# Package 'miRNATarget'

# April 14, 2020

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<b>Title</b> gene target tabale of miRNA for human/mouse used for MiRaGE package
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Description gene target tabale of miRNA for human/mouse used for MiRaGE package
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<b>Depends</b> R ( $>= 2.10$ ), Biobase
License GPL
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# R topics documented:

conv_id
HS_conv_id
HS_refseq_to_affy_hc_g110
HS_refseq_to_affy_hg_focus
HS_refseq_to_affy_hg_u133a
HS_refseq_to_affy_hg_u133a_2
HS_refseq_to_affy_hg_u133b
HS_refseq_to_affy_hg_u133_plus_2
HS_refseq_to_affy_hg_u95a
HS_refseq_to_affy_hg_u95av2
HS_refseq_to_affy_hg_u95b
HS_refseq_to_affy_hg_u95c
HS_refseq_to_affy_hg_u95d
HS_refseq_to_affy_hg_u95e
HS_refseq_to_affy_huex_1_0_st_v2
HS_refseq_to_affy_hugenefl
HS_refseq_to_affy_hugene_1_0_st_v1
HS_refseq_to_affy_u133_x3p
HS_refseq_to_agilent_cgh_44b

2 R topics documented:

HS_refseq_to_agilent_wholegenome	
HS_refseq_to_canonical_transcript_stable_id	
HS_refseq_to_ccds	
HS_refseq_to_codelink	
HS_refseq_to_embl	
HS_refseq_to_ensembl_gene_id	
HS_refseq_to_ensembl_peptide_id	. 23
HS_refseq_to_ensembl_transcript_id	. 23
HS_refseq_to_entrezgene	
HS_refseq_to_hgnc_id	. 25
HS_refseq_to_hgnc_symbol	. 26
HS_refseq_to_hgnc_transcript_name	. 26
HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k	. 27
HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1	. 28
HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2	
HS_refseq_to_HS_refseq_to_ensembl_exon_id	
HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name	
HS_refseq_to_HS_refseq_to_uniprot_sptrembl	
HS_refseq_to_HS_refseq_to_uniprot_swissprot	
HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession	
HS_refseq_to_HS_refseq_to_wikigene_id	
HS_refseq_to_illumina_humanht_12	
HS_refseq_to_illumina_humanwg_6_v1	
HS_refseq_to_illumina_humanwg_6_v2	
HS_refseq_to_illumina_humanwg_6_v3	
HS_refseq_to_interpro	
HS_refseq_to_ipi	
HS_refseq_to_merops	
HS_refseq_to_pdb	
HS_refseq_to_pfam	
HS_refseq_to_phalanx_onearray	
HS_refseq_to_protein_id	
HS_refseq_to_refseq_dna	
HS_refseq_to_refseq_genomic	
HS_refseq_to_refseq_peptide	
HS_refseq_to_rfam	
HS_refseq_to_rfam_gene_name	
HS_refseq_to_rfam_transcript_name	
HS_refseq_to_smart	
HS refseq to tigrfam	
HS_refseq_to_ucsc	
HS_refseq_to_unigene	
HS_refseq_to_uniprot_genename	
HS_refseq_to_wikigene_name	
id_conv	
MM_conv_id	
MM_refseq_to_affy_mg_u74a	
MM_refseq_to_affy_mg_u74av2	
MM_refseq_to_affy_mg_u74b	
MM_refseq_to_affy_mg_u74bv2	
MM_refseq_to_affy_mg_u74c	
MM_refseq_to_affy_mg_u74cv2	. 56

