

Polymorphisms in the *HLA-DMB* region of the human MHC, spanning crossover hotspots *DMB 1,2*

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 L1 repeats plus 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 *DMB 1* and *DMB 2* are also shown.

90759 TGCGATTATTCTCTCCAGTAATCTACGGAAATCTACTGGTTGTTCTGCAGAAAAAGAATT
90819 AAGAGAGACAAGGAGACCTGTTGTCTAAGACTAAGGCAGGATGACGTTTACCTAGTAACT
90879 GATGATGCTAGGCTGAGGCACTCAGTGATTTGTCTCTACATTTGTCCCTGCCTACCTAGC

HLA-DMB exon 1-->

90939 CAATCTGTCCCTGTTTGGGACACTGGACTCCCGTGAGCTGGAAGAACAGATTTAATATC

90999 TAGGGGCTGGGTATCCCCACATCACTCATTTGGGGGGTCAAGGGACCCGGGCAATATAGT
91059 ATTCTGCTCAGTGTCTGGAGATCATCTACCCAGGCTGGGGCTTCTGGGACAGGCGAGGAC
91119 CCACGGACCCTGGAAGAGCTGGTCCAGGGGACTGAACTCCCGGCATCTTTACAGAGCAGA

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91179 GCATGATCACATTCCTGCGCTGCTGCTGGGGCTCAGCCTGGGCTGCACAGGAGCAGGTA

91239 AGGACACTTCTTCTGGGGACTCTCCCTTCCCTGCTCCTGTTTCAGGGTAAGGGTGTTC

91299 GTTTTGTAATTGCATTTGACACCCAGATAGTTTGTCTCCCTGGTATAACATTCCTATAGC

<-----R67.0R----->

91359 ACTTTGTACTTTGTAGCAATTTTAAATGTAATTAATCTGTATAATTAATCTGTGCAGTGTAT
91419 ATTCCTGCTGGAATATAGGCAAGGACAATGTTTCATCTTATTATTGCTGCCTCCTCAGC
91479 TCCTAGCACAGTGCCTTGCATGCAGCAAGTCTTCATAAATATGTGCGAAGTGAATATTT
91539 AATATTTCCAGCACAAATACAAGGCTGACTCTTTCTCTTGACCCTTTTTCTCTCAATAA
91599 TTTGCTTACTGAAGGCTGTGTTCTGGGCAAATGTCATGTTTAAACATGCAAATAATC

91659 TCGGGGGGCTACTCCTATCCCTGTGCTTAGTCTTGCATAAAGAGGAGACTGGATCTAAAA

-----R67.3F----->

91719 ACTTATCTACTACTTCTACTGACTCCCTCAAATCAGACTTTTCAGAACTTCAGTGTATGA
91779 GCTTGGTCAGTAGATGTTCCCTGAGCAGGAAATCTGTGCCAGACTAGCTGGATGTCACCA

91839 AGGCTTAGGTTCTGAGCTGAATATAGGAAAAATCAACTTTTTTTTCTTCTATATGCTACA

<----R67.5R----->

91899 CTCAACACTTCTTTGACCAACTGTGTGAGGTTTTTTTTTTTTTTTACTCATACCAACCA

<-----R67.6R-----> -----R67.8F-

91959 ATTCTCTATATTAGCTGGATATCCTATAAATCAATTCATTGTGACATTAAGTATAGGTT
----->

92019 AACATAGACACCAAAGGTTAAAGACTCAGTCCCATAAAGACTGCCTCCATTTTCAGACACCA
92079 ATCACAAAGTAGTAGGTTCCCAAATFACCCACATCTTCTGTCCAACCTTGCCACAAATCAG
92139 AGGTTCCCATGACCCCTCCTTGGGGTTGGTAATTTGCTAAAGTGGCTTATGGAATCAG
92199 GAAAAGTTTACTTATTATTTGTAGATTTTTTACAAAGGATATTTAATTGATAATAATAAT
92259 TATAAATATTCATGGGGTGGATAATGATGTTTTAGTACATGTAATGTACAGTATCAGAT
92319 CAGATCATCATCTCAATTTATCAATTTCTTTGTGTTGGAAACATTCATATCCTTCTCTAG
92379 CGATTTGAAATGATATAAAGTATTTATGTTAATGACAGTCAATCCACAGTGGTATAGAAC
92439 ACTAGATCATAATTTTGCATCCTTTAACAAAGGATATTTTAAAGCATACAAAGGAACATC
92499 CAGATGAAGAGATACCAGATCTGGAAGGGTCCCAATCACAGGAGCTCTGTCCCCACAGAA
92559 TTGGGGTACTTCACTCCTGGCATGTGGATGTGTTTACCAACTGAGAAGTTCTCTGAACT

