

# Introduction to QDNaseq

Ilari Scheinin

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## 1 Running QDNaseq

This is a short tutorial on how to use the `QDNaseq` package. It covers an example run using the included data set of chromosomes 7–10 of a low grade glioma (LGG) sample. First step is naturally to load the package.

```
> library(QDNaseq)
```

### 1.1 Bin annotations

Then we need to obtain bin annotations. These are available pre-calculated for genome build hg19 and bin sizes 1, 5, 10, 15, 30, 50, 100, 500, and 1000 kbp. They can be downloaded for example with:

```
> bins <- getBinAnnotations(binSize=15)
Downloading bin annotations for genome hg19, bin size 15kbp,
and experiment type SR50 ...
> bins
QDNaseq bin annotations for Hsapiens, build hg19.
Created by Ilari Scheinin with QDNaseq 0.7.5, 2014-02-06 12:48:04.
An object of class 'AnnotatedDataFrame'
 rowNames: 1:1-15000 1:15001-30000 ... Y:59370001-59373566 (206391
   total)
 varLabels: chromosome start ... use (9 total)
 varMetadata: labelDescription
```

After downloading, the bin annotations can be saved locally with `saveRDS`, and in the future be read from the local file with `loadRDS` instead of relying on downloading.

If you are working with another genome build (or another species), see the section on generating the bin annotations.

### 1.2 Processing bam files

Next step is to load the sequencing data from bam files. This can be done for example with one of the commands below.

```

> readCounts <- binReadCounts(bins)
> # all files ending in .bam from the current working directory
>
> # or
>
> readCounts <- binReadCounts(bins, bamfiles='tumor.bam')
> # file 'tumor.bam' from the current working directory
>
> # or
>
> readCounts <- binReadCounts(bins, path='tumors')
> # all files ending in .bam from the subdirectory 'tumors'

```

This will return an object of class `QDNaseqReadCounts`. If the same bam files will be used as input in future R sessions, option `cache=TRUE` can be used to cache intermediate files, which will speed up future analyses. Caching is done with package `R.cache`.

For the purpose of this tutorial, we load an example data set of chromosomes 7–10 of low grade glioma sample LGG150.

```

> data(LGG150)
> readCounts <- LGG150
> readCounts

```

```

QDNaseqReadCounts (storageMode: lockedEnvironment)
assayData: 38819 features, 1 samples
  element names: counts
protocolData: none
phenoData
  sampleNames: LGG150
  varLabels: name reads used.reads
    expected.variance
  varMetadata: labelDescription
featureData
  featureNames: 7:1-15000
    7:15001-30000 ...
    10:135525001-135534747 (38819
    total)
  fvarLabels: chromosome start ...
    use (9 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:

```

Plot a raw copy number profile (read counts across the genome), and highlight bins that will be removed with default filtering (Figure 1).

```
> plot(readCounts, logTransform=FALSE, ylim=c(-50, 200))
Plotting sample LGG150 (1 of 1) ...
> highlightFilters(readCounts, logTransform=FALSE,
+   residual=TRUE, blacklist=TRUE)
Highlighted 3,375 bins.
```

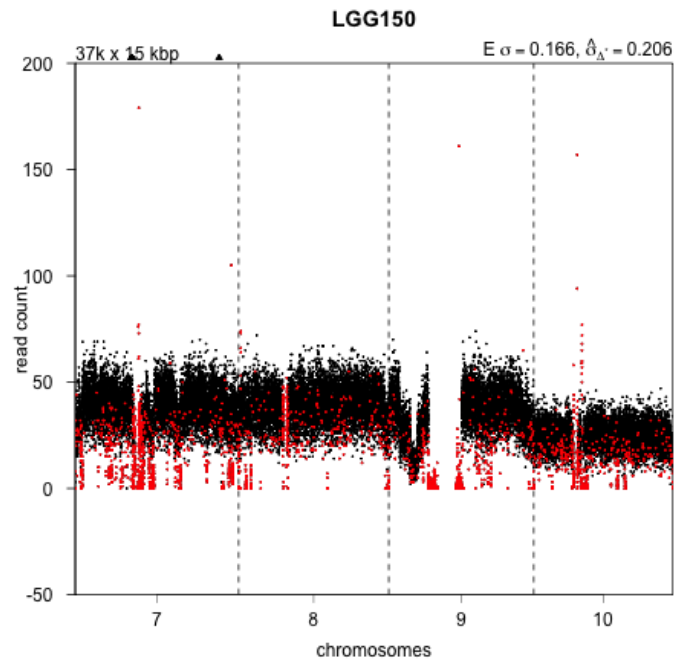


Figure 1: Read counts per bins. Highlighted with red are bins that will be filtered out.

