

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 seven menus, "About", "Input data format", "Single genome plot", "Two genomes plot", "Gallery", "Help" and "Manual".



`shinyChromosome` is a graphical user interface for interactive creation of non-circular whole genome diagrams developed using the R `Shiny` package.

To create single genome plot by aligning genome data along all chromosomes of a single genome, go to the `Single genome plot` menu.

To create two genomes plot for comparison of data across two genomes, go to the `Two genomes plot` menu.

For the detail format of input data, check the `Input data format` menu.

Software references

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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 Yiming Yu and Wen Yao. Please send bugs and feature requests to Yiming Yu (yimingyyu at gmail.com) or Wen Yao (venyao at qq.com). This application uses the shiny package from RStudio.

- The "About" menu gives a brief overview of shinyChromosome.

Menu in shinyChromosome: Input data format

shinyChromosome About **Input data format** Single genome plot Two genomes plot Gallery Help Manual

The detail format of input data for different types of plots are described in the following sections.

1. Single genome plot

1.1 Genome data

The dataset should contain only 2 columns. Column names are **optional**.

1st column: chromosome ID.

2nd column: chromosome length.

```
chr      size
1 43268879
2 35930381
3 36406689
```

1.2 Point

The dataset should contain >=3 columns. Column names are **optional**.

1st column: chromosome ID.

2nd column: chromosome position.

3rd column: data value.

```
chr position    value
1   202360  0.315323
1   213775  1.113439
1   218457  0.393112
```

To control the color of points, add a **color** column to classify data into different groups. Then different colors will be assigned to different groups of data. Column names are **compulsory**.

- The “**Input data format**” menu shows the detail format for different types of plots created by shinyChromosome.

Menu in shinyChromosome: Single genome plot

The screenshot shows the 'Single genome plot' section of the shinyChromosome app. On the left, there's a sidebar with input fields for 'Image type' (radio buttons for 'Concatenated chromosome' and 'Separated chromosome'), 'Chromosome orientation' (radio buttons for 'Horizontal' and 'Vertical'), and 'Upload genome data' (a 'Browse...' button with 'No file selected'). Below these are buttons for 'View example data' and 'Download example data'. A list of data sources from 'Data1' to 'Data10' is provided with checkboxes. At the bottom of the sidebar are 'Plot options' and 'Show Advanced Options' buttons.

The main area has three download buttons: 'Download pdf-file', 'Download svg-file', and 'Download the R scripts to reproduce the plot'. The third button is highlighted with a blue border. To the right of these buttons is the text 'Download scripts'. Below this is a large rectangular region labeled 'Main plot region' with a blue border. To the left of this region is the text 'Download figures'.

At the bottom of the main area, the text 'Upload data and tune plot options' is displayed.

- The “Single genome plot” 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 plot

The screenshot shows the 'Two genomes plot' tab selected in the top navigation bar. On the left, there are three sections for uploading genome data: 'Upload genome1 data', 'Upload genome2 data', and 'Upload main plot data'. Each section includes a 'Browse...' button, a file selection input field ('No file selected'), and 'View example data' and 'Download example data' buttons. Below these is a 'Plot type:' dropdown set to 'point_gradual', a 'Show Advanced Options' button, and a 'Go!' button. To the right of these sections are four large blue-highlighted areas: 'Download scripts' (with download buttons for PDF, SVG, and R scripts), 'Download figures' (with a placeholder box), 'Upload data' (with a placeholder box), and 'Plot options' (with a placeholder box). The overall interface is clean with a dark header and light gray background.

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

Menu in shinyChromosome: Gallery



- 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 Input data format Single genome plot Two genomes plot 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://yimingyu.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 Input data format Single genome plot Two genomes plot 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 single genome plot

Non-circular single genome plots

shinyChromosome About Input data format Single genome plot Two genomes plot Gallery Help Manual

*Image type ?
● Concatenated chromosome
○ Separated chromosome
*Chromosome orientation ?
● Horizontal
○ Vertical
*Upload genome data ?
Browse... genome_data.txt Upload complete
View example data Example data

1.1

Data1
○ NULL
● Upload
Upload data1: ?
Browse... data1_track1_point.txt Upload complete
View example data Example data

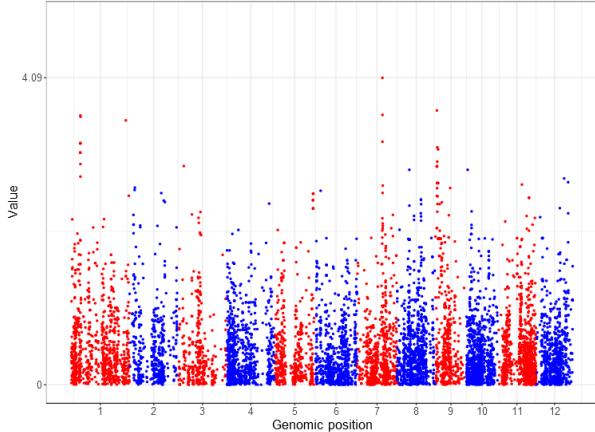
1.2

Track index: ?
track1
Plot type: point
Show Advanced Options
Data2
Data3
Data4
Data5
Data6
Data7
Data8
Data9
Data10

1.3

Go! ?
Plot options Show Advanced Options

1.4



1.5

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 Input data format Single genome plot Two genomes plot Gallery Help Manual

*Image type ?

- Concatenated chromosome
- Separated chromosome

→ All the chromosomes could either be concatenated or separated.

*Chromosome orientation ?

- Horizontal
- Vertical

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

*Upload genome data ?

Browse...

No file selected

Click "Browse" to upload input file. →

View example data

Download Example data

View or download example data.

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.

Upload point data

shinyChromosome About Input data format Single genome plot Two genomes plot Gallery Help Manual

*Image type ?

Concatenated chromosome
 Separated chromosome

*Chromosome orientation ?

Horizontal
 Vertical

*Upload genome data ?

Browse... No file selected

View example data

Data1

NULL
 Upload

Upload data1: ?

Browse... No file selected

View example data

Track index: ?

track1

Plot type:

point

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

Select "Upload"

Upload input file

Set track index

plot type: "point"

- Data assigned 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.

Options

Data1
 NULL
 Upload

Upload data1: [?](#)

[Browse...](#) No file selected

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:
point

Show Advanced Options [?](#)

Color

Data color [?](#)
Random

Color legend [?](#)
Show

Legend title: [?](#)
color

Modify legend labels [?](#)
Yes
a,b,c

Color transparency: [?](#)
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

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

→ Color legend.

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

→ The labels of different colors in the color legend can be 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.

Options

Symbol

Symbol type 

One custom symbol 



Symbol legend 

Show 

Legend title: 

symbol

Modify legend labels 

Yes 

a,b,c

→ The symbol to be used to plot the data, which can be assigned by the application or specified by the "shape" column of the input data.

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

→ Legend for point shape used in specified dataset.

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

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

Options

Size

Point size 

One custom size 



The point size to be used to plot the data, which can be assigned by the application or specified by the "size" column of the input data.

Value used to adjust the size of points.

Size legend 

Show 

Legend for point size used in specified dataset.

Legend title: 

0.2

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

Modify legend labels 

Yes 

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

a,b,c

Y axis label 

Show 

Add tick labels on the Y-axis.

Example 1

The screenshot shows the shinyChromosome R Shiny app interface. On the left, there are several input fields:

- *Image type: Radio buttons for "Concatenated chromosome" (selected) and "Separated chromosome".
- *Chromosome orientation: Radio buttons for "Horizontal" (selected) and "Vertical".
- *Upload genome data: A file input field showing "genome_data.txt" with "Upload complete". Buttons for "View example data" and "Download example data".
- Upload data1: A file input field showing "data1_track1_point.txt" with "Upload complete". Buttons for "View example data" and "Download example data". This field is highlighted with a blue box and has a blue arrow pointing from it to the corresponding table.
- Track index: A dropdown menu showing "track1".
- Plot type: A dropdown menu showing "point".
- Show Advanced Options: A button.

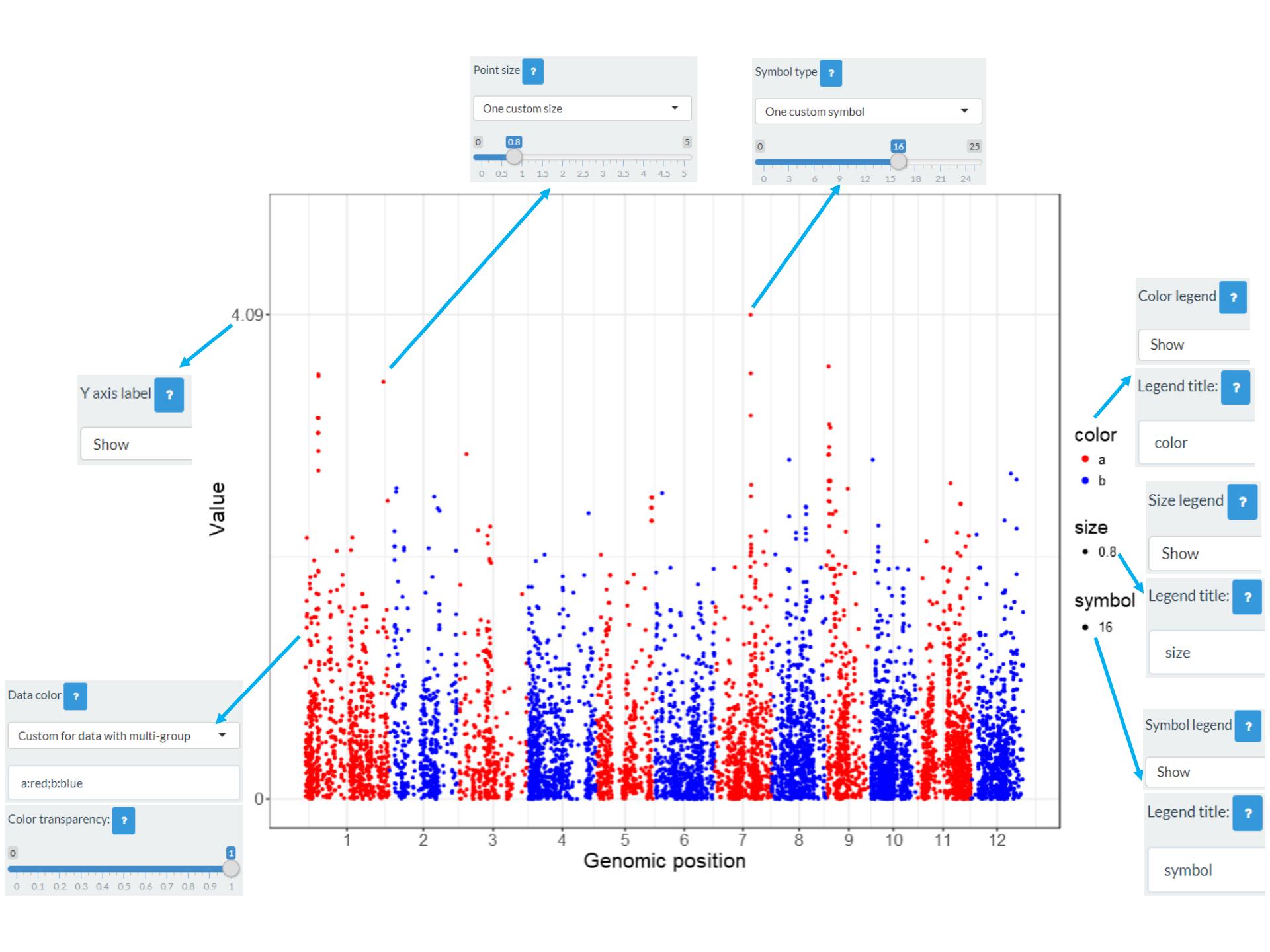
Data format

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.

- 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

*Chromosome orientation ?

Horizontal
 Vertical

*Upload genome data ?

Browse... genome_data.txt
Upload complete

View example data  Example data

Data1
 NULL
 Upload

Upload data1: ?

Browse... data1_track1_point.txt
Upload complete

View example data  Example data

Track index: ?

track1

Plot type:

point

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

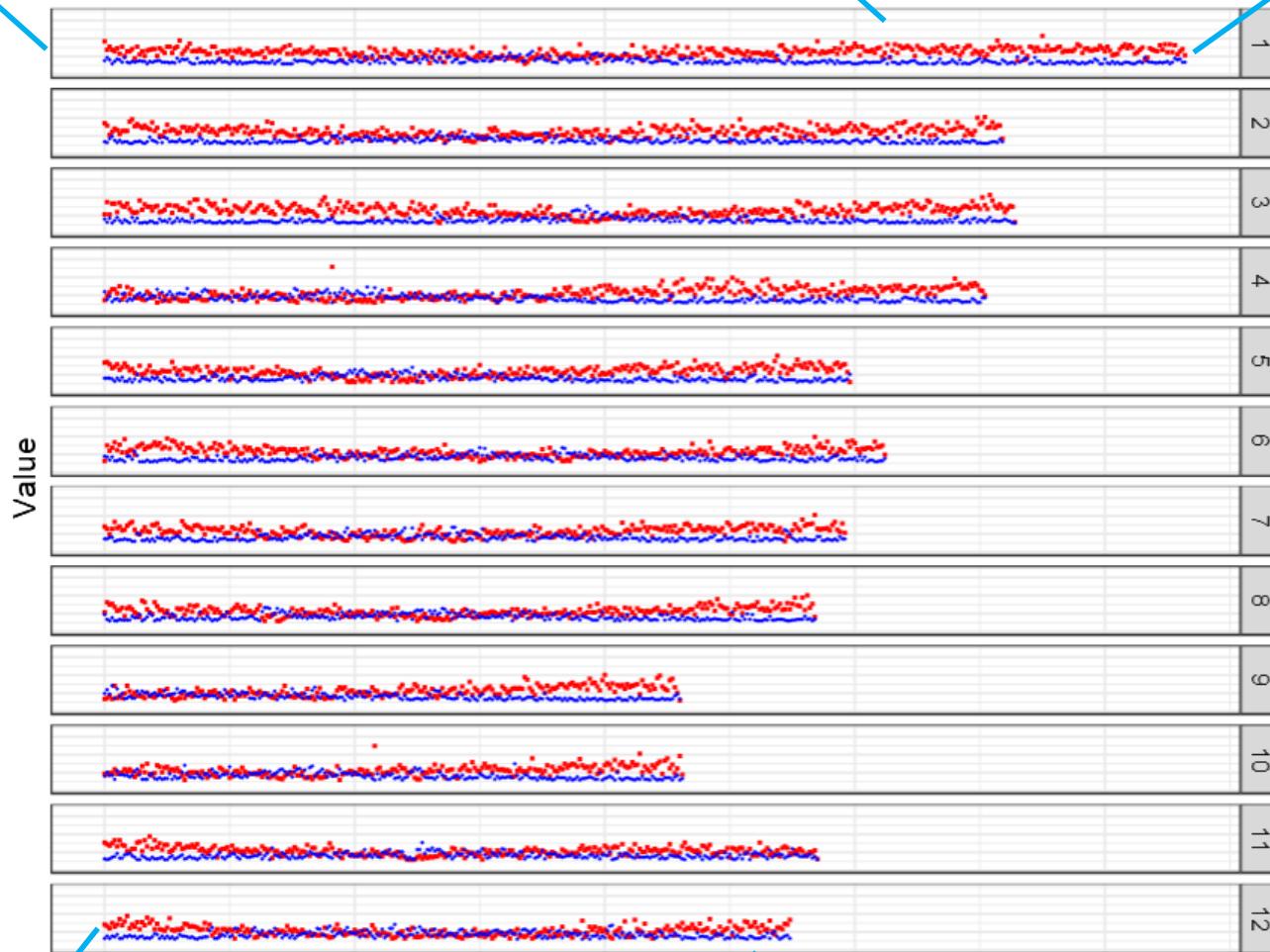
- The “shape” column indicates different symbols used for differing data groups. Applicable value are integers in [0-25]. Type `?pch` in R console for more information.

Y axis label [?](#)

Hide

Image type

- Concatenated chromosome
- Separated chromosome



Point size [?](#)

One custom size

0 0.8 5

0 0.5 1 1.5 2 2.5 3 3.5 4 4.5 5

Symbol type [?](#)

Custom for data with a "shape" column ▾

Data color [?](#)

Custom for data with multi-group

a:red;b:blue

Color transparency: [?](#)

0

0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1

Color legend [?](#)

Show

Legend title: [?](#)

type

type

shape

■ 12

■ 15

• 18

○ 21

Symbol legend [?](#)

Show

Legend title: [?](#)

shape

Size legend [?](#)

Hide

Example 3

*Image type ?

Concatenated chromosome
 Separated chromosomes

*Chromosome orientation ?

Horizontal
 Vertical

*Upload genome data ?

Browse... genome_data.txt
Upload complete

[View example data](#) [Download Example data](#)

Data1
 NULL
 Upload

Upload data1: ?

