

# Package ‘MUGAExampleData’

December 19, 2024

**Type** Package

**Title** Example {M}ouse {U}niversal {G}enotyping {A}rray data for genome reconstruction and quantitative trait locus mapping.

**Version** 1.26.0

**Date** 2013-10-02

**Author** Daniel Gatti <Dan.Gatti@jax.org>

**Maintainer** Daniel Gatti <Dan.Gatti@jax.org>

**Description** This package contains example data for the MUGA array that is used by the R package DOQTL.

**biocViews** ExperimentData, Mus\_musculus\_Data

**Depends** R (>= 2.10.0)

**License** GPL-3

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

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** ae9945c

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2024-12-19

## Contents

call.rate.batch . . . . .	2
FinalReport1 . . . . .	2
FinalReport2 . . . . .	3
geno . . . . .	4
model.probs . . . . .	4
MUGAExampleData . . . . .	5
pheno . . . . .	6
Samples1 . . . . .	6
Samples2 . . . . .	7
x . . . . .	8
y . . . . .	8

<b>Index</b>	<b>10</b>
--------------	-----------

---

call.rate.batch	<i>Call rates and batch information for Svenson et.al samples.</i>
-----------------	--

---

**Description**

The allele call rate and batch information for each sample in the data set.

**Usage**

```
data(call.rate.batch)
```

**Format**

Data.frame with three columns. sample: contains the sample ID. call.rate: contains the allele call rate. batch: contains the batch ID, which is the source directory where the raw files for this batch were stored.

**Details**

This is the summary of the allele call rate and batch from each of the raw data files (FinalReport1 and FinalReport2).

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(call.rate.batch)
```

---

FinalReport1	<i>Allele call and intensity data for the first set of MUGA samples.</i>
--------------	--

---

**Description**

Allele call and intensity data for the first set of MUGA samples.

**Usage**

```
data(FinalReport1)
```

**Format**

Text with tab delimiters.

**Details**

This is the \*\_FinalReport.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(FinalReport1)
```

---

FinalReport2	<i>Allele call and intensity data for the second set of MUGA samples.</i>
--------------	---

---

**Description**

Allele call and intensity data for the second set of MUGA samples.

**Usage**

```
data(FinalReport2)
```

**Format**

Text with tab delimiters.

**Details**

This is the \*\_FinalReport.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. Genetics. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(FinalReport2)
```

geno *Allele calls for Svenson et.al samples.*

---

**Description**

The allele calls for each sample in the data set.

**Usage**

```
data(geno)
```

**Format**

Character matrix containing the allele calls coded as "A", "C", "G", "T", "H" or "-". num.samples x num.snps. Sample names in rownames and SNP IDs in colnames.

**Details**

This is the summary of the allele calls from each of the raw data files (FinalReport1 and FinalReport2).

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(geno)
```

---

model.probs *Founder haplotype probabilities for the Svenson et.al. data.*

---

**Description**

A 3D array containing the eight founder haplotype contributions from each sample at each marker on the array.

**Usage**

```
data(model.probs)
```

**Format**

Numeric 3D array containing founder haplotype probabilities. num.samples x num.founders x num.snps. Sample names in dimnames[[1]], founder letter codes in dimnames[[2]] and SNP IDs in dimnames[[3]].

**Details**

These are reconstructed founder haplotype probabilities for the DO samples in this data set. They were reconstructed using a hidden Markov model based on the MUGA intensities.

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(model.probs)
```

---

MUGAExampleData	<i>Example Mouse Universal Genotyping Array data for genome reconstruction and quantitative trait locus mapping.</i>
-----------------	--

---

**Description**

Example MUGA data for a set of ~150 samples from Svenson et.al., *Genetics*, 2012.

**Details**

Package: MUGAExampleData  
Type: Package  
Version: 1.0  
Date: 2013-10-02  
License: What license is it under?

**Author(s)**

Daniel Gatti <Dan.Gatti@jax.org>

**References**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(FinalReport1)  
data(Samples1)
```

---

pheno	<i>Phenotype data for Svenson et.al samples.</i>
-------	--

---

**Description**

The clinical phenotypes for each mouse in the Svenson et.al. data set.

**Usage**

```
data(pheno)
```

**Format**

Data.frame containing sample IDs, sex, diet and measured clinical phenotypes for 149 DO mice.

**Details**

The clinical phenotypes for each mouse in the Svenson et.al. data set.

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(pheno)
```

---

Samples1	<i>Sample list for the first MUGA data set.</i>
----------	---

---

**Description**

List of samples that correspond to the samples in FinalReport1.

**Usage**

```
data(Samples1)
```

**Format**

Table with tab delimiters.

**Details**

This is the Sample\_Map.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(Samples1)
```

---

Samples2

*Sample list for the second MUGA data set.*

---

**Description**

List of samples that correspond to the samples in FinalReport2.

**Usage**

```
data(Samples2)
```

**Format**

Table with tab delimiters.

**Details**

This is the Sample\_Map.txt file as delivered by GeneSeek. It is unparsed text that contains tab characters and is intended to be written out at text and then read back in to simulate the MUGA genotyping pipeline as the user would experience it.

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(Samples2)
```

---

x

*X allele intensities for Svenson et.al samples.*

---

**Description**

Matrix of allele intensities from the MUGA for each of the Svenson et.al. samples at each marker.

**Usage**

data(x)

**Format**

X allele intensities for each sample at each marker. num.samples x num.snps. Sample names in rownames and SNP IDs in colnames.

**Details**

This is the summary of the X allele intensities from each of the raw data files (FinalReport1 and FinalReport2).

**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

data(x)

---

y

*Y allele intensities for Svenson et.al samples.*

---

**Description**

Matrix of allele intensities from the MUGA for each of the Svenson et.al. samples at each marker.

**Usage**

data(y)

**Format**

Y allele intensities for each sample at each marker. num.samples x num.snps. Sample names in rownames and SNP IDs in colnames.

**Details**

This is the summary of the Y allele intensities from each of the raw data files (FinalReport1 and FinalReport2).



**Source**

High-resolution genetic mapping using the Mouse Diversity outbred population. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, Chesler EJ, Palmer AA, McMillan L, Churchill GA. *Genetics*. 2012 Feb;190(2):437-47. doi: 10.1534/genetics.111.132597. PMID: 22345611

**Examples**

```
data(y)
```

# Index

## \* MUGA

MUGAExampleData, 5

## \* datasets

call.rate.batch, 2

FinalReport1, 2

FinalReport2, 3

geno, 4

model.probs, 4

pheno, 6

Samples1, 6

Samples2, 7

x, 8

y, 8

call.rate.batch, 2

FinalReport1, 2

FinalReport2, 3

geno, 4

model.probs, 4

MUGAExampleData, 5

pheno, 6

Samples1, 6

Samples2, 7

x, 8

y, 8