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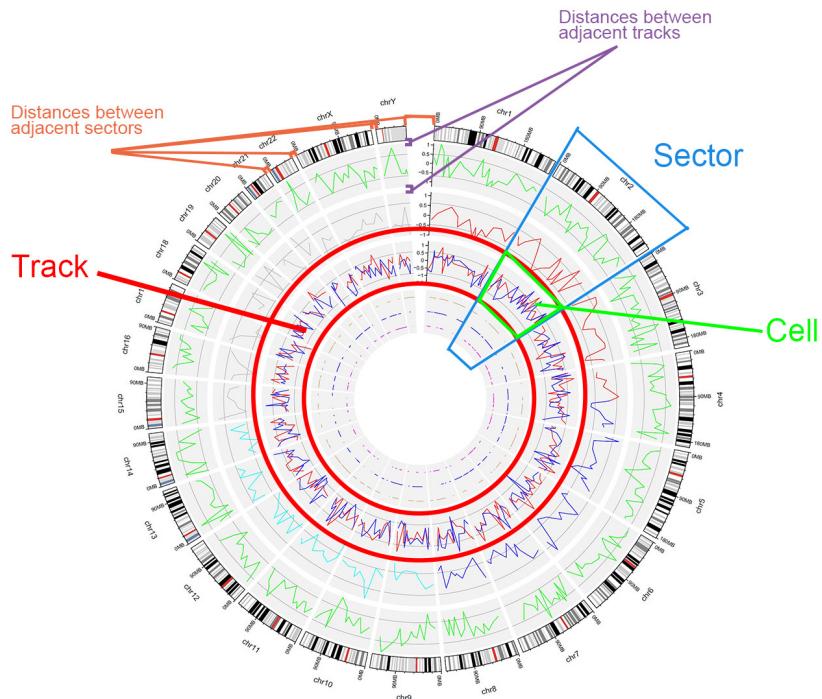
1.Introduction

shinyCircos-V2.0 is an R/shiny application for interactively creating Circos diagrams.

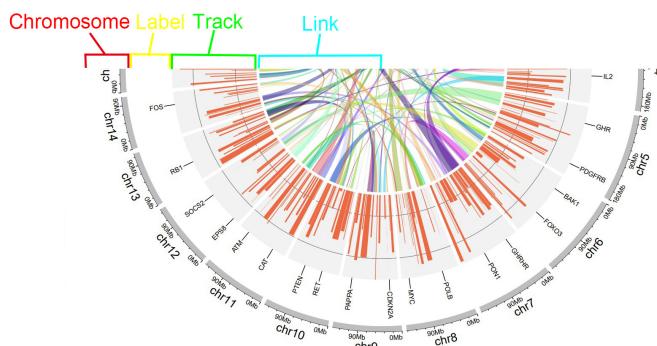
Source code:<https://github.com/YaoLab-Bioinfo/shinyCircos-V2.0>
Use online:<https://venyao.xyz/shinyCircos2.0/>
contact:gentelmanwang@gmail.com or yaowen@henau.edu.cn

shinyCircos-V2.0 is the latest version of [shinyCircos](#). In this version, we have made bold improvements. By sorting out user feedback, we have fixed bugs in the old version, added some useful functions, and used new logic. Now shinyCircos-V2.0 will be one of the best tools for drawing Circos diagrams.

Before using shinyCircos-V2.0, we need to understand the structure of Circos, please read carefully and remember the names of each part of the image, which will help you continue to read and understand the help manual



The structure of a Circos diagram



Track type of Circos diagram(track mean ring here)

2. Input data format

If you are new to shinyCircos-V2.0, then I suggest you read the input data format description carefully, otherwise unknown errors may occur.

We recommend that you upload the file in ".csv" format to shinyCircos-V2.0, because compared with other text files, ".csv" file has a clear standard and is not easy to cause problems when reading. It is worth mentioning that **column names are very important for shinyCircos-V2.0**, and then I will show in detail the different formats of different input data.

2.1 chromosome data

Chromosome data is an essential part of drawing, it determines different sectors without it shinyCircos-V2.0 will not be able to draw graphics. There are two formats of Chromosome data, general data and cell band data, and their formats are different.

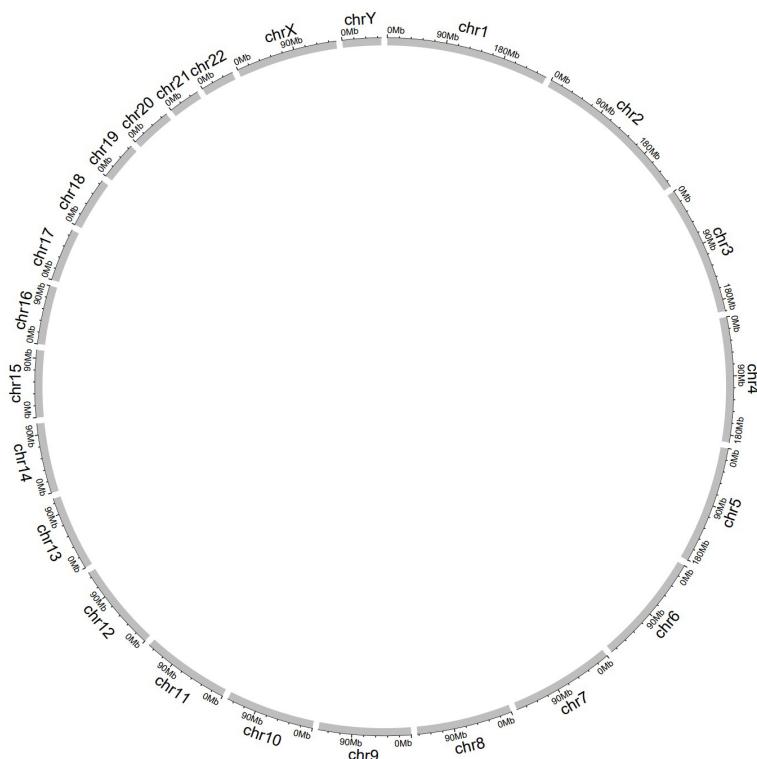
2.1.1 general data

The general data contains three columns, namely chr, start, and end. As shown below:

chr	start	end
chr1	1	249250621
chr2	1	243199373
chr3	1	198022430
chr4	1	191154276
chr5	1	180915260
chr6	1	171115067

general data [↓](#)

When drawing ordinary data, the software will add a gray track by default for aesthetics.



Gray track when the input data is general data

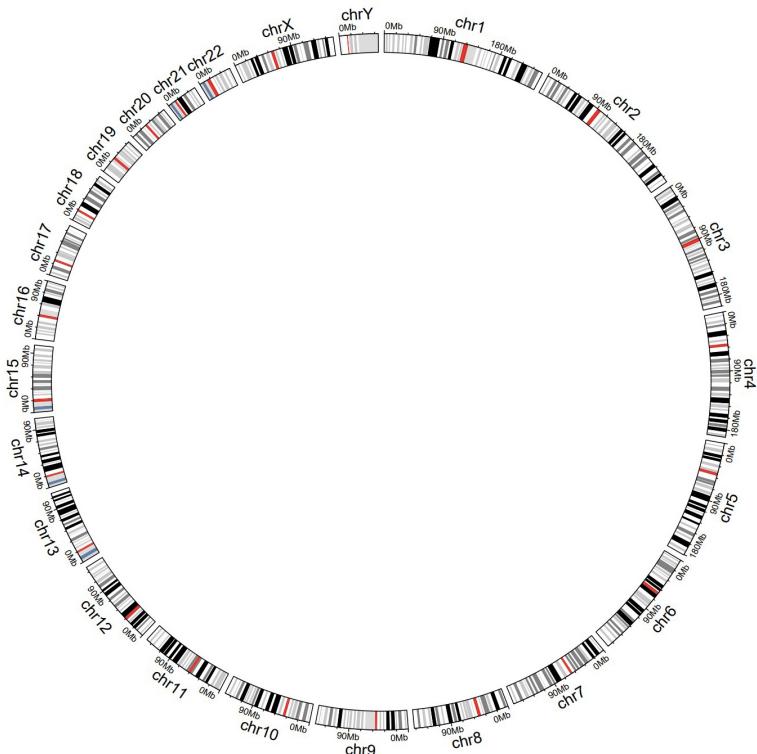
2.1.2 cytoband data

The cytoband data contains five columns, namely chr, start, end, value1, and value2, as shown in the following figure:

chr	start	end	value1	value2
chr1	1	2300000	p36.33	gneg
chr1	2300000	5400000	p36.32	gpos25
chr1	5400000	7200000	p36.31	gneg
chr1	7200000	9200000	p36.23	gpos25
chr1	9200000	12700000	p36.22	gneg
chr1	12700000	16200000	p36.21	gpos50

cytoband data ↴

An Ideogram track will be added when cytoband data is drawn.



Ideogram track when the input data is cytoband data

2.2 track data

Track data is used to draw different Tracks in the Circos diagram. Different types of Tracks often have different input formats, but the first three columns of the data are fixed, namely chr, strat, and end. The different types of Track data will be shown next.

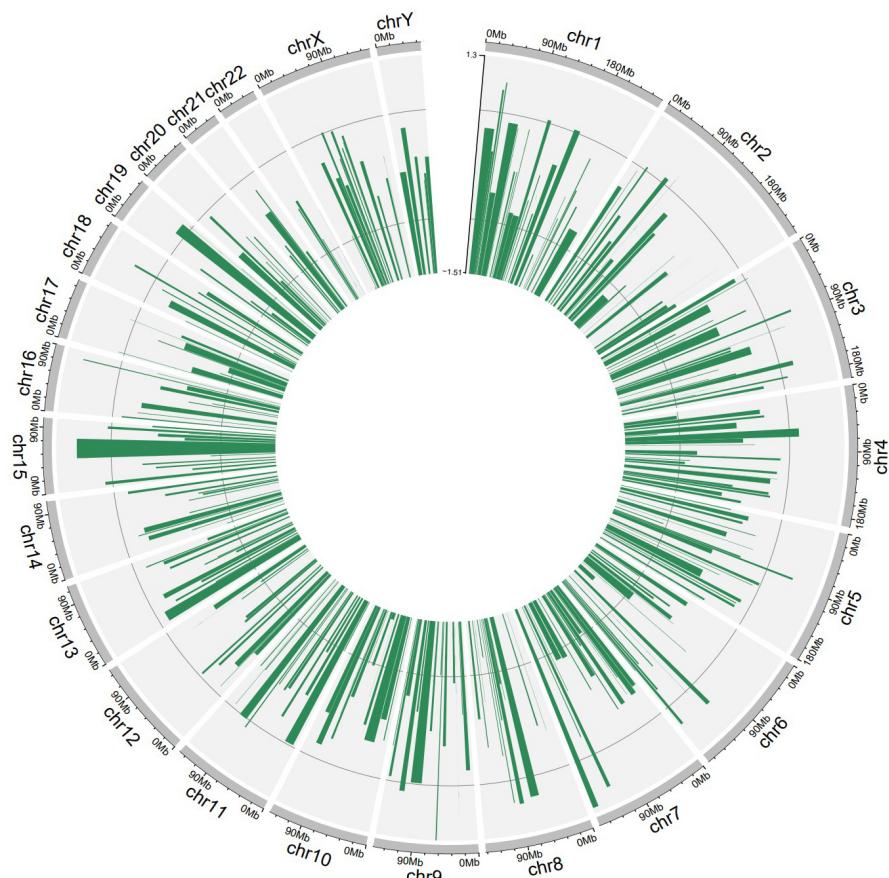
2.2.1 bar

The data used to draw the column chart should have at least four columns, namely chr, start, end and value. It is worth noting that the value of the fourth column can be positive or negative. There are two types of drawing for column charts. They are Unidirectional and Bidirectional respectively, and also supports adding another column of color classification values to the input data. The specific differences are explained below.

Unidirectional data can be used to draw a unidirectional column chart. The minimum value of the column is the minimum value of the value, which can be negative, that is, the starting point of the ordinate can be any value, as shown in the following figure:

chr	start	end	value
chr1	10382554	26901963	0.374
chr1	26901963	30511288	0.084
chr1	30956226	33621691	0.89
chr1	35113388	36674459	0.988
chr1	36674459	47502070	-0.441
chr1	48540858	64361678	0.484

Unidirectional bar data [↓](#)

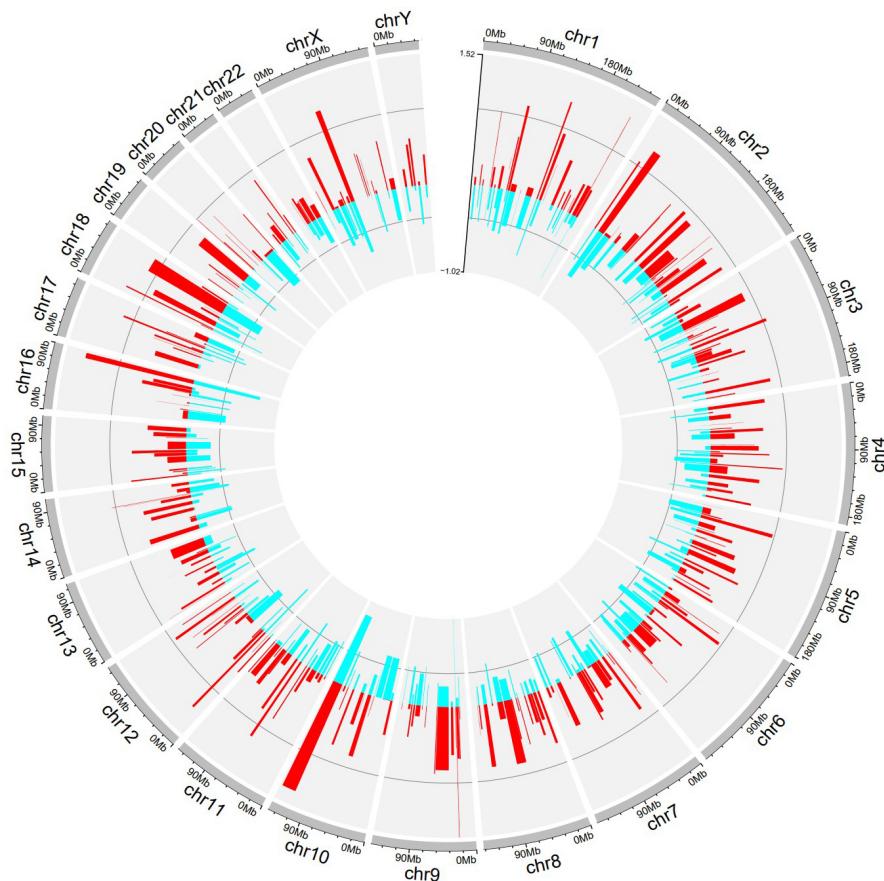


Unidirectional barplot

Bidirectional data is used to draw bidirectional histograms. Generally speaking, the same interval often has two values, and the columns are drawn from 0 by default, as shown in the following figure:

chr	start	end	value
chr1	5622039	9110831	0.095
chr1	5622039	9110831	-0.405
chr1	16816819	18551718	0.247
chr1	16816819	18551718	-0.253
chr1	22908603	24839868	0.077
chr1	22908603	24839868	-0.423

Bidirectional bar data [↓](#)

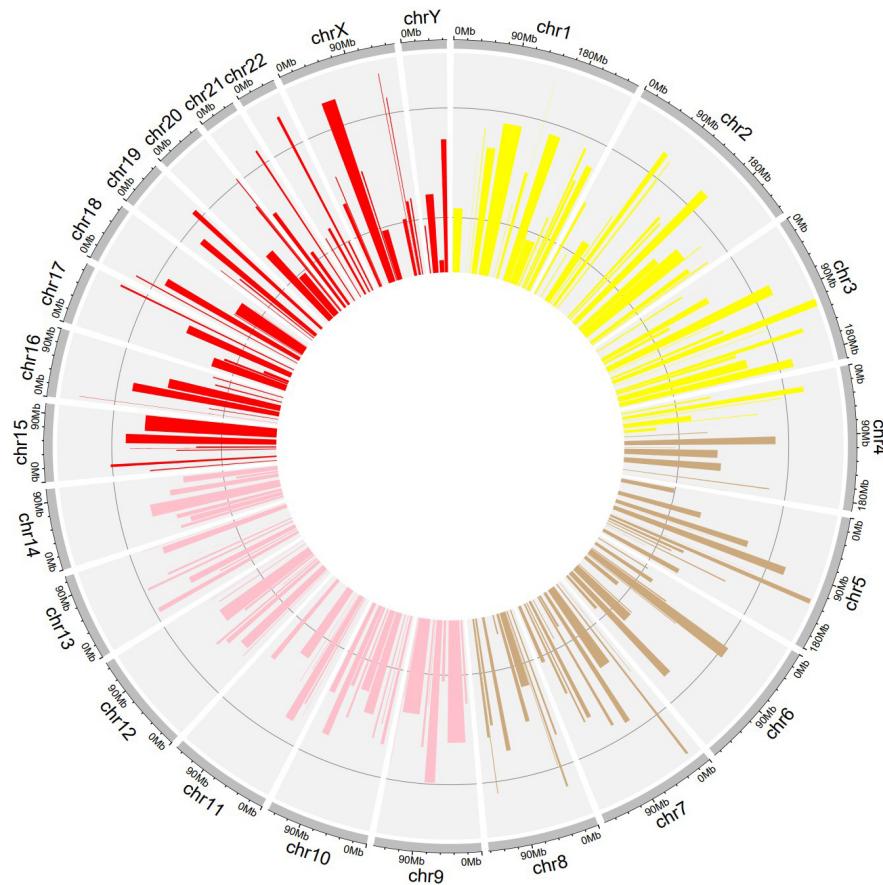


Bidirectional barplot

The color column represents the grouping of colors, such as a, b, c, d

chr	start	end	value	color
chr1	2321390	22775301	-0.52536	a
chr1	43812694	44287183	0.101162	a
chr1	52481565	53897427	0.372158	a
chr1	59354150	74860235	0.160938	a
chr1	81748375	1.12E+08	0.449661	a
chr1	1.27E+08	1.28E+08	-0.38463	a

barplot data with color columns ↴



barplot with color controlled by color column

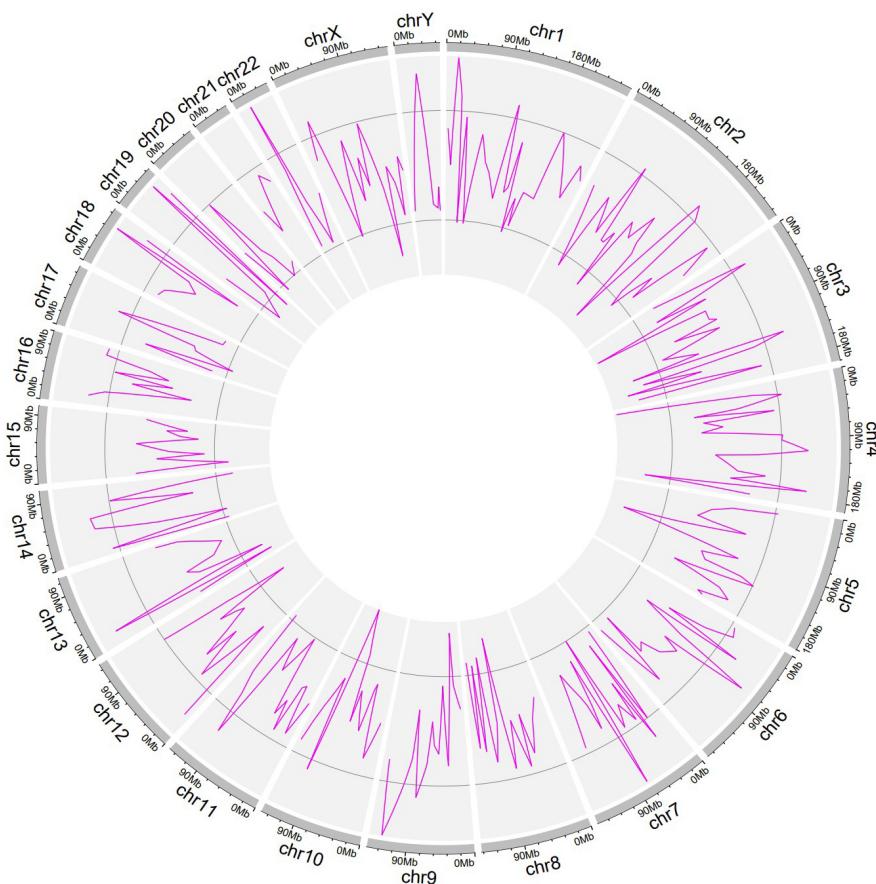
2.2.2 line

The data for drawing line chart should contain at least four columns, in addition to which other columns can be added to enrich the drawing of the line chart.