92619 CCATAGTTCCGGGATTTTTATGGAGGCTTCATCATGTAGGCATGACTGATTATTAECTCA

<-----R68.3R----->

92679 ATCTCCAGCCCTTCCCTTTCAGGGAGTATGGGGATGGGACTAAAAGTTCCAGACTTCT
92739 AATCATGACTTGGTCTTTCTGGTGACCAGCCCTCCTGCAGGAGCCACCAAGGTACCT
92799 CATTAGAACAAGGACACTCCTGTTATCTAGGAAATCTAAGCGATTAGGCACTCTATGT
92859 CAGGAACCAGGTCAAAGACAAAGCTCTGTGCAGAGCTCCTAAATATACGTCTGTATGTT
92919 TTATATATTTATTTTGTGTATATTTATTTATTTATATATTTATTTATTTATTGCCAGGC

HLA-DMB exon 2 --->

92979 CAGTAGAAGACATTGACCTGTTCTCCCTTCCCTGGCTCCTCTAGGTGGCTTCGTGGCCCA

----- R68.7F ----->

93039 TGTGGAAGCACCTGTCTGTGGATGATGCTGGGACTCCAAAGGATTTACATACTGCAT

<-----R68.8R----->

93099 CTCCTTCAACAAGGATCTGCTGACCTGCTGGGATCCAGAGGAGAATAAGATGGCCCTTG

93159 [CGAATTTGGGGTGCTGAATAGCTTGGCGAATGTCCTCTCACAGCACCTCAACCAAAAAGA](#)
93219 [CACCCGTGATGCAGCGCTTGGCGAATGGGCTTCAGAATTGTGCCACACACACCCAGCCCTT](#)
93279 [CTGGGGATCACTGACCAACAGGACACGTGAGGAGAGAGGGGTGCAGAGGGGCTACCAGGA](#)

93339 [AGTGCAGTTAGGAGGGCAGGCCAGGAGGATCCCACAGTGGCCAGGGTTTGTAGATTTG](#)
-----R69.0F----->

JJ1G/A
93399 [AGCAGCAAATAAGAGAAAATGTGTGGATCTGAAATGTAGAAAGACGGAGGATTGAACCTC](#)
A

93459 [AAGGGGAACAAGGTGGCTGACGTGAGTGGAACAGGAGTAAAGAAGGGGAGGTGAGGCTTG](#)
93519 [AACC CGAGGTGCCATGTGGGGAGCTTATGCAGAGGCTGGGGCATCTCAGGATGCATACC](#)
93579 [CAAGATGTTCTTGGCTTGTATCCAGATTTTGTATGTTCCAGATCTGATGTGGGCCAGG](#)
93639 [CATGGGAATATTTGGAATCCCAGGGGATTCTGACACATGCTTTTTCTCACCCCTAAACTC](#)
93699 [TTGCATTGACAATGGCTTGAAGTTTGTGAAAGTAAACTTGAAGATCTCCACAGTACAGAA](#)
93759 [CAGTGTGCTCAAGGGTGGTTTCTGAACCACCTTTCTCAGAAATGCCTGGAGGAGGTGCT](#)
93819 [TGTTAAAGATGCAAGCCCTTAGTACCCTCCAGATCTGTTGAAAGAAAGTATCTGGGGA](#)
93879 [TACAGCCTAGGAAATCTGCATTTTAACATAATTCCCTTGGATTTTATTTAAGATTGTGTT](#)
93939 [TGAAAAATGTCAAGATAGAGGCAAGCAAGAGGATCACCTAGGAGAGTAAATTAGTAAAA](#)