MM_refseq_to_affy_moe430a
MM_refseq_to_affy_moe430b
MM_refseq_to_affy_moex_1_0_st_v1
MM_refseq_to_affy_mogene_1_0_st_v1
MM_refseq_to_affy_mouse430a_2
MM_refseq_to_affy_mouse430_2
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MM_refseq_to_affy_mu11ksubb
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MM_refseq_to_ensembl_peptide_id
MM_refseq_to_ensembl_transcript_id
MM_refseq_to_entrezgene
MM refseq to fantom
MM_refseq_to_illumina_mousewg_6_v1
MM_refseq_to_illumina_mousewg_6_v2
MM_refseq_to_interpro
MM refseq to ipi
MM_refseq_to_merops
MM_refseq_to_mgi_id
MM_refseq_to_mgi_symbol
MM_refseq_to_mgi_transcript_name
MM_refseq_to_mgi_transcript_name 76  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2 78  MM_refseq_to_MM_refseq_to_ensembl_exon_id 79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name 80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl 80  MM_refseq_to_MM_refseq_to_uniprot_swissprot 81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession 82  MM_refseq_to_MM_refseq_to_wikigene_id 83
MM_refseq_to_mgi_transcript_name 76  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2 78  MM_refseq_to_MM_refseq_to_ensembl_exon_id 79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name 80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl 80  MM_refseq_to_MM_refseq_to_uniprot_swissprot 81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession 82  MM_refseq_to_MM_refseq_to_wikigene_id 83  MM_refseq_to_pdb 83
MM_refseq_to_mgi_transcript_name 76  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2 78  MM_refseq_to_MM_refseq_to_ensembl_exon_id 79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name 80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl 80  MM_refseq_to_MM_refseq_to_uniprot_swissprot 81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession 82  MM_refseq_to_MM_refseq_to_wikigene_id 83  MM_refseq_to_pdb 83  MM_refseq_to_pfam 84
MM_refseq_to_mgi_transcript_name 76  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2 78  MM_refseq_to_MM_refseq_to_ensembl_exon_id 79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name 80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl 80  MM_refseq_to_MM_refseq_to_uniprot_swissprot 81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession 82  MM_refseq_to_MM_refseq_to_wikigene_id 83  MM_refseq_to_pdb 83  MM_refseq_to_pfam 84  MM_refseq_to_phalanx_onearray 85
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl  80  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  82  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  84  MM_refseq_to_pfam  84  MM_refseq_to_phalanx_onearray  85  MM_refseq_to_protein_id  86
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_systrembl  80  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  82  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  83  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  84  MM_refseq_to_pfam  85  MM_refseq_to_phalanx_onearray  85  MM_refseq_to_protein_id  86  MM_refseq_to_refseq_dna
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MM_refseq_to_mgi_transcript_name 76  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1 77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2 78  MM_refseq_to_MM_refseq_to_ensembl_exon_id 79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name 80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl 80  MM_refseq_to_MM_refseq_to_uniprot_swissprot 81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession 82  MM_refseq_to_MM_refseq_to_wikigene_id 83  MM_refseq_to_pdb 83  MM_refseq_to_pfam 84  MM_refseq_to_phalanx_onearray 85  MM_refseq_to_protein_id 86  MM_refseq_to_refseq_dna 86  MM_refseq_to_refseq_peptide 87  MM_refseq_to_refseq_peptide 87  MM_refseq_to_refam 88
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl  80  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  82  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  84  MM_refseq_to_pfam  85  MM_refseq_to_phalanx_onearray  MM_refseq_to_protein_id  MM_refseq_to_refseq_dna  MM_refseq_to_refseq_peptide  MM_refseq_to_refseq_peptide  MM_refseq_to_rfam  MM_refseq_to_rfam_gene_name  88  MM_refseq_to_rfam_gene_name
