three columns as chromosome name, start and end position followed by columns of DNA copy number variant data (num.mark and seg.mean).

**Usage**

```
data(RCircos.Line.Data)
```

**Format**

A data frame with 2037 observations on the following 5 variables.

```
chromosome a factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8
          9 X Y
start      a numeric vector
stop       a numeric vector
num.mark   a numeric vector
seg.mean   a numeric vector
```

**Source**

Unpublished data.

---

RCircos.Line.Plot    *Circos-like Line Plot*


---

**Description**

Draw one track of line plot. RCircos core components and graphics device must be initialized before drawing.

**Usage**

```
RCircos.Line.Plot(line.data, data.col, track.num, side)
```

**Arguments**

line.data	A data frame with the first three columns as chromosome names, start position and end position of each data point followed by data values for one or more samples.
data.col	Integer, representing the ordinal number of the column in input dataset that contains the data to be plotted.
track.num	Integer, representing the ordinal number of the plot track where the lines will be plotted.
side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

**Author(s)**

Hongen Zhang

**Examples**

```

# Load RCircos library
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);

# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();

# Load line plot data and plot one track of lines
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Line.Data);
data.col <- 4;
track.num <- 5;
side <- "in";
RCircos.Line.Plot(RCircos.Line.Data, data.col,
                  track.num, side);

```

**Description**

A data frame containing paired genomic position data for each row. The content of each row must be in the order of name, start and end position of chromosome A then name, start and end position of chromosome B. This data frame is directly used to draw link lines without extra processing.

**Usage**

```
data(RCircos.Link.Data)
```

**Format**

A data frame with 71 observations on the following 6 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr14 chr15 chr17 chr19  
chr2 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX

chromStart a numeric vector

chromEnd a numeric vector

Chromosome.1 a factor with levels chr1 chr10 chr11 chr12 chr14 chr15 chr16 chr17  
chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8 chr9  
chrX

chromStart.1 a numeric vector

chromEnd.1 a numeric vector

**Source**

Unpublished data.

---

RCircos.Link.Line *Draw A Circos Link Line*

---

**Description**

Calculate and draw a quadratic Bezier curve between two points with (0,0) as control points. This function is for internal use.

**Usage**

```
RCircos.Link.Line(line.start, line.end, line.color)
```

**Arguments**

line.start	The position (a point) where the Bezier curve starts.
line.end	The position (a point) where the Bezier curve ends.
line.color	Color for the Bezier curve. Any value that represents a R color.

**Author(s)**

Hongen Zhang

---

RCircos.Link.Plot    *Circos-like Link Line Plot*


---

**Description**

Draw lines (quadratic Bezier curves) between paired genomic positions. RCircos core components and graphic device must be initialize before drawing. Link lines are always in the center of plot area.

**Usage**

```
RCircos.Link.Plot(link.data, track.num, by.chromosome = FALSE)
```

**Arguments**

link.data	A data frame with paired genomic positions in each row. The first three columns are for chromosome names, start and end position of one genomic position followed by three columns for chromosome names, start and end position of the second genomic position.
track.num	Integer, representing the ordinal number of the plot track where the link lines will start.
by.chromosome	Logic. If true, red color will be used for links between positions of same chromosomes and blue color for links between different chromosomes. Otherwise, different colors will be automatically assigned for each line.

**Author(s)**

Hongen Zhang

**Examples**

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
```

```

RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);

# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();

# Load link data and plot link lines
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Link.Data);
track.num <- 10;
RCircos.Link.Plot(RCircos.Link.Data, track.num, TRUE);

```

---

```
RCircos.List.Parameters
```

*Print RCircos Parameters to Standard Output*

---

## Description

Display all graphic parameters used by current RCircos session on standard output. RCircos core components must be initialized first.

## Usage

```
RCircos.List.Parameters()
```

## Author(s)

Hongen Zhang

## Examples

```

# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);

```

```

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
num.inside <- 5;
num.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             num.inside, num.outside);

