

NEW ALLELE ALERT

Genomic Full-Length Sequence of the *HLA-DRB1*14:84* Allele, Identified by PacBio Sequencing

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Correspondence: Shu-Tao Pang (qdbc_pst@sina.com)**Received:** 15 April 2025 | **Revised:** 7 May 2025 | **Accepted:** 14 May 2025**Funding:** This study was supported by Qingdao Blood Center Scientific Research Project (2024-xz01).**Keywords:** genomic full length | *HLA-DRB1*14:84* | PacBio sequencing**ABSTRACT**The genomic full-length sequence of the *HLA-DRB1*14:84* allele was identified using a PacBio sequencing approach from China.

Here, we present the first genomic full-length sequence of the *HLA-DRB1*14:84*. The sequence was detected in a bone marrow donor from the China Bone Marrow Bank. As of April 2025, a total of 3,825 HLA-DRB1 alleles have been identified and included in the IPD-IMGT/HLA Database [1]. The *HLA-DRB1*14:84* allele was first detected in a Taiwanese individual in 2009 and assigned the GenBank/ENA accession number FJ594768. But the sequence only covered exon 2 and partial CDS of *DRB1*14:84*. We here report the 13,398 bp full-length genomic sequence of *HLA-DRB1*14:84* using PacBio sequencing methods, a third-generation sequencing platform. The testing was conducted with the informed consent of the donor. In brief, the library was added to the sequencing chip and sequenced using a PacBio Sequel II high-throughput gene sequencer. 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 [2]. Finally, the full-length sequence of the *HLA-DRB1*14:84* allele was confirmed.

The sequence of *DRB1*14:84*, a total of 13,398 bp in length, including the sequence of the 5'-upstream region, all introns, and exons 1, 3, 4, 5, and 6, is first reported here. Compared with *DRB1*14:05:01:02*, there are several nucleotide changes not

only in exons but also in introns. The changes in exons are concentrated in exon 2, including T>C at nucleotide 8644 (codon GCT>GCC, synonymous mutation), G>A at nucleotide 8677 (codon GAG>GAA, synonymous mutation), C>G at nucleotide 8678, G>A at nucleotide 8679, G>C at nucleotide 8680 (codon CGG>GAC, Arginine 99 to Aspartic Acid), G>C at nucleotide 8690, A>T at nucleotide 8691 (codon GAG>CTG, Glutamic Acid 103 to Leucine) and T>C at nucleotide 8704 (codon TAT>TAC, synonymous mutation). The changes within introns include one nucleotide (T) insertion after nucleotide 3073 of intron 1 and two nucleotides (GT) insertion after nucleotide 8851 of intron 2, see Figure 1. The complete HLA typing of the donor is as follows: *HLA-A*02:01:01G, 02:03:01G; -B*13:01:01G, 38:02:01G; -C*03:04, 07:02; -DRB1*14:84, 15:BNK; -DQB1*05:01, DQB1*05:03*.

The full-length nucleotide sequence of this allele has been submitted to GenBank, the accession number is PV208187, and to the IPD-IMGT/HLA Database in March 2025, the accession number HWS10100607. The name was officially assigned by the World Health Organisation (WHO) Nomenclature Committee for Factors of the HLA System in January 2009. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report [3], names will be assigned to new sequences as they are identified. Lists of such new names will be published in the following WHO Nomenclature Report.

