

## NEW ALLELE ALERT

# Genomic Full-Length Sequence of the HLA-DRB1\*03:19 Allele Was Identified in a Chinese Bone Marrow Donor by PacBio Sequencing

B. Han  | Z. Jiang | S.-X. Jiao | Z.-H. Feng | S.-T. Pang

HLA Typing Laboratory, Qingdao Blood Center, Qingdao, Shandong, China

**Correspondence:** S.-T. Pang ([qdbc\\_pst@sina.com](mailto:qdbc_pst@sina.com))

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## ABSTRACT

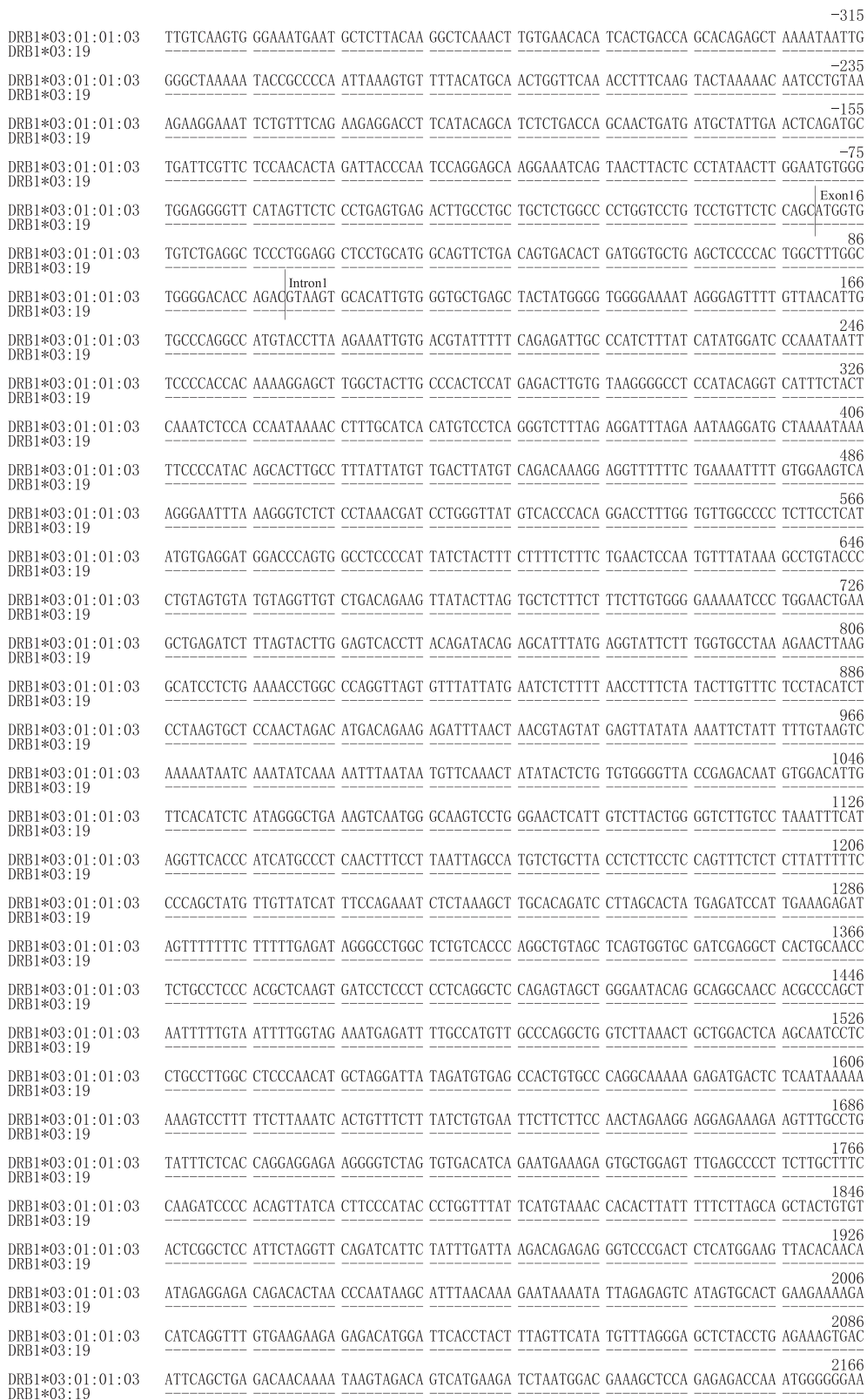
Genomic full-length sequence of HLA-DRB1\*03:19 was identified in a Chinese individual by PacBio sequencing.

The HLA complex, around 4 million bases in length, is located on chromosome 6, 6p21.3. The HLA genes within this region are known to be highly variable [1]. There are currently 41,003 HLA and related alleles described by the HLA nomenclature and included in the IPD-IMGT/HLA Database [2]. Up to December 2024, 3787 *HLA-DRB1* alleles have been identified and included in the IPD-IMGT/HLA Database (<http://www.ebi.ac.uk/imgt/hla/>). *HLA-DRB1\*03:01* is well expressed in the Chinese population, and the allele frequency is 3.69% [3]. The *HLA-DRB1\*03:19* allele was first identified in July 2016 but only contained the sequences of exon 2 and exon 3.

