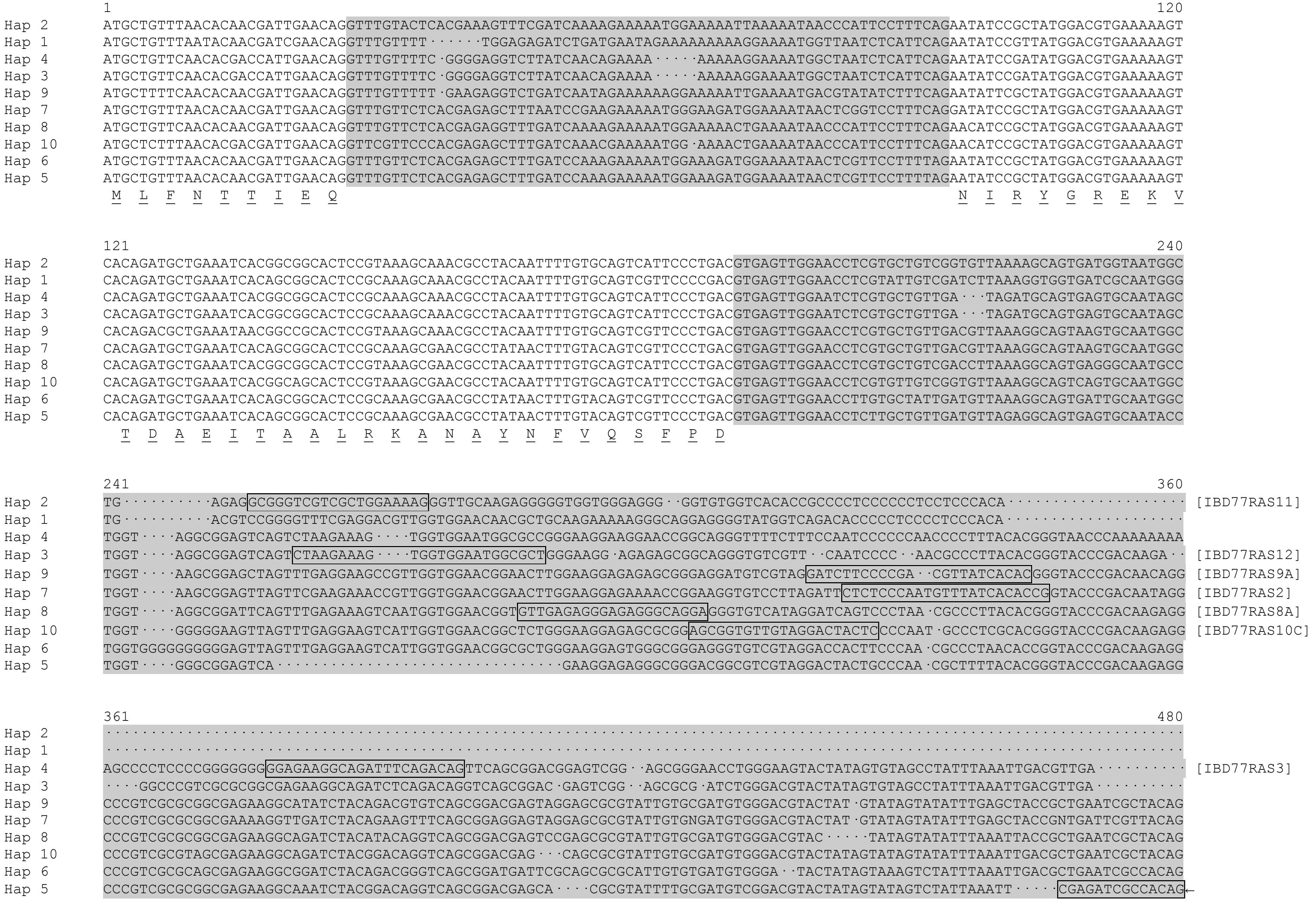

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Hap 2     ATGCTGTTTAACACAACGATTGAACAGGTTTGTACTCACGAAAGTTTCGATCAAAAGAAAAATGGAAAAATTAAAAATAACCCATTCCTTTCAGAATATCCGCTATGGACGTGAAAAAGT
Hap 1     ATGCTGTTTAATACAACGATCGAACAGGTTTGTTTT······TGGAGAGATCTGATGAATAGAAAAAAAAAGGAAAATGGTTAATCTCATTCAGAATATCCGTTATGGACGTGAAAAAGT
Hap 4     ATGCTGTTCAACACGACCATTGAACAGGTTTGTTTTC·GGGGAGGTCTTATCAACAGAAAA·····AAAAAGGAAAATGGCTAATCTCATTCAGAATATCCGATATGGACGTGAAAAAGT
Hap 3     ATGCTGTTCAACACGACCATTGAACAGGTTTGTTTTC·GGGGAGGTCTTATCAACAGAAAA·····AAAAAGGAAAATGGCTAATCTCATTCAGAATATCCGATATGGACGTGAAAAAGT
Hap 9     ATGCTTTTCAACACAACGATTGAACAGGTTTGTTTTT·GAAGAGGTCTGATCAATAGAAAAAAGGAAAAATTGAAAATGACGTATATCTTTCAGAATATTCGCTATGGACGTGAAAAAGT
Hap 7     ATGCTGTTTAACACAACGATTGAACAGGTTTGTTCTCACGAGAGCTTTAATCCGAAGAAAAATGGGAAGATGGAAAATAACTCGGTCCTTTCAGGATATCCGCTATGGACGTGAAAAAGT
Hap 8     ATGCTGTTCAACACAACGATTGAACAGGTTTGTTCTCACGAGAGGTTTGATCAAAAGAAAAATGGAAAAACTGAAAATAACCCATTCCTTTCAGAACATCCGCTATGGACGTGAAAAAGT
Hap 10    ATGCTCTTTAACACGACGATTGAACAGGTTCGTTCCCACGAGAGCTTTGATCAAACGAAAAATGG·AAAACTGAAAATAACCCATTCCTTTCAGAACATCCGCTATGGACGTGAAAAAGT
Hap 6     ATGCTGTTTAACACAACGATTGAACAGGTTTGTTCTCACGAGAGCTTTGATCCAAAGAAAAATGGAAAGATGGAAAATAACTCGTTCCTTTTAGAATATCCGCTATGGACGTGAAAAAGT
Hap 5     ATGCTGTTTAACACAACGATTGAACAGGTTTGTTCTCACGAGAGCTTTGATCCAAAGAAAAATGGAAAGATGGAAAATAACTCGTTCCTTTTAGAATATCCGCTATGGACGTGAAAAAGT
           M  L  F  N  T  T  I  E  Q                                                                     N  I  R  Y  G  R  E  K  V

          121                                                                                                                  240
Hap 2     CACAGATGCTGAAATCACGGCGGCACTCCGTAAAGCAAACGCCTACAATTTTGTGCAGTCATTCCCTGACGTGAGTTGGAACCTCGTGCTGTCGGTGTTAAAAGCAGTGATGGTAATGGC
