

Polymorphisms in the *HLA-DNA* region of the human MHC, spanning crossover hotspots *DNA* 1-3

The sequence is taken from [Beck *et al.* \(1999\)](#) and is orientated centromere to telomere. Coordinates are given relative to SNP DA1+/- located at position 3,260,370 of the [current consensus MHC sequence](#). Exons are shown in blue, Alu repeats in red and microsatellites in green. The locations of PCR primers used for amplification of genomic DNA and for resequencing for SNP discovery are indicated below the sequence. Regions resequenced are underlined. The alternative allele at each SNP is shown below the sequence. The approximate positions of the centres of meiotic crossover hotspots *DNA* 1-3 are also shown.

18319 GGTTTTCGCTGGCCTAGGACTCCAGCTGGCCCTCCTTTCTCTTTACACACATGACACCA
----- R-6.0F ---->

18379 ACACAGATGGCCACTAGTGGGTCAAATAATACCTTTAGGGAGTGCCGACACCTCAAAG
18439 AAAAACAGCAAACAGGACCATCTATGTCCTTGAAGAAGTGGTAGAAAATATAGACCAGC
18499 CGCTTAAAAATGAGCATTAAAAAGTGCACTTTAAAAAGTCAGAAGCTATTATAATATGAAAAA

18559 ATAGAGAATATAGGGAAAACACCTAGAAAGTTCTAGGTGTAAAAAATATATATAATAGTCA
DD15A/C DD19-/+
C |+T

18619 AAGTAAAAGCCACATTAATGGGATAAATAGTGGGAGAGATGCAACTGAAAAACAAAACAG

18679 AAAGATGGAGGACTACACTGAGGAGCTAGTTCAGAACAAAAAGGGGAAGAATTGAGAAGT
18739 CATCAATAGAAAAGTCAGGGGAAAAGGAGGAGAGAATTATCCAATATAGATTATATGAG

18799 TTTCACAAAGACAAAAAATAGAGGAGAAAAATAGTTAAAGAAAATAAAAAAGATGAATTCCC
DD20-/+
|+GAGA

18859 AGAATTTAAAGATAGAGAAGATCCATAATGTCTTACAGAGAGAAGGAAAAACCCACTCTA
18919 GACACACTAGCAAATTTAAAAATATCAAAGACAATGAGAAAATTTAGAAAGATTCCAGC

18979 ATGAAAGACTGACATGGGATTTCTAACTGTGACATTGGATGCAAAAAAAAAAATTTGGA
length polymorphic (A)_n
<---- R-5.3R ----->

19039 ATGATGTTATTTAGAATATTTAAAGGGGAAAAATACTTCAAATAGTATGTAATACACAGCTA
-- R-5.3F ---> - C

19099 AACCTTTATTTCAAAAGTCTGGTATAATTTTAAAAAATTATCAAGCATACAAGACTTTAGA
T A C

19159 AGGTTTGCTATGCAAATCCCACATCTGAAAGGTTTGGGAAGAAGAAATCTAATCAGAGA
DD24G/T DD18T/C
T C

19219 ACGCATTCTAGAAGGTGCCAAAAGATATGAAAAGTAATGTTGACCAATAAATTTGGTGAA

19279 GGAGAAAATATGTGAATAAATTTGAAAGCATGCTAAAGTTCTTATCCAGTCAGAGGGAAG
<----- R-5.0F --->

19339 ATGGAGAAGGTATCGGTAACACTTAAAAAAAAAAAAAGGCAATGAAGATTTAAAAAGAAAA
----- R-5.0R ----->

19399 C TTGGCCGGGTGTGATGGCTCAGCCTGTAATCCTAGCAGTTTGTGAGGCCGAGCCAGGC
19459 AGATTGCCTGAGCTCAGGAGGATAAGCCTGGGCAACACGGTGAAACCCCGTCTCTACTAA
19519 AATACAAAAAAAAAAAAAAAAAATAGCCAAGCATGGTGGCATGCACCTGGAGTCCCAGC
19579 CACTCGGGAAAGCTGAGGAGAATCGCTTGAACCCGGGAAGCAGAGGTTGCAAGTGGCCAGC
19639 CCAGATCATGCCACTACACTCCAGCCTGGCAACAGAGCGGAGACTCCGTCTCAAAAAAAA
19699 CAAAACAAACAAACAAAAAACTTTAAAAAATAGAAAATATTGAAATAAATAAGGTATTACA