Browse... data1_track1_point.txt
Upload complete

[View example data](#) [Download Example data](#)

Track index: ?

track2

Plot type:

point

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

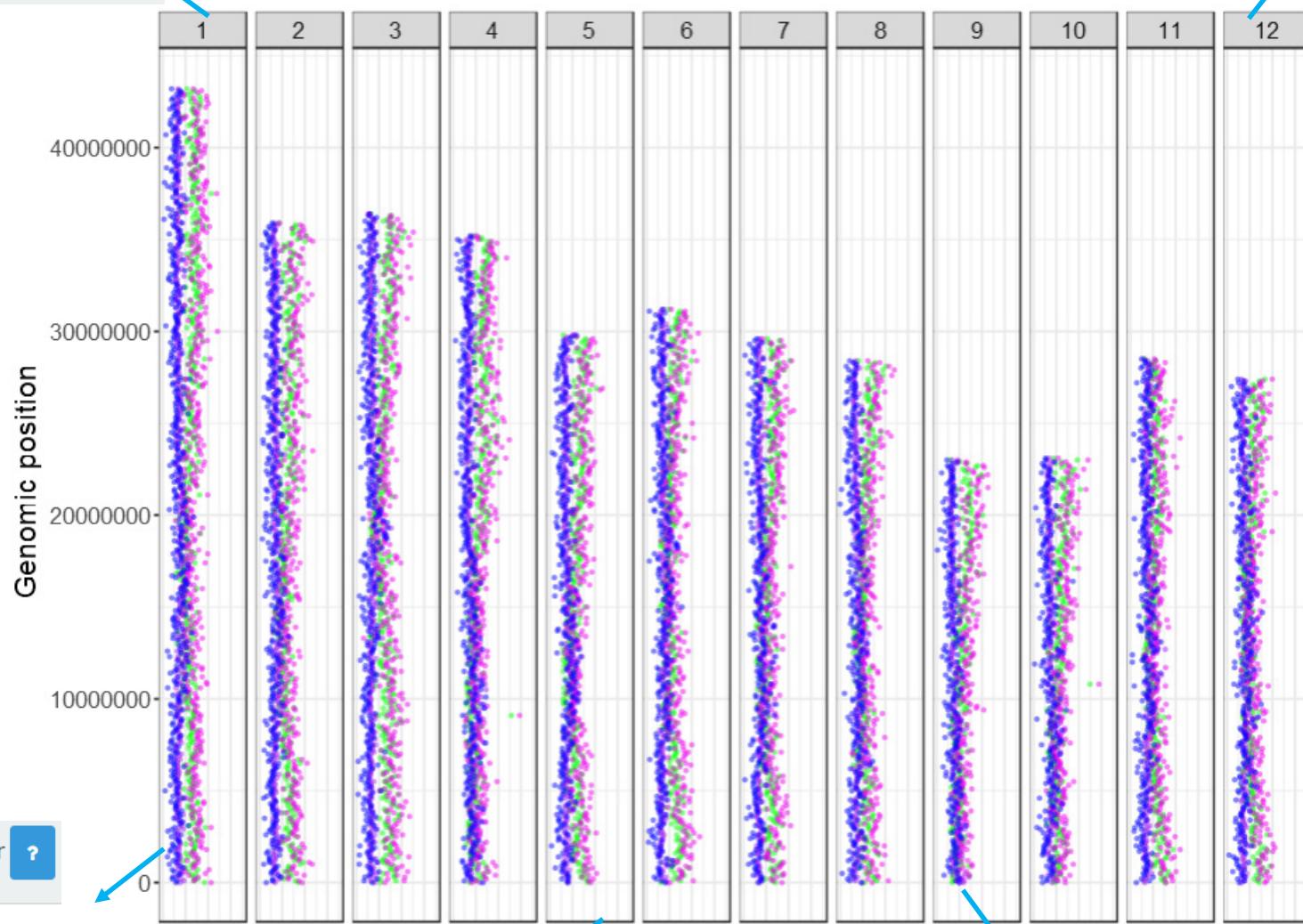
- The “size” column is a **numeric vector** representing different point sizes.
- The names of columns used to specify the color, shape and size of the data should be fixed as “color”, “shape” and “size”.

*Image type ?

- Concatenated chromosome
 Separated chromosome

*Chromosome orientation ?

- Horizontal
 Vertical



Color legend ?

Hide

Symbol legend ?

Hide

Size legend ?

Hide

2.1.2 Plot line

Options

Data1
 NULL
 Upload

Upload data1: [?](#)

[Browse...](#) No file selected

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:

line

Show Advanced Options [▼](#)

Color

Data color [?](#)

Random

Fill area [?](#)

Yes

Area color [?](#)

Identical with lines
 Specific

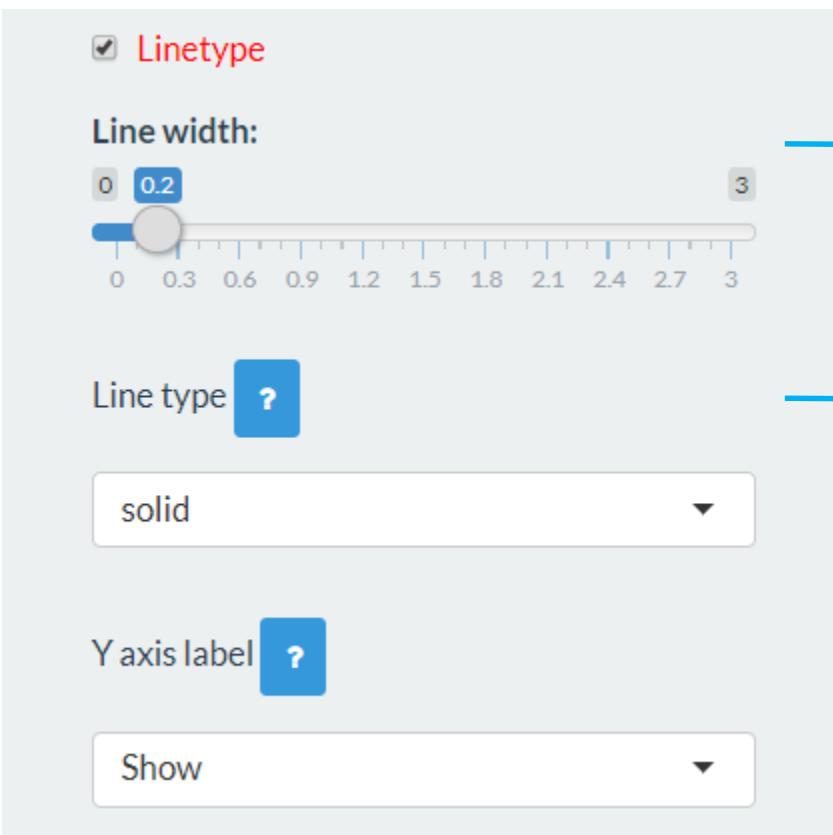
#0000FF

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.

- See section 2.1.1 for more plot options.

Options



- See section 2.1.1 for more plot options.

Example 1

Data1

NULL

Upload

Upload data1: [?](#)

Browse... data1_track1_line.txt Upload complete

[View example data](#) [Download Example data](#)

Track index: [?](#)

track1

Plot type: line

Data2

NULL

Upload

Upload data2: [?](#)

Browse... data1_track1_line.txt Upload complete

[View example data](#) [Download Example data](#)

Track index: [?](#)

track2

Plot type: line

Data format

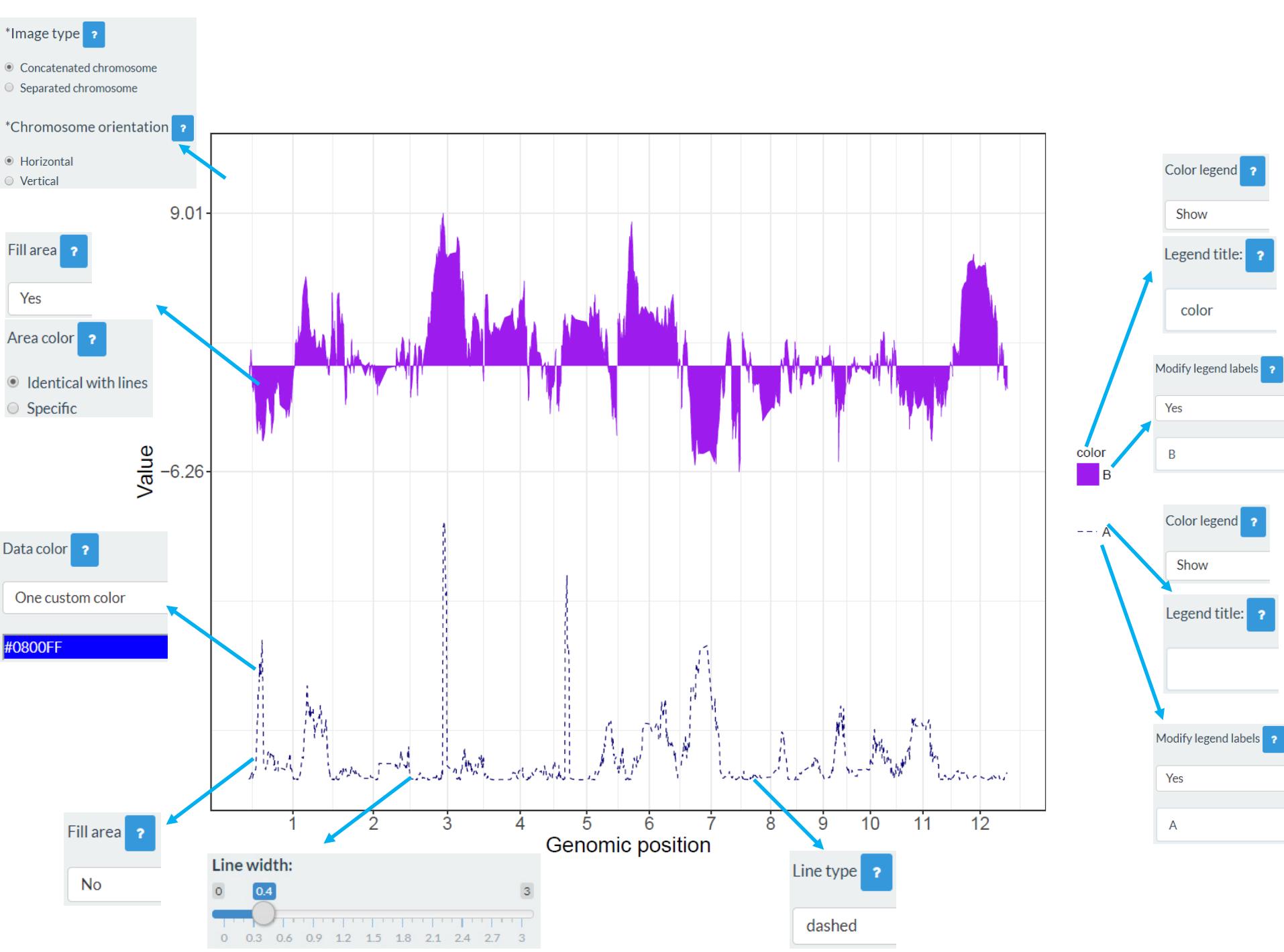
example_10/data1_track1_line.txt

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: [?](#)

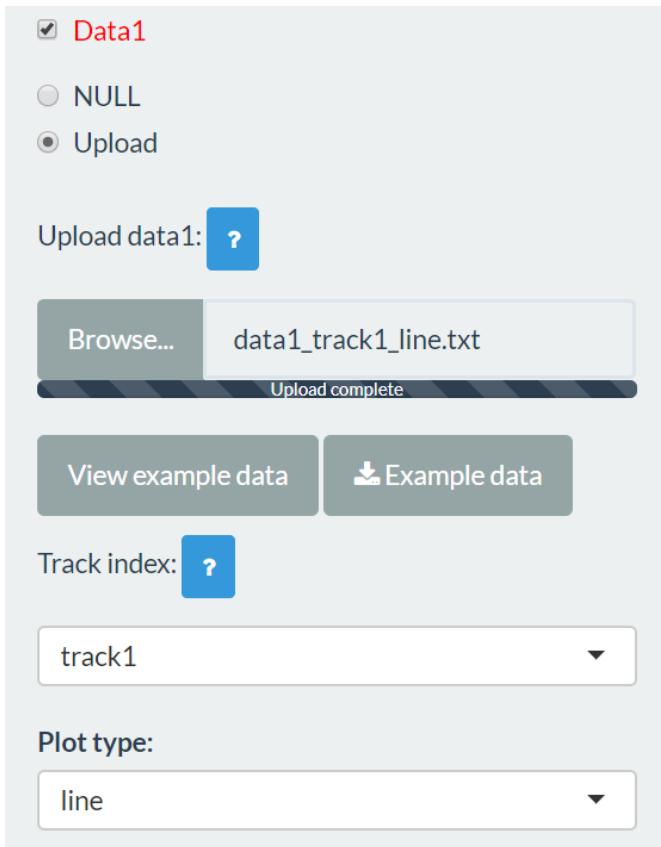
Browse... **data1_track1_line.txt**
Upload complete

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:
line

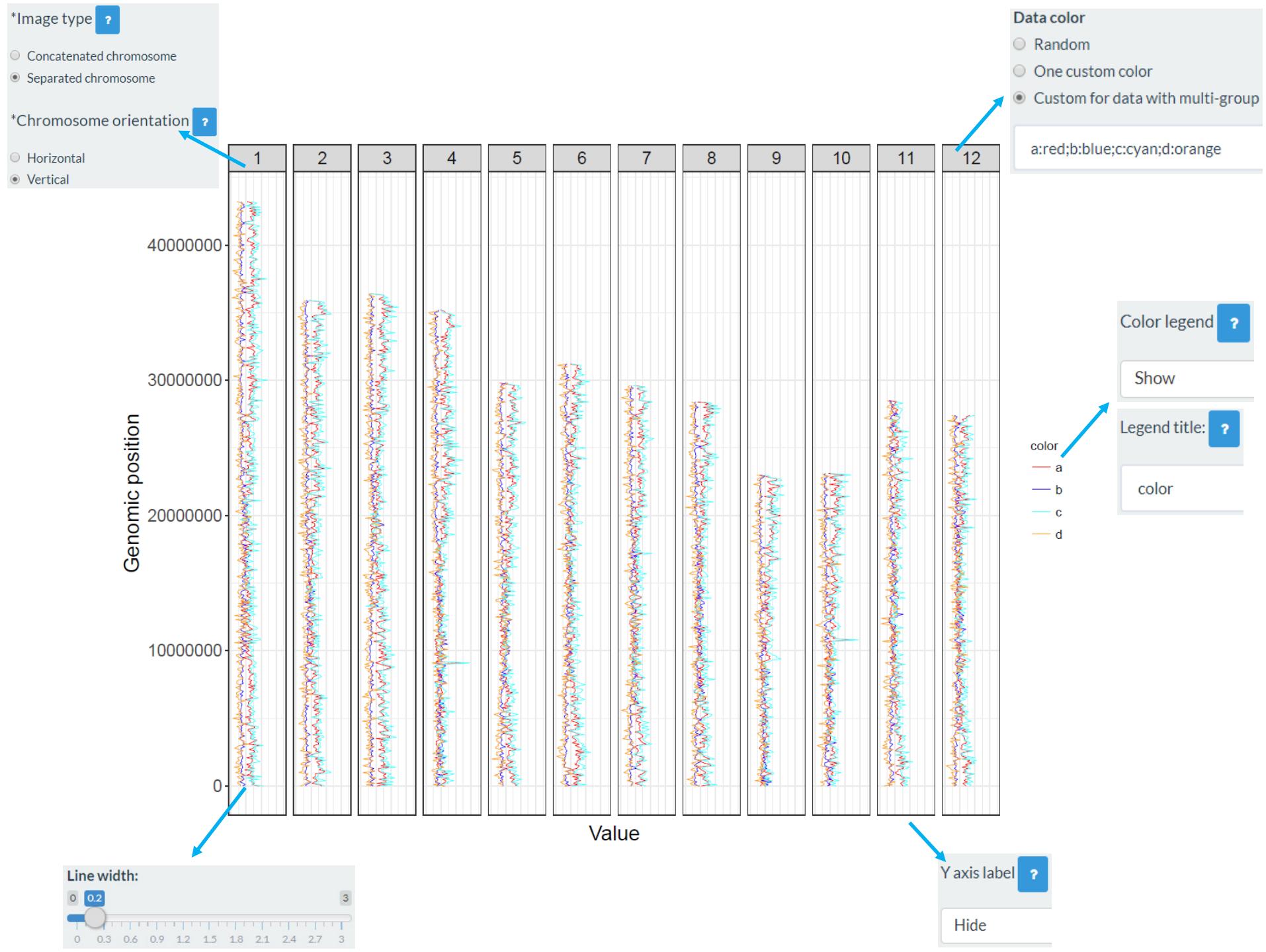


Data format

`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**.



2.1.3 Plot bar

Options

Track index: ?

track1

Plot type:

bar

Show Advanced Options ▾

Color

Data color ?

Random

Color legend ?

Hide

Color transparency: ?

Add cell borders ? →

Yes

Borders color: →

#000000

Add borders to the bars.

The color used for the borders of bars.

- See section 2.1.1 for more plot options.

