ideogram layout and formatting

SESSION 2

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EMBO PRACTICAL COURSE:
BIOINFORMATICS AND COMPARATIVE GENOME ANALYSES
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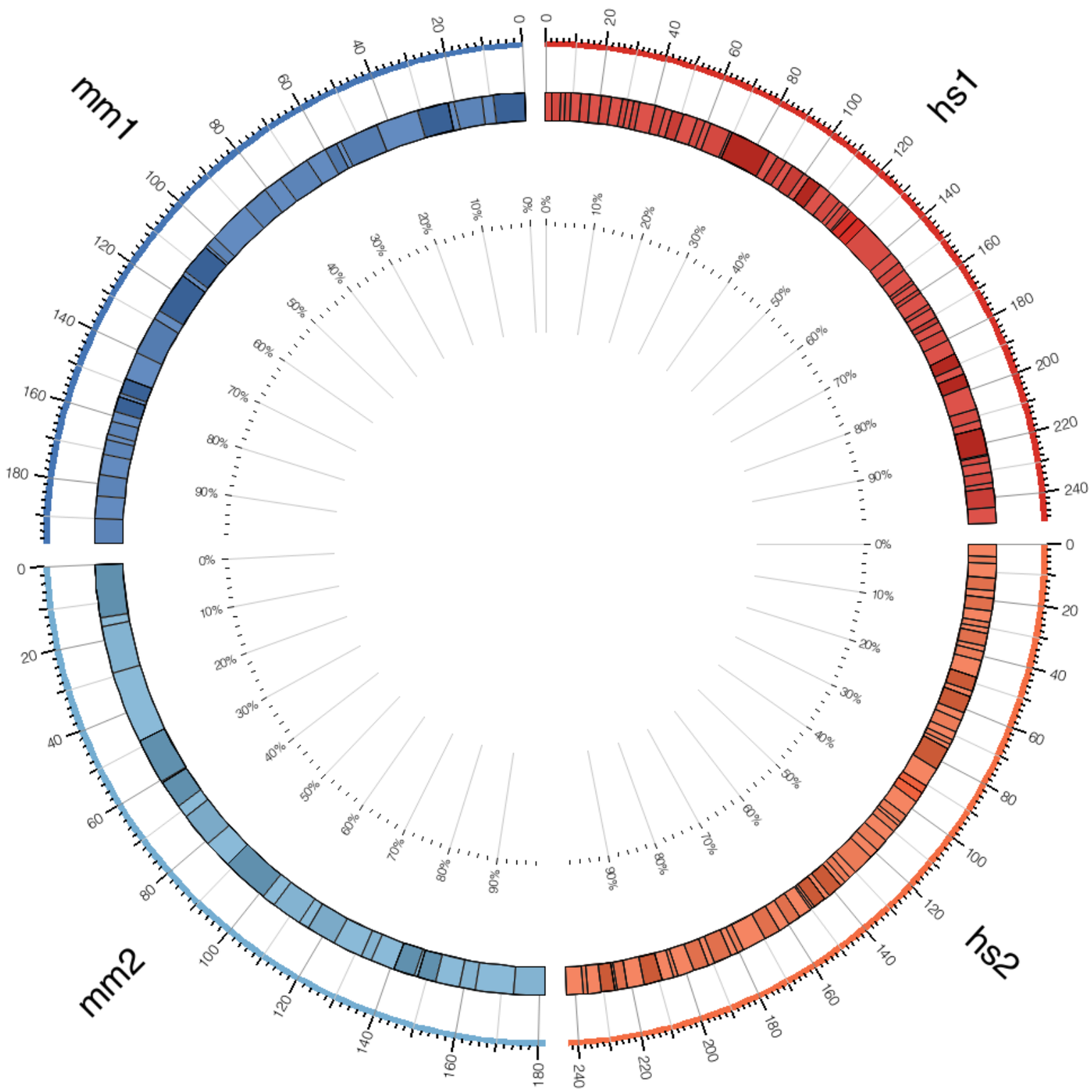
SESSION FINAL IMAGE



drawing and spacing ideograms
relative ideogram spacing
changing ideogram scale
ideogram selection
ideogram order
drawing ideogram regions
chromosome breaks
ordering ideogram regions
cytogenetic bands
drawing multiple genomes
ideogram progression and orientation
relative and absolute ticks

This is the image you will create during this session. It contains chrs 1 & 2 from human and mouse genomes. Each chromosome occupies 1/4 of the figure.

getting ready

PUT ON YOUR UNIX HAT

GO TO SESSION 2 DIRECTORY

```
# You've already copied the course files into
# ~/circos/course session
> cd circos/course/session/2

> ls
drwxr-xr-x   5 martink  users  170  3 May 08:26 1/
drwxr-xr-x   4 martink  users  136  3 May 08:26 10/
drwxr-xr-x   4 martink  users  136  3 May 08:26 11/
drwxr-xr-x   5 martink  users  170  3 May 08:26 12/
drwxr-xr-x   4 martink  users  136  3 May 08:26 2/
drwxr-xr-x   4 martink  users  136  3 May 08:26 3/
drwxr-xr-x   4 martink  users  136  3 May 08:26 4/
drwxr-xr-x   4 martink  users  136  3 May 08:26 5/
drwxr-xr-x   4 martink  users  136  3 May 08:26 6/
drwxr-xr-x   4 martink  users  136  3 May 08:26 7/
drwxr-xr-x   4 martink  users  136  3 May 08:26 8/
drwxr-xr-x   5 martink  users  170  3 May 08:26 9/
drwxr-xr-x   6 martink  users  204  3 May 08:26 data/
drwxr-xr-x   5 martink  users  170  3 May 08:26 etc/
drwxr-xr-x  15 martink  users  510  3 May 08:26 img/
-rwxr-xr-x   1 martink  users   77  3 May 08:45 run
```

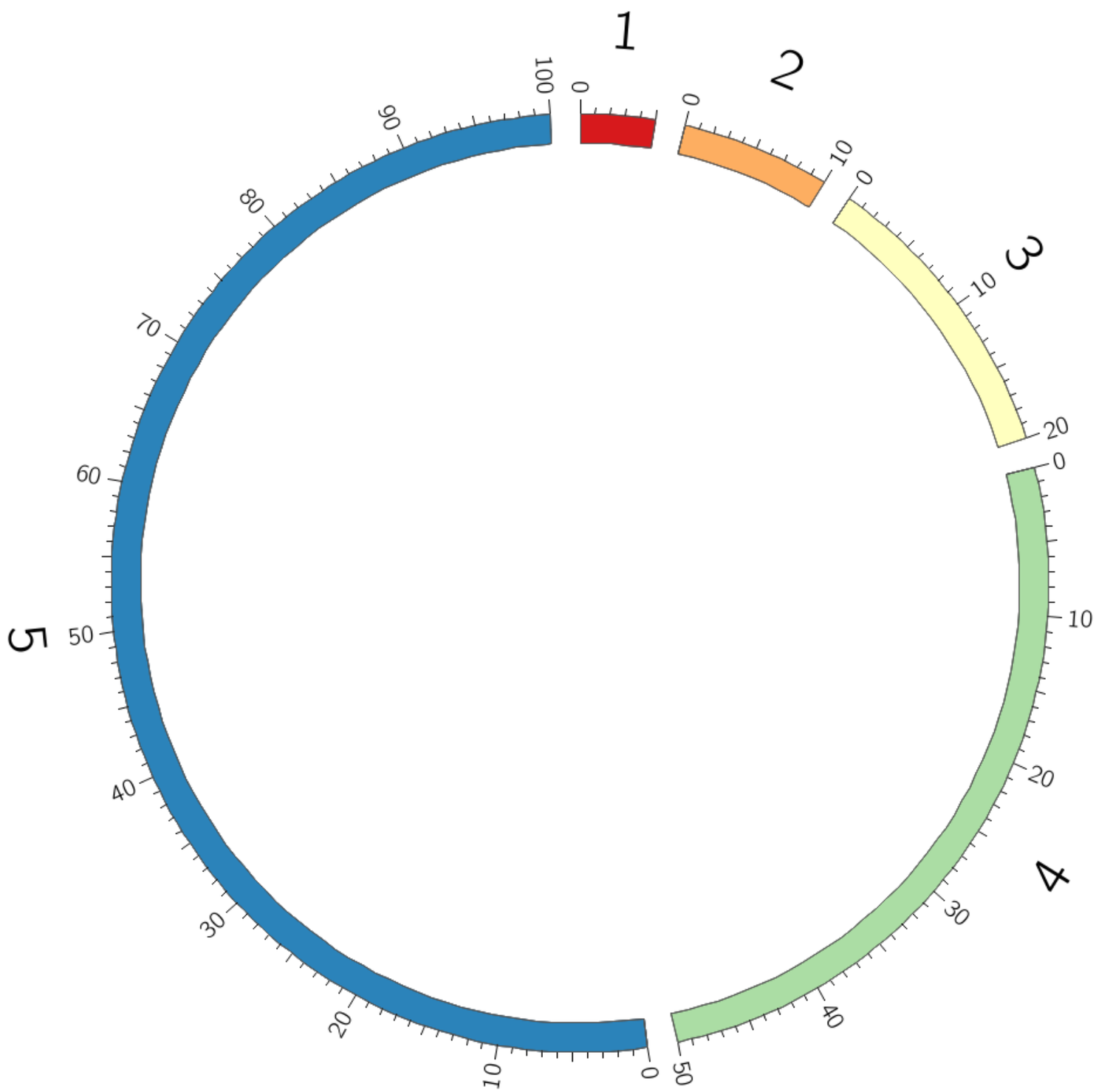
GO TO SESSION 2, LESSON 1 DIRECTORY

```
> cd 1
> ls
-rw-r--r--  1 martink  users  62096  6 May 09:06 circos.png
drwxr-xr-x  7 martink  users    238  5 May 14:51 etc/
```

absolute spacing

LESSON 1

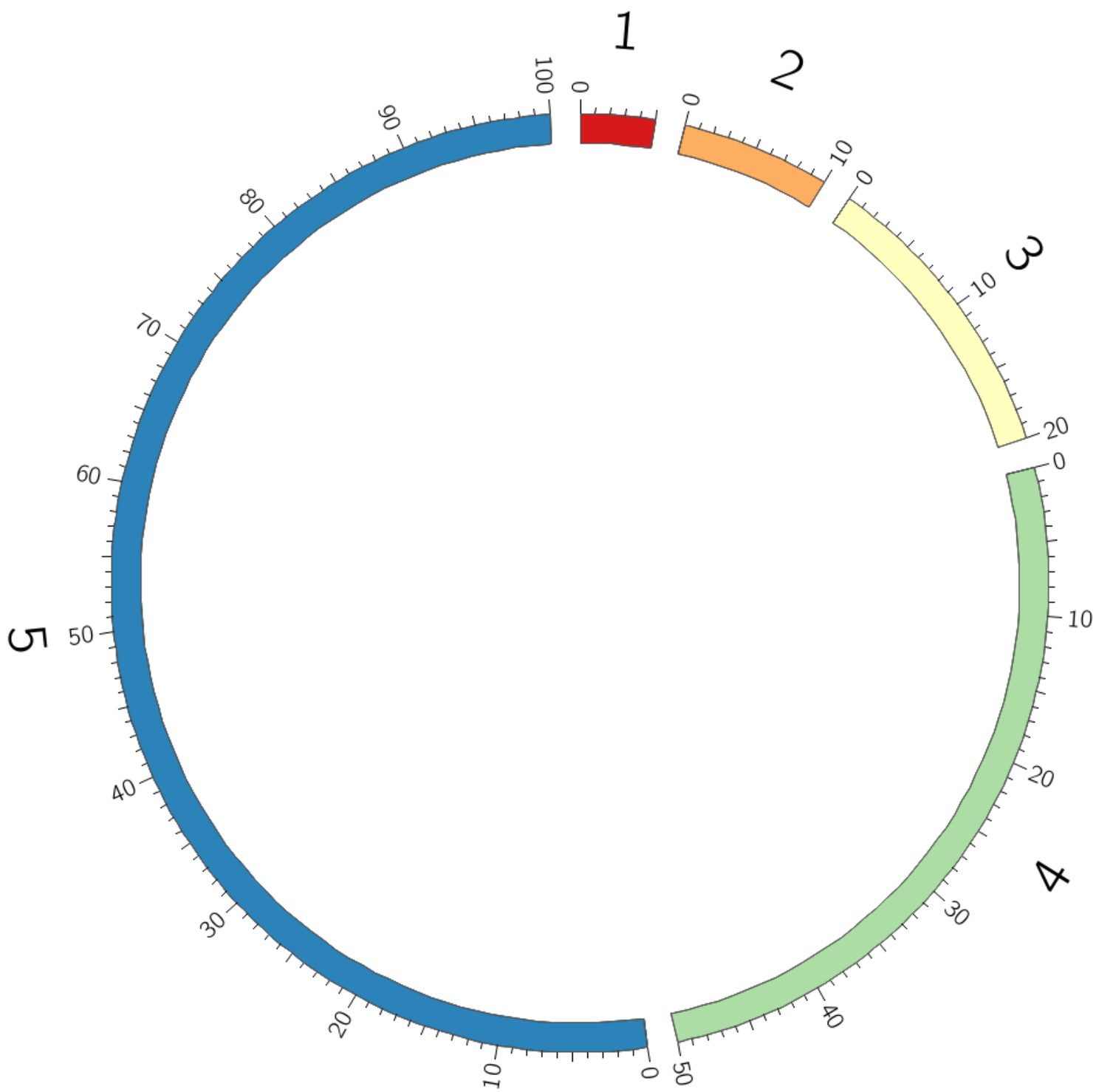
CONFIGURATION FILE




```
# 2/1/etc/circos.conf

karyotype = ../data/karyotype.5chr.txt

chromosomes_units           = 1000000
chromosomes_display_default = yes

<<include ideogram.conf>>

<<include ../etc/ticks.conf>>

<<include ../../etc/image.conf>>
<<include etc/colors_fonts_patterns.conf>>
<<include etc/housekeeping.conf>>
```

.

KARYOTYPE FILE



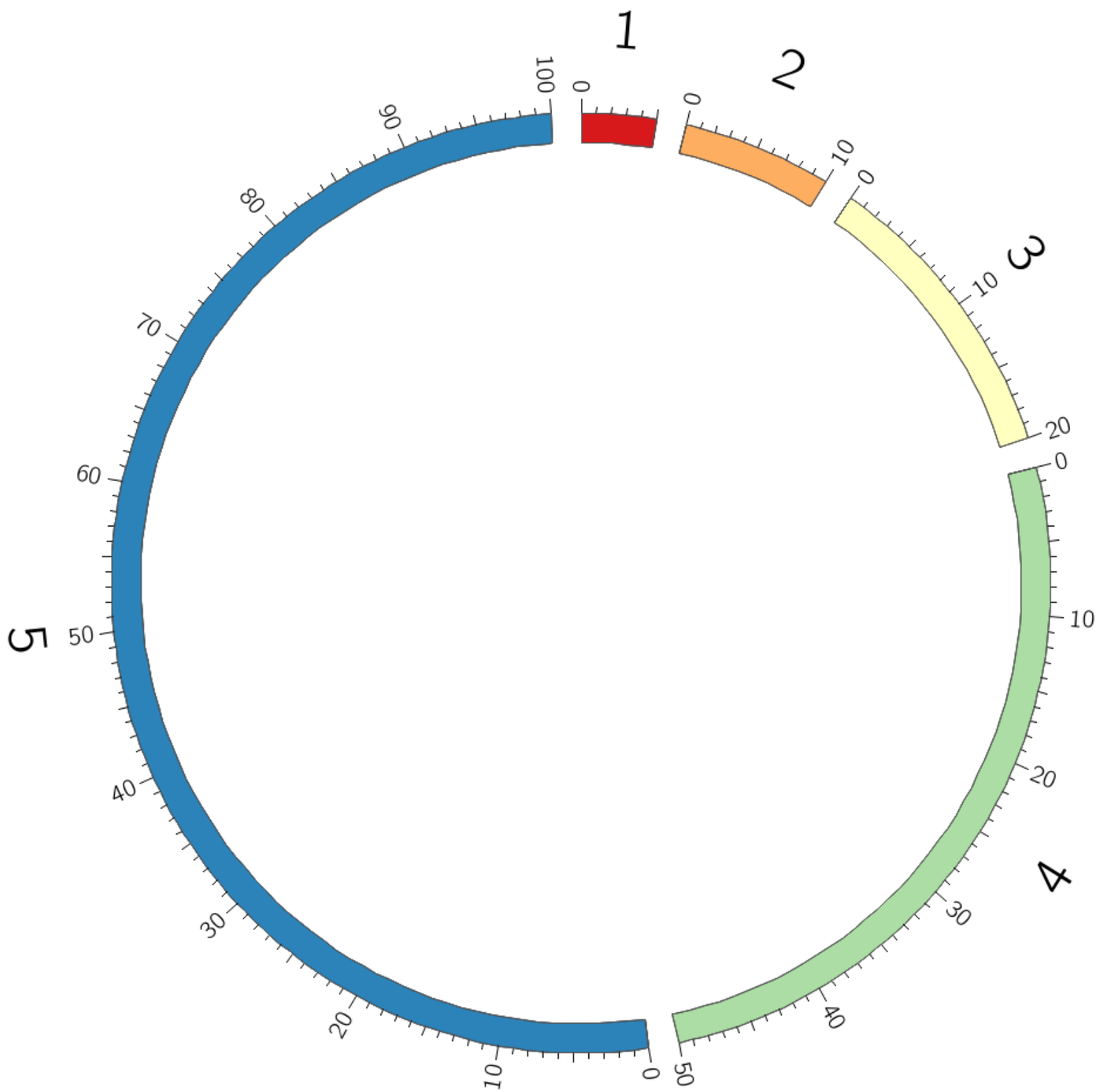

```
# 2/data/karyotype.chr5.txt

chr - chr1 1 0 5000000 spectral-5-div-1
chr - chr2 2 0 10000000 spectral-5-div-2
chr - chr3 3 0 20000000 spectral-5-div-3
chr - chr4 4 0 50000000 spectral-5-div-4
chr - chr5 5 0 100000000 spectral-5-div-5
```

.

CREATE THE IMAGE

```
> circos
debuggroup summary 0.12s welcome to circos v0.67-pre3 2 May 2014
debuggroup summary 0.12s guessing configuration file
debuggroup summary 0.13s found conf file
  /home/martink/circos/course/session/2/1/etc/circos.conf
debuggroup summary 0.38s debug will appear for these features: summary
debuggroup summary 0.38s parsing karyotype and organizing ideograms
debuggroup summary 0.38s applying global and local scaling
debuggroup summary 0.39s allocating image, colors and brushes
debuggroup summary 1.60s drawing highlights and ideograms
debuggroup summary,output 1.80s generating output
debuggroup summary,output 1.89s created PNG image ./circos.png (62 kb)
```

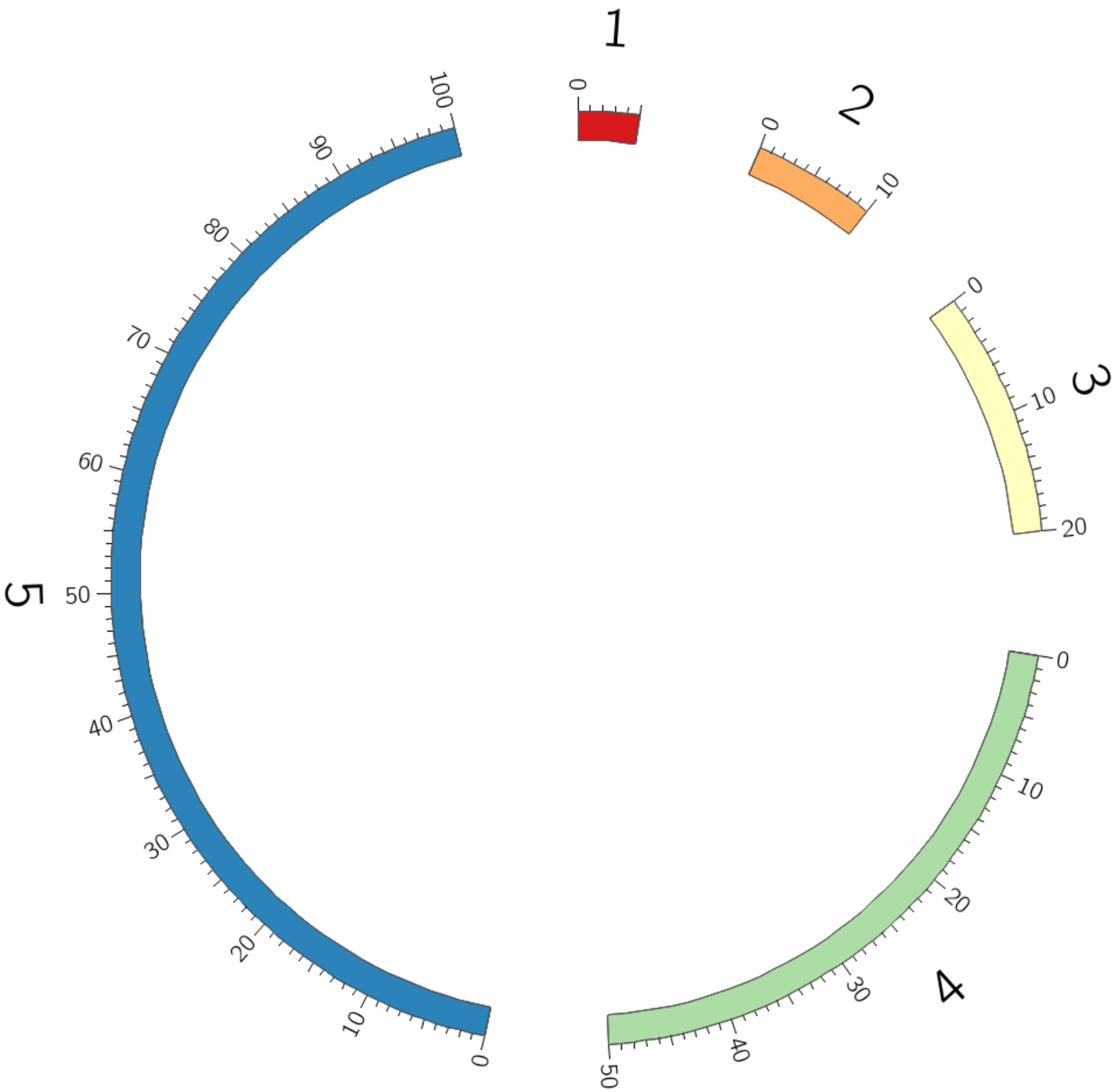
ABSOLUTE SPACING




```
# 2/1/etc/ideogram.conf

<ideogram>

<spacing>

default = 2u

#default = 10u

#<pairwise chr1>
#spacing = 5u
#</pairwise>

#<pairwise chr1 chr2>
#spacing = 15u
#</pairwise>

#<pairwise chr1 chr5>
#spacing = 25u
#</pairwise>

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

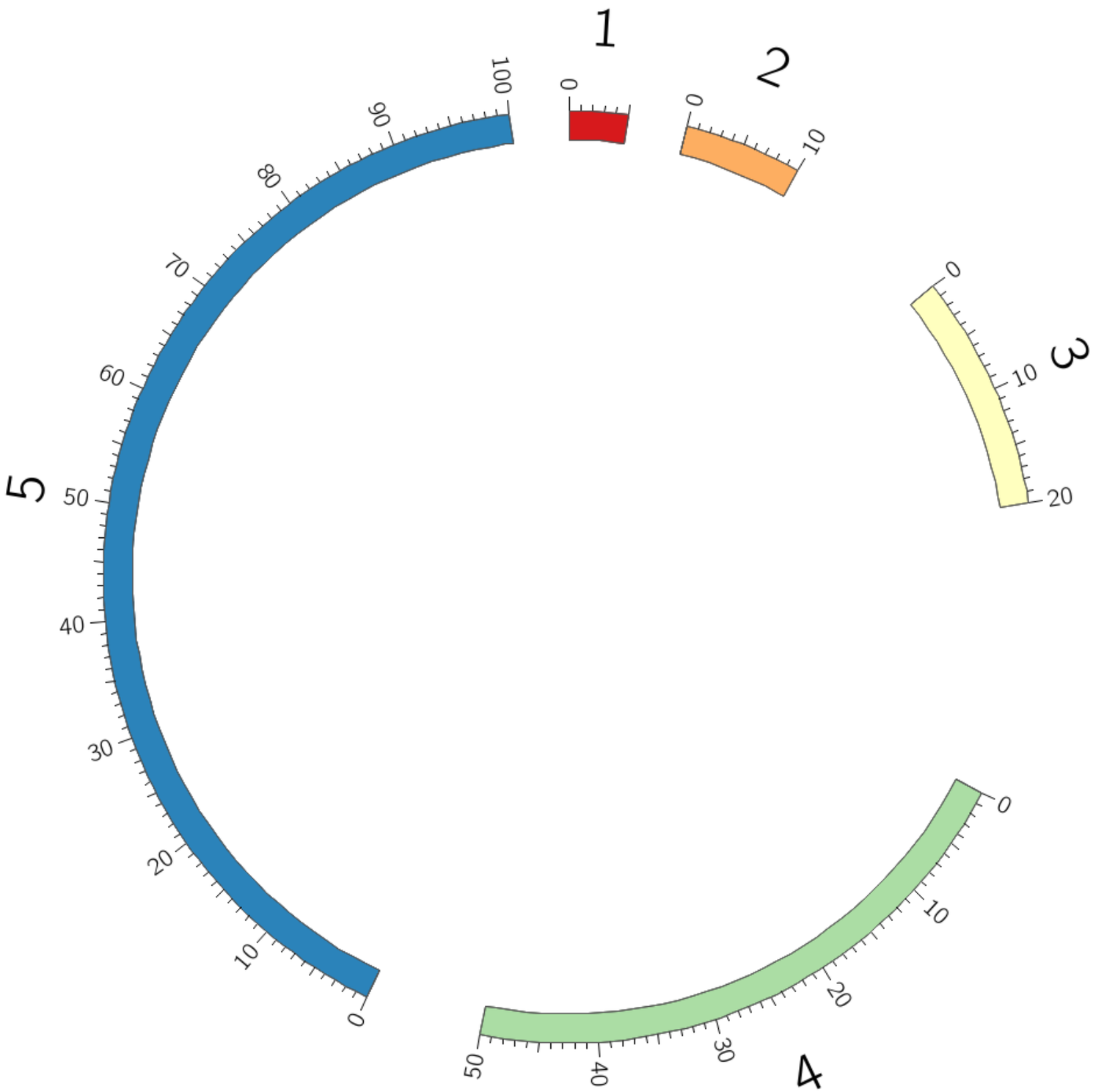
INCREASE ABSOLUTE SPACING




