PREAMBLE TO PRACTICAL SESSIONS

SESSION AND LESSON FILES

The purpose of each session is to learn circos features by creating a complex image.

Each session is divided into multiple lessons.

A lesson will build on the previous lesson.

Each lesson has an independent directory (data, configuration).

For each lesson, you will always be working within the lesson directory

`~/circos/sessions/SESSION/LESSON`

Lesson configuration files are in

`~/circos/sessions/SESSION/LESSON/etc`

UNIX ENVIRONMENT

Your prompt looks something like this

```
[martink@fernbach-26 ~]$
```

When I ask you to enter a command, instead of

```
[martink@fernbach-26 ~]$ pwd
```

you'll see

```
> pwd
```

DESKTOP ENVIRONMENT

I suggest you have three windows opened during each session.

1. a terminal window, from which you'll run circos

2. a text editor to edit configuration files

3. gThumbViewer to look at images

PREPARING LESSON FILES

Lesson files are in a tarball at

```
/home/shared/circos-workshop/circos-workstation-current.tgz
```

untar this into your home directory (check that you're in ~)

```
> cd ~
> pwd
/home/USERNAME
> tar xvfz /home/shared/circos-workshop/circos-workstation-current.tgz
```

Configure environment variable and alias

```
> cd ~/circos/sessions
> . setup.pasteur.sh
Setting up environment for BCGA2010 course.
```

CREATING AN IMAGE

To create the image for session 2 lesson 1

```
> cd ~/circos/sessions/2/1
```

YOU MUST BE IN THE LESSON DIRECTORY TO CREATE THE IMAGE

```
> pwd
/home/USERNAME/circos/sessions/2/1
> circos -conf etc/circos.conf
...
created image at ./s2-1.png
```

An alias has been defined to save time typing

```
> runcircos
...
```

LESSON ORGANIZATION

I will present a part of a configuration file relevant to the lesson.

I won't be showing the entire file – only the immediately interesting parts.

I will ask you to comment/uncomment lines in this configuration file.

take care to comment the a line if you uncomment another

You will then create the image for the lesson and observe the differences.

All variable definitions **must appear on the same line** in the configuration file.

for legibility a line may be broken up into multiple lines on the slides

GAMES FOR BORED STUDENTS

Some parameter names in configuration files have unintuitive names.

There are some legacy elements that no longer seem to make sense.

GAME RULES

For each of these that you find, write them down

+1.0 for each point I agree with
-0.5 for each point I don’t agree with
+1.5 if I don’t agree, but you manage to persuade me to agree

I buy drinks for the 3 students with highest score.

11H00 - 12H30

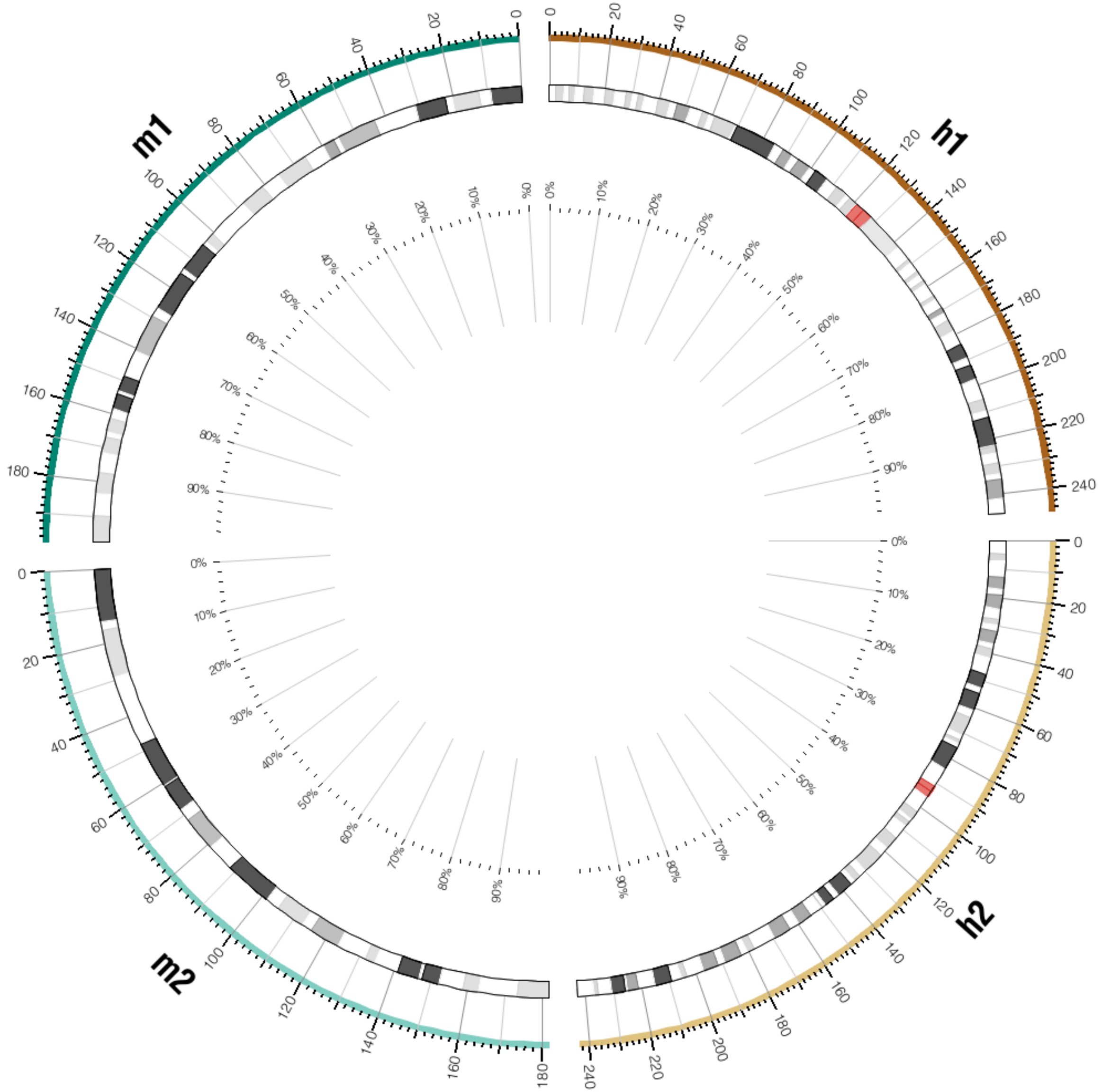
SESSION 2

IDEOGRAM LAYOUT

SESSION PLAN

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

FINAL FIGURE



This is the image you will create during this session.

The figure uses ideogram selection, ordering, scale reversal, global scaling, highlights, grids and absolute and relative tick marks.

LESSON 1

DRAWING IDEOGRAMS

1 SWITCH TO SESSION 2 LESSON 1 DIRECTORY

```
> cd ~/circos/sessions/2/1

> ls
etc      misc      s2-1.png
```

1 CONFIGURATION FILE

sessions/2/etc/circos.conf

```
<<include ideogram.conf>>
<<include ticks.conf>>

<image>
file = s2-1.png
<<include ../etc/image.conf>>
</image>

karyotype = ../data/karyotype.txt

chromosomes_units           = 1000000

chromosomes_display_default = yes

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

The `karyotype` parameter is used to specify the file that defines the chromosome number and size for the genome (or genomes) to be drawn.

1 KARYOTYPE FILE

sessions/2/data/karyotype.txt

```
# first two fields (chr -) are required, followed by
# chromosome name (chr2)
# chromosome label (2)
# chromosome start (0)
# chromosome end (5000000)
# chromosome color (bq1-1)

chr - chr1 1 0   5000000 bq1-1 ●
chr - chr2 2 0  10000000 bq1-2 ●
chr - chr3 3 0  20000000 bq1-3 ●
chr - chr4 4 0  50000000 bq1-4 ●
chr - chr5 5 0 100000000 bq1-5 ●
```

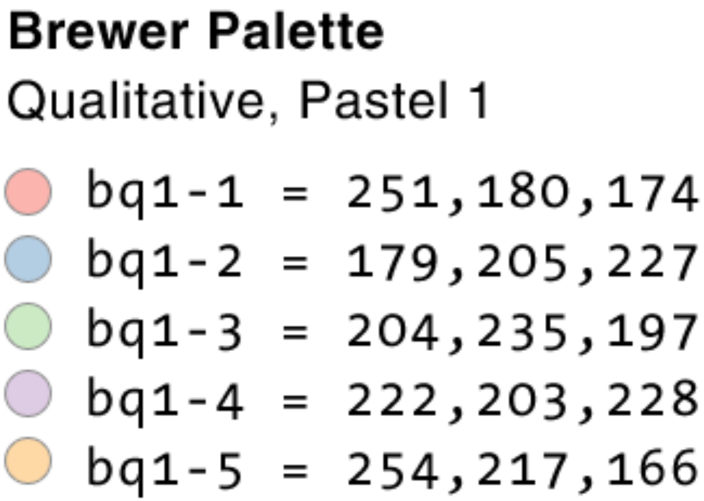
The last field is the color.

Color names `bqN-n` correspond to a Brewer palette.

1 BREWER PALETTES

sessions/etc/brewer.conf

```
# bXN-n
# X=q - qualitative
# X=d - divergent
# X=s - sequential
# N   - palette index
# n   - color index in palette

# 5 color qualitative, pastel 1
bq1-1 = 251,180,174
bq1-2 = 179,205,227
bq1-3 = 204,235,197
bq1-4 = 222,203,228
bq1-5 = 254,217,166

# 3 color sequential, yellow-green-blue
bs8-1 = 237,248,177
bs8-2 = 127,205,187
bs8-3 = 44,127,184
```



Brewer Palette

Qualitative, Pastel 1

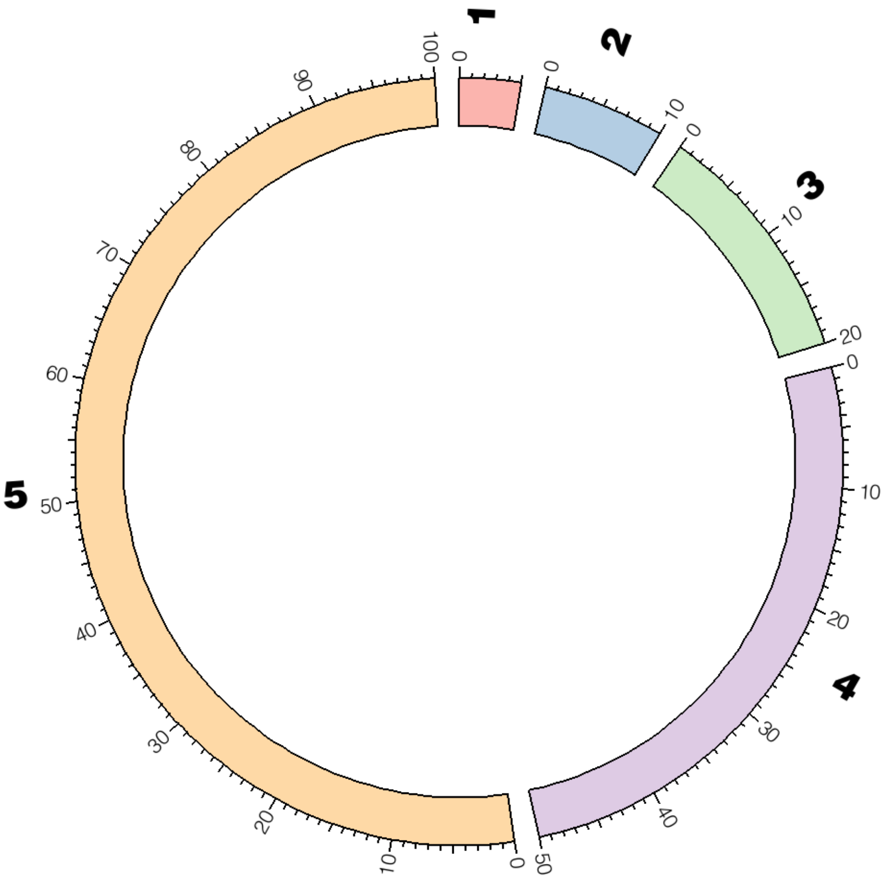
● bq1-1 = 251,180,174
● bq1-2 = 179,205,227
● bq1-3 = 204,235,197
● bq1-4 = 222,203,228
● bq1-5 = 254,217,166

A 5-color qualitative Brewer palette. For other schemes, see *www.colorbrewer.org*

1 FIXED ABSOLUTE SPACING

sessions/2/1/etc/ideogram.conf

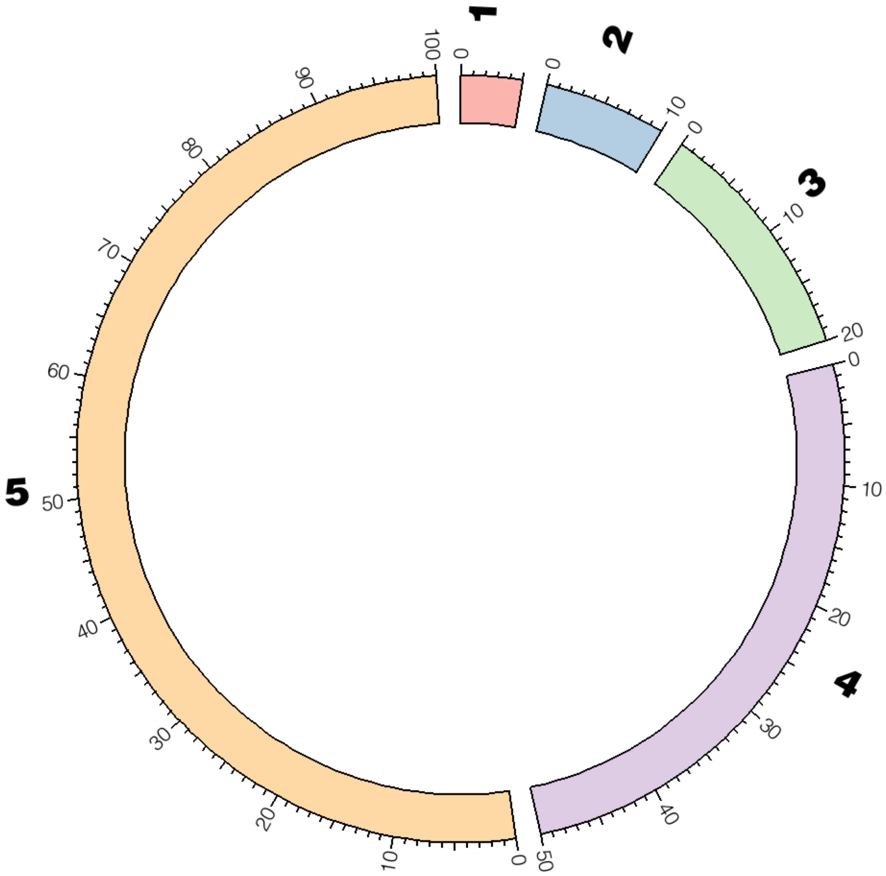
```
<ideogram>

<spacing>

default = 2u

#default = 10u

#<pairwise chr1;chr2>
#spacing = 2u
#</pairwise>

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



Five ideograms, arranged clockwise from 12 o'clock.