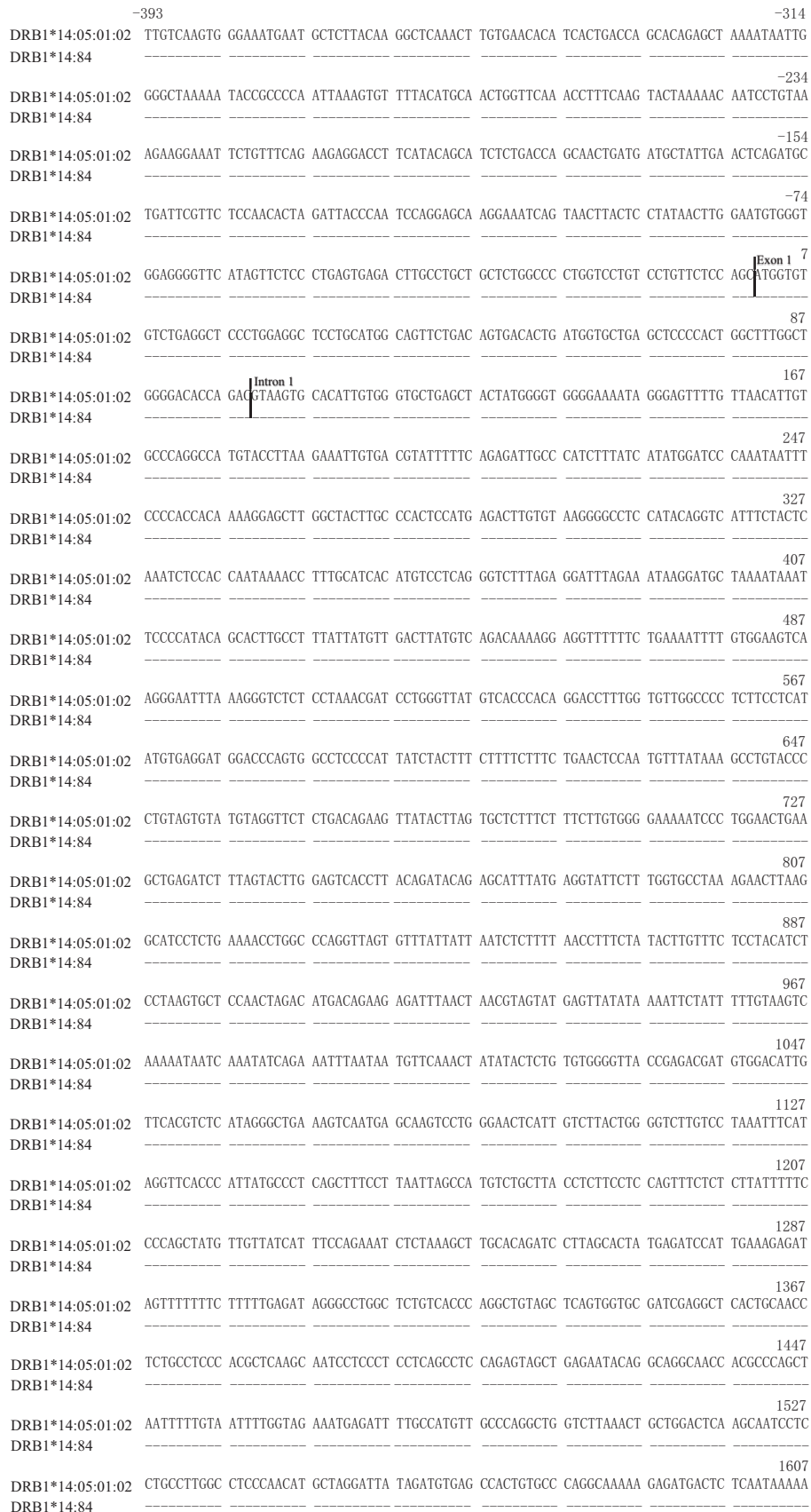


FIGURE 1 | Alignment of the sequence of *DRB1*14:84* with the sequence of *DRB1*14:05:01:02*. Dashes indicate nucleotide identity with the *DRB1*14:05:01:02* sequence. The pipes indicate the exon and intron boundaries.