Hap 1     CACAGATGCTGAAATCACAGCGGCACTCCGCAAAGCAAACGCCTACAATTTTGTGCAGTCGTTCCCCGACGTGAGTTGGAACCTCGTATTGTCGATCTTAAAGGTGGTGATCGCAATGGG
Hap 4     CACAGATGCTGAAATCACGGCGGCACTCCGCAAAGCAAACGCCTACAATTTTGTGCAGTCATTCCCTGACGTGAGTTGGAATCTCGTGCTGTTGA···TAGATGCAGTGAGTGCAATAGC
Hap 3     CACAGATGCTGAAATCACGGCGGCACTCCGCAAAGCAAACGCCTACAATTTTGTGCAGTCATTCCCTGACGTGAGTTGGAATCTCGTGCTGTTGA···TAGATGCAGTGAGTGCAATAGC
Hap 9     CACAGACGCTGAAATAACGGCCGCACTCCGTAAAGCAAACGCCTACAATTTTGTGCAGTCGTTCCCTGACGTGAGTTGGAACCTCGTGCTGTTGACGTTAAAGGCAGTAAGTGCAATGGC
Hap 7     CACAGATGCTGAAATCACAGCGGCACTCCGCAAAGCGAACGCCTATAACTTTGTACAGTCGTTCCCTGACGTGAGTTGGAACCTCGTGCTGTTGACGTTAAAGGCAGTAAGTGCAATGGC
Hap 8     CACAGATGCTGAAATCACGGCGGCACTCCGTAAAGCGAACGCCTACAATTTTGTGCAGTCATTCCCTGACGTGAGTTGGAACCTCGTGCTGTCGACCTTAAAGGCAGTGAGGGCAATGCC
Hap 10    CACAGATGCTGAAATCACGGCAGCACTCCGTAAAGCGAACGCCTACAATTTTGTGCAGTCATTCCCTGACGTGAGTTGGAACCTCGTGTTGTCGGTGTTAAAGGCAGTCAGTGCAATGGC
Hap 6     CACAGATGCTGAAATCACAGCGGCACTCCGCAAAGCGAACGCCTATAACTTTGTACAGTCGTTCCCTGACGTGAGTTGGAACCTTGTGCTATTGATGTTAAAGGCAGTGATTGCAATGGC
Hap 5     CACAGATGCTGAAATCACAGCGGCACTCCGCAAAGCGAACGCCTATAACTTTGTACAGTCGTTCCCTGACGTGAGTTGGAACCTCTTGCTGTTGATGTTAGAGGCAGTGAGTGCAATACC
            T  D  A  E  I  T  A  A  L  R  K  A  N  A  Y  N  F  V  Q  S  F  P  D

          241                                                                                                                  360
Hap 2     TG··········AGAGGCGGGTCGTCGCTGGAAAAGGGTTGCAAGAGGGGGTGGTGGGAGGG··GGTGTGGTCACACCGCCCCTCCCCCCTCCTCCCACA····················  [IBD77RAS11]
Hap 1     TG··········ACGTCCGGGGTTTCGAGGACGTTGGTGGAACAACGCTGCAAGAAAAAGGGCAGGAGGGGTATGGTCAGACACCCCCTCCCCTCCCACA····················
Hap 4     TGGT···AGGCGGAGTCAGTCTAAGAAAG···TGGTGGAATGGCGCCGGGAAGGAAGGAACCGGCAGGGTTTTCTTTCCAATCCCCCCAACCCCTTTACACGGGTAACCCAAAAAAAA