Apply filters and plot median read counts as a function of GC content and mappability (Figure 2). As the example data set only contains a subset of the chromosomes, the distribution looks slithly less smooth than expected for the entire genome.

```
> readCountsFiltered <- applyFilters(readCounts,
+   residual=TRUE, blacklist=TRUE)

38,819      total bins
38,819      of which in selected chromosomes
36,722      of which with reference sequence
33,347      final bins
```

```
> isobarPlot(readCountsFiltered)
```

Plotting sample LGG150 median read counts

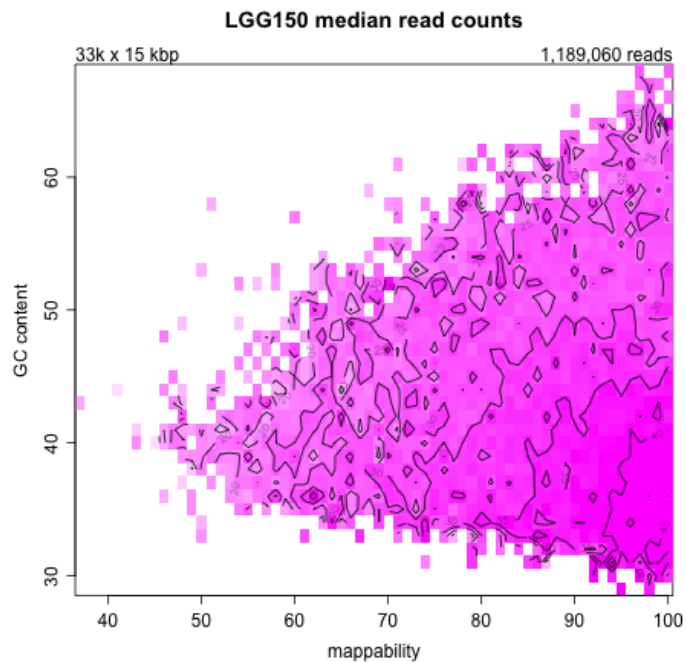


Figure 2: Median read counts per bin shown as a function of GC content and mappability.

Estimate the correction for GC content and mappability, and make a plot for the relationship between the observed standard deviation in the data and its read depth (Figure 3). The theoretical expectation is a linear relationship, which is shown in the plot with a black line. Samples with low-quality DNA will be noisier than expected and appear further above the line than good-quality samples.

```
> readCountsFiltered <- estimateCorrection(readCountsFiltered)
```

Calculating correction for GC content and mappability:

Calculating fit for sample LGG150 (1 of 1) ...

Done.

```
> noisePlot(readCountsFiltered)
```

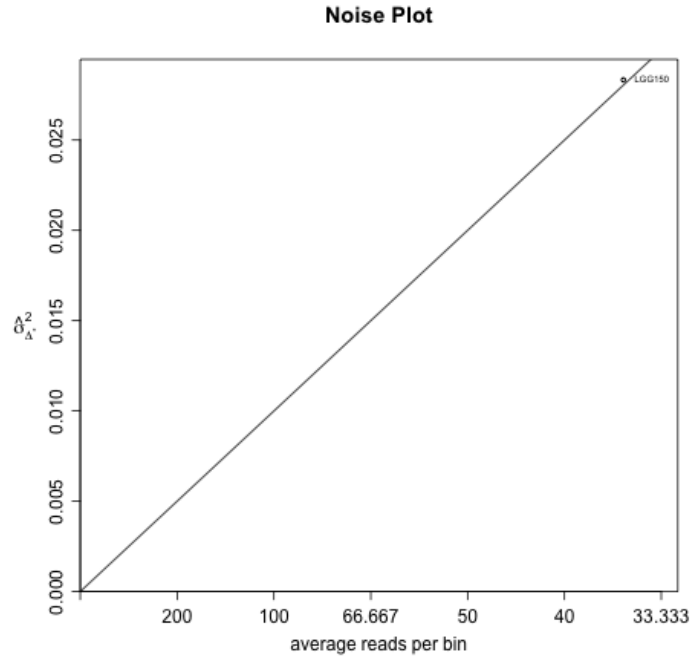


Figure 3: The relationship between sequence depth and noise.