19759 AACAAGCCCAAGTGATCAATATTTACAATAAACACAATCAGAATGCAGCAAAGACAGCG
DD9G/T
T

19819 CCATGTGCTCACCAACCATTATATCTTCTGCACACATAGGTAACGTACATTTTCCAT
19879 CCCCGTGCGCCTATGTGGGGTCATTTTACTTCTTGCCAAATGGAATGTGAGCAGAGATG
19939 GCAAAATAGTTTCTGGTCCAAAACCATGGAAACAATGTGCCTTTCCAGGTTCTCTCTCT

19999 ACCTGCAAAGCTAGGAGTTCATGAAGTCTTTTCAATAATAGAGATGCAAAGTGGAGCTT
DD10C/G DD11T/C
G C

20059 AGCCACCTTGAGGCATGTTTTGGAAAAGAGCTACAGAGTGCCCAACCTGCCTTGAAC
DD12C/G
G

20119 ACGTGGCTAAAAATAAACCTGTGTTTTGTAAACCACTGAGGCTTCAGTGTTTGTCTCT
DD13C/T
T

20179 TGCAGAAACAGTTTTGCTCACTTTGACTACCATATGAATTGAACATAGGTTAGAAGACAG
DD14A/G
G

20239 AGATCGTCAGATTGAATCAGAAGCAAAAATCTATATTTATGACATTTCAAGGGCTACATC
20299 TAAAGCATAAGTACAAAGGAAGAGTAAAAACAAAAGAGTAGAAAAAGATACAGTGAACAA
20359 ATACCCAAAGACAGCTGTAGAACTTATTACTATCAGACAAGACAGAGTAGGACAGAAAGA
----- R-3.9F ----->

20419 TTCTCAGGACAAATTGGGAAAAGGCTCAGTTCACCAAGACTGTAATAAATCCCAAGAGTA
<----- R-3.9R -----

20479 AACACCTTAATAACCTAAATGCAGAGAGGGCAAAAGTTGATTTAAAAATTAGAAACAAGT

20539 TGAAAAACCTACAGTCACAGTTAGAGATTTAAATATACCATTTCATAGGCCAGGAATTGTG
5' truncated Alu -->
<----- R-3.8R -----

20599 GGGCATGCCTATAGTCCCAGCTACTCTGGGAGGCTGAGGCAGGAGGATCGCTTAAGCCCA
DE1C/G
G

20659 GCTGTTTGAGGCTGCAGCGAGCCATGATTACTTCACTGCCCTCCAGCCTGAGCAACAGAG
20719 CAAGGCCCTGTCTCTAAAAATAAATAAATAAATGACACCCTCTTAGTTATGTATAGGCC

20779 AGTCCAAAGATAAAGAAAACCGTAATAAATTAGAATGACAAAATCCACATGCTTGATCCA
DE2G/A
A

20839 ATAAACATGTACATGTATAAAATTTCTGCATCACATTTATTAGAGCCCATGTGAAATATTT
20899 ACAGAAGTTCAACCACACTCCAAGCCATAGAGGATTTATCATGTAATTTAAATTATAAGTTAA
20959 TAACAAAAAACATACTTTAAAAAATCTATGTATGTTTTCAATAAAAAAAAACACCCCGAT

21019 ACTCGACTGTTATTAACCAAAGAAGCAACATTCTTTATCATGAGTTTTTCATGGCTTTCC
- R-3.3F ->

21079 CGTCTTTTCATCTCATGGCTCCAGCTCCCACCTCACTTGGGGGGAGGTGAAGGTGGCAAGG
21139 GTCCCTAACAGGGCAGGACCAAAGCAGTGAAGACACTGTTTCATTTCATGCGCAGGTGTCTC

21199 CTAGGCGCCTATGATGTGCTAGGCATTACGTAGACACTGTGGACTAGAAAACGAAAAA
DE3G/T DE4C/T
T T

21259 AAGATTAGGGCTCCCCATAAACCGGGCCATGCAAATCAATTACTAGCTGTCAATTTGATTA
21319 ATTTGAAGTCAGAAGCTGTGTCTGCCCACTTAAAAATAGGCATCCCTTATTTCATTGAGGA
21379 AAGAGCATTTGGAGCAGGTTTTTACCAGTCCACAGACTACCCGAGAACCACCTGGGGAGCAT