MM_refseq_to_mgi_transcript_name  MM_refseq_to_mMM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl  80  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot  82  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  83  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  84  MM_refseq_to_phalanx_onearray  85  MM_refseq_to_phalanx_onearray  86  MM_refseq_to_refseq_dna  87  MM_refseq_to_refseq_dna  88  MM_refseq_to_refseq_peptide  89  MM_refseq_to_rfam_gene_name  89  MM_refseq_to_rfam_transcript_name
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  82  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  83  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pfam  84  MM_refseq_to_pfam  85  MM_refseq_to_protein_id  86  MM_refseq_to_refseq_dna  87  MM_refseq_to_refseq_dna  88  MM_refseq_to_refam_gene_name  88  MM_refseq_to_rfam_gene_name  89  MM_refseq_to_smart  80  MM_refseq_to_smart
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_systembl  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot  82  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  83  MM_refseq_to_pfam  84  MM_refseq_to_pfam  84  MM_refseq_to_protein_id  86  MM_refseq_to_protein_id  86  MM_refseq_to_refseq_dna  86  MM_refseq_to_refseq_peptide  87  MM_refseq_to_rfam_gene_name  88  MM_refseq_to_rfam_transcript_name  89  MM_refseq_to_smart  90  MM_refseq_to_tigrfam  91
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_sptrembl  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  82  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  83  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pfam  84  MM_refseq_to_pfam  85  MM_refseq_to_protein_id  86  MM_refseq_to_refseq_dna  87  MM_refseq_to_refseq_dna  88  MM_refseq_to_refam_gene_name  88  MM_refseq_to_rfam_gene_name  89  MM_refseq_to_smart  80  MM_refseq_to_smart
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MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_systrembl  80  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot  82  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  83  MM_refseq_to_pfam  84  MM_refseq_to_pfam  84  MM_refseq_to_pfatanx_onearray  85  MM_refseq_to_protein_id  86  MM_refseq_to_refseq_dna  86  MM_refseq_to_refseq_peptide  87  MM_refseq_to_rfam_gene_name  88  MM_refseq_to_rfam_transcript_name  89  MM_refseq_to_smart  90  MM_refseq_to_tigrfam  91  MM_refseq_to_ucsc  92
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_systrembl  80  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  82  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  83  MM_refseq_to_pfam  84  MM_refseq_to_pfam  84  MM_refseq_to_pfatanx_onearray  85  MM_refseq_to_protein_id  86  MM_refseq_to_refseq_dna  86  MM_refseq_to_refseq_peptide  87  MM_refseq_to_rfam_gene_name  88  MM_refseq_to_rfam_transcript_name  89  MM_refseq_to_smart  90  MM_refseq_to_tigrfam  91  MM_refseq_to_unigene  92  MM_refseq_to_unigene
MM_refseq_to_mgi_transcript_name  MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1  77  MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2  78  MM_refseq_to_MM_refseq_to_ensembl_exon_id  79  MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name  80  MM_refseq_to_MM_refseq_to_uniprot_systrembl  80  MM_refseq_to_MM_refseq_to_uniprot_swissprot  81  MM_refseq_to_MM_refseq_to_uniprot_swissprot  82  MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession  83  MM_refseq_to_MM_refseq_to_wikigene_id  83  MM_refseq_to_pdb  84  MM_refseq_to_pfam  85  MM_refseq_to_pfam  86  MM_refseq_to_protein_id  86  MM_refseq_to_protein_id  86  MM_refseq_to_refseq_dna  86  MM_refseq_to_refseq_peptide  87  MM_refseq_to_rfam  88  MM_refseq_to_rfam_transcript_name  89  MM_refseq_to_fram_transcript_name  89  MM_refseq_to_fram_transcript_name  89  MM_refseq_to_to_fram_transcript_name  89  MM_refseq_to_to_fram_transcript_name  89  MM_refseq_to_to_fram_transcript_name  89  MM_refseq_to_unigene  90  MM_refseq_to_unigene  90  MM_refseq_to_uniprot_genename

