

# TALKING IN CIRCOS

RCircos: an R package

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# CIRCOS

- A genomic data visualisation tool: some data patterns are easier to understand when presented in a circular format
- Flexible tool: different data types

# WHERE TO FIND CIRCOS

- Circos software

<http://circos.ca/>

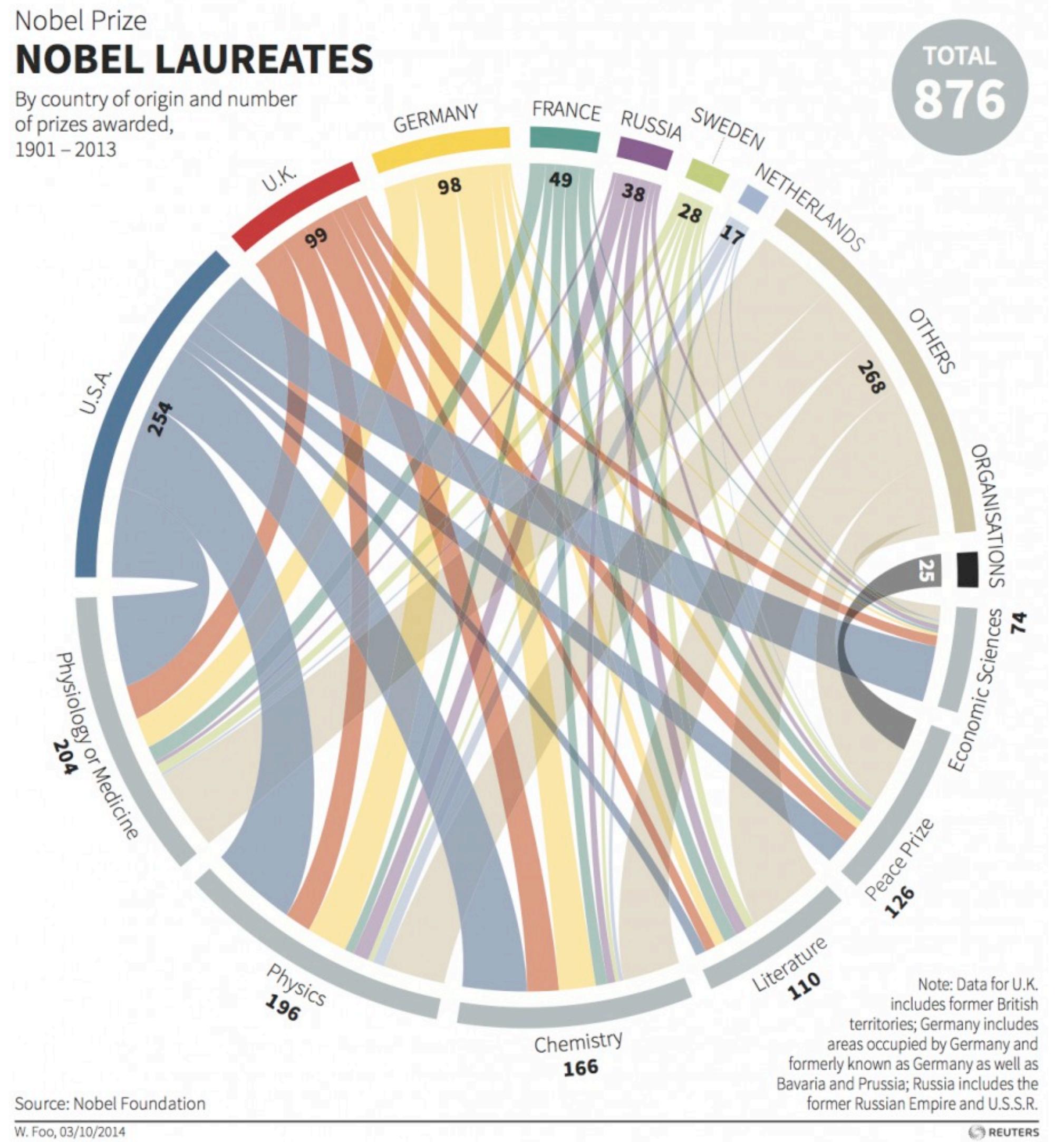
- Circos Online Tool & variants (eg: circosVCF)