Standard line data should contain four columns, chr, start, end and value1, as shown in the following figure:

chr	start	end	value1
chr1	788538	5571920	0.309
chr1	6704086	10962288	-0.075
chr1	13517030	19064946	1.068
chr1	21370275	25642500	0.659
chr1	26160174	27950076	-0.688
chr1	29974329	36789688	0.44

Standard line data ↴

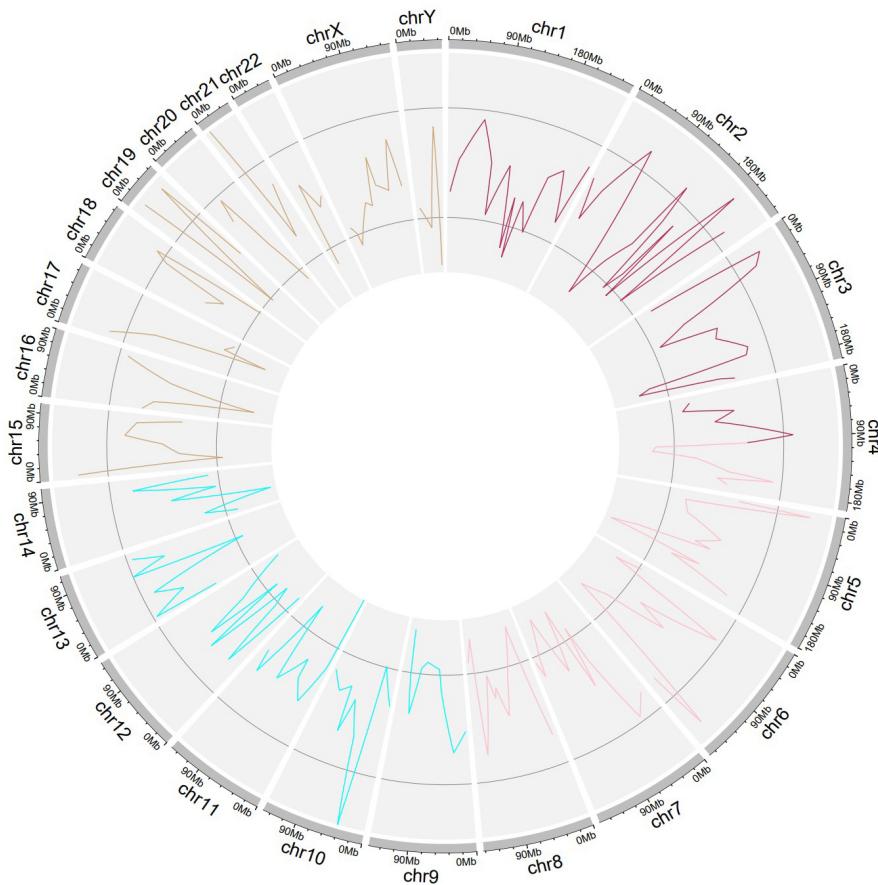


Standard line chart

In addition to the standard four columns of data, you can add a color column or add a value column to draw multiple lines on the same track.

chr	start	end	value	color
chr1	2306857	8605927	-0.207	a
chr1	20851761	21889246	0.121	a
chr1	23158305	28865964	0.163	a
chr1	37301567	80712334	0.53	a
chr1	80874413	81302045	0.115	a
chr1	85048095	85782964	-0.406	a

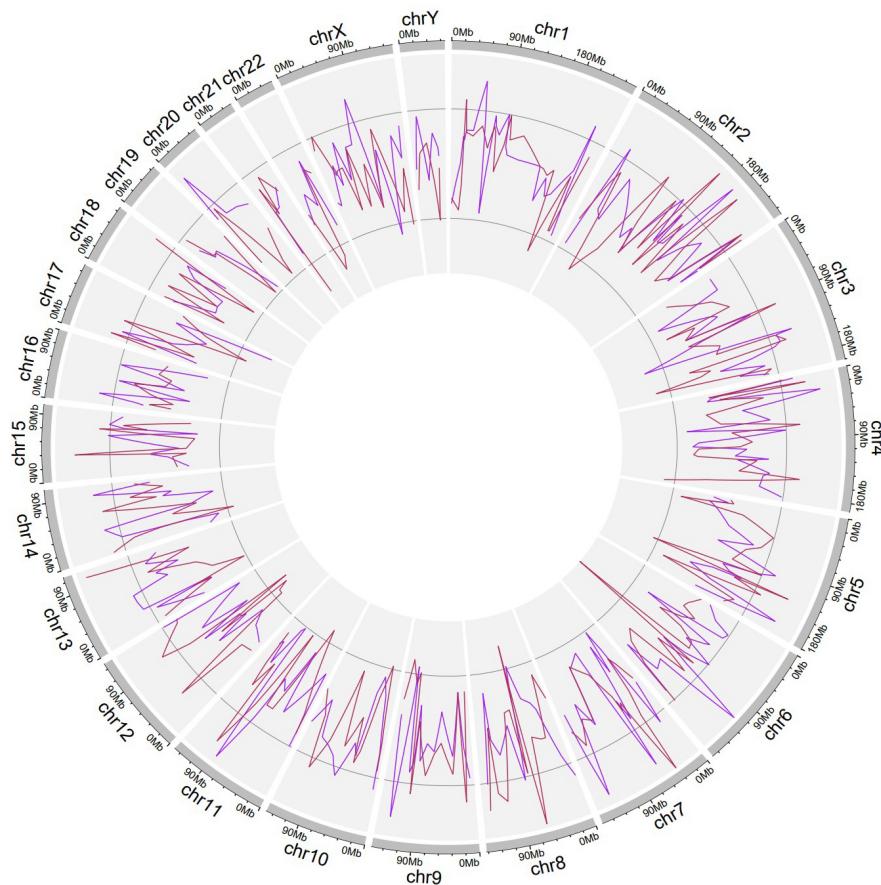
Line data with color column ↓



Line chart with color controlled by color column

chr	start	end	value1	value2
chr1	294540	4666160	-0.66	-0.596
chr1	17589118	18065224	-0.138	-0.747
chr1	21280287	21380873	0.217	-0.419
chr1	22377472	23659781	0.173	0.702
chr1	24230431	27625133	0.304	0.276
chr1	27864815	46726601	0.305	0.233

Line chart data with multiple columns of values ↴



Line chart with multiple lines

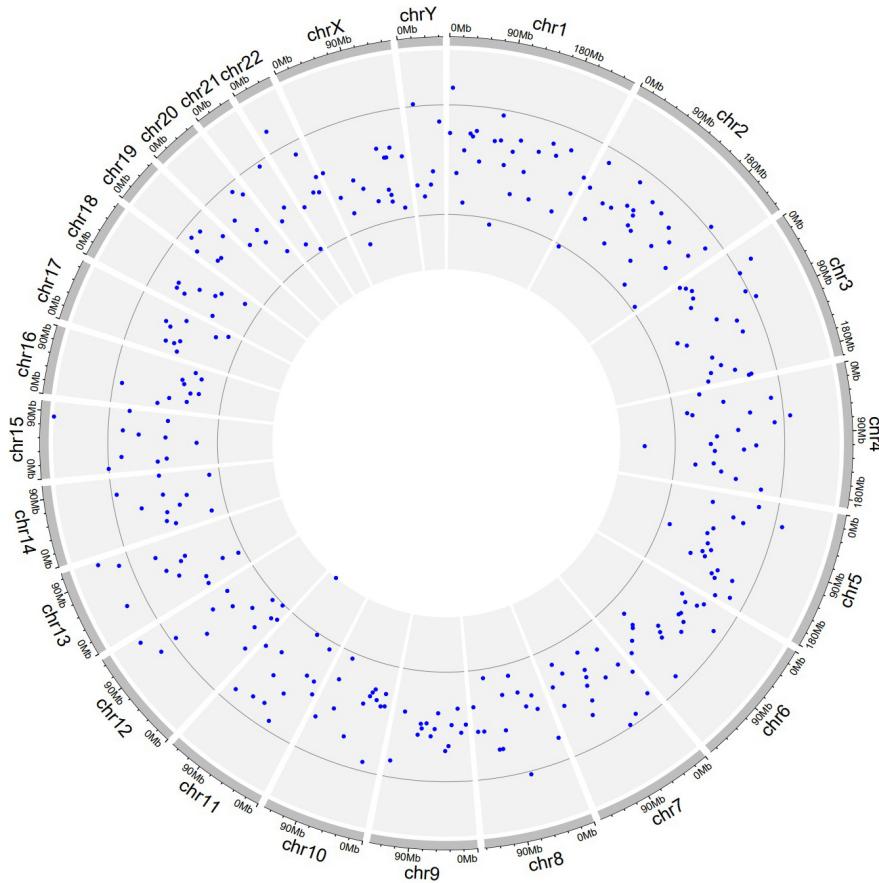
2.2.3 point

Data for point chart is similar to plotting data for a line chart.

Standard point chart data should contain four columns, chr, start, end and value1, as shown in the following figure:

chr	start	end	value1
chr1	1769292	1796134	0.339
chr1	4881594	5495466	1.005
chr1	9076857	21130138	-0.247
chr1	27279764	27941507	0.092
chr1	28351697	32840519	-0.677
chr1	35166605	38111246	0.344

Standard point chart data [↓](#)

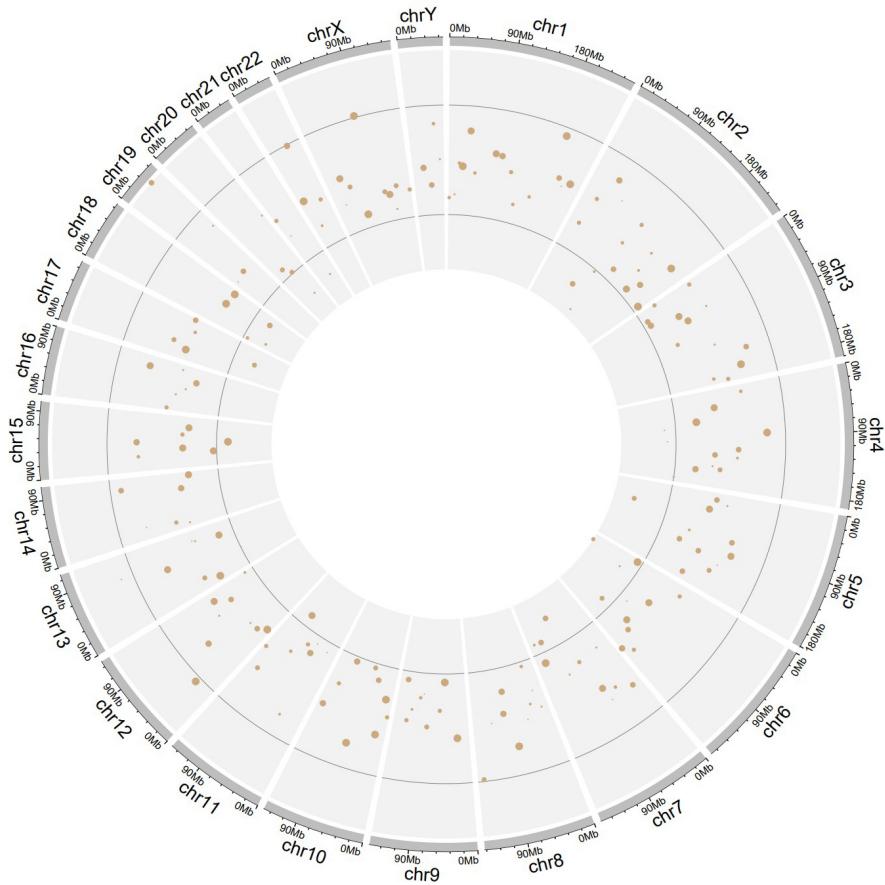


Standard point chart

The data can contain a column to control the size of the points (excessive values can have unpredictable consequences)

chr	start	end	value	cex
chr1	1326341	1845331	-0.374	0.5
chr1	9901462	15656953	-0.321	0.3
chr1	18241935	21630011	0.172	0.5
chr1	24382163	28861398	0.125	1.1
chr1	32942869	41209388	0.685	1
chr1	46216384	55439876	0.035	0.5

point chart data with "cex" column [↓](#)

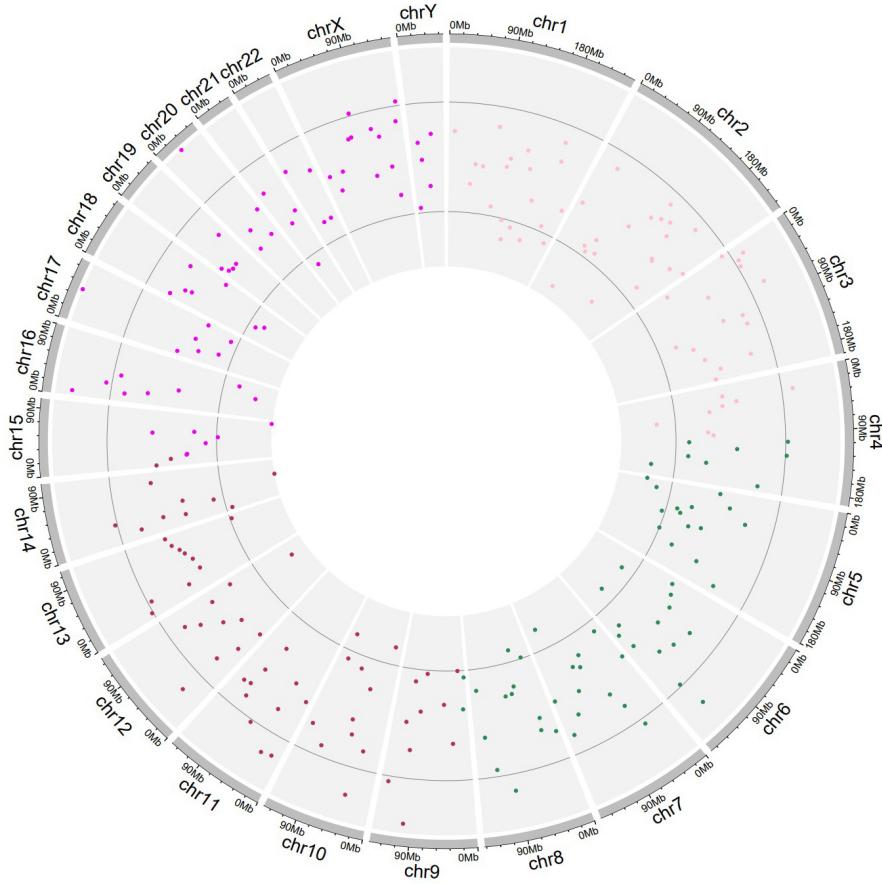


point chart with points of different sizes

Similarly, the point chart also supports the use of color columns to control the color of different points (please use legal color values)

chr	start	end	value	color
chr1	6098636	13915642	0.372	a
chr1	42002814	45209039	-0.253	a
chr1	49351404	52528510	-0.011	a
chr1	64806490	66012454	-0.025	a
chr1	82448410	86862907	0.477	a
chr1	92542207	95289412	-0.489	a

point chart data with "color" column ↴



point chart with points of different colors

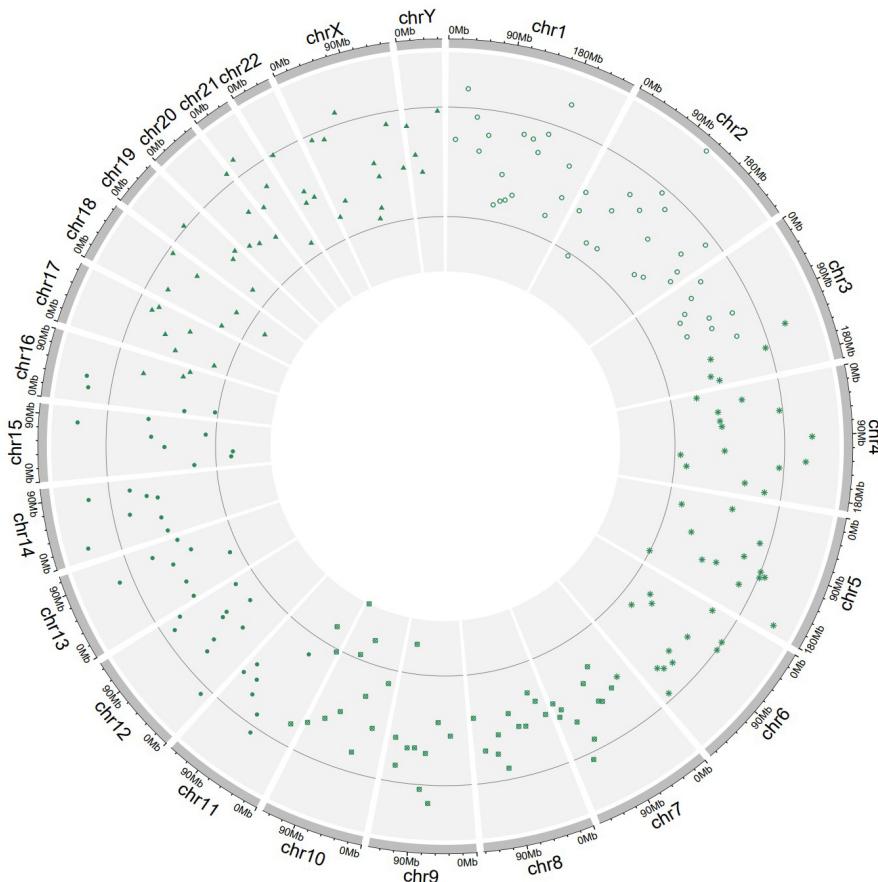
You can also add a column to control the type of point (the different values of pch are as follows)

pch= 0	□	pch= 5	◇	pch= 10	⊕	pch= 15	■	pch= 20	●	pch= 25	▼	pch="0"	0
pch= 1	○	pch= 6	▽	pch= 11	△	pch= 16	●	pch= 21	●	pch=""	*	pch="+"	+
pch= 2	△	pch= 7	☒	pch= 12	田	pch= 17	▲	pch= 22	■	pch=".."	-	pch=".."	-
pch= 3	+	pch= 8	*	pch= 13	⊗	pch= 18	◆	pch= 23	◆	pch="o"	○	pch="T"	
pch= 4	×	pch= 9	◊	pch= 14	☒	pch= 19	●	pch= 24	▲	pch="O"	○		

