

NEW ALLELE ALERT

Genomic Full-Length Sequence of the *HLA-DRB1*04:90* Allele Was Identified by PacBio Sequencing

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Correspondence: Shutao Pang (qdbc_pst@sina.com)**Received:** 7 May 2025 | **Revised:** 26 May 2025 | **Accepted:** 29 May 2025**Funding:** This work was supported by Qingdao Key Medical and Health Discipline Project.**Keywords:** genomic full-length | *HLA-DRB1*04:90* | PacBio sequencing**ABSTRACT**The complete genomic sequence of *HLA-DRB1*04:90* was determined using a PacBio sequencing approach conducted in China.

Here, we present the complete genomic sequence of *HLA-DRB1*04:90*. This sequence was identified in a volunteer donor who took part in the China Marrow Donor Program. As of now, based on the IPD-IMGT/HLA Database Release 3.60 up to April 2025 [1], a total of 3787 HLA-DRB1 alleles have been identified, with 861 of them classified as *DRB1*04* alleles. The *HLA-DRB1*04:90* allele sequence was first submitted to the IPD-IMGT/HLA Database in 2010. At that time, it only covered exon 2. Now, we report the 14,465-base-pair (bp) full-length genomic sequence of *DRB1*04:90* obtained via PacBio sequencing, a third-generation sequencing platform. Briefly, group-specific amplification was carried out using primers located in the 5' untranslated (UT) and 3' UT regions. This was followed by Sanger sequencing using generic primers in both the forward and reverse directions via cycle sequencing [2]. The HLA-DRB1 sequencing result in this sample is rare. To verify this result, the third-generation sequencing platform (Pacific BioSciences) was utilised.

All tests were conducted with the donor's informed consent. Genomic DNA was then extracted from peripheral—blood leukocytes in accordance with the manufacturer's instructions for DNA isolation kits (Life Technologies), and further molecular testing ensued. Briefly, 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 enabled the group to emit fluorescence, and the fluorescence

signal was recorded. Subsequently, we utilised the official PacBio software, Circular Consensus Sequencing (CCS), to process the HiFi data. Next, we partitioned the library according to the presence or absence of barcodes. Afterward, we performed back posting, mutation detection, clustering, typing, and haplotype verification of the results [3]. Finally, the full-length sequence of the *HLA-DRB1*04:90* allele was confirmed.

For the first time, the sequence of *DRB1*04:90*, with a total length of 14,465 bp, encompassing all exons, introns, the 5'-upstream region, and the 3'-downstream region, is reported herein. When compared with *DRB1*04:05:01:04*, *DRB1*04:90* demonstrates three nucleotide changes at nucleotide positions 8573, 8574, and 8575, where T is converted to G, A to T, and C to G. These alterations lead to a coding modification, with the Tyrosine residue at position 107 encoded within exon 2 being transformed into a Histidine. In contrast to *DRB1*04:05:01:04*, a nucleotide A is inserted at position 5262 in the repetitive sequence region of intron 1, and the AGAG fragment is absent after the base at nucleotide 8761 in intron 2, as illustrated in Figure 1. The complete HLA typing of the donor is presented as follows: *HLA-A*02:01, 02:06; -B*35:01:01G, 51:01:01:01; -C*03:03, 14:02; -DRB1*04:90, 11:01; -DQB1*03:01, 04:01*.

The name *DRB1*04:90* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in April 2010. This follows the agreed policy that, subject to the



FIGURE 1 | Alignment of the full-length sequences of the *HLA-DRB1*04:05:01:04* and *HLA-DRB1*04:90* alleles. Dashes denote identity with the *DRB1*04:05:01:04* sequence. The nucleotide positions are numbered in accordance with the full-length genomic sequence alignment in the IPD-IMGT/HLA Database. The *DRB1*04:90* allele exhibits three nucleotide changes from the *DRB1*04:05:01:04* allele at nucleotide positions 8573, 8574, and 8575, where TAC is altered to GTG. These changes lead to a coding modification, with the Tyrosine residue at position 107 encoded within exon 2 being converted to a Histidine. When compared to the *DRB1*04:05:01:04* allele, the *DRB1*04:90* allele has a nucleotide A inserted at position 5262 in the repetitive sequence region of intron 1. In intron 2, the AGAG fragment is absent after the base at nucleotide 8761.