Next, we apply the correction for GC content and mappability. This will return a `QDNaseqCopyNumbers` object, which we then normalize, smooth outliers, and plot the copy number profile (Figure 4).

```
> copyNumbers <- correctBins(readCountsFiltered)
> copyNumbers

QDNaseqCopyNumbers (storageMode: lockedEnvironment)
assayData: 38819 features, 1 samples
  element names: copynumber
protocolData: none
phenoData
  sampleNames: LGG150
  varLabels: name reads ...
    loess.family (6 total)
  varMetadata: labelDescription
featureData
  featureNames: 7:1-15000
    7:15001-30000 ...
    10:135525001-135534747 (38819)
```

```

    total)
  fvarLabels: chromosome start ...
    use (9 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:

> copyNumbersNormalized <- normalizeBins(copyNumbers)

Applying median normalization ...

> copyNumbersSmooth <- smoothOutlierBins(copyNumbersNormalized)

Smoothing outliers ...

> plot(copyNumbersSmooth)

Plotting sample LGG150 (1 of 1) ...

```

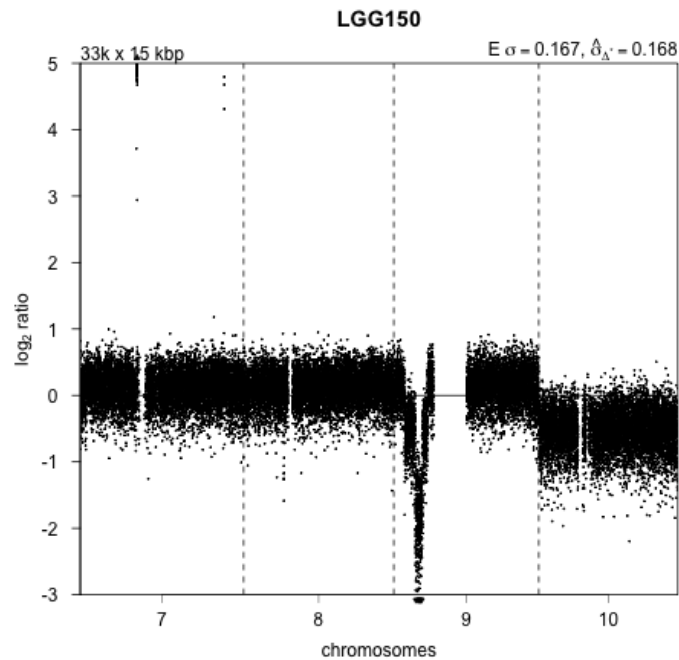


Figure 4: Copy number profile after correcting for GC content and mappability.

Data is now ready to be analyzed with a downstream package of choice. For analysis with an external program or for visualizations in IGV, the data can be exported to a file.

```
> exportBins(copyNumbersSmooth, file="LGG150.txt")
> exportBins(copyNumbersSmooth, file="LGG150.igv", format="igv")
> exportBins(copyNumbersSmooth, file="LGG150.bed", format="bed")
```

### 1.3 Downstream analyses

Segmentation with the CBS algorithm from DNAcopy and calling copy number aberrations with CGHcall have been implemented for convenience.

