

**shinyCircos**

an R/Shiny application for interactive creation of

**Circos plot**

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The source code of shinyCircos is deposited in Github (<https://github.com/venyao/shinyCircos>).

shinyCircos is deployed at <https://yimingyu.shinyapps.io/shinycircos/> and <http://shinycircos.ncpgr.cn/>. Users can use shinyCircos online by accessing either of the two URLs.



Users are encouraged to install and use shinyCircos on local personal computers. Please check the help menu of the shinyCircos application or <https://github.com/venyao/shinyCircos> for the installation of shinyCircos on local computers.

# 1. Interface of shinyCircos

# Menu in shinyCircos: About

- The shinyCircos application contains five menus, "About", "Data upload", "Circos visualization", "Gallery" and "Help".



shinyCircos: an R/Shiny application for interactive creation of Circos plot

- Software references
  - 1. R Development Core Team. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna (2016)
  - 2. RStudio and Inc. *shiny: Web Application Framework for R*. R package version 1.0.0 (2016)
  - 3. Gu, Z. *circlize: Circular Visualization*. R package version 0.4.1 (2017)
  - 4. Neuwirth, E. *RColorBrewer: ColorBrewer palettes*. R package version 1.1-2 (2014)
  - 5. Lawrence, M. *GenomicRanges: Representation and manipulation of genomic intervals and variables defined along a genome*. R package version 1.24.3 (2016)
  - 6. Dowle, M. *data.table: Extension of Data.frame*. R package version 1.9.6 (2015)
  - 7. R Core Team and contributors worldwide. *grDevices: Graphics devices and support for base and grid graphics*. R package version 3.3.3 (2016)
- Further references

This application was created by Wen Yao and Yiming Yu . Please send bugs and feature requests to Wen Yao (ywhzau at gmail.com) or Yiming Yu (yimingyyu at gmail.com). This application uses the shiny package from RStudio .
- **!!Note!!**

Users are encouraged to install and use shinyCircos on local personal computers. Please check the help menu of the shinyCircos application or <https://github.com/venyao/shinyCircos> for the installation of shinyCircos on local computers.

- The "About" menu lists the R packages used in shinyCircos.

# Menu in shinyCircos: Data upload

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, a sidebar titled "Upload data" contains several sections:

- Upload chromosome data**: A file input field showing "No file selected".
- Data type**: Radio buttons for "General" (selected) and "Cytoband".
- Upload label data**: A file input field showing "No file selected".
- Upload data for inner tracks**: A list of checkboxes for "Track1" through "Track10", all of which are unchecked.
- Upload data to create links**: A checkbox for "Links data" which is also unchecked.
- A note: "Data uploaded should use any of the separator in the set [\t;:]".
- A "Go!" button.

The main content area has a blue header bar with tabs: About, Data upload (selected), Circos visualization, Gallery, Help. Below the tabs, there are two main sections:

- Download example data**: A large section containing a list of download links for various data types, each with a download icon:
  - general data
  - cytoband data
  - point data
  - line data
  - barplot data
  - heatmap data
  - ideogram data
  - rect (discrete) data
  - point (multicolumn) data
  - barplot (bidirectional) data
  - rect (gradual) data
  - line (multicolumn) data
  - line (color) data
  - barplot (color) data
  - point (color) data
  - point (pch) data
  - point (color+pch) data
  - point (cex) data
  - point (pch+cex) data
  - point (color+cex) data
  - point (color+pch+cex) data
  - label data
  - point (stack) data
  - line (stack) data
- View uploaded data**: A section titled "Glimpse of data uploaded" which is currently empty.

## Upload data

- The “Data upload” menu allows uploading of input data for Circos plots.
- A glimpse of the uploaded data will be printed on this page.
- Example datasets could be downloaded from this menu.

# Menu in shinyCircos: Circos visualization

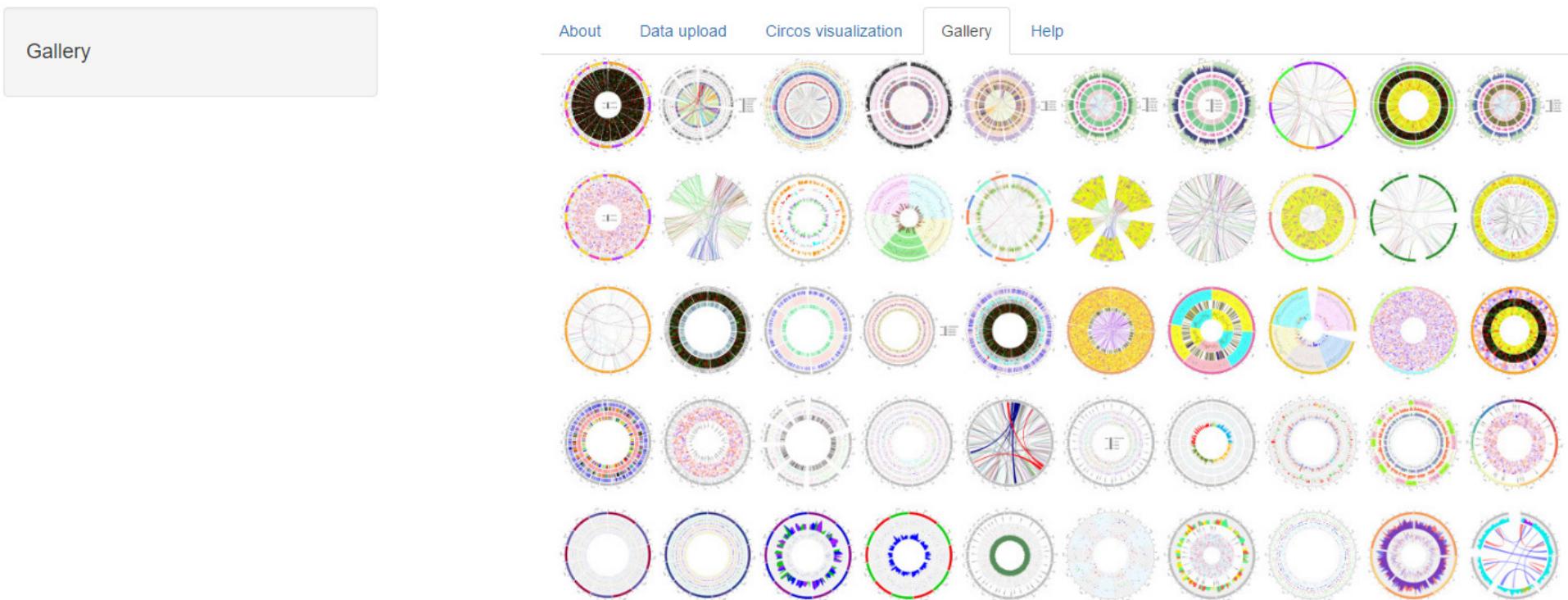
shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, there is a sidebar titled "Plot options" containing checkboxes for "Chromosome" and "Track1" through "Track10", along with options to "Adjust plot size", "Adjust font size", and "Add legend". At the bottom of the sidebar are "Go!" and "?" buttons. The main area has a header with tabs: "About", "Data upload", "Circos visualization" (which is highlighted), "Gallery", and "Help". Below the header are three download buttons: "Download pdf-file", "Download svg-file", and "Download the R scripts to reproduce the Circos plot". The central area contains a large empty box with the placeholder text "Show Pictures". Overlaid on the interface are several blue text annotations: "Download figures" pointing to the download buttons, "Tune plot options" pointing to the sidebar, and "Download scripts" pointing to the third download button.

- After data uploading, the “Circos visualization” menu allows generation of Circos plot.
- Various options are provided to tune the appearance of the Circos plot.

# Menu in shinyCircos: *Gallery*

shinyCircos: an R/Shiny application for interactive creation of Circos plot



- Fifty example figures generated by shinyCircos are listed in the "*Gallery*" menu.

# Menu in shinyCircos: Help

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. At the top, there is a navigation bar with links: About, Data upload, Circos visualization, Gallery, and Help. The 'Help' link is highlighted with a red border. Below the navigation bar, the page title is 'shinyCircos'. A descriptive text follows: 'This is the repository for the Shiny application presented in "shinyCircos: an R/shiny application for creation of Circos plot interactively" (Yu et al. 2017).'. A large red callout box highlights the text 'Help manual for the usage of shinyCircos [Download!]'. Another red callout box highlights the section title 'Use shinyCircos online'. The text below it explains the deployment URLs and activation process. A third red callout box highlights the section title 'Launch shinyCircos directly from R and GitHub (preferred approach)'. The text below it provides instructions for local installation via R and RStudio.

Help

About Data upload Circos visualization Gallery Help

## shinyCircos

This is the repository for the Shiny application presented in "shinyCircos: an R/shiny application for creation of Circos plot interactively" (Yu et al. 2017).

**Help manual for the usage of shinyCircos [Download!]**

### Use shinyCircos online

shinyCircos is deployed at <https://yimingyu.shinyapps.io/shinycircos/> and <http://shinycircos.ncpgr.cn/> for online use. shinyCircos is idle until you activate it by accessing the two URLs. So it may take some time when you access this URL for the first time. Once it was activated, shinyCircos could be used smoothly and easily.

### Launch shinyCircos directly from R and GitHub (preferred approach)

User can choose to run shinyCircos installed locally for a more preferable experience.

**Step 1: Install R and RStudio**

Before running the app you will need to have R and RStudio installed (tested with R 3.3.3 and RStudio 1.0.143). Please check CRAN (<https://cran.r-project.org/>) for the installation of R. Please check <https://www.rstudio.com/> for the installation of RStudio.

**Step 2: Install the R Shiny package and other packages required by shinyCircos**

Start an R session using RStudio and run these lines:

- Instructions for installation of shinyCircos on local computers or web servers are shown in the "Help" menu.

## 2. Usage of shinyCircos

# Step 1: Data uploading

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Upload chromosome data [?](#)

Browse... [chromosome\\_general.csv](#) Upload complete

Data type [?](#)

General  
 Cytoband

Upload label data [?](#)

Browse... No file selected

Upload data for inner tracks [?](#)

Track1  
 NULL  
 Upload

Upload track1 data:

Browse... [point.csv](#) Upload complete

Plot type:

point

Upload label data [?](#)

Browse... No file selected

Track2  
 Track3  
 Track4  
 Track5  
 Track6  
 Track7  
 Track8  
 Track9  
 Track10

Upload data to create links [?](#)

Links data

Data uploaded should use any of the separator in the set [,;].

Go! [?](#)

About Data upload Circos visualization Gallery Help

- Download example data
  - Example chromosomes data
    - general data
    - cytoband data
  - Example tracks data
    - point data
    - line data
    - barplot data
    - heatmap data
    - ideogram data
    - rect (discrete) data
    - point (multicolumn) data
    - barplot (bidirectional) data
    - rect (gradual) data
    - line (multicolumn) data
    - line (color) data
    - barplot (color) data
    - point (color) data
    - point (pch) data
    - point (color+pch) data
    - point (cex) data
    - point (pch+cex) data
    - point (color+cex) data
    - point (color+pch+cex) data
    - label data
    - point (stack) data
    - line (stack) data
  - Example links data
    - links data
    - links (color) data
- Glimpse of data uploaded

Please go to the 'Circos visualization' menu to generate the Circos plot!

  - Chromosomes data
  - Tracks data
    - Track1
  - Links data

## 1.1 Upload chromosome data

## 1.2 Upload track data

- Data from 0 to 10 tracks can be uploaded.
- The first 3 columns of the uploaded data should be the chromosome ID, the start and end coordinates of genomic regions.

## 1.3 Complete uploading

# Step 2: Circos visualization

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

Chromosome

Chromosome band

Show

Hide

Color(s):

grey

Chromosome IDs

Show

Hide

Size units of genomic regions

Show

Hide

Gap width(s):

Legend text

Track1

Track2

Track3

Track4

Track5

Track6

Track7

Track8

Track9

Track10

Adjust plot size

Adjust font size

Add legend

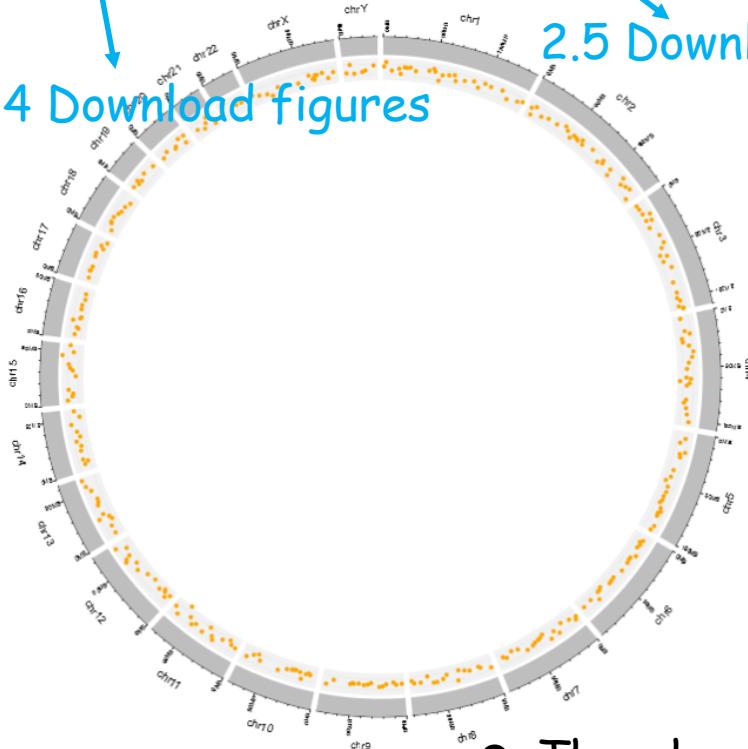
Go!

About Data upload Circos visualization Gallery Help

Download pdf-file  Download svg-file

Download the R scripts to reproduce the Circos plot

2.4 Download figures



2.1 Turn to "Circos visualization" menu

2.5 Download scripts

2.2 Tune plot options

2.3 Make the plot

- The chromosome data is compulsory and defines the frame of a Circos plot.

- Please click the "Go!" button if any options are modified.

## 2.1 Plot chromosomes

# Upload chromosome data

Upload chromosome data ?

Browse... *Click "Browse" to select file*

Data type ?

General

Cytoband

chr	start	end
chr1	1	249250621
chr2	1	243199373
chr3	1	198022430

chr	start	end	value1	value2
chr1	1	2300000	p36.33	gneg
chr1	2300000	5400000	p36.32	gpos25
chr1	5400000	7200000	p36.31	gneg

- Use the “Data upload” menu for data input.
- Chromosome data can be either chromosome ideograms (“Cytoband” type, see example data “chromosome\_cytoband.csv” for detail) or simple definition of chromosome lengths (“General” type, see example data “chromosome\_general.csv” for detail).

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

Chromosome

Chromosome band → Add color band for chromosomes.

Show  
 Hide

Color(s): ? → Colors for chromosome/sector.

grey

Chromosome IDs → Add labels on the outermost circle.

Show  
 Hide

Size units of genomic regions → Add size units of genomic regions on the chromosome axis.

Show  
 Hide

Gap width(s): ? → Gap width between neighboring sectors.

1

Legend text ? → The text to appear in the legend.

About Data upload Circos visualization Gallery Help

[Download pdf-file](#) [Download svg-file](#) [Download the R scripts to reproduce the Circos plot](#)

# Example 1

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Upload chromosome data [?](#)

Browse... chromosome\_general.csv  
Upload complete

Data type [?](#)

General  
 Cytoband

Upload label data [?](#)

Browse... No file selected

Upload data for inner tracks [?](#)

Track1  
 Track2  
 Track3  
 Track4  
 Track5  
 Track6  
 Track7  
 Track8  
 Track9  
 Track10

Upload data to create links [?](#)

Links data

Data uploaded should use any of the separator in the set [,;t ;;].

