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CLUSTAL W (1.83) multiple sequence alignment


human_chr22_NM_001469      -GATCGAGATCTCTTGGCTGTGGTGTTCTATGGTACCGAGAAAGACAAAA
rat_chr7                   CGATCGGGATCTCTTGGCAGTGGTGTTCTATGGTACCGAGAAAGACAAAA
                            ***** *********** *******************************

human_chr22_NM_001469      ATTCAGTGAATTTTAAAAATATTTACGTCTTACAGGAGCTGGATAATCCA
rat_chr7                   ATTCAGTGAACTTCAAAAGTATTTATGTCTTACAAGATCTGGATAACCCA
                           ********** ** **** ****** ******** ** ******** ***

human_chr22_NM_001469      GGTCAGTAATATTTTAAGATCAGCTTTTCCCTTATATATGAGAATATCAG
rat_chr7                   G-------------------------------------------------
                           *

human_chr22_NM_001469      TACTCTGATCAAAGAGGACTGTGGAGAAGGAAGCAAGTTACATCTTGTCT
rat_chr7                   --------------------------------------------------


human_chr22_NM_001469      AGGAGTATGCTTTCCTCCATAAGGGGACCTTGCTCGATGTGGACTTTGTT
rat_chr7                   --------------------------------------------------


human_chr22_NM_001469      AAATGGGTTAAACAGCTCTGGGGTGAAAAAGGGTCCTTCTGTTAGTCTTG
rat_chr7                   --------------------------------------------------


human_chr22_NM_001469      TGGTAAAGGCAGCCACTGACATTCTTCTGATTTTTCTTTCCATTTGACTC
rat_chr7                   --------------------------------------------------


human_chr22_NM_001469      CCTGCCTCTGATCAGGTGCAAAACGAATTCTAGAGCTTGACCAGTTTAAG
rat_chr7                   ---------------GAGCTAAACGAGTGTTAGAGCTTGACCGCTTTAAG
                                          * ** ****** *  ************  ******

human_chr22_NM_001469      GGGCAGCAGGGACAAAAACGTTTCCAAGACATGATGGGCCACGGATCTGA
rat_chr7                   GGACAACAGGGGAAAAAACATTTCCGAGACACAATTGGCCATGGGTCTGA
                           ** ** *****  ****** ***** *****  ** ***** ** *****

human_chr22_NM_001469      CTACTCACTCAGTGA---------
rat_chr7                   CTACTCTTTGAGTGAAGTGCTCTG
                           ******  * *****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr20_NM_181801      -GACACCCAGGGTAACATATGCCTGGACATCCTGAAGGAAAAGTGGTCTG
rat_chr3                   GGACACCCAGGGCAACATCTGCCTGGACATCCTCAAGGACAAGTGGTCTG
                            *********** ***** ************** ***** **********

human_chr20_NM_181801      CCCTGTATGATGTCAGGACCATTCTGCTCTCCATCCAGAGCCTTCTAGGA
rat_chr3                   CACTGTATGATGTCAGGACCATCTTGCTCTCCATCCAGAGCCTGCTAGGA
                           * ********************  ******************* ******

human_chr20_NM_181801      GGTGACTTTAGAGACCACCCCTCCCCTCCATGCAACTTGGGAACCTGTCA
rat_chr3                   G-------------------------------------------------
                           *

human_chr20_NM_181801      GGACTCCCTGGGGTCAGCCTCTTCTACCGCCTTGACCTTCTCTTTCTCTC
rat_chr3                   --------------------------------------------------


human_chr20_NM_181801      CACCCACAGAACCCAACATTGATAGTCCCTTGAACACACATGCTGCCGAG
rat_chr3                   ---------AACCCAACATCGAGAGCCCTTTGAACACACATGCTGCAGAG
                                    ********** ** ** ** ***************** ***

human_chr20_NM_181801      CTCTGGAAAAACCCCACAGGTGAGTCCTCAGTCCTTGAGCCCAGGGTGAT
rat_chr3                   CTCTGGAAAAACCCCACAGGTAGGGCCTTG----TCCAGCTCAGAGTGAC
                           *********************  * ***      *  *** *** ****

human_chr20_NM_181801      CCCTCCCCC------
rat_chr3                   CCTTGCTAACGTACA
                           ** * *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr20_NM_033405      ----TGTGGTCAAGAATGAGCGGCTGCAAAACCTGGGTCTGGACCGGTCT
rat_chr3                   GGCCTGTGGTCAAGAACGAACAGCTGCGAAACCTGGGGATGGACCGGTCA
                               ************ ** * ***** *********  ********** 

human_chr20_NM_033405      CTGTTCGAGCGGTACCACGAGGACGCACATATGCTGGACACTCAGTACCG
rat_chr3                   CTCTTTGAGAGGTACCACAGGGATGCCATCATGCTGGACACACAGTACCG
                           ** ** *** ********  *** **    *********** ********

human_chr20_NM_033405      CATGGTGAGCCCGCCCCACTCAGCCCCCAGCCCACCTGCAGCCCCTGGGG
rat_chr3                   TATG----------------------------------------------
                            ***                                              

human_chr20_NM_033405      GGCCACAACCCCGCGTGGCAGCCTCTGACCAGCGCACATCCTTGCCTGCA
rat_chr3                   --------------------------------------------------
                                                                             

human_chr20_NM_033405      GCATGAGGGCATCTGTGCCTTCCCCTCTGTGGCGTTCTACAAGAGCAAGC
rat_chr3                   -CATAAGGACATCTGCTCCTTTCCCTCCATGGAGTTCTATGGGGGAAAGC
                            *** *** ******  **** *****  *** ******   * * ****

human_chr20_NM_033405      TGAAGACGTGGCAGGGCCTGAGGAGGCCGCCCAGTGTCCTGGGCCACGCT
rat_chr3                   TAAAGACCTGGTCCGACCTGAAGCGTCCACCCAGCCTCCTAGGTCATGTC
                           * ***** ***   * ***** * * ** *****  **** ** ** * 

human_chr20_NM_033405      G-
rat_chr3                   GG
                           * 
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CLUSTAL W (1.83) multiple sequence alignment


human_chr20_NM_032034      ------CGCTTCGCCAGGGACCCTGACAACAATGAGCCCAACTGCAACCT
rat_chr3                   CTAAACCGCTTTGCCCAGGACCCCAACCATGCAGAGCCTGATTGTGACCT
                                 ***** ***  ******  ** *    *****  * **  ****

human_chr20_NM_032034      GGACCTGCTCATGGCCATGCTCTTCACCGATGCCGGGGCACCCATGCGGG
rat_chr3                   GGACCTGCTCATGGCTAAGCTCTTTACAGATGCTGGGGGCCCCATGGAGA
                           *************** * ****** ** ***** ****  ******  *

human_chr20_NM_032034      GTAAAGGTGAGGCCGGTCTCCCGGCCCGGGCGGGGGCGTTGGGAGGGGCT
rat_chr3                   GTAAAG--------------------------------------------
                           ******

human_chr20_NM_032034      GTTGACCCACCACCCTCCCCCTCACTCTTTCCTCAGTCCACCTGCTGTCA
rat_chr3                   ------------------------------------TCCACCTGCTGTCA
                                                               **************

human_chr20_NM_032034      GATACCATCCAAGGGGTCACCGCCACAGTGACAGGGGTGCGGTACCAGCA
rat_chr3                   GATACCATCCAGGGAGTGACCGCCACTGTCAGAGGACTGCAGTACGAGCA
                           *********** ** ** ******** ** * ***  *** **** ****

human_chr20_NM_032034      GTCGTGGCTCTGCATCATGTGAGTTGCCAGGCCACT-
rat_chr3                   GTCATGGCTCTGCATCGTGTGAGTTGCCATCCTACAA
                           *** ************ ************  * **
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CLUSTAL W (1.83) multiple sequence alignment


human_chr20_NM_005560      -CCGTGGCTGCGTCAAAGGCATCAAGGCCCTGGGCAAGTATGTGGACCTC
rat_chr3                   TCCGTGGCTGCATCAAAGGTATCAAGGCTCTGGGCAAGTACGTGGACCTC
                            ********** ******* ******** *********** *********

human_chr20_NM_005560      AAGCGGCTGAACACGACAGGCGTGAGCGCCGGCTGCACCGCCGACCTGCT
rat_chr3                   AAACGACTGAACACCACGGGCATCAGCTTCAGCTGCACCGCTGACCTGCT
                           ** ** ******** ** *** * ***  * ********** ********

human_chr20_NM_005560      GGTGAGCAGCCCTCCCCGGGCTGGGGGTGGCATCTGTGGACATGCAGGGG
rat_chr3                   A-------------------------------------------------
                                                                             

human_chr20_NM_005560      CACCCGCGGGCACTCAGGGATGGCCTCCCCGCAGGTGGGGCGCGCCATGA
rat_chr3                   ----------------------------------ATGGGACGCACCATGA
                                                              **** *** ******

human_chr20_NM_005560      CTTTCCATGGCCACGGCTTCCTTCGCCTGGCGCTCTCGAACGTGGCACCG
rat_chr3                   CTTTCCACGGCCACGGCTTCCTGCCCCTGGCACTTCCCGATGTGGCGCCG
                           ******* ************** * ****** **  *  * ***** ***

human_chr20_NM_005560      CTCACTGGCAACGTCTACTCCGGCTTCGGCTTCC-
rat_chr3                   ATCACTGGAGAGGTCTATTCTGGCTTCGGCTTTCG
                            *******  * ***** ** *********** * 
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_000979      ------------CGGGCCCGCAGCCGCATCCTCAGGGCAGGGGGCAAGAT
rat_chr1                   AGGGTGAGCAGCCGGGCCCGAAGTCGGATCCTCAAGGCTGGGGGTAAGAT
                                       ******** ** ** ******* *** ***** *****

human_chr19_NM_000979      CCTCACTTTCGACCAGCTGGCCCTGGACTCCCCTAAGGGCTGTGGCACTG
rat_chr1                   CCTGACCTTCGACCAGCTGGCCCTGGAGTCTCCCAAGGGCAGGGGCACTG
                           *** ** ******************** ** ** ****** * *******

human_chr19_NM_000979      TCCTGCTCTCCGGTGAGTGATACGTGGTCGACGGGTTTGGACTGAGCTGT
rat_chr1                   TGCTCTTGTCTG--------------------------------------
                           * **  * ** *

human_chr19_NM_000979      GTGGCTACTGGCAGCCTTCACCCTCCTGGATCTGGGAGGCCAGAAGCTGG
rat_chr1                   --------------------------------------------------


human_chr19_NM_000979      GCGCCAGATCCCTGTCTCACCCGGTTCTCCTTCCCCTTCCCTAGGTCCTC
rat_chr1                   --------------------------------------------GTCCTC
                                                                       ******

human_chr19_NM_000979      GCAAGGGCCGAGAGGTGTACCGGCATTTCGGCAAGGCCCCAGGAACCCCG
rat_chr1                   GGAAGGGCCGAGAGGTGTACCGACACTTTGGCAAGGCCCCAGGAACTCCA
                           * ******************** ** ** ***************** **

human_chr19_NM_000979      CACAGCCACACCAAGTGAGTATCAGGCCCCCAGCCCTGCCCTCT-
rat_chr1                   CACAGCCACACCAAGTGAGTAGTGGGGCCTTGTCCTTCGGTAGCT
                           *********************   ** **    ** *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_182513      ---TCACCAGAGAGCTGGAAGAGCTCAAGGAGATTGAGGCGGATCTGGAG
rat_chr8                   AGCTCACCGCAGAGCTGCAGGAGCTCAGGGAGATGGAGGAAGATCTCCAG
                              *****  ******* * ******* ****** ****  *****  **

human_chr19_NM_182513      CGACAGGAGAAGGAGGTCGACGAGGACACGACAGTCACAATCCCCTCGGC
rat_chr8                   CGACAGGAGAGAGACGTGGATGAAGACAACACTGTCACCATCCCCTCTGC
                           **********  ** ** ** ** ****  ** ***** ******** **

human_chr19_NM_182513      CGTGTAGGTTCTGCCAAAACGTGTGCCTGCCTGTGCCTCCTTGTGCAGTC
rat_chr8                   AGT-----------------------------------------------
                            **

human_chr19_NM_182513      CGGCTCTTGGTTGAAGTTGGTGCTGGGTAACTTTCTTTTTTTTTTTTTTT
rat_chr8                   --------------------------------------------------


human_chr19_NM_182513      TTTTTTTGTCTTCCTGTACAGGTACGTGGCTCAACTTTACCACCAAGTTA
rat_chr8                   ---------------------GTATGTGGCGCAGCTCTACCACCAAATTA
                                                *** ***** ** ** ********* ***

human_chr19_NM_182513      GTAAAATTGAGTGGGATTATGAGTGTGAGCCAGGGATGGTCAAAGGCAGT
rat_chr8                   GTAAAATAGAGTGGGATTATGAGTGCGAGCCCGGGATGGTCAAGGGCAGT
                           ******* ***************** ***** *********** ******

human_chr19_NM_182513      ATCCTTTTTGGGGAGCCATTT
rat_chr8                   ATCCTTTGAGAAGTCGGTGT-
                           *******  *  *      *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_001379      TTCCATAGAGGCCAGCCCAGTGGTTGTGCCGGTTCCCGGTGTGGGGCAGG
rat_chr8                   GCCCGTAGAGGCCAGCCCAGTGGTTGTGCCGGTTCCCAGTGTGCGGCAGG
                             ** ******************************** ***** ******

human_chr19_NM_001379      CACCAGGGGATGAGGGTGTTGAACTGCCTGGCTGCGGGGTCGCAGGCTTT
rat_chr8                   CACCAGGGGATGAGCGTGTTGAATTGTCTGGAAGCAGGGTCGCAG-----
                           ************** ******** ** ****  ** *********

human_chr19_NM_001379      GCCGGCTGGAAGACAGGACAGTGATGAGGCTGCAGTTGTGGGATGGGGTA
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      TAGGCTTGGGACAGTGGCTCTTAGAGCTTTGGGAGGCAGAGATGGCACCT
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      CCTGTGCAAGGGGCCCCCTGGGGTGGAGCAGCCAACAATCCTCGTTCTCT
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      GGGCACTGTTTTTATTATTAGTATTATATGTCTCGCTCTGTTGCCCAGGC
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      TGGAGTGCAATGGCATGATCTTGGCTCACTGCAACCTCTGCCTATGGGGT
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      TCAAGCGATTCTCCTGCCTCAGCCTCCCAAATAGCTGGGATTATAGGCGT
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      GCGACACCACGCCCGGCTAATTTTTGTAGTTTTAATAGAGATGGGGTTTC
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      ACCATGTTGGGCAGGCTGATCTCGAGCTCCTGATCTCAAGTGATCTGCCT
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      GCCTTGGCCTCCCAAAGTGCTGGGATTACAGAGGTGAGCCATCGTGCCTG
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      ACCTGCTTTTATTATTTATTTATTGTTTTTTTTTTTTCTTTTTAGAGACA
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      GGGTCTCACTCTGTCTCCCAGGCTGGAGTGCAATGGCACAATCACAGCTC
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      ACTGTAGCCTCCTCAACCTCCCAGGCTCAAGTGATCCTCCCGCCTTGGTT
rat_chr8                   --------------------------------------------------
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human_chr19_NM_001379      TCCCAAAGTGCTGGGATTATAGGTGTGGGCCATGAACCCAGCCTGCTTTT
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      ACTACTCAACATGGTCAGCAGCTACCTTCTCTGGGACACCCAGGCTTGGT
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      GTGTCTGTGCCCTGCCCTGGCCTCCAGGTTCACAGGCCAAAGGCCCAGGG
rat_chr8                   --------------------------------------------------


human_chr19_NM_001379      CTCTGCCTTCCTTCCCCTCAGCCCACCGGGAACCACAACTTACAGGACCC
rat_chr8                   ---------------------------------------------GTCTT
                                                                        * *

human_chr19_NM_001379      ACCTTCCACGCAGGAGCAGACCCCACGGAGGGCCCCAGAGCTGCTGCGGC
rat_chr8                   GCCTTCCGCACAGGAGCAGACCCCACGCAGGGCCCCGGTGCTGCTGCAGC
                            ****** * ***************** ******** * ******** **

human_chr19_NM_001379      CGTTCTTCCTGTCATGGTGGGTATACCGCAGCTTCCTGGCCATGGTGCCG
rat_chr8                   CGTTCTTCGTGTCGTGGAAAGTGTAGCGAAGTTTATTGGTTATGACGCCA
                           ******** **** ***   ** ** ** ** **  ***  ***  *** 

human_chr19_NM_001379      TCTGAGAGCCGCACCT
rat_chr8                   TCTCTCAGCCGCACTT
                           ***   ******** *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_001436      GGAGGCTTCCATTCTGGTGGCAACCGGGGTCG------TGGTCGGGGAGG
rat_chr1                   -----CTTCCAGTCTGGGGGCGGCCGGGGTCGAGGTGGTGGCCGGGGAGG
                                ****** ***** ***  *********      *** ********

human_chr19_NM_001436      AAAAAGAGGAAACCAGTCGGGGAAGAATGTGATGGTGGAGCCGCATCGGC
rat_chr1                   CAAGAGAGGAAACCAGTCAGGGAAGAATGTGATGGTGGAGCCCCATCGGC
                            ** ************** *********************** *******

human_chr19_NM_001436      ATGAGGGTGAGTGAGGAAGGCAGGGAGCCGGCTGAGCTTCGGGGCAGGGA
rat_chr1                   ATGAAG--------------------------------------------
                           **** *

human_chr19_NM_001436      GAGGCTGGGGGTCCTCACCCCTGCTCTGATCCCCTCACCCAGGTGTCTTC
rat_chr1                   ------------------------------------------GAGTCTTT
                                                                     * *****

human_chr19_NM_001436      ATTTGTCGAGGAAAGGAAGATGCACTGGTCACCAAGAACCTGGTCCCTGG
rat_chr1                   ATCTGTCGCGGAAAGGAGGATGCCCTTGTCACAAAGAATCTGGTTCCTGG
                           ** ***** ******** ***** ** ***** ***** ***** *****

human_chr19_NM_001436      GGAATCAGTTTATGGAGAGAAGAGAGTCTCGATTTCGGTGAG-
rat_chr1                   AGAATCTGTGTATGGAGAGAAGAGAGTCTCTATCTCCGTGAGT
                            ***** ** ******************** ** ** *****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_001961      ----CGAGGAGTCGGGAGAGCATATCATCGCGGGCGCCGGCGAGCTGCAC
rat_chr7                   TCATCGAGGAGTCTGGGGAGCACATCATTGCTGGTGCTGGAGAGCTGCAC
                               ********* ** ***** ***** ** ** ** ** *********

human_chr19_NM_001961      CTGGAGATCTGCCTGAAGGACCTGGAGGAGGACCACGCCTGCATCCCCAT
rat_chr7                   CTGGAGATCTGCCTTAAGGACCTGGAGGAGGACCATGCCTGCATCCCCAT
                           ************** ******************** **************

human_chr19_NM_001961      CAAGGTGAGGCGCCAGTGACCAGCCTTCCCCACGCCCCACCCCGGACACC
rat_chr7                   CAAG----------------------------------------------
                           ****

human_chr19_NM_001961      TGCCCTCTGCTTTAAAGCTGAGCTGAGCTAGGCTCTGCAGACGCCTAGAC
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      TTGATCTCGGTCTTGGTCTCAGCTTCTTAAGTTCCTCAAGTTTCTTCTTT
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      GCAGTCTTCCACAGGCATGTGGGGCTGTTTTTGTTGTTGTTGTTGTTTTT
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      TTTGAGATAGTCTCGCTGTGTCATCCAGGCTGGAGTGCAGTGGCGTGATC
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      TTGGCTCGCTAGAACCTCCACCTCCCGGGTTCAAGCGATTCTCTTGCCTC
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      ACTCAGCTTCCTGAGTAACTGGGACTACAGGCGCGTGCTACCACGCCCGG
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      CTAATTTTTTTTTGTATTTTTAGTAGAGGCGGGGTTTCACTGTGTTAGTA
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      AGTCAAGATGGTCTCGATCTCCTGACCTCGTGATCCCCCTGCCTCGGCCT
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      CCCAAAGTGCTGGGATTACAGGTGTGAGCCACCATGCCTGGCCCAGGGCT
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      ATTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAAGAGTCTTGCTCTGT
rat_chr7                   --------------------------------------------------


human_chr19_NM_001961      TGCTTAGGCTGGAGTGCAATGGCGTGATCTTGGCTCACTGCAAGCTCTGC
rat_chr7                   --------------------------------------------------
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human_chr19_NM_001961      TTCCCAGGTTCACGCCATTCTCCTGCCTCAGCCTCCTGTAGCTGGGACTT
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      CAGGCGCCTGCCATCATGCCCGGCTAATTTTTTGCATTTTTAGTAGAGAC
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      GGGGTTTCACCGTGTTAGCCAGGATGGTCTGGATCTCCTGACCTCGTGAT
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      CCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCA
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      CGCCCGGCCTCCGGGGCAGTTTTTGAGTTACATCCTGCTGTCTTCTGTCC
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      ACAAACAACACAAATGCTCTGGAGGGGTTGGGACAGGCCTGCTCCAGACC
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      TCGTTTCTTCCCTGTTAATGCTTAAAATTCCACAAGCCCGTGGTTTCTGC
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      GCCGGAGAGCTCAGTGGAGCCCCTGCTCCTTGTCCTTGTCTGGAGTGAGA
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      TGCGCTTGGCACTGCAACACTGACTCCGCTTCGTTCTGATTGACGTGGCT
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      CTACCAGGCTGTATGAGGTCCGCCTTGCTAGGAAAAGCTTTTAAGGATGC
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      GTCTGTGTGTAAGGTCACCTCTTTCTCCAGGCAAGAGTGGGACTTAACCT
rat_chr7                   --------------------------------------------------

human_chr19_NM_001961      CTTTTTGCAGAAATCTGACCCGGTCGTCTCGTACCGCGAGACGGTCAGTG
rat_chr7                   ----------AAATCTGACCCTGTCGTGTCCTACCGGGAGACAGTCAGTG
                                     *********** ***** ** ***** ***** *******

human_chr19_NM_001961      AAGAGTCGAACGTGCTCTGCCTCTCCAAGTCCCCCAACAAGCACAACCGG
rat_chr7                   AGGAGTCCAACGTGCTCTGTCTTTCCAAGTCCCCAAACAAGCACAACAGG
                           * ***** *********** ** *********** ************ **

human_chr19_NM_001961      CTGTACATGA-
rat_chr7                   CTGTACATGAA
                           **********
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_001961      ----AGGGGGCCAGATCATCCCCACAGCACGGCGCTGCCTCTATGCCAGT
rat_chr7                   GAGGAGGTGGTCAGATCATCCCCACAGCGCGCCGCTGCCTCTATGCCAGT
                               *** ** ***************** ** ******************