Reference value of pch

chr	start	end	value	pch
chr1	8605110	17214753	0.208	1
chr1	22124150	36435838	0.905	1
chr1	43831505	49353791	0.53	1
chr1	50596455	60340980	0.072	1
chr1	65153170	71982950	0.301	1
chr1	97376484	99759071	-0.622	1

point chart data with "pch" column ↴

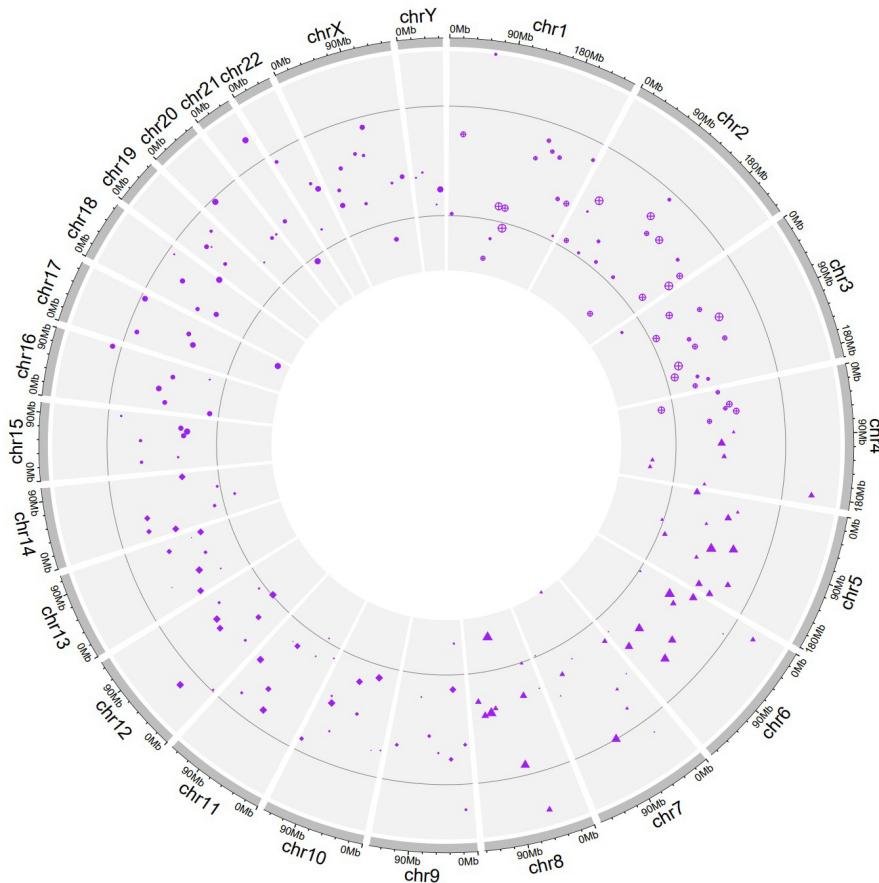


point chart with different types of points

These types of control columns can also be combined arbitrarily

chr	start	end	value	pch	cex
chr1	4049230	11358879	-0.59	10	0.4
chr1	18671867	29619034	0.442	10	0.7
chr1	57445176	66216574	1.511	10	0.3
chr1	96228476	98543344	-1.121	10	0.6
chr1	1.04E+08	1.07E+08	-0.854	10	0.3
chr1	1.09E+08	1.1E+08	-0.421	10	1

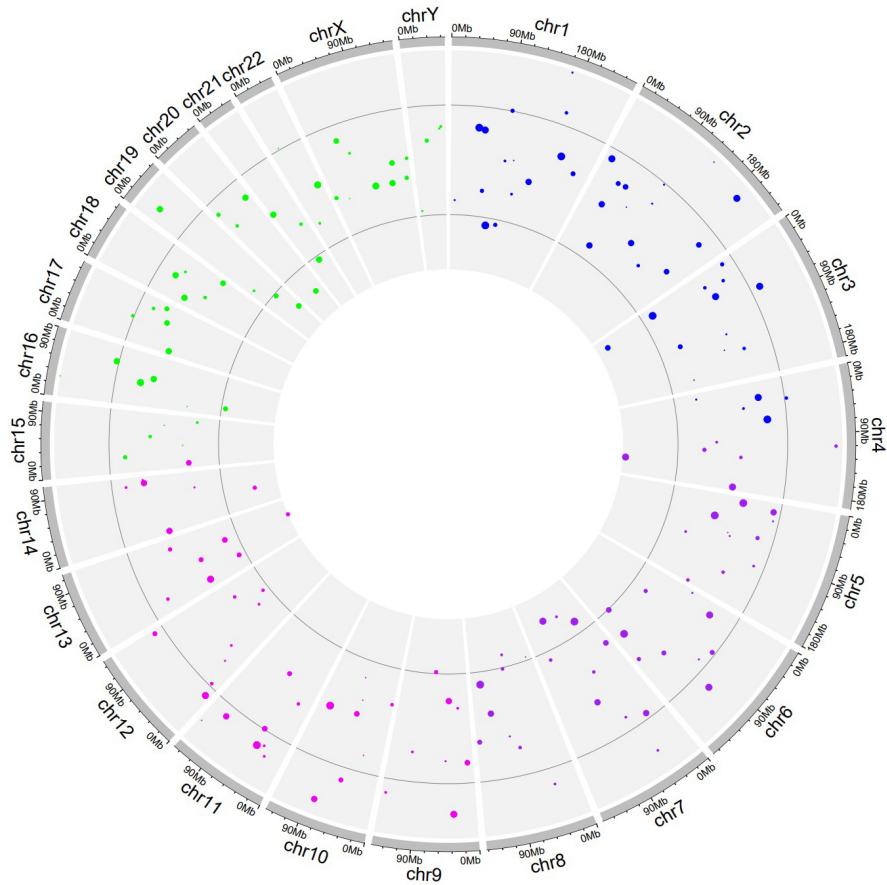
point data with columns "pch", "cex" ↴



point chart with points of different sizes and types

chr	start	end	value	color	cex
chr1	8900700	9211013	-0.6	a	0.3
chr1	38733680	54945292	0.233	a	1.1
chr1	56997278	57258274	0.214	a	1
chr1	63421486	66560161	-0.471	a	0.6
chr1	83102162	84271822	-0.851	a	1.1
chr1	92926675	98678200	0.476	a	0.6

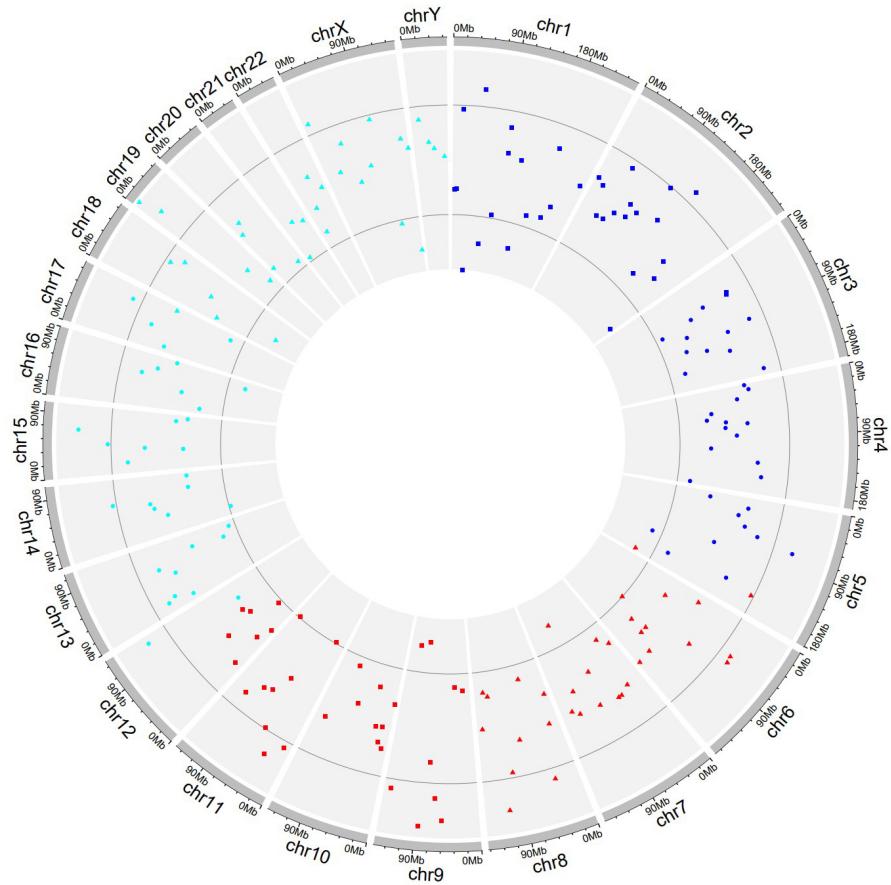
point data with columns "color", "cex" ↴



point chart with points of different colors and sizes

chr	start	end	value	color	pch
chr1	3768320	4851773	-0.416	a	15
chr1	5712552	10112216	-0.41	a	15
chr1	15275256	18873862	0.589	a	15
chr1	28211635	37585705	-1.416	a	15
chr1	46691560	50561898	0.852	a	15
chr1	62357826	74411579	-1.075	a	15

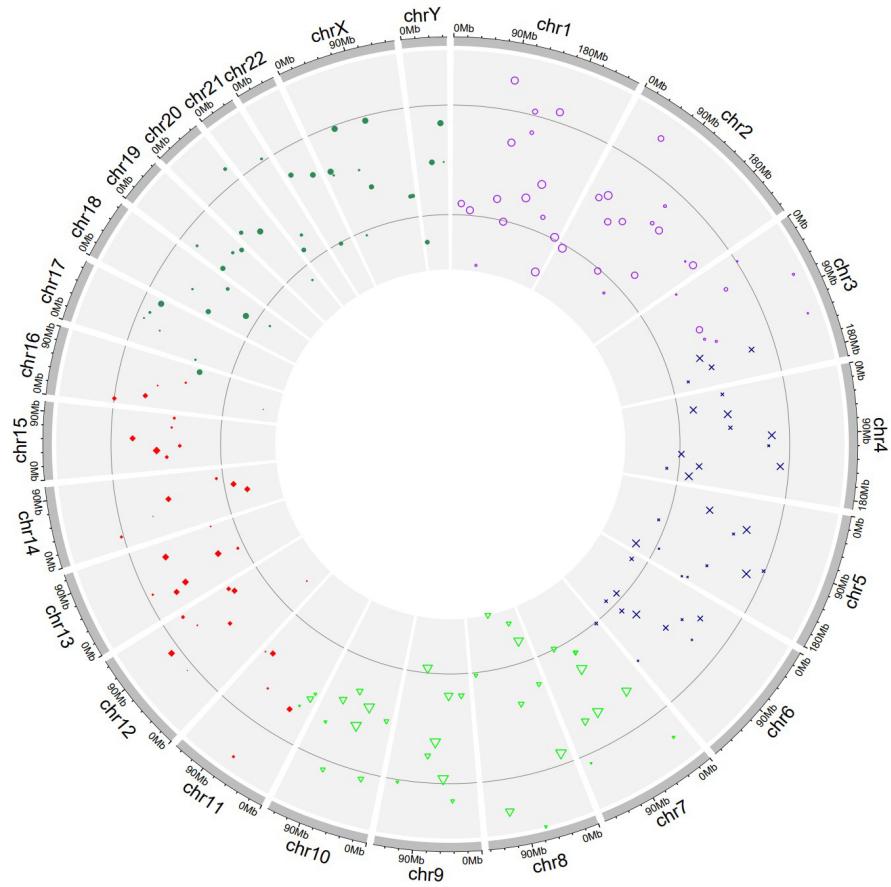
point data with columns "color", "pch" ↴



point chart with points of different colors and types

chr	start	end	value	color	pch	cex
chr1	14053524	24878326	-0.498	a	1	0.9
chr1	29640089	49313488	-0.565	a	1	1
chr1	53970010	87166913	-1.159	a	1	0.3
chr1	87537029	88337021	0.911	a	1	1
chr1	94359096	95393045	-0.402	a	1	1
chr1	100525029	101217751	0.235	a	1	1

point data with columns "color", "pch" and "cex" ↴

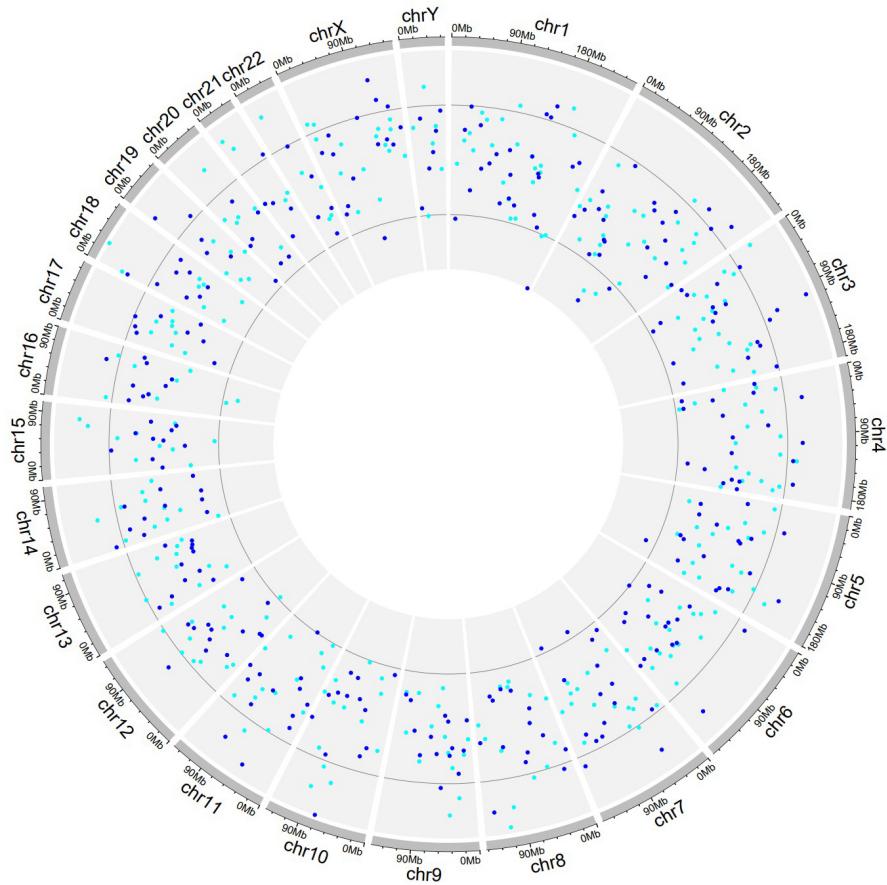


point chart with points of different colors, types and sizes

Of course, point charts can also plot multiple columns of data at the same time like line charts.

chr	start	end	value1	value2
chr1	7224218	16393864	-0.196	-0.955
chr1	21093451	25392112	0.128	0.275
chr1	31462827	31952156	0.234	0.6
chr1	38366450	42030463	0.001	-0.552
chr1	44307009	53690628	0.53	0.355
chr1	58017049	58046561	0.439	-0.24

point data with multiple columns of "value" ↴



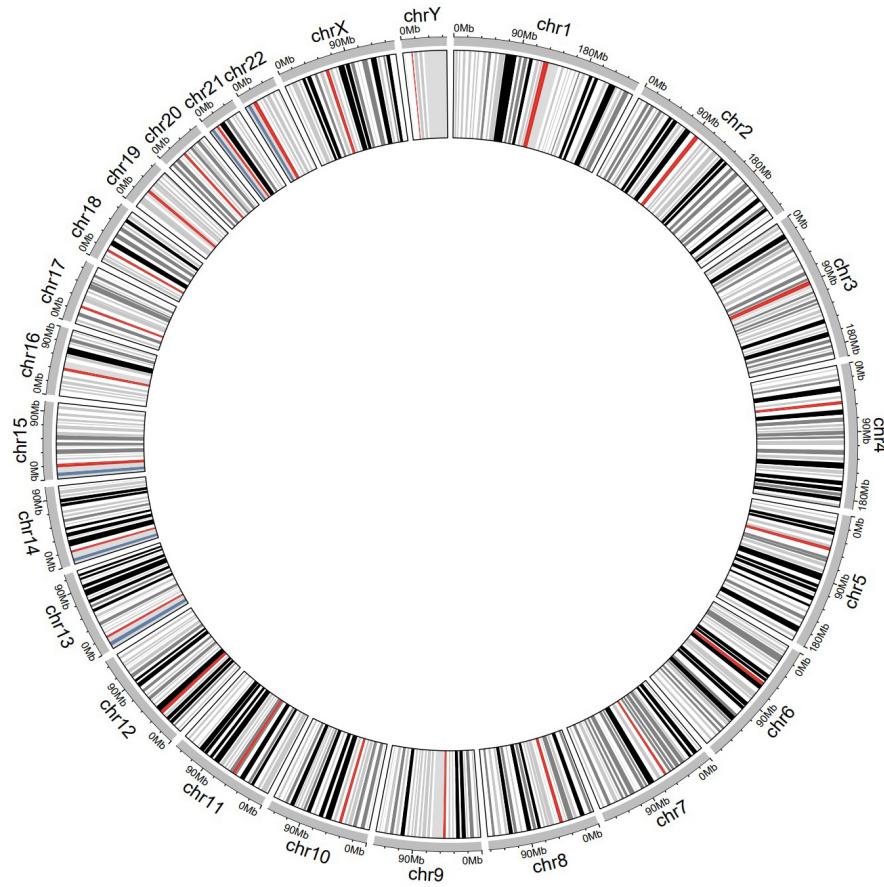
point chart with multiple "values"

2.2.4 ideogram

shinyCircos-V2.0 can also draw chromosome strips on any "Track". The format of chromosome strip data is the same as that of the [cytoband data](#) of chromosomes.

chr	start	end	value1	value2
chr1		1	2300000	p36.33
chr1	2300000	5400000	p36.32	gpos25
chr1	5400000	7200000	p36.31	gneg
chr1	7200000	9200000	p36.23	gpos25
chr1	9200000	12700000	p36.22	gneg
chr1	12700000	16200000	p36.21	gpos50

ideogram data [↓](#)



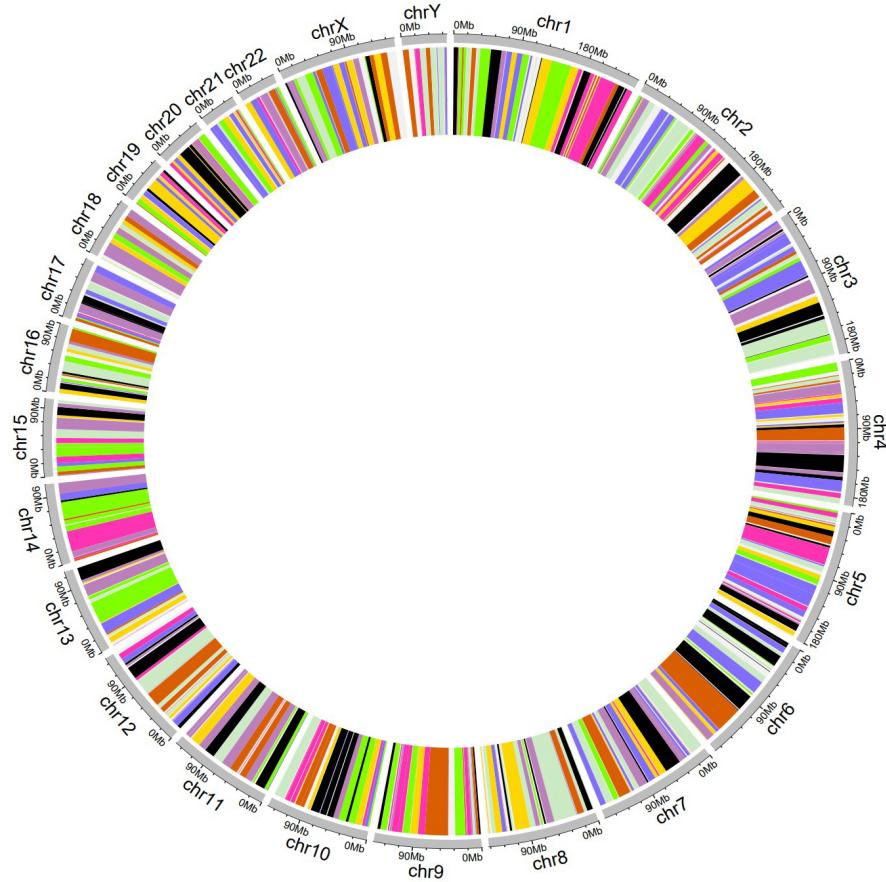
ideogram

2.2.5 rect-discrete

The rect chart can be understood as a single-row heatmap. The discrete histogram data contains four columns: chr, strat, end and group, as shown in the following figure

chr	start	end	group
chr1	1465	5857186	b
chr1	6005405	7051583	c
chr1	7459754	11390112	h
chr1	11461667	11666810	h
chr1	11735789	13740274	a
chr1	13741155	17190699	h

