Size polymorphism and low sequence diversity in the locus encoding the *Plasmodium vivax* rhoptry neck protein 4 (PvRON4) in Colombian isolates

Additional file 2. Aligning the 32 haplotypes identified for *pvron4*.

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                                   *        20         *        40         *        60         *        80         *       100
H1_VCG                  : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H2                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H3                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H4                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H5                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H6                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H7                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H8                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H9                      : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H10                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H11                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H12                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H13                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H14                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H15                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
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H18                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
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H21                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
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H24                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H25                     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H26_Mauritania-I_ref    : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H27_India-VII_refseq    : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H28_Ctg_refsequence     : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H29_Salvador-I_refse    : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H30_NKorea_refsequen    : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H31_P.vivax01_refseq    : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
H32_Brazil-I_refsequ    : ATGTCTCGTAAAAGGGTTTTTCTTCTGTGCATTTTTCTGGCCATTTCCGCCGTTGTTGACGAAGCCGAGTCGTTCAGGAGTAAGCAAAAAGAAAGGAAAAAAAA :  104
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                                 *       120         *       140         *       160         *       180         *       200
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H2                      : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H3                      : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H4                      : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H5                      : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H6                      : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
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H9                   : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCG----------------GTACACACCTGTGCAATGGCGCGTGCCGTATG :  191
H10                  : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H11                  : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H12                  : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H13                  : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
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H16                  : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
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H26_Mauritania-I_ref : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
H27_India-VII_refseq : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
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H29_Salvador-I_refse : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
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H32_Brazil-I_refsequ : GGAGAGATAGGTAGAGAGGGGCATCACACGCAACTGCTATACGCATGCAACTGCGATACGCACGTGACTGCGGTACACACCTGTGCAATGGCGCGTGCCGTATG :  208
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                        *       220         *       240         *       260         *       280         *       300         *
H1_VCG               : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCGGACGCGGCAGCGAA :  312
H2                   : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCGGACGCGGCAGCGAA :  312
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H21                  : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCAGACGCGGCAGCGAA :  312
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H26_Mauritania-I_ref : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCGGACGCGGCAGCGAA :  312
H27_India-VII_refseq : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCGGACGCGGCAGCGAA :  312
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H29_Salvador-I_refse : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCAGACGCGGCAGCGAA :  312
H30_NKorea_refsequen : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCGGACGCGGCAGCGAA :  312
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H32_Brazil-I_refsequ : CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCCGGACGCGGCAGCGAA :  312
                       CATGCTGTCCACGGCGCTCCACCCCCAAAGCAACGAAATAAAAAATAAAAAGTAAATAAATAAATAAATAAATTCCCCCTTTCAGAGCC GACGCGGCAGCGAA

                                 320         *       340         *       360         *       380         *       400         *
H1_VCG               : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H2                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H3                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H4                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H5                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H6                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H7                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H8                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  416
H9                   : CGTCTCCTTCCTGGAGTTCACAGCAGATGGCAACGCTGAAGAGGGGCAGGCGCAGCCAAGTGAACCCATCGTTAACACCCAGCCGCTGCAGGAAAATGTAAGTG :  399
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H7                   : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H8                   : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H9                   : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 503
H10                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H11                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H12                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H13                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H14                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H15                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H16                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H17                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H18                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H19                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H20                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H21                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H22                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H23                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H24                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H25                  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H26_Mauritania-I_ref : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H27_India-VII_refseq : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACGTGACAAAGGTAGTGGC : 520
H28_Ctg_refsequence  : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H29_Salvador-I_refse : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H30_NKorea_refsequen : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H31_P.vivax01_refseq : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
H32_Brazil-I_refsequ : AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACATGACAAAGGTAGTGGC : 520
                       AAGCCGCTCCCCACTCGGAGGAGTCCACTGGGGGAAGCGCGGAGAAGGGAAGTGGCGGCCACGAGGAAACCCCCCACGCAGGAGAACaTGACAAAGGTAGTGGC

