Section 1

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            (1) 1        10        20        30        40        50        60        70              87
      AG1IA (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCASTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      CC7-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      NJ1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      NJ2-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
  ZZYY3-1-2 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      CC2-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      CQ3-2 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCRCCGTGGCCACCTTCAATCTTCGCTGCAAT
        FJ6 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      FJ7-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      GD3-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      GZ4-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      GZ8-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      HB1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
    MA-1-1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
    MB-2-1-1 (1) ATGCGTTTTGCGACCGTRGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      HN2-2 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      WJ1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
  ZZYY2-1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
  HZFY4-1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCACCGTGGCCACCTTCAATCTTCGCTGCAAT
AG1IA-05500 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
        AH3 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
  HZFY5-2-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      FM1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      FM2-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      SY1-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      SY5-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
      WC2-1 (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
  Consensus (1) ATGCGTTTTGCGACCGTAGCCTCTGCTGTGACCGTCTTGGTCAGTGCTGCTGCTCCCGCCGTGGCCACCTTCAATCTTCGCTGCAAT
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Section 2

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                 (88) 88          100       110       120       130       140       150       160           174
      AG1IA (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      CC7-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      NJ1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      NJ2-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
  ZZYY3-1-2 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      CC2-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      CQ3-2 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
        FJ6 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      FJ7-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      GD3-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      GZ4-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      GZ8-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      HB1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
    MA-1-1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
    MB-2-1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      HN2-2 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      WJ1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
  ZZYY2-1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
  HZFY4-1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
AG1IA-05500 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
        AH3 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
  HZFY5-2-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      FM1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      FM2-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      SY1-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      SY5-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
      WC2-1 (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
  Consensus (88) CTCGGAAGCTGGTACTGGAAGGACAAGGACTGCTGCATTAAGGTTGGCGGACCCATATCTCCGCCCAGCCCTCCCTCTGGGAATGCT
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Section 3

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        (175) 175  180       190       200       210       220       230       240       250      261
   AG1IA (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   CC7-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   NJ1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   NJ2-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
ZZYY3-1-2 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   CC2-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   CQ3-2 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
     FJ6 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   FJ7-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   GD3-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   GZ4-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   GZ8-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   HB1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
 MA-1-1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCWCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
 MB-2-1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   HN2-2 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   WJ1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
ZZYY2-1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
HZFY4-1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
AG1IA-05500 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
     AH3 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
HZFY5-2-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   FM1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   FM2-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   SY1-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   SY5-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
   WC2-1 (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
Consensus (175) TGCCCCAACTTGTGGTTCTGGAACAAGGACACCAACTGCTGTGCCCCTCGGTACACTCCCCCTTACAACCAGCCATCGTGCAGCAAC
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Section 4

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            (262) 262     270       280       290       300       310       320       330              348
            AG1IA (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAAYGATTGTGGCGMCAACAAATGG
            CC7-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAAYGATTGTGGCGMCAACAAATGG
            NJ1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAAYGATTGTGGCGMCAACAAATGG
            NJ2-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAAYGATTGTGGCGMCAACAAATGG
        ZZYY3-1-2 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAAYGATTGTGGCGMCAACAAATGG
            CC2-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAAYGATTGTGGCGMCAACAAATGG
            CQ3-2 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAATGATTGTGGCGACAACAAATGG
              FJ6 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAATGATTGTGGCGACAACAAATGG
            FJ7-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAATGATTGTGGCGACAACAAATGG
            GD3-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGACAACAAATGG
            GZ4-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGMCAACAAATGG
            GZ8-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGMCAACAAATGG
            HB1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGMCAACAAATGG
         MA-1-1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGACAACAAATGG
         MB-2-1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGACAACAAATGG
            HN2-2 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAATGATTGTGGCGACAACAAATGG
            WJ1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAATGATTGTGGCGACAACAAATGG
        ZZYY2-1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAATGATTGTGGCGACAACAAATGG
        HZFY4-1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAATGATTGTGGCGACAACAAATGG
      AG1IA-05500 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
              AH3 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
        HZFY5-2-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
            FM1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
            FM2-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
            SY1-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
            SY5-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
            WC2-1 (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCGCCAACAAATGG
        Consensus (262) GGATGGGTCTGGAATCCCAGCACATACTCTTGTCGCCCGCCTGCTACACCCCCACCAAAGAACAACGATTGTGGCG CAACAAATGG
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Section 5

