# Package 'miRNATarget'

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# Description

This miRNA conservation table is for MiRaGE package. Actual name of data files is HS\_conv\_id for human and MM\_conv\_id for mouse, but name of loaded data frame is "conv\_id".

# Usage

data(MM\_conv\_id)

### **Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is two.

### **Details**

The first column includes miRNA names based upon miRBase Release 18 and the second column includes integers which describe miRNA conservation. 2 stands for broadly conserved (in MiRaGE, it corresponds to "conserved"), 1 stands for conserved (in MiRaGE, broadly conserved and conserved correspond to "weakly conserved"), 0 stands for others (in MiRaGE, "all" corresponds to all miRNAs).

### Note

How to generate this table, please see functions in MiRaGE package and vignette.

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### References

For more details about TargetScan, access to http://www.targetscan.org/

### **Examples**

```
data(MM_conv_id)
```

HS\_conv\_id

miRNA conservation table of human

### **Description**

This miRNA conservation table of human is for MiRaGE package, based upon TargetScanHuman 6.1

### Usage

```
data(HS_conv_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is two.

### **Details**

The first column includes miRNA names based upon miRBase Release 18 and the second column includes integers which describe miRNA conservation. 2 stands for broadly conserved (in MiRaGE, it corresponds to "conserved"), 1 stands for conserved (in MiRaGE, broadly conserved and conserved correspond to "weakly conserved"), 0 stands for others (in MiRaGE, "all" corresponds to all miRNAs). Please note that the name of object loaded is not "HS\_conv\_id" but "conv\_id", because of the requirements by MiRaGE package.

### Note

How to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about TargetScanHuman, access to http://www.targetscan.org/vert\_61/

```
data(HS_conv_id)
```

HS\_refseq\_to\_affy\_hc\_g110

Conversion table between RefSeq and affy\_hc\_g110 for human

# **Description**

This gene id conversion table between RefSeq and affy\_hc\_g110 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hc_g110)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hc\_g110. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hc\_g110" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hc_g110)
```

HS\_refseq\_to\_affy\_hg\_focus

Conversion table between RefSeq and affy\_hg\_focus for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_focus is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_focus)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_focus. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_focus" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_focus)
```

HS\_refseq\_to\_affy\_hg\_u133a

Conversion table between RefSeq and affy\_hg\_u133a for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u133a is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u133a)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133a" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u133a)
```

HS\_refseq\_to\_affy\_hg\_u133a\_2

Conversion table between RefSeq and affy\_hg\_u133a\_2 for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u133a\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u133a_2)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133a\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133a\_2" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u133a_2)
```

HS\_refseq\_to\_affy\_hg\_u133b

Conversion table between RefSeq and affy\_hg\_u133b for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u133b is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u133b)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133b" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u133b)
```

HS\_refseq\_to\_affy\_hg\_u133\_plus\_2

Conversion table between RefSeq and affy\_hg\_u133\_plus\_2 for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u133\_plus\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u133_plus_2)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133\_plus\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133\_plus\_2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u133_plus_2)
```

HS\_refseq\_to\_affy\_hg\_u95a

Conversion table between RefSeq and affy\_hg\_u95a for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u95a is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u95a)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95a" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u95a)
```

HS\_refseq\_to\_affy\_hg\_u95av2

Conversion table between RefSeq and affy\_hg\_u95av2 for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u95av2 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u95av2)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95av2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95av2" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u95av2)
```

HS\_refseq\_to\_affy\_hg\_u95b

Conversion table between RefSeq and affy\_hg\_u95b for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u95b is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u95b)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95b" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u95b)
```

HS\_refseq\_to\_affy\_hg\_u95c

Conversion table between RefSeq and affy\_hg\_u95c for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u95c is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u95c)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95c. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95c" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u95c)
```

HS\_refseq\_to\_affy\_hg\_u95d

Conversion table between RefSeq and affy\_hg\_u95d for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u95d is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u95d)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95d. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95d" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u95d)
```

HS\_refseq\_to\_affy\_hg\_u95e

Conversion table between RefSeq and affy\_hg\_u95e for human

# **Description**

This gene id conversion table between RefSeq and affy\_hg\_u95e is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hg_u95e)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95e. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95e" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hg_u95e)
```

HS\_refseq\_to\_affy\_huex\_1\_0\_st\_v2

Conversion table between RefSeq and affy\_huex\_1\_0\_st\_v2 for human

# **Description**

This gene id conversion table between RefSeq and affy\_huex\_1\_0\_st\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_huex_1_0_st_v2)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_huex\_1\_0\_st\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_huex\_1\_0\_st\_v2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_huex_1_0_st_v2)
```

HS\_refseq\_to\_affy\_hugenefl

Conversion table between RefSeq and affy\_hugenefl for human

# **Description**

This gene id conversion table between RefSeq and affy\_hugenefl is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hugenefl)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hugenefl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hugenefl" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_hugenefl)
```

