

# Plotting Idiograms

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April 24, 2017

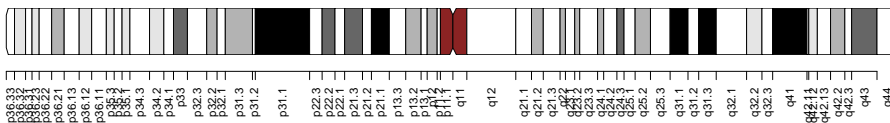
This package is no longer actively developed and maintained largely for historical reasons.

## 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-defined 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, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0))
```



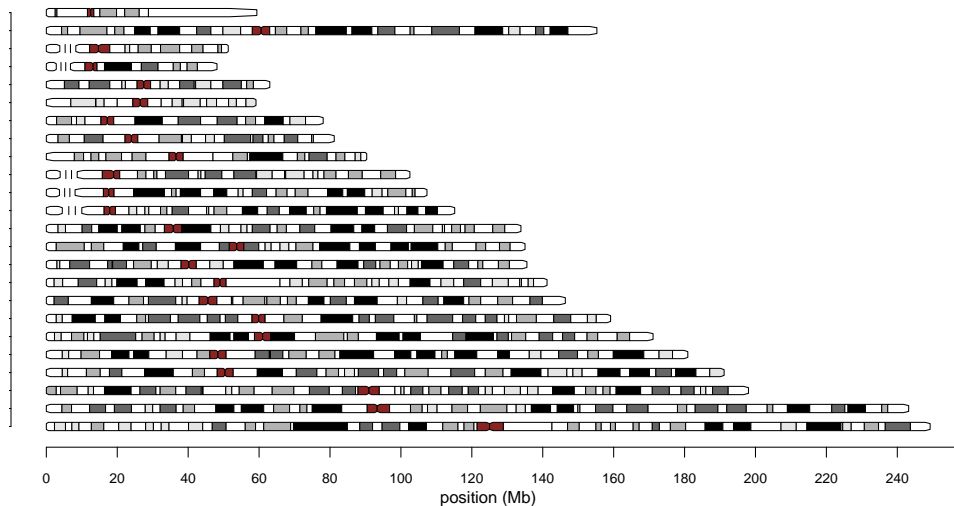
Plot an idiogram for all chromosomes.

```
> 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), cytoband.ycoords=c(0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0))
+   }
+ }
```

```

+             xlim=c(0, max(sl)))
+         }
+         if(i > 1){
+             plotIdiogram(names(sl)[i], build="hg19", cex=0.8, label.cytoband=FALSE, cytoband.ycoord=i)
+         }
+     }
> 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 3.4.0 (2017-04-21), 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 16.04.2 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.5-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.5-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: SNPchip 2.22.0, oligoClasses 1.38.0
- Loaded via a namespace (and not attached): Biobase 2.36.0, BiocGenerics 0.22.0, BiocInstaller 1.26.0, Biostrings 2.44.0, DBI 0.6-1, DelayedArray 0.2.0, GenomeInfoDb 1.12.0, GenomeInfoDbData 0.99.0, GenomicRanges 1.28.0, IRanges 2.10.0, Matrix 1.2-9, RCurl 1.95-4.8, RSQLite 1.1-2, Rcpp 0.12.10, S4Vectors 0.14.0, SummarizedExperiment 1.6.0, XVector 0.16.0,

affyio 1.46.0, bit 1.1-12, bitops 1.0-6, codetools 0.2-15, compiler 3.4.0, digest 0.6.12, ff 2.2-13, foreach 1.4.3, grid 3.4.0, iterators 1.0.8, lattice 0.20-35, matrixStats 0.52.2, memoise 1.1.0, parallel 3.4.0, stats4 3.4.0, tools 3.4.0, zlibbioc 1.22.0