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CLUSTAL O(1.2.4) multiple sequence alignment


NM_001271820.1      -----------------------------------CTGTAACTAGGGGAATCCCCAAAACT      26
NM_011640.3         TTTCCCCTCCCACGTGCTCACCCTGGCTAAAGTTCTGTAGCTTCAGTTCATTGGGACCAT      60
NM_000546.6         -----------------------------------CTCAAAAGTCTAGAGCCACCGT      22
NM_213824.3         --------------------------------------AAAAGTCCAGGGCCACCAT      19
                                                       *          *   *


NM_001271820.1      CC-------ACGCGGATTTGCTTTGTGGATGTCCAATAACCTCCTTGTTTTGGTCAT---      76
NM_011640.3         CCTGGCTGTAGGTAGCGACTACAGTTAGGGGGCACCTAGCATTCAGGCCCTCATCCT---     117
NM_000546.6         CCAGGGAGCAGGTAGCTGCTGGGCTCCGGGGACACTTTGCGTTCGGGCTGGGAGCGTGCT      82
NM_213824.3         CCTTGGCGCAGGTAGCTGCTGGTCTCCGGGGTCACCTGACGTCCGTCTC-GAGCGTGCA      78
                    **        *  *   *       * *  *   * * *  *             * *


NM_001271820.1      --------------------------TCTTTAAGTCGATCGACTACATATCCGGG-----     105
NM_011640.3         -------------CCTCCTTCCCAGCAGGGTGTCACGCTTCTCCGAAGACTGGATGACTG     164
NM_000546.6         TTCCACGACGGTGACACGC--TTCCCTGGATTGGCAGCCAGACTGCCTTCCGGGTCACTG     140
NM_213824.3         TCCCAGGACAGTGACACGCTCTCCTGAGCTTCGGCGGCCACACTCCCCTCCAGGGAGCTG     138
                                        *     *        *        *


NM_001271820.1      CAATCCGAA------AGTCGATAATCGTAGTTTAGTGGAGAGGAGGTCG----GCAAAAT     155
NM_011640.3         CCATGGAGGAGTCACAGTCGGATATCAGCCTCGAGCTCCCTCTGAGCCAGGAGACATTTT     224
NM_000546.6         CCATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTT     200
NM_213824.3         CAATGGAGGAGTCGCAGTCCGAGCTGGGCGTGGAGCCCCCTCTGAGTCAGGAGACATTTT     198
                    * **         ****          *   **          * *       **    *


NM_001271820.1      CAA-TTCTTGCAAAGCAATGGCGCAAAACGACAGCCAAGAGTTCGCGGAGCTCTGGGAGA     214
NM_011640.3         CAGGCTTATGGAAACTACTTCCTCCAGAAGATATCCTGC---CATCACCTCACTGCATGG     281
NM_000546.6         CAGACCTATGGAAACTACTTCCTGAAAACAACGTTCTGT---CCCCCTTGCCGTCCCAAG     257
NM_213824.3         CAGACTTGTGGAAACTGCTTCCTGAAAACAACCTGCTGT---CCTCTGAGCTCTCCCTGG     255
                    **        ** ***    *   *   * * *     *          *    *   *


NM_001271820.1      AGAATTTGATAA---GTATTCAGCCCCCAGGTGGTGGCT----CTTGCT--------GGG     259
NM_011640.3         ACGATC---------TGTTGCTGCCCCAGGATGTTGA------GGAGTT------TTTTG     320
NM_000546.6         CAATGGATGATTT---GATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACC     314
NM_213824.3         CAGCAGTGAACGATCTGCTGCTGTCCCCAGTCACGAA------CTGGCT------GGATG     303
                              * * * ***   *                         * *


NM_001271820.1      ACATCATTAATGATGAGGAGTACTTGCCGGGATCGTTTGACCCCAATTTTTTTG----AA     315
NM_011640.3         AAGGCCCAAGTGAAGCCCTCCGAGTGTCAGGAGCTCCTGCAGCACAGGACCCTGTCACCG     380
NM_000546.6         CAGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCCCGTGGCCCCTGCACCAG     374
NM_213824.3         AAAATCCAGATGACGCCTCCAGAGTGC---------------CAGCGCCTCCTGCAGCAA     348
                         *** *          **           *          **


