

# VAR-Seq workflow template: Some Descriptive Title

**Project ID: VARseq\_PI\_Name\_Organism\_Jul2015**

Project PI: First Last (first.last@inst.edu)

Author of Report: First Last (first.last@inst.edu)

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## Contents

1	Introduction . . . . .	2
1.1	Background and objectives . . . . .	2
1.2	Experimental design . . . . .	2
2	Load workflow environment . . . . .	2
2.1	Load packages and sample data . . . . .	2
2.2	Experiment definition provided by <code>targets</code> file . . . . .	3
3	Read preprocessing . . . . .	4
3.1	Read quality filtering and trimming . . . . .	4
3.2	FASTQ quality report . . . . .	4
4	Alignments . . . . .	5
4.1	Read mapping with <code>BWA</code> . . . . .	5
4.2	Read mapping with <code>gsnap</code> . . . . .	5
4.3	Read and alignment stats . . . . .	6
4.4	Create symbolic links for viewing BAM files in IGV . . . . .	6
5	Variant calling . . . . .	6
5.1	Variant calling with <code>GATK</code> . . . . .	6
5.2	Variant calling with <code>BCFtools</code> . . . . .	7
5.3	Variant calling with <code>VariantTools</code> . . . . .	7
6	Filter variants . . . . .	7
6.1	Filter variants called by <code>GATK</code> . . . . .	8
6.2	Filter variants called by <code>BCFtools</code> . . . . .	8
6.3	Filter variants called by <code>VariantTools</code> . . . . .	8

<i>systemPipeR</i> VAR-Seq Workflow	2	Load workflow environment	8
7	Annotate filtered variants		8
7.1	Annotate filtered variants called by GATK		9
7.2	Annotate filtered variants called by BCFtools		9
7.3	Annotate filtered variants called by <i>VariantTools</i>		9
8	Combine annotation results among samples		9
8.1	Combine results from <i>GATK</i>		9
8.2	Combine results from <i>BCFtools</i>		9
8.3	Combine results from <i>VariantTools</i>		10
9	Summary statistics of variants		10
9.1	Summary for <i>GATK</i>		10
9.2	Summary for <i>BCFtools</i>		10
9.3	Summary for <i>VariantTools</i>		10
10	Venn diagram of variants		10
11	Version Information		11
12	Funding		12
13	References		12

# 1 Introduction

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## 1.1 Background and objectives

This report describes the analysis of a VAR-Seq project studying the genetic differences among several strains ... from *organism* ....

## 1.2 Experimental design

Typically, users want to specify here all information relevant for the analysis of their NGS study. This includes detailed descriptions of FASTQ files, experimental design, reference genome, gene annotations, etc.

# 2 Load workflow environment

---

## 2.1 Load packages and sample data

The *systemPipeR* package needs to be loaded to perform the analysis steps shown in this report (Girke, 2014).

```
library(systemPipeR)
```

Load workflow environment with sample data into your current working directory. The sample data are described [here](#).

```
library(systemPipeRdata)
genWorkenvir(workflow="varseq")
setwd("varseq")
```

In the workflow environments generated by `genWorkenvir` all data inputs are stored in a `data/` directory and all analysis results will be written to a separate `results/` directory, while the `systemPipeVARseq.Rnw` script and the `targets` file are expected to be located in the parent directory. The R session is expected to run from this parent directory. Additional parameter files are stored under `param/`.

To work with real data, users want to organize their own data similarly and substitute all test data for their own data. To rerun an established workflow on new data, the initial `targets` file along with the corresponding FASTQ files are usually the only inputs the user needs to provide.

If applicable users can load custom functions not provided by `systemPipeR`. Skip this step if this is not the case.

```
source("systemPipeVARseq_Fct.R")
```

## 2.2 Experiment definition provided by `targets` file

The `targets` file defines all FASTQ files and sample comparisons of the analysis workflow.

```
targetspath <- system.file("extdata", "targetsPE.txt", package="systemPipeR")
targets <- read.delim(targetspath, comment.char = "#")[,1:5]
targets
```