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              (349) 349        360       370       380       390       400       410       420           435
         AG1IA (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         CC7-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         NJ1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         NJ2-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
     ZZYY3-1-2 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         CC2-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         CQ3-2 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
           FJ6 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         FJ7-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         GD3-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         GZ4-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGRAACAACTGCCCACCCAGTTGG
         GZ8-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGRAACAACTGCCCACCCAGTTGG
         HB1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGRAACAACTGCCCACCCAGTTGG
       MA-1-1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
       MB-2-1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGGAACAACTGCCCACCCAGTTGG
         HN2-2 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         WJ1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
     ZZYY2-1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTMACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
     HZFY4-1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
   AG1IA-05500 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
           AH3 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
     HZFY5-2-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         FM1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         FM2-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         SY1-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         SY5-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
         WC2-1 (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
     Consensus (349) TGGTGGGGTGGTCGCTCTTGCTGTCTTCCTCACGGAAACCCATCGCCGCCGCTCCCTCCTCGCGGAAACAACTGCCCACCCAGTTGG
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                                                                                   Section 6
          (436) 436          450       460       470       480       490       500       510         522
          AG1IA (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          CC7-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          NJ1-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          NJ2-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
      ZZYY3-1-2 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          CC2-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          CQ3-2 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
            FJ6 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          FJ7-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          GD3-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          GZ4-1 (436) TACTGGCATGGACAACAAGGCTGYTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          GZ8-1 (436) TACTGGCATGGACAACAAGGCTGYTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          HB1-1 (436) TACTGGCATGGACAACAAGGCTGYTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
        MA-1-1-1 (436) TACTGGCATGGACAACAAGGCTGYTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
        MB-2-1-1 (436) TACTGGCATGGACAACAAGGCTGTTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          HN2-2 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          WJ1-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
      ZZYY2-1-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
      HZFY4-1-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
    AG1IA-05500 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
            AH3 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
      HZFY5-2-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          FM1-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          FM2-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          SY1-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          SY5-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
          WC2-1 (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
      Consensus (436) TACTGGCATGGACAACAAGGCTGCTGTGTACCTCAGCACCCTCCACCAACGCCTGTTCCGTCTTGCCCTCCCAACTGGGAGTGGAAC
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Section 7

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              (523) 523    530       540       550       560       570       580       590              609
       AG1IA (523) CCTTACACCCAATGCTGCAAGCCTACYCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       CC7-1 (523) CCTTACACCCAATGCTGCAAGCCTACYCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       NJ1-1 (523) CCTTACACCCAATGCTGCAAGCCTACYCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       NJ2-1 (523) CCTTACACCCAATGCTGCAAGCCTACYCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
   ZZYY3-1-2 (523) CCTTACACCCAATGCTGCAAGCCTACYCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       CC2-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       CQ3-2 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACYCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
         FJ6 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       FJ7-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       GD3-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACYCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       GZ4-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCYCCTACTCCACCYGGCCCCCAACCGAGCAAGCGCGCTACTASTGAKACCAAGCGCCAC
       GZ8-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCYCCTACTCCACCYGGCCCCCAACCGAGCAAGCGCGCTACTASTGAKACCAAGCGCCAC
       HB1-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCYCCTACTCCACCYGGCCCCCAACCGAGCAAGCGCGCTACTASTGAKACCAAGCGCCAC
    MA-1-1-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCYCCTACYCCACCYGGCCCCCAACCGAGCAAGCGCGCTACTASTGAKACCAAGCGCCAC
    MB-2-1-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCCCCTACTCCACCCGGCCCCCAACCGAGCAAGCGCGCTACTAGTGAGACCAAGCGCCAC
       HN2-2 (523) CCTTACACCCAATGCTGCAAGCCTACTCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       WJ1-1 (523) CCTTACACCCAATGCTGCAAGCCTACYCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
   ZZYY2-1-1 (523) CCTTACACCCAATGCTGCAAGCCTACYCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
   HZFY4-1-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
 AG1IA-05500 (523) CCTTACACCCAATGCTGCAAGCCTACTCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
         AH3 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
   HZFY5-2-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       FM1-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       FM2-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       SY1-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       SY5-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
       WC2-1 (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACYGATACCAAGCGCCAC
   Consensus (523) CCTTACACCCAATGCTGCAAGCCTACCCCTCCTACTCCACCTGGCCCCCAACCGAGCAAGCGCGCTACTACTGATACCAAGCGCCAC
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Section 8