NM_001271820.1      A-----ATGTGCTTGAAGAACAGCCTCAGCCATCCACTCTCCCACCAACATCCACTGTTC     370
NM_011640.3         AGACCCCTGGGCCAGTGGCCCCTGCCCCAGCCACTCCATGGCCCCTGTCATCTTTTGTCC     440
NM_000546.6         CAGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCC     434
NM_213824.3         CAGCGCCCGCACCAGCTGCCCCCGCACCAGCCACCTCCTGGCCCCTGTCGTCCTTTGTCC     408
                          *   *   *   * *    * * *      ** *    * **    *** *


NM_001271820.1      CGGAGACAAGCGACTATCCCGGCGATCATGGATTTAGGCTCAGGTTCCCGCAGTCTGGCA     430
NM_011640.3         CTTCTCAAAAAAACTTACCAGGGCAACTATGGCTTCCACCTGGGCTTCCTGCAGTCTGGGA     500
NM_000546.6         CTTCCCAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGA     494
NM_213824.3         CTTCTCAGAAGACCTACCCTGGCAGCTATGATTTCCGTCTAGGGTTCCTGCATTCTGGAA     468
                    *         *    ** *  ***    * *  **    ** * *** *** ***** *


NM_001271820.1      CAGCAAAATCTGTAACTTGCACTTATTCACCGGACCTGAATAAACTCTTCTGTCAGCTGG     490
NM_011640.3         CAGCCAAGTCTGTTATGTGCACGTACTCTCCTCCCCTCAATAAGCTATTCTGCCAGCTGG     560
NM_000546.6         CAGCCAAGTCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGG     554
NM_213824.3         CAGCCAAGTCTGTAACCTGCACGTACTCCCCTGCCCTCAATAAGCTGTTTTGCCAGCTGG     528
                    **** ** sequence * alignment ** ** **   *** ** **  * ** ** ** ****


NM_001271820.1      CAAAAACTTGCCCCGTTCAAATGGTGGTGGACGTTGCCCCTCCACAGGGCTCCGTGGTTC     550
NM_011640.3         CGAAGACGTGCCCTGTGCAGTTGTGGGTCAGCGCCACACCTCCAGCTGGGAGCCGTGTCC     620
NM_000546.6         CCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCC     614
NM_213824.3         CCAAGACCTGCCCGGTGCAGCTGTGGGTCAGCTCGCCACCCCCGCCTGGCACCCGTGTCC     588
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NM_001271820.1   GAGCCACTGCCATCTATAAGAAGTCCGAGCATGTGGCTGAAGTGGTCCGCAGATGCCCCC    610
NM_011640.3      GCGCCATGGCCATCTACAAGAAGTCACAGCACATGACGGAGGTCGTGAGACGCTGCCCCC    680
NM_000546.6      GCGCCATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCC    674
NM_213824.3      GCGCCATGGCCATCTACAAGAAGTCAGAGTACATGACCGAGGTGGTGAGGCGCTGTCCCC    648
                 * ****  ********* *** ****  ** *  ** * ** ** **  *  * ** ****

NM_001271820.1   ATCATGAGCGAACCCC---GGATGGAGATAACTTGGCGCCTGCTGGTCATTTGATAAGAG    667
NM_011640.3      ACCATGAGCGCTGCTC---CGATGGTGATGGCCTGGCTCCTCCCCAGCATCTTATCCGGG    737
NM_000546.6      ACCATGAGCGCTGCTC---AGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAG    731
NM_213824.3      ACCATGAGCGCAGCTCTGACTATAGCGATGGTCTGGCCCCTCCCCAGCATCTCATCCGGG    708
                 * ********   * *     ** * ***    **** *** *   *** * **    * *