# List RCircos plot parameters
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.List.Parameters();

```

---

```

RCircos.Mouse.Expr.Data
      Sample Data of Mouse Gene Expression

```

---

## Description

A data frame containing mouse genomic position information and gene expression values.

## Usage

```
data(RCircos.Mouse.Expr.Data)
```

## Format

A data frame with 16499 observations on the following 5 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
chr17 chr18 chr19 chr2 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX chrY

txStart a numeric vector

txEnd a numeric vector

Gene a character vector

Expr.Mean a numeric vector

## Source

Modified from GEO dataset: GSE42081.

---

RCircos.Multiple.Species.Core.Components

*Setup RCircos Core Components with Multiple Species*


---

## Description

Setup RCircos core components with chromosome ideograms of multiple species for visulization of similarity and difference of genomic data between different species.

## Usage

```
RCircos.Multiple.Species.Core.Components(cyto.info.list,
                                         species.list, chr.exclude = NULL,
                                         tracks.inside, tracks.outside)
```

## Arguments

cyto.info.list	A List contains data frames for chromosome ideogram data of different species. All data frames in the list must have same columns.
species.list	Character vector represent multiple species. Each one will be used as prefix of chromosome names for relavant species. The order of species must match the order of the species in cyto.info.list.
chr.exclude	Character vector of chromosome names to be excluded from plot, e.g., chr.exclude <- c("chrX", "chrY");
tracks.inside	Integer, total number of data tracks inside of chromosome ideogram.
tracks.outside	Integer, total number of data tracks outside of chromosome ideogram.

## Author(s)

Hongen Zhang

## Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load mouse and rat chromosome ideograms and make
# a multiple species cytoband data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.Mouse.GRCm38.CytoBandIdeogram);
data(UCSC.Baylor.3.4.Rat.cytoBandIdeogram);
cyto.list <- list(UCSC.Mouse.GRCm38.CytoBandIdeogram,
                  UCSC.Baylor.3.4.Rat.cytoBandIdeogram);
```

```

species <- c("M", "R");

# Set RCircos core components with multiple species
# cytoband data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

tracks.inside <- 5;
tracks.outside <- 0;
RCircos.Multiple.Species.Core.Components(cyto.list,
                                          species, NULL, tracks.inside, tracks.outside);

```

---

RCircos.Multiple.Species.Dataset

*Construct A Dataset from Multiple Genomic Data of Different Species*

---

## Description

Combine plot datasets from different species as one data frame for RCircos plot with multiple sets of chromosome ideogram.

## Usage

```
RCircos.Multiple.Species.Dataset(data.list, species)
```

## Arguments

data.list	A List contains data frames for genomic data of different species. All data frames in the list must have same columns.
species	Character vector represent multiple species. Each one will be used as prefix of chromosome names for relevant species. The order of species must match the order of the species in data.list.

## Value

A data frame contains all input plot data.

## Author(s)

Hongen Zhang

## Examples

```

# Load RCircos library
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load mouse and rat gene expression datasets
# _____

```



```
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(RCircos.Mouse.Expr.Data);
data(RCircos.Rat.Expr.Data);
data.list <- list(RCircos.Mouse.Expr.Data,
                  RCircos.Rat.Expr.Data);
species <- c("M", "R");

# Generate data frome that contains both mouse and
# rat gene expression data
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

new.data <- RCircos.Multiple.Species.Dataset(data.list,
                                              species);
```

---

RCircos.Rat.Expr.Data

*Sample Data of Rat Gene Expression*


---

## Description

A data frame containing rat genes, genomic position and expression values of these genes.

## Usage

```
data(RCircos.Rat.Expr.Data)
```

## Format

A data frame with 11426 observations on the following 5 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
chr17 chr18 chr19 chr2 chr20 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX

txStart a numeric vector

txEnd a numeric vector

Gene a character vector

Expr.Mean a numeric vector

## Source

Modified from GEO dataset: GSE42081.

