single nucleotide substitution (G → A) in exon 2 at gDNA position 3941 (codon 33.a). Complete HLA assignment was as follows: *A*02:01:01:01*, *02:01:01:01; B*27:05:02*, *44:02P; C*02:02:02*, *05:01:01:02; DRB1*08:01P*, *12:01P; DRB3*02:02:01; DQA1*04:01:01:01*, *05:51; DQB1*03:01P*, *04:02:01:01; DPA1* 01:03:01*, *01:03:01; DPB1*03:01P*, *04:01P*.

The names *A*68:288*, *C*07:1012*, *C*12:364*, and *DQA1*05:51* have 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 stated in the most recent Nomenclature Report,[2] names would 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

Evgeny A. Leonov performed the NGS and wrote the article. Alena R. Abdrakhimova and Stanislav P. Khizhinskiy performed the NGS. Ekaterina G. Khamaganova supervised the work and was involved in writing the article. Elena N. Parovichnikova supervised the work and was involved in critical revision of the manuscript.

## CONFLICT OF INTEREST

The authors declare no conflict of interest.

## DATA AVAILABILITY STATEMENT

The data is freely available from the IPD-IMGT/HLA database.

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**How to cite this article:** Leonov EA, Abdrakhimova AR, Khizhinskiy SP, Khamaganova EG, Parovichnikova EN. Characterization of four new HLA alleles: *HLA-A*68:288*, *-C*07:1012*, *-C*13:364*, and *-DQA1*05:51*. *HLA*. 2022;100(5):519-520. doi:10.1111/tan.14717

# The novel HLA class I allele, *HLA-B*14:110*, identified by next-generation sequencing

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The novel HLA-allele *B*14:110*, differs from *B*14:02:01:01*, by one nucleotide substitution, c.T247A in exon 2.

**KEYWORDS**
*HLA-B*14:110*, next-generation sequencing, novel HLA-allele

The numbers of identified HLA-alleles are rapidly increasing since the introduction of sequencing methods such as next-generation sequencing (NGS) for clinical HLA typing. According to IPD-IMGT/HLA Database version 3.47 (2022-01),[1] a total of 8756 HLA-B alleles have been identified. At Aarhus University Hospital we

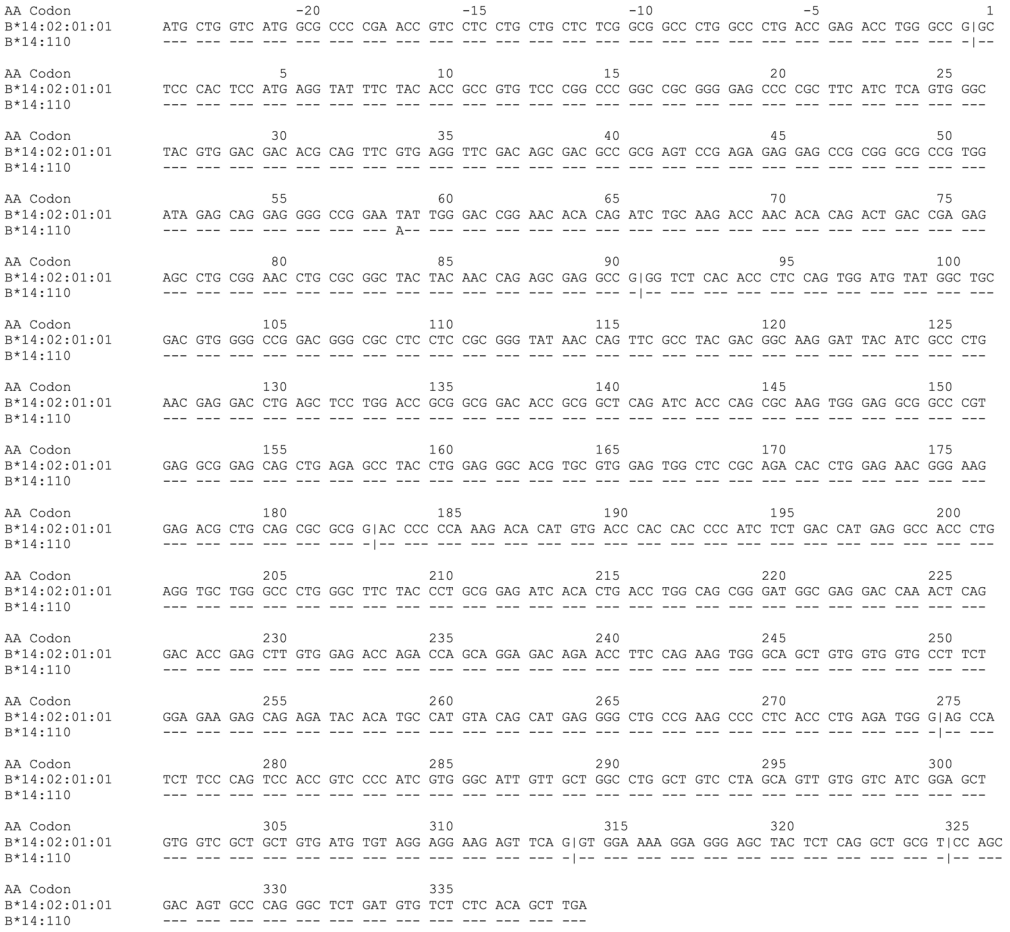


**FIGURE 1** Sequence alignment of *HLA-B*14:02:01:01* and *HLA-B*14:110*, coding sequences (CDS). Identity to the *B*14:02:01:01* allele is shown with dashes (−), the exon boundaries are indicated by pipes (|).