NM_001271820.1   TGGAGGGCAATCAGCGAGCAAATTACAGGGAAGATAACATCACTTTAAGGCATAGTGTTT    727
NM_011640.3      TGGAAGGAAATTTGTATCCCGAGTATCTGGAAGACAGGCAGACTTTTCGCCACAGCGTGG    797
NM_000546.6      TGGAAGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGG    791
NM_213824.3      TGGAAGGGAATTTACGGGCCGAGTACTTGGATGACAGAAACACTTTTCGACACAGCGTTG    768
                 **** ** ***      * **   *** ** *     ***** * ** ** **

NM_001271820.1   TTGTCCCATATGAAGCACCACAGCTTGGTGCTGAATGGACAACTGTGCTACTAAACTACA    787
NM_011640.3      TGGTACCTTATGAGCCACCCGAGGCCGGCTCTGAGTATACCACCATCCACTACAAGTACA    857
NM_000546.6      TGGTGCCCTATGAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACA    851
NM_213824.3      TGGTGCCCTACGAGCCGCCCGAGGTCGGCTCTGACTGTACCACCATCCACTACAACTTCA    828
                 * ** ** ** **  * ** **  **  ** **** * ** **  * *    ** * **

NM_001271820.1   TGTGCAATAGCAGCTGCATGGGGGGGATGAACCGCAGGCCCATCCTCACAATCATCACTC    847
NM_011640.3      TGTGTAATAGCTCCTGCATGGGGGGCATGAACCGCCGACCTATCCTTACCATCATCACAC    917
NM_000546.6      TGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACAC    911
NM_213824.3      TGTGTAACAGCTCCTGCATGGGGGGCATGAACCGGCGGCCCATCCTCACCATCATCACAC    888
                 **** ** **    ********* ** ********  * ** ***** ** ******** *

NM_001271820.1   TGGAGACTCAGGAAGGTCAGTTGCTGGGCCGGAGGTCTTTTGAGGTGCGTGTGTGTGCAT    907
NM_011640.3      TGGAAGACTCCAGTGGGAACCTTCTGGGACGGGACAGCTTTGAGGTTCGTGTTTGTGCCT    977
NM_000546.6      TGGAAGACTCCAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCT    971
NM_213824.3      TGGAAGATGCCAGTGGCAACTTGCTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCT    948
                 ****        **   *   * ***** ***         ******** ***** ***** *

NM_001271820.1   GTCCAGGCAGAGACAGGAAAACTGAGGAGAGCAACTTCAAGAAAGACCAAGAGACCAAAA    967
NM_011640.3      GCCCTGGGAGAGACCGCCGTACAGAAGAAGAAAAATTTCCGCAAAAAGGAAGTCCTTTGCC   1037
NM_000546.6      GTCCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACC   1031
NM_213824.3      GTCCTGGGAGAGACCGCCGCACAGAGGAAGAAAATTTCCTCAAGAAGGGCCAATCTTGCC   1008
                 * ** ** ******* *    ** ** **    ** **    ** *

NM_001271820.1   CCATGGCCAAAACCACCACTGGGACCAAACGTAGTTTGGTGAAAGAATCTTCTTCAGCTA   1027
NM_011640.3      CTGAACTGCCCCCCAGGGA---GCGCAAAGAGAGCGCTGCCCA-----CCTGCACAAGCGC   1089
NM_000546.6      ACGAGCTGCCCCCCAGGGA---GCACTAAGCGAGCACTGCCCA-----ACAACACCAGCTC   1083
NM_213824.3      CCGAGCCTCCCCCCTGGCA---GCACTAAGCGAGCACTGCCCA-----CCAGCACCAGCTC   1060
                     *    *     *  ** *     ** *    *  * *  ***

NM_001271820.1   CATTACGACCTGAGGGGAGCAAAAAGGCCAAGGGCTCCAGCAGCGATGAGGAGATCTTTA   1087
NM_011640.3      ---------CTCTCCCCCGCAAAAGAAA-------AACCACTTGATGGAGAGTATTTCA   1133
NM_000546.6      ---------CTCTCCCCAGCCAAAGAAGA-------AACCACTGGATGGAGAATATTTCA   1127
NM_213824.3      ---------CTCGCCAGTGCAAAAGAAGA-------AGCCACTGGATGGCGAGTATTTCA   1104
                          **        **  ***               ****  **      ** *