---

RCircos.Reset.Plot.Parameters

*Reset RCircos Plot Parameters*


---

## Description

Reset RCircos plot parameters after they were initialized. Also update chromosome ideogram and base positions when necessary. Among the parameters, chromosome padding is automatically calculated with base.per.unit unless the padding is set to zero. Parameters related to radius are automatically adjusted based on radius.

## Usage

```
RCircos.Reset.Plot.Parameters(new.params)
```

## Arguments

`new.params`      An list contains all plot parameters with updated values.

## Author(s)

Hongen Zhang

## Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             tracks.inside, tracks.outside);

# List RCircos plot parameters then get RCircos plot
# parameters, reset base.per.unit to 30000 and then
# reset RCircos plot parameters. List RCircos plot
```

```
# parameters again to see the change
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.List.Parameters();
params <- RCircos.Get.Plot.Parameters();
params$base.per.unit <- 30000;
RCircos.Reset.Plot.Parameters(params);
RCircos.List.Parameters();
```

---

RCircos.Scatter.Data

*Sample Data for Circos Scatter Plot*

---

### Description

A data frame with the first three columns as chromosome name, start and end position followed by columns of DNA copy number variant data (num.mark and seg.mean).

### Usage

```
data(RCircos.Scatter.Data)
```

### Format

A data frame with 1757 observations on the following 5 variables.

```
chromosome a factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8
          9 X Y
start a numeric vector
stop a numeric vector
num.mark a numeric vector
seg.mean a numeric vector
```

---

RCircos.Scatter.Plot

*Circos-like Scatter Plot*

---

### Description

Draw one track of scatter plot. RCircos core components and graphics device must be initialized before drawing.

### Usage

```
RCircos.Scatter.Plot(scatter.data, data.col, track.num,
                    side, by.fold = 0)
```

**Arguments**

<code>scatter.data</code>	A data frame with the first three columns as chromosome name, start position and end position of each data point followed by data values for one or more samples.
<code>data.col</code>	Integer, representing the ordinal number of the column in input dataset that contains the data to be plotted.
<code>track.num</code>	Integer, representing the ordinal number of the plot track where the data will be plotted.
<code>side</code>	Character vector, either "in" or "out", representing the position related to chromosome ideogram.
<code>by.fold</code>	Zero or a positive float number, if it is greater than zero, any data point with a value greater or equal to the <code>by.fold</code> will be plot as red color and data points with values less or equal to negative <code>by.fold</code> will be plot as blue color. Otherwise, black color is used.

**Author(s)**

Hongen Zhang

**Examples**

```
# Load RCircos library
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             tracks.inside, tracks.outside);

# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();
```



**Arguments**

`cyto.info` A data frame with chromosome ideogram data and columns are ordered by chromosome names, start position, end position, band names, and stain intensity for each chromosome band.

`chr.exclude` Character vector of chromosome names to be excluded from plot, e.g., `chr.exclude <- c("chrX", "chrY")`;

`tracks.inside` Integer, total number of data tracks inside of chromosome ideogram.

`tracks.outside` Integer, total number of data tracks outside of chromosome ideogram.

**Author(s)**

Hongen Zhang

**Examples**

```
# Load RCircos libaray
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;

# Set RCircso core components
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             tracks.inside, tracks.outside);
```

---

RCircos.Set.Cytoband.data

*Setup Chromosome Cytoband Data for RCircos Plot*

---

**Description**

Calculate band length (number of base pairs), number of chromosome units (plot points needed to cover the band), relevant locations of each band on the circular layout, and assign colors to chromosome highlights and each band. This function is for internal use.

## Usage

```
RCircos.Set.Cytoband.data(cyto.band.info)
```

## Arguments

cyto.band.info

A data frame with chromosome ideogram data and columns are ordered by chromosome names, start position, end position, band names, and stain intensity for each chromosome band.

**Author(s)**

Hongen Zhang

RCircos.Set.Plot.Area

### Setup Plot Area for RCircos Plot

### Description

Open an new window for plotting. RCircos core components must be initialized before call this function. All four margins are set to 0.25 and window size are set to `plot.radius` in RCircos parameters. This function is optional and could be replaced by call `par()`, `plot.new()`, and `plot.window()` if users want control the plot window by themselves.

## Usage