21439 GCTGAAAACACAGGTTCCCTGGCCCTGCCTTGAAAGGCTAATCTAACCCATTAAGTAAA
DE5G/T
T

21499 GAGGAAACTCAGGAACCGTATTATAACGAACCCCCAGGTGATTCTCATTGGAACCAG

21559 AGACCCGCATGATTTCTTAGCTCCCTCCAAGTTGAAAATCATCGAATTCATGGTCTTTGA
DE6C/T
T

21619 CACATGGCCTAATTTGGTTAGATTTCTCTTTACACAGACGTTAGCTTTACGTTGTTGTTG
DE7A/G
G

21679 TTTGTGTTTTGTTTTGTTTTTTAAATATATATACTGGACTAAATTCTCCAGTGCCTCTTA
----- R-2.6F ----->

21739 TTAGCCGAGCCCAACCAGAAGCCAAGGCAAGGGTGATGCCGTCCCTCCAGCCTGTGTGAC
21799 CCTGGAGGAGGTGCCCGGGTCTGGAGGGACCAACAGAGAGGACCAGCACCTCTGCCCTC
21859 CTCGGGGAGTCCACGGGAGCTCTTTACACTTTGCTTTAGACCAACAACCTCCAACAATTA

21919 CACATTTTTTCTTACACAATGAAATTAATAATAATAAAAGAAAAATAAAATAACATTTT
DE8A/C
C

21979 TGAAAGTGATTTAAAGTTTTAAGAGGTTTTTATTCCATTGTGTAGCCAATGTTTTCTTTT
22039 TAAAGATTATTGGTAAAGTTTTATTTACTTTCTAACTCAAATTTGTCCACGGAAACTTC
22099 TTGGGAAAGTAGGATTCCTGCATCGCAGATGGACATAGAGAGAGGATTTGTTGGAGCTC
22159 AGCTGCGCGGTGCTCTGACGGCCTTTTCTCTCTTTCAGGGGTCCCTTCTTGGAGGACC

22219 TGGTAATAGTTGGTCCAAGCCCCTCCCATCTCCAAAACCTCTTGGCCTCTCTGGGG
DE9T/C
C

22279 GCCCAGTGAATCCTTCCACCTTCTCACCCCGGCTCTTCCCTCTTTACCCAGCAACAGAT

APPROXIMATE CENTRE OF HLA-DNA HOTSPOT 1

22339 ACATTCACTCAGAGAATTTCTGTGATTGGCTGAAGACAGAGAGGGGTCGCCCCATCTCG
DE10A/C
C ---- R-1.9F ----->

22399 AATCTGTTTTCTTCTCTTTACCTCCGCCTTGTTCCTGTCCTCACCACAGGACTGAGAC
HLA-DNA exon 1 --> DE11G/C
C

22459 TGATTTGATTAAAGCACCAGAGTGAATGGCCCTCAGAGCAGGGCTGGTCTGGGGTTCC
DE12T/C ini
C

22519 ACACCCTGATGACCCTCCTGAGCCCGCAGGAGGCAGGGGCCACCAAGGGTGAGTGCGAGG
22579 GCGAGGAGGGTGC GGCGGGGAGCAGAGATTTACGGAGTTGGGTTACATGAGGAGGTGGCA
22639 TGGAGGATGCTTGTTCCTCTCGCTCTCTGGTTTTATGGGCAACTTCCCTCACC AAGAGACA

22699 CCCAATCCCCCTCATCTCTGTACATCCACTCTGGACCTAAATGAAGATGCAGCTCGGTC
DE13C/T DE14C/T
T T

22759 AGCTGCGCAGGTGCCCCAGTCAGCCTTTGCTGACGTTTCTCCTCATTCCTTCTCT
22819 CCTTCTGAGACCCAAACCTCCACCCAACAGATGCCAGCAAGCACCCTGATTTCTCTACC

22879 ACCCTGGCCTGGAATGTGCCGATCAAGTCCAGTTCTGTTGACAGTATTTATGCCCATGC
DE15T/G
G

22939 CGGTAGTTAACTATTTACCTGTCTTTGTTCTTCGGGAGACATGAGCTGGGGTGCGGGTCT

22999 ACAGATGGTTCATCTTTTTTTTTCTTTTATTTCCCTGGCCCCCATTGTGCTGGGTGCATG
DE16C/A
A
C----- R-1.3F ----->

23059 CTAGTTCCCTCAATAACTGTTGCTCAAACAACCTTCATAGAGTTCTACAAGAAITAAAACCTT

23119 AATCCCTAACTTCCAGAAAAC TAGACAACAGTTATGGAAGAGCCACACTCAGTCATAATG
DE17C/T SapI
T

23179 CTCTGAGATGGAGGAATTGGGACATGAACCTTGACTTCTGACTCCTCGTCCAGTGCTCTT
23239 TGTAATGCCTTGAGTTGCCTCTCCCTATCCCCTTGGTCTCTGGGTCACTAACCTTAATTC