JJ3T/A
93999 [ATGGCAGTATTAGCAATCTCTTTAGTTTGGACTACATTCATTCCAAATTTAAGAGTGAGTC](#)
A

94059 [CTAAGTTAGGCTTGTTCCTTGAACATATGTGAGGAGAAAAAGCTTTAACTAGCAAAGAA](#)
94119 [CGTATTAAACAAGATTTGGAGAAAAATCCCTTTCCACCTTAAAAAAACCCAATGTACAA](#)

JJ4T/C
94179 [CTCTGGATTACTCTTAGCTTCTTATTTCAAATACTTTCCAGTTTATGTAAGTGAATAA](#)
C

94239 [ATACAACAACCTCTAGAACAGCTTGCAGTTCAGATCTGGCTTTTACTAATTGTAATCAAA](#)
94299 [CATAATCTGGAGGAGGAAAGAAAGAAAGGGCAATGAAGGAATGGGAGAGAAGAAAGAG](#)
94359 [TAATGCAGGAATACATTTCAACGGTTCCCTTCAAGGGGAGCATGGCAGAGGGGCTGG](#)
94419 [GGTGGAAAGTGGGTTGCAAAATCTACGAAGAGTTGCGATAGGGAAGAAACCAGGTTGAGG](#)

HLA-DMB exon 3 --->
94479 [AAGCAGCCAGAATGTCACCCCTCTCTTAAACATGTTTTTTTTCTCCTATGCAGGGCCACC](#)
<-----R70.2R----->

94539 [ATCTGTGCAAGTAGCCAAAACACTCCTTTTAAACACGAGGGAGCCTGTGATGCTGGCCTG](#)
94599 [CTATGTGTGGGCTTCTATCCAGCAGAAGTGACTATCACGTGGAGGAAGAACGGGAAGCT](#)

JJ5C/A Ala->Glu
94659 [TGTCATGCCTCACAGCAGTGCAGCACAAGACTGCCAGCCCAATGGAGACTGGACATACCA](#)
A

94719 [GACCCCTCTCCATTTAGCCTTAACCCCTCTTACGGGGACACTTACACCTGTGTGGTAGA](#)

94779 [GCACATTGGGGCTCCTGAGCCCATCCTTCGGGACTGGAGTAAGTGTATGGCAGATGGATG](#)
-----R70.5F----->

94839 [GAATTAGGGTCAAAGCAGAGAAAATGAGATGTGGATCGATACATGGTACATGGTAGACAG](#)

94899 [CGAAGTGTGAAAATGGGACTGAGTCTGGAGGAACCTTACGGGGGCTTAGGACCAGAAT](#)
<-----R70.6R----->

94959 [GGGGAAATGGGATAAAGAAATGGAAATATTTAGGTTGGTGCAAAAGTAATTGCAGTTTTT](#)
95019 [GCCATTACTTTTCAGTGGCAAAAACCGCAATTACTTTTGCACCAGTTTAAATTTTGTCTG](#)

JJ6T/C
95079 [TGCTATTGCTGCTCTGGTGGTGGTTGATGTTGCTGCGTCTATGTTTGGGGTGAGAGG](#)
C

JJ7A/C
95139 [GGAGCGTGTCTTGTGAAATGAGGATGTAATTTGGCAATCATATTTTTCAGAACCCCAA](#)
C

95199 [ATTGTAATACACTATTCTAGCCTCCTTAGATTTCAACTATTCTGGTGCCAGAAGCAGATG](#)

