

shinyChromosome

an R/Shiny application for interactive creation of
non-circular plots of whole genomes

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

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



Users are encouraged to install and use shinyChromosome on local personal computers.

Please check the help menu of the shinyChromosome application or <https://github.com/venyao/shinyChromosome> for the installation of shinyChromosome on local computers.

1. Interface of shinyChromosome

Menu in shinyChromosome: About

- The shinyChromosome application contains five menus, "About", "One genome", "Two genomes", "Gallery", "Help" and "Manual".



- Software references

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2. RStudio and Inc. [shiny: Web Application Framework for R](#). R package version 1.0.5 (2017)
3. Lionel Henry and Hadley Wickham. [rlang: Functions for Base Types and Core R and "Tidyverse" Features](#). R package version 0.2.1 (2018)
4. H. Wickham. [ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics](#). R package version 3.0.0 (2018)
5. Gregory R. Warnes, Ben Bolker, Lodewijk Bonebakker, Robert Gentleman, et al. [gplots: Various R Programming Tools for Plotting Data](#). R package version 3.0.1 (2016)
6. Erich Neuwirth. [RColorBrewer: ColorBrewer palettes](#). R package version 1.1-2 (2014)
7. Hadley Wickham. [plyr: Tools for Splitting, Applying and Combining Data](#). R package version 1.8.4 (2016)
8. Jeffrey B. Arnold. [gridthemes: Extra Themes, Scales and Geoms for "ggplot2"](#). R package version 3.4.0 (2017)
9. Christoph Burow, Urs Tilmann Wolpert and Sebastian Kreutzer. [RLumShiny: "Shiny" Applications for the R Package "Luminescence"](#). R package version 0.2.0 (2017)
10. Baptiste Auguie. [gridExtra: Miscellaneous Functions for "Grid" Graphics](#). R package version 2.3 (2017)
11. Hadley Wickham. [reshape2: Flexibly Reshape Data: A Reboot of the Reshape Package](#). R package version 1.4.3 (2017)
12. Matt Dowle and Arun Srinivasan. [data.table: Extension of "data.frame"](#). R package version 1.10.4-3 (2017)
13. JJ Allaire, Jeffrey Horner, Vicent Marti and Natacha Porte. [markdown: "Markdown" Rendering for R](#). R package version 0.8 (2017)

- 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](#).

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

Menu in shinyChromosome: One genome

shinyChromosome About One genome Two genomes Gallery Help Manual

Image type
 Concatenated chromosome
 Separated chromosome

Orientation
 Horizontal
 Vertical

Upload genome data:
 No file selected

Data1
 Data2
 Data3
 Data4
 Data5
 Data6
 Data7
 Data8
 Data9
 Data10

Plot options

 Download pdf-file  Download svg-file

 Download the R scripts to reproduce the plot

Download scripts

Download figures

Show Pictures

Upload data and tune plot options

- The “One genome” menu allows uploading of input data to create non-circular plots along all chromosomes of a single genome.
- Various options are provided to tune the appearance of the generated plot.

Menu in shinyChromosome: Two genomes

The screenshot shows the 'Two genomes' menu of the shinyChromosome application. On the left, there are three input fields for 'Upload genome1 data', 'Upload genome2 data', and 'Upload plot data', each with a 'Browse...' button and a 'No file selected' message. Below these is a 'Plot type:' dropdown set to 'point_gradual' with a 'Show Advanced Options' button. A 'Go!' button is also present. To the right of these controls, the interface is divided into several sections: 'Download figures' (highlighted in blue), 'Upload data' (highlighted in blue), 'Plot options' (highlighted in blue), 'Download scripts' (highlighted in blue), and a large empty rectangular area labeled 'Show Pictures'.

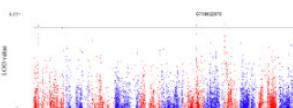
- The “Two genomes” menu allows uploading of input data to create two-dimensional plots for comparison of data across two genomes.
- Various options are provided to tune the appearance of non-circular plots.

Menu in shinyChromosome: Gallery

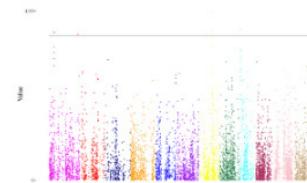
shinyChromosome About One genome Two genomes **Gallery** Help Manual



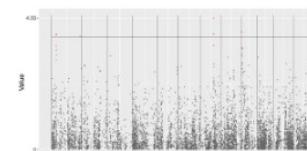
Example 1



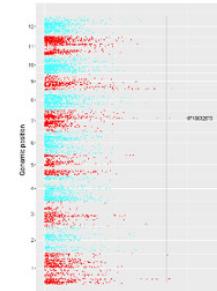
Example 2



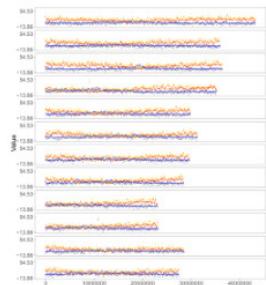
Example 3



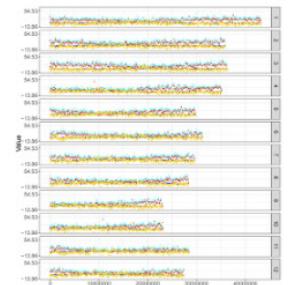
Example 4



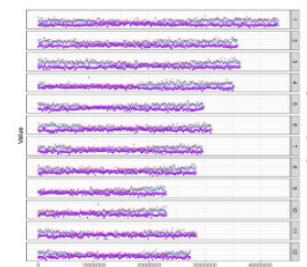
Example 5



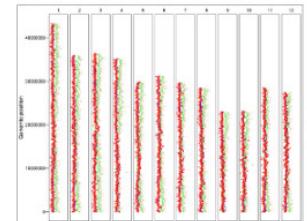
Example 6



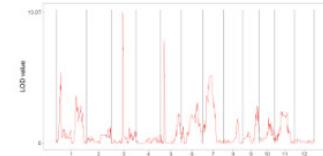
Example 7



Example 8



Example 9



Example 10



- Fifty example figures generated by shinyChromosome are listed in the “*Gallery*” menu.
- Example datasets used to generate the plots are available for download.

Menu in shinyChromosome: Help

shinyChromosome About One genome Two genomes Gallery **Help** Manual

shinyChromosome

This is the repository for the Shiny application presented in "shinyChromosome: an R/Shiny application for interactive creation of non-circular plots of whole genomes" (Yu et al. 2018).

Use shinyChromosome online

shinyChromosome is deployed at <https://yimengyu.shinyapps.io/shinychromosome/> and <http://shinychromosome.ncgr.cn/> for online use.

shinyChromosome 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, shinyChromosome could be used smoothly and easily.

Launch shinyChromosome directly from R and GitHub (preferred approach)

User can choose to run shinyChromosome 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 3.5.0 and RStudio 1.1.419).

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 shinyChromosome

Start an R session using RStudio and run these lines:

```
# try an http CRAN mirror if https CRAN mirror doesn't work
install.packages("shiny")
install.packages("rlang")
install.packages("gplots")
install.packages("ggplot2")
install.packages("plyr")
install.packages("ggthemes")
install.packages("RLumShiny")
install.packages("RColorBrewer")
install.packages("gridExtra")
install.packages("reshape2")
install.packages("data.table")
install.packages("shinythemes")
install.packages("shinyBS")
install.packages("markdown")
```

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

Menu in shinyChromosome: Manual

shinyChromosome About One genome Two genomes Gallery Help **Manual**

shinyChromosome
an R/Shiny application for interactive creation of
non-circular plots of whole genomes

Download this manual for the usage of shinyChromosome

2. Usage of shinyChromosome

2.1 Non-circular plots for one genome

Non-circular plots for one genome

shinyChromosome About One genome Two genomes Gallery Help Manual

1.1

Image type
 Concatenated chromosome
 Separated chromosome

Orientation
 Horizontal
 Vertical

Upload genome data:
Browse... genome_data.txt Upload complete

1.2

Data1
 NULL
 Upload

Upload data1:
Browse... data1_track1_point.txt Upload complete

1.3

Plot type: point

Track index: track1

Show Advanced Options

Data2
 Data3
 Data4
 Data5
 Data6
 Data7
 Data8
 Data9
 Data10

1.4

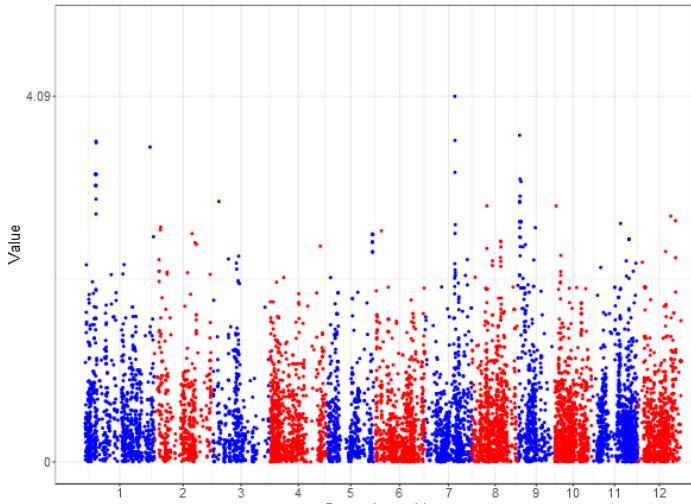
Go!

Plot options

Show Advanced Options

1.5

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



1.5 Download figures and scripts

1.1 Upload genome data

1.2 Upload input data to be distributed into different tracks

1.3 Plot options

- The genome data is compulsory and defines the frame of a non-circular plot.
- 1-10 datasets could be uploaded and displayed in different tracks.
- Please click the "Go!" button, if suitable data is uploaded or any option is modified.

1.4 Submit the data to make the plot

2.1.1 Plot point

Upload genome data

shinyChromosome About

One genome

Two genomes

Gallery

Help

Manual

Image type

Concatenated chromosome
 Separated chromosome

Orientation

Horizontal
 Vertical

Upload genome data:

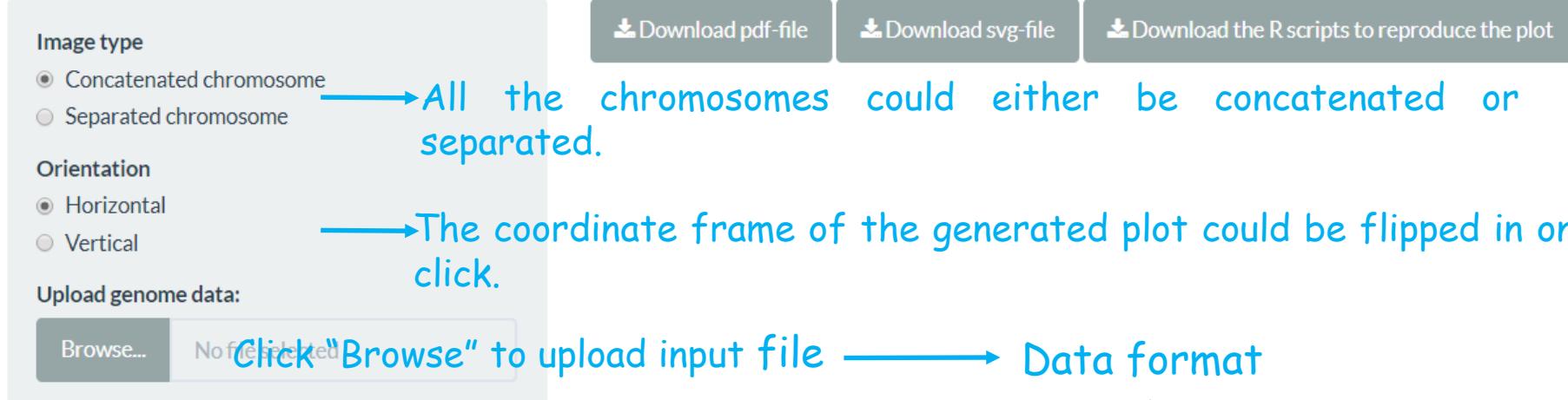
Browse... No file selected

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

All the chromosomes could either be concatenated or separated.

The coordinate frame of the generated plot could be flipped in one click.

Click "Browse" to upload input file → Data format



chr	size
1	43268879
2	35930381
3	36406689
4	35278225
5	29894789

- Genome data can be simple definition of chromosome lengths, which include two columns as chromosome IDs and chromosome lengths (See example data "genome_data.txt" in the "Gallery" menu for more detail).

Upload point data

shinyChromosome About One genome Two genomes Gallery Help Manual

Image type

Concatenated chromosome
 Separated chromosome

Orientation

Horizontal
 Vertical

Upload genome data:

No file selected

Data1
 NULL
 Upload

Upload data1:

No file selected

Plot type:

point

Track index:

track1

Select "Upload"

Upload input file

plot type: "point"

Set track index as "track1"

- Data with the **same track index** will be plotted in the same track, while data with **different track indices** will be displayed in differing tracks.
- The track index can be set at the user's choice, if only one data file is uploaded.

Options

Data1
 NULL
 Upload

Upload data1:

Browse... No file selected

Plot type:

point

Track index:

track1

Show Advanced Options ▾

Data color

Random
 One custom color
 Custom for data with multi-group

Color transparency:

1

Symbol type:

16

Point size:

0.8

→ The color to be used to plot the data, which can be random assigned by the application or specified by the users.

→ A decimal number in $[0, 1]$ to adjust the color transparency. The higher the value, the deeper the color.

→ Symbol used for different points. Applicable values are integers in $[0-25]$.

→ Value used to adjust the size of points.

Options

X-axis rugs

- Show
- Hide

Color:

black

→ Create a set of tick marks along the X-axis.

Y-axis rugs

- Show
- Hide

Color:

black

→ Create a set of tick marks along the Y-axis.

Y label

- Show
- Hide

Add legend

- Yes
- No

Color legend

- Yes
- No

Name:

color

→ Add tick labels on the Y-axis.

→ Add a legend on the right or the bottom of the main plot.

→ Legend for colors used in specified dataset.

→ Title of the color legend. Null value will result in an empty title.

Modify labels

- Yes
- No

a,b,c

→ The labels of different colors in the color legend can be assigned by the application or specified by the users.

Options

Size legend

- Yes
- No

→ Legend for point size used in specified dataset.

Name:

→ Title of size legend. Null value will result in an empty title.

size

Modify labels

- Yes
- No

→ The labels of different point size in the size legend can be assigned by the application or specified by the users.

a,b,c

Shape legend

- Yes
- No

→ Legend for point shape used in specified dataset.

Name:

→ Title of the shape legend. Null value will result in an empty title.

shape

Modify labels

- Yes
- No

→ The labels of different point shape in the shape legend can be assigned by the application or specified by the users.

a,b,c

Example 1

shinyChromosome About One genome Two genomes Gallery Help Manual

Image type
 Concatenated chromosome
 Separated chromosome

Orientation
 Horizontal
 Vertical

Upload genome data:
Browse... genome_data.txt Upload complete

Data1
 NULL
 Upload

Upload data1:
Browse... data1_track1_point.txt Upload complete

Plot type:
point

Track index:
track1

Show Advanced Options

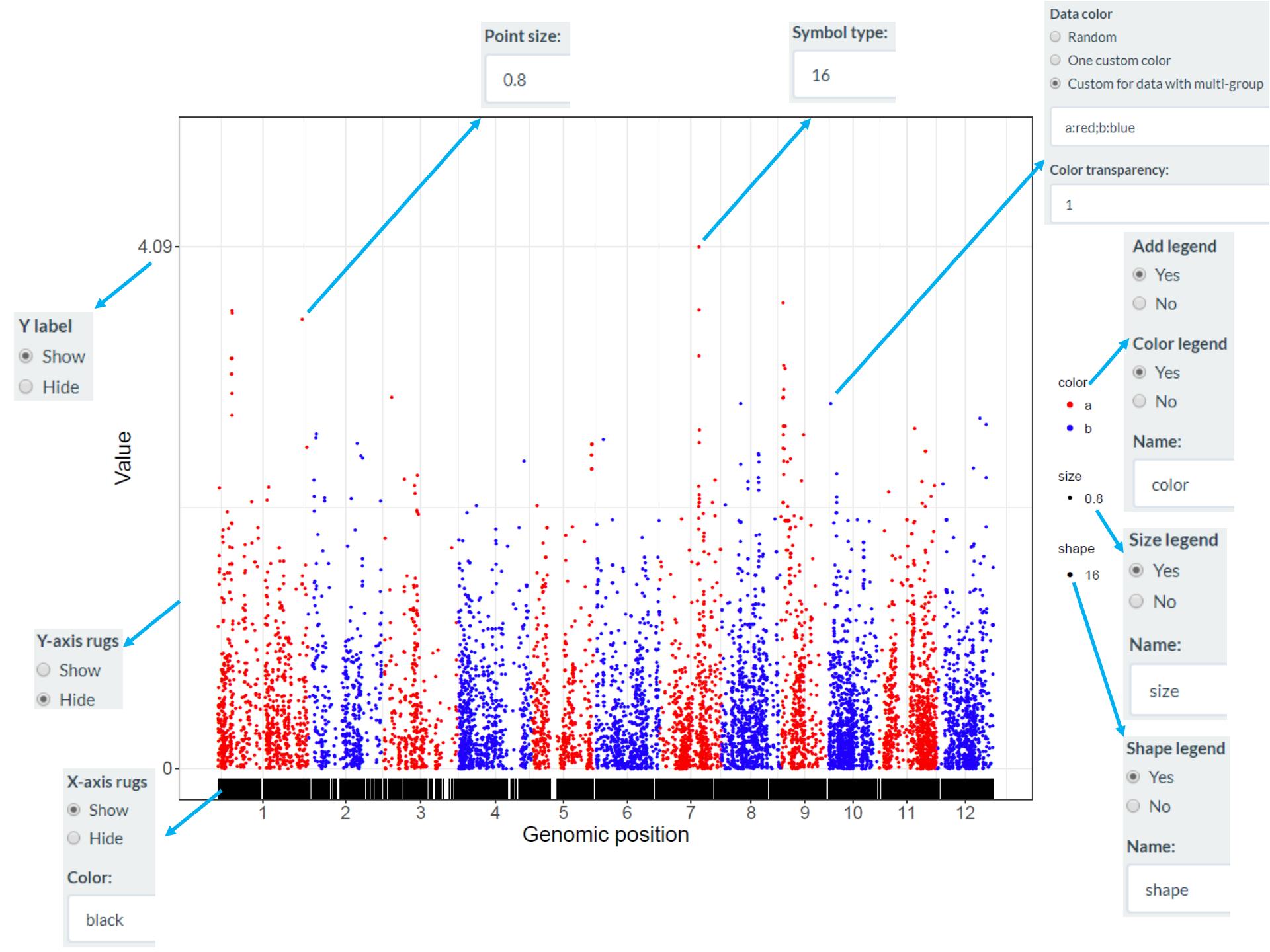
 Download pdf-file  Download svg-file  Download the R scripts to reproduce the plot

Data format example_1/data1_track1_point.txt

chr	position	val	color
1	202360	0.315323	a
1	213775	1.1134394	a
1	218457	0.393112	a
1	223744	0.0231798	a
1	253965	0.4322161	a

The track index can be set at the user's choice, if only one data file is uploaded.

- The "color" column indicates different colors for differing data groups, which is a character vector.
- The simplest dataset to plot point should contain at least 3 columns including the chromosome IDs, genomic positions and numeric values.