<https://omictools.com/circosvcf-tool>

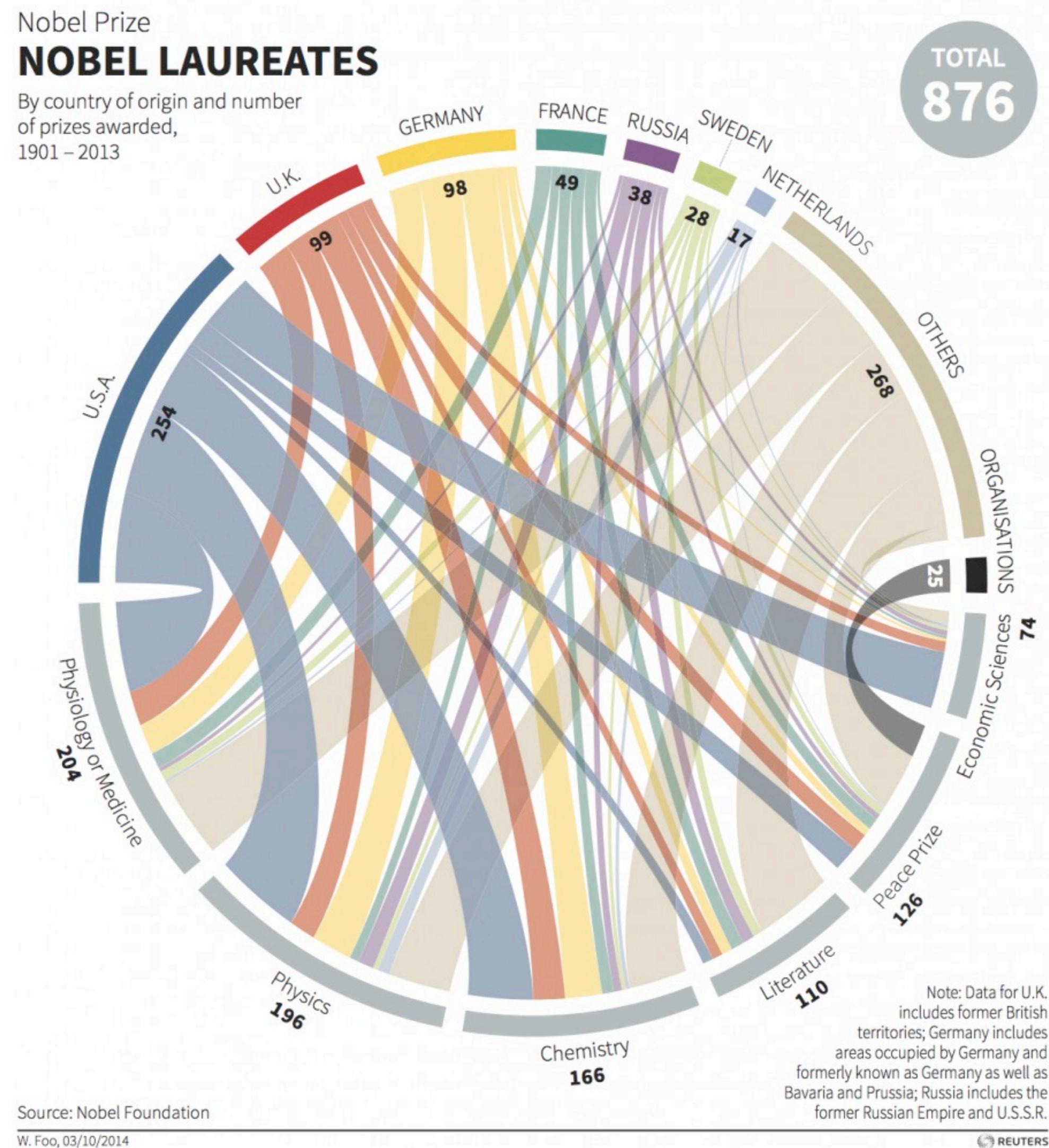
- R-package: RCircos

<https://cran.r-project.org/package=RCircos>

# EXAMPLES



# EXAMPLES

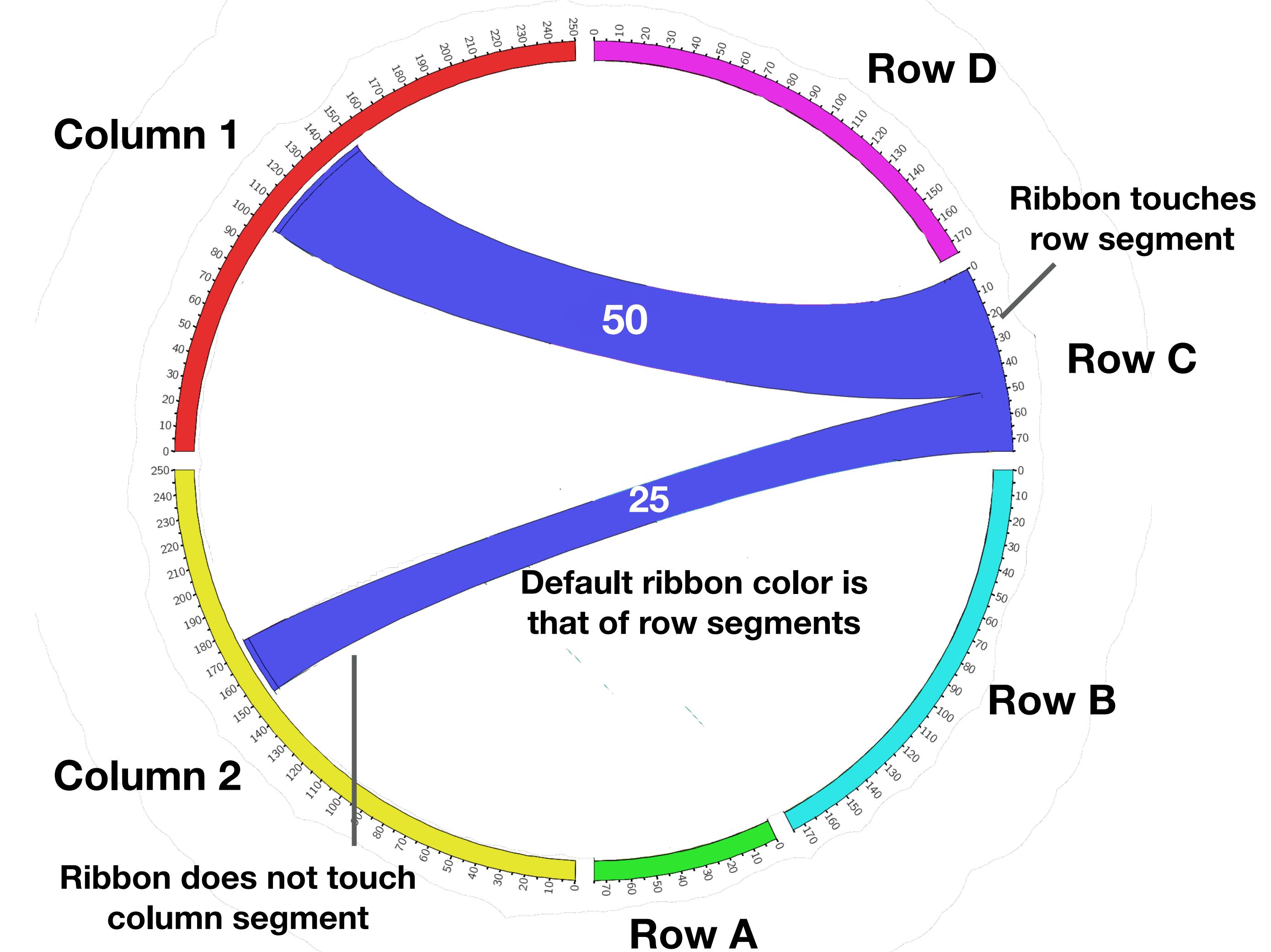


## Global Flow of People 2005-2010



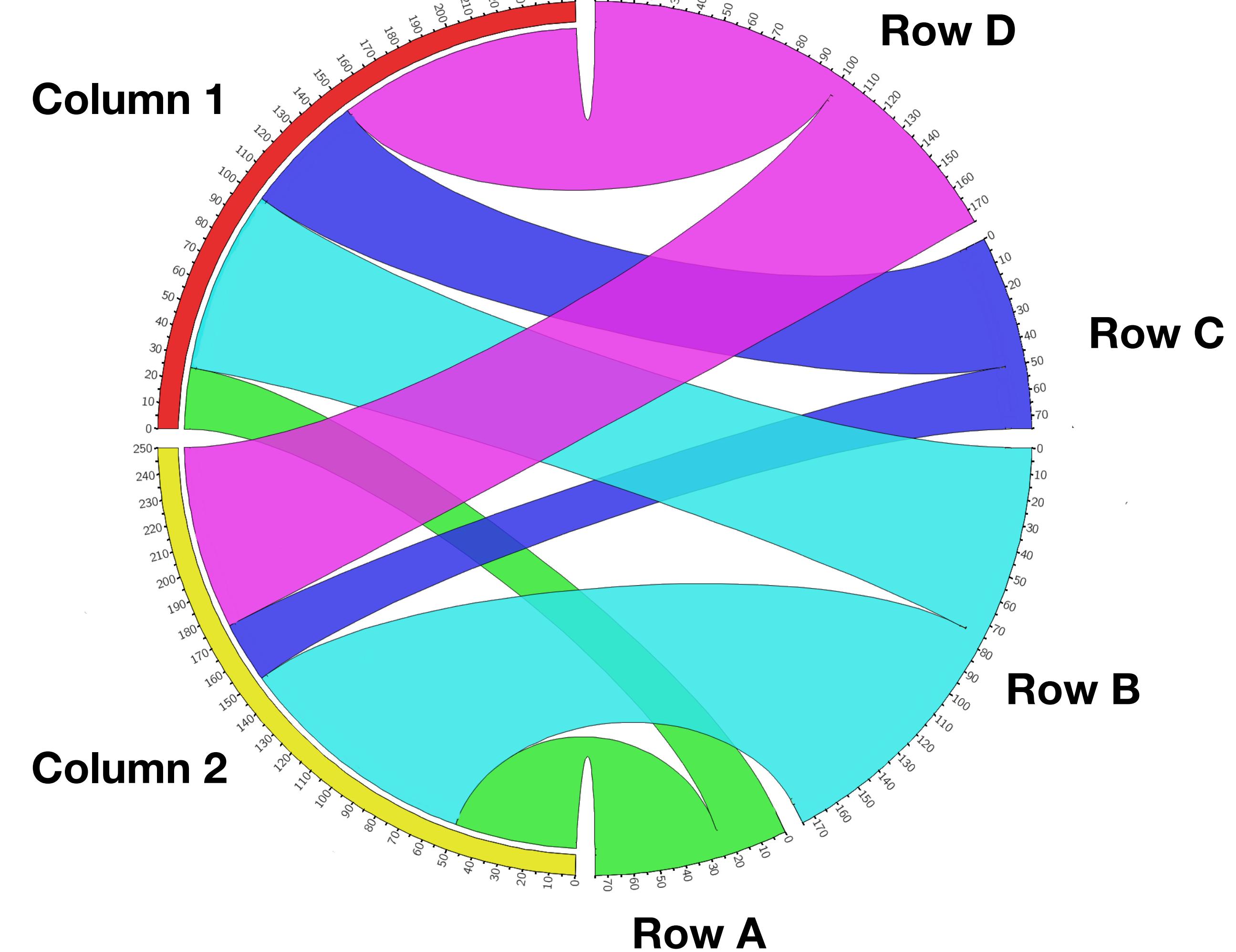
# TABULAR DATA VISUALISATION

	Col 1	Col 2
A	25	50
B	75	100
C	50	25
D	100	75

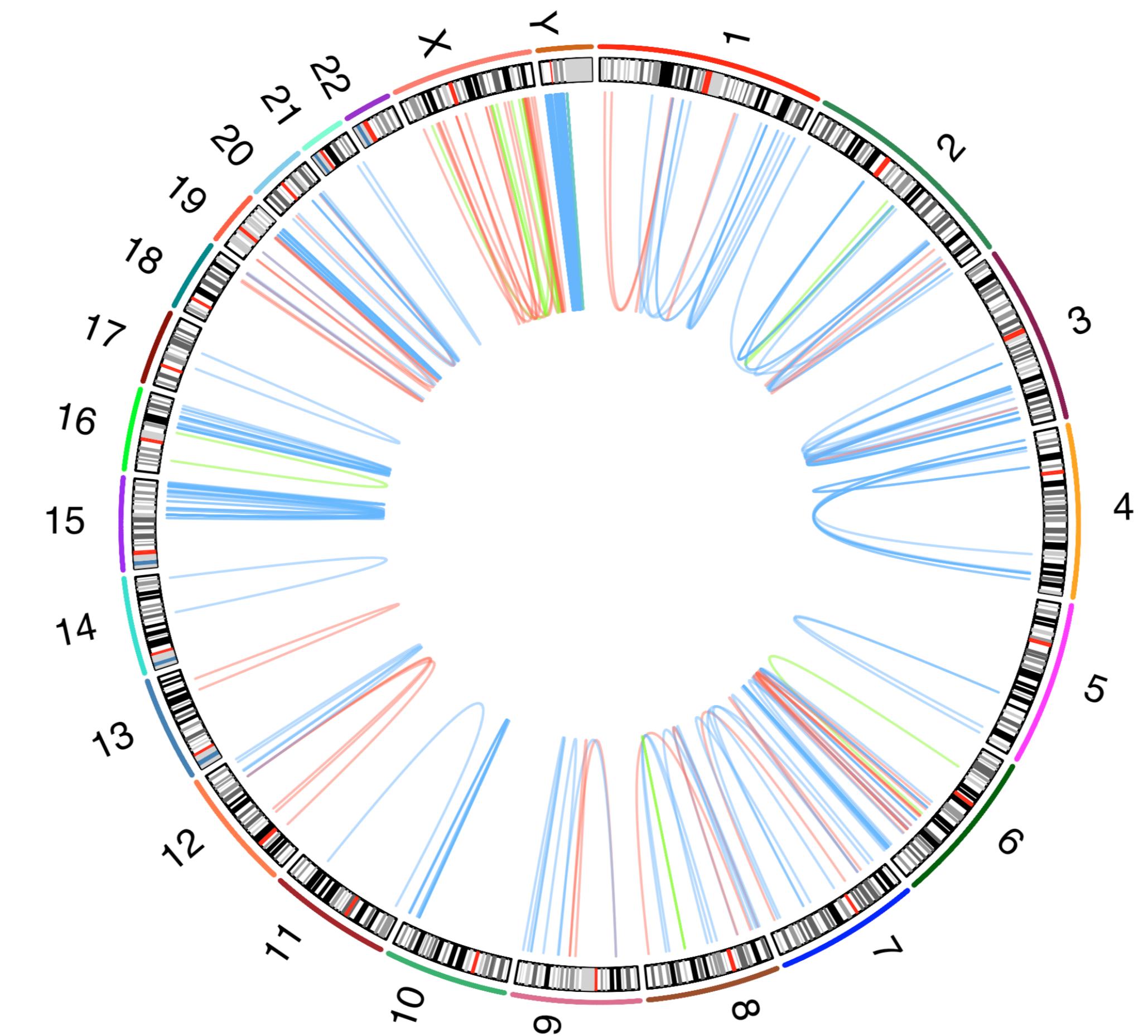


# TABULAR DATA VISUALISATION

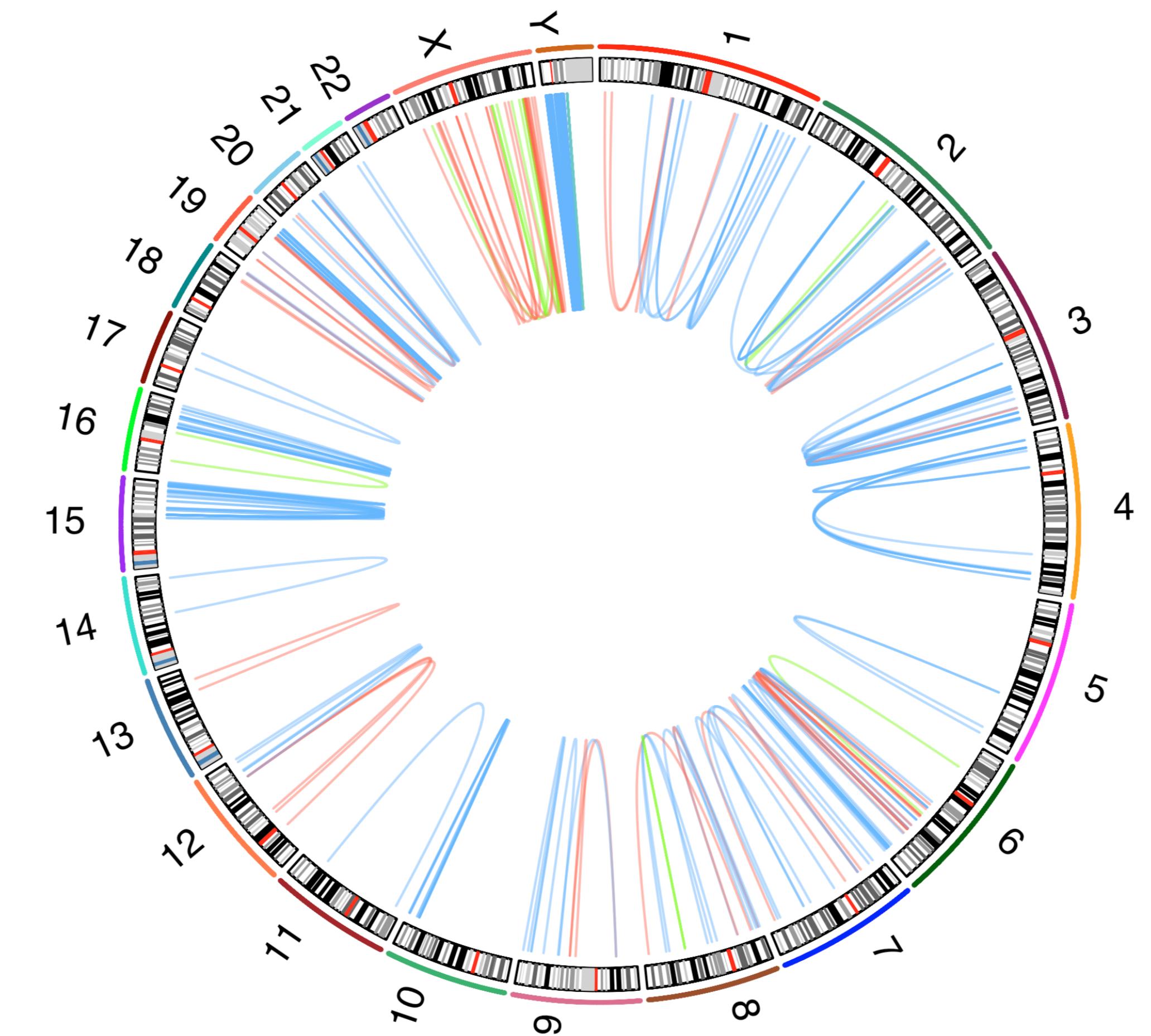
	Col 1	Col 2
A	25	50
B	75	100
C	50	25
D	100	75