DRB1*04:05:01:04	GCTGGAGTGC AATGGCGCGA TCTCGACTCA CTGCAACCTC TGCCCTCTGG GTTCAAGTGA TTCTCCTGCC TCAGCTTCCC	2494
DRB1*04:05:01:04	AAGTAGCTGG GATTACAGGT GCCTGCGACC ATACTCGGCT TATTTTTTTG TATTTTTAGT AGAGACAGGG TATCACCATG	2574
DRB1*04:05:01:04	TTGGCCAGGC TGGTCTCAA CTCTGACCT CAGATAATCT GCCTGGCTTC CCAAAGTGT GAGATTACAG GCGTGAGCCA	2654
DRB1*04:05:01:04	CCATGCCCAA CCTGAATTTT ATTTGAATAG ATATGAGAAG CTACTGTATG GTTACAAGGA CAGTCAATTT ATATTCGATT	2734
DRB1*04:05:01:04	TTTTTTTTTT GAGACAGAGT CTGCTCTGTG TGCCAGGCT AGATTGCAGT GGTACAATCT CAGCTCACTG CAACCTCTGC	2814
DRB1*04:05:01:04	CTCCTGGGTT CCAGCAATTC TCCTGCCTCA GCCTCCAAG TAGCTGAGAC CACAGGTACA TGCCACTACA CCTGGCTAAT	2894
DRB1*04:05:01:04	TTTTTGTTT TTTAGTAGAG ATGGGGTTTC ACCGTGTTAG CCAGGATGGT CTTGATCTCC TGACCTCGTG ATCCACTCCC	2974
DRB1*04:05:01:04	CTCGGCTCC CAAAGTGTG GATTACAGG TGTGAGCCAC CACGCCCGG CTATATTC AAATTAAAAT TAATTCTAGC	3054
DRB1*04:05:01:04	TACTCTGTGG GGATTGGATT GTTGGGTTTC ACAAGTGTG AGGAAGACTA TTTAGGATCA CAGCAGGGAA TTCTCCAGGG	3134
DRB1*04:05:01:04	AAAACAGGCT TGTGGCTTCA TAGAGTGCAT TAGTGATAAA GACAGTGAAA ACGACAAAAGT GGACAGACTA GGCATGTATT	3214
DRB1*04:05:01:04	TTTGCTTAGC TTGTTAATGG ATTACTCTAA AGGGGGTAGA AAAATCAAGC TTATTCCTAA GGATTTTGTG TTGACAATA	3294
DRB1*04:05:01:04	AGTGGATGGT GGTGTTTATT GAGATAGGAA AACTGTGGG AGGAAATGAT TTGAAGTGGG TGGTTGAAA TAAAAGTTTT	3374
DRB1*04:05:01:04	GTTTAAATTT GAGATGATTT ATTGACATTT ATGTGGAGCA ATCCGAAGGT CAATGGCATT TAAGAGACTC ATGGTGAGGT	3454
DRB1*04:05:01:04	GAGGCCAGGG CTCAGGTAT TTAGTTGGC GGCATCAGTA CGTGAATGT GTTAAATCC AGGGAGTGA AGAGGATACA	3534
DRB1*04:05:01:04	TAGGGAGATG GATTGTGTGG AGAAAAAGA AGAGGGTACA GGCCAGCAA GGGGGCTGAG ACAGAGCCCA GGGATGCTGG	3614
DRB1*04:05:01:04	AGAAAACCCA AGAGAACATA ATGGGTGTAA GTCATGGAAA ATAGATTATT TTCAAGGAGA AGGGAGAGGT CAATTTGTGGT	3694
DRB1*04:05:01:04	GAGTACCCT AAGAGGAGG GGAAGTGA ACCTGACAGA GAAGCAAGTG CTGGGTTTG TGGAGTTGAT ATTTGCAGTC	3774
DRB1*04:05:01:04	AATGGAGTAT CCAGGGAGGA AACTGGATTG GACCATTTGA AGAGCAAGTA GAAGTGAAG CGAGGTTAAG GGTGACTATT	3854
DRB1*04:05:01:04	TTAAGTAGAG AGCTTCAGG AAGGACTGTG CTCTGGGTT AGGGAGCCTG CTGGATCTAA AGGAAAAGG CTGAAGAGGC	3934
DRB1*04:05:01:04	TGAAGAGAAG GAGGAGGACC TGTGAACCA AGATACTGAG TTATTATTAG CAAGAAAATA CTAGAGGGTC CCTGTGTGCA	4014
DRB1*04:05:01:04	GTGCTGACTG CTCATGCAAA AGGTCACACA GACAATATTT CACACAGCCA GTATTTATTA GTGACATAGA ATATGCCAGT	4094
DRB1*04:05:01:04	TATTACTCTA GGTCATGAGA ATAGAGTGAT AAATAAAATG AATCTGGTCG CCATCGGTAT ATGCCATGTA ACATTTTGA	4174
DRB1*04:05:01:04	GTGACTGTGT ACCAGGCCTA TGAATTCAG TATGCAATTT CAATAACGAT CCTGTTGTAT CTGTGGTGT TAAAAACATA	4254
DRB1*04:05:01:04	TACATCTCTG GAATCTAAAA TTGAGAGGAT ATAAGTAAAA CCCAGTATTA GAAATTTAGT GCTGGAAATC AGACTGCAGT	4334
DRB1*04:05:01:04	TTAAATCTGA GCATATAGAA AGTCCCTTTC TTCTATGTCA GCAGATGCCT TTTGTGTGAG GTTTAGGTAT ACTACATTAT	4414
DRB1*04:05:01:04	TAGACATAAA CCAGTGATTC TGCCCTATGT TTTGAGAATG ACAATCTTT ATGAAAATA TAGAAGAACA GAAGACAATT	4494
DRB1*04:05:01:04	GCAAAATCAT GATGAAGATG CTAGTGGCTT TAGAACCAAG GAATACAAAA AATAATGTGA GCTGCAGTTA TAGGGATTAT	4574
DRB1*04:05:01:04	AAAAGTAAA ATGGGAATGC ATTTGAGTGT TTATTATGTG ATCAGTGCTA ATAAGAGTCA TCATTTAATT TTACACTTAA	4654
DRB1*04:05:01:04	CAATAATCCT GTGAGGATTA AGCTATTATT AAATGCATTT GATAGATTAC AAAAAGGCTT ACCGTTGGTA AAAATTGACC	4734
DRB1*04:05:01:04	CAAGGGGAAG AGGTCACATT TTTATTCAGA TTTTCTGATT CTAGAGTTTG AGAGTCTGTC CATCATTAGT GAGTAGTGAC	4814
DRB1*04:05:01:04	AATACTGTGT CTAATATATC GACAGAATTT CTGATATTCA TATGTACTAT GTTGTCTTCT AGAGTGTGGG CAGAGATTCA	4894
DRB1*04:05:01:04	GGGCTGCTAG TTCCAATGTA TAGGAGAAAC TTTCAATCAT TTTGCATTTA TCATTTTAAA AGTTCTAGGC TGGCGCGGT	4974
DRB1*04:05:01:04	GGCTCATGCC TGTAATCCCA GCACCTTTGGG AGGCCAAGGC GGGCAGATCA CGAGGTCAGG AGATGAAGAC CATCTGGCT	5054