4			
	TBL2_MM .		96
Index			98
conv	/_id	miRNA conservation table of mouse/hum Mouse/Human 6.1	nan, based upon TargetScan-

# 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.

# References

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

```
data(MM_conv_id)
```

HS\_conv\_id 5

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/

# **Examples**

```
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

```
data(HS_refseq_to_affy_hc_g110)
```

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/

# **Examples**

```
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.

7

#### References

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

# **Examples**

```
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/

# **Examples**

```
{\tt 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

```
data(HS_refseq_to_affy_hg_u133b)
```

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/

# **Examples**

```
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/

# **Examples**

```
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/

# **Examples**

```
{\tt 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

```
data(HS_refseq_to_affy_hg_u95b)
```

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/

# **Examples**

```
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.

13

#### References

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

# **Examples**

```
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/

# **Examples**

```
{\tt 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

```
data(HS_refseq_to_affy_huex_1_0_st_v2)
```

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/

# **Examples**

```
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/

# **Examples**

```
data(HS_refseq_to_affy_hugenefl)
```

```
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/

```
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/

# **Examples**

```
{\tt 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

```
data(HS_refseq_to_agilent_cgh_44b)
```

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/

# **Examples**

```
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/

# **Examples**

```
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/

```
{\tt data(HS\_refseq\_to\_canonical\_transcript\_stable\_id)}
```

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)
```

HS\_refseq\_to\_codelink 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

```
data(HS_refseq_to_codelink)
```

HS\_refseq\_to\_embl 21

#### **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/

# **Examples**

```
data(HS_refseq_to_ensembl_peptide_id)
```

```
{\tt 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

```
data(HS_refseq_to_ensembl_transcript_id)
```

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/

# **Examples**

```
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.

HS\_refseq\_to\_hgnc\_id

25

#### References

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

# **Examples**

```
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/

```
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)
```

```
{\tt 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

```
data(HS_refseq_to_hgnc_transcript_name)
```

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)
```

```
\label{localization} \begin{split} \text{HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k} \\ & \textit{Conversion} \quad \textit{table} \quad \textit{between} \quad \textit{RefSeq} \quad \textit{and} \\ & \textit{HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k} \, \textit{for human} \end{split}
```

# **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\_sure. 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)
```

```
\label{thm:conversion} 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
```

# **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\_who 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/

```
\label{local_data} data (HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1)
```

 $\label{eq:hs_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2} \\ Conversion & table & between & RefSeq & and \\ & HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 \ for \ human \\ \\$ 

# **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\_who 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/

#### **Examples**

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

```
\label{local-conversion} {\it HS\_refseq\_to\_ensembl\_exon\_id} \\ {\it Conversion\ table\ between\ RefSeq\ and\ HS\_refseq\_to\_ensembl\_exon\_id} \\ {\it for\ human}
```

# **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/

### **Examples**

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

```
\label{thm:conversion} HS\_refseq\_to\_uniprot\_genename\_transcript\_name \\ Conversion table between RefSeq and \\ HS\_refseq\_to\_uniprot\_genename\_transcript\_name for human
```

# **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\_genenam. 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\_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/

# **Examples**

```
data(HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name)
```

```
HS_refseq_to_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/

```
{\tt 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/

# **Examples**

```
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 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/

# **Examples**

```
{\tt 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/

# **Examples**

```
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/

# **Examples**

```
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/

# **Examples**

```
data(HS_refseq_to_illumina_humanwg_6_v3)
```

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/

```
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

```
data(HS_refseq_to_merops)
```

HS\_refseq\_to\_pdb 39

#### **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.

#### 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

40 HS\_refseq\_to\_pfam

#### References

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

# **Examples**

```
data(HS_refseq_to_pdb)
```

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/

```
{\tt 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

```
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 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)
```

44 HS\_refseq\_to\_rfam

```
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/

# **Examples**

```
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

```
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 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.

## **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/

```
data(HS_refseq_to_rfam_transcript_name)
```

HS\_refseq\_to\_smart 47

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.

## 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

```
data(HS_refseq_to_tigrfam)
```

48 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 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/

# **Examples**

```
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 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/

```
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

```
data(HS_refseq_to_wikigene_name)
```

id\_conv 51

#### **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/

### **Examples**

```
data(HS_refseq_to_wikigene_name)
```

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.