Here we report the full-length sequence of the *HLA-DRB1\*03:19* allele, which was identified during HLA typing of a Chinese bone marrow donor using PacBio sequencing, a third-generation sequencing platform. The test has been done with the donor's informed consent. The variant was initially recognised by high-resolution HLA-typing technique with SBT kit (Genome Diagnostics BV, Utrecht, The Netherlands). Genomic DNA was extracted from peripheral-blood leukocytes according to the manufacturer's instructions for DNA isolation kits (Life Technologies), and further molecular testing was performed. 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 reverse directions by means of cycle sequencing [4]. 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, the 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 [5]. Finally, the full-length sequence of the *HLA-DRB1\*03:19* allele was confirmed.

The genomic full-length sequence of the *HLA-DRB1\*03:19* included all exons and introns, a total of 13,383bp in length. The overlapping nucleotide sequence was found to be concordant with the available *HLA-DRB1\*03:19* sequence in the IPD-IMGT/HLA Database. The sequence of the 5'-upstream region, all introns, and exons 1, 4, 5, and 6 of *HLA-DRB1\*03:19* was first reported here. Compared with *HLA-DRB1\*03:01:01:03*, the novel *HLA-DRB1\*03:19* has 2 nucleotide changes from *DRB1\*03:01:01:03*; the first change is a T missing at nucleotide 2686 in intron 1, and the second at nucleotide 8280 in exon 2, where C>A (codon CTC>ATC) resulting in a coding change: residue 96 Leucine is changed to Isoleucine. (Figure 1).



**FIGURE 1** | Sequence alignment of the full length of DRB1\*03:01:01:03 and DRB1\*03:19 alleles. Dashes indicate identity with the DRB1\*03:01:01:03 sequence. The pipes indicate the exon and intron boundaries. The nucleotide positions are numbered according to the genomic full-length alignment in the IPD-IMGT/HLA Database. Allele DRB1\*03:19 showed 2 nucleotide changes from DRB1\*03:01:01:03; the first change is a T missing at nucleotide 2686 in intron 1, and the second at nucleotide 8280 in exon 2 where C>A.