Go! [?](#)

About Data upload Circos visualization Gallery Help

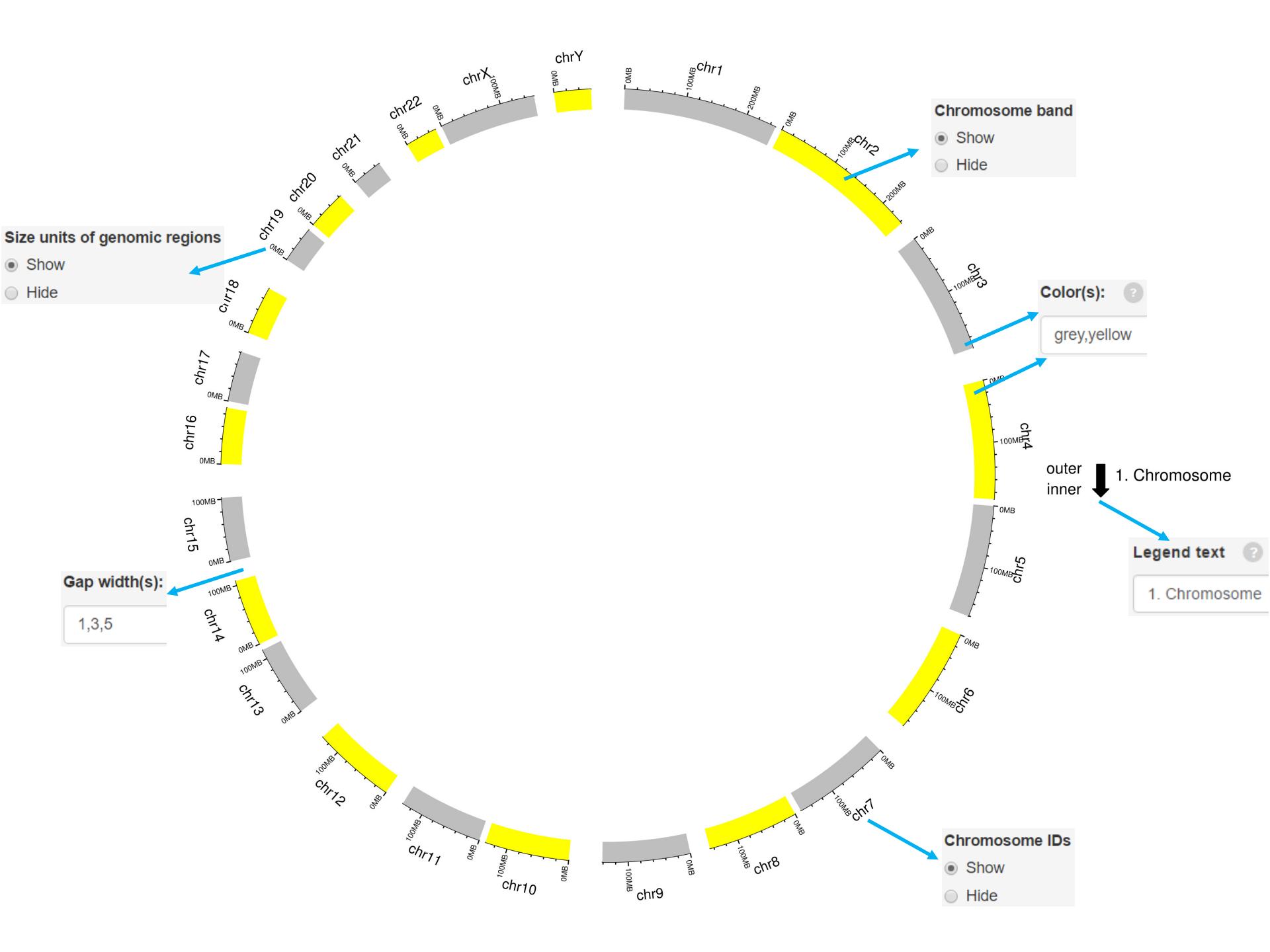
- Download example data
- Example chromosomes data
  - [general data](#)
  - [cytoband data](#)
- Example tracks data
  - [point data](#)
  - [line data](#)
  - [barplot data](#)
  - [heatmap data](#)
  - [ideogram data](#)
  - [rect \(discrete\) data](#)
  - [point \(multicolumn\) data](#)
  - [barplot \(bidirectional\) data](#)
  - [rect \(gradual\) data](#)
  - [line \(multicolumn\) data](#)
  - [line \(color\) data](#)
  - [barplot \(color\) data](#)
  - [point \(color\) data](#)
  - [point \(pch\) data](#)
  - [point \(color+pch\) data](#)
  - [point \(cex\) data](#)
  - [point \(pch+cex\) data](#)
  - [point \(color+cex\) data](#)
  - [point \(color+pch+cex\) data](#)
  - [label data](#)
  - [point \(stack\) data](#)
  - [line \(stack\) data](#)
- Example links data
  - [links data](#)
  - [links \(color\) data](#)
- Glimpse of data uploaded

Please go to the 'Circos visualization' menu to generate the Circos plot!

Chromosomes data		
chr	start	end
chr1	1	249250621
chr2	1	243199373
chr3	1	198022430

## Data format

Chromosome data: chromosome\_general.csv  
Data type: General



# Example 2

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Upload chromosome data [?](#)

Browse... chromosome\_cytoband.csv  
Upload complete

Data type [?](#)

General  
 Cytoband

Upload label data [?](#)

Browse... No file selected

Upload data for inner tracks [?](#)

Track1  
 Track2  
 Track3  
 Track4  
 Track5  
 Track6  
 Track7  
 Track8  
 Track9  
 Track10

Upload data to create links [?](#)

Links data

Data uploaded should use any of the separator in the set [,\t |;:].

Go! [?](#)

About Data upload Circos visualization Gallery Help

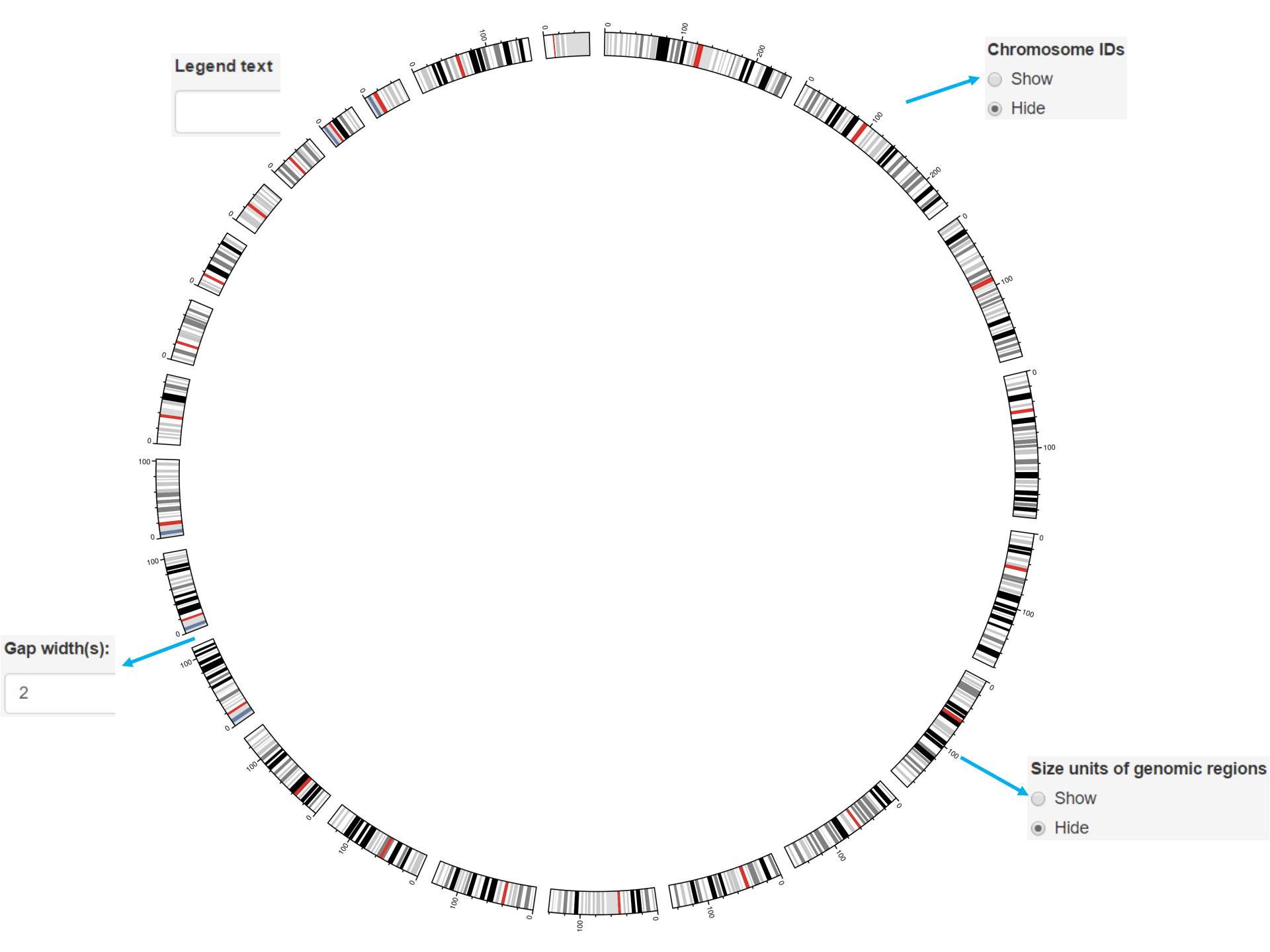
- Download example data
- Example chromosomes data
  - [general data](#)
  - [cytoband data](#)
- Example tracks data
  - [point data](#)
  - [line data](#)
  - [barplot data](#)
  - [heatmap data](#)
  - [ideogram data](#)
  - [rect \(discrete\) data](#)
  - [point \(multicolumn\) data](#)
  - [barplot \(bidirectional\) data](#)
  - [rect \(gradual\) data](#)
  - [line \(multicolumn\) data](#)
  - [line \(color\) data](#)
  - [barplot \(color\) data](#)
  - [point \(color\) data](#)
  - [point \(pch\) data](#)
  - [point \(color+pch\) data](#)
  - [point \(cex\) data](#)
  - [point \(pch+cex\) data](#)
  - [point \(color+cex\) data](#)
  - [point \(color+pch+cex\) data](#)
  - [label data](#)
  - [point \(stack\) data](#)
  - [line \(stack\) data](#)
- Example links data
  - [links data](#)
  - [links \(color\) data](#)
- Glimpse of data uploaded

Please go to the 'Circos visualization' menu to generate the Circos plot!

Chromosomes data				
chr	start	end	value1	value2
chr1	1	2300000	p36.33	gneg
chr1	2300000	5400000	p36.32	gpos25
chr1	5400000	7200000	p36.31	gneg

Data format

Chromosome data: chromosome\_cytoband.csv  
Data type: Cytoband



## 2.2 Plot points

# Upload point data

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Upload chromosome data [?](#)

Browse... No file selected

Data type [?](#)

General  
 Cytoband

Upload label data [?](#)

Browse... No file selected

Upload data for inner tracks [?](#)

Track1  
 NULL  
 Upload

Upload track1 data:  
Browse... No file selected

Plot type:  
point

About Data upload Circos visualization Gallery Help

- Download example data
  - Example chromosomes data
    - [general data](#)
    - [cytoband data](#)
  - Example tracks data
    - [point data](#)
    - [line data](#)
    - [barplot data](#)
    - [heatmap data](#)
    - [ideogram data](#)
    - [rect \(discrete\) data](#)
    - [point \(multicolumn\) data](#)
    - [barplot \(bidirectional\) data](#)
    - [rect \(gradual\) data](#)
    - [line \(multicolumn\) data](#)
    - [line \(color\) data](#)
    - [barplot \(color\) data](#)
    - [point \(color\) data](#)
    - [point \(pch\) data](#)
    - [point \(color+pch\) data](#)
    - [point \(cex\) data](#)
    - [point \(pch+cex\) data](#)
    - [point \(color+cex\) data](#)
    - [point \(color+pch+cex\) data](#)
    - [label data](#)
    - [point \(stack\) data](#)
    - [line \(stack\) data](#)
  - Example links data
    - [links data](#)
    - [links \(color\) data](#)
- Glimpse of data uploaded

Select "Upload"

Select file

Select plot type "point"

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. At the top, there is a navigation bar with links for About, Data upload, Circos visualization (which is highlighted), Gallery, and Help. Below the navigation bar are three download buttons: Download pdf-file, Download svg-file, and Download the R scripts to reproduce the Circos plot.

**Plot options**

- Chromosome
- Track1

**Data color** ? → The color used for data plotting can be randomly assigned by the application or specified by the users.

Random

Custom for data with multi-column

Custom for data with multi-group

**Color transparency:** ? → A decimal number in [0, 1] to adjust the color transparency.  
1

**Y coordinates of baselines:** ? → Decimal numbers in [0, 1] to adjust the y axis coordinates of baselines.  
0.25, 0.75

**Baselines color(s):** ? → The color used for baselines.  
grey

**Background color(s):** ? → The color for the background.  
grey95

**Track height:** ? → Height of the track.  
0.06

**Track margin:** ? → Margin size of the track.  
0.01

**Add borders** ? → Add borders to the different chromosome sectors.

Yes

No

**Legend text** ? →

# Options

Highlight regions 



Genomic regions can be highlighted with specified colors.

Show

Hide

Paste data below: 



Each row should contain four components separated by commas including the chromosome ID, start coordinate, end coordinate and the specified color.

```
chr2,1,100000000,red  
chr3,1,100000000,green
```

Data separated by commas.

Color transparency: 



A decimal number in [0, 1] to adjust the color transparency for the highlighted regions.

1

# Example 1

Track2  
 NULL  
 Upload

Upload track2 data:

Browse... point.csv  
Upload complete

Plot type:  
point

Track3  
 NULL  
 Upload

Upload track3 data:

Browse... point\_multicolumn.csv  
Upload complete

Plot type:  
point

## Data format

- Track2

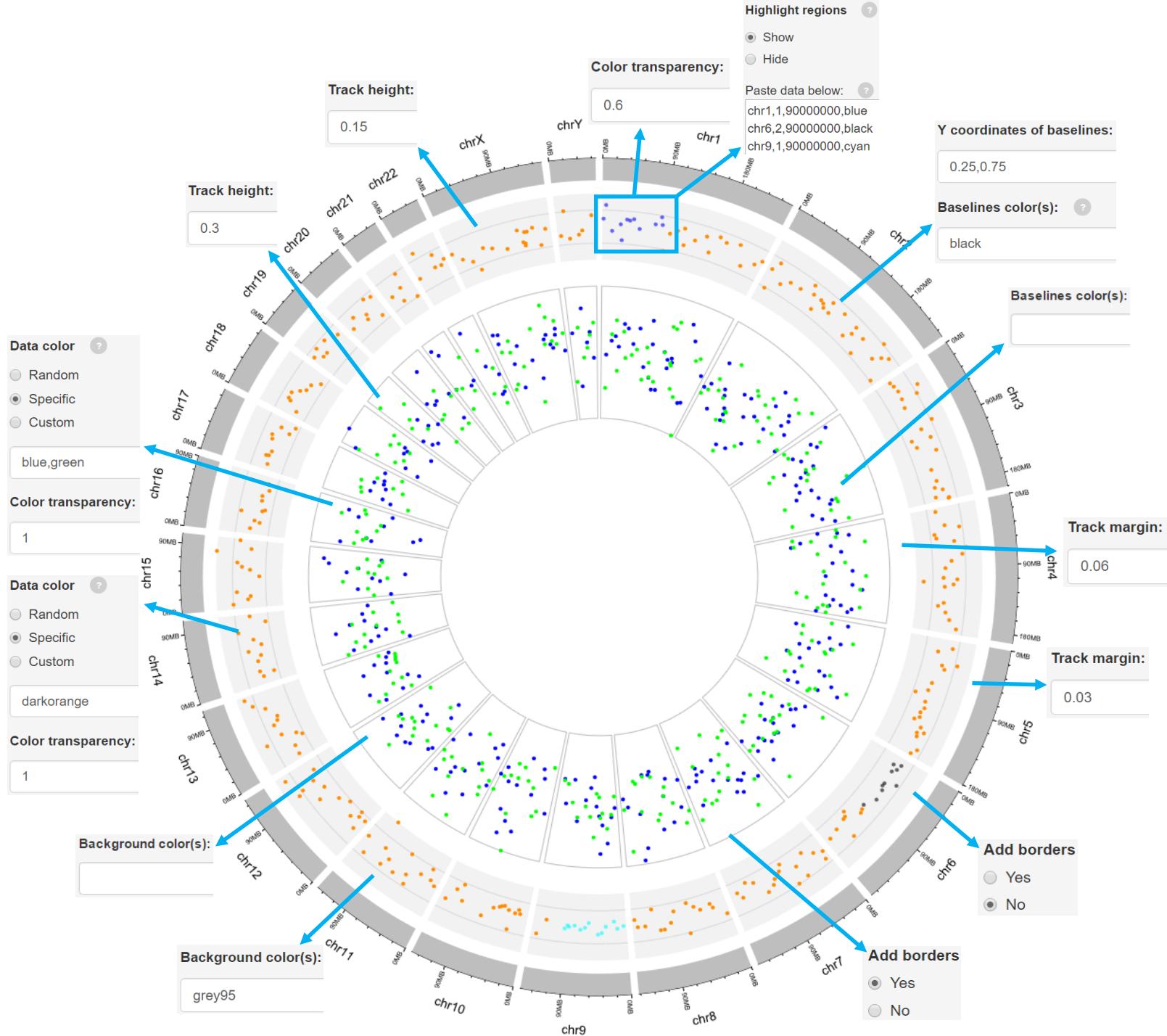
Any track can be used for data uploading.

chr	start	end	value1
chr1	1769292	1796134	0.339
chr1	4881594	5495466	1.005
chr1	9076857	21130138	-0.247

- Track3

chr	start	end	value1	value2
chr1	7224218	16393864	-0.196	-0.955
chr1	21093451	25392112	0.128	0.275
chr1	31462827	31952156	0.234	0.600

- Simplest data to plot point should contain at least 4 columns including the chromosome ID, start coordinate, end coordinate and multiple columns of values.