By default, segmentation uses a  $\log_2$ -transformation, but a  $\sqrt{x + 3/8}$  can also be used as it stabilizes the variance of a Poisson distribution (Anscombe transform):

```
> copyNumbersSegmented <- segmentBins(copyNumbersSmooth, transformFun="sqrt")
```

Performing segmentation:

```
Segmenting: LGG150 (1 of 1) ...
```

```
> copyNumbersSegmented <- normalizeSegmentedBins(copyNumbersSegmented)
```

```
> plot(copyNumbersSegmented)
```

```
Plotting sample LGG150 (1 of 1) ...
```

Tune segmentation parameters and iterate until satisfied. Next, call aberrations, and plot the final results.

```
> copyNumbersCalled <- callBins(copyNumbersSegmented)
```

```
[1] "Total number of segments present in the data: 14"
```

```
[1] "Number of segments used for fitting the model: 11"
```

```
> plot(copyNumbersCalled)
```

```
Plotting sample LGG150 (1 of 1) ...
```

Finally, for other downstream analyses, such as running CGHregions, it might be useful to convert to a cghCall object.

```
> cgh <- makeCgh(copyNumbersCalled)
```

```
> cgh
```

```
cghCall (storageMode: lockedEnvironment)
```

```
assayData: 33347 features, 1 samples
```

```
element names: calls, copynumber, probamp, probdloss, probgain, probloss, probnorm, segmen
```

```
protocolData: none
```

```
phenoData
```

```
sampleNames: LGG150
```

```
varLabels: name reads ...
```

```
loess.family (6 total)
```

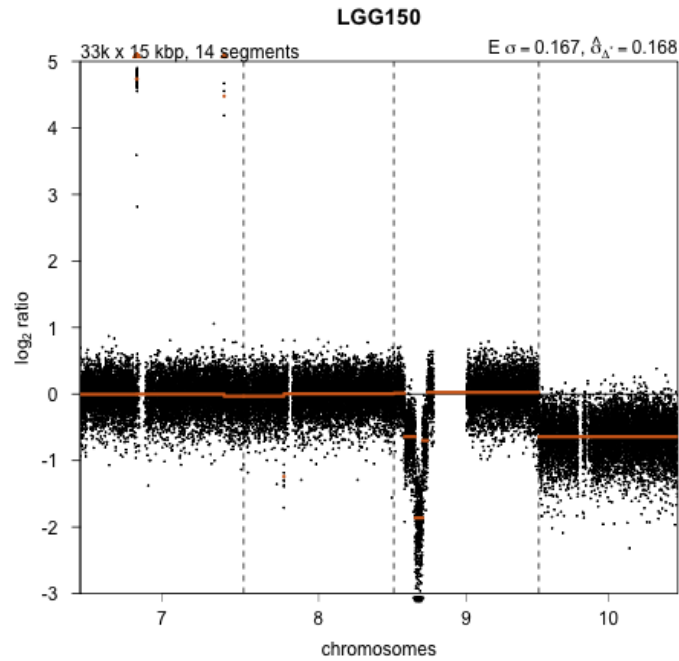


Figure 5: Copy number profile after segmenting.

```

varMetadata: labelDescription
featureData
  featureNames: 7:45001-60000
                7:60001-75000 ...
                10:135420001-135435000 (33347
                total)
  fvarLabels: Chromosome Start ...
              use (9 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
Annotation:

```

This command can also be used to generate `cghRaw` or `cghSeg` objects by running it before segmentation or calling.



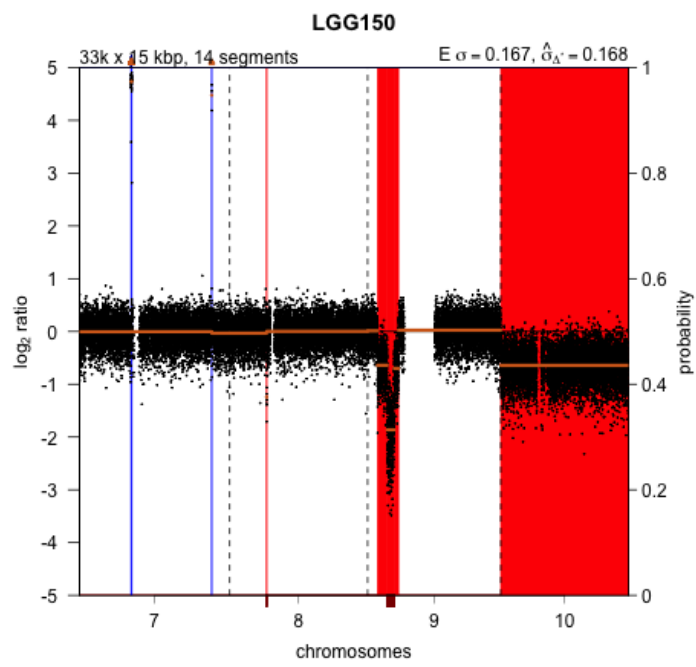


Figure 6: Copy number profile after calling gains and losses.