```
RCircos.Set.Plot.Area()
```

**Author(s)**

Hongen Zhang

## Examples

[illegible]

```
chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
                             tracks.inside, tracks.outside);

# Set plot area, i.e., initialize graphic device
# -----
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
```

---

RCircos.Tile.Data    *Sample Data for Circos Tile Plot*

---

### Description

A data frame containing genomic position data only (chromosome, start and end positions).

### Usage

```
data(RCircos.Tile.Data)
```

### Format

A data frame with 152 observations on the following 3 variables.

Chromosome   a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
               chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8  
               chr9 chrX chrY

chromStart   a numeric vector

chromEnd    a numeric vector

### Source

Unpublished Data.

---

RCircos.Tile.Plot    *Circos-like Tile Plot*

---

### Description

Draw one track of Tiles. RCircos core components and graphics device must be initialized before drawing.

### Usage

```
RCircos.Tile.Plot(tile.data, track.num, side)
```



## Arguments

<code>tile.data</code>	A data frame with three columns as chromosome names, start position and end position of each data point. Columns for data values are optional.
<code>track.num</code>	Integer, representing the ordinal number of the plot track where the data will be plotted.
<code>side</code>	Character vector, either "in" or "out", representing the position related to chromosome ideogram.

**Author(s)**

Hongen Zhang

## Examples

[illegible]

```
track.num <- 6;
side <- "in";
RCircos.Tile.Plot(RCircos.Tile.Data, track.num, side);
```

---

RCircos.Track.Outline

*Draw Outline for A Data Plot Track*


---

## Description

Draw outline with subtracks for one data plot track. RCircos core components and graphic device must be initialized first. This function is mainly for internal use.

## Usage

```
RCircos.Track.Outline(out.pos, in.pos, num.layers)
```

## Arguments

out.pos	Float number, the outside position of a data track.
in.pos	Float number, the inside position of a data track.
num.layers	Integer, total number of subtrack in a data plot track.

## Author(s)

Hongen Zhang

## Examples

```
# Load RCircos libaray
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

library(RCircos);

# Load human chromosome ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

data(UCSC.HG19.Human.CytoBandIdeogram);
cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;

# Set RCircso core components
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

cyto.info <- UCSC.HG19.Human.CytoBandIdeogram;
chr.exclude <- c("chrX", "chrY");
tracks.inside <- 5;
tracks.outside <- 0;
RCircos.Set.Core.Components(cyto.info, chr.exclude,
```

```

        tracks.inside, tracks.outside);

# Initialize graphic device and plot chromosome
# ideogram
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

RCircos.Set.Plot.Area();
RCircos.Chromosome.Ideogram.Plot();

# Plot one track outline
# _____
# xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

side <- "in";
track.num <- 1;
locations <- RCircos.Track.Positions(side, track.num);
out.pos <- locations[1];
in.pos <- locations[2];
subtracks <- 5;
RCircos.Track.Outline(out.pos, in.pos, subtracks);

```

---

RCircos.Track.Positions

*Calculate Data Plot Track Positions*


---

## Description

Calculate inner and outer plot positions for a data track. RCircos core components must be initialized first. This function is for internal use only.

## Usage

```
RCircos.Track.Positions(side, track.num)
```

## Arguments

side	Character vector, either "in" or "out", representing the position related to chromosome ideogram.
track.num	Integer, representing the ordinal number of the plot track

## Author(s)

Honggen Zhang

### Validate Chromosome Ideogram Data

Validate chromosome ideogram information including of chromosome names, order of chromosomes, chromosome start and chromosome end positions for each chromosome band. This function is mainly for internal use.

