

# Package ‘SingleMoleculeFootprintingData’

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**Type** Package

**Title** Data supporting the SingleMoleculeFootprinting pkg

**Version** 1.14.0

**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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`NRF1pair.bam`*SingleMoleculeFootprintingData*

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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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