                                 *       540         *       560         *       580         *       600         *       620
H1_VCG               : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H2                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H3                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H4                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H5                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H6                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H7                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H8                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H9                   : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 607
H10                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H11                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H12                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H13                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H14                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H15                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H16                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H17                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
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H18                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H19                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H20                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H21                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H22                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H23                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H24                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H25                  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H26_Mauritania-I_ref : GG------------------AAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 606
H27_India-VII_refseq : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H28_Ctg_refsequence  : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H29_Salvador-I_refse : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H30_NKorea_refsequen : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H31_P.vivax01_refseq : GGAAGCAACGGGAGCAGCGAAAGCAACGGGAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
H32_Brazil-I_refsequ : GGAAGCAACGGGAGCAGCGAAAGCAACGGAAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG : 624
                       GGaagcaacgggagcagcgaAAGCAACGGaAGCGTCTTGGCTGATGGCCACGCCGAAGAAGCGCCGAACGAGCAGGTGAGTAGCGAGAAGAACGACGGACACAG

                                 *       640         *       660         *       680         *       700         *       720
H1_VCG               : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H2                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H3                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H4                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H5                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H6                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H7                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H8                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H9                   : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 711
H10                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H11                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H12                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H13                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H14                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H15                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H16                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H17                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H18                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H19                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H20                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H21                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
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H24                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H25                  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAAGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H26_Mauritania-I_ref : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 710
H27_India-VII_refseq : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H28_Ctg_refsequence  : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H29_Salvador-I_refse : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H30_NKorea_refsequen : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H31_P.vivax01_refseq : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
H32_Brazil-I_refsequ : TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAGGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA : 728
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                                TGAAAGCAGCACCACGGGCTCACACTCAGATAAGGAgGAGCTGGACTTGTATACGTCCTCCCCCTCCGATAAAGAAGAAAACAGCGCCCCTGCCATGGGTGGTA

                                 *       740         *       760         *       780         *       800         *       820         *
H1_VCG                  : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGGCCCCCATGAAGTGGCAGATAAA :  832
H2                      : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H3                      : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H4                      : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H5                      : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H6                      : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGGCCCCCATGAAGTGGCAGATAAA :  832
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H9                      : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  815
H10                     : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H11                     : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H12                     : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
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H25                     : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
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H27_India-VII_refseq    : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H28_Ctg_refsequence     : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H29_Salvador-I_refse    : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H30_NKorea_refsequen    : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H31_P.vivax01_refseq    : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
H32_Brazil-I_refsequ    : TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGTCCCCCATGAAGTGGCAGATAAA :  832
                          TGCACAACACGGTAGGCCTGAGGGGGGGAAGCGCCTCTGAATCGGCGGCCCCAAGTGAAGAGAAAGCATCCGAAGAGAATGtCCCCCATGAAGTGGCAGATAAA

                                 840         *       860         *       880         *       900         *       920         *
H1_VCG                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H2                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H3                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H4                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H5                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H6                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA-------------------GAGTGGCGGCGAGCACGG :  918
H7                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGAGAGTGGCGAGAGTGGCGAGAGTGGCGGCGAGCACGG :  936
H8                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGAGAGTGGCGAGAGTGGCGAGAGTGGCGGCGAGCACGG :  936
H9                      : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  910
H10                     : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGAGAGTGGCGAGAGTGGCGAGAGTGGCGGCGAGCACGG :  936
H11                     : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H12                     : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
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H13                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H14                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H15                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H16                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H17                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H18                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H19                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H20                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H21                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H22                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H23                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H24                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGAGAGTGGCGAGAGTGGCGAGAGTGGCGGCGAGCACGG :  936
H25                  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H26_Mauritania-I_ref : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA------------------GAGTGGCGGCGAGCACGG :  900
H27_India-VII_refseq : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA------------------GAGTGGCGGCGAGCACGG :  918
H28_Ctg_refsequence  : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H29_Salvador-I_refse : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
H30_NKorea_refsequen : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA------------------GAGTGGCGGCGAGCACGG :  918
H31_P.vivax01_refseq : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA------------------GAGTGGCGGCGAGCACGG :  918
H32_Brazil-I_refsequ : AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA---------GAGTGGCGAGAGTGGCGGCGAGCACGG :  927
                       AATGGGGAGGACACCTCACAGGAGGGTTCCCACGCGGGAGCGCTGTCACCTGCGCATGTGGGTGGCGA         gagtggcgaGAGTGGCGGCGAGCACGG

