```
Mm  ACTGTCCTCAGAATATAGTGTAATTTCACACTCTGTGTCATTTTTTTTA-TCCATTCACG -1074
Rn  ACTTTCCTGAGAATACAGTTTAATTTCAGATTTTGTGTCTTTTTTTTTTCTCCATTCATG -1084
Hs  ACTTTGATC----CATGGTCACAACTCATAATCTTGGAAAAGTGGA------CAGAAAAG -1032
    *** *  *       *  **   *  *** * * *  *     *         **   * *
      TBE IV
Mm  ATATCCAACACTATCAAAAACATCACCTCTCTAGGCAAATAATTTTT--TATCAAACACT -903
Rn  TTATTCAACAGTCAAAAAAAAATCACCTCTCTAGGCAATTAATTTTTATTATCAAGCAAT -907
Hs  ACATTTAGCGTCCCTGCAAATTCTGGCCATC---GCCGCTTCCTT----TGTCCA----- -868
      **  * *        ***      *  **   **   *   **    * ** *
                                                TBE III
Mm  CGTGAAAAGAGTTGCTGATCAAAATGA-TAAAAGCTATGTAACAGCAGGG-GGAAAATAC -676
Rn  TGTGAAA-GAGTTGTTGATCAAAATGA-TAAAAGCTATGTAACAGCAGGGAGGAAAATAC -674
Hs  ----AAGCAACTTAGCTACAAAGATAAATTACAGCTATGTA-CACTGAAG--GTAGCTAT -651
        **   * **    *  ** ** * * * ******** **     *  * *  **
                    TBE II
Mm  TTAGATCCCGGGAGGGGAAGCTGTGACA--CTCTTGAGCTTTTAGGCCCCCACTGGATGC -326
Rn  TCGGATCCCGGGAGGGGAAGCTGTGACATTCTCTTGCTCCTCCGGCCCCCCAGTGGATGC -326
Hs  CGGTATCCCATCCAAGGCGATCAGTCCAG-AACTGGCTCTCGGAAGCGCTCGGGCAA--- -316
        *****      **         **    ** *  *       * * *     *
                                                        TBE I
Mm  GCGACTGGGAGGAAACCGGAGACCCCAAAGAGCGCCAGACTAGGCGCAGACTCAGCGAAC -266
Rn  GGGACTGGGAGGAAACCCGAGACCTCAAAGAGAGCCAGTCTTGGAGCAGGCACAGCGAAC -266
Hs  -AGACTGCGAAGAAGAAAAGACATCTGGCGGAAACCTG---TGCGCCTGGGGCGGTGGAA -260
      ***** ** ***                *    ** *    *   * *   * * * *
                                                    Sp1
                                Sp1
Mm  CACAGGGCGCCTGGAGGGATGGAGAGGGCGGTGCAGCTCTC-TTGGCACCACCTGGGGCA -207
Rn  CACAGGGCGCCTGGAAGGATGCAGAGGGCGGTGCAGCTCTC-TTGGCACCACTTTGGGCA -207
Hs  CTCGGGGAGG--AGAGGGAGGGATCAGACAGGAGAGTGGGGACTACCCCCTCTGCTCCCA -202
    * * *** *    ** *** * *   * * *   **       *  * ** *      **

Mm  GCCAAGGGCAGCTTCCCGGCTTCCTTCGTCTCTCATTTGCGTGGGTAAAAG--CCTGCCG -149
Rn  GCCGAGGGAAGCTTCCTGGCTTCTCTGGGCTC--ATTTGCGTGAGTAAA-G--CCTGCCC -151
Hs  AATTGGGGCAGCTTCCTGGGTTTCCGATTTTCTCATTTCCGTGGGTAAAAAACCCTGCCC -142
         *** ******* ** **         **  **** **** *****    ******
                                          CRE
Mm  TTGGGGAAAGCCTAAGCGGAAAGACAGAGTCACCACTACGTCACGTGGAGTCCGCTTTAC -35
Rn  GTGGGGAAAGCCGAGGCGGAAAGACACAGTCACGAA---GTCACGTGGAGTCCACTTTAC -37
Hs  GTACGAAAAG-----GCGGAAAGAAACAGTCATTTC---GTCACATGGGCTTGGTTTTCA -36
     *  * ****     ********* * *****     ***** ***  *    ***
                                CRE
Mm  --AGACTTAAAAGCAAGGTTCTCCCCATTAGCAGCC                          +1
Rn  TAAGATTTAAAAGCAAGGTTCTCCGGGTTAGCGGCC                          +1
Hs  GTCTTATAAAAAGGAAGGTTCTCTCGGTTAGCGACC                          +1
          * ***** *********    *****  **
      TATA box
```

Supplemental Fig. S1. ClustalW multiple sequence alignment of human and murine COX2 promoters. TBE response elements, as well as recognition sequences for SP1 and CRE transcription factors, and the TATA box are enclosed.