FIGURE 1 | (Continued)

DRB1*04:05:01:04 DRB1*04:90	AACATGGTGA AACCTCGTCT CTAATAAAAA TACAATAAAT TAGCTGGGCG TGGTGGTGTG CACCTGTAGT CCCACTACT	5134
DRB1*04:05:01:04 DRB1*04:90	TGGGAGGCTG AGGCAGGAGA ATGGCATGAA CCTGGGAGGC GGAGCTTGCA GTGAGCTGAG ATCGTGCCAC TGCCTCCAG	5214
DRB1*04:05:01:04 DRB1*04:90	CTCCACCCTG GGCAAAAGAG CGAAACTCCC TCTCAAAAAA AAAAAA*GT TCTATATGTC TGTCATGGCA TATGTGGAAG	5293
DRB1*04:05:01:04 DRB1*04:90	AACACAAGGA AGTATTAAT CACTCCTTCT GAGGTTTGTG TAGCAAGTTG GGCTAGGATT GCCAAATAAA ATACAGGTTT	5373
DRB1*04:05:01:04 DRB1*04:90	CTAGTTAAAT CTGAATTCA GATACACAAC TATAATTAC TGAATAATCCA AATGTAACCT GGCATCCTCT GATTTTATTT	5453
DRB1*04:05:01:04 DRB1*04:90	GCCAAATCTG TCAACCTTAC ATGAGACACA TGAGCATGGA TTACGGTGTG ACCCATGGAA GCCACAGCCA CAGTGACAGC	5533
DRB1*04:05:01:04 DRB1*04:90	GACTTCACAC ATGTTTATTT TTTAACTTTC TCTCTGTAAA GAAAGTGCTT AGATAATTTA GGGATAAAAA GATAGACATT	5613
DRB1*04:05:01:04 DRB1*04:90	GTTTGATCCA GGATGCACCT CTCTCTGCCA TCGTTTCTAA AGGGCAAAGA GAGATTTCCA CAGGTCTTAC TCACAGTCTG	5693
DRB1*04:05:01:04 DRB1*04:90	ACTCACAGTC TGGGGACCTG CTCATGCTTT GAAACTGTCT GTATGAGAAT GTCATTTTCT TGGTTTCTCC CTTTCTGAGG	5773
DRB1*04:05:01:04 DRB1*04:90	GGACTTGACT ACAAACCTGA GAGTTCTACC TCTGGCCAAG GCTGGAATTT TGATGCCTCG TAGTATTGTT GGGAAATGGGA	5853
DRB1*04:05:01:04 DRB1*04:90	GACTGAAATA AATGAGTTAG TTGGGGCATT AAACAGGAAT AAAATAGCTG TGGTTGTGAT TCATTACTAC AATTAGTGGAA	5933
DRB1*04:05:01:04 DRB1*04:90	CTAGTGGCAG AGAAATTAAG AAAGAAGATG ATGTGAGAGA TAAATTATAT GATTTGGTAA GGCAAGGGAA TCAGTAAATC	6013
DRB1*04:05:01:04 DRB1*04:90	TTGGTTCTGA ACAAGTTCAT TTTCTGGAAA GATAGCACTG TACTGGGACC AGAATTCTAC AAAACATCCG TTTTATGTAA	6093
DRB1*04:05:01:04 DRB1*04:90	GACCAAGATT TTCAACAAAT ATTTTTCAT GCAGTTCTCA GCTGCTCCAT AACTAATAGT GACTTATTC A ACACAGATAT	6173
DRB1*04:05:01:04 DRB1*04:90	TTTCAGATGG TTCACACCCA TGTTTCTTAC CCAGGGACAG TTCACCACCC CTCCTTCC CTCCCATCAC TCTTGAGGAA	6253
DRB1*04:05:01:04 DRB1*04:90	CATGTGGCAA TGTTAGAATA ATTTTGGTT GTCACAACAG GGGTTTCTTC TGATATTTAA TGAGCAGAAG CCAGGGACAC	6333