DRB1*03:01:01:03	AGCCCTGGTG TGGGAAATTA TGTGGAGAGA GAGAAAGACG GCTAGAGGGG CTGATGTATA GAAAGTAAGG AAATGGAGAG	2246
DRB1*03:19		
DRB1*03:01:01:03	GCAGAAGATG AGGTAGGACA CAGAGAGAAA GTCAGGAGCC TCATCATTAT AGGCTCTGAT GTCCACGGTA AAAAAATTGA	2326
DRB1*03:19		
DRB1*03:01:01:03	ATTTTATTTT ATTTATTTAT TTATTTATTT ATTTATTTTA TTTATTTATT TATTTATTTT TTTAAGATGG AGTCTCGCTT	2406
DRB1*03:19		
DRB1*03:01:01:03	TGTTGCCAG GCTGGAGTGC AGTGGCGTGA TCTCAGCTCA CTGCAAGCTC CACCTCCTGG GTTCATGCCA TTCTCTGGCC	2486
DRB1*03:19		
DRB1*03:01:01:03	TCAGCCTCCC TAGTAGCTGG GACTACAGGC ACCTGCCACC ACGCCTGGCT AATTTTTAGT ATTTTTAGTA GTGAGGGCAT	2566
DRB1*03:19		
DRB1*03:01:01:03	TTTGTCTGT TAACCAGGGT GGTCTCCATC TCCTGACCTC GTGATCCACC TGCCTCAGCC TCCCAAAGTG CTGAGACTAC	2646
DRB1*03:19		
DRB1*03:01:01:03	AGGTGTGAGC CACCACGCCT GGCCTATTTT TTTT***** GAGACGGAGT TTCGTTCTTG TTGCCCAGGC TGGAGTGCAA	2686 2726
DRB1*03:19		
DRB1*03:01:01:03	TGGTGCAATC TCGGCTCACT GCAACCTTCG CCTCCCTGGT TCAAGTGATT CTCCTGCCTC AGTCTCCCAA GTATCTGAGA	2806
DRB1*03:19		
DRB1*03:01:01:03	TTACAGGCAC CCACCACCAT ACCTGGCTAA TTTTATTTT TTTGTATTTT TAGTAGACAT CGGGTATCAC CATGTTGACC	2886
DRB1*03:19		
DRB1*03:01:01:03	ATGCTGGTCT CGAACTCCTG ACCTCAGATA ATCTGTCTGC CTGGCCTCC CAAAGTGCTG GGATTACAGG CATGAGCCAC	2966
DRB1*03:19		
DRB1*03:01:01:03	CGCGCCGGA CTGAATTTTA TTTAAATAGA TACGAGAAGC TACTGTATGG TTACAAGGAG AGTCAATTTA TATCAATTT	3046
DRB1*03:19		
DRB1*03:01:01:03	ATTTTTATT TATTTTATT TTTGGTGAT GGGTCTTGC TCTGTTGCC AGGCTAGATT GTAGTGGCAC AATCTCGGCT	3126
DRB1*03:19		
DRB1*03:01:01:03	CACTGCAACC TCTGCCTCT GGTTCAGGC GATTCTCCTG ACTCAGCCTC CAGAGTAGCT GGGACCACAG GTACATGCCA	3206
DRB1*03:19		
DRB1*03:01:01:03	CCACACCTGG CTAAGTTTTT GTATTTTTTA GTAGAGACAG GATTCACCA TGTTAGCCAG GATGGTCTCG ATCTCCTGAT	3286
DRB1*03:19		
DRB1*03:01:01:03	CTCGTGATCC ACCCACCTTG GCCTCCCAAA GTGCAGGGAT TACAGGCCTG AGCCACTGCG CCCGGCCTAT ATTCAATTTT	3366
DRB1*03:19		
DRB1*03:01:01:03	TAAACTAAT TCTAGCTACT CTGTGGGGAT TGAATGTTG GGGTTCACAA GTGGTCAGGA AGACTATTTA GGAGCACAGC	3446
DRB1*03:19		
DRB1*03:01:01:03	AGGGAATCT CCAGCGAAAA CAGGCTTGTG GCTTCATGGA GTGCATTAGT GATAAAGACG GTGAAAAAGA TAAAGTGGAC	3526