52 MM\_conv\_id

#### References

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

# **Examples**

```
data(MM_refseq_to_wikigene_name)
```

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/

### **Examples**

```
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

```
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/

## **Examples**

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

# **Examples**

```
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/

### **Examples**

```
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

```
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/

## **Examples**

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

# **Examples**

```
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/

# **Examples**

```
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

```
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/

## **Examples**

```
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

61

#### References

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

# **Examples**

```
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\_mu11ksuba 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/

### **Examples**

```
data(MM_refseq_to_affy_mu11ksuba)
```

```
MM_refseq_to_affy_mu11ksubb
```

Conversion table between RefSeq and affy\_mu11ksubb for mouse

# Description

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

```
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/

## **Examples**

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

## **Examples**

```
data(MM_refseq_to_agilent_wholegenome)
```

```
MM_refseq_to_canonical_transcript_stable_id
```

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

# **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 65

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)
```

MM\_refseq\_to\_codelink 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

```
data(MM_refseq_to_codelink)
```

66 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 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 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/

# **Examples**

```
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

```
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/

## **Examples**

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

# **Examples**

```
data(MM_refseq_to_entrezgene)
```

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/

```
data(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)
```

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

# 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.

MM\_refseq\_to\_ipi 73

#### 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_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

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

```
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**

```
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)
```

# **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\_sure. 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/

#### **Examples**

```
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\_who 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/

#### **Examples**

```
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\_who 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/

### **Examples**

```
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\_ 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\_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/

```
\tt data(MM\_refseq\_to\_MM\_refseq\_to\_ensembl\_exon\_id)
```

# **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\_genena 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\_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**

 $\label{lem:data} data(\texttt{MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_genename\_transcript\_name})$ 

### **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\_sptreml 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/

### **Examples**

```
data(MM_refseq_to_MM_refseq_to_uniprot_sptrembl)
```

### **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\_swisspr 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/

### **Examples**

```
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\_swisspr 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/

```
{\tt data}({\tt 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/

# **Examples**

```
data(MM_refseq_to_MM_refseq_to_wikigene_id)
```

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

```
data(MM_refseq_to_pdb)
```

84 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 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)
```

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/

```
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/

#### **Examples**

```
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

```
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/

### **Examples**

```
{\tt 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.

88 MM\_refseq\_to\_rfam

#### References

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

### **Examples**

```
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/

```
{\tt 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

```
data(MM_refseq_to_rfam_transcript_name)
```

90 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 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/

```
{\tt 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)
```

MM\_refseq\_to\_unigene

Conversion table between RefSeq and unigene for mouse

# Description

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

```
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 95

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)

TBL2\_HS

Target gene table miRNA of human

# **Description**

This target gene table miRNA of human is for MiRaGE package

```
data(TBL2_HS)
```

96 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, 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)
```

# **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.

TBL2\_MM 97

# 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)

# **Index**