DRB1*04:05:01:04 DRB1*04:90	TGCTAGAGAA CCCACAATGT TCAGAAATAGA CTCCATCACC AACCAAGATT TATCTGCTCC AAAATGTCAA TAGTGCTGAG	6413
DRB1*04:05:01:04 DRB1*04:90	GCTGGAAGCA TTGGTTCACA CTGTGCTCTT TCTGAAAAAT GTAGACTCGC TTTTTTTTTT TTTTTTTGAG ATGGGGTCTT	6493
DRB1*04:05:01:04 DRB1*04:90	GCTCTGTCGC CCAGACTGGA GTGCAGTGGC TCCATCTCAG CTCACTACAA CCTCTGCCTC CCAGTTCAA GCGATTCTCC	6573
DRB1*04:05:01:04 DRB1*04:90	TGTCTCAGCC TCCCAGTAG CTGGGATTAC AGGTGCACCC TGCCATGCCG GGCTAATTTT TTGTATTTTA GTAGAGATGG	6653
DRB1*04:05:01:04 DRB1*04:90	GGTTTCACCA TGTTGCCAG GCTGGTCTCG AACTCCTGAG CTCAGGCAAT CCACCCGCTT TGGTCTCCCA AAGTGCTAGG	6733
DRB1*04:05:01:04 DRB1*04:90	ATTACACGCA TGAGCCACCG CGCCCGGCTT AGACTCACAT CTTTTATACA CTACTGCCC AATTCAGTTC TTTATGGTTT	6813
DRB1*04:05:01:04 DRB1*04:90	ATTTTTGCTT GTTTCATTAT AAAAACTAG ACAGTTGCAT AAATTCAACC ACTTACTGTG TGAATCCATT TAGTCAATGC	6893
DRB1*04:05:01:04 DRB1*04:90	AAGCTCAACA TTTTCATATT TATTTTTTGC CTTATGCAAT ATTGTTCAAC ATTTTCATAA GTTGTGGTTC AGCACTATCT	6973
DRB1*04:05:01:04 DRB1*04:90	CTATTAACCT TCAACAGTTT GCCCTTCTAA GTCACAATA GTGATGCTGC TGCAATTATT TTCTACTAAC ATGCCTCAGA	7053
DRB1*04:05:01:04 DRB1*04:90	TTTCTGTAGT GATTCTACAT TTGATATTAT TCACAATGTA AAATGCTTCT ATTTATTATC TTCACTTTTA CCCACAGGAT	7133
DRB1*04:05:01:04 DRB1*04:90	TATTTTTAAG TTATTTTTGT CATTTTCACA CTTCAACCAA ACATAAAGAC AAAAAATCA AAAATATGTA CATAGTGTTA	7213
DRB1*04:05:01:04 DRB1*04:90	TACATAGGTG TATATTTACA CACATATATG CACATATGTT TATATGTATT GAAACTACAG AAGCACATGT CACCAATAAG	7293
DRB1*04:05:01:04 DRB1*04:90	AGCTCTGAGA CACCTTTGAC CACTTACCCT TATCAGATGA GATTTGCCAA ATGAGTTTTG GGAACAAATT TCTTTAACT	7373
DRB1*04:05:01:04 DRB1*04:90	GAATTTCTGA GCTTTGTGGA TTTAGAAATG CAACTGAAAG TTTGTGGACA TTTACGAGGA TCATAGTTTT ATTCTCCTTA	7453
DRB1*04:05:01:04 DRB1*04:90	AAACTCTTCA ATACTTTCCC ATTTGCTTTA GTAATCCAA AATCCTAACA CCACTCACGA GGCTTTTCAA CACTGGCTT	7533
DRB1*04:05:01:04 DRB1*04:90	CTTGTGATTT CTCCAATCTA ACCTTTTACC CTCCTTCCC TCAGCCTCTC TGCTTTAGTG AACTTTGTTT TAGTTTTTTG	7613
DRB1*04:05:01:04 DRB1*04:90	AAGTTCATCA TCAATTCAAG CTTTTGTACA TGGGATTTCC TAAACCTGAA ATGTGCCTCC GGTTTTGTCC AAACAGACAC	7693

FIGURE 1 | (Continued)