human_chr19_NM_001961      GTGCTGACCGCCCAGCCACGCCTCATGGAGCCCATCTACCTTGTGGAGAT
rat_chr7                   GTGCTGACTGCACAGCCCCGCCTCATGGAGCCTATCTACCTGGTGGAGAT
                           ******** ** ***** ************** ******** ********

human_chr19_NM_001961      CCAGGTGAGGTCTACCCGCCCACCGCTGACCCTGCCACCGTCCTGCCCAG
rat_chr7                   TCAG----------------------------------------------
                            ***

human_chr19_NM_001961      CGGCCACTGACAGGTTTTCTTTCCCTTCTGGCAGTGTCCAGAGCAGGTGG
rat_chr7                   ----------------------------------TGTCCTGAGCAAGTGG
                                                             ***** ***** ****

human_chr19_NM_001961      TCGGTGGCATCTACGGGGTTTTGAACAGGAAGCGGGGCCACGTGTTCGAG
rat_chr7                   TGGGCGGAATCTATGGTGTCCTGAACAGGAAGCGTGGCCATGTCTTTGAG
                           * ** ** ***** ** **  ************* ***** ** ** ***

human_chr19_NM_001961      GAGTCCCAGGTGGCCGGCACCCCCATGTTTGTGG-
rat_chr7                   GAGTCCCAGGTAGCTGGGACCCCCATGTTCGTGGT
                           *********** ** ** *********** ****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_002695             ----CATCAAGACCATCAAGGTGTACTGCCAGCGCATGCAGGAGGAGAAC
rat_chr7                          TGGGCATCAAGACCATCAAGGTGTACTGCCAGCGCATGCAGGAGGAGAAC
                                      **********************************************

human_chr19_NM_002695             ATCACACGGGCTCTCATCGTGGTGCAGCAGGGCATGACACCCTCCGCCAA
rat_chr7                          ATCACACGGGCGCTGATCGTGGTGCAGCAGGGCATGACACCCTCCGCCAA
                                  *********** ** ***********************************

human_chr19_NM_002695             GCAGGTGGGCACCCCTGCCCCACCCCGCCAGCCTCTCCCCCTCCCCAGCC
rat_chr7                          GCAG----------------------------------------------
                                  ****

human_chr19_NM_002695             TCCTCCCGCAAGCAGTACCCACAGGCGGCCCACGTGCCTTGGGCTTTGGG
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             CCAGGCCAGCCAGGGTGCCCTGGAGGATGTGGCCGGGATGTCCGGCAAGC
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             CCCGACCGCCTCCCTCCCACCGCGTCCATGGGCCCCACCCCAGGCAGCCG
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             CCGTCCTCCCCCAGCTCTCAGGAGGGGCGTCAGGGCGGAGGGCACTGTGC
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             CTCTCGCCAGCTCCTGTGGGCTCCAGCCCTCGGCCTGGTGCAGATTCCAG
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             GAGCCGGAGGTTCTTTATCCTGAGCTGATGTCCAGGGGGACTTGCAGAGG
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             AGGCCCGGCACGGGGTCCTCCAGGGGCCTATCCGTGTTCCCCGTCTGTCT
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             GTCGGACACTCTGGAGCCAGGCTGCTGTGCTGTGACGGGCAGTCAGCAGA
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             GCAGTTTAGTCCCTGGCCCACCAGCTGTGGGGTTCACGCAGCCACACAGA
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             GCAGCACCCCTGTATGGGGAAGAGGTCGCCCTGCCAGCTCTGAGGGCCGC
rat_chr7                          --------------------------------------------------


human_chr19_NM_002695             CCCTGGAAGCGTGTGATGGATGGAAACACATCCGAGTTTCCACGGCCACT
rat_chr7                          --------------------------------------------------
```

```
human_chr19_NM_002695      TCACTGCTGGATGAGGCTCTCGATGAGCAGAGAGGCTGGGGAGGGGCGGG
rat_chr7                   --------------------------------------------------


human_chr19_NM_002695      CTGTTGAAGGCTCCTGGGCTGGCGGTGGGGTTTTCTGATTCACGACGTGG
rat_chr7                   --------------------------------------------------


human_chr19_NM_002695      GTGTGTTGTTGGGGCACACGAGTAAGCCCCAGGTAGCTTGAGGCAGGAAA
rat_chr7                   --------------------------------------------------


human_chr19_NM_002695      TGGGGTTGGGGTTGTCTGGGCCCCTCCGGGCCGTGCCTTAGAGCCGCTCT
rat_chr7                   --------------------------------------------------


human_chr19_NM_002695      CTTCCAGTCCCTGGTCGACATGGCCCCCAAGTACATCCTGGAGCAGTTTC
rat_chr7                   -------TCCCTGGTAGACATGGCCCCTAAGTACGTGCTAGAACAGTTTC
                                  ******** *********** ****** * ** ** *******

human_chr19_NM_002695      TGCAGCAGGAGCTGCTCATCAACATCACGGAGCACGAGGTGGGCGCGCGC
rat_chr7                   TACAGCAGGAGCTGCTCATCAATATCACAGAACATGAGGTGCGTGTGTCC
                           * ******************** ***** ** ** ****** * * *  *

human_chr19_NM_002695      CGCGGAA-
rat_chr7                   CAGGGAAG
                           *  ****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_002819      -CCGGAAGCTCCCCATCGACGTCACGGAGGGGGAAGTCATCTCCCTGGGG
rat_chr7                   TCCGAAAGCTACCTAGTGATGTCACTGAGGGCGAGGTCATCTCCCTGGGG
                            *** ***** ** *  ** ***** ***** ** ***************

human_chr19_NM_002819      CTGCCCTTTGGGAAGGTCACCAACCTCCTGATGCTGAAGGGGAAAAACCA
rat_chr7                   CTGCCCTTTGGGAAAGTTACCAACCTCCTTATGCTGAAGGGGAAGAACCA
                           ************** ** *********** ************** *****

human_chr19_NM_002819      GGTACCTGAGCCGCGTTTCTCCGGGGTGCTCACACCGTGCAGGCGGGGAC
rat_chr7                   G-------------------------------------------------
                           *

human_chr19_NM_002819      GAGGAGGGCCCAGCGCTCACTGCCTCCCCAACAGGCCTTCATCGAGATGA
rat_chr7                   ----------------------------------GCCTTCATTGAAATGA
                                                             ******** ** ****

human_chr19_NM_002819      ACACGGAGGAGGCTGCCAACACCATGGTGAACTACTACACCTCGGTGACC
rat_chr7                   GCACAGAGGAGGCTGCCAACACTATGGTTAACTACTACACATCGGTGGCG
                            *** ***************** ***** *********** ****** * 

human_chr19_NM_002819      CCTGTGCTGCGCGGCCAGCCCATCTACATCCAGT-
rat_chr7                   CCAGTGCTTCGTGGACAGCCCATCTACATCCAGTT
                           ** ***** ** ** ******************* 
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_003333      -CCACCCTGCACCTGGTGTTGCGCCTGCGAGGTGGCATTATTGAGCCTTC
rat_chr16                  TCCACCTTGCACCTGGTGCTGCGTCTTCGCGGTGGCATCATCGAGCCGTC
                            ***** *********** **** ** ** ******** ** ***** **

human_chr19_NM_003333      TCTCCGCCAGCTTGCCCAGAAATACAACTGCGACAAGATGATCTGCCGCA
rat_chr16                  CCTTCGTCAGCTTGCCCAGAAGTACAACTGTGACAAGATGATCTGCCGCA
                            ** ** ************** ******** *******************

human_chr19_NM_003333      AGTATGTGTGCTCCGATGCTTGGGGGGCTGTGGGGGCTGCCGGAGTCGGG
rat_chr16                  A-------------------------------------------------
                           *

human_chr19_NM_003333      GTATGCCCTCACCCACCCCTCCTGTCTCTGTGCAGGTGCTATGCTCGCCT
rat_chr16                  -----------------------------------GTGCTACGCACGCCT
                                                              ****** ** *****

human_chr19_NM_003333      TCACCCTCGTGCTGTCAACTGCCGCAAGAAGAAGTGTGGTCACACCAACA
rat_chr16                  GCACCCCCGTGCAGTCAACTGCCGCAAGAAGAAGTGCGGCCACACCAACA
                            ***** ***** *********************** ** **********

human_chr19_NM_003333      ACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTGGT----
rat_chr16                  ACCTGCGCCCCAAGAAGAAGGTCAAATAGAGCTGGGCCA
                           ******* ********************  *  *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_003685      -------TGACGGGACAGGGCCCGAGAAGATTGCTCATATAATGGGGCCC
rat_chrUn                  TTTTAGATGACGGGACCGGCCCTGAGAAGATTGCTCACATCATGGGGCCT
                                  ********* ** ** ************** ** ******** 

human_chr19_NM_003685      CCAGACAGGTGCGAGCACGCAGCCCGGATCATCAACGACCTCCTCCAGAG
rat_chrUn                  CCAGATCGGTGTGAGCATGCAGCCCGGATCATCAATGACCTCCTCCAGAG
                           *****  **** ***** ***************** **************

human_chr19_NM_003685      CCTCAGGGTAGGTGGCCCCGGGTGCTGAAGGGGCTGGCAGGGCCTCCAGG
rat_chrUn                  TCTTCGG-------------------------------------------
                            **  **                                           

human_chr19_NM_003685      GGAGTGCAAGACCAGACCGGCTTCCAGGGTTCATCATCCTCCTCCTCCTC
rat_chrUn                  --------------------------------------------------
                                                                             

human_chr19_NM_003685      TTGTCTTGCAGAGTGGTCCCCCAGGTCCTCCAGGGGGTCCAGGCATGCCC
rat_chrUn                  -----------AGTGGGCCCCCAGGTCCTCCAGGGGCCCCTGGCATGCCC
                                      ***** *******************  ** *********

human_chr19_NM_003685      CCGGGGGGCCGAGGCCGAGGAAGAGGCCAAGGCAATTGGGGTCCCCCTGG
rat_chrUn                  CCTGGAGGCCGGGGCCGGGGCCGAGGCCAAGGCAACTGGGGCCCTCCTGG
                           ** ** ***** ***** **  ************* ***** ** *****

human_chr19_NM_003685      CGGGGAGATGA-
rat_chrUn                  AGGGGAGATGAC
                            ********** 
```

```
CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_003938      --TAGACAAGGCAGAGGGTACCACCTACCGTGACGAGCTGCTCACCAAGA
rat_chr7                   CGTGGACAAGGCCGAGGGCACCACCTATCGTGACGAGCTGCTCACCAAGA
                             * ******** ***** ******** **********************

human_chr19_NM_003938      TCATTGACATCTGCAGCCAGTCCAACTACCAGTACATCACCAACTTCGAG
rat_chr7                   TCATTGACATCTGTAGCCAGTCCAACTACCAGCACATCACCAACTTCGAG
                           ************* ****************** *****************

human_chr19_NM_003938      TGGTGCGTCCCGCTCCCAGGGGTGTGGCCGGGGGTTCCGTGGCGCCGCTC
rat_chr7                   TG------------------------------------------------
                           **

human_chr19_NM_003938      ACTCACCGCCTCTGCCCCACAGGTACATCAGCATCCTGGTGGAGCTGACC
rat_chr7                   ----------------------GTACATCAGCATCCTTGTGGAGCTGACA
                                                 *************** ***********

human_chr19_NM_003938      CGGCTGGAGGGCACACGGCACGGCCACCTCATCGCCGCCCAAATGCTGGA
rat_chr7                   AGACTGGAGGGCACCCGGCATGGTCACCTCATTGCTGCACAGATGCTGGA
                            * *********** ***** ** ******** ** ** ** ********

human_chr19_NM_003938      CGTGGCCATCCGCGTGAAGGCC-
rat_chr7                   CGTGGCCATTCGGGTCAAGGCCA
                           ********* ** ** ******
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_015965      -CCACCCCCACCATCGGCCCCATCCCCACAGGACCTTGCAGATGCTTCGG
rat_chr16                  CCTTGAGCTCAGCCATGCCCTGTGACCACAGGACCCTGCAGATTCTTCGG
                            *     *        ****  *  ********** ******* ******

human_chr19_NM_015965      GAGAACCTGGAGGAGGAGGCCATCATCATGAAGGACGTGCCCGACTGGAA
rat_chr16                  GAGAACCTGGAGGAGGAGGCTATCATCATGAAAGATGTGCCCAACTGGAA
                           ******************** *********** ** ****** *******

human_chr19_NM_015965      GGTGGGTCCCGGCTGGGAGGGCAGAGGTGCCAGCCACGGCAGAGACAGGG
rat_chr16                  G-------------------------------------------------
                           *

human_chr19_NM_015965      CCTGGGGTTGGGGAGCTCCCACAGCTTTCTATAGAAACCCCAGGACCAAG
rat_chr16                  --------------------------------------------------


human_chr19_NM_015965      GGGGTGGTGGGTGCCAGGTCCCACAAGGGAAGGCTGTAGCGCCTGCCACG
rat_chr16                  --------------------------------------------------


human_chr19_NM_015965      CACAGGGGCCACTGATCCTGGGGGATGGGTCCTAGCAGGCTGTATATGGG
rat_chr16                  --------------------------------------------------


human_chr19_NM_015965      TGGCTGTGCCTCTACCCATACCCCACTGTCCCCACAGGTGGGGGAGTCTG
rat_chr16                  -------------------------------------GTGGGGGAGTCTA
                                                                ************

human_chr19_NM_015965      TGTTCCACACAACCCGCTGGGTGCCCCCCTTGATCGGGGAGCTGTACGGG
rat_chr16                  TGTTCCATACCACACGATGGGTGCCACCCCTCATCGGCGAGCTTTATGGG
                           ******* ** ** ** ******** *** * ***** ***** ** ***

human_chr19_NM_015965      CTGCGCACCACAGAGGAGGCTCTCCATGCCAGCCACG--
rat_chr16                  TTACGCACCAAGGAGGAGATGGAGAACGCCAACTTCGGC
                            * *******  ******       * **** *  **
```

```
CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_020170      -CCTGGACACCGTGGGCCGGGGCAGCAGCCTGCACCTGCACGTGTCCAAG
rat_chr7                   GCCTGGACACCGTGGGACGTGGCAGCCACCTGCGGCTGCATGTGTCCAAG
                            *************** ** ******  *****  ***** *********

human_chr19_NM_020170      CCGCCTCGGGAGGGCACCCTGCAGCACGCCTTCCTGCGGGAGCTGGAGAC
rat_chr7                   CCTCCGCGGGAGGGGACACTGCAGCATGTCTTCCTGCGCGAGCTGGAGAT
                           ** ** ******** ** ******** * ********* **********

human_chr19_NM_020170      GGTGGGTGCCCCTTTCATGGATGGGTCCGGAGCTCTGCGGAGCACACACA
rat_chr7                   G-------------------------------------------------
                           *

human_chr19_NM_020170      TCGGGGCCGGGTTGGGGCATCCTGTCCCAGGGTGTCCTTGCTGTCCGCCC
rat_chr7                   --------------------------------------------------


human_chr19_NM_020170      CTCAGGCTCTGAGGGCCACACTGTGTCGGGGTCGGGCTGGGGTGTTCTGT
rat_chr7                   --------------------------------------------------


human_chr19_NM_020170      CCTGGGGTGTCCTTGCTGTCCAACCCCGGGGCTCTGAGGGGCACACTGCG
rat_chr7                   --------------------------------------------------


human_chr19_NM_020170      TCAGGGCCGGGCTGGGGTGTCCTGTCCCAGAGTGTCCCCTTGTCCCTCCT
rat_chr7                   --------------------------------------------------


human_chr19_NM_020170      TACCCACTGCTCATTGCCCGCCGGGGCTCCAGCAGGCCTTAGGGGGACCC
rat_chr7                   --------------------------------------------------


human_chr19_NM_020170      CGGGGGCAGGTGGATTTCTCCTCATTTTGCACCCTCGGGGGTTCTGGGAG
rat_chr7                   --------------------------------------------------


human_chr19_NM_020170      GCCCCTGGAGCATTTGGGGAATGGGCTGGGGTGGCCGCCATCCCCGCCTG
rat_chr7                   --------------------------------------------------


human_chr19_NM_020170      CCCTCTGCTAATGGCGCCTCCGGCTGCAGGTGGCCGCGCACCAGTTCCCT
rat_chr7                   -----------------------------GTGGCTGCGCACCAGTTCCCT
                                                        ***** ***************

human_chr19_NM_020170      GAGGTACGGTTCTCCATGGTGCACAAGCGGATCAACCTGGCGGAGGACGT
rat_chr7                   GACGTCAGCTTCTCCATGGTACACAAGAAAATCAATCTAGCAGATGACGT
                           ** **  * *********** ******   ***** ** ** ** *****

human_chr19_NM_020170      GCTGGCCTGGGAGCACGAGCGCTTCGCCA---
rat_chr7                   GCTGGCCTGGGAGCATGAGCGCTTTGCCATCC
                           *************** ******** ****
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_032285      -CTCCCTGCAGATCCTAGACCAGCTGCTGCTGCCCAAGCAGAGCCGCTAC
rat_chr19                  GCTCGCTGCAGATCCTCGACCAGCTGCAGCTGCCGGAGCACTGCCACTAT
                            *** *********** ********** ******  ****  *** ***

human_chr19_NM_032285      GAGGCGGTGGGCTCGGTGCACCAGGCCTGGGAGGCCATCCGCGCCATGAA
rat_chr19                  GAGACGCTGAGCTCCGTGCAGCAGGCCAGGGAAGCGATCCGCGCCATGAA
                           *** ** ** **** ***** ****** **** ** **************

human_chr19_NM_032285      GGTGCAGCGGGGCGGCGGGGCGGCGGGGCGGCGGGGCGGCGGGGCGGCGG
rat_chr19                  G-------------------------------------------------
                           *

human_chr19_NM_032285      GGCGGCGGGGCGGCGGGGCGGCGGGGCGGCGGGGCGGCCGGGTTGGAGGT
rat_chr19                  --------------------------------------------------


human_chr19_NM_032285      GGGAGTGCGCCCGCGCCTGCAGCTTCCGACGCCCAAATCCCTGCCCCGCA
rat_chr19                  --------------------------------------------------


human_chr19_NM_032285      GGTGCGGGGCGCCCCGGCCATAGCCCTGGTGGGCTGTCTCAGCCTCGCCG
rat_chr19                  -GTGCGCGGCGCTCCCGCCATCGCGCTGGTGGGTTGCCTCAGCCTGGCTG
                            ***** ***** ** ***** ** ******** ** ******** ** *

human_chr19_NM_032285      TGGAGCTGCAGGCGGGCGCCGGGGGACCGGGACTCGCCGCGCTCGTGGCC
rat_chr19                  TAGAGCTGCAGGCGGGTGCGGGCGGTCCGGGGCTCGCCGCTCTGGTGGCC
                           * ************** ** ** ** ***** ******** ** ******

human_chr19_NM_032285      T--------
rat_chr19                  TTCGTGCGA
                           *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr1_NM_005216      -
CAGCTCTCAAATGGCAAATGGGTCCCCTTTGATGGCGATGACATTCAGCTGGAGTTTGT
rat_chr5
GCAACTCTCCAATGGTAAGTGGGTCCCCTTTGACGGAGATGACATTCAGCTGGAGTTTGT
                           ** ***** ***** ** ************** **
***********************

human_chr1_NM_005216
CCGCATTGATCCTTTTGTGAGGACCTTCCTGAAGAAGAAAGGTGAGTGTAGTTCCTGCAC
rat_chr5                  ACGCATTGACCCCTTCGTGAGGACCTTCCTGAAGAGGAAGG-------------
------
                           ******** ** ** ****************** *** *

human_chr1_NM_005216
GAGGATGCTGCCAGAAACGGCCCCAGGCCTCACTTGCTCTCGAGGCCCAACCAGGAAAAG
rat_chr5                  ------------------------------------------------------
------


human_chr1_NM_005216
CTCTGGGAAACCCCTCCCGGTTATTCTTGTTGGTTCTTCCGCAGGTGGCAAATACAGTGT
rat_chr5                  --------------------------------------------
GTGGCAAGTACAGTGT
                                                                      *******
********

human_chr1_NM_005216
TCAGTTCAAGTTGCCCGACGTGTATGGTGTATTCCAGTTTAAAGTGGATTACAACCGGCT
rat_chr5
CCAGTTCAAGCTGCCGGACGTGTATGGCGTGTTCCAGTTTAAAGTGGATTACAACCGGCT
                           ********* **** *********** **
*****************************

human_chr1_NM_005216      AGGCTACACACACCTGTACTCTTC-
rat_chr5                  AGGCTACACCCACCTGTACTCCTCC
                          ********* *********** **
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr1_NM_014409      ---
TATAAAACTTTGGAGTTTACGATCCAAGAAGTTAAAATCAGAGCCCCACCAAGTAGA
rat_chr19
CTGCATAAAGCTCTGGAGCTTGCGGTCCAAAAAACTGAAGTCAGAGCCCCACTGTGTGGA
                              ***** ** ***** ** ** ***** **  * ** ************
** **

human_chr1_NM_014409
CGTGTCCCGCATCCATTTGGCTTGTGATATTCTGGAGGAGGAGGTATGAATACCATTTTT
rat_chr19                 CACATCCCGTGTCCGGCTGGCTTGTGACACTCTGGAGGAGGAG-----------
------
                          *   *****  ***   ********** * *************