Upload bar data

Data1
 NULL
 Upload

Upload data1: [?](#)

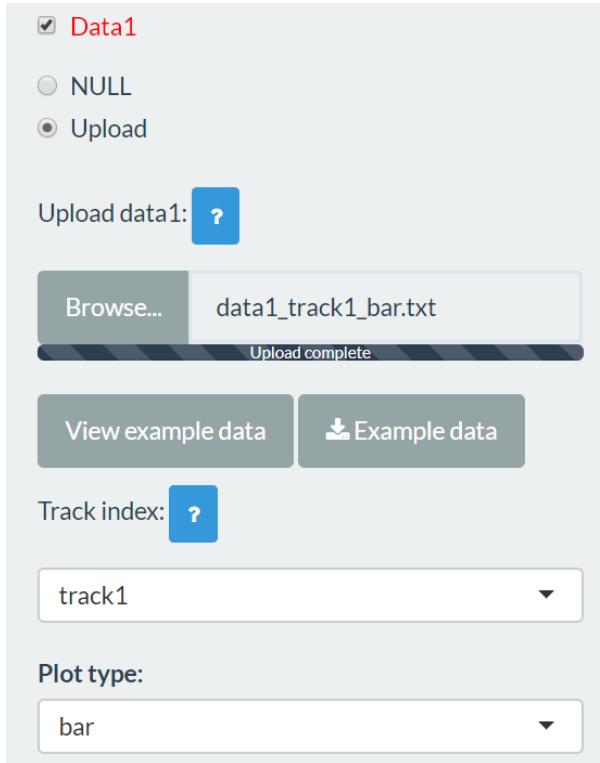
Browse... data1_track1_bar.txt
Upload complete

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:
bar

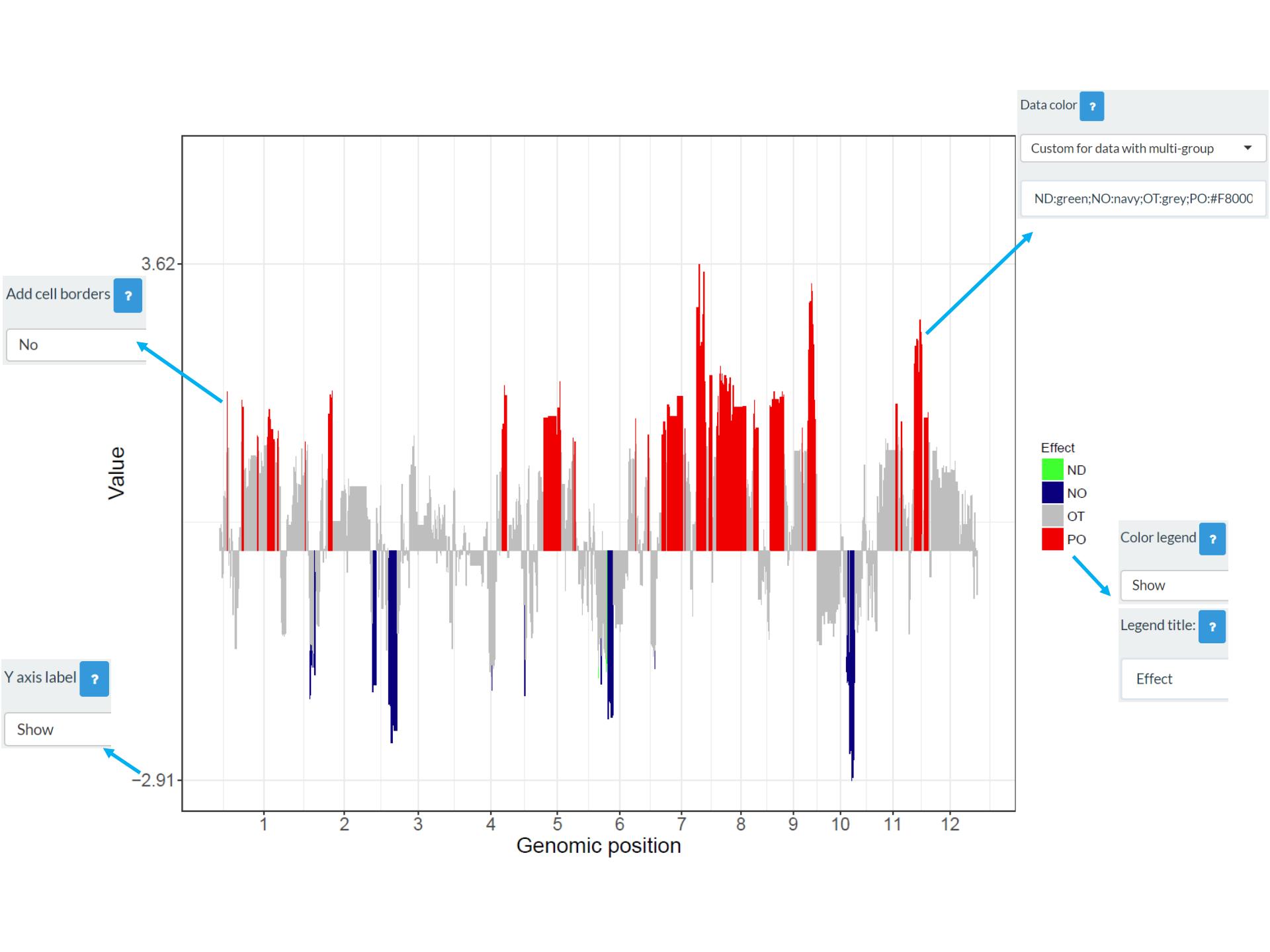


Data format

example_19/data1_track1_bar.txt

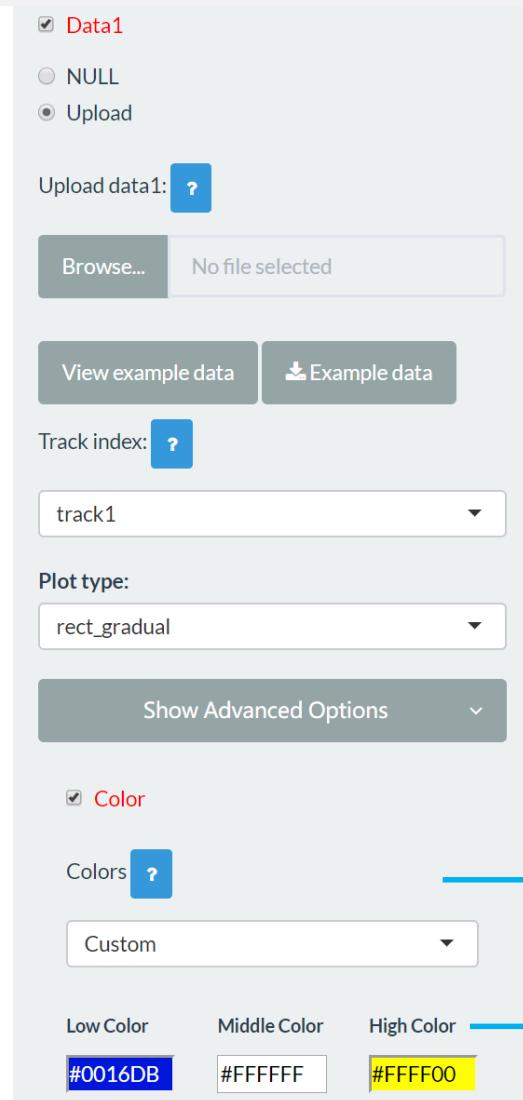
Chr	Start	Stop	D	color
1	0	565000	0.283	OT
1	565000	599000	0.337	OT
1	599000	922000	0.233	OT
1	922000	1075000	-0.12	OT
1	1075000	1147000	-0.339	OT

- Data for bar plot generally includes **4 columns** including the chromosome IDs, start coordinates of genomic regions, end coordinates of genomic 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



Colors to be used for the data, which can be assigned by the application or be specified by the users.

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

[View example data](#) [Example data](#)

Track index: [?](#)

track1

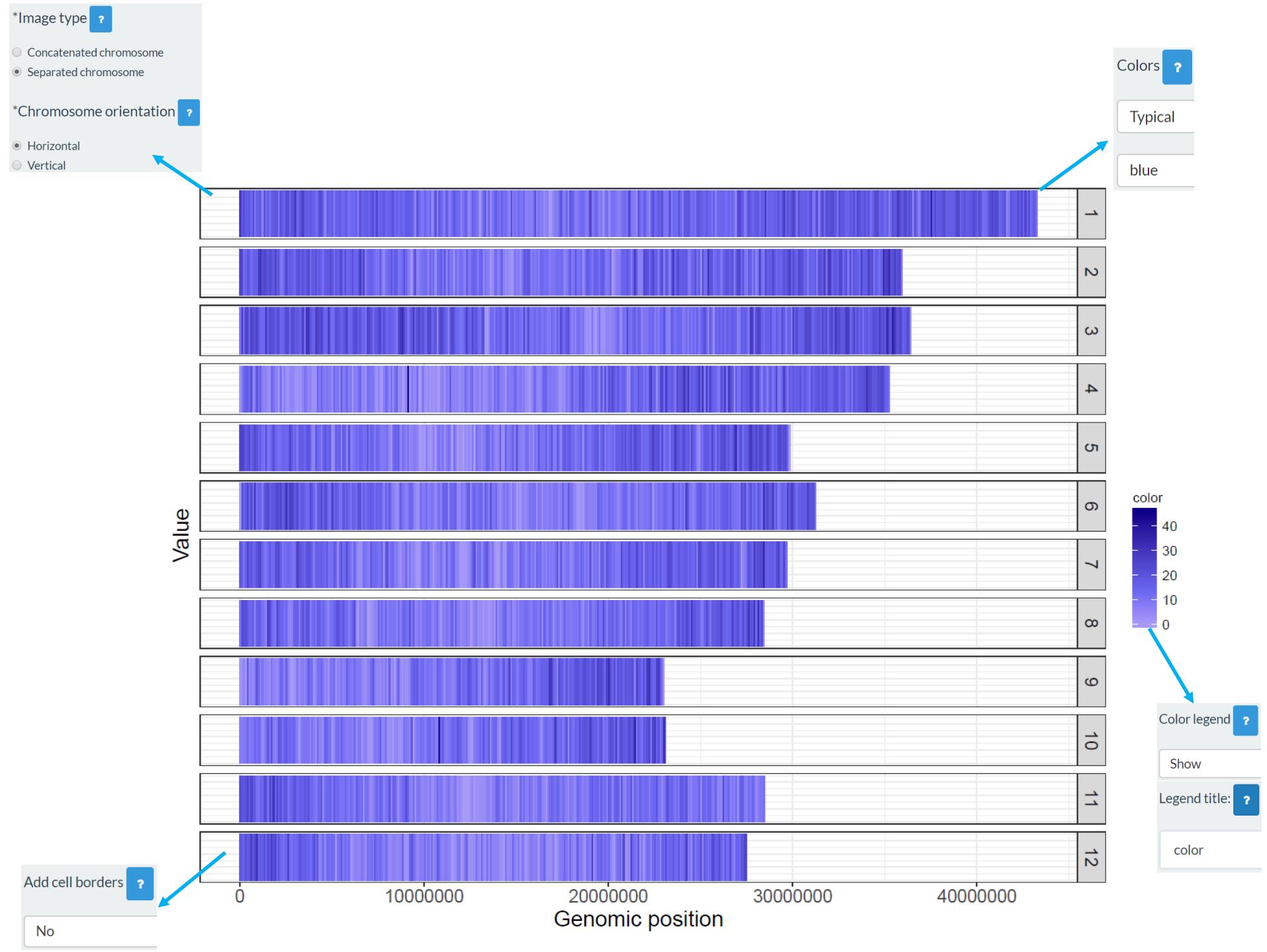
Plot type:
rect_gradual

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 genomic regions, end coordinates of genomic regions and numeric values.
- The last column should be a numeric vector.



2.1.5 Plot rect_discrete

Options

Data1
 NULL
 Upload

Upload data1: [?](#)

[Browse...](#) No file selected

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:

rect_discrete

Show Advanced Options [▼](#)

Color

Data color [?](#)

Random

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

- 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

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:
rect_discrete

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 genomic regions, end coordinates of genomic regions and character values.
- The last column should be a character vector representing discrete variables.

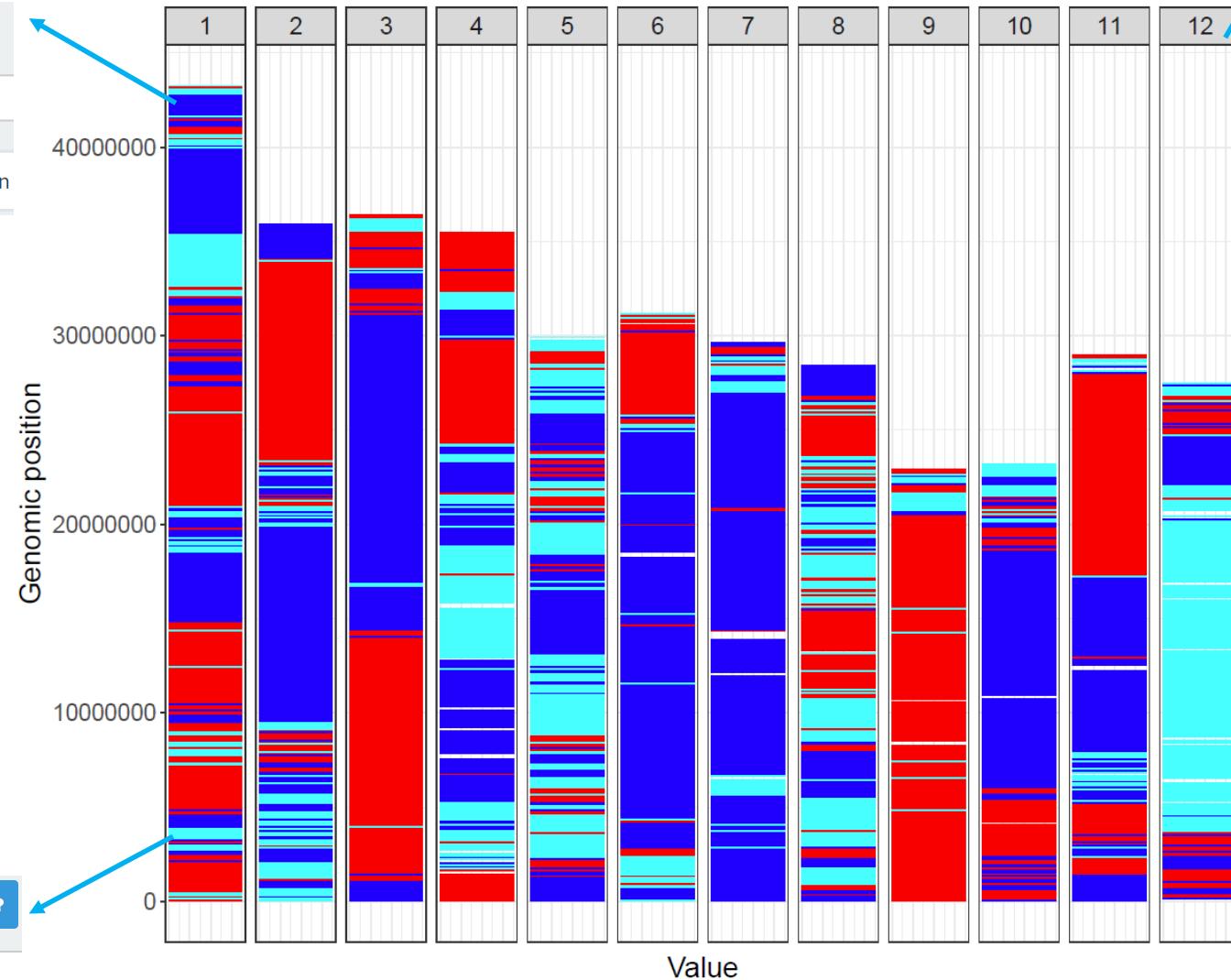
Color transparency:



Data color

Custom

A:red;B:blue;C:cyan



*Image type

Concatenated chromosome

Separated chromosome

*Chromosome orientation

Horizontal

Vertical

color

A

B

C

Color legend

Show

Legend title:

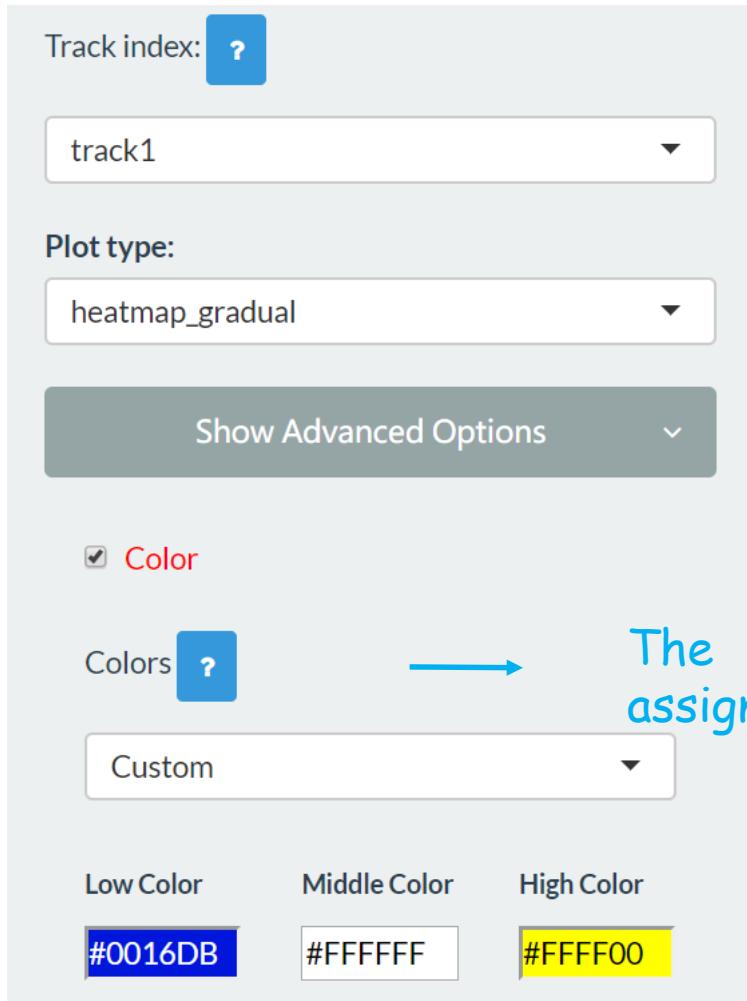
color

Add cell borders

No

2.1.6 Plot heatmap_gradual

Options



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

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:

heatmap_gradual

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 genomic regions and end coordinates of genomic regions.
- Apart from the first three columns, other columns are numeric vectors representing different values.

Colors ?