NM_001271820.1   CCCTGCAGGTGAGGGGGCAGGGAGCGTTATGAAATTTTAAAGAAATTGAACGACAGTCTGG   1147
NM_011640.3      CCCTCAAGATCCGCGGGCGTAAACGCTTCGAGATGTTCCGGGAGCTGAATGAGGCCTTAG   1193
NM_000546.6      CCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTGAATGAGGCCTTGG   1187
NM_213824.3      CCCTCCAGATCCGTGGGCGTGAACGCTTCGAGATGTTCCGAGAGCTGAATGACGCCTTGG   1164
                 ****   ** **  * * ** * * ** *  ** ** **     *  **** **     * *

NM_001271820.1   AGTTAAGTGATGTGGTGCCTGCCTCAGATGCTGAAAAGTATCGTCAGAAATTCATGACAA   1207
NM_011640.3      AGTTAAAGGATGCCCATGCTACAGAGGAGTCTGGAGACAGCAGGGCTCACTCCAGCTACC   1253
NM_000546.6      AACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGGGGGAGCAGGGCTCACTCCAGCCACC   1247
NM_213824.3      AGCTGAAGGATGCCCAGACTGCGCGGGAGTCGGGGGGAAACAGGGCCCACTCCAGCCACC   1224
                 * *  * * **** **      **   **    *  **  *        *    * * **

NM_001271820.1   AAAACAAAA----------------------------AAGAGAATCGTGAATCATCTGA   1238
NM_011640.3      TGAAGACCAAGAAGGGCCAGTCTACTTCCCGCCATAAAAAAACAATGGTCAAGAAAGTGG   1313
NM_000546.6      TGAAGTCCAAAAAAGGGTCAGTCTACCTCCCGCCATAAAAAAACTCATGTTCAAGACAGAAG   1307
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NM_213824.3      TGAAGTCTAAGAAGGGGCAGTCTCCCTCCCGCCATAAAAAACCGATGTTCAAGAGAGAAG      1284
                   **    *                                   **    ** * **


NM_001271820.1   GCCCAAACAGGGAAAGAAG----CTGATGGTGAAGGAC-GAAGGAAGAAG----------      1283
NM_011640.3      GGCCTGACTCAGACTGACTGCCTCTGCATCCCGTCCCCATCACCAGCCTCCCCCCTCTCCT      1373
NM_000546.6      GGCCTGACTCAGACTGACATTCTCCACTTCTTGTTCCCCACTGACAGCCTCCCACCCCCA      1367
NM_213824.3      GACCTGACTCAGACTGATGCCTCCTGCATCCCATCCCCTTTTGAAGT-------------      1331
                 * **   **     **   **      *               *


NM_001271820.1   ---------CGACTCTGATTAAGGTGATGGGATGCTAAGAGAGA------AAGAAACTGG      1328
NM_011640.3      TGCTGTC------------TTATGACTTCAGGGCTGAGACACAATCCTCCCGGTC-----      1416
NM_000546.6      TCTCTCCCTCCCCTGCCATTTTGGGTTTTGGGTCTTTGAACCCTTGCTTGCAATAGGTGT      1427
NM_213824.3      ---------CCCTGGCATTTTGGGGACTCAGGTGCTTAGACCTCTGCTTGGTGCAGGTGT      1382
                          *     *      *     *


NM_001271820.1   GAGTTTTGCTCTTTTTGGACTGCCTTTTTTGCTTTTAT--------TACACCAAAAAAAA      1380
NM_011640.3      ------------CCTTCTGCTGCCTTTTTTACCTTGTAGCTAGGGCTCAGCCCCCTCTCT      1464
NM_000546.6      GCGTCAGAAGCACCCAGGACTTCCATTT--GCTT-TGTCCCGGGGCTCCACTGAACAAGT      1484
NM_213824.3      GCCTTAGAAATGCCCTGGAATTCCTCTATATGCT-TGGCCTGGGGCTCTGCTAAAGAAAT      1441
                             * **  *        *          *        *    *


