```
AA Codon                          280                 285                 290                 295
C*03:03:01:01      AG CCG TCT TCC CAG CCC ACC ATC CCC ATC GTG GGC ATC GTT GCT GGC CTG GCT GTC CTG GCT GTC CTA GCT GTC
C*03:632           -- --- --- --- --- --- --- --- --- --- A-- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AA Codon           300                 305                 310
C*03:03:01:01      CTA GGA GCT GTG GTG GCT GTT GTG ATG TGT AGG AGG AAG AGC TCA G
C*03:632           --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -
```

FIGURE 1 Alignment of the sequence of exon 5 of *HLA-C*03:632* with the sequence of *HLA-C*03:03:01:01*. Dashes indicate nucleotide identity with the *HLA-C*03:03:01:01* allele. Numbers above the sequence indicate codon position.

were analyzed using the TypeStream Visual Software version 3.0 (One Lambda Inc., Canoga Park, California). The nucleotide sequence has been submitted to GenBank (accession number: OQ148664) and in the IPD-IMGT/HLA Database (Submission number: 10064765). The name *C*03:632* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in January 2023. This follows the agreed policy that, subject to the conditions stated in the most recent Nomenclature Report[2] 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.

AUTHOR CONTRIBUTIONS

Charlène Bouthemy, Jean Milhes, and Nicolas Congy-Jolivet performed the data analysis of the Illumina NGS sequencing. Marine Cargou performed the data analysis of the confirmatory NGS sequencing. Charlène Bouthemy performed the submission to "IPD-IMGT/HLA Database" and wrote the paper. Jean Milhes and Nicolas Congy-Jolivet were involved in critical revision of the manuscript.

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CONFLICT OF INTEREST STATEMENT

The authors of this article have no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Characterization of the novel *HLA-C*05:01:01:81Q* allele by sequencing-based typing

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*HLA-C*05:01:01:81Q* differs from *HLA-C*05:01:01:02* by one nucleotide substitution in position 202 in intron 1 (c.74-2A>G, hg19).

