

# Package ‘MMAPPR2data’

October 18, 2022

**Type** Package

**Title** Sample Data for MMAPPR2

**Version** 1.10.0

**Description** Contains data for illustration purposes in the MMAPPR2 package, namely simulated BAM files containing RNA-Seq data for a mutation in the *slc24a5* gene, taken from the GRCz11 genome. Also contains reference sequence and annotation files for the region.

**Depends** R (>= 3.6.0)

**VignetteBuilder** knitr

**Enhances** MMAPPR2

**Suggests** knitr, rmarkdown, BiocStyle, roxygen2, seqinr, readr

**Imports** Rsamtools

**License** GPL-3

**Encoding** UTF-8

**biocViews** RNASeqData, Danio\_rerio\_Data, SequencingData, Genome

**URL** <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3613585/>,  
<https://github.com/kjohnsen/MMAPPR2>

**RoxygenNote** 6.1.1

**git\_url** <https://git.bioconductor.org/packages/MMAPPR2data>

**git\_branch** RELEASE\_3\_15

**git\_last\_commit** ee424d2

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-10-18

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## R topics documented:

MMAPPR2data . . . . . 2

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MMAPPR2data

*MMAPPR2data: Example Data for MMAPPR2*

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## Description

Contains BAM files and indices for example use in MMAPPR2. The data is artificial, meant to simulate sequencing of the zebrafish *slc24a5* gene in mutant and wild-type pools resulting from the cross of a novel mutant from a forward genetics screen with a wild-type line, as described in Hill et al. 2013.

## Usage

`exampleMutBam()`

`exampleWTbam()`

`goldenFasta()`

`goldenGFF()`

## Details

Besides BAM files and indices, the package also contains fasta and gtf files for just the region of the *slc24a5* gene, which are also used in demonstrating MMAPPR2's functionality. They are based on the GRCz11 assembly and were obtained from Ensembl version 95.

## Value

A [BamFile](#) object referencing a BAM file and its index.

A [BamFile](#) object referencing a BAM file and its index.

A path to the bgzipped *slc24a5* fasta file

The path to the bgzipped GFF file

## Functions

- `exampleMutBam`: Easy access to example mutant pool BAM file.
- `exampleWTbam`: Easy access to example wild-type pool BAM file.
- `goldenFasta`: Easy access to example fasta file for *slc24a5* gene.
- `goldenGFF`: Easy access to example GFF file for *slc24a5* gene.

## Examples

```
mutFile <- exampleMutBam()
wtFile <- exampleWTbam()
goldenFasta <- goldenFasta()
goldenGFF <- goldenGFF()
```

# Index

BamFile, [2](#)

exampleMutBam (MMAPPR2data), [2](#)

exampleWTbam (MMAPPR2data), [2](#)

goldenFasta (MMAPPR2data), [2](#)

goldenGFF (MMAPPR2data), [2](#)

MMAPPR2data, [2](#)

MMAPPR2data-package (MMAPPR2data), [2](#)