# Example 2

## Data format

- Track1

chr	start	end	value	pch
chr1	8605110	17214753	0.208	1
chr1	22124150	36435838	0.905	1
chr1	43831505	49353791	0.530	1

→ point\_pch.csv

- The last column "pch" indicates different point types for differing data groups.

- Track2

chr	start	end	value	color
chr1	6098636	13915642	0.372	a
chr1	42002814	45209039	-0.253	a
chr1	49351404	52528510	-0.011	a

→ point\_color.csv

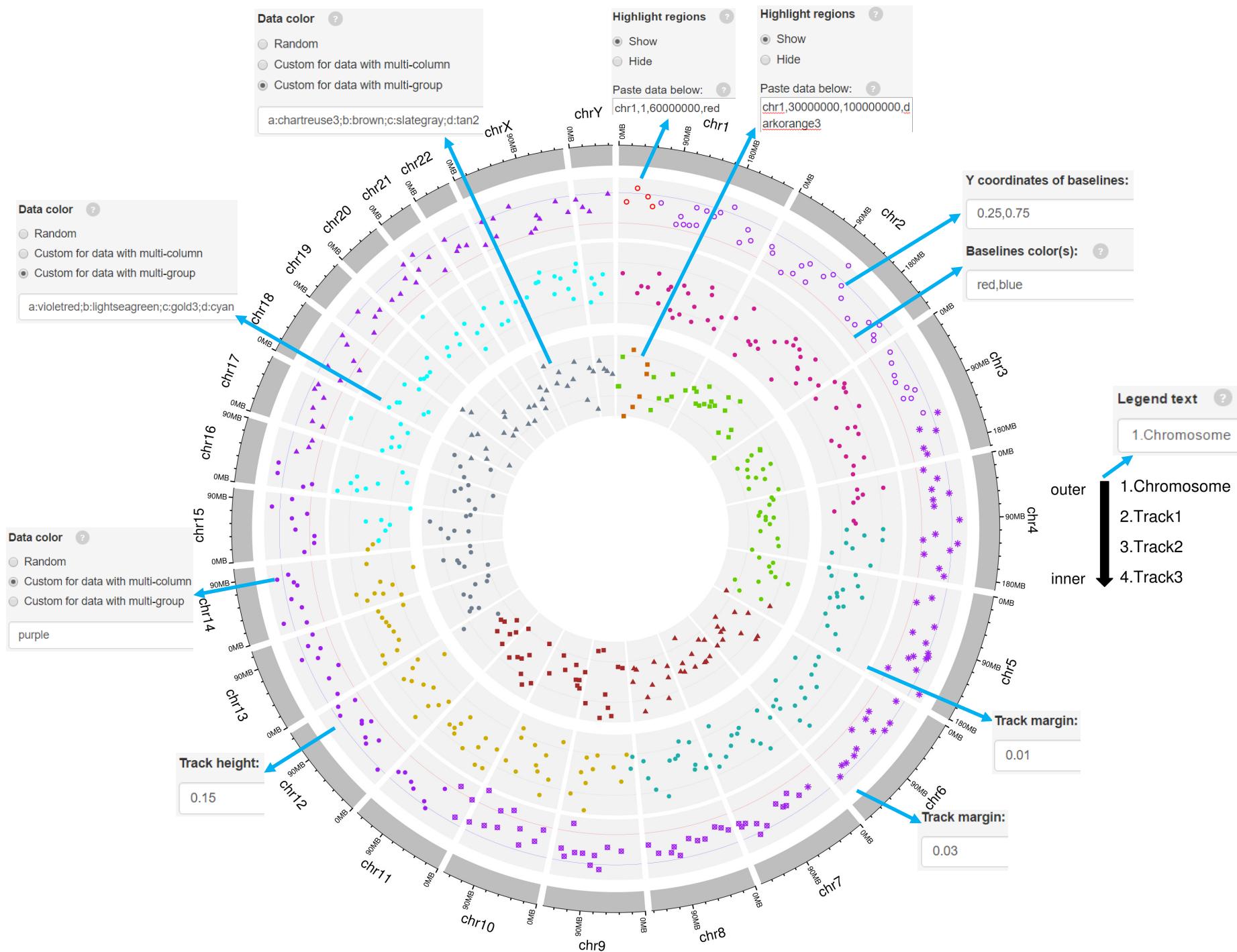
- The last column "color" indicates different colors for differing data groups.

- Track3

chr	start	end	value	color	pch
chr1	3768320	4851773	-0.416	a	15
chr1	5712552	10112216	-0.410	a	15
chr1	15275256	18873862	0.589	a	15

→ point\_color\_pch.csv

- The last columns "color" and "pch" represent different colors and point types for different data groups.



# Example 3

## Data format

- Track1

chr	start	end	value	cex
chr1	1326341	1845331	-0.374	0.500
chr1	9901462	15656953	-0.321	0.300
chr1	18241935	21630011	0.172	0.500

point\_cex.csv

- Track3

chr	start	end	value	color	cex
chr1	8900700	9211013	-0.600	a	0.300
chr1	38733680	54945292	0.233	a	1.100
chr1	56997278	57258274	0.214	a	1.000

point\_color\_cex.csv

- Track2

chr	start	end	value	pch	cex
chr1	4049230	11358879	-0.590	10	0.400
chr1	18671867	29619034	0.442	10	0.700
chr1	57445176	66216574	1.511	10	0.300

point\_pch\_cex.csv

- Track4

chr	start	end	value	color	pch	cex
chr1	14053524	24878326	-0.498	a	1	0.900
chr1	29640089	49313488	-0.565	a	1	1.000
chr1	53970010	87166913	-1.159	a	1	0.300

point\_color\_pch\_cex.csv

- The “cex” column is a numeric vector represents different point size.



# Example 4

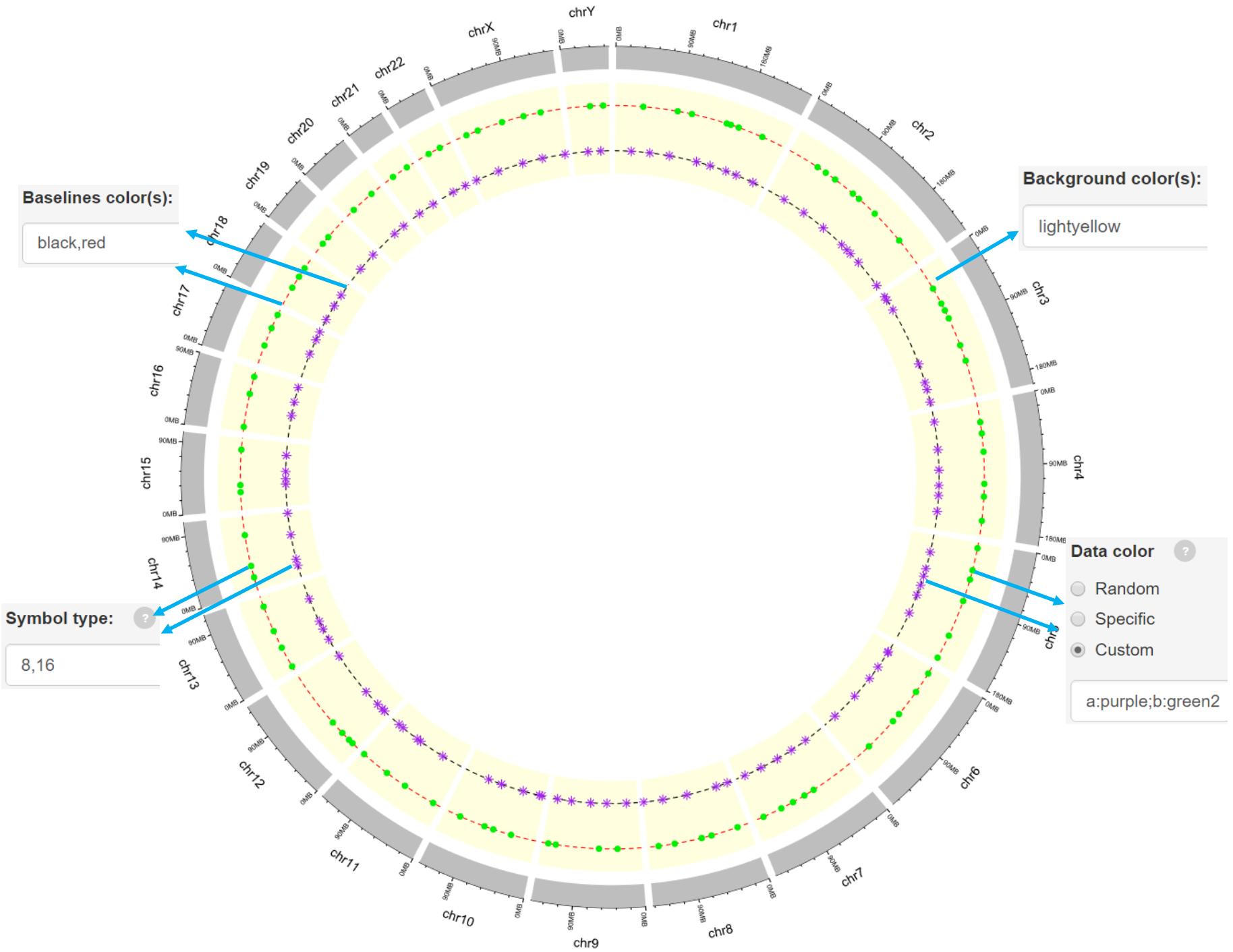
## Data format

- Track1

chr	start	end	stack
chr1	11589909	40133642	a
chr1	52614734	59580026	a
chr1	76931882	99383558	a

[stack\\_point.csv](#)

- The last column "stack" is a numeric vector or a character vector.
- In stack mode, the y-axis is split into several bins with equal height and all data points are put onto different "horizontal" bins based on the "stack" column.



## **2.3 Plot lines**

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, there is a sidebar titled "Plot options" containing several configuration sections:

- Plot options**:
  - Chromosome
  - Track1
- Data color**:
  - Random
  - Custom for data with multi-column
  - Custom for data with multi-group
- Fill area**:
  - Yes
  - NoA blue arrow points from this section to the text "Fill the area below the lines."
- Area color**:
  - Identical with lines
  - SpecificA blue arrow points from this section to the text "Filled the area with color, which can be identical to line color or specified by the user."
- Color transparency:** A text input field containing the value "1".

At the top right, there is a navigation bar with links: "About", "Data upload", "Circos visualization" (which is highlighted), "Gallery", and "Help". Below the navigation bar are three download links:

- [Download pdf-file](#)
- [Download svg-file](#)
- [Download the R scripts to reproduce the Circos plot](#)

- See section 2.2 for more plot options.

# Example 1

## Data format

- Track1

chr	start	end	value1
chr1	788538	5571920	0.309
chr1	6704086	10962288	-0.075
chr1	13517030	19064946	1.068

- Track2

chr	start	end	value1
chr1	788538	5571920	0.309
chr1	6704086	10962288	-0.075
chr1	13517030	19064946	1.068

line.csv

- Track3

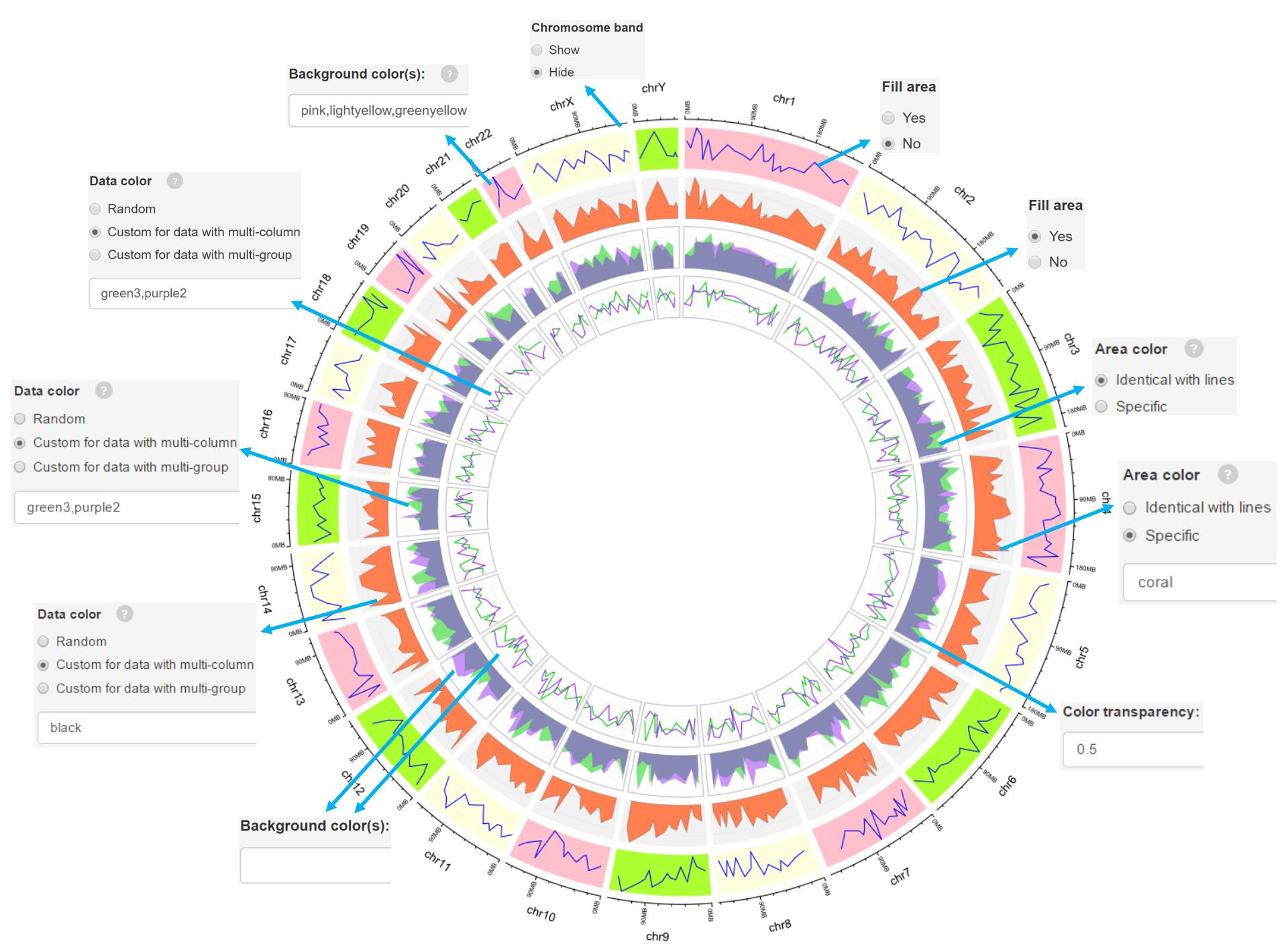
chr	start	end	value1	value2
chr1	294540	4666160	-0.660	-0.596
chr1	17589118	18065224	-0.138	-0.747
chr1	21280287	21380873	0.217	-0.419

- Track4

chr	start	end	value1	value2
chr1	294540	4666160	-0.660	-0.596
chr1	17589118	18065224	-0.138	-0.747
chr1	21280287	21380873	0.217	-0.419

line\_multicolumn.csv

- Simplest data to plot line should contain at least 4 columns including the chromosome ID, start coordinate, end coordinate and multiple columns of values.