1 FIXED ABSOLUTE SPACING

```
> cd ~/circos/sessions/2/1
> runcircos
...
created image at ./s2-1.png
```

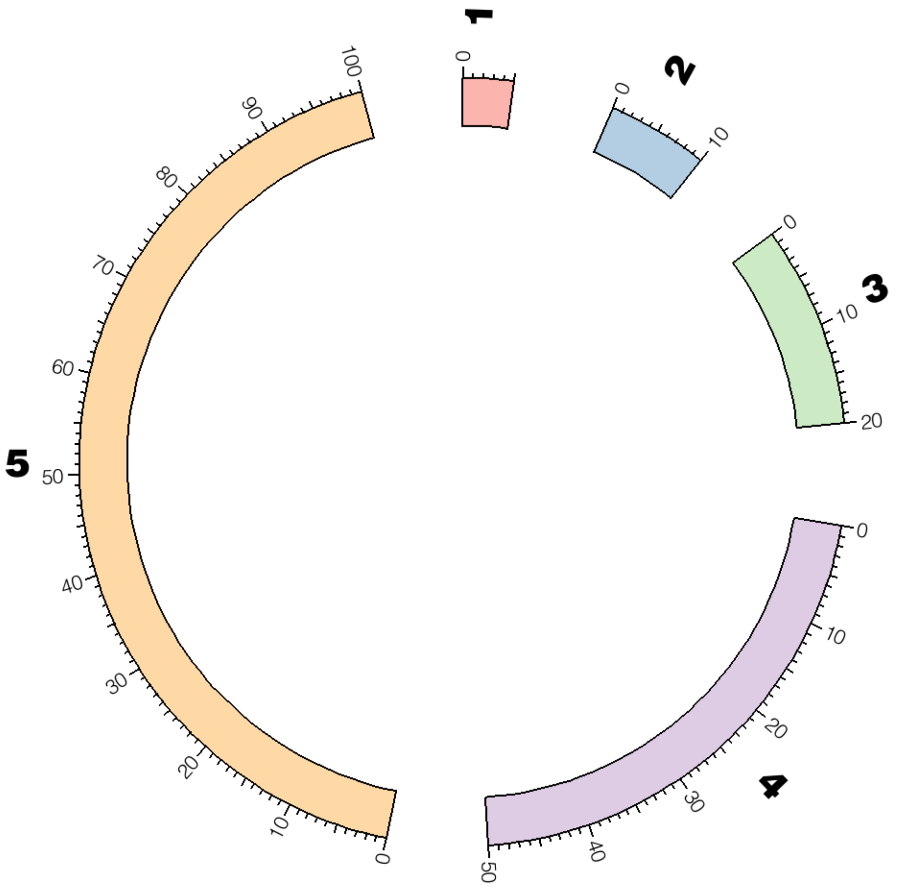


Five ideograms, arranged clockwise from 12 o'clock.

1 INCREASING SPACING

sessions/2/1/etc/ideogram.conf

```
<ideogram>

<spacing>

#default = 2u

default = 10u

#<pairwise chr1;chr2>
#spacing = 2u
#</pairwise>

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

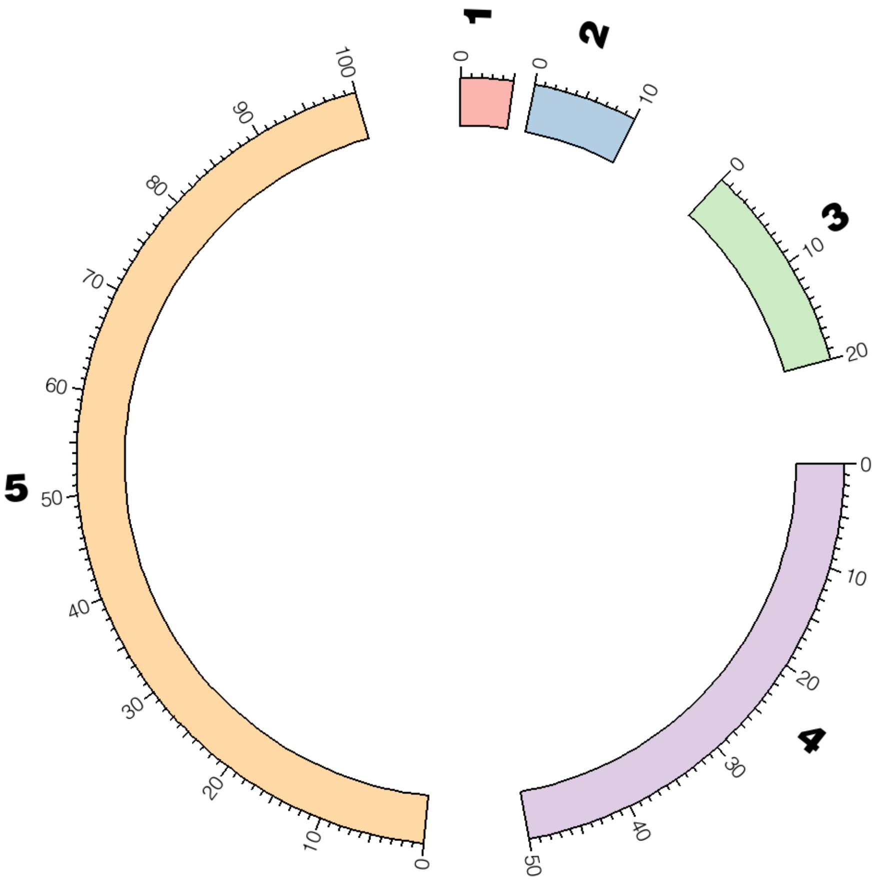


Changing the spacing from 2u to 10u has increased spacing by 5-fold.

1 CHANGING SPACING BETWEEN PAIRS

sessions/2/1/etc/ideogram.conf

```
<ideogram>

<spacing>

#default = 2u

default = 10u

<pairwise chr1;chr2>
spacing = 2u
</pairwise>

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

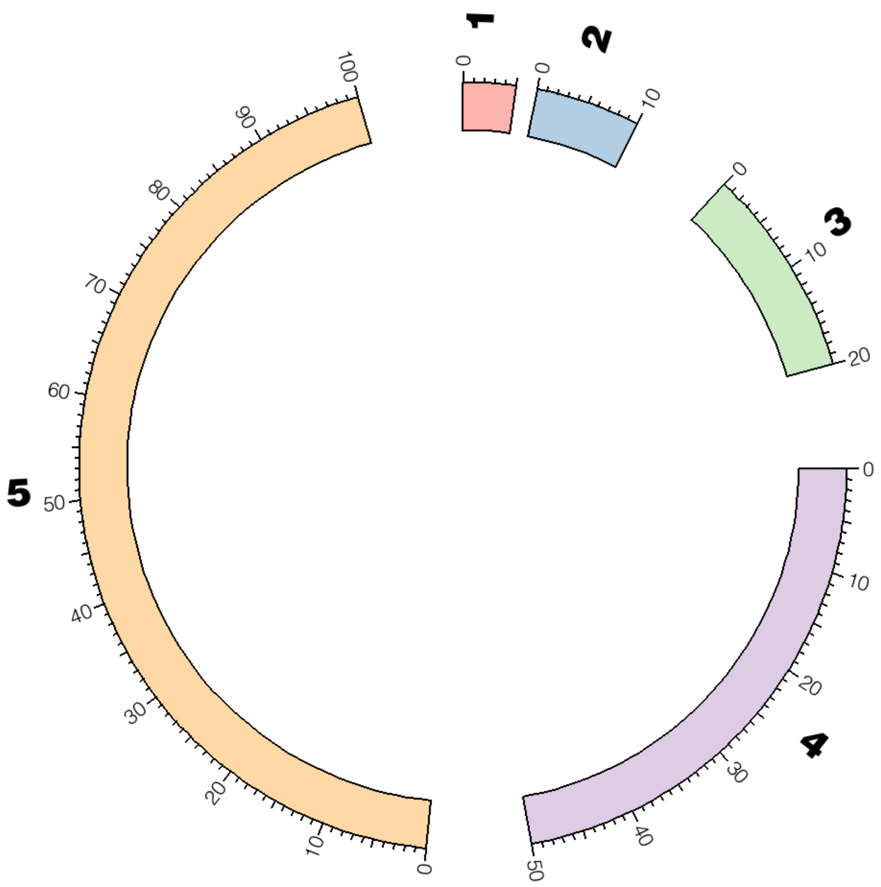


Spacing between individual ideogram pairs can be adjusted independently. This is done using the `<pairwise>` block.

1 CHANGING SPACING BETWEEN PAIRS

sessions/2/1/etc/ideogram.conf

```
<ideogram>

<spacing>

#default = 2u

default = 10u

<pairwise chr1;chr2>
spacing = 2u
</pairwise>

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



Two `<pairwise>` blocks are used to decrease the spacing between chromosomes 1 and 2 to 2u and increase the spacing between chromosomes 5 and 1 to 25u.

LESSON 2

RELATIVE SPACING

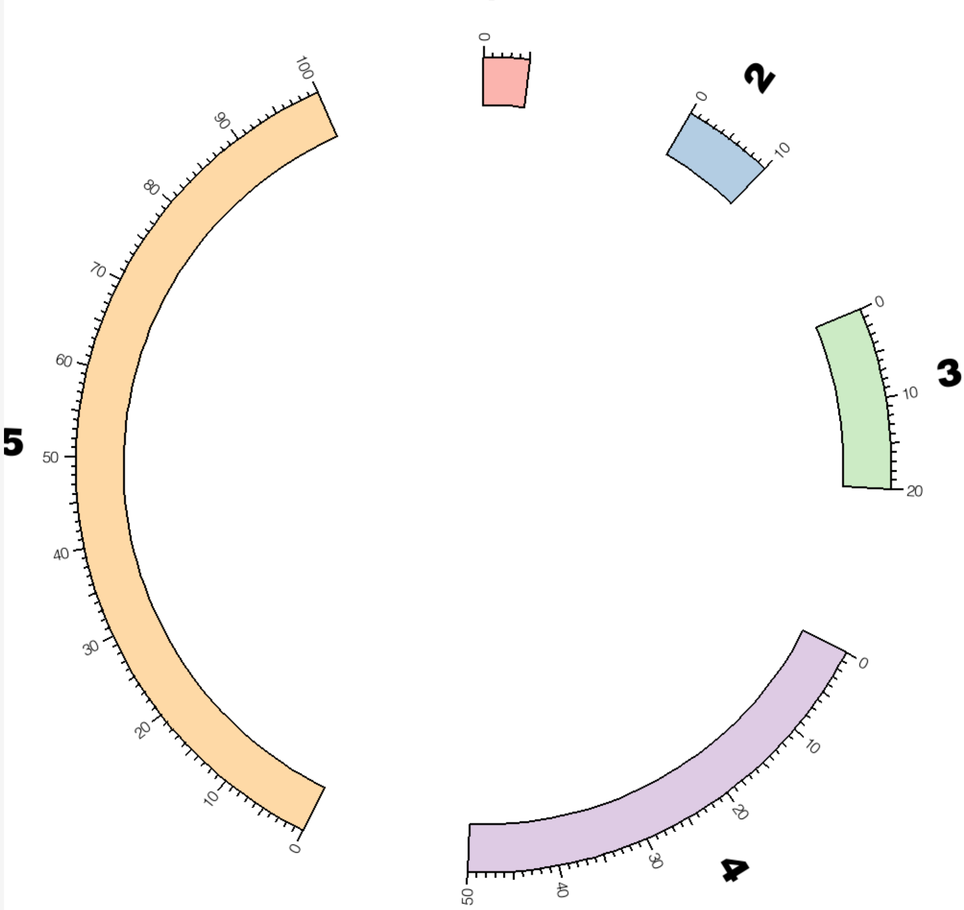
1 SWITCH TO SESSION 2 LESSON 2 DIRECTORY

```
> cd ~/circos/sessions/2/2

> ls
etc        s2-2.png
```

2 RELATIVE SPACING

sessions/2/2/etc/ideogram.conf

```
<ideogram>

<spacing>

#default = 2u

# When spacing unit is "r",
# the fraction is calculated
# relative to the total size of all
  ideograms.
# e.g. if all ideograms total 185 Mb,
# 0.1r spacing is 18.5Mb

default = 0.1r
```

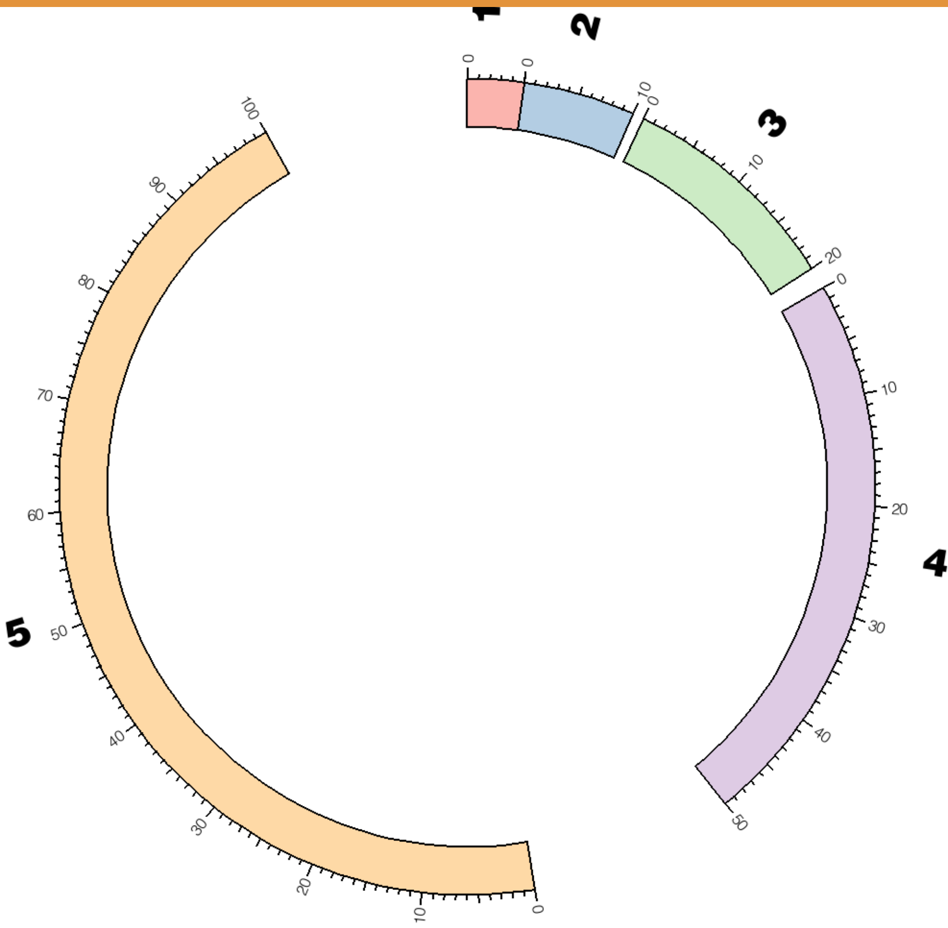


Ideogram spacing can be made relative to total ideogram size by using the *r* suffix. For example, the block below sets each space to 10% of total ideogram size.

2 ABSOLUTE AND RELATIVE SPACING

sessions/2/2/etc/ideogram.conf

```
<ideogram>

<spacing>

default = 0.1r

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

<pairwise chr2;chr3>
spacing = 1u # 1Mb space
</pairwise>

<pairwise chr3;chr4>
spacing = 2u # 2Mb space
</pairwise>

</spacing>
```



Absolute and relative spacing can be used in the same figure. Here, default ideogram spacing is relative (*0.1r*), but spacing between the first four chromosomes is set to *0u*, *1u* and *2u*, respectively.

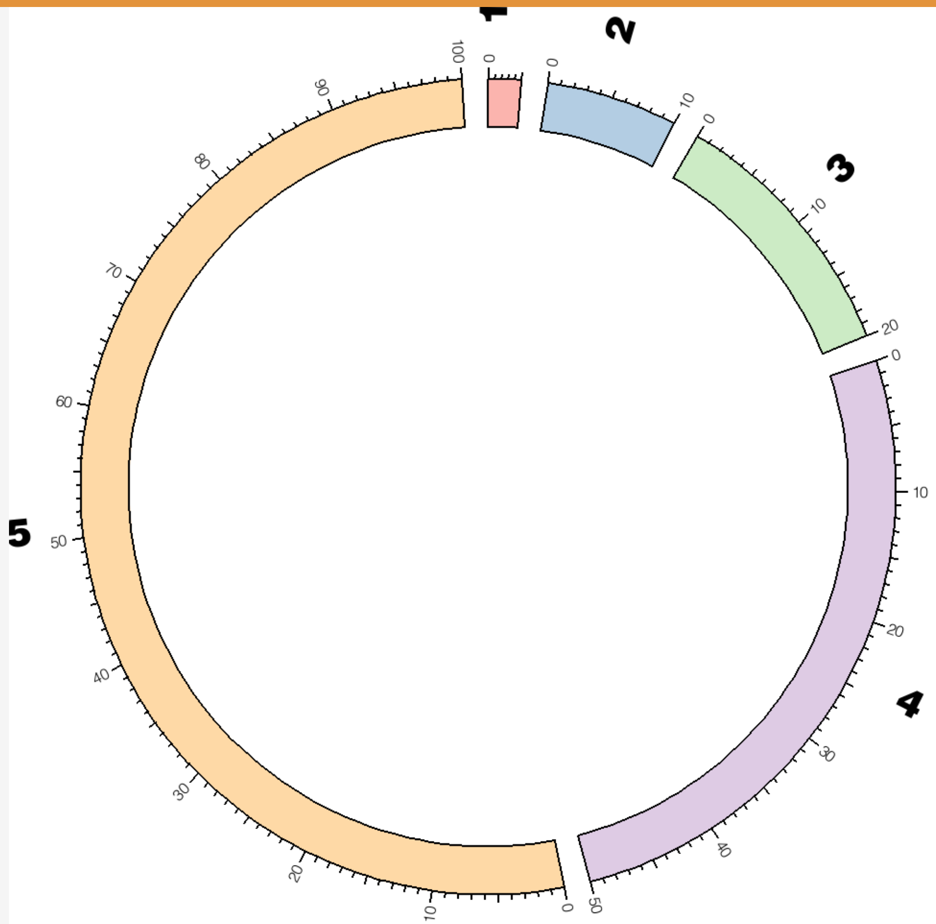
LESSON 3

IDEOGRAM SCALE

3 GLOBAL IDEOGRAM SCALE

sessions/2/3/etc/circos.conf