Hap 3     TGGT···AGGCGGAGTCAGTCTAAGAAAG···TGGTGGAATGGCGCTGGGAAGG·AGAGAGCGGCAGGGTGTCGTT··CAATCCCC··AACGCCCTTACACGGGTACCCGACAAGA··  [IBD77RAS12]
Hap 9     TGGT···AAGCGGAGCTAGTTTGAGGAAGCCGTTGGTGGAACGGAACTTGGAAGGAGAGAGCGGGAGGATGTCGTAGGATCTTCCCCGA··CGTTATCACACGGGTACCCGACAACAGG  [IBD77RAS9A]
Hap 7     TGGT···AAGCGGAGTTAGTTCGAAGAAACCGTTGGTGGAACGGAACTTGGAAGGAGAAAACCGGAAGGTGTCCTTAGATTCTCTCCCAATGTTTATCACACCGGTACCCGACAATAGG  [IBD77RAS2]
Hap 8     TGGT···AGGCGGATTCAGTTTGAGAAAGTCAATGGTGGAACGGTGTTGAGAGGGAGAGGGCAGGAGGGTGTCATAGGATCAGTCCCTAA·CGCCCTTACACGGGTACCCGACAAGAGG  [IBD77RAS8A]
Hap 10    TGGT···GGGGGAAGTTAGTTTGAGGAAGTCATTGGTGGAACGGCTCTGGGAAGGAGAGCGCGGAGCGGTGTTGTAGGACTACTCCCCAAT·GCCCTCGCACGGGTACCCGACAAGAGG  [IBD77RAS10C]
Hap 6     TGGTGGGGGGGGGGAGTTAGTTTGAGGAAGTCATTGGTGGAACGGCGCTGGGAAGGAGTGGGCGGGAGGGTGTCGTAGGACCACTTCCCAA·CGCCCTAACACCGGTACCCGACAAGAGG
Hap 5     TGGT···GGGCGGAGTCA·······························GAAGGAGAGGGCGGGACGGCGTCGTAGGACTACTGCCCAA·CGCTTTTACACGGGTACCCGACAAGAGG

          361                                                                                                                  480
Hap 2     ························································································································
Hap 1     ························································································································
Hap 4     AGCCCCTCCCCGGGGGGGGGAGAAGGCAGATTTCAGACAGTTCAGCGGACGGAGTCGG··AGCGGGAACCTGGGAAGTACTATAGTGTAGCCTATTTAAATTGACGTTGA··········  [IBD77RAS3]
Hap 3     ····GGCCCGTCGCGCGGCGAGAAGGCAGATCTCAGACAGGTCAGCGGAC·GAGTCGG··AGCGCG·ATCTGGGACGTACTATAGTGTAGCCTATTTAAATTGACGTTGA··········
Hap 9     CCCGTCGCGCGGCGAGAAGGCATATCTACAGACGTGTCAGCGGACGAGTAGGAGCGCGTATTGTGCGATGTGGGACGTACTAT·GTATAGTATATTTGAGCTACCGCTGAATCGCTACAG
Hap 7     CCCGTCGCGCGGCGAAAAGGTTGATCTACAGAAGTTTCAGCGGAGGAGTAGGAGCGCGTATTGTGNGATGTGGGACGTACTAT·GTATAGTATATTTGAGCTACCGNTGATTCGTTACAG
