

# Package ‘MMAPPR2data’

July 23, 2024

**Type** Package

**Title** Sample Data for MMAPPR2

**Version** 1.18.0

**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

**PackageStatus** Deprecated

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

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 02075fb

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-07-23

**Author** Kyle Johnsen [aut],  
Jonathon Hill [cre]

**Maintainer** Jonathon Hill <jhill@byu.edu>

## Contents

MMAPPR2data . . . . .	2
<b>Index</b>	<b>4</b>

---

MMAPPR2data	<i>MMAPPR2data: Example Data for MMAPPR2</i>
-------------	--

---

### 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()
```

# Index

BamFile, [2](#)

exampleMutBam (MMAPPR2data), [2](#)

exampleWTbam (MMAPPR2data), [2](#)

goldenFasta (MMAPPR2data), [2](#)

goldenGFF (MMAPPR2data), [2](#)

MMAPPR2data, [2](#)

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