Example 2

Image type
 Concatenated chromosome
 Separated chromosome

Orientation
 Horizontal
 Vertical

Upload genome data:

Browse... genome_data.txt
Upload complete

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_point.txt
Upload complete

Plot type:

point

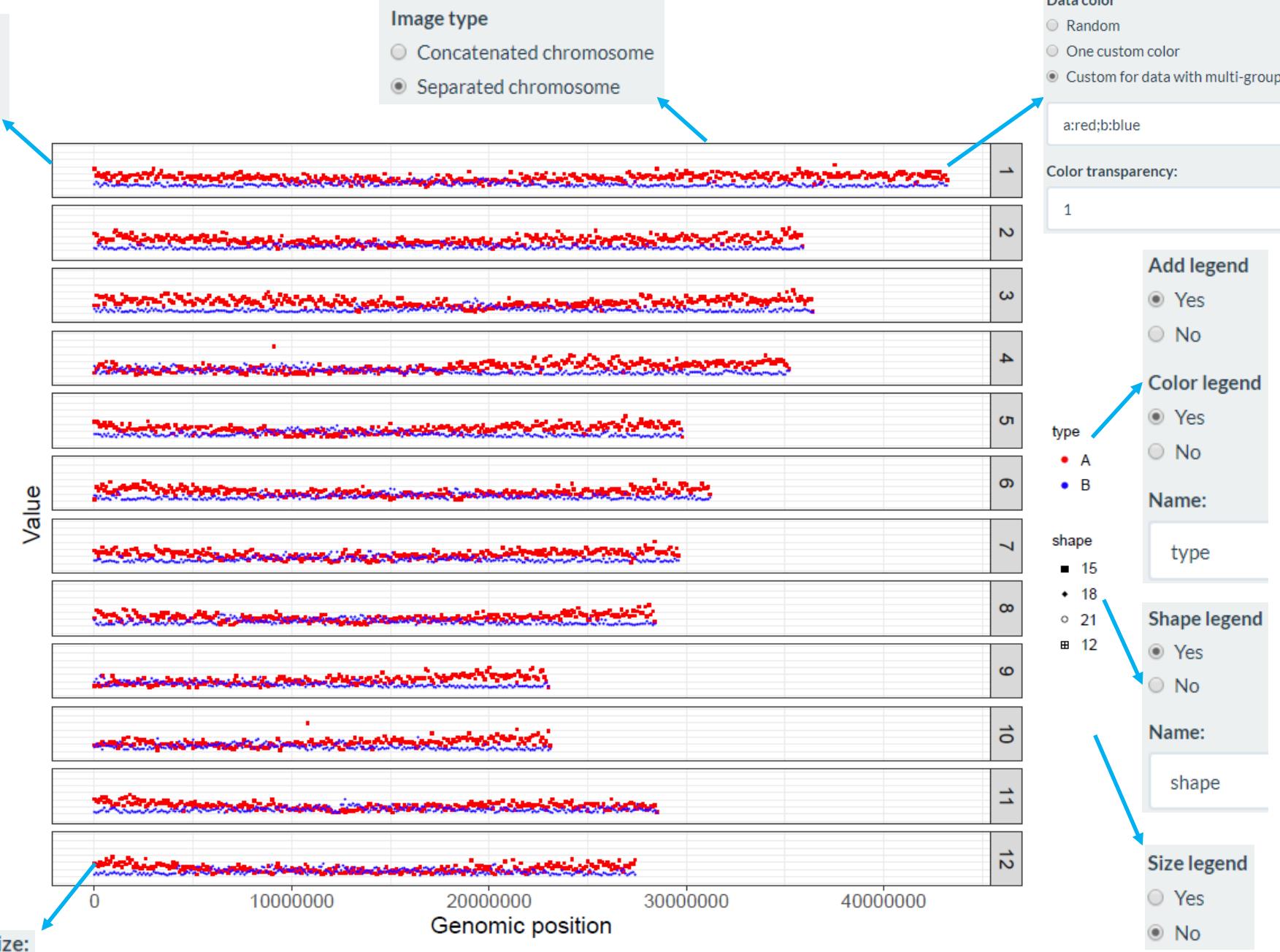
Track index:

track1

Data format
example_7/data1_track1_point.txt

chr	position	count	color	shape
1	1	29	a	15
1	100001	18	a	15
1	200001	22	a	15
1	300001	18	a	15
1	400001	16	a	15

- The “shape” column indicates different point types used for differing data groups. Applicable value are integers in [0-25].



Point size:

0.6

Example 3

Image type
 Concatenated chromosome
 Separated chromosome

Orientation
 Horizontal
 Vertical

Upload genome data:

Browse... genome_data.txt
Upload complete

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_point.txt
Upload complete

Plot type:
point

Track index:

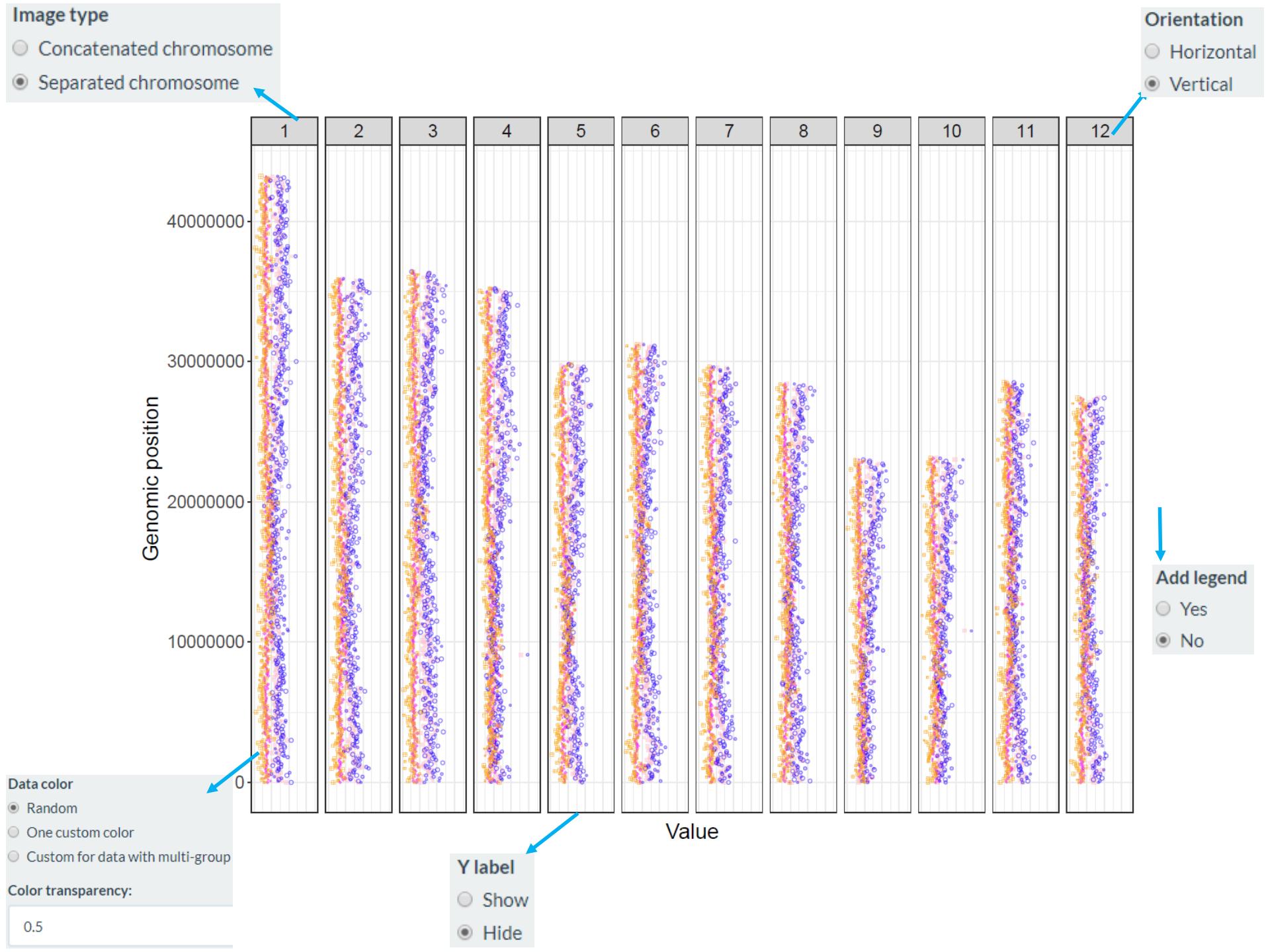
track2

Data format

example_9/data1_track1_point.txt

chr	position	count	color	shape	size
1	1	29	a	15	1.1
1	100001	18	a	15	1
1	200001	22	a	15	1.1
1	300001	18	a	15	0.6
1	400001	16	a	15	0.8

- The “size” column is a **numeric vector** representing different point sizes.
- The names of columns used to specify the “color”, “shape” and “size” of the data should be fixed as “color”, “shape” and “size”.



2.1.2 Plot line

Options

Data1
 NULL
 Upload

Upload data1:

Browse... No file selected

Plot type:

line

Track index:

track1

Show Advanced Options

Data color

Random
 One custom color
 Custom for data with multi-group

Fill area

Yes
 No

Area color

Identical with lines
 Specific

blue

Color transparency:

1

Line width:

0.2

Line type

solid

→ Fill the area below the lines.

→ Fill the area with a given color, which can be identical to line color or specified by the user.

→ Set the line width.

→ Select the line type.

- See section 2.1.1 for more plot options.

Example 1

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_line.txt
Upload complete

Plot type:
line

Track index:
track1

Data2
 NULL
 Upload

Upload data2:

Browse... data1_track1_line.txt
Upload complete

Plot type:
line

Track index:
track2

Data format

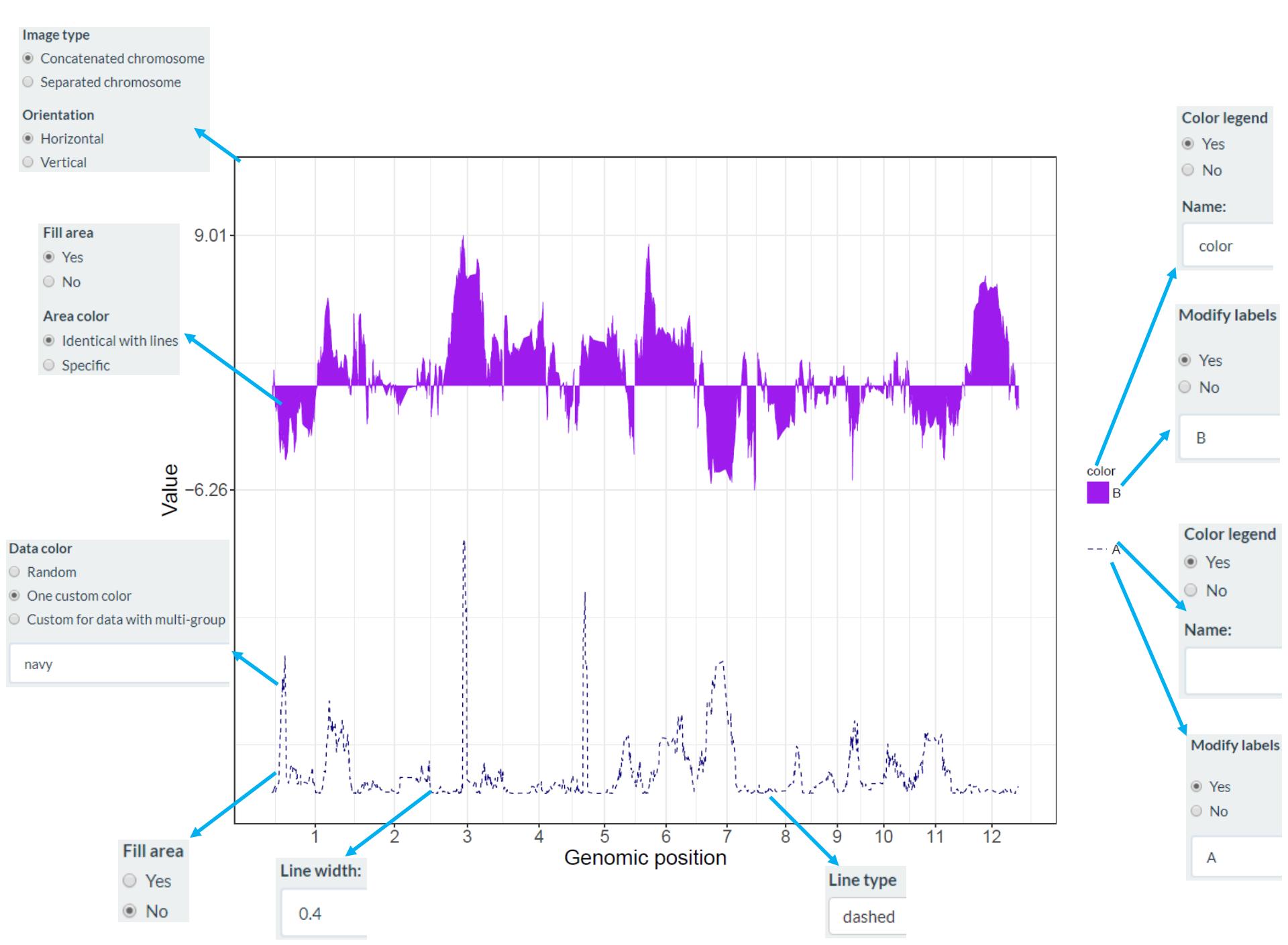
example_10/data1_track1_line.txt

chr	pos	lod
1	0	0.0428
1	565000	0.0522
1	599000	0.0674
1	922000	0.1209
1	1075000	0.2099
1	1147000	0.1348
1	1221000	0.2416

example_11/data1_track1_line.txt

Chr	position	A98
1	283500	-0.653
1	583000	-0.774
1	761500	-0.496
1	999500	0.39
1	1112000	0.879

- Simplest data to plot line should contain at least 3 columns including the chromosome IDs, genomic positions and numeric values.



Example 2

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_line.txt
Upload complete

Plot type:
line

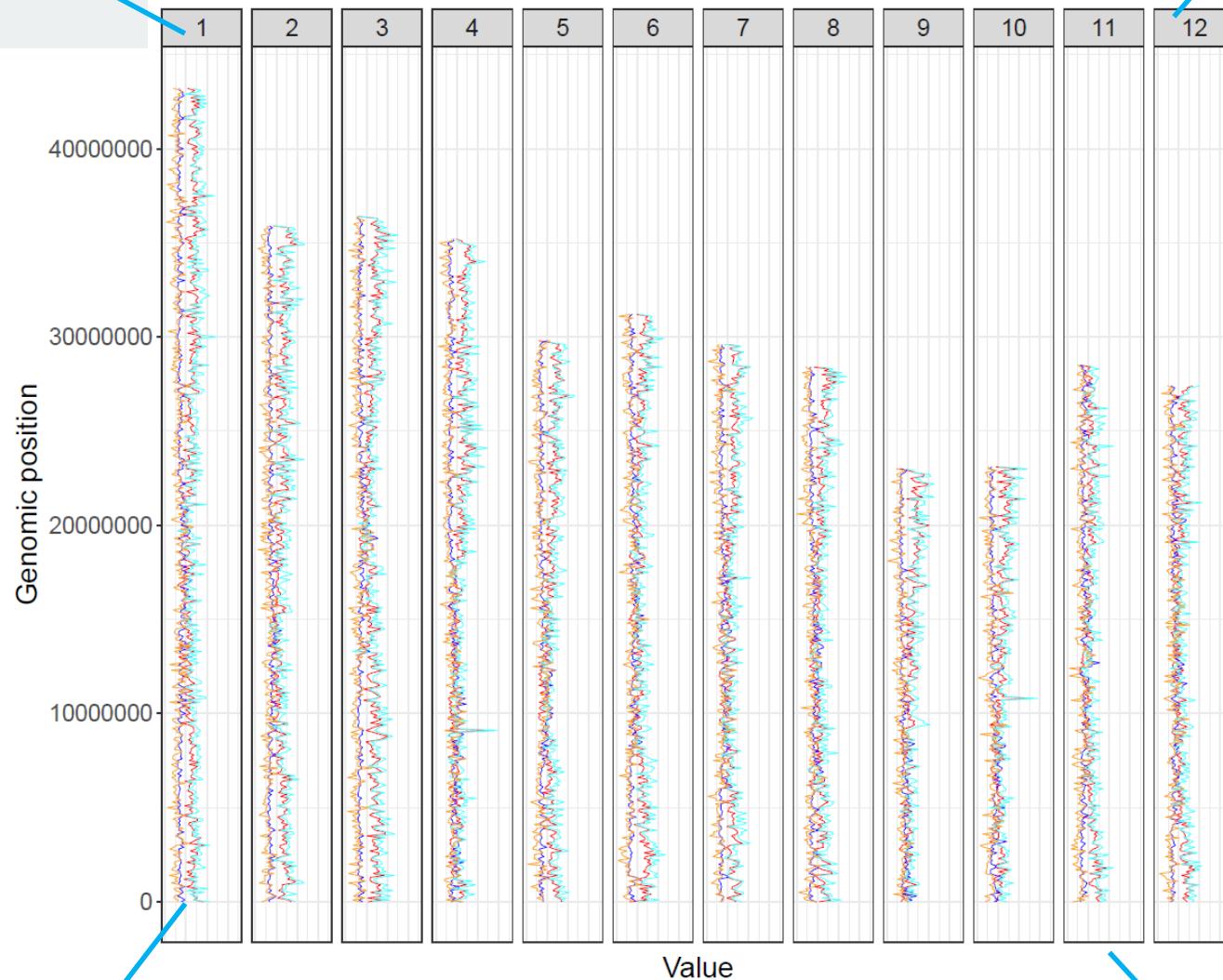
Track index:
track1

Data format

example_15/data1_track1_line.txt

chr	position	count	color
1	1	29	a
1	100001	18	a
1	200001	22	a
1	300001	18	a
1	400001	16	a

- A “color” column can be added to assign colors to different lines, which is a character vector.

Image type Concatenated chromosome Separated chromosome**Orientation** Horizontal Vertical**Data color** Random One custom color Custom for data with multi-group

a:red;b:blue;c:cyan;d:orange

Color legend Yes No

Name:

color

color

a

b

c

d

Y label Show Hide

2.1.3 Plot bar

Options

Data1
 NULL
 Upload

Upload data1:

No file selected

Plot type:

bar

Track index:

track1

Show Advanced Options

Data color

Random
 One custom color
 Custom for data with multi-group

Color transparency:

1

Add cell borders → Add borders to the bars.

Yes
 No

Borders color: → The color used for the borders of bars.

black

- See section 2.1.1 for more plot options.