```
<<include ideogram.conf>>
<<include ticks.conf>>

<image>
file = s2-3.png
<<include ../etc/image.conf>>
</image>

karyotype = ../data/karyotype.txt

chromosomes_units           = 1000000
chromosomes_display_default = yes

chromosomes_scale = chr1:0.5
#chromosomes_scale = chr1:0.5;chr2:2;chr3:10
# chr1 occupies 50% of figure
#chromosomes_scale = chr1:38

# chr1 occupies 75% of figure
#chromosomes_scale = chr1:114
```

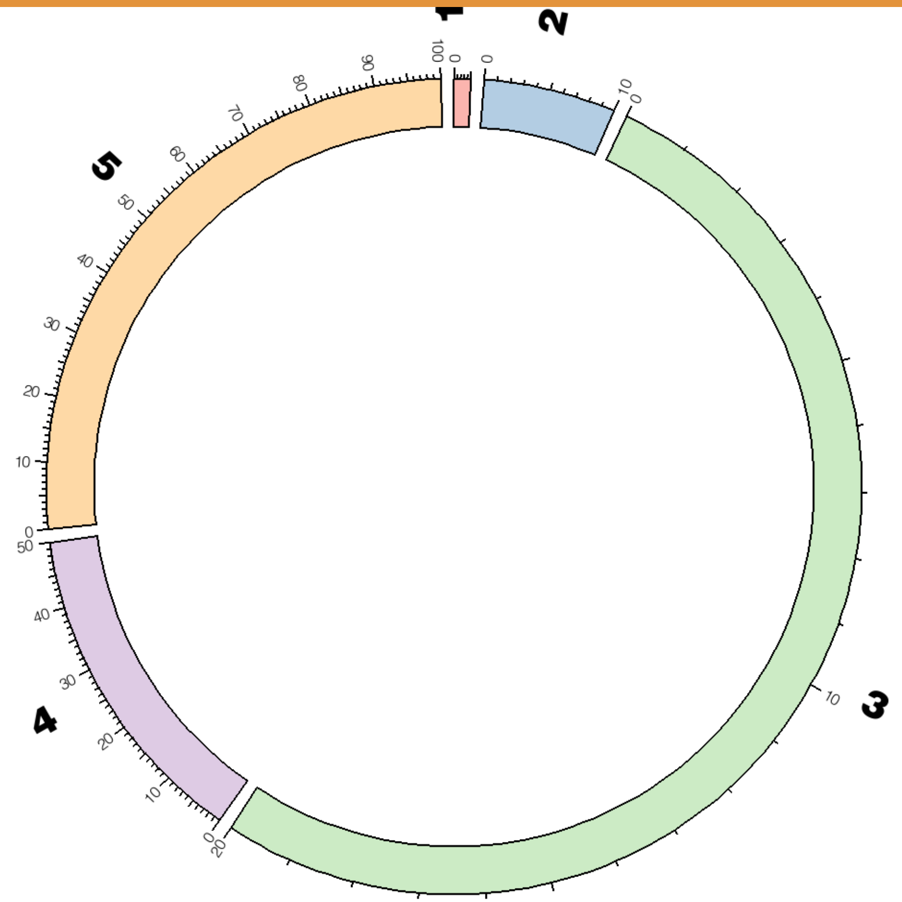


By changing the scale of chromosome 1 to *0.5x* using the chromosomes_scale parameter, the ideogram of this chromosome is shrunk by *2x*.

3 GLOBAL IDEOGRAM SCALE

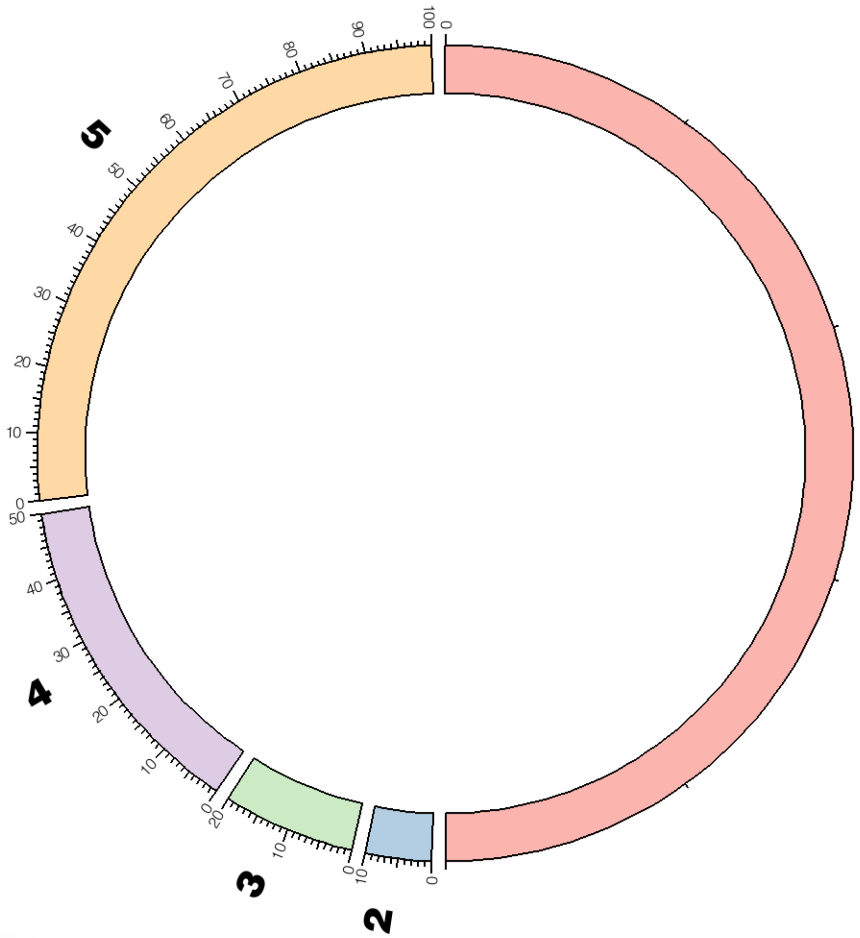
sessions/2/3/etc/circos.conf

```
<<include ideogram.conf>>
<<include ticks.conf>>

<image>
file = s2-3.png
<<include ../etc/image.conf>>
</image>

karyotype = ../data/karyotype.txt

chromosomes_units           = 1000000
chromosomes_display_default = yes

chromosomes_scale = chr1:0.5
chromosomes_scale = chr1:0.5;chr2:2;chr3:10
# chr1 occupies 50% of figure
#chromosomes_scale = chr1:38

# chr1 occupies 75% of figure
#chromosomes_scale = chr1:114
```



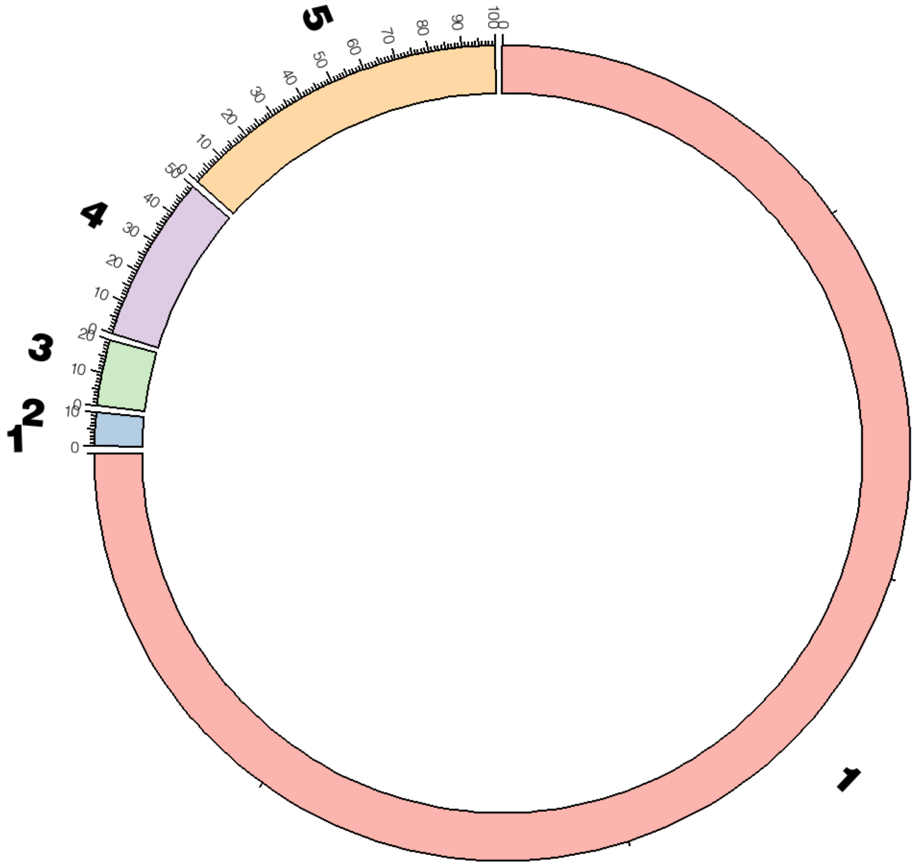
By changing the scale of chromosome 1 to *0.5x*, chromosome 2 to *2x* and chromosome 3 to *10x*, the figure's focus shifts to chromosome 3 (which is now magnified *10x*) and away from chromosome 1 (which is reduced *2x*).

3 FITTING IDEOGRAMS TO FRACTION OF IMAGE



`chromosomes_scale = chr1:38`

By changing the scale of chr1 to 38, it is made to occupy 50% of the figure.



`chromosomes_scale = chr1:114`

By changing the scale of chr1 to 114, it is made to occupy 75% of the figure.

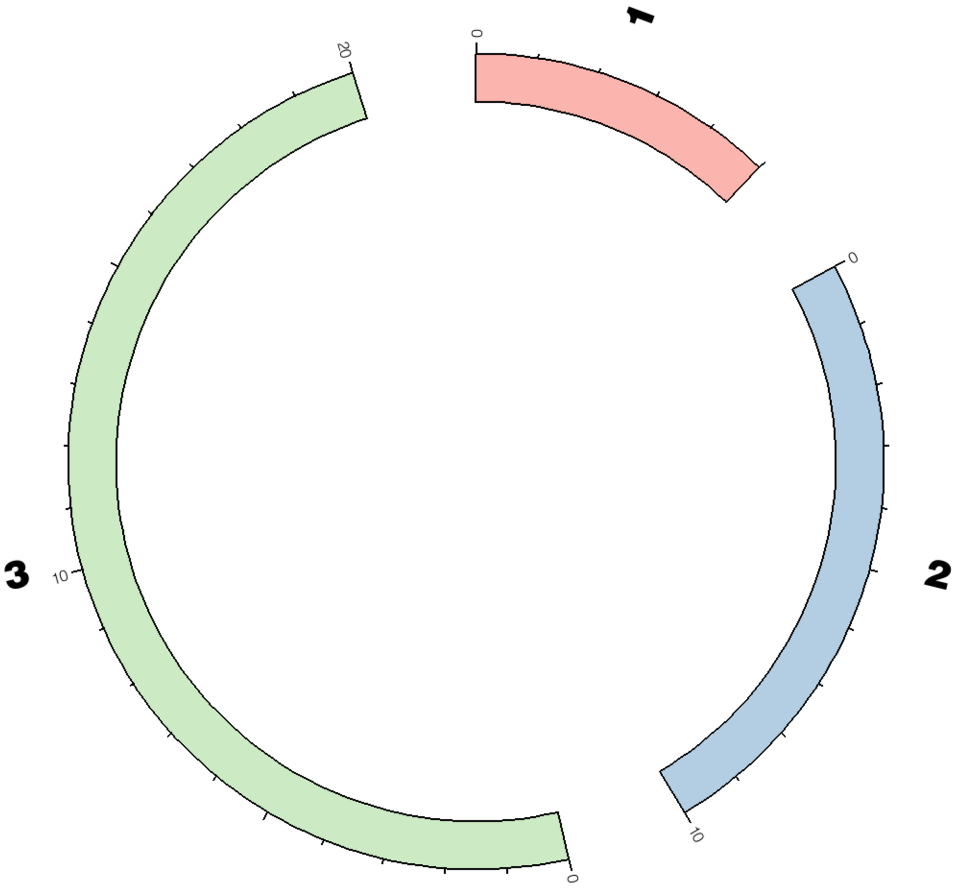
LESSON 4

IDEOGRAM SELECTION

4 SELECTING IDEOGRAMS FOR DISPLAY

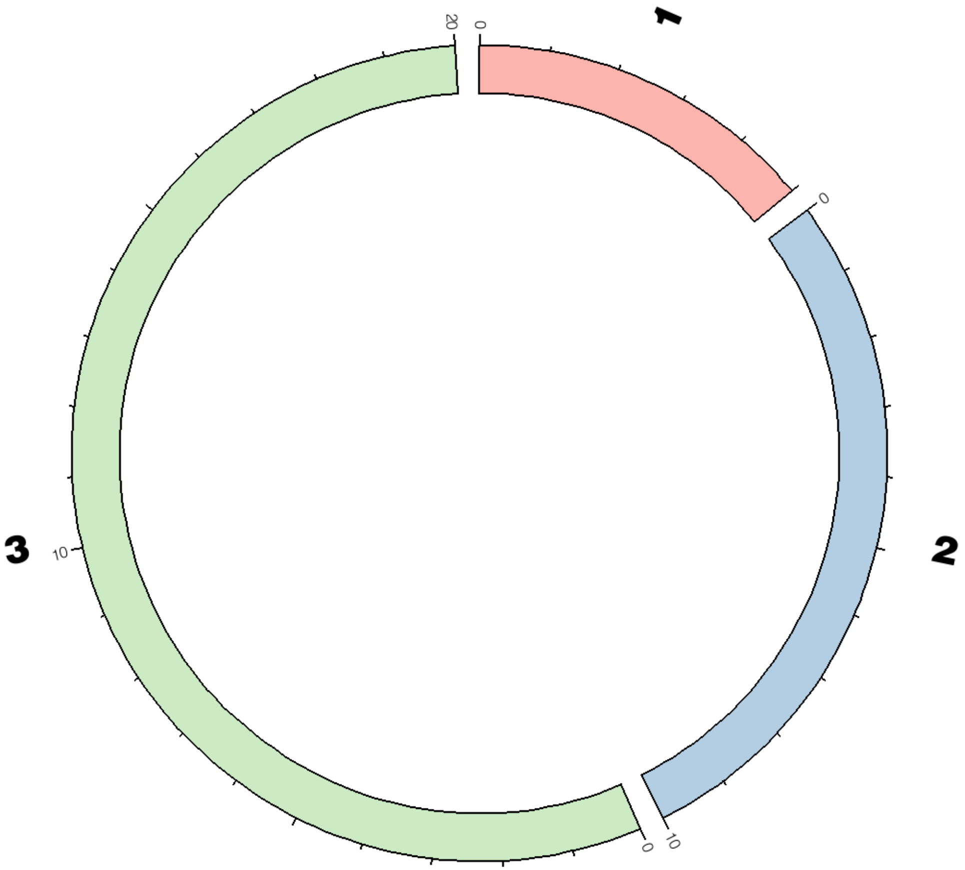
sessions/2/4/etc/circos.conf

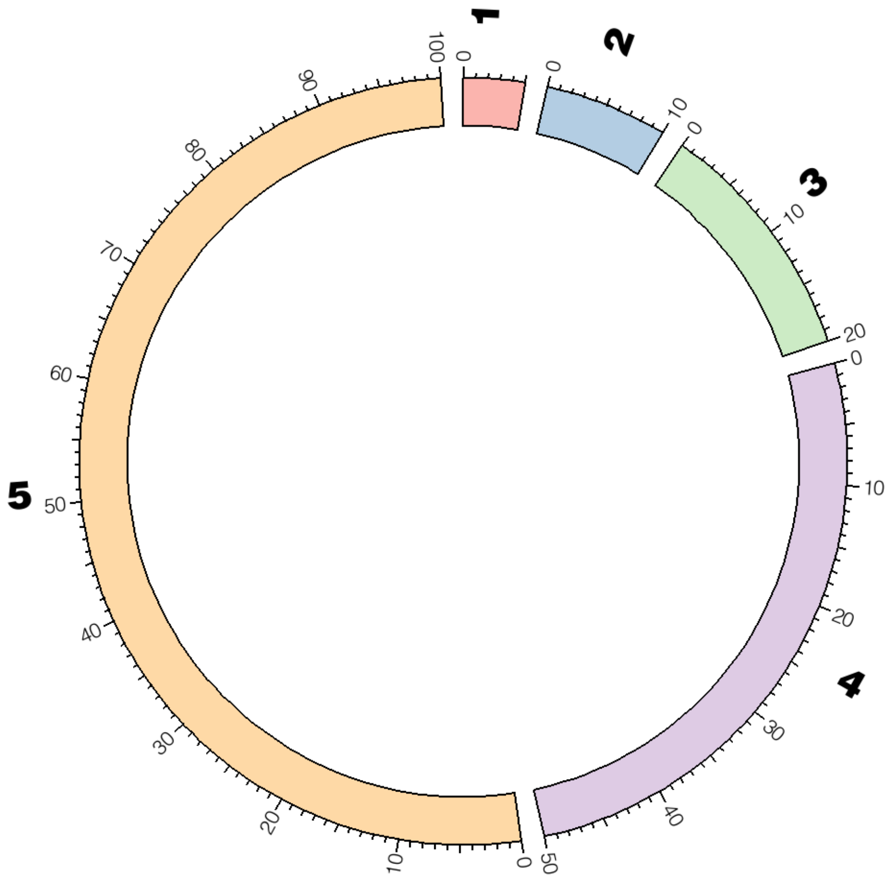
```
#chromosomes_display_default = yes

