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CLUSTAL W (1.83) multiple sequence alignment


human_chr17_NM_004104        -CACACCCAAGGCCAAGTACCATGGCAACGTGATGCTACTGCGCGCCAAG
dog_chr9                     ACACGCCGCAGGCCACCTACCACGGCAATGTGACGCTGCTGCGCGCCAAG
                              *** **  ******  ***** ***** **** *** ************


human_chr17_NM_004104        ACGGGTGGCGCCTACGGCGAGGACCTGGGCGCGGACTACAACCTCTCCCA
dog_chr9                     ACGGGCAGCATGTACGGCGAGGGCCTGGGCGCCGACTACAACCTGTCCCA
                             *****  **    ********** ********* *********** *****


human_chr17_NM_004104        GGTGCGCAAGGGGCCTGACGGGAACGGGGACAGGGACAGGAGTGGGGTGG
dog_chr9                     G-------------------------------------------------
                             *


human_chr17_NM_004104        GACGGCAGCTGATCGCATCCCCTGCAGGTATGCGACGGGAAAGTATCCGT
dog_chr9                     -------------------------GTGTGCGATGGCAAGGTGTCCGT
                                                      ** ***** ** ** ** *****


human_chr17_NM_004104        CCACGTCATCGAGGGTGACCACCGCACGCTGCTGGAGGGCAGCGGCCTGG
dog_chr9                     GCACGTGATCGAGGGTGACCACCGCACGCTGCTGGAGGGCAGCGGCCTAG
                             ***** ****************************************** *


human_chr17_NM_004104        AGTCCATCATCAGCATCATCCACAGCT-
dog_chr9                     AGTCCATCCTCAGCATCATCCACAGCTC
                             ******* *****************
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_002096      ---CGAGCGCGCGCTCATCCTTTGCCATCCCCGTCTTACAGTAGCTCCCA
dog_chr20                  ATGGCCCAGGCCGGCCCTCACCCTCTCGTTCTGTCTTCTAGCAGCTCGCA
                               *   **   * **      *      * *****  ** ***** **

human_chr19_NM_002096      AGAAGAGCCTGAGAGCAAGGCCAAGGCGCCGCAGCAGGAGGAGGGGCCCA
dog_chr20                  GGAGGAGCTGGAGGGCAAGCCCAAGGTCGTCCAGCAGGAGGAGGGGCCCA
                            ** ****   *** ***** ******    ************** ****

human_chr19_NM_002096      AGGGTAGGCGATGGCTGGGCGGGCCGGGGAGATGGGGGCGGTGCTTCCCT
dog_chr20                  AGG-----------------------------------------------
                           ***

human_chr19_NM_002096      GCTCTTGCTCATACCCTGCCCCTCCCAGGTGTCGATGAGCAGAGCGACAG
dog_chr20                  --------------------------GCGTAGACGAGCAGAGCGAGAG
                                                     *  ** ** ********** **

human_chr19_NM_002096      TAGTGAGGAGAGTGAGGAGGAGAAGCCGCCTGAGGAGGACAAGGAGGAGG
dog_chr20                  CAGCGAGGAGAGCGAGGAGGAGAAGCCGCCCGAGGAGGACAAGGAGGAGG
                            ** ******* **************** ********** ******* *****

human_chr19_NM_002096      AGGAGGAGAAGAAGGCACCCACCCCGCA-
dog_chr20                  AGGAGGAGAAGAAGGCGCCCACACCCCAG
                           *************** ***** ** **
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CLUSTAL W (1.83) multiple sequence alignment


human_chr19_NM_025241        ---GCCGCGTCTTCCAGCCCTCGCCCCTGGCCTCGCAGTTCGAACTGCCT
dog_chr20                    AGCGCCGGGTCTTCCGGCCCTCGCCCATGGCCTCCCAGTTTGACCTGCCC
                                **** ******* ********** ******* ***** ** *****

human_chr19_NM_025241        GGGGACTTCTTCAACCTCACAGCAGAGGAGATCAAGCGGGAGCAGAGGCT
dog_chr20                    GGGGACTTCTTTAACCTCACGGCCGAAGAGATCAAGCGGGAACAGAGGCT
                             ********** ******** **  ** ************** ********

human_chr19_NM_025241        CAGGTGGGCCTGACGTCCGCGGAGCAGAGTGGGGCGGGGCGGGGTGGAAG
dog_chr20                    CCG-----------------------------------------------
                             * *

human_chr19_NM_025241        AACCCCGGCCAGCCCTCGTGACCTGGCCCGCGTGTGCAGGTCCGAGGCGG
dog_chr20                    -------------------------------------GTCCGAGGCCG
                                                                  ********* *