                        940         *       960         *       980         *      1000         *      1020         *      1040
H1_VCG               : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACA------------------------------------ :  996
H2                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H3                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H4                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H5                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H6                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACATGGCGAGCACGGTGAA------------------- :  985
H7                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACA------------------------------------ : 1005
H8                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC : 1006
H9                   : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  980
H10                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC : 1006
H11                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H12                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H13                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H14                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H15                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H16                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACATGGCGAGCACGGTGAA------------------- :  994
H17                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H18                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACATGGCGAGCACGGTGAA------------------- :  994
H19                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H20                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H21                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H22                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H23                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H24                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC : 1006
H25                  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  997
H26_Mauritania-I_ref : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA------------------GAGCACGGTGAACA----------------CGCTGAACATGGGGAGCAC :  970
H27_India-VII_refseq : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGGCGAGCACGGTGAA------------------- : 1003
```

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H28_Ctg_refsequence  : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGG------------------------------------------------------------ :  972
H29_Salvador-I_refse : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGA--------------------------------------------------------------------- :  964
H30_NKorea_refsequen : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGT----------------------------------------------------------- :  964
H31_P.vivax01_refseq : ---------TGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACA--------------------------------CGCTGAACATGGGGAGCAC : 979
H32_Brazil-I_refsequ : AGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACA------------------------------------ :  996
                       agagcacggTGAACACGCTGAACATGGGGAGCACGGA                 gagcacggtgaaca

                                 *      1060         *      1080         *      1100         *      1120         *      1140
H1_VCG               : ------------------------------------------------------------------------------------------------------ :    -
H2                   : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H3                   : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H4                   : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H5                   : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H6                   : ------------------------------------------------------------------------------------------------------ :    -
H7                   : ------------------------------------------------------------------------------------------------------ :    -
H8                   : GGAGAGCACGGTGAACAT-------------------------------------------------------------------------------------- : 1024
H9                   : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- :  995
H10                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1021
H11                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H12                  : GGAGAGCACGGTGAACAT-------------------------------------------------------------------------------------- : 1015
H13                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H14                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H15                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H16                  : ------------------------------------------------------------------------------------------------------ :    -
H17                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------CACGCTGA : 1020
H18                  : ------------------------------------------------------------------------------------------------------ :    -
H19                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H20                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H21                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H22                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H23                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H24                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1021
H25                  : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- : 1012
H26_Mauritania-I_ref : GGAGAGCACGGTGAACATGGTGAGCATGGTGAGCACGGTGAGCATGGTGAGCATGGTGAGCACGGTGAACATGGTGAGCATGGGGAGCACGGTGAG-------- : 1066
H27_India-VII_refseq : ------------------------------------------------------------------------------------------------------ :    -
H28_Ctg_refsequence  : ------------------------------------------------------------------------------------------------------ :    -
H29_Salvador-I_refse : ------------------------------------------------------------------------------------------------------ :    -
H30_NKorea_refsequen : ------------------------------------------------------------------------------------------------------ :    -
H31_P.vivax01_refseq : GGAGAGCACGGTGAA----------------------------------------------------------------------------------------- :  994
H32_Brazil-I_refsequ : ------------------------------------------------------------------------------------------------------ :    -

                            *      1160         *      1180         *      1200         *      1220         *      1240
H1_VCG               : ------------------------------------------------------------------------------------------------------ :    -
H2                   : ------------------------------------------------------------------------------------------------------ :    -
H3                   : ------------------------------------------------------------------------------------------------------CACG : 1016
H4                   : ------------------------------------------------------------------------------------------------------ :    -
H5                   : ------------------------------------------------------------------------------------------------------ :    -
H6                   : ------------------------------------------------------------------------------------------------------ :    -
H7                   : ------------------------------------------------------------------------------------------------------ :    -
```