## 2 Generating bin annotations

This section describes how bin annotations have been created for the hg19 build of the human reference genome, and can be applied for other genome builds and species. The first step is to create the bins based on chromosome sizes, and calculate their GC content and proportion of characterized nucleotides (non-N bases in the reference sequence). For this, the corresponding `BSgenome` package is needed.

```
> # load required packages for human reference genome build hg19
> library(QDNAseq)
> library(Biobase)
> library(BSgenome.Hsapiens.UCSC.hg19)
> # set the bin size
> binSize <- 15
> # create bins from the reference genome
> bins <- createBins(bsgenome=BSgenome.Hsapiens.UCSC.hg19, binSize=binSize)
```

The result is a `data.frame` with columns `chromosome`, `start`, `end`, `gc`, and `bases`. Next step is to calculate the average mappabilities, which requires a mappability file in the `bigWig` format and the `bigWigAverageOverBed` binary. The mappability file can be generated with the [GEM library](#) tools from the reference genome sequence. Or it might be available directly, as was the case for hg19, and file `wgEncodeCrgMapabilityAlign50mer.bigWig` downloaded from [ENCODE's download section of the UCSC Genome Browser](#). The `bigWigAverageOverBed` binary can also be downloaded from [UCSC Genome Browser's Other utilities section](#).

```
> # calculate mappabilites per bin from ENCODE mapability tracks
> bins$mappability <- calculateMappability(bins,
+   bigWigFile='/path/to/wgEncodeCrgMapabilityAlign50mer.bigWig',
+   bigWigAverageOverBed='/path/to/bigWigAverageOverBed')
```

If there are genomic regions that should be excluded from analyses, such as ENCODE's Blacklisted Regions, the percentage overlap between these regions can be calculated for each bin as follows. The regions to be excluded need to be in the BED format, like files `wgEncodeDacMapabilityConsensusExcludable.bed` and `wgEncodeDukeMapabilityRegionsExcludable.bed` that were downloaded from [ENCODE's download section of the UCSC Genome Browser](#) for hg19.

```
> # calculate overlap with ENCODE blacklisted regions
> bins$blacklist <- calculateBlacklist(bins,
+   bedFiles=c('/path/to/wgEncodeDacMapabilityConsensusExcludable.bed',
+   '/path/to/wgEncodeDukeMapabilityRegionsExcludable.bed'))
```

To calculate median residuals of the LOESS fit from a control dataset, the following command can be used. For the pre-generated annotations, the control set used is 38 samples from the 1000 Genomes project. See the next section on how those were downloaded.

```

> # load data for the 1000 Genomes (or similar) data set, and generate residuals
> ctrl <- binReadCounts(bins,
+   path='/path/to/control-set/bam/files')
> ctrl <- applyFilters(ctrl, residual=FALSE, blacklist=FALSE,
+   mappability=FALSE, bases=FALSE)
> bins$residual <- iterateResiduals(ctrl)

```

The column `use` specifies whether each bin should be used for subsequent analyses by default. The command `applyFilters` will change its value accordingly. By default, bins in the sex chromosomes, or with only uncharacterized nucleotides (N's) in their reference sequence, are flagged for exclusion.

```

> # by default, use all autosomal bins that have a reference sequence
> # (i.e. not only N's)
> bins$use <- bins$chromosome %in% as.character(1:22) & bins$bases > 0

```

Optionally, the resulting `data.frame` can be converted to an `AnnotateDataFrame` and metadata added for the columns.

```

> # convert to AnnotatedDataFrame and add metadata
> bins <- AnnotatedDataFrame(bins,
+   varMetadata=data.frame(labelDescription=c(
+     'Chromosome name',
+     'Base pair start position',
+     'Base pair end position',
+     'Percentage of non-N nucleotides (of full bin size)',
+     'Percentage of C and G nucleotides (of non-N nucleotides)',
+     'Average mappability of 50mers with a maximum of 2 mismatches',
+     'Percent overlap with ENCODE blacklisted regions',
+     'Median loess residual from 1000 Genomes (50mers)',
+     'Whether the bin should be used in subsequent analysis steps'),
+   row.names=colnames(bins)))