DRB1*04:05:01:04 DRB1*04:90	ACAGGCTCCA CTCTGCCCC TGGCTCACAC CTGCTTAACT TGTTAAGTCA CATCTGTAAC TGTCACTCTT CTCTGGCACC	7773
DRB1*04:05:01:04 DRB1*04:90	CTAAAGGAAT TGAGATCATC CTATTATTCT CTGTTCTAGA ACTCCACACT TCTGAAATTT CTCATTCTCG TCTAAGTCTCT	7853
DRB1*04:05:01:04 DRB1*04:90	TGTGTGTTTG GTTTTTGGCC ATCACTTTCC CTGCTCTTAA AGCTCCCCCA GCGGAGTGGG GAGGTCTGTT TTCCCGTGTT	7933
DRB1*04:05:01:04 DRB1*04:90	TGGATTCTTA GAGGCAGCGC AGGCCTGGCA CAAGGTATC ACTAAGGAAG TGTTACAGG ATGAAAGCGG TGGCTGCTGT	8013
DRB1*04:05:01:04 DRB1*04:90	TTAAGGAAAG GGTAAGCCT TTAATGTTA AAGGGTTGAG AGAAGGAGCA AAGTGCCTTT GGGGTGGAGG CTCCAGGAG	8093
DRB1*04:05:01:04 DRB1*04:90	GAGGCGGCG GGGCTGCGGT GCTGGACGGA TCCTCTCCA GCTCCTGCCT GGAGGTCTCC AGAACAGGCT GGAGGCAGGG	8173
DRB1*04:05:01:04 DRB1*04:90	AGGGGGTCCC AAAAGCCTTG GGATCAGAGG TAGTTTTTCC ACCTGGTCCC CCAGACCCCC GTCCGCCTCA GAAAGACAGA	8253
DRB1*04:05:01:04 DRB1*04:90	GGATGAGCCC CTGGGCTGCG TGTGTGCGGG GTTGCGGGTG GGGCCAGATA GTGTCTTCCC CGGAGGCCGC TTCTGTAACC	8333
DRB1*04:05:01:04 DRB1*04:90	GGATCGTTCT TGTCCCCCA Exon2 GCACGTTTCT TGGAGCAGGT TAAACATGAG TGTCAATTCT TCAACGGGAC GGAGCGGGTG	8413
DRB1*04:05:01:04 DRB1*04:90	CGGTTCTTGG ACAGATACTT CTATCACCAA GAGGAGTACG TGCCTTCCA CAGCGACGTG GGGGAGTACC GGGCGGTGAC	8493
DRB1*04:05:01:04 DRB1*04:90	GGAGCTGGGG CGGCCTAGCG CCGAGTACTG GAACAGCCAG AAGGACTCC TGGAGCAGAG GCGGGCCGCG GTGGACACCT	8573
DRB1*04:05:01:04 DRB1*04:90	ACTGCAGACA CAACTACGGG GTTGGTGA GA GCTTCACAGT GCAGCGGCGA Intron2 GTTGAGCGCG GCGCGGGGCG GGGCCTGAGT	8653
DRB1*04:05:01:04 DRB1*04:90	CCCTGTGAGC GGAGAATCTG AGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGAGAGAG AGAGAGAGAG	8733
DRB1*04:05:01:04 DRB1*04:90	AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGCCCATCT GTGAGCATT AGAATCCTCT CTATCCTGAG CAAGAGATT	8813
DRB1*04:05:01:04 DRB1*04:90	TGCGGGCACA GGTGTGTGTG TAGAGTGTGG ATTTGTCCGT GTCTGTGAGG CTGTTGTGGG AGGGGAGGCA GGAGGGGGCT	8893
DRB1*04:05:01:04 DRB1*04:90	GCTTCTTATT CTGGAGACT TCTGTGGGA GGTGACAAGG GAGGTGGGTG CTGGGGGCTG GAGAGAGAGG CGACCTTGAT	8973