Upload bar data

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_bar.txt
Upload complete

Plot type:
bar

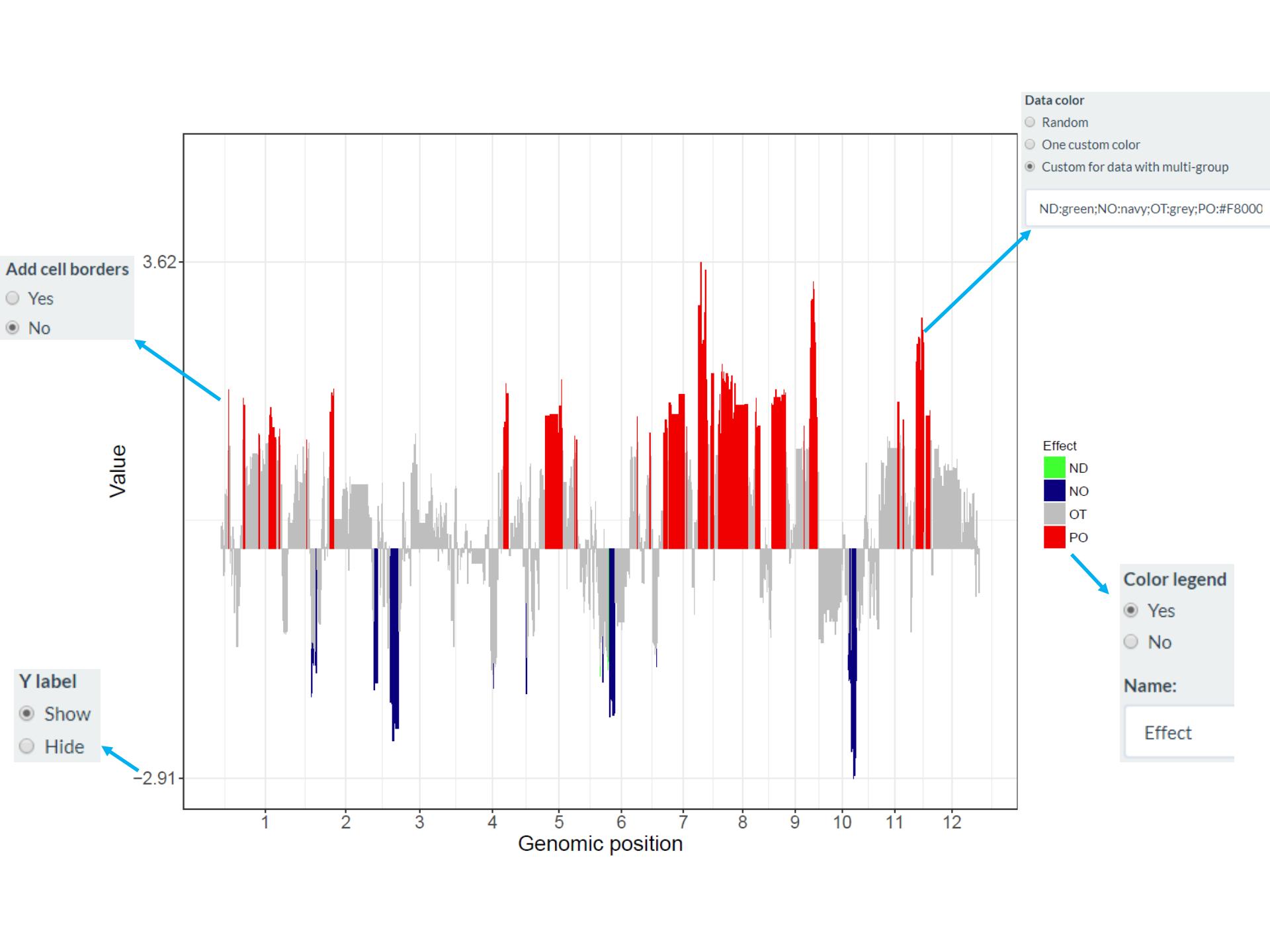
Track index:
track1

Data format

example_19/data1_track1_bar.txt

Chr	Start	Stop	D	color
1	0	565000	0.283	OT
1	565000	599000	0.337	OT
1	599000	922000	0.233	OT
1	922000	1075000	-0.12	OT
1	1075000	1147000	-0.339	OT

- Data for bar plot generally includes 4 columns including the chromosome IDs, start coordinates of regions, end coordinates of regions and numeric values.
- The 4th column is a numeric vector representing the heights of different bars.
- A "color" column can be added to assign colors to different bars, which is a character vector.



2.1.4 Plot rect_gradual

Options

Data1
 NULL
 Upload

Upload data1:

Browse... No file selected

Plot type:

rect_gradual ▾

Track index:

track1 ▾

Show Advanced Options ▾

Data color →

blue ▾

Colors used for the rect plot.

- See section 2.1.1 for more plot options.

Upload rect_gradual data

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_rect_gradual.txt
Upload complete

Plot type:
rect_gradual

Track index:
track1

Data format

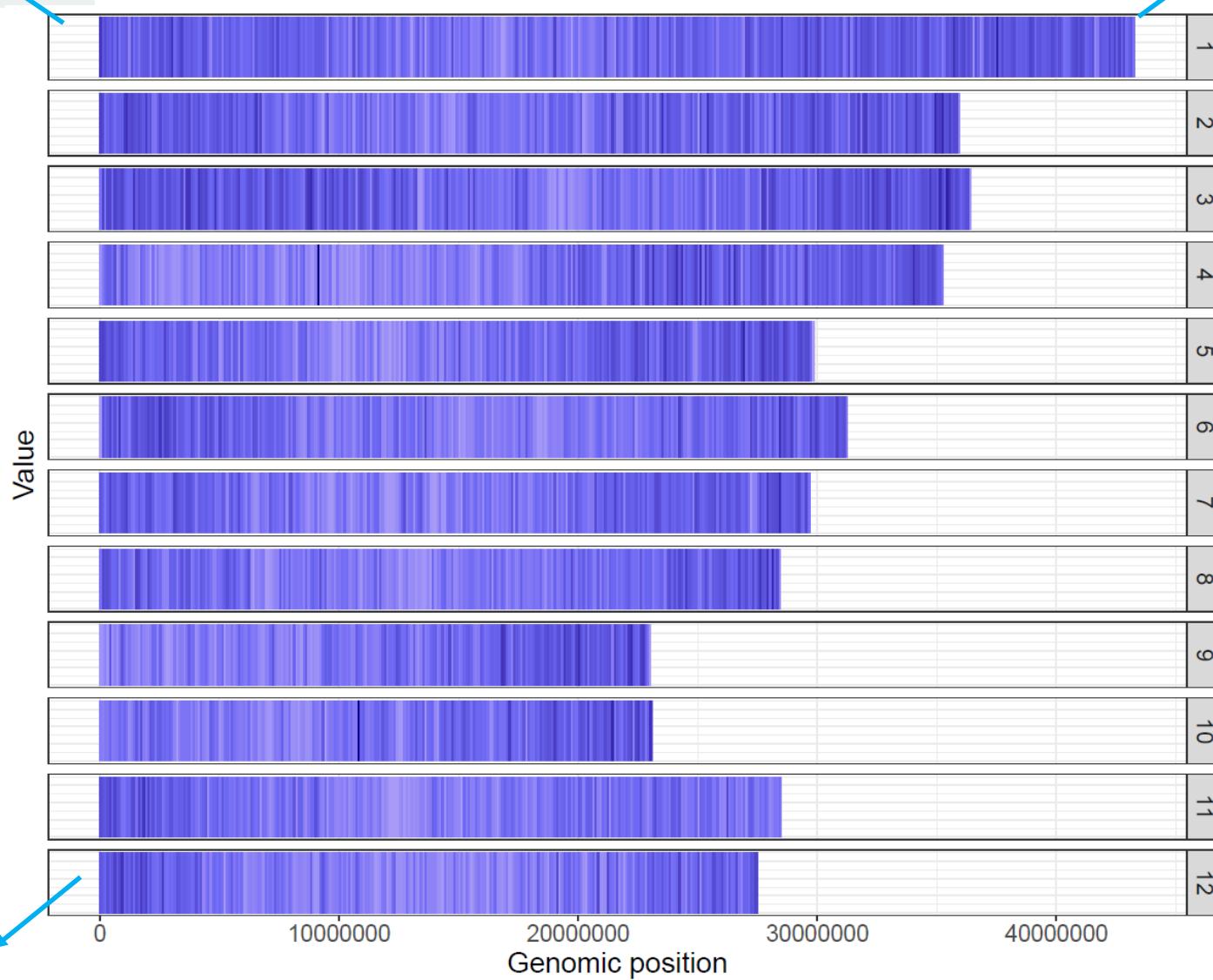
example_26/data1_track1_rect_gradual.txt

chr	i.s	i.e	nt
1	1	100000	29
1	100001	200000	18
1	200001	300000	22
1	300001	400000	18
1	400001	500000	16

- Data for rect_gradual plot includes 4 columns including the chromosome IDs, start coordinates of regions, end coordinates of regions and numeric values.
- The last column should be a numeric vector.

Image type Concatenated chromosome Separated chromosome**Orientation** Horizontal Vertical**Data color**

blue

**Add cell borders** Yes No

2.1.5 Plot rect_discrete

Options

Data1

NULL

Upload

Upload data1:

Browse...

No file selected

Plot type:

rect_discrete

Track index:

track1

Show Advanced Options

Data color

Random

Specific

Custom



The color used in the main plot can be random assigned by the application or specified by the users.

Color transparency:

1

- See section 2.1.1 for more plot options.

Upload rect_discrete data

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_rect_discrete.txt
Upload complete

Plot type:
rect_discrete

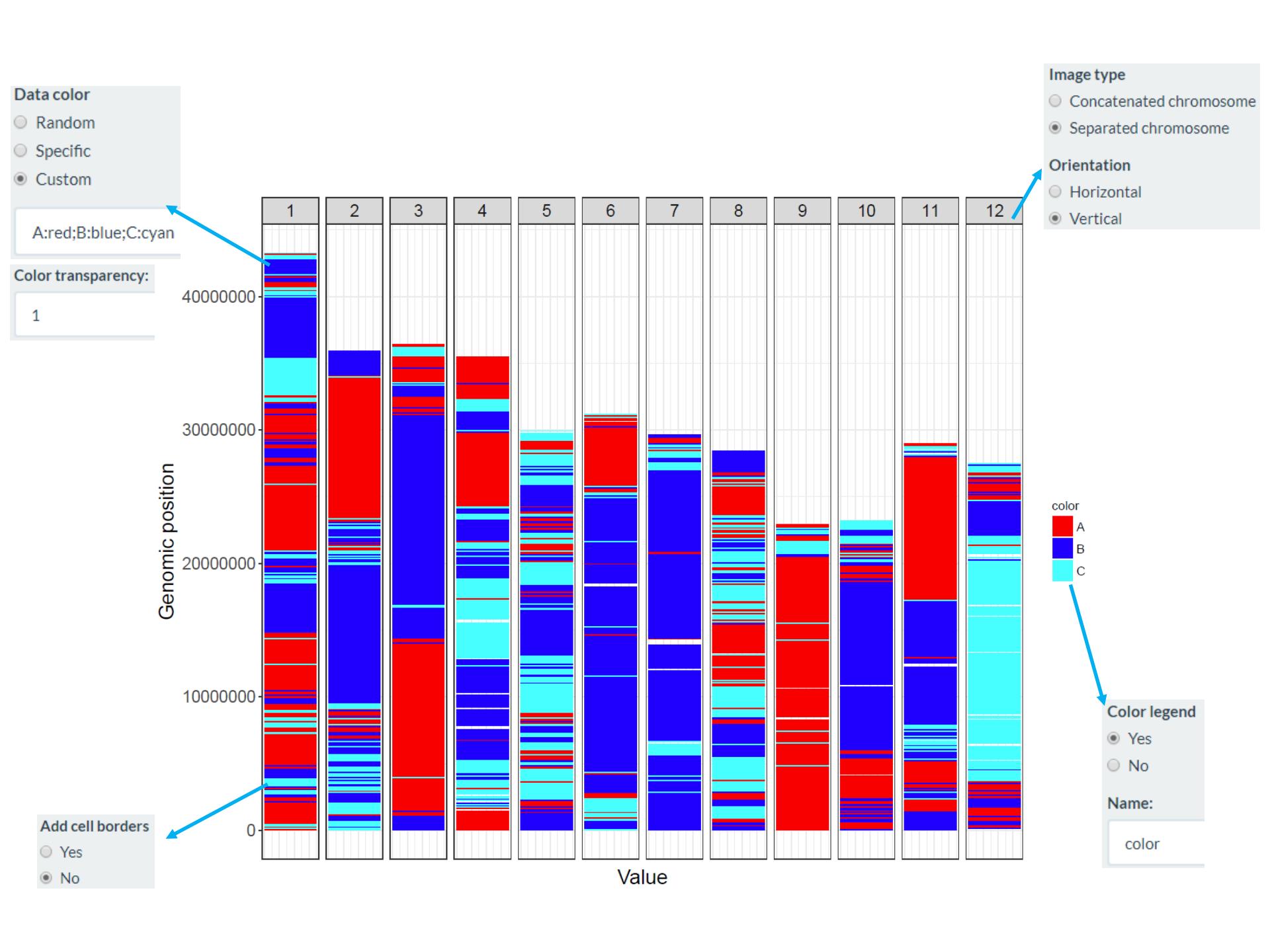
Track index:
track1

Data format

example_24/data1_track1_rect_discrete.txt

chr	start	end	color
1	1	100000	A
1	100001	200000	C
1	200001	300000	A
1	300001	400000	C
1	400001	500000	C

- Data for rect_discrete plot includes 4 columns including the chromosome IDs, start coordinates of regions, end coordinates of regions and character values.
- The last column should be a character vector representing discrete variables.



2.1.6 Plot heatmap_gradual

Options

Data1
 NULL
 Upload

Upload data1:

Browse... No file selected

Plot type:

heatmap_gradual ▾

Track index:

track1 ▾

Show Advanced Options ▾

Colors

Typical
 Custom

Low Color Middle Color High Color

#0016DB #FFFFFF #FFFF00

→ The color used for the heatmap can be random assigned by the application or specified by the users.

- See section 2.1.1 for more plot options.

Upload heatmap_gradual data

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_heatmap_gradual.
Upload complete

Plot type:
heatmap_gradual

Track index:
track1

Data format

example_35/data1_track1_heatmap_gradual.txt

chr	i.s	i.e	te	nt	tr	nr
1	1	100000	4	29	17	45
1	10000001	10100000	9	14	20	28
1	1000001	1100000	1	16	-5	29
1	100001	200000	8	18	16	19
1	10100001	10200000	4	12	13	20

- The 1-3 columns of data for heatmap_gradual plot are the chromosome IDs, start coordinates of regions and end coordinates of regions.
- Apart from the first three columns, other columns are numeric vectors representing different values.

Colors

- Typical
- Custom

Low Color

#0016DB

Middle Color

#919191

High Color

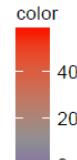
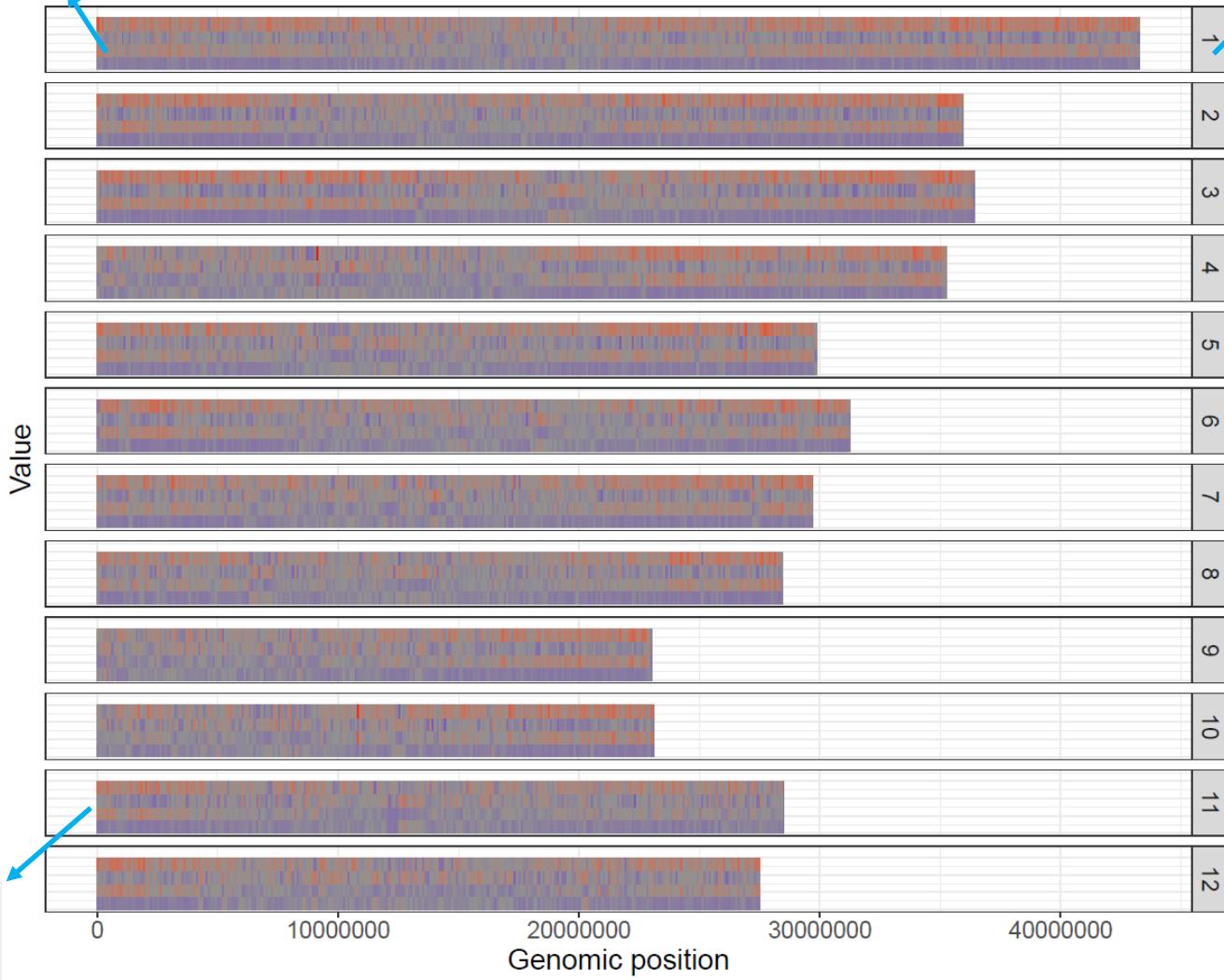
#FF1E05

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical



Add legend

- Yes
- No

Color legend

- Yes
- No

Name:

color

2.1.7 Plot heatmap_discrete

Upload heatmap_discrete data

Data1
 NULL
 Upload

Upload data1:

Browse... data1_track1_heatmap_discrete Upload complete

Plot type:

heatmap_discrete

Track index:

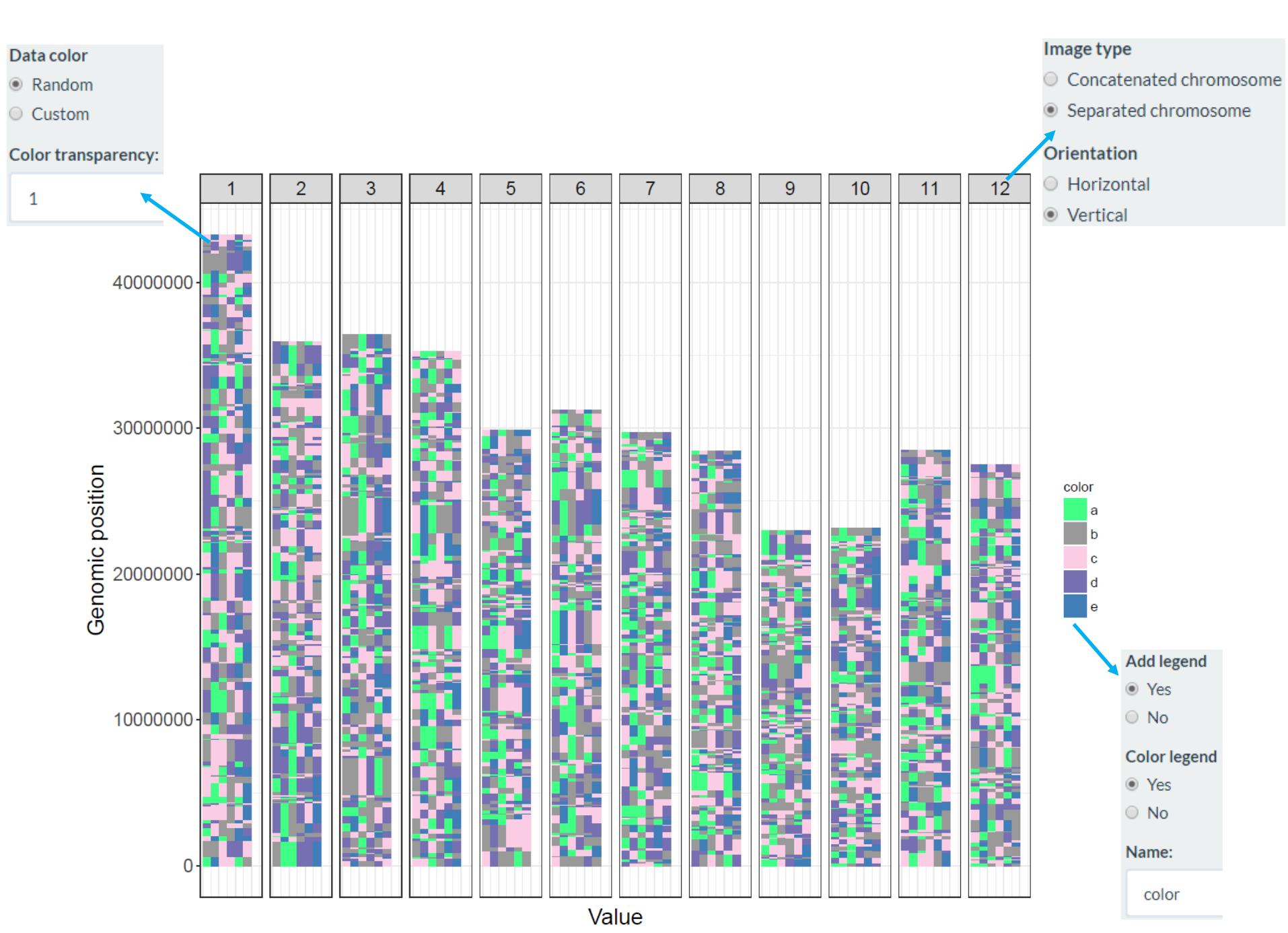
track1

Data format

example_31/data1_track1_heatmap_discrete.txt

chr	start	end	val1	val2	val3	val4	val5	val6
1	0	631164	a	e	c	c	a	b
1	631165	1749192	b	b	c	d	d	c
1	1749193	2077793	c	e	a	b	e	e
1	2077794	2612461	a	c	b	b	e	d
1	2612462	2938491	d	c	b	c	c	b

- The 1-3 columns of data for heatmap_discrete plot are the chromosome IDs, start coordinates of regions, end coordinates of regions.
- Apart from the first three columns, other columns are character vectors representing different categories.



2.1.8 Plot text

Options

Data1
 NULL
 Upload

Upload data1:

Browse... No file selected

Plot type:

text

Track index:

track1

Show Advanced Options ▾

Font color:

black

Font size:

2

Font face:

plain

Font angle:

60

The font color used for the texts.

The font size of texts.

The font face of texts.

The angle of texts relative to the horizontal line.

- See section 2.1.1 for more plot options.

Upload text data

Data1
 NULL
 Upload

Upload data1:
Browse... data1_track1_rect_discrete.txt
Upload complete

Plot type:
rect_discrete

Track index:
track1

Data2
 NULL
 Upload

Upload data2:
Browse... data2_track2_text.txt
Upload complete

Plot type:
text

Track index:
track2

Data format

example_38/data2_track2_text.txt

chr	xpos	ypos	symbol
1	134291	3	OsTLP27
1	2665412	3	MT2D
1	24392841	3	OCPI1
1	26044166	3	SLRL1
1	27906608	3	OsTPC1

- Data for text plot includes 4 columns.
- The 1-3 columns of data for text plot are the chromosome IDs, X-axis coordinates and the Y-axis coordinates of texts.
- The last column should be a character vector representing texts.

Font color:

black

- Image type
 Concatenated chromosome
 Separated chromosome

Orientation
 Horizontal
 Vertical

Genomic position

400000000

300000000

200000000

100000000

0

Font angle:

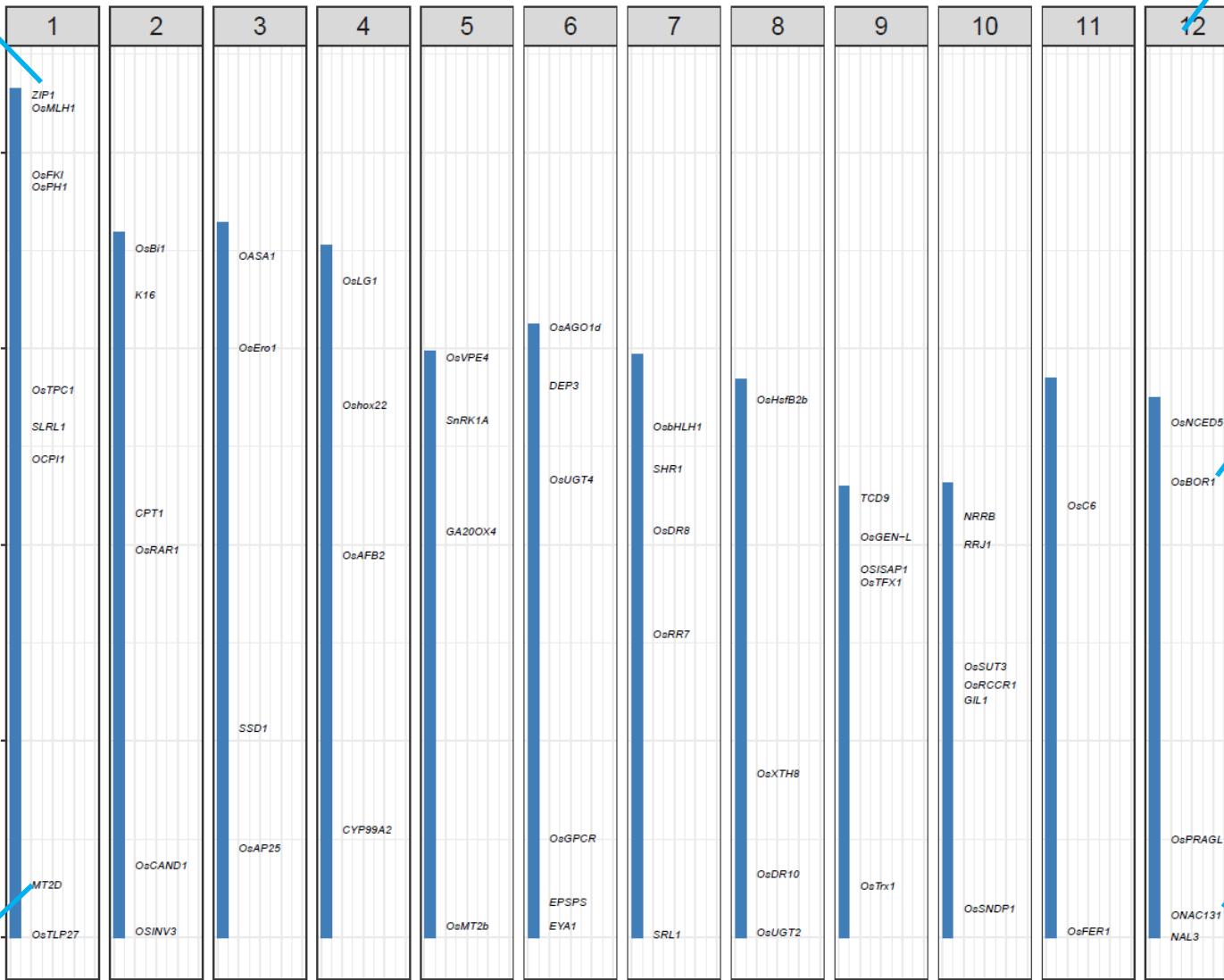
0

Font size:

2

Font face:

italic



Value

2.1.9 Plot segment

Options

Data1
 NULL
 Upload

Upload data1:
 No file selected

Plot type:
segment

Track index:
track1

Show Advanced Options

Data color
 Random
 One custom color
 Custom for data with multi-group

Color transparency:
1

Line width:
0.2

Line type
solid

Add arrow head
 Yes
 No

Arrow position
 Line end
 Line beginning

Arrow size:
0.1

- Set the line width.
- Select the line type.
- Add arrow head for the segment.
- The position of arrow head.
- The size of arrow head.

● See section 2.1.1 for more plot options.

Upload segment data

Data1

NULL
 Upload

Upload data1:

Browse...data1_track1_rect_discrete.txtUpload complete

Plot type:

rect_discrete

Track index:

track1

Data2

NULL
 Upload

Upload data2:

Browse...data2_track2_text.txtUpload complete

Plot type:

text

Track index:

track2

Data3

NULL
 Upload

Upload data3:

Browse...data3_track2_segment.txtUpload complete

Plot type:

segment

Track index:

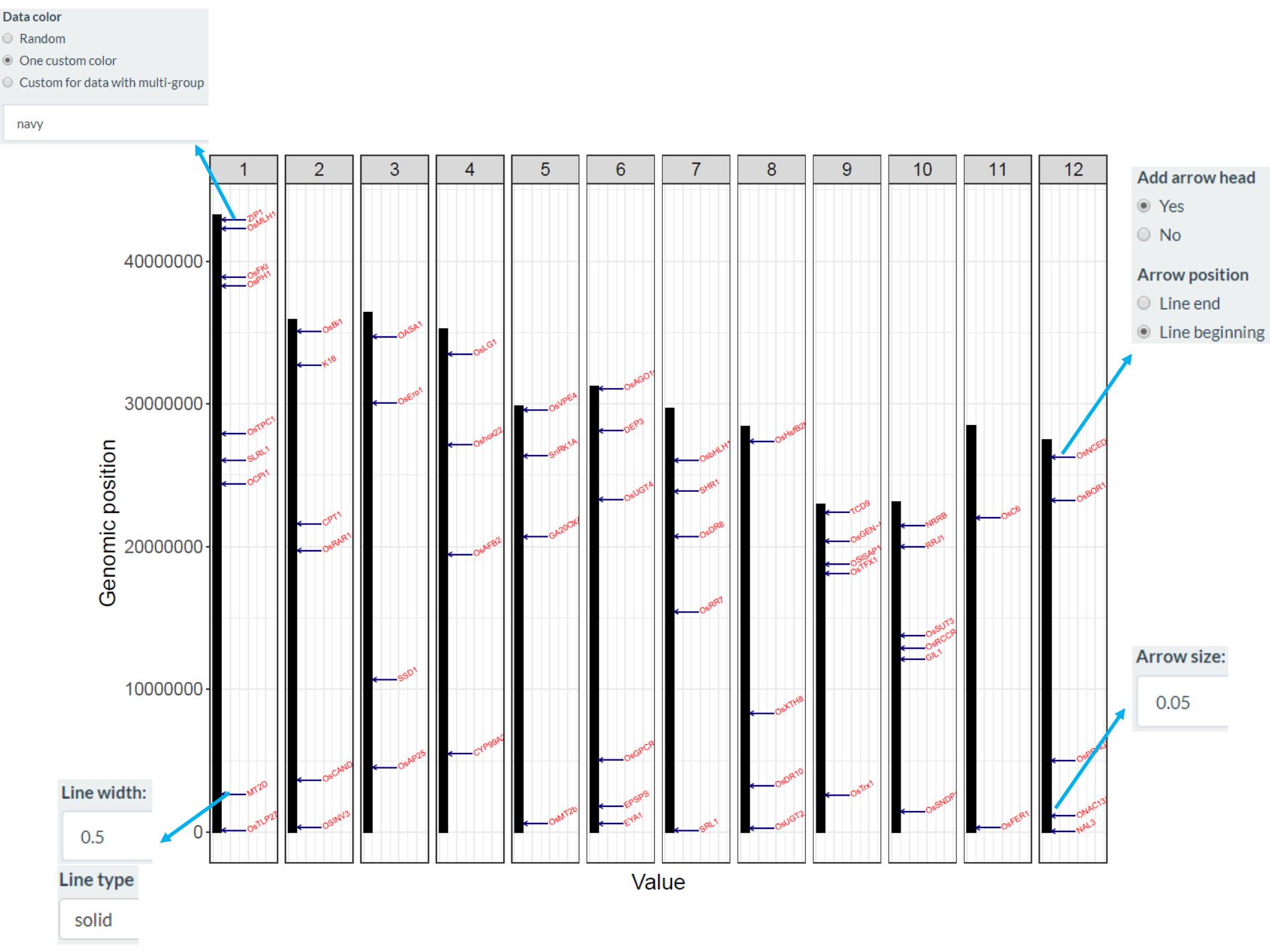
track2

Data format

example_39/data3_track2_segment.txt

chr	xstart	ystart	xend	yend
1	134291	0	134291	2.8
1	2665412	0	2665412	2.8
1	24392841	0	24392841	2.8
1	26044166	0	26044166	2.8
1	27906608	0	27906608	2.8

- Data for segment plot generally includes **5 columns**.
- Columns 2-3 and columns 4-5 represent the positions of the two ends of segment respectively.
- A “color” column can be added to assign colors to different segments, which is a **character vector**.



2.1.10 Plot vertical line or horizontal line

Options

Plot type: vertical line

Track index: track1

Show Advanced Options

Line color: black

Color transparency: 1

Line width: 0.2

Line type: solid

Add legend
 Yes
 No

Color legend
 Yes
 No

Line type legend
 Yes
 No

Name: linetype

Modify labels
 Yes
 No

→ Legend for line type used in specified dataset.

→ Title of line type legend. Null value will result in an empty title.

→ The labels of different line types in the line type legend can be assigned by the application or specified by the users.

- See section 2.1.1 for more plot options.

Upload vertical line or horizontal line data

<input checked="" type="checkbox"/> Data1 <input type="radio"/> NULL <input checked="" type="radio"/> Upload Upload data1: <input type="button" value="Browse..."/> data1_track1_line.txt Upload complete	<input checked="" type="checkbox"/> Data2 <input type="radio"/> NULL <input checked="" type="radio"/> Upload Upload data2: <input type="button" value="Browse..."/> data5_track1_vertical_line.txt Upload complete	<input checked="" type="checkbox"/> Data3 <input type="radio"/> NULL <input checked="" type="radio"/> Upload Upload data3: <input type="button" value="Browse..."/> data6_track2_line.txt Upload complete	<input checked="" type="checkbox"/> Data4 <input type="radio"/> NULL <input checked="" type="radio"/> Upload Upload data4: <input type="button" value="Browse..."/> data10_track2_horizontal_line.txt Upload complete
Plot type: <input type="button" value="line"/>	Plot type: <input type="button" value="vertical line"/>	Plot type: <input type="button" value="line"/>	Plot type: <input type="button" value="horizontal line"/>
Track index: <input type="button" value="track1"/>	Track index: <input type="button" value="track1"/>	Track index: <input type="button" value="track2"/>	Track index: <input type="button" value="track2"/>

Data format

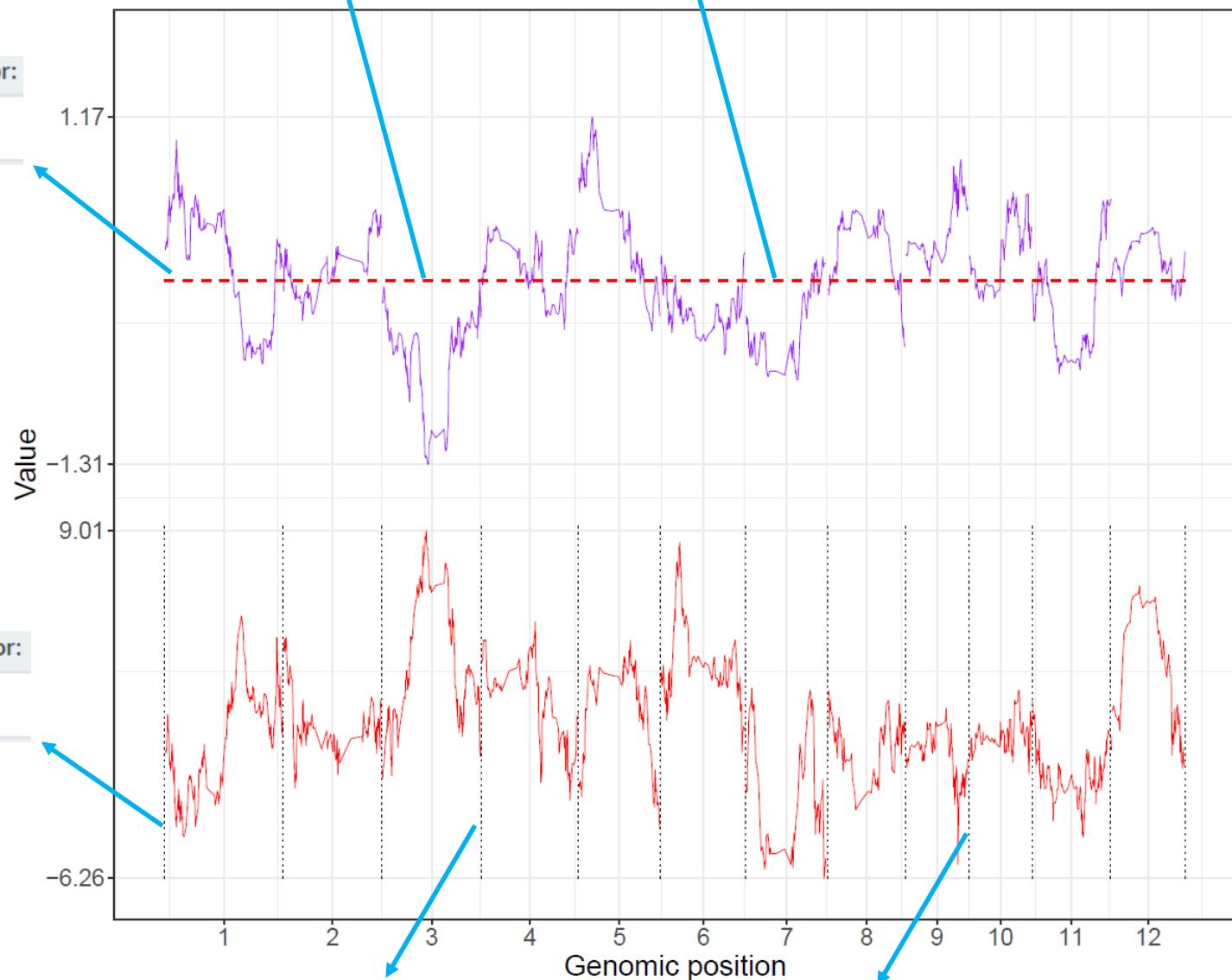
example_12/data5_track1_vertical_line.txt

chr	size
1	0
1	43268879
2	35930381
3	36406689
4	35278225

example_12/data10_track2_horizontal_line.txt

pos
0

- Data for vertical line plot includes **two columns** as chromosome IDs and X-axis coordinate.
- Data for horizontal line plot includes **one column** representing Y-axis coordinate.



