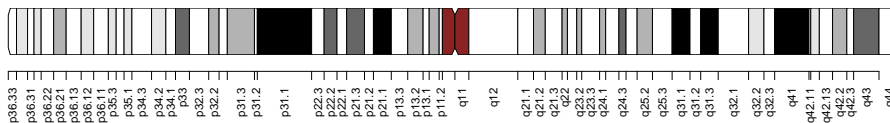# Plotting Idiograms

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This package is no longer actively developed and maintained largely for historical reasons.

1 Simple Usage

```
> library(SNPchip)
```

Plot an idiogram for chromosome 1 with labels for the bands on the x-axis.

```
> plotIdiogram("1", build="hg19", cex=0.8)
```


Suppressing labels:

```
> plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE)
```


With user-definded y-axis limits and y-coordinates for the idiogram:

```
> plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE, ylim=c(0,1), cytoband.ycoords=c(0.1, 0.
```


Plot an idiogram for all chromosomes.

```
> library(oligoClasses)
> sl <- getSequenceLengths("hg19")[c(paste("chr", 1:22, sep=""), "chrX", "chrY")]
> ybottom <- seq(0, 1, length.out=length(sl)) - 0.01
> ytop <- seq(0, 1, length.out=length(sl)) + 0.01
> for(i in seq_along(sl)){
+         chr <- names(sl)[i]
+         if(i == 1){
+                 plotIdiogram("1", build="hg19", cex=0.8, label.cytoband=FALSE, ylim=c(-0.05,1.05), cyt
```

```
+                               xlim=c(0, max(sl)))
+       }
+       if(i > 1){
+               plotIdiogram(names(sl)[i], build="hg19", cex=0.8, label.cytoband=FALSE, cytoband.ycoo
+       }
+ }
> axis(1, at=pretty(c(0, max(sl)), n=10), labels=pretty(c(0, max(sl)), n=10)/1e6, cex.axis=0.8)
> mtext("position (Mb)", 1, line=2)
> par(las=1)
> axis(2, at=ybottom+0.01, names(sl), cex.axis=0.6)
```
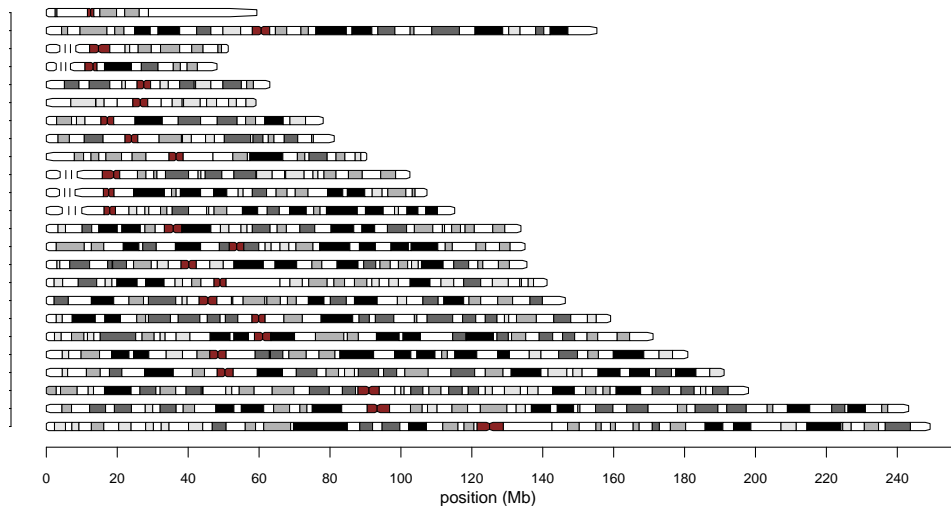

2 Session Information

The version number of R and packages loaded for generating the vignette were:

- R version 3.6.0 (2019-04-26), `x86_64-pc-linux-gnu`

- Locale: `LC_CTYPE=en_US.UTF-8`, `LC_NUMERIC=C`, `LC_TIME=en_US.UTF-8`, `LC_COLLATE=C`, `LC_MONETARY=en_US.UTF-8`, `LC_MESSAGES=en_US.UTF-8`, `LC_PAPER=en_US.UTF-8`, `LC_NAME=C`, `LC_ADDRESS=C`, `LC_TELEPHONE=C`, `LC_MEASUREMENT=en_US.UTF-8`, `LC_IDENTIFICATION=C`

- Running under: `Ubuntu 18.04.2 LTS`

- Matrix products: default

- BLAS: `/home/biocbuild/bbs-3.9-bioc/R/lib/libRblas.so`

- LAPACK: `/home/biocbuild/bbs-3.9-bioc/R/lib/libRlapack.so`

- Base packages: base, datasets, grDevices, graphics, methods, stats, utils

- Other packages: SNPchip 2.30.0, oligoClasses 1.46.0

- Loaded via a namespace (and not attached): Biobase 2.44.0, BiocGenerics 0.30.0, BiocManager 1.30.4, BiocParallel 1.18.0, Biostrings 2.52.0, DBI 1.0.0, DelayedArray 0.10.0, GenomeInfoDb 1.20.0, GenomeInfoDbData 1.2.1, GenomicRanges 1.36.0, IRanges 2.18.0, Matrix 1.2-17, RCurl 1.95-4.12, S4Vectors 0.22.0, SummarizedExperiment 1.14.0, XVector 0.24.0,

affyio 1.54.0, bit 1.1-14, bitops 1.0-6, codetools 0.2-16, compiler 3.6.0, ff 2.2-14, foreach 1.4.4, grid 3.6.0, iterators 1.0.10, lattice 0.20-38, matrixStats 0.54.0, parallel 3.6.0, stats4 3.6.0, tools 3.6.0, zlibbioc 1.30.0