DRB1*03:19		
DRB1*03:01:01:03	AGACTTGGCA TGTATTTTCT CTAGCTTGT TAATGAATTA CTGTAAAGGG GGTAGAACAA TCAAGCTTAT TCCTAAGGAT	3606
DRB1*03:19		
DRB1*03:01:01:03	TTTGTTTTGA CAAATAAGTG GGTGGTAGTG TTGTTATTG AGATAGGAAA AACTATGGGA GGAAATTATT TGAAGTGGGT	3686
DRB1*03:19		
DRB1*03:01:01:03	GGTTGGAAT AAAAGTTTTG TTTAAATTTG AGATGATTTA TTGACATTTA TGTGGAGCAA TCAGAAGGTC AATGGCATT	3766
DRB1*03:19		
DRB1*03:01:01:03	AAGAGACTCA TGGTGAGGCT AGGGCTTCAA GTATTTATGT TGGCGGCATC AATACGTGTA GTGTGTTAAA TTCCAGGGAG	3846
DRB1*03:19		
DRB1*03:01:01:03	TGGAAGAGGA TACATAGGGA GATGGATTGT GTGGAGAAAA AAGAACAGGG CACAGGCCAG CAAAGGGGGC TGAGAAAGAG	3926
DRB1*03:19		
DRB1*03:01:01:03	CCCAGGGATG TTGAGAAAA ATCAAGAGAA CATGATGCGT GTACGCTAAG GAAAATAGAT TTTTTC AAG GAGAAGGGAG	4006
DRB1*03:19		
DRB1*03:01:01:03	AGGCCAATTG TGGTGAGTAC CACTAAGCGG AGGGGGAAGT GAGAACGTGA CAGAGAAGCA AGTGCTGGGT TTGGTGGAGT	4086
DRB1*03:19		
DRB1*03:01:01:03	TGATATTGC AGTCAGTGA GTATCCAGGG AGGAACTGG ATTGGACAAT TTGAAGAGCG AGTAGAAGTG AGGATGAGGT	4166
DRB1*03:19		
DRB1*03:01:01:03	TAAGATTGAC TGTTTTGAGT AGAGAGCTTC AGGGAAGGAC TGCACTCTGG GTTCAGGGAG CCAGCTGGAT CAAAAGGAAA	4246
DRB1*03:19		
DRB1*03:01:01:03	AGGCTAAAGA GGCTGAAGAG AAGCAGGAGG ACCTGTGAAC CAGAGATGCT CAGTCATTAT TAGCAGGAAA ATACTAGAAA	4326
DRB1*03:19		
DRB1*03:01:01:03	GCCCTGTGT GCAGTGATGA CTACTCATGC AGAAGGTCAC ACAGCCAATA TTTAACACAG CCAGTATTTT ACACAGCTAA	4406
DRB1*03:19		
DRB1*03:01:01:03	TATTTATTAG TGACATAGAA TATACCAGTT ATTACTCTAG GTCATGAGAA TGGAGTGATA AATAAAATGA ATCCGGTCCG	4486
DRB1*03:19		
DRB1*03:01:01:03	CATCAGTATA TGCCATGTAA CTTTTGCAG TGACTGTGTA CCAGGCCTGT GAATTCAGT ATGCAATTTT AATAATGATC	4566
DRB1*03:19		
DRB1*03:01:01:03	CTGCTGTATC TGTGGTGTTT AAAAAATAT ACATCTCTGG AATCTAAAAT TGAGAGGTTA TAAGTAAAAA CCAGTATTAC	4646
DRB1*03:19		
DRB1*03:01:01:03	AAATTGAGTG CTGAAATCA GATTGCAGTT TAAATCTGAG CATATAGAAA GTCCCTTCTT TCTATGTGAC CAGATGCTTT	4726
DRB1*03:19		
DRB1*03:01:01:03	TTGTGTGAGG TTTAGCTGGA CTGCATTATT AGACATAAAC CAGTGTCTTCT GCCCTATGTT TTCAGAATGA CAATCTTTTA	4806
DRB1*03:19		

FIGURE 1 | Continued.