# GENOMIC/LINK DATA VISUALISATION

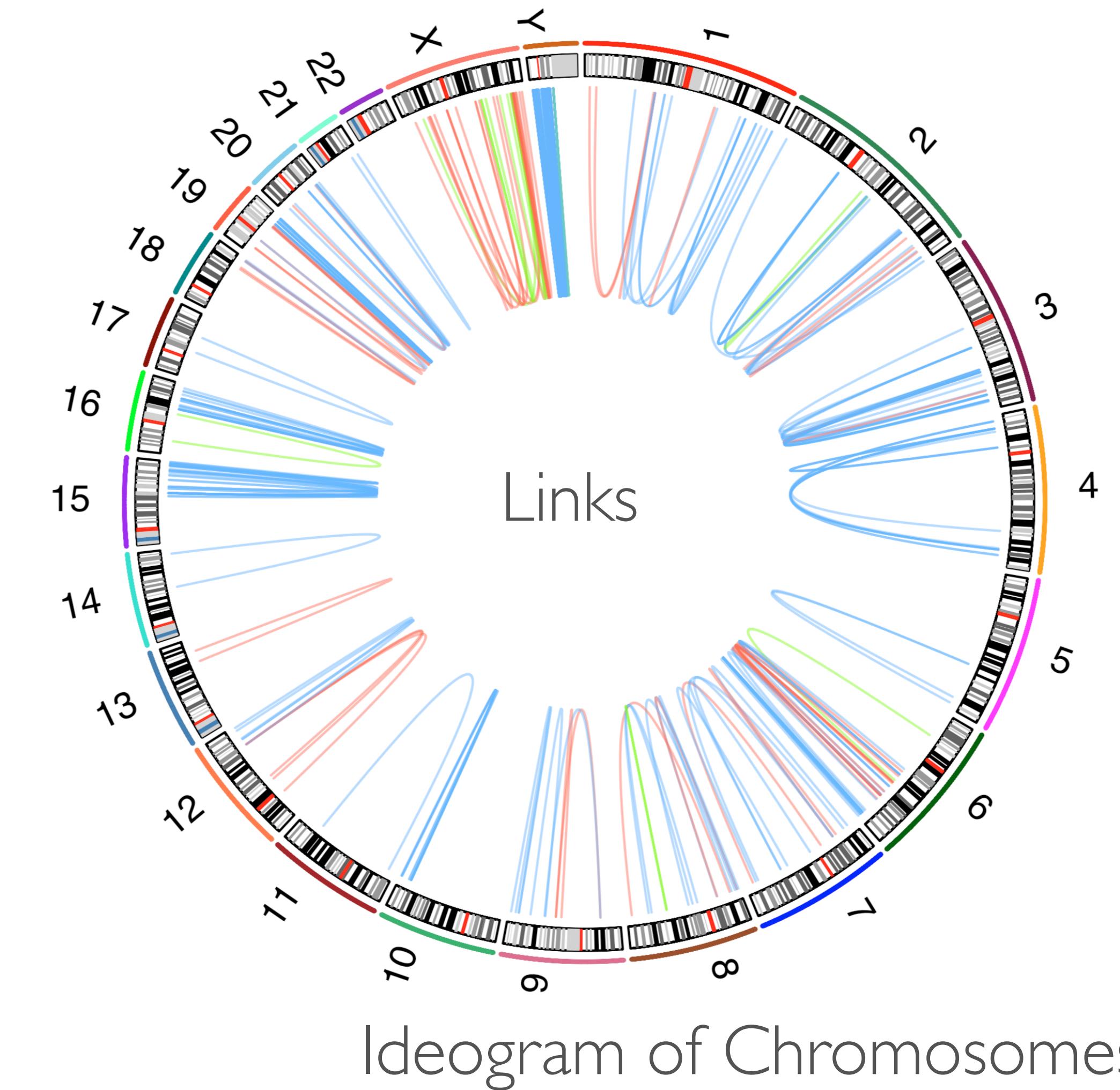


# GENOMIC/LINK DATA VISUALISATION



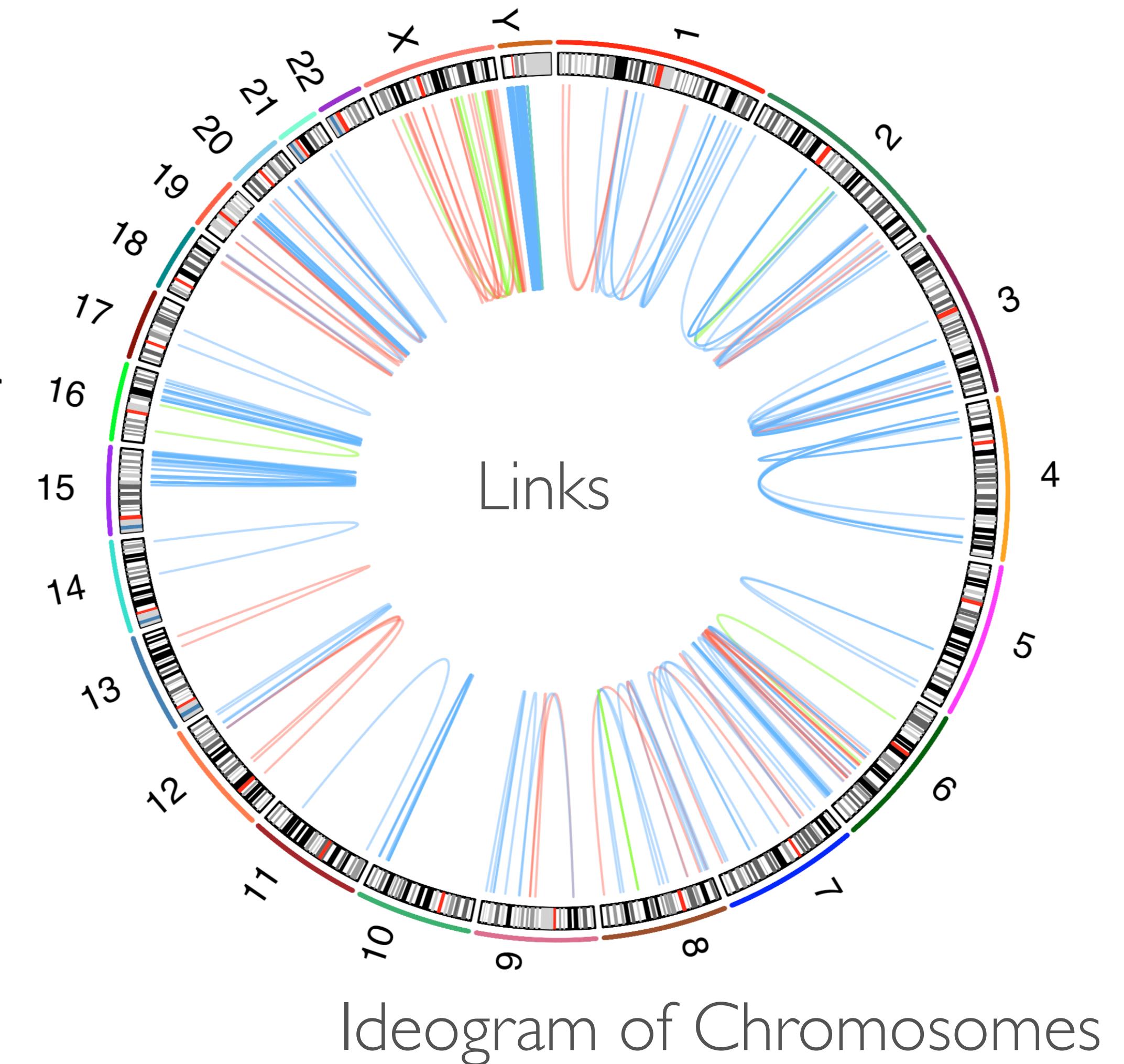
Ideogram of Chromosomes

# GENOMIC/LINK DATA VISUALISATION



# GENOMIC/LINK DATA VISUALISATION

Chromosome	chromStart	chromEnd	Chromosome.1	chromStart.1	chromEnd.1	PlotColor
chr1	166798529	166798530	chr1	167451115	167451116	red
chr16	58245244	58245245	chr16	62304320	62304321	blue
chr8	95604859	95604860	chr8	95734714	95734715	green



# PLOT TYPES

- Paired-location, scatter, line, histogram, heat map, tiles, and text elements plots.
- Plots may be combined in a single figure and multiple tracks are supported.

# R-CIRCOS STEPS

- Install and load RCircos

```
install.packages("RCircos")
```

```
library(RCircos)
```

- Discover package data/load input data

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

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

```
> head(UCSC.HG19.Human.CytoBandIdeogram)
```

	Chromosome	ChromStart	ChromEnd	Band	Stain
1	chr1	0	2300000	p36.33	gneg
2	chr1	2300000	5400000	p36.32	gpos25
3	chr1	5400000	7200000	p36.31	gneg
4	chr1	7200000	9200000	p36.23	gpos25
5	chr1	9200000	12700000	p36.22	gneg
6	chr1	12700000	16200000	p36.21	gpos50

```
> head(RCircos.Gene.Label.Data)
```

	Chromosome	chromStart	chromEnd	Gene
1	chr1	8921418	8934967	EN01
2	chr1	17345375	17380514	SDHB
3	chr1	27022894	27107247	ARID1A
4	chr1	41976121	42501596	HIVEP3
5	chr1	43803519	43818443	MPL
6	chr1	45794977	45805926	MUTYH

```
> head(RCircos.Histogram.Data)
```

	Chromosome	chromStart	chromEnd	Data
1	chr1	45000000	49999999	0.070859
2	chr1	55000000	59999999	0.300460
3	chr1	60000000	64999999	0.125421
4	chr1	70000000	74999999	0.158156
5	chr1	75000000	79999999	0.163540
6	chr1	80000000	84999999	0.342921

```
> head(RCircos.Line.Data)
```

	chromosome	start	stop	num.mark	seg.mean
1	1	61735	16895627	8732	0.1797
2	1	16896821	17212714	105	-0.2117
3	1	17214822	25574471	5321	0.1751
4	1	25574707	25662212	37	0.5064
5	1	25663310	30741496	2400	0.1384
6	1	30741656	30745210	3	-1.4742

```
> head(RCircos.Link.Data)
```

	Chromosome	chromStart	chromEnd	Chromosome.1	chromStart.1	chromEnd.1
1	chr1	8284703	8285399	chr1	8285752	8286389
2	chr1	85980143	85980624	chr7	123161313	123161687
3	chr1	118069850	118070319	chr1	118070329	118070689
4	chr1	167077258	167077658	chr1	169764630	169764965
5	chr1	171671272	171671550	chr1	179790879	179791292
6	chr1	174333479	174333875	chr6	101861516	101861840