Custom

Low Color

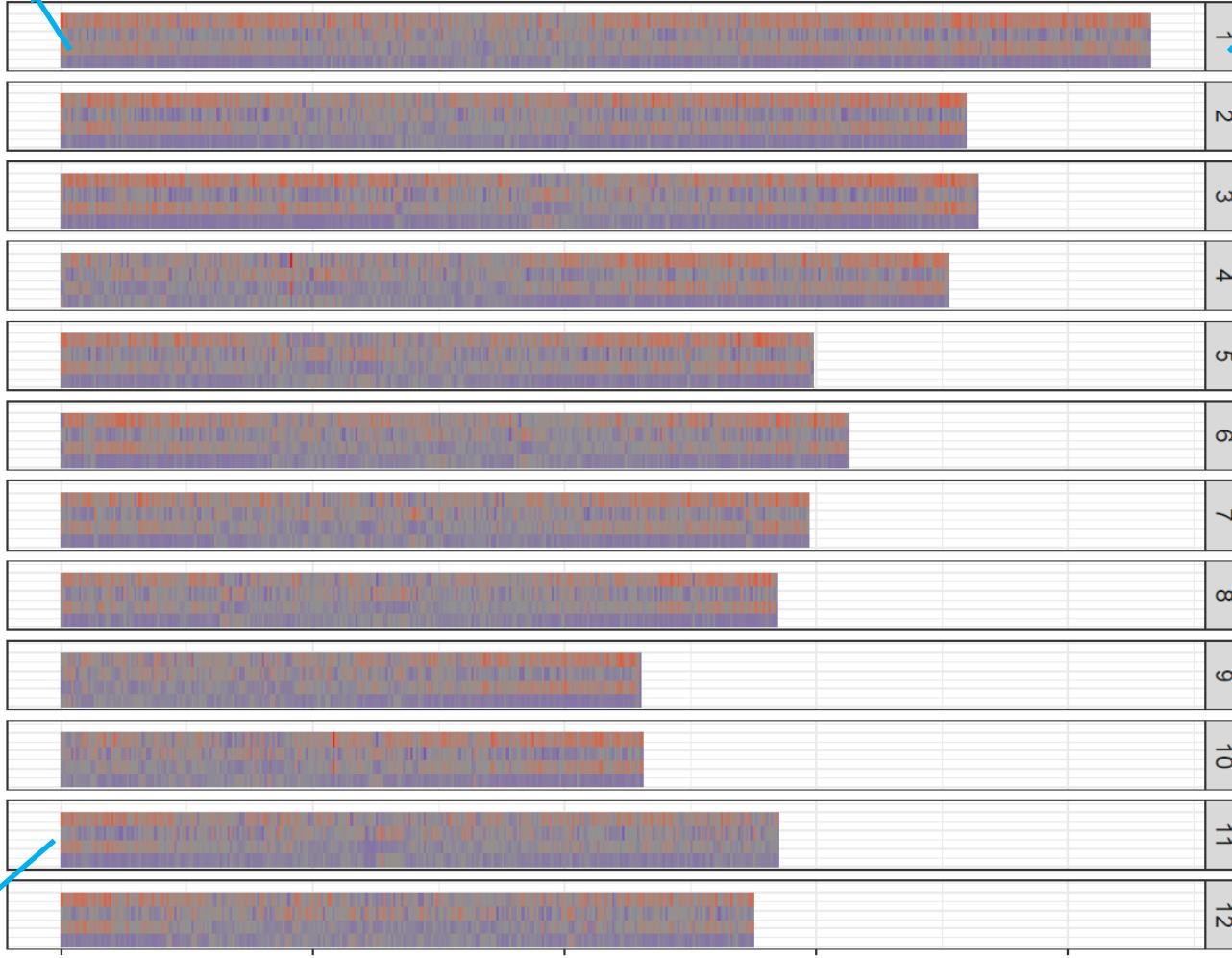
#0016DB

Middle Color

#8A8A8A

High Color

#FF0AOA

*Image type ? Concatenated chromosome Separated chromosome*Chromosome orientation ?

-
- Horizontal
-
-
- Vertical

color

Color legend ? ShowLegend title: ?

color

Add cell borders ?

No

2.1.7 Plot heatmap_discrete

Upload heatmap_discrete data

Data1
 NULL
 Upload

Upload data1: [?](#)

[Browse...](#) data1_track1_heatmap_discrete
Upload complete

[View example data](#) [!\[\]\(df246b58722714e0e756e91d56450201_img.jpg\) Example data](#)

Track index: [?](#)

track1

Plot type:

heatmap_discrete

Data format

example_31/data1_track1_heatmap_discrete.txt

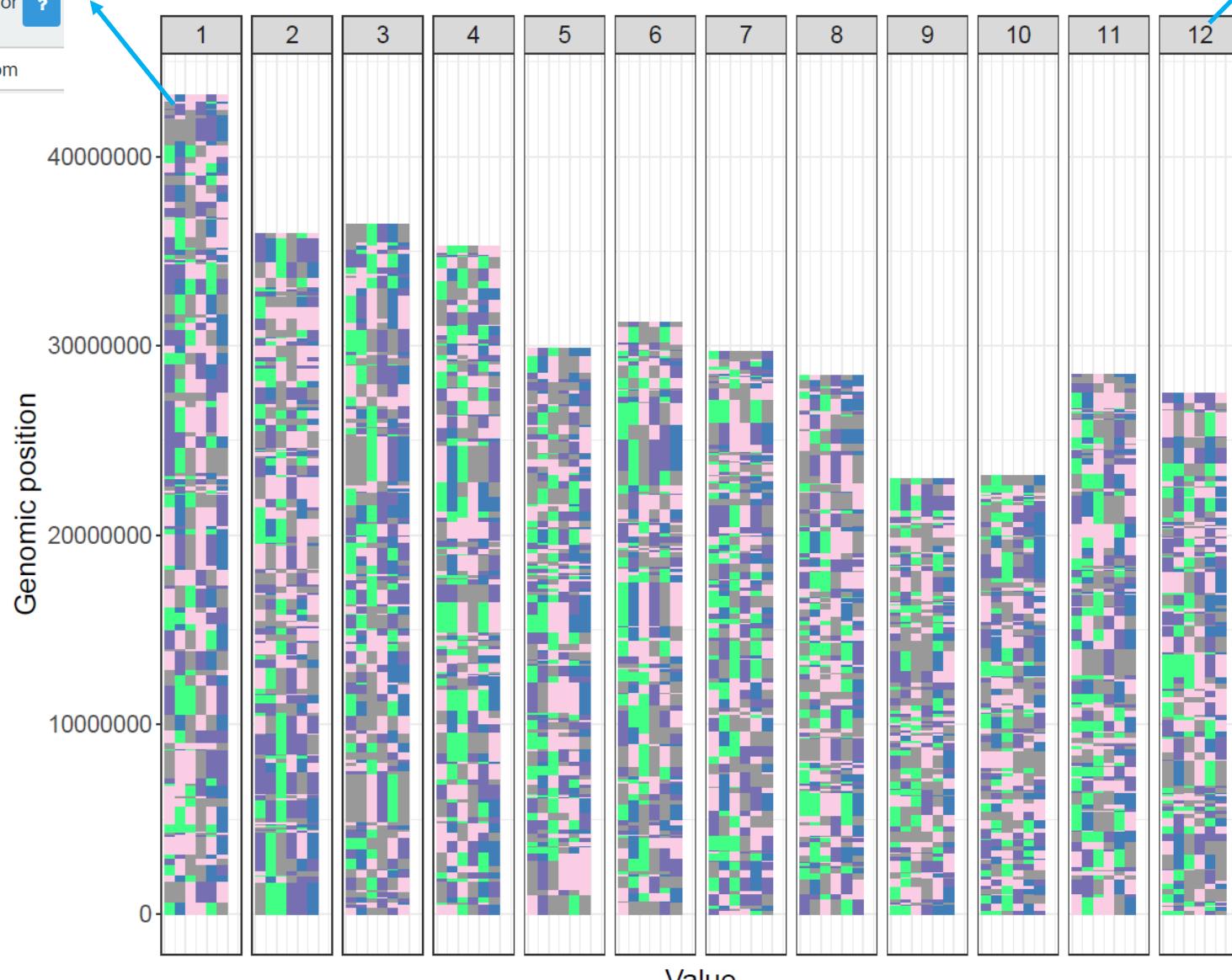
chr	start	end	val1	val2	val3	val4	val5	val6
1	0	631164	a	e	c	c	a	b
1	631165	1749192	b	b	c	d	d	c
1	1749193	2077793	c	e	a	b	e	e
1	2077794	2612461	a	c	b	b	e	d
1	2612462	2938491	d	c	b	c	c	b

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

Color transparency:

Data color

Random



*Image type

Concatenated chromosome

Separated chromosome

*Chromosome orientation

Horizontal

Vertical

color

a

b

c

d

e

Color legend

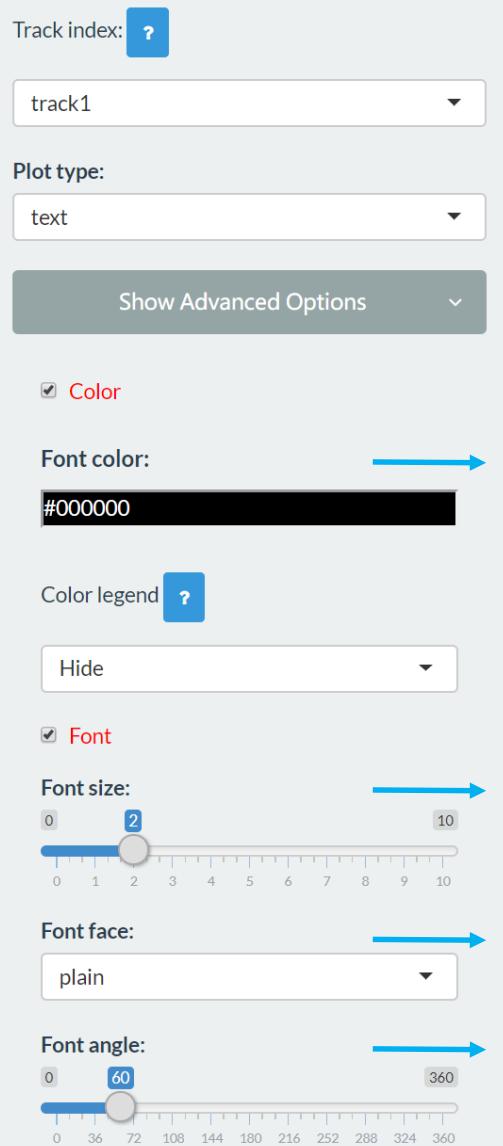
Show

Legend title:

color

2.1.8 Plot text

Options



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

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.

*Image type ?

Concatenated chromosome

Separated chromosome

*Chromosome orientation ?

Horizontal

Vertical

Font face:

italic

Font color:

#000000

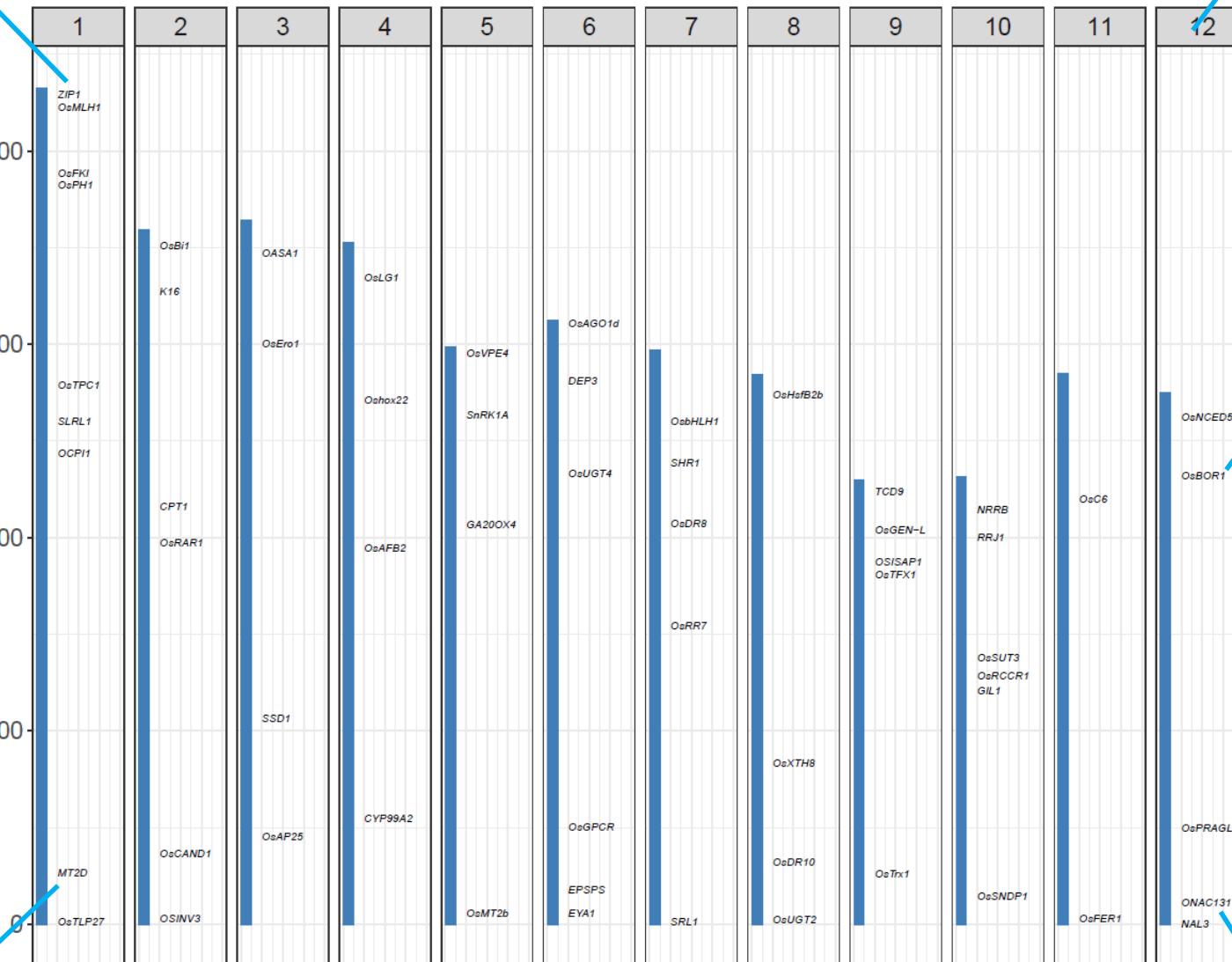
Genomic position

400000000

300000000

200000000

100000000



Font angle:



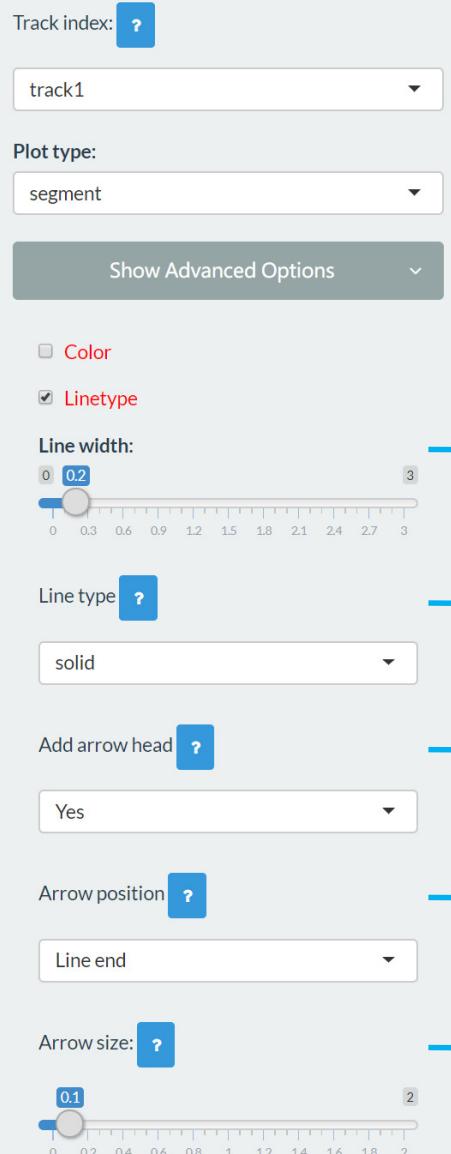
Value

Font size:



2.1.9 Plot segment

Options



Set the line width of segment.

Select the line type of segment.

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

The figure shows three separate upload interfaces, each consisting of a header section and a data entry section. The header sections include checkboxes for 'Data1', 'Data2', and 'Data3', and radio buttons for 'NULL' or 'Upload' (with 'Upload' selected). The data entry sections contain file input fields ('Upload data1', 'Upload data2', 'Upload data3') with 'Browse...' buttons, preview boxes ('data1_track1_rect_discrete.txt', 'data2_track2_text.txt', 'data3_track2_segment.txt'), and 'Upload complete' status indicators. Below each input field are 'View example data' and 'Download example data' buttons. At the bottom of each section are dropdown menus for 'Track index' (with 'track1', 'track2', and 'track2' respectively) and 'Plot type' ('rect_discrete', 'text', and 'segment').