Discrete rect data [↓](#)



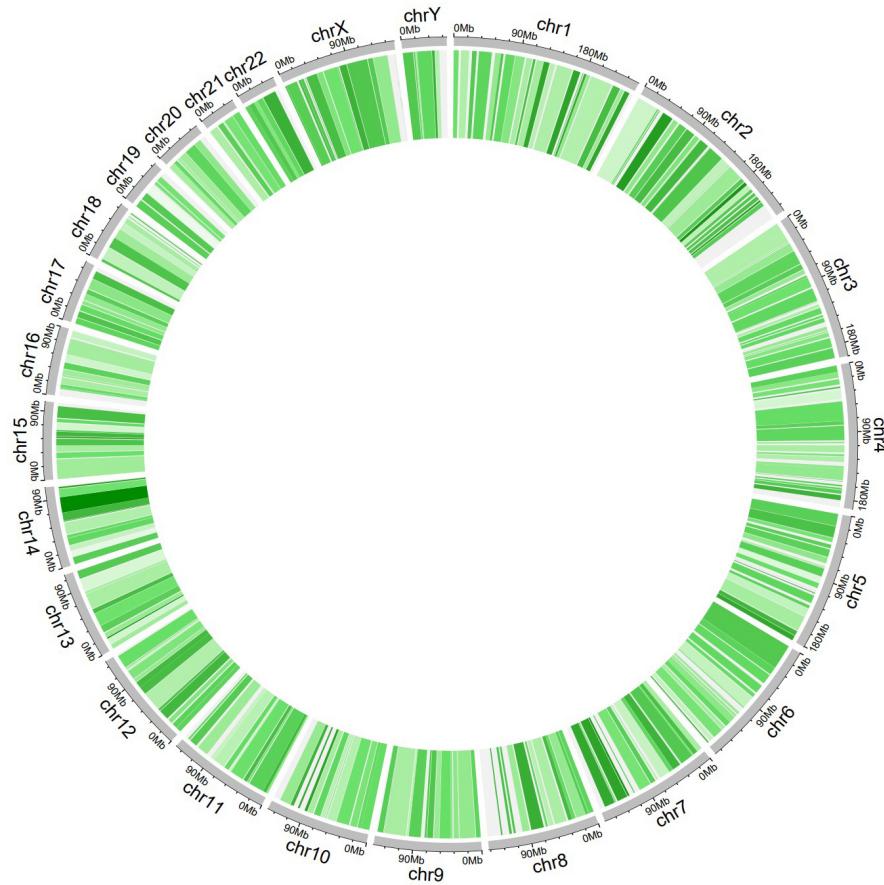
Discrete rect chart

2.2.6 rect-gradual

The gradual rect data contains four columns: chr, strat, end and group, as shown in the following figure

chr	start	end	value
chr1		1	6657591
chr1	9792529	20706145	-0.527
chr1	24807376	30831596	0.355
chr1	31003801	31338988	-0.425
chr1	33917405	51335905	0.216
chr1	55862806	63502192	-0.299

Gradual rect data [↓](#)



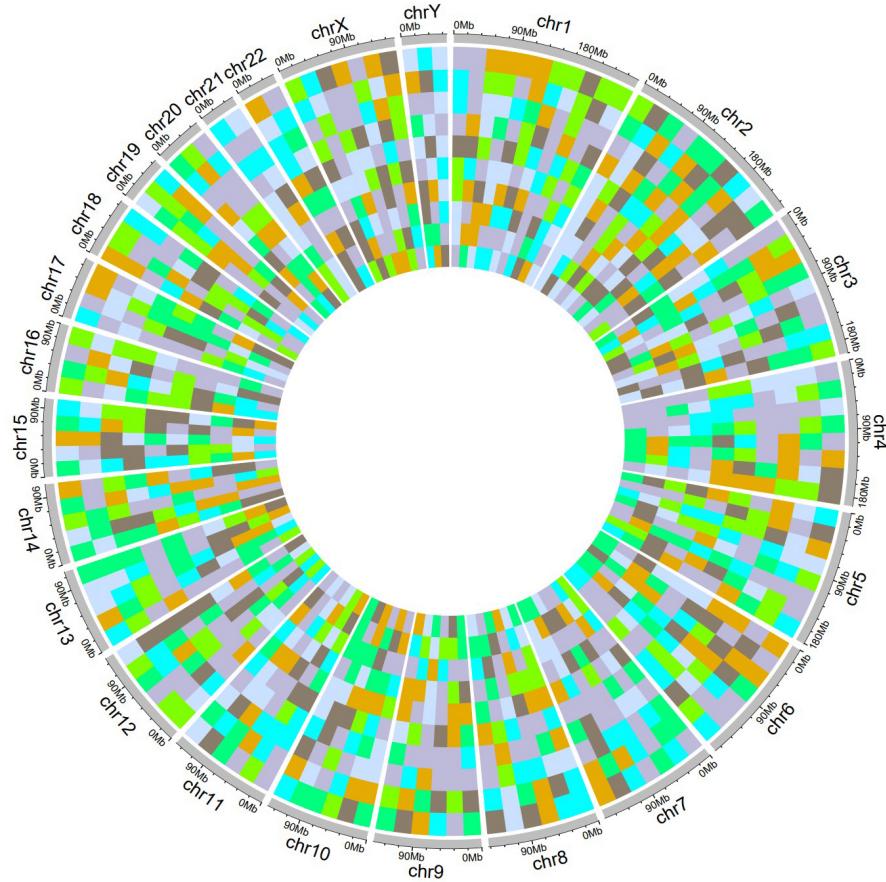
Gradual rect chart

2.2.7 heatmap-discrete

Discrete heatmap data contains at least four columns, namely: chr, strat, end and group1, and there can be multiple group columns, as shown in the following figure

chr	start	end	group1	group2	group3	group4	group5	group6	group7	group8	group9	group10
chr1	20621957	21209624	d	a	a	e	e	c	d	g	g	d
chr1	42967726	53028972	f	b	h	b	g	c	b	h	h	d
chr1	58915991	65942365	a	b	b	c	h	e	a	a	e	b
chr1	67474486	70468059	g	d	b	a	a	d	f	a	e	b
chr1	70834716	93392812	g	h	g	b	a	c	h	g	h	b
chr1	98646692	105744994	a	d	g	c	d	e	e	f	b	b

Discrete heatmap data [↓](#)



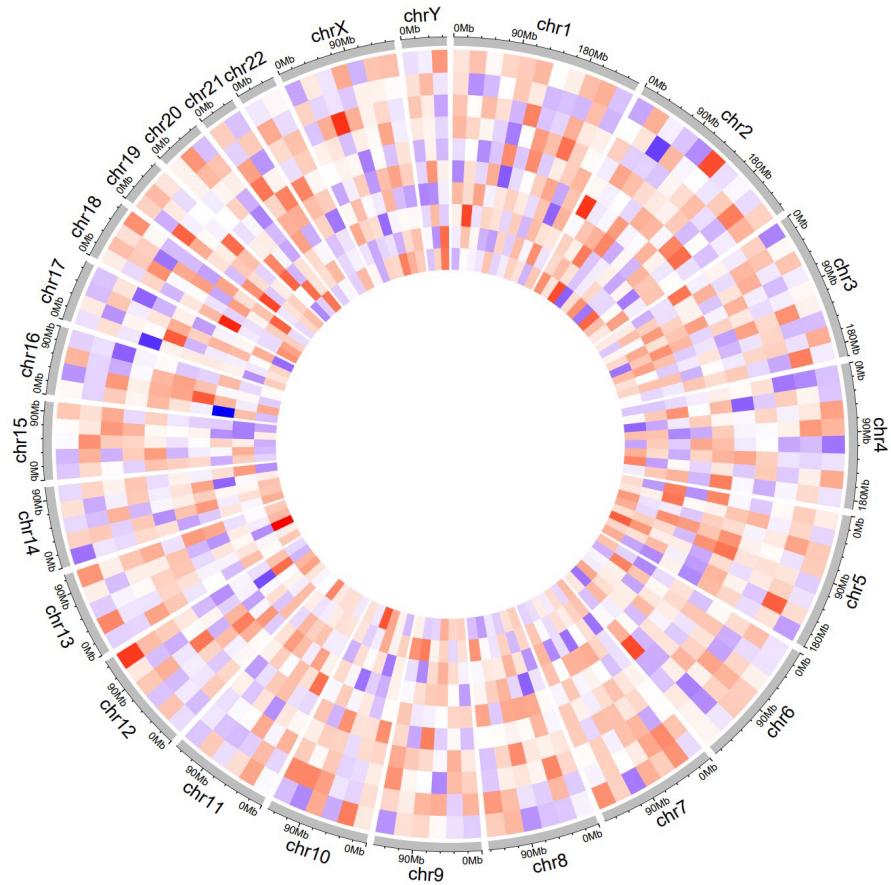
Discrete heatmap

2.2.8 heatmap-gradual

The gradual heatmap data contains at least four columns, namely: chr, strat, end and value1, and there can be multiple value columns, as shown in the following figure

chr	start	end	value1	value2	value3	value4	value5	value6	value7	value8	value9	value10
chr1	20621957	21209624	-0.672	-0.271	-0.001	0.486	-0.986	-0.37	0.48	0.38	0.158	0.108
chr1	42967726	53028972	-0.147	0.387	1.332	0.182	0.16	-0.132	0.234	-0.089	-0.918	0.397
chr1	58915991	65942365	-0.214	-0.059	-0.332	0.654	-0.402	-0.953	-0.046	0.449	-0.615	-0.07
chr1	67474486	70468059	-0.314	-0.67	0.24	-0.221	0.582	-0.536	-0.438	0.153	-0.14	0.242
chr1	70834716	93392812	0.372	-0.812	0.129	0.087	-1.307	0.846	-1.062	-0.653	0.345	0.315
chr1	99846692	1.06E+08	-0.437	0.245	-0.422	0.273	-0.374	-0.522	-0.147	0.924	0.057	0.483

Gradual heatmap data [↓](#)



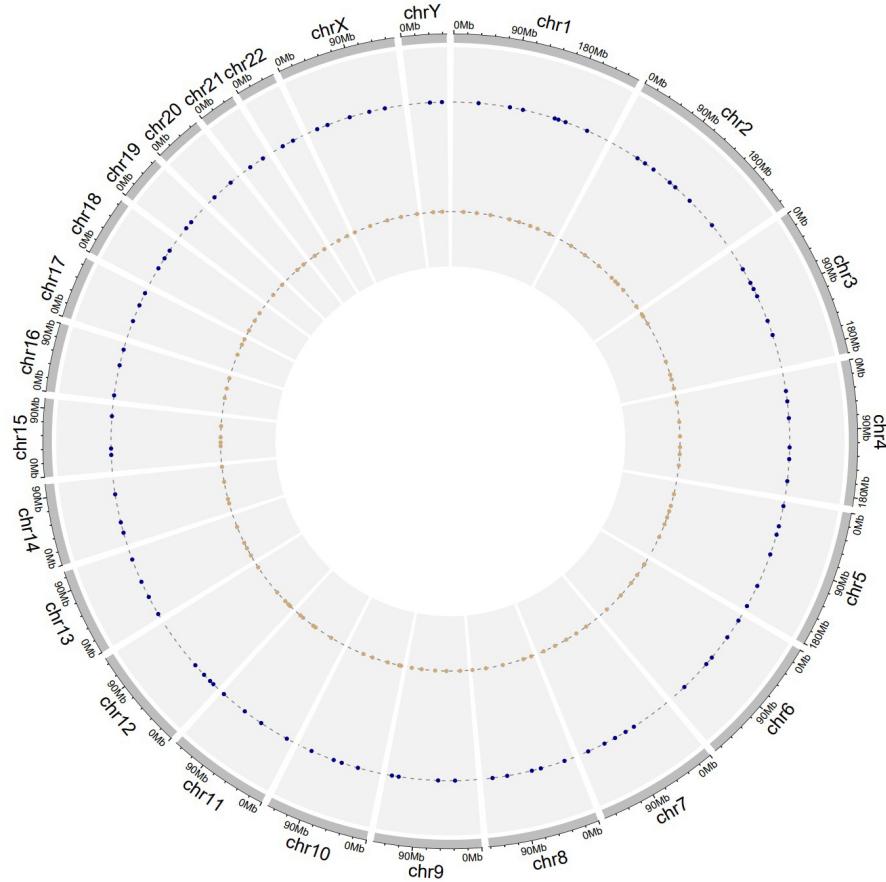
Gradual heatmap

2.2.9 stack-point

shinyCircos-V2.0 can also draw stack point chart. The data should contain four columns, respectively: chr, start, end and stack. It is worth noting that the stack column represents the grouping of the data, and the same group will be plotted on one line, as shown in the image below

chr	start	end	stack
chr1	11589909	40133642	a
chr1	52614734	59580026	a
chr1	76931882	99383558	a
chr1	87453098	89776607	b
chr1	107231283	111232493	b
chr1	157904163	162911422	b

stack point data [↓](#)



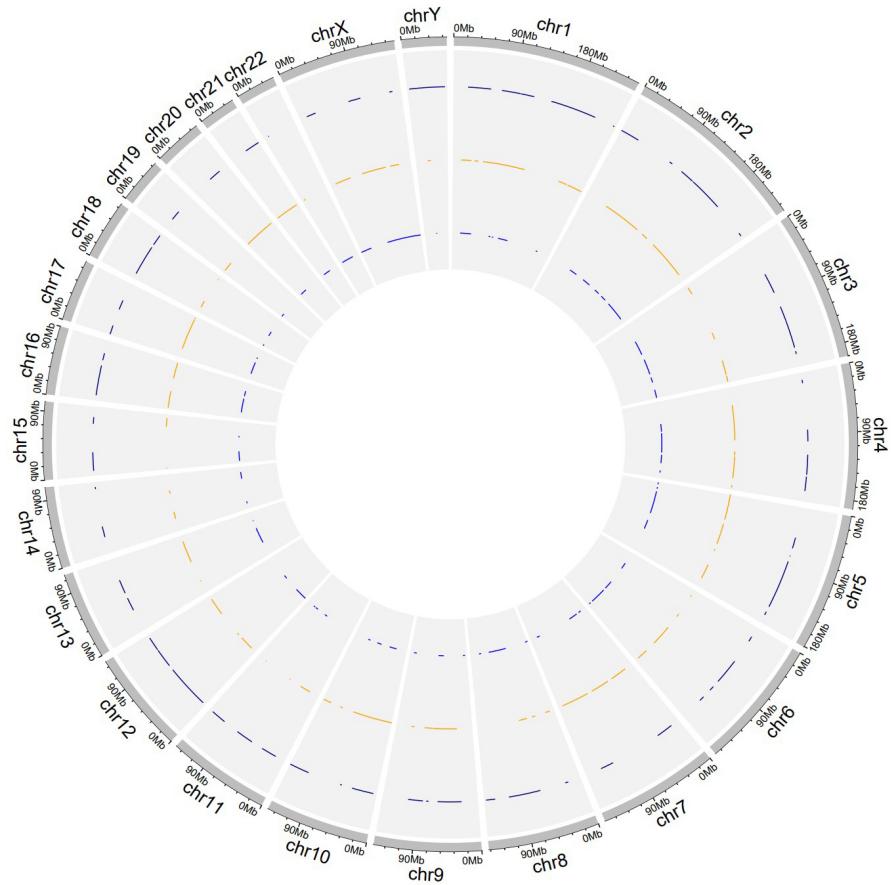
stack point chart

2.2.10 stack-line

The stacked line chart is similar to the stacked point chart, and its data should also contain four columns, respectively: chr, start, end, and stack. It is worth noting that the stack column represents the grouping of the data, and the same group will be drawn in one line, as shown in the image below

chr	start	end	stack
chr1	20646359	46383846	a
chr1	92365687	94981461	a
chr2	55415849	73121067	a
chr1	16051196	33970939	b
chr1	40831033	46774887	b
chr2	43510332	52327672	b

stack line data [↓](#)



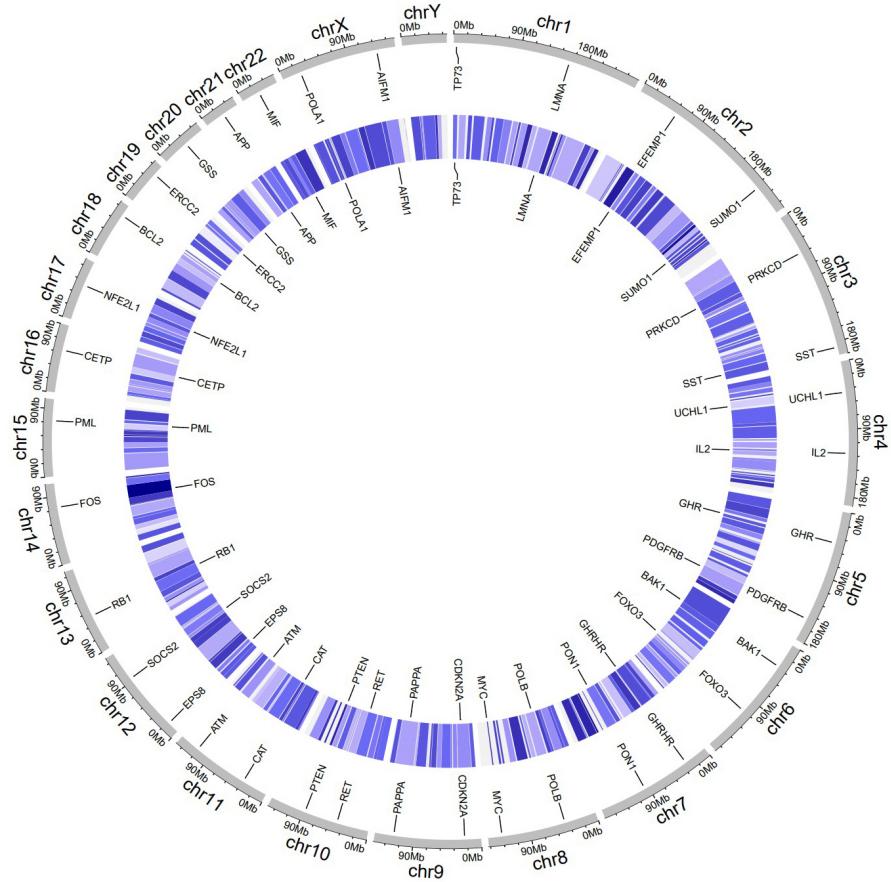
stack line chart

2.3 label data

Label data is the data used to annotate the genome or interpret the track. It will show labels one by one on the graph. The data should contain four columns, as shown in the figure below:

chr	start	end	label
chr1	3698046	3736201	TP73
chr1	1.56E+08	1.56E+08	LMNA
chr2	2.02E+08	2.02E+08	SUMO1
chr2	55865967	55924139	EFEMP1
chr3	1.88E+08	1.88E+08	SST
chr3	53161207	53192717	PRKCD