DRB1*03:01:01:03	TGAAACTCAT AGAAGAACAG AAGACAACCTG CAAAATCATG ATGAAGATAG TAATTGCTTT AGAATTAAGG AATACAAAAA	4886
DRB1*03:19		
DRB1*03:01:01:03	ATAATGTGAG CTGTAGTTAT AGGGATCATA AAAGTTTAAA TGGGAATGTA TTTGAGTATG TGATCAGTGC TAAGAAGAGT	4966
DRB1*03:19		
DRB1*03:01:01:03	CATCATTTAA TTTTACACT AACAGTAATC TCGTGAGGAT TACGCTATTA TTAATGCAT TTGATAGATT ACAAAGAGC	5046
DRB1*03:19		
DRB1*03:01:01:03	TTATGGTTGG TAAAAATGA CCCAAGTAGA AGAGATCATG TTTTATTCA GGTTTTCTGA TTCTAGAGTT TGAGAGTTTG	5126
DRB1*03:19		
DRB1*03:01:01:03	TCCATCATTG GTGAGTAGTG ACTATATTGT GTCTGAATTA TTGACAGAAT TTCTGATATT CATATGTACC AGGTTGTTTC	5206
DRB1*03:19		
DRB1*03:01:01:03	TTAGAGTGGG GATAGAGATG CAAGGGCTGC TAGTCCCGAT GTATTGGGGA AACTTTCATT CATTTTGCAT TTATCATTIT	5286
DRB1*03:19		
DRB1*03:01:01:03	AAAAGTTCTG TATGTCTATA ATGGTCATGT GTTGAAGAAC ACAAGGAAGT ATTAATCACC TCCTTCTTCT AAGGTTTGAC	5366
DRB1*03:19		
DRB1*03:01:01:03	TAGCAAGTTG GGCTAGAGTT ACCAATAAAA ATACATGTTC CTAGTGAAT CTGAATTTCA GATACAAAAA CATAATTTAT	5446
DRB1*03:19		
DRB1*03:01:01:03	TGAAAAATCA AATTTAACTG GGCATCCTCT GGTTTTATTT GCCACATCTG TCAACCTAA GTGTGACACA TGGACATGGA	5526
DRB1*03:19		
DRB1*03:01:01:03	TTACAGTGCT AACCATGCAA GCCACGGTGA CAGCAACTTC ACACATGTTT ATTTTAACT TTCTCTGTAA GAAAGTGCTT	5606
DRB1*03:19		
DRB1*03:01:01:03	AGATAATTTA GGGATAAAAA GATAGACATT GCTTGATCCA GGGTGCACAC CTCTCTGCCA CCATTTCTAA AGGGCAAAGG	5686
DRB1*03:19		
DRB1*03:01:01:03	GAGATTCTG CAGGTCTGG TCACAGTCTG GGGAGCTGCT CATTTTTGTA AAGTGTCTGT ATGAGAATGT CATTTCCTTG	5766
DRB1*03:19		
DRB1*03:01:01:03	GTTCCTCTCT TTCGAGGGG ACTTGACTAC AAAACCAAGA GTTCTGCCTC TGGCCAAGGC TGGTAATTTG ATGCTGCTA	5846
DRB1*03:19		
DRB1*03:01:01:03	GTATTGTTGG GAGTGGGAGA CTGAAAGAAA TGAGTTAGTT GGGGCATTTA ACGGGAATAA AATAGCTGTG GTTGTGACTC	5926
DRB1*03:19		
DRB1*03:01:01:03	ATTACTACAG ATAATTAGTG GACCAGTGGG AGAGAAATTA AGAAAAAGA TGATGTGAAT GATAAATGAT ATGATTAGTG	6006
DRB1*03:19		
DRB1*03:01:01:03	ACTGCTGGT AAGGCAAGGA AATCATTAAA TCTTGGTTCT CATCAAGTTC ATTTTCTGGA AAGATAGCAC TGTATTGGGA	6086
DRB1*03:19		
DRB1*03:01:01:03	GCAGAATCT ACAAACCTT CTTTTTACAT AGGACCAAGA TTTTCAACAA ATATTTTCA ATGCAATTCT CAGCTGCTCC	6166
DRB1*03:19		
DRB1*03:01:01:03	ATAACTAATA GTAGCTTGT CAACACAGAT TTTTFCAGAT GATTACACCC TGTGGTACTT ACCCAGGGAT GGTTCACCAC	6246
DRB1*03:19		
DRB1*03:01:01:03	CCCTCCCTC CCTCTCATCA TCGTTGGGGA ACGGTGACAA TGTTTGAAC AATTTTGGT TGTACAAAC AGGGGTTTCT	6326
DRB1*03:19		
DRB1*03:01:01:03	TCTGATATTC AATGAGTAGA AGCCAGGGAC ACTGCTAGAG AACCCACAAT GTTCAGAACA GCCTCTGCCA TCAACAAGGA	6406
DRB1*03:19		
DRB1*03:01:01:03	ATTATCTGGT CCAAAATGTC AATAGTGTG AGGCTAAGAG CACTGGTTCA CACTGTGCTC TTTCTGAAAA TTCTAGACTC	6486
DRB1*03:19		
DRB1*03:01:01:03	ACATCTGTTA TACTACTACC ACACAGTTA GTCTTTTATT TTTGCTTGT TCAATATAAA CAATAGACA GTTGCAATAA	6566
DRB1*03:19		
DRB1*03:01:01:03	TTCAACCACT TTCTTGTGA ATCCATTAG TCAATGCAAG CTCAATATTT TCATATTTAT TTTTGCCTT ATGCAATATT	6646
DRB1*03:19		
DRB1*03:01:01:03	TTTCAACATT TTCATGAGTT GTCGGTCACT ACTATCTCTA TTAACCTTCA ACAACTTGC CTTGTAAGTC ACAAATAGTG	6726
DRB1*03:19		
DRB1*03:01:01:03	ATGCTGCTGA AATATTCTCT CACTAACATG CCTCAGATT CTGTAGTGAT TCTACATTTG ATATTATTTA CAATGTAATA	6806
DRB1*03:19		
DRB1*03:01:01:03	TGCTCTATT TATTCATTTG GCTTTTACC AAGGATTATT TTTAAGTTAT TTTTGTCAAT TTCACACTTC AAACATAAAG	6886
DRB1*03:19		
DRB1*03:01:01:03	ACAAAAACAT CAAAAATATA GTGTTTTACA TATGTGCATA TTTTACACA TATATGTATG TATATTTATA TGATTGAAA	6966
DRB1*03:19		
DRB1*03:01:01:03	GTACAGAAGC ACATGTCACC AATAAGAGCT CTGAGACACC TTCGACCACT TACCCTATC AGATGAGTTG TGGAAACAAG	7046
DRB1*03:19		
DRB1*03:01:01:03	TTTTTTTAA TGAATTTCTG AGCTTTGTGG ATTTAGAAAT GCAAAGGAAG GTTTGTGGAC ATTCACAGGG ATCATGATTT	7126
DRB1*03:19		
DRB1*03:01:01:03	TATTCTCCT AAAACTCTTC TGTACTTCC AATTGTCTT AGTATAAATC CAAATCCTA ACACCACCA AGAGGCTTTT	7206
DRB1*03:19		
DRB1*03:01:01:03	CAATACCTGG CTCCTGTGAT TTCTCCGGC TAATCTGTTA CCCTCCTTCC CCTCAGCCTC TCTGCTTAG TGAACCTTCT	7286
DRB1*03:19		
DRB1*03:01:01:03	CCTAGTTTT TGAAGAAGTT CATCAATTCA AGCTTTTGTG CATGGGATTT CCTAAACCTG AAATGTGCCT CCCGTTTTGT	7366
DRB1*03:19		
DRB1*03:01:01:03	CCAAACAGAC ACGGGCTCCA CTCTGCCCC TGCTCACAC CTGCTTAACC TGCAAGTCA CATCTGAACC GTCACATTTA	7446
DRB1*03:19		