human_chr1_NM_014409
TTCTTCCCTGCACCCGCCTTCCTAATTTCCTTAGAATGTCCTTACCAAACACGACATATC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TTAGAATGGACTTCCTAGTTTCCCTCATCATATAGCTAAAGCCAGACTAATGACATGTTA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CCTGTAGCCATTGAATTCCTGCACATGCCTAACCTAAGATGCAAAAACAATTTTTAGCAG
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CATTAACTTCTTATTAATGAATGGTCAGTATTTATACTATGTGAAATGTGGATAGCAACA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CTAAGCCTAATGAAAGACCTTTAGCTAATATTGACTTTAGCTGAGATTTGCAGTAAATAT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
ACACTTATGTGTGTGCACATTTGCTCAGGTACAAATAATCGGTAGTAGGATAACTGAGTC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GAAGGGCCTCCATTGTCAACTGTAATGAATATTATTTTCCCCACAGAAGGTTGTGCCATT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TCACAGTCTCAGCAACAGTAGTAAGAATACTGGCATCCCTGCACCCTCACCACACTGGAT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGATGGTATTGGCTTTCTGAGGCCAGTGCATATCCTGTGGCTCCATGTACCCCGGGGTGT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TCCCAGACCCCACTTGGAGAAGTAACACAGGAAGTAGAGTTGCCAGCTCCCCTCCCCCCG
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TCAGTCAGTGTTCAATCTTGTTTGGCTTGTAACCGTTTAGGACAGTCATTGAAAAGGGCA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
GGCGCAGCTTGGGTTTCAGGTCACCAAAAATCACTACCTTAGAAAAAATGTGGGCCAAGG
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
AAGATAGAAATTAAACTTCACAGCATTAACTTTTCTTTAGAGTGGTCCTGAAAAAGCTGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGGCCAAAGTATTTTTGTCTTATCACCACTGAAATTCAGGTAGCTCTGCCTCACATTACT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTGGATGGAAAATTCTTTACACAATGTTGAATAATTAAGGAGCAAAAAAATCACTCTAAT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TAAATTACAGTTAATGATAAGGATGTCAAGAATATTGGGTGCCCTAAATTAAACCATTGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTTCCTGTTCCTGTTTTCTGAGTCCACTTCCAGTTAGGATGGCCTTTGAATTTTTGATTC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTGCAACCGAGACAGTATAATTGAAGGATTTCCTTGTGATGAGTGAAGAGTCTAGATTCC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CATGTAGAAGCTTTAATTTCTAGAATTTTATAGTACTCTCCAAAATATTTTTTATTACAT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTGTATTTGAATTTTCAAACATCTCTTTTCCTTGGAGACAGTTCCCTTTTTGGGAGTTCT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TCTGATAAAACTGAGGAATACTGCCTGCATTTGCTTTCGATTTTCTGTAAATACAAAAAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAATTACACTGACCTTATTAGCTTTGATGATACAGAGTTTGGAGATTATTCTGTGCATTA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAAATTAATATTAAAGAAGATAGCATTATGACATCTGATAACAGTAGACCAAAATAAAAC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ATTTTAAGACTCTGGCCACTACTGGTAACTAGCTCTGTGGCTTGTCCTATGTTTATTTCC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGGTATCAGAAGTGTATCTGAAGACTCAGAAGTGAGGAACCGCATGCGGAATTCCAGGAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CTGAAAGAAATTAAGTATGGCTGGAGTTAGGAGAGGGGCCAAGACAGGAAGTGATGTAGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GACACTGTCTTATATGAGCAATTATGGCGGCCAAACTAGGGTAGTGGCAGTGGCAAAGGA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GACATGGATGGACTAGAGAAGAGCTCGGTTATTCAATTACTGTAGGGGATAAGGGAGAGC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAGCATCAAGGGTGACGTTTGTGTTTCAGGCTTAAACAGTTGGATGTCCATCAAGAAGAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGCAAAAGACGTCATTGGAATGGTGGTTTTGTTTAAGCATTTCTGGCTTTCCATCATGGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TCATACTGAAAGTACTGTAGATGCTAGCTAACCTCTGCCCTTTTTAAGAATAAACCTTTT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTTTAAACTTAAGAACTAAAGCTGAGATTCTCCTATTCTGTTGTTGAGGGGCTTCCTGCA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGCCCGCCCATTTTATCACAGCAATTTGAGAAGTTTTCTTTTTGGTTTCTGACAACAAGC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ATTTGGGGAGAAAGCCAGGCATAAATTAGTTACGATAGTTGGTGTTTAATGTTTCTCCAG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGAAAATTTGGACTTTTCTTTTTCCCTTATAGAATGCATAATTAAAACAGACTATTATTT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGAAATGAAATATTGAATATTAAAAAAAATAAAATAGAGACTCTTAATACAGGAGCCACA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AACTCACATACCTAGAGAAACCAAACAGGTAAAAGCAAGTGGTGAAGCCACATGGATTAA
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rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGAGATGATAGAAAGTACAAAATCACTATGTAAGTCAGATTAAAAAGCCAGCTTGCACTC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TCTGCTTTCATCTTTTTGAAGCAATAACTATTACATAAATCAGTGAATACAGTATTTCTA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CAGTATTTGAAACGGTGTTCACACCCAGCAATTCCACTTCTAGACATATATCCAAGAGAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGGAAAACATGTGCACACAGGCACTTGTACATGAATATTTATGGAAGCATTATTCACAAT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGCCAAAAAGTGGAAACAGTCCAAATGGCCATCAAGATGAATGAATAAATAAAATGTAGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GTGTGCATGCAGTGGAATATTATTTGCCCATAAAAAGAAATGAAGCACTGATGCAGGCTG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CAACATGGATGAACTTGAAAGCTTTATGCTACGTGAAAGAAGCCAGTCATAAAAGGTCAC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CTACTGTTATTCCTTTCATAGGAAATATCCAGATAGGCAAGTCCATAGAGACAGAGAGGA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GAGGAGTGGTTGCCAGGGGCTGGGCAAGGAGAATGAGAGTGACCGCTAATGGGTGTGGCA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTTCTTTGTGAGGTAATGAAAATGTTCTGTATTAGATAGTGGTGATCATTGCACAACTCT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GTGAATGTACTAAAAATCATTGAATTGTACACTTTGAAAGAATTATATAGTATGTAATTA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TATCTCAGTTTAAAAAAAAAAACAGGATAACAGTAACCAAAATCTTCTATGTAAGCTTAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AATTTTCTCTGTTAATTATGCCAAATAAAACTGAATTCACAGCACTGTCCTGTAGCTTCT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GTTGTCTCCCACTTAAAGATCATCTAGGTTAACCTTTGGAAAGGTGTTAAGTGACATAGC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGTCCCTTGCTTTTTACCTTGGTATGAGCAGCCCTCCTCCTGTTTCAGACACTGAGATGA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGAGTGAAACCTTCATTCTCCATCTTTTGTTCTATATGAAATGGAGATAGAAATGATATC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGGCTGGGTGCGGTGGCTCACGCCTGTAATCTCAGCACTTTGGGAGGCCGAGGCAGGTGG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ATCACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAACCCCATCTCTATGA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAAATACAAAAATTAGCTGGGCGTGGTGGCAGACACCTGTAATCCCAGCAACTCAGGAGG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CTGAGGCAGGAGAATCACTTGAACCCAGGCAGCAGGGGTTGCAGTGAGCTGAGACCGCGC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CACTGCACTCCAGCCTGGGCGATAGAGTGAGATTCTGTCTCAAAAAAAAAGAAAAAAAAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAAAAAAGAGATATCCAACCCTTACCCCTGTTGATTGATACCTATGTATTTTTAATATTT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GAGCAACATGGCAAAACCACAGAGATACCAAACCAAGGATTTGCTCTTCTTTCTTTTCAG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CTGTGTGTATGCAGCTACCCTTATCACTACCAGCACCCGCCTCCTTAACTCAGCAGTAAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ACAGCTGTGTGCAATTCATTTATATGTCTGGTGGTTTTGCCCCCAATCTGGTCTTCTTTA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGTTTGAAAAGTAAAGAAGGCAATATTAGCAGCAATACTCAATTCTATAATCTGTGTATC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAATTGTCATTTAGATTAATGCTATCCAATGGGAATATGATGTGAGCCATATAGTAATTT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAATTTTTCTAGTAGCCACATCTAAAAAGGTTAAAAATTTGTTAATTTTAATGATGTATT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TCATTCAAACTAATATGAACAAATTATTTCAGCATGTAAGCAATATAAAAAATCATTCAT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GAAACCTGTTACATACATCTCTTTTGGTCCTAAGTTTTAGAAATCTGATATGTATTTTAC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ATGAACAGCACATGTCAATTCATGCTAGCCAGTATCCAACTTTTCTGTTCTAGTTCAGGC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGCTGTCATCTCCCACGTAGATAGCAGTGATTCACTTGCTTCCAAGTCTAATACACTCAC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AAGTCCAGCCAAATTTAATGTCTTCCTGTTCCACTGACAGCTAATTAGAGAATAGATGGA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGCTAAATTCCAGACCCCAAGAAAGGACCCCTGGTCTGGGGGAAACGTGAGTGTGAGCTC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGAGGTAGTTGGAGCCTCAGAGTCCAGGAGCAGACGGCCATAACAAATCTGAGGTTTTAG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGACTCCATAGTCCAGAGCAGGGGCAGCAAACTACAGCACAAGGGTGCATGAGATGATAC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTGATCTCTTTATGTTTATTTTTCTTGTTAAATTTCTATTTCATGTGTGTTTCATAATGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ATATAATAAGATTTATTATTACATGAATATGCTTTACAAATTAAACATTTCTATTTGGGA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGCATACCCAATTACTGTGGAGTATTCAGGCTGAATCGTAGGGTATGGTATTATCCTGTC
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rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGCAGGAGAGAGAAGTGAAAACCCATGGCGTTGGGCCCTTGTAAATCAGCTGCTCGACCG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TGCTGAGGCCCGTGTGGGACTGGTTGAGCCACACAGAAAATGTGGCTGGGTTATTTTAAG
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CTGTGGTCCTGGCAGAGGGCTGACAGTGATAGCCAACAGGAACATTCTGGTTTCTCCATT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CCTTGGTCTACAGAGTCAGCTGGACACGTTTCCACCAGCCTGGGACAATCATCAAGATCC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CTGGGGAGCACCAGCTGGACTCCCAGCCCATGCTCCTAGCCCATGCACCTTCATCTCCAA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TTGTGATGCCTTCACCACTGAGGAGGTGAAGGCCACTTCCATAGCTTCTTGTTCCAAATG
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
AAGACCACTTACACCTCAGAGGCAGTAACATGTCCTTTAATTCACAGTTAACTTTCACAG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GATCTTTGTTTAATTCATCTGGTGTCATTTTTGTTCCCACAGTCTTTATATAAACTTTCT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGTGTAGAGCAGTGAGTCATTCTTGAAATTTTAAAGTGTTGTTGTAACTTCTTTGGAAAG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GAAAATTACTAATATTCTTGGTAGCACTCAGTAGACCCTTAAGCTCCCAAATACTTAATG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TATTTTTAATGTTGAGTGTTTGGAATAGCCATTGTGAATATTCATGGACATCAGTGTTTA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTTTCTCTCAACTTTTTCTTAAATATGTACACATGGGAGGCATTCATTTTATTTTGAATT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TAACTATTTTCAAGTAGAAAAAAAAAGGTGCCCTTTTCTTATACAAGAACCTAAGGCTGCC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ACAATGAACCAACAAAGCTGACTGGTTTGGGGATCTTCATCATACTCCTTTCTTCTGGTG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTTAATTAAAACCCATTTTAATTGATGAATTCTGGGACAGAAGAGACAGCTGTAGTTTTG
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGGAGTTTATCTATGTGGGAATAAAGGGAAATGAATTTTGAAAACAGATGGTATACTTGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GGGGAGAGGACCAGGAAAGAGGACTCTTTCTGAGTACCATTAGTTGCCGTCTTTTCTGTC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GTCACACACAGGAAATTATTTCGAAGAATCACATGAATCGCTTGGCTTTGCTTCAAGCAC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTCTGAATCCACACCTTGTTTTGTTACGTTGGGGGAGATGTTTTTTGAGACCCTCCAGAA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGTCACTTTAAAAACTTCATTCTTATTTATTTTGAAACACTAAGCAGTTTGTGGCTGGTC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
ACTAGGCAGGGGGAGCTGTGATTTACTAGTAACTGTACCTTTCTAGCTTAGTGTTAATTC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TTAAACATCCAGGTTTTATTTTGGCTAAACTCCTCTGATAGTTCTGGGTTTTGTTTGTGT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
TTGTTTTTGTTTTGGGTTTTTTTGGGCACAGGGTCTTGCTCTGTCCCCCAGGCTGGAGTG
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CAGTGGTGCCATCACAGTTCACTGCAACTTCAACTTCCCAGGCTCAAGTGAGCCTCCTAC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CTTAGCCTCCCAAGTGTCTGGGACCACAGGCATGCGCCACCATGCCCAGCTAATTTTTTA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
AATTTTTTTGGTAAAGAATCTCCCTATGTTTCCCAGGCTGGTCTCCCAACTCCTTAGCTC
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
CAGTGATCCTCCTGCCTTGGCCTCCCAAACTGTTGGGATTACAGTGCGAGCCACCATGCC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TGAACCAATGGTTGTGTGTTAATCTTGAAGTGAGGCTGGGCGCGGTGGCTCATGCCTATA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
ATTCCAGCACTTTGGGAGGCCAAGGCGGGCGGATCACCTGAGGTCGGGAGTTCAAGACCA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GCCTGACCGACATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCGTGGT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
GGCACATGCCTGTAATCCCAGCTACTTGGGATGCTGAGGCAGGAGAATCGCTTGACCCCA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
GGAGTCGGAGGTTGTGGTGAGCCGAGATCACACCATTGCACTCCAGCCTGGGCAACAAGA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
GCGAAACTCCATCTGAAAAAAAAAAATCTTGAAGTGATACCACATCTGCCTTCATGTGTC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
GCTGTGTCCATCATTAACCCCCATCATGGGAGTAAGGAACATGTCAGGACTTAACGAAAT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
GTTGTTGTCAGTTAAATGGAGTAAAAACAGCAGTATGGCTTATAAAGCAGCTAAAACTGA
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TGGATGAAGGCAATGCCCATAGAATAGAACAATCTAAGAGCCTCACGTAAATTCAAAAGT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
AAATATTTTCAAATGGCACACATCAGAATTAACCATACAAGCTATCCTCAATCAAAGGGT
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
AAGGTCCACAGTCATTACTCTGTAATGGCCTTGCATTTCTGTATCTTTTAATCTGATATA
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
GTCTGAGCTGCAAGGTGAATTTAAGGGGAGCAATTTGTAAGTCGTAAGAGACTTTTATTC
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rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGTTATGAGTTATCTTCCTGGGGTAGCGTTCAAGGGCAAGGCCACTGTCATTTGCTGGAT
rat_chr19                 ------------------------------------------------------
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human_chr1_NM_014409
AGATGCTATTTCCCAAGCAGTCTCAGTTCTCTACTTTTTTTTCTCCTGGACTTGTTTTCC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
TTGTCAGACCACTGAACATTTTTTGTGTGTGTTTCTTTTCCCACCCCACCCCACTGTTCC
rat_chr19                 ------------------------------------------------------
------


human_chr1_NM_014409
CAGGATGATGAGGATGATAATGCAGGCACGGAGATGAAGATACTGCGGGGCCACTGCGGA
rat_chr19                 ---
GAGAGCGAAGACGATGACGTAGGCACGGAAATGAAGATTCTGCGGGGACACTGTGGC
                             **    ** ** *** * * ********* ******** ********
***** **

human_chr1_NM_014409      CCAGTGTACAGCACGAGGTTCCTCGCGGACAGCTCAGGGTTGC-
rat_chr19                 CCAGTGTATAGCACACGGTTCCTCGCGGACAGCTCAGGGCTGCT
                          ******** *****  *********************** ***
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr1_NM_024319      ---
GGCGCCATGTTCGGCTCCAGTCGTGGAGGCGTGCGCGGCGGGCAGGACCAGTTCAAC
rat_chr10
TCCAGCACCATGTTCGGCTCCAGTCGCGGCGGCGTGCGTGGCGGGCAAGACCAGTTCAAT
                              ** ******************* ** ******** ********
***********

human_chr1_NM_024319
TGGGAGGACGTGAAGACTGACAAGCAGCGGGAGAACTACCTGGGTGGGTGCGCGCGGTGG
rat_chr10                 TGGGAAGATGTGAAGACTGACAAGCAGAGGGAGAACTACCTGG-----------
------
                          ***** ** ****************** ***************

human_chr1_NM_024319
GCGGGCTCCGGGCTCCGGGCTCCGGGATCCCGGGCGGGCGCTGGACTCACAGCGTCTACG
rat_chr10                 ------------------------------------------------------
------


human_chr1_NM_024319
TCCGCAGGCAACTCGCTGATGGCGCCGGTAGGCCGCTGGCAGAAGGGCCGCGACCTCACC
rat_chr10                 -------
GCAACTCGCTGATGGCACCAGTAGGCCGCTGGCAGAAGGGCCGCGACCTCACC
                                 **************** **
*********************************

human_chr1_NM_024319      TGGTACGCCAAGGGCCGGGCGCCATGCGCGGGCCCGAGCCGCGAGGA-
rat_chr10                 TGGTACGCGAAGGACCGCGCGCCGTGTACCGGCCCGAGCCGTGAAGAA
                          ******** **** *** ***** **  * *********** ** **
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_001747      -
CTATGATCTAGGGCGAAAAGCGAATGAGAAGGAGCGGCAGGCAGCCCTGCAGGTGGCCG
rat_chr4
CCTGTGTTCCAGGGAGAAAAGCCAATGAGAAGGAGCGGCAGGCGGCCCTCCAAGTGGCTG
                           ** ** ** **** ******* ******************** ***** **
***** *

human_chr2_NM_001747
AGGGCTTCATCTCGCGCATGCAGTACGCCCCGAACACTCAGGTGAGGAGATGCGCACAAC
rat_chr4                  ATGGCTTCATCTCTCGAATGAGATATTCCCCAAACACTCAG-------------
------
                          * *********** ** ***   **  **** *********

human_chr2_NM_001747
CACAGCCCTCTTCCTAGGGCTCTTCCTGTGGCCCCTGACCCCTCAAATTGGCCAGGAAGG
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
GCAGGAGAGCCTTGGGCACTGTCAGGAACAACCAGGCCTCCCTCTTAGACCCATCCAGTG
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
GGAAAGCCCATCTCAATCCTTCAAAATGTCAAAATACTTATTATTTTCAAAGAGGATGTT
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
GGGCAGCACTCTCCTGGGTGCCCAGAGAACTGGGTACTCCTCCTCTGGGCCGTTGTCCCT
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
GGCTGGTGCCACCCCTCCTGCCGCAGCACAGTGTCCACAAGTCATCCCGTGGGGAGCTGA
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
CAGGGCTCAGCTACCGTTGGTGGCATTTATTAAACTGTGCACCCACGCCCTTGAAGCAGT
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
CTGTTGCCTCTGTCTGTGTCCCTGAAATCTTGGTTCTCATCTCATGGCTCATCCAGGGGA
rat_chr4                  ------------------------------------------------------
------
```

```
human_chr2_NM_001747
GCTTTCCCAGCCTGGACTGCACATGGATTCAGGCCAGGCGCCCACACCCTCCTCCCTGGC
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
TCTGGCCCCCTCCTGTCCTCCTGGGCAGAGGCAGAGGTGGCAACTTTGTGAACCAGACTT
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_001747
CTCCCCCGCTGTCCCTGCAGGTGGAGATTCTGCCTCAGGGCCATGAGAGTCCCATCTTCA
rat_chr4                  --------------------
GTGGAGATTCTGCCCCAGGGCCGAGAGAGTCCCATCTTCA
                                              ************** *******
****************

human_chr2_NM_001747
AGCAATTTTTCAAGGACTGGAAATGAGGGTGGGCGTCTTCCTGCCCCATGCTCCCCTGCC
rat_chr4
AGCAGTTCTTCAAGGACTGGAAGTGAGGGTGGGTGTCCCCATCCCTGCTCTCCTGCCCCC
                          **** ** ************** ********** ***  * * **   *   *
*  **

human_chr2_NM_001747      -
rat_chr4                  A
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_003400      ---
GTCATGGAAAAATTTGAATACATTGTGTTGGGCAATAGGCTCCATTAGTGGAGCAAT
rat_chr14
ATGGTCATGGAAAAATTTGAATACACTGTGCTGGGCAATAGGCTCCATCAGTGGGGCGAT
                             ********************** **** ***************** *****
** **

human_chr2_NM_003400
GCATGAAGAGGACGAAAAACGATTTCTTGTTACTGTTATAAAGGTATGCAAGGGATAGGT
rat_chr14                 GCACGAGGAGGATGAGAAGCGGTTCCTTGTCACTGTTATCAAG-----------
------
                          *** ** ***** ** ** ** ***** ******** ***

human_chr2_NM_003400
ATGAATTAGAATTGCTAAATAAGTATTATGTTGTTACAATAAATAATACAAATTTGTCTT
rat_chr14                 ------------------------------------------------------
------


human_chr2_NM_003400
ATTTACAGGATCTATTAGGATTATGTGAACAGAAAAGAGGCAAAGATAATAAAGCTATTA
rat_chr14                 --------
GACCTCTTAGGATTATGTGAGCAGAAGAGAGGCAAGGATAATAAAGCCATCA
                                  ** ** ************** ***** ********
*********** ** *

human_chr2_NM_003400      TTGCATCAAATATCATGTACATAGTAGGTCAATACCCACGTTTTTGA-
rat_chr14                 TTGCATCGAATATCATGTACATAGTAGGCCAGTACCCACGGTTTCTGAG
                          ******* ******************** ** ******** *** ***
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_005911      -
CTATCTCCATTTTCCATTATGGTACCTCTCAGAAGAGTGAGAGAGAGCTATTAGAGATT
rat_chr4
TCGATCTCCATTTTCCATTATGGTACTTCTCAGAAGAGTGAGAGAGAGCTATTAGAAATT
                           * ***********************
***************************** ***

human_chr2_NM_005911
GTGAAGAAGAATTTCGATCTCCGCCCTGGGGTCATTGTCAGGTAAAGATGGTAAAGCCTG
rat_chr4                  GTGAAGAATAATTTTGATCTTCGCCCTGGGGTCATTGTCAG-------------
------
                          ******** ***** ***** ********************

human_chr2_NM_005911
TTGCTAGTCAAGTATTGAGGGTGTTGGGTGTGTGTGTATATACTTAAGGCTGAGGAGGTG
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
AAGGTGTGAAGGAAGACTCCTCAAATGGGAATATATTTTAATTCCTGGAACAGTTTTGAA
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
CTGCTGCCTTAGTGAAGACTTAGTTATTTGAGAAATTTAAAATTACGGTGCTCCATGGCT
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
TAGGCTAACCACTCTAGAGAATGTTCCAGATTTGATATTTGAGCTTTGTGCTCTTCTACT
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
TAAGGGTGTTAAGAAAATAGAGATAAAGTGGGTTGCTCAAGGTTTGTTGCAATGTAAAAA
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
CCATGGTAGGGTGTGGGCGGCGGGACCTTGGTAAGTATTGTGTGATCTCAGGTGAGCTTT
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
TTGACAATTGAAATTTCTCAGAATAATGACAAGTTTTCGTATTTGTTGAGCCAGGGACGG
rat_chr4                  ------------------------------------------------------
------
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human_chr2_NM_005911
AAAAACAACTATAGTTACTAATAAGGACTGTGCAAGGAGTTTGGACACCAGGGAAGTAAC
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
ACTTTTGCCACAAATTTTTTTCCTAGCATATCCCAGAGAACTCATTTGCCAGAGCTCTTG
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
AAAATGAGTCTTGCTGATTGTTTTGCTTTATTTTAATTTAATGCTACATATTAAGTTACG
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_005911
GACTTGTATATTCCAGGGATCTGGATCTGAAGAAGCCAATTTATCAGAGGACTGCAGCCT
rat_chr4                  ----------------
GGATCTGGATCTGAAGAAGCCAATTTATCAGAGGACTGCAGCCT