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H8                   : ------------------------------------------------------------------------------------------------------------ :    -
H9                   : ------------------------------------------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACACG : 1035
H10                  : ------------------------------------------------------------------------------------------------------------ :    -
H11                  : ------------------------------------------------------------------------------------------------------------ :    -
H12                  : ------------------------------------------------------------------------------------------------------------ :    -
H13                  : ------------------------------------------------------------------------------------------------------------CACG : 1016
H14                  : ------------------------------------------------------------------------------------------------------------ :    -
H15                  : ------------------------------------------------------------------------------------------------------------ :    -
H16                  : ------------------------------------------------------------------------------------------------------------ :    -
H17                  : ACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACACG : 1124
H18                  : ------------------------------------------------------------------------------------------------------------ :    -
H19                  : ------------------------------------------------------------------------------------------------------------ :    -
H20                  : ------------------------------------------------------------------------------------------------------------ :    -
H21                  : ------------------------------------------------------------------------------------------------------------ :    -
H22                  : ------------------------------------------------------------------------------------------------------------ :    -
H23                  : ------------------------------------------------------------------------------------------------------------ :    -
H24                  : ------------------------------------------------------------------------------------------------------------ :    -
H25                  : ------------------------------------------------------------------------------------------------------------ :    -
H26_Mauritania-I_ref : ------------------------------------------------------------------------------------------------------------ :    -
H27_India-VII_refseq : ------------------------------------------------------------------------------------------------------------ :    -
H28_Ctg_refsequence  : ------------------------------------------------------------------------------------------AGAGCACGGTGAACACG :  989
H29_Salvador-I_refse : ------------------------------------------------------------------------------GAGCACGGAGAGCACGGTGAACACG :  989
H30_NKorea_refsequen : ------------------------------------------------------------------------------------------------------------ :    -
H31_P.vivax01_refseq : ------------------------------------------------------------------------------------------------------------ :    -
H32_Brazil-I_refsequ : ------------------------------------------------------------------------------------------------------------ :    -

                       *      1260         *      1280         *      1300         *      1320         *      1340         *
H1_VCG               : ------------------------------------------------------------------------------------------TGCTGAACAGGAGGAG : 1012
H2                   : ------------------------------------------------------------------CATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1048
H3                   : CTGAACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1120
H4                   : --------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1084
H5                   : --------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1084
H6                   : ------------------------------------------------------------------------------------------CATGCTGAACAGGAGGAG : 1003
H7                   : ------------------------------------------------------------------------------------------TGCTGAACAGGAGGAG : 1021
H8                   : ------------------------------------------------------------------------GGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1057
H9                   : CTGAACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1139
H10                  : ------------------------------------------------------------------CATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1057
H11                  : --------------------------------CACGCTGAACATGGGGAGCACGGAGA------------------GCACGGTGAACATGCTGAACAGGAGGAG : 1066
H12                  : ------------------------------------------------------------------------GGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1048
H13                  : CTGAACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1120
H14                  : --------------------------------CACGCTGAACATGGGGAGCACGGAGA------------------GCACGGTGAACATGCTGAACAGGAGGAG : 1066
H15                  : ------------------------------------------------------------------CATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1048
H16                  : ------------------------------------------------------------------------------------------CATGCTGAACAGGAGGAG : 1012
H17                  : CTGAACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1228
H18                  : ------------------------------------------------------------------------------------------CATGCTGAACAGGAGGAG : 1012
H19                  : --------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAA------------------CATGCTGAACAGGAGGAG : 1066
H20                  : ------------------------------------------------------------------CATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1048
H21                  : --------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1084
H22                  : ------------------------------------------------------------------CATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1048
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H23                  : --------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1084
H24                  : --------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1093
H25                  : ------------------------------------------------------------------CATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1048
H26_Mauritania-I_ref : --------------------------------CACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1138
H27_India-VII_refseq : ------------------------------------------------------------------------------------CATGCTGAACAGGAGGAG : 1021
H28_Ctg_refsequence  : CTGAACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1093
H29_Salvador-I_refse : CTGAACATGGGGAGCACGGAGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1093
H30_NKorea_refsequen : ------------------------------------------------------------------GAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1003
H31_P.vivax01_refseq : --------------CATGGCGAGCACGGTGAACACGCTGAACATGGGGAGCACGGAGAGCACGGTGAACATGGCGAGCACGGTGAACATGCTGAACAGGAGGAG : 1084
H32_Brazil-I_refsequ : ------------------------------------------------------------------------------------TGCTGAACAGGAGGAG : 1012
                                                                                                   caTGCTGAACAGGAGGAG

                                 1360         *      1380         *      1400         *      1420         *      1440         *
H1_VCG               : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1116
H2                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1152
H3                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1224
H4                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1188
H5                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1188
H6                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1107
H7                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1125
H8                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1161
H9                   : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1243
H10                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1161
H11                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1170
H12                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1152
H13                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1224
H14                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1170
H15                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1152
H16                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1116
H17                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1332
H18                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1116
H19                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1170
H20                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1152
H21                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1188
H22                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1152
H23                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1188
H24                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1197
H25                  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1152
H26_Mauritania-I_ref : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1242
H27_India-VII_refseq : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1125
H28_Ctg_refsequence  : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1197
H29_Salvador-I_refse : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1197
H30_NKorea_refsequen : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1107
H31_P.vivax01_refseq : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1188
H32_Brazil-I_refsequ : CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA : 1116
                       CACCAAATCTATGGGACGATTCACCCCGAGGCGGAAGCCTCCATTTTGCCCGCGCTGAAGGAAAAGGGCATCCACGTGTCCAGCCCAGAAAGGGTAATCCTCGA

