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NEW ALLELE ALERT

Genomic Full-Length Sequence of the *HLA-DRB1*13:97:01* Allele Was Identified by PacBio Sequencing

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Received: 8 April 2025 | **Revised:** 10 April 2025 | **Accepted:** 12 April 2025

Funding: This work was supported by Qingdao Key Medical and Health Discipline Project, Qingdao Outstanding Health Professional Development Fund.

Keywords: genomic full-length | *HLA-DRB1*13:97:01* | PacBio sequencing

ABSTRACT

The complete genomic sequence of HLA-DRB1*13:97:01 was determined using a PacBio sequencing approach conducted in China.

Here, we present the complete genomic sequence of *HLA-DRB1*13:97:01*. This sequence was identified in a volunteer donor participating in the China Marrow Donor Program. To date, a total of 3787 HLA-DRB1 alleles have been identified according to the IPD-IMGT/HLA Database Release 3.59 in 2025 [1], amongst which 526 are classified as DRB1*13 alleles. The sequence of the HLA-DRB1*13:97:01 allele was first submitted to the IPD-IMGT/HLA Database in 2009. However, at that time it only encompassed exon 2. Here, we report the 13413 bp full-length genomic sequence of *HLA-DRB1*13:97:01* obtained through PacBio sequencing—a third-generation sequencing platform. In brief, group-specific amplification was performed using primers located in the 5′ untranslated (UT) and 3′ UT regions, followed by Sanger sequencing using generic primers in both forward and reversed directions by means of cycle sequencing [2]. The sequencing results of HLA-DRB1 in this sample did not fully match any allele combination. In order to determine the reason for this difference, third-generation sequencing (Pacific BioSciences) was used. The library was added to the sequencing chip and sequenced using a PacBio Sequel II high-throughput gene sequencer. The excitation wavelength of the instrument could excite the group to emit fluorescence, and the fluorescence signal was recorded. Subsequently, we used the official PacBio software, Circular Consensus Sequencing (CCS), to process the HiFi data. Then we partitioned the library based on the presence or absence of barcodes. Following this, we conducted backposting, mutation detection, clustering, typing and haplotype verification of the results [3]. Finally, the full-length sequence of the HLA-DRB1*13:97:01 allele was confirmed.

The sequence of the *DRB1*13:97:01*, a total of 13413 bp in length, included all exons and introns, 5′-upstream region and 3′-downstream region were first reported here. Compared with the *DRB1*13:02:01:02* allele, the novel *DRB1*13:97:01* has four nucleotide changes from *DRB1*13:02:01:02*, one change is at nucleotide 8190 in exon 2 where A->T (codon AAC->TAC), resulting in a coding change. Asparagine residue 66 is changed to a Tyrosine. The other change is a three nucleotide GAG insertion after nucleotide 8467, which is located in intron 2 as shown in Figure 1. The complete HLA typing of the donor was as follows: HLA-*A*03:01:01*, *30:01:01*; *-B*13:02:01*, *52:01:01:01*; *-C*06:02*, *12:02*; *DRB1*07:01:01*, *13:97:01*; *-DQB1*02:02*, *06:04*.

The full-length nucleotide sequence of this allele has been submitted to the GenBank nucleotide sequence database and was assigned the accession number PV208186, and to the IPD-IMGT/HLA Database, the accession number HWS10100606. The name *HLA-DRB1*13:97:01* was officially assigned by the World Health Organisation (WHO) Nomenclature Committee for Factors of the HLA System in 2009 [4], the sequence extension was submitted in February 2024.