	FileName1	FileName2	SampleName	Factor	SampleLong
1	./data/SRR446027_1.fastq	./data/SRR446027_2.fastq	M1A	M1	Mock.1h.A
2	./data/SRR446028_1.fastq	./data/SRR446028_2.fastq	M1B	M1	Mock.1h.B
3	./data/SRR446029_1.fastq	./data/SRR446029_2.fastq	A1A	A1	Avr.1h.A
4	./data/SRR446030_1.fastq	./data/SRR446030_2.fastq	A1B	A1	Avr.1h.B
5	./data/SRR446031_1.fastq	./data/SRR446031_2.fastq	V1A	V1	Vir.1h.A
6	./data/SRR446032_1.fastq	./data/SRR446032_2.fastq	V1B	V1	Vir.1h.B
7	./data/SRR446033_1.fastq	./data/SRR446033_2.fastq	M6A	M6	Mock.6h.A
8	./data/SRR446034_1.fastq	./data/SRR446034_2.fastq	M6B	M6	Mock.6h.B
9	./data/SRR446035_1.fastq	./data/SRR446035_2.fastq	A6A	A6	Avr.6h.A
10	./data/SRR446036_1.fastq	./data/SRR446036_2.fastq	A6B	A6	Avr.6h.B
11	./data/SRR446037_1.fastq	./data/SRR446037_2.fastq	V6A	V6	Vir.6h.A
12	./data/SRR446038_1.fastq	./data/SRR446038_2.fastq	V6B	V6	Vir.6h.B
13	./data/SRR446039_1.fastq	./data/SRR446039_2.fastq	M12A	M12	Mock.12h.A
14	./data/SRR446040_1.fastq	./data/SRR446040_2.fastq	M12B	M12	Mock.12h.B
15	./data/SRR446041_1.fastq	./data/SRR446041_2.fastq	A12A	A12	Avr.12h.A
16	./data/SRR446042_1.fastq	./data/SRR446042_2.fastq	A12B	A12	Avr.12h.B
17	./data/SRR446043_1.fastq	./data/SRR446043_2.fastq	V12A	V12	Vir.12h.A

```
18 ./data/SRR446044_1.fastq ./data/SRR446044_2.fastq V12B V12 Vir.12h.B
```

## 3 Read preprocessing

### 3.1 Read quality filtering and trimming

The following removes reads with low quality base calls (here Phred scores below 20) from all FASTQ files.

```
args <- systemArgs(sysma="param/trimPE.param", mytargets="targetsPE.txt")[1:4] # Note: subsetting!
filterFct <- function(fq, cutoff=20, Nexceptions=0) {
  qcount <- rowSums(as(quality(fq), "matrix") <= cutoff)
  fq[qcount <= Nexceptions] # Retains reads where Phred scores are >= cutoff with N exceptions
}
preprocessReads(args=args, Fct="filterFct(fq, cutoff=20, Nexceptions=0)", batchsize=100000)
writeTargetsout(x=args, file="targets_PETrim.txt", overwrite=TRUE)
```

### 3.2 FASTQ quality report

The following `seeFastq` and `seeFastqPlot` functions generate and plot a series of useful quality statistics for a set of FASTQ files including per cycle quality box plots, base proportions, base-level quality trends, relative k-mer diversity, length and occurrence distribution of reads, number of reads above quality cutoffs and mean quality distribution. The results are written to a PDF file named `fastqReport.pdf`.

```
args <- systemArgs(sysma="bwa.param", mytargets="targets.txt")
fqlist <- seeFastq(fastq=infile1(args), batchsize=100000, klength=8)
pdf("./results/fastqReport.pdf", height=18, width=4*length(fqlist))
seeFastqPlot(fqlist)
dev.off()
```