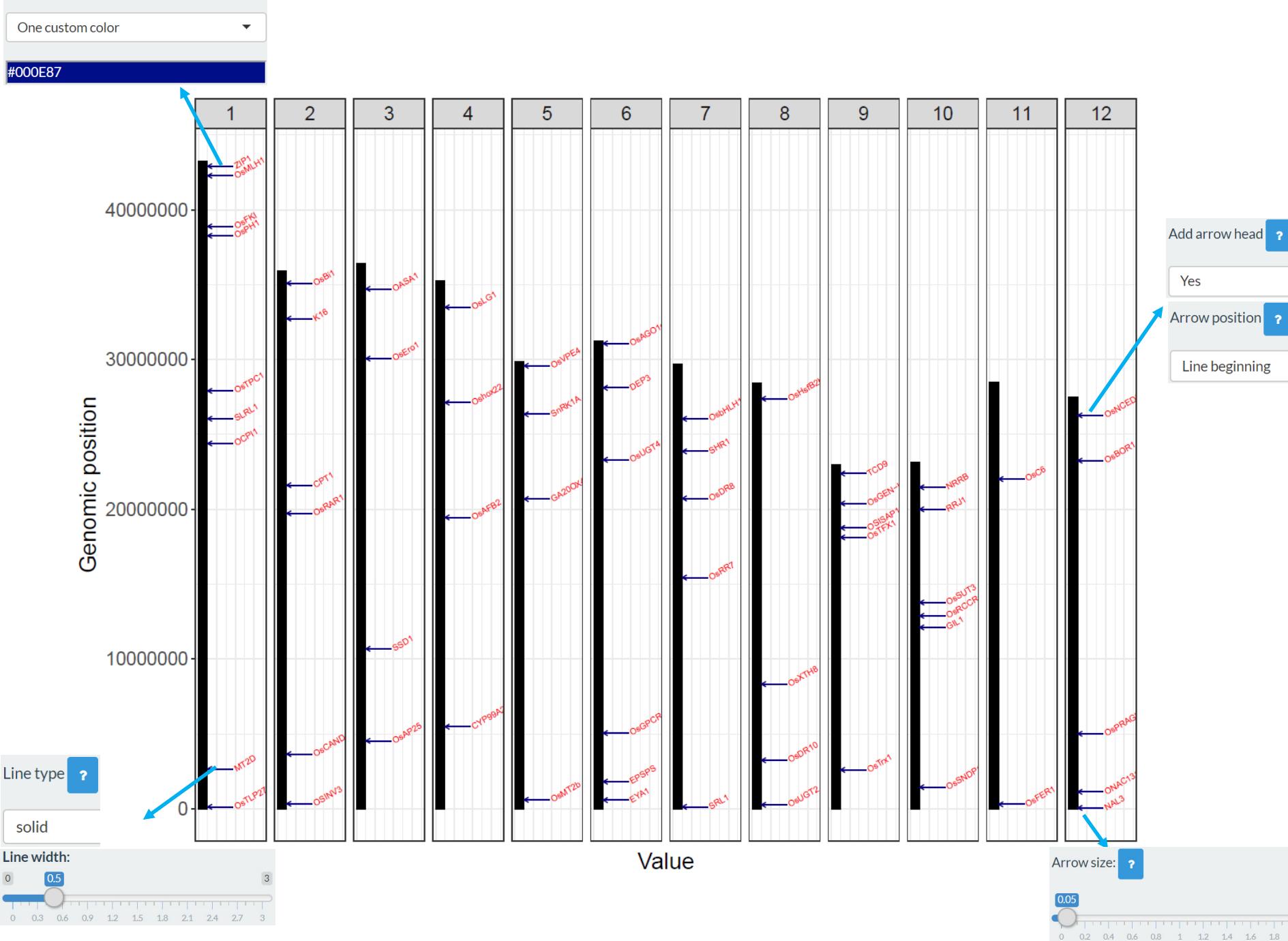
Data format

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

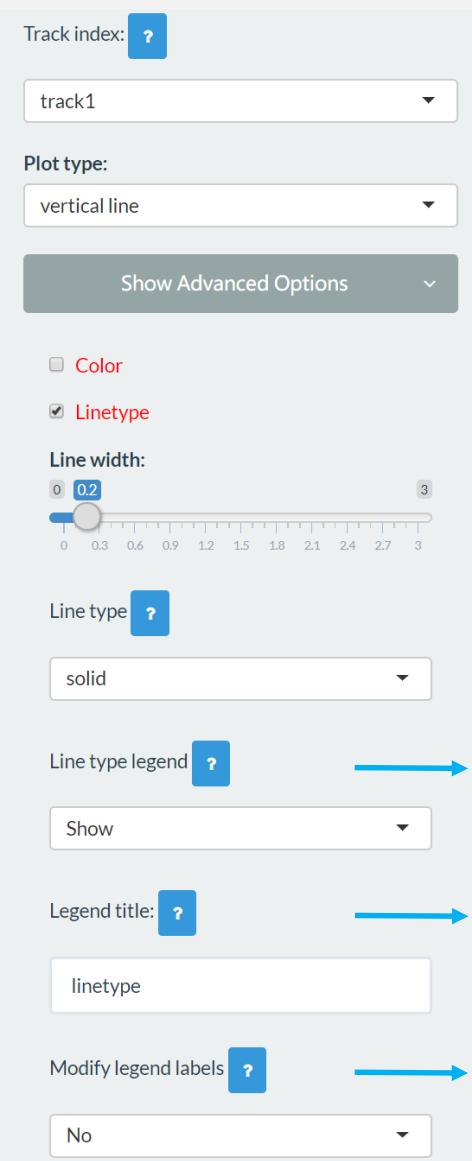
- Data for segment plot generally includes **5 columns**.
- Columns 2-3 and columns 4-5 represent the positions of the two ends of segment respectively.
- A "color" column can be added to assign colors to different segments, which is a **character vector**.

Data color



2.1.10 Plot vertical line or horizontal line

Options



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

Data1
 NULL
 Upload

Upload data1: [?](#)

[Browse...](#) data1_track1_line.txt
Upload complete

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:
line

Data2
 NULL
 Upload

Upload data2: [?](#)

[Browse...](#) data5_track1_vertical_line.txt
Upload complete

[View example data](#) [Example data](#)

Track index: [?](#)

track1

Plot type:
vertical line

Data3
 NULL
 Upload

Upload data3: [?](#)

[Browse...](#) data6_track2_line.txt
Upload complete

[View example data](#) [Example data](#)

Track index: [?](#)

track2

Plot type:
line

Data4
 NULL
 Upload

Upload data4: [?](#)

[Browse...](#) data10_track2_horizontal_line.t
Upload complete

[View example data](#) [Example data](#)

Track index: [?](#)

track2

Plot type:
horizontal line

Data format

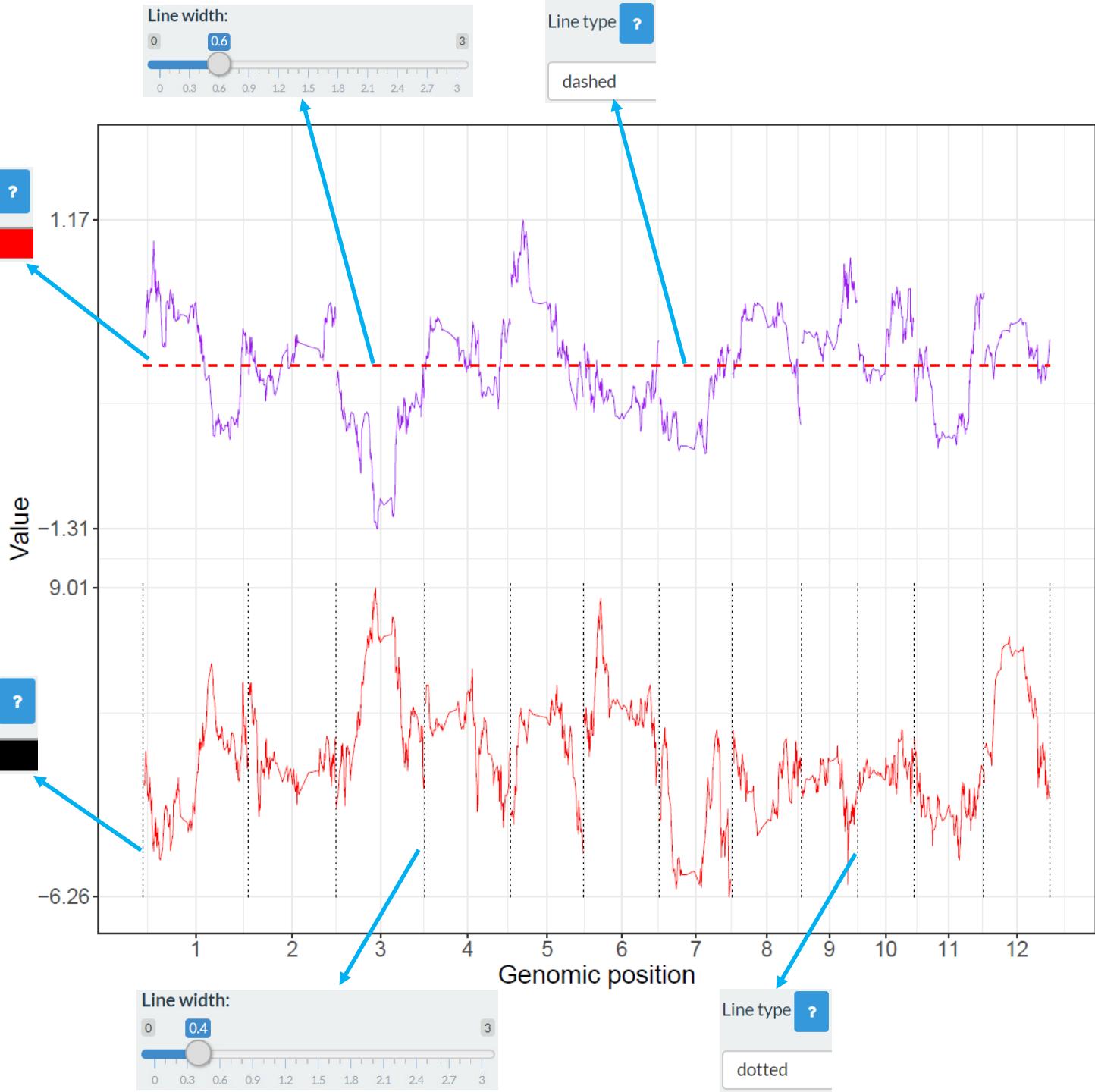
example_12/data5_track1_vertical_line.txt

chr	position
1	0
1	43268879
2	35930381
3	36406689

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 of the horizontal lines.



Line type legend ?

Show

Legend title: ?

linetype

Modify legend labels ?

Yes

dashed

linetype

- - dashed

Line type legend ?

Show

Legend title: ?

linetype

Modify legend labels ?

Yes

dotted

2.2 Non-circular two genomes plots

Non-circular plots for two genomes

shinyChromosome About Input data format Single genome plot Two genomes plot Gallery Help Manual 1.5 Download figures and scripts

*Upload genome1 data: ?

Browse... genome1_data.txt Upload complete

View example data Example data

*Upload genome2 data: ?

Browse... genome2_data.txt Upload complete

View example data Example data

1.1

*Upload main plot data: ?

Browse... plot_data_point_gradual.txt Upload complete

View example data Example data

1.2

Plot type:

point_gradual

Show Advanced Options

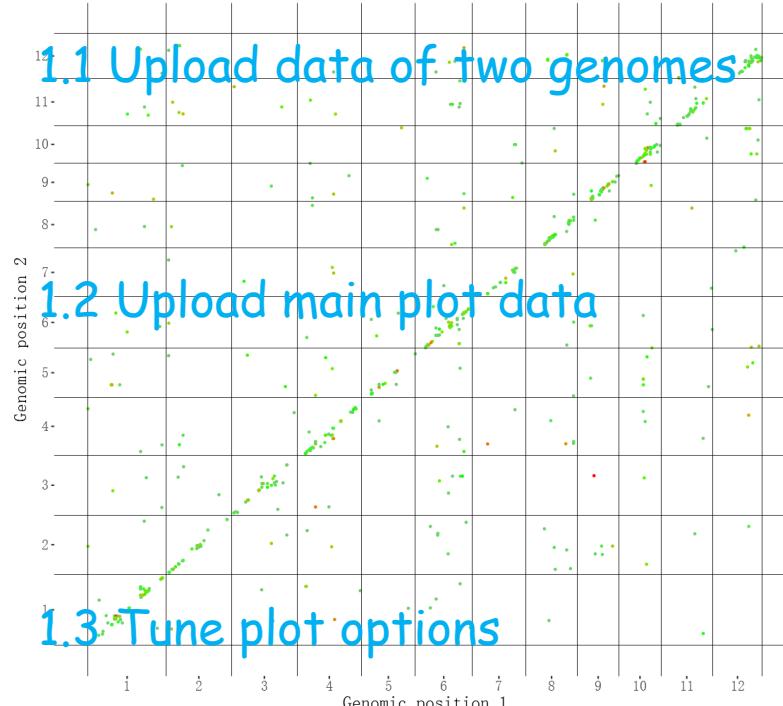
Go!

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 main 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 Input data format Single genome plot Two genomes plot Gallery Help Manual

*Upload genome1 data: ?

Browse...

No file selected



Download pdf-file

Download svg-file

Download the R scripts to reproduce the plot

View example data

Example data

*Upload genome2 data: ?

Browse...

No file selected



View example data

Example data

*Upload main plot data: ?

Browse...

No file selected

View example data

Example data

Plot type:

point_gradual

Data of genome 1 along the X-axis.

Data of genome 2 along the Y-axis.

Data format

chr	size
Chr 01	41185095
Chr 02	34608401
Chr 03	37032663
Chr 04	32359471
Chr 05	29068426

- Genome data is simple definition of chromosome lengths, which include two columns as chromosome IDs and chromosome lengths.

Upload point_gradual data

shinyChromosome About Input data format Single genome plot Two genomes plot Gallery Help Manual

*Upload genome1 data: ?

Browse... No file selected

[View example data](#) [Download example data](#)

*Upload genome2 data: ?

Browse... No file selected

[View example data](#) [Download example data](#)

*Upload main plot data: ?

Browse... No file selected

[View example data](#) [Download example data](#)

Plot type:

point_gradual ▾

Click "Browse" to upload input file

Set plot type as "point_gradual"

Options

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

Show 

Vertical line color:  The color used for the vertical line.

#000000 

Vertical line width:  Line width of the vertical line.

0  0.2 3

Vertical line type  Line type of the vertical line.

solid 

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

Show 

Horizontal line color:  The color used for the horizontal line.

#000000 

Horizontal line width:  Line width of the horizontal line.

0  0.2 3

Horizontal line type  Line type of the horizontal line.

solid 

- See section 2.1.1 for more plot options.

Example 1

shinyChromosome About Input data format Single genome plot Two genomes plot Gallery Help Manual

*Upload genome1 data: [?](#)

Browse... genome1_data.txt
Upload complete

[View example data](#) [Download example data](#)

*Upload genome2 data: [?](#)

Browse... genome2_data.txt
Upload complete

[View example data](#) [Download example data](#)

*Upload main plot data: [?](#)

Browse... plot_data_point_gradual.txt
Upload complete

[View example data](#) [Download example data](#)

Plot type:

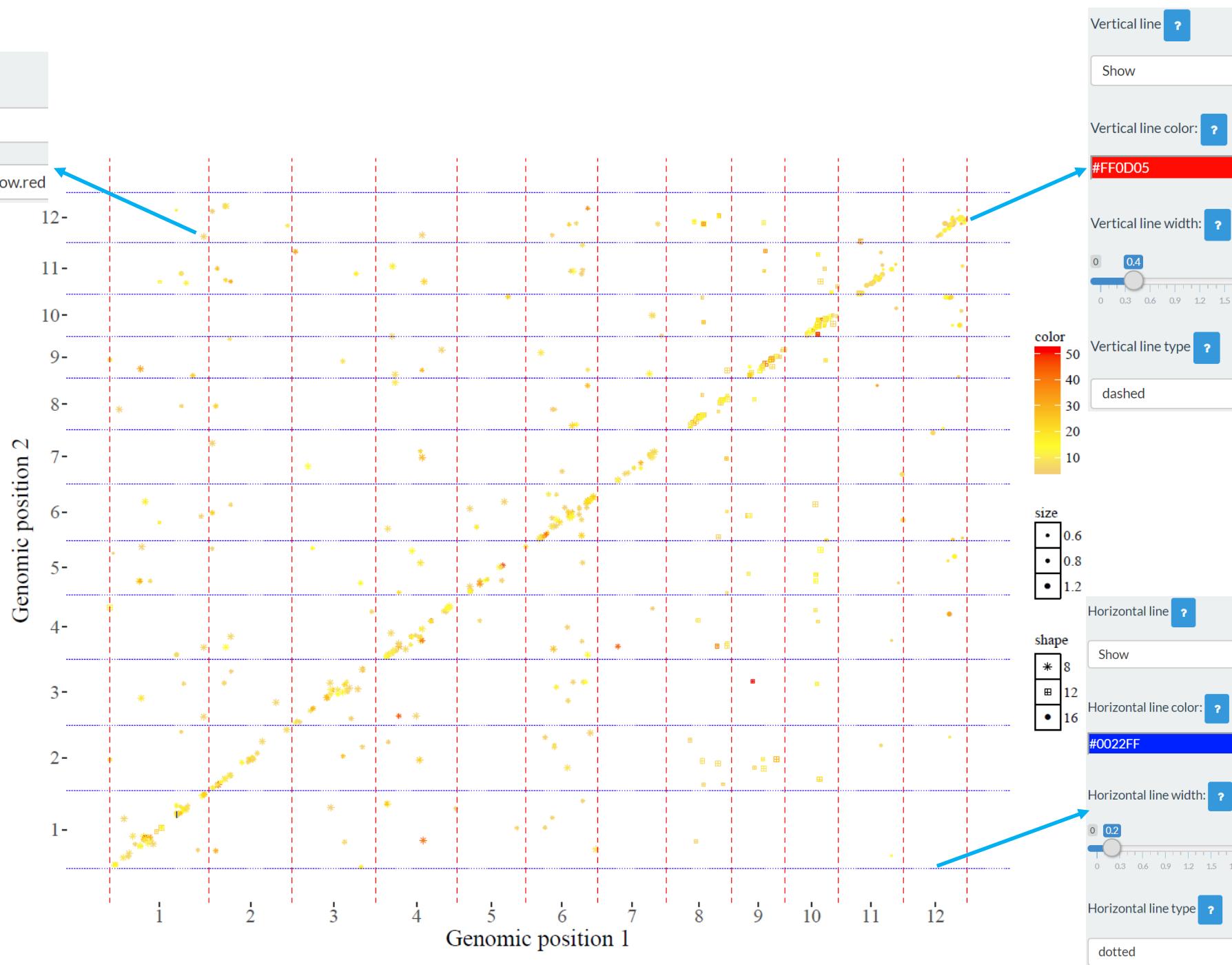
[Download pdf-file](#) [Download svg-file](#) [Download the R scripts to reproduce the plot](#)

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" should be fixed.



2.2.2 Plot point_discrete

Upload point_discrete data

*Upload genome1 data: ?

Browse... genome1_data.txt
Upload complete

View example data Example data

*Upload genome2 data: ?

Browse... genome2_data.txt
Upload complete

View example data Example data

*Upload main plot data: ?

