

Problem 8.4

Jonathan Pevsner, Bioinformatics and Functional Genomics (August, 2015). Modified by kd91 (Feb,2020)

In this exercise we will use the R package **GenomeGraphs** in RStudio to plot the structure of the beta globin gene, and plot the position of this gene on an ideogram of chromosome 11.

```
setwd(getwd())
```

Install GenomeGraphs and open its library.

```
# source("http://bioconductor.org/biocLite.R")
# biocLite("GenomeGraphs")

# if (!requireNamespace("BiocManager", quietly = TRUE))
#   install.packages("BiocManager")
# BiocManager::install(c("GenomicFeatures"))
options(width=100)
library(GenomeGraphs)

## Loading required package: biomaRt

## Warning: package 'biomaRt' was built under R version 3.6.3

## Loading required package: grid

## Warning: Package 'GenomeGraphs' is deprecated and will be removed from
Bioconductor version 3.11
```

Use biomaRt to obtain a gene structure that we will plot.

```
mart <- useMart("ensembl", dataset="hsapiens_gene_ensembl")
gene <- makeGene(id = "ENSG00000128731", type="ensembl_gene_id", biomaRt =
mart)

## Cache found

gdPlot(gene) # save the output as Rplot1 (a .png file)
```



#reference for herc2 gene:

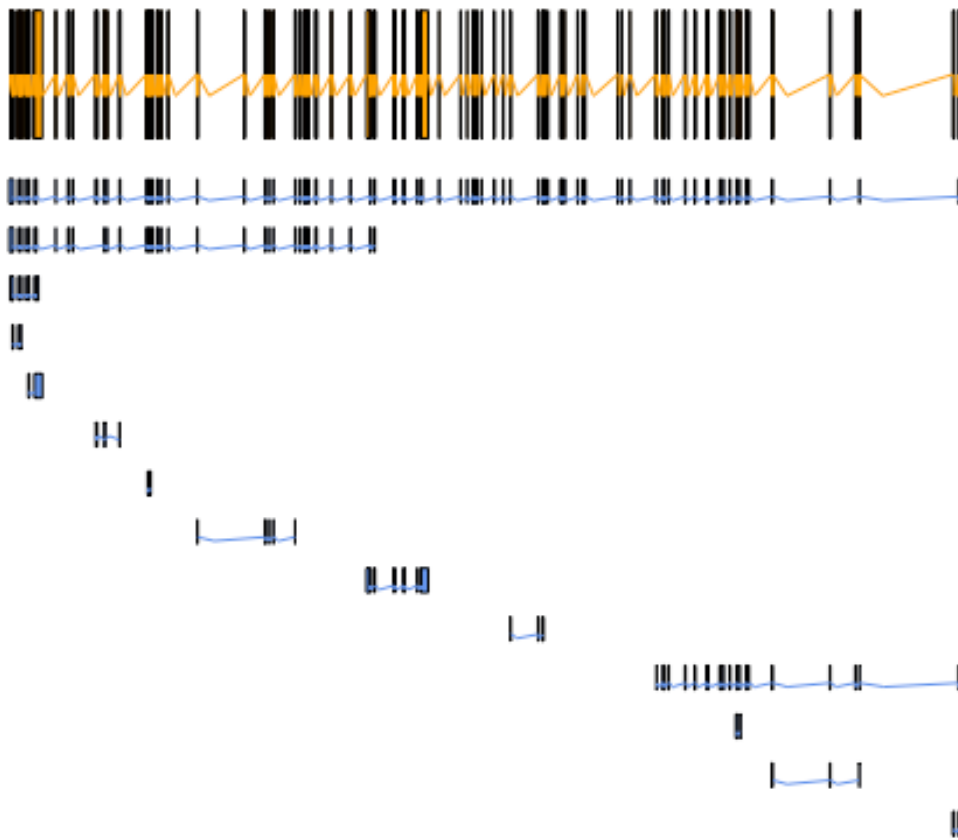
https://uswest.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSG00000128731;r=15:28111040-28322172

Next plot transcripts associated with this gene. Save the output as Rplot2 (a .png file).

```
transcript <- makeTranscript(id = "ENSG00000128731", type="ensembl_gene_id",  
biomart = mart)
```

```
## Cache found
```

```
gdPlot(list(gene, transcript))
```

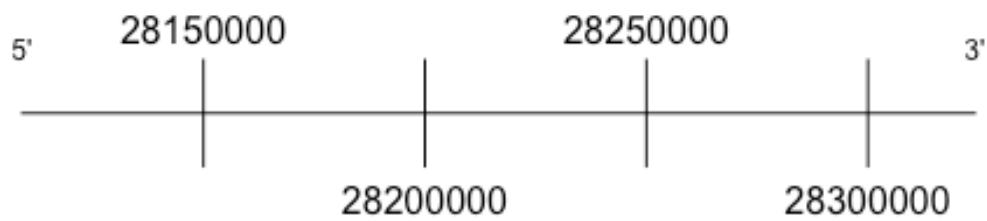


Define the genomic region. The resulting plot has brown boxes for [exons] and genomic coordinates. Save it as Rplot3.

```
minusStrand <- makeGeneRegion(chromosome = 15, start = 28111040, end = 28322172, strand = "-", biomaRt = mart)
```

```
## Cache found
```

```
genomeAxis <- makeGenomeAxis(add53 = TRUE) # Add53 shows 5' and 3' ends
gdPlot(list(genomeAxis, minusStrand))
```

