

AltruType™

Long-Read Sequencing HLA Genotyping

Background

The Human Leukocyte Antigen (HLA) system is encoded by a family of genes located on the short arm of human chromosome 6 and represents one of the most genetically variable regions in the human genome. It plays a central role in cellular immunity against foreign substances by encoding cell surface proteins that distinguish self from non-self. Based on the structure, function, and tissue distribution of their gene products, HLA genes are classified into three categories: Class I, Class II, and Class III.

Given the critical importance of HLA molecules in immune responses, HLA genotyping is widely applied in fields such as transplantation matching, research on immune-related diseases, pharmacogenomics, and platelet transfusion compatibility. Currently, HLA genotyping is performed using a variety of techniques. However, even with high-resolution NGS, commercially available assays still yield ~3% ambiguous results [1] and cannot phase across multiple polymorphisms.

Break the Ambiguity. Resolve with Confidence.

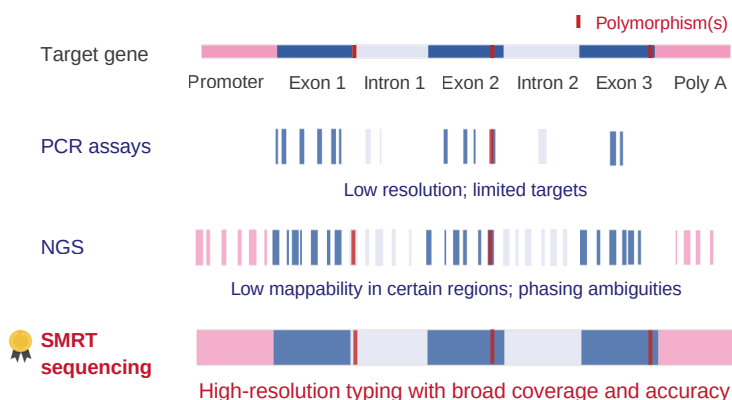
AltruType™ Long-Read Sequencing HLA Genotyping

Powered by PacBio long-read sequencing, Haorui Genomics' AltruType™ offers a complete sample-to-report HLA typing workflow.

It delivers high-resolution results (up to 8-digit) with gold-standard level accuracy and unambiguous calls from high-quality sequencing data. Optimized for ease of use and cost-efficiency, AltruType™ is ideal for commercial laboratories.

By April 2025, Haorui Genomics had completed
> 10,000 long-read HLA typing tests and
identified more than 107 novel alleles.

Coverage of variants by current technologies



Parameters	Description
Technology	Single molecule real-time (SMRT) sequencing, CCS reads
Platform	PacBio Sequel II, Vega and Revio system
gDNA requirement	Total amount: ≥ 60 ng, Concentration: > 30 ng/μL; Fragment size: > 15 kb, intact band without degradation; Purity: A260/A280: 1.8 – 2.0, A260/A230: > 2.0
Test per Batch	Up to 192 tests per SMRT cell
Automation	Supports experimental automation; Automated bioinformatic calling and reporting support with TransMatch™ software
Coverage	11 HLA loci - Class I & II: HLA-A, HLA-B, HLA-C, HLA-DRB1, HLA-DRB3/4/5, HLA-DQA1, HLA-DQB1, HLA-DPA1, and HLA-DPB1 Extended coverage: HLA-E, HLA-F, and HLA-G

	Day 1		Day 2-3		Day 4
	Sample Collection and Nucleic Acid Extraction	PCR amplification for targeted enrichment	Library preparation, purification and QC	SMRT Sequencing and primary analysis	HLA typing analysis and report generation
Hand-on Time	15 minutes	15 minutes	20 minutes	15 minutes	20 minutes
Total Time	1.5 hours	8 hours	3.5 hours	Varies	3.5 hours

Nucleic Acid Extraction Kit

Long-Read Sequencing HLA Genotyping Kit
DNA qualification system

PacBio sequencing system

TransMatch™ software

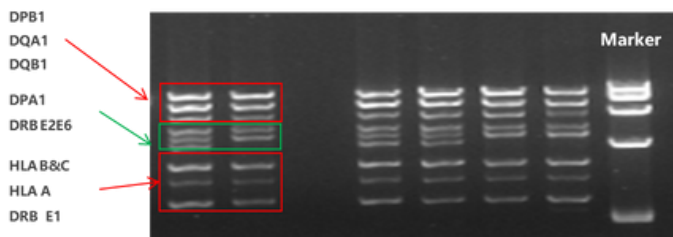
Please note that all working times are approximate and may vary depending on laboratory practices, hardware, and sample number.