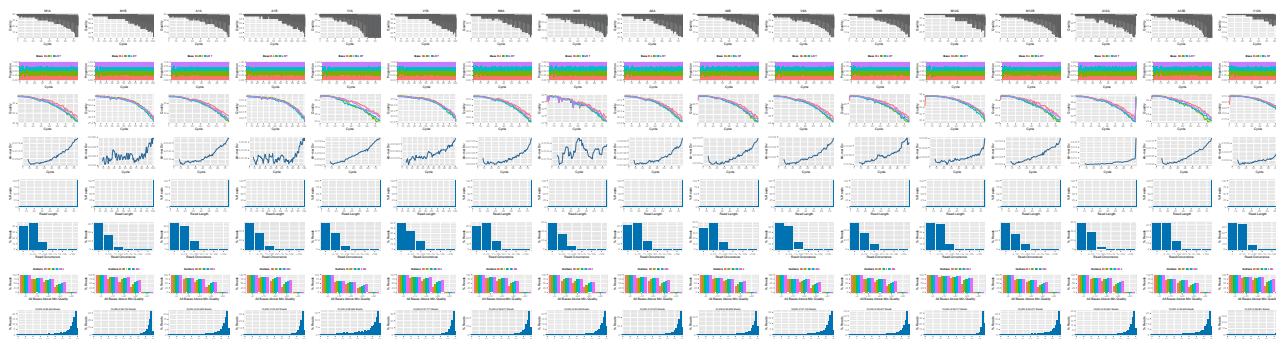


Figure 1: QC report for 18 FASTQ files

## 4 Alignments

### 4.1 Read mapping with BWA

The NGS reads of this project are aligned against the reference genome sequence using the highly variant tolerant short read aligner BWA (Li, 2013; Li and Durbin, 2009). The parameter settings of the aligner are defined in the `bwa.param` file.

```
args <- systemArgs(sysma="bwa.param", mytargets="targets.txt")
sysargs(args)[1] # Command-line parameters for first FASTQ file
```

Runs the alignments sequentially (e.g. on a single machine)

```
bampaths <- runCommandline(args=args)
```

Alternatively, the alignment jobs can be submitted to a compute cluster, here using 72 CPU cores (18 qsub processes each with 4 CPU cores).

```
moduleload(modules(args))
system("bwa index -a bwtsv ./data/tair10.fasta")
resources <- list(walltime="20:00:00", nodes=paste0("1:ppn=", cores(args)), memory="10gb")
reg <- clusterRun(args, conffile=".BatchJobs.R", template="torque.tpl", Njobs=18, runid="01",
  resourceList=resources)
waitForJobs(reg)
```

Check whether all BAM files have been created

```
file.exists(outpaths(args))
```

### 4.2 Read mapping with gsnap

An alternative variant tolerant aligner is `gsnap` from the `gmapR` package (Wu and Nacu, 2010). The following code shows how to run this aligner on multiple nodes of a compute cluster that uses Torque as scheduler.

```
library(gmapR); library(BiocParallel); library(BatchJobs)
gmapGenome <- GmapGenome(reference(args), directory="data", name="gmap_tair10chr", create=TRUE)
args <- systemArgs(sysma="gsnap.param", mytargets="targetsPE.txt")
f <- function(x) {
  library(gmapR); library(systemPipeR)
  args <- systemArgs(sysma="gsnap.param", mytargets="targetsPE.txt")
  gmapGenome <- GmapGenome(reference(args), directory="data", name="gmap_tair10chr", create=FALSE)
  p <- GsnapParam(genome=gmapGenome, unique_only=TRUE, molecule="DNA", max_mismatches=3)
  o <- gsnap(input_a=infile1(args)[x], input_b=infile2(args)[x], params=p, output=outfile1(args)[x])
}
funs <- makeClusterFunctionsTorque("torque.tpl")
param <- BatchJobsParam(length(args), resources=list(walltime="20:00:00", nodes="1:ppn=1", memory="6gb"), cl
register(param)
d <- bplapply(seq(along=args), f)
writeTargetsout(x=args, file="targets_gsnap_bam.txt")
```

## 4.3 Read and alignment stats

The following generates a summary table of the number of reads in each sample and how many of them aligned to the reference.

```
read_statsDF <- alignStats(args=args)
write.table(read_statsDF, "results/alignStats.xls", row.names=FALSE, quote=FALSE, sep="\t")
```

## 4.4 Create symbolic links for viewing BAM files in IGV

The `symLink2bam` function creates symbolic links to view the BAM alignment files in a genome browser such as IGV. The corresponding URLs are written to a file with a path specified under `urlfile`, here `IGVurl.txt`.

```
symLink2bam(sysargs=args, htmldir=c("~/html/", "somedir/"),
            urlbase="http://biocluster.ucr.edu/~tgirke/",
            urlfile="./results/IGVurl.txt")
```

# 5 Variant calling

The following performs variant calling with GATK, BCFtools and *VariantTools* in parallel mode on a compute cluster (McKenna et al., 2010; Li, 2011). If a cluster is not available, the `runCommandline()` function can be used to run the variant calling with GATK and BCFtools for each sample sequentially on a single machine, or `callVariants` in case of *VariantTools*. Typically, the user would choose here only one variant caller rather than running several ones.