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human_chr2_NM_005911
ATGGCCACTTTGGTAGGGACAGCTTCCCATGGGAAGTGCCCAAAAAGCTTAAATAT-
rat_chr4
ATGGCCACTTTGGTAGGGACAGCTTCCCCTGGTAAGTGCCCAAAAAGCTTAAATATT
                          **************************** ***
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_006773      -
GATAATGGGTGGCAGTAACAGATCTGCTGAAGCACAGAAACTTGGTAATGGGATCAACA
rat_chr13
TGATCATGGGTGGCAGTAACAGGTCTGCTGAGGTACAGAAGCTTCTCAATGGGATCAACA
                           *** ***************** ******** * ****** ***
*************

human_chr2_NM_006773
TCATTGTGGCCACACCAGGCCGTCTGCTGGACCATATGCAGGTAAGAGATGTAGTGCTTG
rat_chr13                 TCGTCGTGGCCACCCCAGGCCGGCTCCTAGACCACATGCAG-------------
------
                          ** * ******** ******** ** ** ***** ******

human_chr2_NM_006773
TCTCATTGTCTTGTATGAAACATAAACTGACAACTAATGGTTGTTCTTTGTCCTTTGTTT
rat_chr13                 ------------------------------------------------------
------


human_chr2_NM_006773
TGTTAGAATACCCCAGGATTTATGTATAAAAACCTGCAGTGTCTGGTTATTGATGAAGCT
rat_chr13                 ------
AACACACCAGGGTTTATGTACAAGAACCTGCAGTGTCTGGTTATCGATGAGGCC
                                ** ** ***** ******** ** ********************
***** **

human_chr2_NM_006773      GATCGTATCTTGGATGTGGGGTTTGAAGAGGAATTAAAGCAAATTA--
rat_chr13                 GACCGTATCTTGGATGTTGGGTTTGAAGAAGAATTAAAGCAGATCATT
                          ** ************** *********** *********** ** *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_012290      ----
AATCCTAGGCTTTTGACCTTTATGAACAAAGATATGCTGCTGTGAAGATACATCAG
rat_chr3
TGAATTTTGTAGGCTTTTGACTTGTATGAGCAAAGATATGCTGCTGTGAAGATCCACCAG
                                *  ************ * ***** ***********************
** ***

human_chr2_NM_012290
CTTAATAAAAGCTGGAGAGATGAGAAGAAAGAAAACTACCACAAGTAAATACTAATACTT
rat_chr3                  CTTAATAAAAGCTGGAGAGATGAGAAAAAAGAAAACTACCATAA----------
------
                          ************************** ************** **

human_chr2_NM_012290
TATGGTTTTTTAAAATTGAATATTTTTTGAATGATCATGGAGAATTAATACACTGTCTTC
rat_chr3                  ------------------------------------------------------
------


human_chr2_NM_012290
TCATAGACATGCCTGCAGAGAGTATAGAATACACAAAGAACTGGATCACCCCAGAATAGT
rat_chr3                  ------
ACACGCTTGCAGAGAGTATCGAATACACAAAGAGCTGGACCACCCCAGAATAGT
                                *** ** ************ ************* *****
**************

human_chr2_NM_012290      TAAACTCTATGATTATTTCTCCTTGGATACAGATACGTAAGTGAAT-
rat_chr3                  TAAACTCTATGATTACTTCTCCTTGGACACAGATACGTAAGTAAACA
                          *************** *********** ************** **
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_014670      -
AGCTTTTGCTGTGAAGCTCTTTAAATCATGGATAAATGAAAAAGATATCAATGCAGTAG
rat_chr9
CAGCTTTTGCTGTAAAGCTCTTTAAATCATGGATAAATGAGAAAGACATCAATGCAGTTG
                           ************ ************************** *****
*********** *

human_chr2_NM_014670
CTGCAAGTCTTCGGAAAGTCAGCATGGATAACAGACTGATGGTTGGTAACTTTTTTTCAT
rat_chr9                  CTGCAAGTCTTCGGAAAGTCAGCATGGACAACAGACTGATG-------------
------
                          **************************** ************

human_chr2_NM_014670
TCTTCCCATTCTTGCCAAGGATGTAAATGAGAGAAATTTCTCATTTTTAAGACTGTGAAA
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_014670
AGAAAGTGTTTTTCTTAATCTGATTTAAAGAAAGTTTAACCAGATAAATTCTTCTTTTAG
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_014670
GAACTCTTTCCTGCCAATAAGCAAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCA
rat_chr9
GAGCTGTTCCCTGCCAATAAACAGAGTGTTGAGCACTTCACTAAGTATTTCACTGAGGCA
                          ** ** ** *********** ** ******** ******** ** *****
*********

human_chr2_NM_014670      GGCTTGAAAGAGCTTTCAGAATATGTTCGGAATCAGCAAA-----
rat_chr9                  GGCTTGAAAGAGCTTTCAGAGTATGTCCGCAACCAGCAGACCATT
                          ******************** ***** ** ** ***** *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_014763      -
GCGGCCTGCATTGCAGCGGGGCACTGGGCTGCAATGGGCCTAGGCCGGAGTTTCCAAGC
rat_chr4
GGCGGCCTCCATGGCAGAAAGTTGTAGGGTGTCCATGTACCTGGCCTGGAGCTACCGAAT
                           ******* *** ****   *     ***   * ***  *** * * **** *
** *

human_chr2_NM_014763
CGCCAGGACTCTGCTCCCCCCGCCGGCCTCTATCGCCTGCAGTAAGTGGAGCCGGACTTG
rat_chr4                  GGCCAGGCCACGGCTTGCTGCTCTCGCGTCTGATGCCTGCC-------------
------
                           ****** * * ***  *  * *  ** ***   ******

human_chr2_NM_014763
CGAGCTGGGGCGCGTTAGGGGCCCAGGGTCAGGATGGGGGAGGCGAACCTGGAGATCAGA
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_014763
GGCAACCCCAGCGTTGGTCCCCCGTGGGACGCCGGGTTGGGGGAGATTGCGGGGCTCTGC
rat_chr4                  ------------------------------------------------------
------


human_chr2_NM_014763
GGGATCTCAGGGTTGGCACGAGAGTTCTGACCTCCGTCGTCCGCTCCCGCAGGGGTCCAC
rat_chr4                  ----------------------------------------------------
GTGCCCAC
                                                                              *
* ****

human_chr2_NM_014763
GCGGGGCCTGTCCGGCAGCAGAGCACTGGGCCTTCCGAGCCCGGTGCGTTCCAACCGCCG
rat_chr4
ACGGGCCCAAGTCGGTTTCAGAGCACTGGGCCATCCGAGCCCGGTGGGTTCAAGCCGCCG
                           **** **    ***   ************** ************* **** *
******

human_chr2_NM_014763      CCGAAACCGGTCATCGTGGACAAGCACCGCCC------
rat_chr4                  CCGAAACCTGTCATTGTGGACCGGCGCCGAGCCCCAGA
                          ******** ***** ******  ** ***  *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_016252      -
CAGAATATCTTGCTTTGGGTCGGGGAGCTGCCCTCATTTTCTAGCTGCTGCAACTAAAC
rat_chr6
ACAGAATATCTTGCTTTGGGTCTGGGAGCTGTCCACAGTTTCTAGCTGCTGCTACCAAAC
                           ********************* ******** ** ** **************
** ****

human_chr2_NM_016252
GAGGAAAGATCTGCATATGGGATGTTTCCAAACTTATGAAGGTATGTTTGAATTTTGAAG
rat_chr6                  GTGGGAAGATCTGCATATGGGACGTCTCCAAACTCATGAAG-------------
------
                          * ** ***************** ** ******** ******

human_chr2_NM_016252
TAACAAATTAGTAATTGAAAAAAGATCAGTTGTAAACTTAGGCTTTTCATTTGTTTAGGT
rat_chr6                  ------------------------------------------------------
----GT

**

human_chr2_NM_016252
GCACTTAAAGTTTGAAATTAATGCCTATGATCCAGCAATTGTACAACAGCTTATTCTATC
rat_chr6
GCACTTGAAGTTTGAGATTAATGCCTACGACCCAGTAATTGTGCAACAGTTGATCCTATC
                          ****** ******** *********** ** **** ****** ****** * **
*****

human_chr2_NM_016252      AGGAGACCCAAGCTCAGGAGTTGATTCAAGGAGACCAA--
rat_chr6                  AGGAGATCCAAGTTCAGGAGTTGATTCAAGGAGACCTACT
                          ****** ***** *********************** *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_016516      ------
GTTAATTGTGCACTACATTCCTGTGATCCGGGCTCATTTTGAAGCTCGACTACC
rat_chr14
TTTGCAGCTGATTGTGCACTACATTCCTGTGATCCGGGCTCACTTTGAGGCCCGGCTGCC
                                * * ******************************** ***** ** **
** **

human_chr2_NM_016516
ACCTAAGCAATATAGCATGCTTAGGCATTTTGATCATATCACTAAGGTACTTTTTCATAT
rat_chr14                 CCCCAAGCAGTGGAGCCTGCTTAGGCATTTCGATCACATCACCAAG--------
------
                           ** ***** *  *** ************* ***** ***** ***

human_chr2_NM_016516
ATTTTCTATTGGCGTTTCATAAGTTTAGATCCTTAATTGTTAAGTATTTTAAAAATGTGT
rat_chr14                 ------------------------------------------------------
------


human_chr2_NM_016516
CCCAGGGACTTAAAAATACAATTATCATTTCTCATTGCAGGACTACCATGATCACATAGC
rat_chr14                 ----------------------------------------
GATTACCATGACCATATAGA
                                                                  ** ******** **
****

human_chr2_NM_016516
TGAAATATCAGCTAAGCTTGTAGCGATAATGGATAGCTTATTTGACAAGCTGTTATCTAA
rat_chr14
TGAGATATCATCTAAGCTTGTAGCCATAATGGATAGCCTATTTGATAAGCTGTTATCAAA
                          *** ****** ************* ************ *******
*********** **

human_chr2_NM_016516      GGTAATGATTTATAGAAATT-
rat_chr14                 GGTAACAATATTTTTAAATGA
                          *****  ** * *  ****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr2_NM_145212      -
CGTTGCTTTGTTGTTGTTGTTCACAGGCACATACCCCTCAAGTTCACAAGAATATCCCT
rat_chr9
TCTGTGACCTTGCTCCCCTTGTCCTAGGCACACAGCCCTCAGATCCACAAGAACATCCCG
                           *  **   *        *  **  ******* * ******  * ********
*****

human_chr2_NM_145212
TCAGTGAATGCAAAATTGAAAGTAGTTAAGCATTTGATAAGGTTTGTTGTTTCTTCTCAG
rat_chr9                  TCAGTGAATGCAAAGCTAAAAGTGGTTAAACACTTGATACG-------------
------
                          **************  * ***** ***** ** ****** *

human_chr2_NM_145212
CTCTTTTTAAAATGTATTGCCTAGTGTAATTCTAAATGCATTTTTCTTTTTTCGTTAATG
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_145212
TTCTGAAAAAAACTTTTTAAAAAACTAAAATTTTATTTTGTTTTTTTTTAATTGACACAT
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_145212
AATAATTGTACATATTTATGGGGTACATAGTGACGTTTCAATATATATAAAGTATAGTGA
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_145212
TCCGATCAGGGTAATTGGCATATCCATCATCTCAGACATTTACCATTTCTTCATGTTGGG
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_145212
AACATTCAACATCCTCCTCCTAGCTATTTGAAACTATGTGTTATTGTTAACTGTAGTTAT
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_145212
CCTGCGGGGATATAGAACGCTAGAACGTATTCCTCCTATCTAAACGCATTTTCTTGTGTC
rat_chr9                  ------------------------------------------------------
------


human_chr2_NM_145212
ACAGAATCAAGCCCTTGAAGTTGCCACAAGGACTTCCAGCAGAGGAGAACATGTCTAACA
rat_chr9                  ----
CATCCAGCCCCTGAAGCTGCCACAGGGACTTCCCACAGAAGAGACCATGTCCAGCA
                               *** ***** ***** ******* ********  **** ****
****** * **
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```
human_chr2_NM_145212      CGTGCCTCAAAAGCACTGGGGAGTTAGTAGTGCAGTGGCATCTG-----
rat_chr9                  CGTGCCTCAAGAGCACTGGGGAATTGGTGGTGCAGTGGCATCTGAAGCC
                          ********** *********** ** ** ***************
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CLUSTAL W (1.83) multiple sequence alignment


human_chr3_NM_004953      -
ACCCCCAGTGAGCCCCCTGAAGGCGGCTCTCTCTGAGGAGGAGTTAGAGAAGAAATCCA
rat_chr11
TACCTCCAGTGAGCCCTCCAAAGGCTGCGCTCGCTGTGGATGAGGTGGAGAGGAAGTCGA
                           *** *********** *  ***** ** *** *** *** *** * ****
*** ** *

human_chr3_NM_004953
AGGCTATCATTGAGGAATATCTCCATCTCAATGACATGAAAGTAGGCAGTGGGAGCGGCG
rat_chr11                 AGGCCATCATTGAAGAGTATCTCCATCTCAATGACATGAAG-------------
------
                          **** ******** ** ************************

human_chr3_NM_004953
TGTGATTGAGGAGTGGGCAGGGAGGGATCATGCTGGCAGGCATAGGGGTCCGGGGTCTGG
rat_chr11                 ------------------------------------------------------
------


human_chr3_NM_004953
GTCAGACAGTGACTGGTCTCTTCCTGCTGTGCCCTGCACCCCTCAGGAGGCAGTCCAGTG
rat_chr11                 ----------------------------------------------
GAGGCCGTGCAGTG
                                                                        ***** **
*****

human_chr3_NM_004953
CGTGCAGGAGCTGGCCTCACCCTCCTTGCTCTTCATCTTTGTACGGCATGGTGTCGAGTC
rat_chr11
CGTCCAGGAGCTGGCTTCACCCTCCCTGCTCTTCATCTTTGTACGGCTTGGCATCGAGTC
                          *** *********** ********* ********************* ***
*******

human_chr3_NM_004953      TACGCTGGAGCGCAGTGCCATTGCTC--
rat_chr11                 CACGCTGGAGCGAAGCACCATTGCTCGT
                           *********** **  *********
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr4_NM_006859      -
AATCCTCCTCCACTGGATGCCAGTGAGCCCTACAATACTGCAAAGGCAATTGCAGAATG
rat_chr14
AAATCCCCCTCCATTGGATCCCAGTGAGCCCGACAATACGGCCAGAGCAATCGCAGAGTG
                           ***** ****** ***** *********** ******* ** *  *****
***** **

human_chr4_NM_006859
GGGTCTGGATTATGTTGTCCTGACATCTGTGGATCGAGATGGTTAGTGTGTCATCATGGC
rat_chr14                 GGGTCTGGACTATGTTGTGCTGACGTCTGTGGACCGAGATG-------------
------
                          ********* ******** ***** ******** *******

human_chr4_NM_006859
CTCTACCAGAAACTGGCTCTAAATGATGACATCATCCTGAGCAGTGGATTCTTTTGTTTC
rat_chr14                 ------------------------------------------------------
------


human_chr4_NM_006859
TAGATATGCCTGATGGGGGAGCTGAACACATTGCAAAGACCGTATCATATTTAAAGGAAA
rat_chr14                 ---
ATGTGGTCGATGGGGGAGCTGAGCACATTGCCAAGACAGTGTCATGCTTGAAGGAAA
                             ** **   ************** ******** ***** ** ****   **
*******

human_chr4_NM_006859      GGTACTTATTTTTGCATTTGTGTAATTTAAGGACCTTTTTGGA---
rat_chr14                 GGTACTTGTGTCCCCCCCCCCCCNNNNNNNNNNNNNNNNNNNNNNN
                          ******* * *   *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr4_NM_018115      ---
AGAAAATCCGCATGGCCCAAATGAGAAAAGAACTTGATGCTGCCCCCGGGAAATCCC
rat_chr14
TCCAGAAAATCCGCATGGCCCAGATGAAGAAGGAAATGGACGCTGCCCCGGGGAAAGCCC
                             ******************* ****  ** *** * ** ********
****** ***

human_chr4_NM_018115
AGAAGAGGAAATACATTGAAATAGACAGTGATGAAGAGCCCAGGTAAAATGGCACATCCA
rat_chr14                 AGAAAAGGAAATACTTGGACATGGACAGTGACGAGGAGTCCAG-----------
------
                          **** ********* * ** ** ******** ** *** ****

human_chr4_NM_018115
CTTTAGTACTTCAGTCAGCTCATGTGGTAATGAAAGCATCAGGAAACAGAATTCCATTCT
rat_chr14                 ------------------------------------------------------
------


human_chr4_NM_018115
TGTTTCATGTGTTATTTTTCCCTCACCCCAGGGGTGAATTACTTTCTCTTCGGGACATTG
rat_chr14                 -------------------------------
GGGGGAGTTGCTGTCTCTTCGGGACATTG
                                                         *** ** ** **
****************

human_chr4_NM_018115
AACGCCTTCATAAAAAGCCAAAGTCTGACAAAGAGACAAGACTAGCAACTGCAATGGTGA
rat_chr14
AACGCCTTCATAAAAAGCCCAAGTCCGACAAGGAGACGAGACTAGCAACCGCTATGGTGA
                          ******************* ***** ***** ***** *********** **
*******

human_chr4_NM_018115      GTGAGCATATC-
rat_chr14                 GGGCATATGCCG
                          * *   **  *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr5_NM_002198      ------
CCAGATATCGAGGAGGTGAAAGACCAGAGCAGGAACAAGGGCAGCTCAGCTGTG
rat_chr10
TCCCTACCAGACATCGAGGAAGTGAAGGACCAGAGCAGGAACAAGGGCAGCTCTGCTGTA
                                ***** ******** ***** **************************
*****

human_chr5_NM_002198
CGAGTGTACCGGATGCTTCCACCTCTCACCAAGAACCAGAGAAAAGGTATCCAAGGACTC
rat_chr10                 CGCGTGTACCGGATGCTGCCACCCCTCACCAAGAACCAGAGGAAAG--------
------
                          ** ************** ***** ***************** ****

human_chr5_NM_002198
TGGGTCCTTGGGAAGCCCTCAGGGAGGGAGGGTAGAAGGAGGTCAGCTGGGGCTGGAGAG
rat_chr10                 ------------------------------------------------------
------


human_chr5_NM_002198
CCTGCACCAAGGCTGACAGCCCGTCTGCCCCACAGAAAGAAAGTCGAAGTCCAGCCGAGA
rat_chr10                 -----------------------------------
AGAGAAAGTCCAAGTCCAGCCGTGA
                                                             * ********
*********** **

human_chr5_NM_002198
TGCTAAGAGCAAGGCCAAGAGGAAGGTGAGTGTGGTCCTAAGCAGCCAGGCCTTTGGTCA
rat_chr10
CACTAAGAGCAAAACCAAGAGGAAGGTGAGCTTGACTCTAAGCAGCCCAGCCTTAGGTAG
                            **********  ****************  **    **********  *****
***

human_chr5_NM_002198      CCTGTGGGCCAGGGT-
rat_chr10                 GGGGGCAGTGGGTAAG
                             *   *   *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr5_NM_017676      ---
CACAATCAAAGCATTTCTCTCCAAACACTGTGCTGACCACCCAAACAATTGGGATGA
rat_chr9
CAGCACGGTGAAAACATTCCTCTCCAAACACTGCGCCGAGCACCCCGAGACCTGGGACGA
                             ***  * *** **** ************** ** ** *****  * *
***** **

human_chr5_NM_017676
TCACCTATCAGCTGTTTCATTTGCCTTCAATGTAACTCACTTGGTATGTGCCTTTTTATA
rat_chr9                  GGAGCTGCCAGCTCTCTCCTTTGCCTTCAACGTGACCCGCGTG-----------
------
                            * **  ***** * ** *********** ** ** * * **

human_chr5_NM_017676
ATTCTGTACTTCTGAGTTATGACTATTTCTTGGCCAGATAAATGTTTTATTACAAAATTG
rat_chr9                  ------------------------------------------------------
------


human_chr5_NM_017676
ACGTTTATTTCTTTAAAATAGGAACCTACTAAAAATACACCATATTTTCAAATGTTTAG
rat_chr9                  ----------------------
GAGCCTACTAAAAACTCGCCGTATTTCCAAATGTTCAA
                                                ** ***********  * ** *****
******** *

human_chr5_NM_017676
TCGAAATCCTTATATGCCTGAGACTTCAGATAGTCTTCATGAAGTGGATGGTGATAATAC
rat_chr9                  CCGGAACCCTTGCTTGCTCGAGT---------
GTCCTCATGAAGGGGGAGGCGAAGGCAC
                           ** ** ****   ***  ***          *** ******** **  ** **
**

human_chr5_NM_017676      AA----------
rat_chr9                  AAGCGTGTTCGC
                          **
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr6_NM_001090      -
GATGTACCAGCAGAAGCAGAAAGAACTGCTGAAACAGTATGAGAAGCAAGAGAAAAAGC
rat_chr20
AGATGTACCAGCAGAAGCAGAAGGAGCTGCTGAAGCAGTACGAGAAACAGGAGAAGAAGC
                           ********************* ** ******** ***** ***** **
***** ****

human_chr6_NM_001090
TGAAGGAGCTGAAGGCAGGCGGGAAGTCCACCAAGCAGGCGGTGAGCACCTGAGGGACTT
rat_chr20                 TGAAGGAGCTGAAGGCTGGGGGCAAGTCCACCAAGCAAGCG-------------
------
                          **************** ** ** ************** ***

human_chr6_NM_001090
CTGGGCTGGGGGCCACTGTTCTCTCCTGGCAGTGGAGGAAGAAGGAGACTCTGGAACGCT
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_001090
GGCCTACATTTCAAGGACTGCCGCGCAGGGCTCAGGTTTCTCTTTTTTCCTCTTCCTCTC
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_001090
CAGGAAAAACAAACGAAGGAAGCCCTGACTCGGAAGCAGCAGAAATGCCGACGGAAAAAC
rat_chr20                 ---
GAAAAGCAAACAAAGGAAGTCCTGACTCGAAAACAGCAGAAATGCCGAAGGAAAAAC
                             ***** ***** ******* ********* ** ***************
********

human_chr6_NM_001090      CAAGATGAGGAATCCCAGGAGGCCCCTGAGCTCCTGAAGCGCC---
rat_chr20                 CAGGATGAGGAGTCTCAGGATCCCCCTGAGCTTCTGAAGCGCCCCA
                          ** ******** ** *****  ********** **********
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr6_NM_001634      -
GCCAGATCAAACCTTGGAAATTCTGATGAGTGAGCTTGACCCAGCAGTTATGGACCAGT
rat_chr20
AGCCAGATCAAACCCTGGAAATTCTGATGAGTGAGCTTGACCCAGCAGTTATGGACCAGT
                           *************
*********************************************

human_chr6_NM_001634
TCTACATGAAAGATGGTGTTACTGCAAAGGATGTCACTCGTGTAAGCATTTTTAGTAATA
rat_chr20                 TCTACATGAAAGATGGTGTTACTGCAAAGGATGTCACTCGT-------------
------
                          *****************************************

human_chr6_NM_001634
ATTGTTGCTGGACTCTTCTGCGTGGGGACTAAATTTTATTTTTCATTCTGTAACTTTTAA
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_001634
GTTCAGGGTAACAAGTGCTAGTTTGTTACATAGGTAAACTTGTGTCATGGGGGTTTGTCG
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_001634
TACACAGTATTTCGTCACCCAGGTGTTAAGCCTAGTACCCATTAGTTATTTTTCCTGGTC
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_001634
CTCTCCCTTCTCCCACCCTGGGACTAAATTTTGGACTCAATTGAAGTTTATTTGTCAAAC
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_001634
CCTTGTTAAACTCGGTCTTTTCCCCCCCCAGGAGAGTGGAATTCGTGACCTGATACCAG
rat_chr20                 --------------------------------
GAGAGTGGAATTCGTGACCTGATACCAG