Hap 8     CCCGTCGCGCGGCGAGAAGGCAGATCTACATACAGGTCAGCGGACGAGTCCGAGCGCGTATTGTGCGATGTGGGACGTAC····TATAGTATATTTAAATTACCGCTGAATCGCTACAG
Hap 10    CCCGTCGCGTAGCGAGAAGGCAGATCTACGGACAGGTCAGCGGACGAG···CAGCGCGTATTGTGCGATGTGGGACGTACTATAGTATAGTATATTTAAATTGACGCTGAATCGCTACAG
Hap 6     CCCGTCGCGCAGCGAGAAGGCGGATCTACAGACGGGTCAGCGGATGATTCGCAGCGCGCATTGTGTGATGTGGGA··TACTATAGTAAAGTCTATTTAAATTGACGCTGAATCGCCACAG
Hap 5     CCCGTCGCGCGGCGAGAAGGCAAATCTACGGACAGGTCAGCGGACGAGCA···CGCGTATTTTGCGATGTCGGACGTACTATAGTATAGTCTATTAAATT····CGAGATCGCCACAG←
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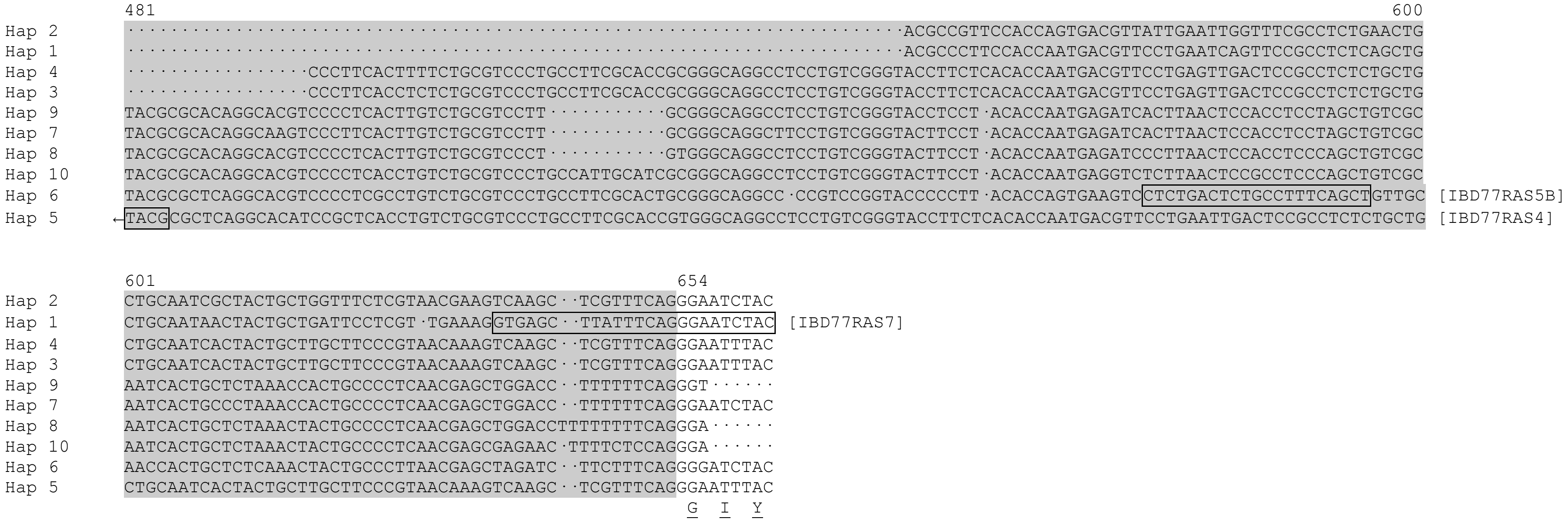

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         481                                                                                                                     600
Hap 2    ························································································ACGCCGTTCCACCAGTGACGTTATTGAATTGGTTTCGCCTCTGAACTG
Hap 1    ························································································ACGCCCTTCCACCAATGACGTTCCTGAATCAGTTCCGCCTCTCAGCTG
Hap 4    ·················CCCTTCACTTTTCTGCGTCCCTGCCTTCGCACCGCGGGCAGGCCTCCTGTCGGGTACCTTCTCACACCAATGACGTTCCTGAGTTGACTCCGCCTCTCTGCTG
Hap 3    ·················CCCTTCACCTCTCTGCGTCCCTGCCTTCGCACCGCGGGCAGGCCTCCTGTCGGGTACCTTCTCACACCAATGACGTTCCTGAGTTGACTCCGCCTCTCTGCTG
Hap 9    TACGCGCACAGGCACGTCCCCTCACTTGTCTGCGTCCTT···········GCGGGCAGGCCTCCTGTCGGGTACCTCCT·ACACCAATGAGATCACTTAACTCCACCTCCTAGCTGTCGC
Hap 7    TACGCGCACAGGCAAGTCCCTTCACTTGTCTGCGTCCTT···········GCGGGCAGGCTTCCTGTCGGGTACTTCCT·ACACCAATGAGATCACTTAACTCCACCTCCTAGCTGTCGC
Hap 8    TACGCGCACAGGCACGTCCCCTCACTTGTCTGCGTCCCT···········GTGGGCAGGCCTCCTGTCGGGTACTTCCT·ACACCAATGAGATCCCTTAACTCCACCTCCCAGCTGTCGC