AltruType™ Long-Read Sequencing HLA Genotyping

Full-length HLA gene enrichment

AltruType™ adopts single-tube LR-PCR enrichment to provide a stable, efficient foundation for downstream analysis.

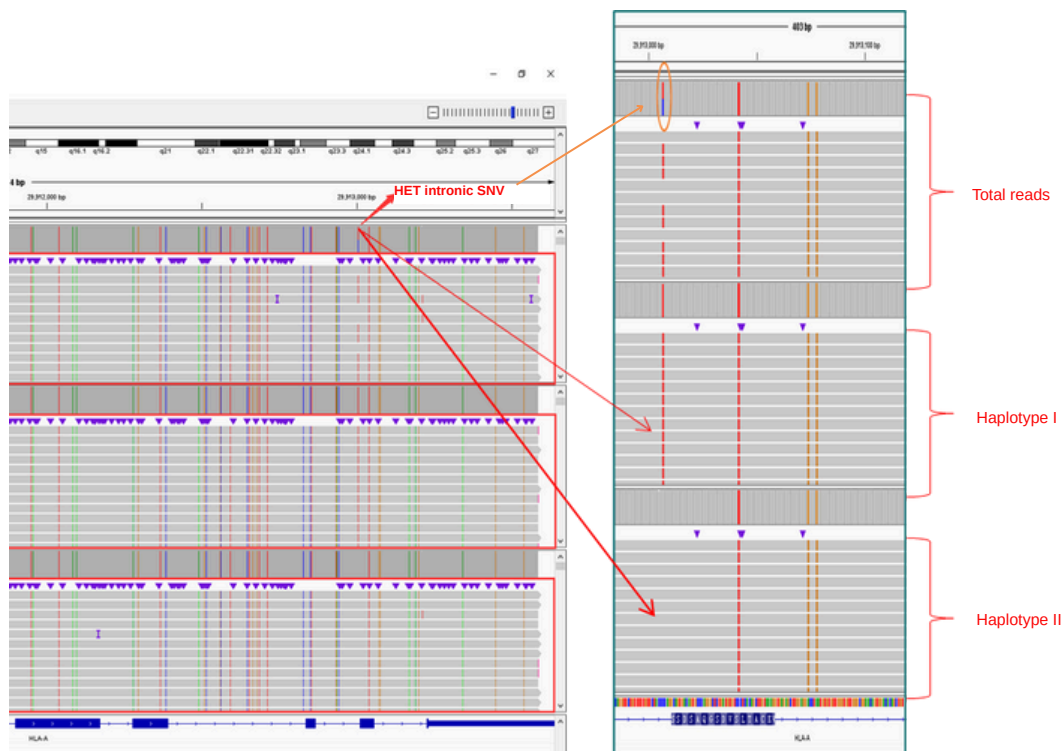
Long-range amplification reduces amplification imbalance, and long-read length span entire genes to minimize phasing ambiguity from alignment errors. This approach reliably distinguishing true homozygosity from potential allelic dropout.



