Supp. Figure S1. Alignment of the H1 hybrid allele sequences of carriers Ci, Cii and Ciii with the human and chimpanzee gene and pseudogene. The Alignment starts at Primer LRPCR4_Fwd and comprises 2718 bp. Paralogue and orthologue discriminating SNPs are highlighted in red and blue, respectively. Those mentioned in Supp. Table S3 are indicated with their names. Pairs of differences involving neither homologues nor paralogues are highlighted in green. SNPs divergent from any of the reference sequences found in this or other H1 sub-haplotypes are encircled and indicated with their names (see Supp. Table S3).

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                                                                PDS2   PDS3
Hs_PMS2                                           AAATTAGTCAGACTTGATGGTGTGTG
Hs_PSD                                            AAATTAGTCAGACTTCATGGTGTATG
Pt_PMS2                                           AAATTAGTCAGACTTGATGGTGTGTG
Pt_PSD                                            AAATTAGTCAGACTTCATGGTGTATG
Ci                                                --------------------------
Cii                                               --------------------------
Ciii                                              --------------------------


Hs_PMS2         CCTGTGGTCCCAGCTATTCGGGAGGCTGAGGTGGGAGGATCGTTTGAGCCCAGGAGATTG
Hs_PSD          CCTGTGGTCCCAGCTATTCGGGAGGCTGAGGTGGGAGGATCGTTTGAGCCCAGGAGATTG
Pt_PMS2         CCTGTGGTCCCAGCTATTCGGGAGGCTGAGGTGGGAGGATCGTTTGAGCCCAGGAGATTG
Pt_PSD          CCTGTGGTCCCAGCTATTCGGAAGGCTGAGGTGGGAGGATCGTT-GAACCCAGGAGAT-G
Ci              ---------CCAGCTATTCGGGAGGCTGAGGTGGGAGGATCGTTTGAGCCCAGGAGATTG
Cii             ----GTGGTCCAGCTATTCGGGAGGCTGAGGTGGGAGGATCGTTTGAGCCCAGGAGATTG
Ciii            ---------CCAGCTATTCGGGAGGCTGAGGTGGGAGGATCGTTTGAGCCCAGGAGATTG


Hs_PMS2         AGGCTGCCATGATCGTGCCACTGCACAGCTCTCCAGCCTGGGTGACAGAGTGAGACAGTG
Hs_PSD          AGGCTGCCATGATCGTGCCACTGCACAGCTCTCCAGCCTGGGTGACAGAGTGAGACAGTG
Pt_PMS2         AGGCTGCCATGATCGTGCCACTGCACAGCTCTCCAGCCTGGGTGACAGAGTGAGACAGTG
Pt_PSD          AGGCTGCCATGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Ci              AGGCTGCCATGATCGTGCCACTGCACAGCTCTCCAGCCTGGGTGACAGAGTGAGACAGTG
Cii             AGGCTGCCATGATCGTGCCACTGCACAGCTCTCCAGCCTGGGTGACAGAGTGAGACAGTG
Ciii            AGGCTGCCATGATCGTGCCACTGCACAGCTCTCCAGCCTGGGTGACAGAGTGAGACAGTG


Hs_PMS2         AGACTCTGTCTCACAAATAAATTAATAAATAAAATAAAATAAAAT-----TTAAAAATTA
Hs_PSD          AGACTCTGTCTCACAAATAAATTAATAAATAAAATAAAATAAAAT-----TTAAAAATTA
Pt_PMS2         AGACTCTGTCTCACAAATAAATTAATAAATAAAATAAAATAAAATAAAATTTAAAAATTA
Pt_PSD          NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN-NNNN------
Ci              AGACTCTGTCTCACAAATAAATTAATAAATAAAACAAAATAAAAT-----TTAAAAATTA
Cii             AGACTCTGTCTCACAAATAAATTAATAAATAAAACAAAATAAAAT-----TTAAAAATTA
Ciii            AGACTCTGTCTCACAAATAAATTAATAAATAAAACAAAATAAAAT-----TTAAAAATTA

                                                               PDSi
Hs_PMS2         TTTTAAGATAGTCACTGCAGAATTTGGTATTTCTCTCTCCTCGGCCAAACTGGAATGTTT
Hs_PSD          TTTTAAGATAGTCACTGCAGAATTTGGTATTTCTCTCTCCTCGGCCAAGCTGGAATGTTT
Pt_PMS2         TTTTAAGATAGTCACTGCAGAATTTGGTATTTCTCTCTCCTCGGCCAAACTGGAATGTTT
Pt_PSD          ------------------------------------------------------------
Ci              TTTTAAGATAGTCACTGCAGAATTTGGTATTTCTCTCTCCTCGGCCAAACTGGAATGTTT
Cii             TTTTAAGATAGTCACTGCAGAATTTGGTATTTCTCTCTCCTCGGCCAAACTGGAATGTTT
Ciii            TTTTAAGATAGTCACTGCAGAATTTGGTATTTCTCTCTCCTCGGCCAAACTGGAATGTTT

                  PDSii                  PDSiii
Hs_PMS2         TACCC-TGACTACTTCACAAAGGTCAGGTGTGATAGTATCATGTAAAACCAAAGTCTTGT
Hs_PSD          TACTC-TGACTACTTCACAAAGGTCAGATGTGATAGTATCATGTAAAACCAAAGTCTTGT
Pt_PMS2         TACCCCTGACTACTTCACAAAGGTCAGGTGTGATAGTATCATGTAAAACCAAAGTCTTGT
Pt_PSD          -----------------------------------------------------GTCTTGT
Ci              TACCC-TGACTACTTCACAAAGGTCAGGTGTGATAGTATCATGTAAAACCAAAGTCTTGT
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Cii             TACCC-TGACTACTTCACAAAGGTCAGGTGTGATAGTATCATGTAAAACCAAAGTCTTGT
Ciii            TACCC-TGACTACTTCACAAAGGTCAGGTGTGATAGTATCATGTAAAACCAAAGTCTTGT

                              PDSiv                                 PDSv
Hs_PMS2         CTTCAGCAAAGTTAGAAGAAGAGGTCATGGATTTTCGTGTGGGAAATTAAACCACGTAGT
Hs_PSD          CTTCAGCAAAGTTATAAGAAGAGGTCATGGATTTTCGTGTGGGAAATTAAACAACGTAGT
Pt_PMS2         CTTCAGCAAAGTTATAAGAAGAGGTCATGGATTTTCGTGTGGGAAATTAAACCACGTAGT
Pt_PSD          CTTCAGCAAAGTTATAAGAAGAGGTCATGGATTTTCATGTGGGAAATTAAACCACGTAGT
Ci              CTTCAGCAAAGTTAGAAGAAGAGGTCATGGATTTTCGTGTGGGAAATTAAACCACGTAGT
Cii             CTTCAGCAAAGTTAGAAGAAGAGGTCATGGATTTTCGTGTGGGAAATTAAACCACGTAGT
Ciii            CTTCAGCAAAGTTAGAAGAAGAGGTCATGGATTTTCGTGTGGGAAATTAAACCACGTAGT


Hs_PMS2         GAAGTAAACTCAGATCCCAACAAGTAGATCCCACATGGAGAAATGTACCACTGAACCTGT
Hs_PSD          GAAGTAAACTCAGATCCCAACAAGTAGATCCCACATGGAGAAATGTACCACTGAACCTGT
Pt_PMS2         GAAGTAAACTCAGATCCCAACAAGCAGATCCCACATGGAGAAATGTACCACTGAACCTGT
Pt_PSD          GAAGTAAACTCAGATCCCGACAAGTAGATCCCACATGGAGAAATGTACCACTGAACCTGT
Ci              GAAGTAAACTCAGATCCCAACAAGTAGATCCCACATGGAGAAATGTACCACTGAACCTGT
Cii             GAAGTAAACTCAGATCCCAACAAGTAGATCCCACATGGAGAAATGTACCACTGAACCTGT
Ciii            GAAGTAAACTCAGATCCCAACAAGTAGATCCCACATGGAGAAATGTACCACTGAACCTGT

                      ODS1                    PDSvi                  PDSvii
Hs_PMS2         GTAGTTTGCTGAGTACTCTCCTGTGTAGTTTACTGAGTACTCTCCTGTGTAGTTTGCTGA
Hs_PSD          GTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTACTGA
Pt_PMS2         GTAGTTTACTGAGTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGA
Pt_PSD          GTAGTTTACTGAGTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGA
Ci              GTAGTTTACTGAGTACTCTCCTGTGTAGTTTACTGAGTACTCTCCTGTGTAGTTTGCTGA
Cii             GTAGTTTACTGAGTACTCTCCTGTGTAGTTTACTGAGTACTCTCCTGTGTAGTTTGCTGA
Ciii            GTAGTTTACTGAGTACTCTCCTGTGTAGTTTACTGAGTACTCTCCTGTGTAGTTTGCTGA