https://doi.org/10.1111/tan.70200

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                                                                                                      -315
DRB1*13:02:01:02   TTGTCAAGTG GGAAATGAAT GCTCTTACAA GGCTCAAACT TGTGAACACA TCACTGACCA GCACAGAGCT AAAATAATTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      -235
DRB1*13:02:01:02   GGGCTAAAAA TACCGCCCCA ATTAAAGTGT TTTACATGCA ACTGGTTCAA ACCTTTCAAG TACTAAAAAC AATCCTGTAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      -155
DRB1*13:02:01:02   AGAAGGAAAT TCTGTTTCAG AAGAGGACCT TCATACAGCA TCTCTGACCA GCAACTGATG ATGCTATTGA ACTCAGATGC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       -75
DRB1*13:02:01:02   TGATTCGTTC TCCAACACTA GATTACCCAA TCCAGGAGCA AGGAAATCAG TAACTTACTC CCTATAACTT GGAATGTGGG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                               |Exon16
DRB1*13:02:01:02   TGGAGGGGTT CATAGTTCTC CCTGAGTGAG ACTTGCCTGC TGCTCTGGCC CCTGGTCCTG TCCTGTTCTC CAGC|ATGGTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----|------
                                                                                                        86
DRB1*13:02:01:02   TGTCTGAGGC TCCCTGGAGG CTCCTGCATG GCAGTTCTGA CAGTGACACT GATGGTGCTG AGCTCCCCAC TGGCTTTGGC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                   |Intron1                                                            166
DRB1*13:02:01:02   TGGGGACACC AGAC|GTAAGT GCACATTGTG GGTGCTGAGC TACTATGCGG TGGGGAAAAT AGGGAGTTTT GTTAACATTG
DRB1*13:97:01      ---------- ----|------ ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       246
DRB1*13:02:01:02   TGCCCAGGCC ATGTACCTTA AGAAATTGTG ACGTATTTTT CAGAGATTGC CCGTCTTTAT CATATGGATC CCAAATAATT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       326
DRB1*13:02:01:02   TCCCCACCAC AAAAGGAGCT TGGCTACTTG CCCACTCCAT GAGACTTGTG TAAGGGGCCT CCATACAGGT CATTTCTACT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       406
DRB1*13:02:01:02   CAAATCTCCA CCAATAAAAC CTTTGCATCA CATGTCCTCA GGGTCTTTAG AGGATTTAGA AATAAGGATG CTAAAATAAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       486
DRB1*13:02:01:02   TTCCCCATAC AGCACTTGCC TTTATTATGT TGACTTAAGT CAGACAAAAG GAGGTTTTTT CTGAAAATTT TGTGGAAGTC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       566
DRB1*13:02:01:02   AAGGGAATTT AAAGGGTCTC TCCCAAACGA TCCTGGGTTA TGTCACCCAC AGGACCTTTG GTGTTGGCCC CTCTTCCTCA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       646
DRB1*13:02:01:02   TATGTGAGGA TGGACCCAGT GGCCTCCCCA TTATCTACTT TCTTTTCTTT CTGAACTCCA ATGTTTATAA AGCCTGTACC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       726
DRB1*13:02:01:02   CCTGTAGTGT ATGTAGGTTG TCTGACAGAA GTTATACTTA GTGCTCTTTC TTTCTTGTGG GGAAAAATCC CTGGAACTGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       806
DRB1*13:02:01:02   AGCTGAGATC TTTAGTACTT GGAGTCACCT TACAGATACA GAGCATTTAT GAGGTATTCT TTGGTGCCTA AAGAACTTAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       886
DRB1*13:02:01:02   GGCATCCTCT GAAAACCTGG CCCAGGTTAG TGTTTATTGT GAATCTCTTT TAACCTTTCT ATACTTGTTT CTCCTACATC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       966
DRB1*13:02:01:02   TCCTAAGTGC TCCAACCAGA CATGACAGAA GAGATTTAAC TAACGTAGTA TGAGTTATAT AAAATTCTAT TTTTGTAAGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1046
DRB1*13:02:01:02   CAAAAATAAT CAAATATCAG AAATTTAATA ATGTTCAAAC TATATACTCT GTGTGGGGTT ACCGAGACAA TGTGGACATT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1126
DRB1*13:02:01:02   GTTCACATCT CATAGGGCTG CAAGTCAATG GGCAAGTCCT GGGAACTCAT TGTCTTACTG GGGTCTTGTC CTAAATTTCA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1206
DRB1*13:02:01:02   TAGGTTCACC CATCATGCCC TCAACTTTCC TTAATTAGCC ATGTCTGCTT ACCTCTTCCT CCAGTTTCTC TCTTATTTTT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1286
DRB1*13:02:01:02   CCCCAGCTAT GTTGTTATCA TTTCCAGAAA TCTCTAAAGC TTGCACAGAT CCTTAGCACT ATGAGATCCA TTGAAAGAGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1366
DRB1*13:02:01:02   TAGTTTTTTT CTTTTTGAGA TAGGGCCTGG CTCTGTCACC CAGGCTGTAG CTCAGTGGTG CGATCGAGGC TCACTGCAAC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1446
DRB1*13:02:01:02   CTCTGCCTCC CACGCTCAAG TGATCCTCCC TCCTCAGGCT CCAGAGTAGC TGGGAATACA GGCAGGCAAC CACGCCCAGC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1526
DRB1*13:02:01:02   TAATTTTTGT AATTTTGGTA GAAATGAGAT TTTGCCATGT TGCCCAGGCT GGTCTTAAAC TGCTGGACTC AAGCAATCCT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1606
DRB1*13:02:01:02   CCTGCCTTGG CCTCCCAACA TGCTAGGATT ATAGATGTGA GCCACTGTGC CCAGGCAAAA AGAGATGACT CTCAATAAAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1686
DRB1*13:02:01:02   AAAAGTCCTT TTTCTTAAAT CACTGTTTCT TTATCTGTGA ATTCTTCTTC CAACTAGAAG GAGGAGAAAG AAGTTTGCCT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1766
DRB1*13:02:01:02   GTATTTCTCA CCAGGAGGAG AAGGGGTCTA GTGTGACATC AGAATGAAAG AGTGCTGGAG TTTGAGCCCC TTCTTGCTTT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1846
DRB1*13:02:01:02   CAAAGATCCC CACAGTTATC ACTTCCCATA CCCTGGTTTA TTCATGTAAA CCACACTTAT TTTTCTTAGC AGCTACTGTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      1926
DRB1*13:02:01:02   TACTCGGCTC CATTCTAGGT TCAGATCATT CTATTTTATT AAGACAGAGA GGGTCCCGAC TCTCATGGAA GTTACACAAC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2006
DRB1*13:02:01:02   AATAGAGGAG ACAGACACTA ACCCAATAAG CATTTAACAA AGAATAAAAT ATTAGAGAGT CATAGTGCAC TGAAGAAAAG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2086
DRB1*13:02:01:02   ACCTCAGGTT TGTGAAGAAG AGAGACATGG ATTCACCTAC TTTAGTTCAT ATGTTTAGGG AGCTCTACCT GAGAAAGTGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2166
DRB1*13:02:01:02   CATTCAGCTG AGACAACAAA ATAAGTAGAC AGTCATGAAG ATCTAATGGA CGAAAGCTCC AGAGAGACCA AATGGGGGTA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
```

FIGURE 1 | Alignment of the full-length sequences of the *HLA-DRB1*13:02:01:02* and *HLA-DRB1*13:97:01* alleles. Dashes indicate identity with the *DRB1*13:02:01:02* sequence. The nucleotide positions are numbered according to the genomic full-length alignment in the IPD-IMGT/HLA Database. The *DRB1*13:97:01* allele showed 4 nucleotide changes from the *DRB1*13:02:01:02* allele; the first change is at nucleotide 8190 in exon 2, and the second is a three-nucleotide GAG insertion after nucleotide 8467.