```
*Topic data
    conv_id, 4
                                                    HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4
    HS_conv_id, 5
    HS_refseq_to_affy_hc_g110, 5
                                                    HS_refseq_to_HS_refseq_to_ensembl_exon_id,
    HS_refseq_to_affy_hg_focus, 6
    HS_refseq_to_affy_hg_u133_plus_2,
                                                    HS_refseq_to_HS_refseq_to_uniprot_genename_transcri
    HS_refseq_to_affy_hg_u133a,7
                                                    HS_refseq_to_HS_refseq_to_uniprot_sptrembl,
    HS_refseq_to_affy_hg_u133a_2,8
                                                    HS_refseq_to_HS_refseq_to_uniprot_swissprot,
    HS_refseq_to_affy_hg_u133b, 8
    HS_refseq_to_affy_hg_u95a, 10
    HS_refseq_to_affy_hg_u95av2, 11
                                                    HS_refseq_to_HS_refseq_to_uniprot_swissprot_access:
    HS_refseq_to_affy_hg_u95b, 11
                                                    HS_refseq_to_HS_refseq_to_wikigene_id,
    HS_refseq_to_affy_hg_u95c, 12
    HS_refseq_to_affy_hg_u95d, 13
                                                    HS_refseq_to_illumina_humanht_12,
    HS_refseq_to_affy_hg_u95e, 14
    HS_refseq_to_affy_huex_1_0_st_v2,
                                                    HS_refseq_to_illumina_humanwg_6_v1,
    HS_refseq_to_affy_hugene_1_0_st_v1,
                                                    HS_refseq_to_illumina_humanwg_6_v2,
    HS_refseq_to_affy_hugenefl, 15
                                                    HS_refseq_to_illumina_humanwg_6_v3,
    HS_refseq_to_affy_u133_x3p, 17
    HS_refseq_to_agilent_cgh_44b, 17
                                                    HS_refseq_to_interpro, 37
    HS_refseq_to_agilent_wholegenome,
                                                    HS_refseq_to_ipi, 38
    {\tt HS\_refseq\_to\_canonical\_transcript\_stable\_id, \ HS\_refseq\_to\_merops, 38}
                                                    HS_refseq_to_pdb, 39
        19
                                                    HS_refseq_to_pfam, 40
    HS_refseq_to_ccds, 20
                                                    HS_refseq_to_phalanx_onearray, 41
    HS_refseq_to_codelink, 20
                                                    HS_refseq_to_protein_id, 41
    HS_refseq_to_embl, 21
                                                    HS_refseq_to_refseq_dna, 42
    HS_refseq_to_ensembl_gene_id, 22
                                                    HS_refseq_to_refseq_genomic, 43
    HS_refseq_to_ensembl_peptide_id,
                                                    HS_refseq_to_refseq_peptide, 44
                                                    HS_refseq_to_rfam, 44
    HS_refseq_to_ensembl_transcript_id,
                                                    HS_refseq_to_rfam_gene_name, 45
    HS_refseq_to_entrezgene, 24
                                                    HS_refseq_to_rfam_transcript_name,
                                                        46
    HS_refseq_to_hgnc_id, 25
                                                    HS_refseq_to_smart, 47
    HS_refseq_to_hgnc_symbol, 26
                                                    HS_refseq_to_tigrfam, 47
    HS_refseq_to_hgnc_transcript_name,
                                                    HS_refseq_to_ucsc, 48
    \label{localization} {\tt HS\_refseq\_to\_efg\_agilent\_surepri} \\ {\tt HS\_gefgeq.8t60lt}, igene, 49
                                                    HS_refseq_to_uniprot_genename, 50
    HS_refseq_to_HS_refseq_to_efg_agilent_wholegeHSmeeffsedkto1wikigene_name, 50
```

INDEX 99