# Example 2

## Data format

- Track1

chr	start	end	stack
chr1	20646359	46383846	a
chr1	92365687	94981461	a
chr1	100852580	102493272	a



stack\_line.csv

- Track2

chr	start	end	stack
chr1	20646359	46383846	a
chr1	92365687	94981461	a
chr1	100852580	102493272	a

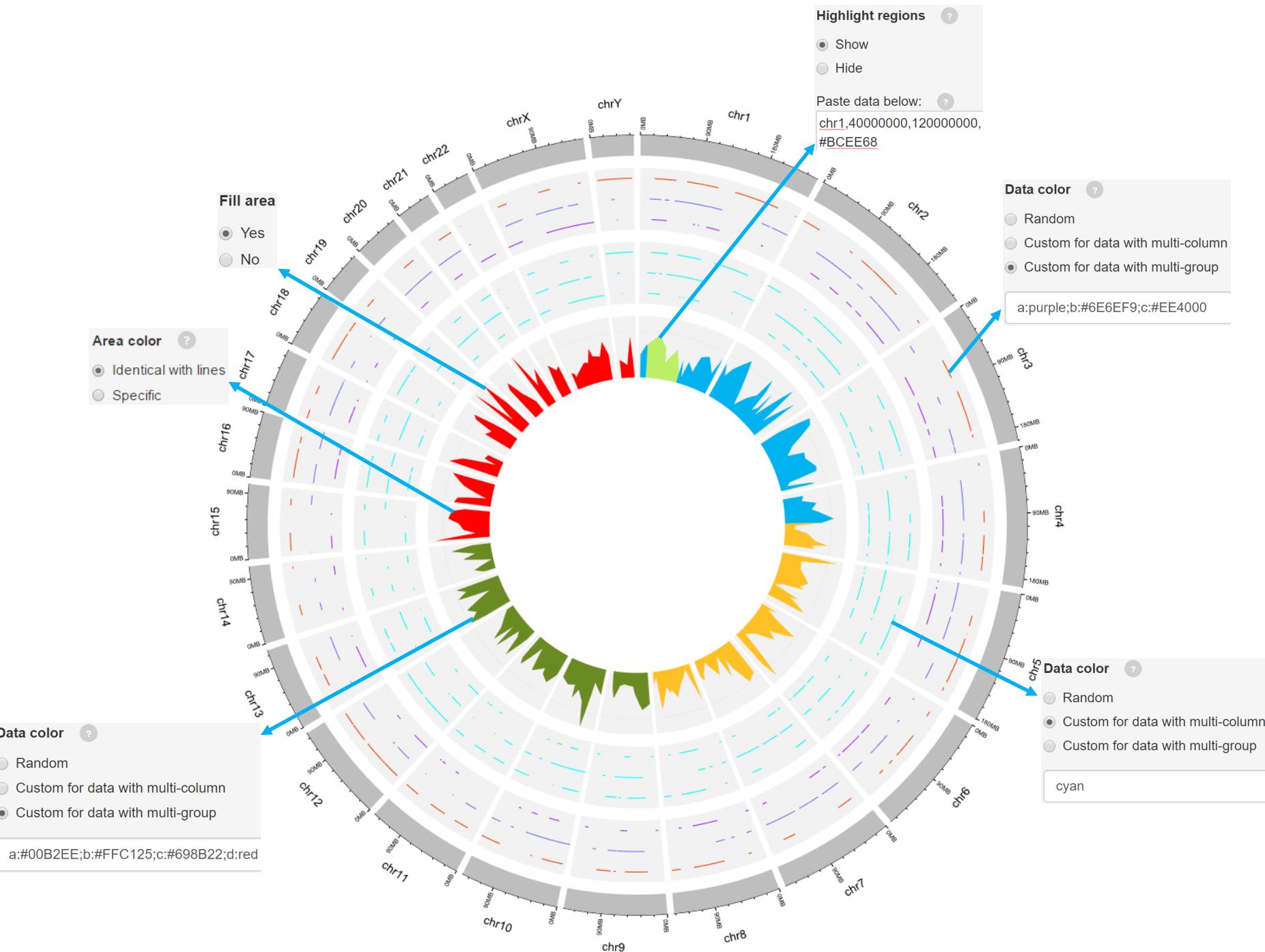


- Track3

chr	start	end	value	color
chr1	2306857	8605927	-0.207	a
chr1	20851761	21889246	0.121	a
chr1	23158305	28865964	0.163	a



line\_color.csv



## **2.4 Plot bars**

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, a sidebar titled "Plot options" contains several configuration fields:

- Chromosome
- Track1
- Bar direction**:  
 Unidirectional  
 Bidirectional
- Boundary value:**
- Outer color:**
- Inner color:**
- Color transparency:**

At the top right, there is a navigation bar with tabs: About, Data upload, **Circos visualization**, Gallery, and Help. Below the tabs are three download buttons:

- [Download pdf-file](#)
- [Download svg-file](#)
- [Download the R scripts to reproduce the Circos plot](#)

Annotations in blue text and arrows highlight specific features:

- An arrow points from the "Bidirectional" radio button to the text: "Bars can be unidirectional or bidirectional. For bidirectional bars, the 4th column with data values will be divided into two groups based on the boundary value."
- An arrow points from the "Outer color" input field to the text: "Color for the outer bars."
- An arrow points from the "Inner color" input field to the text: "Color for the inner bars."

- See section 2.2 for more plot options.

# Example 1

## Data format

- Track1

chr	start	end	value
chr1	10382554	26901963	0.374
chr1	26901963	30511288	0.084
chr1	30956226	33621691	0.890

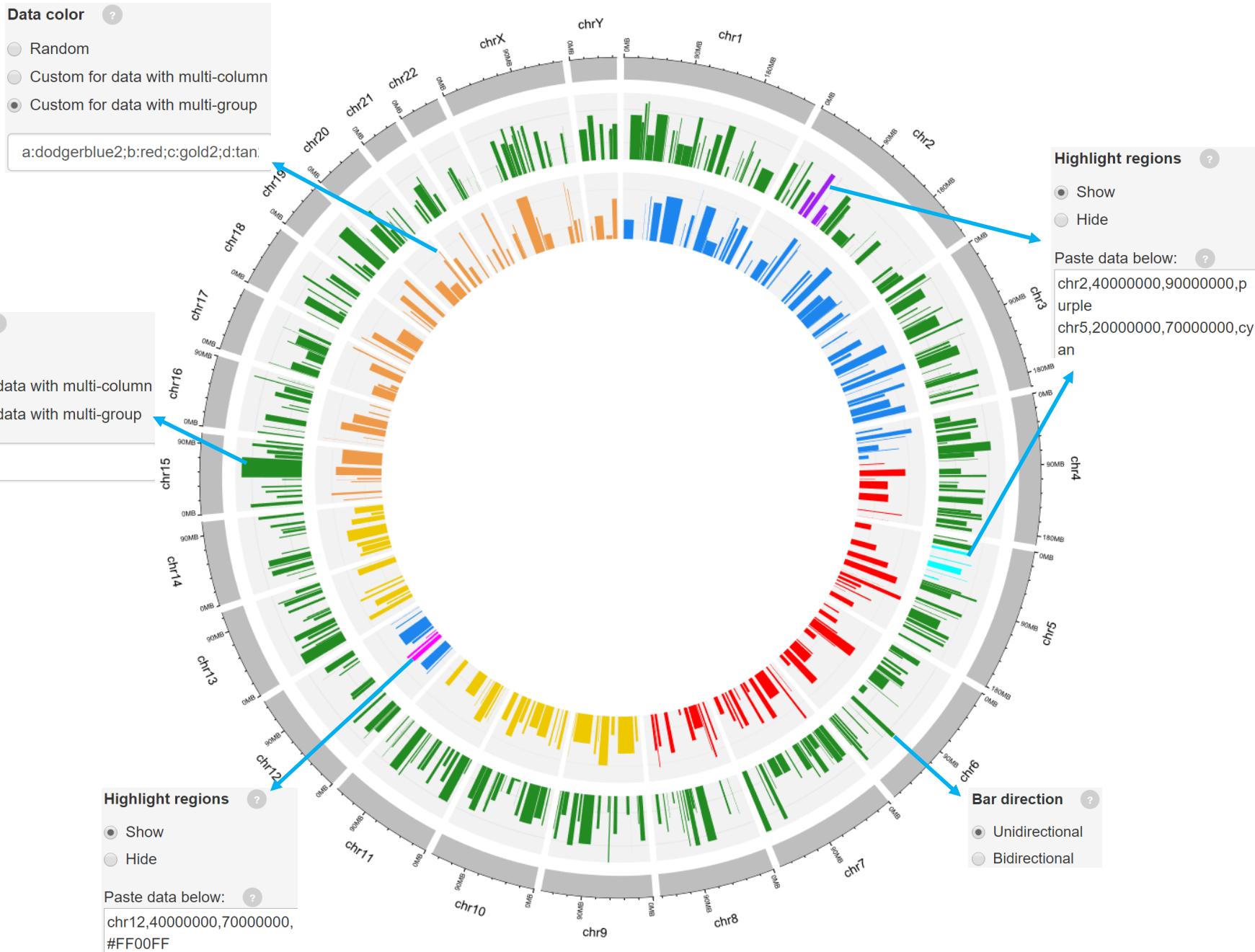
barplot.csv

- Track2

chr	start	end	value	color
chr1	2321390	22775301	-0.525	a
chr1	43812694	44287183	0.101	a
chr1	52481565	53897427	0.372	a

barplot\_color.csv

- Data for bar plot generally includes 4 columns.
- The 4th column is a numeric vector.
- A “color” column can be added to assign color to different bars.



# Example 2

## Data format

- Track1

chr	start	end	value
chr1	10382554	26901963	0.374
chr1	26901963	30511288	0.084
chr1	30956226	33621691	0.890

barplot.csv

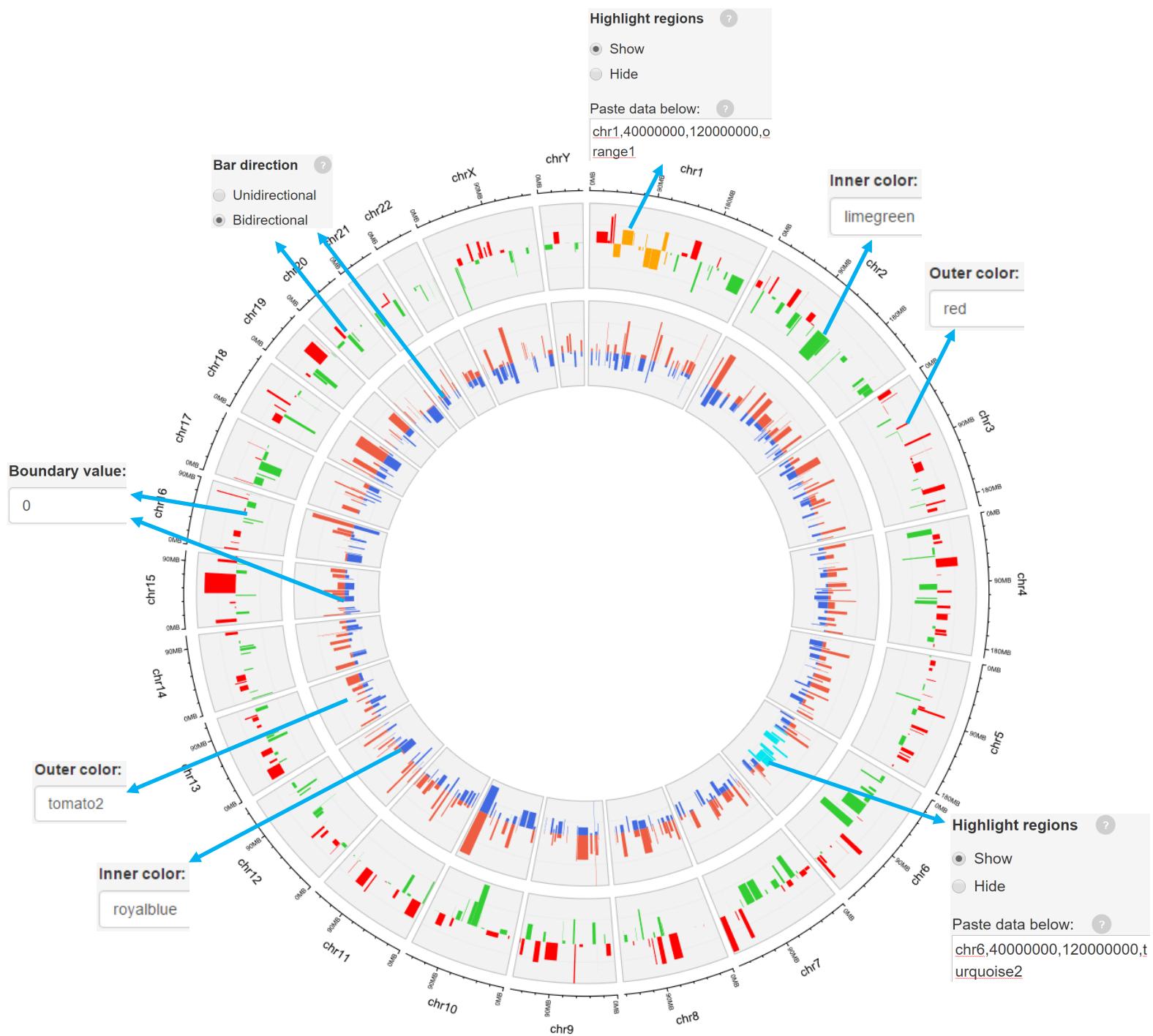
- Track2

chr	start	end	value
chr1	5622039	9110831	0.095
chr1	5622039	9110831	-0.405
chr1	16816819	18551718	0.247

barplot\_bidirectional.csv



- For bidirectional bars, each genomic region corresponds to one or two values.



## 2.5 Plot rects

# Upload rect data

## Data format

- Track1

chr	start	end	value
chr1	1	6657591	0.034
chr1	9792529	20706145	-0.527
chr1	24807376	30831596	0.355

[rect\\_gradual.csv](#)

- Track2

chr	start	end	group
chr1	1465	5857186	b
chr1	6005405	7051583	c
chr1	7459754	11390112	h

- Track3

chr	start	end	group
chr1	1465	5857186	b
chr1	6005405	7051583	c
chr1	7459754	11390112	h

- Track4

chr	start	end	group
chr1	1465	5857186	b
chr1	6005405	7051583	c
chr1	7459754	11390112	h

[rect\\_discrete.csv](#)

- Data for rect plot generally includes four columns.
- The last column should be a numeric vector representing gradual values or a character vector representing discrete variables.

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, there is a sidebar titled "Plot options" containing several configuration options:

- Chromosome
- Track1
- Data type**:  Gradual (disabled)  Discrete
- Select color**:  Random  Specific  Custom. The input field below contains the value "red".
- Color transparency:** A slider input set to 1.
- Background color(s):** An input field containing the value "grey95".