DRB1*04:05:01:04 DRB1*04:90	TGTCTCGGGT CCTTAGAGAT GCAAGGAAGG GAAATGTATG GGGTGTGTGG TTGGGGTAA GGTTTAGGGG AGGAGAGCTG	9053
DRB1*04:05:01:04 DRB1*04:90	AGGGGTAAGG AAGGTTTGGG ATAATGTGAA GAGGCCAGTT TCAGACTGTC CCTGGCACAC ACCCTTCATG TAATCTCTGA	9133
DRB1*04:05:01:04 DRB1*04:90	AATAAAAGTG TGTGCTGTTT GTTTGTA AAA GCATTAGATT AACTTCTAGG GGAATTGAGT AGACCTCTGA GGCACCTCTG	9213
DRB1*04:05:01:04 DRB1*04:90	AAGCTCTTT AGGTATAAAT TTCTGCTAG TTTTGTGTT TCTTAGTGT ATATTTTAC ATAGTTGAAA TGACTGTGAA	9293
DRB1*04:05:01:04 DRB1*04:90	ACTAACTTTT TGAATTAAG TTTGAAAACA CTGTTACTAT TTTATTATAA TGCTAATAAT TTCATAGTTA CTTTTTAAAT	9373
DRB1*04:05:01:04 DRB1*04:90	ATATAATAGT TGTGACACAA ATTACCTCAC TTTCTTGT TTTTTTTTTC TTACTTTTA AGTTTTAGGG TACATGTGCA	9453
DRB1*04:05:01:04 DRB1*04:90	CAACGTGCAG GTTTGTTACA TATGTATACA TGTCCATGT TGGTGTGCTG CACCCATTAA CTCGTCATTT AACATTAGGT	9533
DRB1*04:05:01:04 DRB1*04:90	ATATCTCTTA ATGCTATCCC TCCCCACCC CCCACCCAC AACAGGCCCC AGTGTGTGAT GTTCCCCTTC CTGTGTCCAT	9613
DRB1*04:05:01:04 DRB1*04:90	GTGTTCTCAC TGTTC AATTC CCACCTATGA GTGAGAACAT GCGGTGTTCC GTTTTTTGTC CTGCCATAG TTTGCTGAGA	9693
DRB1*04:05:01:04 DRB1*04:90	ATGATGGTT CCAGCTTCAT CCATGTCCTT ACAAGGACA TGA ACTCATT CTTTTTTGTC GCTGCATAGT ATCCATAGT	9773
DRB1*04:05:01:04 DRB1*04:90	GTATATGTGC CACATTTTCT TAATCCAGTC TATCATTGTT GGACATTTGG GTTGGTTCCA AGTCTTTGCT ATTGTGAAAT	9853
DRB1*04:05:01:04 DRB1*04:90	GTGCCGCAAT AACATACAT GTGCATATGT CTTTATAGCA GCATGATTTA TAATCCTGG GTTATATACC CAGTAATGGG	9933
DRB1*04:05:01:04 DRB1*04:90	ATGGCTGGGT CAAATGGTAT TTCTAGTTCT AGATCCCTGA GGAATCGCCA CACTGACTTC CACAATGGTT GAACTAGTTT	10013
DRB1*04:05:01:04 DRB1*04:90	AGAGTCCAC CAACAGGGTA AAAGTGTTC TATTTCTCCA CATCCTCTCC AGCACCTGTT GCTTCTGAC TTTTAAATGA	10093
DRB1*04:05:01:04 DRB1*04:90	TCGCCATTCT AACTGGTGTG AGATGGTATC TCATTGTGGT TTTGATTGTC AATTCTCTGA TGGCCAGTGA TGATGAGCAT	10173
DRB1*04:05:01:04 DRB1*04:90	TTTTTCATGT GTCTTTTGGC TGCATAAAT TCTTCTTTG AGAAGTGTCT GTTCATGTCC TTTGCCACT TTTGATGGG	10253
DRB1*04:05:01:04 DRB1*04:90	GTATTTTGT TTTTCTTGT AAATTTGTT GAGTTCATTG CAGATTCTGG ATATTAGCCC TTTGTCATAT GAGTAGATTG	10333