```
# 2/1/etc/ideogram.conf

<ideogram>

<spacing>

#default = 2u

default = 10u

#<pairwise chr1>
#spacing = 5u
#</pairwise>

#<pairwise chr1 chr2>
#spacing = 15u
#</pairwise>

#<pairwise chr1 chr5>
#spacing = 25u
#</pairwise>

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

ADJUST SPACING BETWEEN SPECIFIC IDEOGRAM PAIRS



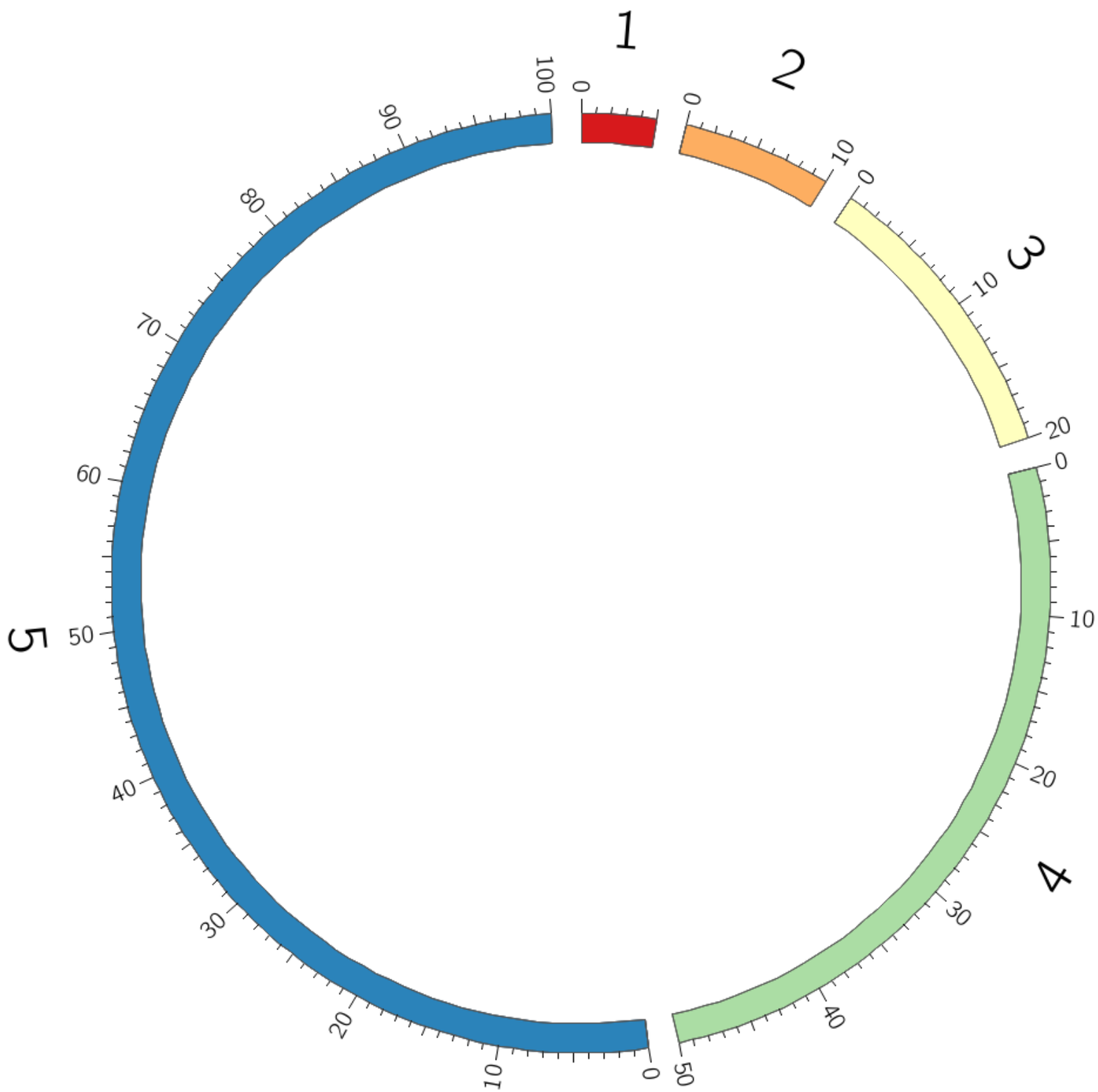

```
# 2/1/etc/ideogram.conf

<ideogram>

<spacing>

#default = 2u

default = 10u

<pairwise chr>
spacing = 5u
</pairwise>

<pairwise chr1 chr2>
spacing = 15u
</pairwise>

<pairwise chr1 chr5>
spacing = 25u
</pairwise>

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

relative spacing

LESSON 2

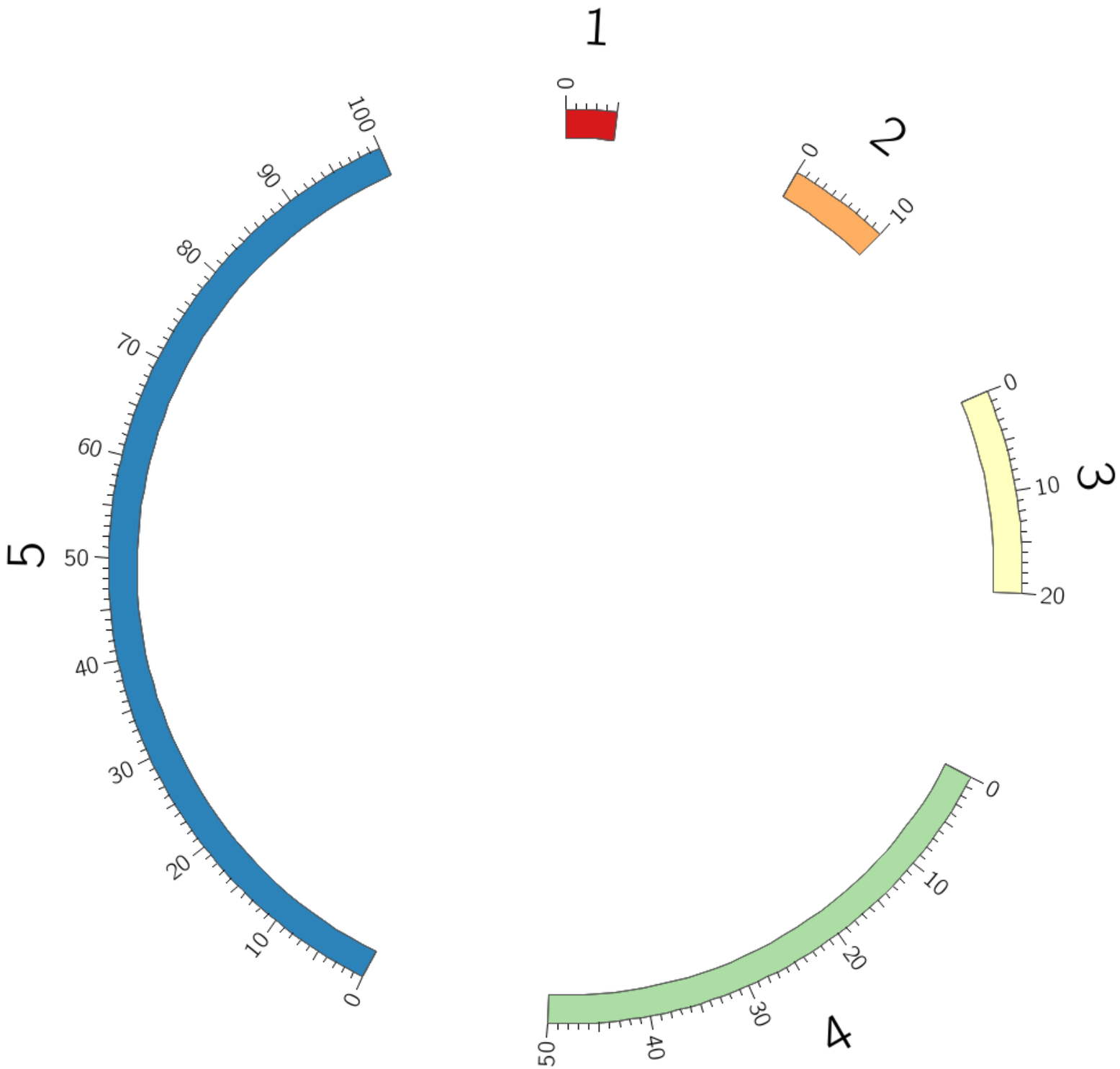
ABSOLUTE SPACING




```
# 2/2/etc/ideogram.conf

<ideogram>

<spacing>

default = 2u

#default = 0.1r

#<pairwise chr1 chr2>
#spacing = 0u # no space
#</pairwise>

#<pairwise chr2 chr3>
#spacing = 2u # 2Mb space
#</pairwise>

#<pairwise chr3 chr4>
#spacing = 2r # 2x default
#</pairwise>

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

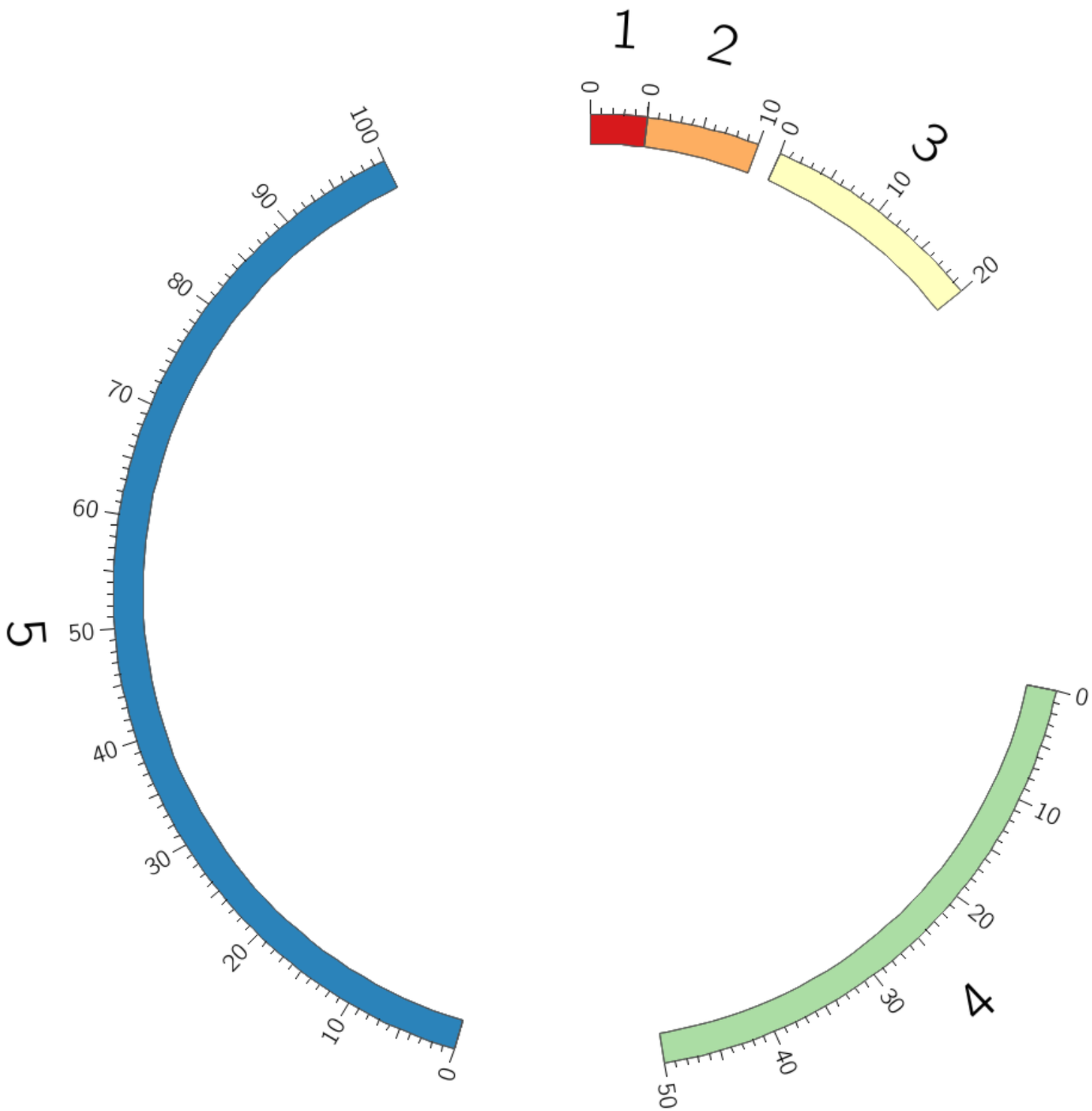
RELATIVE SPACING




```
# 2/2/etc/ideogram.conf

<ideogram>

<spacing>

#default = 2u

default = 0.1r

#<pairwise chr1 chr2>
#spacing = 0u # no space
#</pairwise>

#<pairwise chr2 chr3>
#spacing = 2u # 2Mb space
#</pairwise>

#<pairwise chr3 chr4>
#spacing = 2r # 2x default
#</pairwise>

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

ABSOLUTE AND RELATIVE SPACING COMBINED



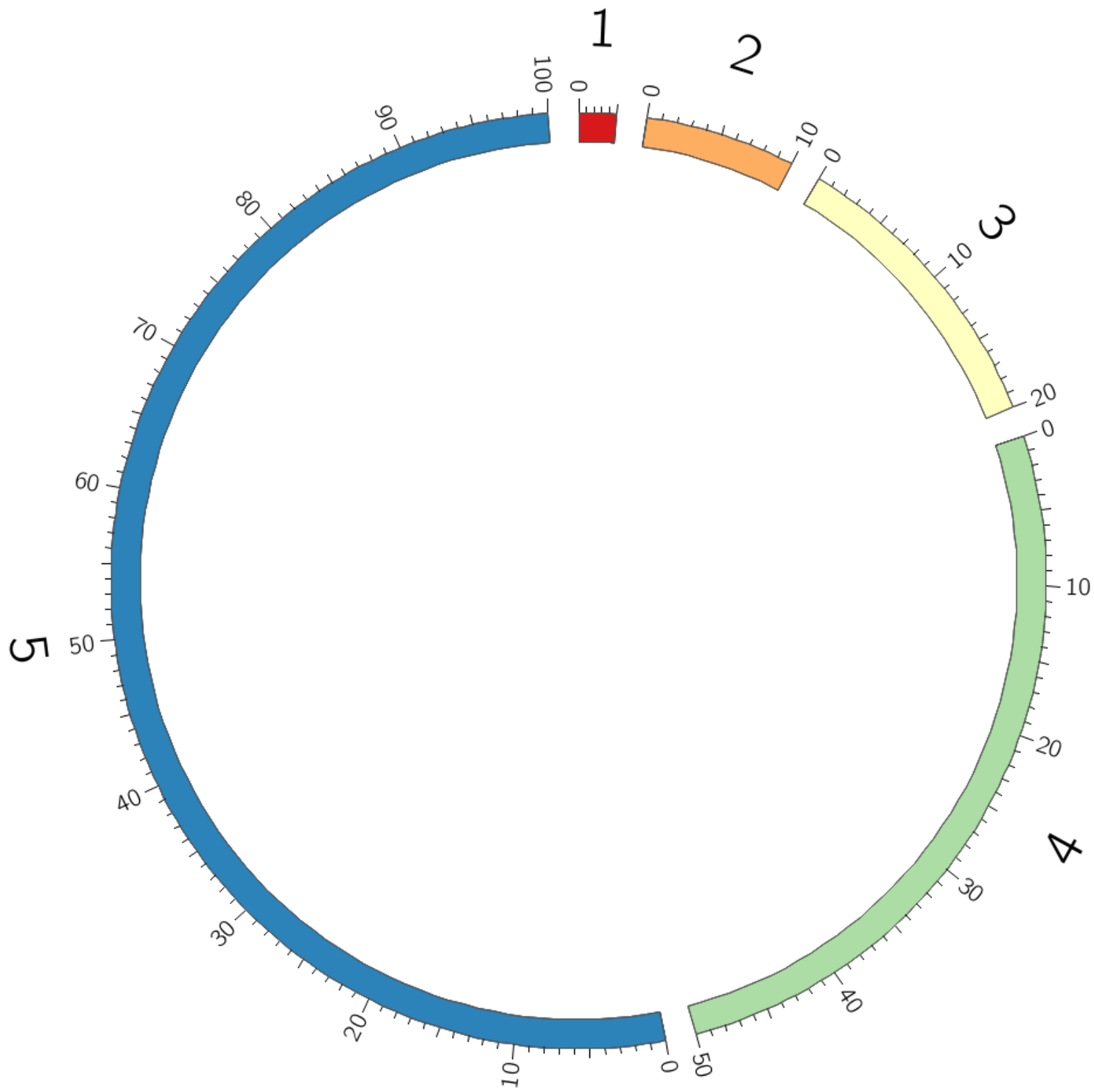

```
# 2/2/etc/ideogram.conf

<ideogram>

<spacing>

#default = 2u

default = 0.1r

<pairwise chr1 chr2>
spacing = 0u # no space
</pairwise>

<pairwise chr2 chr3>
spacing = 2u # 2Mb space
</pairwise>

<pairwise chr3 chr4>
spacing = 2r # 2x default
</pairwise>

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

global scale

LESSON 3

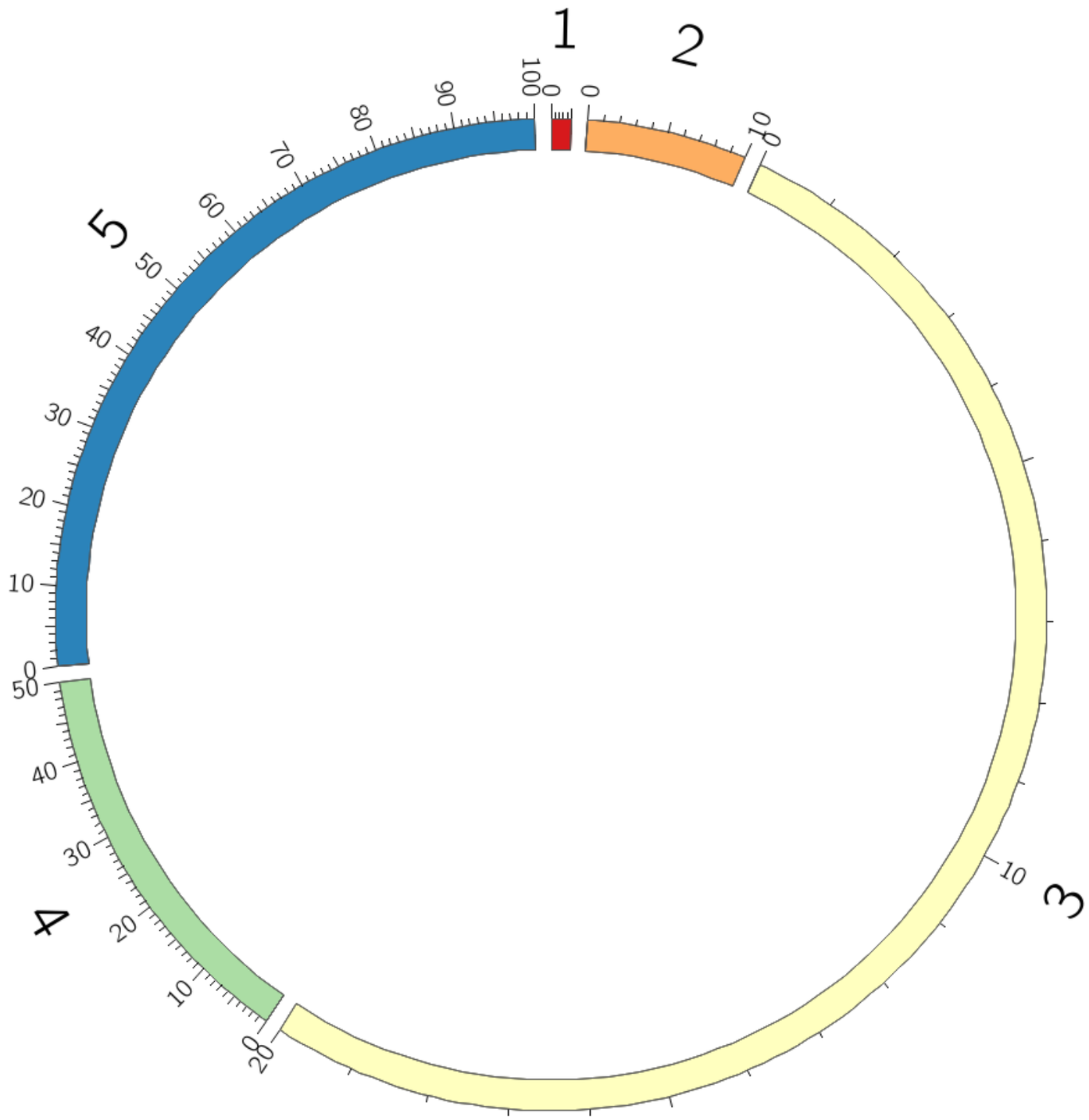
ABSOLUTE IDEOGRAM SCALE




```
# 2/3/etc/circos.conf

chromosomes_scale = chr1=0.5

#chromosomes_scale = chr1=0.5,chr2=2,chr3=10

# chr1 occupies 50% of figure
#chromosomes_scale = chr1=0.5r

# chr5 occupies 25% of figure
# chr4 occupies 25% of figure
#chromosomes_scale = chr5=0.25r,chr4=0.25r

# chr1 chr2 chr3 together occupy 50% of
# figure, and within this region they
# are equally sized
#
# equivalent to
# chr1=0.0833r,chr2=0.0833r,chr3=0.0833r
#chromosomes_scale = /chr[123]/=0.5rn

# all chromosomes equally sized
#chromosomes_scale = /./=1rn
```

.

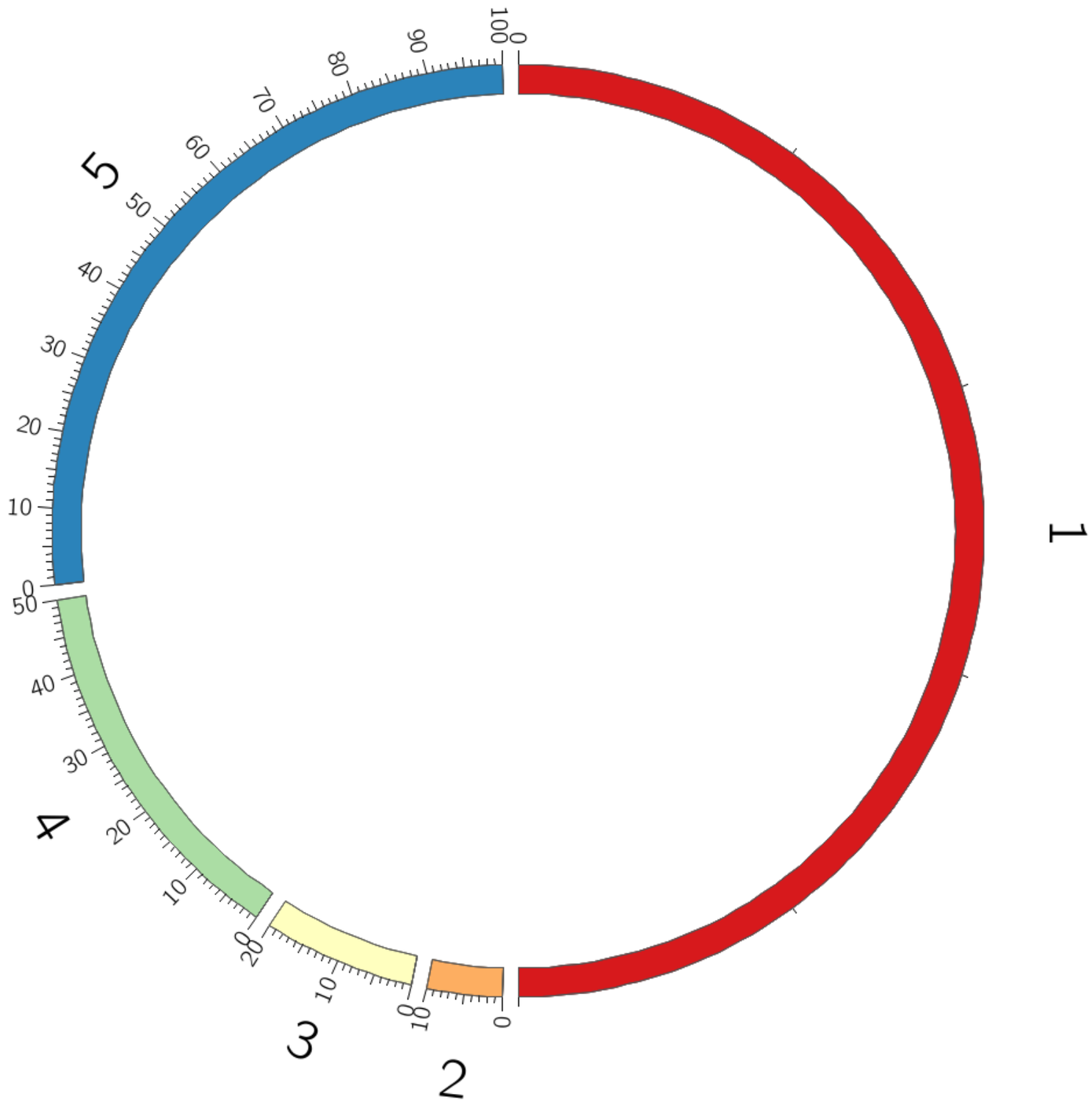
ABSOLUTE SCALE FOR MULTIPLE IDEOGRAMS




```
# 2/3/etc/circos.conf

#chromosomes_scale = chr1=0.5

chromosomes_scale = chr1=0.5,chr2=2,chr3=10

# chr1 occupies 50% of figure
#chromosomes_scale = chr1=0.5r

# chr5 occupies 25% of figure
# chr4 occupies 25% of figure
#chromosomes_scale = chr5=0.25r,chr4=0.25r

# chr1 chr2 chr3 together occupy 50% of
# figure, and within this region they
# are equally sized
#
# equivalent to
# chr1=0.0833r,chr2=0.0833r,chr3=0.0833r
#chromosomes_scale = /chr[123]/=0.5rn

# all chromosomes equally sized
#chromosomes_scale = /./=1rn
```

.

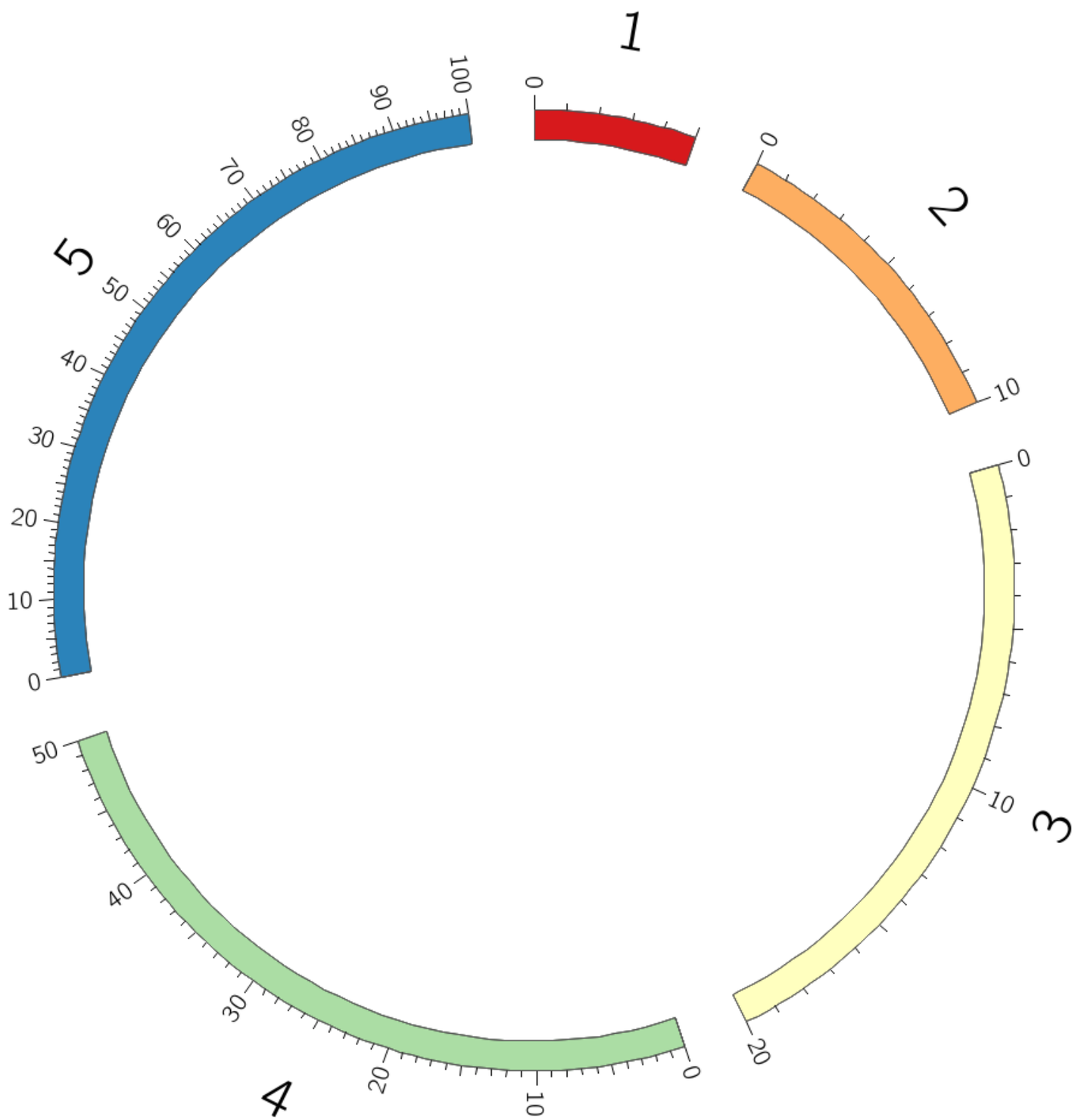
RELATIVE IDEOGRAM SCALE




```
# 2/3/etc/circos.conf

#chromosomes_scale = chr1=0.5

#chromosomes_scale = chr1=0.5,chr2=2,chr3=10

# chr1 occupies 50% of figure
chromosomes_scale = chr1=0.5r

# chr5 occupies 25% of figure
# chr4 occupies 25% of figure
#chromosomes_scale = chr5=0.25r,chr4=0.25r

# chr1 chr2 chr3 together occupy 50% of
# figure, and within this region they
# are equally sized
#
# equivalent to
# chr1=0.0833r,chr2=0.0833r,chr3=0.0833r
#chromosomes_scale = /chr[123]/=0.5rn

# all chromosomes equally sized
#chromosomes_scale = /./=1rn
```

.