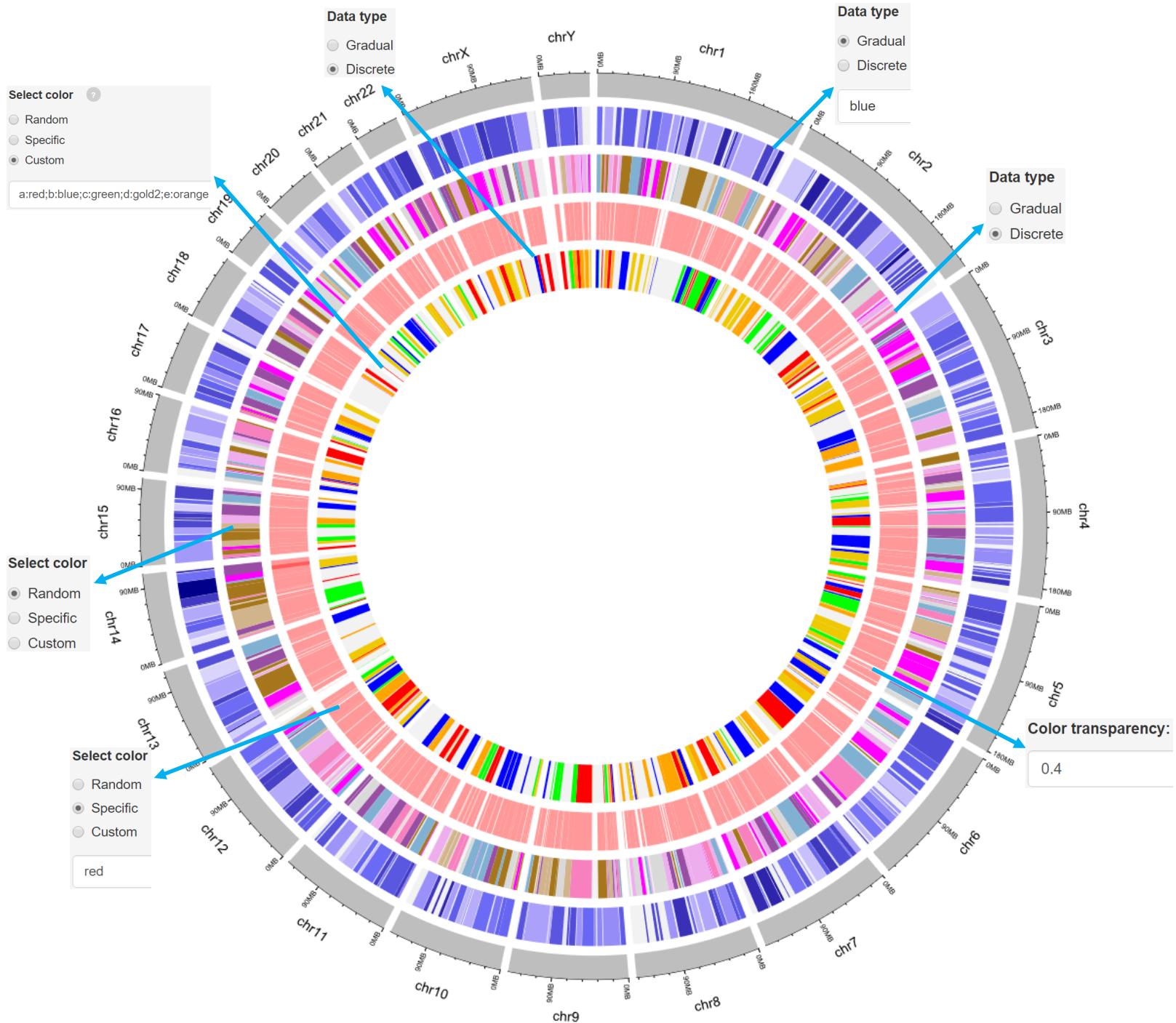
At the top right, there is a navigation bar with tabs: "About", "Data upload", "Circos visualization" (which is active), "Gallery", and "Help". Below the tabs are three download buttons:

- [Download pdf-file](#)
- [Download svg-file](#)
- [Download the R scripts to reproduce the Circos plot](#)

Two annotations are present in blue text with arrows pointing to specific elements:

- An arrow points from the text "The rects are filled with gradual or discrete colors." to the "Data type" section.
- An arrow points from the text "The color used in data plotting can be randomly assigned by the application or specified by the users." to the "Select color" section.

- See section 2.2 for more plot options.



## 2.6 Plot heatmaps

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, there's a sidebar titled "Plot options" containing several configuration settings:

- Colors:** A dropdown menu set to "blue.white.red". An annotation next to it says "Colors used for the heatmap."
- Add position lines:** A radio button group where "Yes" is selected. An annotation next to it says "Add genomic position lines between tracks."
- Position lines height:** A numeric input field set to "0.06". An annotation next to it says "Height of the position lines."
- Position lines margin:** A numeric input field set to "0.01". An annotation next to it says "Margin size of the position lines."
- Track height:** A numeric input field set to "0.06".
- Track margin:** A numeric input field set to "0.01".
- Add cell borders:** A radio button group where "Yes" is selected. An annotation next to it says "Add borders to heatmap grids."
- Borders color:** A dropdown menu set to "black". An annotation next to it says "The color used for the borders of heatmap grids."

At the top right, there's a navigation bar with links: "About", "Data upload", "Circos visualization" (which is highlighted), "Gallery", and "Help". Below the navigation bar are three download buttons: "Download pdf-file", "Download svg-file", and "Download the R scripts to reproduce the Circos plot".

**● See section 2.2 for more plot options.**

# Upload heatmap data

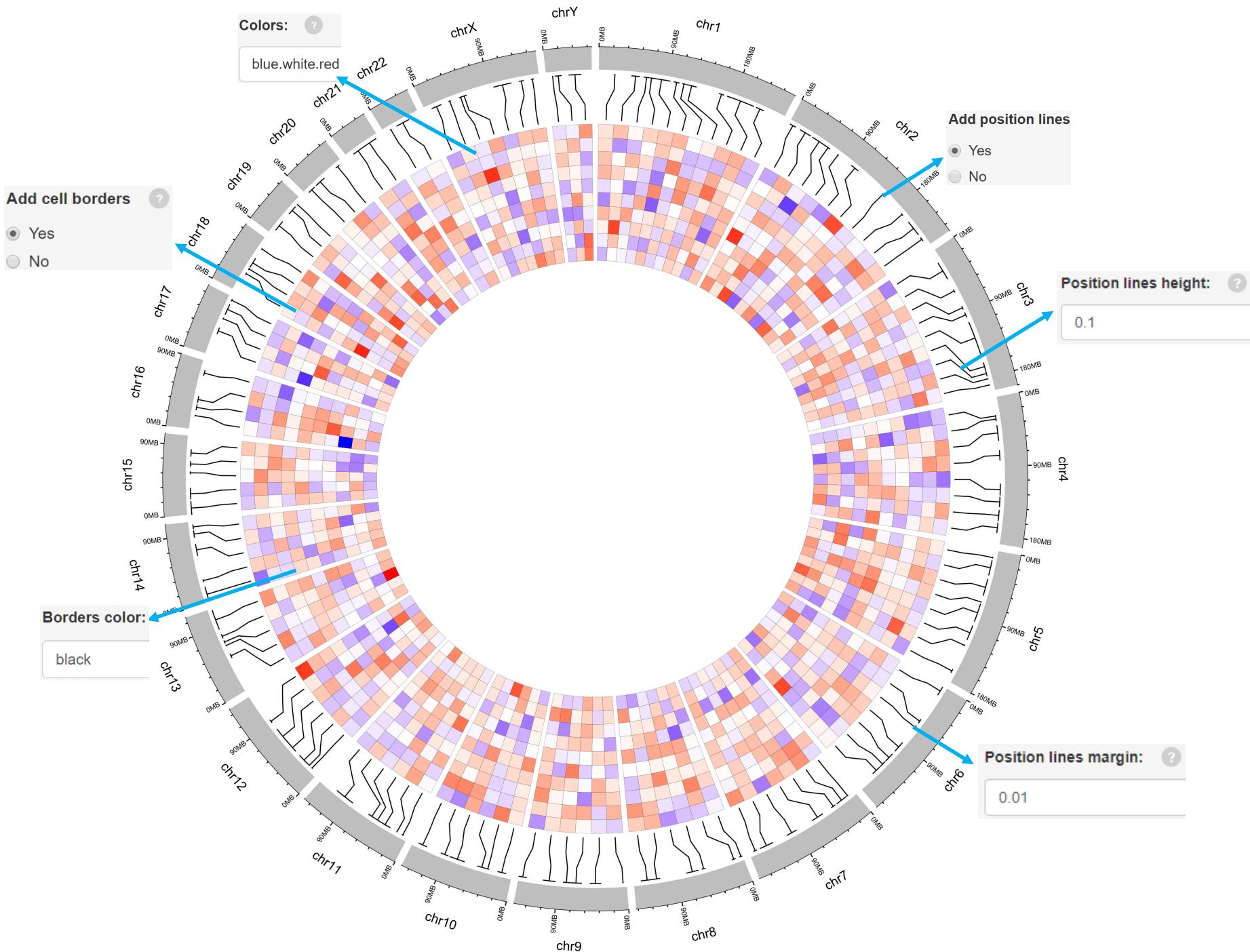
## Data format

- Track1

chr	start	end	value1	value2	value3	value4	value5	value6	value7	value8	value9	value10
chr1	20621957	21209624	-0.672	-0.271	-0.001	0.486	-0.986	-0.370	0.480	0.380	0.158	0.108
chr1	42967726	53028972	-0.147	0.387	1.332	0.182	0.160	-0.132	0.234	-0.089	-0.918	0.397
chr1	58915991	65942365	-0.214	-0.059	-0.332	0.654	-0.402	-0.953	-0.046	0.449	-0.615	-0.070

heatmap.csv

- Apart from the first three columns, other columns are numeric vectors representing different values.



## 2.7 Plot ideogram

# Upload ideogram data

## Data format

- Track1

chr	start	end	value1
chr1	1769292	1796134	0.339
chr1	4881594	5495466	1.005
chr1	9076857	21130138	-0.247

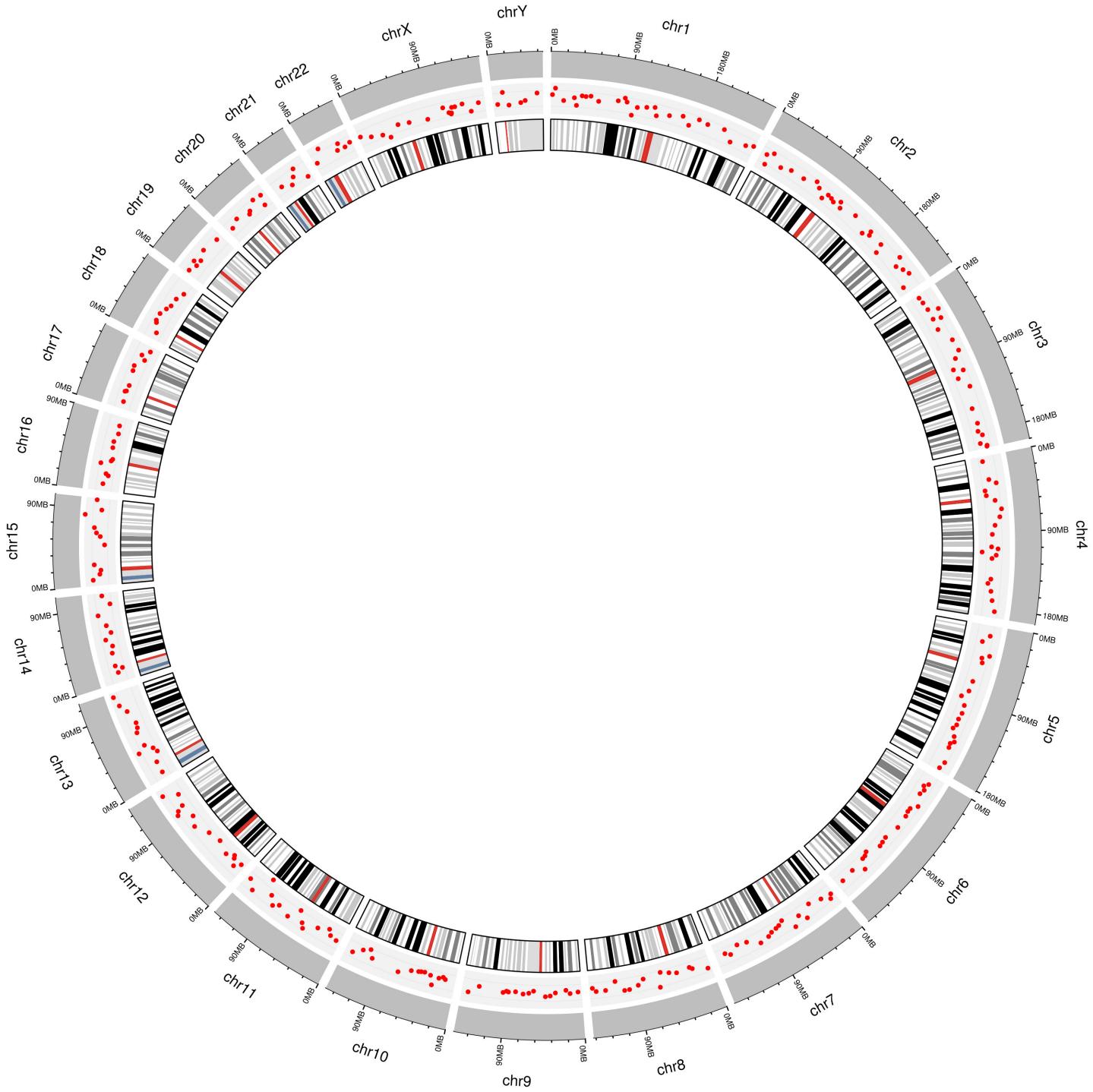
point.csv

- Track2

chr	start	end	value1	value2
chr1	1	2300000	p36.33	gneg
chr1	2300000	5400000	p36.32	gpos25
chr1	5400000	7200000	p36.31	gneg

chromosome\_ideogram.csv

- Data to plot ideogram is the same as "chromosome\_cytoband.csv".
- Ideogram plot can be generated in any track.