LR-PCR enrichment of basic HLA loci (11)
in one-tube reaction



LR-PCR enrichment coverage of HLA loci



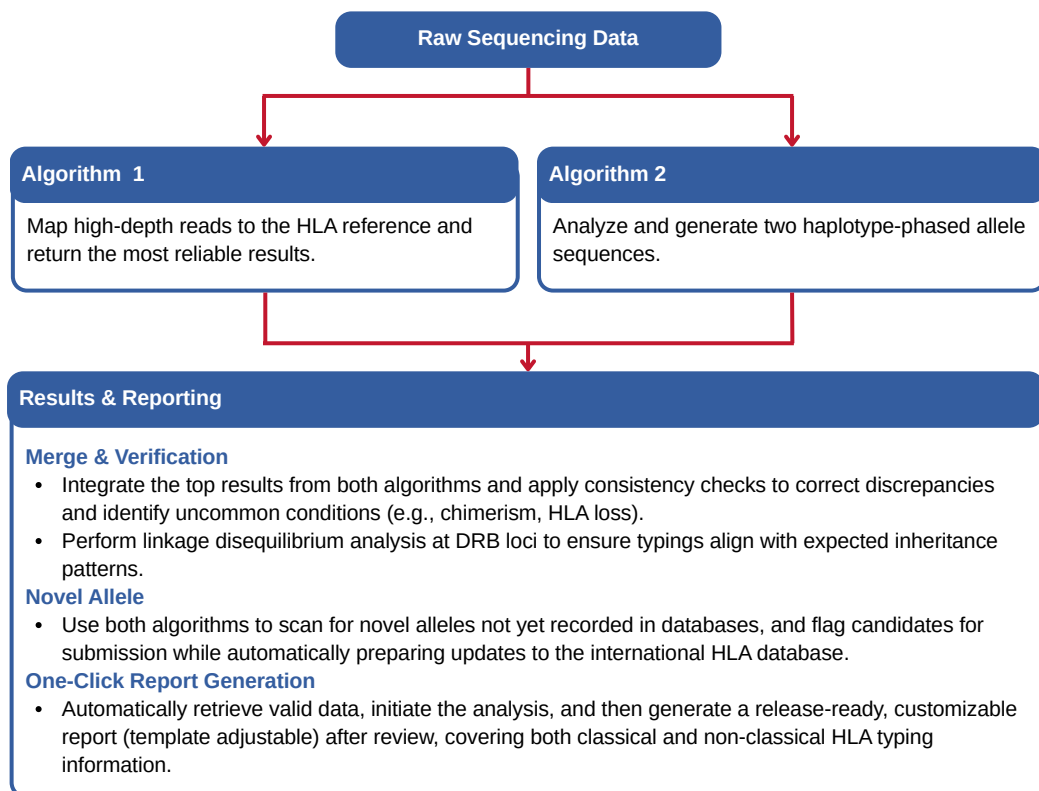
IGV display: HLA-A alleles with homozygous coding exons (CDS) and a heterozygous intronic SNV

AltruType™ Long-Read Sequencing HLA Genotyping

TransMatch™

All-in-one software for sample management, bioinformatics, and reporting

TransMatch™ is a comprehensive platform for HLA sample management and results reporting, delivering true end-to-end analytics and reporting for the service laboratory. Powered by dual-algorithms cross-validation, automated novel allele detection, and one-click reporting function, it achieves exceptional HLA typing accuracy with an efficient workflow. Role-based permissions and full activity logging promote compliance, streamline communication, and enable seamless handoffs across administration, laboratory, reporting, and other teams.



Manual Review

Test Item	Sample ID	Raw Results	QC Thresholds	QC Results	Processing Advice
HLA-A	HLA-A Ratio	HLA-A GeneReads	HLA-A Check	HLA-A1 HLA-A2	HLA-A1 HLA-A2
HLA-B	HLA-B Ratio	HLA-B GeneReads	HLA-B Check	HLA-B1 HLA-B2	HLA-B1 HLA-B2
HLA-C	HLA-C Ratio	HLA-C GeneReads	HLA-C Check	HLA-C1 HLA-C2	HLA-C1 HLA-C2
HLA-DQA1	HLA-DQA1 Ratio	HLA-DQA1 GeneReads	HLA-DQA1 Check	HLA-DQA11 HLA-DQA12	HLA-DQA11 HLA-DQA12
HLA-DQB1	HLA-DQB1 Ratio	HLA-DQB1 GeneReads	HLA-DQB1 Check	HLA-DQB11 HLA-DQB12	HLA-DQB11 HLA-DQB12
HLA-DPA1	HLA-DPA1 Ratio	HLA-DPA1 GeneReads	HLA-DPA1 Check	HLA-DPA11 HLA-DPA12	HLA-DPA11 HLA-DPA12
HLA-DPB1	HLA-DPB1 Ratio	HLA-DPB1 GeneReads	HLA-DPB1 Check	HLA-DPB11 HLA-DPB12	HLA-DPB11 HLA-DPB12