Hs_PMS2         GTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTG-----------------------
Hs_PSD          GTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTACTGAGTACTCTCCTGT
Pt_PMS2         GTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGAGTGCTCTCCTGT
Pt_PSD          GTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGT
Ci              GTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTG-----------------------
Ci              GTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTG-----------------------
Cii             GTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTG-----------------------


Hs_PMS2         ------------------------------------------------------------
Hs_PSD          GTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGA
Pt_PMS2         GTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTG-----------
Pt_PSD          GTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGAGTACTCTCCTGTGTAGTTTGCTGA
Ci              ------------------------------------------------------------
Cii             ------------------------------------------------------------
Ciii            ------------------------------------------------------------


Hs_PMS2         ------------------------------------------------------------
Hs_PSD          GTACTCTCCTGTG-----------------------------------------------
Pt_PMS2         ------------------------------------------------------------
Pt_PSD          GTACTCTCCTGTGTAGTTTGCTGAGTACTCTACTGTGTAGTTTGCTGAGTACTCTCCTGT
Ci              ------------------------------------------------------------
Cii             ------------------------------------------------------------
Ciii            ------------------------------------------------------------
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Hs_PMS2        -------------------------GAATGCGTGAATTGTTTTTATTCTCAGTAGGAGGC
Hs_PSD         -------------------------GAATGCGTGAATTGTTTTTATTCTCAGTAGGAGGC
Pt_PMS2        -------------------------GAATGCGTGAATTGTTTTTATTCTCAGTAGGAGGC
Pt_PSD         GTAGTTTGCTGAGTACTCTCCTGTGGAATGCGTGAATTGTTTTTATTCTCAGTAGGAGGC
Ci             -------------------------GAATGCGTGAATTGTTTTTATTCTCAGTAGGAGGC
Cii            -------------------------GAATGCGTGAATTGTTTTTATTCTCAGTAGGAGGC
Ciii           -------------------------GAATGCGTGAATTGTTTTTATTCTCAGTAGGAGGC


Hs_PMS2        AATGGTAATAATAGACATTTAGTAAGCTACTTTATATCCCTTCCCTGTTCCTCTTAATAG
Hs_PSD         AATGGTAATAATAGACATTTAGTAAGCTACTTTATATCCCTTCCCTGTTCCTCTTAATAG
Pt_PMS2        AATGGTAATAATAGACATTTAGTAAGCTACTTTATATCCCTTCCCTGTTCCTCTTAATAG
Pt_PSD         AATGGTAATAATAGACATTTAGTAAGCTACTTTATATCCCTTCCCTGTTCCTCTTAATAG
Ci             AATGGTAATAATAGACATTTAGTAAGCTACTTTATATCCCTTCCCTGTTCCTCTTAATAG
Cii            AATGGTAATAATAGACATTTAGTAAGCTACTTTATATCCCTTCCCTGTTCCTCTTAATAG
Ciii           AATGGTAATAATAGACATTTAGTAAGCTACTTTATATCCCTTCCCTGTTCCTCTTAATAG


Hs_PMS2        AGGTTTTTTGTTTTTGTGTTTTTGAGACAGAGTTTCACTCTTTCGCCCATACTGGAGTGC
Hs_PSD         AGGTTTTTTGTTTTTGTGTTTTTGAGACAGAGTTTCACTCTTTCGCCCATACTGGAGTGC
Pt_PMS2        AGGTTTTTTGTTTTTGTGTTTTTGAGACAGAGTTTCACTCTTTCGCCCATACTGGAGTGC
Pt_PSD         AGGTTTTTTGTTTTTGTGTTTTTGAGACAGAGTTTCACTCTTTTGCCCATACTGGAGTGC
Ci             AGGTTTTTTGTTTTTGTGTTTTTGAGACAGAGTTTCACTCTTTCGCCCATACTGGAGTGC
cii            AGGTTTTTTGTTTTTGTGTTTTTGAGACAGAGTTTCACTCTTTCGCCCATACTGGAGTGC
Ciii           AGGTTTTTTGTTTTTGTGTTTTTGAGACAGAGTTTCACTCTTTCGCCCATACTGGAGTGC


Hs_PMS2        AGTGATGTGATCTCGGCTTACTGCAACCTCTGCCTCTCGGGTTCAAGTGATTCTCCTGCC
Hs_PSD         AGTGATGTGATCTCGGCTTACTGCAACCTCTGCCTCTCGGGTTCAAGTGATTCTCCTGCC
Pt_PMS2        AGTGATGTGATCTCGGCTCACTGCAACCTCTGCCTCTCGGGTTCAAGTGATTCTCCTGCC
Pt_PSD         AGTGATGTGATCTCGGCTCACTGCAACCTCTGCCTCTCGGGTTCAAGTGATTCTCCTGCC
Ci             AGTGATGTGATCTCGGCTTACTGCAACCTCTGCCTCTCGGGTTCAAGTGATTCTCCTGCC
Cii            AGTGATGTGATCTCGGCTTACTGCAACCTCTGCCTCTCGGGTTCAAGTGATTCTCCTGCC
Ciii           AGTGATGTGATCTCGGCTTACTGCAACCTCTGCCTCTCGGGTTCAAGTGATTCTCCTGCC


Hs_PMS2        TCAGCCTCCCGAGTAGCTGGGATTACAGGCACCCGCCACCACACCTGGCTAATTTTTGGA
Hs_PSD         TCAGCCTCCCGAGTAGCTGGGATTACAGGCACCCGCCACCACACCTGGCTAATTTTTGGA
Pt_PMS2        TCAGCCTCCCGAGTAGCTGGGATTACAGGCGCCTGCCACCACACCTGGCTAATTTTTGGA
Pt_PSD         TCAGCCTCCCGAGTAGCTGGGATTATAGGCGCCCGCCGCCACACCTGGCTAATTTTTGGA
Ci             TCAGCCTCCCGAGTAGCTGGGATTACAGGCACCCGCCACCACACCTGGCTAATTTTTGGA
Cii            TCAGCCTCCCGAGTAGCTGGGATTACAGGCACCCGCCACCACACCTGGCTAATTTTTGGA
Ciii           TCAGCCTCCCGAGTAGCTGGGATTACAGGCACCCGCCACCACACCTGGCTAATTTTTGGA


Hs_PMS2        TTTTTAATAGATAGGGAGTTTTGCC-ATGTTTGTCAGGCTGGTCTTGAACTCCTGACCTC
Pt_PMS2        TTTTTAATAGATAGGGAGTTTTGCCCATGTTTGTCAGGCTGGTCTTGAACTCCTGACCTC
Hs_PSD         TTTTTAATAGATAGGGAGTTTTGCC-ATGTTTGTCAGGCTGGTCTTGAACTCCTGACCTC
Pt_PSD         TTTTTAATAGATAGGGAGTTTTGCC-ATGTTTGTCAGGCTGGTCTTGAACTCCTGACCTC
Ci             TTTTTAATAGATAGGGAGTTTTGCC-ATGTTTGTCAGGCTGGTCTTGAACTCCTGACCTC
Cii            TTTTTAATAGATAGGGAGTTTTGCC-ATGTTTGTCAGGCTGGTCTTGAACTCCTGACCTC
Ciii           TTTTTAATAGATAGGGAGTTTTGCC-ATGTTTGTCAGGCTGGTCTTGAACTCCTGACCTC

                                                            PDS4
Hs_PMS2        AGGTGATCCACCAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCATGC
Hs_PSD         AGGTGATCCACCAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGC
Pt_PMS2        AGGTGATCCACCAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACTATGC
Pt_PSD         AGGTGATCCACCAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGC
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Ci              AGGTGATCCACCAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGC
Cii             AGGTGATCCACCAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGC
Ciii            AGGTGATCCACCAACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGC

                SNP1                                           ODS2
Hs_PMS2         CCGGCTGAGGTCTTGTATTTTTTAGCCATTCGGCAAAGATAACCTCTCATCTGTGACATT
Hs_PSD          CCGGCTGAGGTCTTGTATTTTTTAGCCATTCGGCAAAGATAACCTCTCATCTGTGACATT
Pt_PMS2         CCGGCTGAGGTCTTGTATTTTTTAGCCATTCGGCAAAGATAACCTCTCGTCTGTGACATT
Pt_PSD          CTGGCTGAGGTCTTGTATTTTTTAGCCATTCGGCAAAGATAACCTCTCGTCTGTGACATT
Ci              CTGGCTGAGGTCTTGTATTTTTTAGCCATTCGGCAAAGATAACCTCTCGTCTGTGACATT
Cii             CTGGCTGAGGTCTTGTATTTTTTAGCCATTCGGCAAAGATAACCTCTCGTCTGTGACATT
Ciii            CTGGCTGAGGTCTTGTATTTTTTAGCCATTCGGCAAAGATAACCTCTCGTCTGTGACATT