# SET CORE COMPONENTS

- Call ideogram and decide the data tracks

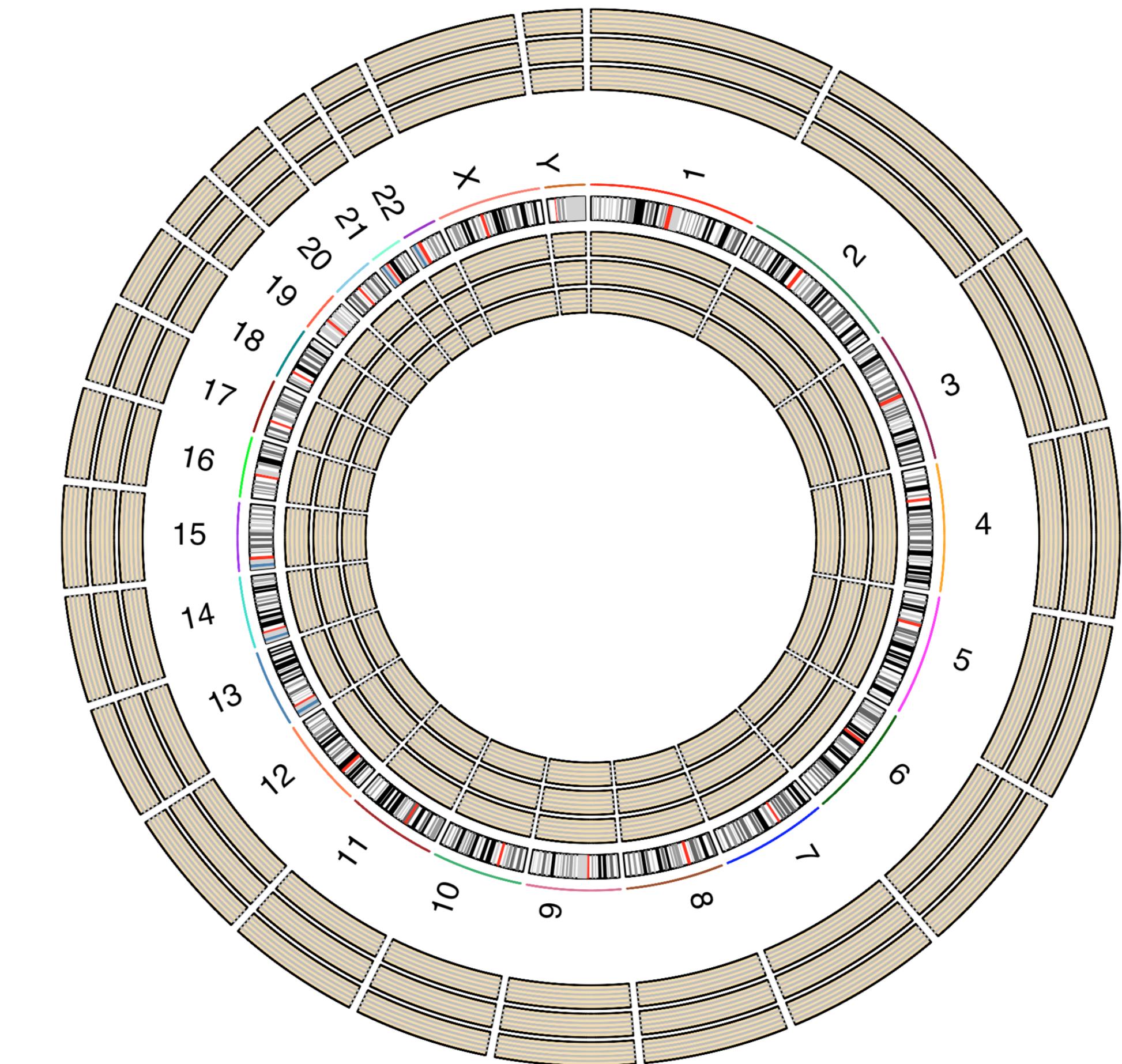
```
cyto.info =  
UCSC.HG19.Human.CytoBandIdeogram
```

```
RCircos.Set.Core.Components(  
  cyto.info,  
  chr.exclude = NULL,  
  tracks.inside = 3,  
  tracks.outside = 3)
```

# SET CORE COMPONENTS

- Call ideogram and decide the data tracks

```
cyto.info =  
UCSC.HG19.Human.CytoBandIdeogram  
  
RCircos.Set.Core.Components(  
cyto.info,  
chr.exclude = NULL,  
tracks.inside = 3,  
tracks.outside = 3)
```