24919 ACATATGTGTCCAGTGTCCCCAG^{F10G/A}GTGCAGAGGCCCCGGGAGTCTGGGGGTGGGGGAGGA
A

24979 AAGTGGATGACTCTGAACAGGACGTGGGTGGAGAATCAGAGATTCTGTTGTGGGGAAAGA
25039 AGTCAGAAAAGAAATGGGCAGGGAGAAAAGAAGCAGAGGTGGGGTGAGAGAGTGAGGTTT
25099 TGGGGGAGGTGGGCACTCAGAGATAGGATCCCAGCATATTGAAATTGAGCAACCTCGATC

HLA-DNA exon 5->
ter

25159 GTATGTTTTCTGCTATTTTAG^{F11C/A}GTAATGATCCTTCTGAGAGAAATGACTTGTGGGAGACAC
A

25219 CCTGCAGATCCTCATGGGTTTGTGACAG^{F11C/A}CCCCTGCGTGCTCAGTGCCCTTTAAGTGCATC
A

25279 CCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCCTACGGGTCCCCTCTTTTTTGGCC

25339 CCAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAACACA^{F5A/C}AA
C

25399 CACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAAATGCTTTGGTGGT^{F6G/A}GTTT
A

25459 G^{F7G/A}CACTGTGTCCTTTCCAGGCCCTTGGCCAGTTCTTCCAGGGGTGAGGCATGTGGTGCTGGG

25519 GATTGGCAGCC^{F7G/A}GTCCCTGGGGCCACACAGGTGTGTCCTTGCTCCATTGGCCCATTTGTGTG
A

25579 TTACTTTGTGAATGAGCCATTTACATGGACTTCATGAAATTTGCCTCCTGAGTTCAGGT
25639 TTACCCTGAAAGGGATGCAGATTATCCTGTTCCCTCACGACCCCTCAGCTAACAACAGTT

25699 CTGAAGGGTGCTGGGACA^{F8A/G}AGACAGGCTCATGGGGACTCCACTCCTGCCTGGGTTTACTCT
G

25759 GTATGAAGAGGCCACTGGTATCCTGCCATGATGTTATCTCCTTTTTTCTACTTTCCCTAGA^{F9-/+}
|+T

25819 GTCCCATGCATGATAAAGAGAGGCCCAAGGCTTGATAAGGTGGCCACTTCCCTCAGTGG
----- R1.5F ----->

25879 AGTCAGTCATGTTAGGTAGGAGGTGGTAGAGTCGGTCTGCA^{FG1A/G}AAGTATCTCGTAAGAGGGG
G <-

25939 AGGTCCACCTAGACACA^{FG2C/T}CTCTAAATATGTGGCCTAGAAGATTTTGGTCTACTTTTCTGTG
T
--- R1.6R -----C

25999 AACAGAAATTTAAACATACAAAGAGATAAATCACCATACCACATAGTTTATGTCAAGACC
26059 AAAATGAGCAATACAGATTACGGTTTTTCAAACCAGAATGCACATAAGAAGTCTTGGGAT

full length Alu---->

26119 CCTTTTAAAAGTACAGGC^{FG3G/A}ATTGGCCTGGTGCAGTGGCTCATTCCTGTAATCCCAGCACTT

26179 TGGGAGGCCAAGGGGACAG^{FG3G/A}CACTGCTTGGGCAAGAGGTGGAACCATCTTGGGCTACA
A

26239 TAGAGAGACCCCATCTCTACAAAGAAAGATTTAAAATTAACCAG^{FG4G/C}GCATGGTGGCTCGCA
C

29899 GCCACCCTGTCCCTGCAGTGCATACCACATTCGCCCTGTGTCAGTTGACTGTGTATGAA

29959 TTTGCCTTTGCCACTAACTGCTCCTCTAAAGCAAGAGAAGGCTGTGTCTTATAGTTCCAA
 <----- R5.7R ----->

30019 CACCCAGAACATAATGGGCATTGAAACACTGTAGAATTCTATTTAATTCAATTTTGTTTG
 30079 CTTCAAATCCAGCCTGGTCCGACTGTCTGCAGCTGGTTTTAATAACATTGGCTACCGTTT
 30139 ACCCAACACATGCAATGTGCCCTGGCCTTAATGCTTTTACGTGTAGTGGATTTGAATCTT
 30199 GGTCCAAAAGATTAATAAGATAGTGCACAGAGTGCAAAAAATAGTAAATGTCTTTAAATA
 30259 ATCGAAAATCTGATTCAAACCTGCTCTTTAAAAAATCTTAAATCTGATTCAAACCCCT