Review of HLA typing results called by Transmatch™

Sample Information

Test Report

HLA Genotyping Results

HLA Locus	A1	A2	B1	B2	C1	C2	DQA1	DQB1	DPA1	DPB1
HLA-A	A*01:01	A*02:01								
HLA-B	B*07:01	B*08:01	B*09:01	B*10:01						
HLA-C	C*01:01	C*02:01	C*03:01	C*04:01	C*05:01	C*06:01				
HLA-DQA1	DQA1*01:01	DQA1*02:01	DQA1*03:01	DQA1*04:01	DQA1*05:01	DQA1*06:01	DQA1*07:01	DQA1*08:01	DQA1*09:01	DQA1*10:01
HLA-DQB1	DQB1*01:01	DQB1*02:01	DQB1*03:01	DQB1*04:01	DQB1*05:01	DQB1*06:01	DQB1*07:01	DQB1*08:01	DQB1*09:01	DQB1*10:01
HLA-DPA1	DPA1*01:01	DPA1*02:01	DPA1*03:01	DPA1*04:01	DPA1*05:01	DPA1*06:01	DPA1*07:01	DPA1*08:01	DPA1*09:01	DPA1*10:01
HLA-DPB1	DPB1*01:01	DPB1*02:01	DPB1*03:01	DPB1*04:01	DPB1*05:01	DPB1*06:01	DPB1*07:01	DPB1*08:01	DPB1*09:01	DPB1*10:01

HLA Genotyping Results

HLA-A: A*01:01, A*02:01

HLA-B: B*07:01, B*08:01, B*09:01, B*10:01

HLA-C: C*01:01, C*02:01, C*03:01, C*04:01, C*05:01, C*06:01

HLA-DQA1: DQA1*01:01, DQA1*02:01, DQA1*03:01, DQA1*04:01, DQA1*05:01, DQA1*06:01, DQA1*07:01, DQA1*08:01, DQA1*09:01, DQA1*10:01

HLA-DQB1: DQB1*01:01, DQB1*02:01, DQB1*03:01, DQB1*04:01, DQB1*05:01, DQB1*06:01, DQB1*07:01, DQB1*08:01, DQB1*09:01, DQB1*10:01

HLA-DPA1: DPA1*01:01, DPA1*02:01, DPA1*03:01, DPA1*04:01, DPA1*05:01, DPA1*06:01, DPA1*07:01, DPA1*08:01, DPA1*09:01, DPA1*10:01

HLA-DPB1: DPB1*01:01, DPB1*02:01, DPB1*03:01, DPB1*04:01, DPB1*05:01, DPB1*06:01, DPB1*07:01, DPB1*08:01, DPB1*09:01, DPB1*10:01

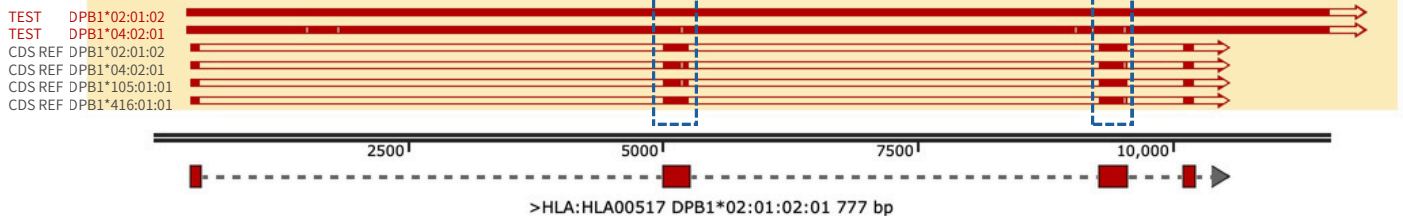
Test report generation preview
(with custom report template)

The system feature and interface may evolve as part of continuous improvements.