                       1460         *      1480         *      1500         *      1520         *      1540         *      1560
H1_VCG               : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1220
H2                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1256
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H3                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1328
H4                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1292
H5                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1292
H6                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1211
H7                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1229
H8                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1265
H9                   : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1347
H10                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1265
H11                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1274
H12                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1256
H13                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1328
H14                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1274
H15                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1256
H16                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1220
H17                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1436
H18                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1220
H19                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1274
H20                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1256
H21                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1292
H22                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1256
H23                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1292
H24                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1301
H25                  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1256
H26_Mauritania-I_ref : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1346
H27_India-VII_refseq : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1229
H28_Ctg_refsequence  : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1301
H29_Salvador-I_refse : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1301
H30_NKorea_refsequen : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1211
H31_P.vivax01_refseq : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1292
H32_Brazil-I_refsequ : GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA : 1220
                       GATCATCGAAAGCGCCAAGGAGGGAATAAAAGGATTGCTGAAGCTCCGGAAGAGCAAAGACACAGGCAAGCTGCTGGAGGAGGCACTAGAAAAGCTAAACATAA

                                 *      1580         *      1600         *      1620         *      1640         *      1660
H1_VCG               : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1324
H2                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1360
H3                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1432
H4                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1396
H5                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1396
H6                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1315
H7                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1333
H8                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1369
H9                   : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1451
H10                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1369
H11                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1378
H12                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1360
H13                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1432
H14                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1378
H15                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1360
H16                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1324
H17                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1540
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H18                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1324
H19                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1378
H20                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1360
H21                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1396
H22                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1360
H23                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1396
H24                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1405
H25                  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1360
H26_Mauritania-I_ref : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1450
H27_India-VII_refseq : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1333
H28_Ctg_refsequence  : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1405
H29_Salvador-I_refse : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1405
H30_NKorea_refsequen : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1315
H31_P.vivax01_refseq : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1396
H32_Brazil-I_refsequ : ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG : 1324
                       ACCAAAGGGATCTGCATGCAAACAATAATTTCATTACCCTAGAAATGTATGACCGGATCCTCTCCGAAATGTTTAAAATATTAACAGAAATGTCATTCTATAAG

                                 *      1680         *      1700         *      1720         *      1740         *      1760
H1_VCG               : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1428
H2                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1464
H3                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1536
H4                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1500
H5                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1500
H6                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1419
H7                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1437
H8                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1473
H9                   : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1555
H10                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1473
H11                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1482
H12                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1464
H13                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1536
H14                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1482
H15                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1464
H16                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1428
H17                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1644
H18                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1428
H19                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1482
H20                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1464
H21                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1500
H22                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1464
H23                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1500
H24                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1509
H25                  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1464
H26_Mauritania-I_ref : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1554
H27_India-VII_refseq : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1437
H28_Ctg_refsequence  : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1509
H29_Salvador-I_refse : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1509
H30_NKorea_refsequen : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1419
H31_P.vivax01_refseq : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1500
H32_Brazil-I_refsequ : GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC : 1428
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                                GATGGCCATTTTTACGAAACGTTAGGTTTGAATAAATCTATACTAAATCAATCGCTGAAAGAAATTAAAATAAAAATGTTGAGGACCATTGGAGTGCCATACAC

                                 *      1780         *      1800         *      1820         *      1840         *      1860         *
H1_VCG                  : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1532
H2                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1568
H3                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1640
H4                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1604
H5                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1604
H6                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1523
H7                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1541
H8                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1577
H9                      : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1659
H10                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1577
H11                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1586
H12                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1568
H13                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1640
H14                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1586
H15                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1568
H16                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1532
H17                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1748
H18                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1532
H19                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1586
H20                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1568
H21                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1604
H22                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1568
H23                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1604
H24                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1613
H25                     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1568
H26_Mauritania-I_ref    : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1658
H27_India-VII_refseq    : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1541
H28_Ctg_refsequence     : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1613
H29_Salvador-I_refse    : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1613
H30_NKorea_refsequen    : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1523
H31_P.vivax01_refseq    : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1604
H32_Brazil-I_refsequ    : GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA : 1532
                          GAAGCTACCGCCAATCGTTAAGAACAAAGAGAAGGAAAGCACATGTGCTGCGAACAATCTCATCATTAGCATTACATCAAAAGAGCTAGCTCAACGAATGGCTA

