Figure S2

Martinez/Needleman-Wunsch DNA Alignment
Minimum Match: 9; Gap Penalty: 1.10; Gap Length Penalty: 0.33

| Seq1(1>1000) mMitfA_promoter.dna | Seq2(1>1000) hMitfA_promoter.dna | Similarity Index | Gap Number | Gap Length | Consensus Length |
|---|---|---|---|---|---|
| (1>971) | (96>1000) | 59.6 | 24 | 222 | 1049 |
| (668>971) | (684>1000) | 22.0 | 10 | 47 | 1049 |

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                v10       v20       v30       v40       v50       v60       v70       v80
Mm  --ACATGTCTAAGATTACACAGGATTTCTTAGAAGAACTAGGAATTTCTGCCATCTTAAAATGCCACCCTTAACTCCAATGTCTCAA
      ACA GTC    A T  A    AT      GAAGAACTAG                                              A
Hs  GAACACGTCCT--ACTGGAGCTAATCAGAGGGAAGAACTAG-------------------------------------------A
        ^100       ^110      ^120      ^130
     v110      v120      v130      v140      v150      v160      v170      v180         v19
Mm  ACATGAAGAGTCCTGCTGGAACTAACCAGAAGACAGGTCTGAACATACAAATGAGCTAAAGTGCGGTCATTT--AATACA-TCACCT
                                                  TACAAATGAGC A A  G  G   TTT  AAT C  T  CCT
Hs  ---------------------------------------------TACAAATGAGCCACAACGGAGAGTTTTAAAATTCTCTTCCCT
                                                    ^140      ^150      ^160      ^170
                                              v220      v230      v240      v250      v260
Mm  ACCGG-----------------------------------CTTGCAATGTTAGGAC-AATCTCATCTGAACTCCCAGCCAACTGAG
    A  GG                                   C TG AATG TAGGAC AATCTCAT TGAACTCCCAG CAACTGAG
Hs  AAGGGGTGGACACTTGTACAGTTCACTTGTACATCTTCACTCCTGAAATGCTAGGACAAATCTCATTTGAACTCCCAGTCAACTGAG
          ^210      ^220      ^230      ^240      ^250      ^260      ^270      ^280
       v290      v300      v310      v320      v330      v340      v350      v360      v370
Mm  TGGTGGTGAAGCTGTTTGGTAACTTGATGTCTTTTAAAATTAACTGAATCCTTCAAGTGCTGCTTTAGATTAGAGGTGACTAATTGG
      G    GA GCT TTT GTAACTT  TG CTTTTAAAATTAAC GAATC TTCAA TGCTGCT TAGATTAGA GTG CTA TTGG
Hs  --GCAACGACGCTATTTTGTAACTTTGTGCCTTTTAAAATTAACCGAATCTTTCAATTGCTGCTGTAGATTAGAAGTGGCTACTTGG
         ^310      ^320      ^330      ^340      ^350      ^360      ^370      ^380      ^
       v400      v410      v420      v430      v440      v450      v460      v470      v480
Mm  CTGATGAAGAGTATTGTGGGAGCTTATACTGAGTTCCAGAAAAAGAACGCACAAGAACAACTCCTCCAATAATGCTTTCATTATAAA
    CTGATGAA A TATTGT   AG   A ACT AGTTC AGAAAA GAACGCACAAGAACAA T CTCCAATAA G TTTCATTA A A
Hs  CTGATGAATACTATTGTAAAAGTCCAGACTTAGTTCTAGAAAAGGAACGCACAAGAACAATTTCTCCAATAACGTTTTCATTACAGA
         ^420      ^430      ^440      ^450      ^460      ^470      ^480      ^490      ^
         v510      v520      v530      v540      v550      v560      v570      v580
Mm  GTTTCAATA-GAGGACAAAATGATGTGTCGCTGCAGTCCAGAAGAGCTCGGGGGCTAATAGAAAGTCCTTTTATTTTAAAAATGGGT
    GTT CAAT  GAGGACAA  TGAT TGTCGC GCAG CCAG   AGC  G G GCT ATAG AAGTCCTTTTATTTTAA  A  GG
Hs  GTTCCAATCCGAGGACAAGCTGATATGTCGCAGCAGCCCAGGGAAGCATGCGAGCTGATAGGAAGTCCTTTTATTTTAAG-ACAGGC
         ^530      ^540      ^550      ^560      ^570      ^580      ^590      ^600
          v620      v630      v640      v650      v660      v670      v680            v69
Mm  AGTTTCAAAACCCCTTAGTGTTTTATTTTTTAAATGAACGCTCGGCGTGTCCTCGCAGATGTCTAAACCAGGAGG-------GACAG
     GT  CAAAACCC T A T TTTTATTTTT AAAT A C CT GGCGTG CCTCGCAGATGTCT A C   GAGG        GA  G
Hs  TGTGCCAAAACCCTTGACTATTTTATTTTTAAAATAAGCACTTGGCGTGCCCTCGCAGATGTCTGAGCTGAGAGGTCGGGGCGATGG
     ^630      ^640      ^650      ^660      ^670      ^680      ^690      ^700      ^710
         v720      v730      v740      v750      v760      v770      v780      v790
Mm  CTTATTAATATTAAACAGCCAGGTCTGTATCCTTGAAGCAAACC-GGAGAGAC-ACGGAGAGGAGCTGCTGACATTGACAAGGAATC
    CTTATT ATATTAA  AGCCA GTCTGTA CCTTGAAGCAA    GGAGAGA  A GGAGAGGAGCTGCTGACATTGACAA GAATC
Hs  CTTATTCATATTAAGTAGCCAAGTCTGTACCCTTGAAGCAAGTGGGGAGAGAGGAGGGAGAGGAGCTGCTGACATTGACAATGAATC
     ^740      ^750      ^760      ^770      ^780      ^790      ^800      ^810      ^820
          v830      v840      v850      v860      v870      v880      v890      v900
Mm  GTACACCACGTTGTCTCTCCCCGGTTTGACCTTCTGGGAGTTGTAGTTTTTGCGGAAGCTGATATCCTGGAGAGCT-GGTGTGCTCT
    GT CACCACGTTG CTCTCCCC G  TG CCTTCTGGGAG TGTAGTTTT G GG AGC G T  CC GG GAGCT GG  TGC C
Hs  GTCCACCACGTTGCCTCTCCCCCGCCTGGCCTTCTGGGAGCTGTAGTTTTCGTGGGAGCGGCTCCCCAGGCGAGCTGGGAATGCCCC
     ^850      ^860      ^870      ^880      ^890      ^900      ^910      ^920      ^930
          v920      v930      v940      v950      v960      v970
Mm  AGGCGGAACCACAAATCCCAGGGCGCACCGGGCTCAGCCCCTCCCGCTCTGGTGTGAGA
    AGGCGG   C C   TC   GG CGC        CAGCCCCTCCCGC C GGTG GAG
Hs  AGGCGG---CGC---TC---GGCCGC--------CAGCCCCTCCCGCCCGGGTGCGAGT
     ^960              ^970              ^980      ^990      ^1000
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