AltruType™ Long-Read Sequencing HLA Genotyping

Case Study

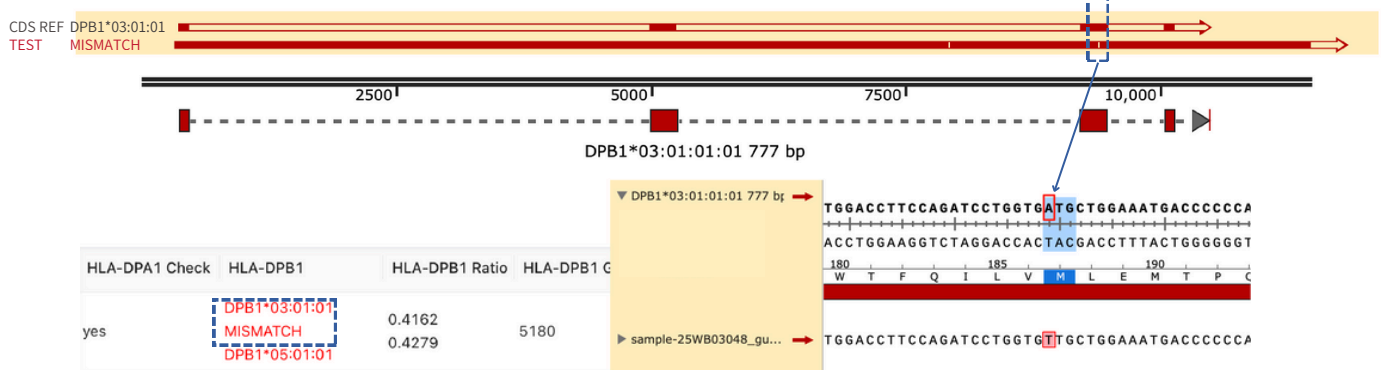
Full-length phasing eliminates ambiguity



In this sample, two key exonic SNPs were detected in DPB1 exon 2 and 3.

- For NGS assays, it is unlikely to resolve the cis/trans configuration of the SNPs due to short read-length, resulting in four possible typing outcomes: DPB1*02:01:02, DPB1*04:02:01, DPB1*105:01:01, and DPB1*416:01:01.
- Using long-read sequencing, full-length HLA sequences with phasing can be constructed, confirming that the SNPs are in cis and provide a definitive typing result for this sample: DPB1*02:01:02 / DPB1*04:02:01.

Novel allele discovery



In this sample, one allele is typed as DPB1*05:01:01, and the other shows a mismatch in DPB1.

- Compared with the closest match, DPB1*03:01:01, the mismatched allele has an A → T substitution at exon 3. This is a missense variant that alters the amino acid sequence.
- TransMatch™ can identify potential novel alleles by flagging “mismatch” candidates and reporting their closest HLA nomenclature.

Ordering Information

- AltruType™ Long-Read Sequencing HLA Genotyping Kit (24/48/96/192 reactions)** - For 11 HLA Loci (HLA-A, HLA-B, HLA-C, HLA-DRB1, HLA-DRB3/4/5, HLA-DQA1, HLA-DQB1, HLA-DPA1, and HLA-DPB1)
- AltruType™ Long-Read Sequencing HLA-E/F/G Genotyping Kit (24/48/96/192 reactions)** - For HLA-E, HLA-F and HLA-G
- TransMatch™ Data Analysis Software**

Customization is supported. Please contact us for details.

Reagents for library preparation and purification, along with workflow management and data analysis software, will be provided. Sequencing instruments and related reagents will be supplied by a local PacBio representative. An on-site hardware server and DNA quantification reagent/equipment will need to be prepared by the laboratory. All products are for research use only.

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References: [1] Weimer ET, Montgomery M, Petrarola R, Crawford J, Schmitz JL. Performance Characteristics and Validation of Next-Generation Sequencing for Human Leucocyte Antigen Typing. *J Mol Diagn*. 2016;18(5):668-675. INT_LRSLAV1

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