DRB1*14:05:01:02	AAGTCCTTT	TCTTAAATCA	CTGTTTCTTT	ATCTGTGAAT	TCTTCTCCA	ACTAGAAGGA	GGAGAAAGAA	GTTTGCCTGT	1687
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	ATTTCTCACC	AGGAGGAGAA	GGGGTCTAGT	GTGACATCAG	AATGAAAGAG	TGCTGGAGTT	TGAGCCCCCT	CTTGCTTTCC	1767
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	AAGATCCCCA	CAGTGATCAG	TTCCCATACC	CTGGTTTATT	CATGTA AAC	ACACTTATTT	TTCTTAGCAG	CTACTGTGTA	1847
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	CTCGGCTCCA	TTCTAGGTTT	AGATCATTCT	ATTTGATTAA	GACAGAGAGG	GTCCCGACTC	TCATGGAAGT	TACACAACAA	1927
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	TAGAGGAGAC	AGACACTAAC	CCAATAAGCA	TTTAAACAAAG	AATAAAATGT	TAGAGAGTCA	TAGTGCCTG	AAGAAAAGAC	2007
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	ATCAGGTTTG	TGAAGAAGAG	AGACATGGAT	TCATCTACTT	TAGTTCATAT	GTTTAGGGAG	CTCTACCTGA	GAAAGTGACA	2087
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	TTCAGCTGAG	ACAACAAAAT	AAGTAGACAG	TCATGAAGAT	CTAATGGACG	AAAGCTCCAG	GGAGACAAA	TGGGGGAAA	2167
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	GCCCTGGTGT	GGGAAATTAT	GTGGAGAGAG	AGAAAAGAGG	CTAGAGGGGC	TGATGTATAG	AAAGTAAGGA	AATGGAGAGG	2247
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	CAGAAGATGA	GGTAGGACAC	AGAGAGAAAG	TCAGGAGCCT	CATGATTATA	GGCTCTGATG	TCCACGGTAA	AAAATTTGAA	2327
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	TTTTATTTTA	TTTATTTTAT	TATTTATTTT	ATTTTATTTA	TTTATTTATT	TTTTGAGATG	GAGTCTCGCT	TTGTGCCCCA	2407
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	GGCTGGAGTG	CAGTGGCGCG	ATCTCAGCTC	ACTGCAAGCT	CCACCTCCTG	GGTTCATGCC	ATTCTCTGCG	CTCAGCCTCC	2487
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	CTAGTAGCTG	GGACTACAGG	CACCCGCCAC	CACGCCTGGC	TAATTTTTAG	TATTTTTAGT	AGTGAGGGCG	TTTCGTCATG	2567
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	TTAGCCAGGG	TGGTCTCCAT	CTCCTGACCT	CGTGATCCAC	CTGCCCCGGC	CTCCCAAAGT	GCTGAGACTA	CAGGTGTGAG	2647
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	CCACCACGCC	TGGCCTATTT	TTTTTTTTTT	TTT*GAGACG	GAGTTTCGTT	CTTGTTGCC	AGGCTGGAGT	GCAATGGTGC	2727
DRB1*14:84	-----	-----	-----	-----T-----	-----	-----	-----	-----	
DRB1*14:05:01:02	AATCTCGGCT	CACTGCAACC	TTCGCCTCCC	TGGTCAAGT	GATTCTCCTG	CCTCAGCTTC	CCAAGTATCT	GAGATTACAG	2807
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	GCACCCACCA	CCATACCTGG	CTAATTTTTA	TTTTTTTGTA	TTTTTAGTAG	ACATGGGGTA	TCACCATGTT	GACCATGCTG	2887
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	GTCTCGAACT	CCTGACCTCA	GATAATCTGT	CTGCCTTGGC	CTCCCAAAGT	GCTGGGATTA	CAGGCATGAG	CCACGGCGGC	2967
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	CGGACTGAAT	TTTATTTAAA	TAGATACGAG	AAGCTACTGT	ATGGTTACAA	GGAGAGTCAA	TTTATATCCA	ATTTATTTTT	3047
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	ATTTTATTTT	ATTTTTTTGG	TGATGGGGTC	TTGCTCTGTT	GCCCAGGCTA	GATTGTAGTG	GCACAATCTC	GGCTCACTGC	3127
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	AACCTCTGCC	TTCTGGGTTT	AGGCGATTCT	CCTGACTCAG	CCTACAGAGT	AGCTGGGACC	ACAGGTACAT	GCCACCACAC	3207
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	CTGGCTAAGT	TTTTGTATTT	TTTAGTAGAG	ACAGGATTTT	ACCGTGTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	3287
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	ATCCACCCAC	CTTGGCTCC	CAAAGTGACG	GGATTACAGG	CGTGAGCCAC	TGCGCCCGGC	CTATATTCAA	TTTTTAAAA	3367
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	TAATTCTAGC	TACTCTGTGG	GGATTGGAAT	GTTGGGGTTC	ACAAGTGGTC	AGGAAGACTA	TTTAGGAGCA	CAGCAGGGAA	3447
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	TTCTCCAGCG	AAAACAGGCT	TGTGGCTTCA	TGGAGTGAT	TAGTGATAAA	GACGGTGAAA	AAGATAAAGT	GGACAGACTT	3527
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	
DRB1*14:05:01:02	GGCATGTATT	TTTGCTTAGC	TTGTTAATGA	ATTACTGTAA	AGGGGGTAGA	ACAATCAAGC	TTATTCCTAA	GGATTTTGT	3607
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	

FIGURE 1 | (Continued)