Hap 10   TACGCGCACAGGCACGTCCCCTCACCTGTCTGCGTCCCTGCCATTGCATCGCGGGCAGGCCTCCTGTCGGGTACTTCCT·ACACCAATGAGGTCTCTTAACTCCGCCTCCCAGCTGTCGC
Hap 6    TACGCGCTCAGGCACGTCCCCTCGCCTGTCTGCGTCCCTGCCTTCGCACTGCGGGCAGGCC·CCGTCCGGTACCCCCTT·ACACCAGTGAAGTCCTCTGACTCTGCCTTTCAGCTGTTGC [IBD77RAS5B]
Hap 5   ←TACGCGCTCAGGCACATCCGCTCACCTGTCTGCGTCCCTGCCTTCGCACCGTGGGCAGGCCTCCTGTCGGGTACCTTCTCACACCAATGACGTTCCTGAATTGACTCCGCCTCTCTGCTG [IBD77RAS4]

         601                                       654
Hap 2    CTGCAATCGCTACTGCTGGTTTCTCGTAACGAAGTCAAGC··TCGTTTCAGGGAATCTAC
Hap 1    CTGCAATAACTACTGCTGATTCCTCGT·TGAAAGGTGAGC··TTATTTCAGGGAATCTAC [IBD77RAS7]
Hap 4    CTGCAATCACTACTGCTTGCTTCCCGTAACAAAGTCAAGC··TCGTTTCAGGGAATTTAC
Hap 3    CTGCAATCACTACTGCTTGCTTCCCGTAACAAAGTCAAGC··TCGTTTCAGGGAATTTAC
Hap 9    AATCACTGCTCTAAACCACTGCCCCTCAACGAGCTGGACC··TTTTTTCAGGGT······
Hap 7    AATCACTGCCCTAAACCACTGCCCCTCAACGAGCTGGACC··TTTTTTCAGGGAATCTAC
Hap 8    AATCACTGCTCTAAACTACTGCCCCTCAACGAGCTGGACCTTTTTTTTCAGGGA······
Hap 10   AATCACTGCTCTAAACTACTGCCCCTCAACGAGCGAGAAC·TTTTCTCCAGGGA······
Hap 6    AACCACTGCTCTCAAACTACTGCCCTTAACGAGCTAGATC··TTCTTTCAGGGGATCTAC
Hap 5    CTGCAATCACTACTGCTTGCTTCCCGTAACAAAGTCAAGC··TCGTTTCAGGGAATTTAC
                                                     G  I  Y
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S6 Fig. Multiple-alignment of partial sequences of *Tci-pgp-9-IBDA* haplotypes showing introns (shaded), amino acid translation (underlined) and locations of allele-specific reverse primers used in genotyping reactions (boxed). *Tci-pgp-9-IBDA* haplotypes were identified based on PCR clones (n=66) amplified from gDNA preparations. “Allele-specific” primers were designed to differentiate between each of the haplotypes using a nested PCR strategy to allow genotyping of individual male worms from the S_{inbred} and RS^3 strains of *T. circumcincta*.