Hs_PMS2         TCAAGTTGGCCCAGGTAATCACAGACCACTTAGGGTCCCAGATGGACCACACTTCAAGAT
Hs_PSD          TCAAGTTGGCCCAGGTAATCACAGACCACTTAGGGTCCCAGATGGACCACACTTCAAGAT
Pt_PMS2         TCAAGTTGGCCCAGGTAATCACAGACCACTTAGGGTCTCAGATGGACCACACTTCAAGAT
Pt_PSD          TCAAGTTGGCCCAGGTAATCACAGACCACTTAGGGTCCCAGATGGACCACACTTCAAGAT
Ci              TCAAGTTGGCCCAGGTAATCACAGACCACTTAGGGTCCCAGATGGACCACACTTCAAGAT
Cii             TCAAGTTGGCCCAGGTAATCACAGACCACTTAGGGTCCCAGATGGACCACACTTCAAGAT
Ciii            TCAAGTTGGCCCAGGTAATCACAGACCACTTAGGGTCCCAGATGGACCACACTTCAAGAT


Hs_PMS2         TAAAGGATAAAGACCCAGTTCCACCCTGCCCTGCCAGCCCCTGTGTAGGGTGGCCCTGTT
Hs_PSD          TAAAGGATAAAGACCCAGTTCCACCCTGCCCTGCCAGCCCCTGTGTAGGGTGGCCCTGTT
Pt_PMS2         TAAAGGATGAAGACCCAGTTCCACCCTGCCCTGCCAGCCCCTGTGTAGGGTGGCCCTGTT
Pt_PSD          GAAAGGATGAAGACCCAGTTCCACCCTGCCCTGCCAGCCCCTGTGTAGGGTGGCCCTGTT
Ci              TAAAGGATAAAGACCCAGTTCCACCCTGCCCTGCCAGCCCCTGTGTAGGGTGGCCCTGTT
Cii             TAAAGGATAAAGACCCAGTTCCACCCTGCCCTGCCAGCCCCTGTGTAGGGTGGCCCTGTT
Ciii            TAAAGGATAAAGACCCAGTTCCACCCTGCCCTGCCAGCCCCTGTGTAGGGTGGCCCTGTT


Hs_PMS2         GACCTCTGTAGCTTTTCCCGTTCGTCTTCCCCTTGTTCCCTGTACTCAA-GCCTCT--CT
Hs_PSD          GACCTCTGTAGCTTTTCCCGTTCGTCTTCCCCTTGTTCCCTGTACTCAA-GCCTCT--CT
Pt_PMS2         GGCCTCTGTAGCTTTTCCTGTTCATCTTCCCCTTGTTCCCTGTACTCAATGCCTCTGGCT
Pt_PSD          GAC-TCTGTAGCTTTTCCCGTTCGTCTTCCCCTTGTTCCCTGTACTCAA-GCCTCT--CT
Ci              GACCTCTGTAGCTTTTCCCGTTCGTCTTCCCCTTGTTCCCTGTACTCAA-GCCTCT--CT
Cii             GACCTCTGTAGCTTTTCCCGTTCGTCTTCCCCTTGTTCCCTGTACTCAA-GCCTCT--CT
Ciii            GACCTCTGTAGCTTTTCCCGTTCGTCTTCCCCTTGTTCCCTGTACTCAA-GCCTCT--CT


Hs_PMS2         GGCTGTCTTTCTTTTTCCCTTG-GCAGGCCT--GATGAAT-CCCTATGTGGCCACTAAGC
Hs_PSD          GGCTGTCTTTCTTTTTCCCTTG-GCAGGCCT--GATGAAT-CCCTATGTGGCCACTAAGC
Pt_PMS2         GGCTGTCTTTCTTTTTCCCTTGAGCAGGCCTCTGATGAATGCCCTATGTGGCCACTAAGC
Pt_PSD          GGCTGTCTTTCTTTTTCCCTTG-GCAGGCCT--GATGAAT-CCCTATGTGGCCACTAAGC
Ci              GGCTGTCTTTCTTTTTCCCTTG-GCAGGCCT--GATGAAT-CCCTATGTGGCCACTAAGC
Cii             GGCTGTCTTTCTTTTTCCCTTG-GCAGGCCT--GATGAAT-CCCTATGTGGCCACTAAGC
Ciii            GGCTGTCTTTCTTTTTCCCTTG-GCAGGCCT--GATGAAT-CCCTATGTGGCCACTAAGC


Hs_PMS2         AGAATGAAGGATATCTTTATGTGTGGCTCTGCAAACATCAGCGGTCCATCCTGGGGCTTG
Hs_PSD          AGAATGAAGGATATCTTTATGTGTGGCTCTGCAAACATCAGCGGTCCATCCTGGGGCTTG
Pt_PMS2         AGAATGAAAGATATCTTTATGTGTGGCTCTGCAAACATCAGCGGTCCATCCTGGGGCTTG
Pt_PSD          AGAATGAAGGATATCTTTATGTGTGGCTCTGCAAACATCAGCGGTCCATCCTGGGGCTTG
Ci              AGAATGAAGGATATCTTTATGTGTGGCTCTGCAAACATCAGCGGTCCATCCTGGGGCTTG
Cii             AGAATGAAGGATATCTTTATGTGTGGCTCTGCAAACATCAGCGGTCCATCCTGGGGCTTG
Ciii            AGAATGAAGGATATCTTTATGTGTGGCTCTGCAAACATCAGCGGTCCATCCTGGGGCTTG
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Hs_PMS2         GCACAGATTGTTGTCCCTGTCTAGAATACTTGTCCTGCACCCTGCACCCACTTCTCCCCC
Hs_PSD          GCACAGATTGTTGTCCCTGTCTAGAATACTTGTCCTGCACCCTGCACCCACTTCTCCCCC
Pt_PMS2         GCACAGATTGTTGTCCCTGTCTAGAATACTTGTCCTGCACCCTGCACCCACTTCTCCCCC
Pt_PSD          GCACAGATTGTTGTCCCTGTCTAGAATACTTGTCCTGCACCCTGCACCCACTTCTCCCCC
Ci              GCACAGATTGTTGTCCCTGTCTAGAATACTTGTCCTGCACCCTGCACCCACTTCTCCCCC
Cii             GCACAGATTGTTGTCCCTGTCTAGAATACTTGTCCTGCACCCTGCACCCACTTCTCCCCC
Ciii            GCACAGATTGTTGTCCCTGTCTAGAATACTTGTCCTGCACCCTGCACCCACTTCTCCCCC


Hs_PMS2         GTTACCTGATTAACTCTCTTATCCCCGGACTCAGCTCAAAGGTCACTTCCTGACCCCAGG
Hs_PSD          GTTACCTGATTAACTCTCTTATCCCCGGACTCAGCTCAAAGGTCACTTCCTGACCCCAGG
Pt_PMS2         ATTACCTGATTAACTCTCTTATCCCCGGACTCAGCTCAAAGGTCACTTCCTGACCCCAGG
Pt_PSD          ATTACCTGATTAACTCTCTTATCCCCGGACTCAGCTCAAAGGTCACTTCCTGACCCCAGG
Ci              GTTACCTGATTAACTCTCTTATCCCCGGACTCAGCTCAAAGGTCACTTCCTGACCCCAGG
Cii             GTTACCTGATTAACTCTCTTATCCCCGGACTCAGCTCAAAGGTCACTTCCTGACCCCAGG
Ciii            GTTACCTGATTAACTCTCTTATCCCCGGACTCAGCTCAAAGGTCACTTCCTGACCCCAGG

Hs_PMS2         GTGAAGTCTCTCTATGACACTGGCTGCTTTTTCTTCCTGACCTTCCTGTCGTTTCTCATC
Hs_PSD          GTGAAGTCTCTCTATGACACTGGCTGCTTTTTCTTCCTGACCTTCCTGTCGTTTCTCATC
Pt_PMS2         GTGAAGTCTCTCTATGACACTGGCTGCTTTTTCTTCCTGACCTTCCTGTCATTTCTCATC
Pt_PSD          GTGAAGTCTCTCTATGACACTGGGTGCTTTTTCTTCCTGACCTTCCTGTCGTTTCTCATC
Ci              GTGAAGTCTCTCTATGACACTGGCTGCTTTTTCTTCCTGACCTTCCTGTCGTTTCTCATC
Cii             GTGAAGTCTCTCTATGACACTGGCTGCTTTTTCTTCCTGACCTTCCTGTCGTTTCTCATC
Ciii            GTGAAGTCTCTCTATGACACTGGCTGCTTTTTCTTCCTGACCTTCCTGTCGTTTCTCATC