30319 GCCATGAGGCTGGTTTTAAGTTCAATCTGTCTTTATTGGGGCTTCTGGTCTCTTACAGTT
 GA6G/A
 A

30379 GTTCCAAGGTCTGCGCCCTGACACAGTGCTGAGGCCTTGGAGAAGCCCTGTGTCTTC
 GA7G/T
 T

30439 TCCAGTCCAGACTGTTTACTCCAAGCATGCTTAGGGCTTAACCTGTATGCTCTTTTCCAA
 SphI

30499 GTGGAAGCTCTGCTGCTTCTGCACTAGGCTTGGGGCAGGGGAATCTTTAGTGAGGAGTGA
 30559 TCCCCAGTGCCTGGGAGCAGGACTGCAAAGATGCACCATACGGCCAACCTTCCCCGTCCCT

30619 GGGAGGCCTCCCCACCTGCCTTGGCTGTGCAAGGAAGCAGGGCTTTTCAGACCCACAG
 GA8C/T
 <----- R6.3R -----> T

30679 GCCACTGTGCCTTCCTCAGTTTGGGAGAACCTTCCCCCTTTGCCTGTCAAAGGCATTCCC
 30739 CTCTCTCTCTGCGACAATGTCTGGGACACCTGGCATAATGTCAAGTGAGCTTCAGATT
 30799 TTGGGAAATCCAAAGCCAGAAGAGGAAAGGCCTTGGCGGTGACATGTGCTATTGTCTTGT

30859 GTGACAAACCTAAATACAAACAAAGGAAAAAGAAAAGCATCATTCTGCCATACATGAATT
 GA9A/C
 C

30919 ATTTTCATTTCTTCTTATGACCAATCTGCAAGTTAAGTATAATGATTTTATATAAG
 GA10C/T
 T

30979 AAGGAAGCTAGGATTCAAATTACCTAACTTGCCCAAGGTCAAACAGCTAGGAGGTGGTTG

31039 GAAGGTCTGTGTGATGCTAGAGCCCATGTTCTTTTCCACTGCACTGTCTACTCAGCAGCG
 <----- R6.7R ----->

31099 AATCGAGACCAGCTTGTGAGACATGAGGCAGGATGAACAGGGTCAGACATCAGCATTACT
 GA11G/A
 A

31159 AGGAAATGTGTAGGAGGAGGTATTCCTCAACTTTGGGAAACAACTTCTTCTGAGGCTTCAG
 GA12C/T
 T

31219 CAGCAACAGGCTGCAGGGAATGAGGTGAGCTTGAAGAATGACTGGGGATGGAATTACTGA
 ----- R6.9F ----->

31279 AGAGATTTTCTTCTCCTCCTGGAT-CAGTCTGAAGCACTCCCCAGTTTCAGACTTTCTTT
 mismatch with EMBL seq | A1C/T
 T <----- R7.0R ----->