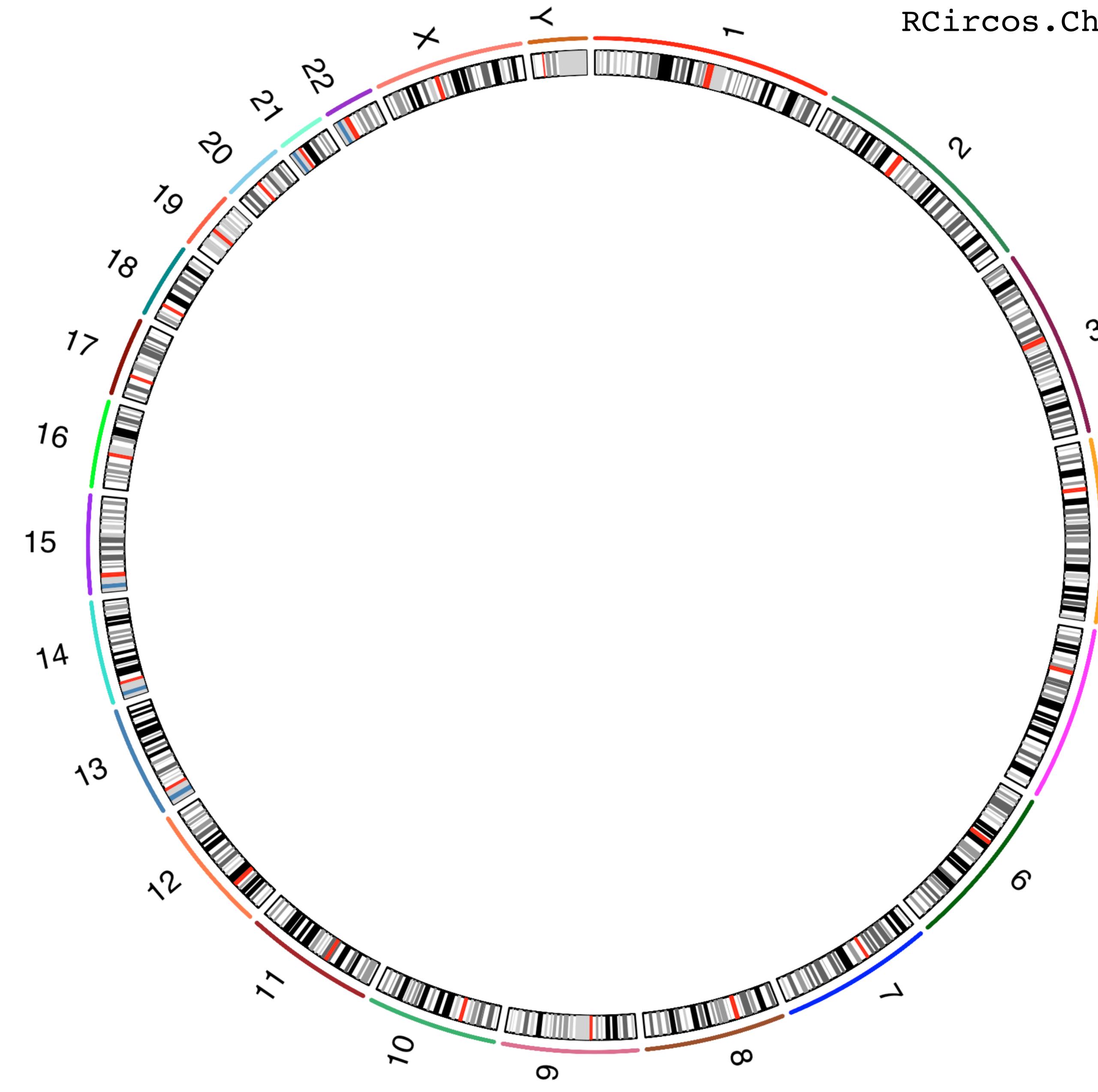


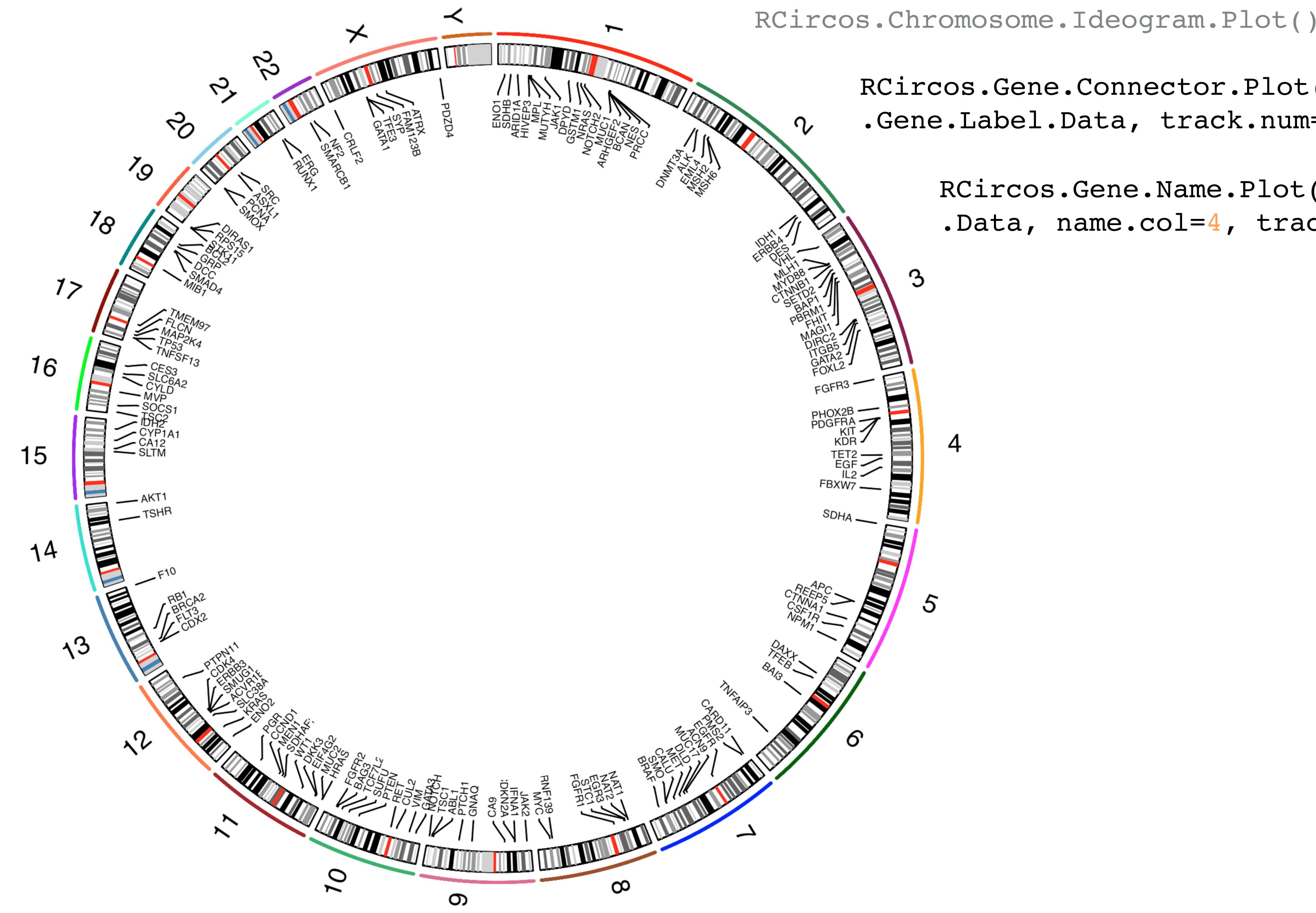
# SET PLOT AREA

- Setup plot area for RCircos plot

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

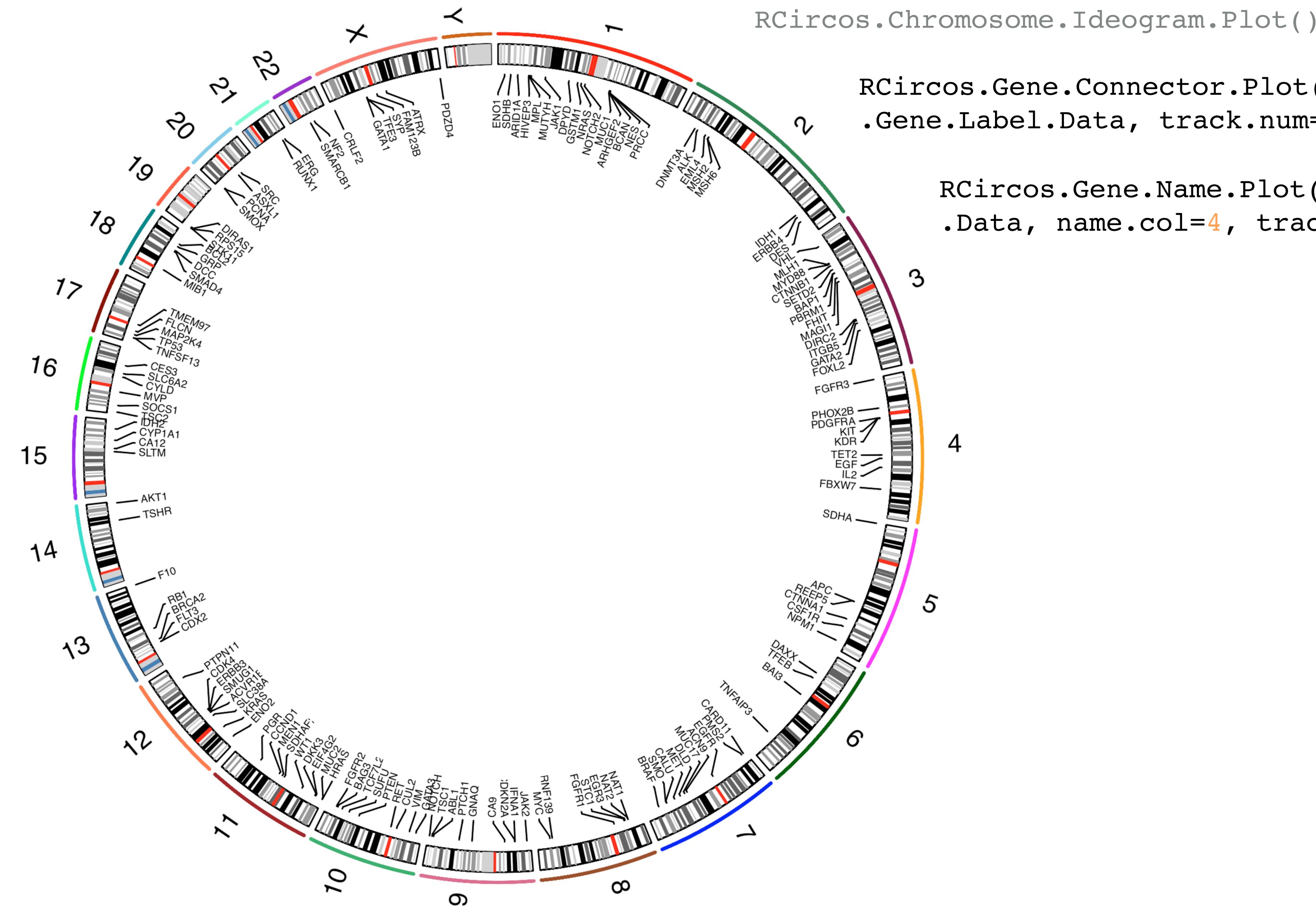
RCircos.Chromosome.Ideogram.Plot()





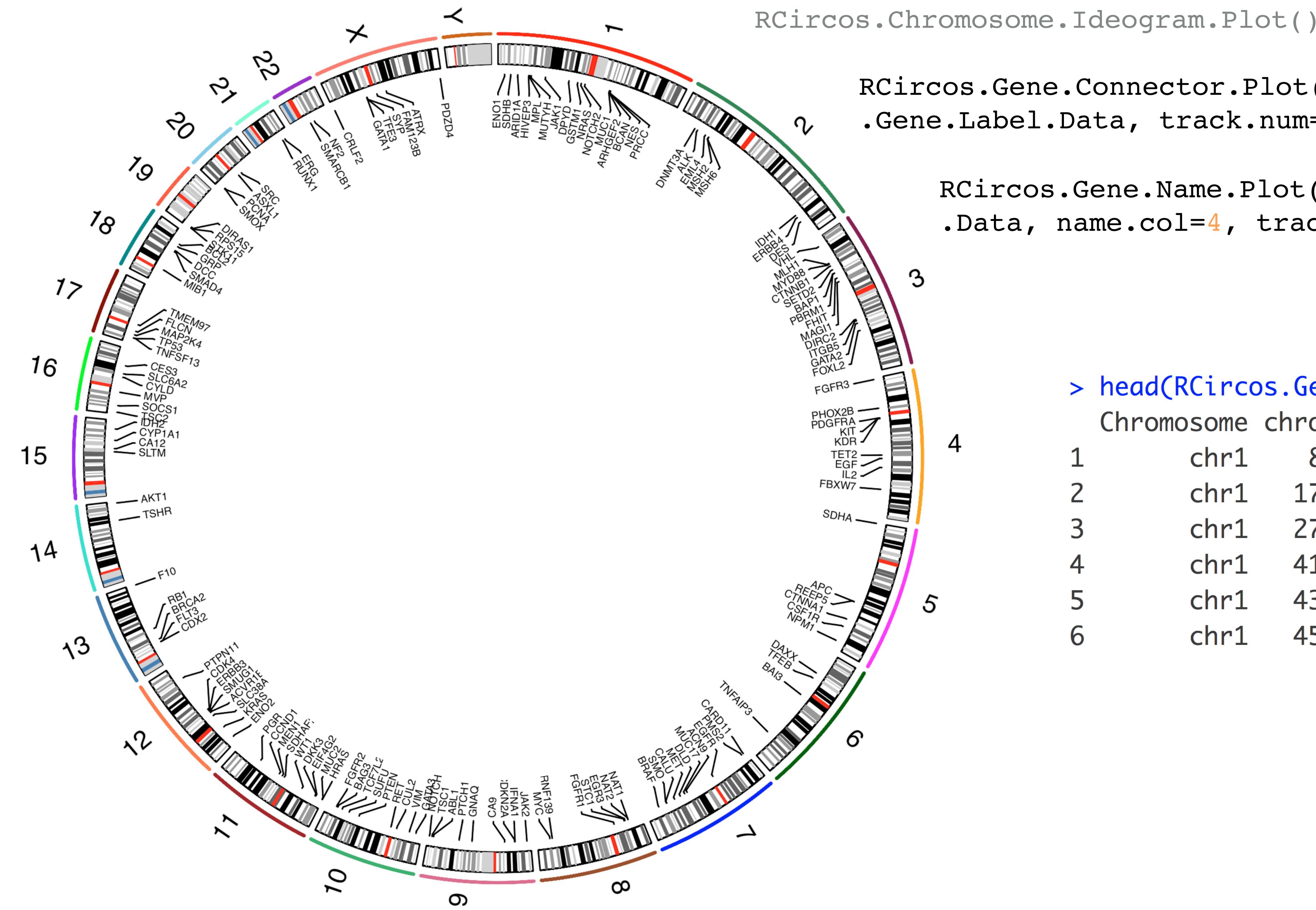
RCircos.Gene.Connector.Plot(genomic.data=RCircos.Gene.Label.Data, track.num=1, side="in")

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



RCircos.Gene.Connector.Plot(genomic.data=RCircos  
.Gene.Label.Data, track.num=1, side="in")

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

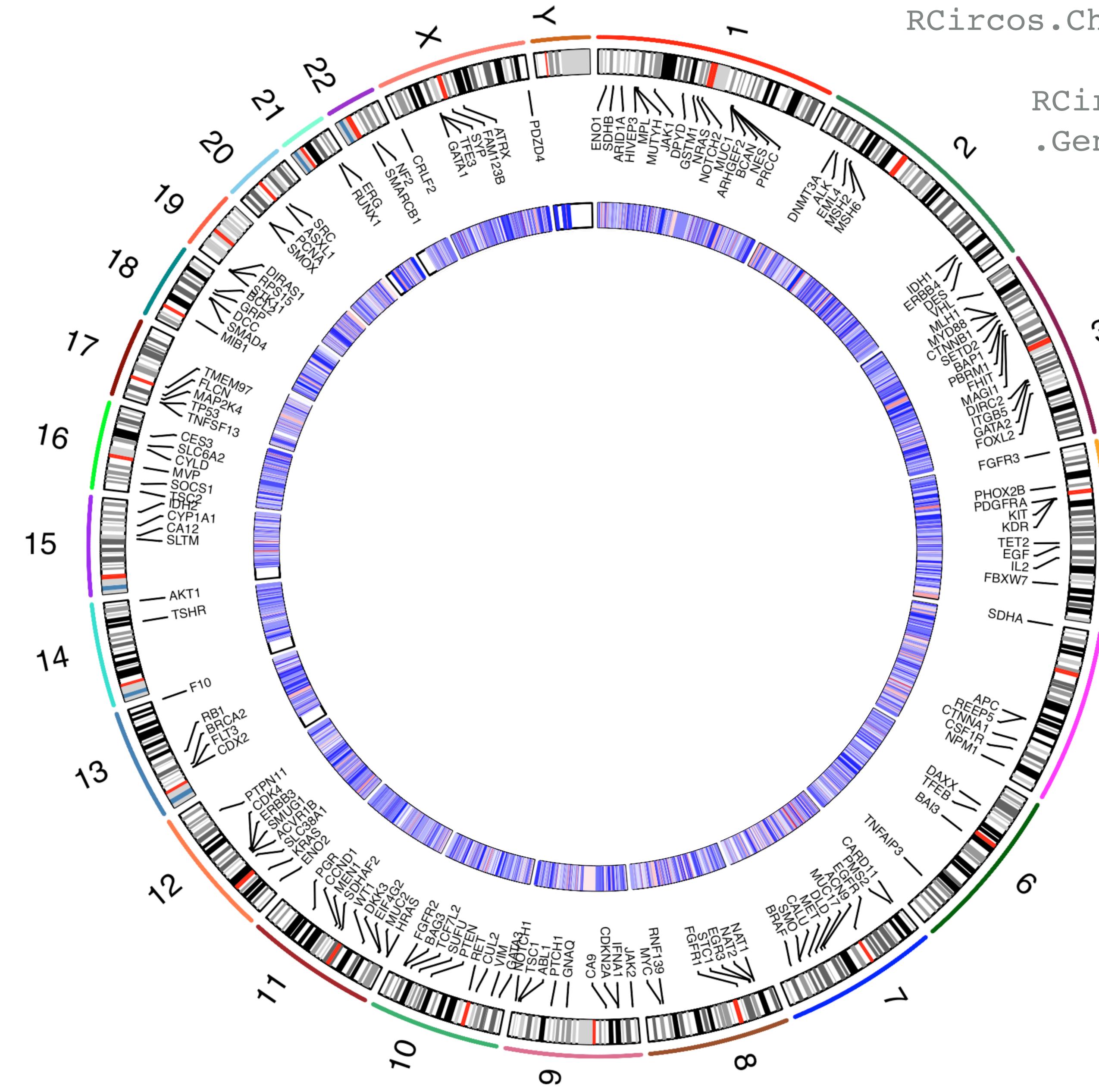


RCircos.Gene.Connector.Plot(genomic.data=RCircos  
.Gene.Label.Data, track.num=1, side="in")

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

> head(RCircos.Gene.Label.Data)

	Chromosome	chromStart	chromEnd	Gene
1	chr1	8921418	8934967	EN01
2	chr1	17345375	17380514	SDHB
3	chr1	27022894	27107247	ARID1A
4	chr1	41976121	42501596	HIVEP3
5	chr1	43803519	43818443	MPL
6	chr1	45794977	45805926	MUTYH