DRB1*14:05:01:02	TTGACAAATA AGTGGGTGGT AGTGTGTGTT ATTGAGATAG GAAAAACTAT GGGAGGAAAT TATTTGAAGT GGGTGGTTGG	3687
DRB1*14:84	-----	-----
DRB1*14:05:01:02	AAATAAAGT TTTGTTAAA TTTGAGATGA TTTATTGACA TTTATGTGGA GCAATCAGAA GGTCATGGC ATTTAAGAGA	3767
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CTCATGGTGA GGCTAGGGCT TCAAGTATTT ATGTTGGCGG CATCAATACA TGTAGTGTGT TAAATTCCAG GGAGTGAAG	3847
DRB1*14:84	-----	-----
DRB1*14:05:01:02	AGGATACATA GGGAGATGGA TTGTGTGGAG AAAAAAGAAC AGGGCACAGG CCAGCAAAGG GGGCTGAGAA AGAGCCCAGG	3927
DRB1*14:84	-----	-----
DRB1*14:05:01:02	GATGTTGGAG AAAAATCAAG AGAACATGAT GCGTGTACGT CAAGGAAAAAT AGATTTTTTT CAAGGAGAAG GGAGAGGCCA	4007
DRB1*14:84	-----	-----
DRB1*14:05:01:02	ATTGTGGTGA GTACCTATAA GAGGAGGGGG AAGTGAGAAC GTGACAGAGA AGCAAGTGCT GGGTTTGGTG GAGTTGATAT	4087
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TTGCAGTAG TGGAGTATCC AGGGAGGAAA CTGGATTGGA CAATTTGAAG AGCGAGTAGA AGTGAGGATG AGGTTAAGGT	4167
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TGACTGTTTT GAGTAGAGAG CTTCAGGGAA GGAAGTCACT CTGGGTTGAG GGGGCCAGCT GGATCAAAAG GAAAAGGCTA	4247
DRB1*14:84	-----	-----
DRB1*14:05:01:02	AAGAGGCTGA AGAGAAGCAG GAGGACCTGT GAACCAGAGA TGCTCAGTCA TTATTAGCGA GGAATACTA GAGAGCCCTT	4327
DRB1*14:84	-----	-----
DRB1*14:05:01:02	GTGTGCAGTG ATGACTACTC ATGCAGAAGG TCACACAGCC AATATTTAAC ACAGCCAGTA TTTCACACAG CTAATATTTA	4407
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TTAGTGACAT AGAATATACC AGTTATTACT CTAGGTCATG AGAATGGAGT GATAAATAAA ATGAATCCGG TCGCCATCAG	4487
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TATATGCCAT GTAACATTTT GCAGTGACTG TGTACCAGC CTGTGAATTT CAGTATGCAA TTTCAATAAT GATCCTGCTG	4567
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TATCTGTGGT GTTTAAAAAC ATATACATCT CTGGAATCTA AAATTGAGAG GTTATAAGTA AAACCCAGTA TTACAAATTG	4647
DRB1*14:84	-----	-----
DRB1*14:05:01:02	AGTGCTGGAA ATCAGATTGC AGTTTAAATC TGAGCATATA GAAAGTCCCT TTCTTCTATG TCAGCAGATG CCTTTTGTGT	4727
DRB1*14:84	-----	-----
DRB1*14:05:01:02	GAGGTTTAGC TGGACTGCAT TATTAGACAT AAACAAGTGT TTCTGCCCTA TGTTTTCAGA ATGACAATTC TTTATGAAAC	4807
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TAATAGAAGA ACAGAAGACA ACTGCAAAAT CATGATGGAG ATAGTAATTG CTTTAGAATT AAGGAATACA AAAAATAATG	4887
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TGAGCTGTAG TTATAGGGAT CATAAAAGTT TAAATGGGAA TGTATTGAG TATGTGATCA GTGCTAAGAA GAGTCATCAT	4967
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TTAATTTTAC ACTTAACAGT AATCTCGTGA GGATTACGCT ATTATTAAT GCATTGATA GATTACAAAA AGGCTTATGG	5047
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TTGGTAAAA TTGACCCAAG TAGAAGAGAT CATGTTTTA TTCAGGTTTT CTGATTCTAG AGTTTGAGAG TTTGTCATC	5127
DRB1*14:84	-----	-----
DRB1*14:05:01:02	ATTAGTGAGT AGTGACTATA TTGTGCTGA ATTATTGACA GAATTTCTGA TATTCATATG TACCAGGTTG TTTCTTAGAG	5207
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TGGGGATAGA GATGCAAGG CTGCTAGTTC CGATGTATTG GGGAAACTTT CATTCAATTT GCATTTATCA TTTTAAAAAGT	5287
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TCTGTATGTC TATAATGGTC ATGTGTTGAA GAACACAAGG AAGTATTAAT TCACTCCTTC TTCTAAGGTT TGACTAGCAA	5367
DRB1*14:84	-----	-----
DRB1*14:05:01:02	GTTGGGCTAG AGTTACAAA TAAAATACAT GTTCTAGTG AAATCTGAAT TTCAGATACA AAACCATAAT TTATTGAAAA	5447
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TCCAAATTTA ACTGGGCATC CTCTGGTTTT ATTTGCCACA TCTGTCAACC CTAATGTGA CACATGGACA TGGATTACAG	5527
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TGCTAACCAT GCAAGCCAGG GTGACAGCAA CTTACACAT GTTTATTTTT AACTCTCTCT GTAAGAAAGT GCTTAGATAA	5607
DRB1*14:84	-----	-----

FIGURE 1 | (Continued)