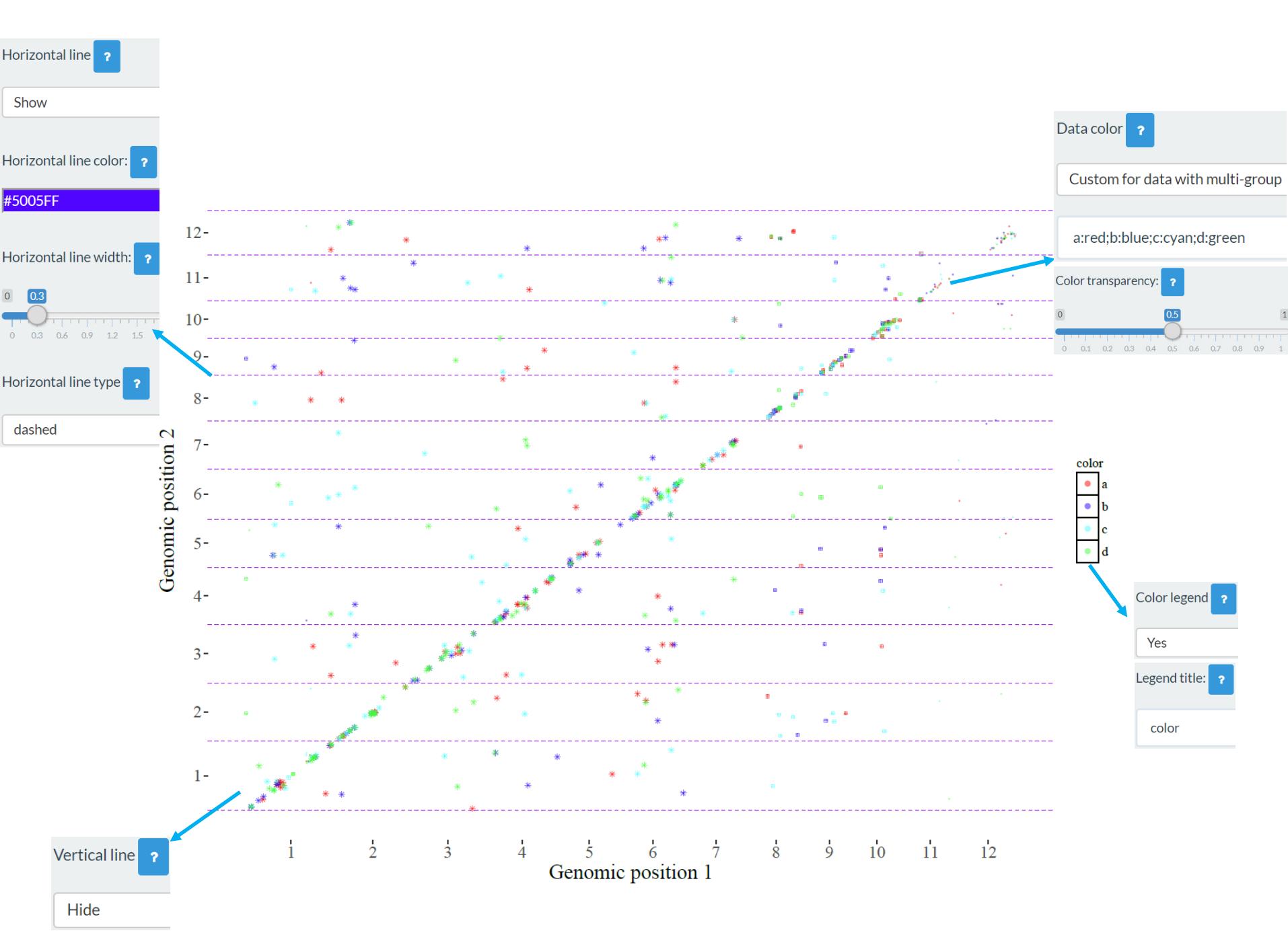
Browse... plot_data_point_discrete.txt
Upload complete

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" should be fixed.



2.2.3 Plot segment

Upload segment data

*Upload genome1 data: ?

Browse... genome1_data.txt
Upload complete

[View example data](#) [Example data](#)

*Upload genome2 data: ?

Browse... genome2_data.txt
Upload complete

[View example data](#) [Example data](#)

*Upload main plot data: ?

Browse... plot_data_segment.txt
Upload complete

[View example data](#) [Example data](#)

Plot type:

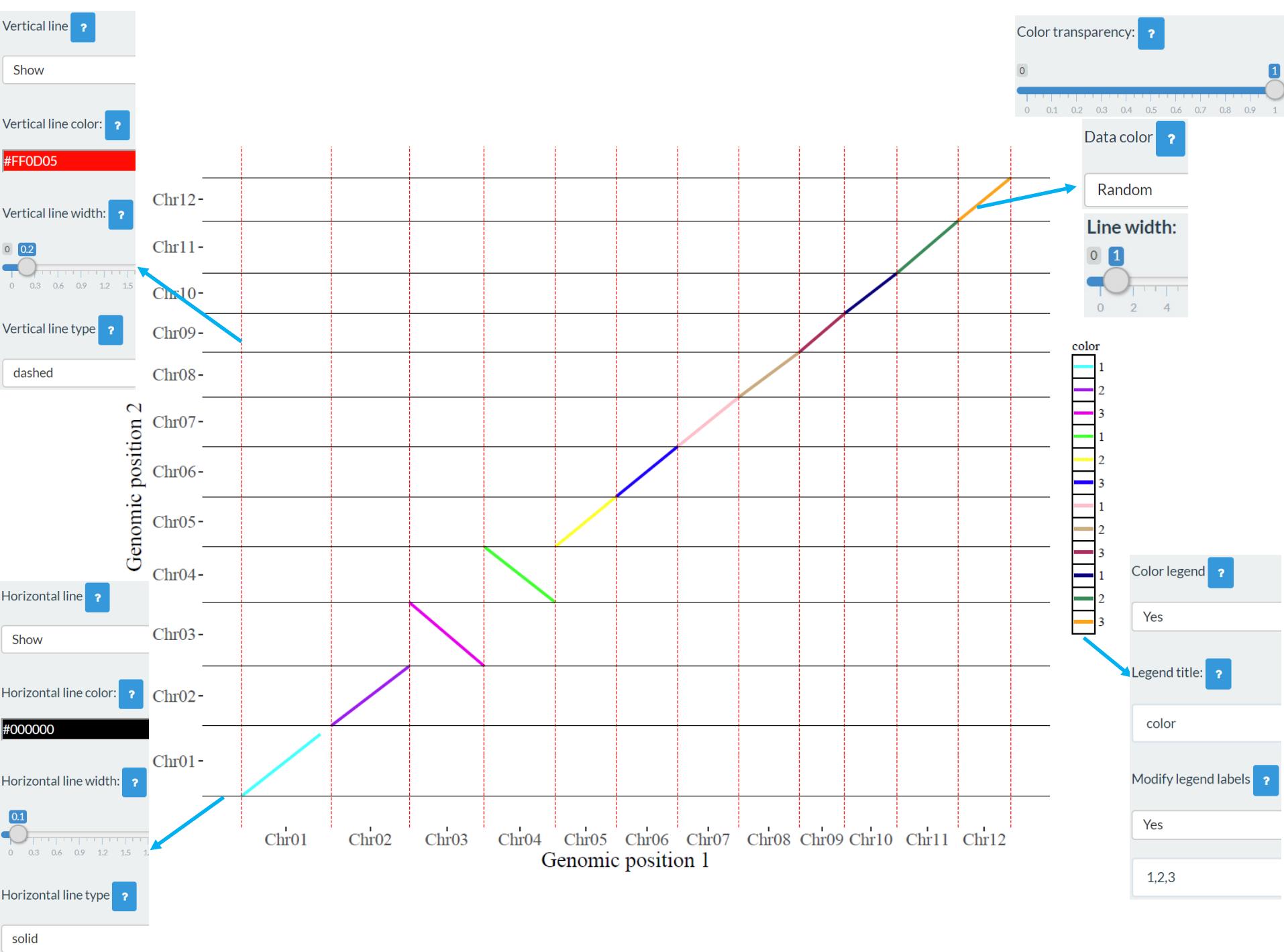
segment

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**.



2.2.4 Plot rect_gradual

Upload rect_gradual data

*Upload genome1 data: ?

Browse... genome1_data.txt
Upload complete

[View example data](#) [Example data](#)

*Upload genome2 data: ?

Browse... genome2_data.txt
Upload complete

[View example data](#) [Example data](#)

*Upload main plot data: ?

Browse... plot_data_rect_gradual.txt
Upload complete

[View example data](#) [Example data](#)

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

Vertical line color: ?

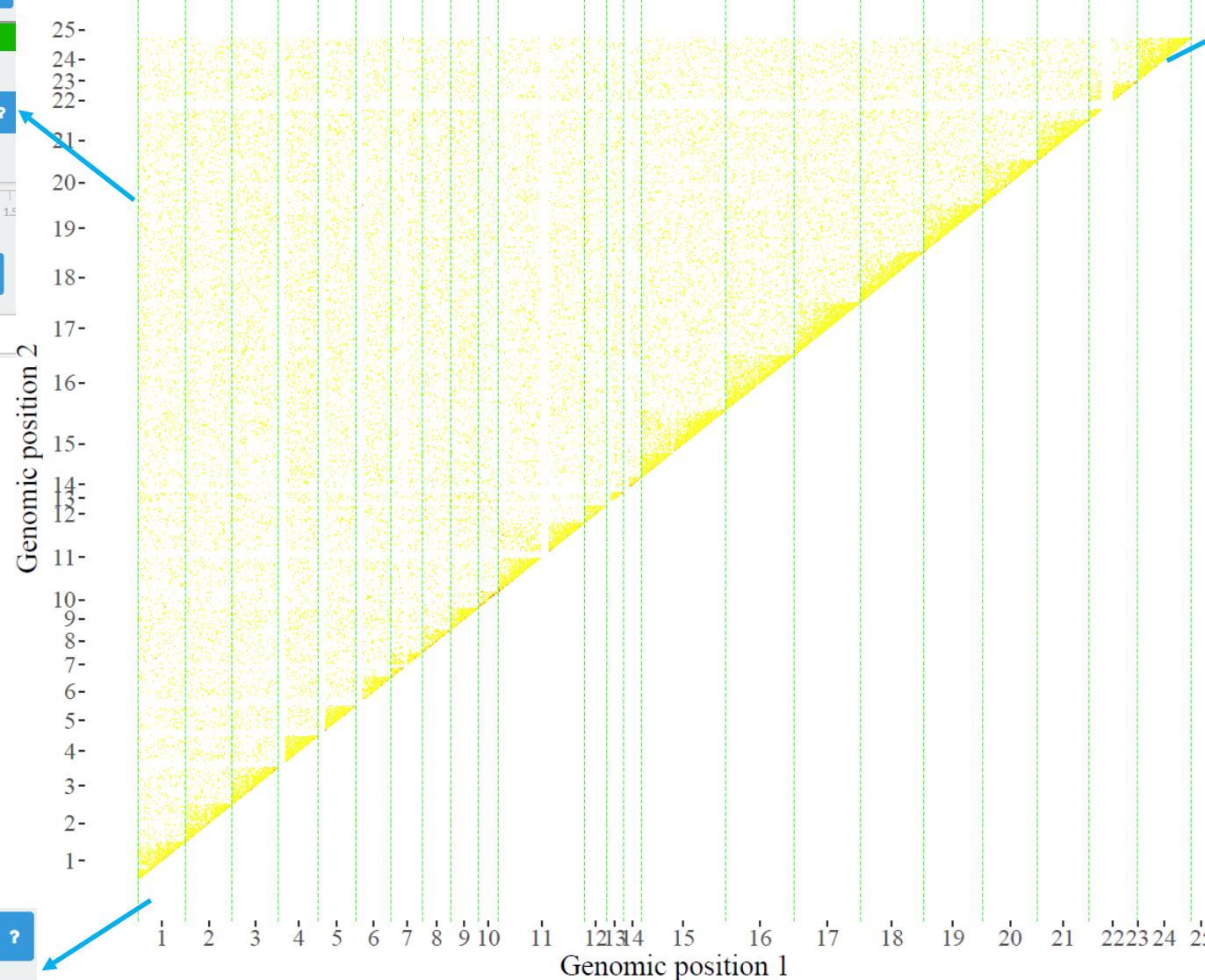
#12B800

Vertical line width: ?

0 0.2

Vertical line type: ?

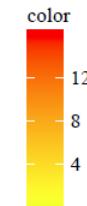
dashed



Colors ?

Typical

green.yellow.red



Color legend ?

Yes

Legend title: ?

color

Horizontal line ?

Hide

2.2.5 Plot rect_discrete

Upload rect_discrete data

*Upload genome1 data: ?

Browse... genome1_data.txt
Upload complete

[View example data](#) [Example data](#)

*Upload genome2 data: ?

Browse... genome2_data.txt
Upload complete

[View example data](#) [Example data](#)

*Upload main plot data: ?

Browse... plot_data_rect_discrete.txt
Upload complete

[View example data](#) [Example data](#)

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

Vertical line color: ?

#000000

Vertical line width: ?

0 0.2

Vertical line type ?

solid

Horizontal line ?

Show

Horizontal line color: ?

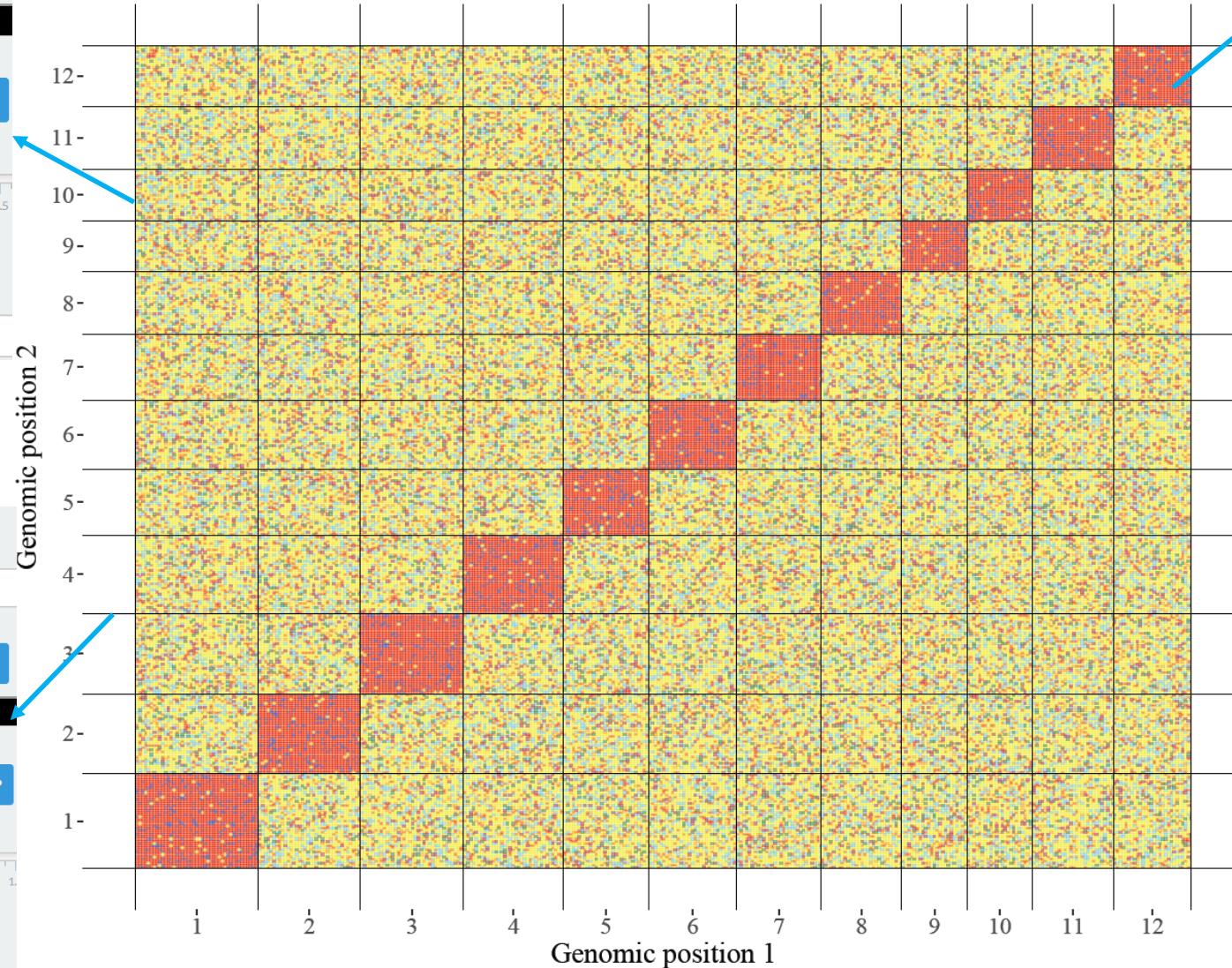
#000000

Horizontal line width: ?

0 0.2

Horizontal line type ?

solid



Data color ?

Random

Color transparency: ?

0 0.5

color
a
b
c
d
e
f
g

Color legend ?

Yes

Legend title: ?