```
id_conv, 51
                                                   80
MM_conv_id, 52
                                               MM_refseq_to_MM_refseq_to_uniprot_sptrembl,
MM_refseq_to_affy_mg_u74a, 53
                                               MM_refseq_to_MM_refseq_to_uniprot_swissprot,
MM_refseq_to_affy_mg_u74av2, 53
{\tt MM\_refseq\_to\_affy\_mg\_u74b,}\, {\tt 54}
                                               MM_refseq_to_MM_refseq_to_uniprot_swissprot_access:
MM_refseq_to_affy_mg_u74bv2, 55
MM_refseq_to_affy_mg_u74c, 56
                                               MM_refseq_to_MM_refseq_to_wikigene_id,
MM_refseq_to_affy_mg_u74cv2, 56
MM_refseq_to_affy_moe430a, 57
                                               MM_refseq_to_pdb, 83
MM_refseq_to_affy_moe430b, 58
                                               MM_refseq_to_pfam, 84
MM_refseq_to_affy_moex_1_0_st_v1,
                                               MM_refseq_to_phalanx_onearray, 85
                                               MM_refseq_to_protein_id, 86
MM_refseq_to_affy_mogene_1_0_st_v1,
                                               MM_refseq_to_refseq_dna, 86
    59
                                               MM_refseq_to_refseq_peptide, 87
MM_refseq_to_affy_mouse430_2, 61
                                               MM_refseq_to_rfam, 88
MM_refseq_to_affy_mouse430a_2, 60
                                               MM_refseq_to_rfam_gene_name, 89
MM_refseq_to_affy_mu11ksuba, 62
                                               MM_refseq_to_rfam_transcript_name,
MM_refseq_to_affy_mu11ksubb, 62
                                                   89
MM_refseq_to_agilent_wholegenome,
                                               MM_refseq_to_smart, 90
                                               MM_refseq_to_tigrfam, 91
MM_refseq_to_canonical_transcript_stable_id,
                                               MM_refseq_to_ucsc, 92
                                               MM_refseq_to_unigene, 92
MM_refseq_to_ccds, 65
                                               MM_refseq_to_uniprot_genename, 93
MM_refseq_to_codelink, 65
                                               MM_refseq_to_wikigene_name, 94
MM_refseq_to_embl, 66
                                               TBL2, 95
MM_refseq_to_ensembl_gene_id, 67
                                               TBL2_HS, 95
MM_refseq_to_ensembl_peptide_id,
                                               TBL2_MM, 96
MM_refseq_to_ensembl_transcript_id,
                                           conv_id, 4
MM_refseq_to_entrezgene, 69
                                           HS_conv_id, 5
MM_refseq_to_fantom, 70
                                           HS_refseq_to_affy_hc_g110,5
MM_refseq_to_illumina_mousewg_6_v1,
                                           HS_refseq_to_affy_hg_focus, 6
                                           HS_refseq_to_affy_hg_u133_plus_2,9
MM_refseq_to_illumina_mousewg_6_v2,
                                           HS_refseq_to_affy_hg_u133a, 7
    71
                                           HS_refseq_to_affy_hg_u133a_2,8
MM_refseq_to_interpro, 72
                                           HS_refseq_to_affy_hg_u133b, 8
MM_refseq_to_ipi, 73
                                           HS_refseq_to_affy_hg_u95a, 10
MM_refseq_to_merops, 74
                                           HS_refseq_to_affy_hg_u95av2, 11
MM_refseq_to_mgi_id, 74
                                           HS_refseq_to_affy_hg_u95b, 11
MM_refseq_to_mgi_symbol, 75
                                           HS_refseq_to_affy_hg_u95c, 12
MM_refseq_to_mgi_transcript_name,
                                           HS_refseq_to_affy_hg_u95d, 13
                                           HS_refseq_to_affy_hg_u95e, 14
MM_refseq_to_MM_refseq_to_efg_agilent_sur@priefts@d_ge_&&f0khuex_1_0_st_v2, 14
                                           HS_refseq_to_affy_hugene_1_0_st_v1, 16
MM_refseq_to_MM_refseq_to_efg_agilent_wholl@geen6smeq4te44tfff.hugenefl, 15