DRB1*14:05:01:02	TTTAGGGATA AAAAGATAGA CATTGCTTGA TCCAGGGTGC ACACCTCTCT GCCACCATT CTAAAGGGCA AAGGGAGATT	5687
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TCCGCAGGTC TTGCTCACAG TCTGGGAGC TGCTCATTTT TGTAAGTGT CTGTATGAGA ATGTCATTTT CTTGTTTCC	5767
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TCCTTTACGA GGGGACTTGA CTACAAAACC AAGAGTTCTG CCTCTGGCCA AGGCTGGTAA TTTGATGCCT GCTAGTATTG	5847
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TTGGGAGTGG GAGACTGAAA GAAATGAGTT AGTTGGGGCA TTTAACGGGA ATAAAATAGC TGTGGTTGTG ATTCATTACT	5927
DRB1*14:84	-----	-----
DRB1*14:05:01:02	ACAGATAATT AGTGGACCAG TGGCAGAGAA ATTAAGAAAA AAGATGATGT GAACGATAAA TGATATGATT AGTGACTGCT	6007
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TGGTAAGGCA AGGAAATCAT TAAATCTTGG TTCTCATCAA GTTCATTTTC TGGAAAGATA GCACTGTATT GGGAGCAGAA	6087
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TTCTACAAA CCTTCTTTT ACATAGGACC AAGATTTTCA ACAAATATTT TTCAATGCAA TTCTCAGCTG CTCCATAACT	6167
DRB1*14:84	-----	-----
DRB1*14:05:01:02	AATAGTAGCT TGTCAACAC AGATTTTTTC AGATGATTCA CACCTGTGGT ACTTACCCAG GGATGGTTCA CCACCCCTCC	6247
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CTTCCCTCTC ATCATCGTTG GGGAAACGGT ACAATGTTG GAACAATTTT TGGTTGTAC AACAGGGGT TTCTTCTGAT	6327
DRB1*14:84	-----	-----
DRB1*14:05:01:02	ATTCAATGAG TAGAAGCCAG GGACACTGCT AGAGAACCCA CAATGTTTCA AACAGCCTCT GCCATCAACA AGGAATTATC	6407
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TGGTCCAAAA TGTCAATAGT GCTGAGGCTA AGAGCACTGG TTCACACTGT GCTCTTCTA AAAATTCTAG ACTCACATCT	6487
DRB1*14:84	-----	-----
DRB1*14:05:01:02	GTTATACACT CACCACACAG TTTAGTCTTT TATTTTGTCT TGTTTCATTA TAAACAATTA GACAGTTGCA TAAATTC AAC	6567
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CACTTTCTTG TTGAATCCAT TTAGTCAATG CAAGCTCAAT ATTTTCATAT TTATTTTCTG CCTTATGCAA TATTTTTC AA	6647
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CATTTTTCATG AGTTGTCGGT CATCACTATC TCTATTA ACT TTCAACA ACT TGCCCTTGTA AGTCACAAAT AGTGATGCTG	6727
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CTGAAATTAT TTCTCACTAA CATGCCTCAG ATTTCTGTAG TGATTCTACA TTTGATATTA TTCACAATGT AAAATGCCTC	6807
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TATTTATTCA TTTGCTTTT ACCCAAGGAT TATTTTAAAG TTATTTTGTG GTTTTCACAC TTCAAACATA AAGACAAAAA	6887
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CATCAAAAAT ATAGTGT TTTT ACATATGTGC ATATTTTAC ACATATATGT ATGTATATTT ATATGTATTG AAACACAGAA	6967
DRB1*14:84	-----	-----
DRB1*14:05:01:02	AGCACATGTC ACCAATAAGA GCTCTGAGAC ACCTTCGACC ACTTACCCTT ATCAGATGAG TTGTGGAAC AAGTTTTTTT	7047
DRB1*14:84	-----	-----
DRB1*14:05:01:02	AACTGAATTT CTGAGTTTTG TGGATTAGA AATGCAAAGG AAGGTTTGTG GACATTCACA GGGATCATGA TTTTATTCTC	7127
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CTTAAAACTC TTCTATACTT TCCAATTGTC CTTAGTATAA ATCCAAAAAT CTAACACCAC CCAAGAGGCT TTTCAATACC	7207
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TGGCTCCTGT GATTCTCCG GGCTAATCTT TTACCCTCT TCCCTCAGC CTCTCTGCTT TAGTGA ACT TCTCCTAGTT	7287
DRB1*14:84	-----	-----
DRB1*14:05:01:02	TTTTGAAGAA GTTCATCAAT TCAAGCTTTT GTACATGGGA TTTCTTAAAC CTGAAATGTG CCTCCCGTTT TGTCCAAACA	7367
DRB1*14:84	-----	-----
DRB1*14:05:01:02	GACACGGGCT CCACTCTGCC CCTGGTCA CACCTGTTA ACCTGTCAAG TCACATCTGA ACCGTCAC TAAGAGGGT	7447
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CCTTCTCTGG CACCCTAATG TAATTGAGAT CATCTATTA TTCTCTGTTC TAGAACTCCA CACTTCCGAC ATTTCTCATT	7527
DRB1*14:84	-----	-----
DRB1*14:05:01:02	CCTGTCTAAG CTCTGTGTG TTTGGTGTG GGCCATCACT TTCACTGCTC TTTAAGTCC CCCAGCGGAG TGGAGAGGTC	7607
DRB1*14:84	-----	-----

FIGURE 1 | (Continued)

7687
DRB1*14:05:01:02 TGTTCCTT CGTTTGATT CCTAGAGGCA GCGCAGACCA GGCACAAGT CAGCACTAAG GAAGGGTTCA CAGGATGAAC
DRB1*14:84 -----

7767
DRB1*14:05:01:02 GCGGTGGGTG CTGTTAAGG AACCGTAAA CGTGTGGAT GAGAGAAGGA GCAGAGAGTG TCTTTGGGT GGAGGCTCCC
DRB1*14:84 -----

7847
DRB1*14:05:01:02 AGGAGGAGC GCGCGGGCT GCGTGCGGG GCGGATCCTC CTCCAGTCC TGCTTGAGG TCTCCAGAAC AGGCTGGAGG
DRB1*14:84 -----

7927
DRB1*14:05:01:02 TAGGGAGGG GGTCCAAAA GCCTGGGGAT CAGACGTGT TTTCCGCCT GGTCCCTCAG GCCCCCTTC GCCTCAGGAA
DRB1*14:84 -----

8007
DRB1*14:05:01:02 GACAGAGGAG GAGCCCTGG GCTGCAGATG GTGGGCTTG CGGCGGGGC CGGTTAAGT TCCAGTGCC TGACCCCGC
DRB1*14:84 -----

8087
DRB1*14:05:01:02 CCAGGGAGCC CCGGATGGT GCGTCACTGT CAGTGTCTC TCAGGAGCC GCCTGTGTGA CTGGATCGTT CGTGCCCCA
DRB1*14:84 -----