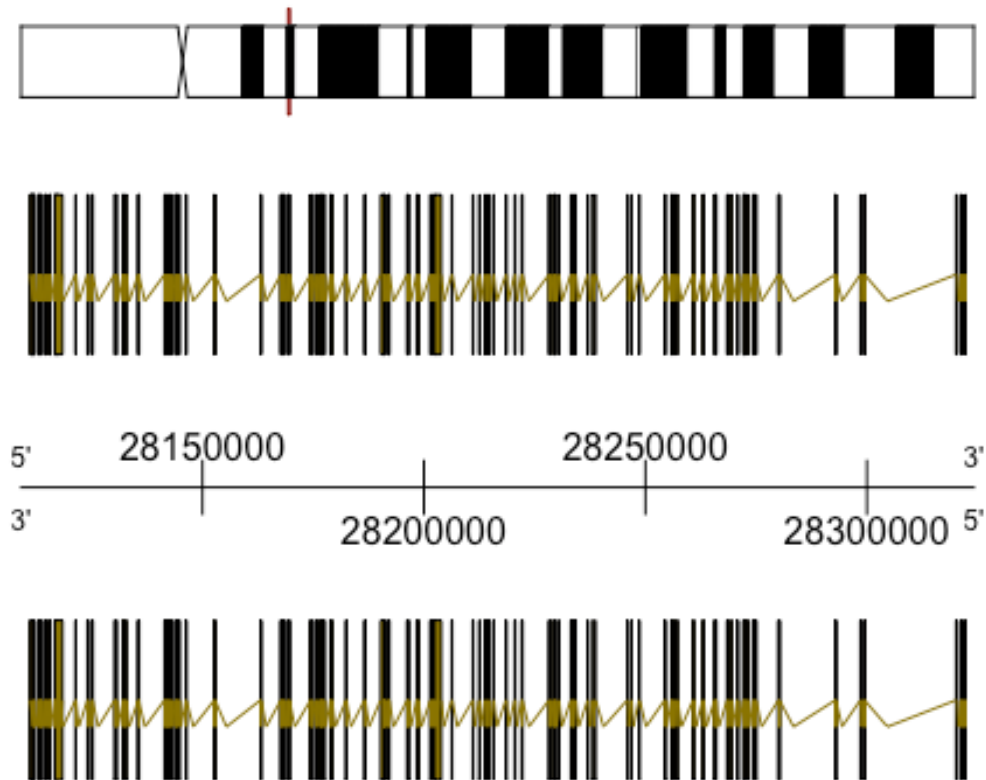


Add an ideogram of chromosome 15 to the plot.

```
minStrand <- makeGeneRegion( chromosome = 15, start = 28111040, end =
28111040, strand = "-", biomaRt = mart)
```

```
## Cache found
```

```
ideogram <- makeIdeogram(chromosome = 15)
genomeAxis <- makeGenomeAxis(add53=TRUE, add35=TRUE)
gdPlot(list(ideogram, minStrand, genomeAxis, minStrand))
```



save as Rplot4.png

Show the session information

`sessionInfo()`

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.5
##
## Matrix products: default
## BLAS:
## /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK:
## /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] grid      stats    graphics grDevices utils    datasets methods
## base
##
## other attached packages:
```

```

## [1] GenomeGraphs_1.46.0 biomaRt_2.42.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.4          pillar_1.4.3        compiler_3.6.1
dbplyr_1.4.3
## [5] prettyunits_1.1.1   tools_3.6.1         progress_1.2.2
digest_0.6.25
## [9] bit_1.1-15.2        lifecycle_0.2.0     tibble_3.0.1
RSQLite_2.2.0
## [13] evaluate_0.14       memoise_1.1.0       BiocFileCache_1.10.2
pkgconfig_2.0.3
## [17] rlang_0.4.5         DBI_1.1.0           curl_4.3
yaml_2.2.1
## [21] parallel_3.6.1      xfun_0.13           dplyr_0.8.5
stringr_1.4.0
## [25] httr_1.4.1          knitr_1.28          rappdirs_0.3.1
S4Vectors_0.24.4
## [29] vctrs_0.2.4         askpass_1.1         IRanges_2.20.2
hms_0.5.3
## [33] tidyselect_1.0.0    stats4_3.6.1        bit64_0.9-7
glue_1.4.0
## [37] Biobase_2.46.0      R6_2.4.1            AnnotationDbi_1.48.0
XML_3.99-0.3
## [41] rmarkdown_2.1       purrr_0.3.4         blob_1.2.1
magrittr_1.5
## [45] codetools_0.2-16    ellipsis_0.3.0      htmltools_0.4.0
BiocGenerics_0.32.0
## [49] assertthat_0.2.1    stringi_1.4.6       openssl_1.4.1
crayon_1.3.4

```