## **2.8 Plot labels**

# Upload label data

**Upload chromosome data** ?

Browse... chromosome\_general.csv

Upload complete

**Data type** ?

General  
 Cytoband

**Upload label data** ?

Browse... gene\_label.csv

Upload complete

**Upload data for inner tracks** ?

Track1  
 NULL  
 Upload

**Upload track1 data:**

Browse... point.csv

Upload complete

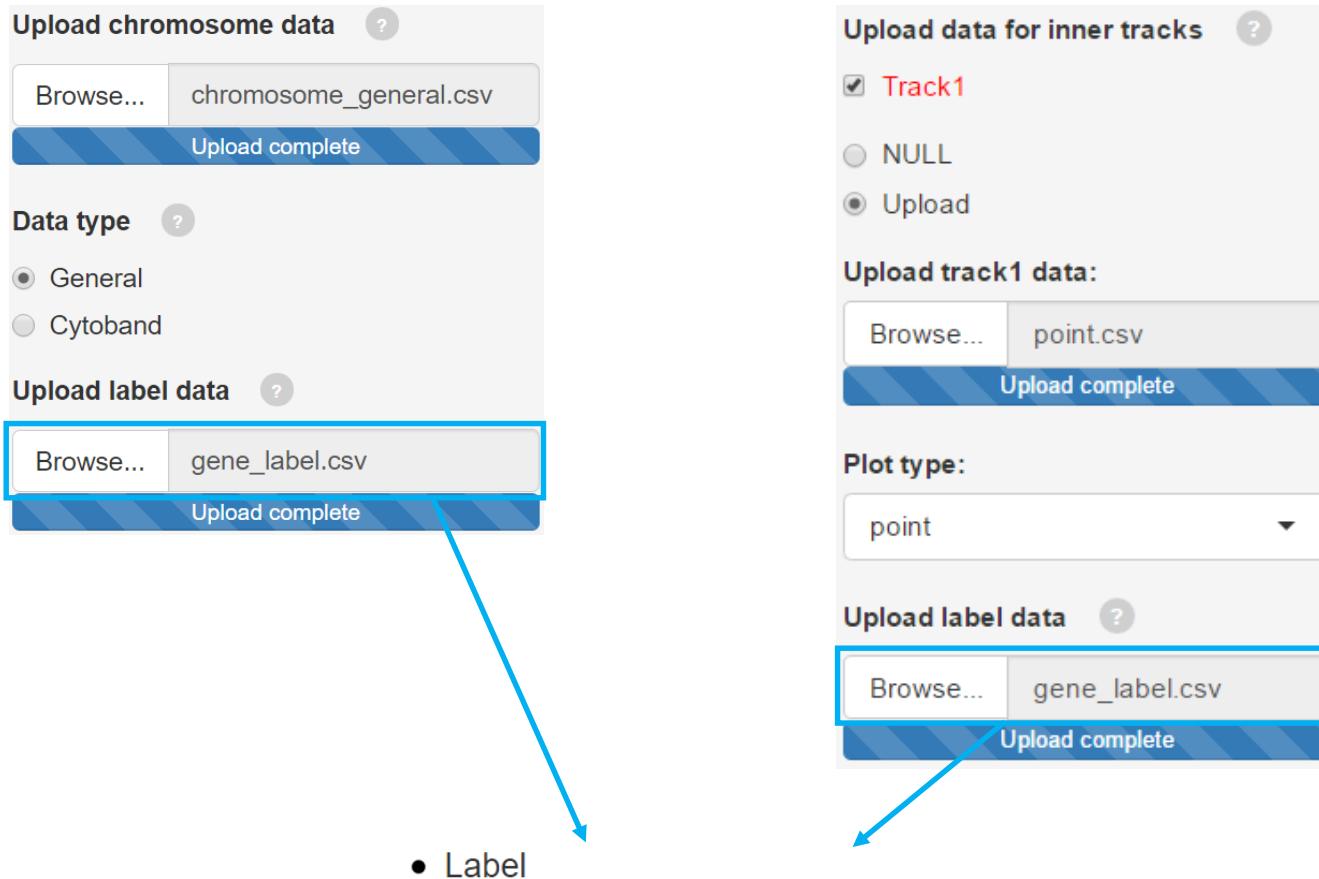
**Plot type:**

point

**Upload label data** ?

Browse... gene\_label.csv

Upload complete



- Label

chr	start	end	label
chr1	3698046	3736201	TP73
chr1	156114670	156140089	LMNA
chr2	202206180	202238599	SUMO1

# Options

## shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, there is a sidebar with several configuration sections:

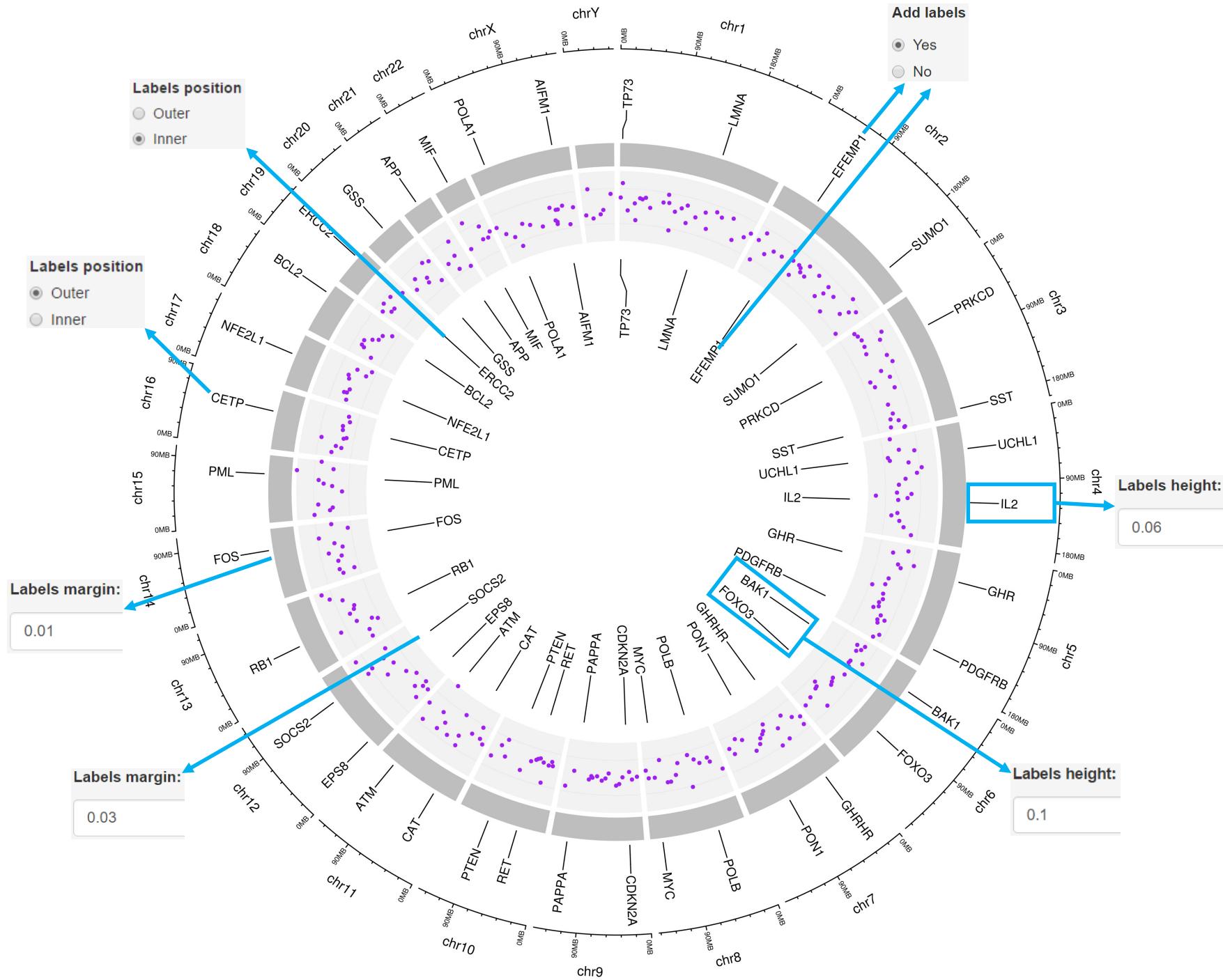
- Plot options**:
  - Chromosome
- Chromosome band**:
  - Show
  - Hide
- Color(s):** grey
- Chromosome IDs**:
  - Show
  - Hide
- Size units of genomic regions**:
  - Show
  - Hide
- Gap width(s):** 1
- Add labels**:
  - Yes
  - No
- Labels position**:
  - Outer
  - Inner
- Labels height:** 0.06
- Labels margin:** 0.01

At the top right, there is a navigation bar with links: About, Data upload, Circos visualization (which is highlighted), Gallery, Help, and download buttons for PDF, SVG, and R scripts.

Annotations in blue text explain some of the settings:

- Add labels**: Add labels to mark genes or genomic regions for this track using data uploaded in the "Data upload" menu.
- Labels position**: Specify labels positions relative to the track.
- Labels height**: Height of the labels.
- Labels margin**: Margin size of the labels.

● See section 2.2 for more plot options.



## **2.9 Plot links**

# Upload links data

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Upload chromosome data [?](#)

Browse... No file selected

Data type [?](#)

General  
 Cytoband

Upload label data [?](#)

Browse... No file selected

Upload data for inner tracks [?](#)

Track1  
 Track2  
 Track3  
 Track4  
 Track5  
 Track6  
 Track7  
 Track8  
 Track9  
 Track10

Upload data to create links [?](#)

Links data

Upload region data:

Browse... No file selected

About Data upload Circos visualization Gallery Help

- Download example data
  - Example chromosomes data
    - [general data](#)
    - [cytoband data](#)
  - Example tracks data
    - [point data](#)
    - [line data](#)
    - [barplot data](#)
    - [heatmap data](#)
    - [ideogram data](#)
    - [rect \(discrete\) data](#)
    - [point \(multicolumn\) data](#)
    - [barplot \(bidirectional\) data](#)
    - [rect \(gradual\) data](#)
    - [line \(multicolumn\) data](#)
    - [line \(color\) data](#)
    - [barplot \(color\) data](#)
    - [point \(color\) data](#)
    - [point \(pch\) data](#)
    - [point \(color+pch\) data](#)
    - [point \(cex\) data](#)
    - [point \(pch+cex\) data](#)
    - [point \(color+cex\) data](#)
    - [point \(color+pch+cex\) data](#)
    - [label data](#)
    - [point \(stack\) data](#)
    - [line \(stack\) data](#)
  - Example links data
    - [links data](#)
    - [links \(color\) data](#)
- Glimpse of data uploaded

Data to plot links should include 6 or 7 columns.

Select "Links data" and upload file.

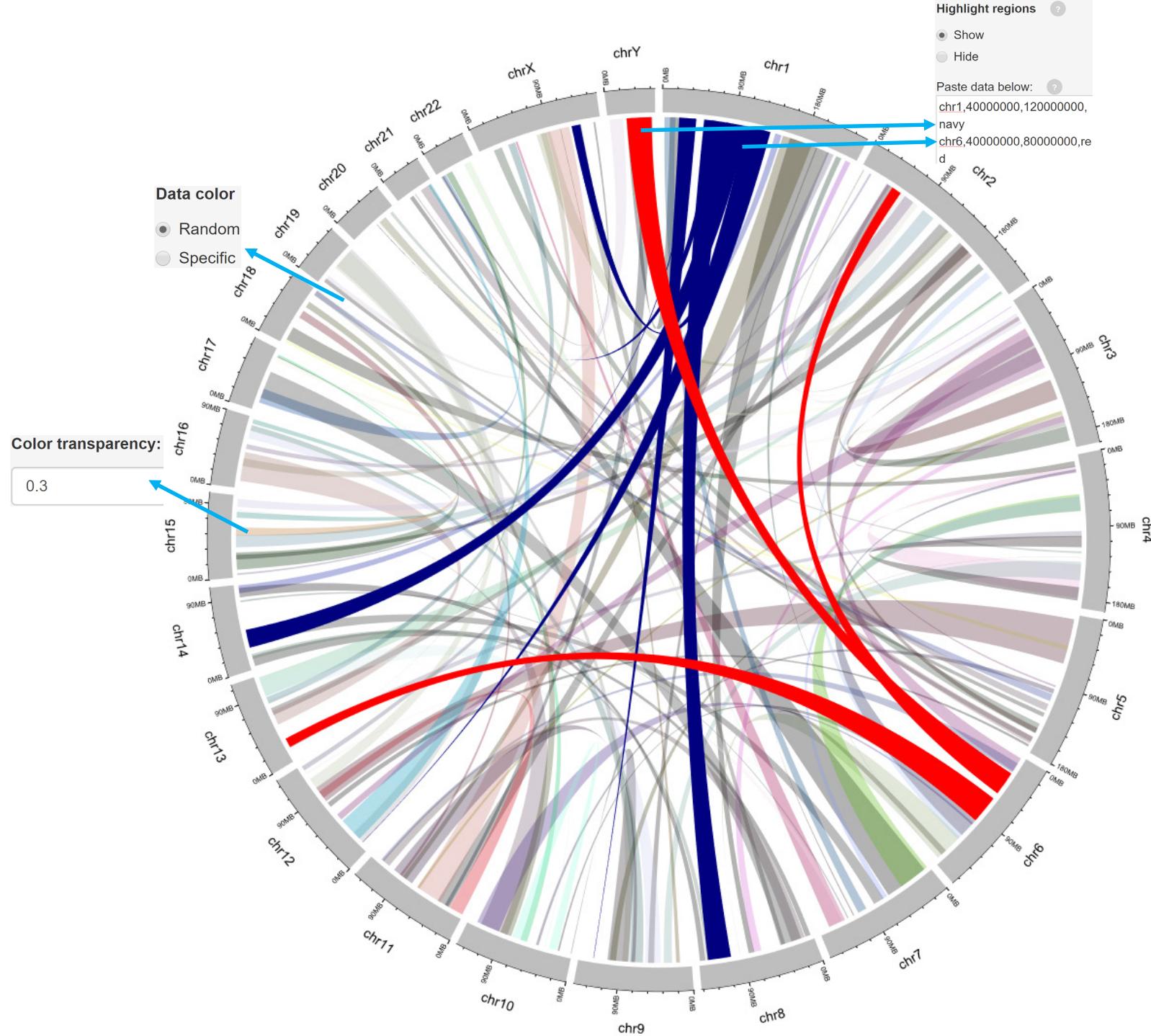
# Example 1

## Data format

chr1	start1	end1	chr2	start2	end2
chr20	37720821	47419255	chr5	162124929	168434522
chr8	76179361	83302661	chr1	162049212	213797379
chr2	38375277	49805216	chr11	19060895	36294068

links.csv

- Data with 6 columns.
- Columns 1-3 and columns 4-6 represent the two ends of connectors respectively.