FIGURE 1 | (Continued)

DRB1*04:05:01:04	CAAAAATTTT TCCCATTCT GTAGGTGCC TCTTCACTCT GATGGTAGTT TCTTTGCTG TGCAGAACT CTTTAGTTTA	10413
DRB1*04:05:01:04	ATTAGATCCC ATTTGTCCAT TTTGGCTTTT GTTGCCATTG CTTTGGTGT TTTAGACATG AAGTTCTTGC CCATGCCTAT	10493
DRB1*04:05:01:04	GTCTGAATG GTATTGCCTA GGTTTTCTTC TAGGGTTTTT ATGGTTTCAG GTCTAACATT TAAGTCTTTA ATCCATCTTG	10573
DRB1*04:05:01:04	AATTAATTTT TGTATAAGCA AATTACGTC CTTTCCCAT TGATGACCTT TATTATGACA TTCACCAATA GTTGAAAATG	10653
DRB1*04:05:01:04	TATGTTTCTG GTTAATTTT GATTATATT TTTTGATT GTAATTATT TGAATTATT TGACCTATT ATTGGCCAGT	10733
DRB1*04:05:01:04	TGTAATTACT GCTCTGCTCT ACGAATTACC TGTGTATTT GGTAGGTAAT GGACAATGAT CTATTGTCTC TTATCTTTAG	10813
DRB1*04:05:01:04	GGCTTAGTAT TTTTCTCAGT GACTTTGTGG GTTTGTGTA CTGTAAGATT ATTAACACTT TATTGATATT TGATTCAGTA	10893
DRB1*04:05:01:04	TTTTCTCCAG TTTGTGGTAT GTATATTTT AAAATCTTT TCCATGTTAA GAATTTGAAC ATTTTATT AATAAAATAT	10973
DRB1*04:05:01:04	ATTGCAAAAT GTTAATTAAT GATTACAAA CTAGCTCAAG TCTACCATT TGTGGTATTG ATGTCTCCAG GTTCTCTCTT	11053
DRB1*04:05:01:04	CCTTCTAAA AAAAAATGTA TTTATTGAGA GTATGCTAGT GTCAGGGATT TCCCTAGGCA TAAGCACTCC AAGTAATGAG	11133
DRB1*04:05:01:04	TCCAGACAC TGCCTTGATC CAAATGTCAT TCTGGAAAGA AAAATCATT TACAGTGATA AGCCTAATAA TAGTTATACT	11213
DRB1*04:05:01:04	TGTTTTGCCT GGGAGATGCA TTGATCAGCT AAATGTAAT ATAAGAACTT TCAAACTAA AATGACGTTT CTTAATCTTT	11293
DRB1*04:05:01:04	CTCTCTGCTT TAGGAATCAT GCTTCTTAG GAACTAAAG ATTTGGAGAA TCATTTCTGT CTGTCCACC TCCCCAGGAG	11373
DRB1*04:05:01:04	CATAACCATT TCTGTGGTGT TCTAAGGTG GAGTGCATGG CAGTAGTATT CCTAAAAATC CATATTCAGT TTCCTCATGT	11453
DRB1*04:05:01:04	GCCCTACTCC GTCCCTTCT CTATCCACAT TGCTTTAAAT CATATTTTCT TCTCAAGGTG TACAAGGATG ATAAATAGGT	11533
DRB1*04:05:01:04	GCCAAGTGG AACCCTAAGT GTGACGAGCC CTCTCACAGT AGAATGGAGT GAGAAGCTTT CTGACCTCAT AAATTTGAAGG	11613
DRB1*04:05:01:04	CTATCGTAAT TCATTCTTTT ATATATTTTA CTGCATTAA TCCTCATATA ACCTCAAGAG GTAAATTAAT ATAATTATCC	11693
DRB1*04:05:01:04	TCCATTATTG GAGAGAAAGT TGAGACACAA AAGAATCAAA AACTCTTCCA GGATCAACCA GTAAAAGGCA GACCTTGGAT	11773
DRB1*04:05:01:04	TTGAACCAGG CAACCTGGCT CAGAAGTCAG TTTTAATTAC CACACTCTGT ACTTTCAAAG ATTTGTAAAC GCTTTGACAA	11853
DRB1*04:05:01:04	TGCATGTCAA TTCAAGCTA TGAAGAGCCA AACATAATTT TTCACAATAT CTCTCAAATC TAATGGGTCC CCACATAAAA	11933
DRB1*04:05:01:04	GATTAATTC CAGGCTGATG ACACTGTGAG GCCACATGGC CAGCTGTGCT GGAGGCCTGC TCAAGGCCAG AGCCTAGGTT	12013
DRB1*04:05:01:04	TACAGAGAAG CAGACAAAAA GCTAAACAAG GAGACTTACT CTGTCTGCAT GACTTATTCC CTCTACCTTG TTTTCTCTTA	12093
DRB1*04:05:01:04	GTCTATCCTG AGGTGACTGT GTATCCTGCA AAGACCAGC CCCTGCAGCA CCACAACCTC CTGGTCTGCT CTGTGAATGG	12173
DRB1*04:05:01:04	TTTCTATCCA GGCAGCATTG AAGTCAGGTG GTTCCGGAAC GGCCAGGAAG AGAAGACTGG GGTGGTGTCC ACAGGCCTGA	12253
DRB1*04:05:01:04	TCCAGAATGG AACTGGACC TTCCAGACCC TGGTGTGCT GAAACAGTT CCTCGGAGTG GAGAGGTTA CACCTGCCAA	12333
DRB1*04:05:01:04	GTGGAGCACC CAAGCTGAC GAGCCCTCTC ACAGTGAAT GGAGTGAGCA GCTTTCTGAC TTCATAAATT TCTACCCAC	12413
DRB1*04:05:01:04	CAAGACGCGA ACTTTACTAA TCCCTGAGTA TCAGGCTTCT CCTATCCCAC ATCCTATTTT CATTGTCTCC ACGTTCTCAT	12493
DRB1*04:05:01:04	CTCCATCAGC ACAGGTCAC TGGGGGTAGC CCTGTAATAC TTTCTAGAAA CACCTGTACC CCCTGGGAA GCAGTCATGC	12573
DRB1*04:05:01:04	CTGCCAGGCA GGAGAGGCTG TCCCTCTTTT GAACCTCCCC ATGATGTCAC AAGTCGGGT CACCTGTCTG CTGTGGGCTC	12653
DRB1*04:05:01:04	CAGGCCCTGC CTCTGGTCT GAGACTGAGT TTCTGGTACT GTTGTCTGTA GTCGTTTGT GTAATCTGAG AAGAGGAGAA	12733
DRB1*04:05:01:04	GTATAGGGAC CTTCTGACA TGAGGGGAGT CCAATCTCAG CTCCGCTTT TATTAGTCT GCACTCTAG GCAACTACTT	12813
DRB1*04:05:01:04	AACCTCATTG GGTCTCAGC TTTCTGTCA TCAGATGTTG AAGTCCTGTC TTACATCAAG GCTGTAATAT TTGAATGAGT	12893
DRB1*04:05:01:04	TTGATGACTG AACCTGTAA CTGTTCACTG TGATTTGAAA ACCTTTCTCA AGAAATGGTC AGTTATTTTA GTTCTTGAC	12973

FIGURE 1 | (Continued)