95259 GGAGCTGAAGGAATGATGAAGGTTGAAGAAGGGGGCTTTTCTTGGTGTGGGGCAGTACT

95319 GCATTTGGCCTGCTCTACCAAGCATACGGGAGTAGTAAAGCCACGGCTGGCAGACCATTT
 -----RU71.1F-----
 ----- R71.0F ----->

95379 GGCATGCATGCTCAGGGGCCAGTGGATAAAGAATTACTTACAGTTCAAACACTGTTTGAA
 ----->
 <----- R71.1R -----

95439 CTCAGTGTCCGGAGTAGTTAAAGGTATCGTGAGAAGTTGCACACAGCTTTGGGGACTCTT
 <-----R71.2Rs-----

95499 GGAAAAGAAAGAGGAAGAAATGAGGAAGAGGAGGTTGCTACAAAGGGCCAGAGAACAG

95559 GATCTCAGATCAGCTGCTGTAACCAGGTTTCCCTTGTGGGAAGTGTGTTTCTTGCTGG

95619 GCAGTTGGGAAGGAATGGAGAACAGAGAAGAGAGTGGAAATCAGTGCCTCATTGAACT

95679 TTCCITGGGGAACGTCTCCTCACAGCGTGCACAAGAGCCTCCCTTTTGAAAATGGAGTGTTC
 J8A/G J1A/T
 G T

95739 ATTTTATCATGGGAAAAGAAATCTGAGTGGGACATGATTCAGAACAGGACCGGCCAAAGGA
 ---- R71.5F -

95799 AGTGCAGGGGCTGTGGAGTGGGATGGAGACAAGCTCTGAAAGGACACATGGGAGATCTAG
 ----->

95859 ATGTAGAGGTACACAAGTAGTAGGATAACTCACAGGATGGATCCACTGGAGGTTAAGAC
 J2A/G
 G

95919 ATGTGGTAAGACAGTGTAAATAGGAAGCTGCTCAGTTGGAGAAAGTAAGGAAGCAAACATT

95979 GTTACCGTGGGGCAATGGAGAGGACAGTGGAGAGCCCTTTATCCTGATAAGGGTGGCTT

96039 TGAGGTAAAGGAAGGAAAGAGGATGCCTTGAGAGGCCCCACTGTATTAGAGAGGACCTGG
 J3A/G
 G

96099 AAGCCAGGATGCTAATTCTGGGGAGATGGATTCGCCAGGCTTACTCTAGGAGTAGAGGTC
 J4A/G
 G

96159 CATGGGACGAGGTTTGATTTGAGAAAGATCATTTTCTTGGGAGTGGGTGGTGTGAGCTA

96219 GACCTTGGAGCTGGGATAAAGGACCTTTTAACCCACTGAGAGGTGGCTGCAATAAATGG

96279 AATTGCCCTGGGGTGTAGCAACAGAACTGGGTCAAGTAAGTTTCTATTTTTTGCAGCAC
 HLA-DMB exon 4->

APPROXIMATE CENTRE OF HLA-DMB HOTSPOT 1

96339 CTGGGCTGTCCCCATGCAGACCCTGAAGGTTTCTGTGTCTGCAGTGACTCTGGGCCTGG

96399 GCCTCATCATCTTCTCTCTTGGTGTGATCAGCTGGCGGAGAGCTGGCCACTCTAGTGAGT

96459 GACTCGCTGAACTCCCACTCCCACTCTTGGTCCCACTCTCTGCTTACTTTCTGTTTGTGA

96519 TTAACTCTCTCCTTCCCTACTGCATTTGCTATGAATACTGCTAGATATTTTATCCACAAA

96579 GACTGGTATAATCAAGTATCTTCCCTCTCTTAGGTTACACTCCCTCTCCITGGGTCCAATTA
 HLA-DMB exon 5 ->

96639 TTCAGAAGGTAAACATCTCTGTTGGTCTGTTTCCCTACTTGCCCTTTGGTAGGGGTGCGGG

96699 TTAGAGGGTCAAGTGTGGGTTCAACTAATCTTGATTATTATATGGGTGAGCTTCCATGA

96759 GGATCTAGGCAAGGGCATGATTTAAGCTGCCATTGCTAGGATTAAGAGCAGGAAGGAGCA

96819 TCCTCTCTTCTACCAAGTGGGATGTCTGTGGAGAGGAGGCTGAAGGTGCTTCCCTTTGTA

96879 TTAGTTGTTGGTGCCTGGAGTTTTCAGTATCACTGTATTAAGGCATGGGATGGTTACAG

96939 TGACAAACGATGGGGCAAGTTGGGTTGAAGCCTCATTTATCTCCCTTTTATTTATCTGT

HLA-DMB exon 6-> ter

96999 AGGATGGCACATTTTCCTAGAGGCAGAATCCTACAACCTCCACTCCAAGTGAGAAGGAGAT
 <----- R72.7R ----->

97059 TCAAACCTCAATGATGCTACCATGCCTCTCCAACATCTTCAACCCCTGACATTATCTTGG
 97119 ATCCTATGGTTTCTCCATCCAATCTTTGAATTTCCAGTCTCCCCTATGTAAACTTAG

