

# Package ‘SingleMoleculeFootprintingData’

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**Type** Package

**Title** Data supporting the SingleMoleculeFootprinting pkg

**Version** 1.19.0

**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

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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](mailto:guido.barzaghi@embl.de)>

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## 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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