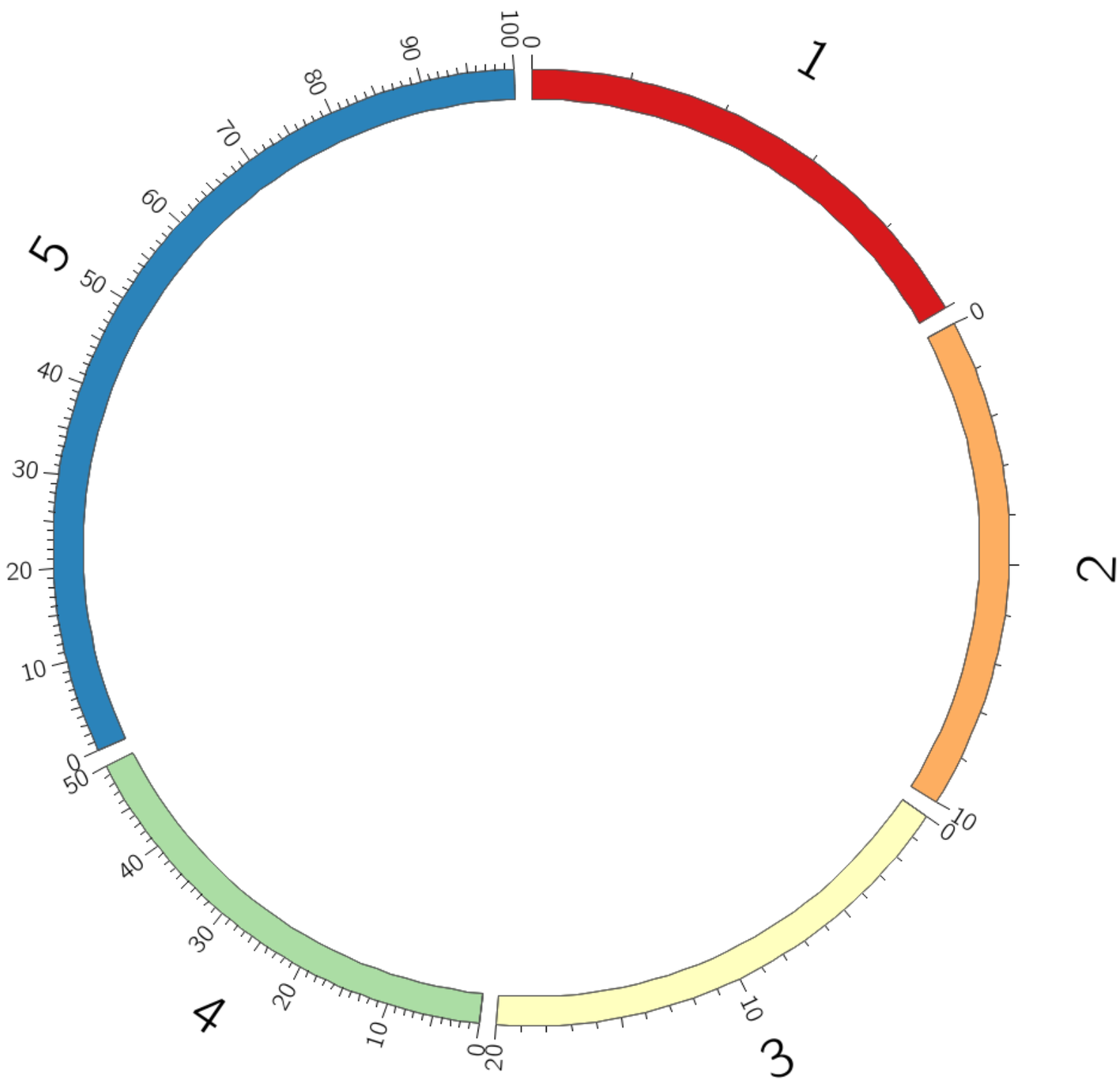
RELATIVE SCALE FOR MULTIPLE IDEOGRAMS




```
# 2/3/etc/circos.conf

#chromosomes_scale = chr1=0.5

#chromosomes_scale = chr1=0.5,chr2=2,chr3=10

# chr1 occupies 50% of figure
#chromosomes_scale = chr1=0.5r

# chr5 occupies 25% of figure
# chr4 occupies 25% of figure
chromosomes_scale = chr5=0.25r,chr4=0.25r

# chr1 chr2 chr3 together occupy 50% of
# figure, and within this region they
# are equally sized
#
# equivalent to
# chr1=0.0833r,chr2=0.0833r,chr3=0.0833r
#chromosomes_scale = /chr[123]/=0.5rn

# all chromosomes equally sized
#chromosomes_scale = /./=1rn
```

.

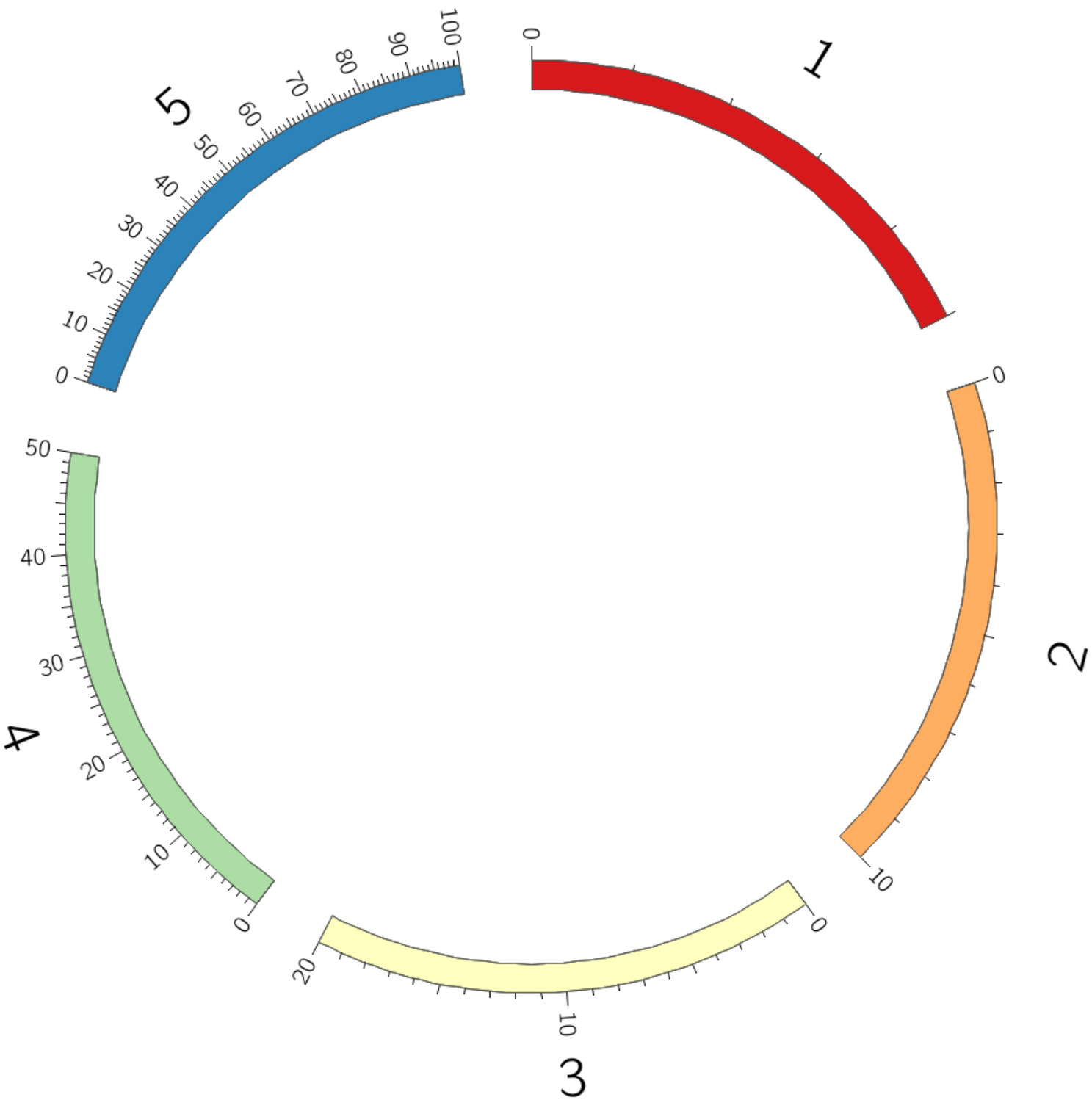
RELATIVE SCALE FOR MULTIPLE IDEOGRAMS




```
# 2/3/etc/circos.conf

#chromosomes_scale = chr1=0.5

#chromosomes_scale = chr1=0.5,chr2=2,chr3=10

# chr1 occupies 50% of figure
#chromosomes_scale = chr1=0.5r

# chr5 occupies 25% of figure
# chr4 occupies 25% of figure
#chromosomes_scale = chr5=0.25r,chr4=0.25r

# chr1 chr2 chr3 together occupy 50% of
# figure, and within this region they
# are equally sized
#
# equivalent to
# chr1=0.0833r,chr2=0.0833r,chr3=0.0833r
chromosomes_scale = /chr[123]/=0.5rn

# all chromosomes equally sized
#chromosomes_scale = /./=1rn
```

.

RELATIVE SCALE FOR MULTIPLE IDEOGRAMS



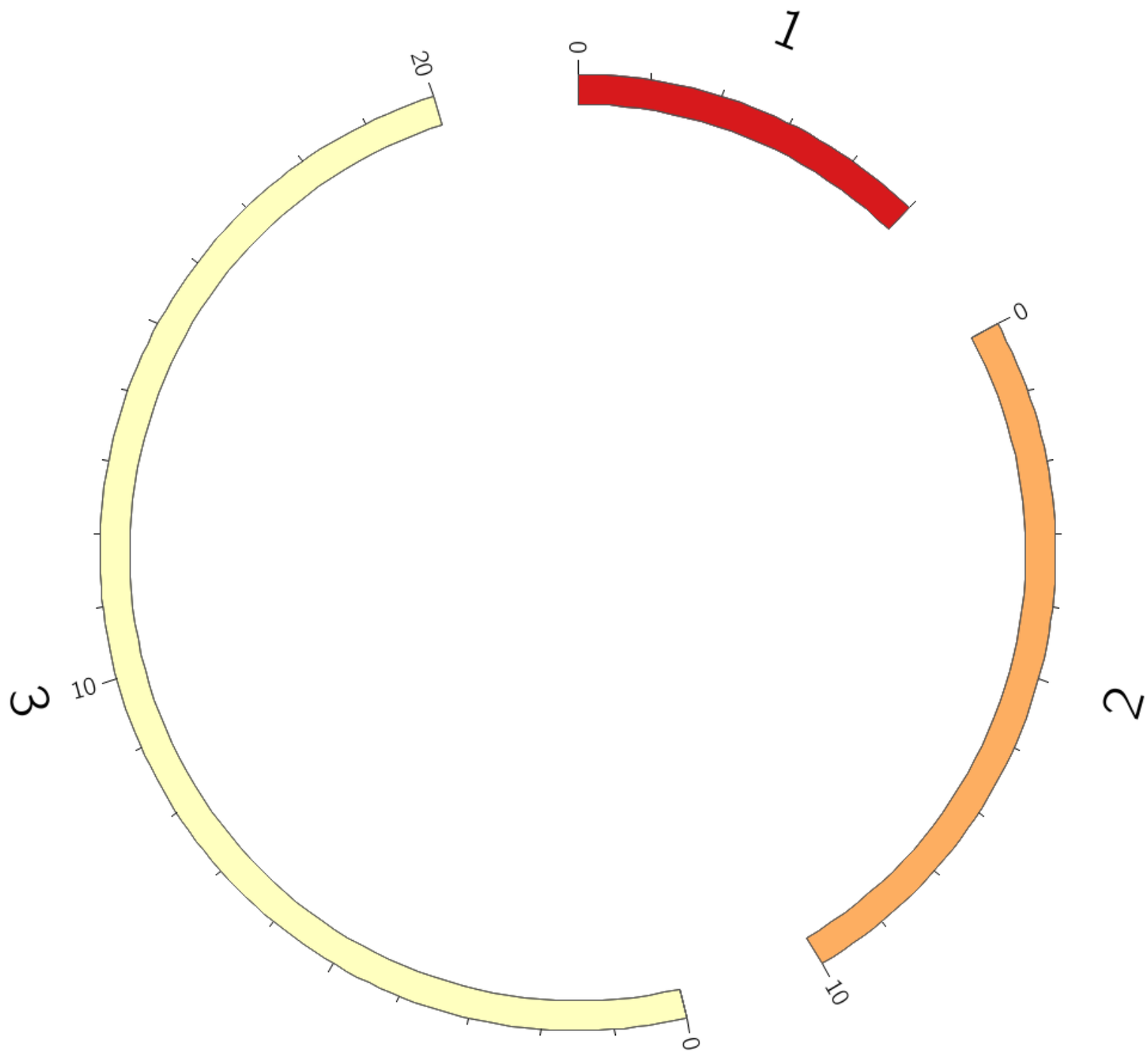

```
# 2/3/etc/circos.conf

#chromosomes_scale = chr1=0.5

#chromosomes_scale = chr1=0.5,chr2=2,chr3=10

# chr1 occupies 50% of figure
#chromosomes_scale = chr1=0.5r

# chr5 occupies 25% of figure
# chr4 occupies 25% of figure
# chromosomes_scale = chr5=0.25r,chr4=0.25r

# chr1 chr2 chr3 together occupy 50% of
# figure, and within this region they
# are equally sized
#
# equivalent to
# chr1=0.0833r,chr2=0.0833r,chr3=0.0833r
#chromosomes_scale = /chr[123]/=0.5rn

# all chromosomes equally sized
chromosomes_scale = /./=1rn
```

.

filtering

LESSON 4

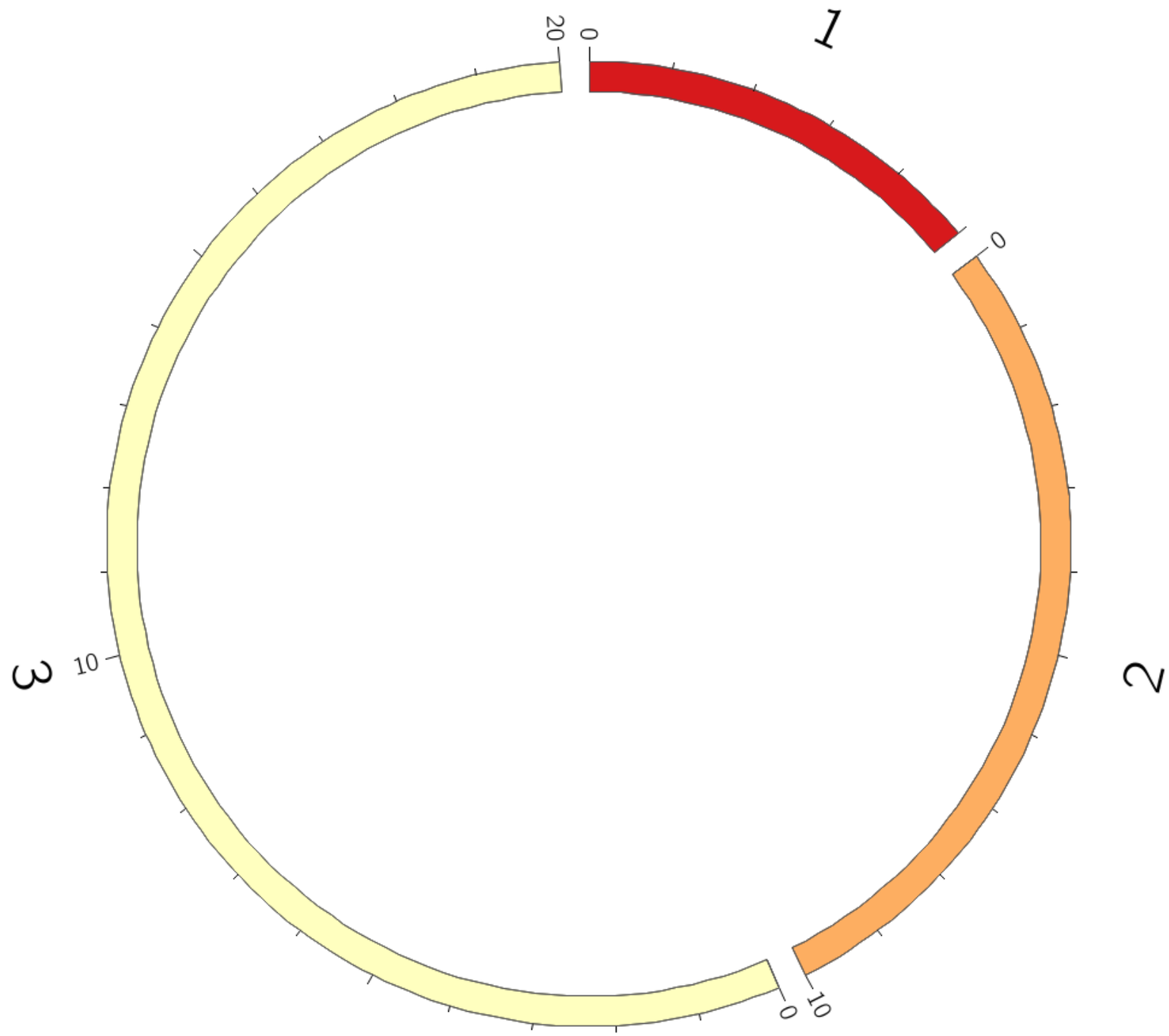
DRAWING SPECIFIC IDEOGRAMS




```
# 2/4/etc/circos.conf

chromosomes_units            = 1000000
#chromosomes_display_default = yes

chromosomes_display_default  = no
chromosomes                  = chr1;chr2;chr3

# 2/4/etc/ideogram.conf

<ideogram>

<spacing>

default = 2u

#default = 0.01r

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

RELATIVE SPACING



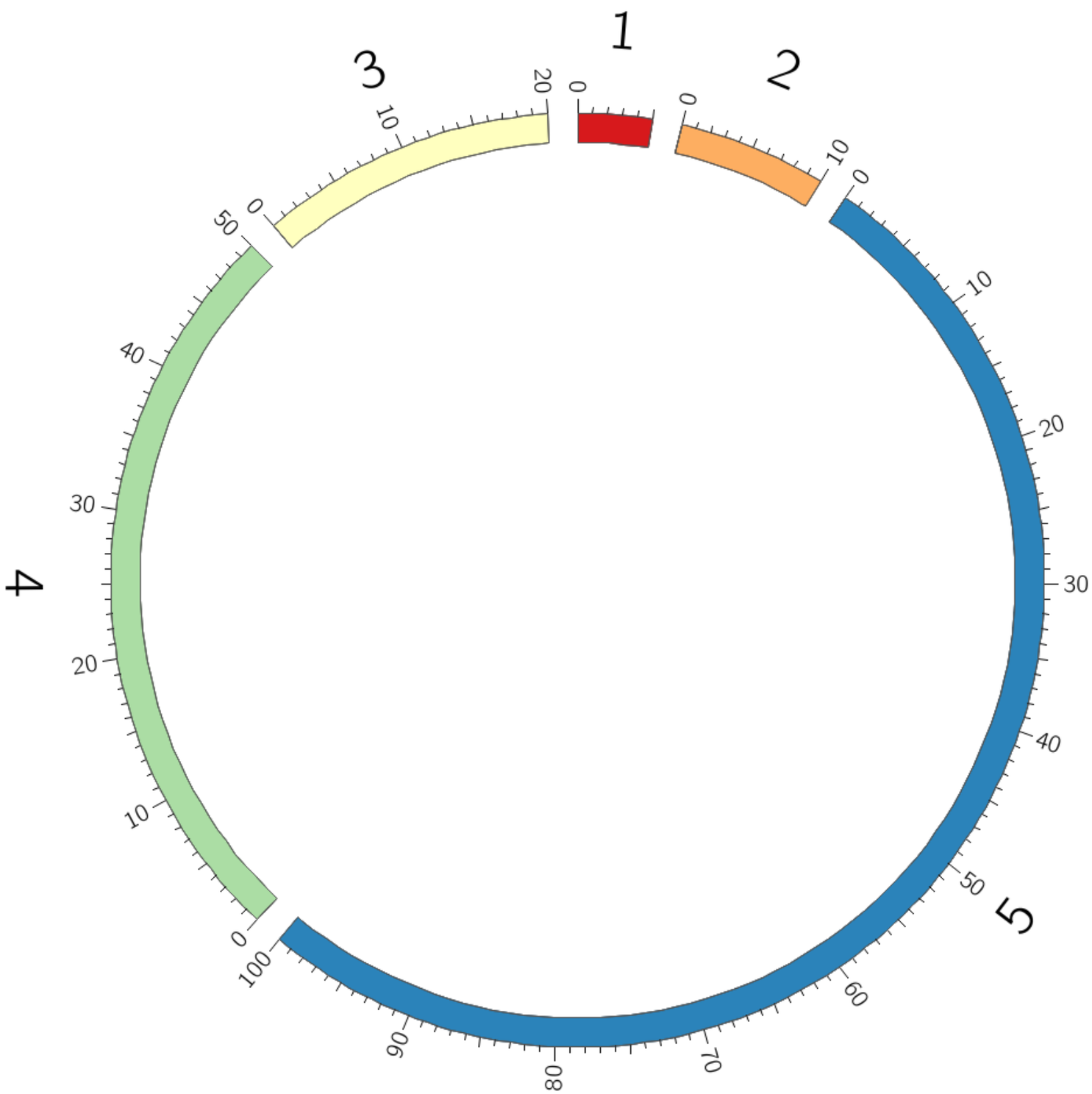

```
# 2/4/etc/circos.conf

chromosomes_units            = 1000000
#chromosomes_display_default = yes

chromosomes_display_default  = no
chromosomes                  = chr1;chr2;chr3

# 2/4/etc/ideogram.conf

<ideogram>

<spacing>

#default = 2u

default = 0.01r

</spacing>

<<include ../../etc/ideogram.conf>>

</ideogram>
```

.

order

LESSON 5

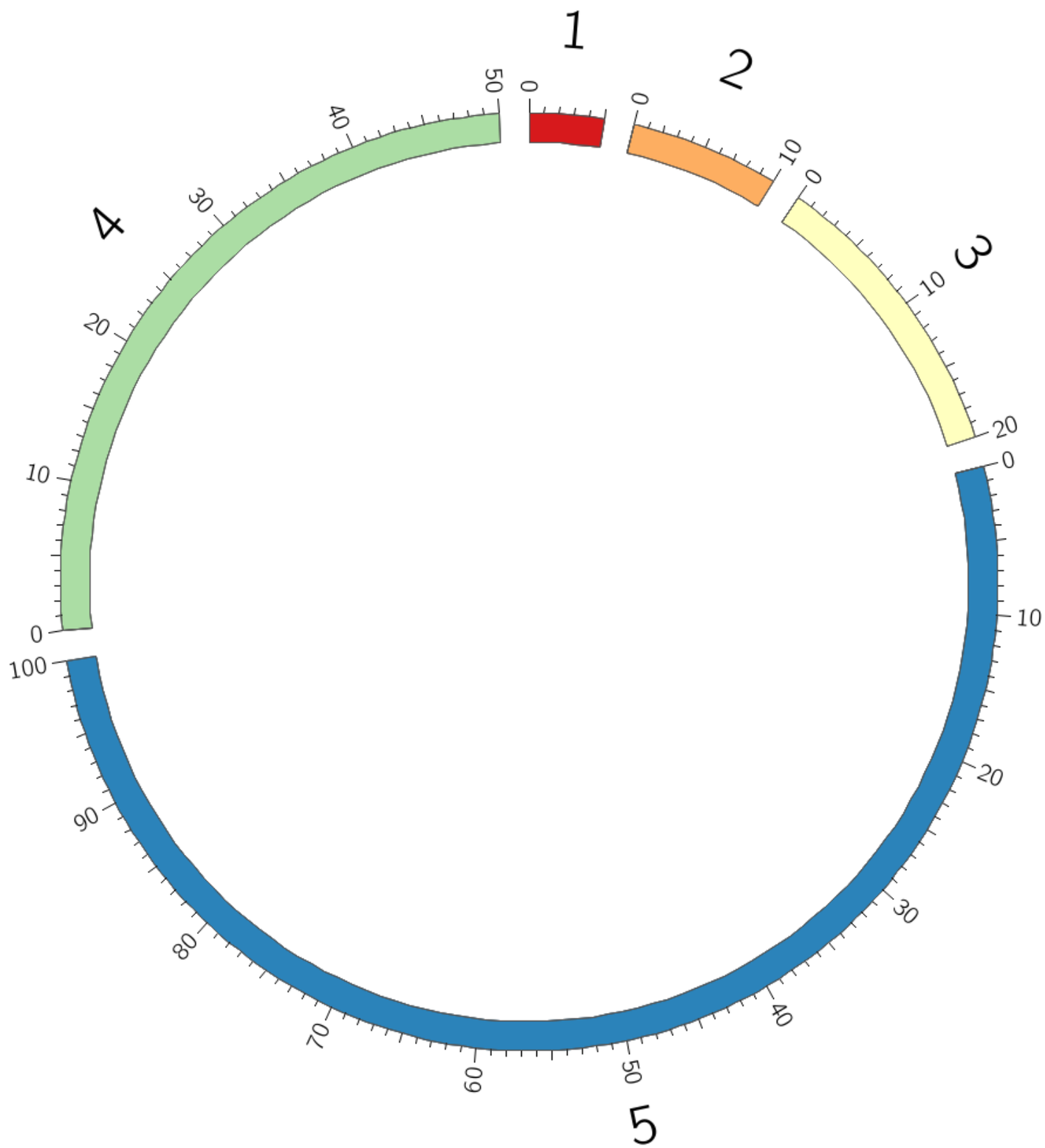
IDEOGRAM ORDER




