

# Package ‘SingleMoleculeFootprintingData’

June 6, 2023

**Type** Package

**Title** Data supporting the SingleMoleculeFootprinting pkg

**Version** 1.8.0

**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>

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## R topics documented:

NRF1pair.bam . . . . . 2

**Index****3**

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NRF1pair.bam	<i>SingleMoleculeFootprintingData</i>
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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)
```

# Index

AllCs.rds (NRF1pair.bam), [2](#)

EnrichmentRegions\_mm10.rds  
(NRF1pair.bam), [2](#)

NRF1pair.bam, [2](#)

ReferenceMethylation.rds  
(NRF1pair.bam), [2](#)