chromosomes_display_default = no
chromosomes = chr1;chr2;chr3
```



By turning off default chromosome display and setting the chromosomes parameter, you can control which chromosomes are drawn.

4 BENEFIT OF RELATIVE SPACING





When ideogram spacing is set to relative, the fraction of the ideogram circle occupied by spaces is the same regardless of the total ideogram size.

left Spacing is set to *0.01r* and the total ideogram size is 35Mb.

right Spacing is also *1u* but ideogram size is 185Mb.

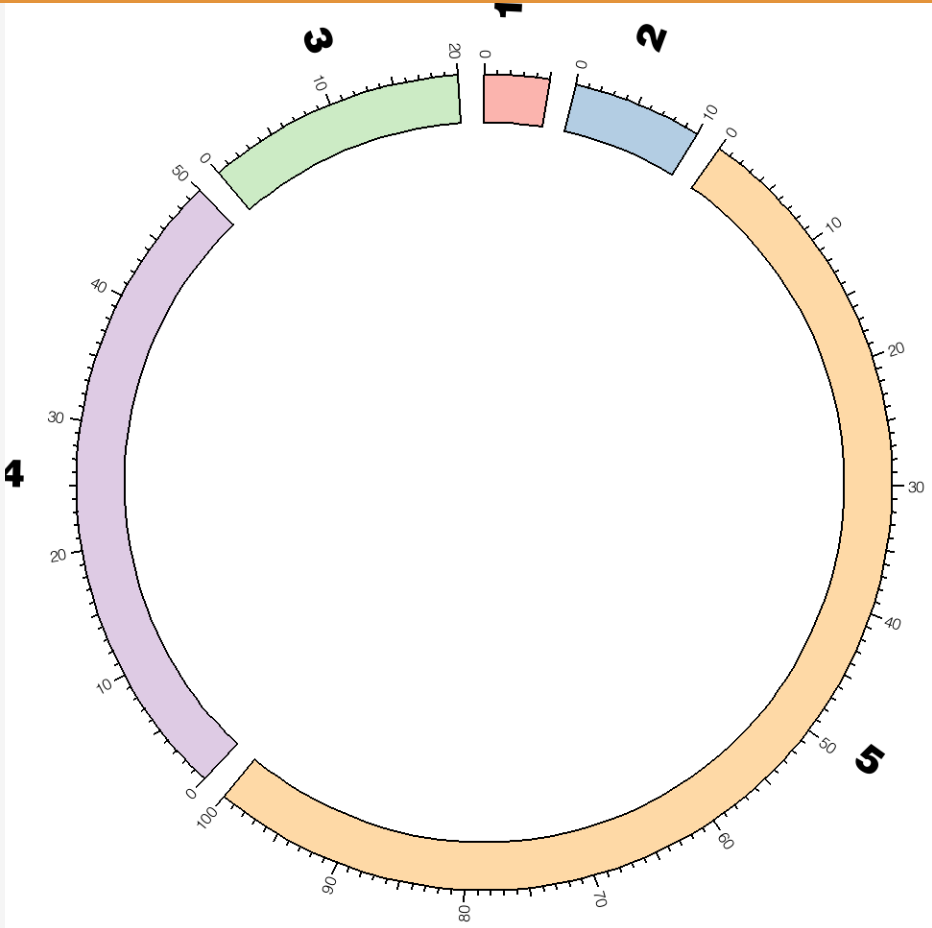
LESSON 5

IDEOGRAM ORDER

5 ORDERING IDEOGRAMS

sessions/2/5/etc/circos.conf

```
chromosomes_units           = 1000000
chromosomes_display_default = yes

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

# relative order
#chromosomes_order = chr3,chr5

# relative order
#chromosomes_order = chr1,chr4,-,chr3,chr5

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

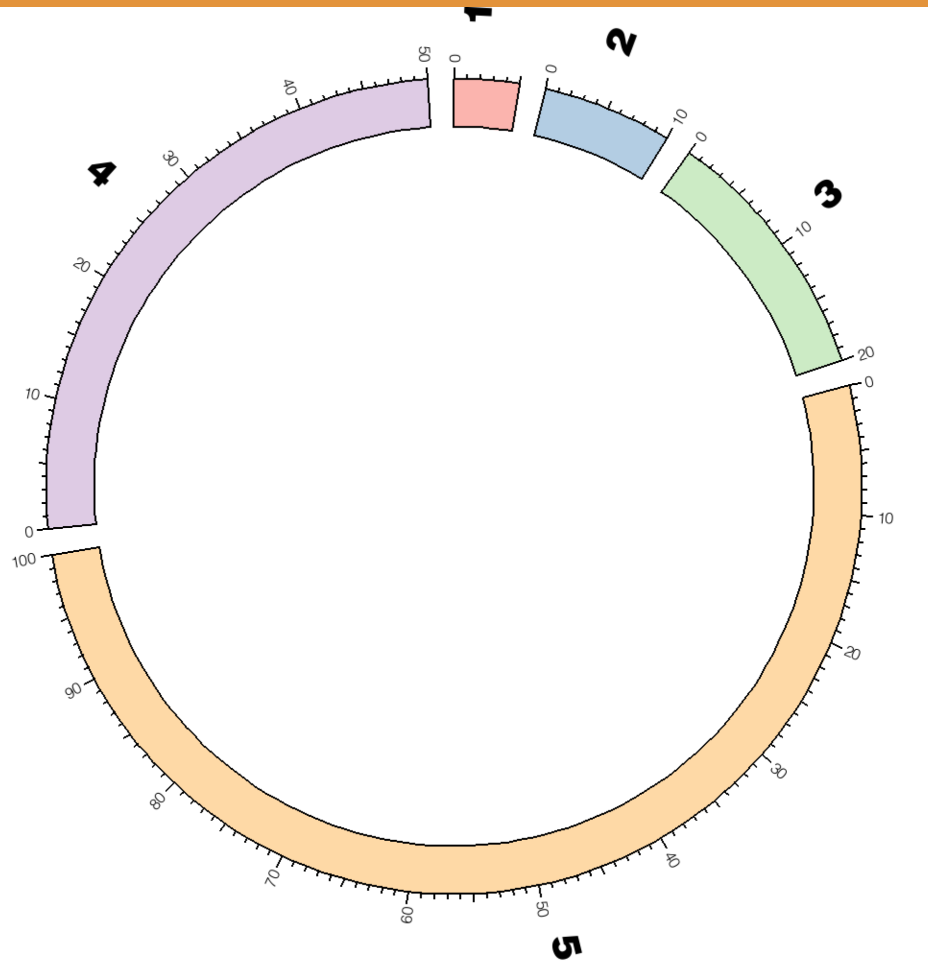


Ideogram order can be adjusted using `chromosomes_order`.

5 ORDERING IDEOGRAM SUBSET

sessions/2/5/etc/circos.conf

```
chromosomes_units            = 1000000
chromosomes_display_default = yes

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

# relative order
chromosomes_order = chr3,chr5

# relative order
#chromosomes_order = chr1,chr4,-,chr3,chr5

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

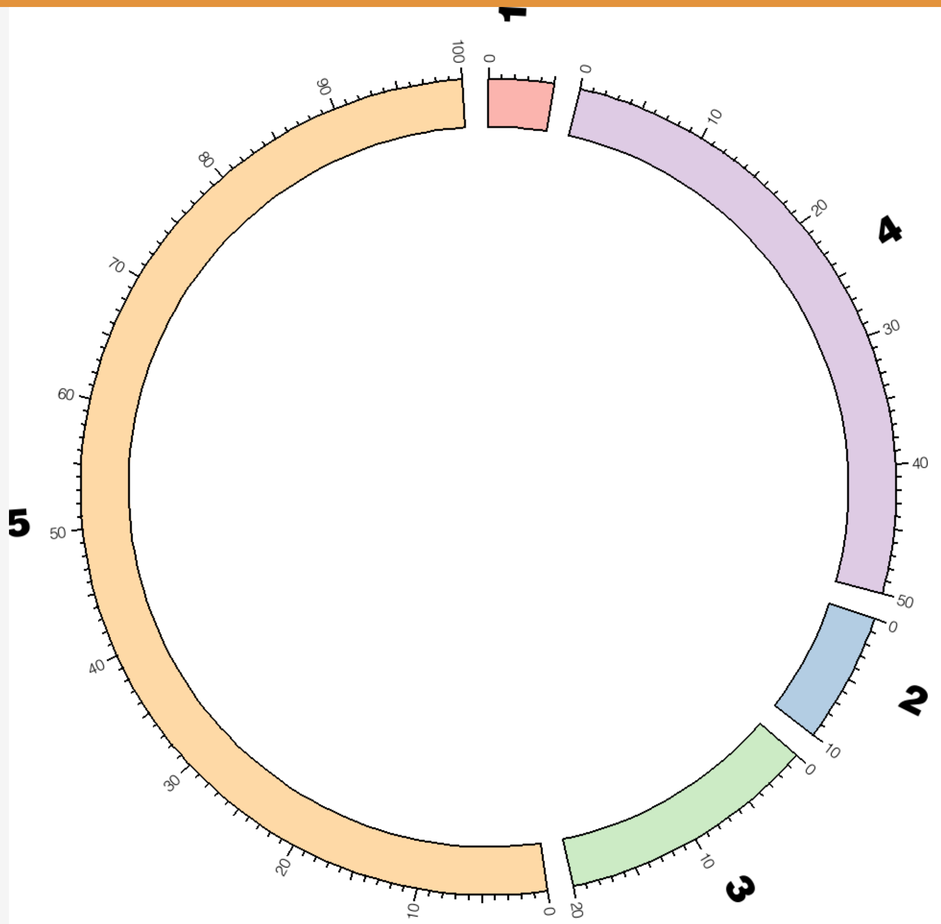


To change the order of a subset of ideograms, set `chromosomes_order` to the order of the subset. You do not need to specify the order of the full set.

5 ORDERING MULTIPLE IDEOGRAM SUBSETS

sessions/2/5/etc/circos.conf

```
chromosomes_units           = 1000000
chromosomes_display_default = yes

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

# relative order
#chromosomes_order = chr3,chr5

# relative order
chromosomes_order = chr1,chr4,-,chr3,chr5

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



To change the order of a several ideogram subsets, separate the order of subsets by a “`-`“ in `chromosomes_order`.

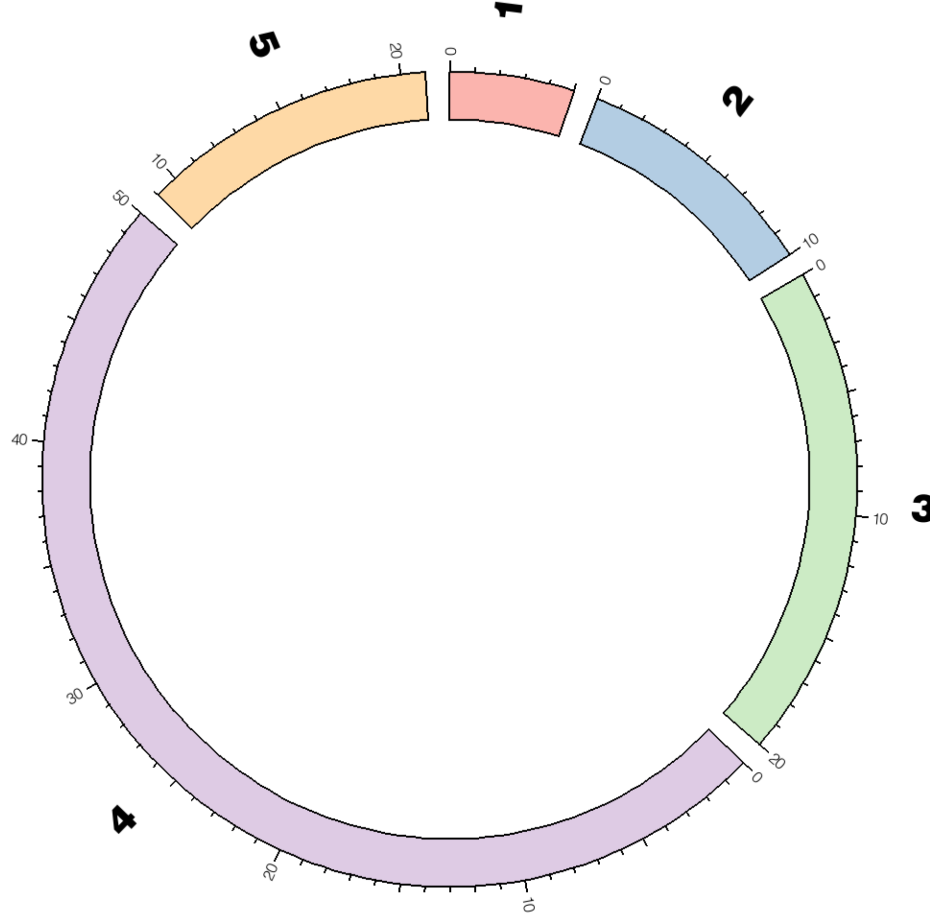
LESSON 6

IDEOGRAM REGIONS

6 CROPPING IDEOGRAMS

sessions/2/6/etc/circos.conf

```
chromosomes_units           = 1000000
chromosomes_display_default = yes

chromosomes   = chr5:9-21
```

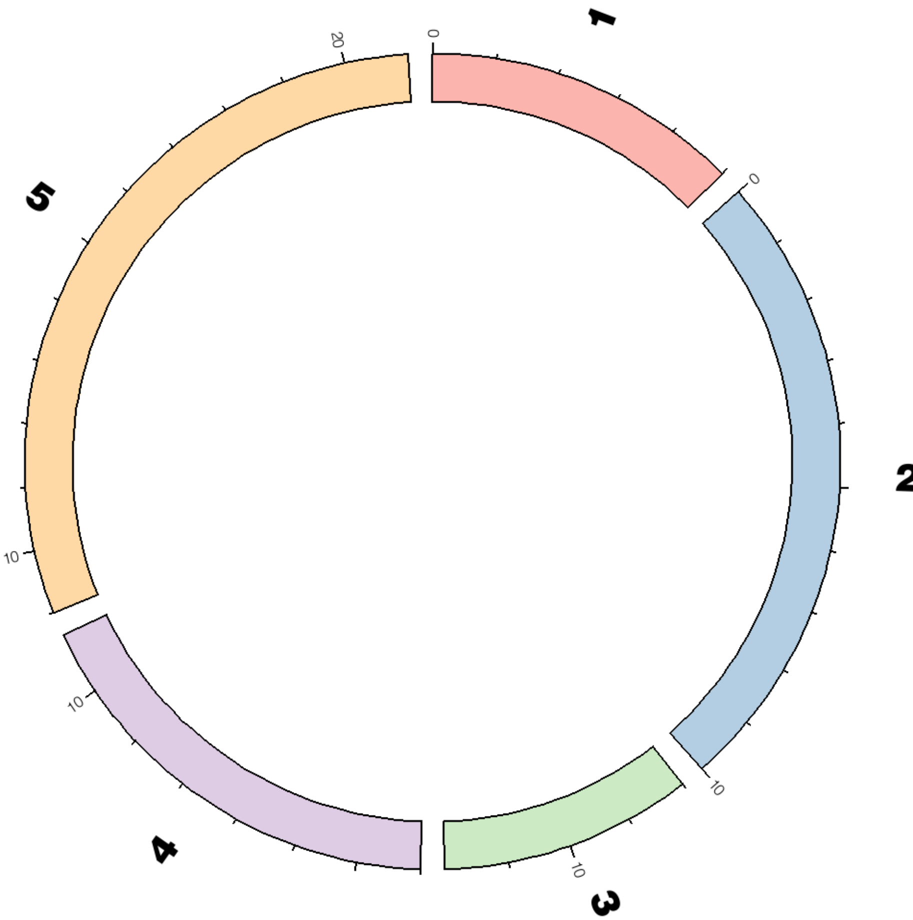


Ideograms can be cropped by using the chromosomes parameter. Here, ideogram of chromosome 5 cropped to the 9-21 Mb region.