```
\label{localization} HS\_refseq\_to\_affy\_hugene\_1\_0\_st\_v1 \\ Conversion \ table \ between \ RefSeq \ and \ affy\_hugene\_1\_0\_st\_v1 \ for \ human
```

# **Description**

This gene id conversion table between RefSeq and affy\_hugene\_1\_0\_st\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_hugene_1_0_st_v1)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hugene\_1\_0\_st\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hugene\_1\_0\_st\_v1" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
\tt data(HS\_refseq\_to\_affy\_hugene\_1\_0\_st\_v1)
```

HS\_refseq\_to\_affy\_u133\_x3p

Conversion table between RefSeq and affy\_u133\_x3p for human

# **Description**

This gene id conversion table between RefSeq and affy\_u133\_x3p is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_affy_u133_x3p)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_u133\_x3p. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_u133\_x3p" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_affy_u133_x3p)
```

```
HS_refseq_to_agilent_cgh_44b
```

Conversion table between RefSeq and agilent\_cgh\_44b for human

# **Description**

This gene id conversion table between RefSeq and agilent\_cgh\_44b is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_agilent_cgh_44b)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding agilent\_cgh\_44b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_agilent\_cgh\_44b" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_agilent_cgh_44b)
```

HS\_refseq\_to\_agilent\_wholegenome

Conversion table between RefSeq and agilent\_wholegenome for human

# **Description**

This gene id conversion table between RefSeq and agilent\_wholegenome is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_agilent_wholegenome)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# **Details**

The first column includes RefSeq gene id and the second column includes corresponding agilent\_wholegenome. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_agilent\_wholegenome" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_agilent_wholegenome)
```

HS\_refseq\_to\_canonical\_transcript\_stable\_id

Conversion table between RefSeq and canonical\_transcript\_stable\_id

for human

# **Description**

This gene id conversion table between RefSeq and canonical\_transcript\_stable\_id is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_canonical_transcript_stable_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding canonical\_transcript\_stable\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_canonical\_transcript\_stable\_id" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_canonical_transcript_stable_id)
```

HS\_refseq\_to\_ccds 25

HS\_refseq\_to\_ccds

Conversion table between RefSeq and ccds for human

# **Description**

This gene id conversion table between RefSeq and ccds is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_ccds)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ccds. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ccds" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(HS_refseq_to_ccds)
```

 ${\tt HS\_refseq\_to\_codelink} \ \ \textit{Conversion table between RefSeq and codelink for human}$ 

### Description

This gene id conversion table between RefSeq and codelink is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_codelink)
```

26 HS\_refseq\_to\_embl

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding codelink. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_codelink" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(HS_refseq_to_codelink)
```

HS\_refseq\_to\_embl

Conversion table between RefSeq and embl for human

### **Description**

This gene id conversion table between RefSeq and embl is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_embl)
```

# **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding embl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_embl" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(HS_refseq_to_embl)
```

HS\_refseq\_to\_ensembl\_gene\_id

Conversion table between RefSeq and ensembl\_gene\_id for human

# **Description**

This gene id conversion table between RefSeq and ensembl\_gene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_ensembl_gene_id)
```

# **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_gene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ensembl\_gene\_id" but "id\_conv", because of the requirements by MiRaGE package.

# Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_ensembl_gene_id)
```

HS\_refseq\_to\_ensembl\_peptide\_id

Conversion table between RefSeq and ensembl\_peptide\_id for human

# **Description**

This gene id conversion table between RefSeq and ensembl\_peptide\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_ensembl_peptide_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_peptide\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ensembl\_peptide\_id" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_ensembl_peptide_id)
```

HS\_refseq\_to\_ensembl\_transcript\_id

Conversion table between RefSeq and ensembl\_transcript\_id for human

# **Description**

This gene id conversion table between RefSeq and ensembl\_transcript\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_ensembl_transcript_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# **Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_transcript\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ensembl\_transcript\_id" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_ensembl_transcript_id)
```

HS\_refseq\_to\_entrezgene

Conversion table between RefSeq and entrezgene for human

# **Description**

This gene id conversion table between RefSeq and entrezgene is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_entrezgene)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding entrezgene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_entrezgene" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_entrezgene)
```

HS\_refseq\_to\_hgnc\_id Conversion table between RefSeq and hgnc\_id for human

# Description

This gene id conversion table between RefSeq and hgnc\_id is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_hgnc_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding hgnc\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_hgnc\_id" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(HS_refseq_to_hgnc_id)
```

HS\_refseq\_to\_hgnc\_symbol

Conversion table between RefSeq and hgnc\_symbol for human

# **Description**

This gene id conversion table between RefSeq and hgnc\_symbol is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_hgnc_symbol)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding hgnc\_symbol. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_hgnc\_symbol" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(HS_refseq_to_hgnc_symbol)
```

```
HS_refseq_to_hgnc_transcript_name
```