Line type legend
● Yes
○ No

Name:

linetype

Modify labels
● Yes
○ No

dashed

linetype

— dashed

linetype

··· dotted

Line type legend
● Yes
○ No

Name:

linetype

Modify labels
● Yes
○ No

dotted

2.2 Non-circular plots for two genomes

Non-circular plots for two genomes

shinyChromosome About One genome Two genomes Gallery Help Manual

1.5 Download figures and scripts

Upload genome1 data:

Browse... genome1_data.txt 1.1
Upload complete

Upload genome2 data:

Browse... genome2_data.txt 1.1
Upload complete

Upload plot data:

Browse... plot_data_point_gradual.txt 1.2
Upload complete

Plot type:

point_gradual

Show Advanced Options 1.4

Go! 1.4

Plot options

Adjust plot size

Figure theme

Font size

Axis title

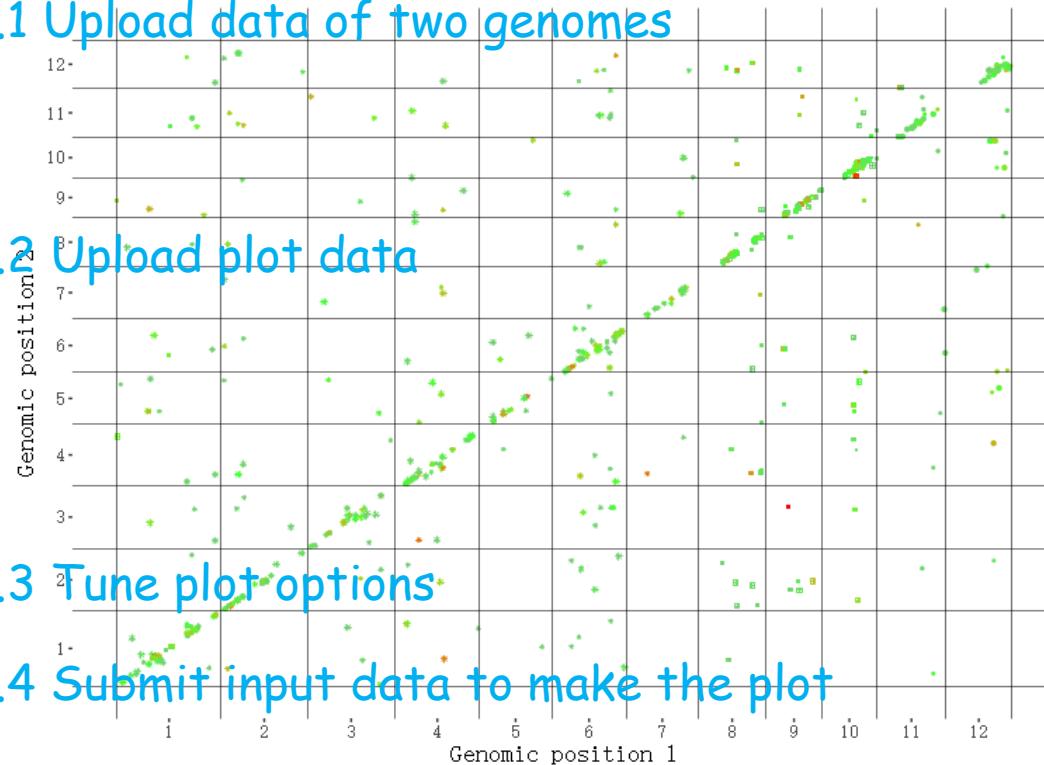
Axis label

Legend

1.3

[Download pdf-file](#) [Download svg-file](#) [Download the R scripts to reproduce the plot](#) 1.5

1.1 Upload data of two genomes



1.2 Upload plot data

1.3 Tune plot options

1.4 Submit input data to make the plot

- The genome data is compulsory and defines the frame of the non-circular plot.
- Please click the "Go!" button if suitable input data is uploaded or any options are modified.

2.2.1 Plot point_gradual

Upload genome data

shinyChromosome About One genome

Two genomes

Gallery

Help

Manual

Upload genome1 data:

Download pdf-file

Download svg-file

Download the R scripts to reproduce the plot

Browse...

No file selected

Data of genome 1 along the X-axis.

Upload genome2 data:

Browse...

No file selected

Data of genome 2 along the Y-axis.

Upload plot data:

Browse...

No file selected

Plot type:

point_gradual

Data format

chr	size
1	43268879
2	35930381
3	36406689
4	35278225
5	29894789

- Genome data can be simple definition of chromosome lengths, which include two columns as chromosome IDs and chromosome lengths (See example data "genome_data.txt" in the "Gallery" menu for more detail).

Upload point_gradual data

shinyChromosome

About

One genome

Two genomes

Gallery

Help

Manual

Upload genome1 data:

Browse...

No file selected

Upload genome2 data:

Browse...

No file selected

Upload plot data:

Browse...

No file selected

Click "Browse" to upload input file

Plot type:

point_gradual

Set plot type as "point_gradual"

Download pdf-file

Download svg-file

Download the R scripts to reproduce the plot

Options

Vertical line

- Show
- Hide

→ Create a set of vertical lines across X-axis to separate chromosomes of genome 1.

Vertical line color:

black

→ The color used for the vertical line.

Vertical line width:

0.2

→ Line width of the vertical line.

Vertical line type

solid

→ Line type of the vertical line.

Horizontal line

- Show
- Hide

→ Create a set of horizontal lines across the Y-axis to separate chromosomes of genome 2.

Horizontal line color:

black

→ The color used for the horizontal line.

Horizontal line width:

0.2

→ Line width of the horizontal line.

Horizontal line type

solid

→ Line type of the horizontal line.

- See section 2.1.1 for more plot options.

Example 1

shinyChromosome About One genome Two genomes Gallery Help Manual

Upload genome1 data:

Browse... genome1_data.txt
Upload complete

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

Upload genome2 data:

Browse... genome2_data.txt
Upload complete

Upload plot data:

Browse... plot_data_point_gradual.txt
Upload complete

Plot type:

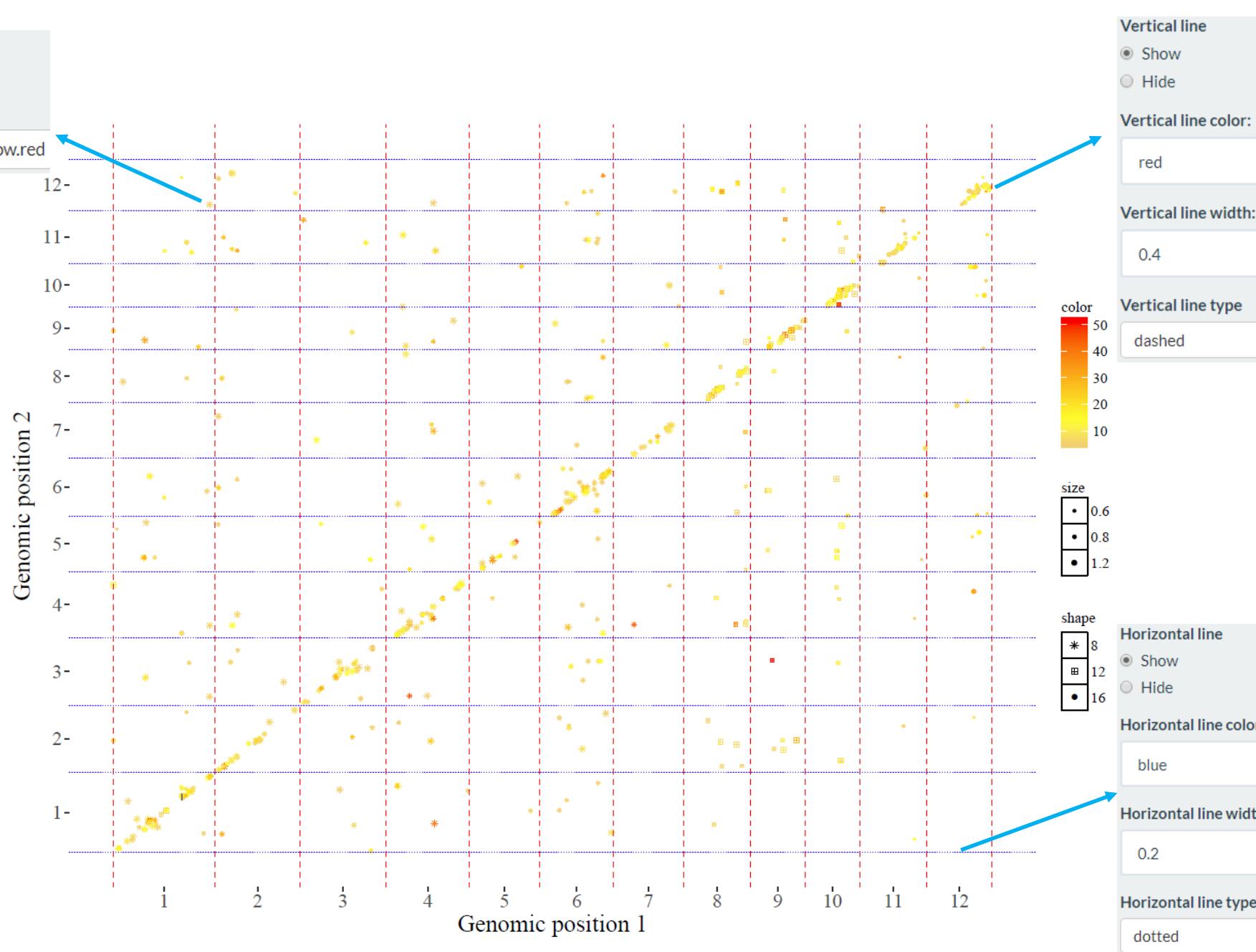
point_gradual

Data format

example_43/plot_data_point_gradual.txt

ChrX	startX	ChrY	startY	color	shape	size
1	15414550	1	17415683	21.477	12	0.6
1	2314068	1	2291658.5	29.537	12	0.8
1	2583523	1	2546653.5	10.966	12	0.6
1	33396049	1	33278033	19.967	12	0.8
1	17988456	1	15622836	10.852	12	0.6

- Simplest data to plot point should contain at least **5 columns** including the chromosome ID of x-axis, coordinate of x-axis, chromosome ID of y-axis, coordinate of y-axis and "color" column representing different values.
- The "shape" and "size" columns can be used to specify the shape and size of data points.
- The "color" column should be a **numeric vector** representing gradual values.
- The names of the columns "color", "shape" and "size" are fixed.



2.2.2 Plot point_discrete

Upload point_discrete data

Upload genome1 data:

Browse... genome1_data.txt
Upload complete

Upload genome2 data:

Browse... genome2_data.txt
Upload complete

Upload plot data:

Browse... plot_data_point_discrete.txt
Upload complete

Plot type:

point_discrete

Data format

example_44/plot_data_point_discrete.txt

ChrX	startX	ChrY	startY	color	shape	size
1	15414550	1	17415683	a	12	1.2
1	2314068	1	2291658.5	a	12	1.2
1	2583523	1	2546653.5	c	12	1.2
1	33396049	1	33278033	d	12	1.2
1	17988456	1	15622836	a	12	1.2

- Simplest data to plot point should contain at least **4 columns** including the chromosome ID of x-axis, coordinate of x-axis, chromosome ID of y-axis and coordinate of y-axis.
- The "color" column indicates different colors for differing data groups, which is a **character vector**.
- The names of columns "color", "shape" and "size" are fixed.

Horizontal line

○ Show

Hide

Horizontal line color:

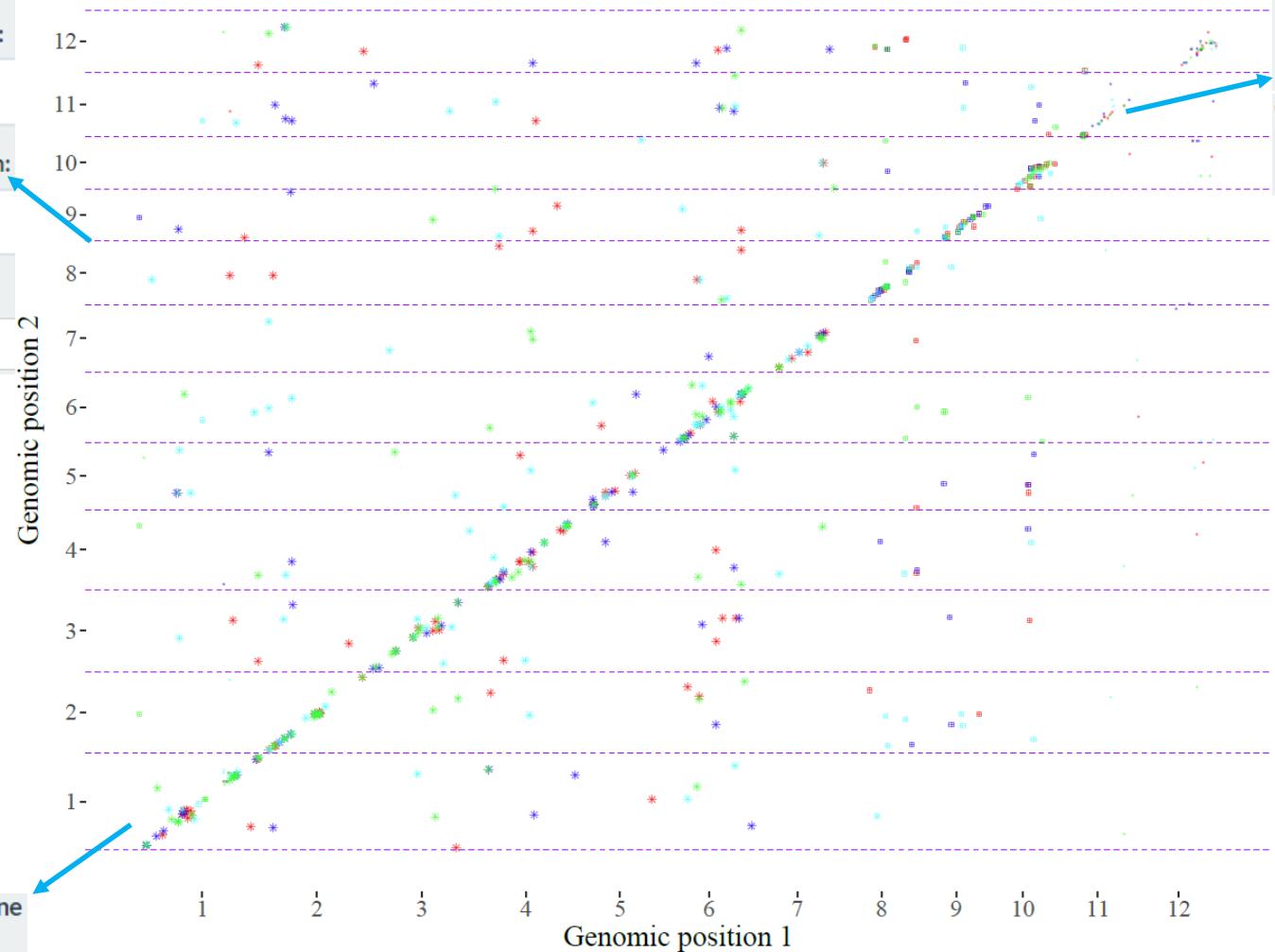
purple

Horizontal line width:

03

Horizontal line type

dashed



Data color

Random

- One custom color

Custom for data with multi

Color transparency:

05

color

Color legend

Yes

○ No

Name:

color

2.2.3 Plot segment

Upload segment data

Upload genome1 data:

Browse... genome1_data.txt
Upload complete

Upload genome2 data:

Browse... genome2_data.txt
Upload complete

Upload plot data:

Browse... plot_data_segment.txt
Upload complete

Plot type:

segment ▾

Data format

example_45/plot_data_segment.txt

ChrX	startX	stopX	ChrY	startY	stopY	color
Chr01	1	35619588	Chr01	1	36185095	a
Chr02	35140161	1	Chr02	34608401	1	b
Chr03	1	33736842	Chr03	37032663	1	c
Chr04	32024326	1	Chr04	1	32359471	d
Chr05	1	27379772	Chr05	1	29068426	e

- Simplest data to plot segment should contain at least **6 columns** including the chromosome ID of x-axis, start coordinate of x-axis, stop coordinate of x-axis, chromosome ID of y-axis, start coordinate of y-axis and stop coordinate of y-axis.
- The "color" column indicates different colors for differing data groups, which is a **character vector**.