6 CROPPING MULTIPLE IDEOGRAMS

sessions/2/6/etc/circos.conf

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



Multiple ideograms can be cropped. Here ideograms are cropped to chr3:8-12, chr4:4-11, chr5:9-21.

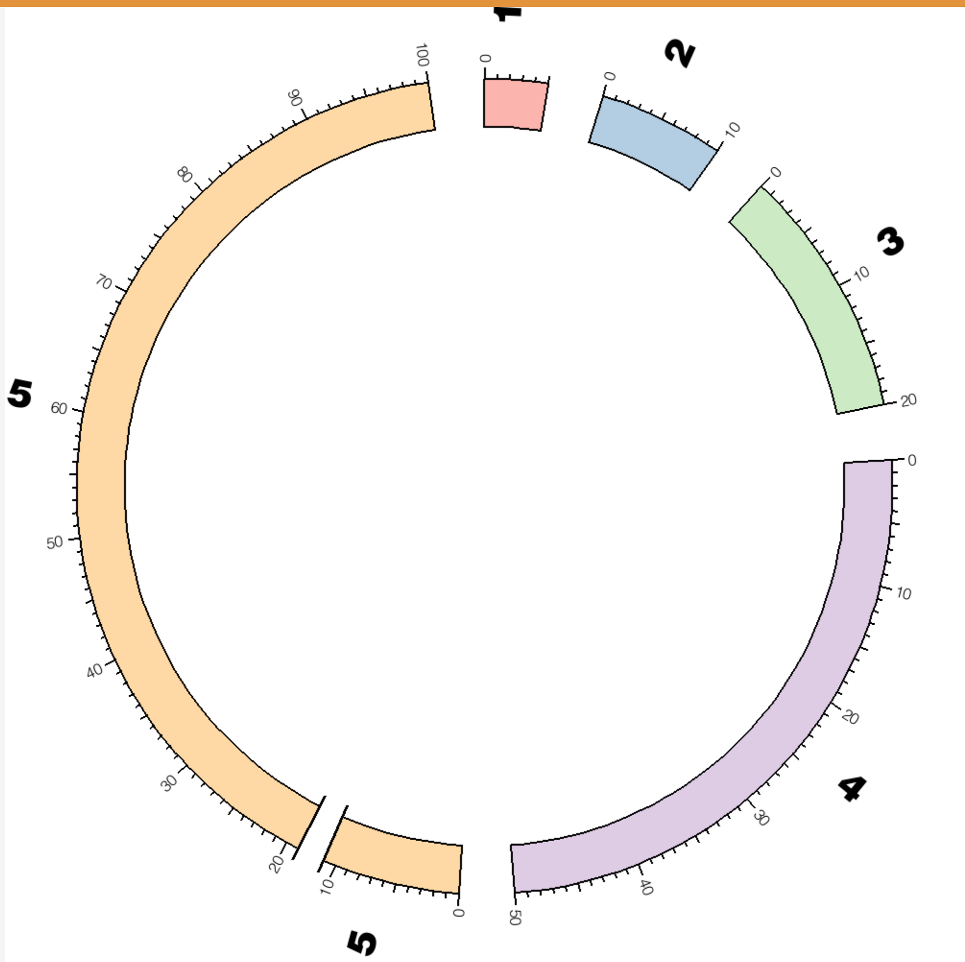
LESSON 7

CHROMOSOME BREAKS

7 AXIS BREAKS

sessions/2/7/etc/circos.conf

```
chromosomes_breaks  = -chr5:11-19
```

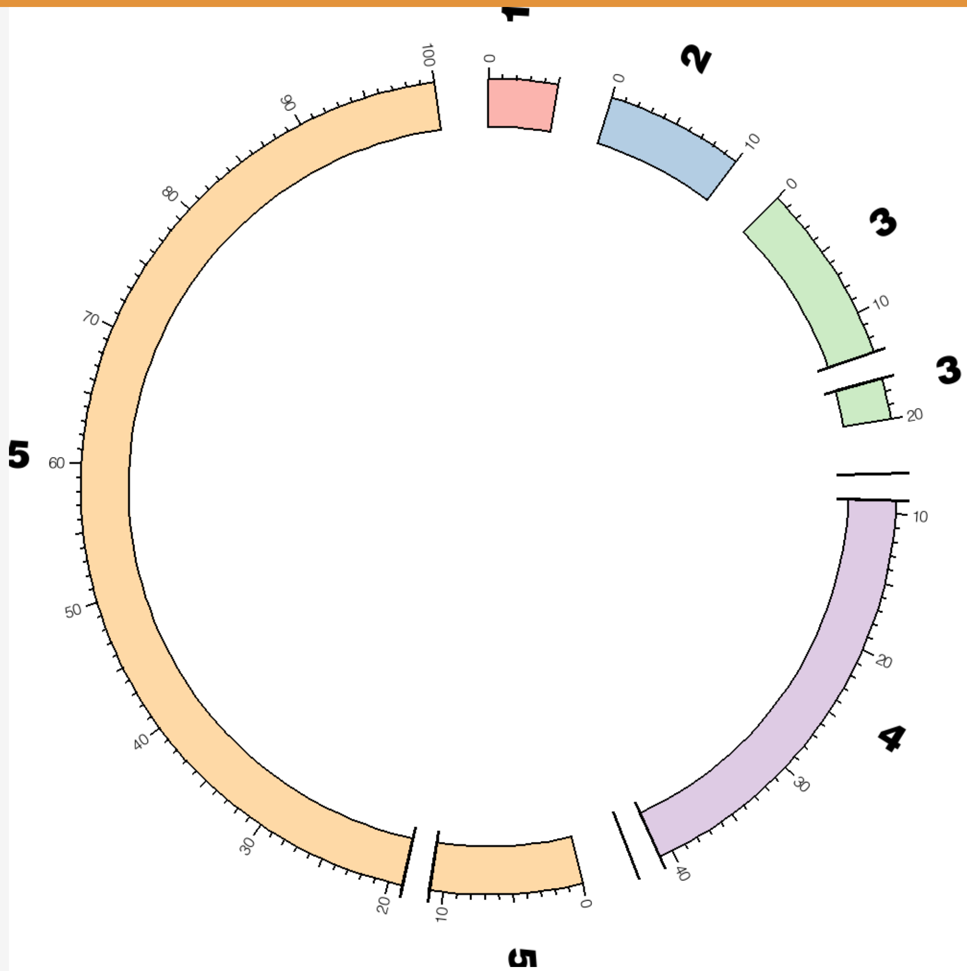


Regions of chromosomes can be removed from the display by using `chromosomes_breaks`. In this figure region chr5: 11-19 Mb is removed and replaced by an axis break.

7 MULTIPLE AXIS BREAKS

sessions/2/7/etc/circos.conf

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



Multiple breaks are defined. Regions removed are chr3:13-17, chr4:start-9, chr4:41-end, chr5:11-19

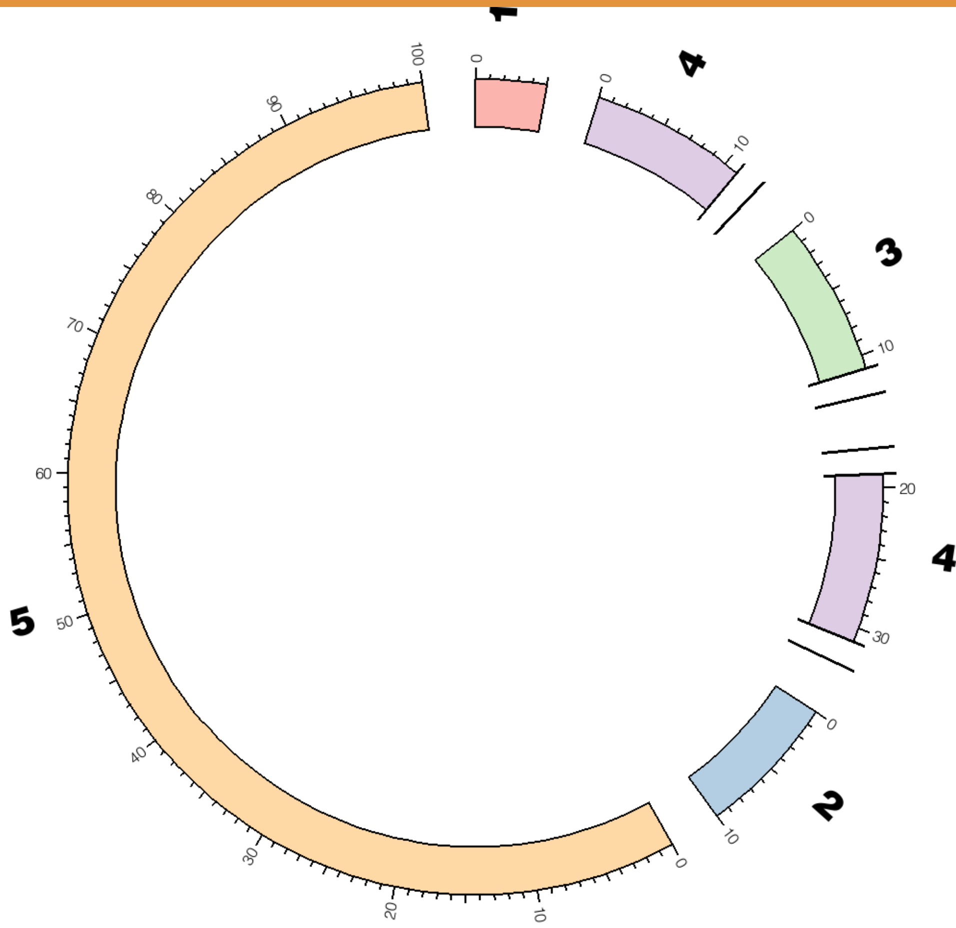
LESSON 8

ORDERING REGIONS

8 REORDERING IDEOGRAM SEGMENTS

sessions/2/8/etc/circos.conf

```
chromosomes       =
  chr3:0-11;chr4[a]:0-11;chr4[b]:19-31

chromosomes_order = ^,chr1,a,chr3,b
```

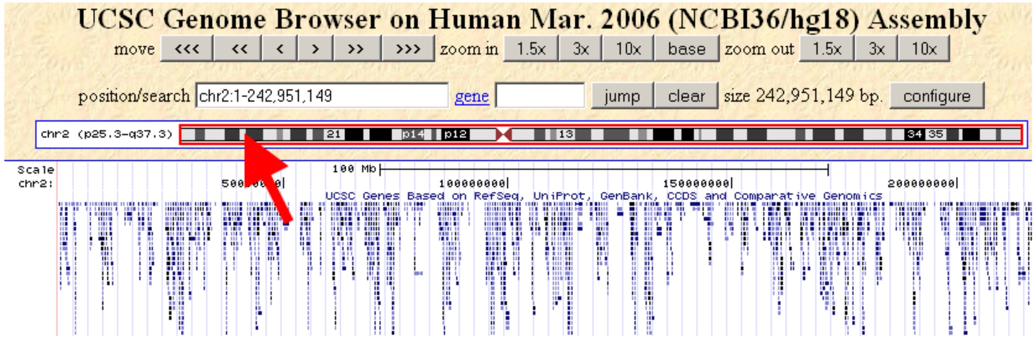


A chromosome can be split into multiple, independently ordered ideograms by using *tags* in the chromosomes parameter to associate a unique name to each ideogram. Chromosome 4 is split into two pieces (a and b) which correspond to 0-11 Mb and 19-31 Mb of the chromosome.

LESSON 9

CYTOGENETIC BANDS

9 CYTOGENETIC BANDS

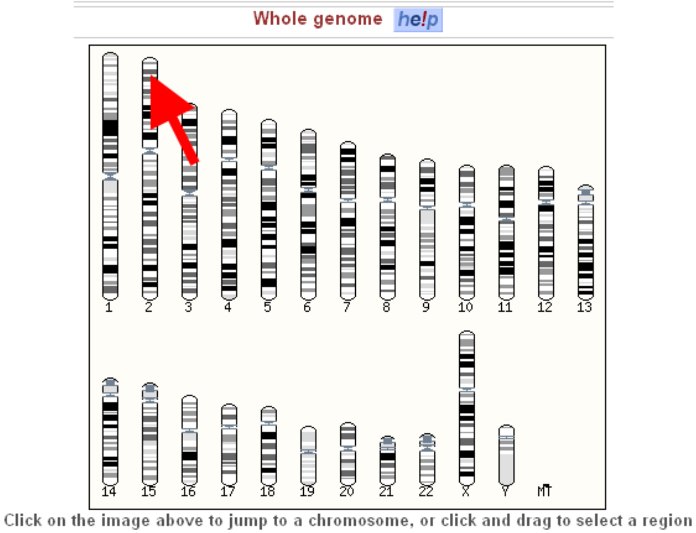


UCSC Genome Browser on Human Mar. 2006 (NCBI36/hg18) Assembly

position/search chr2:1-242,951,149

size 242,951,149 bp.

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

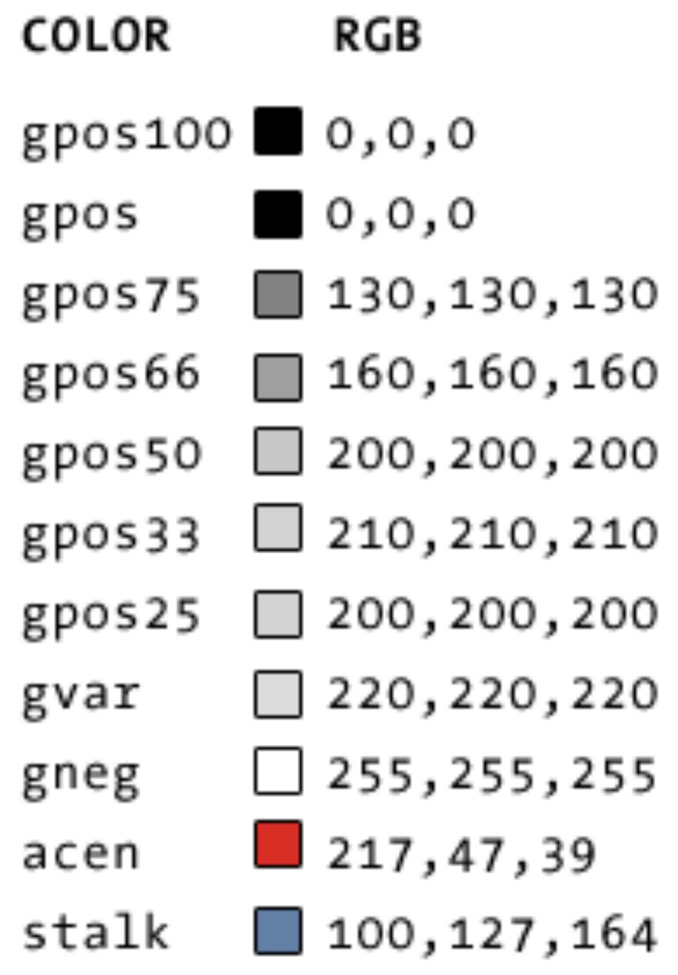


Click on the image above to jump to a chromosome, or click and drag to select a region

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

Views showing cytogenetic bands in UCSC and Ensembl browsers (same band position is indicated by a red arrow).