Conversion table between RefSeq and hgnc\_transcript\_name for human

# Description

This gene id conversion table between RefSeq and hgnc\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_hgnc_transcript_name)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding hgnc\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_hgnc\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(HS_refseq_to_hgnc_transcript_name)
```

# Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

### Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_efg\_agilent\_sureprint It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

```
\begin{tabular}{lll} HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1\\ & Conversion & table & between & RefSeq & and \\ & HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1 & for human \end{tabular}
```

# **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_efg\_agilent\_wholege. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

 $\label{eq:hs_refseq_to_efg_agilent_wholegenome_4x44k_v2} Knew Example 1 & Conversion & table & between & RefSeq & and & HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 & for human & RefSeq & table &$ 

# **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_efg\_agilent\_wholege. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

# **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_ensembl\_exon\_id is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_ensembl\_exon\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_ensembl\_exon\_id" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

 $\begin{tabular}{lll} HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_genename\_transcript\_name \\ & Conversion & table & between & RefSeq & and \\ & HS\_refseq\_to\_uniprot\_genename\_transcript\_name & for human \\ \end{tabular}$ 

## **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_genename\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_genename\_transcript name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_genename\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name)
```

 $\label{local-conversion} HS\_refseq\_to\_uniprot\_sptrembl\\ Conversion\ table\ between\ RefSeq\ and\ HS\_refseq\_to\_uniprot\_sptrembl\\ for\ human$ 

## **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_sptrembl is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_sptrembl)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_sptrembl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_sptrembl" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_HS_refseq_to_uniprot_sptrembl)
```

HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot

Conversion table between RefSeq and

HS\_refseq\_to\_uniprot\_swissprot for human

## **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_swissprot is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_swissprot. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

## **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_swissprot\_accession is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_swissprot\_act It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot\_accession" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

## **Examples**

data(HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot\_accession)

HS\_refseq\_to\_HS\_refseq\_to\_wikigene\_id

Conversion table between RefSeq and HS\_refseq\_to\_wikigene\_id for
human

## **Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_wikigene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_HS_refseq_to_wikigene_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_wikigene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_wikigene\_id" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_HS_refseq_to_wikigene_id)
```

HS\_refseq\_to\_illumina\_humanht\_12

Conversion table between RefSeq and illumina\_humanht\_12 for human

# Description

This gene id conversion table between RefSeq and illumina\_humanht\_12 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_illumina_humanht_12)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanht\_12. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanht\_12" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_illumina_humanht_12)
```

```
HS_refseq_to_illumina_humanwg_6_v1
```

Conversion table between RefSeq and illumina\_humanwg\_6\_v1 for human

## **Description**

This gene id conversion table between RefSeq and illumina\_humanwg\_6\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_illumina_humanwg_6_v1)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanwg\_6\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanwg\_6\_v1" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_illumina_humanwg_6_v1)
```

HS\_refseq\_to\_illumina\_humanwg\_6\_v2

Conversion table between RefSeq and illumina\_humanwg\_6\_v2 for human

## **Description**

This gene id conversion table between RefSeq and illumina\_humanwg\_6\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_illumina_humanwg_6_v2)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanwg\_6\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanwg\_6\_v2" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_illumina_humanwg_6_v2)
```

```
HS_refseq_to_illumina_humanwg_6_v3
```

Conversion table between RefSeq and illumina\_humanwg\_6\_v3 for human

## **Description**

This gene id conversion table between RefSeq and illumina\_humanwg\_6\_v3 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_illumina_humanwg_6_v3)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanwg\_6\_v3. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanwg\_6\_v3" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_illumina_humanwg_6_v3)
```

46 HS\_refseq\_to\_ipi

HS\_refseq\_to\_interpro Conversion table between RefSeq and interpro for human

## **Description**

This gene id conversion table between RefSeq and interpro is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_interpro)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding interpro. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_interpro" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(HS_refseq_to_interpro)
```

 $HS\_refseq\_to\_ipi$ 

Conversion table between RefSeq and ipi for human

## Description

This gene id conversion table between RefSeq and ipi is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_ipi)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ipi. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ipi" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

## **Examples**

```
data(HS_refseq_to_ipi)
```

HS\_refseq\_to\_merops

Conversion table between RefSeq and merops for human

### **Description**

This gene id conversion table between RefSeq and merops is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_merops)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding merops. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_merops" but "id\_conv", because of the requirements by MiRaGE package.

48 HS\_refseq\_to\_pdb

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(HS_refseq_to_merops)
```

HS\_refseq\_to\_pdb

Conversion table between RefSeq and pdb for human

# Description

This gene id conversion table between RefSeq and pdb is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_pdb)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding pdb. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_pdb" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_pdb)
```

HS\_refseq\_to\_pfam 49

HS\_refseq\_to\_pfam

Conversion table between RefSeq and pfam for human

# Description

This gene id conversion table between RefSeq and pfam is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_pfam)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding pfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_pfam" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

## **Examples**