FIGURE 1 | Continued.

DRB1*03:01:01:03 DRB1*03:19	AGAGGGTCCT TCTCTGGCAC CCTAATGTAA TTGAGATCAT CCTATTATTC TCTGTTCTAG AACTCCACAC TTCCGACATT	7526
DRB1*03:01:01:03 DRB1*03:19	TCTCATTCTT GTCTAAGCTC TTGTGTGTTT GGTGTTGGGC CATCACTTTC ACTGCTCTTT AAGCTCCCC AGCGGAGTGG	7606
DRB1*03:01:01:03 DRB1*03:19	AGAGGTCTGT TTTCCCTCGT TTGGATTCTT AGAGGCAGCG CAGACCAGGC ACAAGGTCAG CACTAAGGAA GGGTTCAGAG	7686
DRB1*03:01:01:03 DRB1*03:19	GATGAACCGG GTGGGTGCTG TTTAAGGAAC CGGTAACAT GTGGGATGAG AGAAGGAGCA GAGTGTCTTT GGGGTGGGAG	7766
DRB1*03:01:01:03 DRB1*03:19	CTCCCAGGAG GAGGCGGCGC GGGCTGCGGT GCTGGGCGGA TCCTCCTCCA GCTCCTGCTT GGAGGTCTCC AGAACAGGCT	7846
DRB1*03:01:01:03 DRB1*03:19	GGAGGTAGGG AGGGGGGTCC CAAAAGCCTG GGGATCAGAC GTGGTTTTCC GCCTGGTCC CCCAGGCCCC CTTTCGCCCT	7926
DRB1*03:01:01:03 DRB1*03:19	AGGAAGACAG AGGAGGAGCC CCTGGGCTGC TGGTGGTGGG CGTTGCGGCG GGGGCCGGTT AAGGTTCCCA GTGCCCGCAC	8006
DRB1*03:01:01:03 DRB1*03:19	CCCACCCAGG GAGCCCCGGA TGCCGCGCTC ACTGTCAGTG TCTTCTCAGG AGGCCGCCTG TGTGACTGGA TCGTTCGTT	8086
DRB1*03:01:01:03 DRB1*03:19	CCCCACAGCA CGTTTCTTGG AGTACTCTAC GTCTGAGTGT CATTCTTCA ATGGGACGGA GCGGGTGGCG TACCTGGACA	8166
DRB1*03:01:01:03 DRB1*03:19	GATACTTCCA TAACCAGGAG GAGAACGTGC GCTTCGACAG CGACGTGGGG GAGTCCGGG CGGTGACGGA GCTGGGGCGG	8246
DRB1*03:01:01:03 DRB1*03:19	CCTGATGCCG AGTACTGGAA CAGCCAGAAG GACCTCCTGG AGCAGAAGCG GGGCCGGGTG GACAACTACT GCAGACACAA	8280
DRB1*03:01:01:03 DRB1*03:19	CTACGGGTT GTGGAGAGCT TCACAGTGCA GCGGCGAGT GAGCGCGGCG GGGGCGGGG CCTGAGTCCC TGTGAGCTGG	8406
DRB1*03:01:01:03 DRB1*03:19	GAATCTGAGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGAGA GAGAGAGACA GAGAGACAGA GAGAGAGAGC	8486
DRB1*03:01:01:03 DRB1*03:19	GCCATCTGTG AGCATTTAGA ATCCTCTCTA TCCTGAGCAA GGAGTCTGA GGGCACAGGT GTGTGTGTAG AGTGTGGATT	8566
DRB1*03:01:01:03 DRB1*03:19	TGTTCTGTGC TGTGAGGCTG TTGTGGGAGG GGAGGCAGGA GGGGGCTGCT TCTTATTCTT GGAGGACTCT GTGGGAGGTT	8646
DRB1*03:01:01:03 DRB1*03:19	GACAAGGGAG GTGGGTGCGG GCGGCTGGAG AGAGAGGTGA CCTTGATTGT CTCGGGTCTT TAGAGATGCA GGAAGGGGAA	8726
DRB1*03:01:01:03 DRB1*03:19	ATGTAAGGGG TGTGTGGTTG GGGTGAAGTT TTAGGGGAGG AGAGCTGAGG GGAAGGAAG GTTTGGGATA ATGTGAGGAG	8806
DRB1*03:01:01:03 DRB1*03:19	GCCAGTCCA GACTGTCCCT GGCACACACC CTTCATGTAA TCTCTGAAAT AAAAGTGTGT GCTGTTTGTG TGTAAGAACA	8886
DRB1*03:01:01:03 DRB1*03:19	TTAGATTAAT TTCTAGGGGA ATTGAGGAGA CCTCTGAGGC ATCTCTGAAG CTTCTTTAGG TCTAAATTC TTGCTAGTTT	8966
DRB1*03:01:01:03 DRB1*03:19	TTTGTTTTT ATTGTGTATA TTTTACATA GTAGAAATGA CTGTAAACT AACTTTTTGA ATTAAGATT TAACACAGTT	9046
DRB1*03:01:01:03 DRB1*03:19	ACTATTTTAT TATAATGCTA ATAGTTTCTT AGTAGTTACA TATTATTCTT TTATATATA TAGTTGTGAC ACAACTTACC	9126
DRB1*03:01:01:03 DRB1*03:19	TCACTTTCCA CTTTGTGAC CTTTATTATG ACATTACCA AAATTTGAAA ATGTATGTTT CTGGTAATT TTTAATTTAT	9206
DRB1*03:01:01:03 DRB1*03:19	ATTTTTTCA TTTATAATTC TTTGAATTA TTTGACCTA TTTATTGGCC AGTTTTAATA ACTGCTGTAA GAATTCCTTA	9286
DRB1*03:01:01:03 DRB1*03:19	TTGATTGG TAGGGAATGG ACAATGATCT ACTGCTAAT ATCTCGAGGG CTAGTATT TTCTCAGTA CTTTGTGGT	9366
DRB1*03:01:01:03 DRB1*03:19	TCTTTGACT GTGAGATTAT TAACACTTA TTGATATTG ATTCAGCATT TGCTCCAGTT TGTGGTTGT ATGTTGATT	9446
DRB1*03:01:01:03 DRB1*03:19	TGAAAATCT TTTCCATGTT AAGAATTGA ACATTTTAT ATAATAAAT ATGTTGCAA ATTTTATTA ATGATTACA	9526
DRB1*03:01:01:03 DRB1*03:19	ATCCATCTTA AATCTGCCAT TTTGTGTAT TGTGTCTCC AGGTTTCTCC TTACTTCTAA AAAAAATGC ATTTATTGAG	9606
DRB1*03:01:01:03 DRB1*03:19	AGTCTGCTAG TGTTAGGGAT TTTCTGGGC ATAAGCACCC CAAGTGACGA GTCCAGACA CTGCCTAAT CCAAAATGTA	9686
DRB1*03:01:01:03 DRB1*03:19	TTCTGGAAG AAAAATCATT TTACAATGAT AGGCCTAATA ATAATTAAGC TTGTGTTGCA TGGGAGATGC ATTGATCAGC	9766
DRB1*03:01:01:03 DRB1*03:19	TAAATGTAAA TATAAGAACT TTCAAACCTA AAATGACGTT CCTTAATCCT TCTCTCTGCT TTATGACTCA TGCTTTTCTG	9846
DRB1*03:01:01:03 DRB1*03:19	GGAAAGTAAA AATTTGGAGA ATCATTCTG TCTGTCCAC CTCCAGGG GCAGAACCAT TTCTGTGGT TTCTAAGGTG	9926
DRB1*03:01:01:03 DRB1*03:19	TGAGTGCATG GCGGTAGTAT TCCTAAAAAT TCATATTCGG TTTGTCATG TACCAACTC TGTCCTGTTA TCTATCAACA	10006
DRB1*03:01:01:03 DRB1*03:19	TTGTTTTAAA TCATATATTT CTGTCAAGGT GTACAAGGAT GATAAATAGG TGCCAAGTGG AGCACCCAAG TGTGATGAGC	10086

FIGURE 1 | Continued.

