

Package ‘SingleMoleculeFootprintingData’

May 28, 2026

Type Package

Title Data supporting the SingleMoleculeFootprinting pkg

Version 1.21.0

Description This Data package contains data objects relevant 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

git_url <https://git.bioconductor.org/packages/SingleMoleculeFootprintingData>

git_branch devel

git_last_commit cfcbed2

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-28

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>

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`NRF1pair.bam`*SingleMoleculeFootprintingData*

Description

This Data package contains `r` objects 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 containing 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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