Vertical line
 Show
 Hide

Vertical line color:

red

Vertical line width:

0.2

Vertical line type

dashed

Horizontal line

Show

Hide

Horizontal line color:

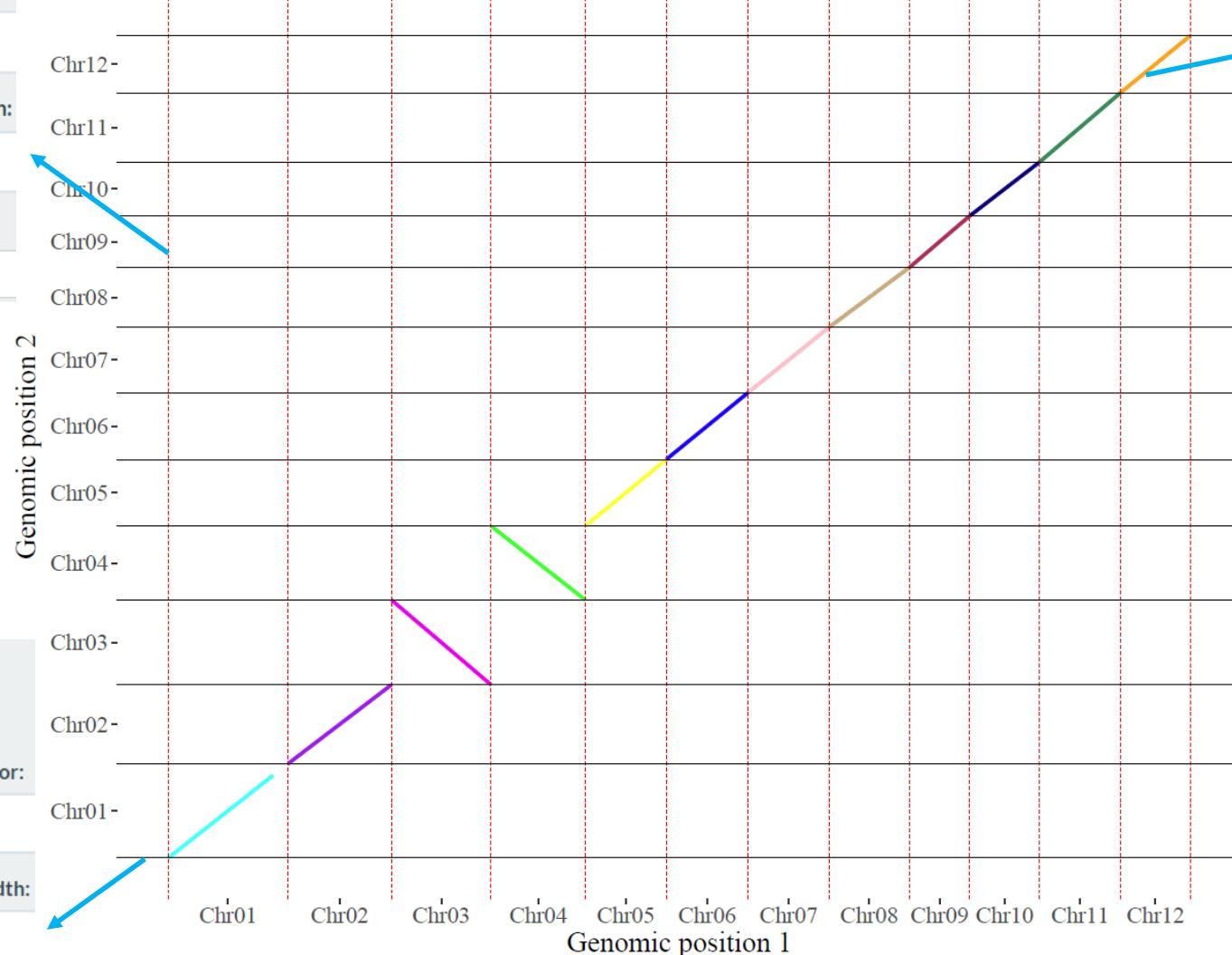
black

Horizontal line width:

0.1

Horizontal line type

solid



Data color
 Random
 One custom color
 Custom for data with multi-group

Color transparency:

1

Line width:

1

color	1	2	3
1	cyan		
2		magenta	
3			yellow

Color legend

- Yes
 No

Name:

color

Modify labels

- Yes
 No

1,2,3

2.2.4 Plot rect_gradual

Upload rect_gradual data

Upload genome1 data:

Browse... genome1_data.txt
Upload complete

Upload genome2 data:

Browse... genome2_data.txt
Upload complete

Upload plot data:

Browse... plot_data_rect_gradual.txt
Upload complete

Plot type:

rect_gradual

Data format

example_47/plot_data_rect_gradual.txt

chrX	startX	stopX	chrY	startY	stopY	color
1	117000000	117500000	11	108000000	108500000	0.520087
1	81000000	81500000	11	71000000	71500000	1.940479
1	46000000	46500000	11	74000000	74500000	2.48548
1	121000000	121500000	11	247000000	247500000	1.171732
1	57500000	58000000	11	217500000	218000000	0.967213

- Simplest data to plot gradual rectangles should contain **7 columns** including the chromosome ID of x-axis, start coordinate of x-axis, stop coordinate of x-axis, chromosome ID of y-axis, start coordinate of y-axis, stop coordinate of y-axis and "color" column representing different values.
- The "color" column should be a **numeric vector** representing gradual values.

Vertical line

- Show
- Hide

Vertical line color:

green

Vertical line width:

0.2

Vertical line type

dashed

Genomic position 2

25
24
23
22
21
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25

Genomic position 1

Horizontal line

- Show
- Hide

Colors

- Typical
- Custom

green.yellow.red

**Color legend**

- Yes
- No

Name:

color

2.2.5 Plot rect_discrete

Upload rect_discrete data

Upload genome1 data:

Browse... genome1_data.txt
Upload complete

Upload genome2 data:

Browse... genome2_data.txt
Upload complete

Upload plot data:

Browse... plot_data_rect_discrete.txt
Upload complete

Plot type:

rect_discrete ▾

Data format

example_50/plot_data_rect_discrete.txt

chrX	startX	stopX	chrY	startY	stopY	color
1	1	1000000	1	1	1000000	b
1	1	1000000	1	1000001	2000000	b
1	1	1000000	1	2000001	3000000	b
1	1	1000000	1	3000001	4000000	b
1	1	1000000	1	4000001	5000000	b

- Simplest data to plot discrete rectangles should contain at least 6 columns including the chromosome ID of x-axis, start coordinate of x-axis, stop coordinate of x-axis, chromosome ID of y-axis, start coordinate of y-axis and stop coordinate of y-axis.
- The "color" column indicates different colors for differing data groups, which is a character vector.

Vertical line

- Show
 Hide

Vertical line color:

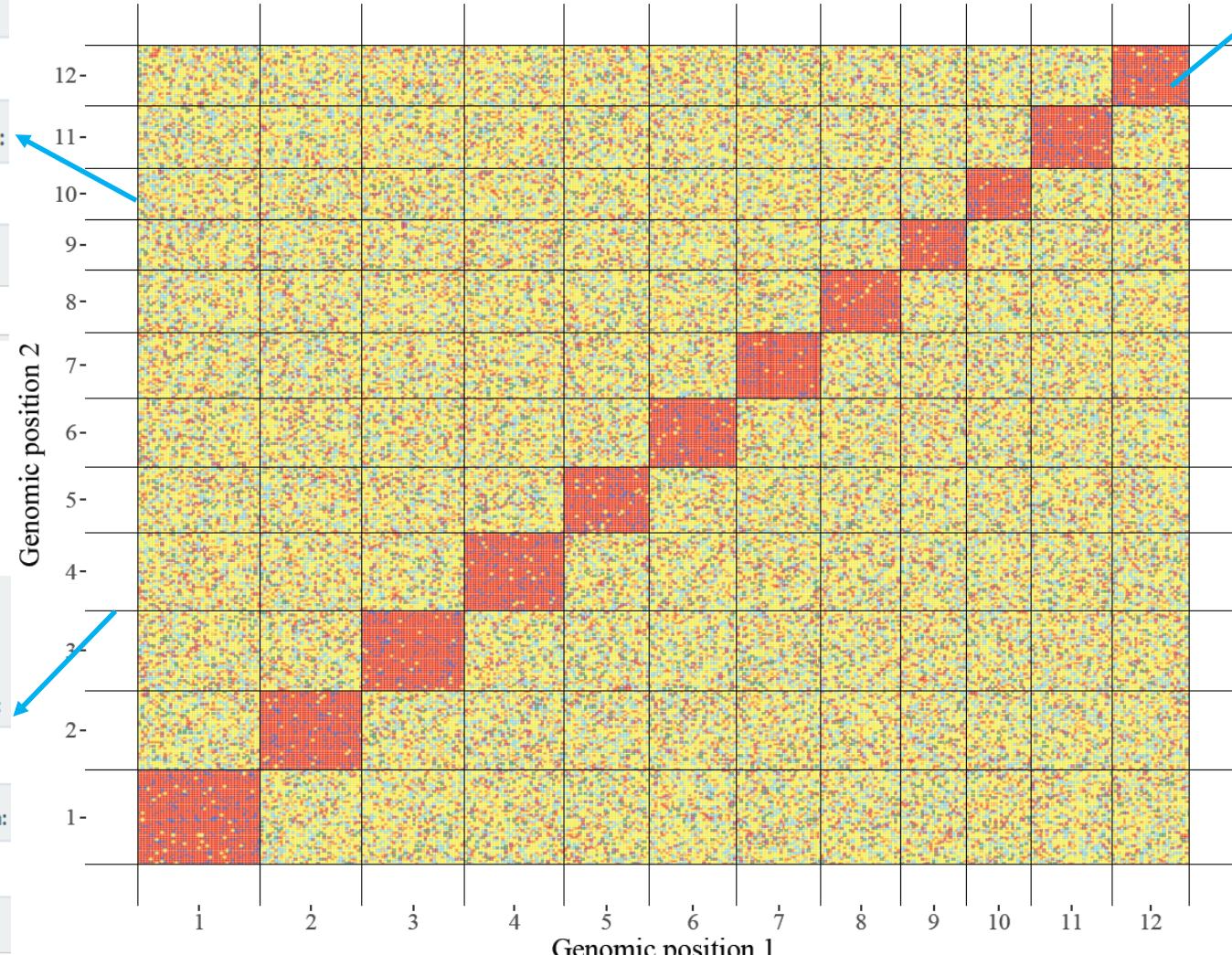
black

Vertical line width:

0.2

Vertical line type

solid

**Data color**

- Random
 One custom color
 Custom for data with multi-group

Color transparency:

0.5

**Color legend**

- Yes
 No

Name:

color

3. Other features

3.1 Figure size

Options

Plot options

Show Advanced Options ▾

Adjust plot size

Plot height:

550

Plot width:

750

Figure theme

Font size

Axis title

X axis label

Legend

Users can adjust the height and width of the non-circular plot.

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

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

Upload genome data:

genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

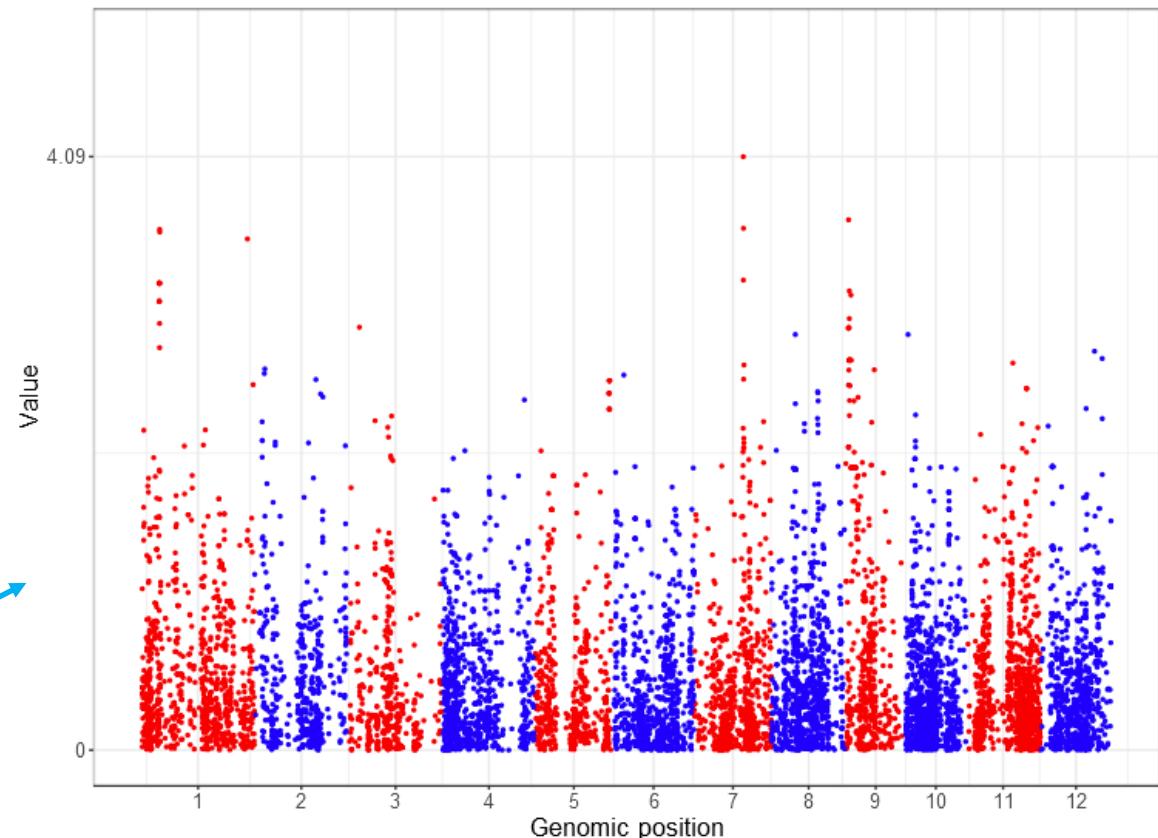


Image type

- Concatenated chromosome
- Separated chromosome

Orientation

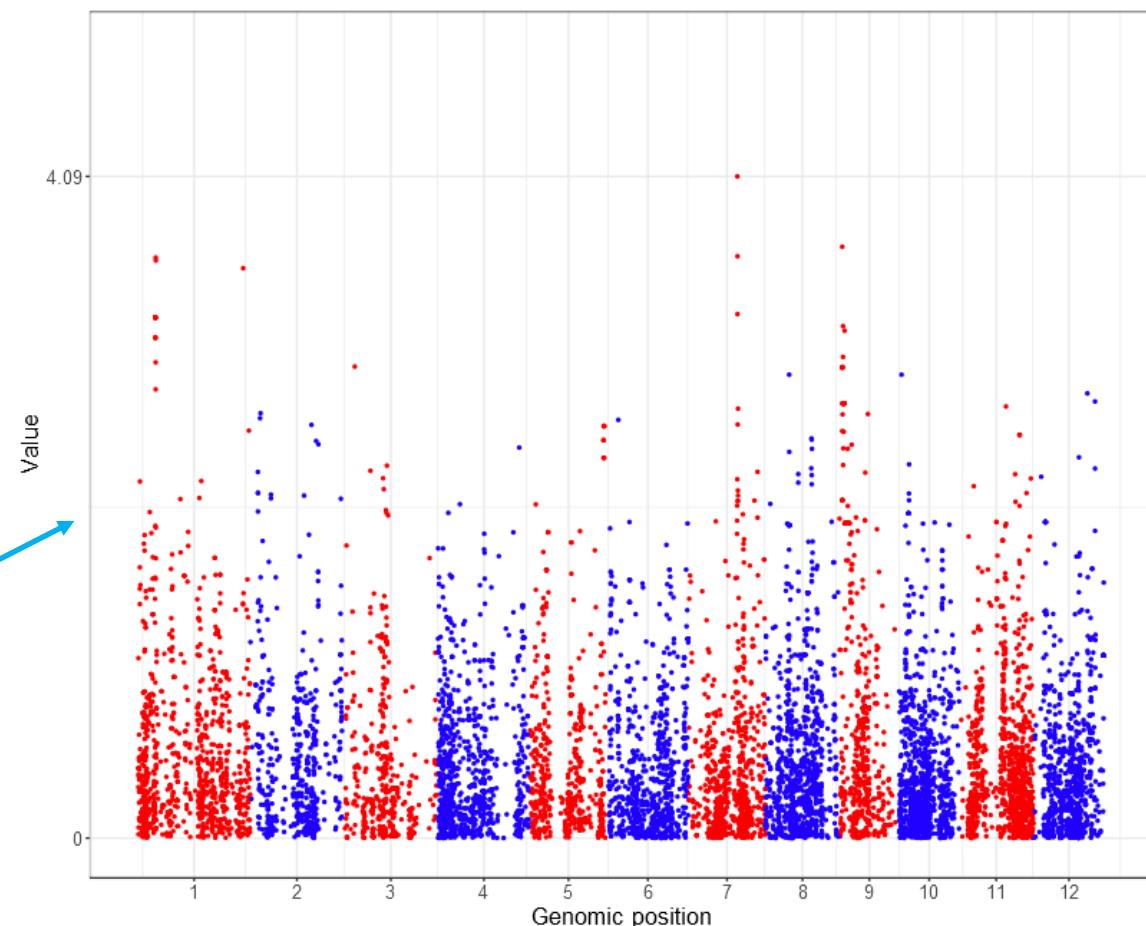
- Horizontal
- Vertical

Upload genome data:

genome_data.txt

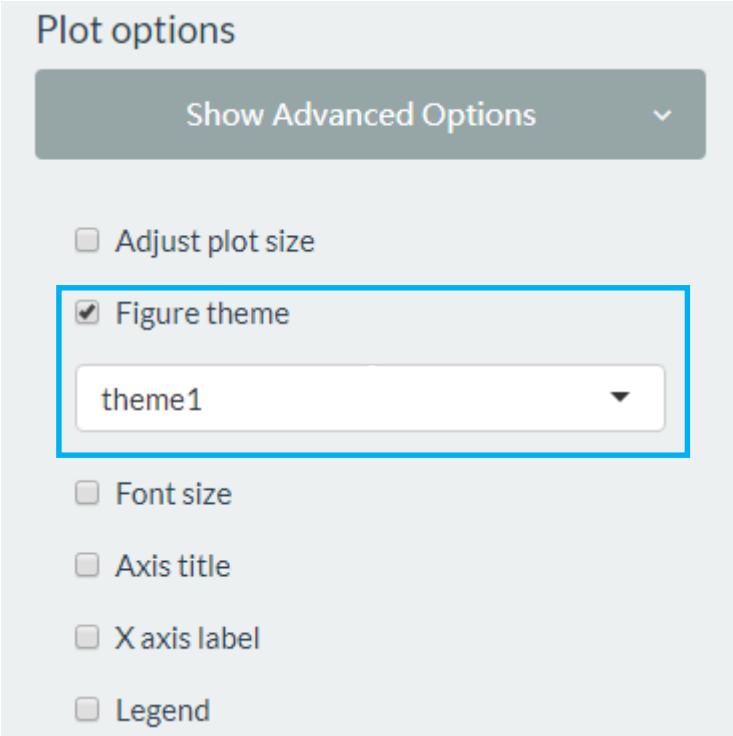
Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

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

3.2 Figure theme

Options



Select a theme for the plot.

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

Upload genome data:

genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

 Figure theme

theme1

Go!