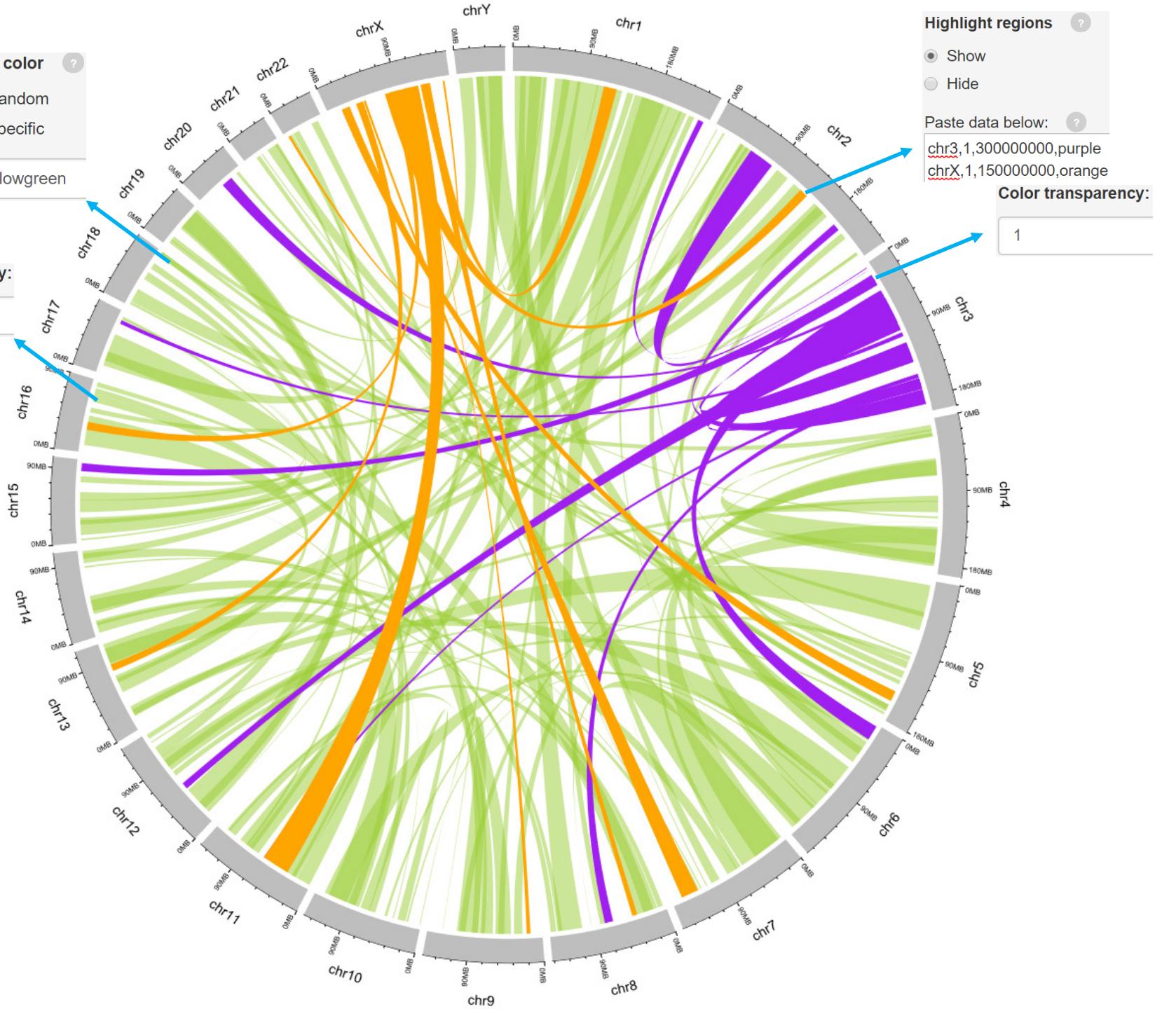
**Data color**

- Random
- Specific

yellowgreen

**Color transparency:**

0.5



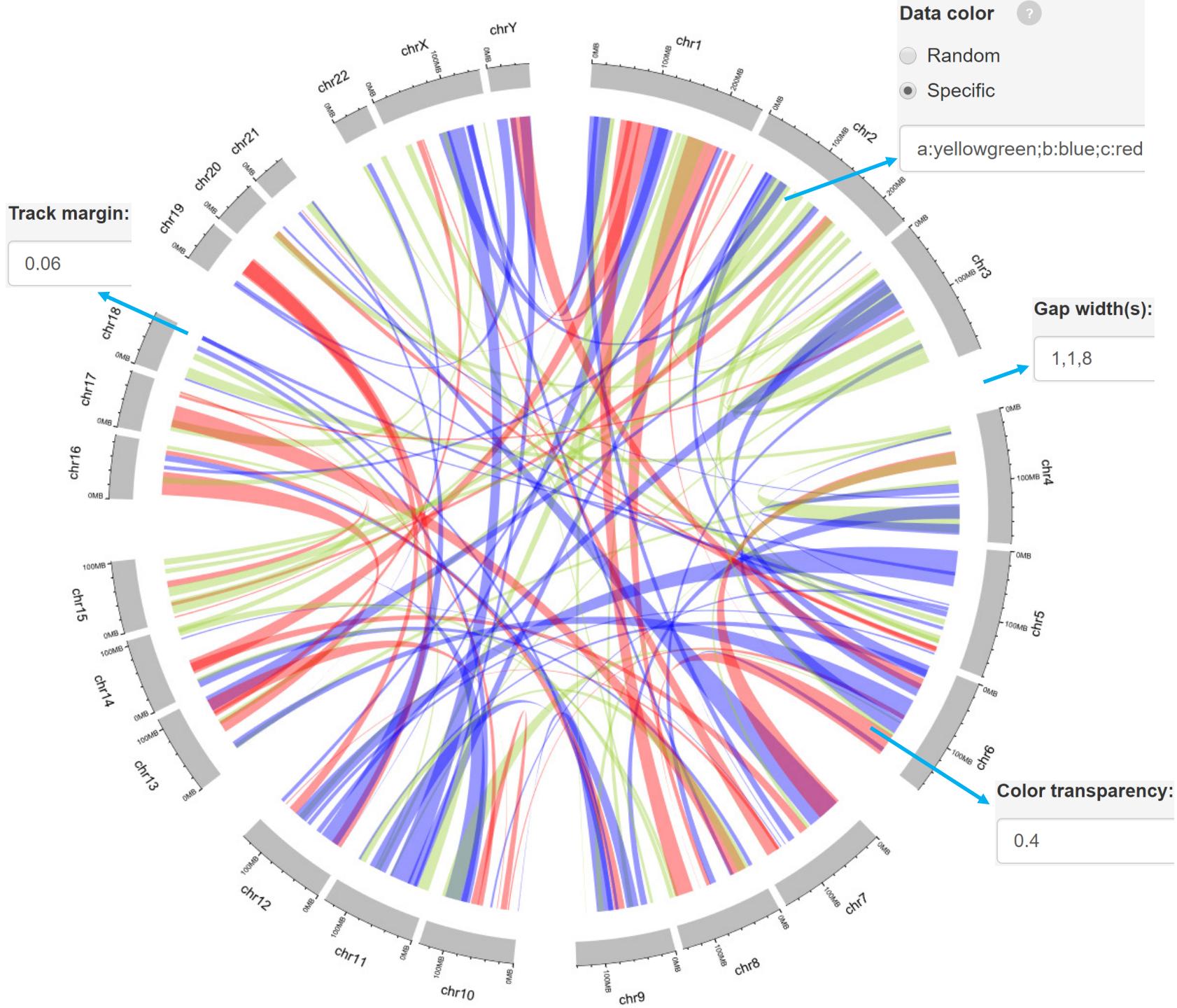
# Example 2

## Data format

chr1	start1	end1	chr2	start2	end2	color
chr20	37720821	47419255	chr5	162124929	168434522	c
chr8	76179361	83302661	chr1	162049212	213797379	c
chr2	38375277	49805216	chr11	19060895	36294068	b

[links\\_color.csv](#)

- Data with 7 columns.
- A “color” column representing different groups of data with differing colors can be added.



## Highlight regions

?

 Show Hide

Paste data below:

?

Color transparency:

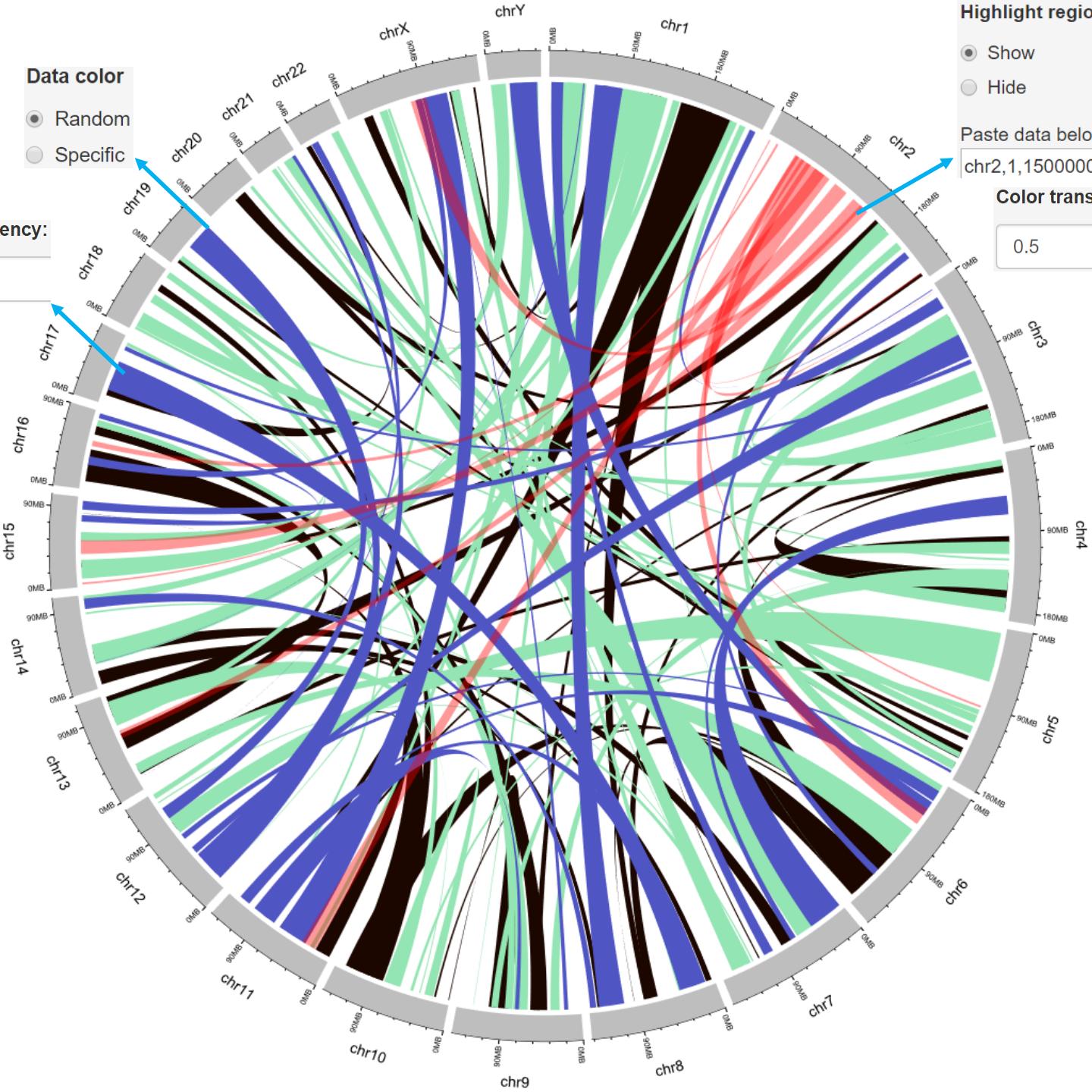
0.5

## Data color

- Random
- Specific

Color transparency:

1



### **3. Other features**

## 3.1 Figure size

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

The screenshot shows the shinyCircos application interface. On the left, a sidebar titled "Plot options" contains checkboxes for "Chromosome" and "Track1" through "Track10". Below these is a section with a checked checkbox for "Adjust plot size" and two input fields: "Plot height" set to 750 and "Plot width" set to 750. At the top right, there is a navigation bar with links for "About", "Data upload", "Circos visualization" (which is highlighted), "Gallery", and "Help". Below the navigation bar are three download buttons: "Download pdf-file", "Download svg-file", and "Download the R scripts to reproduce the Circos plot". A blue box highlights the "Adjust plot size" section. Two blue arrows point from the text annotations to this highlighted area.

Plot options

- Chromosome
- Track1
- Track2
- Track3
- Track4
- Track5
- Track6
- Track7
- Track8
- Track9
- Track10

Adjust plot size

Plot height:  
750

Plot width:  
750

About Data upload Circos visualization Gallery Help

[Download pdf-file](#)  [Download svg-file](#)  [Download the R scripts to reproduce the Circos plot](#)

Users can adjust the height and width of the Circos plot.

The figure size in both the browser and the download files would be affected.

# shinyCircos: an R/Shiny application for interactive creation of Circos plot

**Plot options**

- Chromosome
- Track1
- Track2
- Track3
- Track4
- Track5
- Track6
- Track7
- Track8
- Track9
- Track10
- Adjust plot size

**Plot height:**  
600

**Plot width:**  
600

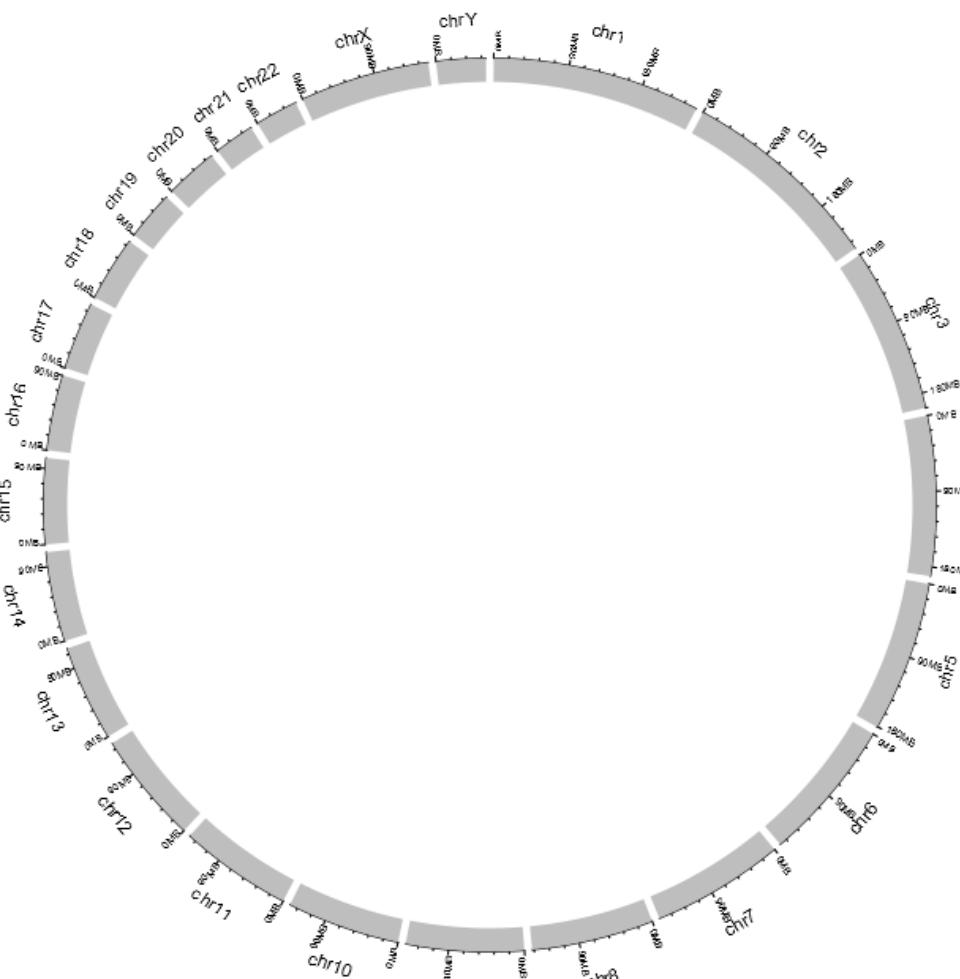
Adjust font size

Add legend

**Go!** ?

[About](#) [Data upload](#) [Circos visualization](#) [Gallery](#) [Help](#)

[Download pdf-file](#)  [Download svg-file](#)  [Download the R scripts to reproduce the Circos plot](#)



# shinyCircos: an R/Shiny application for interactive creation of Circos plot

**Plot options**

- Chromosome
- Track1
- Track2
- Track3
- Track4
- Track5
- Track6
- Track7
- Track8
- Track9
- Track10
- Adjust plot size

**Plot height:**

**Plot width:**

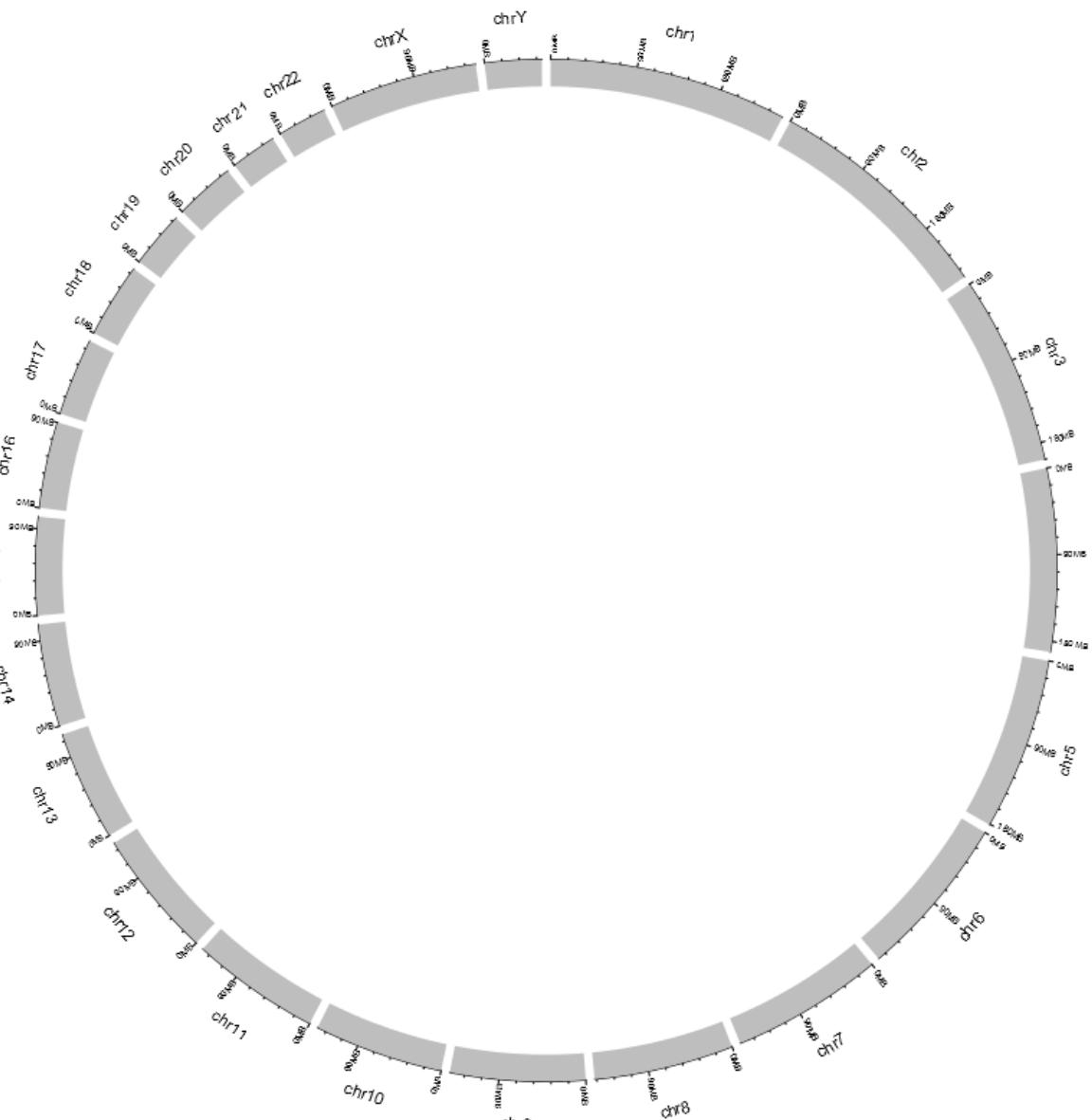
Adjust font size

Add legend

**Go!** ?

[About](#) [Data upload](#) [Circos visualization](#) [Gallery](#) [Help](#)