```
RCircos.Validate.Cyto.Info(cyto.info, chr.exclude)
```

<code>cyto.info</code>	A data frame with chromosome ideogram data includes chromosome names, start position, end position, band names, and stain intensity for each chromosome band.
<code>chr.exclude</code>	Character vector of chromosome names to be excluded from plot, e.g., <code>chr.exclude &lt;- c("chrX", "chrY");</code>

Data frame with validated chromosome ideogram information.

## Hongen Zhang

### Validate Genomic Data for RCircos Plot

Validate input dataset for correct chromosome names, chromosome start, and chromosome end positions. Chromosome names will be converted to character vectors if they are factor variables. This function is for internal use.

[illegible]

**Arguments**

- `genomic.data` A data frame with the first three columns as chromosome names, start and end positions. Following columns may be another set of chromosome names, start and end positions then zero or more data columns.
- `plot.type` Character vector either "plot" for dataset with one set of genomic position data or "link" for dataset with paired genomic position data .

**Value**

The validated data frame.

**Author(s)**

Hongen Zhang

---

RCircos.Workflow      *Print Out RCircos Workflow*

---

**Description**

Display RCircos plot workflow on standard output device for a quick guide.

**Usage**

```
RCircos.Workflow()
```

**Author(s)**

Hongen Zhang

**Examples**

```
library(RCircos);
RCircos.Workflow();
```

---

UCSC.Baylor.3.4.Rat.cytoBandIdeogram  
*Cytoband Information for Rat Chromosome Ideogram*

---

**Description**

A data frame containing chromosome name, start and end position, band name, and intensity of Giemsa stains for each cytoband.

**Usage**

```
data(UCSC.Baylor.3.4.Rat.cytoBandIdeogram)
```

**Format**

A data frame with 246 observations on the following 5 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
chr17 chr18 chr19 chr2 chr20 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX

ChromStart a numeric vector

ChromEnd a numeric vector

Band a factor with levels p11 p12 p13 p14 p15 p16 p21 p22 q11 q12 q12.1 q12.2  
q12.3 q12.4 q12.5 q13 q14 q15 q16 q21 q22 q23 q24 q25 q26 q27 q31 q32  
q32.1 q32.2 q32.3 q33 q34 q35 q36 q37 q38 q41 q42 q43 q44 q45 q51 q52  
q53 q54 q55

Stain a factor with levels gneg gpos gvar

**Source**

<http://genome.ucsc.edu>

---

UCSC.HG19.Human.CytoBandIdeogram

*Cytoband Information for Human Chromosome Ideogram*

---

**Description**

A data frame containing chromosome name, start and end position, band name, and intensity of Giemsa stains for each cytoband.

**Usage**