DRB1*03:01:01:03	CCCCTCACAG TGGAAATGGAG TGTGAAGCTT TATGACCTCA TAAATTGAAG GTTATCTTCA GGCATTGTTT TATAATATTT	10166
DRB1*03:19		
DRB1*03:01:01:03	ACATGCATTA ATCCTCATAT AATCCCAAGA GGTAATATTAG TATAATTATC CTTTATTATA GGTGACAAA TTAGACACACA	10246
DRB1*03:19		
DRB1*03:01:01:03	GAAGAATCAA ACTCTTAAGG CAGACCTTGG ATTTGAACCA GGCAACCTGG CTCAGATATC AGTTTTAATT ACTACACTCT	10326
DRB1*03:19		
DRB1*03:01:01:03	GTACTTTCAA AGATTTGTAA ACACTTTGAC AATGCATGAC AATTTCAAGC TATGAAGAAA CAAACACAAT TTTTCACAAT	10406
DRB1*03:19		
DRB1*03:01:01:03	ATCTCTCAA TCTAATAGGT CCTCACTATC AAGATTAAGT TCCAGGCTGA TGACACTGTA AGGCCACATG GCCACGCTGTG	10486
DRB1*03:19		
DRB1*03:01:01:03	CTGGAGGCCT GGTC AAGGTC AGAGCCTGGG TTTGCAGAGA AGCAGACAAA CAGCCAAAACA AGGAGACTTA CTCTGTCTTC	10566
DRB1*03:19		
DRB1*03:01:01:03	ATGACTCATT CCCTCTACCT TTTTCTCTCT   Exon3 AGTCCATCCT AAGGTGACTG TGTATCCTTC AAAGACCCAG CCCTGTCAGC	10646
DRB1*03:19		
DRB1*03:01:01:03	ACCATAACCT CCGTGTCTGT TCTGTGAGTG GTTTCATCC AGGCAGCATT GAAGTCAGGT GGTTCGGGAA TGGCCAGGAA	10726
DRB1*03:19		
DRB1*03:01:01:03	GAGAAGACTG GGGTGGTGC CACAGGCCTG ATCCACAATG GAGACTGGAC CTTCCAGACC CTGGTGTATG TGGAAACAGT	10806
DRB1*03:19		
DRB1*03:01:01:03	TCCTCGGAGT GGAGAGGTTT ACACCTGCCA AGTGGAGCAC CCAAGCGTGA CAAGCCCTCT CACAGTGGAA TGGAGTGAGC	Intron3
DRB1*03:19		
DRB1*03:01:01:03	AGCTTCTGA CTTCATAAAT TTCTCACCCA CCAAGAAGGG GACTGTGCTC ATCCCTGAGT GTCAGGTTTC TCCTCTCCGA	10966
DRB1*03:19		
DRB1*03:01:01:03	CATCCTATTT TCATTTGCTC CATGTTCTCA TCTCCATCAG CACAGGTCAC TGGGGGTAGC CTTGTAGGTG TTTCTAGAAA	11046
DRB1*03:19		
DRB1*03:01:01:03	CACCTGTACC TCCTGGAGAA GCAGTCTCGC CTGCCAGGCA GGAGAGGCTG TCCCTCTTTT GAACCTCCCC ATGATGTCAC	11126
DRB1*03:19		
DRB1*03:01:01:03	AGGTGAGGCT CACCCACCCT CCCCAGGCTC CAGGCATCGC CTCTGGGTCT GAGACTGAGT TTCTGGTCTG GTTGATCTGA	11206
DRB1*03:19		
DRB1*03:01:01:03	GTTATTTGTT GTGATCTGGG AAGAGGAGAA GTGTAGGGGC CTTCTGACA TGAGGGGAGT CCAATCTCAG CTCTGCCTTT	11286
DRB1*03:19		
DRB1*03:01:01:03	TATTAGTCTG GTCACCTAG ACAAACTACT TAGCCTCATT GAGTCTCAGG CTTTCTGTGG ATCAGATGTT GAACTCTTGC	11366
DRB1*03:19		
DRB1*03:01:01:03	CTTACATCAA GGCTGAATA TTTGAATGAG TTTGATGCTT GAACCTTGTA ACTGTTGAGT GTGATTGAA ATCCTTTTTT	11446
DRB1*03:19		
DRB1*03:01:01:03	TCTCCAGAAA TGGCTAGTTA TTTTGTCTCT TGTGGGTGAG ACTTCTTCCC CATTTTCAA GCTCTGAATC TTAGAGTCTC	11526
DRB1*03:19		
DRB1*03:01:01:03	AATTAAGAG GTTCAATTTG GAATAAACAC TAAACCTGGC TTCCTCTCTC   Exon4 AGGAGCACGG TCTGAATCTG CACAGAGCAA	11606
DRB1*03:19		
DRB1*03:01:01:03	GATGCTGAGT GGAGTCGGGG GCTTTGTGCT GGGCCTGCTC TTCCTGGGG CCGGGCTGTT CATCTACTTC AGGAATCAGA	11686
DRB1*03:19		
DRB1*03:01:01:03	Intron4 AAGGTGAGGA GCCTTTGGTA GCTGGCTCTC TCCATAGGCT TTTCTGGAGG AGGAATATG GCTTTGCTGA GGTTAGTTCT	11766
DRB1*03:19		
DRB1*03:01:01:03	CAGTATATGA GTGGCCCTGA ATAAAGCCTT TCTTCCCCA AACGGCTCTA ATGTCCTGCT AATCCAGAAA TCATCAGTGC	11846
DRB1*03:19		