****************************

human_chr6_NM_001634
GTTCTGTCATTGATGCCACAATGTTCAATCCTTGTGGGTATTCGATGAATGGAATGAAAT
rat_chr20
GTTCTGTCATTGATGCCACACTGTTCAATCCTTGTGGCTACTCAATGAATGGAATGAAAT
                          ******************** **************** ** **
****************

human_chr6_NM_001634      CGGATGTGAGTA-----
rat_chr20                 CGGATGTGAGTGGCTCG
                          ***********
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr6_NM_004381      ----
CAGCCCAAACCTGTAGTGCTAACCACTGTCCCAATGCCATCCAGAGCTGTGCCTCC
rat_chr20
ACTGCAGCCCAAGCCTGTGGTGCTAACCACAGTTCCGGTGCCACCTAGAGCTGGGCCTGC
                              ******** ***** *********** ** **  ***** * *******
**** *

human_chr6_NM_004381
CAGCACCACAGTCCTTCTGCAGTCCCTCGTCCAGCCACCCCCAGGTACTGAAGAAGGAGA
rat_chr20                 CAGCACTGCTGTCCTTCTGCAGCCCCTGGTCCAGCAGCCCGCAG----------
------
                          ******  * ************ **** *******  *** ***

human_chr6_NM_004381
AAAGGGCCGGGCATGGTGGCTCACGCCGGTAATCCCAGCACTTTGGGAGGCTGAGGCGGG
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
CGAATCACCTGAGGTCAGAAGTTTAAGACCAGCCTGGCCAACGTGGTGAAACCTTGTCTC
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
TACTAAAAATACAAAAATTAGCGTGGAGTGGTGGCAGGCGCCTGTAATCCCAGCTCCTCG
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
GGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGAT
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
CATGCCACTGCACTCCAGCCTGGGCGACAAAGCGAGACTTTGTCTCAAAAAAAAAAAAAA
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
GAAAAAAGAAAAACCAAAAAATAAAAATAAAAATTAATTAATTAATTAAAAAAAAAAGGC
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
CAGGCACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGCAGGCCAAGGCAGGCGGATCA
rat_chr20                 ------------------------------------------------------
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human_chr6_NM_004381
CAAGGTCAGGAGATCGAGACCATCCTGACTAACACAGTGAAACCCCGTCTCTACTAAAAA
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
TACAAAAAAATTAGCCAGGCGTGGTGGCGTGCGTCTGTAGTTCCAGCTGCTGGGGAGGCT
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
GAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGCACCA
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
CTGCACTCCAGCCTGGTCGACAGAGCAAGACTGCATCTCAAAAAAGAAAAAAAGGAGAAA
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
AGGAGGCGGGCTGCATTGACCCTGTCAGAGAGCTTGCAGCCATTGAGGCTGCCCAATCCT
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
TGGGTGCTCTTGTGTGGGTGTGGACACAAGGACCCCACCCAGCGCACAGCCCTCTGACCT
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_004381
CTGCTCACTTGCCCCAGTGTCCCCAGTTGTCCTCATCCAGGGTGCTATTCGAGTCCAGCC
rat_chr20                 -----------------
TATCCCCGGTGGTTCTCATCCAAGGTGCTATCCGAGCCCAGCC
                                           * ***** ** ** ******** ******** ****
******

human_chr6_NM_004381
TGAAGGGCCGGCTCCCTCTCTACCACGGCCTGAGAGGAAGAGCATCGTTCCCGCTCC-
rat_chr20
TGAAGGGCCAGCTCCGGCAGCCCCTCGGCCTGAGAGGAAGAGCATTGTCCCAGCCCCT
                          ********* *****  *    ** ******************** ** ** **
**
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CLUSTAL W (1.83) multiple sequence alignment


human_chr6_NM_007355      -
CCATCTTAAAGAAGATCAGACAGAGTACCTAGAAGAGAGGCGGGTCAAAGAAGTAGTGA
rat_chr9
TTCACCTCAAAGAAGACCAGACAGAGTACTTAGAGGAGAGGAGGGTCAAGGAGGTGGTGA
                            ** ** ******** ************ **** ****** ******* **
** ****

human_chr6_NM_007355
AGAAGCATTCTCAGTTCATAGGCTATCCCATCACCCTTTATGTGAGTATGGACTTTTAAA
rat_chr9                  AGAAACACTCACAGTTCATAGGCTACCCCATCACCCTCTAT-------------
------
                          **** ** ** ************** *********** ***

human_chr6_NM_007355
TCTTTTACACTTAACGTGCAGGATGTTTCCTGTTCTGGAGAATCTCATTGTCCCTGGCTT
rat_chr9                  ------------------------------------------------------
------


human_chr6_NM_007355
TTGCTTTCCCTGGTAGTGTTTTGTACTCCAAGGCTAACTTCTGTTTTTGTTACTTAGTTG
rat_chr9                  ------------------------------------------------------
---CTG

**

human_chr6_NM_007355
GAGAAGGAACGAGAGAAGGAAATTAGTGATGATGAGGCAGAGGAAGAGAAAGGTGAGAAA
rat_chr9
GAGAAGGAACGCGAGAAGGAGATCAGTGATGATGAGGCAGAGGAAGAGAAAGGGGAGAAG
                          *********** ******** ** *****************************
*****

human_chr6_NM_007355      GAAGAGGAAGATAAAGATGATGAAGAAAAACCCAAGA-----
rat_chr9                  GAGGAGGAAGATAAGGAGGATGAGGAGAAGCCTAAGATTGAG
                          ** *********** ** ***** ** ** ** ****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr6_NM_015153      -
GAGTGCTTAATGTACATCCTGCTGCTTCTGCTTCCAAGCCTTCTGCAGATCAGATCAGG
rat_chr9
GGACCTAATGTGCACCCTCCTGCCGCTGCTGCCATCAAGCCTTCTGCAGATCAGATCAGA
                           **     *      * ****** *** ****
************************

human_chr6_NM_015153
CAAAGTGTCAGACATTCTCTCAAAGACATTCTTATGAAGAGGTAACATATATTTTTATTA
rat_chr9                  CAGAGTGTCCGGCACTCCCTTAAGGATATTCTTATGAAAAG-------------
------
                          ** ****** * ** ** ** ** ** *********** **

human_chr6_NM_015153
TAGAAGTATCAATAATTATGCTTTATACATTTGAAAAATAATTGAATTGTTCTAATTTTA
rat_chr9                  ------------------------------------------------------
------


human_chr6_NM_015153
AGACTTACAGACTCAAATTTGAAGGTACCAGAGGAAAAGGCAGCAAAAGTTGCCACAAAA
rat_chr9                  --
ACTTACGGACTCAAACTTGAAGATCCCAGAGGAAAAGTCAGCAAAGGTTGCCACAAAA
                            ****** ******** ****** * ************ *******
************

human_chr6_NM_015153      ATTGAGAAAGAGCTTTTCTCTTTTTTTCGGGACACAGATGCT-
rat_chr9                  ATTGAAAAGGAACTTTTCTCTTTTTTTCGGGACACAGATGCCA
                          ***** ** ** *****************************
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr6_NM_022551      -
TCACTTCATTCAGGGTGTGGGCCGAAGATATGCTCATGTGGTGTTGAGGAAAGCAGACA
rat_chr20
AACTCTAACATCAGGGTGTGGGGCGGAGATACGCTCATGTGGTGTTGAGGAAAGCAGACA
                            * **    ************ ** *****
****************************

human_chr6_NM_022551
TTGACCTCACCAAGAGGGCGGGAGAACTCACTGAGGATGAGGTGAGGACAAGGAAGGGGG
rat_chr20                 TTGACCTCACCAAGAGGGCTGGGGAGCTCACGGAGGACGAG-------------
------
                          ******************* ** ** ***** ***** ***

human_chr6_NM_022551
CTGGGGGTGGGGTCAGCCTCAGAAAGGGGTCCATCTAGATCTGACCTTGGTCTGCCTGCC
rat_chr20                 ------------------------------------------------------
------


human_chr6_NM_022551
AGGTGGAACGTGTGATCACCATTATGCAGAATCCACGCCAGTACAAGATCCCAGACTGGT
rat_chr20                 --
GTGGAGCGTGTGATCACCATCATGCAGAACCCACGACAATACAAGATCCCTGACTGGT
                            ***** ************** ******** ***** ** ***********
*******

human_chr6_NM_022551      TCTTGAACAGACAGAAGGATGTAAAGGATGGAAAATACAGCC--
rat_chr20                 TCTTGAACAGACAGAAGGACGTGAAGGATGGGAAGTATAGCCAG
                          ******************* ** ******** ** ** ****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr8_NM_000971      -----
AGCTTCTTCGCCTTCGTCAAATCTTCAATGGAACCTTTGTGAAGCTCAACAAGGC
rat_chr5
GCTGCAGCTGCTCCGTCTCCGGCAGATCTTCAATGGCACCTTTGTGAAGCTCAACAAGGC
                               **** ** ** ** ** ** ***********
***********************

human_chr8_NM_000971
TTCGATTAACATGCTGAGGATTGTAGAGCCATATATTGCATGGGGGTAAGTCTCTTTTCT
rat_chr5                  TTCAGTGAACATGCTGAGGATCGTGGAGCCCTACATTGCATGGGG---------
------
                          ***  * ************** ** ***** ** ***********

human_chr8_NM_000971
CCTTTGATTTCTATTTGATAAATTGGTTATGTAGCAACATGAATTTTAGATGTTTTAACA
rat_chr5                  ------------------------------------------------------
------


human_chr8_NM_000971
GTGGTCACCTTATTTATGTTTGCTTTTTCACTTCAGGTACCCCAATCTGAAGTCAGTAAA
rat_chr5                  ------------------------------------
GTACCCCAACCTGAAGTCAGTAAA
                                                              *********
**************

human_chr8_NM_000971
TGAACTAATCTACAAGCGTGGTTATGGCAAAATCAATAAGAAGCGAATTGCTTTGACAGA
rat_chr5
CGAGCTCATCTACAAACGAGGCTATGGCAAAATCAATAAAAAGCGCATTGCCTTGACAGA
                           ** ** ******** ** ** ***************** ***** *****
********

human_chr8_NM_000971      TAACGCTTTGATTGCT-
rat_chr5                  TAACTCCTTGGTTGCTC
                          **** * *** *****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr9_NM_001010      ------
GCAGCACAAACGGCGGCGTATTGCTCTGAAGAAGCAGCGTACCAAGAAAAATAA
rat_chr5
TGTCCTGCAACACAAACGCCGACGTATTGCTCTGAAGAAGCAACGCACTAAGAAAAACAA
                                *** ******** ** ******************** ** **
******** **

human_chr9_NM_001010
AGAAGAGGCTGCAGAATATGCTAAACTTTTGGCCAAGAGAATGAAGGTTAGTCTAAGATG
rat_chr5                  GGAGGAGGCTGCAGAATATGCTAAACTTTTGGCCAAGAGAATGAAG--------
------
                           ** ******************************************

human_chr9_NM_001010
ATTTGAGGGGGTGGGAGGAGTTCGACCTGGCTTTGGATTTGCGTCTTTAACCCAGAAAGG
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_001010
CCTTAACTGTTTGCTGTTTTGTTTTGTTTAGGAGGCTAAGGAGAAGCGCCAGGAACAAAT
rat_chr5                  -------------------------------
GAAGCCAAAGAGAAGCGCCAGGAACAGAT
                                                         ** ** **
***************** **

human_chr9_NM_001010
TGCGAAGAGACGCAGACTTTCCTCTCTGCGAGCTTCTACTTCTAAGTCTGAATCCAGTCA
rat_chr5
TGCCAAGAGACGTAGGCTGTCTTCGCTGAGAGCTTCTACTTCTAAATCTGAGTCCAGTCA
                          *** ******** ** ** ** ** *** **************** *****
********

human_chr9_NM_001010      GAAATAAGATT-
rat_chr5                  AAAATAAGTCTT
                           *******  *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr9_NM_018449      ---
CTGTCCAGTAGCATGAACACCGCGAACAGCCTCTGTCTGGGTGGGACCCCCGCGAGT
rat_chr5                  
GCCCTGCCTGGGAGCATGAGCACCGTGAGCAGCCTGTGCCTGGGTGGGACCACTGTGAGC
                             *** *  * ******* ***** ** ****** ** ************ *
* ***

human_chr9_NM_018449      
GCATCCAGCAGCAGTAGCAGGGCCGCGCCCTTGGTGACCTCAGGTATTTGCTCCAGAGGC
rat_chr5                  GCACCTAGCAGCAGTACCAGGGCCACAGCCTTGGTGACCTCAG-----------
------
                          *** * ********** ******* *  ***************

human_chr9_NM_018449      
CTTTCCTGCCCACCCCTGAGCCCCTCAAAGGTGCCTGCTTGGCGTCCCAGGAAGGCAGTG
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449      
CAGGTGTCAGGAGAGTCTCAGGCCCGCCGAGTGCGCTGCGTGTTCCACTGACCTTGAGGC
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449      
CCAATCTCCCCACCCCTGATGGGGATGAATTCTTCCTTGCAGGATTCCTGGCCTCTGCGT
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449      
GCTTCTAGCTTTTCAGTCTTTCCTCTTTGTTCTTTCCTGGAGCCGAGTTGACATTGTGAC
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449      
TTGGAGGGGCCAGGGATGACTTATGGTGGGCTCCACGACTGCAGACCTAGGCTGTCTGTA
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449      
GGCCCAGCAGACTATGATTTGATGGTCGCTGCTAAAACCGACTTCGAACTCAGCCTGTCC
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449      
CTCTCCTGGCACTGCATGGCTTCCTTGCCCTCTTTGGAGGAGGCAGATTCTTTTTATATT
rat_chr5                  ------------------------------------------------------
------
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human_chr9_NM_018449
TCTCTTTGCTCAGTGCAGTGGGACCTTAGGGACTGGGGGAAAGGGGCTGCTTTTGTCTGG
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449
GCCCGGAACTCTCTGACGTTGAAACAACCTCAGTGTGGTGGCCGGGCTTTCTGTCTCCCC
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449
TTCACTGCTTTGTAGAATGACCCTCTGCCTCATTCGGCCACTGCCCTTCTTTGAACCCAT
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449
CTGGGGTAGCTCAGTGACTGTGCCTCCTCCTGAAGCAGCTGAGGACTCTCACTCTTTGTG
rat_chr5                  ------------------------------------------------------
------


human_chr9_NM_018449
GTGACCATTTCACTCCATTTGATTTTTCCCTCTATACAGGCAAAGCACCCCCAAACTTAC
rat_chr5                  ---------------------------------------
GCAAAGCACCCCCAAACCTTC

***************** * *

human_chr9_NM_018449
CTCAGGGGGTGCCTCCCCTGCTGCACAACCAGTACCTCGTAGGTCCCGGAGGACTGCTTC
rat_chr5
CTCAAGGGGTGCCTCCTCTGCTACACAATCAGTACCTCGTGGGCCCTGGAGGGCTGCTTC
                          **** *********** ***** ***** *********** ** ** *****
*******

human_chr9_NM_018449      CTGCCTACCCGGTGAGTGT-
rat_chr5                  CTGCTTACCCGGGAGTAGAT
                          **** *******     *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr10_NM_003375      -CTTGGAGACCAAATACAAGTGGTGTGAGTATGGTCTGACTTTCACAGAA
rat_chr15                  CCTTGGAGACCAAGTACAAATGGTGTGAGTATGGTCTGACTTTCACAGAG
                            ************ ***** ***************************** 

human_chr10_NM_003375      AAGTGGAACACTGATAACACTCTGGGAACAGAAATCGCAATTGAAGACCA
rat_chr15                  AAATGGAACACTGACAACACTCTGGGGACGGAGATTGCAATTGAAGACCA
                           ** *********** *********** ** ** ** **************

human_chr10_NM_003375      GGTAACATTTTGAAAATTTTAGTATTAATTTTATTAATTTATTTTTGTAT
rat_chr15                  G-------------------------------------------------
                           *                                                 

human_chr10_NM_003375      TTCAAAAAAAGAAAACAAATTACTTTTCTTTCAAAATAGATTTGTCAAGG
rat_chr15                  ---------------------------------------ATTTGTCAAGG
                                                                  ***********

human_chr10_NM_003375      TTTGAAACTGACATTTGATACTACCTTCTCACCAAACACAGGGTAAGCAC
rat_chr15                  TTTGAAACTGACCTTTGACACCACGTTTTCACCAAACACAGGGTAAGTGC
                           ************ ***** ** ** ** *******************  *

human_chr10_NM_003375      AGACATTTTTATCTGTATTACATTTAAAAGTATTTCTCT--
rat_chr15                  TGGTGTTGGTGCACGCTGTGCTTACAGGCCTCGTCTGCTCA
                            *   **  *    *   * * *  *    *  *   **  
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CLUSTAL W (1.83) multiple sequence alignment


human_chr10_NM_003591      ------GAAGTCAGCGAAAGGGATGACAGAGAATGAAGTGGAAGACAGGC
rat_chr17                  GCTAAAGAAGTCAGCAAAGGGGATGACGGAGAATGAAGTAGAGGACAAGC
                                 ********* ** ******** *********** ** **** **

human_chr10_NM_003591      TCACGAGCTTCATCACAGTGTTCAAATACATTGATGACAAGGACGTCTTT
rat_chr17                  TTACCAGCTTCATCACAGTTTTCAAGTACATCGATGACAAGGACGTCTTT
                           * ** ************** ***** ***** ******************

human_chr10_NM_003591      CAAAAGGTATGTTGTGAACAGAAAAGTTTCATTTGTATTTTGGTCAACTT
rat_chr17                  CAGAAG--------------------------------------------
                           ** ***

human_chr10_NM_003591      TATTTCTGAATGCTAAATCATTAGAAAGGAAGTAATCTTTTAAAATATTT
rat_chr17                  --------------------------------------------------


human_chr10_NM_003591      TTAAATGTAGTTCTACGCAAGAATGCTGGCAAAACGTTTAATTCATGGGT
rat_chr17                  ----------TTCTATGCAAGAATGCTAGCAAAACGTCTAATTCACGGGC
                                     ***** *********** ********* ******* ***

human_chr10_NM_003591      TATCCATGTCTATGGACTCTGAAGAAGCCATGATCAACAAATTAAAGGTA
rat_chr17                  TGTCTATGTCTATGGATTCTGAAGAAGCCATGATCAATAAATTAAAGGTA
                           * ** *********** ******************** ************

human_chr10_NM_003591      ATGTAAGTCT-
rat_chr17                  ACATAAATCTT
                           *  *** ***
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr10_NM_018237      -GTAGTGCTCCGTGAATCTTGCTTTTACCGGAAATTAACAGACACCTCAA
rat_chr20                  AGTAGTGCTCCGAGAATCGTGCTTCTATCGGAAATTAACAGACACCTCAA
                            *********** ***** ***** ** **********************

human_chr10_NM_018237      AAGATGAAGAGAACCATGAAGAGTCTGAGTCATTGCAGGAAGATATGCTA
rat_chr20                  AAGACGGCGAGAGCCATGACGAGCCAGAGTCGCTGCAGG--GGGACACGA
                           **** *  **** ****** *** * *****  ******  *  *  * *

human_chr10_NM_018237      GGTCTGAGTAATATTAAGATTTTGCTTTTTAATAAATATACTAGTAATTA
rat_chr20                  CG-CTGG----------------------------------------------
                           ** ***

human_chr10_NM_018237      AAGAAGAAAAATAACTTACTAAAATATGGTATATTTTATATTATAGGAAA
rat_chr20                  ----------------------------------------------GAAA
                                                                         ****

human_chr10_NM_018237      CAGATTATTACTTCCAACACCAACAGTAAAGCAGGAATCAAAGGATGTGG
rat_chr20                  CAGGTTACTACTTCCCACACCAACAGTGAAGCAGGAATCGAAGGATGGAG
                           *** *** ******* *********** *********** *******  *

human_chr10_NM_018237      AAGAAAATGTTGGCCTCATTGTGTACAATGGTGCAATGGTAGATGT
rat_chr20                  AAGAAAACGTAGGGCTTATTGTGTACAACGGTGCAATGGTGGATGT
                           ******* ** ** ** *********** *********** *****
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CLUSTAL W (1.83) multiple sequence alignment


human_chr10_NM_001001973      -GAAAGCCCCCCACTTTTGGAGATGCGTCAGTCATTGCCCTTGAATTACT
rat_chr17                     CGGAAGCCCCCTACTTTTGGAGATGCATCGGTCATTGCCTTGGAGTTGTT
                               * ******** ************** ** ********* * ** **  *

human_chr10_NM_001001973      AAATTCTGGATATGAATTTGATGAAGGCTCCATCATCTTTAATAAATTCA
rat_chr17                     AAATTCGGGATATGAATTTGATGAAGGCTCTATTATCTTTAATCAGTTCA
                              ****** *********************** ** ********* * ****

human_chr10_NM_001001973      GGCAAGACAGATTTAGAAATCAAAGCTTTTTTATGTTCATGCTTTTGTTC
rat_chr17                     A-------------------------------------------------


human_chr10_NM_001001973      ATATTTTGAAATAACAGTTTAAAAATTATTTTGAGATTTACATTTGTTTT
rat_chr17                     --------------------------------------------------


human_chr10_NM_001001973      TGTCAATTCTAGGTCTGTCATCTCCTATAAGACAGAAGAAAAGCCCATCT
rat_chr17                     ------------GTCTGTTATCTCCTACAAGACAGAAGAGAAGCCCATCT
                                          ****** ******** *********** **********

human_chr10_NM_001001973      TTTCCCTTAATACCGTTGCAAGTGCTGGTAAGTAGTTTTTCTATGATACA
rat_chr17                     TCTCTTTCAGTACCGTCGTGGCTGCTGGTAAGCCGCCTTCACACGGCAGG
                              * **  * * ****** *     **********  *  **   * *  *

human_chr10_NM_001001973      TATTTTTTGGCA--
rat_chr17                     TGTGGCGACTGGGA
                              * *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr10_NM_001011663      ----CGCCTGATTAATCTCTCTGAGCTGACCCCATACATCTTGTGTTCCA
rat_chr1                      ACAGCGCCTGATCAACCTGGTTGAGCTGACCCCCTACATCTTGTGCTCCA
                                  ******** ** **   ************ *********** ****