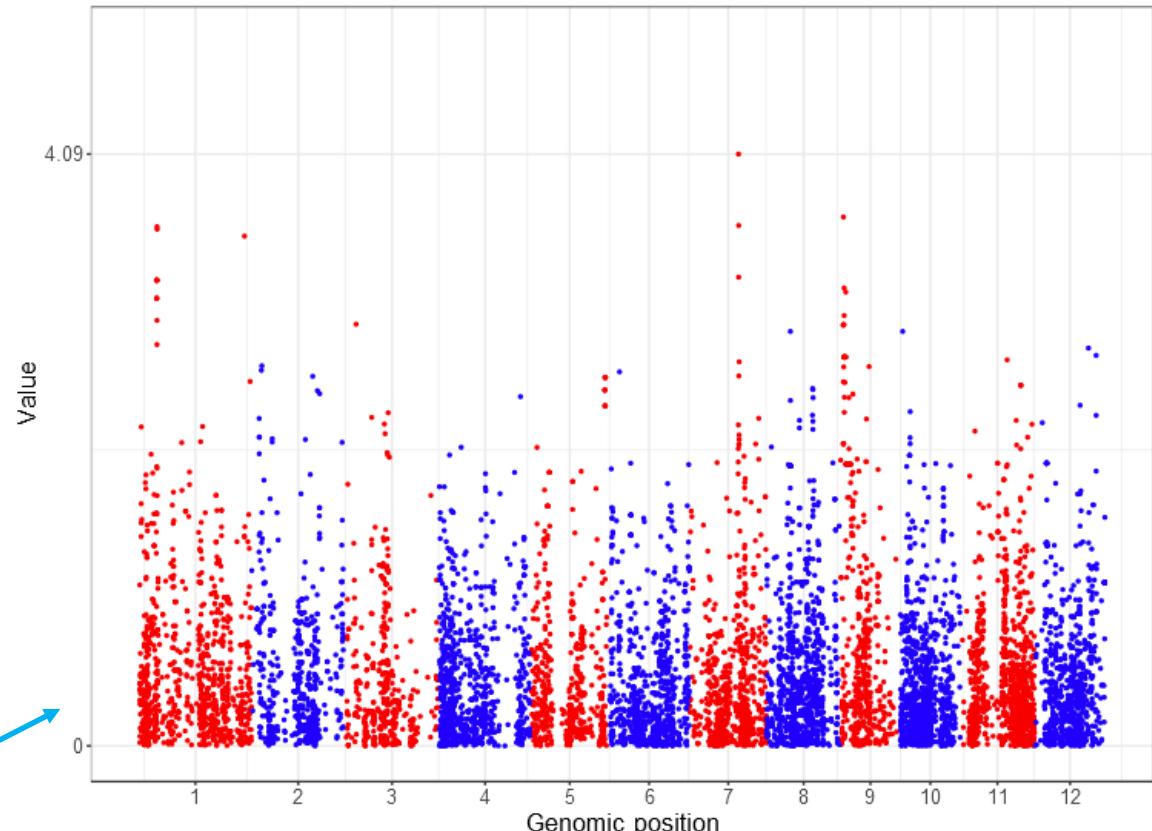
 [Download pdf-file](#) [Download svg-file](#) [Download the R scripts to reproduce the plot](#)

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

Upload genome data:

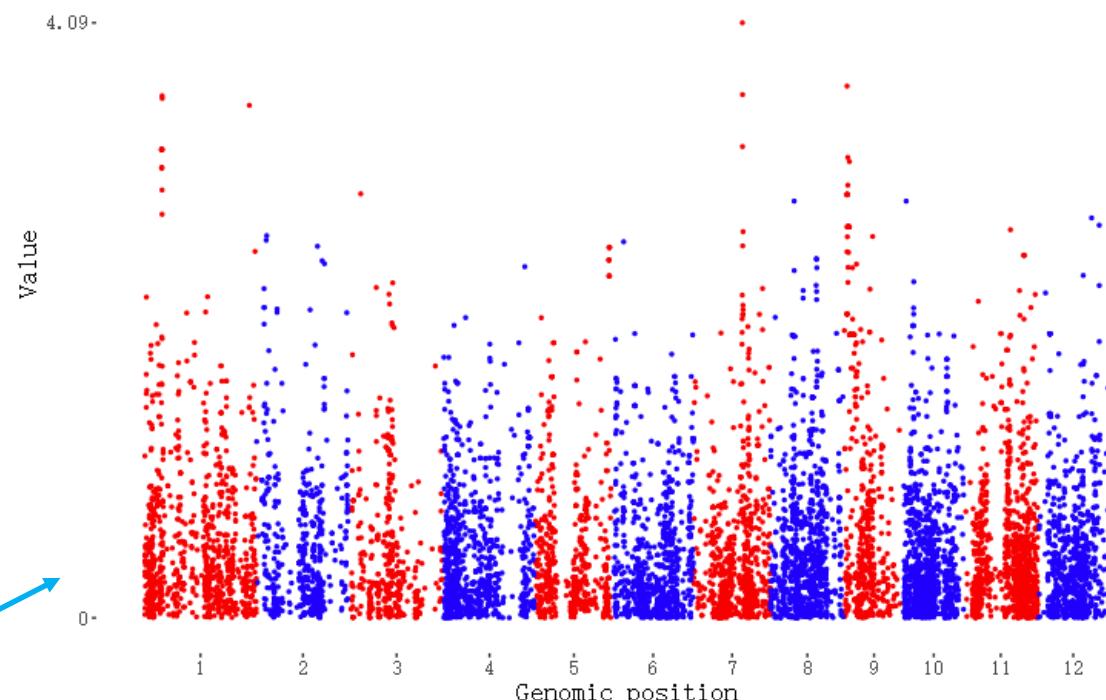
 genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

 Figure theme

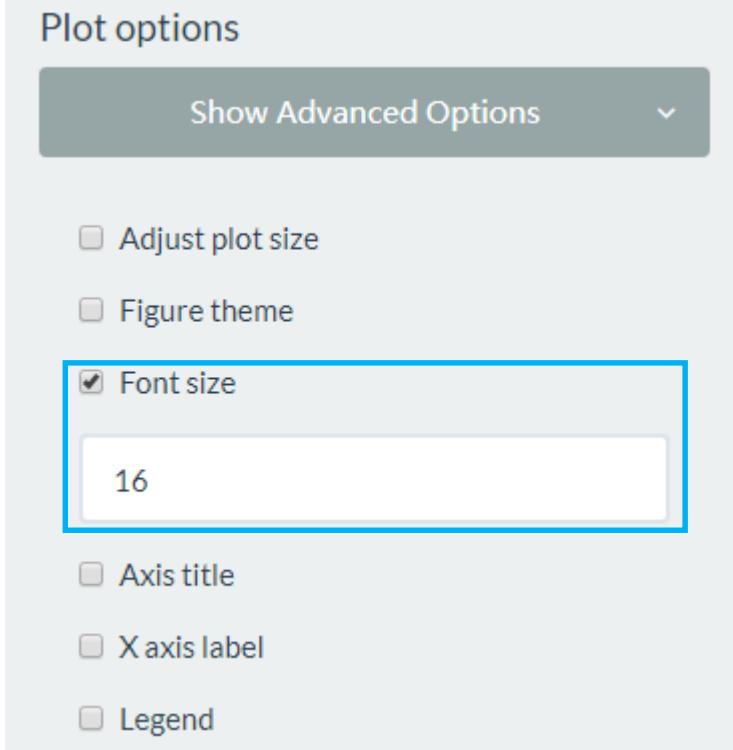
theme6



Go!

3.3 Font size

Options



Adjust font size used in the main plot.

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

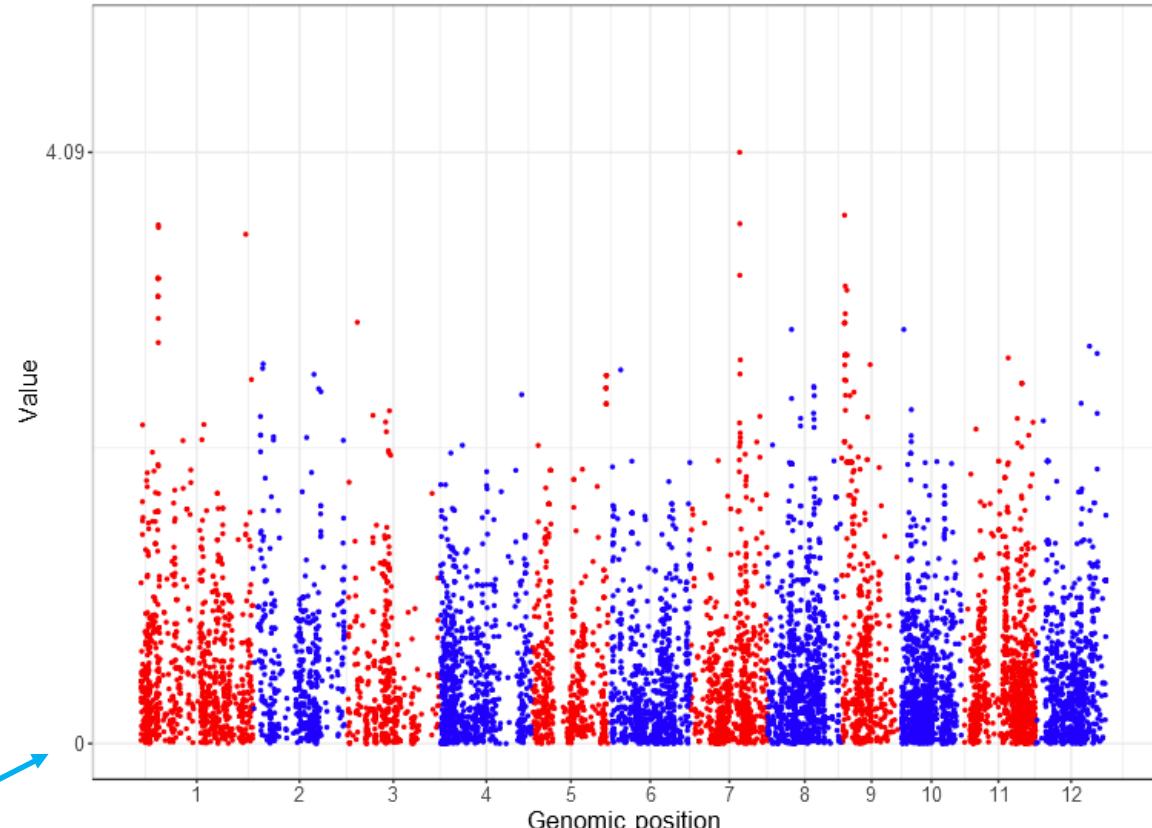
- Horizontal
- Vertical

Upload genome data:

 genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

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

16

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

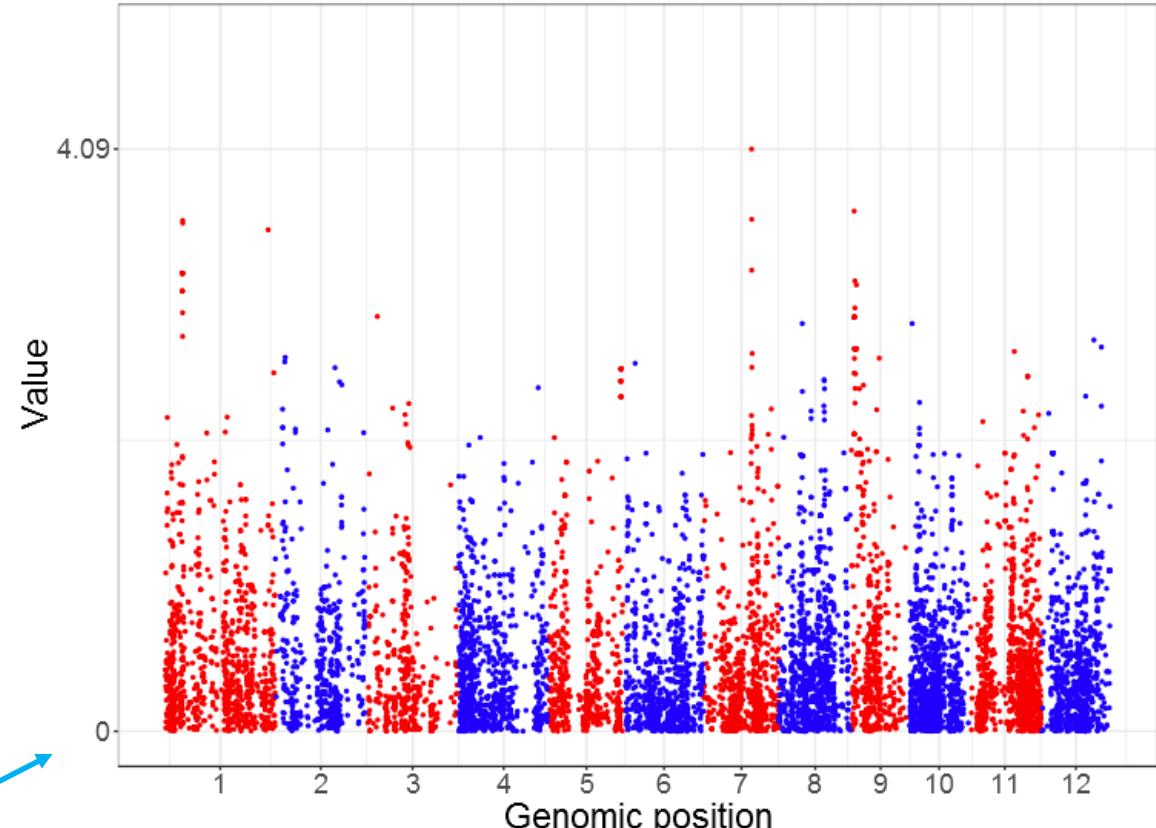
- Horizontal
- Vertical

Upload genome data:

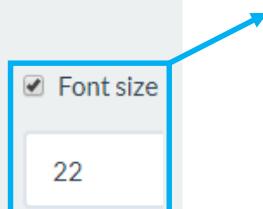
genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

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

22



3.4 Axis title

Options

Plot options

Show Advanced Options ▾

- Adjust plot size
- Figure theme
- Font size
- Axis title

X title:

Genomic position

Y title:

a

Value

Font face:

plain ▾

Modify axis title of non-circular plot.

Adjust font face of axis title.

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

Upload genome data:

 genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

Go!

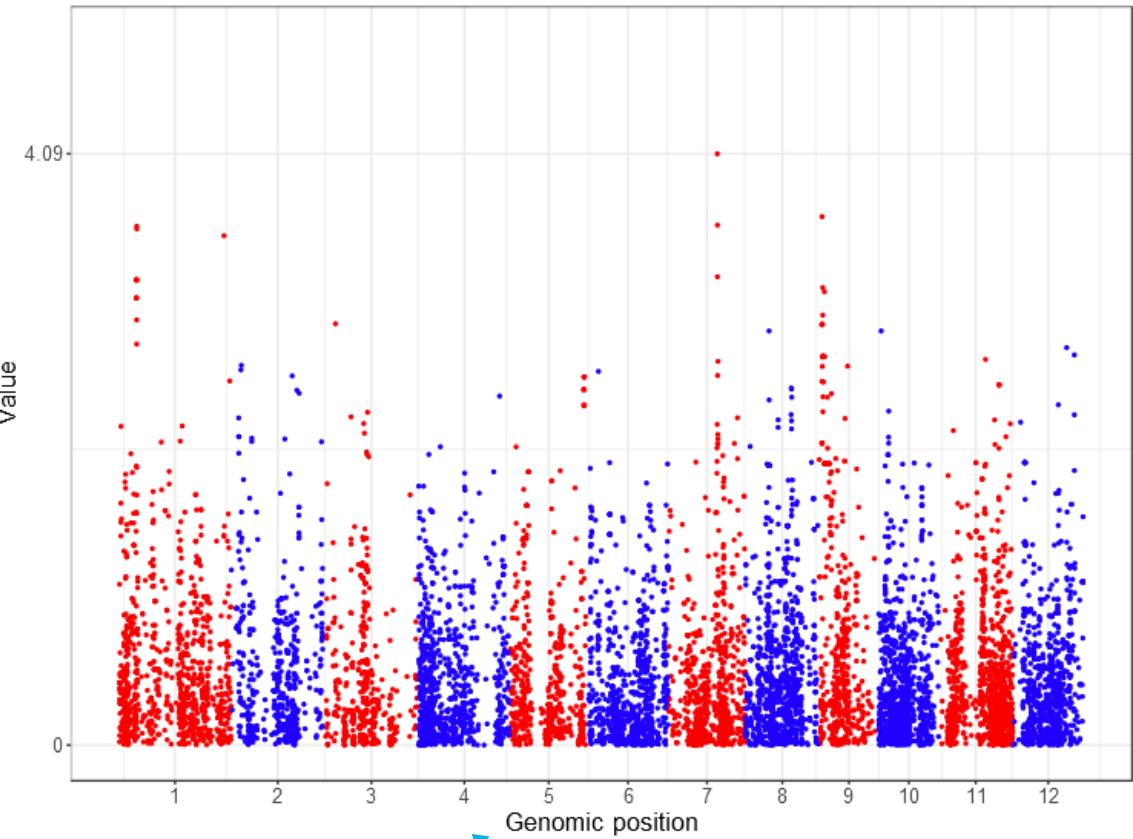
 [Download pdf-file](#) [Download svg-file](#) [Download the R scripts to reproduce the plot](#)

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

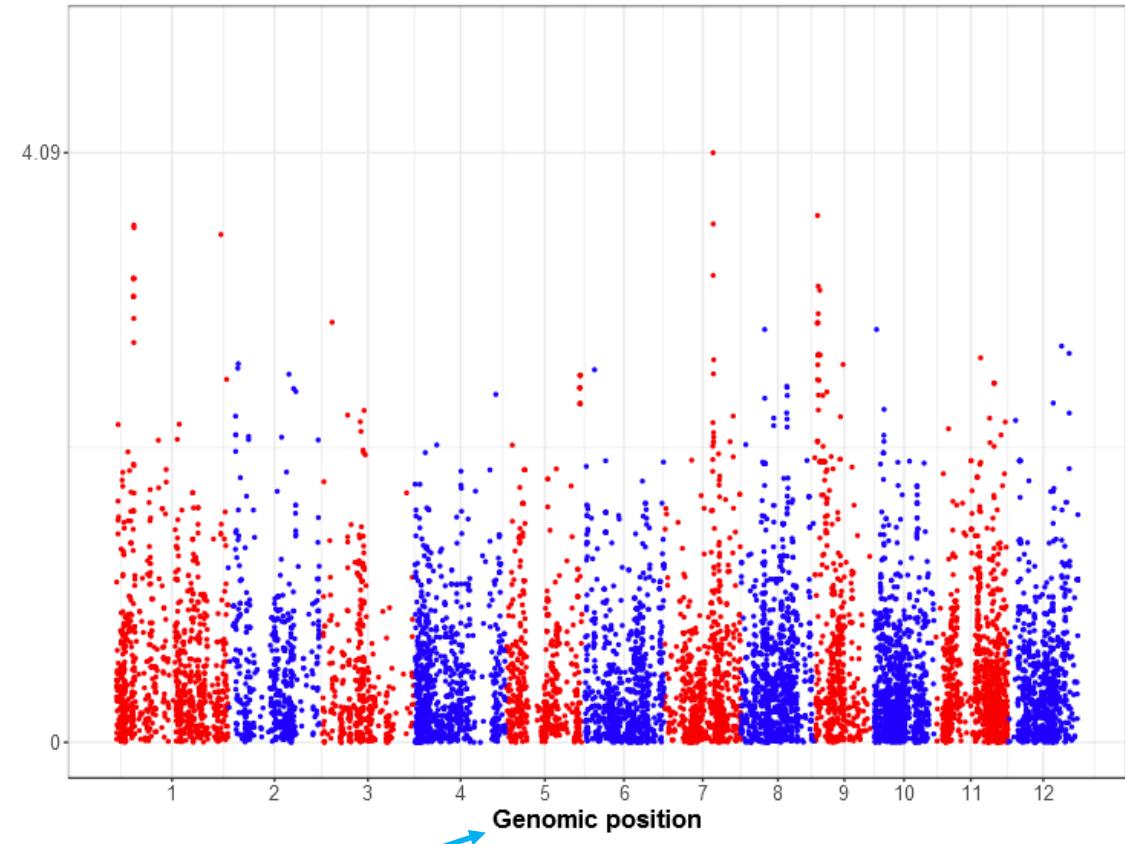
- Horizontal
- Vertical

Upload genome data:

genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

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

3.5 Axis label

Options

One genome plot

Plot options

Show Advanced Options ▾

- Adjust plot size
- Figure theme
- Font size
- Axis title
- X axis label
 - Show a
 - Hide
- Legend

Two genomes plot

Plot options

- Adjust plot size
- Figure theme
- Font size
- Axis title
- Axis label
 - Show a
 - Hide
- X label
 - Show a
 - Hide
- Y label
 - Show a
 - Hide

Add tick labels on x-axis of non-circular plot for one genome.

Add tick labels on x/y-axis of non-circular plot for two genomes.