```
                                                                                                      2246
DRB1*13:02:01:02   AAGCCCTGGT GTGGGAAATT ATGTGGAGAG AGAGAAAGAA GGCTAGAGGG GCTGACGTAT AGAAAGTAAG GAAATGGAGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2326
DRB1*13:02:01:02   GGCAGAAGAT GAGGTAGGAC ACAGAGAGAA AGTCAGGAGC CTCATCATTA TAGGCTCTGA TGTCCACGGT AAAAAATTTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2406
DRB1*13:02:01:02   AATTTTATTT TATTTATTTA TTTTATTTTA TTTATTTATT TATTTATTTA TTTTTTGAGA TGGAGTCTCG CTTTGTTGCC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2486
DRB1*13:02:01:02   CAGGCTGGAG TGCAGTGGCG TGATCTCAGC TCACTGCAAG CTCCACCTCC TGGGTTCATG CCATTCTCCT GCCTCAGCCT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2566
DRB1*13:02:01:02   CCCTAGTAGC TGGGACTACA GGCACCTGCC ACCACGCCTG GCTAATTTTT AGTATTTTTA GTAGTGAGGG CATTTCGTCA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2646
DRB1*13:02:01:02   TGTTAGCCAG GGTGGTCTCC ATCTCCTGAC CTCGTGATCC ACCTGCCTCA GCCTCCCAAA GTGCTGAGAC TACAGGTGTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2726
DRB1*13:02:01:02   AGCCACCACG CCTGGCCTAT TTTTTTTTTT TTTTTGAGAC GGAGTTTCGT TCTTGTTGCC CAGGCTGGAG TGCAATGGTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2806
DRB1*13:02:01:02   CAATCTCGGC TCACTGCAAC CTTCGCCTCC CTGGTTCAAG TGATTCTCCT GCCTCAGCTT CCCAAGTATC TGAGATTACA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2886
DRB1*13:02:01:02   GGCACCCACC ACCATACCTG GCTAATTTTT ATTTTTTTGT ATTTTTAGTA GACATAGGGT ATCACCATGT TGACCATGCT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      2966
DRB1*13:02:01:02   GGTCTCGAAC TCCTGACCTC AGATAATCTG TCTGCCTTGG CCTCCCAAAG TGCTGGGATT ACAGGCGTGA GCCACCGCGG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3046
DRB1*13:02:01:02   CCGGACTGAA TTTTATTTAA ATAGATACGA GAAGCTACTG TATGGTTACA AGGAGAGTCA ATTTATATTC AATTTATTTT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3126
DRB1*13:02:01:02   TATTTTATTT TATTTTTTTG GTGATGGGGT CTTGCTCTGT TGCCCAGGCT AGATTGTAGT GGCACAATCT CGGCTCACTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3206
DRB1*13:02:01:02   CAACCTCTGC CTTCTGGGTT CAGGCGATTC TCCTGACTCA GCCTCCAGAG TAGCTGGGAC CACAGGTACA TGCCACCACA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3286
DRB1*13:02:01:02   CCTGGCTAAG TTTTTGTATT TTTTAGTAGA GACAGGATTT CACCATGTTA GCCAGGATGG TCTCGATCTC CTGACCTCGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3366
DRB1*13:02:01:02   GATCCACCCA TCTTGGCCTC CCAAAGTGCA GGGATTACAG GCCTGAGCCA CTGCGCCCGG CCTATATTCA ATTTTTAAAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3446
DRB1*13:02:01:02   CTAATTCTAG CTACTCTGTG GGGATTGGAA TGTTGGGGTT CACAAGTGGT CAGGAAGACT ATTTAGGAGC ACAGCAGGGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3526
DRB1*13:02:01:02   ATTCTCCAGC GAAAACAGGC TTGTGGCTTC ATGGAGTGCA TTAGTGATAA AGACGGTGAA AAAGATAAAG TGGACAGACT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3606
DRB1*13:02:01:02   TGGCATGTAT TTTTCCTTAG CTTGTTAATG AATTACTGTA AAGGGGGTAG AACAATCAAG CTTATTCCTA AGGATTTTGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3686