                              1880         *      1900         *      1920         *      1940         *      1960         *
H1_VCG                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1636
H2                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1672
H3                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1744
H4                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1708
H5                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1708
H6                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1627
H7                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1645
H8                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1681
H9                      : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1763
H10                     : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1681
H11                     : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1690
H12                     : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1672
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H13                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1744
H14                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1690
H15                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1672
H16                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1636
H17                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1852
H18                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1636
H19                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1690
H20                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1672
H21                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1708
H22                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1672
H23                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1708
H24                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1717
H25                  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1672
H26_Mauritania-I_ref : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1762
H27_India-VII_refseq : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1645
H28_Ctg_refsequence  : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1717
H29_Salvador-I_refse : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1717
H30_NKorea_refsequen : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1627
H31_P.vivax01_refseq : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1708
H32_Brazil-I_refsequ : TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA : 1636
                       TCATGTTCGCAAAATGGCTAGCTCCAGAAGAATACGGGTCTGTCGTCGATTTAGATAAAAGCATAGAATTAAATGTCCTCTGCGCAGGGGCACCTATCCTAGTA

                       1980         *      2000         *      2020         *      2040         *      2060         *      2080
H1_VCG               : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1740
H2                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1776
H3                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1848
H4                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1812
H5                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1812
H6                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1731
H7                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1749
H8                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1785
H9                   : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1867
H10                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1785
H11                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1794
H12                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1776
H13                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1848
H14                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1794
H15                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1776
H16                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1740
H17                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1956
H18                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1740
H19                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1794
H20                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1776
H21                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1812
H22                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1776
H23                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1812
H24                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1821
H25                  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1776
H26_Mauritania-I_ref : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1866
H27_India-VII_refseq : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1749
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H28_Ctg_refsequence  : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1821
H29_Salvador-I_refse : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1821
H30_NKorea_refsequen : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1731
H31_P.vivax01_refseq : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1812
H32_Brazil-I_refsequ : CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG : 1740
                       CAGCAATGGAAATATTACCAAAACATGTTAGGGTTCGAAACGGGAAATGAACATGCCTTCTTAAACCTCATCGATGAGTTGCTAGTCATCGACAAGAGACACAG

                                 *      2100         *      2120         *      2140         *      2160         *      2180
H1_VCG               : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1844
H2                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1880
H3                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1952
H4                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1916
H5                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1916
H6                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1835
H7                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1853
H8                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1889
H9                   : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1971
H10                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1889
H11                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1898
H12                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1880
H13                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1952
H14                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1898
H15                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1880
H16                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1844
H17                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 2060
H18                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1844
H19                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1898
H20                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1880
H21                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1916
H22                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1880
H23                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1916
H24                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1925
H25                  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1880
H26_Mauritania-I_ref : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1970
H27_India-VII_refseq : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1853
H28_Ctg_refsequence  : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1925
H29_Salvador-I_refse : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1925
H30_NKorea_refsequen : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1835
H31_P.vivax01_refseq : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1916
H32_Brazil-I_refsequ : TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC : 1844
                       TAACAATGAAGCGTATTCAAAAGTGATAAGGAAAATAAAAAAATCGAAAGCCTTTAATTATTGTACTAAAGTTATGAGGATTGCAGGGAATATTTCTTCCATTC

                            *      2200         *      2220         *      2240         *      2260         *      2280
H1_VCG               : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1948
H2                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1984
H3                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2056
H4                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2020
H5                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2020
H6                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1939
H7                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1957
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H8                    : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1993
H9                    : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2075
H10                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1993
H11                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2002
H12                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1984
H13                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2056
H14                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2002
H15                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1984
H16                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1948
H17                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2164
H18                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1948
H19                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2002
H20                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1984
H21                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2020
H22                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1984
H23                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2020
H24                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2029
H25                   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1984
H26_Mauritania-I_ref  : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2074
H27_India-VII_refseq  : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1957
H28_Ctg_refsequence   : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2029
H29_Salvador-I_refse  : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2029
H30_NKorea_refsequen  : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1939
H31_P.vivax01_refseq  : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 2020
H32_Brazil-I_refsequ  : CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT : 1948
                        CATTTAATCATGAAAATAATAAAACGCCTAGCTACTCCATCATCGGGTCGTTAGGTAACCTGGTGAAGGCTCACATGGGGAACTACTACGTTGCCATTGCTAAT

