

# Package: NanoporeRNASeq (via r-universe)

October 10, 2026

**Type** Package

**Title** Nanopore RNA-Seq Example data

**Version** 1.22.0

**Description** The NanoporeRNASeq package contains long read RNA-Seq data generated using Oxford Nanopore Sequencing. The data consists of 6 samples from two human cell lines (K562 and MCF7) that were generated by the SG-NEx project. Each of these cell lines has three replicates, with 1 direct RNA sequencing data and 2 cDNA sequencing data. Reads are aligned to chromosome 22 (Grch38) and stored as bam files. The original data is from the SG-NEx project.

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Depends** R(>= 4.0.0), ExperimentHub (>= 1.15.3)

**Suggests** knitr, bambu, ggbio, BSgenome.Hsapiens.NCBI.GRCh38, circlize, ComplexHeatmap, apeglm, rlang, rmarkdown, GenomicAlignments, Rsamtools

**Enhances** parallel

**biocViews** ExperimentHub, ExperimentData, RNASeqData, Genome, SequencingData

**bugReports** <https://github.com/GoekeLab/NanoporeRNASeq/issues>

**URL** <https://github.com/GoekeLab/NanoporeRNASeq>

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**Config/pak/sysreqs** libicu-dev libpng-dev libssl-dev zlib1g-dev

**Repository** Bioconductor 3.23

**Date/Publication** 2026-04-28 12:34:34 UTC

**RemoteUrl** <https://github.com/bioc/NanoporeRNASeq>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** cd1349ff6679e3d3b29caa77ba1a072b1f1ec21e

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|------------------------|-----------------------------------------------------------------|
| HsChr22BambuAnnotation | <i>BambuAnnotation of the first half of Human Sapiens Chr22</i> |
|------------------------|-----------------------------------------------------------------|

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Description

Annotation GRangesList prepared from bambu for Granges of human genome (Grch38) chromosome 22 (1:25409234)

Usage

```
data("HsChr22BambuAnnotation")
```

Format

SummarizedExperiment

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|                |                                                                  |
|----------------|------------------------------------------------------------------|
| NanoporeRNASeq | <i>NanoporeRNASeq package with long-read RNA sequencing data</i> |
|----------------|------------------------------------------------------------------|

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Description

The NanoporeRNASeq package contains long-read RNA-Seq data generated using Oxford Nanopore Sequencing. The data consists of 6 samples from two human cell lines (K562 and MCF7). Each of these cell lines has three replicates, with 1 direct RNA sequencing data and 2 cDNA sequencing data. Reads are aligned to chromosome 22 (Grch38) and stored as bam files. The original data is from the SG-NEx project. Please see the package vignette for examples and use cases.

Details

Data objects include:

- [SGNexSamples](#) - sample information of the bam files
- [HsChr22BambuAnnotation](#) - annotation GRangesList

For detailed information on usage, see the package vignette, by typing `vignette("NanoporeRNASeq")`, or the workflow linked to on the first page of the vignette.

Author(s)

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SGNexSamples

*SG-Nex samples from Nanopore RNA-Seq*

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**Description**

Sample information description for K562 and MCF7 samples from SG-Nex

**Usage**

```
data("SGNexSamples")
```

**Format**

DataFrame

**Details**

SGNexSamples is a DataFrame containing the following information:

- sample\_id - sample names of the bam files
- Platform - sequencing platform
- cellLine - cell line used
- protocol - sequencing protocols
- cancer\_type- cancer type of the cell line

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