DRB1*13:02:01:02   TTTGACAAAT AAGTGGGTGG TAGTGTTGTT TATTGAGATA GGAAAAACTA TGGGAGGAAA TTATTTGAAG TGGGTGGTTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3766
DRB1*13:02:01:02   GAAATAAAAG TTTTGTTTAA ATTTGAGATG ATTTATTGAC ATTTATGTGG AGCAATCAGA AGGTCAATGG CATTTAAGAG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3846
DRB1*13:02:01:02   ACTCATGGTG AGGTGAAGCT AGGGCTTCAA GTATTTATGT TGGCGGCATC AATACGTGTA GTGTGTTAAA TTCCAGGGAG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      3926
DRB1*13:02:01:02   TGGAAGAGGA TACATAGGGA GATGGATTGT GTGGAGAAAA AAGAACAGGG CACAGGCCAG CAAAGGGGGC TGAGAAAGAG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4006
DRB1*13:02:01:02   CCCAGGGATG TTGGAGAAAA ATCAAGAGAA CATGATGCAT GTAAGTCAAG GAAAATAGAT TTTTTTCAAG GAGAAGGGAG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4086
DRB1*13:02:01:02   AGGCCAATTG TGGTGAGTAC CACTAAGCGG AGGGGGAAGT GAGAACGTGA CAGAGAAGCA AGTGCTGAGT TTGGTGGAGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4166
DRB1*13:02:01:02   TGATATTTGC AGTCAGTGGA GTATTCAGGG AGGAAACTGG ATTGGACAAT TTGAAGAGCG AGTAGAAGTG AGGATGAGGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4246
DRB1*13:02:01:02   TAAGATTGAC TGTTTTGAGT AGAGAGCTTC AGGGAAGGAC TGCACTCTGG GTTCAGGGAG CCAGCTGGAT CAAAAGGAAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4326
DRB1*13:02:01:02   AGGCTAAAGA GGCTGAAGAG AAGCAGGAGG ACCTGTGAAC CAGAGATGCT CAGTCATCAT TAGCGAGGAA ATACTAGAGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4406
DRB1*13:02:01:02   GCCCCTGTGT GCAGTGATGA CTACTCATGC AGAAGGTCAC ACAGCCAATA TTTAACACAG CCAGTATTTC ACACAGCTAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4486
DRB1*13:02:01:02   TATTTATTAG TGACATAGAA TATACCAGTT ATTACTCTAG GTCATGAGAA TGGAGTGATA AATAAAATGA ATCCGGTCGC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4566
DRB1*13:02:01:02   CATCAGTATA TGCCATGTAA CATTTTGCAG TGACTGTGTA CCAGGCCTAT GAATTTCTGT ATGCAATTTC AATAATGATC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4646
DRB1*13:02:01:02   CTGCTGTATC TGTGGTGTTT AAAAACATAT ACATCTCTGG AATCTAAAAT TGAGAGGTTA TAAGTAAAAC CCAGTATTAC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      4726
DRB1*13:02:01:02   AAATTGAGTG CTGGAAATCA GATTGCAGTT TAAATCTGAG CATATAGGAA ATCCCTTTCT CCTATGTCAG CAGATGCCTT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
```

FIGURE 1 | Continued

```
                                                                                                       4806
DRB1*13:02:01:02    TTGTGTGAGG TTTAGCTGGA CTGCATTATT AGACATAAAC CAGTGTTTCT GCCCTATGTT TTCAGAATGA CAATTCTTTA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       4886
DRB1*13:02:01:02    TGAAACTCAT AGAAGAACAG AAGACAACTG CAAAATCATG ATGAAGATAG TAATTGCTTT AGAATTAAGG AATACAAAAA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       4966
DRB1*13:02:01:02    ATAATGTGAG CTGTAGTTAT AGGGATCATA AAAGTTTAAA TGGGAATGTA TTTGAGTATG TGATCAGTGC TAAGAAGAGT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5046
DRB1*13:02:01:02    CATCATTTAA TTTTACACTT AACAGTAATC TCGTGAGGAT TACGCTATTA TTAAATGCAT TTGATAGATT ACAAAAAGGC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5126
DRB1*13:02:01:02    TTATGGTTGG TAAAAATTGA CCCAAGTAGA AGAGATCATG TTTTTATTCA GGTTTTCTGA TTCTAGAGTT TGAGAGTTTG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5206
DRB1*13:02:01:02    TCCATCATTA GTGAGTAGTG ACTATATTGT GTCTGAATTA TTGACAGAAT TTCTGATATT CATATGTACC AGGTTGTTTC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5286
DRB1*13:02:01:02    TTAGAGTGGG GATAGAGATG CAAGGGCTGC TAGTTCCGAT GTATTGGGGA AACTTTCATT CATTTTGCAT TTATCATTTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5366
DRB1*13:02:01:02    AAAAGTTCTG TATGTCTATA ATGGTCATGT GTTGAAGAAC ACAAGGAAGT ATTAAATCAC TCCTTCTTCT AAGGTTTGAC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5446
DRB1*13:02:01:02    TAGCAAGTTG GGCTAGAGTT ACCAAATAAA ATACATGTTC CTAGTGAAAT CTGAATTTCA GATACAAAAC CATAATTTAT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5526
DRB1*13:02:01:02    TGAAAATCCA AATTTAACTG GGCATCCTCT GGTTTTATTT GCCACATCTG TCAACCCTAA GTGTGACACA TGGACATGGA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5606
DRB1*13:02:01:02    TTACAGTGCT AACCATGCAA GCCACGGTGA CAGCAACTTC ACACATGTTT ATTTTTAACT TTCTCTGTAA GAAAGTGCTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5686
DRB1*13:02:01:02    AGATAATTTA GGGATAAAAA GATAGACATT GCTTGATCCA GGGTGCACAC CTCTCTGCCA CCATTTCTAA AGGGCAAAGG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5766
DRB1*13:02:01:02    GAGATTTCTG CAGGTCTTGC TCACAGTCTG GGGAGCTGCT CATTTTTGTA AAGTGTCTGT ATGAGAATGT CATTTTCTTG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5846
DRB1*13:02:01:02    GTTTCCTCCT TTCCGAGGGG ACTTGACTAC AAAACCAAGA GTTCTGCCTC TGGCCAAGGC TGGTAATTTG ATGCCTGCTA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       5926
DRB1*13:02:01:02    GTATTGTTGG GAGTGGGAGA CTGAAAGAAA TGAGTTAGTT GGGGCATTTA ACGGGAATAA AATAGCTGTG GTTGTGACTC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6006
DRB1*13:02:01:02    ATTACTACAG ATAATTAGTG GACCAGTGGC AGAGAAATTA AGAAAAAAGA TGATGTGAAT GATAAATGAT ATGATTAGTG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6086
DRB1*13:02:01:02    ACTGCTTGGT AAGGCAAGGA AATCATTAAA TCTTGGTTCT CATCAAGTTC ATTTTCTGGA AAGATAGCAC TGTATTGGGA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6166
DRB1*13:02:01:02    GCAGAATTCT ACAAAACCTT CTTTTTACAT AGGACCAAGA TTTTCAACAA ATATTTTTCA ATGCAATTCT CAGCTGCTCC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6246
DRB1*13:02:01:02    ATAACTAATA GTAGCTTGTT CAACACAGAT TTTTTCAGAT GATTCACACC TGTGGTACTT ACCCAGGGAT GGTTCACCAC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6326

