

# Package ‘NanoporeRNASeq’

August 11, 2022

**Type** Package

**Title** Nanopore RNA-Seq Example data

**Version** 1.7.0

**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

## SystemRequirements

**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>

**git\_branch** master

**git\_last\_commit** c7f0335

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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*

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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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