**Codes for examples**

The codes used to get the Fig. 1 and 2 using example data contained in the package *RIdeogram*. For more detailed information about the parameter settings and general applications of this package, users can refer to the tutorial vignette (vignette("RIdeogram")).

**Figure 1**

First, we load the package:

>library(RIdeogram)

Then, we load the human karyotype information, gene density data and positions of 500 random RNAs:

>data(human_ karyotype, package = "RIdeogram")
>data(gene_density, package = "RIdeogram")
>data(Random_RNAs_500, package = "RIdeogram")

Next, we can use the function to *ideogram* get the SVG file:

>ideogram(karyotype = human_karyotype, overlaid = gene_density, label = Random_RNAs_500)

And, we will get a SVG file in the current working directory. We can get the current working directory information using the following code:

>getwd()

We can use the software Adobe Illustrator or Inkscape to view this SVG file that contains a vector graphic. Or, we can use the function *convertSVG* to convert this SVG file into an image file:

> convertSVG("chromosome.svg", device = "png")

Finally, we will get the gene distribution plot which is displayed in Fig. 1.

**Figure 2**

First, we load the package:

>library(RIdeogram)

Then, we load the human karyotype information, gene and LTR density data:

>data(human_ karyotype, package = "RIdeogram")
>data(gene_density, package = "RIdeogram")
>data(LTR_density, package = "RIdeogram")

Next, we use the function to *ideogram* get the SVG file:

> ideogram(karyotype = human_karyotype, overlaid = gene_density, label = LTR_density,
colorset1 = c("#fee090", "#fdae61", "#f46d43", "#d73027", "#a50026"), colorset2 = c("#e0f3f8",
"#abd9e9", "#74add1", "#4575b4", "#313695"))

After that, we use the function *convertSVG* to convert this SVG file into an image file:

> convertSVG("chromosome.svg", device = "png")

Finally, we get the comparison plot of gene and LTR distribution which is displayed in Fig. 2.