DRB1*13:02:01:02    CCCTCCCTTC CCTCTCATCA TCGTTGGGGA ACGGTGACAA TGTTTGGAAC AATTTTTGGT TGTCACAAAC AGGGGTTTCT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6406
DRB1*13:02:01:02    TCTGATATTC AATGAGTAGA AGCCAGGGAC ACTGCTAGAG AACCCACAAT GTTCAGAACA GCCTCTGCCA TCAACAAGGA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6486
DRB1*13:02:01:02    ATTATCTGGT CCAAAATGTC AATAGTGCTG AGGCTAAGAG CACTGGTTCA CACTGTGCTC TTTCTGAAAA TTCTAGACTC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6566
DRB1*13:02:01:02    ACATCTGTTA TACACTCACC ACACAGTTTA GTTTTTTATT TTTGCTTGTT TCATTATAAA CAATTAGACA GTTGCATAAA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6646
DRB1*13:02:01:02    TTCAACCACT TTCTTGTTGA ATCCATTTAG TCAATGCAAG CTCAATATTT TCATATTTAT TTTTTGCCTT ATGCAATATT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6726
DRB1*13:02:01:02    TTTCAACATT TTCATGAGTT GTCGGTCATC ACTATCTCTA TTAACTTTCA ACAACTTGCC CTTGTAAGTC ACAAATATTG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6806
DRB1*13:02:01:02    ATGCTGCTGA AATTATTTCT CACTAACATG CCTCAGATTT CTGTAGTGAT TCTACATTTG ATATTATTCA CAATGTAAAA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6886
DRB1*13:02:01:02    TGCTTCTATT TATTCATTTC GCTTTTACCC AAGGATTATT TTTAAGTTAT TTTTGTCATT TTCACACTTC AAACATAAAG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       6966
DRB1*13:02:01:02    ACAAAAACAT CAAAAATATA GTGTTTTACA TATGTGCATA TTTTCACACA TATATGTATG TATATTTATA TGTATTGAAA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7046
DRB1*13:02:01:02    CTACAGAAGC ACATGTCACC AATAAGAGCT CTGAGACACC TTCGACCACT TACCCTTATC AGATGAGTTG TGGAAACAAG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7126
DRB1*13:02:01:02    TTTTTTTAAC TGAATTTCTG AGCTTTGTGG ATTTAGAAAT GCAAAGGAAG GTTTGTGGAC ATTCACAGGG ATCATGATTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7206
DRB1*13:02:01:02    TATTCTCCTT AAAACTCTTC TGTACTTTCC AATTGTCCTT AGTATAAATC CAAAATCCTA ACACCACCCA AGAGGCTTTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7286
DRB1*13:02:01:02    CAATACCTGG CTCCTGTGAT TTCTCCGGGC TAATCTTTTA CCCTCCTTCC CCTCAGCCTC TCTGCTTTAG TGAACTTTCT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7366
DRB1*13:02:01:02    CCTAGTTTTT TGAAGAAGTT CATCAATTCA AGCTTTTGTA CATGGGATTT CCTAAACCTG AAATGTGCCT CCCGTTTTGT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
```

FIGURE 1 | Continued