human_chr19_NM_025241        TGGAGCGGCTGAGCGTGCTGCGGACCAAGGCCATGCGGGAGAAGGAGGAG
dog_chr20                    TGGAGCGGCTGAGCGTGCTGCGGACCAAGGCCATGCGGGAGAGGGAGGAG
                             ****************************************** *******

human_chr19_NM_025241        CAGCGGGGGCTGCGCAAGTACAACTACACGCTGCTGCGC-
dog_chr20                    CAGAGAGAGCTACGCAAGTACACCTACACGCTGCTGCGCG
                             *** * * *** ********* **************
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CLUSTAL W (1.83) multiple sequence alignment


human_chr10_NM_012207      -GATATTGGAGCTGATGGCAGAGCCACAGGAGAAGCAGATGTAGAGTTTG
dog_chr28                  TGAGATTGGCCCTGATGGAAGAGTGACGGGTGAAGCTGATGTTGAGTTTG
                            ** *****  ******* ****  ** ** ***** ***** *******


human_chr10_NM_012207      TGACACATGAAGATGCAGTAGCTGCCATGTCTAAAGATAAAAATAACATG
dog_chr28                  CCACTCACGAAGAAGCTGTGGCAGCTATGTCCAAAGACCGGGCCAACATG
                            ** ** ***** ** ** ** ** ***** *****       ******


human_chr10_NM_012207      CGTAAGTGGTGTCTTTGGCACACAATCTTATTTCCTAAACGTGAATTTAT
dog_chr28                  C-------------------------------------------------
                           *


human_chr10_NM_012207      AAAATAAGAGGCTCTAAGATCTGTAGGTAACGCTTGGCAGTTGTTGGGAT
dog_chr28                  --------------------------------------------------


human_chr10_NM_012207      TTAAAACCATTTGACCTCTATAATGGCTTTCTGTGGGCTTTATATATCGC
dog_chr28                  --------------------------------------------------


human_chr10_NM_012207      TGTACTAGTAATTAATAAGCATACTTTGTTTAATATTACTTAATTGATCT
dog_chr28                  --------------------------------------------------


human_chr10_NM_012207      TTTTTACAAAGCTTGTATTGATGAATTTTATCCATCATTCCTTTCTCCCC
dog_chr28                  --------------------------------------------------


human_chr10_NM_012207      TGTTACTCTTTCTTTTTTTCTTAAAGAACATCGATATATTGAACTCTTCT
dog_chr28                  -----------------------AACACAGATACATAGAACTTTTCC
                                                  ****  **** ** ***** ***


human_chr10_NM_012207      TGAATTCTACTCCTGGAGGCGGCTCTGGCATGGGAGGTTCTGGAATGGGA
dog_chr28                  TGAATTCCACAACTGGGGCCAGCAATGGGGCATATAGCAGCCAGATGATG
                           ******* **  **** * * **   ***         *        ***


human_chr10_NM_012207      GGCTACGGAAGAGATGGAATGGGTAT-----
dog_chr28                  CAAGGCATGGGAGTGTCAGCCCAGTCGACTT
                                  *    ***     *
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CLUSTAL W (1.83) multiple sequence alignment


human_chr15_NM_018445      ---TGTTTCTCAGCTTGAAGAAGAAAAAAGGAGACAGAAGATTGAAATGT
dog_chr3                   AATTCTTTCTTAGCTTGAGGAACAAAAAAGGAGACAGAAGATTGAAATGT
                            * ***** ******* *** ************************

human_chr15_NM_018445      GGGACAGCATGCAAGAAGGAAAAAGTTACAAAGGAAATGCAAAGAAGCCC
dog_chr3                   GGGATAGCATGCAAGAAGGGAAAAGTTACAAAGGAAATGCAAGAAAGCAT
                           **** ************* ******************  ****

human_chr15_NM_018445      CAGGTGACTGGAGACCTCGGCCGGCTGGCATGCGGTAGATGAAGATTGCC
dog_chr3                   CCG-----------------------------------------------
                           * *

human_chr15_NM_018445      AAGTAGAATGTTTTAATTGCTTCTTACACTACTGTGTGTGTTCAAACAGG
dog_chr3                   -------------------------------------------------G
                                                                            *

human_chr15_NM_018445      AGGAAGACAGTCCTGGGCCTTCCACTTCATCTGTCCTG---AAACGGAAA
dog_chr3                   AAGAAGACAGTCCTGGGCCTTCTACTTCATCAGTCCTGCCGAAACGGAAA
                           * ******************* ******** ******   *********