[Download pdf-file](#)  [Download svg-file](#)  [Download the R scripts to reproduce the Circos plot](#)



## **3.2 Font size**

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

Plot options

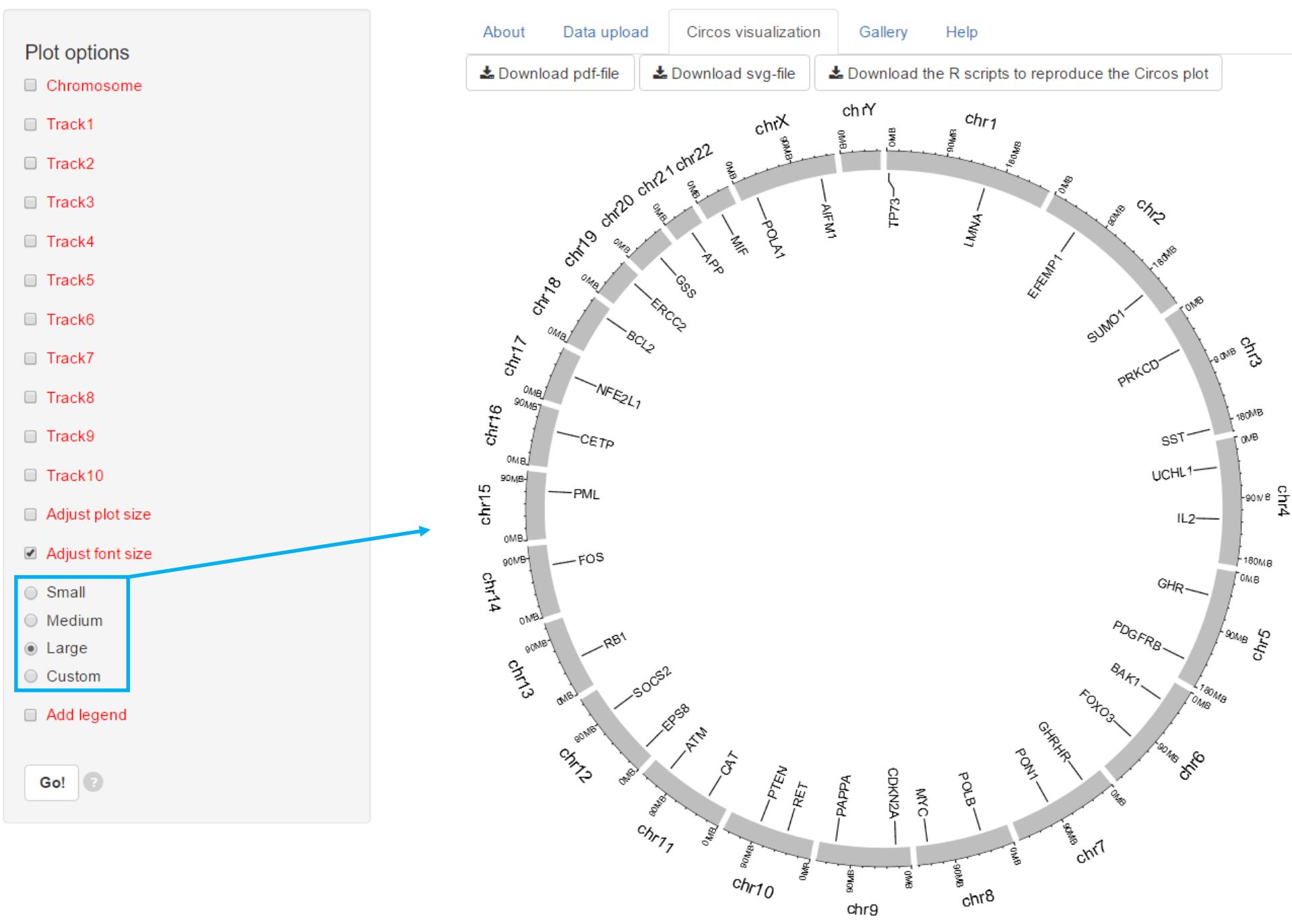
- Chromosome
- Track1
- Track2
- Track3
- Track4
- Track5
- Track6
- Track7
- Track8
- Track9
- Track10
- Adjust plot size
- Adjust font size
  - Small
  - Medium
  - Large
  - Custom

About    Data upload    Circos visualization    Gallery    Help

[Download pdf-file](#)     [Download svg-file](#)     [Download the R scripts to reproduce the Circos plot](#)

The font size can be 'small', 'medium', 'large' or specified by the user.

# shinyCircos: an R/Shiny application for interactive creation of Circos plot



shinyCircos: an R/Shiny application for interactive creation of Circos plot

## Plot options

- Chromosome
  - Track1
  - Track2
  - Track3
  - Track4
  - Track5
  - Track6
  - Track7
  - Track8
  - Track9
  - Track10
  - Adjust plot size

Adjust font size

- Small
  - Medium
  - Large
  - Custom

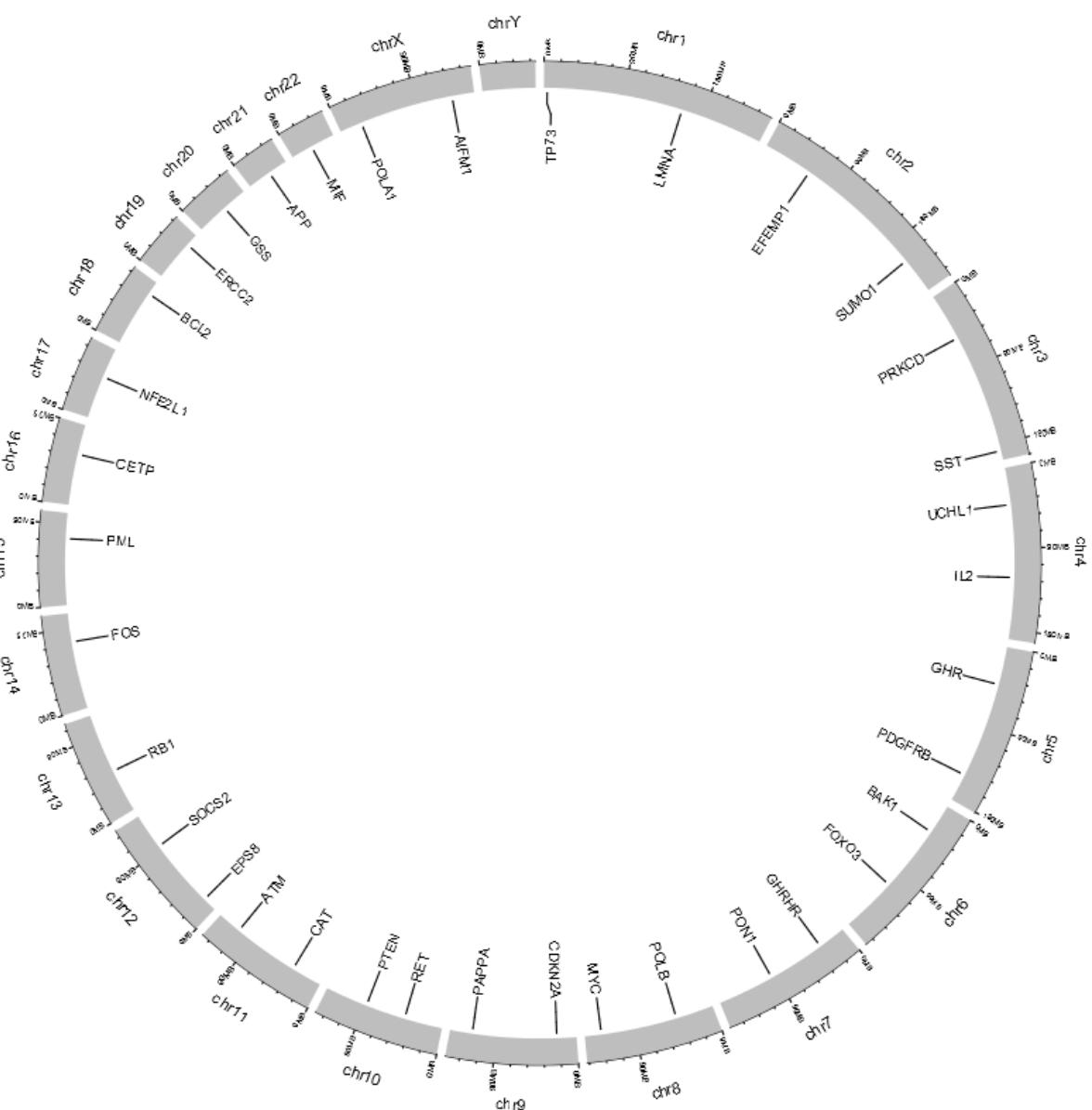
1

Add legend

Go!

About Data upload Circos visualization Gallery Help

 Download pdf-file    Download svg-file    Download the R scripts to reproduce the Circos plot



### 3.3 Legend

# Options

shinyCircos: an R/Shiny application for interactive creation of Circos plot

## Plot options

Chromosome

Track1

Track2

Track3

Track4

Track5

Track6

Track7

Track8

Track9

Track10

Adjust plot size

Adjust font size

Add legend

Yes

No

## Legend position

Right

Center

About

Data upload

Circos visualization

Gallery

Help

 Download pdf-file

 Download svg-file

 Download the R scripts to reproduce the Circos plot

Legend can be added at the right or the center of the Circos plot.

# shinyCircos: an R/Shiny application for interactive creation of Circos plot

## Plot options

Chromosome

## Chromosome band

- Show
- Hide

## Color(s):

grey

## Chromosome IDs

- Show
- Hide

## Size units of genomic regions

- Show
- Hide

## Gap width(s):

1

## Legend text

1.Chromosome

- Track1
- Track2
- Track3
- Track4
- Track5
- Track6
- Track7
- Track8
- Track9
- Track10

## Add legend

- Yes
- No

## Legend position

- Right
- Center

Go!

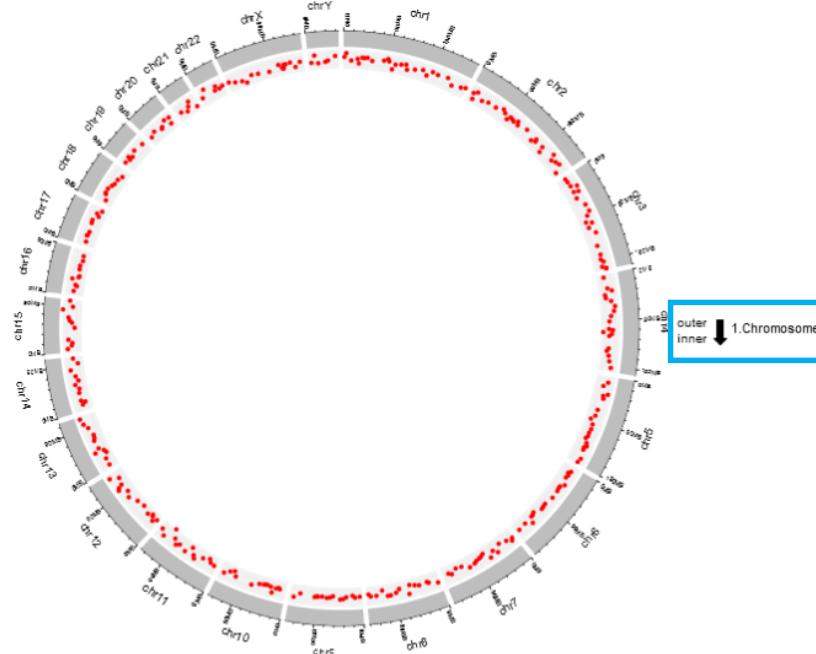


About Data upload Circos visualization Gallery Help

[Download pdf-file](#)

[Download svg-file](#)

[Download the R scripts to reproduce the Circos plot](#)



Input  
legend text

Legend option

# shinyCircos: an R/Shiny application for interactive creation of Circos plot

## Plot options

Chromosome

## Chromosome band

- Show
- Hide

## Color(s):

grey

## Chromosome IDs

- Show
- Hide

## Size units of genomic regions

- Show
- Hide

## Gap width(s):

1

## Legend text

1.Chromosome

- Track1
- Track2
- Track3
- Track4
- Track5
- Track6
- Track7
- Track8
- Track9
- Track10
- Adjust plot size
- Adjust font size

## Add legend

- Yes
- No

## Legend position

- Right
- Center

About

Data upload

Circos visualization

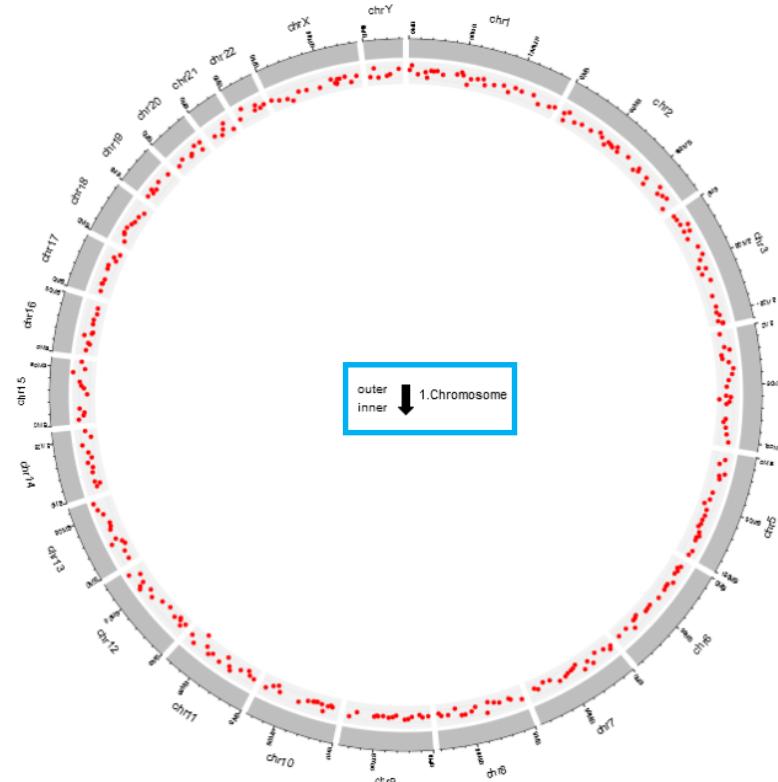
Gallery

Help

 Download pdf-file

 Download svg-file

 Download the R scripts to reproduce the Circos plot



Input  
legend text

Legend option