label data ↴



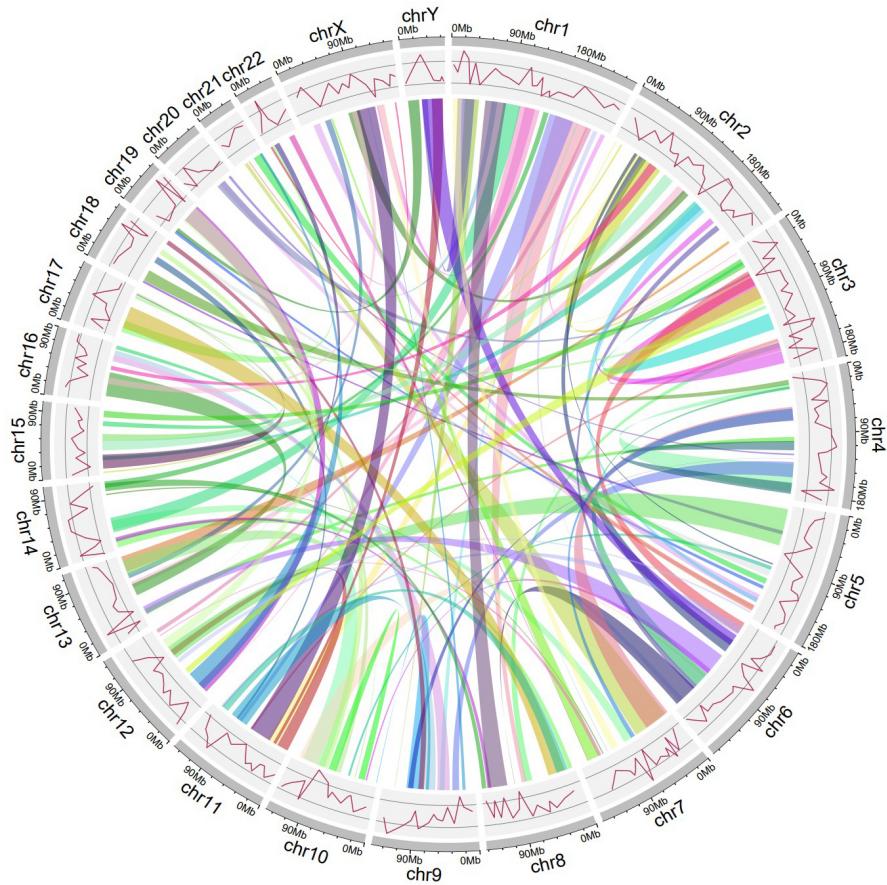
labels for Circos diagrams

2.4 links data

The link data should contain at least six columns, which represent the head and tail of the connection line respectively. The specific format is shown in the figure below:

chr1	start1	end1	chr2	start2	end2
chr20	37720821	47419255	chr5	162124929	168434522
chr8	76179361	83302661	chr1	162049212	213797379
chr2	38375277	49805216	chr11	19060895	36294068
chr2	120255288	134792772	chr13	62362083	71502856
chr4	95199225	102508113	chr13	16327889	24910342
chr15	83769167	83992136	chr10	83790329	119443216

standard link data ↴

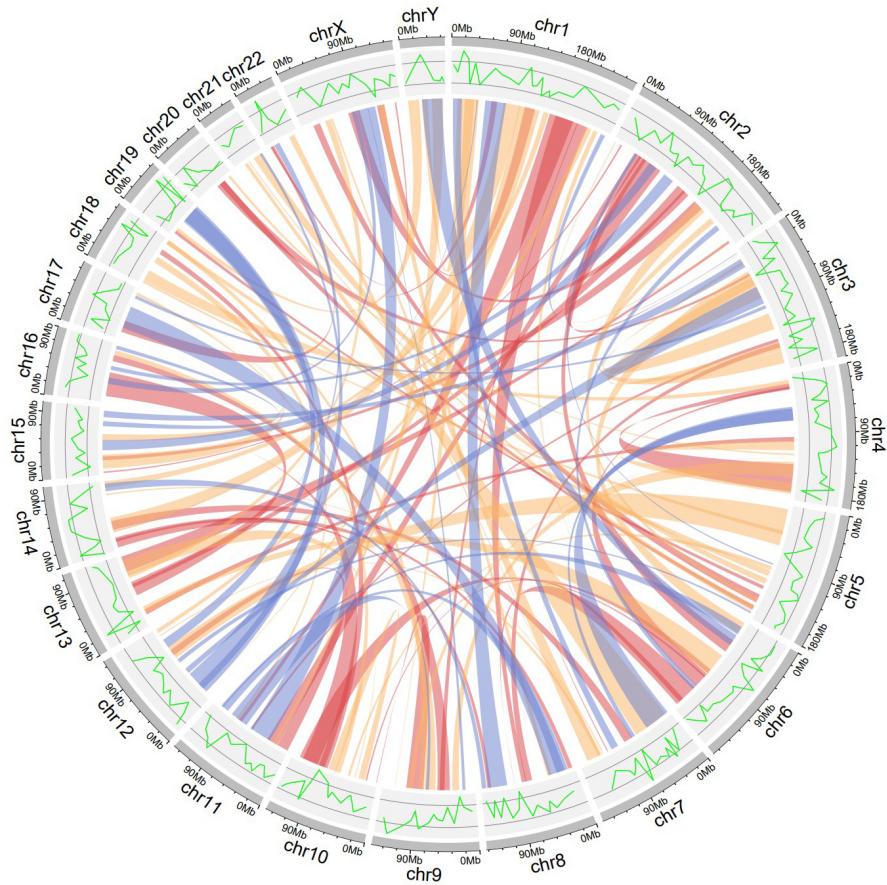


link for Circos diagram

In addition to the necessary six columns of data, you can also add another column to control the color of the link. Two formats are supported to adjust the color of the link, discrete values and continuous values, as shown in the following figure:

chr1	start1	end1	chr2	start2	end2	color
chr20	37720821	47419255	chr5	1.62E+08	1.68E+08	c
chr8	76179361	83302661	chr1	1.62E+08	2.14E+08	c
chr2	38375277	49805216	chr11	19060895	36294068	b
chr2	1.2E+08	1.35E+08	chr13	62362083	71502856	a
chr4	95199225	1.03E+08	chr13	16327889	24910342	a
chr15	83769167	83992136	chr10	83790329	1.19E+08	b

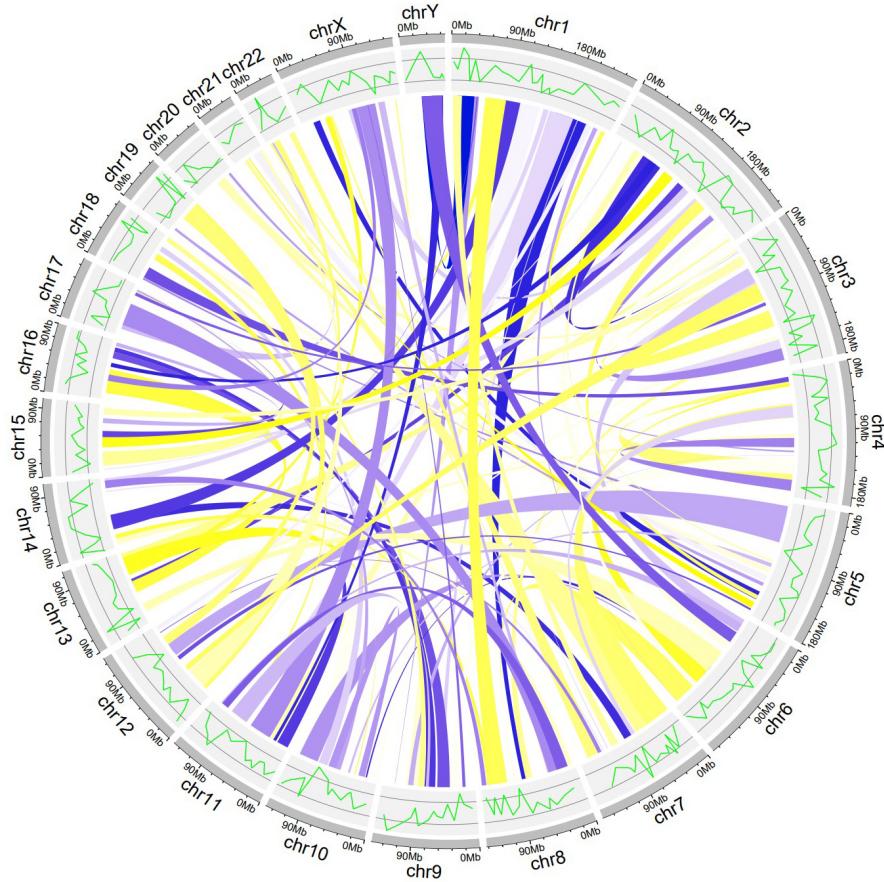
link data with discrete color values [↓](#)



link for Circos graph (discrete color values)

chr1	start1	end1	chr2	start2	end2	color
chr20	37720821	47419255	chr5	1.62E+08	1.68E+08	217
chr8	76179361	83302661	chr1	1.62E+08	2.14E+08	7
chr2	38375277	49805216	chr11	19060895	36294068	206
chr2	1.2E+08	1.35E+08	chr13	62362083	71502856	27
chr4	95199225	1.03E+08	chr13	16327889	24910342	189
chr15	83769167	83992136	chr10	83790329	1.19E+08	161

link data with gradual color values ↴



link for Circos graph (gradual color values)

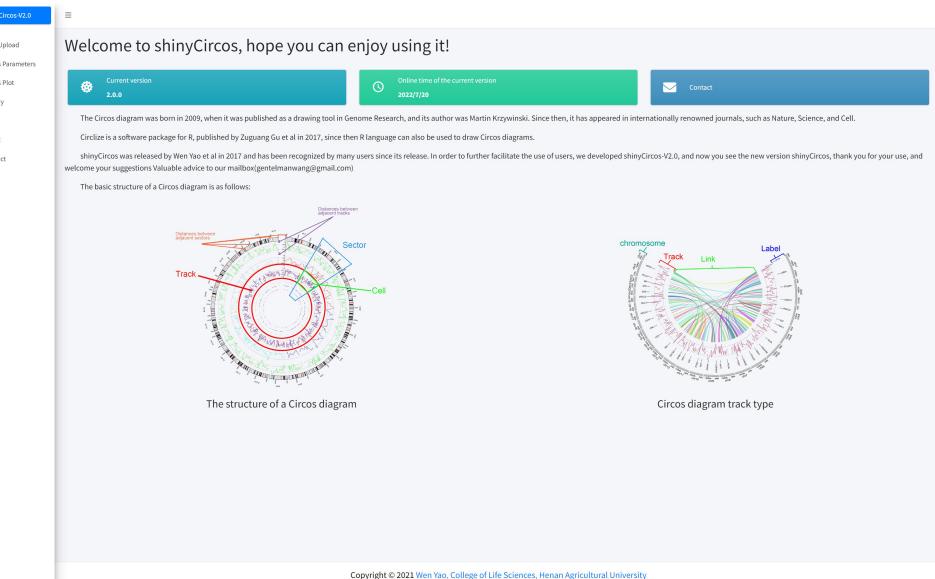
3.Using help

3.1 Use shinyCircos-V2.0 online

The URL to use shinyCircos-V2.0 online is <https://venyao.xyz/shinyCircos2.0/>. When users visit shinyCircos-V2.0 for the first time, the loading speed of the website may be relatively slow. On the one hand, it may be a network problem. On the other hand, in order to save resources, when the website is inactive, shinyCircos-V2.0 will enter hibernation to save resources, which leads to a slower loading speed for the first access after a period of time. Therefore, the first visit may take some time, once the website is activated, shinyCircos-V2.0 can be used smoothly and conveniently.

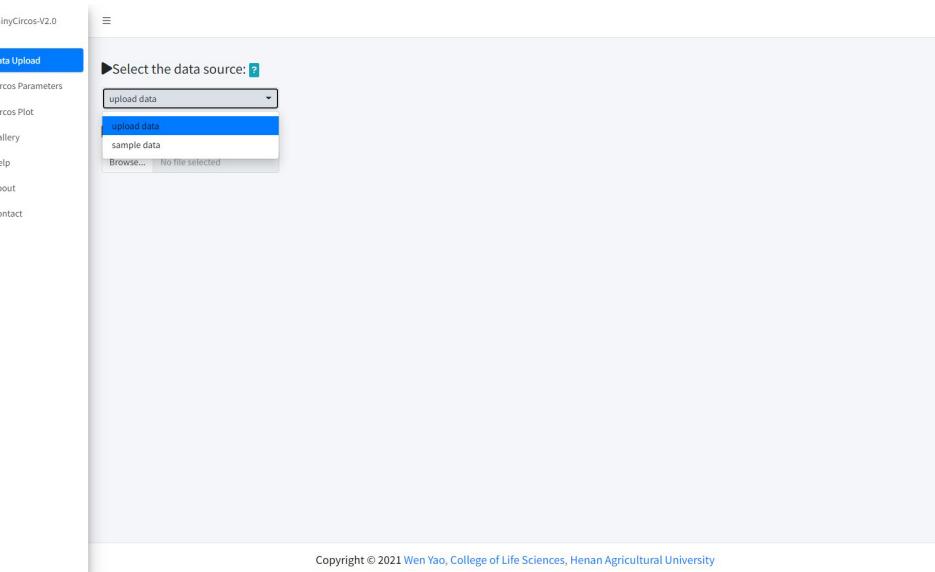
3.2 Interface of shinyCircos-V2.0

The shinyCircos-V2.0 application contains 8 main menus: "shinyCircos-V2.0", "Data Upload", "Circos Parameters", "Circos Plot", "Gallery", "Help", "About" and "Contact" (See below). The "shinyCircos-V2.0" menu lists the basic introduction to the Circos diagram that the current version of the shinyCircos-V2.0 application has had.



The main page of shinyCircos-V2.0

The "Data Upload" menu allows the user to upload input data or load sample data (as shown below).



Choose a data source

Different input data will display different interfaces. If you select "upload data", the data classification interface will appear after uploading the data (as shown in the figure below). After dragging the data into the appropriate box, click "Save data" to connect. You can continue to upload data or click "Submit!", the application will jump to the next interface after checking that the data is correct.

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Upload data yourself

If "sample data" is selected, the user can select a sample data set and click "Submit!" (as shown in the figure below), and the application will jump to the next interface.

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Use sample data

The "Circos Parameters" menu will list all the data uploaded by the user or the loaded sample data (as shown in the figure below), and the parameter configuration will also be loaded when loading the sample data. The Circos Parameters menu has four sections, namely Chromosome data, Track data, Label data, Links data, corresponding to different classification boxes on the previous page, users can click the little eye after the file name to preview the data, or click the small gear at the end of each row to configure the

parameters, all parameters are configured. After the user can click "Submit! " button to draw, and the application will check whether the parameter configuration is reasonable, if there is no error, it will jump to the "Circos Plot" menu (Note: The jumping process may not be very smooth, because the program has already started to draw the image).

The screenshot shows the 'Circos Parameters' page of the shinyCircos-v2.0 application. It includes sections for Chromosome data, Track data, Label data, and Link data. Each section has a 'File name' dropdown, a 'Type' or 'Format' dropdown, and a 'Track index' or 'Label index' dropdown. A 'SUBMIT!' button is at the bottom.

- Chromosome data:**
 - File name: chromosome_general.csv
 - Type: general
- Track data:**
 - File name: barplot.csv
 - Type: bar
 - Index: 1
 - File name: chromsome_ideogram.csv
 - Type: ideogram
 - Index: 2
 - File name: heatmap-gradual.csv
 - Type: heatmap-gradual
 - Index: 3
 - File name: line.csv
 - Type: line
 - Index: 4
 - File name: point.csv
 - Type: point
 - Index: 5
 - File name: rect_discrete.csv
 - Type: rect-discrete
 - Index: 6
- Label data:**
 - File name: gene_label.csv
 - Type: Data without 'color' column
 - Index: 0
 - File name: gene_label1.csv
 - Type: Data without 'color' column
 - Index: 3
- Link data:**
 - File name: links.csv
 - Type: Data without 'color' column

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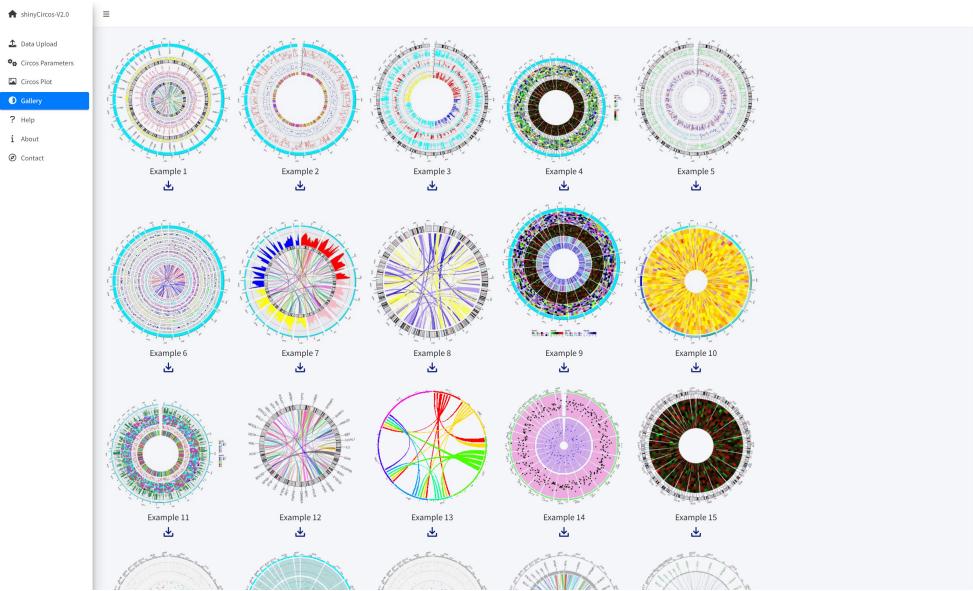
Circos Parameters page

The "Circos Plot" menu will select and output the corresponding image according to the user's input data and parameters, and provide download and fine-tuning parameters. The user can finally adjust the image, such as adding a legend, highlighting areas, etc. (as shown in the figure below). After adjustment, don't forget To update the image, click "Update".



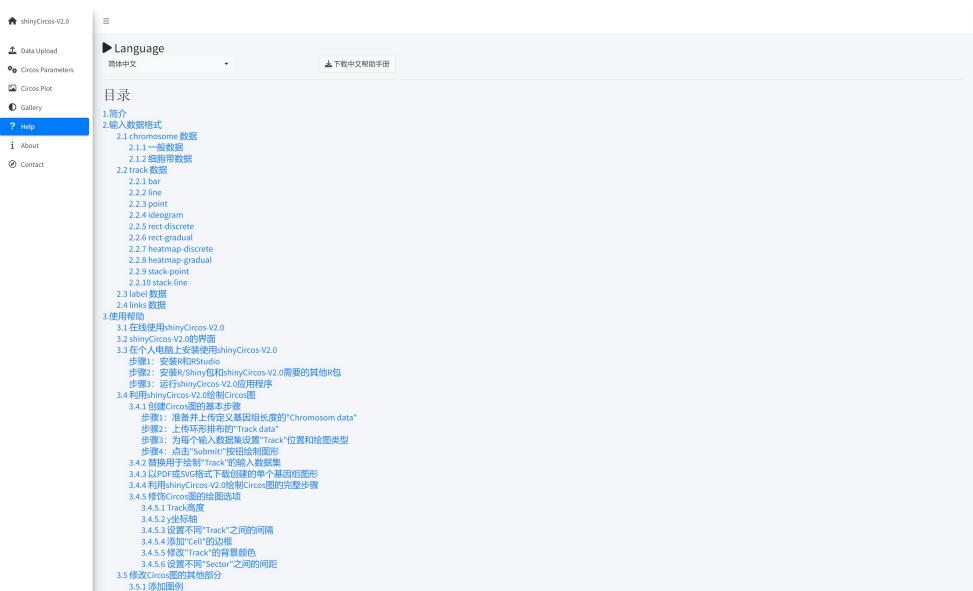
Circos Plot page

Thirty sample graphics created with shinyCircos-V2.0 are listed in the "Gallery" menu of the shinyCircos-V2.0 application (pictured below). The dataset used to generate each example plot is also provided for download, containing all input files, each appropriately named, indicating the track and plot type for each file in the dataset. **The sample data of the first ten sample graphs is the same as the sample file configuration provided by the "Data Upload" interface.**



Gallery page

In the "Help" menu of the shinyCircos-V2.0 application program, we have compiled the help documents of the software in detail. Users can refer to the corresponding parts to learn according to the catalogue, support Chinese and English switching, and also support download.