8167
DRB1*14:05:01:02 CAGCACGTTT CTTGGAGTAC TCTACGTCTG AGTGTCAATT CTTCAATGGG ACGGAGCGGG TCGGTTCTT GCACAGATAC
DRB1*14:84 -----
| Exon 2

8247
DRB1*14:05:01:02 TTCCATAACC AGGAGGAGTT CGTGCCTTC GACAGCGACG TGGGGAGTA CCGGGCGGTG ACGGAGCTGG GCGCGCTGA
DRB1*14:84 -----

8327
DRB1*14:05:01:02 TGCTGAGTAC TGAACAGCC AGAAGGACCT CCTGGAGCGG AGGCGGGCCG AGGTGGACAC CTATTGCAGA CACAACACTG
DRB1*14:84 ---C-----AGAC-----C T-----C-----

8407
DRB1*14:05:01:02 GGTTGTGGA GAGCTTACA GTGCAGCGG GAGGTGAGCG CGGCGGGGG CGGGCCCTGA GTCCCTGTGA GCTGGGAATC
DRB1*14:84 -----
| Intron 2

8487
DRB1*14:05:01:02 TGAGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG T**GAGAGAG AGAGAGAGAG AGAGACAGAG
DRB1*14:84 -----GT-----

8567
DRB1*14:05:01:02 AGAGAGAGAG CGCCATCTGT GAGCATTAG AATCCTCTCT ATCCTGAGCA AGGAGTCTG AGGGCACAGG TGTGTGTGA
DRB1*14:84 -----

8647
DRB1*14:05:01:02 GAGTGTGGAT TTGCTGTGT CTGTGAGGCT GTTGTGGAG GGGAGGCAGG AGGGGGCTGC TTCTTATTCT TGGAGGACTC
DRB1*14:84 -----

8727
DRB1*14:05:01:02 TGTGGGGAGG TGACAAGGA GGTGGGTGCG GCGCGTGGG GAGAGAGGTG ACCTTGATTG TCCTGGGTCC TTAGAGATGC
DRB1*14:84 -----

8807
DRB1*14:05:01:02 AGGGAAGGGA AATGTAAGG GTGTGTGTT GGGTGAAGG TTTAGGGGAG GAGAGCTGAG GGGTAAGGAA GGTTTGGGAT
DRB1*14:84 -----

8887
DRB1*14:05:01:02 AATGTGAGGA GGCCGGTCC AGACTGTCCC TGGCACACAC CCTTCATGTA ATCTCTGAAA TAAAAGTGTG TGCTGTTTGT
DRB1*14:84 -----

8967
DRB1*14:05:01:02 TTGTAAGGC ATTAGATTAA TTTCTAGGGG AATTGAGGAG ACCTCTGAGG CATCTCTGAA GCTTCTTTAG GTCTAAATTT
DRB1*14:84 -----

9047
DRB1*14:05:01:02 CTGCTAGTT TTTGTTTTT TATTGTAT ATTTTTACAT AGTAGAAATG ACTGTGAAAC TAACTTTTGT AATTAAGTT
DRB1*14:84 -----

9127
DRB1*14:05:01:02 TTAACACAGT TACTATTTTA TTATAATGCT AATAGTTTC TAGTAGTAC ATATTATTCT TTTATATATA ATAGTTGTGA
DRB1*14:84 -----

9207
DRB1*14:05:01:02 CACAACCTAC CTCACCTTCC CCTTTGTTGA CCTTTATTAT GACATTCACC AAAAGTGA AATGTATGTT TCTGGTTAAT
DRB1*14:84 -----

9287
DRB1*14:05:01:02 TTTTAATTA TATTTTTTC ATTTATAATT CTTTGAATT ATTTGACCT ATTTATTGGC CAGTTTAAAT AACTGCTGTA
DRB1*14:84 -----

9367
DRB1*14:05:01:02 AGAATCCCT ATTGTATTG GTAGGGAATG GACAATGATC TACTGCCTAA TATCTCGAGG GCTTAGTATT TTTCTCAGT
DRB1*14:84 -----

9447
DRB1*14:05:01:02 ACTTTTGGG TTCTTTGTAC TGTGAGATTA TTAACACTTT ATTGATATTT GATTCAGCAT TTGCTCCAGT TTGTGGTTG
DRB1*14:84 -----

9527
DRB1*14:05:01:02 TATGTTGATT TTGAAAATC TTTCCATGT TAAGAATTG AACATTTTAA TATAATAAAA TATGTTGCAA AATTTTATT
DRB1*14:84 -----

9607
DRB1*14:05:01:02 AATGATTAC AATCCATCTT AAATCTGCCA TTTTGTGTA TTGTTGTCTC CAGGTTTCTC CTTACTTCTA AAAAAAATTG
DRB1*14:84 -----

FIGURE 1 | (Continued)