```
data(HS_refseq_to_pfam)
```

HS\_refseq\_to\_phalanx\_onearray

Conversion table between RefSeq and phalanx\_onearray for human

## **Description**

This gene id conversion table between RefSeq and phalanx\_onearray is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_phalanx_onearray)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding phalanx\_onearray. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_phalanx\_onearray" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

## **Examples**

```
data(HS_refseq_to_phalanx_onearray)
```

```
HS_refseq_to_protein_id
```

Conversion table between RefSeq and protein\_id for human

# Description

This gene id conversion table between RefSeq and protein\_id is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_protein_id)
```

### Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding protein\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_protein\_id" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(HS_refseq_to_protein_id)
```

HS\_refseq\_to\_refseq\_dna

Conversion table between RefSeq and refseq\_dna for human

## **Description**

This gene id conversion table between RefSeq and refseq\_dna is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(HS_refseq_to_refseq_dna)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding ref-seq\_dna. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_refseq\_dna" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(HS_refseq_to_refseq_dna)
```

HS\_refseq\_to\_refseq\_genomic

Conversion table between RefSeq and refseq\_genomic for human

# Description

This gene id conversion table between RefSeq and refseq\_genomic is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_refseq_genomic)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding ref-seq\_genomic. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_refseq\_genomic" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_refseq_genomic)
```

HS\_refseq\_to\_refseq\_peptide

Conversion table between RefSeq and refseq\_peptide for human

# **Description**

This gene id conversion table between RefSeq and refseq\_peptide is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_refseq_peptide)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ref-seq\_peptide. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_refseq\_peptide" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_refseq_peptide)
```

HS\_refseq\_to\_rfam

Conversion table between RefSeq and rfam for human

# Description

This gene id conversion table between RefSeq and rfam is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_rfam)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_rfam" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

## **Examples**

```
data(HS_refseq_to_rfam)
```

 $HS\_refseq\_to\_rfam\_gene\_name$ 

Conversion table between RefSeq and rfam\_gene\_name for human

## **Description**

This gene id conversion table between RefSeq and rfam\_gene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_rfam_gene_name)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_gene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_rfam\_gene\_name" but "id\_conv", because of the requirements by Mi-RaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

## **Examples**

```
data(HS_refseq_to_rfam_gene_name)
```

```
HS_refseq_to_rfam_transcript_name
```

Conversion table between RefSeq and rfam\_transcript\_name for human

# Description

This gene id conversion table between RefSeq and rfam\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_rfam_transcript_name)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

HS\_refseq\_to\_smart

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_rfam\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(HS_refseq_to_rfam_transcript_name)
```

HS\_refseq\_to\_smart

Conversion table between RefSeq and smart for human

### **Description**

This gene id conversion table between RefSeq and smart is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_smart)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding smart. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_smart" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

HS\_refseq\_to\_tigrfam

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### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

## **Examples**

```
data(HS_refseq_to_smart)
```

### **Description**

This gene id conversion table between RefSeq and tigrfam is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_tigrfam)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding tigrfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_tigrfam" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_tigrfam)
```

HS\_refseq\_to\_ucsc

Conversion table between RefSeq and ucsc for human

## **Description**

This gene id conversion table between RefSeq and ucsc is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_ucsc)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ucsc. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ucsc" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(HS_refseq_to_ucsc)
```

## **Description**

This gene id conversion table between RefSeq and unigene is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_unigene)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding unigene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_unigene" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(HS_refseq_to_unigene)
```

HS\_refseq\_to\_uniprot\_genename

Conversion table between RefSeq and uniprot\_genename for human

### **Description**

This gene id conversion table between RefSeq and uniprot\_genename is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_uniprot_genename)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding uniprot\_genename. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_uniprot\_genename" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

#### **Examples**

```
data(HS_refseq_to_uniprot_genename)
```

HS\_refseq\_to\_wikigene\_name

Conversion table between RefSeq and wikigene\_name for human

## **Description**

This gene id conversion table between RefSeq and wikigene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_wikigene_name)
```

## **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding wikigene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_wikigene\_name" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(HS_refseq_to_wikigene_name)
```

id\_conv 61

id\_conv

Conversion table between refseq and various gene id/probe id

## **Description**

This gene id conversion table between RefSeq and gene id/probe id is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_wikigene_name)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding gene id. It can be made out of getBM function in biomaRt package. Actual names of data file is HS\_refseq\_to\_[gene id/probe id] for human and MM\_refseq\_to\_[gene id/probe id] for mouse. [gene id/probe id] stands for various gene id / probe id, but loaded data frame has the name "id\_conv".