annually perform approximately 1000 high resolution HLA typing using NGS.

We report here a novel *HLA-B*14*-allele, now officially named *B*14:110*. The allele was identified in a patient HLA typed prior to listing for renal transplantation.

The novel allele was determined by NGS applying the Holotype HLA protocol (Omixon, Hungary) and the Illumina MiSeq platform (Illumina, USA). Data was aligned using HLA Twin software 4.4.1 (Omixon). The novel allele was verified with the AllType NGS protocol (One Lambda, USA).

The novel *B*14:110* allele has one nucleotide change when compared to the *B*14:02:01:01* allele at coding position c.247 T > A in exon 2. This non-synonymous codon change, TAT > AAT, results in an amino acid substitution from Tyrosine to Asparagine, both of which are neutral polar amino acids (Figure 1A). This novel position is located in the α1 helix of the peptide binding groove, which defines affinity to presented peptides. As the amino acid is located in the α1 helix and not pointing towards the peptide binding site, it is not expected to be directly involved in peptide binding (Figure 1B).[2]

The patient carrying the novel allele had the following extended genotype: *HLA-A*23:01:01:01*, *24:02:01G*; *B*14:110*, *35:02:01G*; *C*02:02:02G*, *04:01:01:06*; *DRB1*01:02:01:01*, *11:04:01*; *DQB1*03:01:01:02*, *05:01:01:01*; *DQA1*01:01:02*, *05:05:01:09*; *DPA1*01:03:01G*, *01:03:01G*; *DPB1*02:01:02:03*, *04:01:01:27*.

The novel sequence was submitted to GenBank under accession number OM687206. The name *B*14:110* 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 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.

## AUTHOR CONTRIBUTIONS

**Marie Quach Lam, Maja Nørgaard:** performed the analyses; **Maja Nørgaard, Marie Quach Lam, Mira Marie Laustsen:** handled and analyzed data; **Nicklas Heine Staunstrup, Mira Marie Laustsen, Pernille Koefoed-Nielsen:** wrote the paper; **Nicklas Heine Staunstrup, Pernille Koefoed-Nielsen:** supervision.

## 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.

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**How to cite this article:** Laustsen MM, Nørgaard M, Lam MQ, Koefoed-Nielsen P, Staunstrup NH. The novel HLA class I allele, *HLA-B*14:110*, identified by next-generation sequencing. *HLA*. 2022;100(5):520-522. doi:10.1111/tan.14721

# The *HLA-B*15:02:01:05* allele identified by two next-generation sequencing methods in a Japanese individual

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**Funding information**
Japan Agency for Medical Research and Development, Grant/Award Numbers: JP20fk0108104, JP20kk0205012; National Center for Global Health and Medicine, Grant/Award Number: 20A2002D

*HLA-B*15:02:01:05* differs from *HLA-B*15:02:01:01* by four nucleotides in 3′UTR at positions 3435, 3457, 3472, and 3511.

**KEYWORDS**
*B*15:02:01:05*, *B*15:02:01:01*, Japanese

The *HLA-B*15:02* allele is the 36th most common HLA-B allele in the Japanese population[1] with an allele frequency of 0.041%. Here, we are reporting a novel *HLA- HLA-B*15:02:01:01* variant allele, now officially named as *HLA-B*15:02:01:05* by World Health Organization (WHO) Nomenclature Committee for Factors of the HLA System in December 2020. *HLA-B*15:02:01:05* was discovered in the project to evaluate the potential association of HLA alleles with the severity of Japanese COVID-19.[2]

Here, we report the first genomic full-length sequence of *B*15:02:01:05* with a total amplicon length of 4093 bp genotyped by using AllType™ NGS Assays (One Lambda, West Hills, CA) on the Ion GeneStudio S5 (Thermo Fisher Scientific, Waltham, MA). Concordant HLA genotype assignments were carried out using both NGSengine® (2.22.0.22581) by the GenDX company (GenDX, Utrecht, the Netherlands) and HLATypeStream Visual (TSV v2.0; One Lambda).

Confirmation of novel HLA alleles were carried out by Pacbio Sequel sequencing using in-house primers developed in conjunction with H.U.Group Research Institute (Tokyo, Japan). Pacbio subreads and consensus