DRB1*14:05:01:02	CATTTATTGA	GAGTCTGCTA	GTGTTAGGGA	TTTTCTGGG	CATAAGCACC	CCAAGTGACG	AGTCCCAGAC	ACTGCCTTAA	9687
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	TCCAAATGTG	ATTCTGAAA	GAAAAATCAT	TTTACAATGA	TAGGCCTAAT	AATAATTAAG	CTTGTGTGC	ATGGGAGATG	9767
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	CATTGATCAG	CTAAATGTAA	ATATAAGAAC	TTTCAAACT	AAAATGACGT	TCCTTAATCC	TTCTCTCTGC	TTTATGAATC	9847
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	ATGCTTTTCT	GGGAAAGTAA	AAATTTGGAG	AATCATTCT	GTCTGTCCCA	CCTTCCCAGG	GGCAGAACCA	TTTCTGTAGT	9927
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	GTTCTAAGGT	GTGAGTGCAT	GGCAGTAGTA	TTCTAAAAA	TTCATATTCG	GTTTCGTCAT	GTACCCAAC	CTGTCCCGTT	10007
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	ATCTATCCAC	ATTGTTTTAA	ATCATATATT	TCTGTCAAGG	TGTACAAGGA	TGATAAATAG	GTGCCAAGTG	GAGCACCCAA	10087
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	GTGTGATGAG	CCCCCTCACA	GTGGAATGGA	GTGTGAAGCT	TTATGACCTC	ATAAATTGAA	GGTTATCTTC	AGTCATTGTT	10167
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	TTATATATTT	TACATGCATT	AATCCTCATA	TAATCCCAAG	AGGTAAATTA	GTATAATTAT	CCTTCATTAT	AGGTGACAAA	10247
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	GTTGAGACAC	AGAAGAATCA	AACTCTTAAG	GCAGACCTTG	GATTTGAACC	AGGCAACCTG	GCTCAGATAT	CCGTTTTAAT	10327
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	TACTACACTC	TGTACTTTCA	AAGATTGTGA	AACACTTTGA	CAATGCATGA	CAATTTCAAG	CTATGAAGAA	ACAACACAAA	10407
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	TTTTTCACAA	TATCTCTCAA	ATCTAATGGG	TCCTCACTAT	CAAGATTAAG	TTCCAGGCTG	ATGACACTGT	AAGGCCACAT	10487
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	GGCCAGCTGT	GCTGGAGGCC	TGGTCAAGGT	CAGAGCCTGG	GTTTGCAGAG	AAGCAGACAA	ACAGCCAAAC	AAGGAGACTT	10567
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	ACTCTGTCTT	CATGACTCAT	TCCCTTACC	TTTTTCTCC	TAGTCCATCC	TAAGGTGACT	GTGTATCCTT	CAAAGACCCA	10647
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	GCCCCCTGCAG	CACCACAACC	TGCTGGTCTG	TTCTGTGAGT	GGTTTCTATC	CAGGCAGCAT	TGAAGTCAGG	TGGTTCCGGG	10727
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	ATGGCCAGGA	AGAGAAGACT	GGGGTGGTGT	CCACAGGCCT	GATCCACAAT	GGAGACTGGA	CCTTCCAGAC	CCTGGTGATG	10807
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	CTGAAACAG	TTCCTCGGAG	TGGAGAGGTT	TACACCTGCC	AAGTGGAGCA	CCCAAGCGTG	ACAAGCCCTC	TCACAGTGGA	10887
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	ATGGAGTGTGAG	CAGCTTTCTG	ACTTCATAAA	TTTCTCACCC	ACCAAGAAGG	GGACTGTGCT	CATCCCTGAG	TGTCAGGTTT	10967
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	CTCCTCTCCG	ACATCCTATT	TTCATTGCT	CCATGTTCT	ATCTCCATCA	GCACAGGTCA	CTGGGGTAGC	CCTGTAGGT	11047
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	GTTTCTAGAA	ACACCTGTAC	CTCCTGGAGA	AGCAGTCTCG	CCTGCCAGGC	AGGAGAGGCT	GTCCCTTTT	TGAACCTCCC	11127
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	CATGATGTCA	CAGGTCAGGG	TCACCCACCC	TCCCCGGGCT	CCAGGCACTG	CCTCTGGGTC	TGAGACTGAG	TTTCTGGTGC	11207
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	TGTTGATCTG	AGTTATTTGT	TGTGATCTGG	GAAGAGGAGA	AGTGTAGGGG	CCTTCTGAC	ATGAGGGGAG	TCCAATCTCA	11287
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	GCTCTGCCTT	TTATTAGCTC	TGTCACTCTA	GACAAACTAC	TTAGCCTCAT	TGAGTCTCAG	GCTTTCTGTG	GATCAGATGT	11367
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	TGAACTCTTG	CCTTACATCA	AGGCTGTAAT	ATTTGAATGA	GTTTGATGTC	TGAACCTTGT	AACTGTTTCA	TGTGATTTGA	11447
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	AATCCTTTTT	TTCTCCAGAA	ATGGCTAGTT	ATTTTAGTTC	TTGTGGGGCA	GACTTCTTCC	CCATTTTCAA	AGCTCTGAA	11527
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----
DRB1*14:05:01:02	CTTAGAGTCT	CAATTAAGA	GGTTCAATTT	GGAATAAGCA	TCACTAAACC	TGGCTTCTCT	TCTCAGGAGC	ACGGTCTGAA	11607
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----	-----