```
# 2/5/etc/circos.conf

# explicitly define order
chromosomes_order = chr1,chr2,chr5,chr4,chr3

# relative order
#chromosomes_order = chr3,chr5

# relative order
#chromosomes_order = chr1,chr4,-,-,chr2
```

.

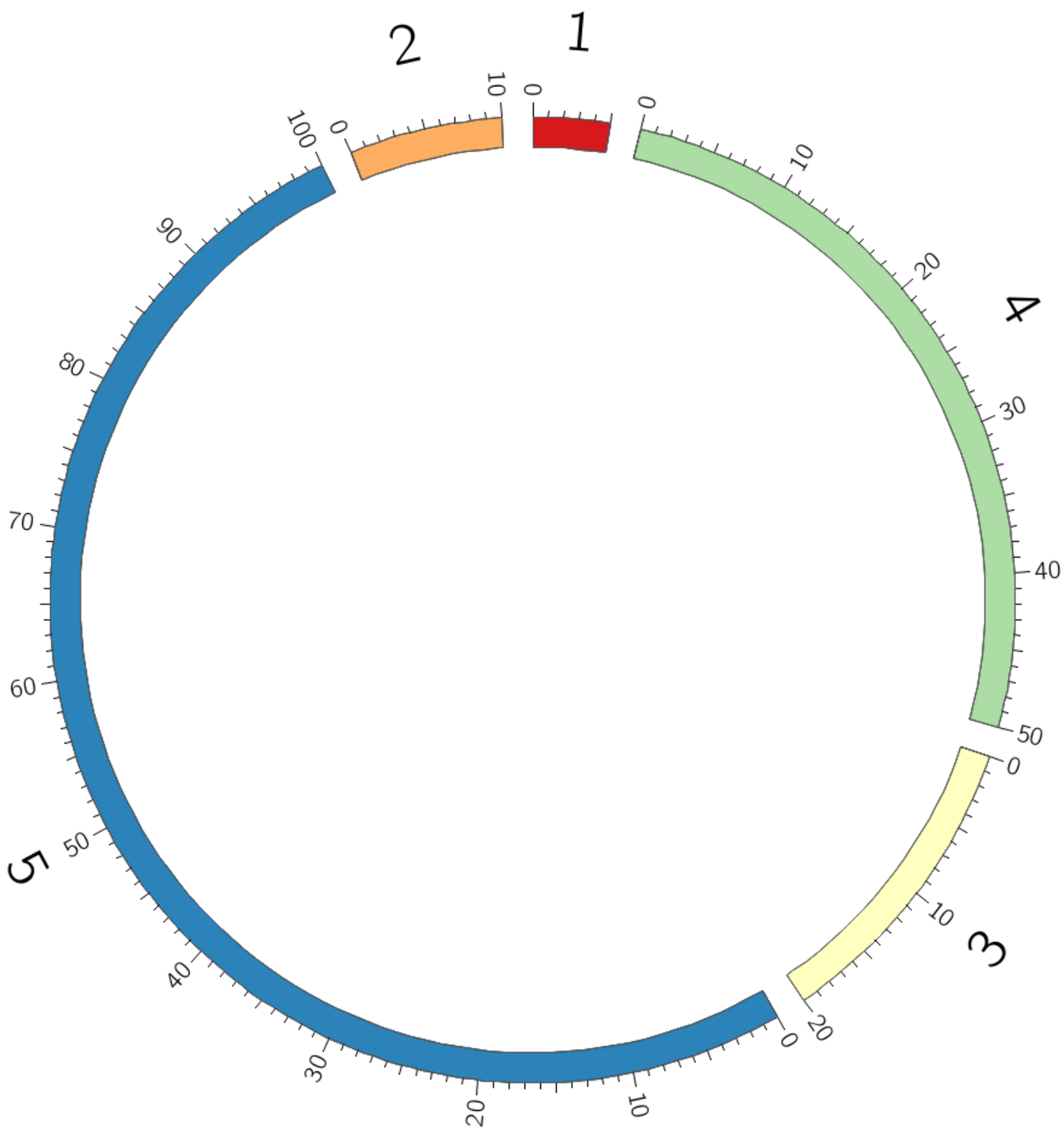
IDEOGRAM ORDER




```
# 2/5/etc/circos.conf

# explicitly define order
#chromosomes_order = chr1,chr2,chr5,chr4,chr3

# relative order
chromosomes_order = chr3,chr5

# relative order
#chromosomes_order = chr1,chr4,-,-,chr2
```

.

IDEOGRAM ORDER



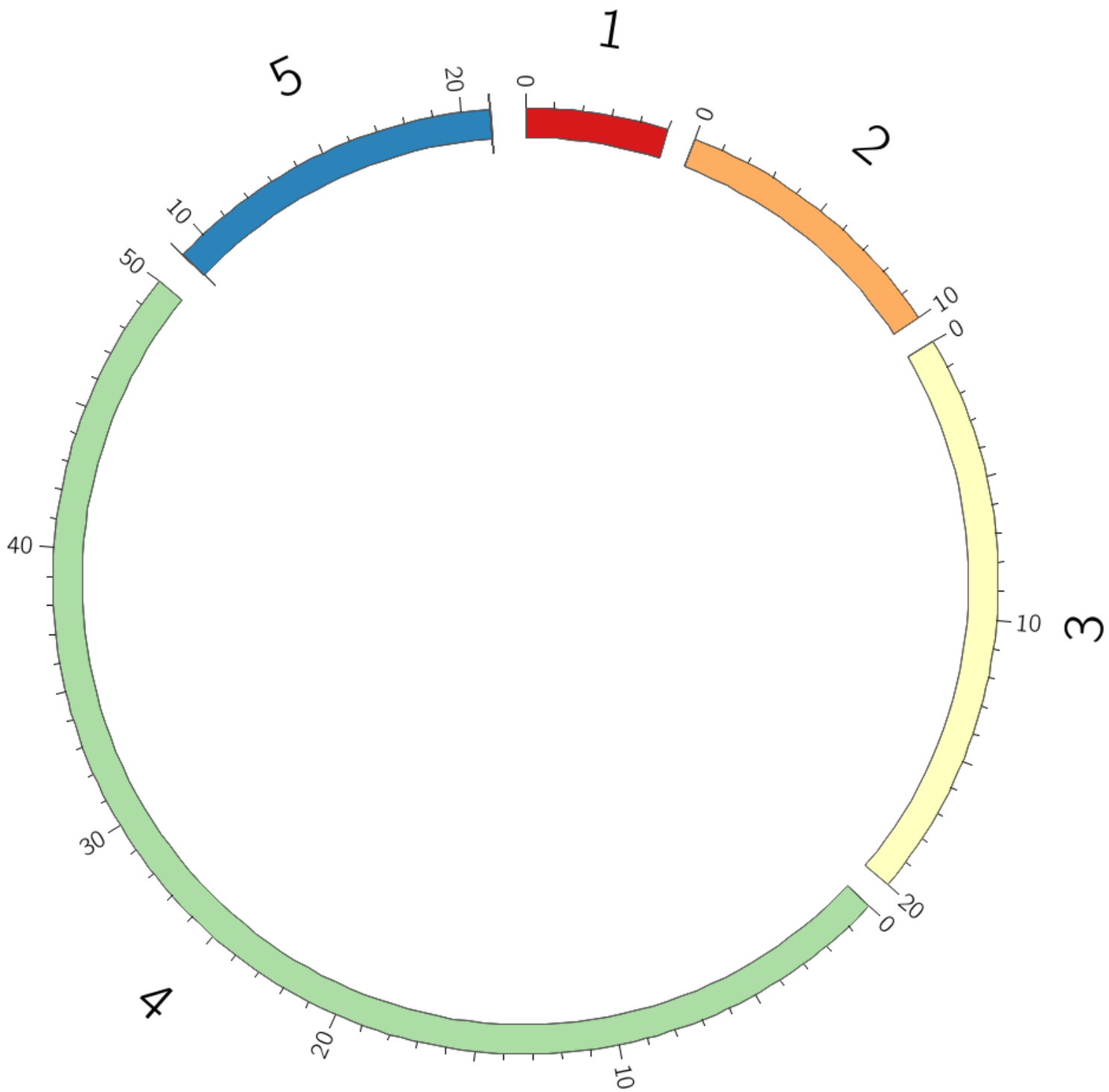

```
# 2/5/etc/circos.conf

# explicitly define order
#chromosomes_order = chr1,chr2,chr5,chr4,chr3

# relative order
#chromosomes_order = chr3,chr5

# relative order
chromosomes_order = chr1,chr4,-,-,chr2
```

.

cropping

LESSON 6

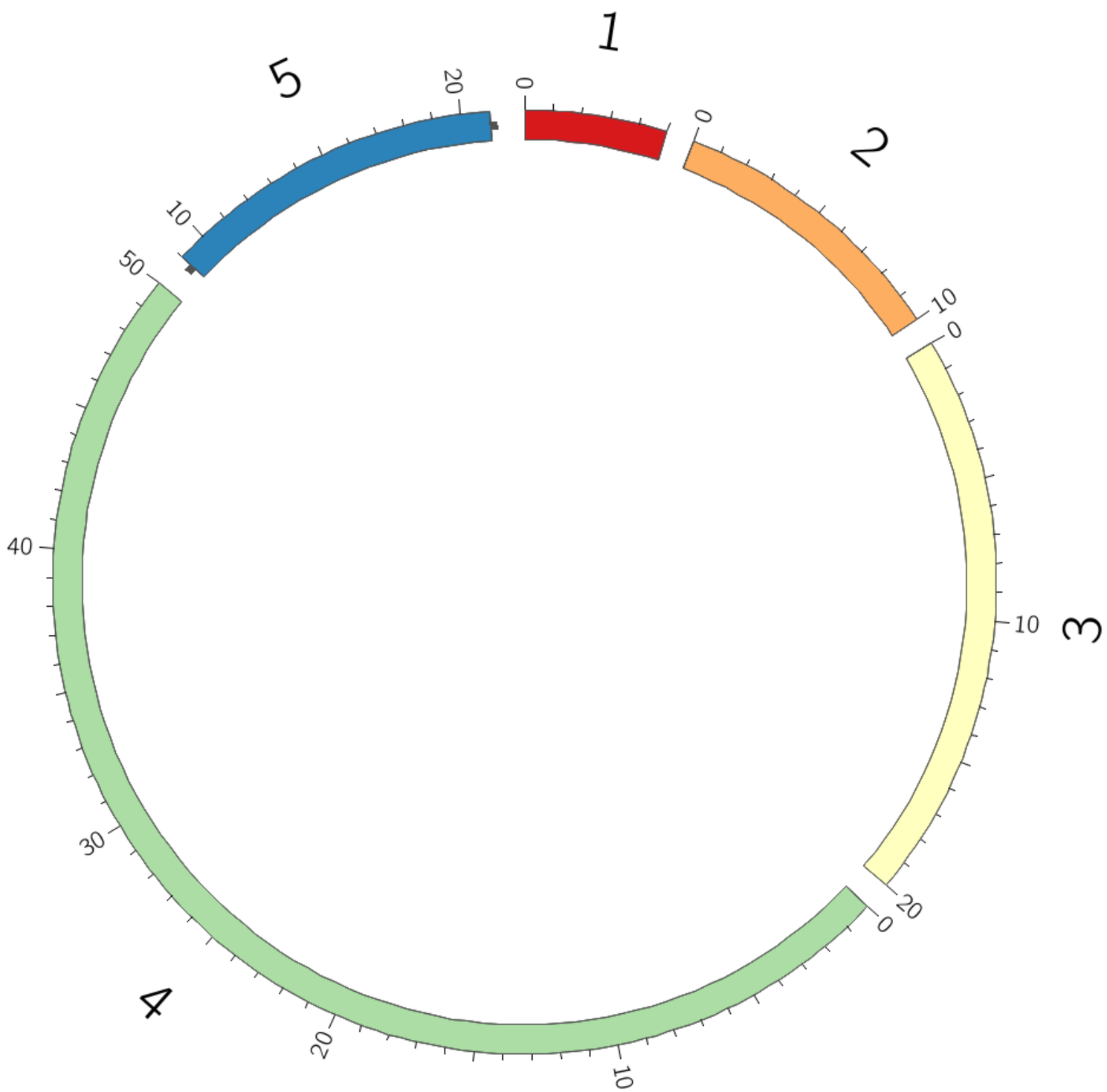
CROPPING IDEOGRAMS




```
# 2/6/etc/circos.conf

chromosomes  = chr5=9-21
#chromosomes = chr3=8-12;chr4=4-11;chr5=9-21


# 2/6/etc/ideogram.conf

<spacing>

default = 0.01r
break   = 0.25r

<<include break.conf>>

</spacing>

# 2/6/etc/break.conf

axis_break         = yes
axis_break_at_edge = yes
axis_break_style   = 2

<break_style 1>
stroke_color = vdgrey
fill_color   = vdgrey
thickness    = 0.25r
</break_style>

<break_style 2>
stroke_color     = vdgrey
stroke_thickness = 2
thickness        = 2r
</break_style>
```

.

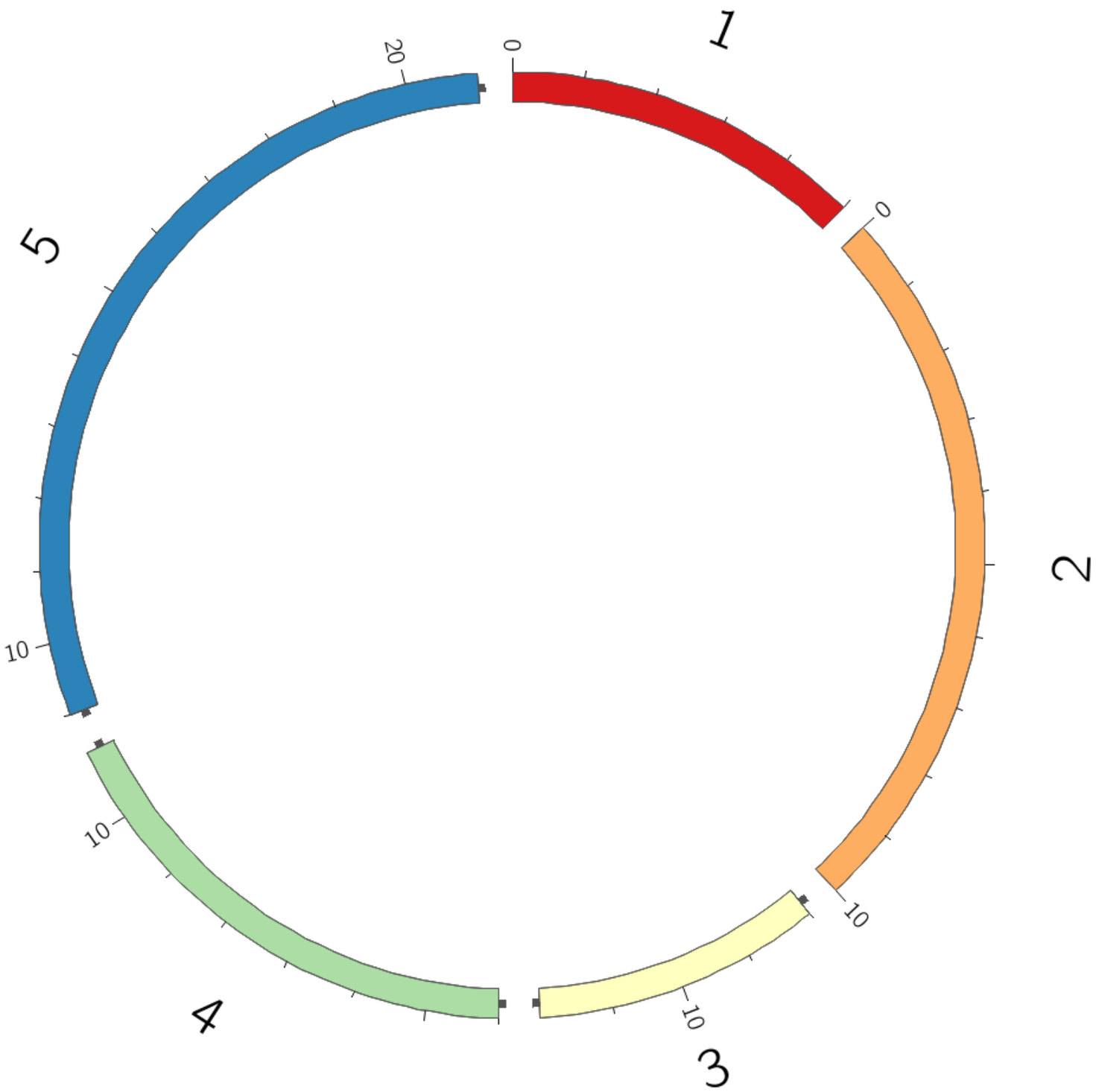
CROPPING IDEOGRAMS




```
# 2/6/etc/circos.conf

chromosomes  = chr5=9-21
#chromosomes = chr3=8-12;chr4=4-11;chr5=9-21


# 2/6/etc/ideogram.conf

<spacing>

default = 0.01r
break   = 0.25r

<<include break.conf>>

</spacing>

# 2/6/etc/break.conf

axis_break_style   = 1
```

.

CROPPING IDEOGRAMS



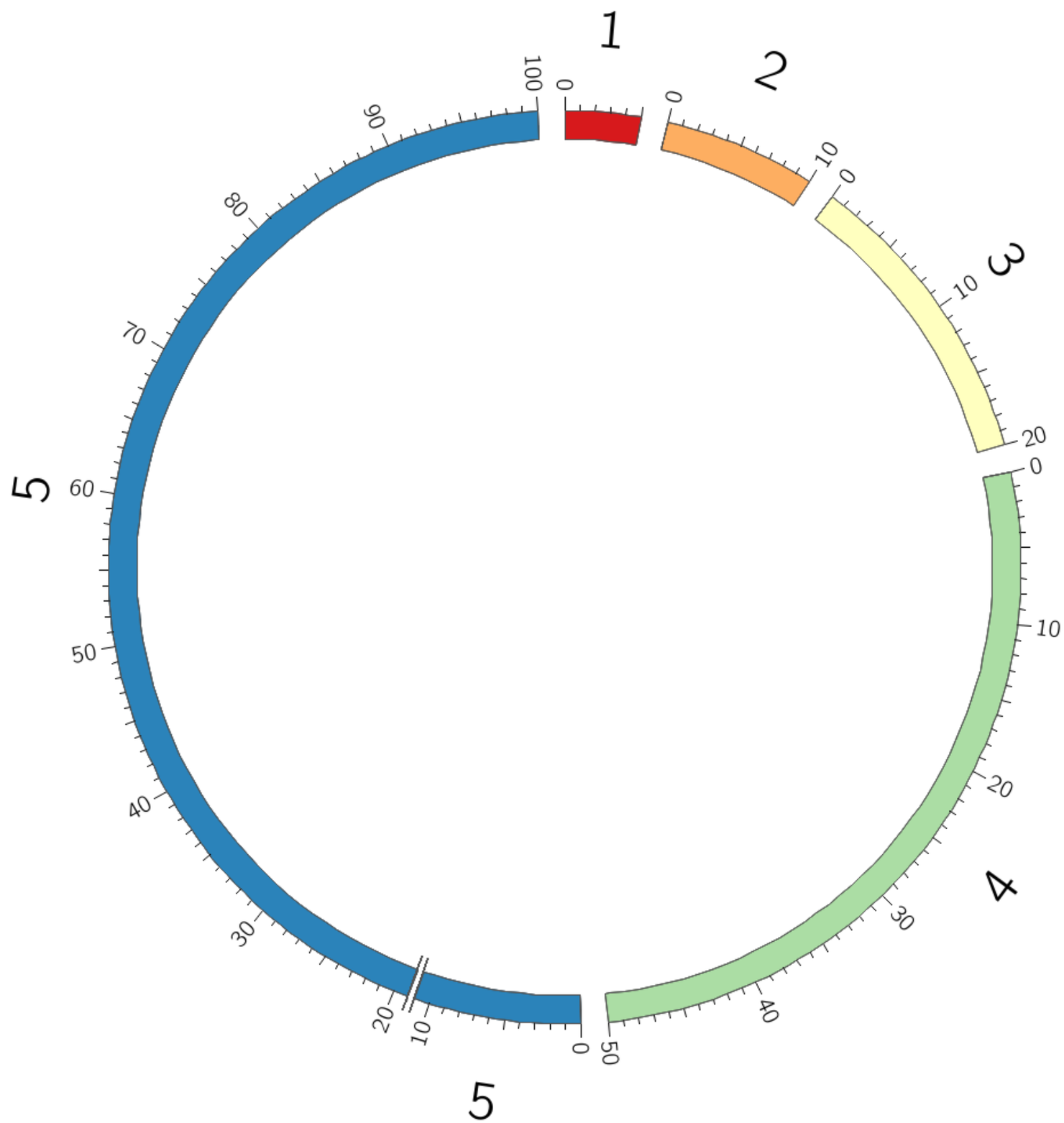

```
# 2/6/etc/circos.conf

#chromosomes  = chr5=9-21
chromosomes = chr3=8-12;chr4=4-11;chr5=9-21
```

.

axis breaks

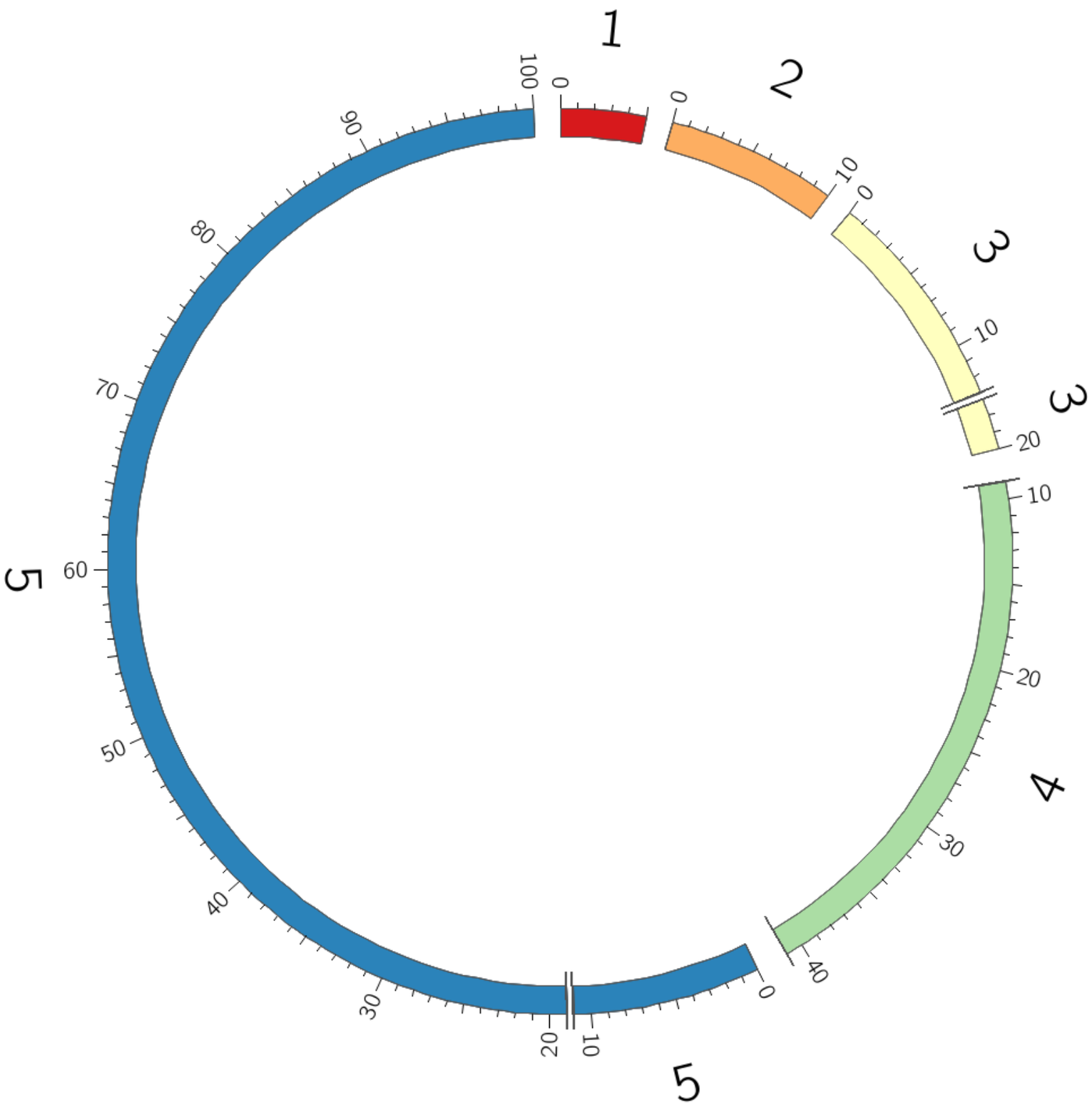
LESSON 7

IDEOGRAM BREAKS




```
# 2/7/etc/circos.conf

chromosomes_breaks = -chr5=11-19
#chromosomes_breaks = -chr3=13-17;
                      -chr4=(-9;-chr4=41-);
                      -chr5=11-19

# 2/7/etc/ideogram.conf

<spacing>

default = 0.01r
break   = 0.25r

<<include break.conf>>

</spacing>

# 2/7/etc/break.conf

axis_break         = yes
axis_break_at_edge = yes
axis_break_style   = 2

<break_style 1>
stroke_color = vdgrey
fill_color   = vdgrey
thickness    = 0.25r
</break_style>

<break_style 2>
stroke_color     = vdgrey
stroke_thickness = 2
thickness        = 2r
</break_style>
```

IDEOGRAM BREAKS



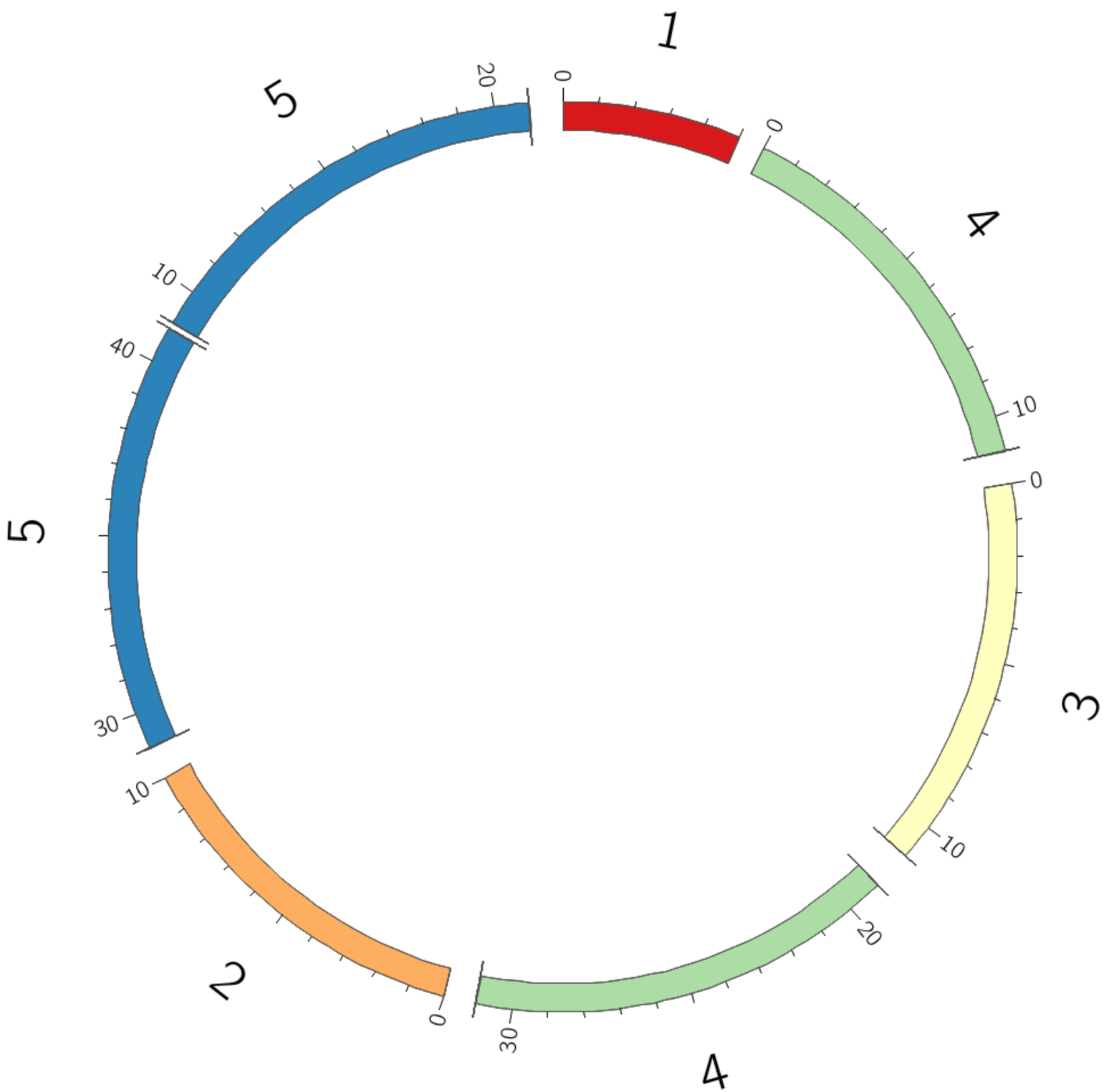