                         *      2300         *      2320         *      2340         *      2360         *      2380         *
H1_VCG                : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2052
H2                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2088
H3                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2160
H4                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2124
H5                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2124
H6                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2043
H7                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2061
H8                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2097
H9                    : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2179
H10                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2097
H11                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2106
H12                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2088
H13                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2160
H14                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2106
H15                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2088
H16                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2052
H17                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2268
H18                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2052
H19                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2106
H20                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2088
H21                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2124
H22                   : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2088
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H23                  : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2124
H24                  : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2133
H25                  : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2088
H26_Mauritania-I_ref : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2178
H27_India-VII_refseq : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2061
H28_Ctg_refsequence  : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2133
H29_Salvador-I_refse : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2133
H30_NKorea_refsequen : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2043
H31_P.vivax01_refseq : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2124
H32_Brazil-I_refsequ : AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA : 2052
                       AGGATTAACTCCTATTTTGCCTATGCCGAGAAGAGGAACAAAAAAAACAGCCCCTTAAAAGTTGTCTCCGTCTGTACTCTCCTTCATTTGACCGACATGCTCCA

                           2400         *      2420         *      2440         *      2460         *      2480         *
H1_VCG               : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2156
H2                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2192
H3                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2264
H4                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2228
H5                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2228
H6                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2147
H7                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2165
H8                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2201
H9                   : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2283
H10                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2201
H11                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2210
H12                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2192
H13                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2264
H14                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2210
H15                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2192
H16                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2156
H17                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2372
H18                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2156
H19                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2210
H20                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2192
H21                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2228
H22                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2192
H23                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTATGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2228
H24                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2237
H25                  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2192
H26_Mauritania-I_ref : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2282
H27_India-VII_refseq : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2165
H28_Ctg_refsequence  : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2237
H29_Salvador-I_refse : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2237
H30_NKorea_refsequen : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2147
H31_P.vivax01_refseq : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2228
H32_Brazil-I_refsequ : CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTCTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA : 2156
                       CAATTGCTCTGATGAACATTTAAAGAATATTTTGGACCTCAACACTTTGAAGCTTAACATTcTGAACATGCAGGGCAGGCGCGTGCTGCAGCCCCTCGTCAAGA

                       2500         *      2520         *      2540         *      2560         *      2580         *      2600
H1_VCG               : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2260
H2                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2296
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H3                    : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2368
H4                    : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2332
H5                    : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2332
H6                    : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2251
H7                    : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2269
H8                    : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2305
H9                    : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2387
H10                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2305
H11                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2314
H12                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2296
H13                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2368
H14                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2314
H15                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2296
H16                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2260
H17                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2476
H18                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2260
H19                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2314
H20                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2296
H21                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2332
H22                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2296
H23                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2332
H24                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2341
H25                   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2296
H26_Mauritania-I_ref  : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2386
H27_India-VII_refseq  : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2269
H28_Ctg_refsequence   : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGACGACCTCCATGGGGGGCT : 2341
H29_Salvador-I_refse  : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGACGACCTCCATGGGGGGCT : 2341
H30_NKorea_refsequen  : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2251
H31_P.vivax01_refseq  : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2332
H32_Brazil-I_refsequ  : TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGCGACCTCCATGGGGGGCT : 2260
                        TGAGCTTCCTCGGCGCCGCGCAGAACCCCGCCCTCAAGGAGATCTGCGAGCCGAGCAACCACCTAGTGGGTGAGTGACGGGGGGGgCGACCTCCATGGGGGGCT

                                  *      2620         *      2640         *      2660         *      2680         *      2700
H1_VCG                : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2364
H2                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2400
H3                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2472
H4                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2436
H5                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2436
H6                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2355
H7                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2373
H8                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2409
H9                    : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2491
H10                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2409
H11                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2418
H12                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2400
H13                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2472
H14                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2418
H15                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2400
H16                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2364
H17                   : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2580
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H18                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2364
H19                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2418
H20                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2400
H21                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2436
H22                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2400
H23                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2436
H24                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2445
H25                  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2400
H26_Mauritania-I_ref : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2490
H27_India-VII_refseq : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2373
H28_Ctg_refsequence  : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2445
H29_Salvador-I_refse : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2445
H30_NKorea_refsequen : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2355
H31_P.vivax01_refseq : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2436
H32_Brazil-I_refsequ : GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC : 2364
                       GCTATTCCAGCGCGGTGATCCACGCAGTGATCCGCGCAGCTGCTTTATTGGAAGCGCTTTACTCGAACTGCCTTCCTTCATTCGAACTTCCTTCCTTCATTCGC