#### Note

How to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_wikigene_name)
```

62 MM\_conv\_id

MM\_conv\_id

miRNA conservation table of mouse

### **Description**

This miRNA conservation table of mouse is for MiRaGE package, based upon TargetScanMouse 6.1

### Usage

```
data(MM_conv_id)
```

#### **Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is two.

### **Details**

The first column includes miRNA names based upon miRBase Release 18 and the second column includes integers which describe miRNA conservation. 2 stands for broadly conserved (in MiRaGE, it corresponds to "conserved"), 1 stands for conserved (in MiRaGE, broadly conserved and conserved correspond to "weakly conserved"), 0 stands for others (in MiRaGE, "all" corresponds to all miRNAs). Please note that the name of object loaded is not "MM\_conv\_id" but "conv\_id", because of the requirements by MiRaGE package.

### Note

How to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about TargetScanMouse, access to http://www.targetscan.org/mmu\_61/

```
data(MM_conv_id)
```

MM\_refseq\_to\_affy\_mg\_u74a

Conversion table between RefSeq and affy\_mg\_u74a for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_mg\_u74a is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_mg_u74a)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74a" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mg_u74a)
```

MM\_refseq\_to\_affy\_mg\_u74av2

Conversion table between RefSeq and affy\_mg\_u74av2 for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_mg\_u74av2 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_mg_u74av2)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74av2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74av2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mg_u74av2)
```

MM\_refseq\_to\_affy\_mg\_u74b

Conversion table between RefSeq and affy\_mg\_u74b for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_mg\_u74b is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_mg_u74b)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74b" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mg_u74b)
```

MM\_refseq\_to\_affy\_mg\_u74bv2

Conversion table between RefSeq and affy\_mg\_u74bv2 for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_mg\_u74bv2 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_mg_u74bv2)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74bv2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74bv2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mg_u74bv2)
```

MM\_refseq\_to\_affy\_mg\_u74c

Conversion table between RefSeq and affy\_mg\_u74c for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_mg\_u74c is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_mg_u74c)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74c. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74c" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mg_u74c)
```

MM\_refseq\_to\_affy\_mg\_u74cv2

Conversion table between RefSeq and affy\_mg\_u74cv2 for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_mg\_u74cv2 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_mg_u74cv2)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74cv2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74cv2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mg_u74cv2)
```

MM\_refseq\_to\_affy\_moe430a

Conversion table between RefSeq and affy\_moe430a for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_moe430a is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_moe430a)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_moe430a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_moe430a" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_moe430a)
```

MM\_refseq\_to\_affy\_moe430b

Conversion table between RefSeq and affy\_moe430b for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_moe430b is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_moe430b)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_moe430b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_moe430b" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_moe430b)
```

MM\_refseq\_to\_affy\_moex\_1\_0\_st\_v1

Conversion table between RefSeq and affy moex 1 0 st v1 for mouse

## **Description**

This gene id conversion table between RefSeq and affy\_moex\_1\_0\_st\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_moex\_1\_0\_st\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_moex\_1\_0\_st\_v1" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

```
MM_refseq_to_affy_mogene_1_0_st_v1

Conversion table between RefSeq and affy_mogene_1_0_st_v1 for mouse
```

# Description

This gene id conversion table between RefSeq and affy\_mogene\_1\_0\_st\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_affy_mogene_1_0_st_v1)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mogene\_1\_0\_st\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mogene\_1\_0\_st\_v1" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mogene_1_0_st_v1)
```

MM\_refseq\_to\_affy\_mouse430a\_2

Conversion table between RefSeq and affy\_mouse430a\_2 for mouse

# **Description**

This gene id conversion table between RefSeq and affy\_mouse430a\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_affy_mouse430a_2)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mouse430a\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mouse430a\_2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mouse430a_2)
```

MM\_refseq\_to\_affy\_mouse430\_2

Conversion table between RefSeq and affy\_mouse430\_2 for mouse

# **Description**

This gene id conversion table between RefSeq and affy\_mouse430\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_affy_mouse430_2)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mouse430\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mouse430\_2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mouse430_2)
```

MM\_refseq\_to\_affy\_mu11ksuba

Conversion table between RefSeq and affy\_mullksuba for mouse

# **Description**

This gene id conversion table between RefSeq and affy\_mu11ksuba is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_affy_mu11ksuba)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mu11ksuba. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mu11ksuba" but "id\_conv", because of the requirements by Mi-RaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mu11ksuba)
```

MM\_refseq\_to\_affy\_mu11ksubb

Conversion table between RefSeq and affy\_mullksubb for mouse

# **Description**

This gene id conversion table between RefSeq and affy\_mu11ksubb is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_affy_mu11ksubb)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mu11ksubb. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mu11ksubb" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_affy_mu11ksubb)
```