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            (610) 610       620       630       640       650       660       670       680           696
      AG1IA (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      CC7-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      NJ1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      NJ2-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
   ZZYY3-1-2 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      CC2-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      CQ3-2 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCYCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
        FJ6 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCYCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      FJ7-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCYCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      GD3-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCTCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      GZ4-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCRACTGCYCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      GZ8-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCRACTGCYCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      HB1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCRACTGCTCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
   MA-1-1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCTCAGTACACCGARCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
   MB-2-1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCAACTGCTCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      HN2-2 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      WJ1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
  ZZYY2-1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
  HZFY4-1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
AG1IA-05500 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
        AH3 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCYCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
  HZFY5-2-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCYCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      FM1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      FM2-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      SY1-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      SY5-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
      WC2-1 (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
  Consensus (610) AATGCTGTCCCTCAGCACAAGAAGAAGGCGACTGCCCAGTACACCGAGCTCGAGGCTTTCTTCTGCCCCGCGGGCATGACCGCTTGC
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Section 9

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            (697) 697         710       720       730       740       750       760       770             783
       AG1IA (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       CC7-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       NJ1-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       NJ2-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
   ZZYY3-1-2 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       CC2-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       CQ3-2 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
         FJ6 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       FJ7-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       GD3-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       GZ4-1 (697) CCTATCGGSGGRATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       GZ8-1 (697) CCTATCGGSGGRATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       HB1-1 (697) CCTATCGGSGGRATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
     MA-1-1-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
     MB-2-1-1 (697) CCTATCGGGGGAATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       HN2-2 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       WJ1-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
   ZZYY2-1-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
   HZFY4-1-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
 AG1IA-05500 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
         AH3 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
   HZFY5-2-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       FM1-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       FM2-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       SY1-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       SY5-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
       WC2-1 (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
   Consensus (697) CCTATCGGCGGGATCTTCAGCACCGAGTCTGAATGCTTCGATACGCTTTCCGACCTGAAATCTTGCGGAGGTTGCGCTTCGGTGGGC
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Section 10

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                (784) 784   790       800       810       820       830       840       850       860       870
        AG1IA (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        CC7-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        NJ1-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        NJ2-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
     ZZYY3-1-2 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        CC2-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        CQ3-2 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
          FJ6 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCRTGCGAGAGCGGCGGTTGYACTGTCTTGTCTTGCAACGAAGGT
        FJ7-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCRTGCGAGAGCGGCGGTTGYACTGTCTTGTCTTGCAACGAAGGT
        GD3-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCRTGCGAGAGCGGCGGTTGYACTGTCTTGTCTTGCAACGAAGGT
        GZ4-1 (784) GCTGGRCAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCWCTGTCTTGTCTTGCAACGAAGGT
        GZ8-1 (784) GCTGGRCAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCWCTGTCTTGTCTTGCAACGAAGGT
        HB1-1 (784) GCTGGRCAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCWCTGTCTTGTCTTGCAACGAAGGT
      MA-1-1-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
      MB-2-1-1 (784) GCTGGRCAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGYACTGTCTTGTCTTGCAACGAAGGT
        HN2-2 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        WJ1-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
     ZZYY2-1-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
     HZFY4-1-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
   AG1IA-05500 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
          AH3 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
     HZFY5-2-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        FM1-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        FM2-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        SY1-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        SY5-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
        WC2-1 (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
    Consensus (784) GCTGGACAAGATTGCTCTGCGATCCCCAACGTTAGCGTCTCGTCGTGCGAGAGCGGCGGTTGCACTGTCTTGTCTTGCAACGAAGGT
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            (871) 871      880       890       900       912
       AG1IA (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       CC7-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       NJ1-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       NJ2-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
   ZZYY3-1-2 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       CC2-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       CQ3-2 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
         FJ6 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       FJ7-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       GD3-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       GZ4-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       GZ8-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       HB1-1 (871) TATACCRTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
     MA-1-1-1 (871) TATACCRTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
     MB-2-1-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       HN2-2 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       WJ1-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
   ZZYY2-1-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
   HZFY4-1-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
 AG1IA-05500 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
         AH3 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
   HZFY5-2-1 (871) TATACCRTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       FM1-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       FM2-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       SY1-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       SY5-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
       WC2-1 (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
   Consensus (871) TATACCGTTAGCGAAGACAAACAATCGTGCGTTGCCATCTAA
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