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

*Chromosome orientation [?](#)

- Horizontal
- Vertical

*Upload genome data [?](#)

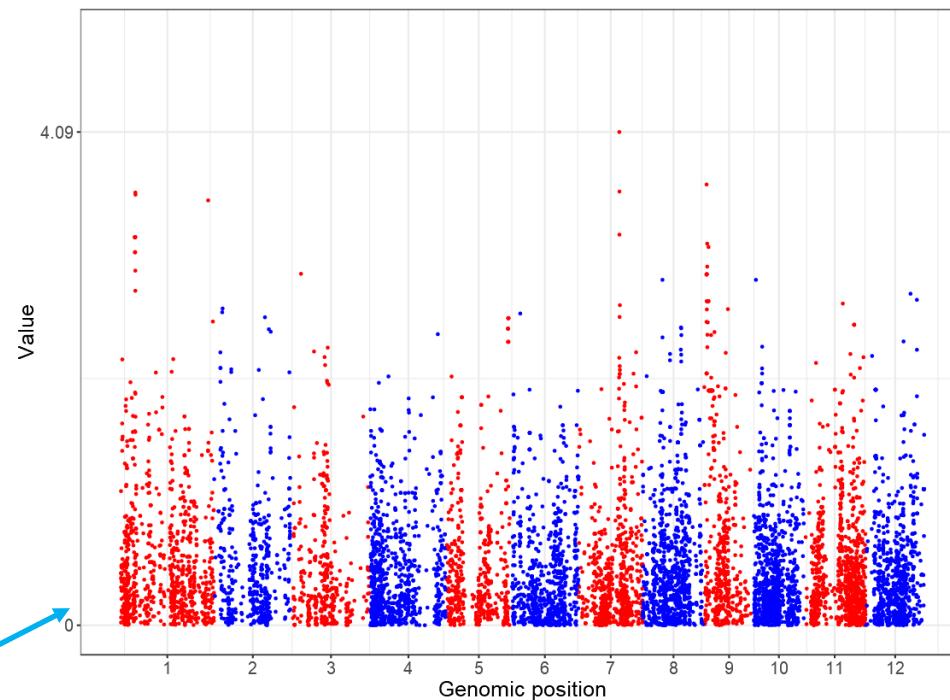
Browse... genome_data.txt
Upload complete

[View example data](#) [Download example data](#)

- 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](#)



Adjust plot size

Plot height:

550

Plot width:

750

*Image type [?](#)

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation [?](#)

- Horizontal
- Vertical

*Upload genome data [?](#)[Browse...](#) genome_data.txt

Upload complete

[View example data](#)[Download Example data](#)

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

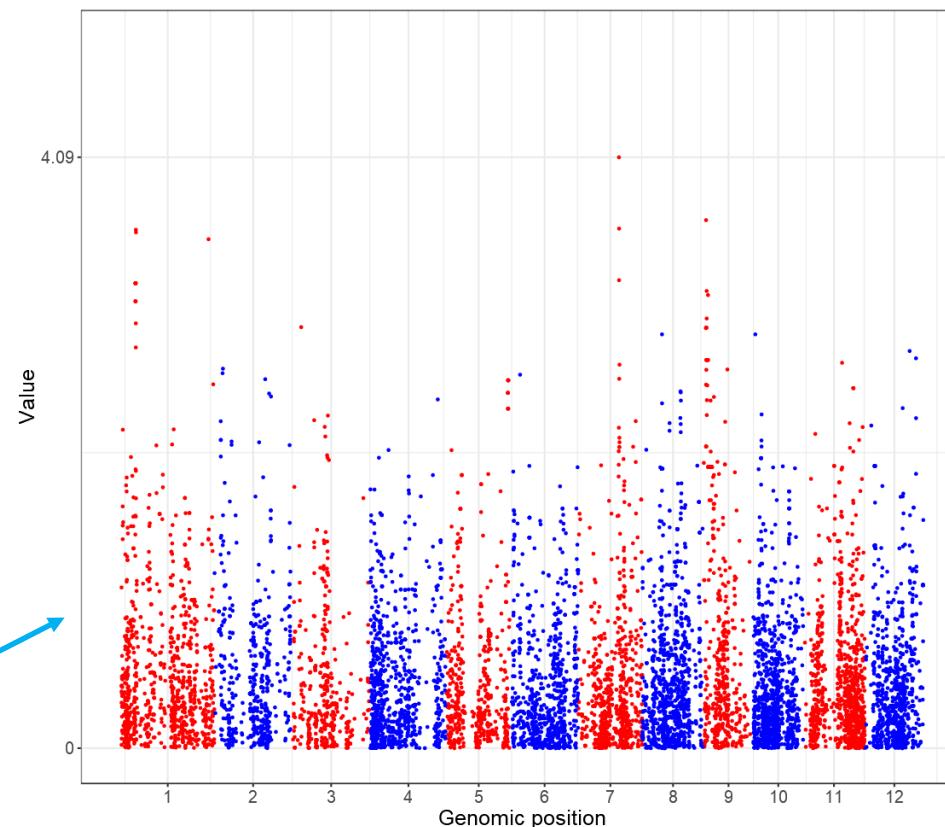
 Adjust plot size

Plot height:

650

Plot width:

750

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

3.2 Figure theme

Options

Plot options

Show Advanced Options ▾

Adjust plot size

Figure theme

theme1 ▾

Font size

Axis title

X axis label

Legend

Select a theme for the plot.

*Image type [?](#)

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation [?](#)

- Horizontal
- Vertical

*Upload genome data [?](#)[Browse...](#) genome_data.txt

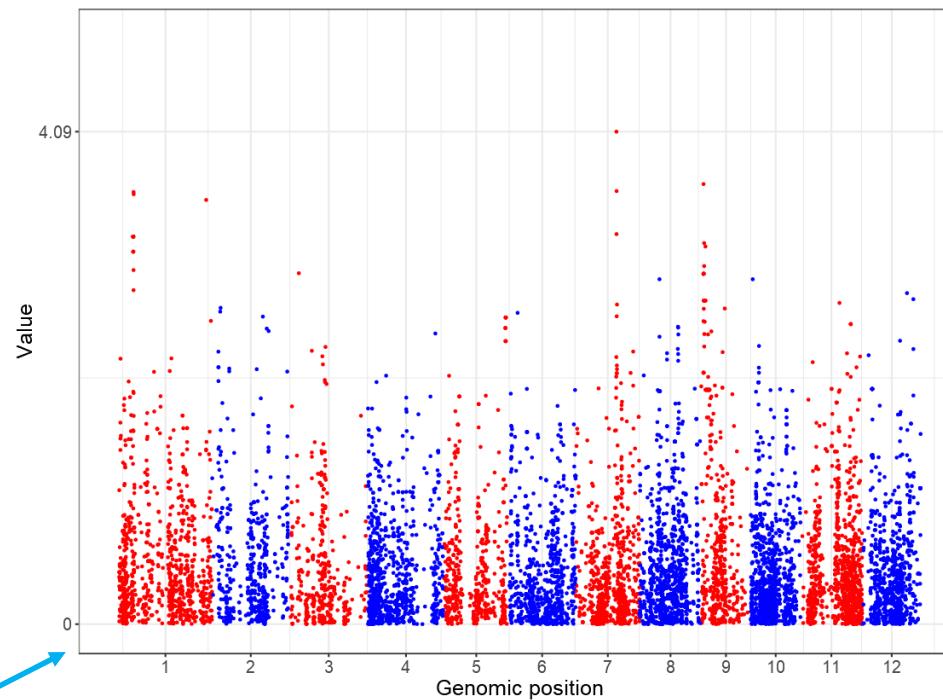
Upload complete

[View example data](#)[Download Example data](#)

- 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

*Chromosome orientation ?

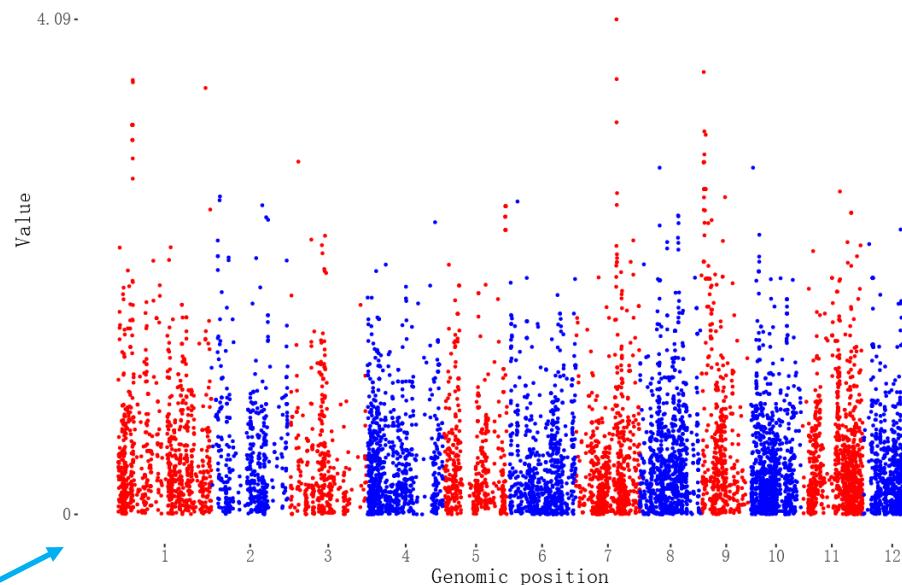
- Horizontal
- Vertical

*Upload genome data ?

Browse... Upload complete

View example data Download Example data

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

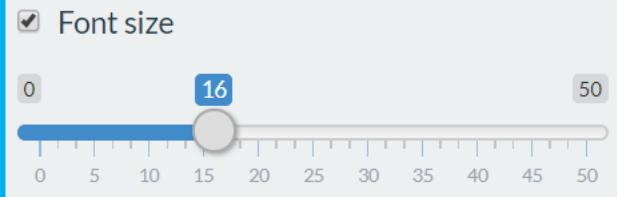
Figure themetheme6Go!Download pdf-file Download svg-file Download the R scripts to reproduce the plot

3.3 Font size

Options

Plot options

Show Advanced Options ▾

- Adjust plot size
- Figure theme
- Font size
 - 0
 - 15
 - 50
- Axis title
- X axis label
- Legend

Adjust font size used in the main plot.

*Image type [?](#)

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation [?](#)

- Horizontal
- Vertical

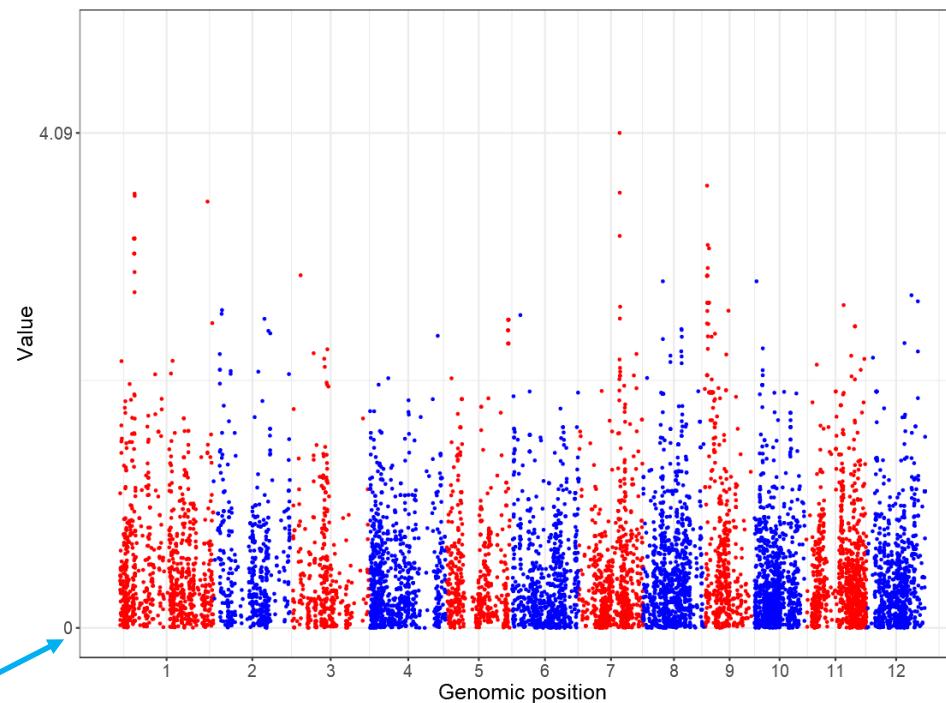
*Upload genome data [?](#)

Browse... genome_data.txt

Upload complete

[View example data](#)[Download Example data](#)

- 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](#)

Font size

0 16

0 5 10 15

Font size

0

16

0

5

10

15

0 16

0 5 10 15

0

16

0

5

10

15

*Image type ?

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation ?

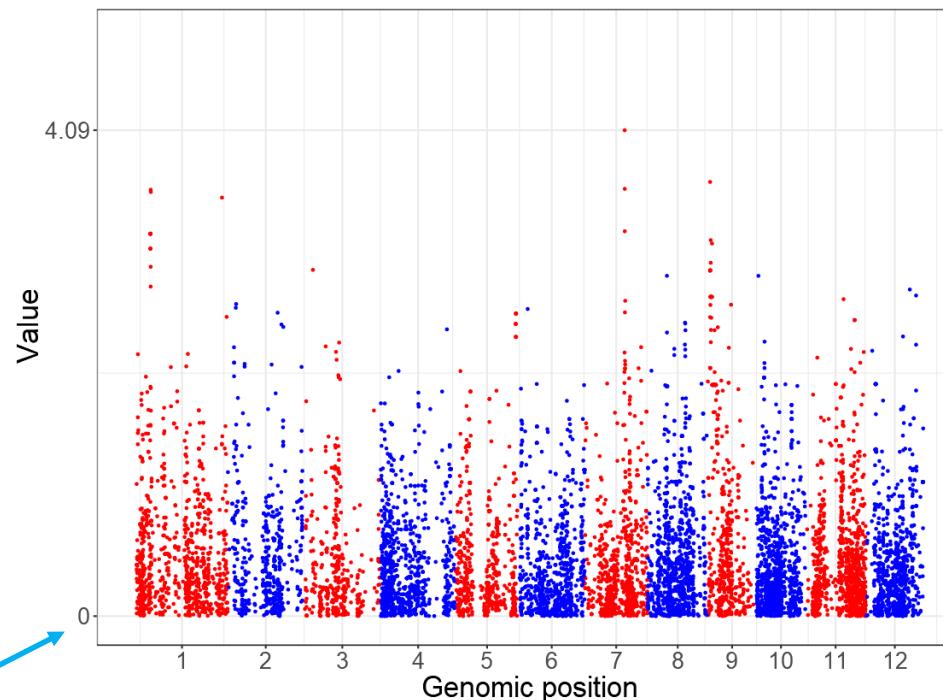
- Horizontal
- Vertical

*Upload genome data ? genome_data.txt

Upload complete

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

Font size
 22

? 

3.4 Axis title

Options

Plot options

Show Advanced Options ▾

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

X title:

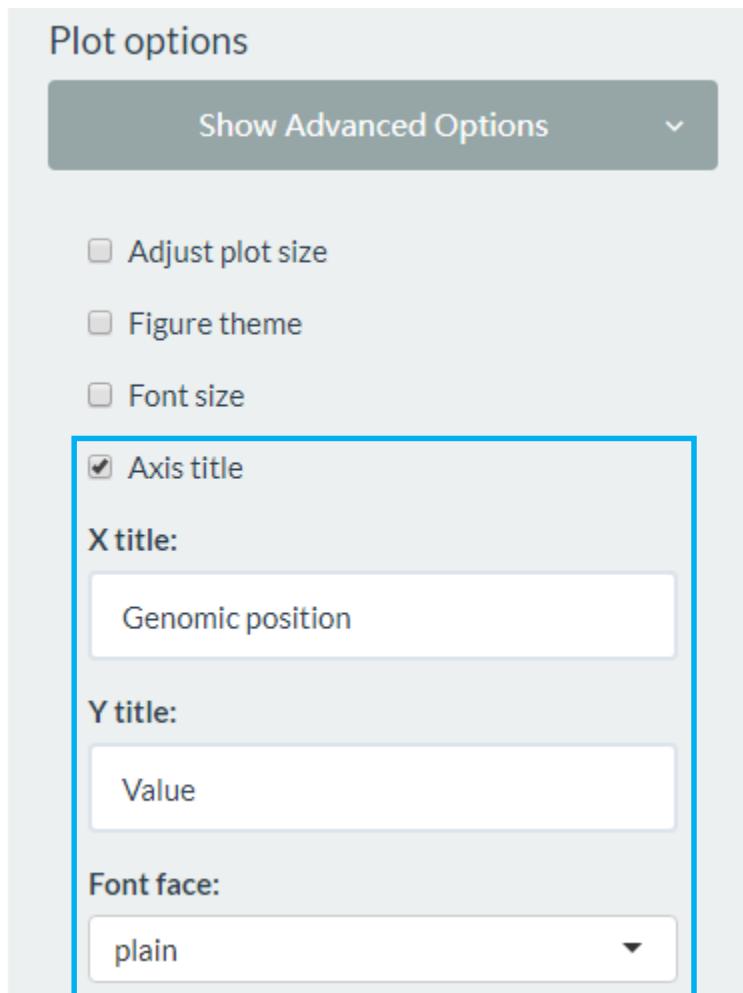
Genomic position

Y title:

Value

Font face:

plain ▾



The screenshot shows a 'Plot options' dialog with a 'Show Advanced Options' button. Under 'Advanced Options', there are four checkboxes: 'Adjust plot size', 'Figure theme', 'Font size', and 'Axis title'. The 'Axis title' checkbox is checked and highlighted with a blue border. Below it, there are fields for 'X title' (containing 'Genomic position') and 'Y title' (containing 'Value'). At the bottom, there is a 'Font face' dropdown menu set to 'plain'.

Modify axis title of non-circular plot.

Adjust font face of axis title.

*Image type [?](#)

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation [?](#)

- Horizontal
- Vertical

*Upload genome data [?](#)

Browse... genome_data.txt

Upload complete

[View example data](#)

[Download Example data](#)

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

Axis title

X title:
Genomic position

Y title:

Value

Font face:

plain

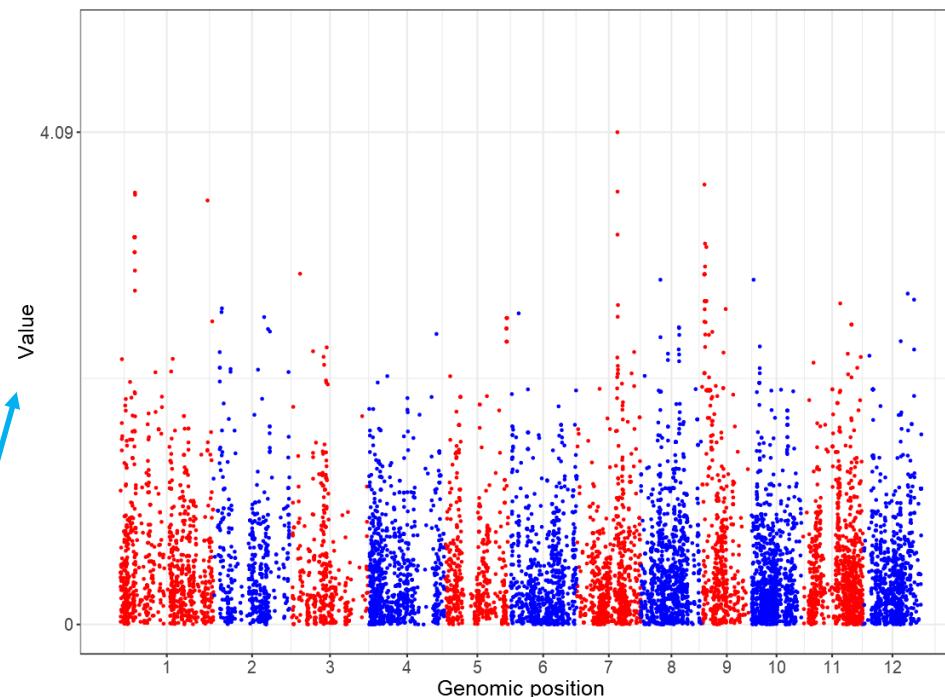
Go!