Help page

In the "About" menu of shinyCircos-V2.0 we declare the R packages used and our details.

The screenshot shows the 'About' page of the shinyCircos-V2.0 application. On the left, a sidebar lists navigation options: Data Upload, Circos Parameters, Circos Plot, Gallery, Help, About (which is selected and highlighted in blue), and Contact. The main content area displays a detailed list of R packages used in the application, starting with 'Software references' and including items like 'shiny' (version 1.0.0), 'gridExtra' (version 2.3.0), and 'shinyWidgets' (version 0.6.4). It also lists 'Further references' and 'Please cite' sections. At the bottom of this section, it says 'This application was created by Wen Yao and Yazhou Wang. Please send bugs and feature requests to Wen Yao (yaowen@henu.edu.cn) or Yazhou Wang (gentelmanwang@gmail.com). This application uses the shiny package from RStudio.' Below this, there's a footer with logos for Henan Agricultural University, Wen Yao's lab, and a citation for 'Wang et al. 2022'. To the right is a small world map image.

About page

Users can find our contact information in the "Contact" menu of shinyCircos-V2.0.

The screenshot shows the 'Contact' page of the shinyCircos-V2.0 application. The sidebar on the left is identical to the 'About' page, with 'Contact' being the selected option. The main content area contains a section titled 'Contact us' with the following text: 'If you have any problem, comments or suggestions about shinyCircos, please contact us. e-mail: yaowen@henu.edu.cn and gentelmanwang@gmail.com. We really appreciate all your suggestions for shinyCircos.' Below this, there's a copyright notice: 'Copyright © 2021 Wen Yao, College of Life Sciences, Henan Agricultural University'.

Contact page

3.3 Install and use shinyCircos-V2.0 on PC

Users can choose to install and run shinyCircos-V2.0 on a personal computer (Windows, Mac or Linux) without uploading data to an online server. shinyCircos-V2.0 is a

cross-platform application, i.e. shinyCircos-V2.0 can be installed on any platform with an available R environment. The installation of shinyCircos-V2.0 consists of three steps.

Step 1:Install R and RStudio

Check out CRAN (<https://cran.r-project.org/>) for the R installation process.

Step 2:Install the R/Shiny package and other R packages required by shinyCircos-V2.0

Start an R session with RStudio and run the following lines of code:

```
# try an http CRAN mirror if https CRAN mirror doesn't work
install.packages("shiny")
install.packages("circlize")
install.packages("bs4Dash")
install.packages("DT")
install.packages("RColorBrewer")
install.packages("shinyWidgets")
install.packages("data.table")
install.packages("shinyBS")
install.packages("sortable")
install.packages("shinyjqui")
install.packages("shinycssloaders")
install.packages("colourpicker")
install.packages("gridBase")
install.packages("BiocManager")
BiocManager::install("ComplexHeatmap")
BiocManager::install("GenomicRanges")
```

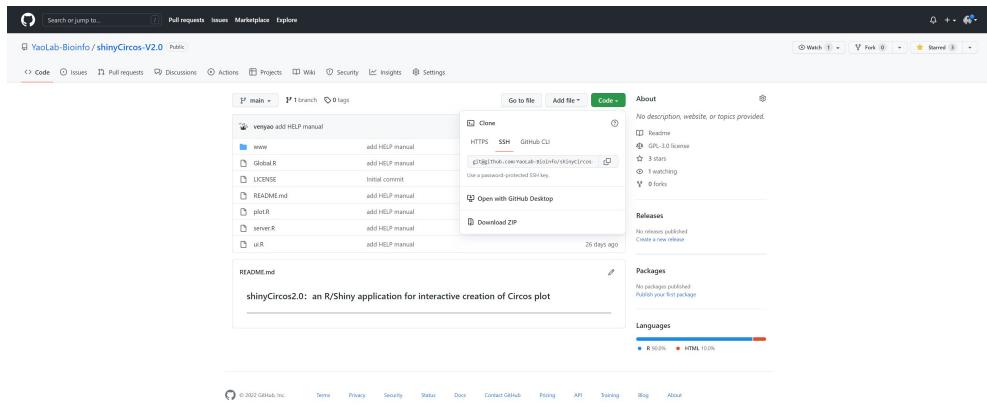
Step 3: Run the shinyCircos-V2.0 application

Start an R session with RStudio and run the following lines of code:

```
shiny::runGitHub("shinyCircos-V2.0", "YaoLab-Bioinfo")
```

This command will download the source code of shinyCircos-V2.0 from GitHub to a temporary directory on your computer, then launch the shinyCircos-V2.0 application in a web browser. **The downloaded shinyCircos-V2.0 code will be deleted from your computer once the web browser is closed. The next time you run this command in RStudio, it will download the source code of shinyCircos-V2.0 from GitHub again to a temporary directory.** This process is cumbersome because it takes some time to download the shinyCircos-V2.0 code from GitHub.

We recommended that users download the source code of shinyCircos-V2.0 from GitHub to a fixed directory on your computer, such as "E:\apps" on Windows, follow the steps shown in the **below**, a name A zip file named "shinyCircos-V2.0-master.zip" will be downloaded to your computer. Move this file to "E:\apps" and extract this file. Then a directory named "shinyCircos-V2.0-master" will be generated in "E:\apps". The scripts "server.R" and "ui.R" can be found in "E:\apps\shinyCircos-V2.0-master". You can then start the shinyCircos-V2.0 application by running the following lines of script in RStudio.



Download source code from GitHub

```
library(shiny)
runApp("E:/apps/shinyCircos-V2.0-master", launch.browser = TRUE)
```

The shinyCircos-V2.0 application will then open in your computer's default browser.

3.4 Drawing Circos diagram with shinyCircos-V2.0

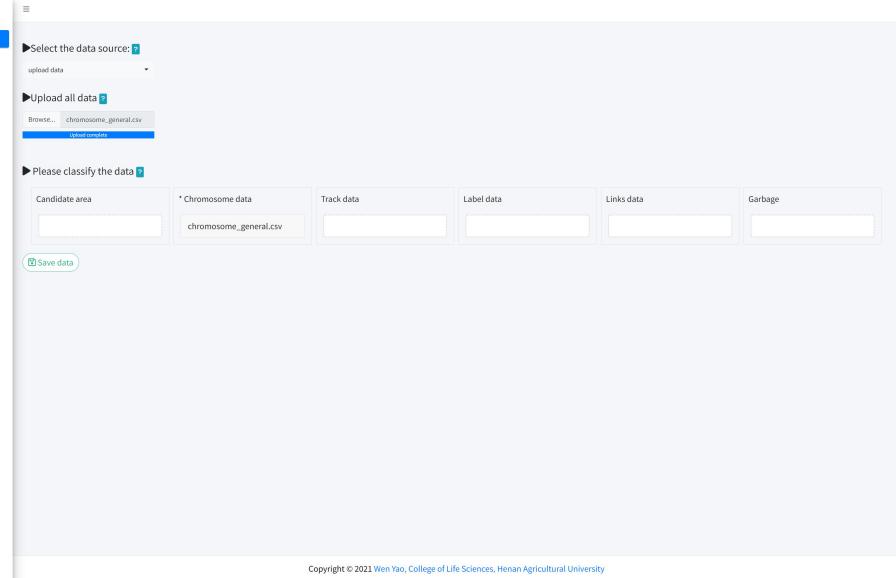
Users can use the shinyCircos-V2.0 application to create Circos diagrams. When making a Circos plot, you must enter a file that defines the length of each chromosome in the genome, as well as several input data arranged along the genome. In this section, we will demonstrate all the basic steps to create a Circos diagram using the example dataset in shinyCircos-V2.0.

3.4.1 Basic steps to create a Circos diagram

Step 1: Prepare and upload "Chromosom data" that defines the length of the genome

The genomic data is a mandatory input file, which defines the frame of the Circos diagram, the scale of the "Sector" (the example dataset can be obtained in the unpacked source file `www\example_data`). Genome data is a text file containing **three or five columns**, three columns for general data and five columns for cell band data. The detailed format of the genomic data is detailed in the "[Input Data Format](#)" section above.

Now, we've prepared this file and stored it on disk (eg "E:/" on Windows). Next, we need to upload this file to the shinyCircos-V2.0 application through the "Data Upload" menu in the shinyCircos-V2.0 application, and select "upload data" as the data source (as shown in the figure below).



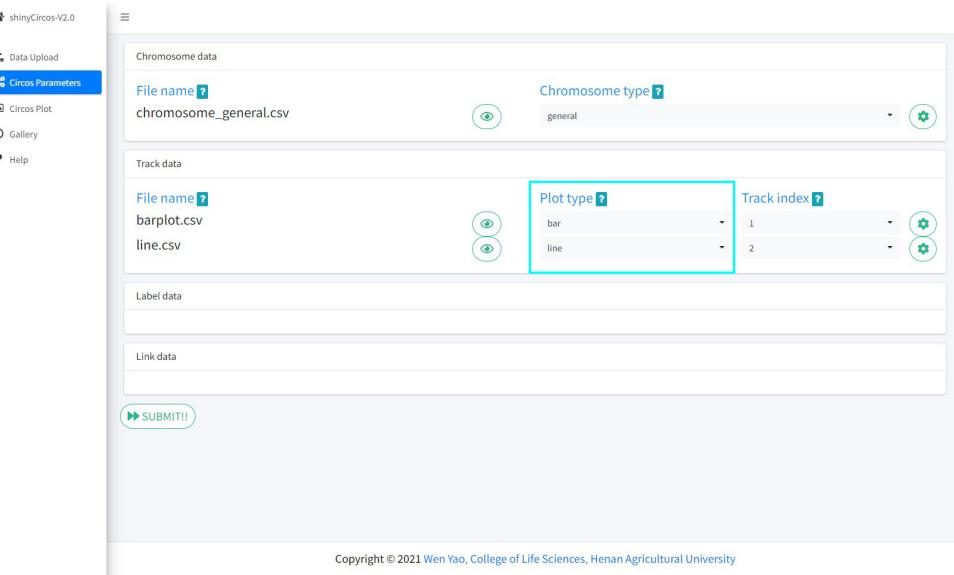
upload chromosome data

Step 2:Upload the "Track data" arranged in a ring

Users can upload several datasets, which are arranged in a circle along the genomic data uploaded in step 1. The "Track data" box in the category box of the "Data Upload" menu is provided for this purpose (see image above). Here, we use two input datasets (barplot.csv and line.csv) to demonstrate the process. The detailed format for creating input files of different types of "Tracks" is detailed in the "[Input Data Format](#)" section above. First, we prepare two files and store them on disk (for example, "E:/" on Windows). To upload the files "barplot.csv" and "line.csv" into the software, then drag and drop them into "Track data", **click "Save" data** and **"Submit!"**.

Step 3:Set the "Track" location and plot type for each input dataset

By default, the order of dragging and dropping into the selection box is the order in which "Tracks" are drawn, and the default drawing type for each input dataset is "point". Because we want to use the file "barplot.csv" to create a bar chart, we need to set the "Plot type" corresponding to the file "barplot.csv" to "bar" (as shown below), and the same "line.csv" corresponds to "Plot type" is set to "line".



parameter setting interface of shinyCircos-V2.0

Step 4: Click the "Submit!" button to draw the graph

After all the input datasets have been successfully uploaded to the shinyCircos-V2.0 application and the track positions and plot types are set correctly, we need to click the "Submit!" button at the bottom of the "Circos Parameters" menu to tell shinyCircos-V2.0 to draw the graph . **By default, shinyCircos-V2.0 will use random colors or predefined colors when drawing graphics.**

3.4.2 Replace the input dataset used to draw "Track"

Circos diagrams usually consist of several basic types of diagrams distributed on different orbits. Each graph is created using a user-uploaded input dataset. From time to time, we may need to replace one or more of these input files so that we can update some components of a single genome graph without recreating the entire graph. For example, we want to create a discrete histogram by replacing Track2's "line.csv" with a new input file "rect_discrete.csv". To achieve this, we can go to "Data Upload" and upload "rect_discrete.csv" to the software, replace "line.csv" in the "Track data" category box with "rect_discrete.csv", and replace the original Drag "line.csv" to the "Garbage" category box, then click "Save data", then "Submit!". At the same time, we need to set the plot type of the newly imported data to "rect_discrete". Finally, we need to click the "Go!" button at the bottom of the "Circos Parameters" panel to tell shinyCircos-V2.0 to update the corresponding plot results.

3.4.3 Download the created single genome graph in PDF or SVG format

After the Circos graph is generated, users can use the widgets "Download PDF-file" and "Download SVG-file" above the "Circos Plot" menu panel to download the plot results in PDF or SVG format (as shown below). By default, the two files downloaded are named "shinyCircos.pdf" and "shinyCircos.svg". The downloaded PDF file "shinyCircos.pdf" can be opened in Adobe Acrobat, and the downloaded SVG file "shinyCircos.svg" can be opened

in Google Chrome browser. We do not recommend you to right-click to save the image. To ensure clarity, we recommend You use PDF files to store images and then convert to bitmaps.

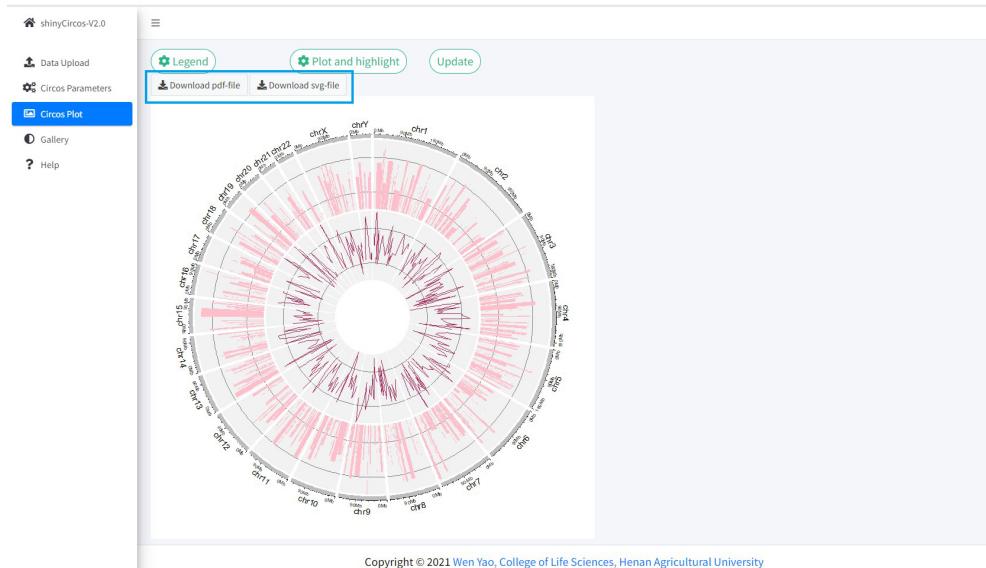


Image download

3.4.4 Complete steps to draw Circos diagram with shinyCircos-V2.0

Using shinyCircos-V2.0 you can create 10 different types of graphs, including point, line, bar, stack-line, stack-point, rect-gradual, rect-discrete, heatmap-gradual, heatmap-discrete and ideogram. To create a Circos graph, at least one input data file is required, that is, a genome data file that defines the length of the genome, so that the output graph has only the chromosome part. In this section, we will show the key steps in drawing a Circos diagram (as shown below). Different drawing types and specific drawing parameters are not described here, and users can learn by referring to the sample data.

shinyCircos-V2.0: an R/Shiny application for interactive creation of Circos plot

- Software references

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10. Andrie de Vries. *sortable*: Enables drag-and-drop behaviour in Shiny apps. R package version 0.4.5 (2021)
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14. Gu, Z. *ComplexHeatmap*: efficient to visualize associations between different sources of data sets and reveal potential patterns. R package version 2.10.0 (2015)

- Further references
- Please cite

This application was created by [Wen Yao](#) and [Yazhou Wang](#). Please send bugs and feature requests to Wen Yao (ywhzau@gmail.com) or Yazhou Wang (gentelemanwang@gmail.com). This application uses the [shiny package from RStudio](#).

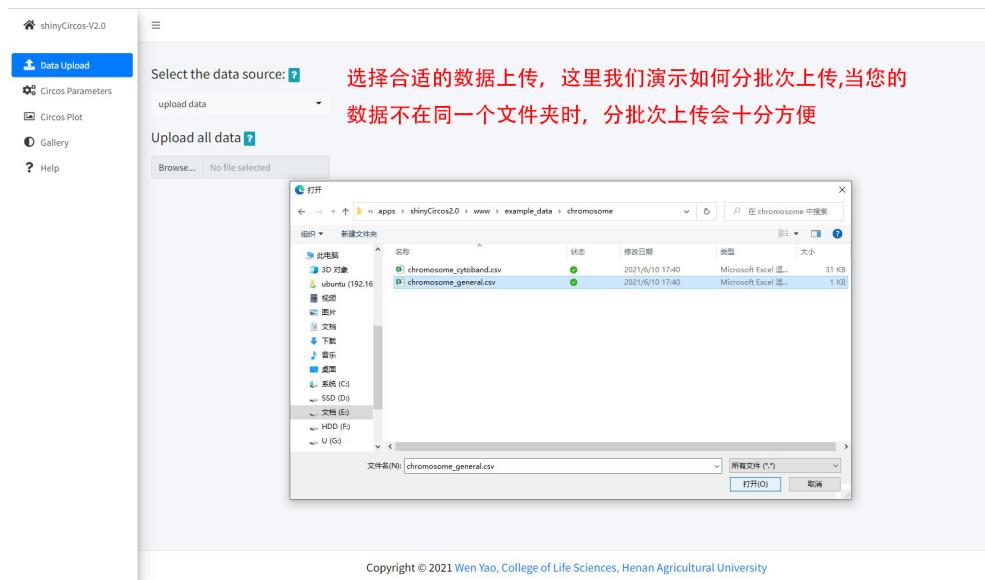
Henan Agricultural University 	Wen Yao's lab Web site GitHub Google Scholar ResearchGate ORCID	Citation Wang et al. 2022
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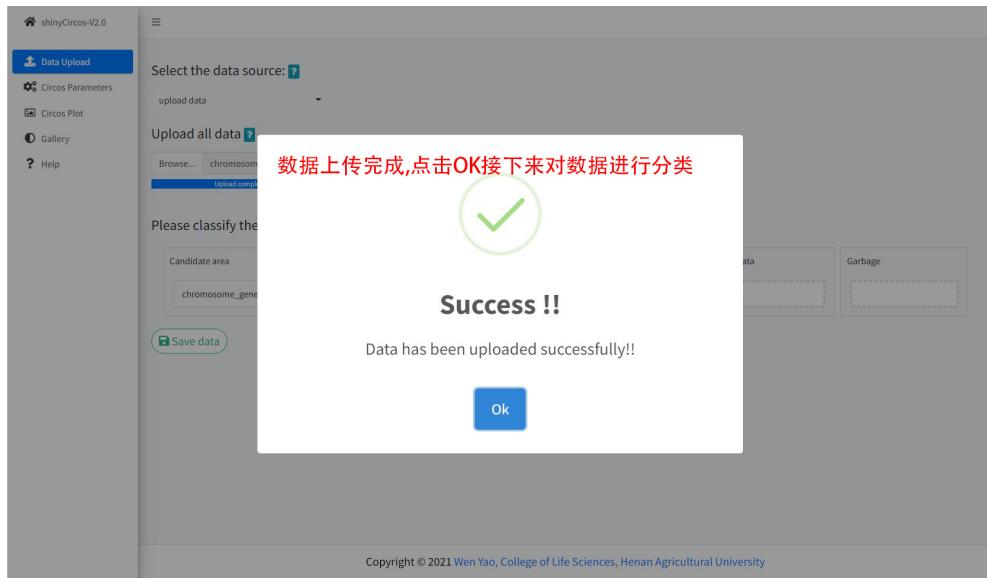
Run the software and enter the "Data Upload" page