## 5.1 Variant calling with GATK

The following creates in the initial step a new targets file (`targets_bam.txt`). The first column of this file gives the paths to the BAM files created in the alignment step. The new targets file and the parameter file `gatk.param` are used to create a new `SYSargs` instance for running GATK. Since GATK involves many processing steps, it is executed by a bash script `gatk_run.sh` where the user can specify the detailed run parameters. All three files are expected to be located in the current working directory. Samples files for `gatk.param` and `gatk_run.sh` are available in the subdirectory `./inst/extdata/` of the source file of the *systemPipeR* package. Alternatively, they can be downloaded directly from [here](#).

```
writeTargetsout(x=args, file="targets_bam.txt")
system("java -jar CreateSequenceDictionary.jar R=./data/tair10.fasta O=./data/tair10.dict")
# system("java -jar /opt/picard/1.81/CreateSequenceDictionary.jar R=./data/tair10.fasta O=./data/tair10.dict")
args <- systemArgs(sysma="gatk.param", mytargets="targets_bam.txt")
resources <- list(walltime="20:00:00", nodes=paste0("1:ppn=", 1), memory="10gb")
reg <- clusterRun(args, conffile=".BatchJobs.R", template="torque.tpl", Njobs=18, runid="01",
                 resourceList=resources)
waitForJobs(reg)
writeTargetsout(x=args, file="targets_gatk.txt")
```

## 5.2 Variant calling with BCFtools

The following runs the variant calling with BCFtools. This step requires in the current working directory the parameter file `sambcf.param` and the bash script `sambcf_run.sh`.

```
args <- systemArgs(sysma="sambcf.param", mytargets="targets_bam.txt")
resources <- list(walltime="20:00:00", nodes=paste0("1:ppn=", 1), memory="10gb")
reg <- clusterRun(args, conffile=".BatchJobs.R", template="torque.tpl", Njobs=18, runid="01",
  resourceList=resources)
waitForJobs(reg)
writeTargetsout(x=args, file="targets_sambcf.txt")
```

## 5.3 Variant calling with VariantTools

```
library(gmapR); library(BiocParallel); library(BatchJobs)
args <- systemArgs(sysma="vartools.param", mytargets="targets_gsnap_bam.txt")
f <- function(x) {
  library(VariantTools); library(gmapR); library(systemPipeR)
  args <- systemArgs(sysma="vartools.param", mytargets="targets_gsnap_bam.txt")
  gmapGenome <- GmapGenome(systemPipeR::reference(args), directory="data", name="gmap_tair10chr", create=FALSE)
  tally.param <- TallyVariantsParam(gmapGenome, high_base_quality = 23L, indels = TRUE)
  bfl <- BamFileList(infile1(args)[x], index=character())
  var <- callVariants(bfl[[1]], tally.param)
  sampleNames(var) <- names(bfl)
  writeVcf(asVCF(var), outfile1(args)[x], index = TRUE)
}
funs <- makeClusterFunctionsTorque("torque.tpl")
param <- BatchJobsParam(length(args), resources=list(walltime="20:00:00", nodes="1:ppn=1", memory="6gb"), cluster=funs)
register(param)
d <- bplapply(seq(along=args), f)
writeTargetsout(x=args, file="targets_vartools.txt")
```

## 6 Filter variants

The function `filterVars` filters VCF files based on user definable quality parameters. It sequentially imports each VCF file into R, applies the filtering on an internally generated `VRanges` object and then writes the results to a new subsetted VCF file. The filter parameters are passed on to the corresponding argument as a character string. The function applies this filter to the internally generated `VRanges` object using the standard subsetting syntax for two dimensional objects such as: `vr[filter, ]`. The parameter files (`filter_gatk.param`, `filter_sambcf.param` and `filter_vartools.param`), used in the filtering steps, define the paths to the input and output VCF files which are stored in new `SYSargs` instances.

## 6.1 Filter variants called by GATK

The below example filters for variants that are supported by  $\geq x$  reads and  $\geq 80\%$  of them support the called variants. In addition, all variants need to pass  $\geq x$  of the soft filters recorded in the VCF files generated by GATK. Since the toy data used for this workflow is very small, the chosen settings are unreasonably relaxed. A more reasonable filter setting is given in the line below (here commented out).

```
library(VariantAnnotation)
args <- systemArgs(sysma="filter_gatk.param", mytargets="targets_gatk.txt")
filter <- "totalDepth(vr) >= 2 & (altDepth(vr) / totalDepth(vr) >= 0.8) & rowSums(softFilterMatrix(vr))>=1"
# filter <- "totalDepth(vr) >= 20 & (altDepth(vr) / totalDepth(vr) >= 0.8) & rowSums(softFilterMatrix(vr))>=1"
filterVars(args, filter, varcaller="gatk", organism="A. thaliana")
writeTargetsout(x=args, file="targets_gatk_filtered.txt")
```