CYTOGENETIC BAND COLORS



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

Band colors are defined in `color.conf` to correspond to the color scheme of the UCSC genome browser and the names given to the bands in the UCSC Karyotype table. For example, *acen* is used for centromeres, typically shown in red.

9 CYTOGENETIC BAND DEFINITION

sessions/2/data/karyotype.banded.txt

```
# the first field must be “band”
# the second field is the band’s chromosome
# the next two fields are the name and
# label of the band (not used, but must be present)
# the last three fields are the start,
# end and color of the band.
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

band chr3 band1 band1 0 1000000 stalk
band chr3 band2 band2 1000000 5000000 gpos50
band chr3 band3 band3 5000000 7500000 gpos100
band chr3 band4 band4 7500000 10000000 gvar
band chr3 band5 band5 10000000 15000000 acen
band chr3 band7 band7 15000000 19000000 gneg
band chr3 band8 band8 19000000 20000000 stalka
```

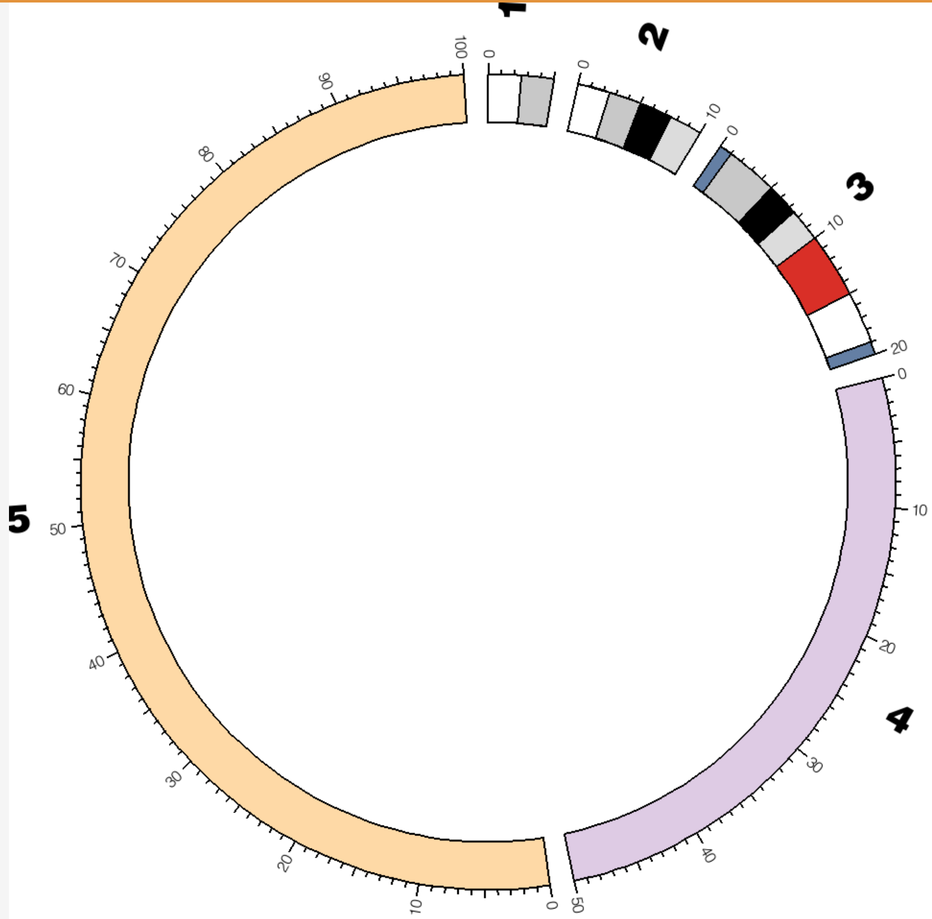
Bands are defined together with chromosomes in the karyotype file.

The syntax for a band is the same as for a chromosome, except that the line starts with “band” and the second field now defines the parent chromosome.

9 CYTOGENETIC BANDS

`sessions/2/data/karyotype.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

band chr3 band1 band1 0 1000000 stalk
band chr3 band2 band2 1000000 5000000 gpos50
band chr3 band3 band3 5000000 7500000 gpos100
band chr3 band4 band4 7500000 10000000 gvar
band chr3 band5 band5 10000000 15000000 acen
band chr3 band7 band7 15000000 19000000 gneg
band chr3 band8 band8 19000000 20000000 stalk
```

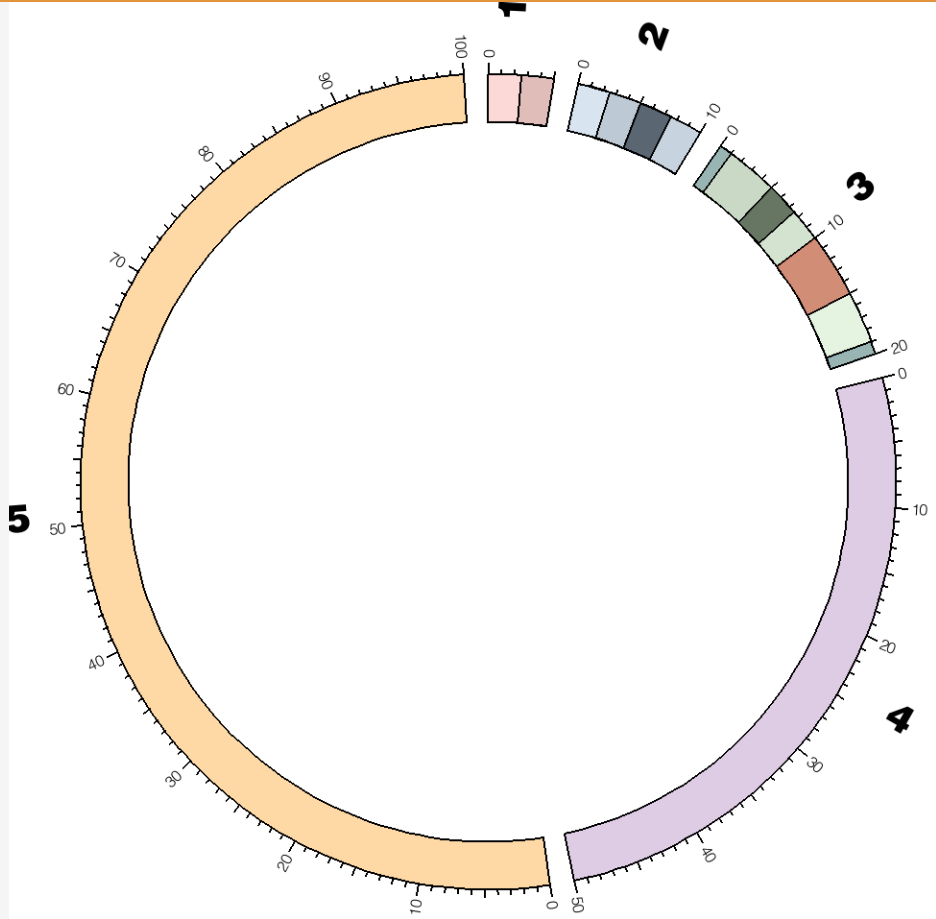


Cytogenetic bands appear as stripes within the ideogram segment.

9 ADDING TRANSPARENCY TO BANDS

sessions/2/9/etc/ideogram.conf

```
band_transparency = 3
```



By changing `band_transparency` in the `<ideogram>` block, the band pattern can be made semi-transparent to allow the color of the ideogram to show through. Using this parameter you can combine the ideogram color and the band pattern.

LESSON 10

MULTIPLE GENOMES

10 HUMAN GENOME KARYOTYPE

sessions/2/data/karyotype.human.txt

```
chr - hs1 1 0 247249719 chr1
chr - hs2 2 0 242951149 chr2
chr - hs3 3 0 199501827 chr3
chr - hs4 4 0 191273063 chr4
chr - hs5 5 0 180857866 chr5
chr - hs6 6 0 170899992 chr6
chr - hs7 7 0 158821424 chr7
...
```

sessions/2/data/karyotype.mouse.txt

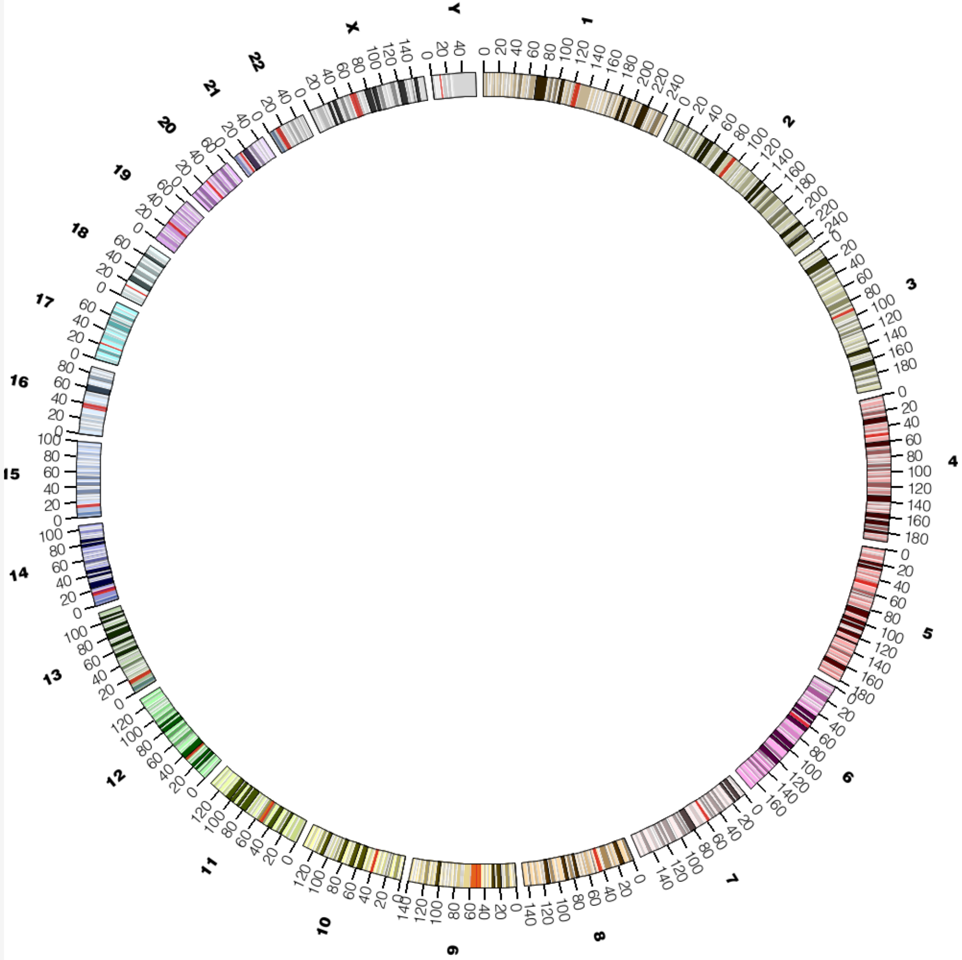
```
chr - mm1 1 0 197195432 white
chr - mm2 2 0 181748087 white
chr - mm3 3 0 159599783 white
chr - mm4 4 0 155630120 white
chr - mm5 5 0 152537259 white
chr - mm6 6 0 149517037 white
chr - mm7 7 0 152524553 white
..
```

You can download karyotype definitions from UCSC Genome Browser table viewer (karyotype table).

10 DRAWING THE HUMAN GENOME

sessions/2/10/etc/circos.conf

```
karyotype = ../data/karyotype.human.txt
#karyotype = ../data/karyotype.mouse.txt
#karyotype = ../data/
  karyotype.human_mouse.txt
#karyotype = ../data/
  karyotype.human_mouse_labels.txt
```



All chromosomes in the human genome. The figure uses the human karyotype file which defines 24 chromosomes (1..22, X, Y) and the cytogenetic bands. Bands are drawn with transparency.

10 CONVENTIONAL HUMAN CHROMOSOME COLORS

$CIRCOS/etc/colors.conf

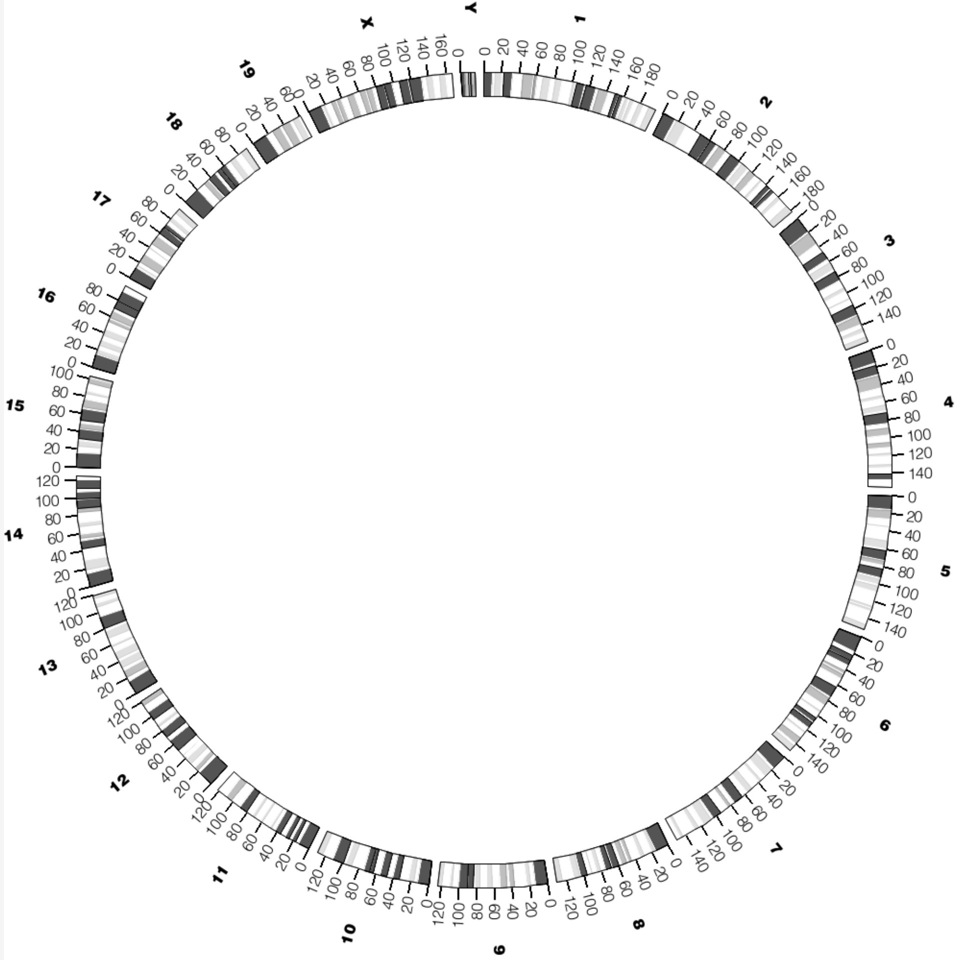
```
# UCSC genome browser RGB
# colors for human chromosomes
chr1 = 153,102,0
chr2 = 102,102,0
chr3 = 153,153,30
chr4 = 204,0,0
chr5 = 255,0,0
chr6 = 255,0,204
chr7 = 255,204,204
chr8 = 255,153,0
chr9 = 255,204,0
chr10 = 255,255,0
chr11 = 204,255,0
chr12 = 0,255,0
chr13 = 53,128,0
...
chr21 = 204,153,255
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
```

Conventional color palette for the human genome used by the UCSC genome browser. These colors are defined in the `color.conf` file, named after the chromosome name, but with a "chr" prefix (e.g. hs1 has color chr1).

10 DRAWING THE MOUSE GENOME

sessions/2/10/etc/circos.conf