human_chr10_NM_001011663      TTTGCAAAGGTTACTTAATAGATGCAACTACCATCACAGAATGTCTTCAT
rat_chr1                      TTTGCAAAGGTTACTTGATAGATGCCACCACTATTACAGAATGTCTCCAC
                              **************** ******** ** ** ** *********** **

human_chr10_NM_001011663      ACCTGTAAGCATACCGATCACATTTCTGAATAATTTTTCAGTTTTTGAAA
rat_chr1                      ACCT----------------------------------------------
                              ****

human_chr10_NM_001011663      TGTCTTGAAAGCATCCTGACTTCAACATTCTTTTTCAACAGTTTGTAAAA
rat_chr1                      -----------------------------------------TCTGTAAAA
                                                                       * *******

human_chr10_NM_001011663      GCTGCATCGTAAGACATTTTTACTACAGCAACAGATGTCCAAAATGCAAT
rat_chr1                      GCTGCATTGTGAGACATTTTTACTATAGCAACAGATGCCCCAAATGCAAC
                              ******* ** ************** *********** ** ******** 

human_chr10_NM_001011663      ATAGTAGTACATCAGACACAACCTCTTTATAACATAAGGTA-
rat_chr1                      ATAGTCGTCCACCAGACTCAGCCTCTTTATAATATAAGGTAA
                              ***** ** ** ***** ** *********** ********
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr11_NM_000920      ---TCACTGCTGGCCACTCGTGTGCGCACCCACGATCTCAAAAAGATCGC
rat_chr1                   CAGTCACTACTTGCCACTAGAGTGCGCACACACGATCTCAAAAAGATTGC
                              ***** ** ****** * ******** ***************** **

human_chr11_NM_000920      CCCCTATGTTGCCCACAACTTCAGCAAGCTCTTCAGCATGGAGAACTGGG
rat_chr1                   ACCCTACGTTGCCCACAACTTCAACAACCTCTTCAGCATAGAGAACTGGG
                            ***** **************** *** *********** **********

human_chr11_NM_000920      GAGGTAGGCTGGCATGCTGCGCAGCGCCTGGTAGGAATGGGCGCCCGCTC
rat_chr1                   GAG-----------------------------------------------
                           ***

human_chr11_NM_000920      TGTGGCCAGTCCCACAGGCTTAGGCCACTGGGGACAAGCTAGAGACGCTG
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      ACACGAAGAACACCAAAGAGGAAGGACCGAAGAAGGCACAGCGCCCTCTC
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      CGGCCAGGCCTGGTGCCGGCACGAGGTTGCAGAGCTGAGACCAGGTGCAT
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      CCTGGGAGGTCCAGGGTCAGGAGGAGACACCTGCCTGTTAATTATAGCAC
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      AGAGAGGTAGAGGAGAAGATGGGATTATAAAGGGGGCATAGAAGGGACAC
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      AAATGAGCCTGGTCTCCCCCTTAGAGATCAGACAAGGGAAAAATCTGTGG
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      GGGTTGGAGCAGGGAACACAGGTATGGCGAAGATGAGCAGGACCTGGTAT
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      TGGGGCCAGAGGCTTGTGCTGCAGAGCTAGCTCCAAGGCCTGGTGGAGTT
rat_chr1                   --------------------------------------------------


human_chr11_NM_000920      CCCCAGGCATGCAGAGCTGATCTGGGCCTCTCGGTTCCTGTGCAGGAGCC
rat_chr1                   ---------------------------------------------GAGCC
                                                                        *****

human_chr11_NM_000920      ACGTTTGACGTCGCCATGCGCTTCCTGTATGAGTGCCCCTGGCGGCGGCT
rat_chr1                   ACATTTGACGTGGCCATGCGCTTCTTGTATGAGTGCCCCTGGCGGCGGCT
                           ** ******** ************ *************************

human_chr11_NM_000920      GCAGGAGCTCCGGGAGCTCATCCCCAACATCCCTTTCCAGATGCT-
rat_chr1                   CCAGGAGCTCCGGGAGCTCATCCCCAACATCCCATTCCAGATGCTA
                            ******************************** ***********
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr11_NM_001166      -ATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCATCTA
rat_chr8                   TATGCAGACACACTCTGCTCGGATGAGGACGTTTCTGTACTGGCCATCGA
                            ***********  * ***** ***** ** *** ************* *

human_chr11_NM_001166      GTGTTCCAGTTCAGCCTGAGCAGCTTGCAAGTGCTGGTTTTTATTATGTG
rat_chr8                   GTGTTCTTGTTCAGCCTGAGCAGCTTGCAAGTGCTGGATTTTATTATGTG
                           ******  ***************************** ************

human_chr11_NM_001166      GGTAAGAAGCAAATAACTATACATTTTATCATTTTATTTTAATTTACATA
rat_chr8                   G-------------------------------------------------
                           *

human_chr11_NM_001166      TTAGAACATACGTGTTTTCAATATTTAGTCTTTTTTTTCCTGAAGGTCGC
rat_chr8                   ---------------------------------------------ATCAC
                                                                        ** *

human_chr11_NM_001166      AATGATGATGTCAAATGCTTTTGTTGTGATGGTGGCTTGAGGTGTTGGGA
rat_chr8                   AATGATGATGTCAAATGCTTTTGTTGTGATGGTGGCTTGAGATGTTGGGA
                           **************************************** *********

human_chr11_NM_001166      ATCTGGAGATGATCCATGGGTAGAACATGCCAAGTGGTTTCCAAG---
rat_chr8                   ACCCGGAGATGACCCCTGGATAGAACATGCCAAATGGTTTCCAAGGTA
                           * * ******** ** *** ************* ***********
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr11_NM_004357      -CCGCGCCCCGCAGGGCGGCTGCATCACCAAGTTGGAGACCTTCATCCAG
rat_chr1                   TTATCTCCCGCTAGGGTGGCTGCATCACTAAGCTGGAGTCCTTCATTCAG
                               * ***   **** *********** *** ***** ******* ***

human_chr11_NM_004357      GAGCACCTGAGGGTCATTGGGGCTGTGGGGATCGGCATTGCCTGTGTGCA
rat_chr1                   GAGCACCTGCGGGTCATCGGGGCCGTGGGCATTGGCATCGCCTGTGTGCA
                           ********* ******* ***** ***** ** ***** ***********

human_chr11_NM_004357      GGTGAGGGCACATGGGGGTGGCGGTCATCTTGTTGGGGACACGGGGCAGG
rat_chr1                   G-------------------------------------------------
                           *

human_chr11_NM_004357      GCGGTGGCTGGTGGCCCCATGACGTCTGCTTACGCCCACCCGGCTCTGCA
rat_chr1                   --------------------------------------------------


human_chr11_NM_004357      CACAGGTCTTTGGCATGATCTTCACGTGCTGCCTGTACAGGAGTCTCAAG
rat_chr1                   -----GTCTTCGGCATGATCTTCACCTGCTGCTTGTACAGAAGCCTCAAG
                                ***** ************** ****** ******* ** ******

human_chr11_NM_004357      CTGGAGCACTACTGACCCTGCCTTGGGCCTTGCTGCTGCTGCACCCAACT
rat_chr1                   CTGGAGCACTACTGACCATGGTGCCAGGCCAGAAGGCCAGCCTCGCGCTG
                           ***************** **      * *  *  *      * * *

human_chr11_NM_004357      ACTGA-
rat_chr1                   TGTCCC
                             *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr11_NM_005146      -CGCCGCCGAGTGTCCGAAGTGGAGGAGGAGAAGGAGCCTGTGCCTCAGC
rat_chr1                   AGTGGAGGAGGAGGCCCTTGAGGATGAAGAGAAGGACCCTGTGGCCCAGC
                                     * * **   * *** ** ******** ****** * ****

human_chr11_NM_005146      CCCTGCCGTCGGACGACACCCGAGTGGAGAACATGGACATCAGTGATGAG
rat_chr1                   CGCCACCATCAGATGACACTCGCGTAGAGAACATGGACATCAGTGATGAG
                           * *  ** ** ** ***** ** ** ************************

human_chr11_NM_005146      GGTGAGGGCCCGGCCAGGGGGTGGGAGGGGCAGGGACAGGAGCCGCGGGT
rat_chr1                   G-------------------------------------------------
                           *

human_chr11_NM_005146      TGGAGGAGATGGTCTGAGCAGGCATCCCCTGTGTTTCCCCCAGAGGAAGG
rat_chr1                   -------------------------------------------AGGATGG
                                                                      **** **

human_chr11_NM_005146      TGGAGCTCCACCGCCGGGGTCCCCGCAGGTGCTGGAGGAGGACGAGGCGG
rat_chr1                   GGGGGCTCTTCCCTCGGGGCCCCCA---GAGCTGGAGGAGGACGAAGCGG
                            ** ****  **  ***** ****    * *************** ****

human_chr11_NM_005146      AGCTGGAGCTGCAGAAGCAGCTGGAGAAGGGACGCCGGCTGCG-----
rat_chr1                   AGCTGGAGCTGCAGAAGCAGCTGGAGAAGGGGCGCCGGCTGCGGCAGC
                           ******************************* ***********
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CLUSTAL W (1.83) multiple sequence alignment


human_chr11_NM_006842      -AAGTGAGACACCTCAGCTCTTCACTGTGTTGCCAGAGAAGAGAACAGCC
rat_chr1                   GGAGCGAGACACCTCAGTTGTTCACTGTATTGCCAGAGAAGAGGACAGCC
                             ** ************ * ******** ************** ******

human_chr11_NM_006842      ACTGTTGGAGGGGCCATGATGGGATCAACCCACATTTATGACATGTCCAC
rat_chr1                   ACTGTTGGTGGGGCCATGATGGGATCTACCCACATTTATGACATGTCCAC
                           ******** ***************** ***********************

human_chr11_NM_006842      GGTGAGTACTTGGAGGATACTGCTTTTGGAGGCTGAGAAAGGCAGCAGAA
rat_chr1                   G-------------------------------------------------
                           *

human_chr11_NM_006842      GCTAGGGCTTCTCTGACTCTTTGGAGATGACCAGGCCCTGATCTCCTTTC
rat_chr1                   --------------------------------------------------


human_chr11_NM_006842      CAGGTTATGAGCCGGAAGGGCCCGGCTCCTGAGCTGCAAGGTGTGGAAGT
rat_chr1                   ---GTTATGAGCCGGAAGGGCCCGGCCCCTGAGTTGCAAGGTGTGGAAGT
                              *********************** ****** ****************

human_chr11_NM_006842      GGCGCTGGCGCCTGAAGAGTTGGAGCTGGATCCTATGGCCATGACCCAGA
rat_chr1                   AGCACTGGCTCCCGAGGAGTTGGAGTTGGACCCCATGGCCATGACCCAGA
                            ** ***** ** ** ********* **** ** ****************

human_chr11_NM_006842      AGT------
rat_chr1                   AGTATGAGG
                           ***
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr11_NM_015104      -----------CCAGGCGCCGCCGGTGGACGTGCATCAGCCGCCTGCCTT
rat_chr1                   CGGGACCCAAGCCAGGCACCACCTGTGGACGTGCACCAGCCACCTGCCTT
                                      ****** ** ** *********** ***** ********

human_chr11_NM_015104      CCTGCACAAGCTGCTGCAGCTGGCAGGGGTCCGCCTGCACTACGAGGAGC
rat_chr1                   CTTGCACAAGCTGCTGCAGCTGACTGGGGTCTGCCTGTACTTTGAAGAGC
                           * ******************** * ****** ***** ***  ** ****

human_chr11_NM_015104      TCCCGGCACAGGTGAGCGGGCTCTGATTCCCACAGCCCCTGTCTCCTCTC
rat_chr1                   TGCCCTCCCAG---------------------------------------
                           * **  * ***

human_chr11_NM_015104      CCTTGAGCCCATTGAGCCCCTCCCATCCTTTCTGACCATCTCTGACTCCA
rat_chr1                   --------------------------------------------------


human_chr11_NM_015104      TTTTCTCAACCTTTCCCTCTTGTATCCTCCCGTCTCCCAGGAAGAGCCTC
rat_chr1                   ----------------------------------------GTGGACCCGC
                                                                   *  ** ** *

human_chr11_NM_015104      CAGAGCCCCCCTTGCAGATCGGCAGCTGCTCAGGGTACATGGAGCTGATG
rat_chr1                   CAAAGCCACCTTTGCAAATCGGCAGCTGCACAGGGTACATGGAGCTCATG
                           ** **** ** ***** ************ **************** ***

human_chr11_NM_015104      GTGAAGTTGAAGCAAAATGAGGCCTTCCCTGGCCCCAAGG-
rat_chr1                   GTGAAGCTGAAACAGAATGAGGCCTTCCCGGGGCCCAAGGT
                           ****** **** ** ************** ** *******
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CLUSTAL W (1.83) multiple sequence alignment


human_chr11_NM_020680      -GACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGAGAGTGGAG
rat_chr1                   TGACAGAGGCTGTGACCCCACTGGGAACATACCTCAAGGCACGAGCAGAA
                            ******************  ****** ************  ***  ** 

human_chr11_NM_020680      GCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGT
rat_chr1                   GCAGGTGGTCTGAAGGAGCAGGAGCTGTCATGGGGGTTACACCAGATCGT
                           ** ***** ********** **** * ** ****** *************

human_chr11_NM_020680      GGTGAGGTGGGGGGCAGTGGTGATGAGAGCAGGGATGGGGGGTTGCAGGT
rat_chr1                   G-------------------------------------------------
                           *                                                 

human_chr11_NM_020680      GCTGGGGCGTGATGGCTCCTTTTGCCCCCAGAAAGCCCTCAGCTTCCTGG
rat_chr1                   -------------------------------AAAGCCCTCAGCTTCCTGG
                                                          *******************

human_chr11_NM_020680      TCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCGCCGTGTTC
rat_chr1                   TCAACGACTGCAACCTCATCCACAACAATGTCTGCATGGCTGCTGTGTTT
                           ************ *************************** ** ***** 

human_chr11_NM_020680      GTGGACCGAGCTGGCGAGTGGAAGCTTGGGG---
rat_chr1                   GTGGACAAGGCTGGCGAGTGGAAACTTGGGGGTC
                           ******   ************** *******   
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CLUSTAL W (1.83) multiple sequence alignment


human_chr12_NM_002046      -ATTTGGTCGTATTGGGCGCCTGGTCACCAGGGCTGCTTTTAACTCTGGT
rat_chr4                   GATTTGGCCGTATCGGACGCCTGGTTACCAGGGCTGCCTTCTCTTGTGAC
                            ****** ***** ** ******** *********** **    * **  

human_chr12_NM_002046      AAAGTGGATATTGTTGCCATCAATGACCCCTTCATTGACCTCAACTACAT
rat_chr4                   AAAGTGGACATTGTTGCCATCAACGACCCCTTCATTGACCTCAACTACAT
                           ******** ************** **************************

human_chr12_NM_002046      GGTGAGTGCTACATGGTGAGCCCCAAAGCTGGTGTGGGAGGAGCCACCTG
rat_chr4                   G-------------------------------------------------
                           *                                                 

human_chr12_NM_002046      GCTGATGGGCAGCCCCTTCATACCCTCACGTATTCCCCCAGGTTTACATG
rat_chr4                   -----------------------------------------GTCTACATG
                                                                    ** ******

human_chr12_NM_002046      TTCCAATATGATTCCACCCATGGCAAATTCCATGGCACCGTCAAGGCTGA
rat_chr4                   TTCCAGTATGACTCTACCCACGGCAAGTTCAACGGCACAGTCAAGGCTGA
                           ***** ***** ** ***** ***** *** * ***** ***********

human_chr12_NM_002046      GAACGGGAAGCTTGTCATCAATGGAAATCCCATCACCATCT---
rat_chr4                   GAATGGGAAGCTGGTCATCAACGGGAAACCCATCACCATCTTCC
                           *** ******** ******** ** ** *************   
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr12_NM_002046      -GAGCCAAAAGGGTCATCATCTCTGCCCCCTCTGCTGATGCCCCCATGTT
rat_chr4                   GGGGCCAAAAGGGTCATCATCTCCGCCCCTTCCGCTGATGCCCCCATGTT
                            * ******************** ***** ** *****************

human_chr12_NM_002046      CGTCATGGGTGTGAACCATGAGAAGTATGACAACAGCCTCAAGATCATCA
rat_chr4                   TGTGATGGGTGTGAACCACGAGAAATATGACAACTCCCTCAAGATTGTCA
                            ** ************** ***** *********  *********  ***

human_chr12_NM_002046      GGTGAGGAAGGCAGGGCCCGTGGAGAAGCGGCCAGCCTGGCACCCTATGG
rat_chr4                   G-------------------------------------------------
                           *

human_chr12_NM_002046      ACACGCTCCCCTGACTTGCGCCCCGCTCCCTCTTTCTTTGCAGCAATGCC
rat_chr4                   -------------------------------------------CAATGCA
                                                                      ******

human_chr12_NM_002046      TCCTGCACCACCAACTGCTTAGCACCCCTGGCCAAGGTCATCCATGACAA
rat_chr4                   TCCTGCACCACCAACTGCTTAGCCCCCCTGGCCAAGGTCATCCATGACAA
                           *********************** **************************

human_chr12_NM_002046      CTTTGGTATCGTGGAAGGACTCATGGTATGAGAGCTGGGGAAT-
rat_chr4                   CTTTGGCATCGTGGAAGGGCTCATGGTATGTAGGCAATGGAGAC
                           ****** *********** ***********   **   ***
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr12_NM_002898      --TCCTATTCTCACTCAAGGGCTCACAATGTGAACACTGTGTTCTTTCTT
rat_chr7                   GGGGCATATGGGTACTCCGGGCTGGCAATATGGACGCTGCATTCTTTCTT
                               *   *         *****  **** ** ** ***  *********

human_chr12_NM_002898      TATAGGGCGTCATGGCCTTGACCTATGACCCCACCACAGCTCTTCAGAAT
rat_chr7                   -ACAGGGTGGAATGGCCTTGACCTATGACCCCACCACAGCTCTTCAGAAT
                            * **** *  ***************************************

human_chr12_NM_002898      GGGTAAGGTTTTATATAATCAAGCCACCTGAAAATGATAATGGCCTGTGT
rat_chr7                   GG------------------------------------------------
                           **

human_chr12_NM_002898      CCAGACACTCAAATGATTCATCTTGATTCTCTCTATTTGAAAGTCAAGGG
rat_chr7                   --------------------------------------------------


human_chr12_NM_002898      AACGTTGGCTGTGCCTATCAGTTGGGACCCTTCCCTTGTGGTTTCCTGTG
rat_chr7                   --------------------------------------------------


human_chr12_NM_002898      ACTCAGTACTGATTGAGGTTCCTTCCCACAGGTTTTACCCAGCCCCCTAT
rat_chr7                   -------------------------------GTTCTACACAGCTCCTTAC
                                                          *** *** **** ** **

human_chr12_NM_002898      AACATCACCCCCAACAGGATGCTTGCTCAGTCTGCACTCTCCCCATACCT
rat_chr7                   AGTCTCGCCCACAGCAGAATGCTCGCTCAGTCTGCACTAGCCCCGTATCT
                           *   ** *** ** *** ***** **************  **** ** **

human_chr12_NM_002898      TTCCTCTCCTGTGTCTTCGTATCAGGTATGT---
rat_chr7                   TCCATCGCCCGTGTCTTCCTACCAGGTGAGGTGC
                           * * ** ** ******** ** *****  *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr12_NM_007062      -AATTTTTCTTACAGATGCTGAGACTCTTGGTGAATCTCTCTTGGGTCTT
rat_chr7                   GGATCCTGATTACAGATGCTGAGACCATTGGAGAATCTCTGTTGGGGCTT
                             **  *  ****************  **** ******** ***** ***

human_chr12_NM_007062      ACGGTCTACGGGAGTAATGATCAAGATCCTTACGTTACTCTGAAAGATAC
rat_chr7                   ACGGTCTATGGCAGTAACGATCAGGATCCATACGTCACCCTCAAAGACAC
                           ******** ** ***** ***** ***** ***** ** ** ***** **

human_chr12_NM_007062      AGTAAGTATTTACATCTTTTTTCTAATTATGCTCTTAAGTGTTCAAAAAA
rat_chr7                   G-------------------------------------------------
                                                                             

human_chr12_NM_007062      CCTTACTGGCTCTCTGCTTCTAGTCAATGACATTTTTTTCCTCTCACTTA
rat_chr7                   --------------------------------------------------
                                                                             

human_chr12_NM_007062      GGAACAATATGAACGTGAAGATTTCTTGATTAAGCCCAGTGATAATCTTA
rat_chr7                   -GAACAGTACGAGCACGAAGACTTCTTGATTAAGCCGACCGACAACCTCA
                            ***** ** ** *  ***** ************** *  ** ** ** *

human_chr12_NM_007062      TAGTTTGTGGCCGAGCTGAACAGGACCAGTGCAATTTAGAGGTGCATGGT
rat_chr7                   TCGTCTGTGGCCGTGCAGAACAAGAGCAGTGTAACTTAGAGGTGCACGGT
                           * ** ******** ** ***** ** ***** ** *********** ***

human_chr12_NM_007062      A---
rat_chr7                   GAGT
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr12_NM_013449      -----GCGCCAGACCCTCGAGCGGTGCCGGAGCGCAGCCCAGGTGTGCTT
rat_chr7                   GTCTGGCGGCAGACACTTGAGAGGTGCCGCAGTGCAGCCCAAGTGTGCCT
                                *** ***** ** *** ******* ** ******** ****** *

human_chr12_NM_013449      GTGCCTGGGCCAGCTGGAGAGGTCCATTGCCTGGGAGAAGTCTGTCAACA
rat_chr7                   GTGCGTGGGCCAGCTGGAAAGGTCCATCGC-TGGGAGAAGTCTGTCAACA
                           **** ************* ******** ** *******************

human_chr12_NM_013449
AAGTGGTAAGAGGCTGAGAGAGCCTGGAGAGGCTGAGGGGCCAGCCAGCAGGGGC
rat_chr7                   AAGTG------------------------------------------------
--
                           *****

human_chr12_NM_013449      GGGGTGGGGTCACTGGCAGGTAGAGGCTGGAGAGCTCATTCTGCCTCCTC
rat_chr7                   --------------------------------------------------


human_chr12_NM_013449      ACAACCTTGGTCCAG-ACATGTCT-AGTCT-GCCGGAA-GGGTG-ACAAT
rat_chr7                   ---------------GACCTGTCTGGGTCTTGTCGGAAGGGGTGTACAAT
                                           ** *****  **** * ***** ***** *****

human_chr12_NM_013449      GATGAGTTTCTTCTGCTTT-GTGATGGGTGTGACCGTGGCTGCCACATTT
rat_chr7                   GACGAGTTTCTCCTGCTTTTGTGATGGGTGTGACCGAGGCTGCCACATTT
                           ** ******** ******* **************** *************

human_chr12_NM_013449      ACTGCCATCGTCCCAAGATGG
rat_chr7                   ACTGTCATCGCCCCAAG----
                           **** ***** ******
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr12_NM_053275      ---GCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACC
rat_chr12                  TCCGCATGTCCCTCCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACC
                              ********** ************************************