                                 *      2720         *      2740         *      2760         *      2780         *      2800
H1_VCG               : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2468
H2                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2504
H3                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2576
H4                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2540
H5                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2540
H6                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACTCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2459
H7                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2477
H8                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2513
H9                   : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2595
H10                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2513
H11                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2522
H12                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2504
H13                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2576
H14                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2522
H15                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2504
H16                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2468
H17                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2684
H18                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2468
H19                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2522
H20                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACTCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2504
H21                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACTCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2540
H22                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACTCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2504
H23                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2540
H24                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2549
H25                  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2504
H26_Mauritania-I_ref : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2594
H27_India-VII_refseq : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2477
H28_Ctg_refsequence  : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2549
H29_Salvador-I_refse : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2549
H30_NKorea_refsequen : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCGTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2459
H31_P.vivax01_refseq : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2540
H32_Brazil-I_refsequ : ACCGCCTTCTTTCACCCCCCTCAGACGAGACCCTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC : 2468
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                                ACCGCCTTCTTTCACCCCCCTCAGACGAGACccTCTCCAAGCTGCTCAACCTGCTCTCGACCGGTTCGCACGAACTCCTCGCGGCCGAGGTGGAAAAGCGCGGC

                                 *      2820         *      2840         *      2860         *      2880         *      2900         *
H1_VCG                  : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2572
H2                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2608
H3                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2680
H4                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2644
H5                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2644
H6                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2563
H7                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2581
H8                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2617
H9                      : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2699
H10                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2617
H11                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2626
H12                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2608
H13                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2680
H14                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2626
H15                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2608
H16                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2572
H17                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2788
H18                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2572
H19                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2626
H20                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2608
H21                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2644
H22                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2608
H23                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2644
H24                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2653
H25                     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2608
H26_Mauritania-I_ref    : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2698
H27_India-VII_refseq    : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2581
H28_Ctg_refsequence     : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2653
H29_Salvador-I_refse    : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2653
H30_NKorea_refsequen    : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2563
H31_P.vivax01_refseq    : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2644
H32_Brazil-I_refsequ    : TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA : 2572
                          TTCGACGAGGACTACATCCAGGAGGAAATCAAAAACATAAACGAAAGCGACAACAACGTTCGGGACAAGGGCGAAGACGAAGTGGAAAATCTCATTTTTGAAGA

H1_VCG                  : CTTGTGA : 2579
H2                      : CTTGTGA : 2615
H3                      : CTTGTGA : 2687
H4                      : CTTGTGA : 2651
H5                      : CTTGTGA : 2651
H6                      : CTTGTGA : 2570
H7                      : CTTGTGA : 2588
H8                      : CTTGTGA : 2624
H9                      : CTTGTGA : 2706
H10                     : CTTGTGA : 2624
H11                     : CTTGTGA : 2633
H12                     : CTTGTGA : 2615
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H13                   : CTTGTGA : 2687
H14                   : CTTGTGA : 2633
H15                   : CTTGTGA : 2615
H16                   : CTTGTGA : 2579
H17                   : CTTGTGA : 2795
H18                   : CTTGTGA : 2579
H19                   : CTTGTGA : 2633
H20                   : CTTGTGA : 2615
H21                   : CTTGTGA : 2651
H22                   : CTTGTGA : 2615
H23                   : CTTGTGA : 2651
H24                   : CTTGTGA : 2660
H25                   : CTTGTGA : 2615
H26_Mauritania-I_ref  : CTTGTGA : 2705
H27_India-VII_refseq  : CTTGTGA : 2588
H28_Ctg_refsequence   : CTTGTGA : 2660
H29_Salvador-I_refse  : CTTGTGA : 2660
H30_NKorea_refsequen  : CTTGTGA : 2570
H31_P.vivax01_refseq  : CTTGTGA : 2651
H32_Brazil-I_refsequ  : CTTGTGA : 2579
                        CTTGTGA
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