```
# 2/7/etc/circos.conf

#chromosomes_breaks = -chr5=11-19
chromosomes_breaks = -chr3=13-17;
                     -chr4=(-9;-chr4=41-);
                     -chr5=11-19
```

.

ordering cropped regions

LESSON 8

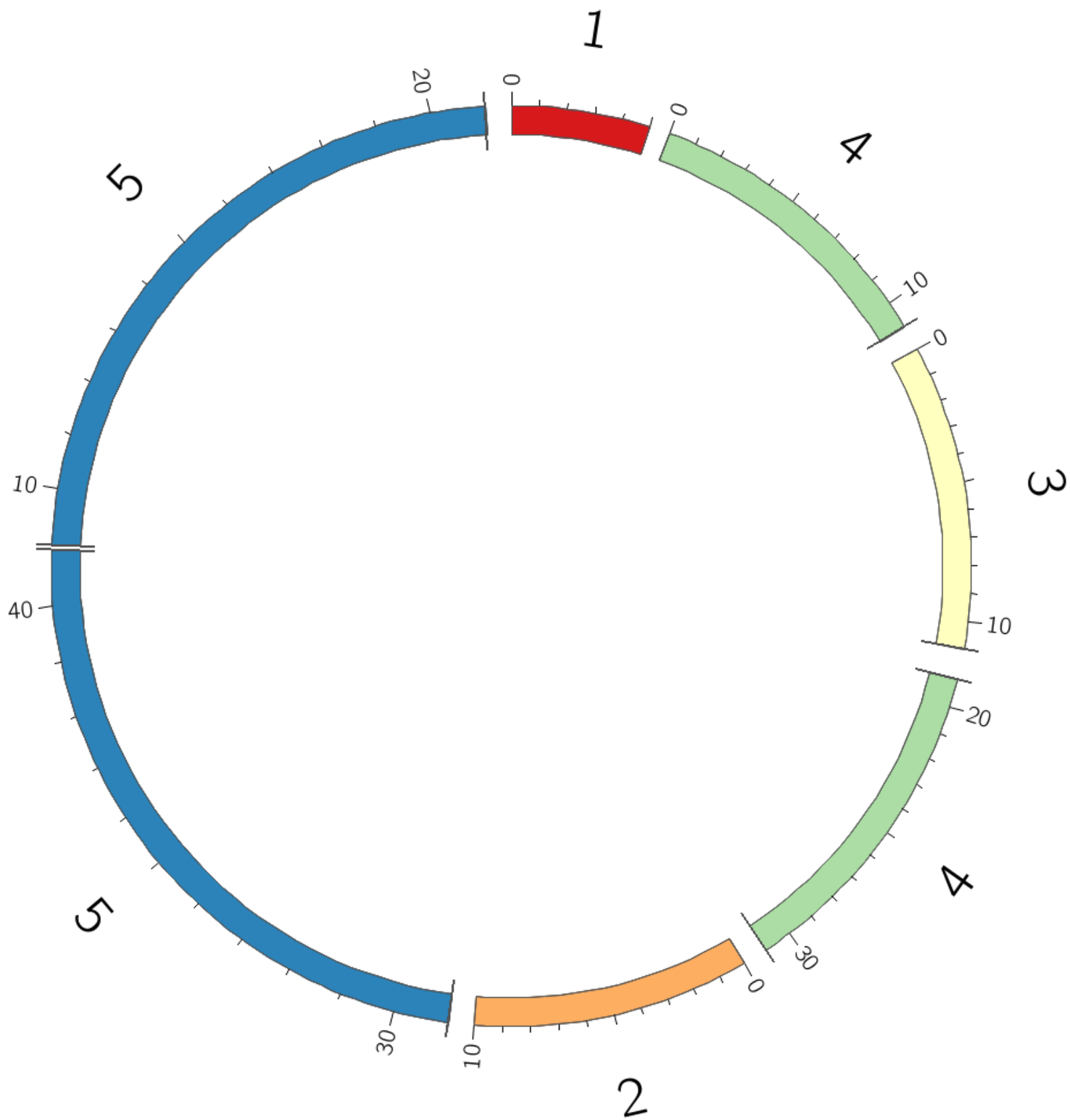
ORDERING CROPPED IDEOGRAMS




```
# 2/8/etc/circos.conf

chromosomes        = chr3:0-11;
                     chr4[4a]:0-11;
                     chr4[4b]:19-31;
                     chr5[5a]:9-21;
                     chr5[5b]:29-41;

chromosomes_order = ^,chr1,4a,chr3,4b,-,5b,5a

#chromosomes_scale = 5a=2,5b=2
```

.

ORDERING AND SCALING CROPPED IDEOGRAMS



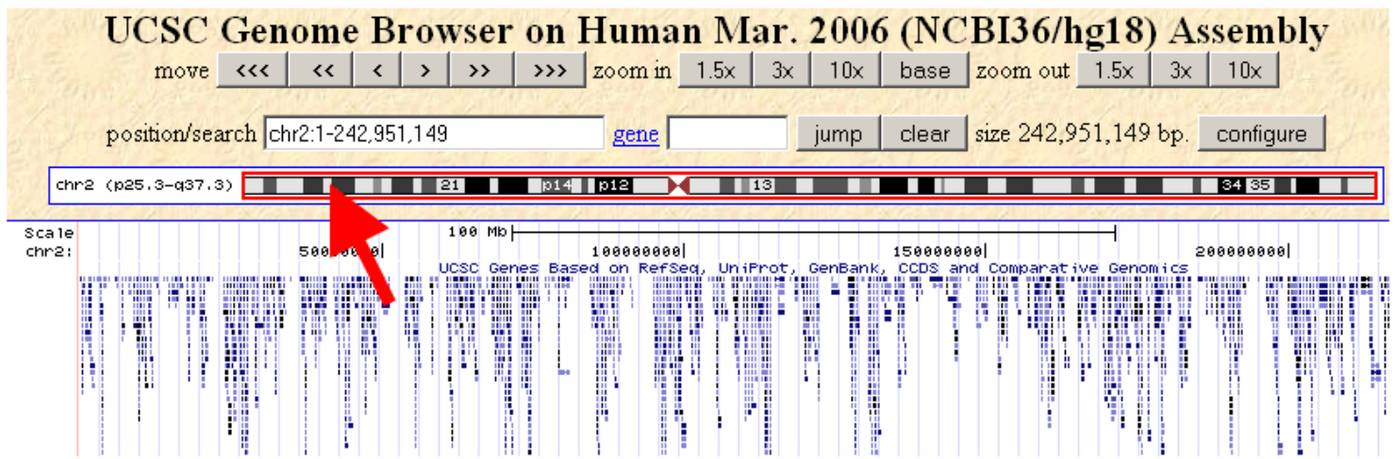

```
# 2/8/etc/circos.conf

chromosomes       = chr3:0-11;
                    chr4[4a]:0-11;
                    chr4[4b]:19-31;
                    chr5[5a]:9-21;
                    chr5[5b]:29-41;

chromosomes_order = ^,chr1,4a,chr3,4b,-,5b,5a

chromosomes_scale = 5a=2,5b=2
```

.

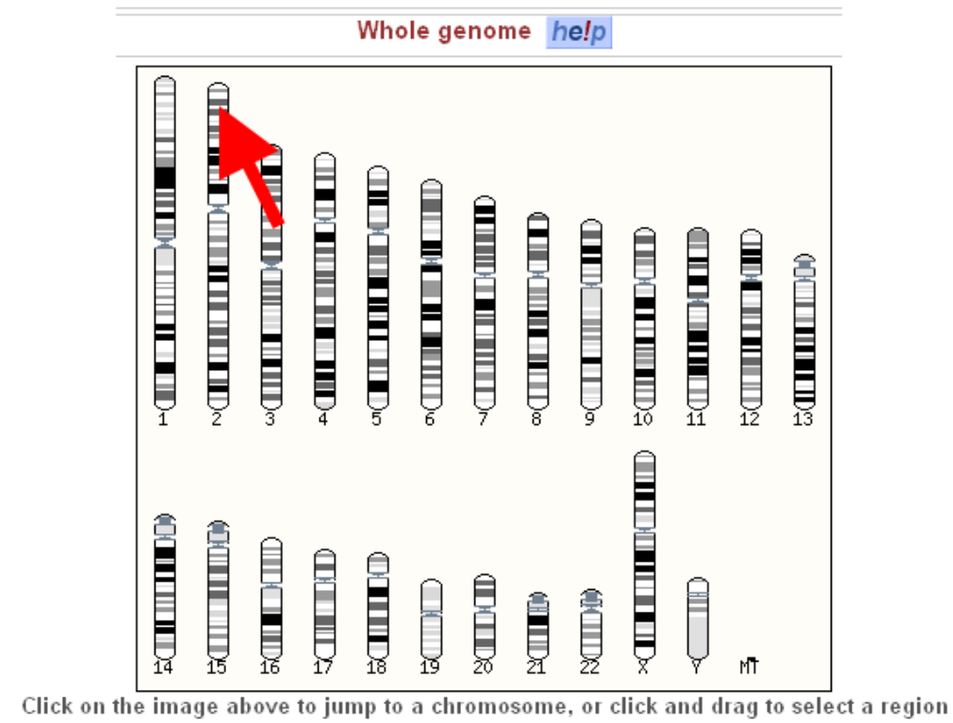
cytogenetic bands

LESSON 9

CYTOGENETIC BANDS IN BROWSERS



human chr2 at UCSC Genome Browser
http://genome.ucsc.edu



karyotype entry point to human genome at Ensembl
http://www.ensembl.org/Homo_sapiens/Location/Genome

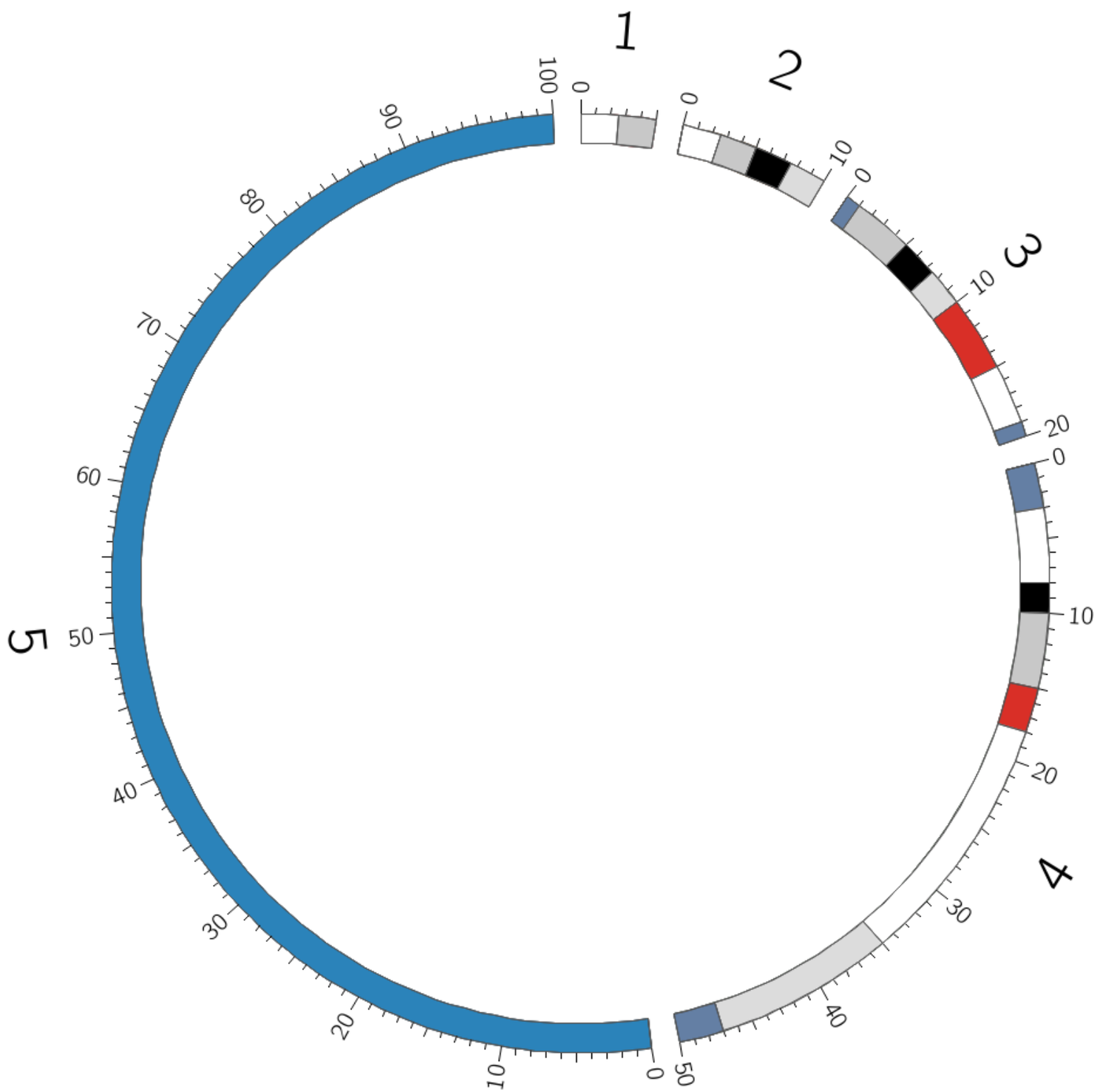
.

CONVENTIONAL BAND COLOR SCHEME

COLOR	RGB
gpos100	0,0,0
gpos	0,0,0
gpos75	130,130,130
gpos66	160,160,160
gpos50	200,200,200
gpos33	210,210,210
gpos25	200,200,200
gvar	220,220,220
gneg	255,255,255
acen	217,47,39
stalk	100,127,164

.

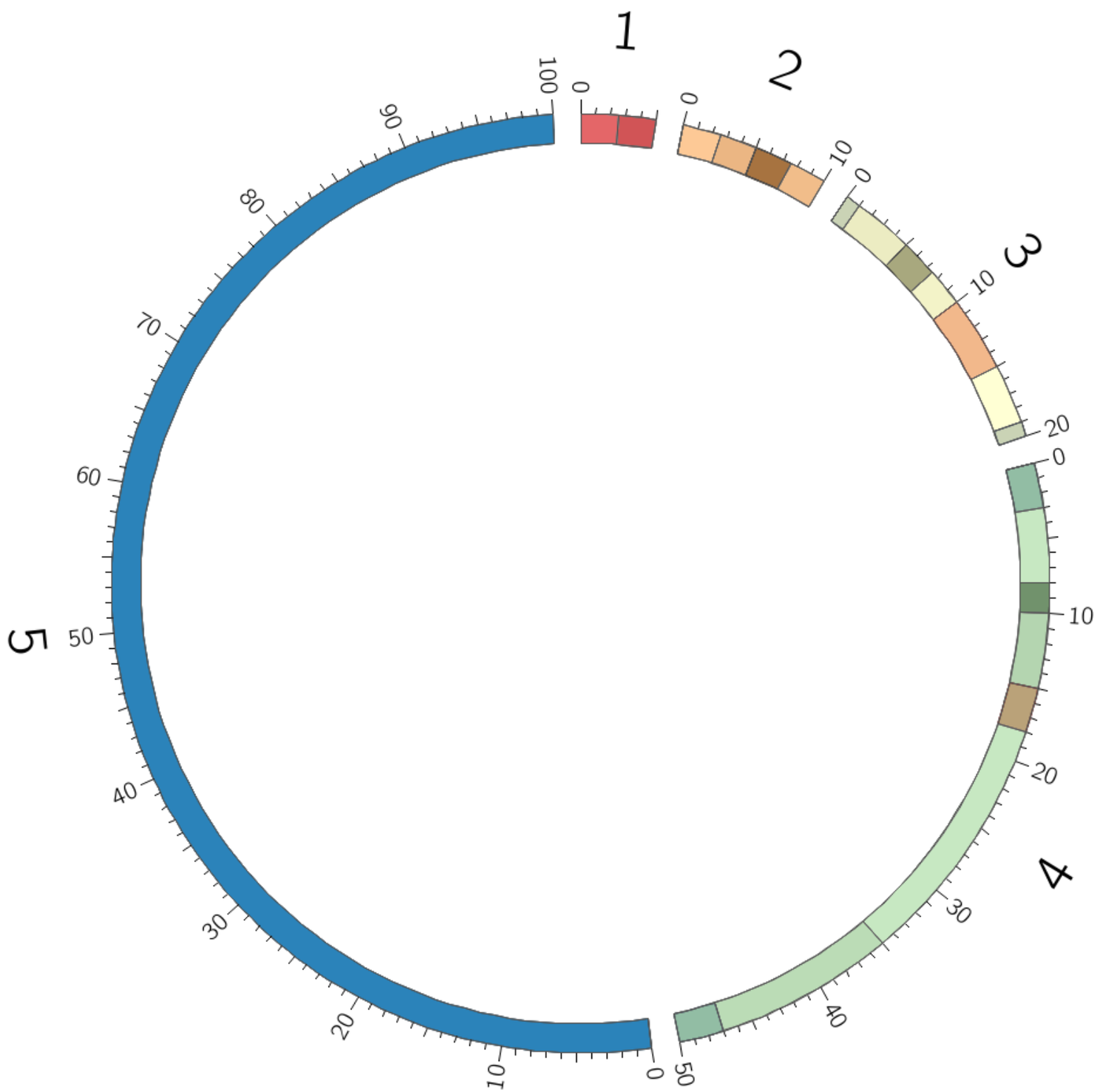
DEFINING AND DRAWING BANDS




```
# 2/9/etc/circos.conf

karyotype = ../data/karyotype.5chr.banded.txt

# 2/data/karyotype.5chr.banded.txt

band chr1 band1 band1 0 2500000 gneg
band chr1 band2 band2 2500000 5000000 gpos25

band chr2 band1 band1 0 2500000 gneg
band chr2 band2 band2 2500000 5000000 gpos25
band chr2 band3 band3 5000000 7500000 gpos100
band chr2 band4 band4 7500000 10000000 gvar

# 2/9/ideogram.conf

<<include ../../etc/ideogram.conf>>
band_transparency* = 0

# 2/etc/ideogram.conf

show_bands            = yes
fill_bands            = yes
band_stroke_thickness = 1
band_transparency     = 1
```

.

DEFINING AND DRAWING BANDS



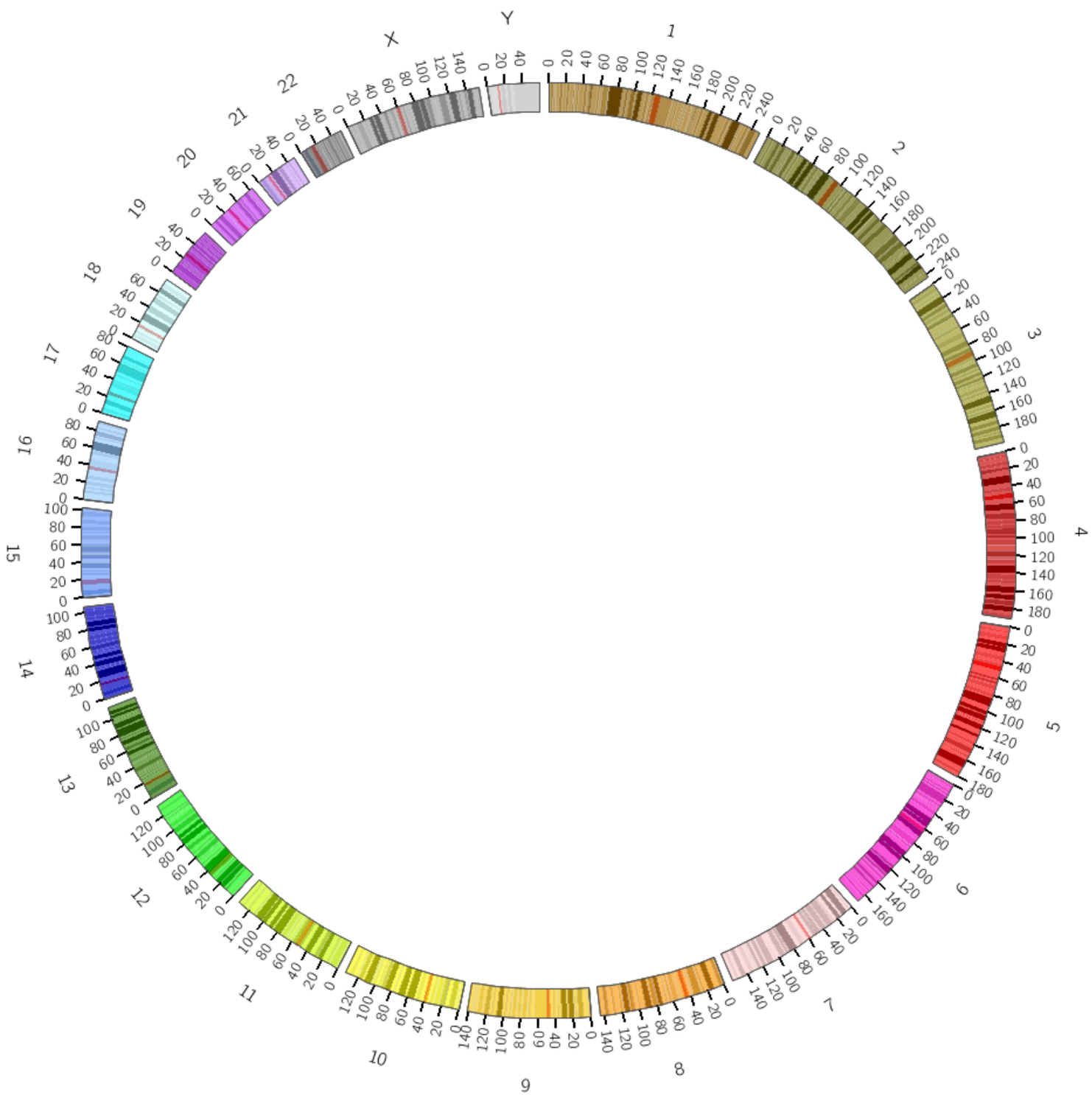

```
# 2/9/etc/circos.conf

karyotype = ../data/karyotype.5chr.banded.txt

# 2/data/karyotype.5chr.banded.txt

band chr1 band1 band1 0 2500000 gneg
band chr1 band2 band2 2500000 5000000 gpos25

band chr2 band1 band1 0 2500000 gneg
band chr2 band2 band2 2500000 5000000 gpos25
band chr2 band3 band3 5000000 7500000 gpos100
band chr2 band4 band4 7500000 10000000 gvar

# 2/9/ideogram.conf

<<include ../../etc/ideogram.conf>>
band_transparency* = 4

# 2/etc/ideogram.conf

show_bands            = yes
fill_bands            = yes
band_stroke_thickness = 1
band_transparency     = 1
```

.

whole genome karyotypes

LESSON 10

HUMAN GENOME IDEOGRAMS




```
# 2/10/etc/circos.conf

karyotype = data/karyotype/
            karyotype.human.txt
#karyotype = data/karyotype/
             karyotype.mouse.txt
#karyotype = data/karyotype/
             karyotype.human.txt,
             data/karyotype/
             karyotype.mouse.txt
```

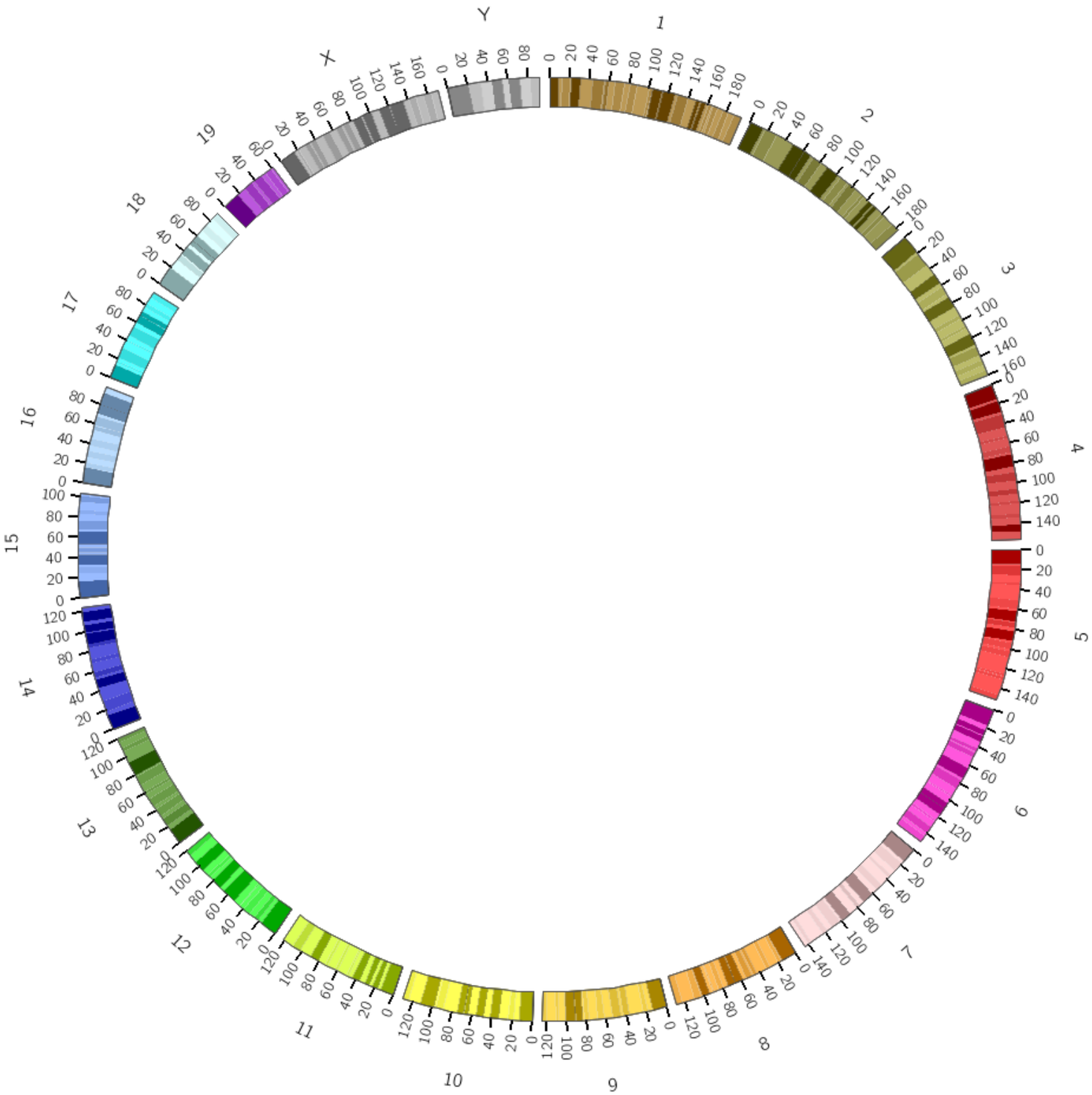
.

CONVENTIONAL IDEOGRAM COLOR SCHEME


