Using the PACViR Pipeline

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1 Introduction

The PACViR pipeline generates a visualization of a plastome in a circular fashion. This vignette provides two examples of how to execute PACViR via the R function 'PACViR.complete()' and via bash.

2 Requirements

To execute PACViR several requirements have to be installed.

```
>       #require(PACViR)
>       require(RCircos)
>       require(genbankr)
>       require(optparse)
```

3 PACViR via R-function

PACViR can be easily executed via the PACViR.complete() function in R. Therefore one can load the provided data from the package.

```
>       gbk.file <- "./SCHM2.gb"
>       bam.file <- "./SCHM2.bam"
>       windowSize <- 250
>       mosdepthCmd <- "mosdepth"
>       threshold <- 25
>       outDir <- "./output"
>       #PACViR.complete(gbk.file, bam.file, windowSize, mosdepthCmd, threshold, outDir)
```
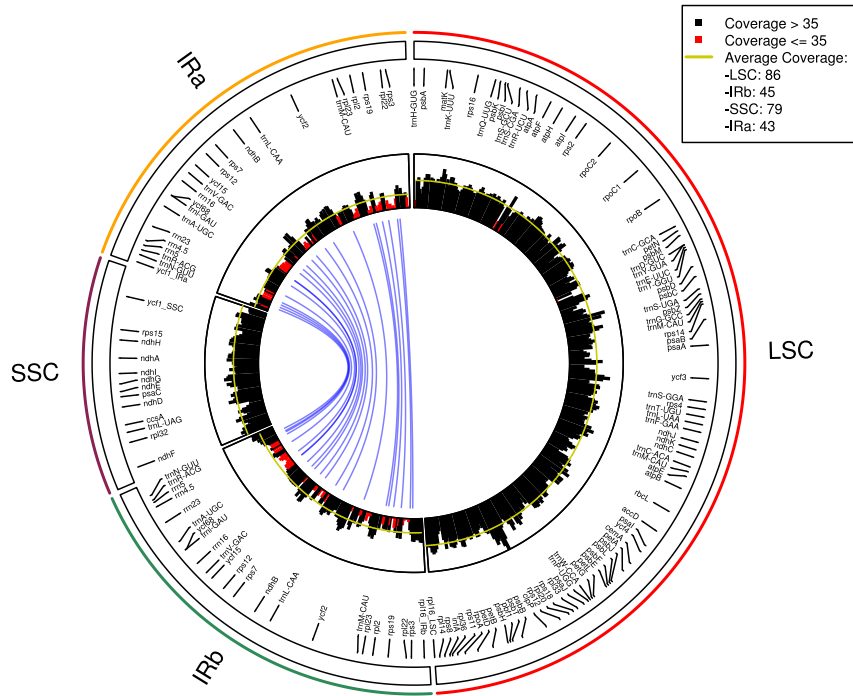
Figure 1: Visualization of SCHM2 plastome with PACViR.complete()

4 PACViR via command line

Execute PACViR_Rscript.R via command line with Rscript.

```
Rscript PACViR_Rscript.R  -k ../inst/extdata/DAS01.gb -b ../inst/extdata/DAS01.bam
```
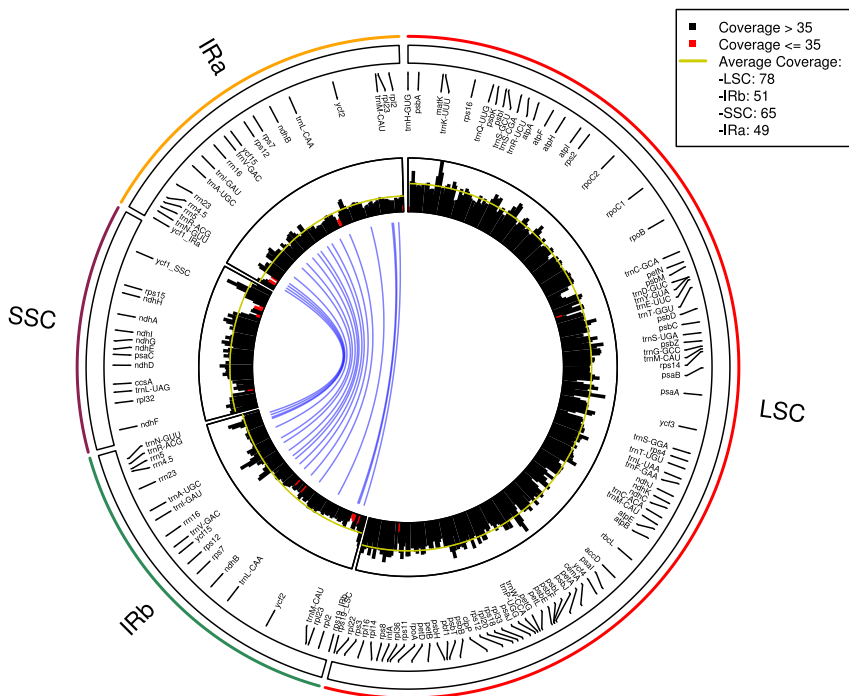
Figure 2: Visualization of DAS01 plastome with Rscript

5 Modifying parameters

Depending on which system PACViR will be executed

6 More Information

7 sessionInfo

```
> sessionInfo()

R version 3.3.3 (2017-03-06)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Debian GNU/Linux 9 (stretch)

locale:
[1] C
```

```
attached base packages:
[1] stats      graphics  grDevices utils     datasets
[6] methods    base

other attached packages:
[1] optparse_1.6.0 genbankr_1.2.1 RCircos_1.2.0

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.0                AnnotationDbi_1.36.2
 [3] XVector_0.14.1           GenomicAlignments_1.10.0
 [5] GenomicRanges_1.26.4     BiocGenerics_0.20.0
 [7] zlibbioc_1.20.0          IRanges_2.8.2
 [9] getopt_1.20.2            BiocParallel_1.8.2
[11] bit_1.1-14               BSgenome_1.42.0
[13] lattice_0.20-35          blob_1.1.1
[15] GenomeInfoDb_1.10.3      tools_3.3.3
[17] grid_3.3.3               SummarizedExperiment_1.4.0
[19] parallel_3.3.3           Biobase_2.34.0
[21] DBI_1.0.0                bit64_0.9-7
[23] digest_0.6.11            Matrix_1.2-7.1
[25] rtracklayer_1.34.1       S4Vectors_0.12.2
[27] bitops_1.0-6             RCurl_1.95-4.8
[29] biomaRt_2.30.0           memoise_1.1.0
[31] RSQLite_2.1.1            Rsamtools_1.26.2
[33] GenomicFeatures_1.26.2   Biostrings_2.42.1
[35] stats4_3.3.3             XML_3.98-1.5
[37] VariantAnnotation_1.20.2
```