                                                                  SNP2
Hs_PMS2         ATAATCGACTTGCCTGAGTATTTGCTCAACGTCTTTCTTCCCCGGTAATCTGTTGGCTCC
Hs_PSD          ATAATCGACTTGCCTGAGTATTTGCTCAACGTCTTTCTTCCCCGGTAATCTGTTGGCTCC
Pt_PMS2         ATAATTGACTTGCCGGAGTATTTGCTGAACGTCTTTCTTCCCCGGTAATCTGTTGGCTCC
Pt_PSD          ATAATTGACTTGCCTGAGTATTTGCTGAACGTCTTTCTTCCCCGGTAATCTGTTGGCTCC
Ci              ATAATCGACTTGCCTGAGTATTTGCTCAACGTCTTTCTTCCCCGGTAATCTGTTGGCTCC
Cii             ATAATCGACTTGCCTGAGTATTTGCTCAACGTCTTTCTTCCCCGGTAATCTGTTGGCTCC
Ciii            ATAATCGACTTGCCTGAGTATTTGCTCAACGTCTTTCTTCCCCGGTAATCTGTTGGCTCC


Hs_PMS2         AGGACCAAGCCTGTGTTTGCTCACCAGCTGTCTCCTGCCTTGAGCAGTGTTTGTCTTATC
Hs_PSD          AGGACCAAGCCTGTGTTTGCTCACCAGCTGTCTCCTGCCTTGAGCAGTGTTTGTCTTATC
Pt_PMS2         AGGACCAAGCCTGTGTTTGCTCACCAGCTGTCTCCTGCCTTGAGCAGTGTTTGTCTTATC
Pt_PSD          AGGACCAAGCCTGTGTTTGCTCACCAGCTGTCTCCTGCCTTTAGCAGTGTTTGTCTTATC
Ci              AGGACCAAGCCTGTGTTTGCTCACCAGCTGTCTCCTGCCTTGAGCAGTGTTTGTCTTATC
Cii             AGGACCAAGCCTGTGTTTGCTCACCAGCTGTCTCCTGCCTTGAGCAGTGTTTGTCTTATC
Ciii            AGGACCAAGCCTGTGTTTGCTCACCAGCTGTCTCCTGCCTTGAGCAGTGTTTGTCTTATC


Hs_PMS2         CAGCACTCAGGACCAGATGCAGTGGCTCACACTCGTAATCCCAGCACTTTGGGAGGCTGA
Hs_PSD          CAGCACTCAGGACCAGATGCAGTGGCTCACACTCGTAATCCCAGCACTTTGGGAGGCTGA
Pt_PMS2         CAGCACTCAGGACCAGATGCAGTGGCTCACACTTGTAATCCCAGCACTTTGGGAGGCTGA
Pt_PSD          CAGCACTCAGGACCGGATGCAGTGGCTCACACTTGTAATCCCAGCACTTTGGGAGGCTGA
Ci              CAGCACTCAGGACCAGATGCAGTGGCTCACACTCGTAATCCCAGCACTTTGGGAGGCTGA
Cii             CAGCACTCAGGACCAGATGCAGTGGCTCACACTCGTAATCCCAGCACTTTGGGAGGCTGA
Ciii            CAGCACTCAGGACCAGATGCAGTGGCTCACACTCGTAATCCCAGCACTTTGGGAGGCTGA

                                                                        SNP3
Hs_PMS2         AGTGGAAGGATCGCTTGAGCCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGTGAGACCC
Hs_PSD          AGTGGAAGGATCGCTTGAGCCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGTGAGACCC
Pt_PMS2         AGTGGAAGGATCCCTTGAGCCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGTGAGACCC
Pt_PSD          AGTGGAAGGATCGCTTGAGCCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGTGAGACCC
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Ci              AGTGGAAGGATCGCTTGAGCCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGTGAGACCC
Cii             AGTGGAAGGATCGCTTGAGCCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGTGAGACCC
Ciii            AGTGGAAGGATCGCTTGAGCCCAGGAGTTTGAGAGCAGCCTGGGCAACATAGTGAGACCC

                                                                PDSviii
Hs_PMS2         TGTCTCTATCTTTGAAAAAAATAACGAAAGGTTAAAAAAAAA------CAAACAGTAAAT
Hs_PSD          TGTCTCTATCTTTGAAAAAAATAACGAAAGGTTAAAAAAAAAAA---GCACTCAGTAAAT
Pt_PMS2         TGTCTCTATCTTTGAAAAAAATAACAAAAAGTTAAAAAAAAAAAA--GCACTCAGTAAAT
Pt_PSD          TGTCTCTATCTTTGAAAAAAATAACAAAAGGTTAAAAAAAAAAAAAAACACTCAGTAAAT
Ci              TGTCTCTATCTTTGAAAAAAATAACGAAAGGTTAAAAAAAAAAR------CTCAGTAAAT
Cii             TGTCTCTATCTTTGAAAAAAATAACGAAAGGTTAAAAAAAAAAR------CTCAGTAAAT
Ciii            TGTCTCTATCTTTGAAAAAAATAACGAAAGGTTAAAAAAAAAAR------CTCAGTAAAT

                           PDSix                PDSx
Hs_PMS2         CCAGGAGGAGAGAGGGATGGAGATATAATACAGGCAGAGGAAGGAACAGGATAGCAAAAT
Hs_PSD          CCAGGAGGAGAGAAGGATGGAGATATAATACAGGGAGAGGAAGGAACAGGATAGCAAAAT
Pt_PMS2         CCAGGAGGAGAGAAGGATGGAGATATAATACAGGCAGAGGAAGGAACAGGATAGCAACAT
Pt_PSD          CCAGGAGGAGAGAAGGATGGAGATATAATACAGGCAGAGGAAGGAACAGGATAGCAAAAT
Ci              CCAGGAGGAGAGAAGGATGGAGATATAATACAGGGAGAGGAAGGAACAGGATAGCAAAAT
Cii             CCAGGAGGAGAGAAGGATGGAGATATAATACAGGGAGAGGAAGGAACAGGATAGCAAAAT
Ciii            CCAGGAGGAGAGAAGGATGGAGATATAATACAGGGAGAGGAAGGAACAGGATAGCAAAAT
                 PDSxi
Hs_PMS2         AAAAGCTGTCTGTTCATTCTGTTTACAAATGCTGGCAATGACCTAACCCAGTGTTTCAAA
Hs_PSD          AAATGCTGTCTGTTCATTCTGTTTACAAATGCTGGCAATGACCTAACCCAGTGTTTCAAA
Pt_PMS2         AAATGCTGTCTGTTCAT---------AAATGCTGGCAATGACCTAACCCAGTGTTTCAAA
Pt_PSD          AAATGCTGTCTGTTCATTCTGTTTACAAATGCTGGCAATGACCTAACCCAGTGTTTCAAA
Ci              AAATGCTGTCTGTTCATTCTGTTTACAAATGCTGGCAATGACCTAACCCAGTGTTTCAAA
Cii             AAATGCTGTCTGTTCATTCTGTTTACAAATGCTGGCAATGACCTAACCCAGTGTTTCAAA
Ciii            AAATGCTGTCTGTTCATTCTGTTTACAAATGCTGGCAATGACCTAACCCAGTGTTTCAAA

                  PDSxii      PDSxiii
Hs_PMS2         TTCTGTATTAGAAGGAGGAAAAATAGCATTTTTGTGATACTGTTATCCTTAAGGAAAGGA
Hs_PSD          TTCTCTATTAGAAGGAGAAAAAATAGCATTTTTGTGATACTGTTATCCTTAAGGAAAGGA
Pt_PMS2         TTCTCTATTAGAAGGAGAAAAAATAGCATTTTTGTGATATTGTTATCCTTAAGGAAAGGA
Pt_PSD          TTCTGTATTAGAAGGAGGAAAAATAGCATTTTTGTGATATTGTTATCCTTAAGGAAAGGA
Ci              TTCTCTATTAGAAGGAGAAAAAATAGCATTTTTGTGATACTGTTATCCTTAAGGAAAGGA
Cii             TTCTCTATTAGAAGGAGAAAAAATAGCATTTTTGTGATACTGTTATCCTTAAGGAAAGGA
Ciii            TTCTCTATTAGAAGGAGAAAAAATAGCATTTTTGTGATACTGTTATCCTTAAGGAAAGGA