DRB1*03:01:01:03	ATGGTTACTA TGTGAAGACA TAATAGCTTG TGGCCTGAGC AGACAAGAGG AAGGTTAACA AGTAGGGGTC CTTTGGTTTG	11926
DRB1*03:19		
DRB1*03:01:01:03	AGATCTTGA GCGATTAAG GAAGAGCCAC TAAGACTAAT GGAATTACAC TGGATCCTGT GCAGACACTC TTACCCTTCA	12006
DRB1*03:19		
DRB1*03:01:01:03	TGGGTACAT GGTCTGTTTC TGCTCTCTC TGCCCTGGCT GGTGTGGGTT GTAGTGACAG AGAACTCTCC GGTGGGAGAT	12086
DRB1*03:19		
DRB1*03:01:01:03	CTGGGGCTGG GACATTGTGT TGGAAAGACAG ATTTGCTTCC ATAAATTTTA AGTGTATATA TTTTCTCTTT TTTCCAGGA	Exon5
DRB1*03:19		
DRB1*03:01:01:03	CACCTCTGAC TTCAGCCAAG AGGTAATACC TTTTAATCCT CTTTGTAGAA CAGATACGGT TTCCTAGTGT AGAGGTGAAG	Intron5
DRB1*03:19		
DRB1*03:01:01:03	CCAGCTGGAC TTCTGGGTGC GGTAGGACT TGCAGAACTT TCCTGTCTTA GGAGAGGTTT CTAATGCAC CAATCAGTGC	12326
DRB1*03:19		
DRB1*03:01:01:03	TCTGTAATA CACACCAATT GGCACCTGCT GGCTAGATAG ATGTTTGTAA AATGGACTAA TCAGCACTCT GTAAAATGGA	12406
DRB1*03:19		
DRB1*03:01:01:03	GCAATCCACA CTTGTGTAATA TGGACCAATC AATGCTCTTT AAAATGGACC AATCAGCAGG ACATGGGCGG GGACAATAA	12486
DRB1*03:19		
DRB1*03:01:01:03	GGGAATACAA GCTGGCCACC CCAGCCAGCA GCAGCAACCC GCTCAGGTCG CCTTCCATCG TGTGGAAGCT TTGTTCTTTT	12566
DRB1*03:19		
DRB1*03:01:01:03	GCTCTTACA ATAAATCTTG CTGTTGCTCA CTCTCGGGT CTGTGCCACC TTTAAGAGCT GTAACACTCA CTGTGAAGAT	12646
DRB1*03:19		
DRB1*03:01:01:03	TGCGGGCTTC ATTCTTGAAG TCAGCGAAAC CACGAACCCA CCGGAAGGAA CAAACTCTGG ACACACTAGA ATTGATGGTA	12726
DRB1*03:19		
DRB1*03:01:01:03	GAGGTGATAA GGCATGAGAC AGAAATAATA GGAAAGACTT TGGATCCAAA TTTCTGATCA GGCAATTTAC ACCAAAACCTC	12806
DRB1*03:19		
DRB1*03:01:01:03	CTCCTCTCCA CTTAGAAAAG GCCTGTGCTC TGTGGGACTA TTGGCTCTGG GAGACTCAGG AACTGTTTTT TCTTCTCTCT	12886
DRB1*03:19		
DRB1*03:01:01:03	GCAGTCTCTC CATCTGAGTC CCTGAAAGAG AGGAAAAGAA ACTGTTAGTA GAGTCAGGTT GAAAACAACA CTCTCTCTCTG	12966
DRB1*03:19		
DRB1*03:01:01:03	TCTTTTGCAG   Exon6 GATTCCTGAG CTGA	12990
DRB1*03:19		

FIGURE 1 | Continued.

The complete HLA typing of the donor is as follows: HLA-A\*02:06:01, 24:02:01:01; -B\*13:02:01, 39:01:01:01; -C\*03:04, 06:02; -DQB1\*02:01, 03:01; -DRB1\*03:19, 11:01.

The sequence data has been submitted to GenBank and the IPD-IMGT/HLA Database (PQ811753-HWS10100124); the name was officially assigned by the World Health Organisation (WHO) Nomenclature Committee for Factors of the HLA System. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report [6], names will be assigned to new sequences as they are identified.

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### Conflicts of Interest

The authors declare no conflicts of interest.

### Data Availability Statement

The genomic full-length sequence of the new allele is available at GenBank (accession number PQ811753) and submitted to the IPD-IMGT/HLA Database (submission number HWS10100124).

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