```
# UCSC genome browser RGB
# colors for human chromosomes
chr1 = 153,102,0
chr2 = 102,102,0
chr3 = 153,153,30
chr4 = 204,0,0
chr5 = 255,0,0
chr6 = 255,0,204
chr7 = 255,204,204
chr8 = 255,153,0
chr9 = 255,204,0
chr10 = 255,255,0
chr11 = 204,255,0
chr12 = 0,255,0
chr13 = 53,128,0
...
chr21 = 204,153,255
chr22 = 102,102,102
chr23 = 153,153,153
chrX  = 153,153,153
chr24 = 204,204,204
chrY  = 204,204,204
chrM  = 204,204,153
chr0  = 204,204,153
chrUn = 121,204,61
chrNA = 255,255,255

hs1 = chr1
hs2 = chr2
hs3 = chr3
...
```

.

MOUSE GENOME IDEOGRAMS




```
# 2/10/etc/circos.conf

#karyotype = ../../data/karyotype/
             karyotype.human.txt
karyotype = ../../data/karyotype/
            karyotype.mouse.txt
#karyotype = ../../data/karyotype/
             karyotype.human.txt,
             ../../data/karyotype/
             karyotype.mouse.txt
```

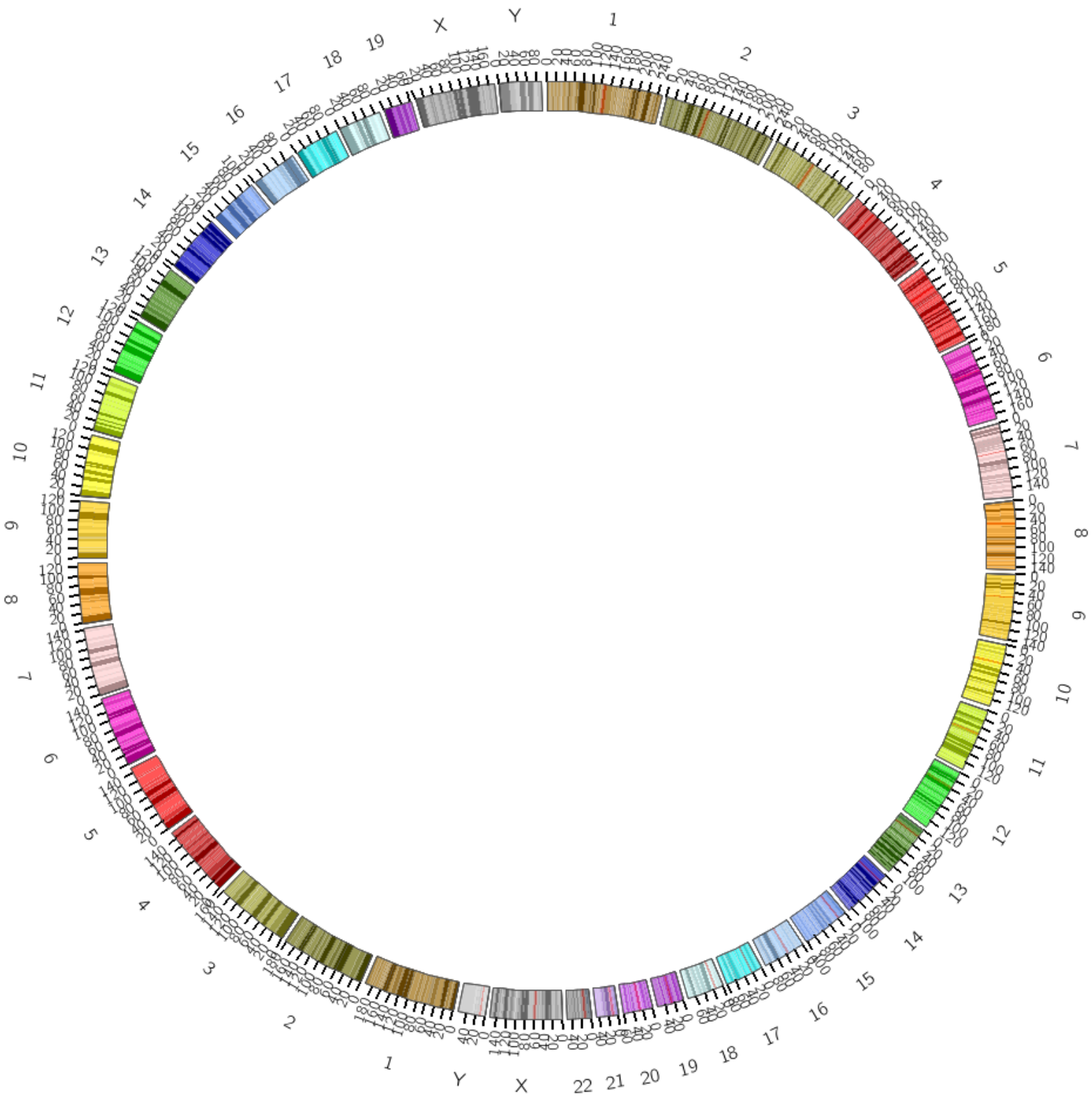
.

HG & MM KARYOTYPE DEFINITIONS

```
# data/karyotype/karyotype.human.hg19.txt

chr - hs1 1 0 249250621 chr1
chr - hs2 2 0 243199373 chr2
chr - hs3 3 0 198022430 chr3
chr - hs4 4 0 191154276 chr4
chr - hs5 5 0 180915260 chr5
chr - hs6 6 0 171115067 chr6
chr - hs7 7 0 159138663 chr7
chr - hs8 8 0 146364022 chr8
chr - hs9 9 0 141213431 chr9
chr - hs10 10 0 135534747 chr10
chr - hs11 11 0 135006516 chr11
chr - hs12 12 0 133851895 chr12
chr - hs13 13 0 115169878 chr13
chr - hs14 14 0 107349540 chr14
chr - hs15 15 0 102531392 chr15
chr - hs16 16 0 90354753 chr16
chr - hs17 17 0 81195210 chr17
chr - hs18 18 0 78077248 chr18
chr - hs19 19 0 59128983 chr19
chr - hs20 20 0 63025520 chr20
chr - hs21 21 0 48129895 chr21
chr - hs22 22 0 51304566 chr22
chr - hsX x 0 155270560 chrx
chr - hsY y 0 59373566 chry
```

```
# data/karyotype/karyotype.mouse.mm10.txt

chr - mm1 1 0 195471971 chr1
chr - mm2 2 0 182113224 chr2
chr - mm3 3 0 160039680 chr3
chr - mm4 4 0 156508116 chr4
chr - mm5 5 0 151834684 chr5
chr - mm6 6 0 149736546 chr6
chr - mm7 7 0 145441459 chr7
chr - mm8 8 0 129401213 chr8
chr - mm9 9 0 124595110 chr9
chr - mm10 10 0 130694993 chr10
chr - mm11 11 0 122082543 chr11
chr - mm12 12 0 120129022 chr12
chr - mm13 13 0 120421639 chr13
chr - mm14 14 0 124902244 chr14
chr - mm15 15 0 104043685 chr15
chr - mm16 16 0 98207768 chr16
chr - mm17 17 0 94987271 chr17
chr - mm18 18 0 90702639 chr18
chr - mm19 19 0 61431566 chr19
chr - mmX x 0 171031299 chrx
chr - mmY y 0 91744698 chry
```

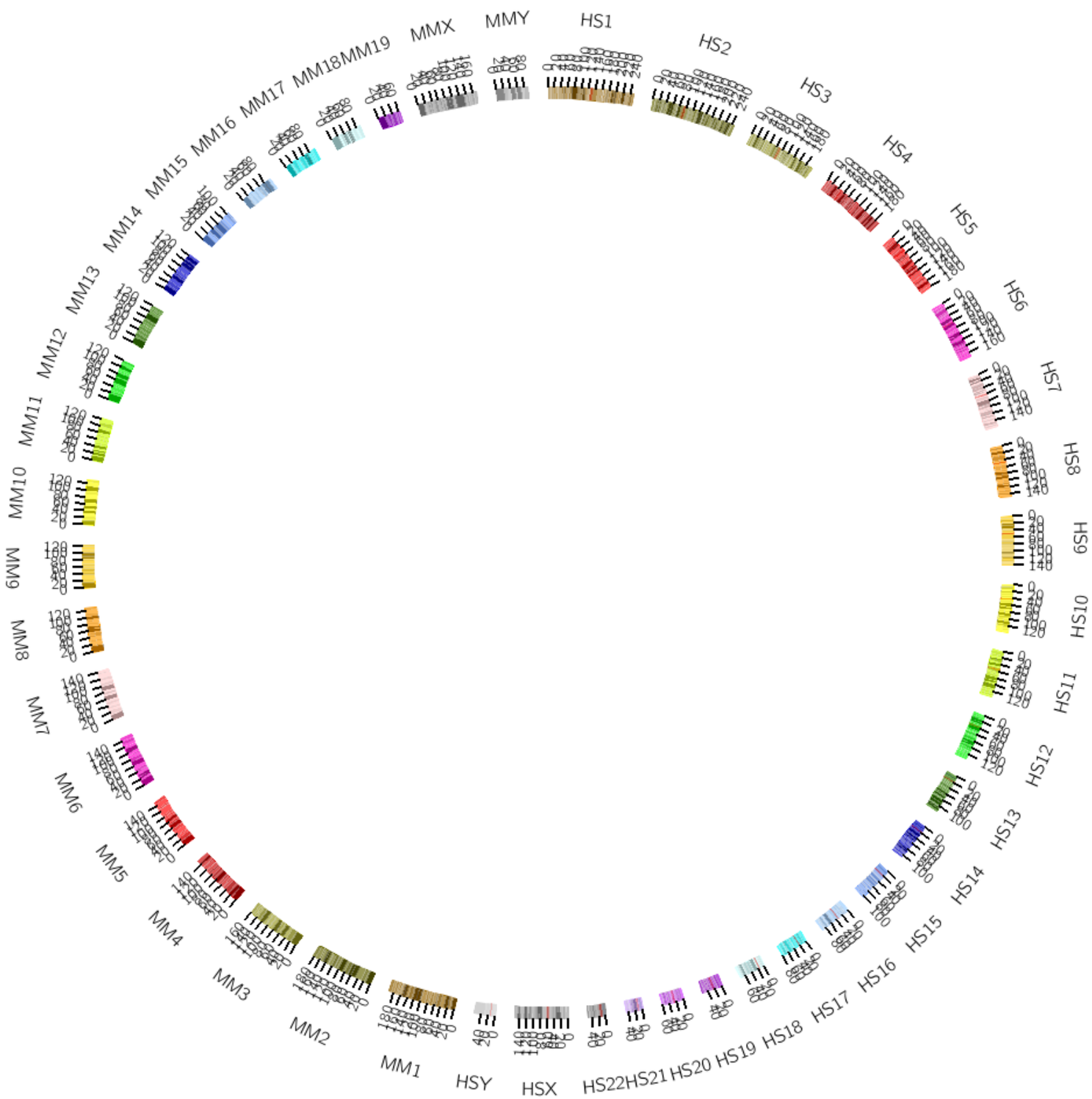
DRAWING MULTIPLE KARYOTYPES



```
# 2/10/etc/circos.conf

#karyotype = ../../data/karyotype/
             karyotype.human.txt
#karyotype = ../../data/karyotype/
             karyotype.mouse.txt
karyotype = ../../data/karyotype/
            karyotype.human.txt,
            ../../data/karyotype/
            karyotype.mouse.txt
```

.

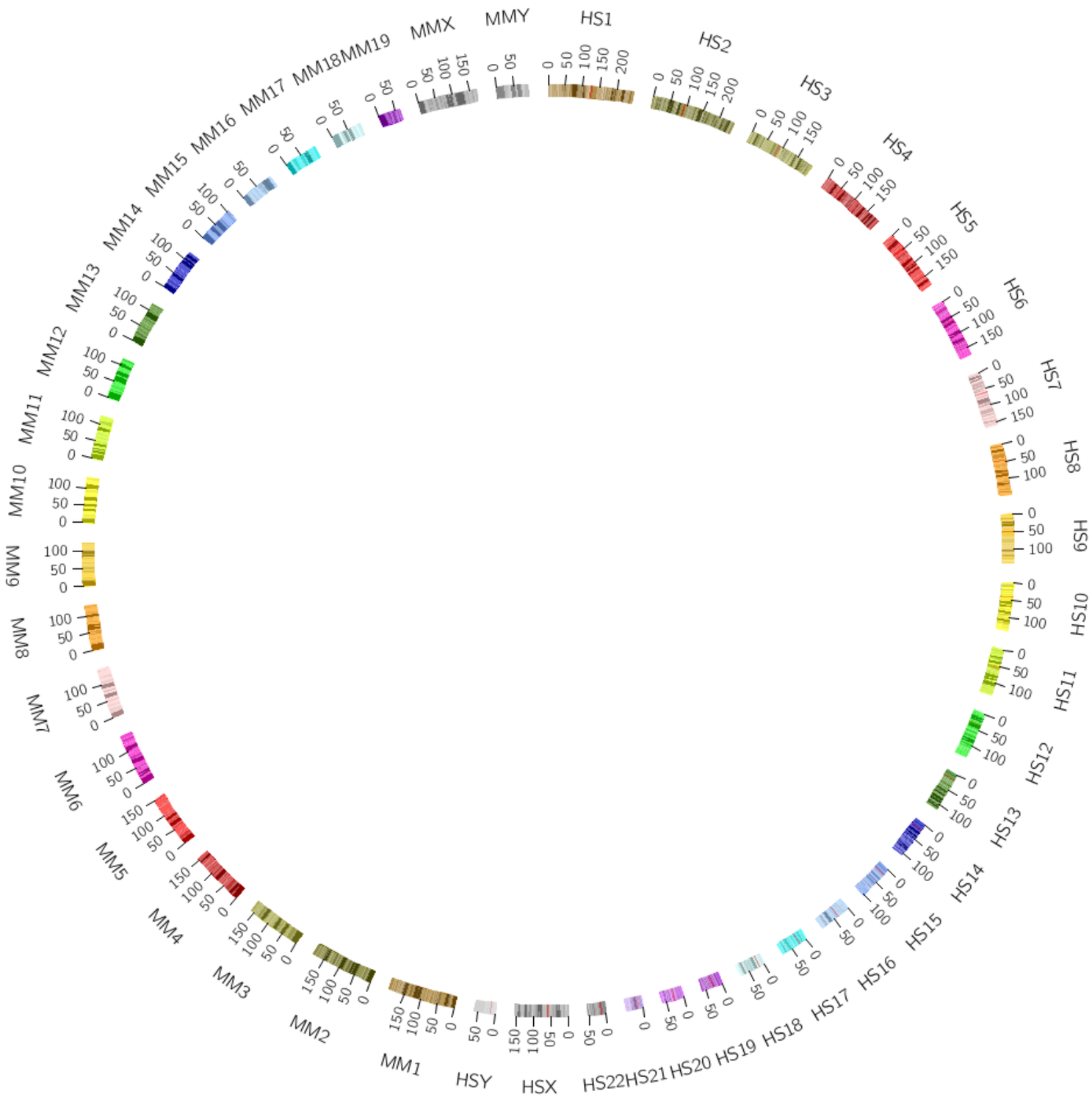
DRAWING MULTIPLE KARYOTYPES




```
# 2/10/etc/circos.conf

#karyotype = ../../data/karyotype/
             karyotype.human.txt
#karyotype = ../../data/karyotype/
             karyotype.mouse.txt
karyotype = ../../data/karyotype/
            karyotype.human.txt,
            ../../data/karyotype/
            karyotype.mouse.txt

# 2/10/etc/ideogram.conf

<spacing>
#default = 10u
default = 0.01r
</spacing>

thickness*        = 10p
stroke_thickness* = 0

label_format = eval(sprintf("%s",var(chr)))
```

.

DRAWING MULTIPLE KARYOTYPES




```
# 2/10/etc/circos.conf

#karyotype = ../../data/karyotype/
             karyotype.human.txt
#karyotype = ../../data/karyotype/
             karyotype.mouse.txt
karyotype = ../../data/karyotype/
            karyotype.human.txt,
            ../../data/karyotype/
            karyotype.mouse.txt

# 2/10/etc/ticks.conf

<tick>
spacing     = 50u
size        = 8p
thickness   = 1p
</tick>
```

.

GENOME.UCSC.EDU

Home | Genomes | Genome Browser | Blat | Tables | Gene Sorter | PCR | Session | FAQ | Help

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA seq
queries, and the OpenHelix Table Browser tutorial for a narrated presentation of the software features and usage. For more complex queries,
for the list of contributors and usage restrictions associated with these data.

clade: Mammal **genome:** Human **assembly:** Feb. 2009 (GRCh37/hg19)

group: Mapping and Sequencing Tracks **track:** Chromosome Band (Ideogram) add custom tracks

table: cytoBandIdeo describe table schema

region: genome position chr21:33031597-33041570 lookup define regions

identifiers (names/accessions): paste list upload list

filter: create

intersection: create

correlation: create

output format: all fields from selected table Send output to Galaxy GREAT

output file: (leave blank to keep output in browser)

file type returned: plain text gzip compressed

get output summary/statistics

To reset **all** user cart settings (including custom tracks), click here.

.

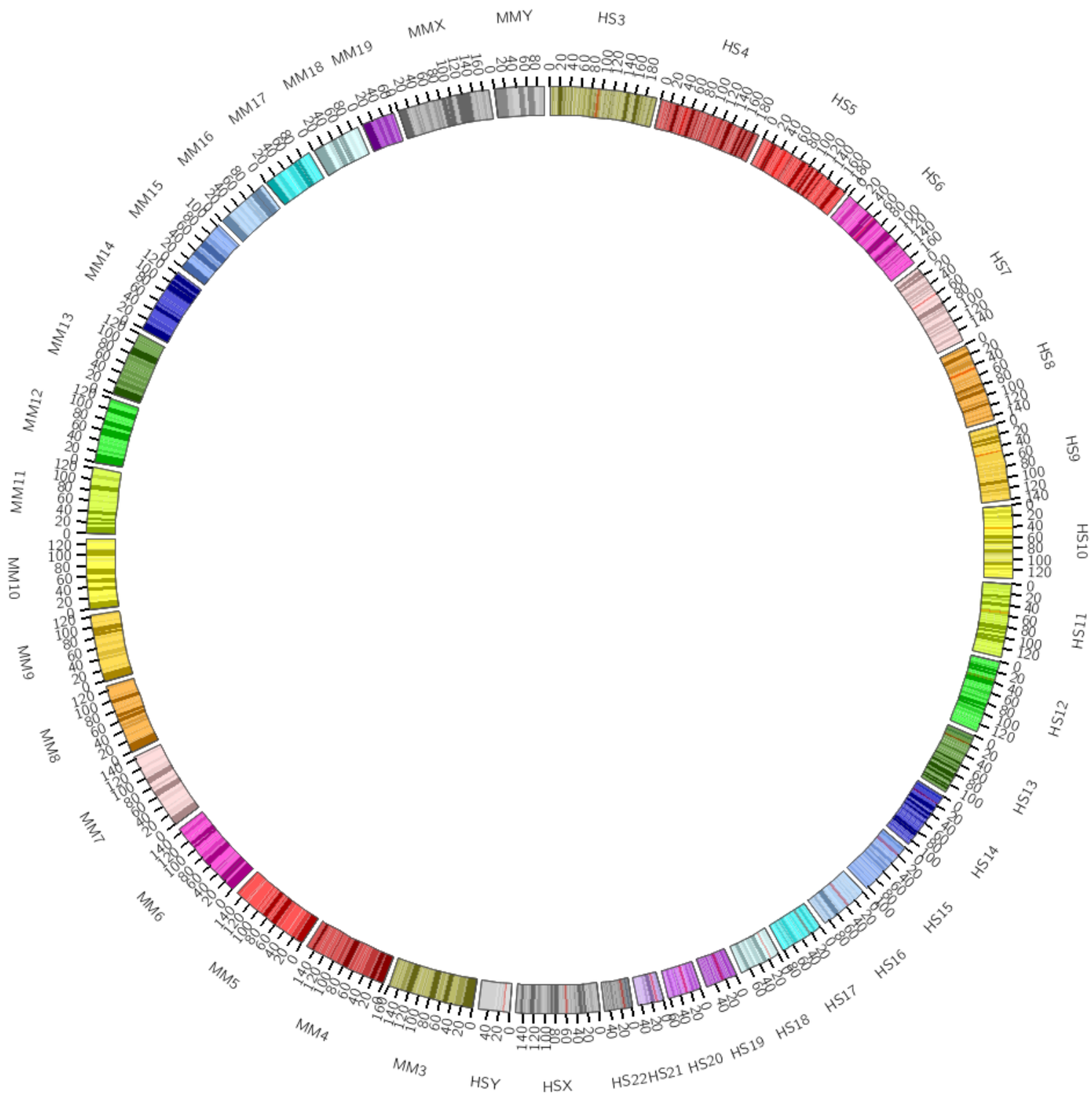
UCSC KARYOTYPE TABLE

#chr	chrStart	chrEnd	name	gieStain
chr1	0	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
chr1	16200000	20400000	p36.13	gneg
chr1	20400000	23900000	p36.12	gpos25
chr1	23900000	28000000	p36.11	gneg
chr1	28000000	30200000	p35.3	gpos25
chr1	30200000	32400000	p35.2	gneg
...				
chr1	227000000	230700000	q42.13	gneg
chr1	230700000	234700000	q42.2	gpos50
chr1	234700000	236600000	q42.3	gneg
chr1	236600000	243700000	q43	gpos75
chr1	243700000	249250621	q44	gneg
chr2	0	4400000	p25.3	gneg
chr2	4400000	7100000	p25.2	gpos50
chr2	7100000	12200000	p25.1	gneg
chr2	12200000	16700000	p24.3	gpos75
chr2	16700000	19200000	p24.2	gneg
chr2	19200000	24000000	p24.1	gpos75
...				

regex filtering, color, progression & orientation

LESSON 11

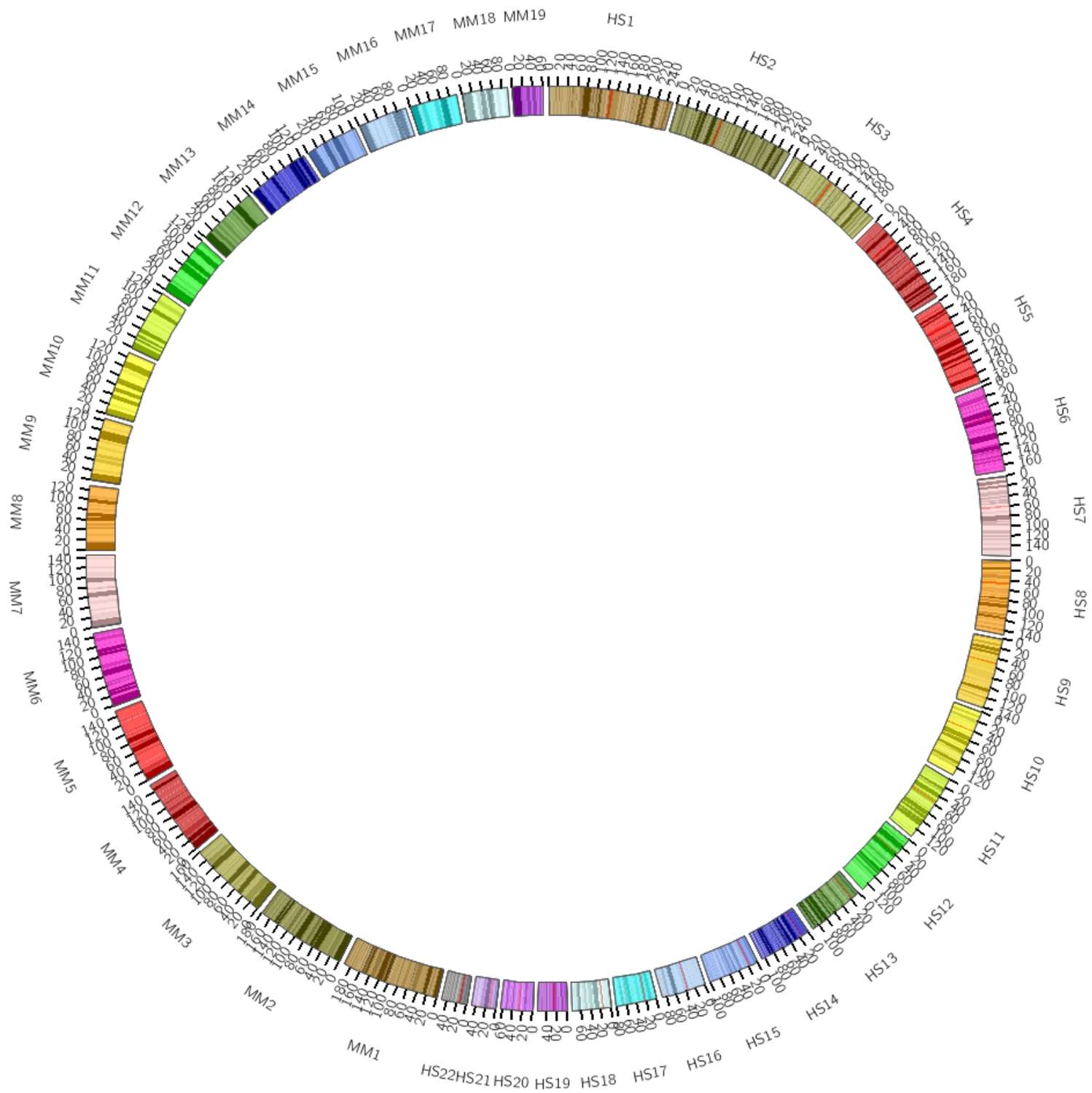
IDEOGRAM REGEX FILTERING




```
# 2/11/etc/circos.conf

# all ideograms displayed,
# except hs1, hs2, mm1, mm2
chromosomes_display_default = yes
chromosomes = -hs1;-hs2;-mm1;-mm2

# all ideograms displayed, except
# those matching regular expression [XY]
#chromosomes_display_default = yes
#chromosomes                 = -/[XY]/

# all ideograms displayed, except
# hs1, hs2 and those those matching
# regular expressions Y or \d\d
#chromosomes_display_default = yes
#chromosomes = -hs1;-hs2;-/Y/;-/\d\d/;