                     SNP4
Hs_PMS2         TTCAGAAAAAGTGGGAGTCATTGGCGTGGCAGGCTGAGGAAAAAGCAAACTACTTTTGTA
Hs_PSD          TTCAGAAAAAGTGGGAGTCATTGGCGTGGCAGGCTGAGGAAAAAGCAAACTACTTTTGTA
Pt_PMS2         TTCAGAAAAAGTGGGAGTCATTGGGGTGGCAGGCTGAGGAAAAAGCAAACTACTTTTGTA
Pt_PSD          TTCAGAAAAAGTGGGAGTCATTGGCGTGGCAGGCTGAGGAAAAAGCAAACTACTTTTGTA
Ci              TTCAGAAAAAGTGGGAGTCATTGGCGTGGCAGGCTGAGGAAAAAGCAAACTACTTTTGTA
Cii             TTCAGAAAAAGTGGGAGTCATTGGCGTGGCAGGCTGAGGAAAAAGCAAACTACTTTTGTA
Ciii            TTCAGAAAAAGTGGGAGTCATTGGCGTGGCAGGCTGAGGAAAAAGCAAACTACTTTTGTA

                     PDSxiv                    PDSxv
Hs_PMS2         GCTACTTGAACTTTTTTTTTTTTTTT----GAGACAGAGTCTTGCCCTGTTGCCCAGGCT
Hs_PSD          GCTACTTTAACTTTTTTTTTTTTTTTT---GAGTCAGAGTCTTGCCCTGTTGCCCAGGCT
Pt_PMS2         GCTACTTTAACTTTTTTTTTTTTTTT----GAGTCAGAGTCTTGCCCTGTTGCCCAGCCT
Pt_PSD          GTTACTTTAACTTTTTTTTTTTTTTTTTTTGAGACAGGGTCTTGCCCTGTTGCCCAGGCT
Ci              GCTACTTGAACTTTTTTTTTTTTTTT----GAGTCAGAGTCTTGCCCTGTTGCCCAGGCT
Cii             GCTACTTGAACTTTTTTTTTTTTTTT----GAGTCAGAGTCTTGCCCTGTTGCCCAGGCT
Ciii            GCTACTTGAACTTTTTTTTTTTTTTT----GAGTCAGAGTCTTGCCCTGTTGCCCAGGCT
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Hs_PMS2         GGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTC
Hs_PSD          GGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTC
Pt_PMS2         GGAGTGCAGTGGTGTGATCTCAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTC
Pt_PSD          GGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTC
Ci              GGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTC
Cii             GGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTC
Ciii            GGAGTGCAGTGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTC


Hs_PMS2         TAGTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGAGCCACCACTTCCAGCTAAT
Pt_PMS2         TAGTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGAGCCACCACTTCCAGCTAAT
Hs_PSD          TAGTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGAGCCACCACTTCCAGCTAAT
Pt_PSD          TAGTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGAGCCACCACTTCCAGCTAAT
Ci              TAGTGCCTCAGCCTCCCGAGTAGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Cii             TAGTGCCTCAGCCTCCCGAGTAGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Ciii            TAGTGCCTCAGCCTCCCGAGTAGCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

                        PDSxvi
Hs_PMS2         TTTTGTTTTTATGGGTGTTTTTTTTTTTTTTTTTTTTTT-----GAGACAGAGTCTTGTT
Hs_PSD          TTTTGTTTTTGTGGGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTTGTT
Pt_PMS2         TTTTGTTTTTGTGGGTTTTTTTTTTTTTTTTTTTT---------GAGACAGAGTCTTGTC
Pt_PSD          TTTTGTTTTTGTGGGTGTTTTTTTTTTTTTTTTTT---------GAGACAGAGTCTTGTT
Ci              NNNNNNNNNNNNNNGTGTTTTTTTTTTTTTTTTTTTTTT-----GAGACAGAGTCTTGTT
Cii             NNNNNNNNNNNNNNNNNTTTTTTTTTTTTTTTTTTTTTT-----GAGACAGAGTCTTGTT
Ciii            NNNNNNNNNNNNNNGTGTTTTTTTTTTTTTTTTTTTTTT-----GAGACAGAGTCTTGTT

Hs_PMS2         GTGTCGCCCAGGCTGGAGTACAGTGGCGTGATCTTGGCTCTCACTACAACCTCTGCCTCC
Hs_PSD          GTGTCGCCCAGGCTGGAGTACAGTGGCGTGATCTTGGCTCTCACTACAACCTCTGCCTCC
Pt_PMS2         ATGTCATCCAGGCTGGAGTATAGTGGCGTGATCTTGGCT--CACTGCAACCTCTGCCTCC
Pt_PSD          GTGTGACCCAGGCTGGAGTATAGTGGTGTGATCTTGGCTCTCACTGCAACCTCTGCCTCC
Ci              GTGTCGCCCAGGCTGGAGTACAGTGGCGTGATCTTGGCTCTCACTACAACCTCTGCCTCC
Cii             GTGTCGCCCAGGCTGGAGTACAGTGGCGTGATCTTGGCTCTCACTACAACCTCTGCCTCC
Ciii            GTGTCGCCCAGGCTGGAGTACAGTGGCGTGATCTTGGCTCTCACTACAACCTCTGCCTCC


Hs_PMS2         CTCCTGGGTTCAAACGAATCTCATGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGTG
Hs_PSD          CTCCTGGGTTCAAACGAATCTCATGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGTG
Pt_PMS2         ----TGGGTTCAAACGAATCTCCTGCCTAAGCCTCCCAAGGAGCTGGGACTACAGGCGTG
Pt_PSD          ----TGGGTTCAAACGAATCTCCTGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGTG
Ci              CTCCTGGGTTCAAACGAATCTCATGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGTG
Cii             CTCCTGGGTTCAAACGAATCTCATGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGTG
Ciii            CTCCTGGGTTCAAACGAATCTCATGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGTG

                                           SNP5         PDSxvii  SNP6 PDSxviii
Hs_PMS2         CGCCAC-CATGCC-TGGCCTAATTTTTATATTTTTAGTAGAGAGAGTGTTTCGCTGTGTT
Hs_PSD          CGCCAC-CATGCC-TGGCCTAATTTTTATATTTTTAGTAGAGAGAGGGTTTCGCCGTGTT
Pt_PMS2         CGCCACGCATGCCCTGGCTTAATTTTTATATTTTTAGTAGAGAGAGGGTTTCGCCGTGTT
Pt_PSD          CGCCACGCATGCCCTGGCTTAATTTTTATATTTTTAGTAGAGAGAGGGTTTCGCCGTGTT
Ci              CGCCAC-CATGCC-TGGCCTAATTTTTATATTTTTAGTAGAGAGAGGGTTTCGCCGTGTT
Cii             CGCCAC-CATGCC-TGGCCTAATTTTTATATTTTTAGTAGAGAGAGGGTTTCGCCGTGTT
Ciii            CGCCAC-CATGCC-TGGCCTAATTTTTATATTTTTAGTAGAGAGAGGGTTTCGCCGTGTT

                   PDSxix PDSxx                     PDSxxi PDSxxii
Hs_PMS2         GACCAGGCCGGTCTCAAACTCCTGGCCTCAAGAGATCTGCCTGCCTCGGGCTCCTAAAGT
Hs_PSD          GACCAGGCTGATCTCAAACTCCTGGCCTCAAGAGATCTGCCTGCCTCAGCCTCCTAAAGT
Pt_PMS2         GACCAGGCTGATCTCAAACTCCTGGCCTCAAGAGATCTGCCTGCCTCGGGCTCCTAAAGT
Pt_PSD          GACCAGGCTGATCTCAAACTCCTGGCCTCAAGAGATCTGCCTGCCTCGGGCTCCTAAAGT
Ci              GACCAGGCTGATCTCAAACTCCTGGCCTCAAGAGATCTGCCTGCCTCAGCCTCCTAAAGT
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Cii             GACCAGGCTGATCTCAAACTCCTGGCCTCAAGAGATCTGCCTGCCTCAGCCTCCTAAAGT
Ciii            GACCAGGCTGATCTCAAACTCCTGGCCTCAAGAGATCTGCCTGCCTCAGCCTCCTAAAGT

                                                        PDSxxiii
Hs_PMS2         GCTGAGATTACAGGCGTGAGCCACCGCACCTGGCCTGTAGCTACTTTAACTTCTAAAAAG
Hs_PSD          GCTGAGATTACAGGCGTGAGCCACCGCACCTGGCCTGTAGCTATTTTAACTTCTAAAAAG
Pt_PMS2         GCTGAGATTACAGGTGTGAGCCACCGCACCCGGCCTGTAGCTATTTTAACTTCTAAAAAG
Pt_PSD          GCTGAGATTACAGGTGTGAGCCACCGCACCCGGCCTGTAGCTATTTTAACTTCTAAAAAG
Ci              GCTGAGATTACAGGCGTGAGCCACCGCACCTGGCCTGTAGCTATTTTAACTTCTAAAAAG
Cii             GCTGAGATTACAGGCGTGAGCCACCGCACCTGGCCTGTAGCTATTTTAACTTCTAAAAAG
Ciii            GCTGAGATTACAGGCGTGAGCCACCGCACCTGGCCTGTAGCTATTTTAACTTCTAAAAAG