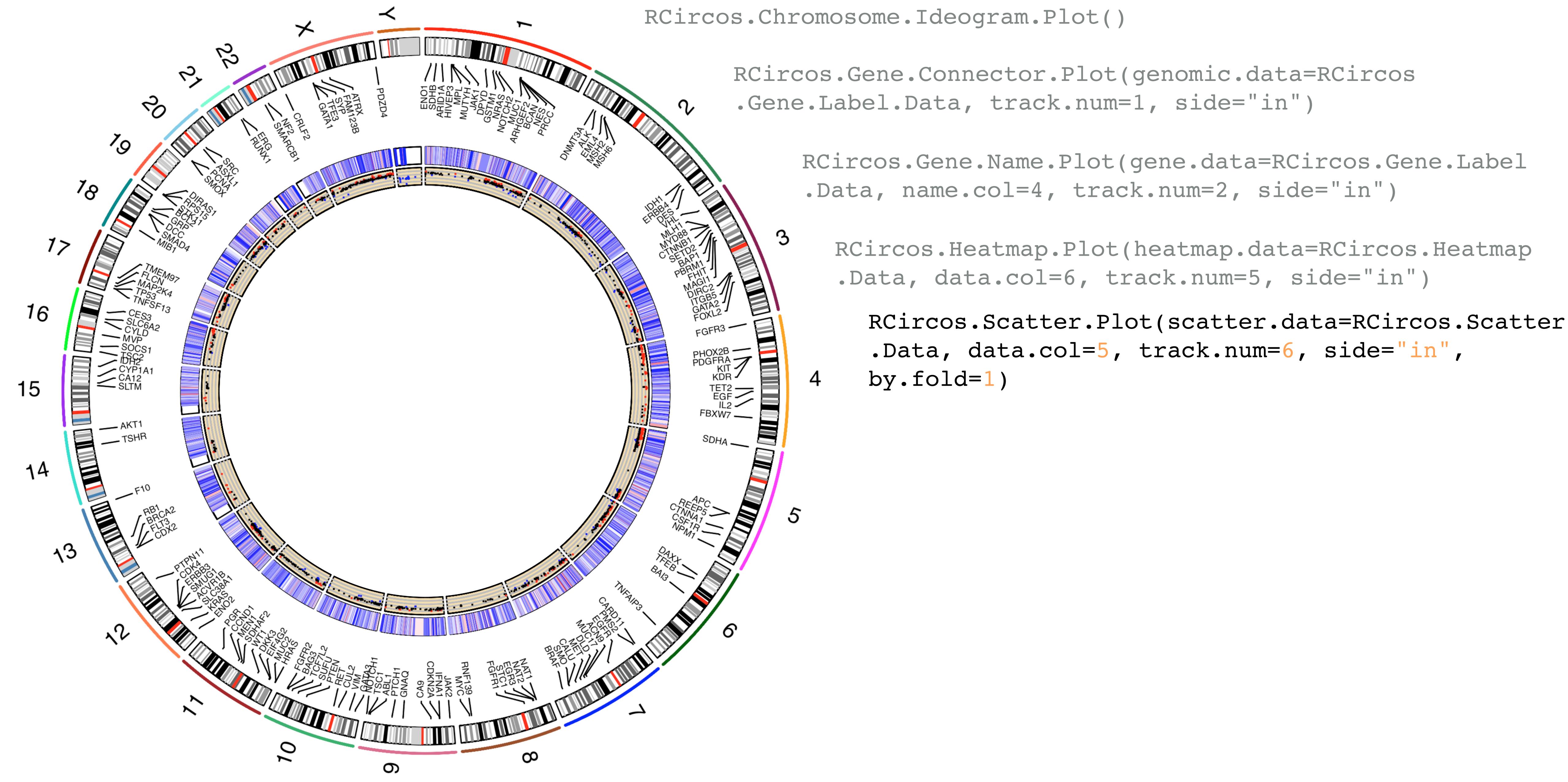


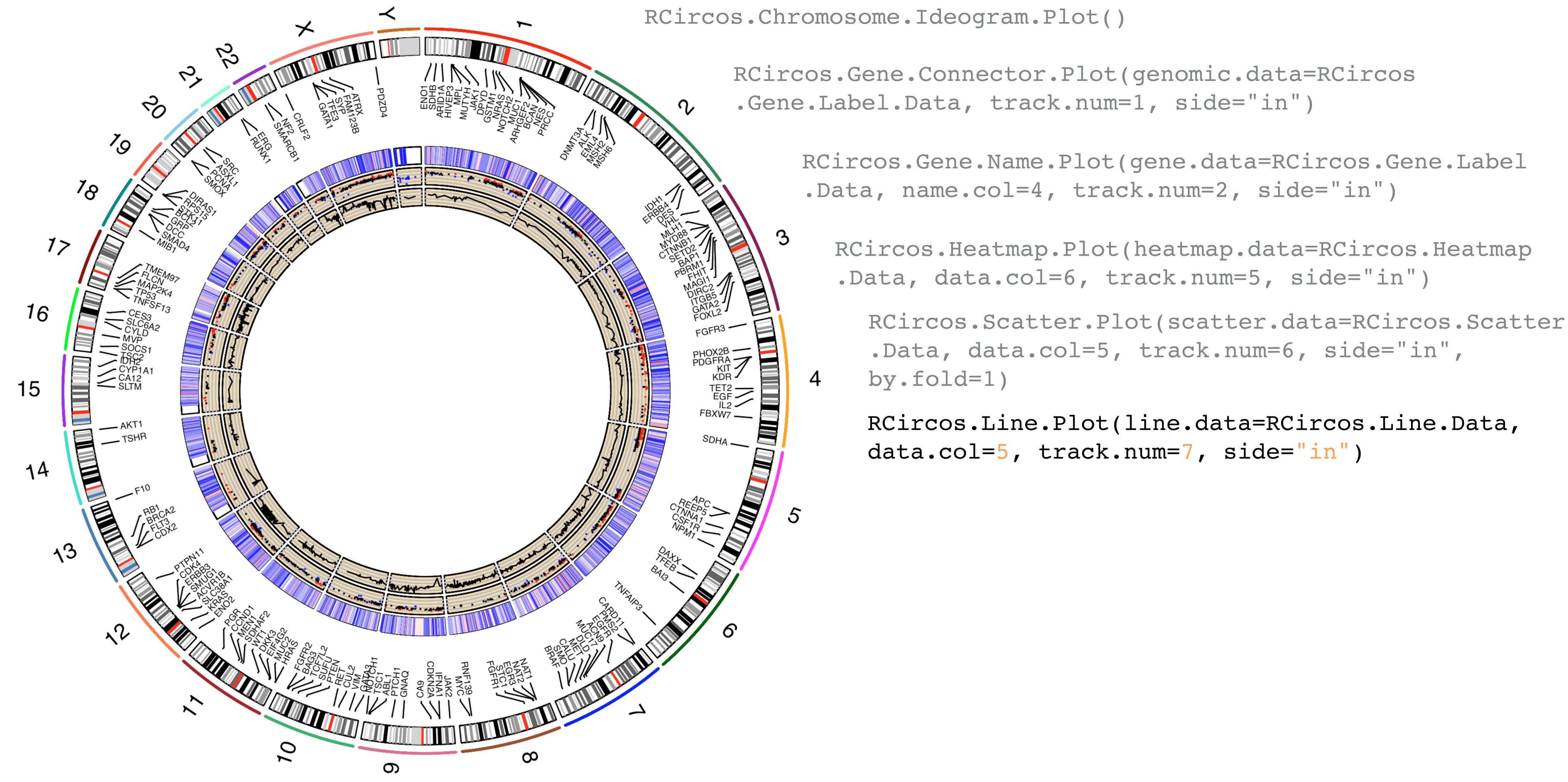
## RCircos.Chromosome.Ideogram.Plot( )

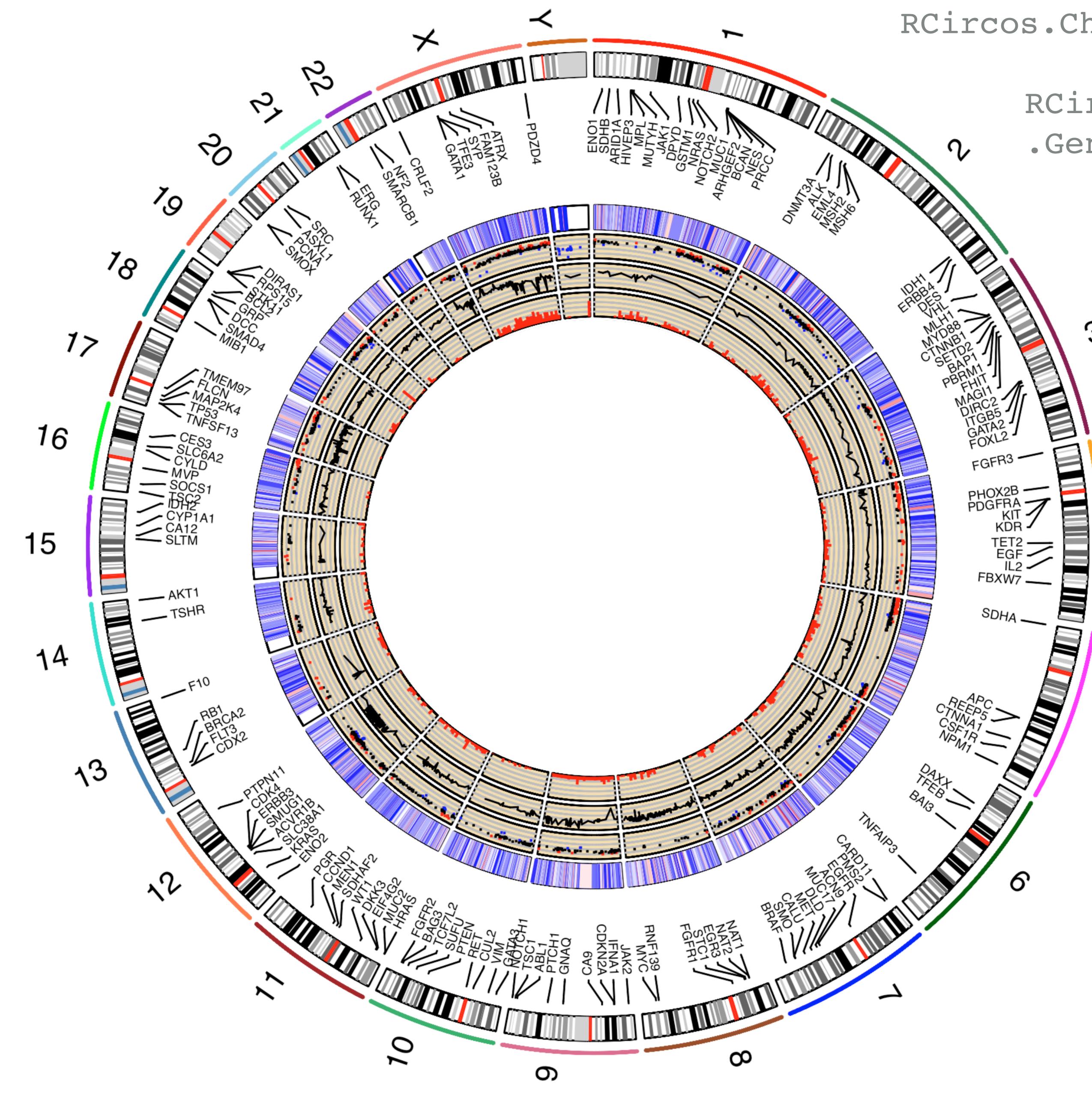
```
RCircos.Gene.Connector.Plot(genomic.data=RCircos  
.Gene.Label.Data, track.num=1, side="in")
```

```
RCircos.Gene.Name.Plot(gene.data=RCircos.Gene.Label  
.Data, name.col=4, track.num=2, side="in")
```

```
RCircos.Heatmap.Plot(heatmap.data=RCircos.Heatmap  
.Data, data.col=6, track.num=5, side="in")
```







RCircos.Chromosome.Ideogram.Plot()

RCircos.Gene.Connector.Plot(genomic.data=RCircos.Gene.Label.Data, track.num=1, side="in")

