PacBio

Long-Read Sequencing for Immunohematology and Histocompatibility

HLA · KIR · MIC · Blood Group · HPA

Product Catalog

Ready to upgrade? Send a message to us.

HAORUI GENOMICS 浩瑞基因 XCELOM

About Haorui Genomics

Founded in 2019, Haorui Genomics is a pioneer in applying long-read sequencing (LRS) to transplantation and transfusion medicine, delivering advanced molecular solutions for diverse clinical needs.

Backed by an expert technical team and substantial LRS capacity (including 7 PacBio Sequel II and 3 Revio systems), we are advancing high-resolution genotyping in histocompatibility and immunohematology. Our end-to-end ecosystem spans assay development, bioinformatics, and clinical implementation, empowering laboratories to translate long-read technology into measurable clinical value.

We offer proven, locally deployable (on-premises) LRS genotyping solutions that are already in routine clinical use. Our flagship products include AltruType™ for HLA/MIC/KIR genotyping and HemoSure™ for comprehensive red blood cell and HPA typing. Engineered to resolve highly complex genomic regions that confound conventional methods, our high-throughput workflows deliver production-scale, high-accuracy results for both routine screening and complex case resolution.

Trusted by over 100 blood centers and hospitals in China and worldwide, our collaborative research has driven numerous peer-reviewed publications addressing real-world challenges. To ensure seamless integration into your laboratory, we provide comprehensive quality documentation, hands-on training, and responsive technical support for reliable, ongoing clinical operations.

Xcelom Limited is the authorized sole representative of Berry Genomics for overseas business operations and the authorized distributor for Haorui Genomics solutions.

Service

Send-Out Service

Ship your samples to our receiving hub and we handle the rest. We accept whole blood (≥2 mL in EDTA tube) or extracted high molecular weight gDNA (total amount ≥60 ng, concentration >30 ng/μL, fragment size >15 kb with intact band and no degradation). Samples must be shipped on dry ice, and we recommend delivery within 72 hours of collection.

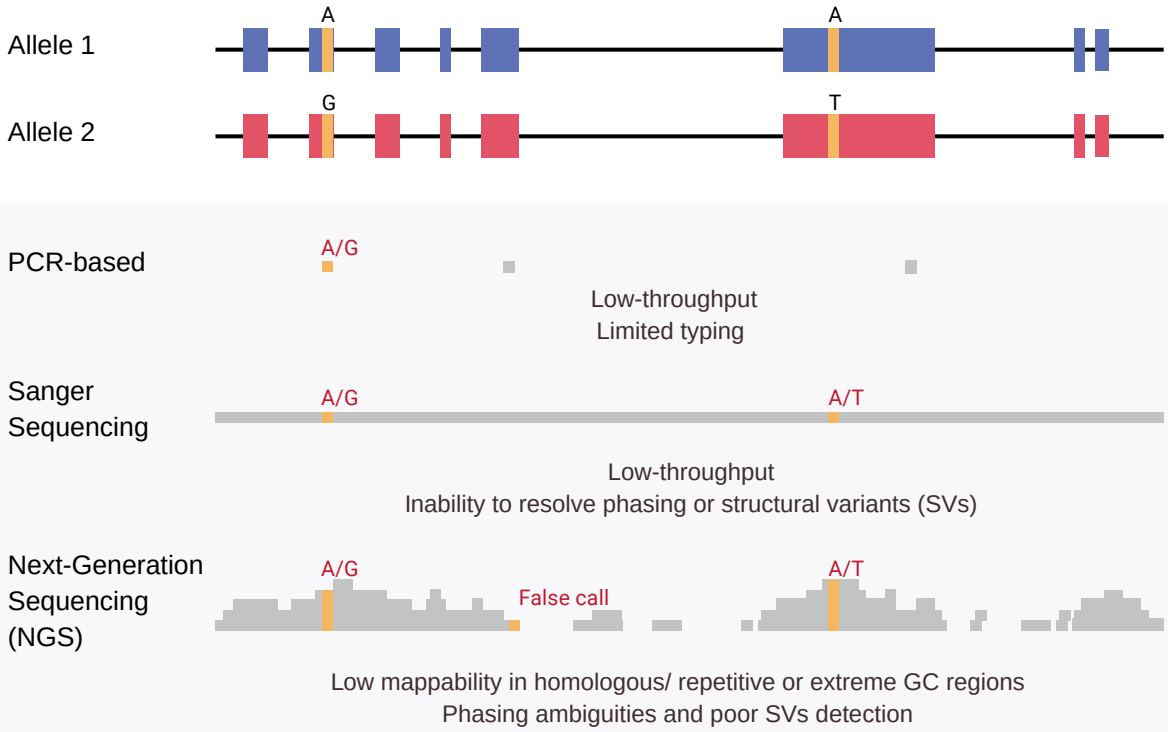
End-to-End Technology Transfer (Turnkey Solution)