                    SNP7
Hs_PMS2         AACTTTAAGAAAGAGAAAATTAAAAGGAACTTCTCAGGAAGTTTTGTGACACTTAGCTGA
Hs_PSD          AACTTTAAGAAAGAGAAAATTAAAAGGAACTTCTCAGGAAGTTTTGTGACACTTAGCTGA
Pt_PMS2         AACTTTAAGAAAGAGAAAATTAAAAGGAACTTCTCAGGAAGTTTTGTGACACTTAGCTGA
Pt_PSD          AACTTTAAGAAAGAGAAAATTAAAAGGAACTTCTCAGGAAGTTTTGTGACACTTAGCTGA
Ci              AACTTTAAGAAAGAGAAAATTAAAAGGAACTTCTCAGGAAGTTTTGTGACACTTAGCTGA
Cii             AACTTTAAGAAAGAGAAAATTAAAAGGAACTTCTCAGGAAGTTTTGTGACACTTAGCTGA
Ciii            AACTTTAAGAAAGAGAAAATTAAAAGGAACTTCTCAGGAAGTTTTGTGACACTTAGCTGA

          PDSxxiv PDSxxv  PDSxxvi
Hs_PMS2         GTAGTGTTGTTATTTGTGTTGTTATTTTGACATGAATTCAAAATACAGTATTGTTGTTTT
Hs_PSD          ATTATGTTGTTATTCGTGTTGTTATTTTGACATGAATTCAAAATACAGTATTGTTGTTTT
Pt_PMS2         ATAATGTTGTTATTCGTGTTGTTATTTTGACATGAATTCAAAATACAGTATTGTTGTTTT
Pt_PSD          ATAATGTTGTTATTCGTGTTGTTATTTTGACATGAATTCAAAATACAGTATTGTTGTTTT
Ci              ATTATGTTGTTATTCGTGTTGTTATTTTGACATGAATTCAAAATACAGTATTGTTGTTTT
Cii             ATTATGTTGTTATTCGTGTTGTTATTTTGACATGAATTCAAAATACAGTATTGTTGTTTT
Ciii            ATTATGTTGTTATTCGTGTTGTTATTTTGACATGAATTCAAAATACAGTATTGTTGTTTT
                                   SNP8
Hs_PMS2         CATTTCATTTCTGCTGTAAAGCTAAATGTTTGACTTCAGGATATGGTTTGAATCATTTTT
Hs_PSD          CATTTCATTTCTGCTGTAAAGCTAAATGTTTGACTTCAGGATATGGTTTGAATCATTTTT
Pt_PMS2         CATTTCATTTCTGCTGTAAAGCTAAATGTTTGACTTCAGGATATGGTTTGAATCATTTCT
Pt_PSD          CATTTCATTTCTGCTGTAAAGCTAAATGTTTGACTTCAGGATATGGTTTGAATCATTTCT
Ci              CATTTCATTTCTGCTGTAAAGCTAAATGTTTGACTTCAGGATATGGTTTGAATCATTTTT
Cii             CATTTCATTTCTGCTGTAAAGCTAAATGTTTGACTTCAGGATATGGTTTGAATCATTTTT
Ciii            CATTTCATTTCTGCTGTAAAGCTAAATGTTTGACTTCAGGATATGGTTTGAATCATTTTT


Hs_PMS2         GTGTTTTTCAG
Hs_PSD          GTGTTTTTCAG
Pt_PMS2         GTGTTTTTCAG
Pt_PSD          GTGTTTTTCAG
Ci              GTGTTTTTCAG
Cii             GTGTTTTTCAG
Ciii            GTGTTTTTCAG
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Supp. Table S1. List of primers

Name	Location	Orientation	PCR/Seq	Sequence
cDNA sequencing of *PMS2* and *PMS2CL*				
PMS2B_F[1]	Ex 11	Fwd	PCR	5’-CAGCCACTGCTGGATGTTGAAGG-3’
PMS2B_R[1]	Ex 15	Rev	PCR	5’-GGTTTGAAAAGGTTCTCAAGATCAC-3’
PMS2CLB_F	Ex 9/Ex 11	Fwd	PCR	5’-CTTAACATTTCTGTTGATTCAGGTAAC-3’
PMS2A_R	Ex 11	Rev	Seq	5’-CTTTCTCCTGAGAGTCCACATG-3’
PMS2_6	Ex 11	Fwd	Seq	5’-TCTGACAAAGGCGTCCTGAG-3’
PMS2_7	Ex 11	Fwd	Seq	5’-TCTCAGGTTGATGTAGCTGTG-3’
PMS2_8	Ex 12/Ex13	Fwd	Seq	5’-GGCTCATAGCACCTCAGACTCTC-3’
ODS1-specific PCR				
PMS2in12_ODS1AF	IVS 12	Fwd	PCR	5’-CCACTGAACCTGTGTAGTTTA-3’
PMS2in12_8F	IVS 12	Fwd	PCR	5’-CTGCAGAATTTGGTATTTCTCTC-3’
PMS2in12_8R	IVS 12	Rev	PCR	5’-CTATTAAGAGGAACAGGGAAGGG-3’
ODS2-specific PCR				
PMS2in12_ODS2GR	IVS 12	Rev	PCR	5’-CCAACTTGAAATGTCACAGAC-3’
PMS2in12_PDS2GF	IVS 12	Fwd	PCR	5’-CAAATGTAAAAAATTAGTCAGACTTG-3’
PMS2in12_PDS2CF	IVS 12	Fwd	PCR	5’-CAAATGTAAAAAATTAGTCAGACTTC-3’
***17C-specific PCR**				
PMS2_*17CF	Ex 15	Fwd	PCR	5’-AACTGACCGTAGTCACTGTATGC-3’
PMS2_15_1F	Ex 15	Fwd	PCR	5’-GAAGGCCAACCATGAGACAC-3’
PMS2B_R[1]	Ex 15	Rev	PCR	5’-GGTTTGAAAAGGTTCTCAAGATCAC-3’
H1 allele specific multiplex PCR				
PMS2in12_ODS1AF	IVS 12	Fwd	PCR	5’-CCACTGAACCTGTGTAGTTTA-3’
PMS2in12_ODS2GR	IVS 12	Rev	PCR	5’-CCAACTTGAAATGTCACAGAC-3’
PMS2_*17CF	Ex 15	Fwd	PCR	5’-AACTGACCGTAGTCACTGTATGC-3’
PMS2B_R[1]	Ex 15	Rev	PCR	5’-GGTTTGAAAAGGTTCTCAAGATCAC-3’
PMS2in14_1F	IVS 14	Fwd	PCR	5’-GAAGTGGAATGAATAACCTGACAG-3’
Characterization of the 5’ breakpoint				
PMS2c2253G_R	Ex 13	Rev	PCR/Seq	5’-CCATTTTCATCGATAACAAAATCG-3’
PMS2c2253A_R	Ex 13	Rev	PCR/Seq	5’-CATTTTCATCGATAACAAAATCA-3’
LRPCR4_Fwd[2]	IVS 12	Fwd	PCR/Seq	5’-AAATTAGTCAGACTTGATGGTGTG-3’
PMS2in12_PDS2CF	IVS 12	Fwd	PCR/Seq	5’-CAAATGTAAAAAATTAGTCAGACTTC-3’
PMS2in12_ODS1AF	IVS 12	Fwd	PCR/Seq	5’-CCACTGAACCTGTGTAGTTTA-3’
PMS2in12_2F	IVS 12	Rev	Seq	5’-CACCACACCTGGCTAATTTTTG-3’
PMS2in12_2R	IVS 12	Fwd	Seq	5’-CTGGCAGGGCAGGGTGGAAC-3’
PMS2in12_univ.1F	IVS 12	Fwd	Seq	5’-ATACTTGTCCTGCACCCTGC-3’
PMS2in12_univ.2F	IVS 12	Fwd	Seq	5’-AGGCAGAGGAAGGAACAGG-3’
PMS2in12_univ.3R	IVS 12	Rev	Seq	5’-CAAAAATTAGCTGGAAGTGG-3’
Characterization of the 3’ breakpoint				
PMS2_*17CF	Ex 15	Fwd	PCR	5’-AACTGACCGTAGTCACTGTATGC-3’
LRPCR4_Rev[2]	3’ UTR	Rev	PCR	5’-CTTCCATCTCCAAAACCAGCAAGA-3’
PMS2_15_2F	3’ UTR	Fwd	Seq	5’-GTGTGTCCAGGCAAGAACAC-3’
PMS2_15_2R	3’ UTR	Rev	Seq	5’-CTGTTATCCTGCCACAGCTC-3’
c.2340T-specific PCR				
Clend14F[2]	IVS 13	Fwd	PCR	5’-GGTCTGTATCTCCTGACCTCATGAT-3’
PMS2c2340_TR	Ex 14	Rev	PCR	5’-CAGTTCATCGACGTCCTGA-3’

PCR=Primer for PCR, Seq = Primer for sequencing, IVS= Intron, Ex=Exon,[1] Etzler et al., 2008 (note that primer PMS2B_R contained an erroneous sequence in Etzler et al., 2008), [2] Primer designed by Clendenning et al. (2006)

Supp. Table S2. Genotypes in PMS2 exons 11-15 of 150 individuals from 3 different ethnic backgrounds.