# only the specified ideograms displayed:
# hs1-hs5, hs10, mm10-mm15, mmX
#chromosomes_display_default = no
#chromosomes = /hs[1-5]$/;hs10;/mm1[0-5]/;mmX
```

.

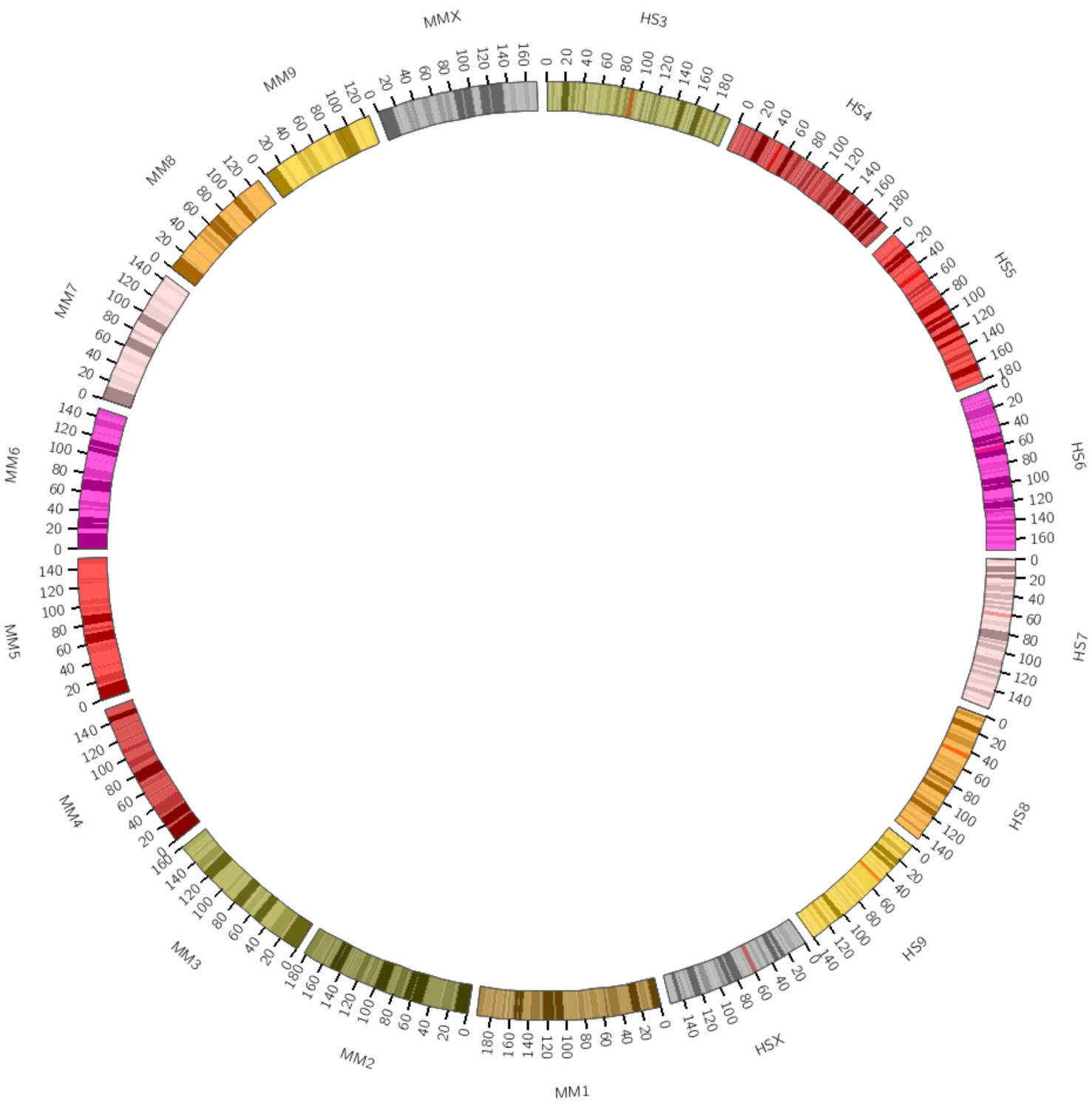
IDEOGRAM REGEX FILTERING




```
# 2/11/etc/circos.conf

# all ideograms displayed,
# except hs1, hs2, mm1, mm2
#chromosomes_display_default = yes
#chromosomes = -hs1;-hs2;-mm1;-mm2

# all ideograms displayed, except
# those matching regular expression [XY]
chromosomes_display_default = yes
chromosomes                 = -/[XY]/

# all ideograms displayed, except
# hs1, hs2 and those those matching
# regular expressions Y or \d\d
#chromosomes_display_default = yes
#chromosomes = -hs1;-hs2;-/Y/;-/\d\d/;

# only the specified ideograms displayed:
# hs1-hs5, hs10, mm10-mm15, mmX
#chromosomes_display_default = no
#chromosomes = /hs[1-5]$/;hs10;/mm1[0-5]/;mmX
```

.

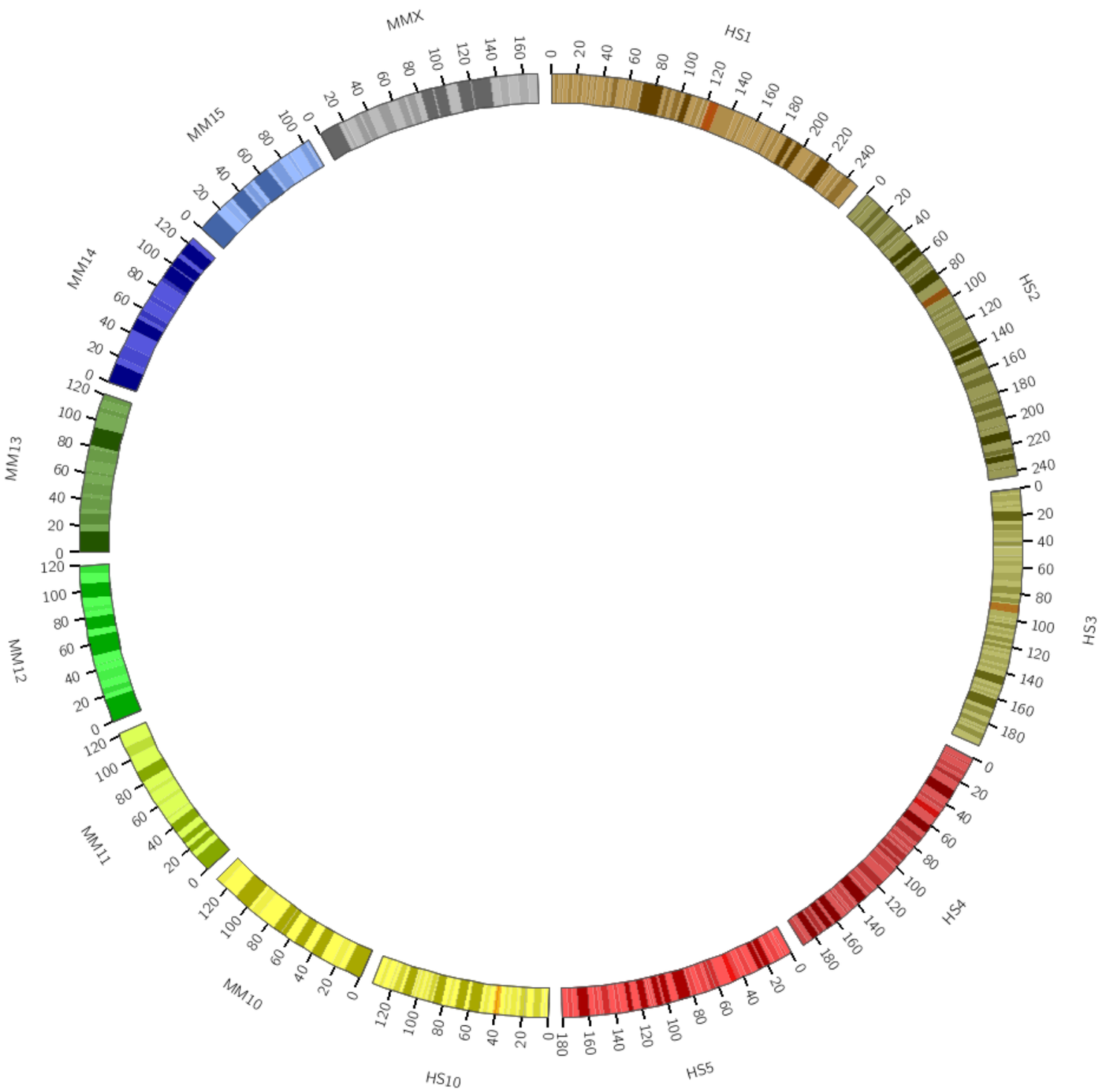
IDEOGRAM REGEX FILTERING




```
# 2/11/etc/circos.conf

# all ideograms displayed,
# except hs1, hs2, mm1, mm2
#chromosomes_display_default = yes
#chromosomes = -hs1;-hs2;-mm1;-mm2

# all ideograms displayed, except
# those matching regular expression [XY]
#chromosomes_display_default = yes
#chromosomes                 = -/[xy]/

# all ideograms displayed, except
# hs1, hs2 and those those matching
# regular expressions Y or \d\d
chromosomes_display_default = yes
chromosomes = -hs1;-hs2;-/Y/;-/\d\d/;

# only the specified ideograms displayed:
# hs1-hs5, hs10, mm10-mm15, mmX
#chromosomes_display_default = no
#chromosomes = /hs[1-5]$/;hs10;/mm1[0-5]/;mmX
```

.

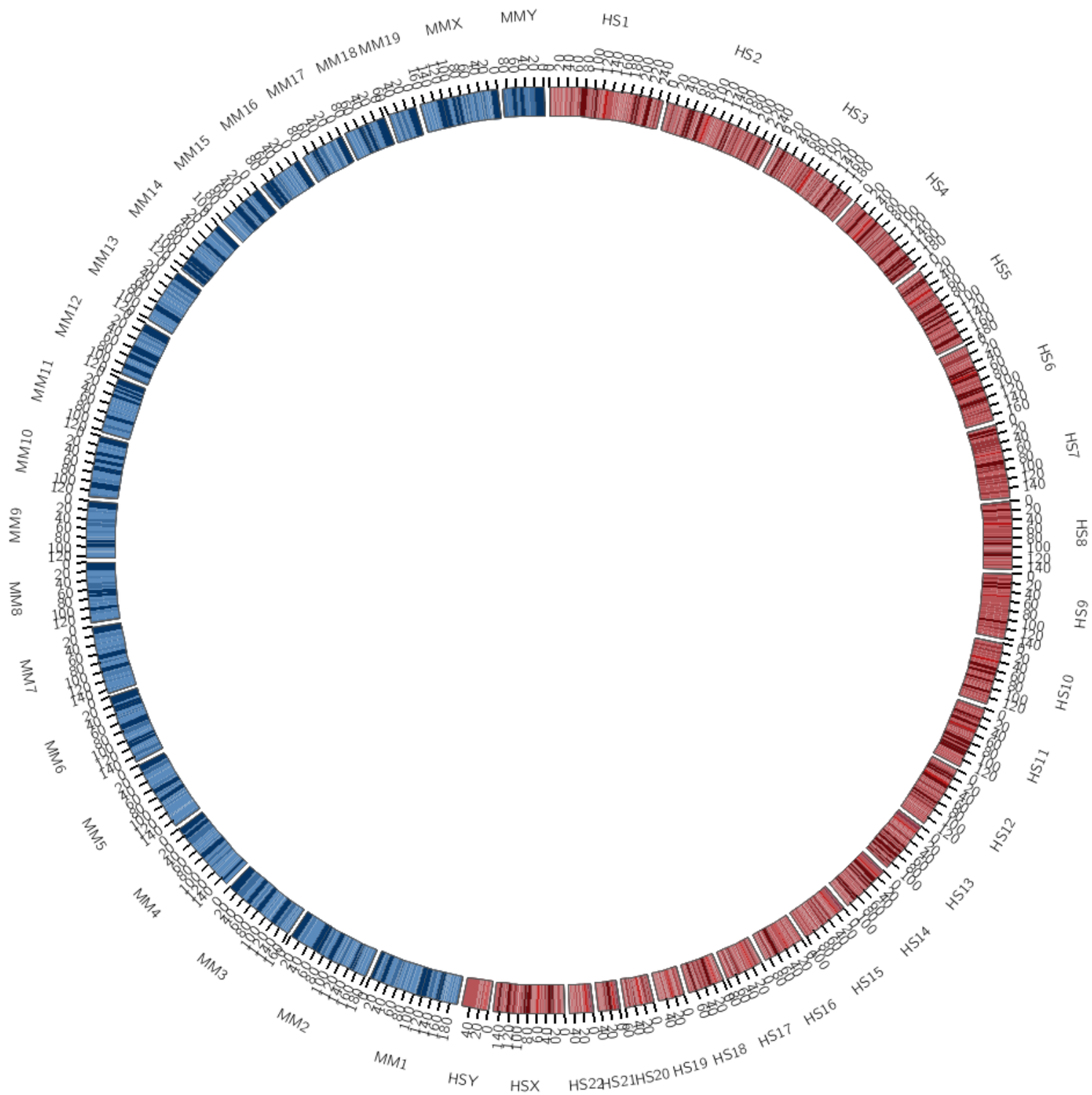
IDEOGRAM REGEX FILTERING




```
# 2/11/etc/circos.conf

# all ideograms displayed,
# except hs1, hs2, mm1, mm2
#chromosomes_display_default = yes
#chromosomes = -hs1;-hs2;-mm1;-mm2

# all ideograms displayed, except
# those matching regular expression [XY]
#chromosomes_display_default = yes
#chromosomes                 = -/[XY]/

# all ideograms displayed, except
# hs1, hs2 and those those matching
# regular expressions y or \d\d
#chromosomes_display_default = yes
#chromosomes = -hs1;-hs2;-/Y/;-/\d\d/;

# only the specified ideograms displayed:
# hs1-hs5, hs10, mm10-mm15, mmX
chromosomes_display_default = no
chromosomes = /hs[1-5]$/;hs10;/mm1[0-5]/;mmX
```

.

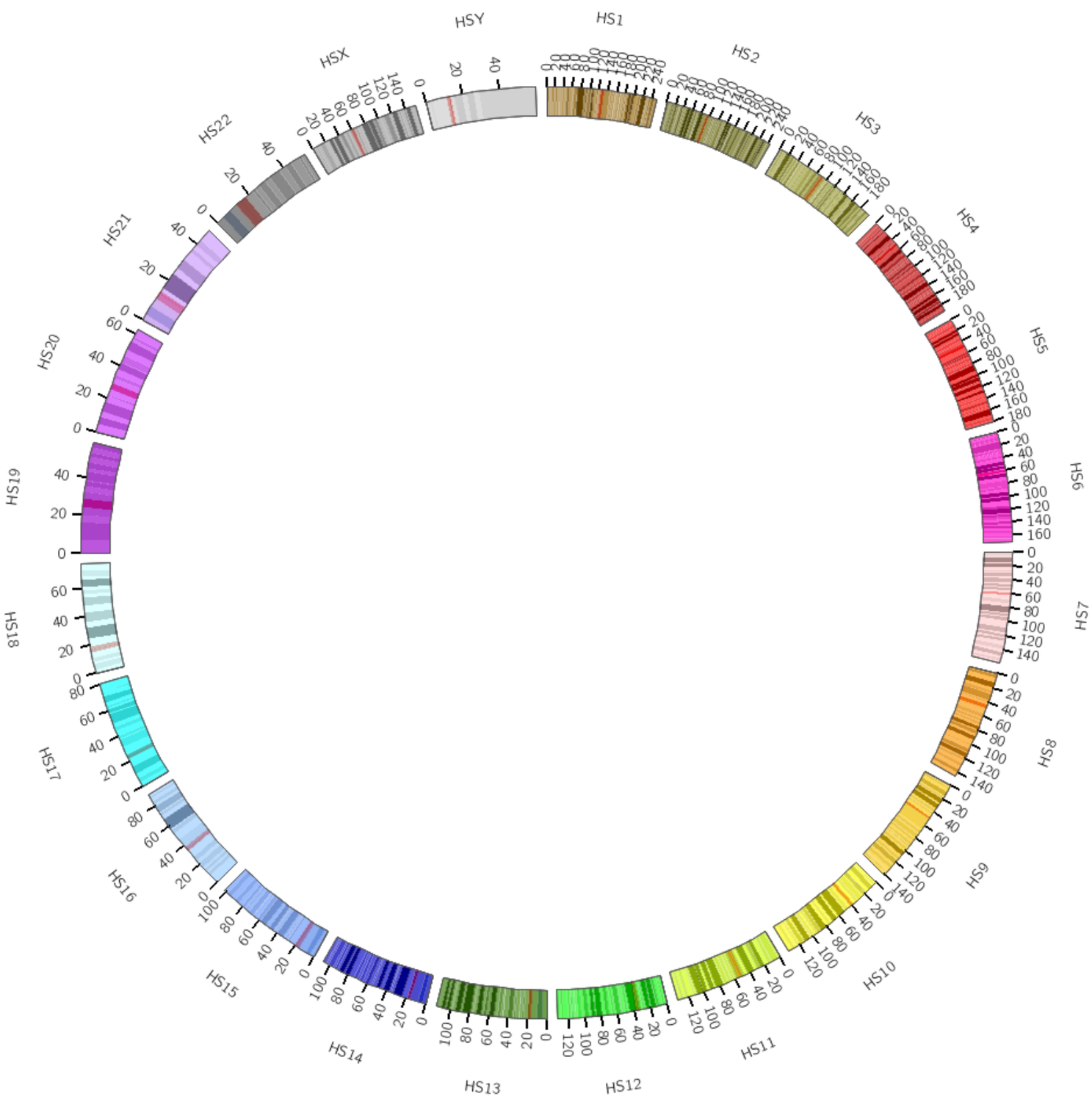
COLOR, PROGRESSION & ORIENTATION




```
# 2/11/etc/circos.conf
# human chromosomes: red
# mouse chromosomes: blue
# mouse chromosomes are reversed
chromosomes_display_default = yes
chromosomes_color   = /hs/=reds-5-seq-5,
                      /mm/=blues-5-seq-5
chromosomes_reverse = /mm/

# only human chromosomes are shown,
# each occupying 1/24th of the image
#chromosomes_display_default = no
#chromosomes = /hs/
#chromosomes_scale = /hs/=1rn

# 5 human (hs1...hs5) and 3 mouse
# (mm17...mm19) chromosomes are shown
# human chromosomes occupy 50%
# of the image (each occupies 10%)
# mouse chromosomes occupy 50%
# of the image (each occupies 16.7%)
#chromosomes_display_default = no
#chromosomes = /hs[1-5]$/;/mm1[7-9]/
#chromosomes_scale = /hs/=0.5rn,/mm/=0.5rn

#chromosomes_display_default = no
#chromosomes          = hs1;hs2;mm1;mm2
#chromosomes_order    = hs1,hs2,mm2,mm1
#chromosomes_reverse = /mm/
#chromosomes_scale    = /./=1rn
#chromosomes_color    =
 hs1:rdylbu-11-div-2,
 hs2:rdylbu-11-div-3,
 mm1:rdylbu-11-div-10,
 mm2:rdylbu-11-div-9
```

.

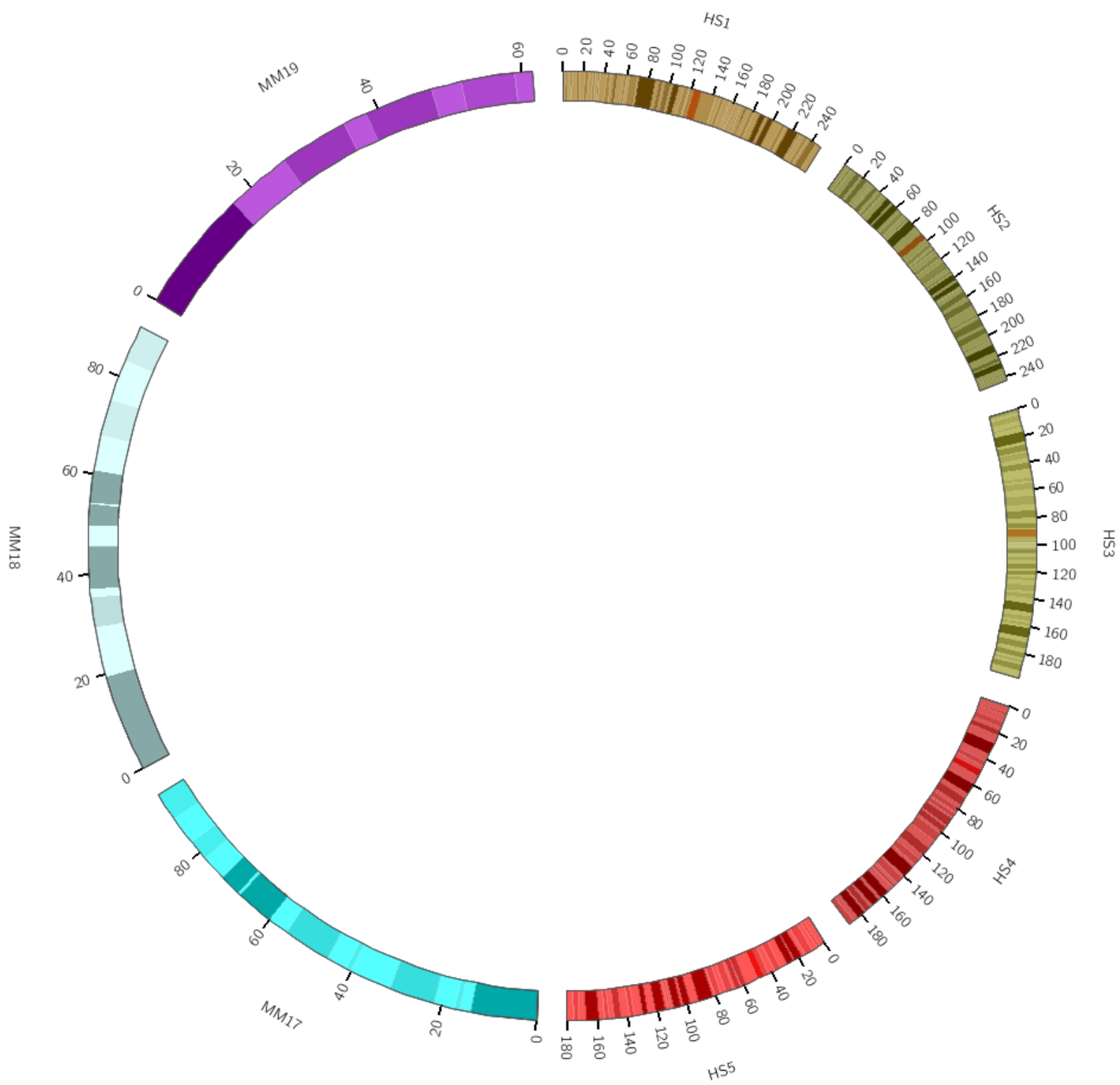
COLOR, PROGRESSION & ORIENTATION




```
# 2/11/etc/circos.conf
# human chromosomes: red
# mouse chromosomes: blue
# mouse chromosomes are reversed
#chromosomes_display_default = yes
#chromosomes_color    = /hs/=reds-5-seq-5,
                        /mm/=blues-5-seq-5
#chromosomes_reverse = /mm/

# only human chromosomes are shown,
# each occupying 1/24th of the image
chromosomes_display_default = no
chromosomes = /hs/
chromosomes_scale = /hs/=1rn

# 5 human (hs1...hs5) and 3 mouse
# (mm17...mm19) chromosomes are shown
# human chromosomes occupy 50%
# of the image (each occupies 10%)
# mouse chromosomes occupy 50%
# of the image (each occupies 16.7%)
#chromosomes_display_default = no
#chromosomes = /hs[1-5]$/;/mm1[7-9]/
#chromosomes_scale = /hs/=0.5rn,/mm/=0.5rn

#chromosomes_display_default = no
#chromosomes          = hs1;hs2;mm1;mm2
#chromosomes_order    = hs1,hs2,mm2,mm1
#chromosomes_reverse = /mm/
#chromosomes_scale    = /./=1rn
#chromosomes_color    =
 hs1:rdylbu-11-div-2,
 hs2:rdylbu-11-div-3,
 mm1:rdylbu-11-div-10,
 mm2:rdylbu-11-div-9
```

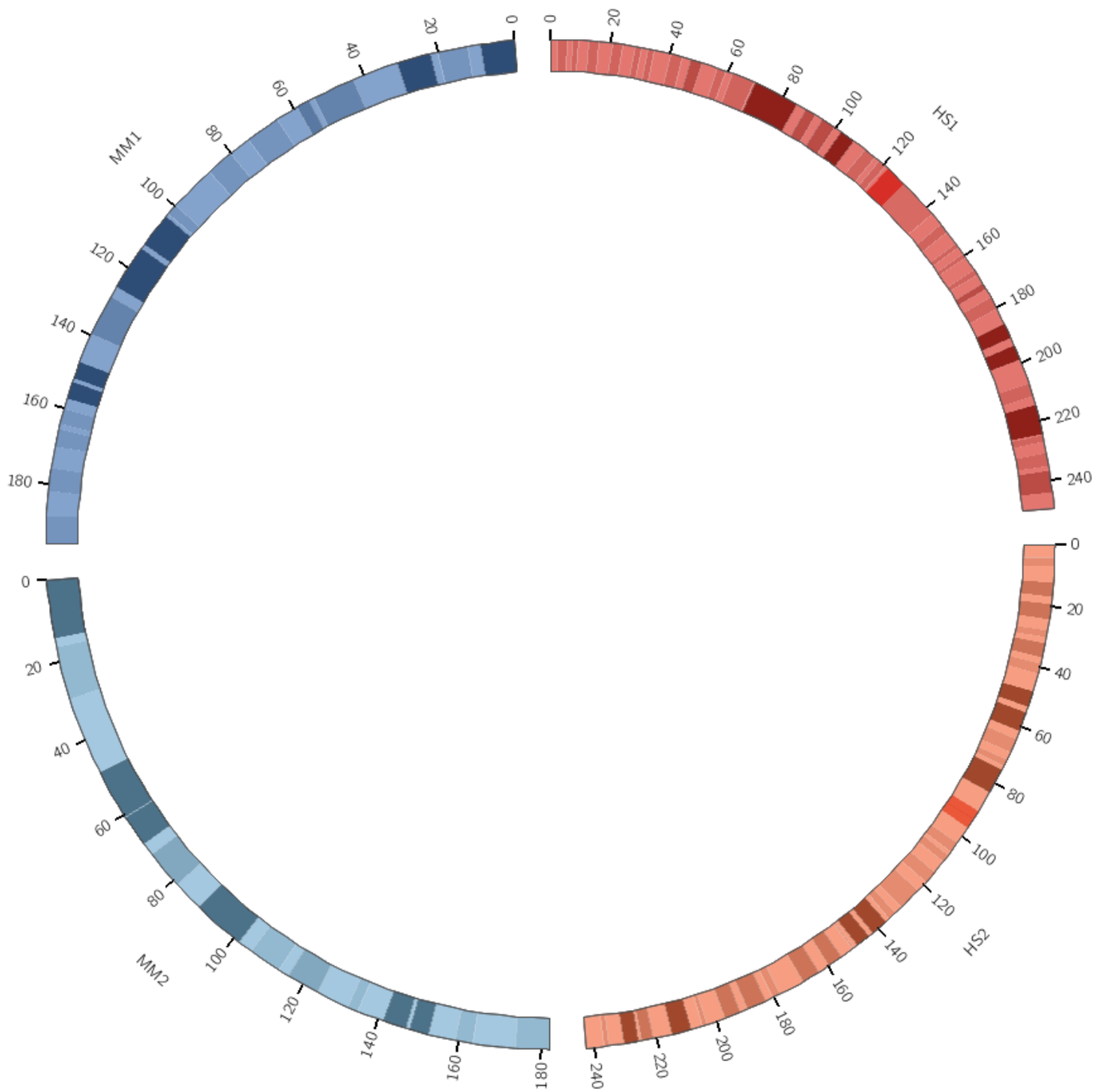
.

COLOR, PROGRESSION & ORIENTATION




```
# 2/11/etc/circos.conf
# human chromosomes: red
# mouse chromosomes: blue
# mouse chromosomes are reversed
#chromosomes_display_default = yes
#chromosomes_color    = /hs/=reds-5-seq-5,
                       /mm/=blues-5-seq-5
#chromosomes_reverse = /mm/

