Package ‘SingleMoleculeFootprintingData’

May 19, 2026

Type Package

Title Data supporting the SingleMoleculeFootprinting pkg

Version 1.21.0

Description This Data package contains data objcets relevanat for the SingleMoleculeFootprinting package. More specifically, it contains one example of aligned sequencing data (.bam & .bai) necessary to run the SingleMoleculeFootprinting vignette. Additionally, we provide data that are essential for some functions to work correctly such as BaitCapture() and SampleCorrelation().

biocViews ExperimentHub, ExperimentData, SequencingData

License GPL-3

Encoding UTF-8

LazyData true

Imports ExperimentHub, utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.1.1

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Author Guido Barzaghi [aut, cre] (ORCID: <`https://orcid.org/0000-0001-6066-3920`>), Arnaud Krebs [aut] (ORCID: <`https://orcid.org/0000-0001-7999-6127`>), Mike Smith [ctb] (ORCID: <`https://orcid.org/0000-0002-7800-3848`>)

Maintainer Guido Barzaghi <`guido.barzaghi@embl.de`>

Contents

`NRF1pair.bam` *SingleMoleculeFootprintingData*

Description

This Data package contains r objcets necessary to run some of the functions from the SingleMoleculeFootprinting package. SingleMoleculeFootprinting is an R package providing functions to analyze Single Molecule Footprinting (SMF) data.

Usage

```
NRF1pair.bam(metadata = FALSE)
NRF1pair.bam.bai(metadata = FALSE)
EnrichmentRegions_mm10.rds(metadata = FALSE)
ReferenceMethylation.rds(metadata = FALSE)
AllCs.rds(metadata = FALSE)
```

Arguments

`metadata`	FALSE (default) returns data. TRUE returns metadata

Value

Returns respectively: NRF1pair.bam - Bam file contanining reads covering example NRF1 pair binding locus used for SingleMoleculeFootprinting vignette. NRF1pair.bam.bai - Bam index file to Bam file used as example data in SingleMoleculeFootprinting vignette EnrichmentRegions_mm10.rds - GRanges obj of mouse genomic regions enriched for SMF signal in genome-wide capture experiments. Can be used to compute bait capture efficiency ReferenceMethylation.rds - Reference matrix of genome-wide bulk SMF values for published experiments in mouse cell lines AllCs.rds - GRanges obj referencing the genomic context cytosines for mm10

Examples

```
NRF1pair.bam(metadata = TRUE)
NRF1pair.bam.bai(metadata = TRUE)
EnrichmentRegions_mm10.rds(metadata = TRUE)
ReferenceMethylation.rds(metadata = TRUE)
AllCs.rds(metadata = TRUE)
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