All sites in exons 11-15 showing sequence variations in 150 control individuals from three different ethnic backgrounds, i.e.Caucasians (C), Hispanics (H) and African-Americans (A), are listed. SNPs listed in dbSNP as polymorphic variants in the gene are indicated with +. C to T transitions at CpG-dinucleotides are indicated with a star. Allele frequencies of the SNPs in this cohort are given at the bottom of the table. Individuals are named according to their ethnic origin with initials C, H or A and consecutive Arabic numbers.

Exon	11												13	14		15							
nucleotide position	c.1266G>A (p.A423T)	c.1408C>T (p.P470S)	c.1437C>G (p.H479Q)	c.1454C>A (p.T485K)	c.1488C>T (p.H496H)	c.1531A>C (p.T511P)	c.1532C>T (p.T511M)	c.1557T>C (p.Y519Y)	c.1621G>A (p.E541K)	c.1711C>A (p.L571I)	c.1789A>T (p.T597S)	c.1866G>A (p.M622I)	c.2253T>C (p.F571F)	c.2324A>G (p.N775S)	c.2340C>T (p.P780P)	c.2466T>C (p.L822L)	c.2570G>C (p.G857A)	c.*17G>C (3'UTR)	c.*92dupA (3'UTR)	Deduced haplotype as given in table S3		ODS 1-specific PCR	c.*17-specific PCR
CpG					*		*						*										
dbSNP	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+				
ID																				Allele 1	Allele 2		
A02	G	C	C	C	C	A	C	T	G	C	A	G	C	G	Y	Y	G	S	A,A	H1-A	H1-A	+	+
A31	G	C	C	C	C	A	C	T	R	C	A	G	Y	R	C	Y	G	G	(-),A	H1-A	N	+	-
A40	G	C	C	C	C	A	C	T	G	C	A	G	Y	R	C	Y	S	G	(-),A	H1-A	N	+	-
C28	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
C47	G	C	C	C	C	A	C	T	R	C	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
C06	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
C08	G	C	C	M	C	A	C	T	G	C	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
H02	G	C	C	C	C	A	C	T	G	C	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
H37	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
A45	G	C	C	C	C	A	C	T	G	C	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
C17	G	C	C	C	C	A	C	T	G	C	A	G	Y	R	Y	Y	G	G	(-),A	H1-A	H2	+	-
H20	G	C	C	C	C	A	C	T	G	M	A	G	Y	R	Y	T	S	G	(-),(-)	H1-A	N	+	-
A12	G	Y	C	C	C	A	C	T	G	M	A	G	Y	R	Y	Y	G	S	A,A	H1-A	H3	+	+
A34	G	C	C	C	C	A	C	T	R	M	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
A46	G	C	C	C	Y	A	C	T	G	M	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
C16	G	C	C	C	C	A	C	T	G	M	A	G	Y	R	Y	Y	G	S	(-),A	H1-A	N	+	+
A17	G	C	C	C	C	A	Y	T	G	C	A	G	C	G	C	Y	G	G	A,A	H1-B	H1-C2	+	-
A36	G	Y	C	C	C	A	Y	T	G	C	A	G	Y	R	C	C	G	G	A,A	H1-B	H2	+	-

A50	G	Y	C	C	C	A	Y	T	G	C	A	G	Y	R	C	T	G	G	(-),A	H1-B	N	+	-
A06	G	Y	C	C	C	A	Y	T	G	C	A	G	Y	R	C	T	G	G	(-),A	H1-B	N	+	-
H36	R	Y	C	C	C	A	Y	T	G	C	A	G	Y	R	C	Y	G	G	A,A	H1-B1	H3	+	-
A13	R	C	C	C	C	A	Y	T	G	C	A	G	Y	R	C	Y	G	G	(-),A	H1-B1	N	+	-
A04	G	C	C	C	Y	A	C	T	G	C	A	G	Y	R	C	T	G	G	(-),A	H1-C	N	+	-
A22	G	C	C	C	C	A	C	T	G	C	A	G	Y	R	C	T	S	G	(-),A	H1-C1	N	+	-
A30	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	C	Y	G	G	A,A	H1-C1	H3	+	-
A43	G	C	C	C	C	A	C	T	G	C	A	G	Y	R	C	T	G	G	(-),A	H1-C1	N	+	-
A35	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	C	Y	G	G	A,A	H1-C2	H3	+	-
A33	G	Y	C	C	C	A	C	T	G	C	A	G	C	G	C	Y	G	G	A,A	H1-C2	H1-C2	+	-
A11	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	C	T	G	G	A,A	H1-C2	H3	+	-
A28	G	C	C	M	C	A	C	T	G	C	A	G	Y	R	C	T	G	G	(-),A	H1-C2	N	+	-
A29	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	C	T	G	G	(-),A	H1-C2	N	+	-
A08	G	Y	C	C	C	A	C	T	G	C	A	G	Y	R	C	T	G	G	(-),A	H1-C2	N	+	-
H17	G	Y	C	C	C	A	Y	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	+	-
A38	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	S	G	(-),A	H2	N	-	-
A07	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	S	G	(-),A	H2	N	-	-
C31	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	S	G	(-),A	H2	N	-	-
C50	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	S	G	(-),A	H2	N	-	-
H41	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	S	G	(-),A	H2	N	-	-
A16	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
A23	G	C	S	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
A25	G	C	S	C	Y	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C11	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C18	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C19	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C21	G	Y	C	M	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C23	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C32	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C34	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C35	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C36	G	Y	C	C	C	A	C	T	G	C	A	R	T	A	C	Y	G	G	(-),A	H2	N	-	-
C37	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C03	G	T	C	C	C	A	C	T	G	C	W	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C41	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C04	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C09	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H10	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H11	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H12	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H24	G	Y	C	M	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H29	G	Y	C	M	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H33	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-

H34	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H40	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H42	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
H47	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	(-),A	H2	N	-	-
C10	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	C	G	G	A,A	H2	H2	-	-
H16	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	C	G	G	A,A	H2	H2	-	-
H07	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	A,A	H2	H3	-	-
H09	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	Y	G	G	A,A	H2	H3	-	-
C38	G	C	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),A	H3	N	-	-
A20	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
A24	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
A26	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
A37	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
A03	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
A44	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
C01	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
C26	G	C	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
H23	G	C	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
H32	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
H38	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
H03	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
H43	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
H44	G	Y	C	M	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),A	H3	N	-	-
C29	G	Y	C	C	C	R	C	T	G	C	A	G	T	A	C	Y	G	G	(-),(-)	N	N	-	-
H26	G	C	C	M	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A41	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	N	G	(-),(-)	N	N	-	-
A10	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
A01	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
A27	G	C	C	C	C	A	C	Y	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
A39	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
A42	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
A47	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
A05	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
C24	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
C02	G	C	C	M	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
C39	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
C40	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
C43	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
H27	G	Y	C	C	C	A	C	T	G	C	W	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
H30	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
H39	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
H50	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
H46	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	C	G	(-),(-)	N	N	-	-

A49	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	S	G	(-),(-)	N	N	-	-
A14	G	C	C	C	Y	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A15	G	Y	C	C	C	R	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A18	G	C	C	M	C	A	C	Y	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A19	G	C	C	C	Y	A	C	Y	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A21	G	C	C	C	Y	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A32	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A48	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
A09	G	Y	C	C	C	A	C	Y	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C12	G	Y	C	C	C	R	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C13	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C14	G	C	C	C	C	R	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C07	G	C	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C15	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C20	G	Y	C	C	C	A	C	T	G	C	A	R	T	A	C	T	G	G	(-),(-)	N	N	-	-
C22	G	Y	C	C	C	A	C	T	G	C	W	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C25	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C27	G	C	C	C	C	R	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C30	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C33	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C42	G	Y	C	C	C	A	C	T	G	C	A	R	T	A	C	T	G	G	(-),(-)	N	N	-	-
C44	G	Y	C	C	C	R	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C45	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C46	G	C	C	C	C	R	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C48	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C49	G	Y	C	C	C	R	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
C05	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H13	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H14	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H15	G	C	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H18	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H19	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H01	G	Y	C	M	C	A	C	T	G	C	W	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H21	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H22	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H25	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H28	G	Y	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H31	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H35	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H45	G	Y	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H48	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H49	G	C	C	C	C	A	C	T	R	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H04	G	C	C	M	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-