Upload data at "Upload all data" page



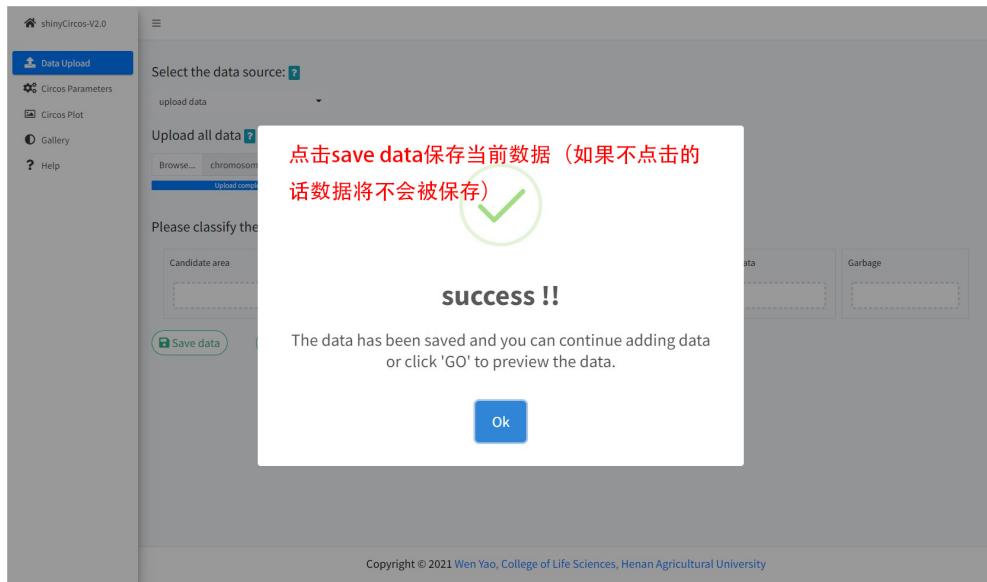
Select data to upload



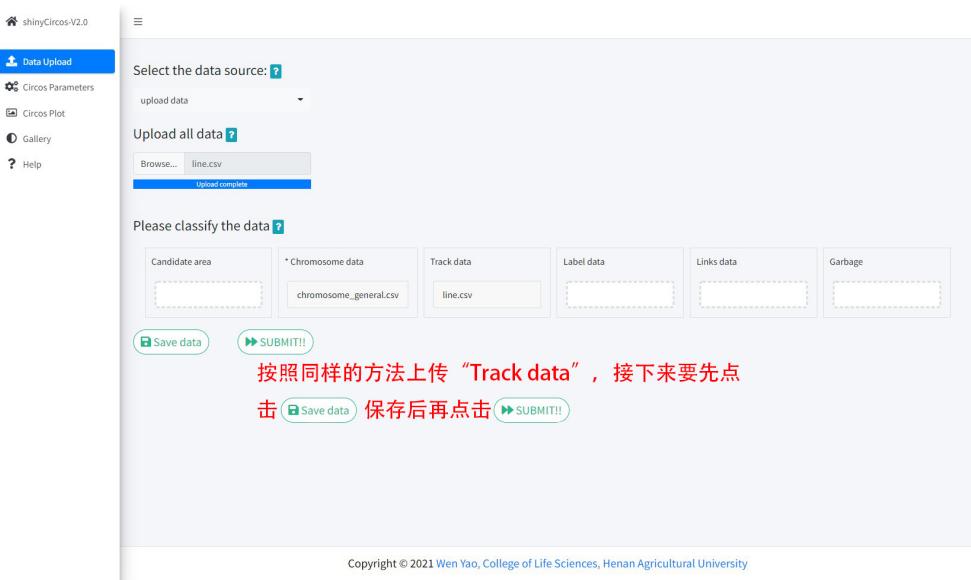
data upload successfully



Distribute data



Drag the data to the appropriate category box and click "Save data"



Add "Track data"

Chromosomes data

File name: chromosome_general.csv

Chromosome type: general

Track data

File name: line.csv

Plot type: line

Track index: 1

Label data

Link data

▶ SUBMIT!!

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Adjust drawing type

this track plot type is:line

Data color: Random

Fill area: Yes

Area color: #808080

Color transparency: 1

Y coordinates of baselines: 0.25,0.75

Baselines color(s): #808080

Background color(s): #F2F2F2

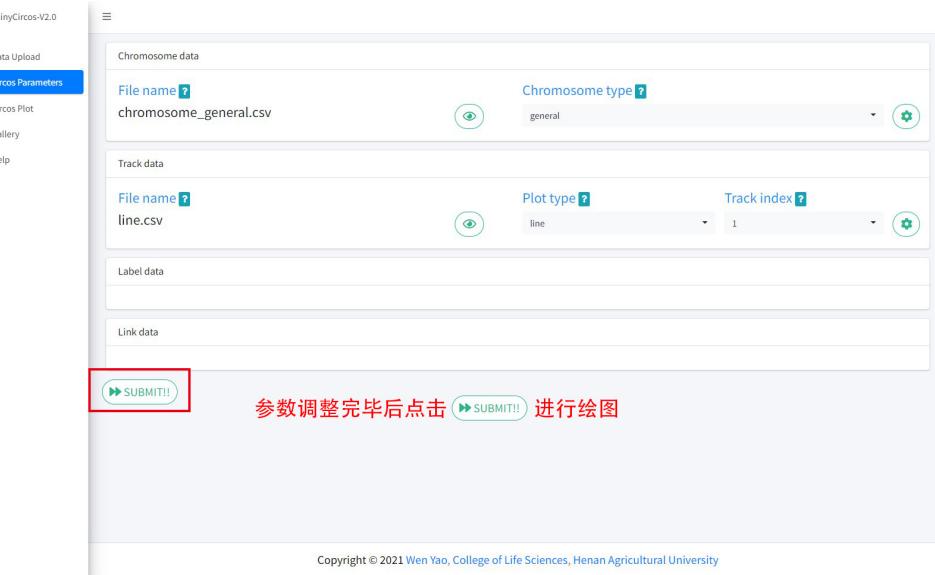
Track height: 0.5

Distance from the next section: 0.01

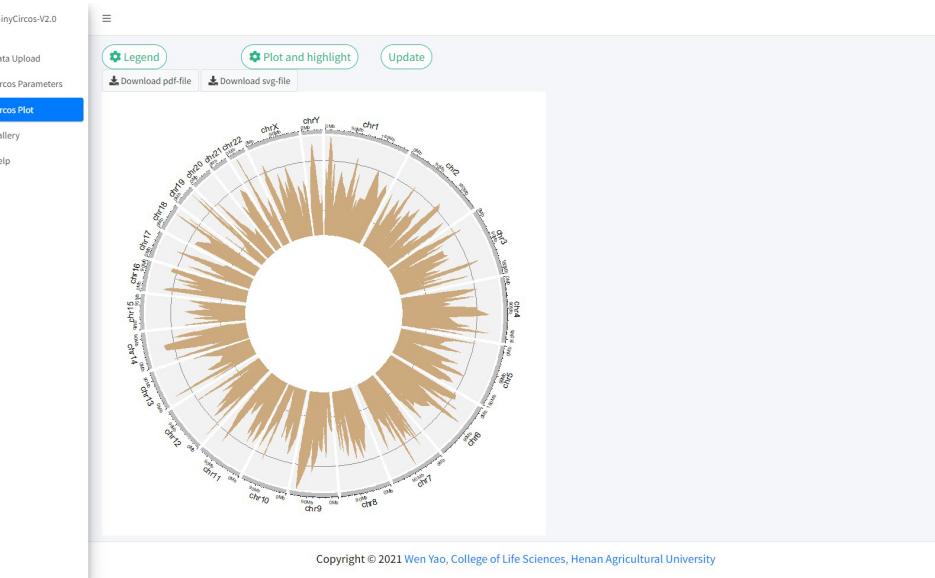
Add borders: No

Add y-axis: Yes

Adjust some parameters of "Track"



After the parameter setting is completed, click the "SUBMIT!!" button to start the drawing process



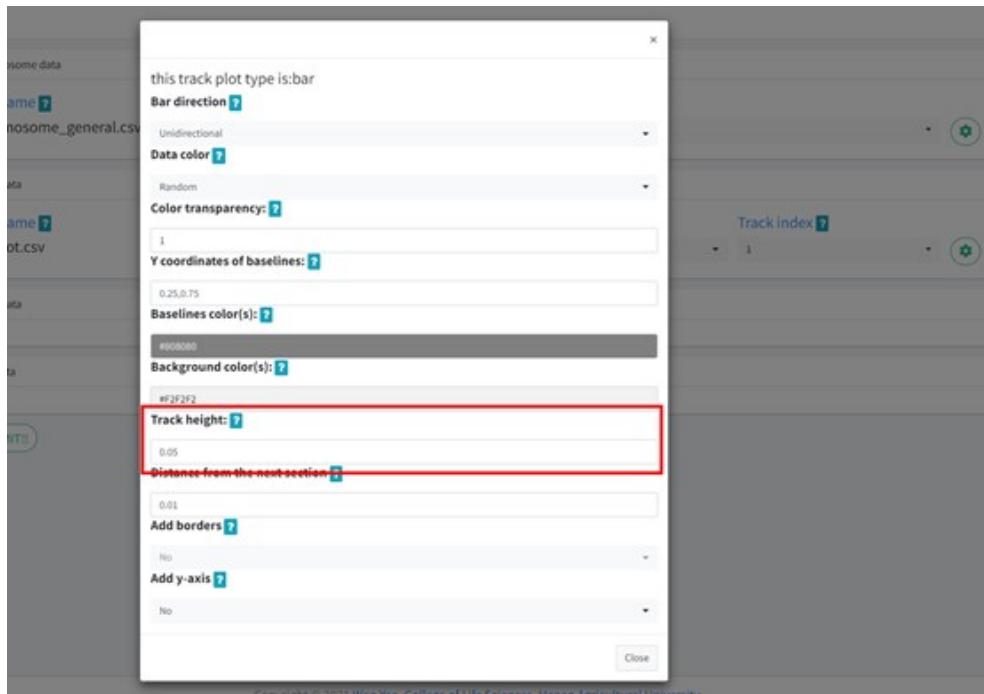
Finally get the Circos diagram

3.4.5 Plot options for decorating Circos diagrams

The small gear button on the right side of each row of data in the "Circos Parameters" menu will pop up a prompt box for specific parameters after the user clicks it. The settings for some of these options are demonstrated below.

3.4.5.1 Plot options for decorating Circos diagrams

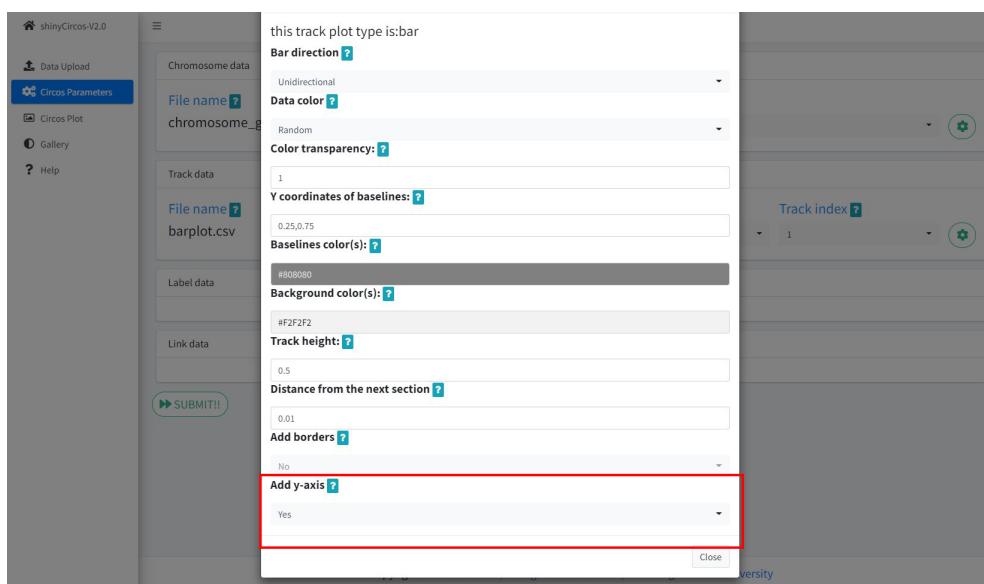
The default Track height of shinyCircos-V2.0 is only 0.1, which is 5% of the unit circle radius. This value may not be suitable, so it needs to be adjusted by the user. The adjustment of the Track height is very simple, just need the user to click the corresponding Track data. Gear icon, adjust "Track height" in the pop-up menu (as shown below).



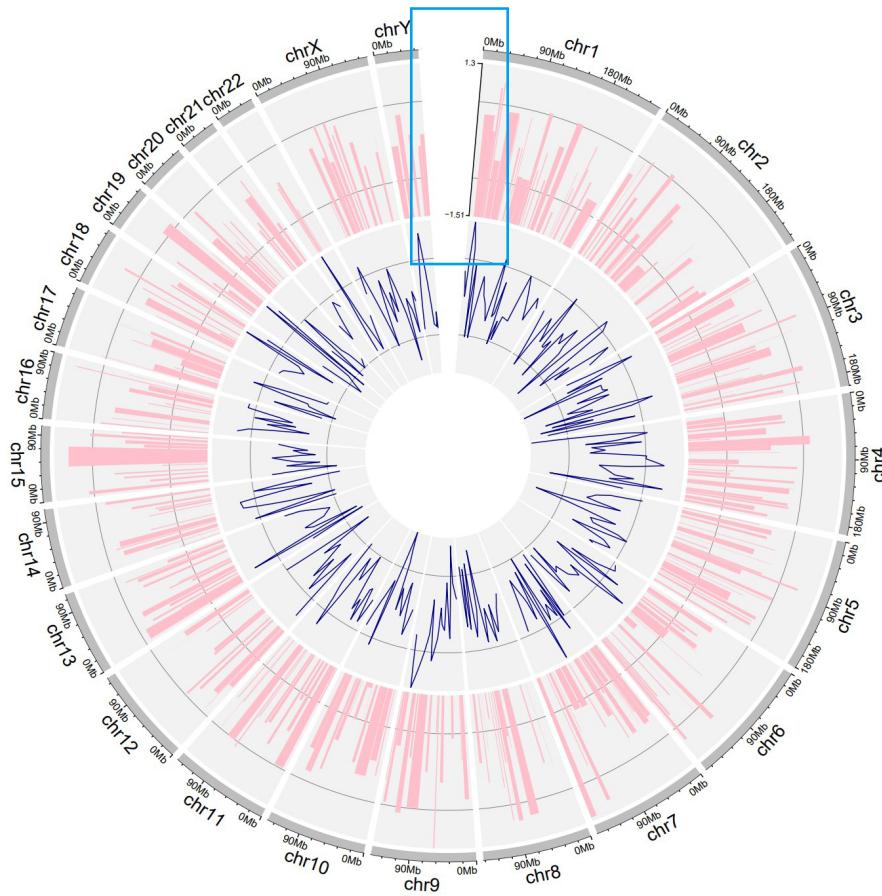
Adjust the height of the "Track"

3.4.5.2 y-axis

shinyCircos-V2.0 adds the function of adding the y-axis to the track, so that the range of the y-axis can be displayed. Users can select "yes" in "Add y-axis" in the pop-up parameter box and then update the drawing to get The image with the y-axis added (as shown below).



add y-axis



Circos plot with y-axis

3.4.5.3 Distances between adjacent tracks

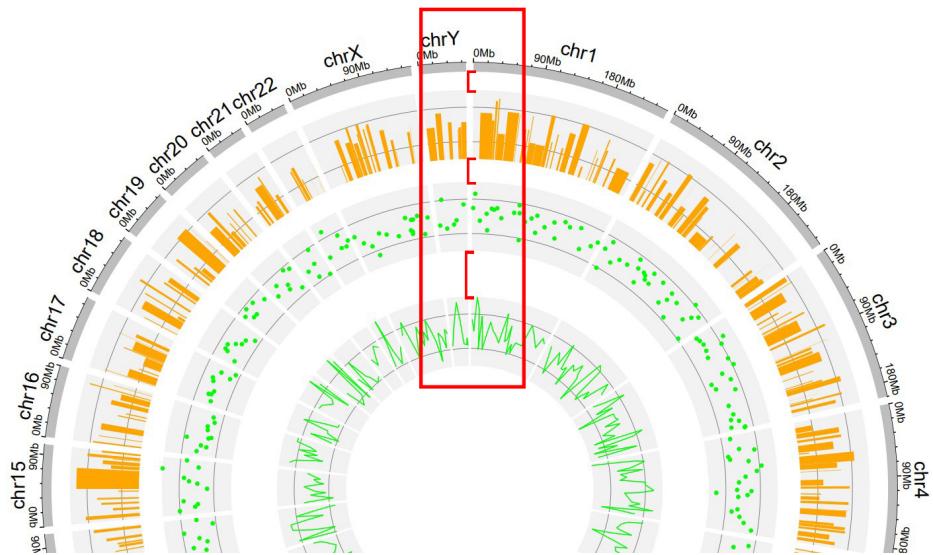
In the process of using shinyCircos-V2.0, users can adjust the spacing of different tracks according to their needs. Users can input the appropriate value in "Distance to the next track" in the pop-up parameter box and click the "SUBMIT!!" button Draw according to the current configuration (as shown below).

The screenshot shows the shinyCircos-V2.0 web application. On the left, there's a sidebar with links like 'shinyCircos-V2.0', 'Data Upload', 'Circos Parameters' (which is currently selected), 'Circos Plot', 'Gallery', and 'Help'. The main area is titled 'Circos Parameters' and contains several configuration fields:

- Chromosome data**: File name: chromosome.gff, Symbol type: 16, Point size: 0.6.
- Track data**: File name: barplot.csv.
- Label data**.
- Link data**.
- Background color(s)**: #008080.
- Track height**: 0.05.
- Distance from the next section**: 0.01 (this field is highlighted with a red border).
- Add borders**: No.
- Add y-axis**: No.

At the bottom left is a green 'SUBMIT!' button, and at the bottom right is a 'Close' button.

Adjust the distances between adjacent tracks

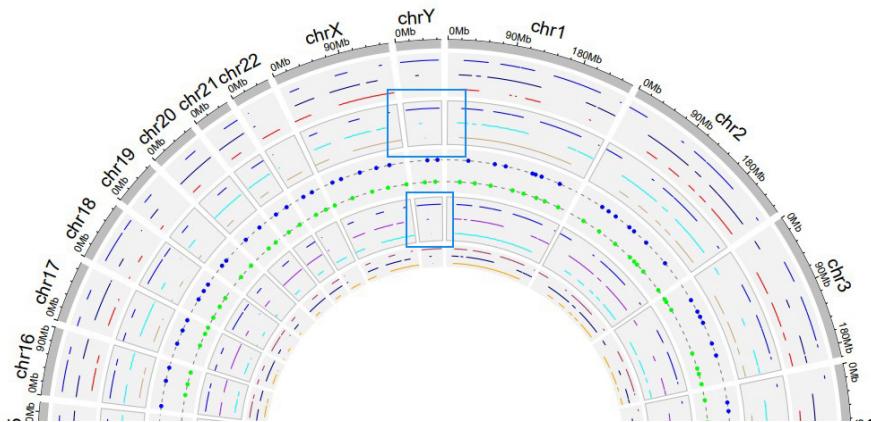


Different distances between adjacent tracks

3.4.5.4 Cell border

In shinyCircos-V2.0, users can add borders to different "Tracks" to emphasize a certain "Track". Users can input appropriate values in "Add borders" in the pop-up parameter box and click "SUBMIT!" !" button to draw according to the current configuration (as shown below).