```
                                                                                                       7446
DRB1*13:02:01:02    CCAAACAGAC ACGGGCTCCA CTCTGCCCCC TGGCTCACAC CTGCTTAACC TGTCAAGTCA CATCTGAACC GTCACTATTA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7526
DRB1*13:02:01:02    AGAGGGTCCT TCTCTGGCAC CCTAATGTAA TTGAGATCAT CCTATTATTC TCTGTTCTAG AACTCCACAC TTCCGACATT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7606
DRB1*13:02:01:02    TCTCATTCCT GTCTAAGCTC TTGTGTGTTT GGTGTTGGGC CATCACTTTC ACTGCTCTTT AAGCTCCCCC AGCGGAGTGG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7686
DRB1*13:02:01:02    AGAGGTCTGT TTTCCCTCGT TTGGATTCCT AGAGGCAGCG CAGACCAGGC ACAAGGTCAG CACTAAGGAA GTGTTCACAG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7766
DRB1*13:02:01:02    GATGAACGCG GTGGGTGCTG TTTAAGGAAC CGGTAAACGT GTGGGATGAG AGAAGGAGCA GAGTGTCTTT GGGGTGGAGG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7846
DRB1*13:02:01:02    CTCCCAGGAG GAGGCGGCGC GGGCTGCGGT GCGGGGCGGA TCCTCCTCCA GCTCCTGCTT GGAGGTCTCC AGAACAGGCT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       7926
DRB1*13:02:01:02    GGAGGTAGGG AGGGGGGTCC CAAAAGCCTG GGGATCAGAC GTGGTTTTCC CGCCTGGTCC CCCAGGCCCC CTTTCGCCTC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       8006
DRB1*13:02:01:02    AGGAAGACAG AGGAGGAGCC CCTGGGCTGC AGGTGGTGGG CGTTGCGGCG GCGGCCGGTT AAGGTTCCCA GTGCCCGCAC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       8086
DRB1*13:02:01:02    CCGGCCCAGG GAGCCCCGGA TGGCGGCGTC ACTGTCAGTG TCTTCTCAGG AGGCCGCCTG TGTGACTGGA TCGTTCGTGT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                            |Exon2                                                                     8166
DRB1*13:02:01:02    CCCCACAG|CA CGTTTCTTGG AGTACTCTAC GTCTGAGTGT CATTTCTTCA ATGGGACGGA GCGGGTGCGG TTCCTGGACA
DRB1*13:97:01       --------|-- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                             8190                                                      8246
DRB1*13:02:01:02    GATACTTCCA TAACCAGGAG GAGAACGTGC GCTTCGACAG CGACGTGGGG GAGTTCCGGG CGGTGACGGA GCTGGGGCGG
DRB1*13:97:01       ---------- ---------- ---T------ ---------- ---------- ---------- ---------- ----------
                                                                                                       8326
DRB1*13:02:01:02    CCTGATGCCG AGTACTGGAA CAGCCAGAAG GACATCCTGG AAGACGAGCG GGCCGCGGTG GACACCTACT GCAGACACAA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                             |Intron2                                  8406
DRB1*13:02:01:02    CTACGGGGTT GGTGAGAGCT TCACAGTGCA GCGGCGAG|GT GAGCGCGGCG CGGGGCGGGG CCTGAGTCCC TGTGAGCTGG
DRB1*13:97:01       ---------- ---------- ---------- --------|-- ---------- ---------- ---------- ----------
                                                                                  8468-8470            8486
DRB1*13:02:01:02    GAATCTGAGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT G***AGAGAG AGAGAGAGAG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- -GAG------ ----------
                                                                                                       8566
DRB1*13:02:01:02    AGAGACAGAG AGACAGAGAG AGAGAGAGCG CCATCTGTGA GCATTTGGAA TCCTCTCTAT CCTGAGCAAG GAGTTCTGAG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       8646
DRB1*13:02:01:02    GGCACAGGTG TGTGTGTAGA GTGTGGATTT GTCTGTGTCT GTGAGGCTGT TGTGGGAGGG GAGGCAGGAG GGGGCTGCTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       8726
DRB1*13:02:01:02    CTTATTCTTG GAGGACTCTG TGGGGAGGTG ACAAGGGAGG TGGGTGCGGG CGGCTGGAGA GAGAGGTGAC CTTGATTGTC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       8806
DRB1*13:02:01:02    TCGGGTCCTT AGAGATGCAG GGAAGGGAAA TGTAAGGGGT GTGTGGTTGG GGTGAAGGTT TAGGGGAGGA GAGCTGAGGG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       8886
DRB1*13:02:01:02    GTAAGGAAGG TTTGGGATAA TGTGAGGAGG CCAGTTCCAG ACTGTCCCTG GCACACACCC TTCATGTAAT CTCTGAAATA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       8966

DRB1*13:02:01:02    AAAGTGTGTG CTGTTTGTTT GTAAAAGCAT TAGATTAATT TCTAGGGGAA TTGAGGAGAC CTCTGAGGCA TCTCTGAAGC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9046
DRB1*13:02:01:02    TTCTTTAGGT CTAAATTTCT TGCTAGTTTT TTGTTTTTTA TTGTGTATAT TTTTACATAG TAGAAATGAC TGTGAAACTA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9126
DRB1*13:02:01:02    ACTTTTTGAA TTAAAGTTTT AACACAGTTA CTATTTTATT ATAATGCTAA TAGTTTTCTA GTAGTTACAT ATTATTCTTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9206
DRB1*13:02:01:02    TATATATAAT AGTTGTGACA CAACTTACCT CACTTTCCCC TTTGTTGACC TTTATTATGA CATTCACCAA AATTTGAAAA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9286
DRB1*13:02:01:02    TGTATGTTTC TGGTTAATTT TTAATTTATA TTTTTTTCAT TTATAATTCT TTTGAATTAT TTTGACCTAT TTATTGGCCA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9366
DRB1*13:02:01:02    GTTTTAATAA CTGCTGTAAG AATTCCCTAT TGTATTTGGT AGGGAATGGA CAATGATCTA CTGCCTAATA TCTCGAGGGC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9446
DRB1*13:02:01:02    TTAGTATTTT TCTCAGTGAC TTTGTGGGTT CTTTGTACTG TGAGATTATT AACACTTTAT TGATATTTGA TTCAGCATTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9526
DRB1*13:02:01:02    GCTCCAGTTT GTGGTTTGTA TGTTGATTTT GAAAATTCTT TTCCATGTTA AGAATTTGAA CATTTTTATA TAATAAAATA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9606
DRB1*13:02:01:02    TGTTGCAAAA TTTTTATTAA TGATTTACAA TCCATCTTAA ATCTGCCATT TTGTGGTATT GTTGTCTCCA GGTTTCTCCT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9686
DRB1*13:02:01:02    TACTTCTAAA AAAAATTGCA TTTATTGAGA GTCTGCTAGT GTTAGGGATT TTCCTGGGCA TAAGCACCCC AAGTGACGAG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9766
DRB1*13:02:01:02    TCCCAGACAC TGCCTTAATC CAAATGTGAT TCTGGAAAGA AAAATCATTT TACAATGATA GGCCTAATAA TAATTAAGCT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9846
DRB1*13:02:01:02    TGTGTTGCAT GGGAGATGCA TTGATCAGCT AAATGTAAAT ATAAGAACTT TCAAAACTAA AATGACGTTC CTTAATCCTT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                       9926
DRB1*13:02:01:02    CTCTCTGCTT TATGACTCAT GCTTTTCTGG GAAAGTAAAA ATTTGGAGAA TCATTTCTGT CTGTCCCACC TTCCCAGGGG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
```

FIGURE 1 | Continued