human_chr12_NM_053275      ATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGA
rat_chr12                  ATGATGCGCAAGGCCATCCGGGGCCACCTGGAGAACAACCCCGCTCTGGA
                           ******************** ** ******** ******** ********

human_chr12_NM_053275      GAAGTCAGTTCCCCTGGCAGTTTTGTCCTTTCTCCCCAGTGCCCGTCTCC
rat_chr12                  GAA-----------------------------------------------
                           ***

human_chr12_NM_053275      CTCTTCCTGGAGAATGGTGCTGAAAGGTGATTGTCTCCCATAAACTTCTC
rat_chr12                  --------------------------------------------------


human_chr12_NM_053275      TTTGCAGACTGCTGCCTCATATCCGGGGGAATGTGGGCTTTGTGTTCACC
rat_chr12                  -------GCTGCTGCCTCACATCCGGGGGAACGTGGGCTTTGTGTTCACC
                                   *********** *********** ******************

human_chr12_NM_053275      AAGGAGGACCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTAAG
rat_chr12                  AAGGAGGACCTCACCGAGATTAGGGACATGCTGCTGGCCAATAAGGTAAG
                           ************** ***** ********* *******************

human_chr12_NM_053275      GGGACAA-
rat_chr12                  GGGCGGTA
                           ***
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr13_NM_002271      -TGCAAAATCCTTGGAAAAGAATTTCAGCAATACCTTCCAGTGGTTATGG
rat_chr15                  GTGCAAAATCCTTGGGAAAGAATTCCAGCAGTACCTTCCTGTGGTTATGG
                            ************** ******** ***** ******** **********

human_chr13_NM_002271      GGCCTTTAATGAAGACGGCTTCAATTAAGCCCGAAGTAGCCCTTTTAGAT
rat_chr15                  GGCCACTGATGAAGACCGCTTCAATTAAGCCTGAAGTGGCCCTTCTAGAC
                           ****  * ******** ************** ***** ****** ****

human_chr13_NM_002271      AGTAGGTGTCTTTAGAAGGAGCTATCGGTTATAATAGTTCTCTCTTTGTT
rat_chr15                  A-------------------------------------------------
                           *

human_chr13_NM_002271      ATTATTTTTCATATGCATTTGTTTTCTTCTCCGTTAATAGCCCAAGACAT
rat_chr15                  ----------------------------------------CCCAGGACAT
                                                                   **** *****

human_chr13_NM_002271      GGAGAATATGAGTGATGATGATGGTTGGGAATTTGTGAACCTTGGAGATC
rat_chr15                  GGAGAATATGAGTGACGACGATGGTTGGGAATTTGTAAACCTTGGAGATC
                           *************** ** ***************** *************

human_chr13_NM_002271      AGCAAAGCTTTGGTATTAAAACTGCAGGACTAGAAGAAAA----
rat_chr15                  AGCAGAGTTTTGGTATTAAAACTGCAGGACTGGAGGAGAAGTCA
                           **** ** *********************** ** ** **
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CLUSTAL W (1.83) multiple sequence alignment


human_chr13_NM_002271      -ATGGGAGATGGATGCCTTAATAATGAACACTTTGAAGAACTGGGAGGTA
rat_chr15                  GATGGGAGATGGGTGTCTCAACAATGAACACTTCGAGGAACTGGGAGGTA
                            *********** ** ** ** *********** ** *************

human_chr13_NM_002271      TATTGAAAGCAAAGCTTGAAGAACATTTTAAAAATCAAGAATTACGACAA
rat_chr15                  TACTGAAGGCGAAGCTCGAGGAACATTTCAAAAATCAAGAGTTGCGGCAA
                           ** **** ** ***** ** ******** *********** ** ** ***

human_chr13_NM_002271      GGTAAGTTTTCCATGCTTTTATTTCTGAATATAATCCTTGACCATCTTGG
rat_chr15                  G-------------------------------------------------
                           *

human_chr13_NM_002271      CAATCATTTAAAACATTTATTTGGGTGTGTTTTAGTTAAAAGACAAGATG
rat_chr15                  -----------------------------------TTAAAAGACAAGATG
                                                              ***************

human_chr13_NM_002271      AAGACTATGATGAACAGGTCGAAGAGTCACTACAAGATGAGGTAAGTTAT
rat_chr15                  AAGACTACGACGAACAGGTTGAAGAGTCGCTACAAGATGAAGTGAGTCAG
                           ******* ** ******** ******** *********** ** *** *

human_chr13_NM_002271      TCCCTTTGGAACTTACTTACGTGACCACTTGCATC--
rat_chr15                  GCCTTCAGAACTGCACTCCCATGACGTTGCACCTGAG
                            ** *  * *    ***  * ****      * *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr13_NM_007111      -GAAGGTGCAGAGGAAAGGGACCACTTCCTACAACGAAGTGGCAGACGAG
rat_chr16                  AGAAGGTGCAGAGGAAAGGGACGACCTCCTACAATGAGGTGGCCGACGAG
                            ********************* ** ******** ** ***** ******

human_chr13_NM_007111      CTGGTTGCGGAGTTCAGTGCTGCCGACAACCACATCTTACCAAACGAGTC
rat_chr16                  CTGGTTGCCGAGTTCAGCGCCGCTGACAACCACATCTTACCCAACGAGTC
                           ******** ******** ** ** ***************** ********

human_chr13_NM_007111      AGTAAGTGTGTGCCGGGGGCCGAGAGGCTGGGGTGGCGGAGCCCAGCGGT
rat_chr16                  C-------------------------------------------------


human_chr13_NM_007111      GTGGTACGTTTCGCTCTTTTAATATCGGGAACAGTTAAAACCATACAGAA
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      AATGCCAAGTACAGCATAAAAGAATTTTTACCAAACGAGTCAGTAAGTGT
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      GTGCCGGGGGCCGAGAGGCTGGGGTGGCGGAGCCCAGCGGTGTGGTACGTT
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      TCGCTCTTTTAATATCGGGAACAGTTAAAACCATACAGAAAATGCCAAGT
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      ACAGCATAAAAGAATTTTTCCGATCCATTTGCTGGCACGATGCTTTGTCA
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      ACTCCAGTGAGTGAGCACGTGGGCTGGCTCTGCACGTCTAGCGGCCCAGA
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      AATGCACAAATGCCCACCTCACCAGCTGGGCTCGACACCCGAGAGCCCCC
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      GGCTCTCCTTCTGGAACACACTCAGGCTTCGCACAGCCCCGTCTTGCCCT
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      GCGTCATCTGTGGGGTGGGAGCGCTCCCTGAGGGCATGTTGGGGTGGCGG
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      CTCCGTGAGCGGGGTGCCCCTTTGAGCCAGTGCCCATGGTCTACAGTTTA
rat_chr16                  --------------------------------------------------


human_chr13_NM_007111      AGGATCCACCGGCCTTTTTGGATCATTTGGAAACTCCACTCCCTGTCATC
rat_chr16                  --------------------------------------------------
```

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human_chr13_NM_007111      CCCAGGCTTATGACCAGAAAAACATAAGACGGCGCGTCTACGATGCCTTA
rat_chr16                  -----GCCTACGACCAGAAGAACATCCGGCGGCGTGTGTACGATGCCTTA
                                ** ** ******** *****  * ***** ** ************

human_chr13_NM_007111      AACGTGCTAATGGCCATGAACATCATCTCCAAGGAGAAGAAGGAGATCAA
rat_chr16                  AATGTGCTGATGGCCATGAACATCATCTCCAAGGAGAAGAAGGAGATCAA
                           ** ***** *****************************************

human_chr13_NM_007111      GTGGA----
rat_chr16                  GTGGATCGG
                           *****
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr14_NM_001312      -CTCAGCCGAGAAGGTGAGCTCCCTGGGGAAGGACTGGCACAAGTTCTGC
rat_chr6                   CTACAGCCGAGAAGGTGAGCTCCCTGGGCAAGGACTGGCACAAGTTCTGC
                              ************************* *********************

human_chr14_NM_001312      CTCAAGTGCGAGCGCTGCAGCAAGACGCTGACGCCCGGGGGCCACGCCGA
rat_chr6                   CTCAAGTGTGAGCGCTGCAACAAGACACTGACGCCTGGCGGCCATGCTGA
                           ******** ********** ****** ******** ** ***** ** **

human_chr14_NM_001312      GGTGAGCCCCACTGCGCGGCGCGGGCGGGGGCGGGGGTCGCGACTCCCGC
rat_chr6                   G-------------------------------------------------
                           *

human_chr14_NM_001312      CACCCTCAGGCAGGGTCCTGACCCGCGCCCCTCTGCGCAGCATGACGGGA
rat_chr6                   ----------------------------------------CATGATGGGA
                                                                   ***** ****

human_chr14_NM_001312      AGCCGTTCTGCCACAAGCCGTGCTACGCCACCCTGTTCGGACCCAAAGGT
rat_chr6                   AACCCTTCTGCCACAAGCCCTGTTATGCCACACTGTTTGGACCCAAAGGT
                           * ** ************** ** ** ***** ***** ************

human_chr14_NM_001312      GAGCTCCGGCTGCCCTCGGCCTGCCCTGGGACCTGCTGGG--
rat_chr6                   AAGCAGGGTCCCAGACAGGCCTCAGATGATCTGGGACAGCTC
                            ***   * *       *****    **      *   *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr14_NM_002892      -GAAGGTCTCTGTGAGAGGGAATCGGCAAATGGATTTGAAACTAATGTTG
rat_chr6                   GGAAGGCCTGTGTGAGAGGGAATCAGCAAACGGATTTGAAGCCAGCGTCA
                            ***** ** ************** ***** ********* * *  **  

human_chr14_NM_002892      CCTCTGGTACCTGTAGTATAATTGTACAAGAGAGAGAGAGCAGAGAGAAG
rat_chr6                   CCTCTGGCGCCTGTGGCATGATCGTCCACGAGAGAGAGAGCAGAGAGAAG
                           *******  ***** * ** ** ** ** *********************

human_chr14_NM_002892      GGTAAGGACTTTCTAGGGAAAAGTAAGTGTTTATATGAAACCAAAAATCA
rat_chr6                   G-------------------------------------------------
                           *                                                 

human_chr14_NM_002892      AAACTGTTGAGTTTCAGGTACTGTTGATCTGTAAAGTACTTTCTTTTTCT
rat_chr6                   --------------------------------------------------
                                                                             

human_chr14_NM_002892      TTTCTCTCTTCTTTTCTTATTAAAAAGAAAGAAATGTCAGTGTAGTCTGT
rat_chr6                   --------------------------------------------------
                                                                             

human_chr14_NM_002892      TGAATAATATACTTGCTCTTTTTTTTTTTTTTTTTTTTTTCAACATTCTC
rat_chr6                   --------------------------------------------------
                                                                             

human_chr14_NM_002892      TCTTTCCCCTTATTTCAGGTCAGAAGAGGCCAAGTGATGGAAATAGTGGA
rat_chr6                   ------------------GTCAGAAAAGGCCAAGCGATGCAAACAGTGGG
                                             ******* ******** **** *** ***** 

human_chr14_NM_002892      TTAATGGCAAAAAAGCAAAAGCGTACCCCAAAGCGAACAAGTGCTGCAGC
rat_chr6                   CTAATGGCAAAAAAGCAAAAGCGAACCCCAAAGCGGACGAGTGCTGCAGC
                            ********************** *********** ** ***********

human_chr14_NM_002892      CAAAAATGAAAAGAATGG---
rat_chr6                   CAAGAGTGAGAAGAACGGAGC
                           *** * *** ***** **   
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CLUSTAL W (1.83) multiple sequence alignment


human_chr14_NM_207661      -TTTGTTAGCAGTTGCACCACCAGCACCACCTTCCAGTAGTCAGCTCTGC
rat_chr6                   TCTTGTCAGCAGTGTCGTCACCAGCGCCATCTTCTAATGGCCAGCTCTGC
                             **** ******  *  ******* *** **** * * * *********

human_chr14_NM_207661      CGTTACTTCCCTGCTTGTAAGAAGATGGAATGTCCCTTCTATCATCCAAA
rat_chr6                   CGTTACTTCCCTGCCTGTAAGAAAATGGAGTGTCCCTTCTACCACCCCAA
                           ************** ******** ***** *********** ** ** **

human_chr14_NM_207661      AGTAAGAACTTCTATTTTCTCAAATCAATTTAGTGACAACATCTCAATTT
rat_chr6                   A-------------------------------------------------
                           *

human_chr14_NM_207661      CCTCATTTAACTTCTTTTTTGTCAGAGTTACTACATTGGTGCAAAAGTAA
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      TTGCGATTTTTGCCAGTAAAACTATTAAGTTGTTCCTCGTCACTGAACCT
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      CCATCTGGCCCCTTAGGCCAAGTGGTCTGAAACTGTTCAATGTTAGTATC
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      CCAAGCACTCAGTGGGGGGAAGCATATCTTTGCTAGTCACATTTTCCATT
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      ATTCCCTGCATTTAAGTATATGGATGGGTTTTAGCGGGGGCTGGGGGGCA
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      GTTTGAACCTAATGTCAGAACTGAGATGAAGAAATCCAGTAGGTACTGCT
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      TAAAACCATCCAAACTTGTACTGATGATGGTTGATGAATCTCCAGATGTT
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      TAGTTGGTCAAAATGAATTATCTCCTTCTTGCCCCGGTAGCTTGAGGACC
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      ATATGAAGGCCTTCACTTGCCCCCATCTGTAACTGGGCGTAGATGAGGGT
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      ACTCAGTGAAGAGTGTAAGGGATAATTAGAAGTTTTTGTGGTATGCTAAA
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      CTACCTTTTGAAATTGTACTTGCTGTGATTCTTTGACTAGAATTTTGTGT
rat_chr6                   --------------------------------------------------
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human_chr14_NM_207661      CTCAAGGTTAAGTCCATTTTTCAAGGCTTCACTAGTATTAAAATGGTCCT
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      TATAGATGGAATCTCTTACTCTGTTAATGGTTAGGGTGGGCTGGTTATTG
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      TCTCCTAAGTTGTATGTTGGCCAGGTGAGGTGGGTCAGGCCTGCTATCCT
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      AGTACTTTGGGAGGTAGAGGCAGAAGTGGAAGGATCGTTTGAGCCCGGGA
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      GTTTGAAACCAGCCTAGGCAACATTTAAGAGACCCCATCTCTTAAAAAAA
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      AAAAAAACAGGCTTGGTAGCACACGCCTGTAGTCCCAGCTACTCGGGAGA
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      CTGAGGCAAGAGGTCATGCCACTTCACTCCAGCCTGGGTGACAGAGTGAG
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      ACCCTGTCTCAAATAATAAAATAATGTGTTTACTTATATTAGCCTTGTGG
rat_chr6                   --------------------------------------------------


human_chr14_NM_207661      ATATTGTTGAAGCTCTGTTATCTCTATTCAGCATTGTAGGTTTAACACTC
rat_chr6                   -------------------------------CACTGTAGGTTTAATACCC
                                                          ** *********** ** *

human_chr14_NM_207661      AATGTACAAGACCGGACTGCACATTCTACCATCCCACCATTAATGTCCCA
rat_chr6                   AGTGTACAAGACCAGACTGTACGTTTTATCACCCCACTATTACTGTGCCA
                           * *********** ***** ** ** ** ** ***** **** *** ***

human_chr14_NM_207661      CCACGACATGCCTTGAAATGGATTCGACCTC----
rat_chr6                   CCAAGACATGCCTTGAAATGGATTCGACCTCAAAC
                           *** ***************************
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CLUSTAL W (1.83) multiple sequence alignment


human_chr15_NM_001003      -ATTGGGAGCCTCATCTGCAATGTAGGGGCCGGTGGACCTGCTCCAGCAG
rat_chr8                   CATTGGAAGCCTCATCTGCAATGTAGGGGCTGGTGGGCCAGCTCCAGCCG
                            ***** *********************** ***** ** ******** *

human_chr15_NM_001003      CTGGTGCTGCACCAGCAGGAGGTCCTGCCCCCTCCACTGCTGCTGCTCCA
rat_chr8                   CTGGGGCTGCGCCTGCTGGTGGTCCTGCTCCATCTGCCGCCGCTGCCCCA
                           **** ***** ** ** ** ******** ** **  * ** ***** ***

human_chr15_NM_001003      GGTAGGAAACATGGAGTTTTTAGTATTGGGAGGAGTGTAGAGATTTTTTA
rat_chr8                   G-------------------------------------------------
                           *

human_chr15_NM_001003      AAAAATAGTATTATAGACAAAATTGCCATTAATTTTTCACAAGTATATGA
rat_chr8                   --------------------------------------------------


human_chr15_NM_001003      AGTATGGAAATCCTAACACCTGATTGACTTTTTTTTTCTAGCTGAGGAGA
rat_chr8                   -----------------------------------------CTGAGGAGA
                                                                    *********

human_chr15_NM_001003      AGAAAGTGGAAGCAAAGAAAGAAGAATCCGAGGAGTCTGATGATGACATG
rat_chr8                   AGAAAGTAGAAGCAAAGAAGGAAGAATCTGAAGAATCCGAGGATGACATG
                           ******* *********** ******** ** ** ** ** *********

human_chr15_NM_001003      GGCTTTGGTCTTTTTGACTAAACCTCTTTTATAACATGTTC--
rat_chr8                   GGCTTTGGTCTTTTTGACTAAACTGCTTTTGTTAACATGTCCA
                           ***********************  ***** * *     **
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CLUSTAL W (1.83) multiple sequence alignment


human_chr15_NM_005926      -----AGTGACAGTTCAAGAACGTGAAGCCGAAGCATTGAAACAGAAGGA
rat_chr3                   GATCGTGTGACAGTTCAAGAACGAGAAGCTGAGGCATTGAGACAGAAGGA
                                 ***************** ***** ** ******* *********

human_chr15_NM_005926      GCTGGAGCAGGAAGCAAAACGCATGGCTGAGGAAAGGCGCAAGTACACAC
rat_chr3                   ATTGGAGCAGGAAGCAAAACGCATGGCTGAGGAGCGGCGCAAGTACACCC
                             *******************************  ************* *

human_chr15_NM_005926      TCAAGGTACTGGGGAGTGGTTGCAAGGAATGAGTACAAGAAATAGTGTAA
rat_chr3                   TCAAG---------------------------------------------
                           *****

human_chr15_NM_005926      TCAGGTTTGTCTGAGGAGAGTAAGGAAGTCCAAGCTGAATTGTTCTCCCT
rat_chr3                   --------------------------------------------------


human_chr15_NM_005926      ATCCAGATTGTCGAAGAGGAAACCAAAAAAGAGCTGGAAGAGAACAAGCG
rat_chr3                   ------ATTGTAGAAGAAGAGACCAAGAAAGAGCTGGAGGAGAACAAGCG
                                 ***** ***** ** ***** *********** ***********

human_chr15_NM_005926      ATCCCTGGCTGCATTGGATGCACTCAATACTGATGATGAAAATGATGAGG
rat_chr3                   GTCCCTTGCCGCCCTGGATGCACTCAATACAGATGATGAAAATGACGAGG
                            ***** ** **  **************** ************** ****

human_chr15_NM_005926      AGGAAT-
rat_chr3                   AGGAGTA
                           **** *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr15_NM_020990      -TGTTGTGGTGGATGCACTGAGTGGCCTGAAGGGTGACCTGGCTGGACGT
rat_chr3                   GTGTTGTGGTGGACGCGCTGAGTGGCCTGAAGGGCGACCTGGCTGGACGG
                            ************ ** ***************** ************** 

human_chr15_NM_020990      TACTATAGGCTCAGTGAGATGACAGAGGCTGAACAGCAGCAGCTTATTGA
rat_chr3                   TACTACAGGCTCAGTGAGATGACAGAGGCTGAGCAGCAGCAGCTTATTGA
                           ***** ************************** *****************

human_chr15_NM_020990      TGTGAGGGCCTTAAGAGGGTGCTGGTTGGTGGGAGCAGATGGGGAAGGCT
rat_chr3                   C-------------------------------------------------
                                                                             

human_chr15_NM_020990      GGGCCAGATGAGACATGGGCTCTGAAAGGCCCAGGGGCCACCATGAAGAT
rat_chr3                   --------------------------------------------------
                                                                             

human_chr15_NM_020990      TCTTAACCCAAGTCCCGTTACTCTTCCCAGGACCACTTTCTGTTTGATAA
rat_chr3                   ------------------------------GACCATTTCCTGTTTGATAA
                                                         ***** ** ***********

human_chr15_NM_020990      GCCTGTGTCCCCGTTGCTGACTGCAGCAGGAATGGCTCGAGACTGGCCAG
rat_chr3                   ACCTGTGTCCCCATTGCTGACAGCAGCAGGCATGGCTCGAGACTGGCCAG
                            *********** ******** ******** *******************

human_chr15_NM_020990      ATGCTCGTGGAATTTGGTATGAAGCTGCTC----
rat_chr3                   ATGCCCGAGGAATCTGGTACGAGGCCGATCCACC
                           **** ** ***** ***** ** ** * **    
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr16_NM_002952      --CATCCGTGGGGCCATCATCCTGGCCAAGCTCTCCATCGTCCCCGTGCG
rat_chr10                  GCCATCCGAGGGGCCATCATCCTGGCCAAGCTTTCGATCGTCCCAGTGCG
                             ****** *********************** ** ******** *****

human_chr16_NM_002952      CAGAGGCTACTGGGGGAACAAGATCGGCAAGCCCCACACTGTCCCTTGCA
rat_chr10                  GAGAGGCTACTGGGGGAACAAGATTGGCAAGCCCCACACTGTGCCATGCA
                            *********************** ***************** ** ****

human_chr16_NM_002952      AGGTAGGCTGGTGGCAGGTGATGGGCCTGCCGTGGGGCAGGCTCCCTCGG
rat_chr10                  AG------------------------------------------------
                           **

human_chr16_NM_002952      GCCCCCGTCTCCTGACTCCTTCCCTCACCAGGTGACAGGCCGCTGCGGCT
rat_chr10                  -------------------------------GTGACAGGCCGCTGTGGCT
                                                          ************** ****

human_chr16_NM_002952      CTGTGCTGGTACGCCTCATCCCTGCACCCAGGGGCACTGGCATCGTCTCC
rat_chr10                  CTGTGCTGGTTCGTCTCATCCCTGCCCCCAGAGGCACTGGCATTGTCTCT
                           ********** ** *********** ***** *********** *****

human_chr16_NM_002952      GCACCTGTGCCTAAGAAGCTGCTCATGATGG-
rat_chr10                  GCTCCTGTGCCCAAGAAGCTACTGATGATGGC
                           ** ******** ******** ** *******
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr16_NM_005881      -CGCCCCGTGTCCGCATCAATGGCCATGTGGCTGCCCGGTTCCCCTTCAT
rat_chr1                   GCCCCTAGAGTCCGCATCAATGGGCACGTGGCTGCCCGTTTCCCCTTCAT
                            * **  * ************** ** *********** ***********

human_chr16_NM_005881      CCCTATGCCACTGGACTACATCCTGCCGGAGCTGCTCAAGAATGCCATGA
rat_chr1                   TCCTATGCCGCTGGACTATATCCTGCCTGAGCTGCTCAAGAACGCCATGA
                            ******** ******** ******** ************** *******

human_chr16_NM_005881      GGTGGGGTGGCTTGATGTGCTGGCTTGGGGGCGGACAGGAACCGGGGTGC
rat_chr1                   G-------------------------------------------------
                           *

human_chr16_NM_005881      TTGTACCTACTGGTCTTTCCCCTCTGCATAGAGCCACAATGGAGAGTCAC
rat_chr1                   -------------------------------AGCCACAATGGAGAGTCAC
                                                          *******************

human_chr16_NM_005881      CTAGACACTCCCTACAATGTCCCAGATGTGGTCATCACCATCGCCAACAA
rat_chr1                   CTAGACACGCCCTACAATGTTCCTGATGTGGTCATCACCATCGCCAATAA
                           ******** *********** ** *********************** **

human_chr16_NM_005881      TGATGTCGATCTGATCATCAGGTTTGCCCTG--
rat_chr1                   CGATGTGGATCTCATCATCAGGTTTGCTCAAAC
                            ***** ***** ************** *
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr16_NM_024860      -CTTATCTCAGGTGGCGGGGCCCGTGGACGGCGGCGACCTGGATCCTGTG
rat_chr19                  TGCCGCTCCCGGCGGGGCCCAGCGGCCACGAGCCCGAGAGTGACGCAGTG
                                   * ** ** *     **   ***    ***    **  * ***

human_chr16_NM_024860      GCCTGCTTCCTGAGCTGGTGCCGGCGGGTGGGGCTGGAGCTGAGTCCCAA
rat_chr19                  GCCGGCTTCCTGCGCTGGTGCACGCGAGTGGGGCTGGAGCTGAGTCCCAA
                           *** ******** ********  *** ***********************

human_chr16_NM_024860      GGTGAGCGAGCGAGCCGGCGGGCGGAGGACCCGCGGCGGGGCGCGGGCTG
rat_chr19                  G-------------------------------------------------
                           *

human_chr16_NM_024860      CCCTGACCAGCCCTCCTGCTCAGGTGGCGGTCAGCCGGCAGGGCACGGTG
rat_chr19                  -----------------------GTGCTGGTGAGCCGGCAGGGCACGGTG
                                                  ***  *** ******************

human_chr16_NM_024860      GCCGGCTACGGCATGGTGGCCCGGGAGAGCGTGCAGGCCGGAGAGCTGTT
rat_chr19                  GCCGGCTACGGCATGGTGGCGCGGGAGAGCGTGCAGCCCGGGGAGCTGCT
                           ******************** *************** **** ****** *

human_chr16_NM_024860      GTTCGTGGTGCCGCGGGCCGCGC--------
rat_chr19                  GTTCGCAGTGCCGCGGTCCGCGCTCCTGTCT
                           *****  ********* ******
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CLUSTAL W (1.83) multiple sequence alignment


human_chr17_NM_000546      -TCAGCATCTTATCCGAGTGGAAGGAAATTTGCGTGTGGAGTATTTGGAT
rat_chr10                  CCCAACATCTTATCCGGGTGGAAGGAAATCCGTATGCTGAGTATCTGGAC
                             ** *********** ************  *  **  ****** ****

human_chr17_NM_000546      GACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTATGAGCCGCCTGA
rat_chr10                  GACAGGCAGACTTTTCGGCACAGCGTGGTGGTACCGTATGAGCCACCTGA
                           *****  * ******** ** ** ******** ** ******** *****

human_chr17_NM_000546      GGTCTGGTTTGCAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGTGGTTGT
rat_chr10                  G-------------------------------------------------
                           *

human_chr17_NM_000546      CAGTGGCCCTCCAGGTGAGCAGTAGGGGGGCTTTCTCCTGCTGCTTATTT
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      GACCTCCCTATAACCCCATGAGATGTGCAAAGTAAATGGGTTTAACTATT
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      GCACAGTTGAAAAAACTGAAGCTTACAGAGGCTAAGGGCCTCCCCTGCTT
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      GGCTGGGCGCAGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAA
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      GGCAGGCGGATCACGAGGTTGGGAGATCGAGACCATCCTGGCTAACGGTG
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      AAACCCCGTCTCTACTGAAAAATACAAAAAAAAATTAGCCGGGCGTGGTG
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      CTGGGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGAAGGAGAATGGC
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      GTGAACCTGGGCGGTGGAGCTTGCAGTGAGCTGAGATCACGCCACTGCAC
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      TCCAGCCTGGGCGACAGAGCGAGATTCCATCTCAAAAAAAAAAAAAAAAG
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      GCCTCCCCTGCTTGCCACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTG
rat_chr10                  --------------------------------------------------


human_chr17_NM_000546      GGCCTGTGTTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTACA
rat_chr10                  -------------------GTCGGCTCCGACTATACCACTATCCACTACA
                                              ** ***** **** ****** **********
```

```
human_chr17_NM_000546      ACTACATGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCATC
rat_chr10                  AGTACATGTGCAACAGCTCCTGCATGGGGGGCATGAACCGCCGGCCCATC
                           * ******** ***** *********** ***********  ********

human_chr17_NM_000546      CTCACCATCATCACACTGG-
rat_chr10                  CTTACCATCATCACGCTGGA
                           ** *********** ****
```