NM_001271820.1   AAGCTTGTC-ACAGGGGTCATTTGGGGA--------------------------------      1407
NM_011640.3      GAGTAGTGGTTCCTGGCCCAAGTTGGGGAATAGGTTGATAGTTGTCAG-GTCTCTGCTGG      1523
NM_000546.6      TGGCCTGCACTGGTGTTTTGTTGTGGGGAGGAGGATGGGGAGTAGGAC------------      1532
NM_213824.3      TGGCCTGCACTGGTGGGTTGCGGGGGTGGGGGGTGGGGGGTGGATAAGGGGTACTGGGGG      1501
                   *           *         **


NM_001271820.1   -ACT---GCGATACATGTGATCCATTAGTCCTGTTTG-----------------------      1440
NM_011640.3      CCCAGCGAAATTCTATCCAGCCAGTTGTTGGACCCTGGCACCTACAAT------------      1571
NM_000546.6      -ATA-CCAGCTTAGATTTTAA-GGTTTTTACTGTGAGGGATGTTTGGGAGATGTAAGAAA      1589
NM_213824.3      CCTT-CCGGCTTAGCTTTTTAAGGGGTTTTTGTATTTT----TTTTATTAAATTTTTTTCA      1556
                        *    *          * *


NM_001271820.1   ------TCATGTTTCTTCTTGTTCACTCCACTGGGACCTTTGTTGCTGGACACTGATTTT      1494
NM_011640.3      -------GAAATCTCACCCTACCCCACACCCTGTAAGATTCTATCTTGGGCCCTCATAGG      1624
NM_000546.6      TGTTCTTGCAGTTAAGGGGTTAGTTTACAATCAGCCACATTCTAGGTAGGGGCCCACTTCA      1649
NM_213824.3      TTTTTTTAAAGTTTAAAGTATAGTTGCTGTTTCCGTGTGTTT--------------TTAA      1602
                         *                              *              *


NM_001271820.1   GC-AGTGTTTTACCAGCACTGGCG-----AGGGCTAA--GACTAGCCTGACGTTTTACAG      1546
NM_011640.3      GTCCATATCCTCCAGGGCCTACTTTCCTTCCATTCTGCAAAGCCTGTCTGCATTTATCCA      1684
NM_000546.6      C--CGTACTAACC-AGGGAAGCTGTCCCTCACTGTTG--AATTTTCTCTAACTTCAAGGC      1704
NM_213824.3      ---AGGGTTTTAT-TGGTAAAATGTTCAGAGAGGTAGGAAAATGTTCCTGCGTATCAGGA      1658
                            *                      *               *


NM_001271820.1   ACCCGTT----AAATGAACGTTCAGGAACGAAGTTTACCTGTGACTTTTGTAAATTGTAA      1602
NM_011640.3      CCCC-------------CCACCCTGTCTCCCTCTT---T-TTTTTTTTTTTACCCCTTTT      1727
NM_000546.6      CCATATCTGTGAAATGCTGGCATTTGCACCTACCTCACA-GAGTGCATTGTGAGGGTTAA      1763
NM_213824.3      ACAGGTTACCACCAGCCATACACTGGGTCGGA--------AGCCCAGTTCTCCACCGTAA      1710
                   *                       *              ** *         *