# only human chromosomes are shown,
# each occupying 1/24th of the image
#chromosomes_display_default = no
#chromosomes = /hs/
#chromosomes_scale = /hs/=1rn

# 5 human (hs1...hs5) and 3 mouse
# (mm17...mm19) chromosomes are shown
# human chromosomes occupy 50%
# of the image (each occupies 10%)
# mouse chromosomes occupy 50%
# of the image (each occupies 16.7%)
chromosomes_display_default = no
chromosomes = /hs[1-5]$/;/mm1[7-9]/
chromosomes_scale = /hs/=0.5rn,/mm/=0.5rn

#chromosomes_display_default = no
#chromosomes          = hs1;hs2;mm1;mm2
#chromosomes_order    = hs1,hs2,mm2,mm1
#chromosomes_reverse = /mm/
#chromosomes_scale    = /./=1rn
#chromosomes_color    =
 hs1:rdylbu-11-div-2,
 hs2:rdylbu-11-div-3,
 mm1:rdylbu-11-div-10,
 mm2:rdylbu-11-div-9
```

COLOR, PROGRESSION & ORIENTATION



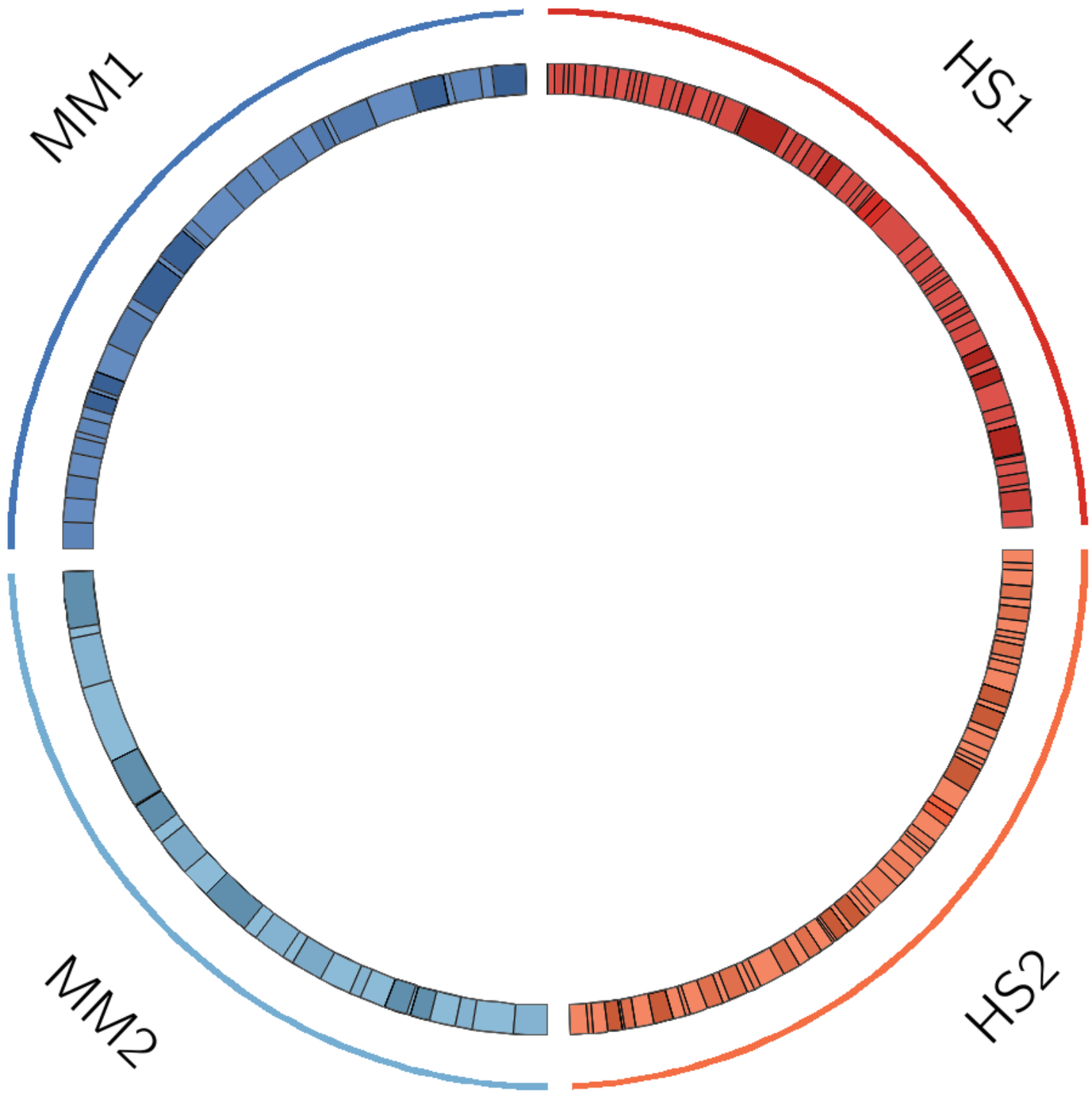

```
# 2/11/etc/circos.conf
# human chromosomes: red
# mouse chromosomes: blue
# mouse chromosomes are reversed
#chromosomes_display_default = yes
#chromosomes_color    = /hs/=reds-5-seq-5,
                       /mm/=blues-5-seq-5
#chromosomes_reverse = /mm/

# only human chromosomes are shown,
# each occupying 1/24th of the image
#chromosomes_display_default = no
#chromosomes = /hs/
#chromosomes_scale = /hs/=1rn

# 5 human (hs1...hs5) and 3 mouse
# (mm17...mm19) chromosomes are shown
# human chromosomes occupy 50%
# of the image (each occupies 10%)
# mouse chromosomes occupy 50%
# of the image (each occupies 16.7%)
#chromosomes_display_default = no
#chromosomes = /hs[1-5]$/;/mm1[7-9]/
#chromosomes_scale = /hs/=0.5rn,/mm/=0.5rn

chromosomes_display_default = no
chromosomes          = hs1;hs2;mm1;mm2
chromosomes_order    = hs1,hs2,mm2,mm1
chromosomes_reverse = /mm/
chromosomes_scale    = /./=1rn
chromosomes_color    =
 hs1:rdylbu-11-div-2,
 hs2:rdylbu-11-div-3,
 mm1:rdylbu-11-div-10,
 mm2:rdylbu-11-div-9
```

.

ticks & grids

LESSON 12

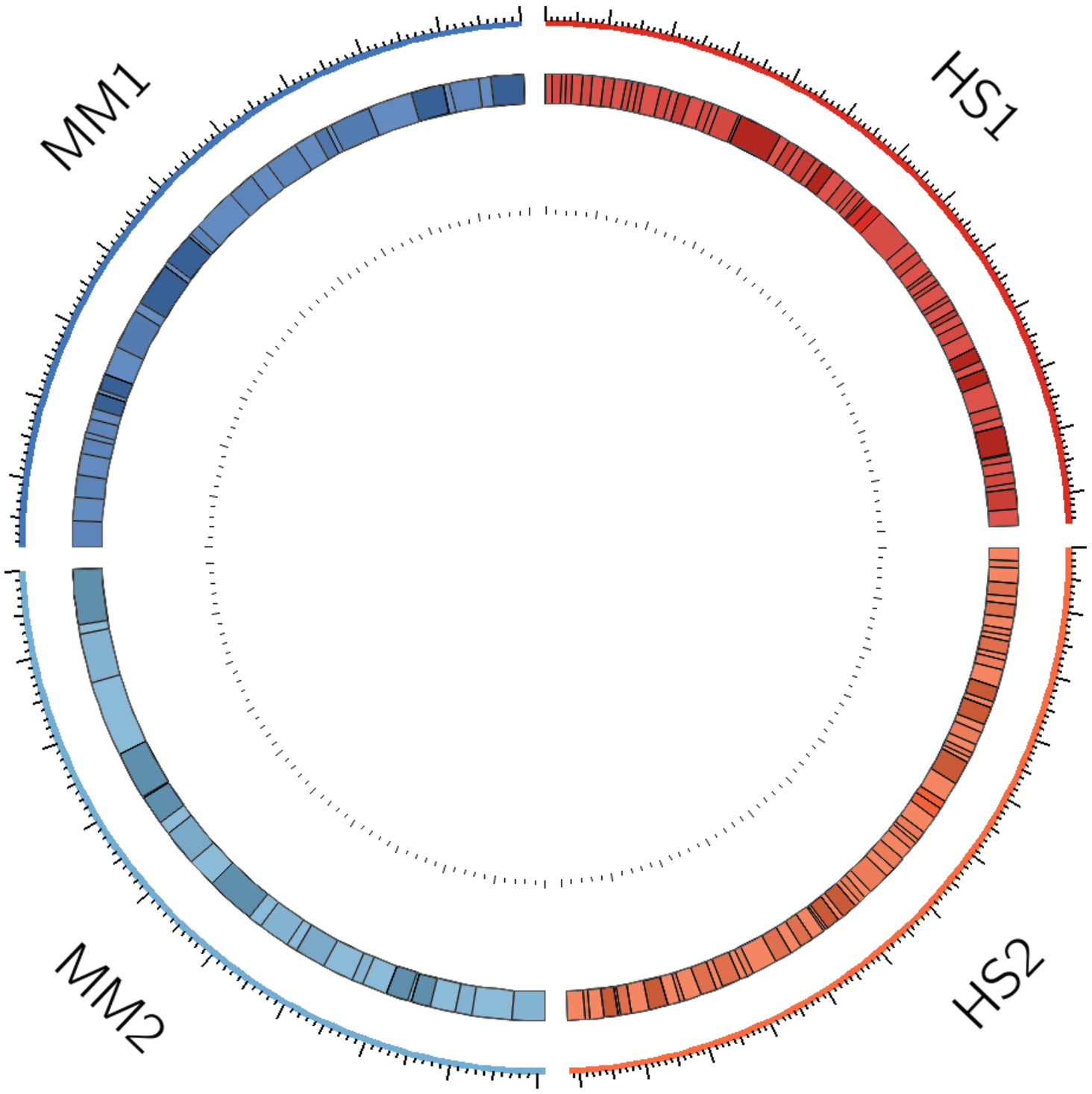
TICKS AND GRIDS




```
# 2/12/etc/circos.conf

chromosomes_display_default = no

chromosomes         = hs1;hs2;mm1;mm2
chromosomes_order   = hs1,hs2,mm2,mm1
chromosomes_color   =
  hs1=rdylbu-11-div-2,
  hs2=rdylbu-11-div-3,
  mm1=rdylbu-11-div-10,
  mm2=rdylbu-11-div-9

chromosomes_reverse = mm1,mm2
chromosomes_scale   = /./=0.25r

<highlights>
<highlight>
file = ../data/highlight.txt
r0   = 1r+40p
r1   = 1r+45p
</highlight>
</highlights>

# 2/12/etc/ticks.conf

show_ticks        = no
show_tick_labels  = no
show_grid         = no
```

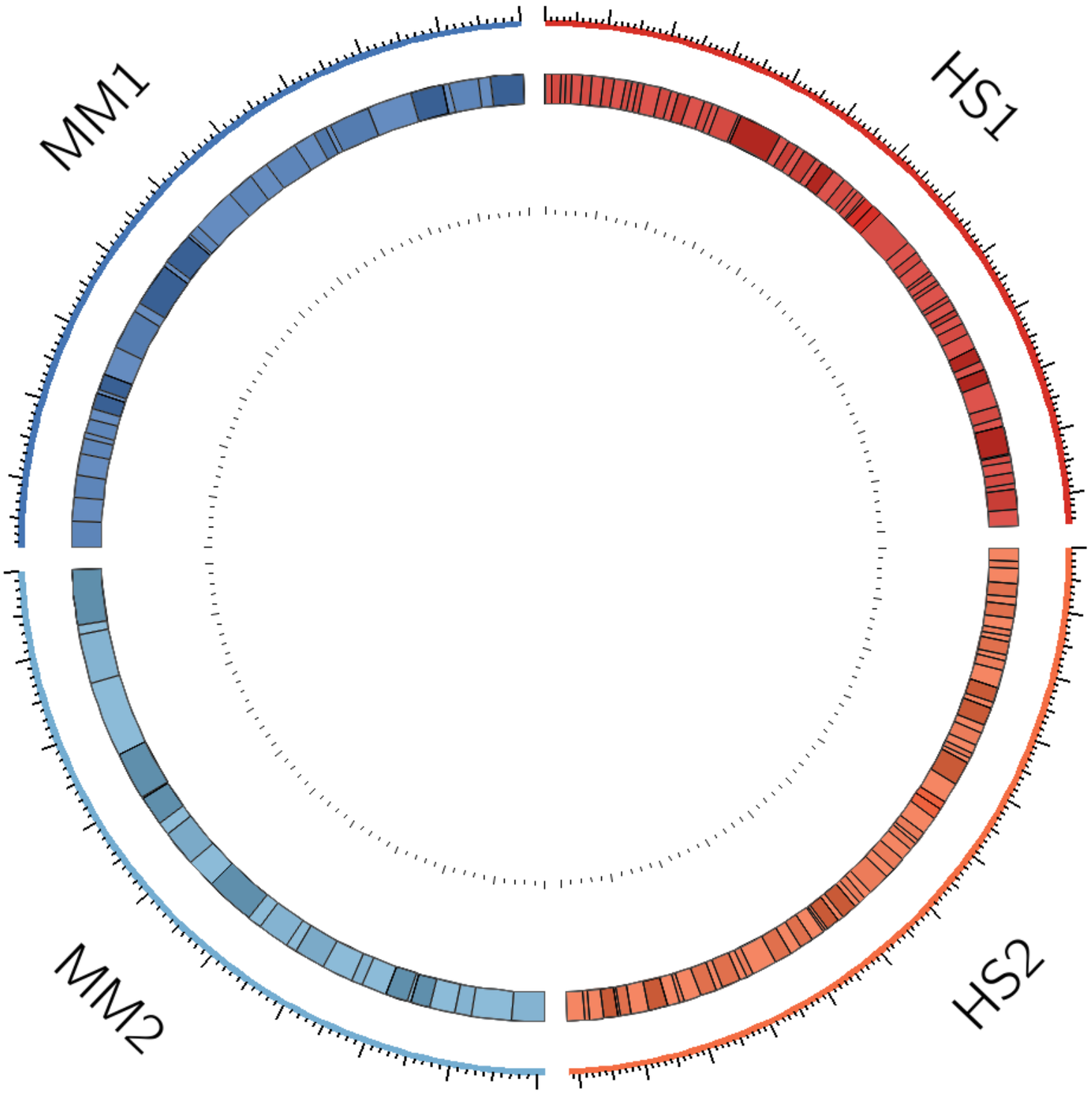
.

TICKS AND GRIDS




```
# 2/12/etc/ticks.conf

show_ticks        = yes

<ticks>
radius = dims(ideogram,radius_outer) + 45p
color  = black
...

# absolute tick groups

<tick>
spacing        = 20u
size           = 12p
thickness      = 2p
...
</tick>

<tick>
spacing        = 10u
size           = 7p
thickness      = 2p
...
</tick>

<tick>
spacing        = 2u
size           = 3p
thickness      = 2p
...
</tick>

...

</ticks>
```

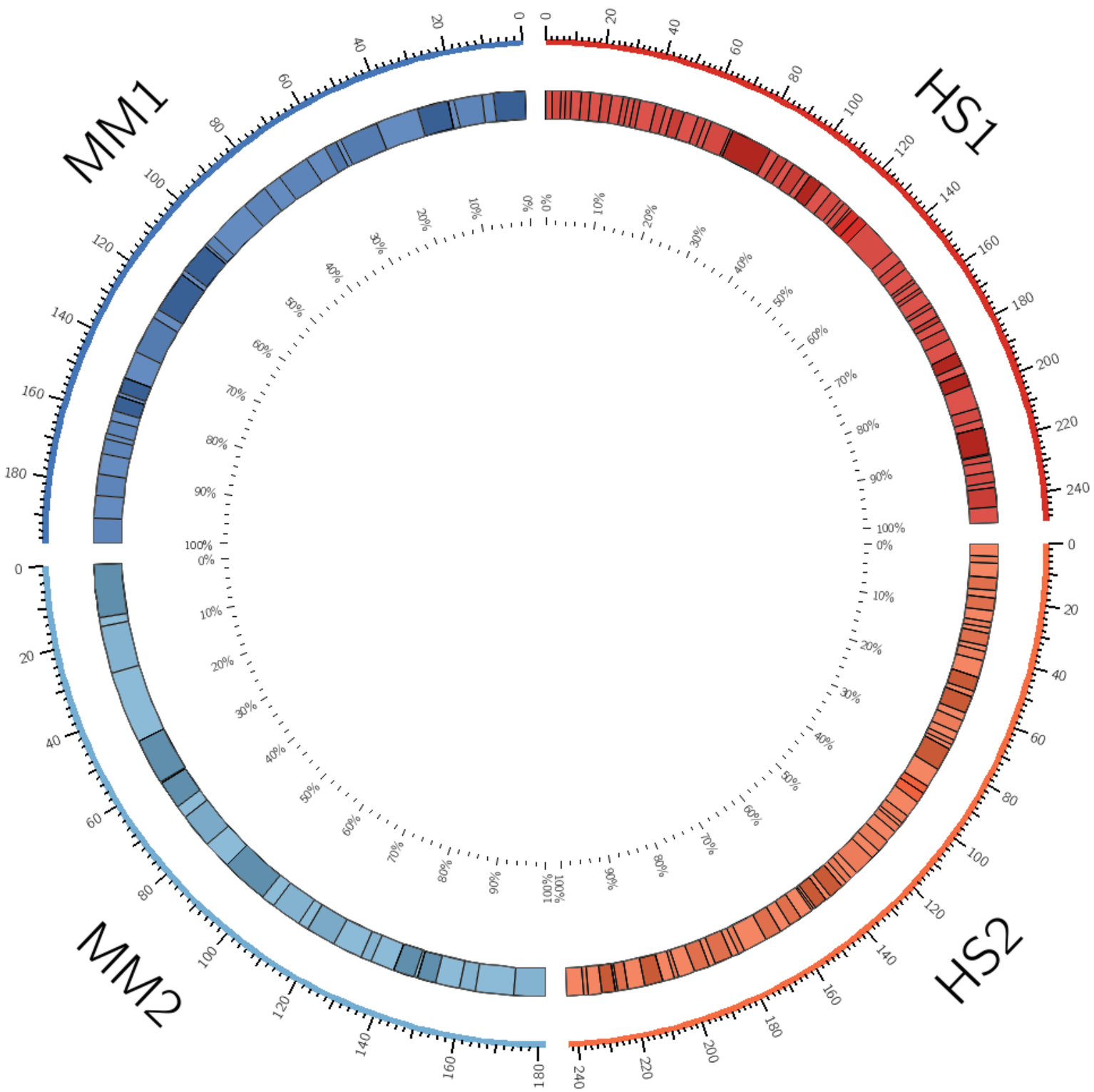
TICKS AND GRIDS




```
# 2/12/etc/ticks.conf

...

# relative tick groups

<tick>
radius          = 0.75r
spacing_type    = relative
rspacing        = 0.02
size            = 3p
thickness       = 1p
</tick>

<tick>
radius          = 0.75r
spacing_type    = relative
rspacing        = 0.10
size            = 6p
thickness       = 1p
</tick>
```

.

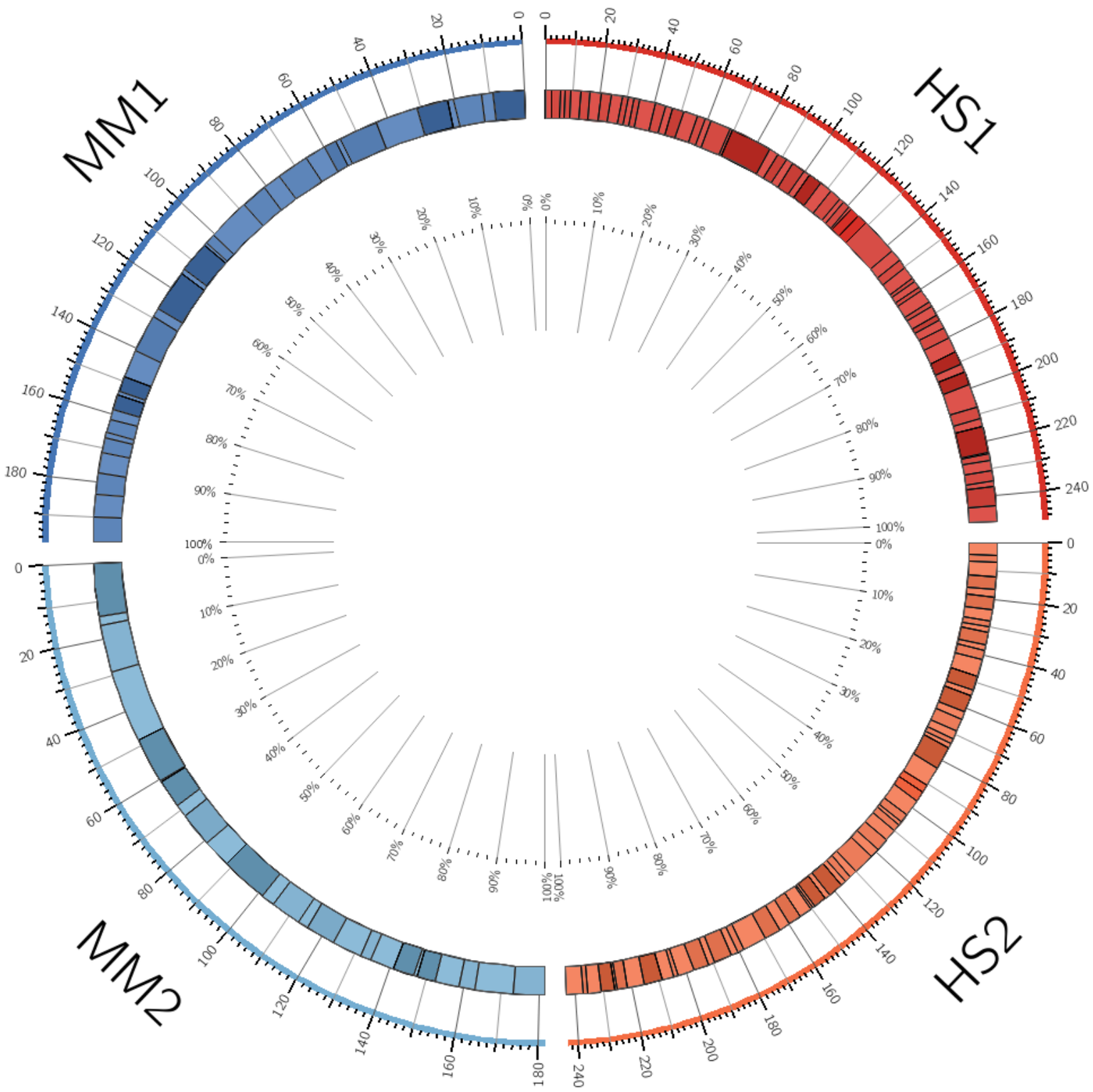
TICKS AND GRIDS




```
# 2/12/etc/ticks.conf

show_ticks          = yes
show_tick_labels    = yes
show_grid           = no

<ticks>
label_offset     = 5p
label_size       = 8p
multiplier       = 1e-6
...

<tick>
spacing          = 20u
size             = 12p
thickness        = 2p
show_label       = yes
label_size       = 10p
format           = %d
</tick>

...

</ticks>
```

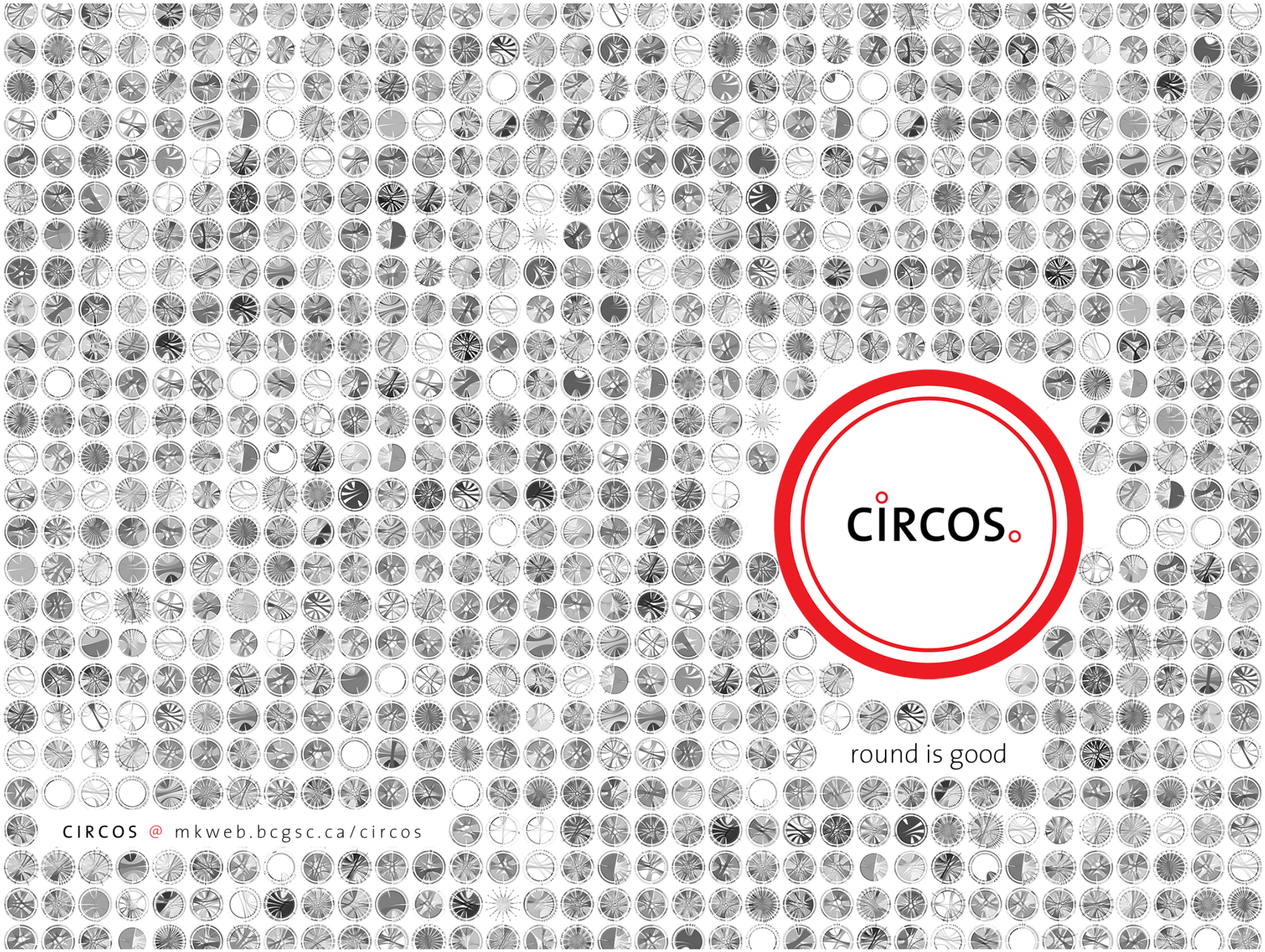
.

TICKS AND GRIDS




```
# 2/12/etc/ticks.conf

show_ticks        = yes
show_tick_labels  = yes
show_grid         = yes

<ticks>
...

<tick>
spacing        = 20u
...
grid_start     = 1r
grid_end       = 1r+45p
grid_color     = vdgrey
grid_thickness = 1p
grid           = yes
</tick>

...

</ticks>
```

.


CIRCOS.
round is good
CIRCOS @ mkweb.bcgsc.ca/circos

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