```
#karyotype = ../data/karyotype.human.txt
karyotype = ../data/karyotype.mouse.txt
#karyotype =
  ../data/karyotype.human_mouse.txt
#karyotype =
  ../data/karyotype.human_mouse_labels.txt
```

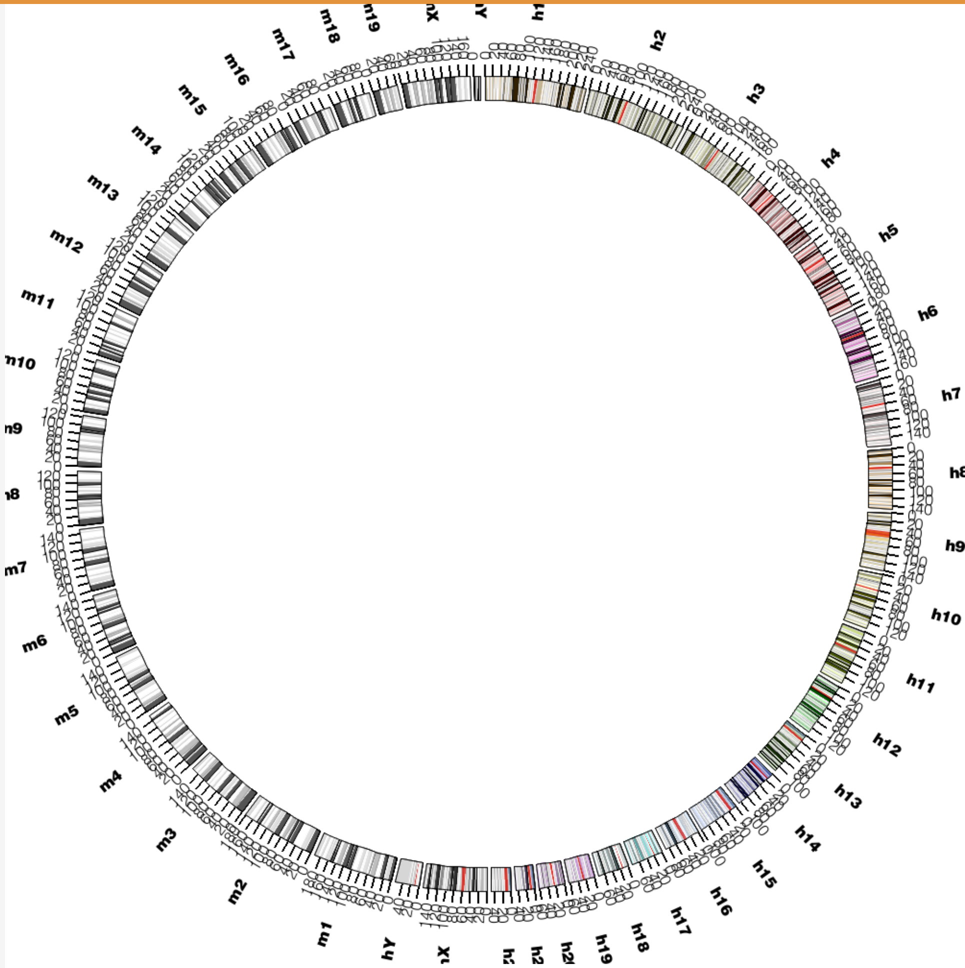


All chromosomes in the mouse genome. The figure uses the human karyotype file which defines 21 chromosomes (1..19, X, Y) and the cytogenetic bands.

10 DRAWING MULTIPLE GENOMES

sessoins/2/10/etc/circos.conf

```
#karyotype = ../data/karyotype.human.txt
#karyotype = ../data/karyotype.mouse.txt
#karyotype =
  ../data/karyotype.human_mouse.txt
karyotype =
  ../data/karyotype.human_mouse_labels.txt
```



Ideograms of all human (labeled hN) and mouse (labeled mN) chromosomes.

Human ideograms are shaded by the UCSC genome browser color convention.

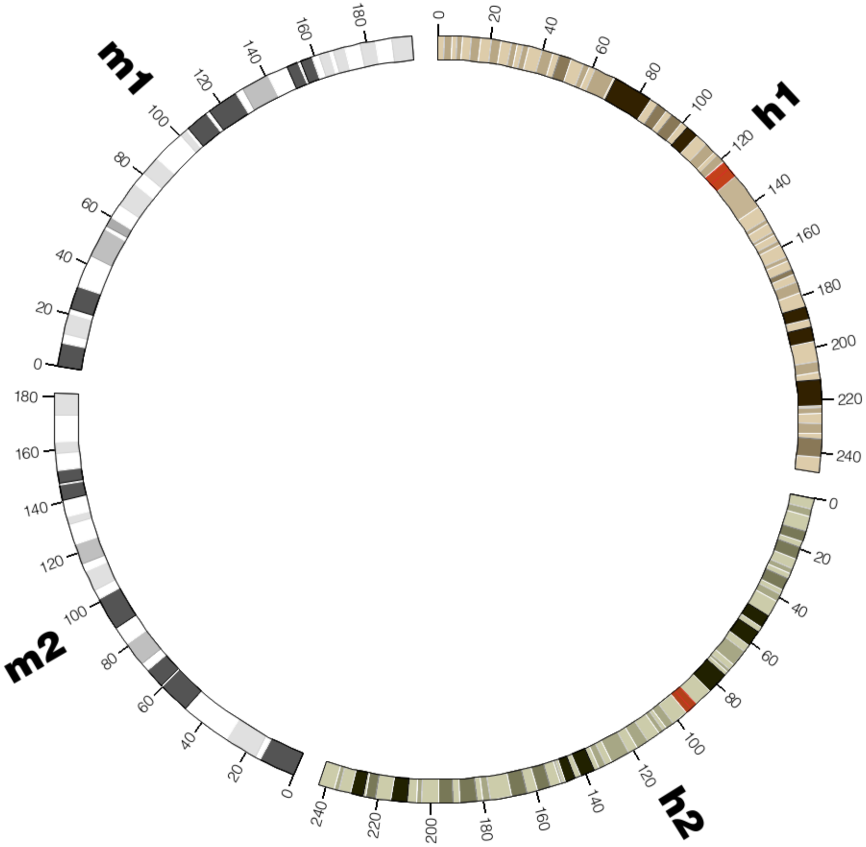
LESSON 11

PROGRESSION & ORIENTATION

11 IDEOGRAM SELECTION

sessions/2/11/etc/circos.conf

```
karyotype =
  ../data/karyotype.human_mouse_labels.txt

chromosomes_display_default = no

chromosomes       = hs1;hs2;mm1;mm2
chromosomes_order = hs1;hs2;mm2;mm1
```



Chromosomes 1,2 of human and mouse genomes.

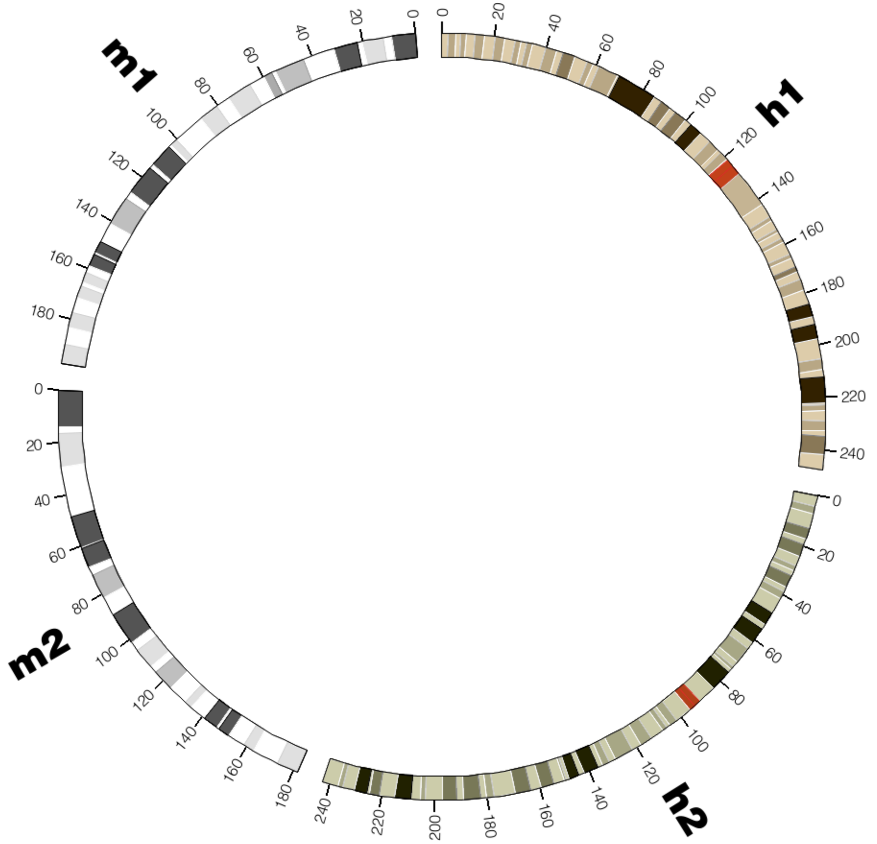
The ideograms start the top of the figure and progress clockwise.

The scale of each ideogram is oriented clockwise.

11 SCALE REVERSAL

sessions/2/11/etc/circos.conf

```
chromosomes_reverse = mm2;mm1
```

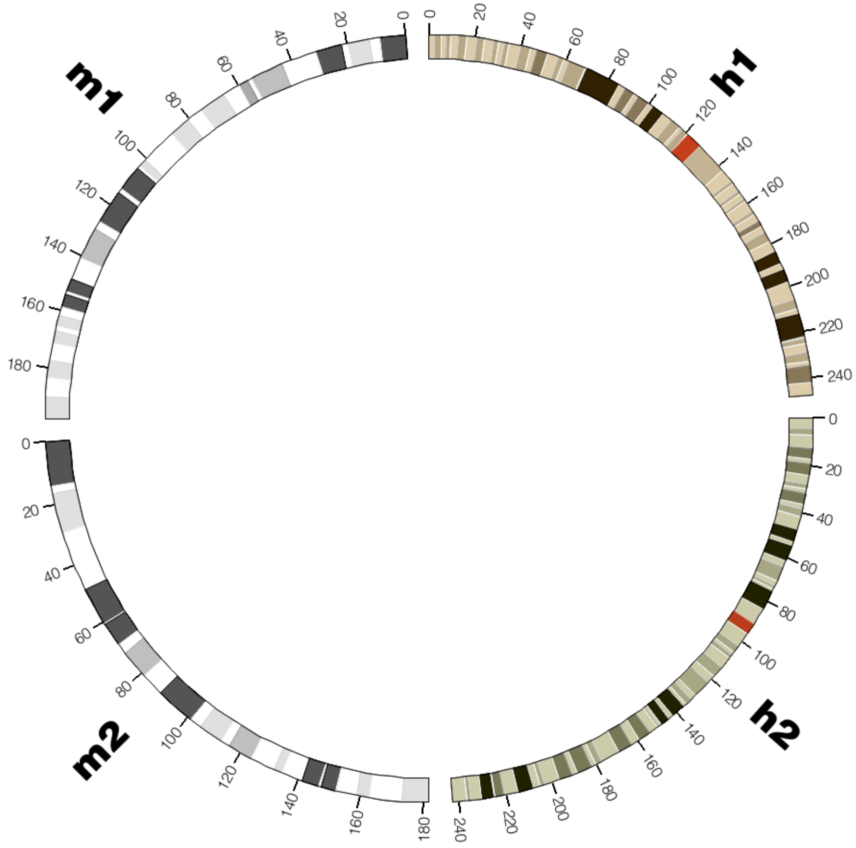


Scale on mouse ideograms is oriented counter-clockwise, opposite to the scale on the human ideograms. This makes adjacent the start and end of chromosomes 1 and 2 from the two species.

11 FITTING IDEOGRAMS TO 25% OF FIGURE

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

```
chromosomes_scale    =
   hs2:1.018;mm1:1.254;mm2:1.360
```



Scale of each ideogram has been adjusted so that it occupies ¼ of the figure.

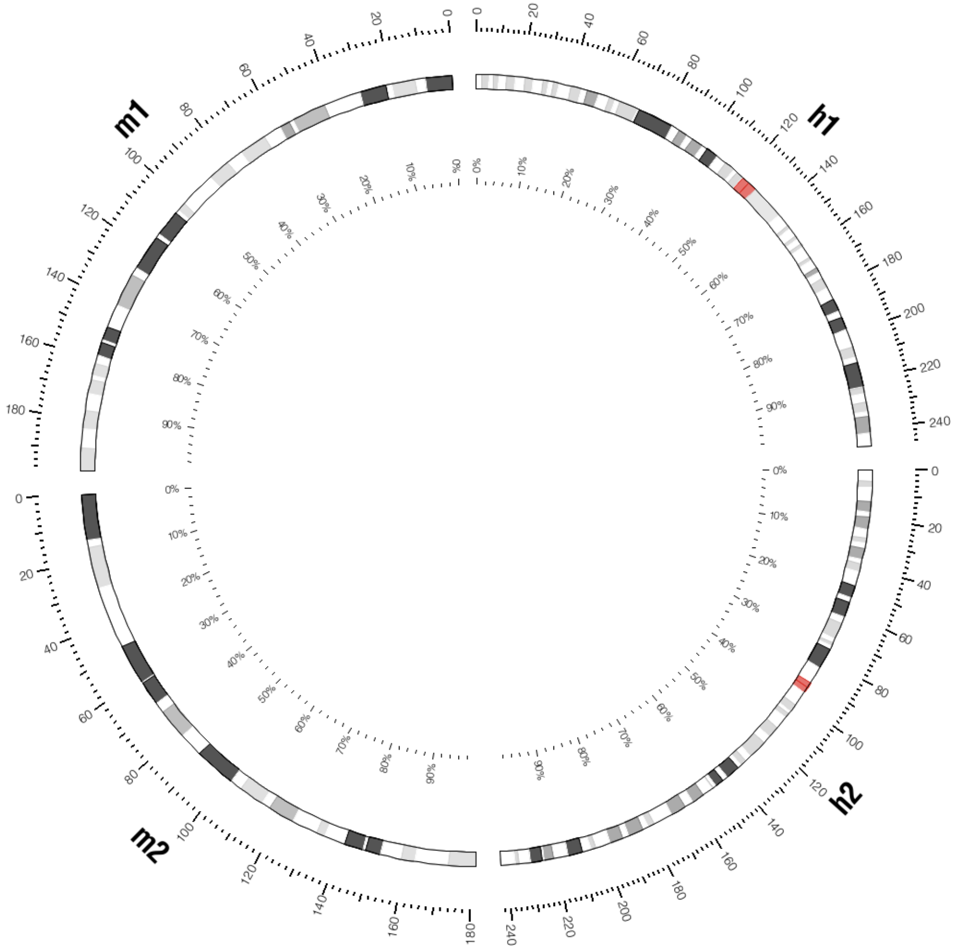
LESSON 12

RELATIVE & ABSOLUTE TICKS

ABSOLUTE TICKS – 20 MB SPACING

sessions/2/12/etc/ticks.conf

```
show_ticks          = yes
show_tick_labels    = yes

<ticks>

radius          =
  dims(ideogram,radius_outer) + 45p

# absolute ticks (spacing is
# defined by parameter “spacing”)

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

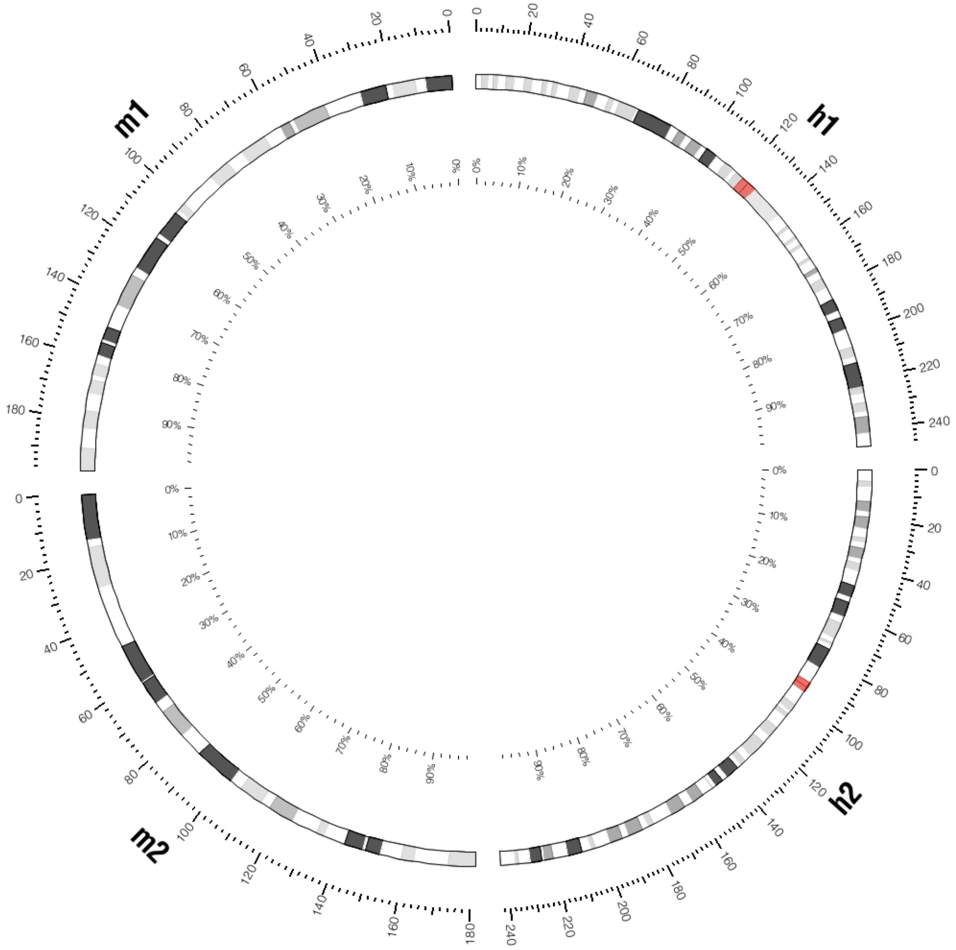


Ticks have been added inside (relative ticks) and outside (absolute ticks) the ideogram circle.