human_chr15_NM_018445      TCGGACAGAAAGCCTTTGCGGGGAGGAGGTAAGCACCACTGATGTCAAAT
dog_chr3                   CCTGATCGAAAGCCTCTGCGGGGAGGTGGTGAGTACCAGATATTAACGTA
                            * **   ******* ********** *** ** ****    **

human_chr15_NM_018445      GT
dog_chr3                   --
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CLUSTAL W (1.83) multiple sequence alignment


human_chr15_NM_025234      ----AGGAACTCATGTCGGGAAAGTGAACATTTTTGGTGTGGAAAGTGGG
dog_chr3                   CCACAGGAACTCATGTGGGGAAAATGAACATTTTTGGTGTGGAAAGTGGG
                               *********** ****** ************************

human_chr15_NM_025234      AAAAAGGAATATTCTTTGGACACGAGAGGAAAATTCATTCTTAGTATTGC
dog_chr3                   AAAAAGGAATATTCTCTGGACACAAGAGGAAAATTCATTCTTAGTATTGC
                           *************** ******* ************************

human_chr15_NM_025234      ATATGTAAGGAAACATTGCTCTCTGTTCTCCTTCTGATTCTTTCAGTTTA
dog_chr3                   ATAT----------------------------------------------
                           ****

human_chr15_NM_025234      CCCTTCCAGCCTGTTGCAGTCCTTGCCACAGATTCTGTCTTGGTCTGGTC
dog_chr3                   --------------------------------------------------


human_chr15_NM_025234      AGGCAGCTGCTGTCTCACTGGTGTGGTTTGCCAAGTAGCCAGTTAGACCT
dog_chr3                   --------------------------------------------------


human_chr15_NM_025234      GTAGATAGCAGGAGGTTTGCTTGTGTTTGGTAGGGACAGCTTAACAACAC
dog_chr3                   --------------------------------------------------


human_chr15_NM_025234      GGAGTCTGAAAGTGCTAATTTCTCCATATGTTCTCTGAACAGAGTCCTGA
dog_chr3                   ----------------------------------------AGCTCTGA
                                                                   **   ****

human_chr15_NM_025234      TGGGAAATACCTAGCCAGTGGAGCCATAGATGGAATCATCAATATTTTTG
dog_chr3                   TGGGAAGTATCTGGCCAGTGGATCCATGAATAGGATCATCAATATTTT-G
                           ****** ** ** ******** ****   ** * ************* *

human_chr15_NM_025234      ATATTGCAACTGGAAAACTTCTGCATACCCTGGAAGGTATAT--
dog_chr3                   ATATTGCAACTGGAAAACTTCTGCACACGCTGGGAGGCCATGCT
                           ************************ ** **** ***
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CLUSTAL W (1.83) multiple sequence alignment


human_chr16_NM_032259      ------GCCGCGCCGTCAGCTGCCTCAACCAGGCCTCCACCACCCTGCAC
dog_chr6                   GCACCAGCCGCGCCATCAGCTGCCTCAACCAGGCGTCCACCACCCTGCAT
                                 ******* ******************* **************

human_chr16_NM_032259      GTCAACTGCAGCCACTGCAAGCGGCCCATGAGCAGCCGGGGCTGGGTCTG
dog_chr6                   GTCAACTGCAGCCACTGCAAGCGGCCCATGAGCAGCCGCGGCTGGGTCTG
                           ************************************** ***********

human_chr16_NM_032259      CGACAGGTGGGGCAGTGGGGTCGGGAGGTGGGGCAGGGGCCTGCAGGCAG
dog_chr6                   TGACCG--------------------------------------------
                            *** *

human_chr16_NM_032259      CGCAGCAGCCCCCGCTGAGGCACCCTCCCTCCCGCCCGCCCCCAGGTGCC
dog_chr6                   ---------------------------------------------CTGCC
                                                                        ****

human_chr16_NM_032259      ACCGCTGCGCCAGCATGTGTGCCGTCTGCCACCACGTAGTCAAGGGTCTC
dog_chr6                   ACCGCTGCGCCAGTATGTGCGCCGTGTGCCACCACGTGGTCAAGGGGCTG
                           ************* ***** ***** *********** ******** **

human_chr16_NM_032259      TTCGTGTGGTGCCAGGGCTGCAGCCACGGCGGCCACCTGCAGCAC-
dog_chr6                   TTCGTGTGGTGCCAGGGCTGCAGTCACGGCGGCCACCTGCAGCACA
                           *********************** **************************
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