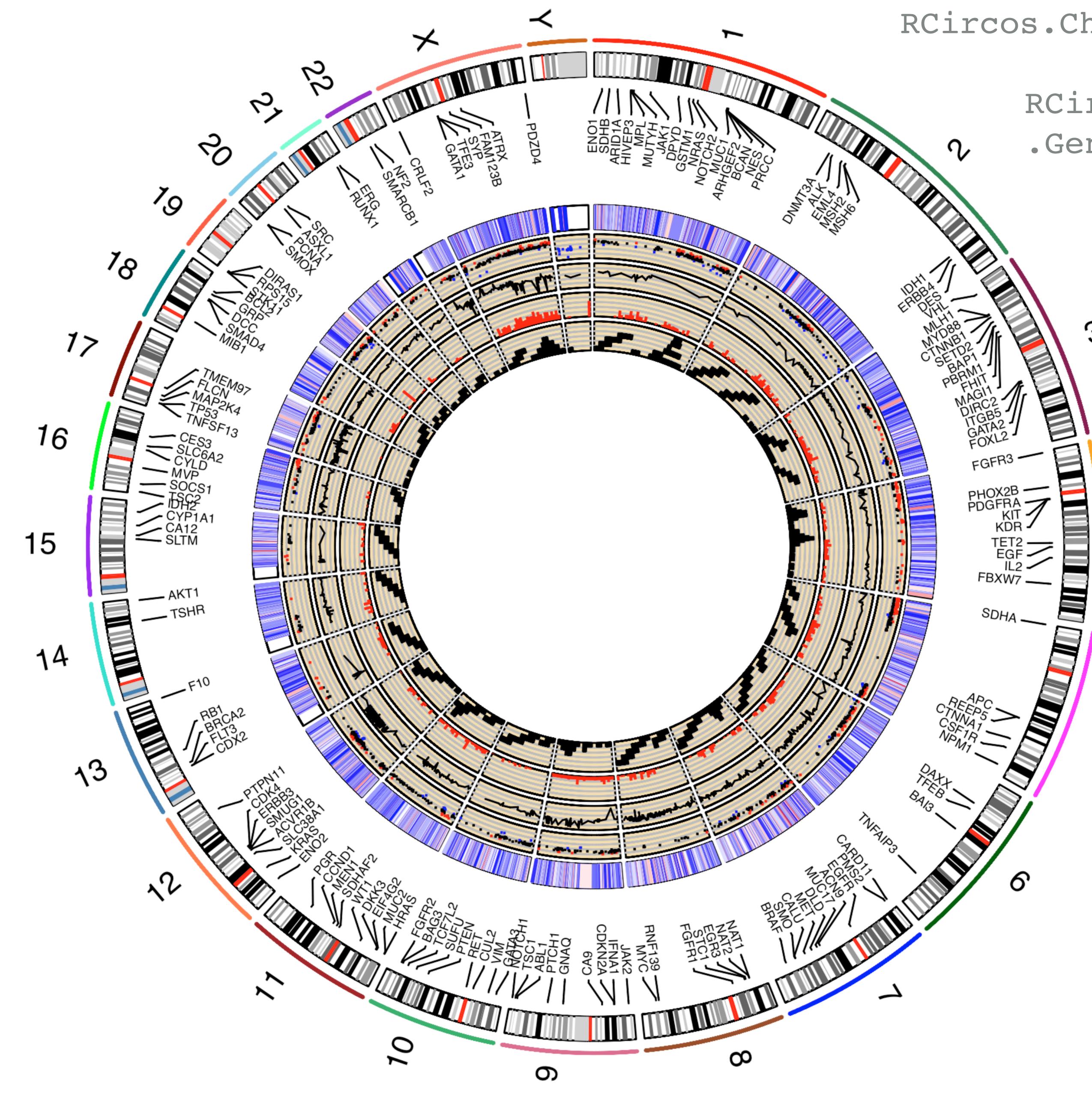
RCircos.Gene.Name.Plot(gene.data=RCircos.Gene.Label.Data, name.col=4, track.num=2, side="in")

RCircos.Heatmap.Plot(heatmap.data=RCircos.Heatmap.Data, data.col=6, track.num=5, side="in")

RCircos.Scatter.Plot(scatter.data=RCircos.Scatter.Data, data.col=5, track.num=6, side="in", by.fold=1)

RCircos.Line.Plot(line.data=RCircos.Line.Data, data.col=5, track.num=7, side="in")

RCircos.Histogram.Plot(hist.data=RCircos.Histogram.Data, data.col=4, track.num=8, side="in")



RCircos.Chromosome.Ideogram.Plot()

RCircos.Gene.Connector.Plot(genomic.data=RCircos  
.Gene.Label.Data, track.num=1, side="in")

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

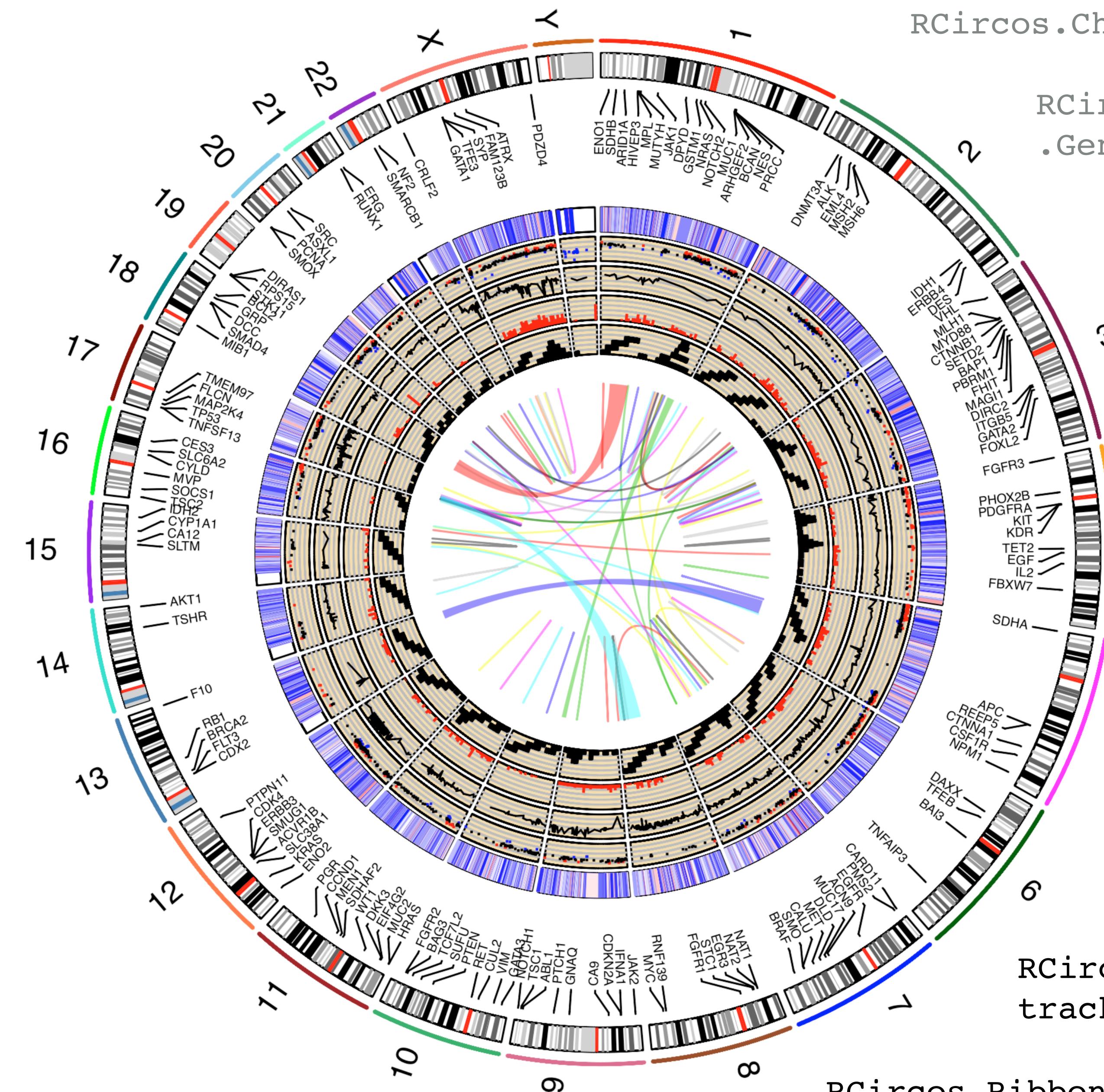
RCircos.Heatmap.Plot(heatmap.data=RCircos.Heatmap  
.Data, data.col=6, track.num=5, side="in")

RCircos.Scatter.Plot(scatter.data=RCircos.Scatter  
.Data, data.col=5, track.num=6, side="in",  
by.fold=1)

RCircos.Line.Plot(line.data=RCircos.Line.Data,  
data.col=5, track.num=7, side="in")

RCircos.Histogram.Plot(hist.data=RCircos.Histogram  
.Data, data.col=4, track.num=8, side="in")

RCircos.Tile.Plot(tile.data=RCircos.Tile.Data,  
track.num=9, side="in")



`RCircos.Chromosome.Ideogram.Plot()`

`RCircos.Gene.Connector.Plot(genomic.data=RCircos  
.Gene.Label.Data, track.num=1, side="in")`

`RCircos.Gene.Name.Plot(gene.data=RCircos.Gene.Label  
.Data, name.col=4, track.num=2, side="in")`

`RCircos.Heatmap.Plot(heatmap.data=RCircos.Heatmap  
.Data, data.col=6, track.num=5, side="in")`

`RCircos.Scatter.Plot(scatter.data=RCircos.Scatter  
.Data, data.col=5, track.num=6, side="in",  
by.fold=1)`

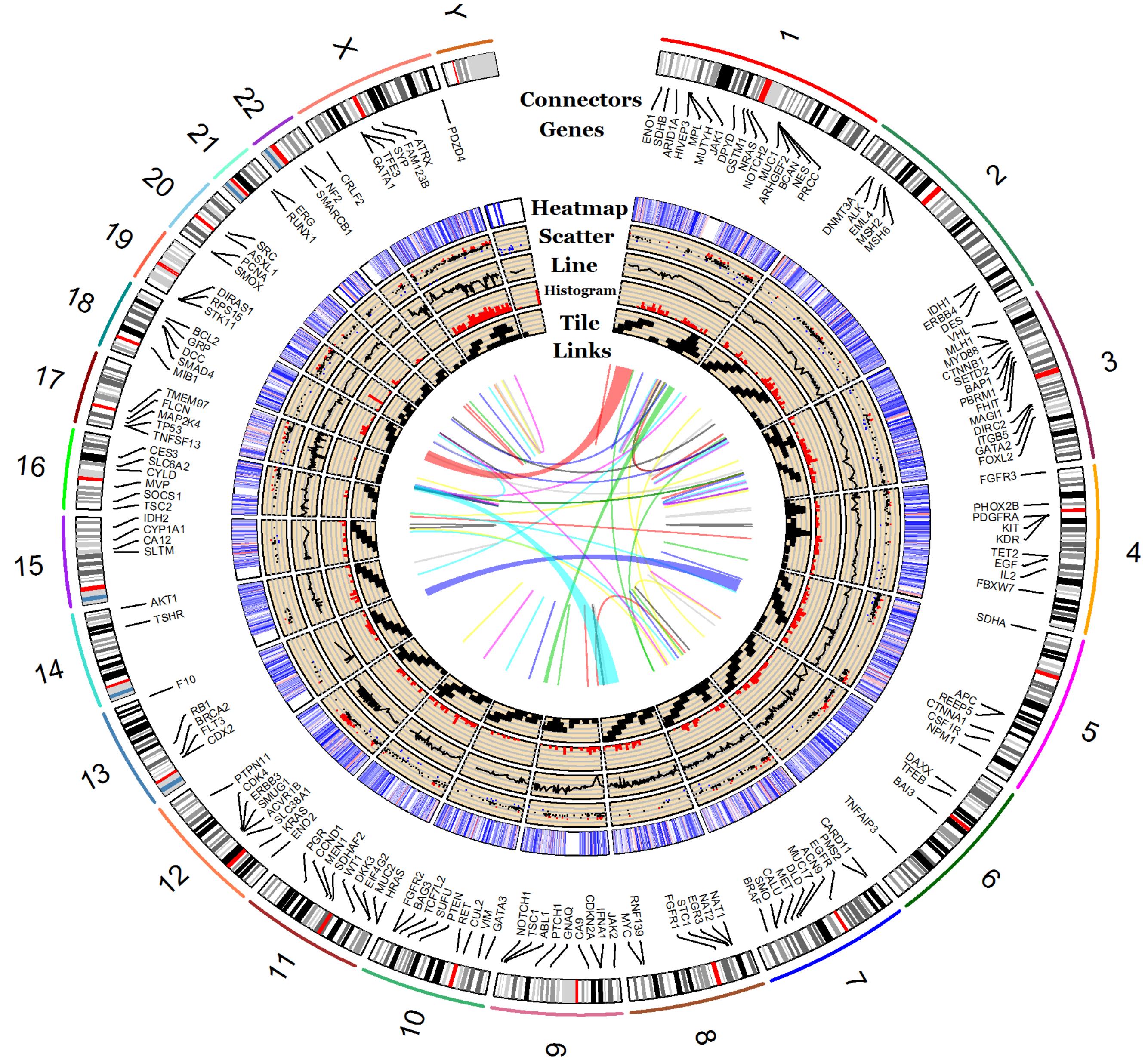
`RCircos.Line.Plot(line.data=RCircos.Line.Data,  
data.col=5, track.num=7, side="in")`