```
                                                                                                     10006
DRB1*13:02:01:02   CAGAACCATT TCTGTGGTGT TCTAAGGTGT GAGTGCATGG CGGTAGTATT CCTAAAAATT CATATTCGGT TTCGTCATGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10086
DRB1*13:02:01:02   ACCCAACTCT GTCCCGTTAT CTATCAACAT TGTTTTAAAT CATATATTTC TGTCAAGGTG TACAAGGATG ATAAATAGGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10166
DRB1*13:02:01:02   GCCAAGTGGA GCACCCAAGT GTGATGAGCC CCCTCACAGT GGAATGGAGT GTGAAGCTTT ATGACCTCAT AAATTGAAGG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10246
DRB1*13:02:01:02   TTATCTTCAG TCATTGTTTT ATATATTTTA CATGCATTAA TCCTCATATA ATCCCAAGAG GTAAATTAGT ATAATTATCC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10326
DRB1*13:02:01:02   TTCATTATAG GTGACAAAGT TGAGACACAG AAGAATCAAA CTCTTAAGGC AGACCTTGGA TTTGAACCAG GCAACCTGGC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10406
DRB1*13:02:01:02   TCAGATATCA GTTTTAATTA CTACACTCTG TACTTTCAAA GATTTGTAAA CACTTTGACA ATGCATGACA ATTTCAAGCT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10486
DRB1*13:02:01:02   ATGAAGAAAC AAACACAATT TTTCACAATA TCTCTCAAAT CTAATAGGTC CTCACTATCA AGATTAAGTT CCAGGCTGAT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10566
DRB1*13:02:01:02   GACACTGTAA GGCCACATGG CCAGCTGTGC TGGAGGCCTG GTCAAGGTCA GAGCCTGGGT TTGCAGAGAA GCAGACAAAC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                       Exon3                                         10646
DRB1*13:02:01:02   AGCCAAACAA GGAGACTTAC TCTGTCTTCA TGACTCATTC CCTCTACCTT TTTTCTCCTA GTCCATCCTA AGGTGACTGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10726
DRB1*13:02:01:02   GTATCCTTCA AAGACCCAGC CCCTGCAGCA CCACAACCTC CTGGTCTGTT CTGTGAGTGG TTTCTATCCA GGCAGCATTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10806
DRB1*13:02:01:02   AAGTCAGGTG GTTCCGGAAT GGCCAGGAAG AGAAGACTGG GGTGGTGTCC ACAGGCCTGA TCCACAATGG AGACTGGACC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     Intron3
DRB1*13:02:01:02   TTCCAGACCC TGGTGATGCT GGAAACAGTT CCTCGGAGTG GAGAGGTTTA CACCTGCCAA GTGGAGCACC CAAGCGTGAC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     10966
DRB1*13:02:01:02   AAGCCCTCTC ACAGTGGAAT GGAGTGAGCA GCTTTCTGAC TTCATAAATT TCTCACCCAC CAAGAAGGGG ACTGTGCTCA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11046
DRB1*13:02:01:02   TCCCTGAGTG TCAGGTTTCT CCTCTCCGAC ATCCTATTTT CATTTGCTCC ATGTTCTCAT CTCCATCAGC ACAGGTCACT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11126
DRB1*13:02:01:02   GGGGGTAGCC CTGTAGGTGT TTCTAGAAAC ACCTGTACCT CCTGGAGAAG CAGTCTCGCC TGCCAGGCAG GAGAGGCTGT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11206
DRB1*13:02:01:02   CCCTCTTTTG AACCTCCCCA TGATGTCACA GGTCAGGGTC ACCCACCCTC CCCGGGCTCC AGGCACTGCC TCTGGGTCTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11286
DRB1*13:02:01:02   AGACTGAGTT TCTGGTGCTG TTGATCTGAG TTATTTGTTG TGATCTGGGA AGAGGAGAAG TGTAGGGGCC TTCCTGACAT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11366
DRB1*13:02:01:02   GAGGGGAGTC CAATCTCAGC TCTGCCTTTT ATTAGCTCTG TCACTCTAGA CAAACTACTT AGCCTCATTG AGTCTCAGGC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11446
DRB1*13:02:01:02   TTTCTGTGGA TCAGATGTTG AACTCTTGCC TTACATCAAG GCTGTAATAT TTGAATGAGT TTGATGTCTG AACCTTGTAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11526
DRB1*13:02:01:02   CTGTTCAGTG TGATTTGAAA TCCTTTTTTT CTCCAGAAAT GGCTAGTTAT TTTAGTTCTT GTGGGGCAGC CTTCTTCCCC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                             Exon4                   11606
DRB1*13:02:01:02   ATTTTCAAAG CTCTGAATCT TAGAGTCTCA ATTAAAGAGG TTCAATTTGG AATAAACACT AAACCTGGCT TCCTCTCTCA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11686
DRB1*13:02:01:02   GGAGCACGGT CTGAATCTGC ACAGAGCAAG ATGCTGAGTG GAGTCGGGGG CTTTGTGCTG GGCCTGCTCT TCCTTGGGGC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                       Intron4                                                                       11766
DRB1*13:02:01:02   CGGGCTGTTC ATCTACTTCA GGAATCAGAA AGGTGAGGAG CCTTTGGTAG CTGGCTCTCT CCATAGGCTT TTCTGGAGGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11846
DRB1*13:02:01:02   GGAACTATGG CTTTGCTGAG GTTAGTTCTC AGTATATGAG TGGCCCTGAA TAAAGCCTTT CTTTCCCCAA ACGGCTCTAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     11926
DRB1*13:02:01:02   TGTCCTGCTA ATCCAGAAAT CATCAGTGCA TGGTTACTAT GTGAAAGCAT AATAGCTTGT GGCCTGCAGA GACAAGAGGA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     12006
DRB1*13:02:01:02   AGGTTAACAA GTAGGGGTCC TTTGGTTTGA GATCTTGGAG CAGATTAAGG AAGAGCCACT AAGACTAATG GAATTACACT
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     12086
DRB1*13:02:01:02   GGATCCTGTG ACAGACACTT CACCCTTCAT GGGTCACATG GTCTGTTTCT GCTCCTCTCT GCCCTGGCTG GTGTGGGTTG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                         Exon5
DRB1*13:02:01:02   TAGTGACAGA GAACTCTCCG GTGGGAGATC TGGGGCTGGG ACATTGTGTT GGAAGACAGA TTTGCTTCCA TAAATTTTAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                            Intron5                                                  12246
DRB1*13:02:01:02   GTGTATATAT TTTCCTCTTT TTCCCAGGAC ACTCTGGACT TCAGCCAAGA GGTAATACCT TTTAATCCTC TTTTAGAAAC
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     12326
DRB1*13:02:01:02   AGATACGGTT TCCCTAGTGA GAGGTGAAGC CAGCTGGACT TCTGGGTCGG GTAGGGACTT GCAGAACTTT CCTGTCTTAG
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                     12406
DRB1*13:02:01:02   GAGAGGTTTC TAAATGCACC AATCAGTGCT CTGTAAAAAC ACACCAATTG GCACTCTGTG GCTAGATAGA TGTTTGTAAA
DRB1*13:97:01      ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
```

FIGURE 1 | Continued