J13C/T
 97179 CAACTTGGGGGACCTCATTCTGGGACTATGCTGTAACCAAATATTGTCCAAGGCTATA
 T

97239 TTTCTGGGATGAATATAAATCTGAGGAAGGGAGTTAAAGACCCTCCTGGGGCTCTCAGTGT

polyA signal
 97299 GCCATAGAGGACAGCAACTGGTGATTGTTTCAGAGAAATAAACTTTGGTGGAAATATTGT
 97359 TTTTCCATGCTTCTTCTCCTGGGGCCCTGGGGAAGGAATATGGGCAAAGCAGGGACTGAGG
 97419 TTAATCTCTTCTGCTTGAGTAGGGGAGAAATCAATGCCTTCTTCCATTTTCCCACTTAG
 97479 ACATGACAGAAATTTGGGGCCGTTTTCTGATTTATAATTCATAAGGAGAAATCAACTGTG
 97539 GTGGGTGGAGTCACAGAGTATGGGCAAGGAAGGAATTAACAGCTTACTCACCTCATAC
 <----- R73.2R ----->

J14G/C
 97599 AGGATCTTATGAGGATTAATGAGTTCATACTTGTAATGGCTAAGAACACCCGCCAGGCA
 C ----->

97659 CATAGCCAGCCTGCAATAGTGACGTTAGCTATATTGATTATTCAACTTCTGGCCAGGC
 --R73.3F----->

Jjk1C/T
 97719 ATTGTACCAGGTGCTTTGATCCTCATCACAACCGTAAGGCAGACCCTCATACCCTCAG
 T

Jjk2C/T
 97779 GATTCAGGGGACAGAGCTTAACTCCAGATTGAGTTCTAGACAGTTATTTCTTCCATACCC
 <-----R73.5R-----> T

97839 TGAATGCAGAAGGGAACATAGCTTGAGTGATTATTATGTCTTAGGCACTGGTCTCAGACC
 97899 TTTATATTTGTAGCTCATTCTCTCTCACAATAACCACACAAGGGACAGATTGTTTCCCT
 97959 CTATGTTACAGACAAAAGATGTGAGGCTCAGAGACATTTAAGTGAATTTGTTCAAGGTCAA

98019 AGAACAGATTTCTGTAGGATGTTTGTCTACCTGAGCTGGAAGTAGCAGATTACTTTATTTC
 -

98079 TGAAGACCCTCATGCTGGTGAGCACACATCTCTTCAGAGCCACCGTTCATTCCCTTCTA
 -----R73.8F----->

98139 CCCCAAGACCAAGGAGAGCCCTTTGGGGGAATGACTCCACCCTAAGGAAGAGAGGATGC
 98199 TGGCTGGTGGTTTGTGTGCCACGAAGGGCGACACCTGCTGGACACAGAAACCTAGGGTG
 98259 TGGAATGTTTTTGGAAATFAGAGCTAGATACTAGAATATGGGTAAGAAAAGAAACCAAG

98319 AAATGAGTTGATTTGGAACACCTCCATAAATTTCTTCAGAAGCATCCTTGAATTAGAGCA

Jjk13G/A
 98379 TCTCTTCTGGAAGGGGTTAACAGAAGAAGTCAGTGGGAAGAACTTAATCTCTACATTTTA
 -----R74.1F-----> A

98439 CCATTTTTATGTTTCATTTTCATTTTTCTATTCACTGTTTTTGTTTTTATTTTTGTTTTG
 98499 TTTGACAAAGCAAATTCCTTTTGAAATTTCTAGTTTACTAGGAATGGGGGCTTTGGGC
 98559 CTTGCTATATCTGGGCAGTTTTATTTATTTATTTTATTTTATTTATTTATTTTTCG
 98619 AGACAGAGTTTTGCTCTTGTGCCCCAGGCTGGAGTGAATGGCGTGATCTCGGCTTATTG

98679 CAACTTCTGCCTCCCATGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGAGAT

Jjk15T/C Jjk16G/C
 98739 TACAGCGTGCACCACCATGCCTGGCTAATTTTGTATTTTCTTAGTAGGGATGGGTTTC
 ----R74.4F-----> C C

98799 ACCATGTTGGTCAGGCTGGTCTCGATCTCCTGACCTCAAGTGATCCACCTGCCTCAGCCT

<---- full length Alu element

98859 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCACTAGGCCTATCTGGACAGTTTTAA

Jjk3G/A

98919 AGGAGAAGCTGCAGATCTGAAGGTCTAGTTCTAGTCACAGCAGTGGGAATCAAAGTGGC
A

98979 AGGATCCCAGAGAAAGGAAGTAGAGAGTTAGCTAATGGGACGGCTTCCAGTTCCTTTTCT
<----- R74.7R -----

Jjk5T/C

99039 AGAGATTCCAGTGCAGGCTTTTCTCTGCCCTAACTTTGTAGGTTTTTTTGTATATAGGA
C

Jjk9C/T Jjk4G/A Jjk18G/C

99099 AAGGCTGTCCCTTCCAGGTAAGGAATAGGGAAAAGTATATGTAGGTCTCTAGGATCCA
T A C
<-----S--R74.8R--

Jjk14G/A

99159 GAAAGTCAGAATACTATAGGTAGAAAGGGAGTTCCTTACACAGGGGAATGAGTGGTACTT
A

-

99219 GAAAGGAAGGTGGAAGAAGGGTGATGGTGCACCAATTGTAGGAGGATGAGGAGAAGAGAA

Jjk10C/T

99279 TGGATGCTGCATGAGGAGAATGGAATGTAAACATAATGGATTGCCAAAAAGGAGTCCGT
-----R74.9F-----> T

Jjk11+/- Jjk12+/-

99339 GTGTGTGTGTGTGTGTGTGTGCACTTGAGCACATGTGAGAGAAAGAGAGAAAAAAGAG
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<-----R75.0R-----

Jjk6G/A

99399 AAGGAGTGGAAGAGAGTAAGAGAGAGGGAGCAAAGGGTGAGAGGAGAGAAGTGGAGTGG
- A

99459 GAGAAAGAAGGAGAGGGACATAGAGAGAGGGAGGGAGGGAGCGGGGAAGAGAGAGAGA

99519 GCTGGACTTTCGGGTTATACATAATCCAAGCTGCACAAAGAATGTTTTTCGCCCTTCAAT

APPROXIMATE CENTRE OF HLA-DMB HOTSPOT 2

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99579 GTCTTGTGTTTTTAAAGCTGAACTTGGAGCTAGAATTTGGTTTTTAAAGGTCATCTAGTCC
C

Jjk7G/C

99639 ACCTCCCCTCCCATGAAAGAAGCTGGGCCTGTGTTAACAAGGGCACACACAGTGCAGGGAG

Jjk8C/G

99699 TTCTTCAACACTTGGGGCAGATAACAATATTTTAGAGAAACGCGTTGACCCACATTTG
----R75.4F-----> G

99759 AGCTTCTTCTTTTGACCATTAAGACAATGAGAATAAATCTCAAATACACCACGGGAGGT
<-----

99819 GGTATCCTTGGCATTTTTTTTTTCCCTGAGGGAGAGCATGTTCCTAGGTTCCAGGTTCTC
---R75.5R---- <-----R75.5Fs----->

99879 TTTGCTCCCTACCCACGAACACATGCATGTGAAAGAAACAGACAAGATTGACATTTAAT

99939 CCCAATGTCTATTTATGAAAATTATCTTTAGGCCATTTCTCAAGTTTTTCTCTTTCCAA

99999 AGTAAAATTGGGCAAATCAGATGAAAACGAGGGTGGAGTTCAACCCCATCTCAAATCC

100059 TTTTTTTTTTTTGGCTTGAGTGTCTGTCAATCCCAAGAGCCCTCCAACCTGCCTTGAAGCA

100119 AGGCATGGGGGATTTCTCCGTGGTGCTTCTGCCACTACTTGGCCAGACCAGTCTCCAGG
-----75.8F----->

100179 GGTTTCAGAGAGTGGAGAGGCCCAAACCTATAGAGACTACTCCAGATGGGGGGCTCCT
<-----RU75.9R-----
<-----R75.9R-----

