# Package ‘NanoporeRNASeq’

August 26, 2025

**Type** Package

**Title** Nanopore RNA-Seq Example data

**Version** 1.18.0

**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

**git_url** https://git.bioconductor.org/packages/NanoporeRNASeq

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# Contents

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## `HsChr22BambuAnnotation` *BambuAnnotation of the first half of Human Sapiens Chr22*

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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` *NanoporeRNASeq package with long-read RNA sequencing data*

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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*

### 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

# Index