```
                                                                                                      12486
DRB1*13:02:01:02    ATGGACTAAT CAGCACTCTG TAAAATGGAG CAATCCACAC TCTGTAAAAT GGACCAATCA ATGCTCTTTA AAATGGACCA
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      12566
DRB1*13:02:01:02    ATCAGCAGGA CATGGGCGGG GACTAATAAG GGAATACAAG CTGGCCACCC CAGCCAGCAG CAGCAACCCG CTCAGGTCGC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      12646
DRB1*13:02:01:02    CTTCCATGCT GTGGAAGCTT TGTTCTTTTG CTCTTCACAA TAAATCTTGC TGTTGCTCAC TCTTCGGGTC TGTGCCACCT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      12726
DRB1*13:02:01:02    TTAAGAGCTG TAACACTCAC TGTGAAGATT CGCGGCTTCA TTCTTGAAGT CAGCGAAACC ACGAACCCAC CGGAAGGAAC
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      12806
DRB1*13:02:01:02    AAACTCTGGA CACACTAGAA TTGATGGTAG AGGTGATAAG GCATGAGACA GAAATAATAG GAAAGACTTT GGATCCAAAT
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      12886
DRB1*13:02:01:02    TTCTGATCAG GCAATTTACA CCAAAACTCC TCCTCTCCAC TTAGAAAAGG CCTGTGCTCT GTGGGACTAT TGGCTCTGGG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                                                                                                      12966
DRB1*13:02:01:02    AGACTCAGGA ACTTGTTTTT CTTCTTCCTG CAGTGCTCTC ATCTGAGTCC CTGAAAGAGA GGAAAAGAAA CTGTTAGTAG
DRB1*13:97:01       ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
                               |Exon6                                     13019
DRB1*13:02:01:02    AGTCAGGTTG |AAAACAACAC TCTCCTCTGT CTTTTGCAGG ATTCCTGAGC TGA
DRB1*13:97:01       ---------- |---------- ---------- ---------- ---------- ---
```

FIGURE 1 | Continued

Author Contributions

Xiaoyun Chi: performed full-length sequencing test; wrote the paper. **Zhi Jiang:** performed full-length sequencing test. **Li Liu:** performed full-length sequencing test. **Bin Han:** performed PCR-SBT test. **Shuxian Jiao:** performed PCR-SBT test. **Shutao Pang:** designed test scheme and reviewed this paper.

Acknowledgements

All the experiments comply with the regulations in China. This work was supported by the Qingdao Key Medical and Health Discipline Project and the Qingdao Outstanding Health Professional Development Fund.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are openly available in IPD-IMGT/HLA at https://www.ebi.ac.uk/ipd/imgt/hla/.

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