FIGURE 1 | (Continued)

										11687
DRB1*14:05:01:02	TCTGCACAGA	GCAAGATGCT	GAGTGGAGTC	GGGGGCTTTG	TGCTGGGCCT	GCTCTTCCTT	GGGGCCGGGC	TGTTCATCTA		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										11767
DRB1*14:05:01:02	CTTCAGGAAT	CAGAAAGCTG	AGGAGCCTTT	GGTAGCTGCC	TCTCTCCATA	GCCTTTTCTG	GAGGAGGAAC	TATGGCTTTG		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										11847
DRB1*14:05:01:02	CTGAGGTTAG	TTCTCAGTAT	ATGAGTGGCC	CTGAATAAAG	CCTTCTTCTC	CCCAAACGGC	TCTAATGTCC	TGCTAATCCA		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										11927
DRB1*14:05:01:02	GAAATCATCA	GTGCATGGTT	ACTATGTGAA	AGCATAATAG	CTTGTGGCCT	GCAGAGACAA	GAGGAAGGTT	AACAAGTAGG		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12007
DRB1*14:05:01:02	GGTCCTTTGG	TTTGAGATCT	TGGAGCAGAT	TAAGGAAGAG	CCACTAAGAC	TAATGGAATT	ACACTGGATC	CTGTGACAGA		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12087
DRB1*14:05:01:02	CACCTCACCC	TTCATGGGTC	ACATGGTCTG	TTTCTGTCC	TCTCTGCCCT	GGCTGGTGTG	GGTTGTAGTG	ACAGAGAACT		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12167
DRB1*14:05:01:02	CTCCGGTGGG	AGATCTGGGG	CTGGGACATT	GTGTTGGAAG	ACAGATTTCG	TTCCATAAAT	TTTAAGTGTG	TATATTTTCC		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12247
DRB1*14:05:01:02	TCTTTTTCCC	AGGACACTCT	GGACTTCAGC	CAAGAGCTAA	TACCTTTTAA	TCCTCTTTTA	GAACACAGATA	CGGTTTCCCT		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12327
DRB1*14:05:01:02	AGTGAGAGGT	GAAGCCAGCT	GGACTTCTGG	GTCGGGTAGG	GACTTGCAGA	ACTTTTCTGT	CTTAGGAGAG	GTTTCTAAAT		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12407
DRB1*14:05:01:02	GCACCAATCA	GTGCTCTGTA	AAAACACACC	CATTGGCACT	CTGTGGCTAG	ATAGATGTTT	GTAATAATGGA	CTAATCAGCA		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12487
DRB1*14:05:01:02	CTCTGTAATA	TGGAGCAATC	CACACTCTGT	AAAATGGGCC	AATCAATGCT	CTTTAAATG	GACCAATCAG	CAGGACATGG		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12567
DRB1*14:05:01:02	GCGGGGACAA	ATAAGGGAAT	ACAAGCTGGC	CACCCAGCC	AGCAGCAGCA	ACCCGCTCAG	GTCGCCTTCC	ATGCTGTGGA		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12647
DRB1*14:05:01:02	AGCTTTGTTC	TTTTGCTCTT	CACAATAAAT	CTTGCTGTG	CTCACTCTTC	GGGTCTGTGC	CACCTTTAAG	AGCTGTAACA		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12727
DRB1*14:05:01:02	CTCACTGTGA	AGATTGCGG	CTTCATTCTT	GAAGTCAGCA	AAACCACGAA	CCCACCGGAA	GGAACAAACT	CTGGACACAC		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12807
DRB1*14:05:01:02	TAGAATTGAT	GGTAGAGGTG	ATAAGGCATG	AGACAGAAAT	AATAGGAAAG	ACTTTGGATC	CAAATTTCTG	ATCAGGCAAT		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12887
DRB1*14:05:01:02	TTACACAAA	ACTCCTCCTC	TCCAATTAGA	AAAGGCCTGT	GCTCTGTGGG	ACTATTGGCT	CTGGGAGACT	CAGGAACITG		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										12967
DRB1*14:05:01:02	TTTTTCTTCT	TCCTGCAGTG	CTCTCATCTG	AGTCCCTGAA	AGAGAGGAAA	AGAAACTGTT	AGTAGAGTCA	GGTTGAAAAC		
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		
										13005
DRB1*14:05:01:02	AACACTCTCC	TCTGTCTTTT	GCAAGATTCC	TGAGCTGA						
DRB1*14:84	-----	-----	-----	-----	-----	-----	-----	-----		

FIGURE 1 | (Continued)

Author Contributions

Yu-Li Zhu analysed the sequencing data, wrote the manuscript, and developed the figure. Ying-Chun Wang collected the peripheral blood of this volunteer donor for China Marrow Donor Program. Zhi-Hui Feng sequenced by PacBio sequencing approach. Shu-Xian Jiao and Shu-Tao Pang revised the manuscript.

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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/>, reference number HWS10100607.

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