DRB1*04:05:01:04	AGCAGCCTTC TTTCTCATT TCAAAGCTCT GAATCTCAAG GTGTCAATTA AAGAGGTTCC ATTTGGGATA AAAATCACTA	13053
DRB1*04:90	-----	
DRB1*04:05:01:04	AACCTGGCTT CCTCTCTCAG ^{Exon4} GAGCACGGTC TGAATCTGCA CAGAGCAAGA TGCTGAGTGG AGTCGGGGGC TTCGTGCTGG	13133
DRB1*04:90	-----	
DRB1*04:05:01:04	GCCTGCTCTT CCTTGGGGCC GGGCTGTTC TCTACTTCAG GAATCAGAAA ^{Intron4} GGTGAGGAGC CTTTGGTAGC TGGCTGTCTC	13213
DRB1*04:90	-----	
DRB1*04:05:01:04	CATACGCTTT TCTGGAGGAG GAACATATGCC TTTGCTGAAG TTGGTTCTCA GCATATGAAT GGCCCTGGAT AAAGCCTCTC	13293
DRB1*04:90	-----	
DRB1*04:05:01:04	TACTCCAAA TGACCTCCAA TGTCTGCAA ATCCAGAAAT CATCAGTGA TGTTGCTAT GTCAAAGCAT AATAGCTTGT	13373
DRB1*04:90	-----	
DRB1*04:05:01:04	GGCCTACAGA GATAACAGAA AGATTAACAG GTATAGTGC TTTGGTTGAG ATCGTGGAGC AAATTAAGGA AGAGCAACTA	13453
DRB1*04:90	-----	
DRB1*04:05:01:04	AAGCTAATAC AATTACACTG GATCCTGTGA CAGACACTTC ACACTTCATG GGTACATGG TCTGTTTCTG CTCCTCTCTG	13533
DRB1*04:90	-----	
DRB1*04:05:01:04	CCCTGGCTGG TGTGGGTTGT GGTGTCAGAG AACTCTCAGG TGGGAGATCT GGAGCTGGGA CATTGTGTTG GAGGACAGAT	13613
DRB1*04:90	-----	
DRB1*04:05:01:04	TTGCTTCCAT ATCCTTTAAG TGTATATCTT CTCTTTTTCC ^{Exon5} TAGGACACTC TGGACTTCAG ^{Intron5} CCAACAGGTA ATACCTTTTC	13693
DRB1*04:90	-----	
DRB1*04:05:01:04	ATCCTCTTTA AGAAACAGAT TTGGAGGCCA GGCGCAGTGG CTCACGCCTG TAATCCAGC ACTTTGGGAG GCCCGAGGGCG	13773
DRB1*04:90	-----	
DRB1*04:05:01:04	GCGAATCATG AGGTCAGGAG TTCGAGACCA GCCTGACCAA CGTGGTGAAA CCCCGTCTCT ACTAAAAATA CAAAAAATA	13853
DRB1*04:90	-----	
DRB1*04:05:01:04	TCAGTCGGGC GTGGTGGTGT GCGCCTGTAA TCCCAGTAC TCAGGAGGCC AAGGCAGGAG AATCGCTGGA ACCCGGGAGG	13933
DRB1*04:90	-----	
DRB1*04:05:01:04	CAGAGGTTGC AGTGAGCCGA GATTGGGCCA CTGCACTCCA GCCTAGGTGA CAGAGTGAGA CCCCATCTCA AAAAAACAAA	14013
DRB1*04:90	-----	
DRB1*04:05:01:04	AAAAAGAAAG AAAGAAACAG ATTTCTTTC CCTAGAATGA TGGTAGAGGT AATAAGGCAT GAGACAGAAG TAATAGCAAA	14093
DRB1*04:90	-----	
DRB1*04:05:01:04	GACATTGGAT CCAAATTCT GATCAGGCAA TTTACACCAG AACTCCTCCT CTCCTTAG AAAAGGCTG TGCTCTGCAG	14173
DRB1*04:90	-----	
DRB1*04:05:01:04	GAGTATTGAC TCATGGAGAC TTCAGAACTT GTTTTCTTC TTCCTGCAGT GCTCTCATCT GAGTCTTGA AAGAGGGCAA	14253
DRB1*04:90	-----	
DRB1*04:05:01:04	AATAAACTGT TAGTAGAGCC AGGTCTGAAA ACAACACTTT CTTGCGTCTC TGCAGGATTC ^{Exon6} CTGAGCTGA	14322
DRB1*04:90	-----	

FIGURE 1 | (Continued)

conditions stated in the most recent Nomenclature Report, 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 [4].

The full-length nucleotide sequence of this allele was submitted to the GenBank nucleotide sequence database in January 2025 and was assigned the accession number PQ811754. It was also submitted to the IPD-IMGT/HLA Database, and the assigned accession number is HWS10100158.

Author Contributions

Bin Hu: perform PacBio sequencing test and write the paper. Qi Yu: perform PacBio sequencing test. Li Liu: perform PacBio sequencing test. Zhihui Feng: perform PCR-SBT test. Shutao Pang: design test scheme and review this paper.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The name *DRB1*04:90* was officially assigned by the World Health Organisation (WHO) Nomenclature Committee for Factors of the HLA System in 2010. The full-length nucleotide sequence of this allele is available at European Nucleotide Archive GenBank accession number PQ811754 and to the IPD-IMGT/HLA Database (submission number HWS10100158).

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