```

For the pre-generated annotations, some additional descriptive metadata has also been added.

```

> attr(bins, "QDNaseq") <- list(
+   author="Ilari Scheinin",
+   date=Sys.time(),
+   organism="Hsapiens",
+   build="hg19",
+   version=packageVersion("QDNaseq"),
+   url=paste0(
+     "http://cdn.bitbucket.org/ccagc/qdnaseq/downloads/QDNaseq.hg19.",
+     binsize, "kbp.SR50.rds"),
+   md5=digest::digest(bins@data),
+   sessionInfo=sessionInfo())

```

### 3 Downloading 1000 Genomes Samples

This section defines the criteria that were used to download samples from the 1000 Genomes project for the pre-generated bin annotations.

```
> # download table of samples
> server <- "ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/"
> g1k <- read.table(paste0(server, "sequence.index"),
+   header=TRUE, sep="\t", as.is=TRUE, fill=TRUE)
> # keep cases that are Illumina, low coverage, single-read, and not withdrawn
> g1k <- g1k[g1k$INSTRUMENT_PLATFORM == 'ILLUMINA', ]
> g1k <- g1k[g1k$ANALYSIS_GROUP == 'low coverage', ]
> g1k <- g1k[g1k$LIBRARY_LAYOUT == 'SINGLE', ]
> g1k <- g1k[g1k$WITHDRAWN == 0, ]
> # keep cases with read lengths of at least 50 bp
> g1k <- g1k[!g1k$BASE_COUNT %in% c("not available", ""), ]
> g1k$BASE_COUNT <- as.numeric(g1k$BASE_COUNT)
> g1k$READ_COUNT <- as.integer(g1k$READ_COUNT)
> g1k$readLength <- g1k$BASE_COUNT / g1k$READ_COUNT
> g1k <- g1k[g1k$readLength > 50, ]
> # keep samples with a minimum of one million reads
> readCountPerSample <- aggregate(g1k$READ_COUNT,
+   by=list(sample=g1k$SAMPLE_NAME), sum)
> g1k <- g1k[g1k$SAMPLE_NAME %in%
+   readCountPerSample$sample[readCountPerSample$x >= 1e6], ]
> g1k$fileName <- basename(g1k$FASTQ_FILE)
> # download fastq files
> for (i in rownames(g1k)) {
+   sourceFile <- paste0(server, g1k[i, "FASTQ_FILE"])
+   destFile <- g1k[i, "fileName"]
+   if (!file.exists(destFile))
+     download.file(sourceFile, destFile)
+ }
```

Next, reads were trimmed to 50 bp, and the multiple files for each sample (as defined by column SAMPLE\_NAME) were combined by concatenating the FASTQ together. Finally, they were aligned with BWA allowing two mismatches and end-trimming of bases with qualities below 40 (options -n 2 -q 40).

### 4 Session Information

The version number of R and packages loaded for generating the vignette were:

R version 3.1.2 (2014-10-31)

Platform: x86\_64-apple-darwin13.4.0 (64-bit)

```
locale:  
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

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

```
other attached packages:  
[1] QDNAseq_1.2.4
```

```
loaded via a namespace (and not attached):
```

```
[1] Biobase_2.26.0  
[2] BiocGenerics_0.12.1  
[3] Biostrings_2.34.1  
[4] CGHbase_1.26.0  
[5] CGHcall_2.28.0  
[6] DNACopy_1.40.0  
[7] GenomeInfoDb_1.2.4  
[8] GenomicRanges_1.18.4  
[9] IRanges_2.0.1  
[10] R.methodsS3_1.6.1  
[11] R.oo_1.18.0  
[12] R.utils_1.34.0  
[13] Rsamtools_1.18.2  
[14] S4Vectors_0.4.0  
[15] XVector_0.6.0  
[16] bitops_1.0-6  
[17] impute_1.40.0  
[18] limma_3.22.4  
[19] marray_1.44.0  
[20] matrixStats_0.13.0  
[21] parallel_3.1.2  
[22] stats4_3.1.2  
[23] tools_3.1.2  
[24] zlibbioc_1.12.0
```