                                           HS_refseq_to_affy_u133_x3p, 17
MM_refseq_to_MM_refseq_to_efg_agilent_wholl@gea6seq4te44tgivlent_cgh_44b, 17
                                           HS_refseq_to_agilent_wholegenome, 18
MM_refseq_to_MM_refseq_to_ensembl_exon_idHS_refseq_to_canonical_transcript_stable_id,
MM_refseq_to_MM_refseq_to_uniprot_genenames_trafiseq_ipt_oads, 20
```

100 INDEX

HS_refseq_to_codelink, 20	MM_conv_id, 52
HS_refseq_to_embl, 21	MM_refseq_to_affy_mg_u74a, 53
HS_refseq_to_ensembl_gene_id, 22	MM_refseq_to_affy_mg_u74av2, 53
HS_refseq_to_ensembl_peptide_id, 23	MM_refseq_to_affy_mg_u74b, 54
HS_refseq_to_ensembl_transcript_id, 23	MM_refseq_to_affy_mg_u74bv2, 55
HS_refseq_to_entrezgene, 24	MM_refseq_to_affy_mg_u74c, 56
HS_refseq_to_hgnc_id, 25	MM_refseq_to_affy_mg_u74cv2, 56
HS_refseq_to_hgnc_symbol, 26	MM_refseq_to_affy_moe430a, 57
HS_refseq_to_hgnc_transcript_name, 26	MM_refseq_to_affy_moe430b, 58
HS_refseq_to_HS_refseq_to_efg_agilent_surepr	iMN_g&fgeq8x60&ffy_moex_1_0_st_v1,59
27	MM_refseq_to_affy_mogene_1_0_st_v1, 59
${\tt HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegerseq\_to\_efg\_agilent\_whole$	e <b>Mo<u>m</u>eeflydd</b> ktහ <u>1</u> affy_mouse430_2,61
28	MM_refseq_to_affy_mouse430a_2,60
${\tt HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholeger} \\$	
29	MM_refseq_to_affy_mu11ksubb, 62
HS_refseq_to_HS_refseq_to_ensembl_exon_id,	MM_refseq_to_agilent_wholegenome, 63
29	MM_refseq_to_canonical_transcript_stable_id,
HS_refseq_to_HS_refseq_to_uniprot_genename_t	ranscript64ame,
30	MM_refseq_to_ccds, 65
HS_refseq_to_HS_refseq_to_uniprot_sptrembl,	MM_refseq_to_codelink, 65
31	MM_refseq_to_embl, 66
${\tt HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot},$	MM_refseq_to_ensembl_gene_id, 67
32	MM_refseq_to_ensembl_peptide_id, 68
${\tt HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot\_def} \\$	ୟୟୟ <u>୍ଟ୍ରେମ୍ଟ୍ରେମ୍</u> ଡ୍ରେମ୍ବ୍ରେମ୍ବ୍ରେମ୍ବର୍
32	MM_refseq_to_entrezgene, 69
HS_refseq_to_HS_refseq_to_wikigene_id,	MM_refseq_to_fantom, 70
33	MM_refseq_to_illumina_mousewg_6_v1,71
HS_refseq_to_illumina_humanht_12, 34	MM_refseq_to_illumina_mousewg_6_v2,71
HS_refseq_to_illumina_humanwg_6_v1,35	MM_refseq_to_interpro,72
HS_refseq_to_illumina_humanwg_6_v2, 35	MM_refseq_to_ipi,73
HS_refseq_to_illumina_humanwg_6_v3,36	MM_refseq_to_merops, 74
HS_refseq_to_interpro, 37	MM_refseq_to_mgi_id, 74
HS_refseq_to_ipi, 38	MM_refseq_to_mgi_symbol, 75
HS_refseq_to_merops, 38	MM_refseq_to_mgi_transcript_name, 76
HS_refseq_to_pdb, 39	MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_
HS_refseq_to_pfam, 40	77
HS_refseq_to_phalanx_onearray, 41	MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44
HS_refseq_to_protein_id, 41	77
HS_refseq_to_refseq_dna, 42	MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44
HS_refseq_to_refseq_genomic, 43	78
HS_refseq_to_refseq_peptide, 44	MM_refseq_to_MM_refseq_to_ensembl_exon_id,
HS_refseq_to_rfam, 44	79
HS_refseq_to_rfam_gene_name, 45	MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_
HS_refseq_to_rfam_transcript_name, 46	80
HS_refseq_to_smart, 47	MM_refseq_to_MM_refseq_to_uniprot_sptrembl,
HS_refseq_to_tigrfam, 47	80
HS_refseq_to_ucsc, 48	MM_refseq_to_MM_refseq_to_uniprot_swissprot,
HS_refseq_to_unigene, 49	81
${\tt HS\_refseq\_to\_uniprot\_genename,} \ 50$	MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession,
HS_refseq_to_wikigene_name, 50	82
	MM_refseq_to_MM_refseq_to_wikigene_id,
id_conv, 51	83

INDEX 101

```
MM_refseq_to_pdb, 83
MM_refseq_to_pfam, 84
{\tt MM\_refseq\_to\_phalanx\_onearray},\, 85
MM_refseq_to_protein_id, 86
MM_refseq_to_refseq_dna, 86
MM_refseq_to_refseq_peptide, 87
\texttt{MM\_refseq\_to\_rfam}, \textcolor{red}{88}
MM_refseq_to_rfam_gene_name, 89
MM_refseq_to_rfam_transcript_name, 89
{\tt MM\_refseq\_to\_smart}, \textcolor{red}{90}
MM_refseq_to_tigrfam, 91
MM_refseq_to_ucsc, 92
MM_refseq_to_unigene, 92
MM_refseq_to_uniprot_genename, 93
{\tt MM\_refseq\_to\_wikigene\_name}, 94
TBL2, 95
TBL2_HS, 95
TBL2_MM, 96
```