KEYWORDS
HLA, *HLA-C*05:01:01:81Q*, novel allele, sequencing-based typing

We report here a novel *HLA-C*05* allele, now named *HLA-C*05:01:01:81Q* that carries one nucleotide substitution in acceptor splice site of intron 1 (c.74-2A>G) when compared with the *HLA-C*05:01:01:02* allele, identified in a volunteer bone marrow donor. The genomic coordinates (GRCh37) of the variant are Chr6(GRCh37):g.31239647T>C. The HLA typing was performed using Next Generation Sequencing (AllType NGS, One Lambda, Canoga Park, CA) on the Ion S5 system platform (ThermoFisher Scientific, Waltham, MA),[1] from exons 1 to 8. The reads were analyzed using the TypeStream Visual Software version 2.1 (One Lambda). This patient was found to have a new *C*05* allele and was consequently typed *A*02:01, 29:02*; *B*40:01, 57:01*; *C*05:01:01:81Q, 16:01:01:01*; *DRB1*07:01, 07:01*; *DRB4*01:01, 01:03:01:02N*; *DQA1*02:01, 02:01*; *DQB1*02:02, 03:03*; *DPA1*02:01, 02:02*; *DPB1*01:01, 11:01*. Using the IPD-IMGT/HLA Database,[2] nucleotide sequence alignment with HLA-C alleles shows that this new allele has one nucleotide change from *C*05:01:01:02* in acceptor splice site of intron 1 (c.74-2A>G) (Figure 1). Three softwares predicted a change at acceptor site 2 bps downstream (MaxEnt, NNSPLICE and SSF) with a score of 1 and SpliceAI software with a score of 0.57, resulting in a high probability of abolition of the splice site. This nucleotide change was confirmed using other NGS reagents provided by Immucor (Mia Fora NGS Flex, Norcross, GA) run on the Illumina MiSeq system (San Diego, CA) and analyzed with the Mia Fora Flex software (version 5.1). We were very confident in the phasing as the sample displayed a mean read length of 304 base pairs over all the loci, the mismatched G base was attributed 229 times to the new *HLA-C*05* allele and can be only attributed to this allele because it was possible to discriminate from the associated *HLA-C*16:01:01:01* allele by virtue of 2 variant positions each distant by less than 100 base pairs. *C*05:01:01:81Q* was not evaluated easily with T or B cell flow cytometry crossmatch (FCXM).[3,4] Furthermore none LCT Typing kit is available to demonstrate the lack of expression of this antigen. Despite these drawbacks, it is highly probable that the abolition of the splice site leads to a frameshift variant and a truncated protein. As such this could have an importance in both allogeneic hematopoietic stem cell transplantation and solid organ transplantation. The coding nucleotide sequence of the new allele has been submitted to the GenBank database (Accession No. OM913145) and to the IPD-IMGT/HLA Database (Submission No. HWS10060752). The name *C*05:01:01:81Q* has been officially assigned by the WHO Nomenclature Committee for Factors of the HLA System in March 2022. This follows the agreed policy that, subject to the conditions

```
gDNA                    10         20         30         40         50         60         70         80         90         100
C*05:01:01:02      |ATGCGGGTCA TGGCGCCCCG AACCCTCATC CTGCTGCTCT CGGGAGCCCT GGCCCTGACC GAGACCTGGG CCT|GTGAGTG CGAGGTTGGG AGGGAAACGG
C*05:01:01:81Q     |---------- ---------- ---------- ---------- ---------- ---------- ---------- ---|------- ---------- ----------

gDNA                   110        120        130        140        150        160        170        180        190        200
C*05:01:01:02      CCTCTGCGGA GAGGAGCGAG GGGCCCGCCC GGCGAGGGCG CAGGACCCGG GGAGCCGCGC AGGGAGGAGG GTCGGGCGGG TCTCAGCCCC TCCTCGCCCC
C*05:01:01:81Q     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

gDNA                   210        220        230        240        250        260        270        280        290        300
C*05:01:01:02      CAG|GCTCCCA CTCCATGAGG TATTTCTACA CCGCCGTGTC CCGGCCCGGC CGCGGAGAGC CCCGCTTCAT CGCAGTGGGC TACGTGGACG ACACGCAGTT
C*05:01:01:81Q     -G-|------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

gDNA                   310        320        330        340        350        360        370        380        390        400
C*05:01:01:02      CGTGCAGTTC GACAGCGACG CCGCGAGTCC AAGAGGGGAG CCGCGGGCGC CGTGGGTGGA GCAGGAGGGG CCGGAGTATT GGGACCGGGA GACACAGAAG
C*05:01:01:81Q     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

gDNA                   410        420        430        440        450        460        470        480        490        500
C*05:01:01:02      TACAAGCGCC AGGCACAGAC TGACCGAGTG AACCTGCGGA AACTGCGCGG CTACTACAAC CAGAGCGAGG CCG|GTGAGTG ACCCCGGCCC GGGGCGCAGG
C*05:01:01:81Q     ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---|------- ---------- ----------
```

FIGURE 1 Alignment of the sequence of exon 1, intron 1, exon 2 and partial intron 2 of *HLA-C*05:01:01:81Q* with the sequence of *HLA-C*05:01:01:02*. Dashes indicate nucleotide identity with the *HLA-C*05:01:01:02* allele. Numbers above the sequence indicate nucleotide position. Pipes (|) are used to indicate the exon, intron boundary.

stated in the most recent Nomenclature Report,[5] 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.

AUTHOR CONTRIBUTIONS

Marine Cargou and Jonathan Visentin contributed to the design of the study. Marine Cargou and Jonathan Visentin participated in the writing of the paper. Marine Cargou, Vincent Elsermans, Virginie Raclet, Elodie Wojciechowski, and Jonathan Visentin participated in the performance of the research. Marine Cargou, Vincent Elsermans, Virginie Raclet, Elodie Wojciechowski, and Jonathan Visentin participated in data analysis. Vincent Elsermans, Virginie Raclet, and Elodie Wojciechowski were involved in critical revision of the manuscript.

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CONFLICT OF INTEREST STATEMENT

The authors confirm that there are no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions. The sequence is freely available in the IPD-IMGT/HLA Database.

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A novel *HLA-C*06* allele, *HLA-C*06:02:96*, identified by next-generation sequencing in a Chinese family

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*HLA-C*06:02:96* differs from *HLA-C*06:02:01:01* (924C → A, I284I), resulting in a synonymous change in exon 5.

KEYWORDS

HLA, new allele, next-generation sequencing