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CLUSTAL W (1.83) multiple sequence alignment


human_chr18_NM_024805      -CTTATGTAACTTTTTGACTTTGCCATCACTAACATAATGCTTATTTTCT
rat_chr18                  TCCTGAGCTGTTTCTCCAGCCTCCCCTCCCAACCTAATTTCTGTTTGCT
                            * *  *    ** *  *   * **    * *** ****   * *** **

human_chr18_NM_024805      CCCCAAAGAAAAAAGGTTTGGTATGAAAGTCCTTCCTTGGGTTCTCACTC
rat_chr18                  TGACACAGAAAGAAGTTTTGGTATGAAGCTCCATCCCTGGGGTCTCACTT
                              ** ***** *** ***********  *** *** **** *******

human_chr18_NM_024805      GGTGAGTATAAGCCATGAGCCACTTTATAATCTTGATGGGAGTGAGGGTT
rat_chr18                  G-------------------------------------------------
                           *

human_chr18_NM_024805      TAAAAGTTGGCAAAACTCTTACCTGGAGGTCTTTCCATTTCTGTATTGGA
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      GGGGATAGTGTCTATGTGGATGCGACTGGATGCCATTGGCAACATGGAGT
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      TTTGATCTTTTCAAAAAAAAATGTACTGACATTAATGTTTTCTGGAAAGT
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      CATATCTTTTATCAAATTATAATATGGTAATATCCATTCAGTTTTTAGTG
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      TGTGTGTACTGTAAAAGTTTATACAATATATGGCTCCCATTCTGAAAAAT
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      AAATACATCACGTTTCCAAAAAATTACTGAATTATTCCCTTTAGCACGGT
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      GAACTTTATGGTATGTGAATTATATCTCAACAAAAACTTTTTTTGAGAAA
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      ATATTTACTGGCAGTACTTTTAATCTTGGAGGGTTACCAGGTAAAATTTA
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      AAAGGATCCCGGTTTATAAAACTTTATCTTAATGAAAGCTGAGGCAGCTG
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      AGAGTGATAGCTGCTGTTGATCTGGTTGCCCATCCAGCCCTCCCCCAGCC
rat_chr18                  --------------------------------------------------


human_chr18_NM_024805      CCTGCTGTGTGACTTGGTGAGTTTGGAGTTGTAACGCTGCCCTTGGGGTG
rat_chr18                  --------------------------------------------------
```

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human_chr18_NM_024805      TGCTCTTCTTCCTGATGGAGACTTACAAACCATCCAAGTTGGAATTCCTC
rat_chr18                  --------------------ACTCACAAGCCATCCAAGTATGAGTTCCTC
                                               *** **** **********  ** ******

human_chr18_NM_024805      ATGAGGAGCACCTCAAAGAAAACCAGGAAGGAAGACCATGCGCGCCTGAG
rat_chr18                  ACGAAGAACACGTTAAAGAAGACTAGGAAGGAGGACACTATACGCCTAAG
                           * ** ** *** * ****** ** ******** ***  *   ***** **

human_chr18_NM_024805      GGCCCTGAACGGCCTCCTCT----
rat_chr18                  GGTCCTGAACGGCCTTCTCCACAA
                           ** ************ ***
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CLUSTAL W (1.83) multiple sequence alignment


human_chr22_NM_014303      --CCCGCGGACTGGCAAGTGCCACGTGCAGACCATTCAGCTGTGCCGCCG
rat_chr14                  TTCCCTCGGACGGGCAAGTGCCACGTGCAGACCATCCAGCTGTGCCGCCG
                             *** ***** *********************** **************

human_chr22_NM_014303      GCTCACTGTGGAGTTCATGCACTACATTATCGCTGCCCGTGCCCTGCGCA
rat_chr14                  CCTCACCGTGGAGTTCATGCACTACGTCATTGCTGCCCGAGCCCTGCGCA
                            ***** ****************** * ** ******** **********

human_chr22_NM_014303      AGGTGAGCCTGGGACTGCCCGGCTGGCATCCCACCCTGCCCCCTCTCCTG
rat_chr14                  AG------------------------------------------------
                           **

human_chr22_NM_014303      CCACCCCATGGTCTTCACCCAGATGTCTCCTCCTCTCCCCTAGGTCTTCC
rat_chr14                  -------------------------------------------GTCTTCC
                                                                      *******

human_chr22_NM_014303      TGTCCATCAAAGGCATTTACTACCAGGCCGAGGTACTGGGGCAGCCCATC
rat_chr14                  TGTCCATCAAAGGCATCTACTATCAGGCTGAGGTGCTGGGTCAGCCCATC
                           **************** ***** ***** ***** ***** *********

human_chr22_NM_014303      GTGTGGATCACTCCCTATGCCTTCTCCCATGACGTGAGTGTGC-
rat_chr14                  GTGTGGATTGCACCCTACGCTTTCTCCCATGATGTAAGTGTGCT
                           ********  * ***** ** *********** ** *******
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CLUSTAL W (1.83) multiple sequence alignment


human_chr22_NM_007098      --CTATGACAAGTACGAGGAGTATGACAATGCTGTGCTCACCATGATGAG
rat_chr10                  CTGTATGACAAGTATGAAGAGTATGATAATGCCATCATCACTATGATGAA
                              *********** ** ******** *****  *  **** *******

human_chr22_NM_007098      CCACCCCACTGAGGCCTGGAAGGAGGGTCAGTTCAAGGACATCATTACCA
rat_chr10                  TCACCCCACCGACGCATGGAAGGAAGGGCAGTTCAAAGACATCATCACCA
                            ******** ** ** ******** ** ******** ******** ****

human_chr22_NM_007098      AGGTAAGAGGGGATACAGAGCGCTGGCTCCTGCCAGCCTCTGCCAGGCCC
rat_chr10                  AG------------------------------------------------
                           **

human_chr22_NM_007098      TATTCTGGGTGCAGGGGAATGGGCAGGTGGGAGTGGAATGAGTACCAGCA
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TGCCCCCATGCTGTGTGTGCGTTCACTTGTATGAGTCCACCACCCTCTGG
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      GCAGATGGTAGTAATTCCATCTTTGAAGGGAACTGACACTTAAGAAGGGC
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      AGGTGACCCGTCTAGCGATGCACAGCTGAGCTGCGGGCAGGGTCAGGCCA
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      GCATGCAGCCGTGGCCCTGTGGCCCTGCCTGCCCGCCCCTCCCACCATAC
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      CACGCCCCTTGTGGCCAGGCCTCAGTTCGTTCTTCCTTCTGCCCTGTCAGC
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TCAGGGCTCCCACCCCCACTTCCTGTGGTTATTGTTCACCATCGGACCTT
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TTTTTTTTTTAGTTCATGTCTCTCCCCAGCACCAGCGGCCTTACCTGTCT
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      GGGAGTGGGCCTCCATCCTGTAGCCTAACTGGGCTAAACCGGGACCCGAG
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TTTCTCTGTCAGCAGCCACACTGTTGGGTGGTGTCGGGTTTGGGTGCCAT
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      GGTCAAGTGAGCCTTTGTTATTTTGTTTCCGGTCTCTTAGAGAGTTCAAC
rat_chr10                  --------------------------------------------------
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human_chr22_NM_007098      CTCAGGACCCACCCCTCTCCAGCTCTGTATGTGAGTTTGGTGAAGGGGCT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GGAATTCTTTATCCTCAGCCCCCATCCCTTTGCATTGGGTATCTGCGCTT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TGTGCCATGGTCTTTGGGTAACTAACTTGTCACAGTCGGCTTGTGACTGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AGTGGCACAGCAGTGAGCTGTGGCCTCGCTCATGCACCTCTTTTCCACAT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GCGGCTACTGAGGGTGGGCGCGAGTGGCACGTGTGCTGCCAGGTGAGCCT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCAGCCTCTGCCTTTCCTGGGAACTATTTGAAGGAACCCAGTATTGAGCA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CCAGGCCACAAGCCCGAGCTTCTTGTTGGAGGACATCCATGTTACTGGGC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      ATGGTGGTACGTGAAAGTGGGGGCCTTTGATGGGGCGTCCCACCCTGAGC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AGAGTCTGCAGGTTGCTGGAGGGAGTGCGGCCAGGTCATACCTTACTGTG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GCCTGGCACACGTGGCTGCTGCCTTGTAGATTTGTCTGTGTGCTGGAAAA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCCATACTTGATCAATCCTGTGTGTATTTTATTCACATTGTAACTCCTCT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GATATTAGGGTGTTTTTAAAAATTGCTGAGCCGTGGTGGAAGTGGCCATG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CTTTTGTTTCTTACTGGCATATAAAATAATAGCAGGACAGCTGAGACTCA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CTGTGTGGGAGAGCAGCATCTCTCATCTGGTGCCTGCAGGGCTGATGGCT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GAGTCCAGTTCCTTGTGTGATTCATGATGCTTCTACTACACCCTGCCGTG
rat_chr10                  --------------------------------------------------
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human_chr22_NM_007098      TGGGAGACAGACACTGTCAGCTCAGGTGTGAAGGGGGTAGGAGGATACTC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GCCAGTGCAGGGGTCCAATCAGATGGACGACATCCAATCTGTATTTGGGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CACACGATAGCAGGAATCCACTTAGCCATAGGGCTGGGCCAGCAGCAGCC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TGAGCAGGGGAGCTTGCTAACTCACACGGGGGGCACCCCAGCTCAGCCAT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCACTGTCTCTCTCCATGTGGGCTAGGGGTGTCACCGCTGTGAACCTCGT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TATCCCATCCATACAATGGACATCATGTTTCCTCCCGACCAAGTGGTCCA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TGGCAGGTGCCTGGCATCCGGTGGGCGCTTCTTTCAGGTTGTGCAGCACA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GCACGCCAACCAGCTATCCTGGAGCTTGTGGCGGAATCTCAGCTTCAGTT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TTCTCTTCTTTTTTTGTTTTATTATTATTTTTCTTGAAACGGAGTCTCAC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCTGTCACTCAGGCTGGAGTGCAGTGGCGCGATCTTGGCTCACTGCAACC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCCGCCTCCCAGCCTCGAGCGATTCTCCTGCCTCAGCCTCCAGAGTAGCT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GGGATTACAGGTGCCTGCCACCACGCCCGGCTCATTTTTGTATTTTTAAT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AGATACAGGGTTTTACCATGTTGGGCAGGCTGTTCTCAAACTCCTGACCT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CAGGTGATCTTGAGAGGTGACGCCACCTGGACTTCTTGGGTCGGGTGGGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      ACTTGGAGAAATTTTGTGTCCAGCTAAAGGATTGTAAGTACACCAATCAG
rat_chr10                  --------------------------------------------------
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human_chr22_NM_007098      CACTCTGCATCTAGCTAAAGGATTGTAAATGCACCAATCAGCACTCTGTA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AAAAACGTACCAATCAGCACTCTGTAAAATGGGCCAATCAGCACTCTGTA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GAATGGACCAATTAGCGCTCTGTAAAATGGGCCAATCAGCAGGATGTGGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TGGGGCCAAATAAGGGAATAAAAGCTGGCCATGCGAGCCAGCAGTGCAAC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CTGTTCGGGTCTTTTTCCATGTTGTGGGAGCTTTGTTCTTTTGCTTTTCA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CAATCAGTCTTGCTGCTGCTCACTCATTGAGTCTGCACTAGGTTTAAAAG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CTGTAACACTCACTGCGAAGGTCTGGAGCTTCATTTGTGAAGTCAGCCAG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      ATCACGAACCCACCAGAAGGAAGAAACTCACACCTCTCAACATCTGAAGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AACAAACTCTGGACACAACATCTTTAAGAGCTGTAACACTCACCATGAGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GTCTGTGGCTTCATTCTTGAAGTCAGTGAGACCAAGAACCCACCGGAAGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AATAAATTACAGACACAATCCGCCTGCCTTGGCCTCCCAAAGTGCTGGGA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TTACAGGCGTGAGCCACCACGCCCAGCCTTCAGTTTTCCCTTGTATAAAA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CAGGGATACTACCATGTCTTCTGGGGTGCTGGCTGTCCTTGCTGACCATG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CTAGTGGGCACGGGCCTGCCAGTGCTCCATGTCCTGGCGCGTGGCTAGTG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GACTCACCCCATCCTGTCTTTCAGCTTGGATCTGGAGGACGCTCCAGAGG
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rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GGCCCCGCCGCTCCATTCCTCCTGTAGTGCAGAGGGCTCCAGATCCCAGC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AGCTGAGCCCAACAGAGATGTGTGTCCCTGCAGGCCTCAACACCAGAGGA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      ACTGGGTGGGAACATGGCAGTTATACTCCACCTTAAACGGCATTCCGGCC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      ATGCTGCATGGACCTGTTGAAAGGGCCAAGAGTGCACATGGTACCAGGTG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCCCACAAGGGAAGCTAGGACTGCTGGTGCCCCACTTCAAGTCTGTCCAC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCGCGTGATACCTGCAAGAGTCTCTGAAATGGGCTTGTCCTTGGATGGTT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CCTCTCCTTCACGGGAGGCCTGAGGAGCCTTGTGGTTGGTGGGGAAGCAG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GTGGGGCTTTGAGGAGGTGATTCGCCACAGAAGATGAACTTGAGTCCCTA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CCCTTCTCTTCAGCCCCACATCACATCCTGACTGCTCTCTGCTTCTTCAG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TGTCTAGTTGAGGCCCCCATGTCCTGGCCCTGCTGCTGAGTAAAGGGCCA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GCCTAGAAGGCTGACAGGTGCTAGAGCTCCAATAGGAGTGGACCCACAGT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GGCCTGTGGCAGAGTCTGGGGGCCCACCAGTGCCATAGGTGAAGCTTTGT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GATGCGGCCAGTTCACCGTTTTGCTCTGAATCCATGGTGGCGGGTACTAG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GGACCCTGCTGCCTGTCTGGGTCAGAATCTCTGGTGACAGTGAGTGCTCT
rat_chr10                  --------------------------------------------------
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human_chr22_NM_007098      AGCACAAAAGGAAAAGAGAAGGAGAAAGAAGACACCCTGAAGTGGCCAGT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AAGCCATAGTGGGACCATTAGACCCCTTTTAGTCAGAAGACCCCATCGGG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CCCCACATTTTTGCCAGGTCACCCAAACCCAGCAGTGCTGGAGGCTCCAG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TGGTGATCACCCTGGGATCCCAGCATGACTTTAGCTCCAGCTGTGCCCTG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TGCACATCCCGGGACCCCCACACTCACGCAGACACATTCATCACCACTGT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      CTTGGTTCATGCCCATCTGGCTTGCATGCTCCCTGAACAGAGCTGTGTCC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AGGCCCTGGACATCGATGCCACAGTCAGCAAGCCACCAAATGACATCGCC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AGGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GAGGTGGGGAGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACAC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GGTGAAACCCCGGCTCTACTAAAAATACAAAAAATTAGCCGGGCATGGTG
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GCAGCTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      ATGAACCCAGGAGGCAGAGCTTGCAGTGAGCAGAGATCGCACCACTGCAC
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      TCCAGCCTGGGCGACAGAGTGAGACTCCGTCTCAAAAAAAAAAAAAAAAA
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      AAAGATGACATCGCCCAGCAAGAGAATGGTGGCAGACCAGTGGGGAAAGT
rat_chr10                  --------------------------------------------------

human_chr22_NM_007098      GCTAAGAGANACAGCAGCCTGGCCAAATCTCGAGACCCAGGAGCACAGGC
rat_chr10                  --------------------------------------------------
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human_chr22_NM_007098      ACAGGGTCCACCCAGAGTGGTCCACTCTCTGCATGGGCTGGCCTTCAGGT
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      CTCACCCAGGGTCTGAGCACCACAGTGTTTCAGCTCAAAAGCTCTGGTGA
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TGTCACAGGACATGCTGTCCACTTGGTTATGGCTCAGGCTGAGGCCTCCA
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      AGGAAAGCTGGAGTAATCTTGCTTGGATGGAAACATACTCTGTTGTTTGG
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TTTTGCTGTGGGGCTTCATTCTGACTGATTACACTTCATTCATTCAGCCG
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      ATACTGAGTGATCGTGGACCCTGCATCAGATACTGGTCTAGGTGCTGGGT
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TGAGGCAGGAAACCCTGAGGCTGGCCTCTTAAGAAAAATGCTCAGTGTGT
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      CAGTGCTGGGGGACAAAATACCTCAGGGATGAGAGGAGGCACCTTCACAG
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      GCCATTGAGTCTTATAGGGGGTAGTCATGGCAGGCCTCAGTAGTAAAGTG
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      TCATTTGAGCAAAAACTGGAAGGAGCCCTGGGGTATCTGGAGACAGCGGC
rat_chr10                  --------------------------------------------------


human_chr22_NM_007098      AGGGACTGACCCTCAGCTTTGCTCACCACAGGTTGCCAACGTCGAGCTCT
rat_chr10                  -------------------------------GTGGCTAATGTGGAACTGT
                                                          ** ** ** ** ** ** *

human_chr22_NM_007098      GTTACAGAGCCCTGCAGTTCTATTTGGATTACAAACCACTGCTCATCAAT
rat_chr10                  ACTACAAAGCAATCCAGTTCTACTTAGAATTCAAGCCCTTGTTGTTAAAT
                             **** ***  * ******** ** ** * *** **  ** *  * ***

human_chr22_NM_007098      GACCTGCTGCTGGTGCTTTCACCCCGGCTGG-
rat_chr10                  GACTTGCTCATGGTGCTGTCTCCACGGTTGGA
                           *** ****  ******* ** ** *** ***
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