MM\_refseq\_to\_agilent\_wholegenome

Conversion table between RefSeq and agilent\_wholegenome for mouse

# **Description**

This gene id conversion table between RefSeq and agilent\_wholegenome is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_agilent_wholegenome)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding agilent\_wholegenome. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_agilent\_wholegenome" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_agilent_wholegenome)
```

 $\begin{tabular}{ll} MM\_refseq\_to\_canonical\_transcript\_stable\_id \\ Conversion \ table \ between \ RefSeq \ and \ canonical\_transcript\_stable\_id \\ for \ mouse \end{tabular}$ 

# **Description**

This gene id conversion table between RefSeq and canonical\_transcript\_stable\_id is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding canonical\_transcript\_stable\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_canonical\_transcript\_stable\_id" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

MM\_refseq\_to\_ccds 79

MM\_refseq\_to\_ccds

Conversion table between RefSeq and ccds for mouse

# **Description**

This gene id conversion table between RefSeq and ccds is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_ccds)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ccds. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ccds" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(MM_refseq_to_ccds)
```

 ${\tt MM\_refseq\_to\_codelink} \ \ \textit{Conversion table between RefSeq and codelink for mouse}$ 

### Description

This gene id conversion table between RefSeq and codelink is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_codelink)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding codelink. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_codelink" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(MM_refseq_to_codelink)
```

MM\_refseq\_to\_embl

Conversion table between RefSeq and embl for mouse

### **Description**

This gene id conversion table between RefSeq and embl is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_embl)
```

# **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding embl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_embl" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

#### **Examples**

```
data(MM_refseq_to_embl)
```

MM\_refseq\_to\_ensembl\_gene\_id

Conversion table between RefSeq and ensembl\_gene\_id for mouse

# **Description**

This gene id conversion table between RefSeq and ensembl\_gene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_ensembl_gene_id)
```

# **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_gene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ensembl\_gene\_id" but "id\_conv", because of the requirements by MiRaGE package.

# Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_ensembl_gene_id)
```

MM\_refseq\_to\_ensembl\_peptide\_id

Conversion table between RefSeq and ensembl\_peptide\_id for mouse

# **Description**

This gene id conversion table between RefSeq and ensembl\_peptide\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_ensembl_peptide_id)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_peptide\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ensembl\_peptide\_id" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_ensembl_peptide_id)
```

MM\_refseq\_to\_ensembl\_transcript\_id

Conversion table between RefSeq and ensembl\_transcript\_id for mouse

# **Description**

This gene id conversion table between RefSeq and ensembl\_transcript\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_ensembl_transcript_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# **Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_transcript\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ensembl\_transcript\_id" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_ensembl_transcript_id)
```

MM\_refseq\_to\_entrezgene

Conversion table between RefSeq and entrezgene for mouse

# **Description**

This gene id conversion table between RefSeq and entrezgene is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_entrezgene)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding entrezgene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_entrezgene" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_entrezgene)
```

MM\_refseq\_to\_fantom

MM\_refseq\_to\_fantom

Conversion table between RefSeq and fantom for mouse

### **Description**

This gene id conversion table between RefSeq and fantom is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_fantom)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding fantom. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_fantom" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
{\tt data}({\tt MM\_refseq\_to\_fantom})
```

```
MM_refseq_to_illumina_mousewg_6_v1
```

Conversion table between RefSeq and illumina\_mousewg\_6\_v1 for mouse

### **Description**

This gene id conversion table between RefSeq and illumina\_mousewg\_6\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_mousewg\_6\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_illumina\_mousewg\_6\_v1" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

```
MM_refseq_to_illumina_mousewg_6_v2
```

Conversion table between RefSeq and illumina\_mousewg\_6\_v2 for mouse

# Description

This gene id conversion table between RefSeq and illumina\_mousewg\_6\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_mousewg\_6\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_illumina\_mousewg\_6\_v2" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

MM\_refseq\_to\_interpro Conversion table between RefSeq and interpro for mouse

# **Description**

This gene id conversion table between RefSeq and interpro is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_interpro)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding interpro. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_interpro" but "id\_conv", because of the requirements by MiRaGE package.

# Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

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### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(MM_refseq_to_interpro)
```

MM\_refseq\_to\_ipi

Conversion table between RefSeq and ipi for mouse

### **Description**

This gene id conversion table between RefSeq and ipi is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_ipi)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ipi. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ipi" but "id\_conv", because of the requirements by MiRaGE package.

# Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_ipi)
```

MM\_refseq\_to\_merops

MM\_refseq\_to\_merops

Conversion table between RefSeq and merops for mouse

# **Description**

This gene id conversion table between RefSeq and merops is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_merops)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding merops. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_merops" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# Examples

```
data(MM_refseq_to_merops)
```

MM\_refseq\_to\_mgi\_id

Conversion table between RefSeq and mgi\_id for mouse

### Description

This gene id conversion table between RefSeq and mgi\_id is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_mgi_id)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding mgi\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_mgi\_id" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

#### **Examples**

```
data(MM_refseq_to_mgi_id)
```

```
MM_refseq_to_mgi_symbol
```

Conversion table between RefSeq and mgi\_symbol for mouse

### **Description**

This gene id conversion table between RefSeq and mgi\_symbol is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_mgi_symbol)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding mgi\_symbol. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_mgi\_symbol" but "id\_conv", because of the requirements by Mi-RaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
{\tt data(MM\_refseq\_to\_mgi\_symbol)}
```