## 6.2 Filter variants called by BCFtools

The following shows how to filter the VCF files generated by *BCFtools* using similar parameter settings as in the previous filtering of the GATK results.

```
args <- systemArgs(sysma="filter_sambcf.param", mytargets="targets_sambcf.txt")
filter <- "rowSums(vr) >= 2 & (rowSums(vr[,3:4])/rowSums(vr[,1:4]) >= 0.8)"
# filter <- "rowSums(vr) >= 20 & (rowSums(vr[,3:4])/rowSums(vr[,1:4]) >= 0.8)"
filterVars(args, filter, varcaller="bcftools", organism="A. thaliana")
writeTargetsout(x=args, file="targets_sambcf_filtered.txt")
```

## 6.3 Filter variants called by VariantTools

The following shows how to filter the VCF files generated by *VariantTools* using similar parameter settings as in the previous filtering of the GATK results.

```
args <- systemArgs(sysma="filter_vartools.param", mytargets="targets_vartools.txt")
filter <- "(values(vr)$n.read.ref + values(vr)$n.read.pos) >= 2 & (values(vr)$n.read.pos / (values(vr)$n.read.ref + values(vr)$n.read.pos) >= 0.8)"
# filter <- "(values(vr)$n.read.ref + values(vr)$n.read.pos) >= 20 & (values(vr)$n.read.pos / (values(vr)$n.read.ref + values(vr)$n.read.pos) >= 0.8)"
filterVars(args, filter, varcaller="vartools", organism="A. thaliana")
writeTargetsout(x=args, file="targets_vartools_filtered.txt")
```

# 7 Annotate filtered variants

The function `variantReport` generates a variant report using utilities provided by the *VariantAnnotation* package. The report for each sample is written to a tabular file containing genomic context annotations (e.g. coding or non-coding SNPs, amino acid changes, IDs of affected genes, etc.) along with confidence statistics for each variant. The parameter file `annotate_vars.param` defines the paths to the input and output files which are stored in a new `SYSargs` instance.



## 7.1 Annotate filtered variants called by GATK

```
library("GenomicFeatures")
args <- systemArgs(sysma="annotate_vars.param", mytargets="targets_gatk_filtered.txt")
txdb <- loadDb("../data/tair10.sqlite")
fa <- FaFile(systemPipeR::reference(args))
variantReport(args=args, txdb=txdb, fa=fa, organism="A. thaliana")
```

## 7.2 Annotate filtered variants called by BCFtools

```
args <- systemArgs(sysma="annotate_vars.param", mytargets="targets_sambcf_filtered.txt")
txdb <- loadDb("../data/tair10.sqlite")
fa <- FaFile(systemPipeR::reference(args))
variantReport(args=args, txdb=txdb, fa=fa, organism="A. thaliana")
```

## 7.3 Annotate filtered variants called by VariantTools

```
args <- systemArgs(sysma="annotate_vars.param", mytargets="targets_vartools_filtered.txt")
txdb <- loadDb("../data/tair10.sqlite")
fa <- FaFile(systemPipeR::reference(args))
variantReport(args=args, txdb=txdb, fa=fa, organism="A. thaliana")
```

# 8 Combine annotation results among samples

---

To simplify comparisons among samples, the `combineVarReports` function combines all variant annotation reports referenced in a `SYSargs` instance (here `args`). At the same time the function allows to consider only certain feature types of interest. For instance, the below setting `filtercol=c(Consequence="nonsynonymous")` will include only nonsynonymous variances listed in the Consequence column of the annotation reports. To omit filtering, one can use the setting `filtercol="All"`

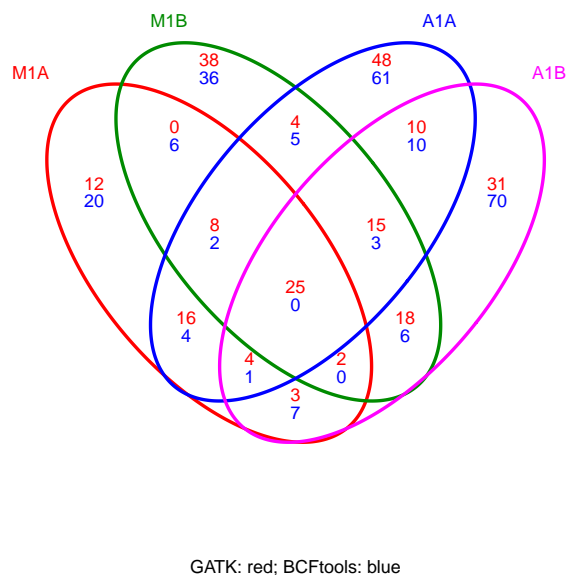
## 8.1 Combine results from GATK

```
args <- systemArgs(sysma="annotate_vars.param", mytargets="targets_gatk_filtered.txt")
combinedDF <- combineVarReports(args, filtercol=c(Consequence="nonsynonymous"))
write.table(combinedDF, "../results/combinedDF_nonsyn_gatk.xls", quote=FALSE, row.names=FALSE, sep="\t")
```