H05	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H06	G	T	C	C	C	A	C	T	G	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
H08	G	C	C	C	C	A	C	T	A	C	A	G	T	A	C	T	G	G	(-),(-)	N	N	-	-
frequency	0.0067	0.35	0.0067	0.037	0.02	0.027	0.023	0.013	0.18	0.017	0.013	0.001	0.117	0.117	0.0467	0.21	0.097	0.04	0.32				

Supplementary Table S3: Variants defining H1-hybrid-allele haplotypes

	Exon 11			Intron 12 (2393 bp)																	
nuclotide position	c.1266G>A (p.A423T)	c.1532C>T (p.T511M)	c.1711C>A (p.L571I)	c.2174+1857G>A	c.2174+1881A>G	c.2174+1905G>A	c.2174+1851-1957 4xrep.> 8xrep.	c.2175-1802T>C	c.2175-1786C>T	c.2175-1739A>G	c.2175-1203G>C	c.2175-1017C>A	c.2175-969-970AA>CT	c.2175-947G>A	c.2175-926C>G	c.2175-897A>T	c.2175-836G>C	c.2175-823G>A	c.2175-774A>G	c.2175-713G>T	c.2175-691A>T	c.2175-534A>G
name of variant				ODS1	PDSvi	PDSvii	24-bp repeat	PDS4	SNP1	ODS2	SNP2	SNP3	PDSviii	PDSix	PDSx	PDSxi	PDSxii	PDSxiii	SNP4	PDSxiv	PDSxv	PDSxvi
CpG		*						*	*													
dbSNP	-	g	g	-	-	-	-	g/p	-	g/p	p	-	g	p	p	g	p	p	-	p	g/p	g/p
RefSeq. *PMS2*				G	A	G	4x	T	C	A	G	C	AA	G	C	A	G	G	A	G	A	A
RefSeq. *PMS2CL*				G	G	A	8x	C	C	A	G	C	CT	A	G	T	C	A	A	T	T	G
ID																						
Ci	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
Cii	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
Ciii	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A45	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
C28	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
C47	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
C06	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
C08	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
H02	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
H37	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A02(i)	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
C17	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A12	G	C	A	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A34	G	C	A	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A46	G	C	A	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
C16	G	C	A	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
H20	G	C	A	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A02(ii)	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A31	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A40	G	C	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A13	A	T	C	A	A	G	4x	C	T	G	G	A	CT	A	G	T	C	A	A	G	T	-
H36	A	T	C	A	A	G	4x	C	T	G	G	A	CT	A	G	T	C	A	A	G	T	-
A06	G	T	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A50	G	T	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A36	G	T	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A17(i)	G	T	C	A	A	G	4x	C	T	G	G	C	CT	A	G	T	C	A	A	G	T	-
A17(ii)	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A11	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A28	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A29	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A08	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A33(i)	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A33(ii)	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A35	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
A30	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	G	G	A	-
A43	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	G	G	A	-
A22	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	G	G	A	-
A04	G	C	C	A	A	G	4x	C	T	G	C	C	CT	A	G	T	C	A	A	G	A	-
H17	G	T	C	A	A	G	4x	C	T	G	G	C	AA	G	C	T	G	G	A	G	A	-

	Intron 12 (2393 bp)																Exon						
																	13	14	14	15	15	15	
nuclotide position	c.2175-426_2175-429delCTCC	c.2175-407A>C	c.2175-343T>C	c.2175-325T>G	c.2175-320C>T	c.2175-317T>C	c.2175-303C>T	c.2175-301G>A	c.2175-264G>A	c.2175-262G>C	c.2175-208C>T	c.2175-186T>C	c.2175-131G>A	c.2175-128-129AG>TA	c.2175-117T>C	c.2175-51G>C	c.2253T>C (p.F751F)	c.2324A>G (p.N775S)	c.2340C>T (p.P780P)	c.2466T>C (p.L822L)	c.*17G>C (3'UTR)	c.*92dupA (3'UTR)	Haplotypes for phylogenetic analysis
name of variant	ODS3	ODS4	SNP5	PDSxvii	SNP6	PDSxviii	PDSxix	PDSxx	PDSxxi	PDSxxii	PDSxxiii	SNP7	PDSxxiv	PDSxxv	PDSxxvi	SNP8							
CpG					*	*	*		*						*		*						
dbSNP	-	p	p	g	-	-	-	-	g/p	g/p	-	-	-	-	-	-	g/p	g/p	g/p	g/p	-	g/p	
RefSeq. *PMS2*	CTCC	A	T	T	C	T	C	G	G	G	C	T	G	AG	T	G	T	A	T	T	G	(-)	
RefSeq. *PMS2CL*	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	T	G	A	
ID																							
Ci	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
Cii	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
Ciii	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
A45	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
C28	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
C47	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
C06	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
C08	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
H02	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
H37	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
A02(i)	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
C17	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	T	G	(-)	H1-A
A12	CTCC	A	T	C	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
A34	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
A46	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
C16	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	C	C	A	H1-A
H20	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	T	T	G	(-)	H1-A
A02(ii)	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	C	T	G	A	H1-A
A31	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	C	C	G	A	H1-A
A40	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	C	C	G	A	H1-A
A13	CTCC	A	T	G	T	C	T	A	A	C	T	T	A	TA	C	C	C	G	C	C	G	A	H1-B1
H36	CTCC	A	T	G	T	C	T	A	A	C	T	T	A	TA	C	C	C	G	C	C	G	A	H1-B1
A06	CTCC	A	T	G	T	C	T	A	A	C	T	T	A	TA	C	C	C	G	C	T	G	A	H1-B
A50	CTCC	A	T	G	T	C	T	A	A	C	T	T	A	TA	C	C	C	G	C	T	G	A	H1-B
A36	CTCC	A	T	G	T	C	T	A	A	C	T	T	A	TA	C	C	C	G	C	C	G	A	H1-B
A17(i)	CTCC	A	T	G	T	C	T	A	A	C	T	T	A	TA	C	C	C	G	C	C	G	A	H1-B
A17(ii)	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	T	G	A	H1-C2
A11	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	T	G	A	H1-C2
A28	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	T	G	A	H1-C2
A29	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	T	G	A	H1-C2
A08	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	T	G	A	H1-C2
A33(i)	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	T	G	A	H1-C2
A33(ii)	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	C	G	A	H1-C2
A35	CTCC	A	T	G	C	C	T	A	A	C	T	C	A	TA	C	G	C	G	C	C	G	A	H1-C2
A30	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	C	C	G	A	H1-C1
A43	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	C	T	G	A	H1-C1
A22	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	C	T	G	A	H1-C1
A04	CTCC	A	T	G	C	C	T	A	A	C	T	T	A	TA	C	G	C	G	C	T	G	A	H1-C
H17	Δ	C	C	G	C	C	T	A	A	C	T	T	A	TA	C	G	T	A	C	Y	G	(-)	

H1 haplotypes in the exonic regions are deduced from the genotypes as assessed by cDNA sequencing. SNPs listed in dbSNP as polymorphic variants in the gene (g) or pseudogene (p) are indicated. C to T transitions at CpG-dinucleotides are indicated with a star. One PDS was not analyzed, -, due to its location close to mononucleotide repeats. Haplotypes of individuals from our first Caucasian cohort are named Ci-iii. Those from individuals of our second cohort are named as in Supp. Table S2. Haplotypes from individuals compound heterozygous for two H1 alleles were given an extension i or ii for the first and the second allele. Haplotypes were grouped into six sub-haplotypes, H1-A - H1-C2. PDSs are indicated with gray and ODSs with lightblue underlay. All discriminatory SNPs are with colored underlay. Individual H17 was positive for ODS1 in the multiplex PCR assay but lacked PSVs in exons 13-15.

Supp. Table S4. H1 hybrid allele frequencies in CRC patients

Cancer and control cohorts	Carrier frequency		
PMS2-deficient CRC patients	2/22 (9%)	P = 0.58	P = 0.68
Sporadic CRC patients	19/142 (13%)		
Age and sex matched controls	38/267 (14%)		

CRC = colorectal cancer