```
MM_refseq_to_mgi_transcript_name
```

Conversion table between RefSeq and mgi\_transcript\_name for mouse

# **Description**

This gene id conversion table between RefSeq and mgi\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_mgi_transcript_name)
```

# **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### Details

The first column includes RefSeq gene id and the second column includes corresponding mgi\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_mgi\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

# Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_mgi_transcript_name)
```

 $\begin{tabular}{lll} MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k \\ & Conversion & table & between & RefSeq & and \\ & MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k & for mouse \\ \end{tabular}$ 

# Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_efg\_agilent\_sureprint It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_efg\_agilent\_wholeg It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

#### **Usage**

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_efg\_agilent\_wholeg It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_ensembl\_exon\_id is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_MM_refseq_to_ensembl_exon_id)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_ensembl\_exon\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_ensembl\_exon\_id" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_ensembl_exon_id)
```

 $\begin{tabular}{lll} MM\_refseq\_to\_mM\_refseq\_to\_uniprot\_genename\_transcript\_name \\ & Conversion & table & between & RefSeq & and \\ & MM\_refseq\_to\_uniprot\_genename\_transcript\_name & for mouse \\ \end{tabular}$ 

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_genename\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

#### **Usage**

```
data(MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_genename\_ It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_genename\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name)
```

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_sptrembl is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_sptrembl)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_sptrembl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_sptrembl" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_uniprot_sptrembl)
```

MM\_refseq\_to\_uniprot\_swissprot

Conversion table between RefSeq and

MM\_refseq\_to\_uniprot\_swissprot for mouse

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_swissprot is for Mi-RaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_swissprot. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_swissprot" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot)
```

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_swissprot\_accession is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_swissprot\_a It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_swissprot\_accession" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession)
```

MM\_refseq\_to\_MM\_refseq\_to\_wikigene\_id

Conversion table between RefSeq and MM\_refseq\_to\_wikigene\_id for

mouse

# **Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_wikigene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_MM_refseq_to_wikigene_id)
```

### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# **Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_wikigene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_wikigene\_id" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_MM_refseq_to_wikigene_id)
```

MM\_refseq\_to\_pdb

MM\_refseq\_to\_pdb

Conversion table between RefSeq and pdb for mouse

# **Description**

This gene id conversion table between RefSeq and pdb is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_pdb)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding pdb. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_pdb" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(MM_refseq_to_pdb)
```

 ${\tt MM\_refseq\_to\_pfam}$ 

Conversion table between RefSeq and pfam for mouse

### Description

This gene id conversion table between RefSeq and pfam is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_pfam)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding pfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_pfam" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

#### **Examples**

```
data(MM_refseq_to_pfam)
```

MM\_refseq\_to\_phalanx\_onearray

Conversion table between RefSeq and phalanx\_onearray for mouse

### **Description**

This gene id conversion table between RefSeq and phalanx\_onearray is for MiRaGE package, based upon BioMart Gene ID Converter

#### Usage

```
data(MM_refseq_to_phalanx_onearray)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding phalanx\_onearray. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_phalanx\_onearray" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

#### **Examples**

```
data(MM_refseq_to_phalanx_onearray)
```

MM\_refseq\_to\_protein\_id

Conversion table between RefSeq and protein\_id for mouse

# **Description**

This gene id conversion table between RefSeq and protein\_id is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_protein_id)
```

# **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding protein\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_protein\_id" but "id\_conv", because of the requirements by MiRaGE package.

# Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_protein_id)
```

MM\_refseq\_to\_refseq\_dna

Conversion table between RefSeq and refseq\_dna for mouse

# **Description**

This gene id conversion table between RefSeq and refseq\_dna is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_refseq_dna)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ref-seq\_dna. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_refseq\_dna" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_refseq_dna)
```

MM\_refseq\_to\_refseq\_peptide

Conversion table between RefSeq and refseq\_peptide for mouse

# **Description**

This gene id conversion table between RefSeq and refseq\_peptide is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_refseq_peptide)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ref-seq\_peptide. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_refseq\_peptide" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

# References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_refseq_peptide)
```

MM\_refseq\_to\_rfam

Conversion table between RefSeq and rfam for mouse

# Description

This gene id conversion table between RefSeq and rfam is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_rfam)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_rfam" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(MM_refseq_to_rfam)
```

MM\_refseq\_to\_rfam\_gene\_name

Conversion table between RefSeq and rfam\_gene\_name for mouse

### **Description**

This gene id conversion table between RefSeq and rfam\_gene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_rfam_gene_name)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_gene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_rfam\_gene\_name" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(MM_refseq_to_rfam_gene_name)
```

```
MM_refseq_to_rfam_transcript_name
```

Conversion table between RefSeq and rfam\_transcript\_name for mouse

# Description

This gene id conversion table between RefSeq and rfam\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_rfam_transcript_name)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_rfam\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(MM_refseq_to_rfam_transcript_name)
```