`RCircos.Histogram.Plot(hist.data=RCircos.Histogram  
.Data, data.col=4, track.num=8, side="in")`

`RCircos.Tile.Plot(tile.data=RCircos.Tile.Data,  
track.num=9, side="in")`

`RCircos.Link.Plot(link.data=RCircos.Link.Data,  
track.num=11, by.chromosome=FALSE)`

`RCircos.Ribbon.Plot(ribbon.data=RCircos.Ribbon.Data,  
track.num=11, by.chromosome=FALSE, twist=FALSE)`



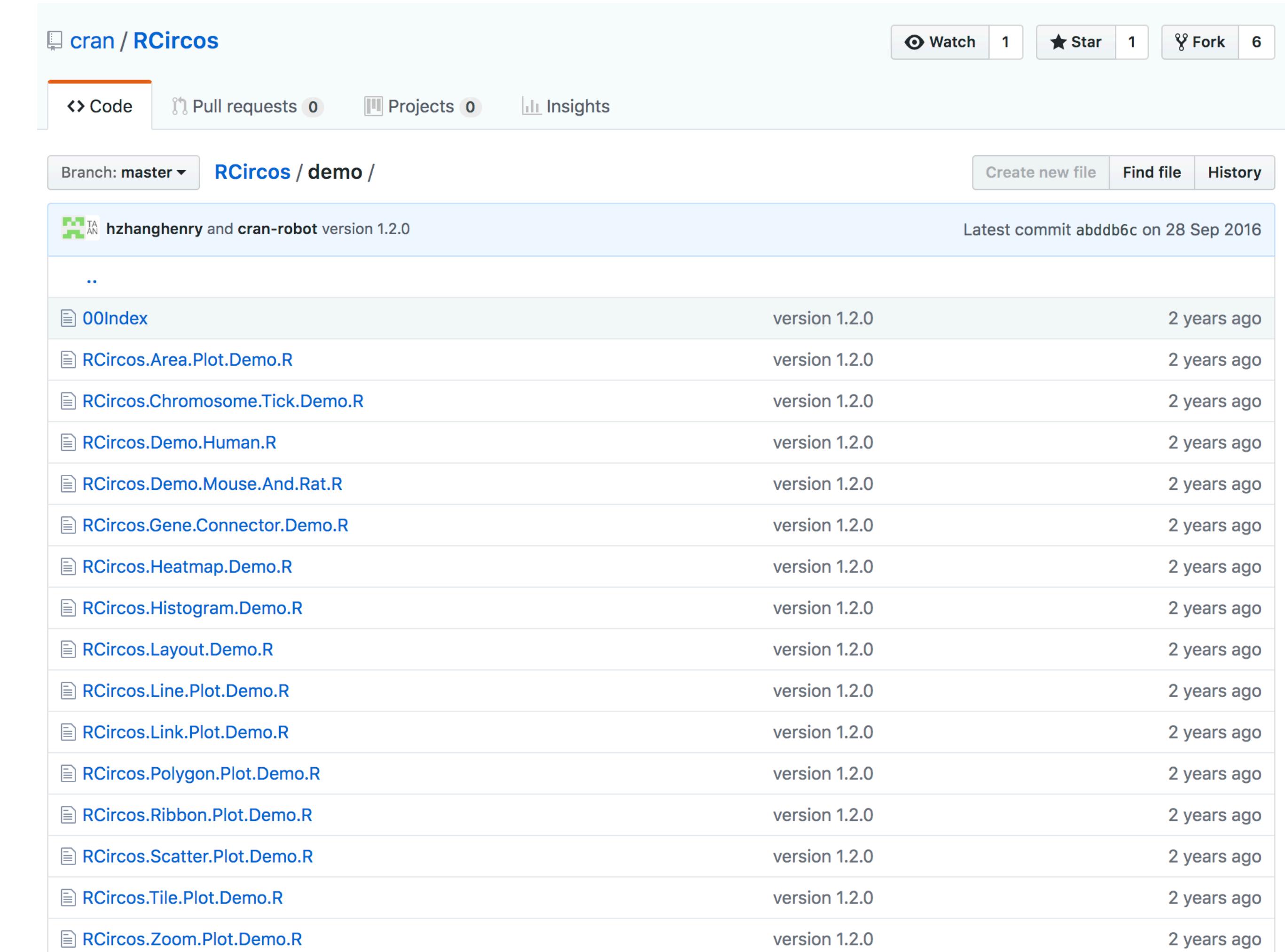
# USEFUL RESOURCES

- Circos software tutorials

[http://circos.ca/software/  
download/tutorials/](http://circos.ca/software/download/tutorials/)

- RCircos GitHub Demo

[https://github.com/cran/  
RCircos/tree/master/demo](https://github.com/cran/RCircos/tree/master/demo)

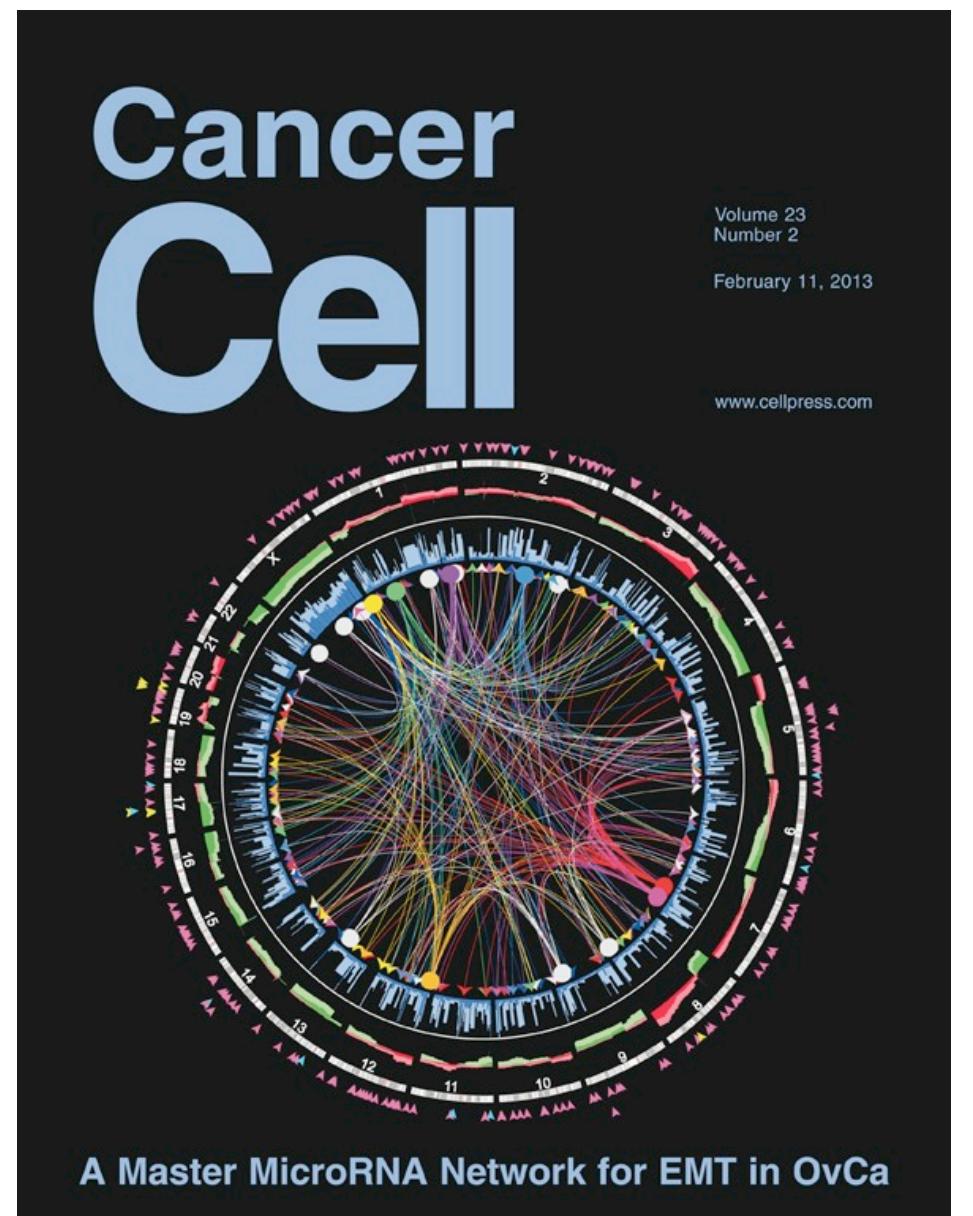


A screenshot of a GitHub repository page for 'cran / RCircos'. The repository has 1 watch, 1 star, and 6 forks. The 'Code' tab is selected. The branch is 'master'. The repository path is 'RCircos / demo /'. The latest commit was on 28 Sep 2016. The table lists 15 demo files, all of which are version 1.2.0 and were committed 2 years ago.

File	Version	Committed
00Index	version 1.2.0	2 years ago
RCircos.Area.Plot.Demo.R	version 1.2.0	2 years ago
RCircos.Chromosome.Tick.Demo.R	version 1.2.0	2 years ago
RCircos.Demo.Human.R	version 1.2.0	2 years ago
RCircos.Demo.Mouse.And.Rat.R	version 1.2.0	2 years ago
RCircos.Gene.Connector.Demo.R	version 1.2.0	2 years ago
RCircos.Heatmap.Demo.R	version 1.2.0	2 years ago
RCircos.Histogram.Demo.R	version 1.2.0	2 years ago
RCircos.Layout.Demo.R	version 1.2.0	2 years ago
RCircos.Line.Plot.Demo.R	version 1.2.0	2 years ago
RCircos.Link.Plot.Demo.R	version 1.2.0	2 years ago
RCircos.Polygon.Plot.Demo.R	version 1.2.0	2 years ago
RCircos.Ribbon.Plot.Demo.R	version 1.2.0	2 years ago
RCircos.Scatter.Plot.Demo.R	version 1.2.0	2 years ago
RCircos.Tile.Plot.Demo.R	version 1.2.0	2 years ago
RCircos.Zoom.Plot.Demo.R	version 1.2.0	2 years ago

# TAKE HOME MESSAGES

- ◆ Easy to plot, format and layer your data
  - ◆ Looks pretty
  - ◆ Strong online community + tutorials
- 
- RCircos goes hand-in-hand with Adobe Illustrator



**Thank you for your attention!**