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

Upload genome data:

 genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

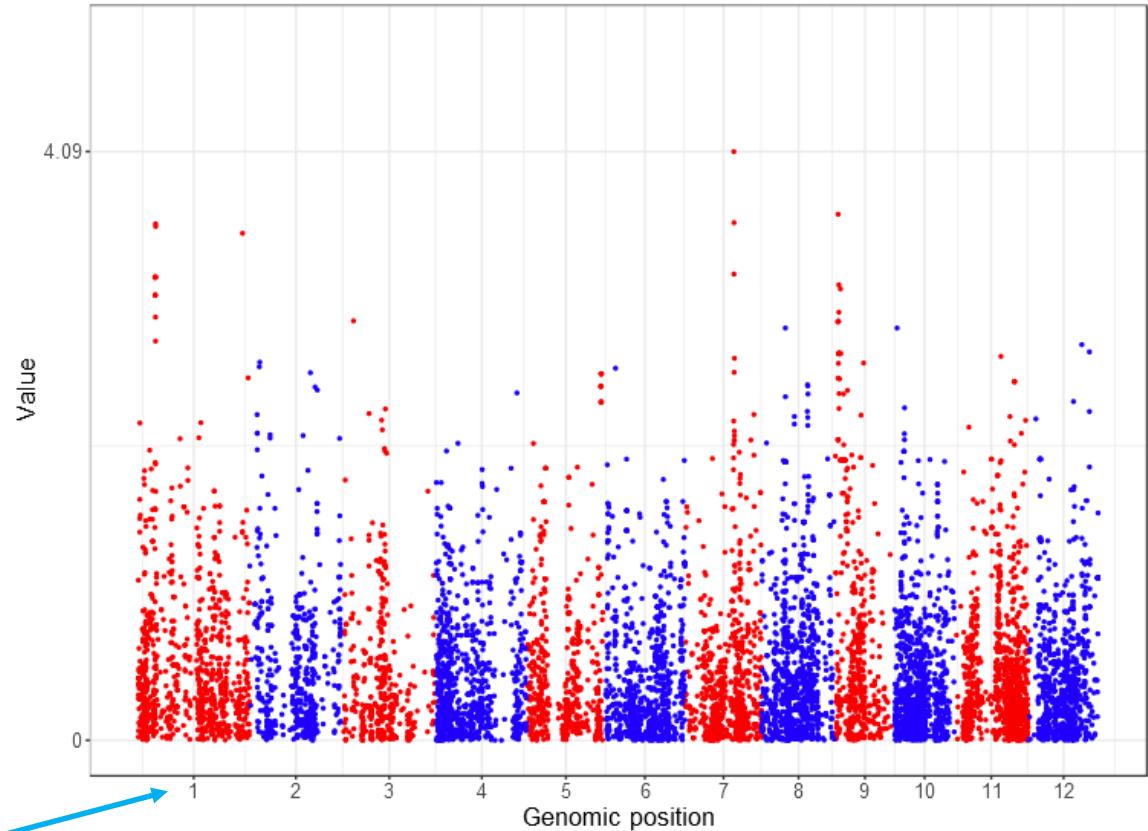
 [Download pdf-file](#) [Download svg-file](#) [Download the R scripts to reproduce the plot](#) X axis label Show Hide

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

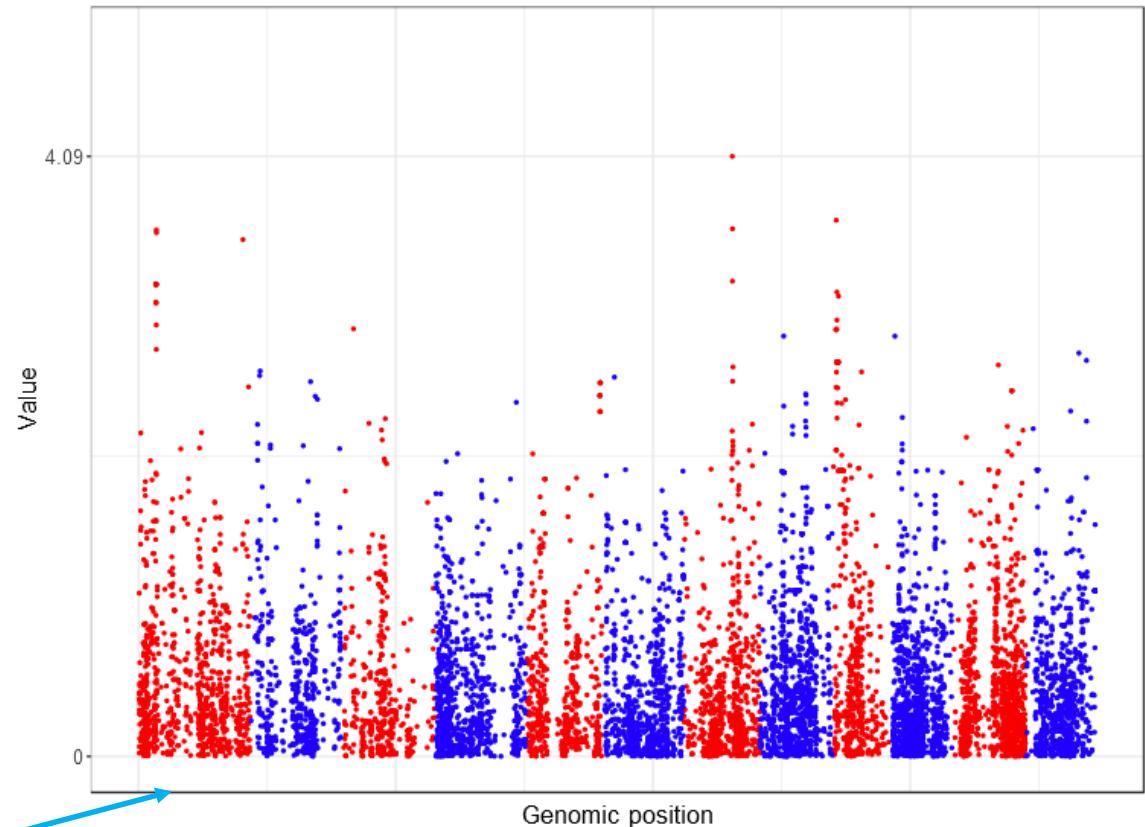
Upload genome data:

 genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

Go!

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

- Show
- Hide

Upload genome1 data:

Browse... genome1_data.txt
Upload complete

Upload genome2 data:

Browse... genome2_data.txt
Upload complete

Upload plot data:

Browse... plot_data_point_gradual.txt
Upload complete

Plot type:

point_gradual

Show Advanced Options

Go!

Plot options

Adjust plot size

Figure theme

Font size

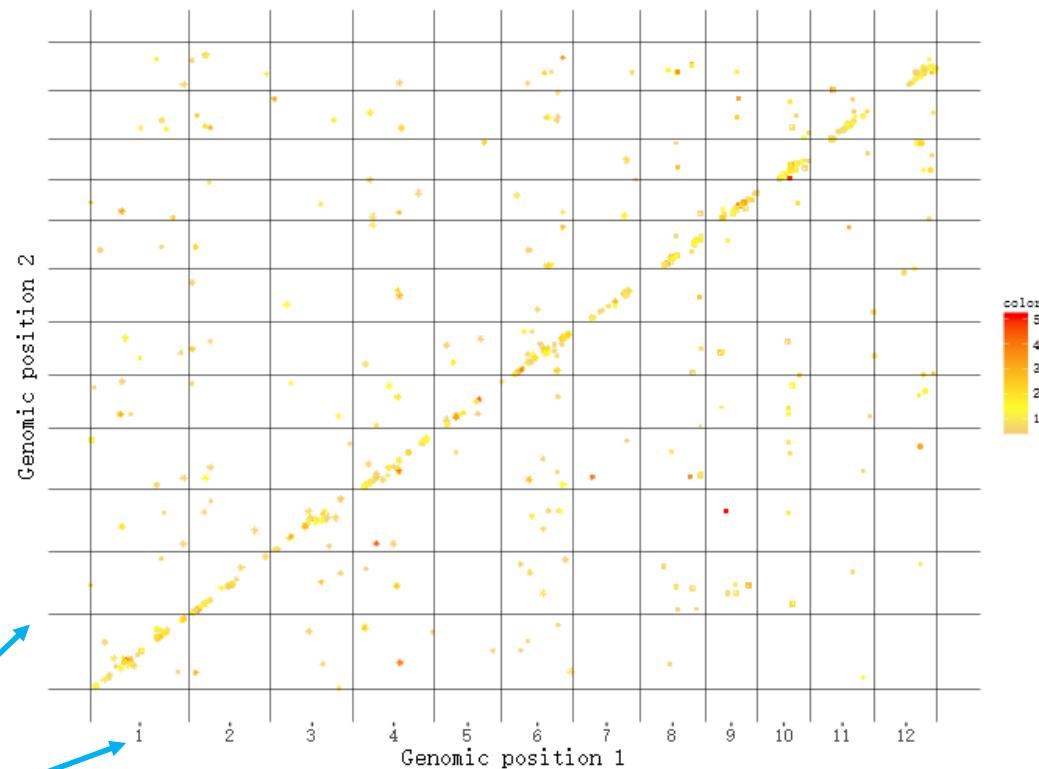
Axis title

Axis label

X label
 Show
 Hide

Y label
 Show
 Hide

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



3.6 Legend

Options

Plot options

Show Advanced Options ▾

- Adjust plot size
- Figure theme
- Font size
- Axis title
- X axis label
- Legend

Position

- Right
- Bottom

Space size

0.04

Intra-spacing

15

Title size

10

Title font face:

plain

Label size

10

Label font face:

plain

→ The position to place the legend.

→ Percent of legend size relative to the main plotting region. Applicable values are numbers in [0-1].

→ Intra-spacing between different legends.

→ The font size of legend title.

→ The font face of legend title.

→ The font size of legend tick label.

→ The font face of legend tick label.

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

Upload genome data:

 genome_data.txt

Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

Go!

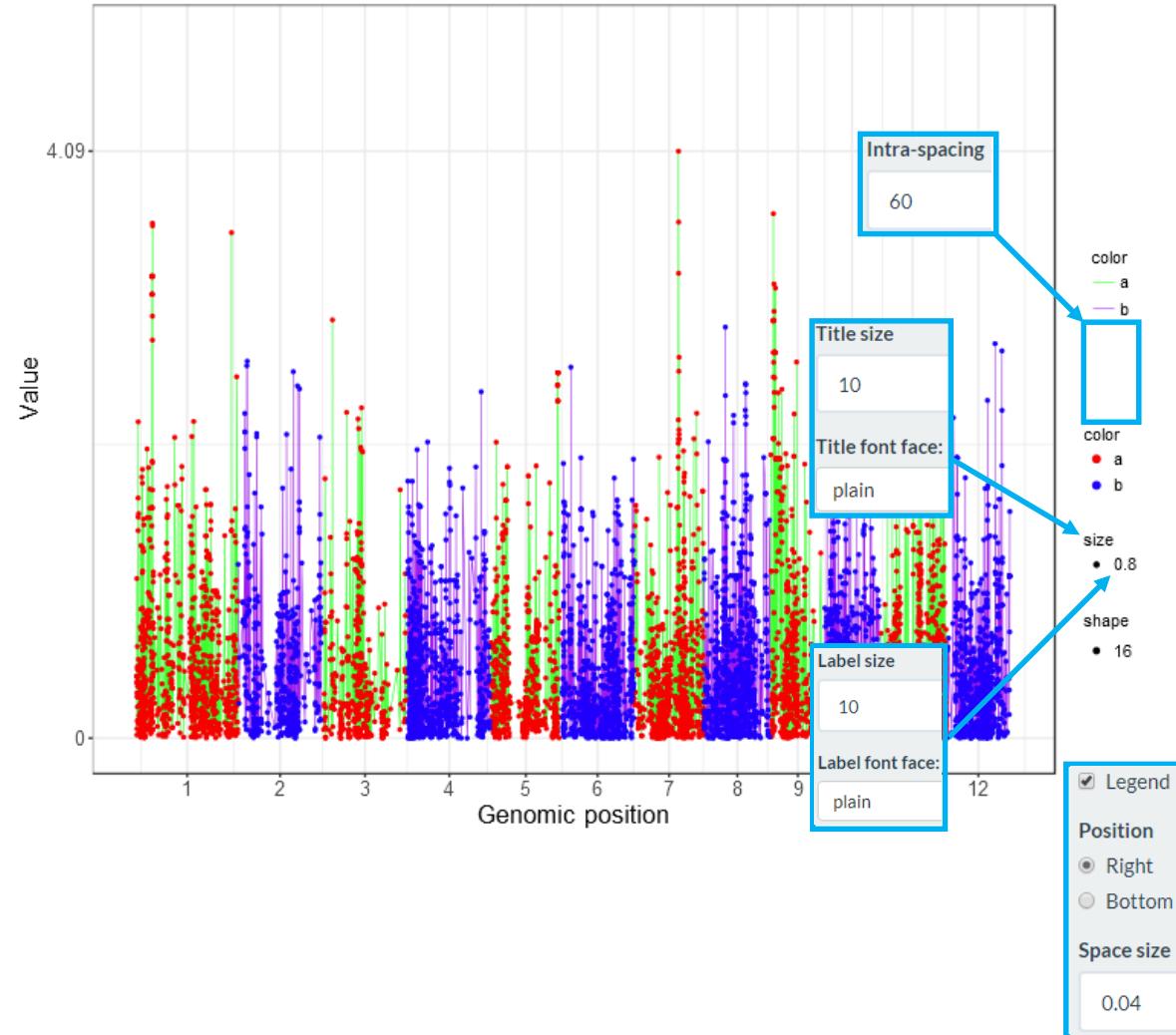
 [Download pdf-file](#) [Download svg-file](#) [Download the R scripts to reproduce the plot](#)

Image type

- Concatenated chromosome
- Separated chromosome

Orientation

- Horizontal
- Vertical

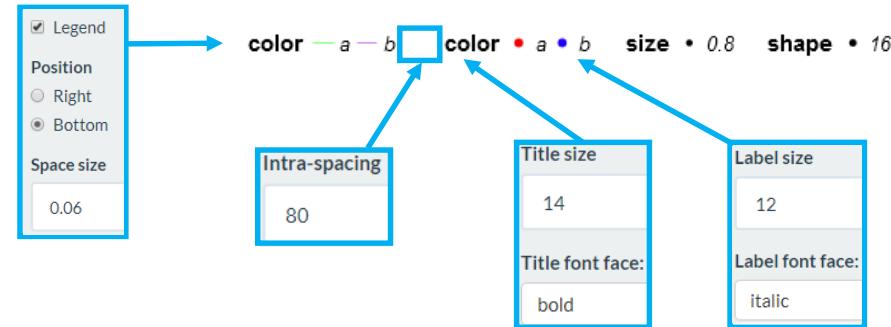
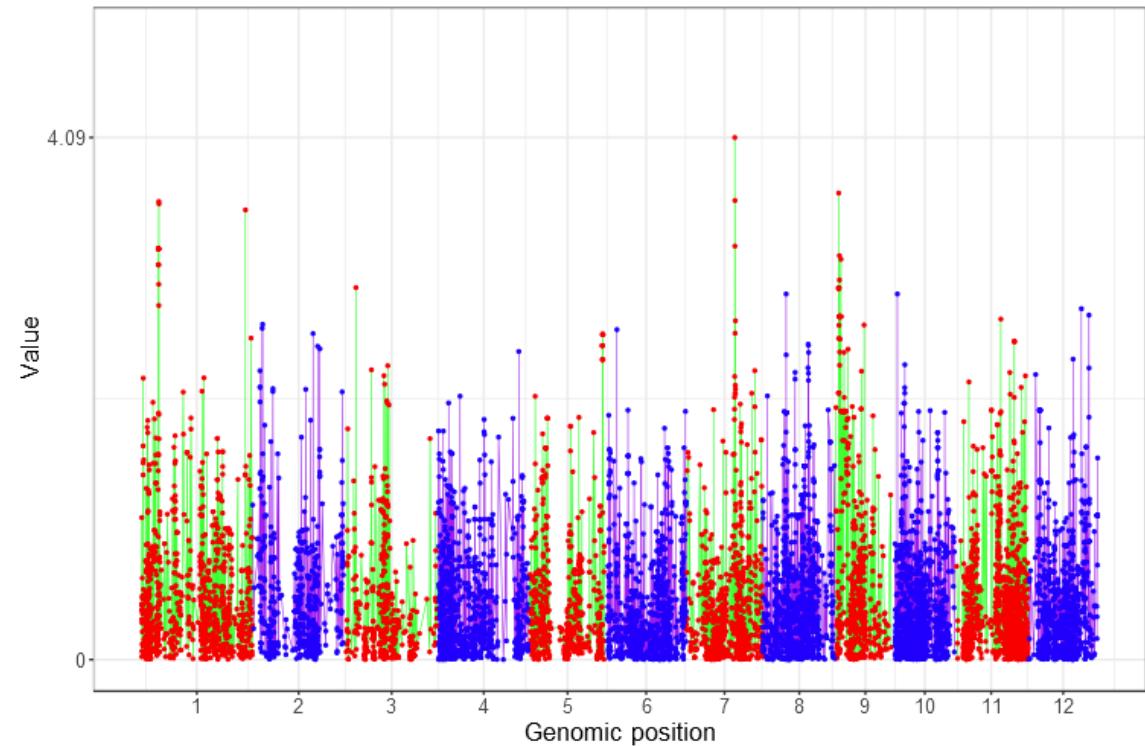
Upload genome data:

Browse... genome_data.txt
Upload complete

- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

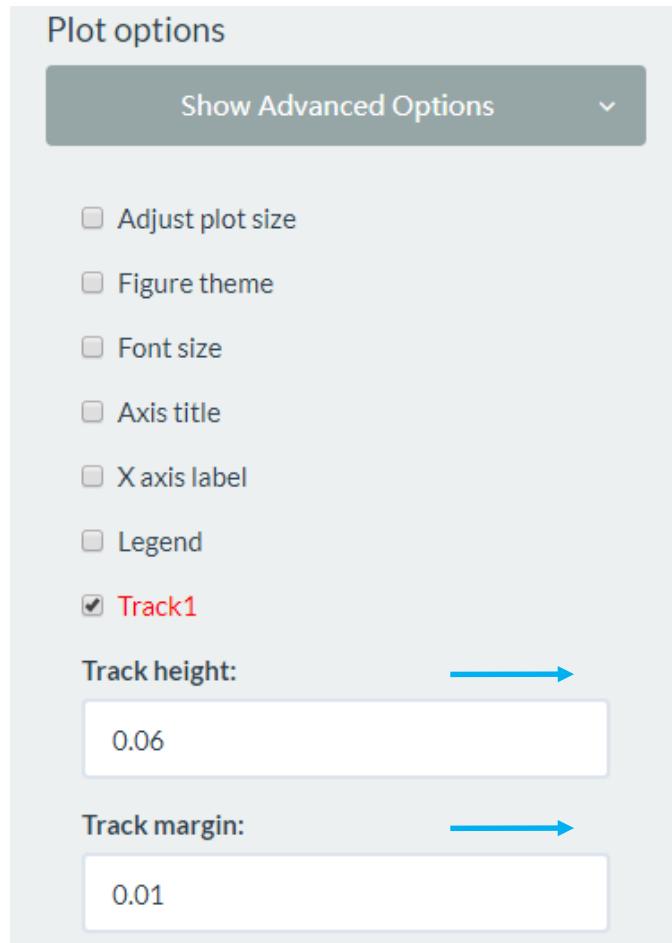
Go!

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



3.8 Height and width of different tracks

Options



Height of the track for one genome plot.

Margin of the track for one genome plot.

- These options are only available for one genome plot.

