

Plotting Idiograms

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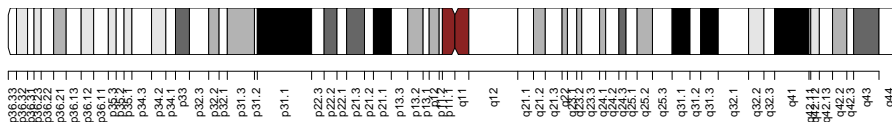
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1 Simple Usage

```
> 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))
```



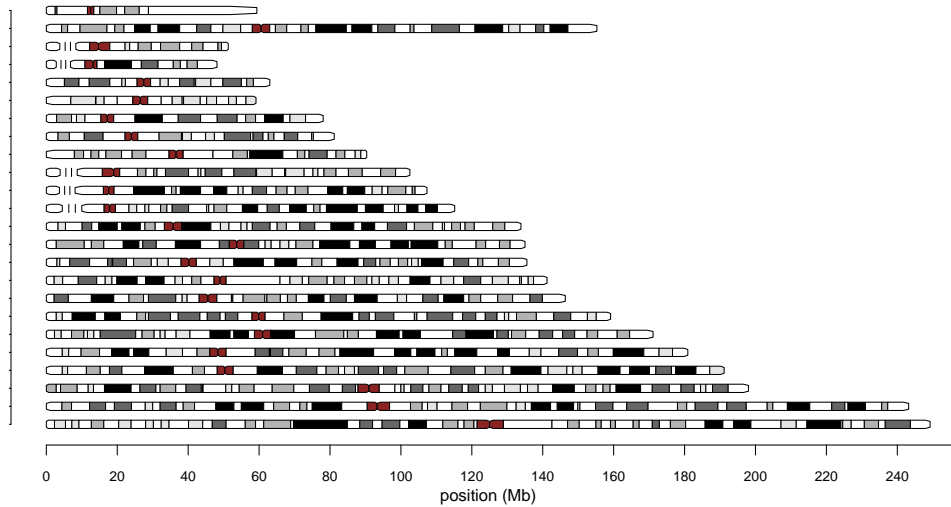
Plot an idiogram for all chromosomes.

```
> 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), cy
+       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 3.2.0 RC (2015-04-08 r68161), x86_64-apple-darwin10.8.0
- Locale: en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: oligoClasses 1.30.0, SNPchip 2.14.0
- Loaded via a namespace (and not attached): affyio 1.36.0, Biobase 2.28.0, BiocGenerics 0.14.0, BiocInstaller 1.18.1, Biostrings 2.36.0, bit 1.1-12, codetools 0.2-11, DBI 0.3.1, ff 2.2-13, foreach 1.4.2, GenomeInfoDb 1.4.0, GenomicRanges 1.20.0, grid 3.2.0, IRanges 2.2.0, iterators 1.0.7, lattice 0.20-31, parallel 3.2.0, RSQLite 1.0.0, S4Vectors 0.6.0, stats4 3.2.0, tools 3.2.0, XVector 0.8.0, zlibbioc 1.14.0