```
data(UCSC.HG19.Human.CytoBandIdeogram)
```

**Format**

A data frame with 862 observations on the following 5 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8  
chr9 chrX chrY

ChromStart a numeric vector

ChromEnd a numeric vector

Band a factor with levels p11 p11.1 p11.11 p11.12 p11.2 p11.21 p11.22 p11.23  
p11.3 p11.31 p11.32 p11.4 p12 p12.1 p12.2 p12.3 p12.31 p12.32 p12.33  
p13 p13.1 p13.11 p13.12 p13.13 p13.2 p13.3 p13.31 p13.32 p13.33 p14  
p14.1 p14.2 p14.3 p15 p15.1 p15.2 p15.3 p15.31 p15.32 p15.33 p15.4  
p15.5 p16.1 p16.2 p16.3 p21 p21.1 p21.2 p21.3 p21.31 p21.32 p21.33  
p22 p22.1 p22.11 p22.12 p22.13 p22.2 p22.3 p22.31 p22.32 p22.33 p23  
p23.1 p23.2 p23.3 p24.1 p24.2 p24.3 p25.1 p25.2 p25.3 p26.1 p26.2  
p26.3 p31.1 p31.2 p31.3 p32.1 p32.2 p32.3 p33 p34.1 p34.2 p34.3 p35.1  
p35.2 p35.3 p36.11 p36.12 p36.13 p36.21 p36.22 p36.23 p36.31 p36.32  
p36.33 q11 q11.1 q11.2 q11.21 q11.22 q11.221 q11.222 q11.223 q11.23

q12 q12.1 q12.11 q12.12 q12.13 q12.2 q12.3 q13 q13.1 q13.11 q13.12  
 q13.13 q13.2 q13.3 q13.31 q13.32 q13.33 q13.4 q13.41 q13.42 q13.43  
 q13.5 q14 q14.1 q14.11 q14.12 q14.13 q14.2 q14.3 q15 q15.1 q15.2 q15.3  
 q16.1 q16.2 q16.3 q21 q21.1 q21.11 q21.12 q21.13 q21.2 q21.21 q21.22  
 q21.23 q21.3 q21.31 q21.32 q21.33 q22 q22.1 q22.11 q22.12 q22.13 q22.2  
 q22.3 q22.31 q22.32 q22.33 q23 q23.1 q23.2 q23.3 q23.31 q23.32 q23.33  
 q24 q24.1 q24.11 q24.12 q24.13 q24.2 q24.21 q24.22 q24.23 q24.3 q24.31  
 q24.32 q24.33 q25 q25.1 q25.2 q25.3 q25.31 q25.32 q25.33 q26 q26.1  
 q26.11 q26.12 q26.13 q26.2 q26.3 q26.31 q26.32 q26.33 q27 q27.1 q27.2  
 q27.3 q28 q28.1 q28.2 q28.3 q29 q31.1 q31.2 q31.21 q31.22 q31.23 q31.3  
 q31.31 q31.32 q31.33 q32 q32.1 q32.11 q32.12 q32.13 q32.2 q32.3 q32.31  
 q32.32 q32.33 q33 q33.1 q33.2 q33.3 q34 q34.1 q34.11 q34.12 q34.13  
 q34.2 q34.3 q35 q35.1 q35.2 q35.3 q36.1 q36.2 q36.3 q37.1 q37.2 q37.3  
 q41 q42.11 q42.12 q42.13 q42.2 q42.3 q43 q44

Stain a factor with levels acen gneg gpos100 gpos25 gpos50 gpos75 gvar stalk

## Source

<http://genome.ucsc.edu>

---

UCSC.Mouse.GRCm38.CytoBandIdeogram

*Cytoband Information for Mouse Chromosome Ideogram*

---

## Description

A data frame containing chromosome name, start and end position, band name, and intensity of Giemsa stains for each cytoband.

## Usage

```
data(UCSC.Mouse.GRCm38.CytoBandIdeogram)
```

## Format

A data frame with 403 observations on the following 5 variables.

Chromosome a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16  
 chr17 chr18 chr19 chr2 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX chrY

ChromStart a numeric vector

ChromEnd a numeric vector

Band a factor with levels qA qA1 qA1.1 qA1.2 qA1.3 qA2 qA3 qA3.1 qA3.2 qA3.3 qA4  
 qA5 qA5.1 qA5.2 qA5.3 qA6 qA7.1 qA7.2 qA7.3 qB qB1 qB1.1 qB1.2 qB1.3  
 qB2 qB2.1 qB2.2 qB2.3 qB3 qB3.1 qB3.2 qB3.3 qB4 qB5 qB5.1 qB5.2 qB5.3  
 qC qC1 qC1.1 qC1.2 qC1.3 qC2 qC3 qC3.1 qC3.2 qC3.3 qC4 qC5 qC6 qC7 qD  
 qD1 qD2 qD2.1 qD2.2 qD2.3 qD3 qE qE1 qE1.1 qE1.2 qE1.3 qE2 qE2.1 qE2.2  
 qE2.3 qE3 qE3.1 qE3.2 qE3.3 qE4 qE5 qF qF1 qF2 qF2.1 qF2.2 qF2.3 qF3  
 qF4 qF5 qG1 qG1.1 qG1.2 qG1.3 qG2 qG3 qH1 qH2 qH2.1 qH2.2 qH2.3 qH3 qH4  
 qH5 qH6

Stain a factor with levels gneg gpos100 gpos33 gpos66 gpos75

**Source**

<http://genome.ucsc.edu>



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