### Package ‘NanoporeRNASeq’

**Type**  Package  
**Title**  Nanopore RNA-Seq Example data  
**Version**  1.14.0  
**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  
**git_branch**  RELEASE_3_19  
**git_last_commit**  ca3b82a  
**git_last_commit_date**  2024-04-30  
**Repository**  Bioconductor 3.19  
**Date/Publication**  2024-06-27
HsChr22BambuAnnotation

BambuAnnotation of the first half of Human Sapiens Chr22

Description

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

Usage

data("HsChr22BambuAnnotation")

Format

SummarizedExperiment

NanoporeRNASeq

NanoporeRNASeq package with long-read RNA sequencing data

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.

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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
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