MM\_refseq\_to\_smart

Conversion table between RefSeq and smart for mouse

### **Description**

This gene id conversion table between RefSeq and smart is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_smart)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding smart. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_smart" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(MM_refseq_to_smart)
```

### **Description**

This gene id conversion table between RefSeq and tigrfam is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_tigrfam)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

# **Details**

The first column includes RefSeq gene id and the second column includes corresponding tigrfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_tigrfam" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_tigrfam)
```

MM\_refseq\_to\_ucsc

Conversion table between RefSeq and ucsc for mouse

# **Description**

This gene id conversion table between RefSeq and ucsc is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_ucsc)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### **Details**

The first column includes RefSeq gene id and the second column includes corresponding ucsc. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ucsc" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

# **Examples**

```
data(MM_refseq_to_ucsc)
```

### **Description**

This gene id conversion table between RefSeq and unigene is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_unigene)
```

#### **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding unigene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_unigene" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

### **Examples**

```
data(MM_refseq_to_unigene)
```

MM\_refseq\_to\_uniprot\_genename

Conversion table between RefSeq and uniprot\_genename for mouse

### **Description**

This gene id conversion table between RefSeq and uniprot\_genename is for MiRaGE package, based upon BioMart Gene ID Converter

#### **Usage**

```
data(MM_refseq_to_uniprot_genename)
```

# Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

#### **Details**

The first column includes RefSeq gene id and the second column includes corresponding uniprot\_genename. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_uniprot\_genename" but "id\_conv", because of the requirements by MiRaGE package.

#### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

#### **Examples**

```
data(MM_refseq_to_uniprot_genename)
```

MM\_refseq\_to\_wikigene\_name

Conversion table between RefSeq and wikigene\_name for mouse

# **Description**

This gene id conversion table between RefSeq and wikigene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

# Usage

```
data(MM_refseq_to_wikigene_name)
```

# **Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### Details

The first column includes RefSeq gene id and the second column includes corresponding wikigene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_wikigene\_name" but "id\_conv", because of the requirements by MiRaGE package.

# Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

#### References

For more details about BioMart Gene ID Converter, access to http://www.ensembl.org/biomart/martview/

```
data(MM_refseq_to_wikigene_name)
```

TBL2

TBL2

Target gene table miRNA

# **Description**

This target gene table of miRNA is for MiRaGE package. Actual name of data file is either TBL2\_MM (for mouse) or TBL2\_HS (for human), but name of data frame loaded is "TBL2"

### Usage

data(TBL2\_MM)

### **Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is the number of RefSeq gene id.

#### **Details**

This target gene table is generated by simple seed match between 3' UTR RefSeq gene and 5' UTR of miRNAs. 3' UTR RefSeq gene sequence is taken from genome table. miRNA mature sequences are taken from miRBase Release 18. Row names are miRNA names and column names are RefSeq gene id.

### Note

How to generate this table, please see functions in MiRaGE package and vignette.

### References

M, Yoshizawa, Y-h. Taguchi and J. Yasuda, Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method, Int. J. Mol. Sci. 2011, 12(12), 9265-9276

# **Examples**

data(TBL2\_MM)

114 TBL2\_MM

TBL2\_HS

Target gene table miRNA of human

# Description

This target gene table miRNA of human is for MiRaGE package

### Usage

data(TBL2\_HS)

### **Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is the number of RefSeq gene id.

#### **Details**

This target gene table is generated by simple seed match between 3' UTR RefSeq gene and 5' UTR of miRNAs. 3' UTR RefSeq gene sequence is taken from genome table, from hg19 genome sequence. miRNA mature sequences are taken from miRBase Release 18. Row names are miRNA names and column names are RefSeq gene id.

# Note

How to generate this table, please see functions in MiRaGE package and vignette.

### References

M, Yoshizawa, Y-h. Taguchi and J. Yasuda, Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method, Int. J. Mol. Sci. 2011, 12(12), 9265-9276

# **Examples**

data(TBL2\_HS)

TBL2\_MM

Target gene table miRNA of mouse

# **Description**

This target gene table miRNA of mouse is for MiRaGE package

### Usage

data(TBL2\_MM)

TBL2\_MM 115

# **Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is the number of RefSeq gene id.

# **Details**

This target gene table is generated by simple seed match between 3' UTR RefSeq gene and 5' UTR of miRNAs. 3' UTR RefSeq gene sequence is taken from genome table, from mm9 genome sequence. miRNA mature sequences are taken from miRBase Release 18. Row names are miRNA names and column names are RefSeq gene id.

### Note

How to generate this table, please see functions in MiRaGE package and vignette.

### References

M, Yoshizawa, Y-h. Taguchi and J. Yasuda, Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method, Int. J. Mol. Sci. 2011, 12(12), 9265-9276

# **Examples**

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