NM_001271820.1   TAATGCCAGTATTCGGTTGTTTTGT-AAGCAGCAT------------------------      1636
NM_011640.3      T-----------------------------------------------------------      1728
NM_000546.6      TGAAATAATGTACATCTGGCCTTGA-AACCACCTTTTATTACATGGGGTCTAGAACTTGA      1822
NM_213824.3      TAGGCAGAAGAGTGCCTTTCCCTGATAACCTCCCTCCCCATGCTGGTTGGGAGAATTT-A      1769
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NM_001271820.1   -------------TTTTTTTTATTTTTATAAAGAAATGAGTATTAGACTAATTGGAACAAA      1684
NM_011640.3      ----------------------------ATATATCAATTTCCTATT--TTACAATAAA      1756
NM_000546.6      CCCCCTTGAGGGTGCTTGTTCCCTCTCCCTGTTGGTCGGTGGGTTGGT--AGTTTCTACA      1880
NM_213824.3      TGAAATAATGT-ATTGTTTTCTTTTTATATGT--------TTCTTATT--TTCCAATAAA      1818
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NM_001271820.1   CCATCGGAATTGGTT-GCAAGCCGATTATGTAA---TAAAAATACCAAAGCAAAACCGTT      1740
NM_011640.3      ATTTTGTTATCACTTAAAAAAAAAA-----------------------------------      1781
NM_000546.6      GTTGGGCAGCTGGTTAGGTAGAGGGAGTTGTCAAGTCTCTGCTGGCCCAGCCAAACCCTG      1940
NM_213824.3      ATA-----GTGTGGTAGCAAAAAAAAAAAAAAAAAAA-----------------------      1849
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NM_001271820.1   TTGTATCTTATATTTTTTTATGTTAATTACTGCTGTTCCTATTTTTGTATTTTAGCTAAT   1800
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      TCTGACAACCTCTTGGTGAACCTTAGTACC---------TAAAAGGAAATCTCACCCCAT   1991
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   AAGAGAAGCTGCC---------CTTTATAACACGCTTTTAGATTTAGTACAACCATTGTT   1851
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      CCCACACCCTGGAGGATTTCATCTCTTGTATATGATGATCTGGATCCACCAAGACTTGTT   2051
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   --CTTTTTCAATTGAAGTAGTTGTTGATTTACTCTTGTGATTGTTGTTGAGTAATGTGGC   1909
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      TTATGCTCAGGGTCAATTTCTTTTTTCTTTTTTTTTTTTTTTTTTCT--TTTTCTTTGAG   2109
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   ACAGATAAGCTCATAAGTGGCCAGTCTGTTTTGACATGTGCTTGTGCAAATGGTTATGGA   1969
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      ACTGGGTCTCGCTTTGTTGCCCAGGCTGGAGTGGAGTGGCGTGAT-CTTGGCTTACTGCA   2168
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   TTGGATGTCTAAATATGAGCAAATGAAATGTCAAATACTCAGGGCA----TGTACAAGTC   2025
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      GCCTTTGCCTCCCCGGCTCGAGCAGTCCTGCCTCAGCCTCCGGAGTAGCTGGGACCACAG   2228
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   CCTCCTGGAAATCTTGATAAAACTCTTCTACTGTTTTACCTGCTATAGA-------TTT   2077
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      GTTCATGCCACCATGGCCAGCCAACTTTTGCATGTTTTGTAGAGATGGGGTCTCACAGTG   2288
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   TATGCTGGTTTTGTTTCTTATTACTGTTTACACGCATTTGCCTTTTATAAATATATAAGC   2137
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      TTGCCCAGGCTGGTCTCAAACTCCTGGGCTCAGGCGATCCACCTGTCTCAGCCTCCCAGA   2348
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   GT----------------------------------------------------------   2139
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      GTGCTGGGATTACAATTGTGAGCCACCACGTCCAGCTGGAAGGGTCAACATCTTTTACAT   2408
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   -----------GCATTTATTTGTAGCTAGCTGAATCATTTATAATTTTTCTTTTTAAGAG   2188
NM_011640.3      ------------------------------------------------------------   1781
NM_000546.6      TCTGCAAGCACATCTGCATTTTCACCCCACCCTTCCCCTCC---TTCTCCCTTTTTATAT   2465
NM_213824.3      ------------------------------------------------------------   1849


NM_001271820.1   AAATGTTTTAAAATACACTCTTTAAAAAAAAAAAAAAAAAAAAAAAAAA   2236
NM_011640.3      ------------------------------------------------   1781
NM_000546.6      CCCATTTTTATATCGATCTCTTATTTTACAATAAAACTTTGCTGCCA-   2512
NM_213824.3      ------------------------------------------------   1849
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