12 ABSOLUTE TICKS – 10 AND 2 MB SPACING

sessions/2/12/etc/ticks.conf

```
<tick>
spacing        = 10u
size           = 7p
thickness      = 2p
show_label     = no
</tick>

<tick>
spacing        = 2u
size           = 3p
thickness      = 2p
show_label     = no
</tick>
```

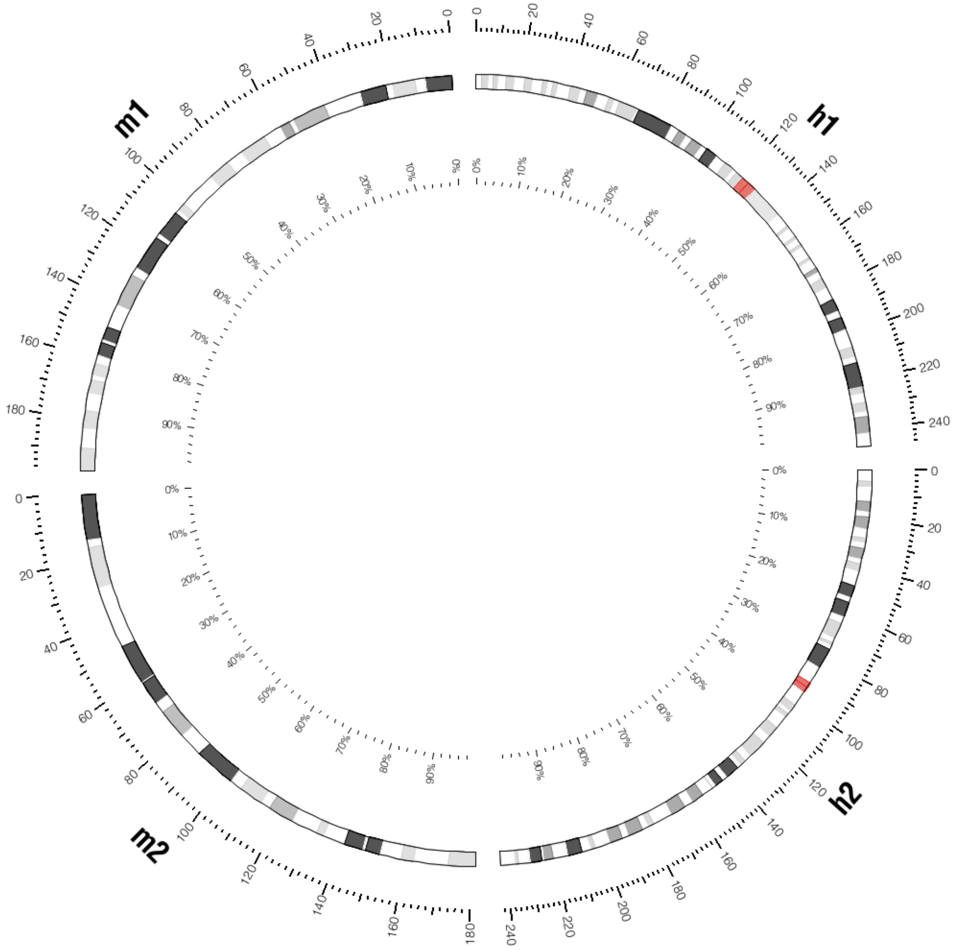


Chromosomes 1,2 of human and mouse genomes, with adjusted format parameters to make the ideograms thinner, shrink the ideogram circle and remove ideogram color.

12 RELATIVE TICKS – 10 AND 2 % SPACING

sessions/2/12/etc/ticks.conf

```
<tick>
radius         = 0.75r
spacing_type   = relative
rspacing       = 0.02
size           = 3p
thickness      = 1p
show_label     = no
</tick>

<tick>
radius         = 0.75r
spacing_type   = relative
rspacing       = 0.10
size           = 6p
thickness      = 1p
show_label     = yes
label_relative = yes
rmultiplier    = 100
format         = %d
suffix         = %
</tick>
```

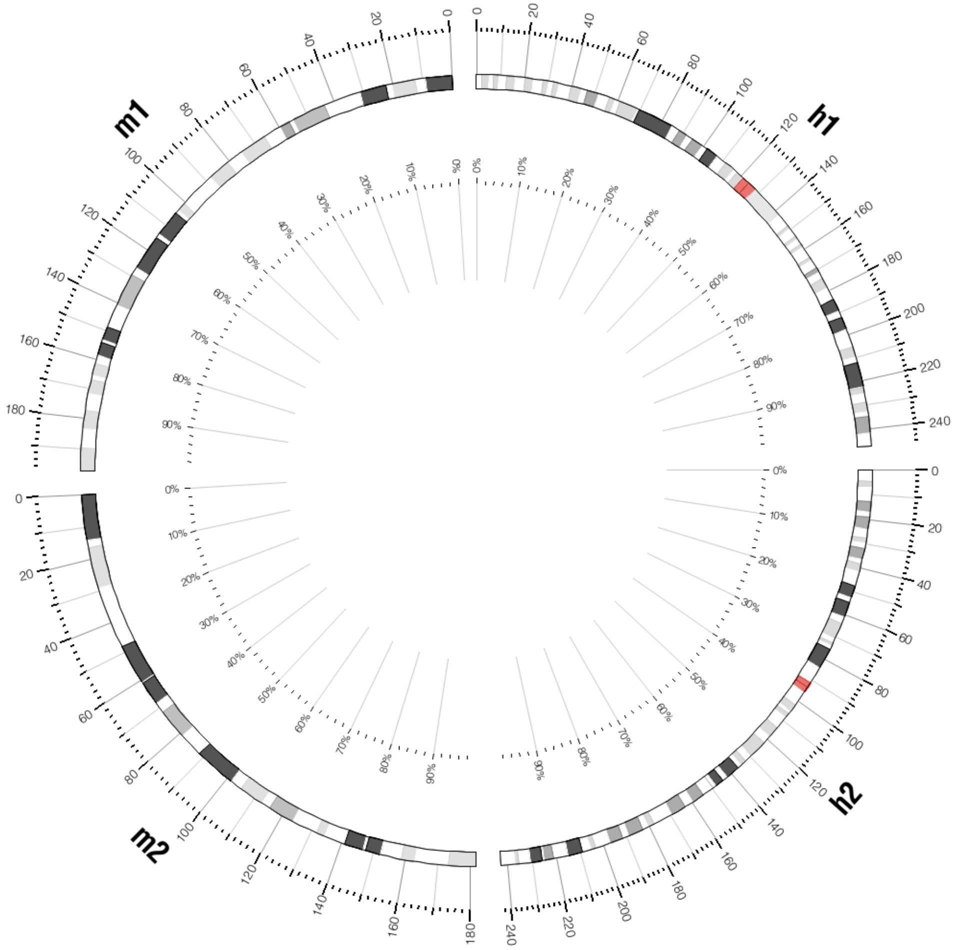


Chromosomes 1,2 of human and mouse genomes, with adjusted format parameters to make the ideograms thinner, shrink the ideogram circle and remove ideogram color.

12 GRIDS

sessions/2/12/etc/ticks.conf

```
show_grid       = yes

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

grid_start     = 1r
grid_end       = 1r+45p
grid_color     = vdgrey
grid_thickness = 1p
grid           = yes
</tick>
```



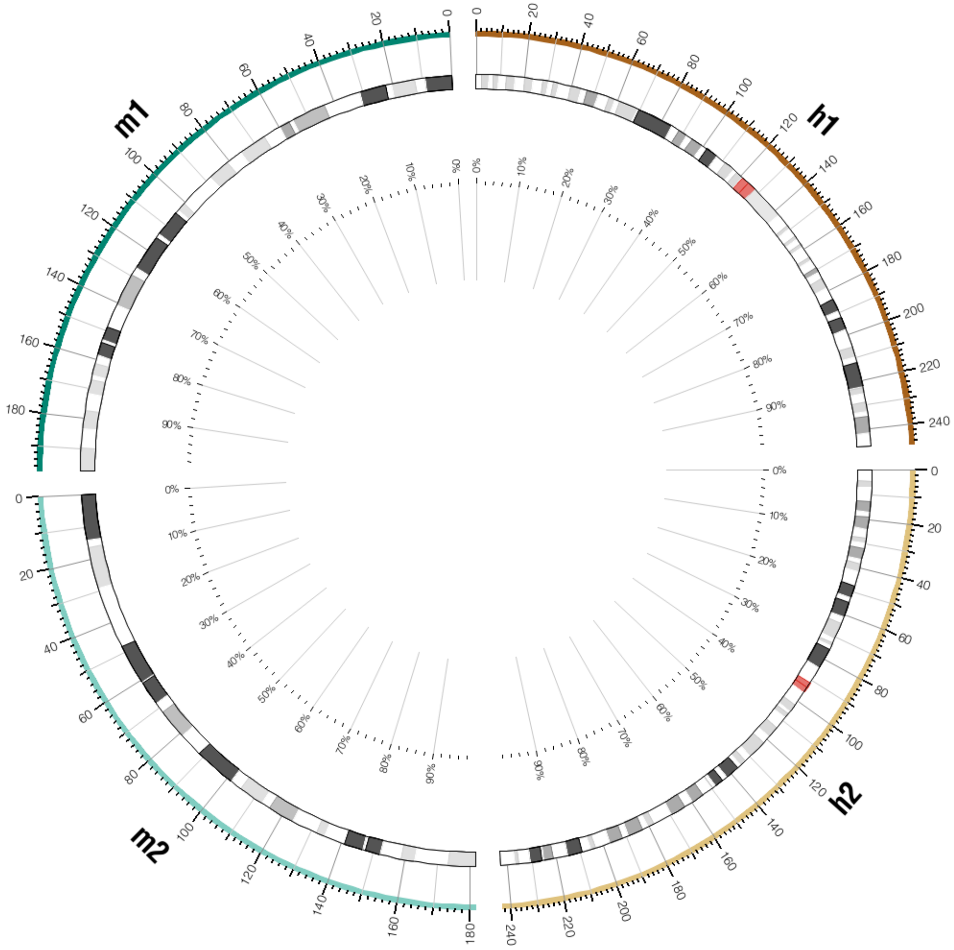
12 HIGHLIGHTS

sessions/2/12/etc/circos.conf

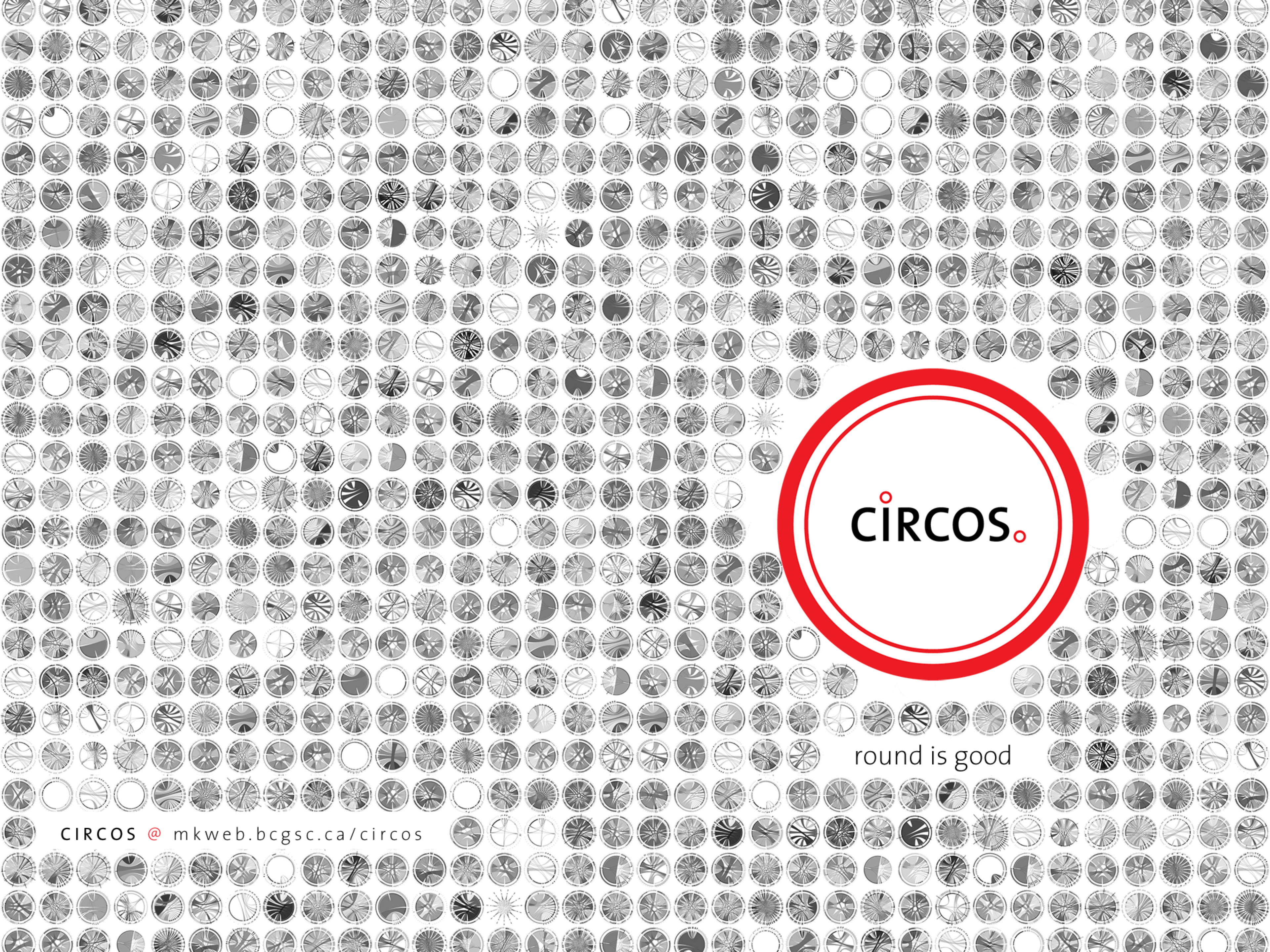
```
<highlights>
<highlight>
file = ../data/highlight.txt
r0   = 1r+40p
r1   = 1r+45p
</highlight>
</highlights>
```

sessions/2/data/highlight.txt

```
hs1 0 247249719 fill_color=bd2-1
hs2 0 242951149 fill_color=bd2-2
mm1 0 197195432 fill_color=bd2-4
mm2 0 181748087 fill_color=bd2-3
```



Highlight regions placed immediately inside the outer tick ring provide a visual color index for the ideograms.



circos

round is good

CIRCOS @ mkweb.bcgsc.ca/circos