31339 CTTGCTTAGTCTAAATTCCTCCTGGTCAACAAGACTCTATATGATCTGGCGCTGCATGT
 A2A/G
 G

31399 GTCTTCATCTTACTTCCCTCTACTCTTCTTCTTTCATTAAGCAATAGCCACACTATCT
 A3C/G
 G

31459 TCCCCAGAATTCCTTAACATTAATGCCTCCAATTCATCACCCATTCACTCGTGTG

34579 AAAGAAAAAAAAAAAAAAAAAAAAAGAACTAAGATTTTCATGTATAAAAAAGCAAGTAAAAGT

34639 AGCTGAATTAATAATAATATTAGAAAAATATTTGAACTAGAACTGTCAATTTTAACT
SspI SspI

34699 AATGATTCACTAACATATATGTCCTGCTCTAGCAAATGAAAGAGCCTAATAGTAGCCCT
AB14C/T AB8T/C
T C

34759 GTAGCAATGAGCATCCTCAATGCACAGATTGTAGTGTGTAATATCATTTCCCACTCAA

34819 GGAAATTAGAGCTTCTTGAGAGAAGTGACCAGTTCCAGGCCTGAGTTATGGAAAATACAAAG
AB9T/C AB10G/C
C C

34879 CAAGTGTGAGTATCTCATTGTTTTTATAAAAACAAGGCACTGTTCAAAGACTAATAGAGTC

34939 ATGTCAAAAAAACAGGTCAGCCAGTTTGAAGGAGCTTCCATGGCCAAAACCTGGAAACAAC
AB11-/+
|+A

34999 TCAGACATCAAAAAGATGACTATAATATAATTAACACATTGAGTATATAAAAATCCATG
<---

35059 GGTTCCTATTAATAGTCGAATACAGATTTTAAAAAGAAAGCAACAACAACCCATTGATAT
AB6A/T
----- R10.7R ----- T

35119 TACCACTGGATGTGATCTTCCAATTCATAACACAGGAAATTGGTGCTAAAGAAAACAAG
35179 TATATATCCTGACATTTCAAGGAAATGTTCCACTGATGAAAAAGGCTACCCTTCAG
35239 AGTACCAGTGAATAAATGTTGGGAAAAATAACAGAATTAGAAAACCAGCATTTTGTAAAGC
35299 CTAATGTGATCATTGATTCAGGGAAGGCATCATATATGTTAAAACCATAGGAGAATAGA

35359 CAGTGAGGAACAAGAGAGTCACATCATGCCAAAGTATCATGGTCATAGATTATTTGCTAT
----- R11.1F ----->

35419 TGTCAAATGGGAGAAATACCTTTACAGAGGTGATGGCTGTCATCACCTCGACTGAGTGAT
<----- R11.1R -----

35479 CAAGTTTAGCCTCACCAATAATAGGACAAGACATTAAGCATATGCTTCCTAATAAGATGA
B2G/A B3A/G
A G

35539 AATGCAAAGTACACAGCAATACCTATGAAGAATTATTGTCAAAAATCTTTCATCTAAATC
B4-/+
|+A

35599 TAGTCAAGCCTTTGTTTTCAAAAAGTTCTAGTCTATAAAAAAATACATTGGATAGAGGAA
35659 TAAGTCAAATGAAACCACAAAGAACCAATCACACAAATTCAAAATGTGAGAGATTCTACT
35719 GGCCTTGTCTCTCTAAAAAGATGCTGTTTTAAAAAATGGGTGGAATAGTGGGAATTAAGAG
35779 ACATTACAATCAAATTTAGTGAATGATTCTTGGCAATATCTTTGAGGAAAAACAGATATA

35839 AAAGCACTTTTTCAGACAAATGGGAAATTTGAATATGAACTGGTAATCGATGATATTAGA
B8C/A
A

35899 GAGCTGTTTTCAGTTTTGTTTAGTATGATTACAGTACCACGGTTATGTATCAAGTCATCT

35959 TTATGCTAAAGTATTTAGGGATGAAATGCTAGATCTCTAATTTACTTCCGAATGAATTCA
B9G/A
A

36019 GAATACACACACAGTTCAAACAAACACAGCAAAATCTTGACAGTTGTTGAATCTATATGA

36079 TGGGTATTTGTCTTAGTCCATTTGTGTTGCCATAACAGAATACCCAGACTAGGTAATT
<---- R11.8R ---

38059 GGTACTAAGTTTCCAAAATCTTAAAAAGTCTTTATAGTTTTTAAATCTCCTTCTTATGTA
-- R13.7F --->

38119 GTCAACGCAAGCCCAGACGCACGCCTACCCCTACCCCAGCTTTCCTCTCACCATCCATC
BC4C/T
T

38179 TCCTACAATCCAGTTCCTCAGGCCTCTCTTCCCTCACAAGGTCCAGTGTCTAAGCCA
38239 AGCCTGAAGGTATGGTTAGGATGAATGGTAGGTATGAATAGTTACCATTTAGAAATTACG
38299 CAGTCTAAAGCGAATATTAATAGTTCAACTTAGCCTGGTTTCTCTTCGTGCAGCAAAGC

38359 CATCACTGGAATTTCTTTACTTACATTATGGAATGAAGTCGTTTCGTTTCTTATTTGTG
BC5C/T BC6C/T
T T

38419 TCTTCACACTTCTTAATAGTTCTCCAGCTAAGCTAAATTAATTGGGCTTGGTGAAAAAAA
38479 TAAAATTTTCTACAGTATGCAGGAATCTTGTGTAGAAGCTGCATTTAAGAACATAGAAGA
38539 AAATGGAGACATTACAACCTGACACTATAGAAATACAAAAGATCATCTAAGAATACTATAA