[?](#)

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*Image type [?](#)

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation [?](#)

- Horizontal
- Vertical

*Upload genome data [?](#)

Browse... genome_data.txt
Upload complete

[View example data](#)[Download example data](#)

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

 Axis title

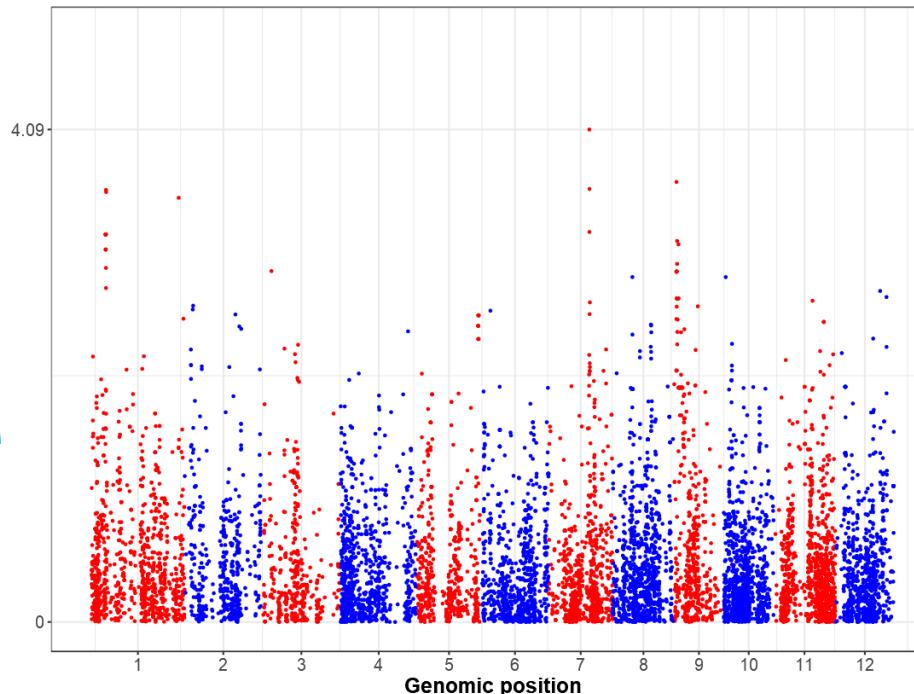
X title:

Genomic position

Y title:

Font face:

bold

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3.5 Axis label

Options

Single genome plot

Plot options

Show Advanced Options ▾

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

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

Two genomes plot

Plot options

- Adjust plot size
- Figure theme
- Font size
- Axis title
- Axis label
 - X axis label ?
 - Show ▾
 - Y axis label ?
 - Show ▾

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

*Image type ?

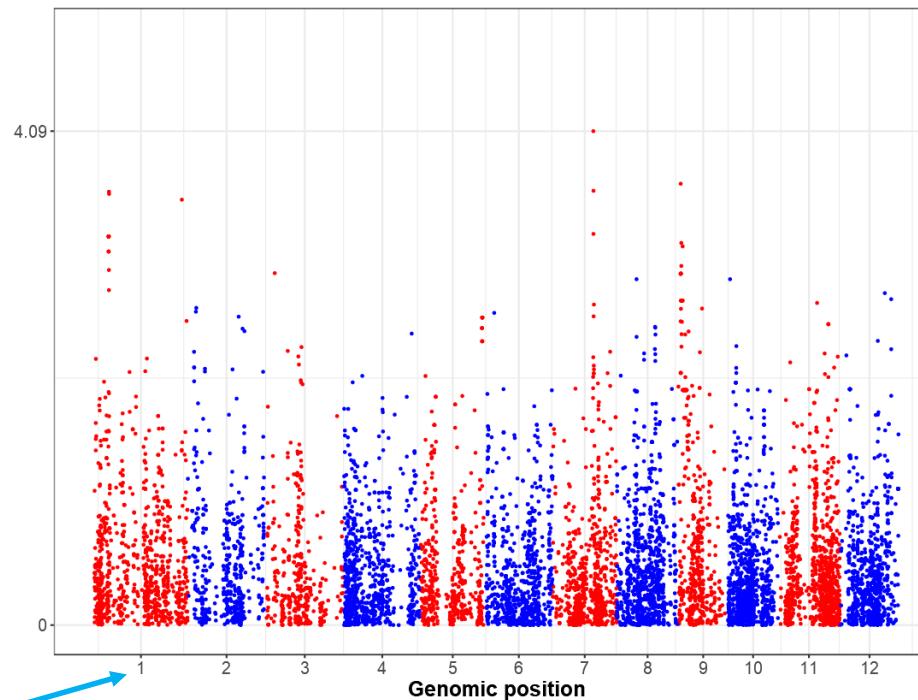
- Concatenated chromosome
- Separated chromosome

*Chromosome orientation ?

- Horizontal
- Vertical

*Upload genome data ?Browse... genome_data.txt
Upload completeView example dataDownload Example data

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

X axis labelShowGo!?Download pdf-file Download svg-file Download the R scripts to reproduce the plot

*Image type [?](#)

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation [?](#)

- Horizontal
- Vertical

*Upload genome data [?](#)

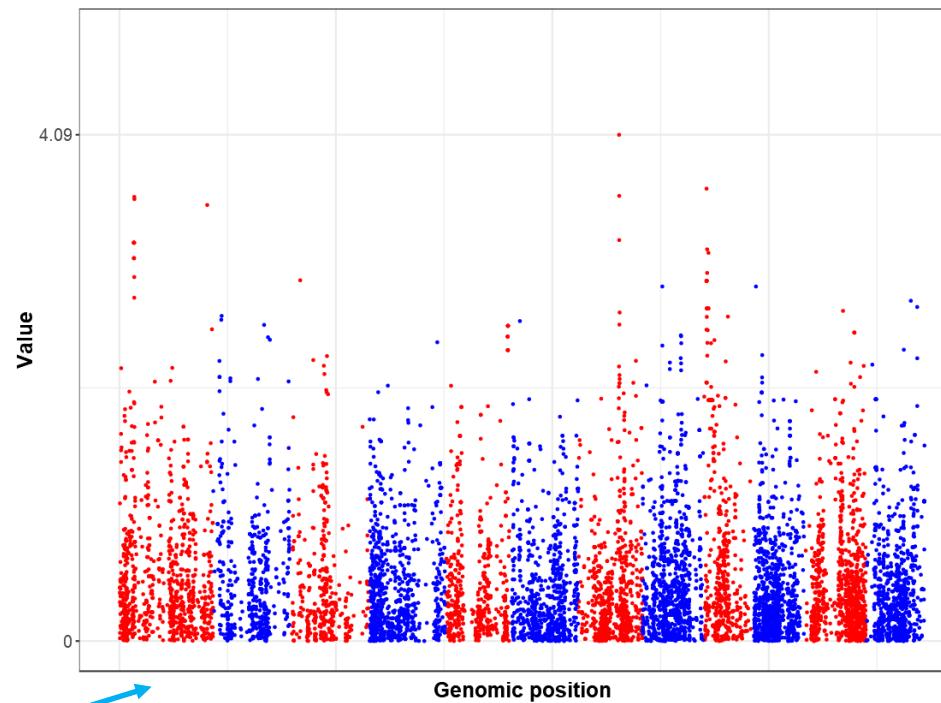
Browse... genome_data.txt

Upload complete

[View example data](#) [Download Example data](#)

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

Go! [?](#)

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X axis label

[Hide](#)

*Upload genome1 data: ?

Browse... genome1_data.txt Upload complete

View example data Example data

*Upload genome2 data: ?

Browse... genome2_data.txt Upload complete

View example data Example data

*Upload main plot data: ?

Browse... plot_data_point_gradual.txt Upload complete

View example data Example data

Plot type:

point_gradual

Show Advanced Options

Go! ?

Plot options

Adjust plot size

Figure theme

Font size

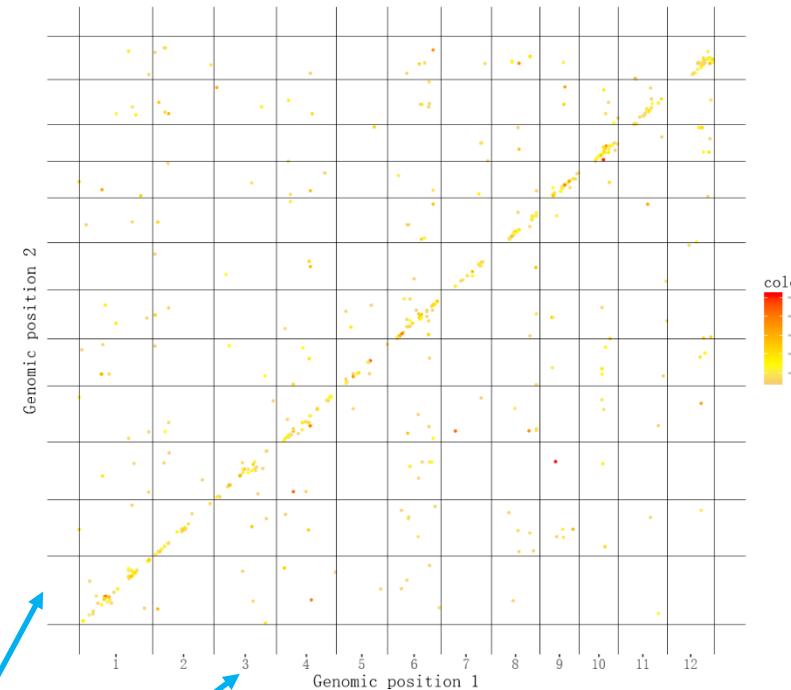
Axis title

Axis label

X axis label ? Show

Y axis label ? Hide

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3.6 Legend

Options

Plot options

Show Advanced Options ▾

Adjust plot size

Figure theme

Font size

Axis title

X axis label

Legend

Legend position 

Right 

Legend region size 



Intra-spacing 



Title font size 



Title font face: 

plain 

Label font size 



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 size of legend tick label.

The font face of legend tick label.

*Image type ?

- Concatenated chromosome
- Separated chromosome

*Chromosome orientation ?

- Horizontal
- Vertical

*Upload genome data ?

Browse... genome_data.txt Upload complete

[View example data](#) [Download example data](#)

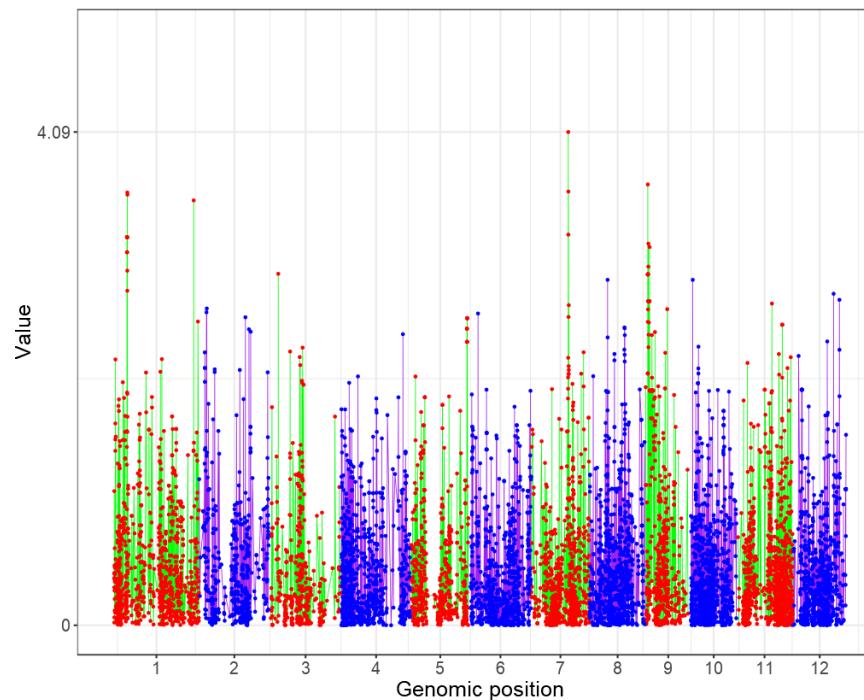
- Data1
- Data2
- Data3
- Data4
- Data5
- Data6
- Data7
- Data8
- Data9
- Data10

Go! ?

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Intra-spacing ?
0 15 30 45 60

color
● a
● b

Title font size ?
0 4 8 12 16
Title font face: plain

size
● 0.8

Label font size ?
0 4 8 12 16
Label font face: plain

Legend position ?
Right
Legend region size ?
0.04

*Image type [?](#)

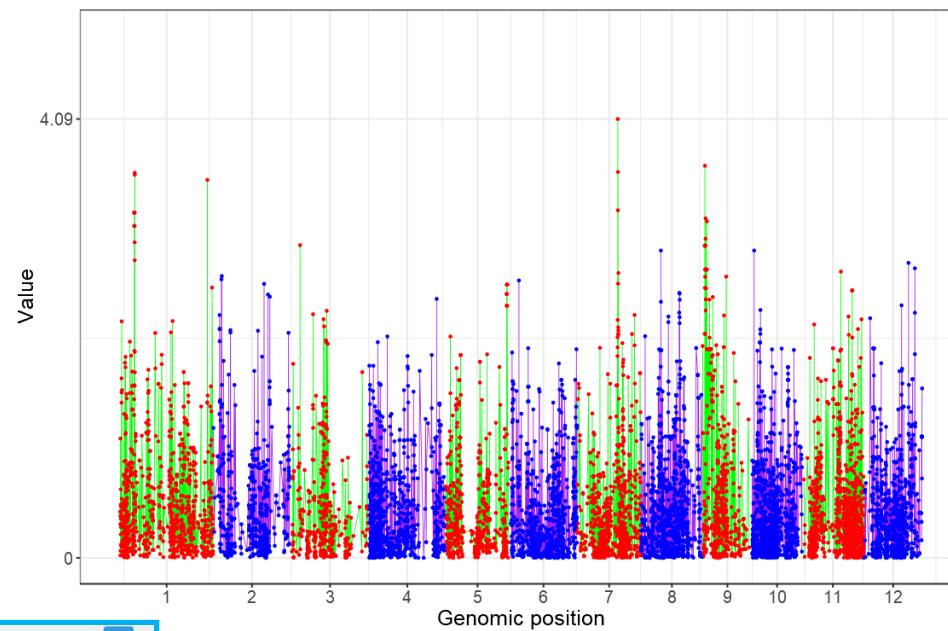
- Concatenated chromosome
- Separated chromosome

*Chromosome orientation [?](#)

- Horizontal
- Vertical

*Upload genome data [?](#)[Browse...](#) genome_data.txt

Upload complete

[View example data](#)[Download example data](#) 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](#)Legend position [?](#)

Bottom

Legend region size [?](#)

0.06



color

a

b

color

●

a

b

size

•

0.8

symbol

•

16

Title font size [?](#)

14

0

4

8

12

16

Title font face: [?](#)

bold

Label font size [?](#)

12

0

4

8

12

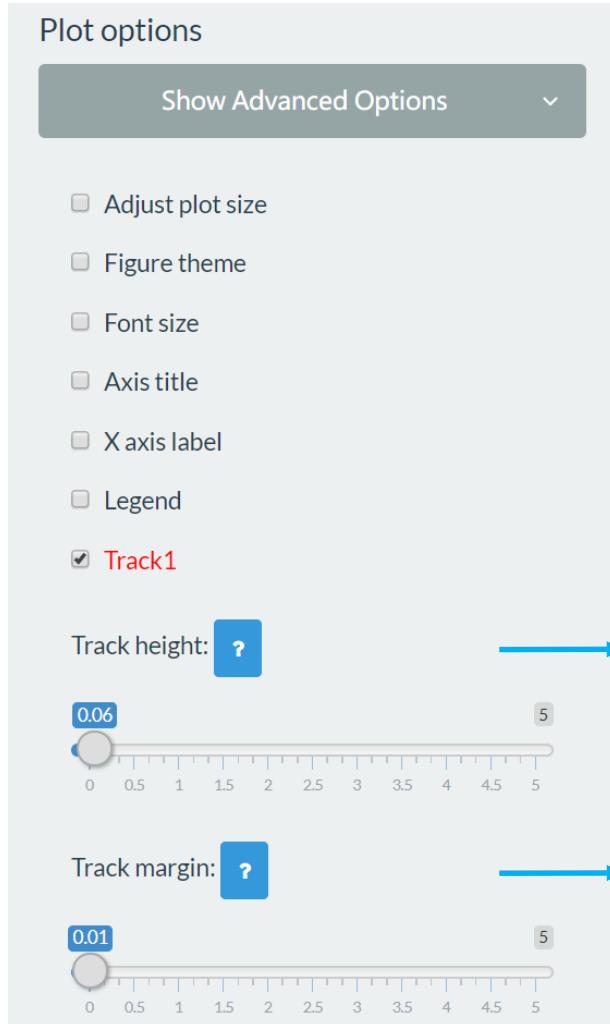
16

Label font face: [?](#)

italic

3.8 Height and width of different tracks

Options



Height of the track in single genome plot.

Margin of the track in single genome plot.

- These options are only available for single genome plot.

*Image type ?

Concatenated chromosome

Separated chromosome

*Chromosome orientation

Horizontal

Vertical

*Upload genome data ?

Browse... genome_data

Upload completed

View example data

Download pdf-file

Download svg-file

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Data1

Data2

Data3

Data4

Data5

Data6

Data7

Data8

Data9

Data10

Track margin: ?

0 0.5 1 1.5 2

Track height: ?

0.03 0 0.5 1 1.5 1.5

Track margin: ?

0.01 0 0.5 1 1.5 2

Track height: ?

0.06 0 0.5 1 1.5 2

Value

4.09

0

1 2 3 4 5 6 7 8 9 10 11 12

Genomic position

Track2

Track1