Add cell borders

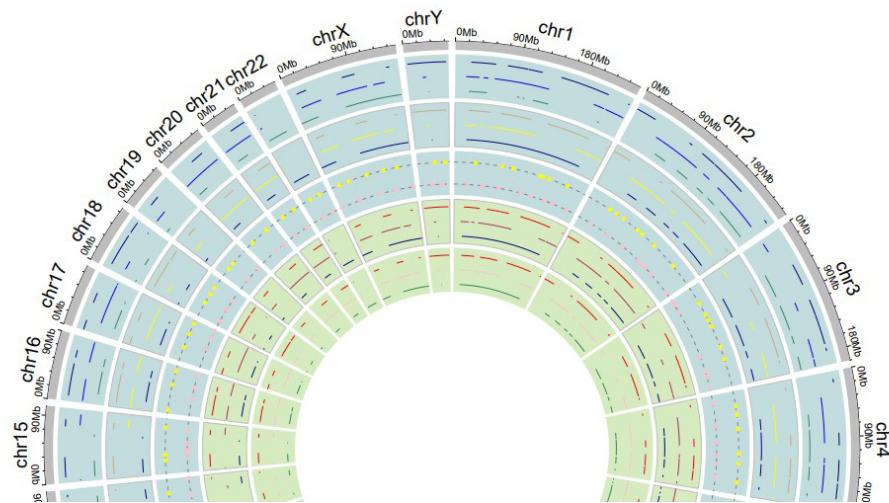


"Cell" with border

3.4.5.5 background color of "Track"

In shinyCircos-V2.0, users can adjust the background color of different "Track" (some drawing types do not support background color adjustment) to group "Track". Select the appropriate color in "color(s)" or input the appropriate value to adjust the color of the "Track". After the adjustment, click the "SUBMIT!!" button to draw according to the current configuration (as shown in the figure below).

Change the background color of "Track"

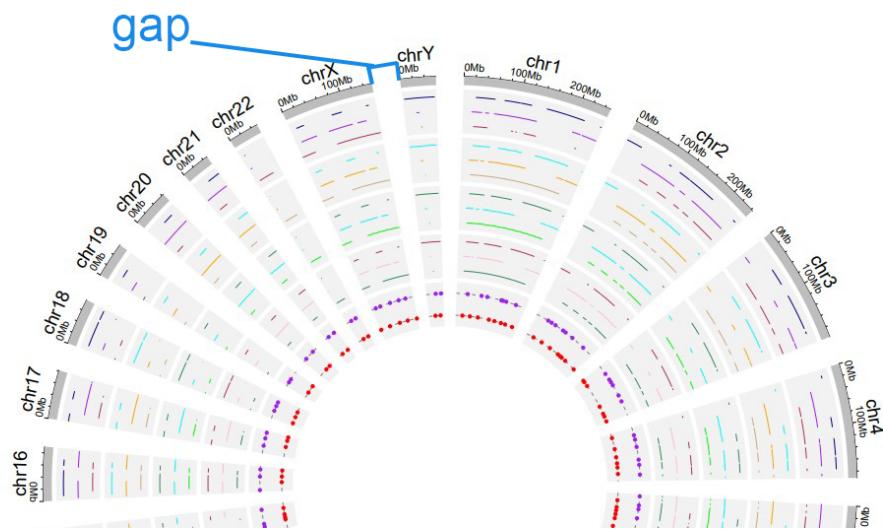


"Track" with different background colors

3.4.5.6 Distances between adjacent sectors

In shinyCircos-V2.0, users can adjust the spacing between each "Sector" on the parameter adjustment page of chromosome data. Just enter the value to flexibly adjust the spacing between each "Sector", and the adjustment is completed. Then click the "SUBMIT!!" button to draw according to the current configuration (as shown below).

Adjust the distances between adjacent setcors



Different distances between adjacent sectors

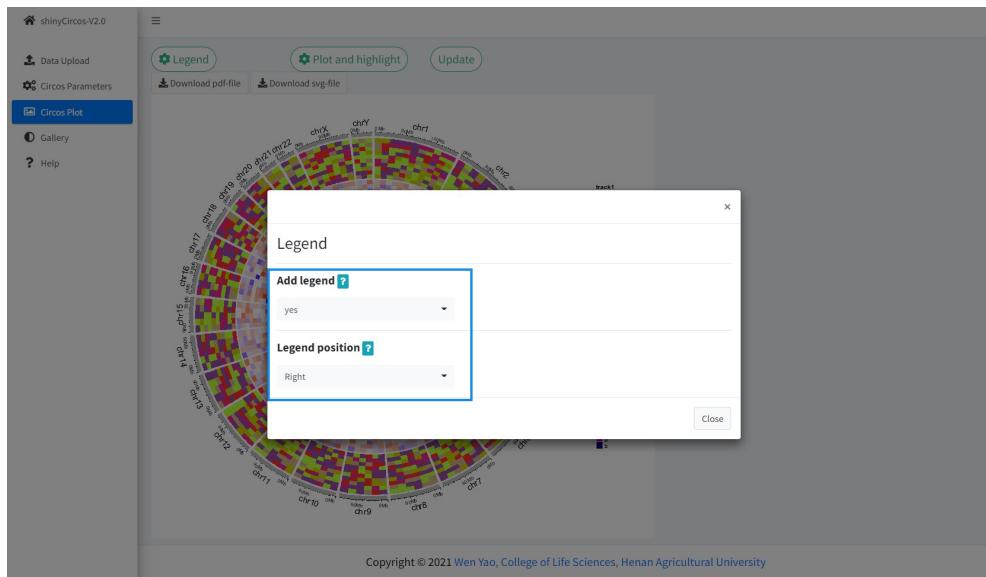
3.5 Modify other parts of the Circos diagram

Compared with the old version of shinyCircos, in addition to the changes in the interface and usage logic, we have also improved some functions, added support for some graphic legends, and supported highlighted areas.

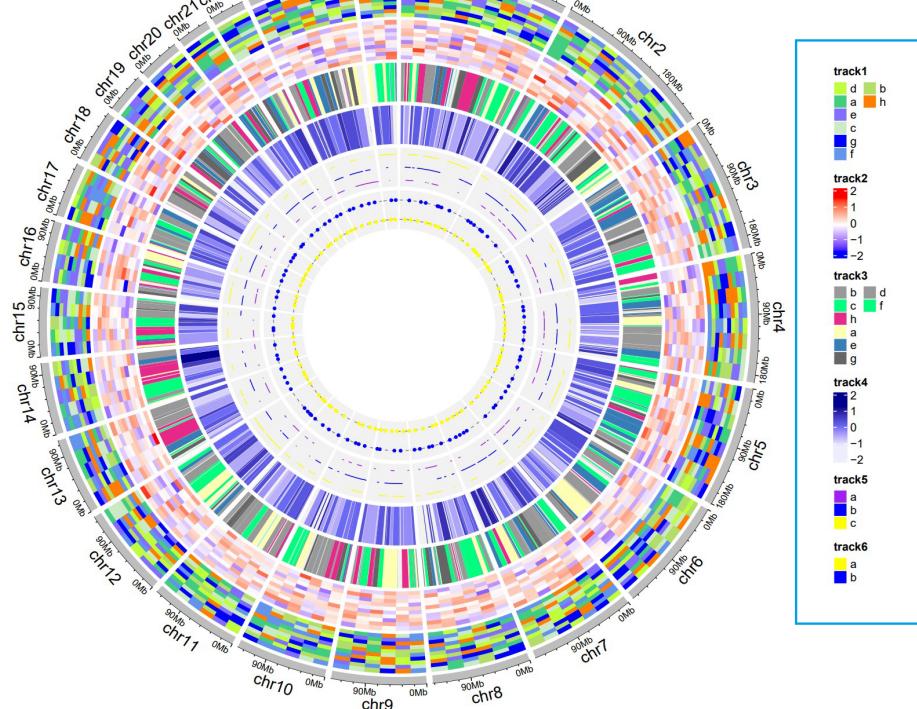
3.5.1 Add legend

When the user draws six types of "Track", "stack-line", "stack-point", "heatmap-gradual", "heatmap-discrete", "rect-gradual" and "rect-discrete", the user You can click the

"Legend" button in the "Circos Plot" menu to add a legend, which supports drawing the legend at the bottom or right side of the Circos plot (see the figure below).



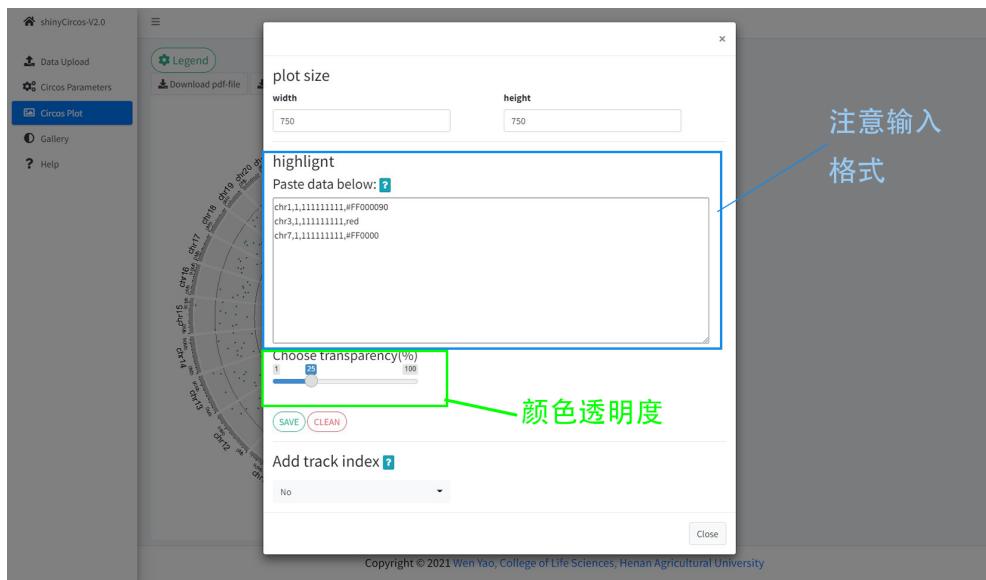
Add legend



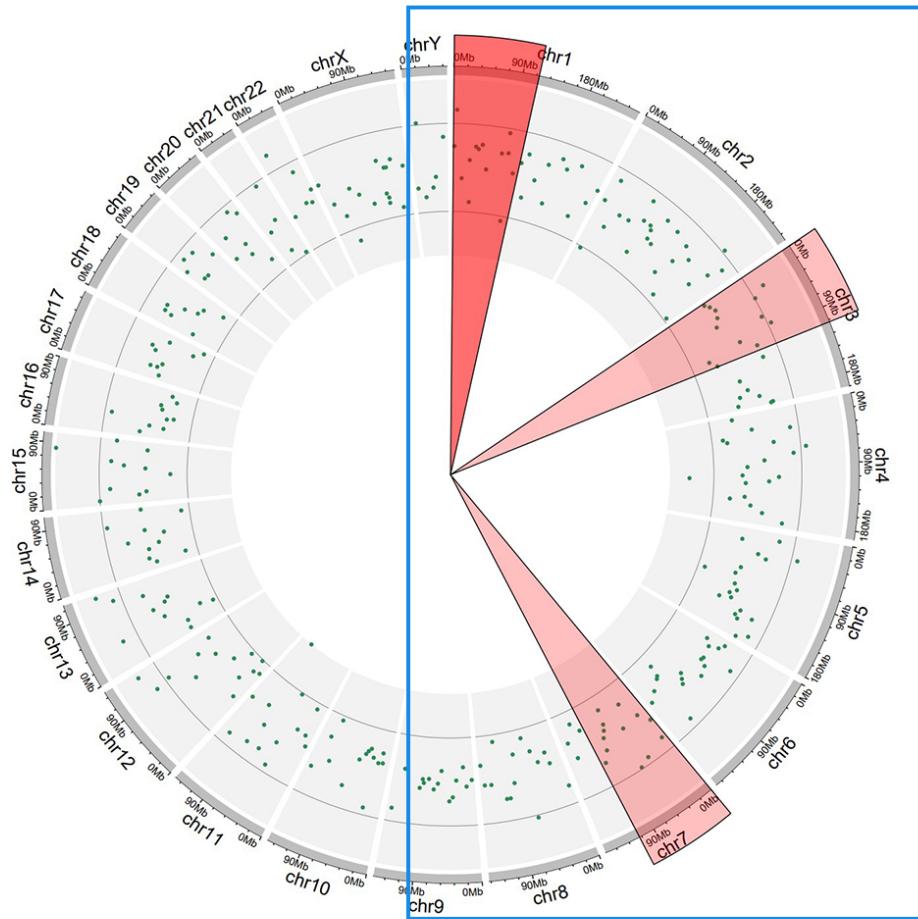
Legend for circos diagram

3.5.2 Highlight specific genomic regions

The new version of shinyCircos-V2.0 supports highlighting some areas, helping users to highlight some areas or classifying some "Sectors", helping users to display their own data according to their needs. Users can click the "Plot and highlight" button in the "Circos Plot" menu to add highlighted areas. As shown in the figure, three color input formats are supported. When inputting a hexadecimal color code with transparency, the transparency selection below will not be applied.



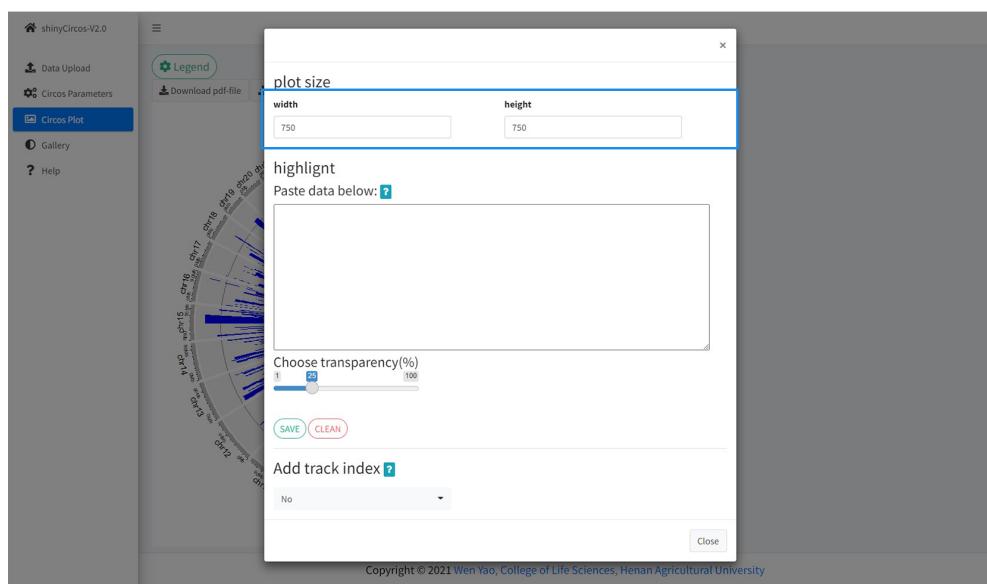
Add highlighted area



Circos diagram with highlighted areas

3.5.3 Adjust plotsize

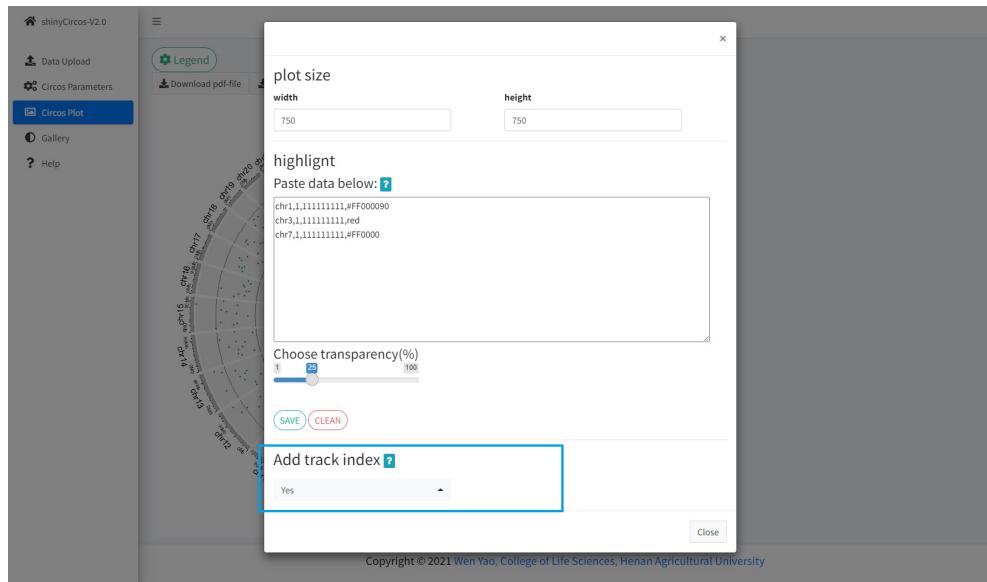
shinyCircos-V2.0 supports resizing of images, and users can easily adjust the height and width of images. (As shown below)



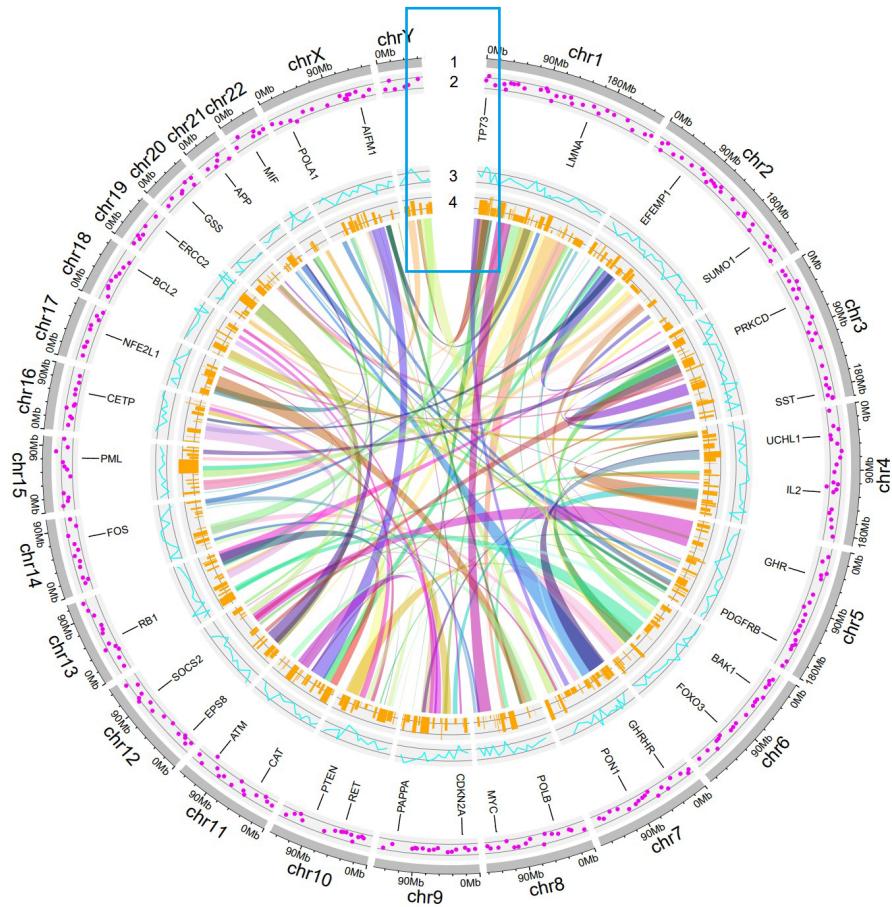
Adjust the Circos Plot

3.5.4 Add "Track index"

"Track index" is the index of "Track", which can add labels to different "Tracks" to facilitate users to make subsequent comments. Users can click the "Plot and highlight" button in the "Circos Plot" menu and then choose whether to add the "Track" index at "Add track index" (as shown in the figure below).



Add Track index



Circos diagram with Track index