## 8.2 Combine results from BCFtools

```
args <- systemArgs(sysma="annotate_vars.param", mytargets="targets_sambcf_filtered.txt")
combinedDF <- combineVarReports(args, filtercol=c(Consequence="nonsynonymous"))
write.table(combinedDF, "../results/combinedDF_nonsyn_sambcf.xls", quote=FALSE, row.names=FALSE, sep="\t")
```





**Figure 2: Venn Diagram for 4 samples from GATK and BCFtools**

## 11 Version Information

```
toLatex(sessionInfo())
```

- R version 3.4.2 (2017-09-28), 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 16.04.3 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.6-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, stats4, utils
- Other packages: Biobase 2.38.0, BiocGenerics 0.24.0, BiocParallel 1.12.0, BiocStyle 2.6.0, Biostrings 2.46.0, DESeq2 1.18.0, DelayedArray 0.4.0, GenomInfoDb 1.14.0, GenomicAlignments 1.14.0, GenomicRanges 1.30.0,

IRanges 2.12.0, Rsamtools 1.30.0, S4Vectors 0.16.0, ShortRead 1.36.0, SummarizedExperiment 1.8.0, XVector 0.18.0, ape 5.0, ggplot2 2.2.1, knitr 1.17, matrixStats 0.52.2, systemPipeR 1.12.0

- Loaded via a namespace (and not attached): AnnotationDbi 1.40.0, AnnotationForge 1.20.0, BBmisc 1.11, BatchJobs 1.6, Category 2.44.0, DBI 0.7, Formula 1.2-2, GO.db 3.4.2, GOstats 2.44.0, GSEABase 1.40.0, GenomInfoDbData 0.99.1, GenomicFeatures 1.30.0, Hmisc 4.0-3, Matrix 1.2-11, R6 2.2.2, RBGL 1.54.0, RColorBrewer 1.1-2, RCurl 1.95-4.8, RMySQL 0.10.13, RSQLite 2.0, Rcpp 0.12.13, Rgraphviz 2.22.0, XML 3.98-1.9, acepack 1.4.1, annotate 1.56.0, assertthat 0.2.0, backports 1.1.1, base64enc 0.1-3, biomaRt 2.34.0, bit 1.1-12, bit64 0.9-7, bitops 1.0-6, blob 1.1.0, bookdown 0.5, brew 1.0-6, checkmate 1.8.5, cluster 2.0.6, codetools 0.2-15, colorspace 1.3-2, compiler 3.4.2, data.table 1.10.4-3, digest 0.6.12, edgeR 3.20.0, evaluate 0.10.1, fail 1.3, foreign 0.8-69, genefilter 1.60.0, geneplotter 1.56.0, graph 1.56.0, grid 3.4.2, gridExtra 2.3, gtable 0.2.0, highr 0.6, htmlTable 1.9, htmltools 0.3.6, htmlwidgets 0.9, hwriter 1.3.2, labeling 0.3, lattice 0.20-35, latticeExtra 0.6-28, lazyeval 0.2.1, limma 3.34.0, locfit 1.5-9.1, magrittr 1.5, memoise 1.1.0, munsell 0.4.3, nlme 3.1-131, nnet 7.3-12, pheatmap 1.0.8, pkgconfig 2.0.1, plyr 1.8.4, prettyunits 1.0.2, progress 1.1.2, rjson 0.2.15, rlang 0.1.2, rmarkdown 1.6, rpart 4.1-11, rprojroot 1.2, rtracklayer 1.38.0, scales 0.5.0, sendmailR 1.2-1, splines 3.4.2, stringi 1.1.5, stringr 1.2.0, survival 2.41-3, tibble 1.3.4, tools 3.4.2, xtable 1.8-2, yaml 2.1.14, zlibbioc 1.24.0

## 12 Funding

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## 13 References

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