Bring the service in-house with full support from our team. We provide reagents, analysis pipeline, SOPs, hands-on training, and ongoing implementation support to get your facility up and running with confidence. We also offer reagent kit customization to match your lab's specific assay requirements and workflows.

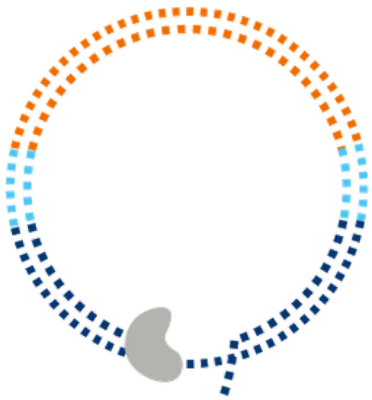
Our Solution

Product Line	Service	Coverage
AltruType™	HLA Typing	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*
	KIR Typing	17 Genes: *KIR2DL1*, *KIR2DL2*, *KIR2DL3*, *KIR2DL4*, *KIR2DL5A*, *KIR2DL5B*, *KIR3DL1*, *KIR3DL2*, *KIR3DL3*, *KIR2DS1*, *KIR2DS2*, *KIR2DS3*, *KIR2DS4*, *KIR2DS5*, *KIR3DS1*, *KIR2DP1*, and *KIR3DP1*
	MIC Typing	*MICA* and *MICB* genes
HemoSure™	ABO Typing	*ABO*, *FUT1*, and *FUT2* genes (Antigen: A, B, and H)
	Rh Typing	*RHD*, *RHCE*, and *RHAG* genes (Antigen: D, C, c, E, e, Duclos, Ol^a ...)
	RBC Typing (Panel 1)	ABO, Rh, MNS, Kidd, Duffy Blood Group Systems (7 Genes): *ABO*, *RHD*, *RHCE*, *GYPA*, *GYPB*, *SLC14A1*, and *ACKR1* (Antigen: A, B, D, C, c, E, e, M, N, S, s, Mur, Mi^a, Jk^a, Jk^b, Fy^a, Fy^b ...)
	RBC Typing (Panel 2)	ABO, Rh, MNS, Kidd, Duffy, P1PK, Kell, Lewis, Diego Blood Group Systems (13 Genes): *ABO*, *RHD*, *RHCE*, *GYPA*, *GYPB*, *SLC14A1*, *ACKR1*, *A4GALT*, *B3GALNT1*, *KEL*, *FUT2*, *FUT3*, and *SLC4A1* (Antigen: A, B, D, C, C, E, e, M, N, S, s, Mur, Mi^a, Jk^a, Jkb, Fy^a, Fy^b, P1, Pk, K, k, Kp^a, Kp^b, Le^a, Leb, Di^a, Di^b, Wr^a ...)
	RBC Typing (Extended)	H, GLOB, JR, LAN, Vel, Lutheran, Dombrock, Knops, Chido/Rodgers, XG, Kx, LW, CD36 13 Blood Group Systems (17 Genes): *FUT1*, *FUT2*, *B3GALNT1*, *ABCG2*, *KLF1*, *ABCB6*, *SMIM1*, *BCAM*, *ART4*, *CR1*, *C4A*, *C4B*, *XG*, *CD99*, *XK*, *ICAM4*, *CD36* (Antigen: H, P, Jr, Lan, Vel, Lu^a, Lu^b, Do^a, Do^b, Hy, Jo^a, Gy^a, Kn^a, Kn^b, McC^a, Ch1, Ch2, Xg^a, CD99, Kx, LW^a, LW^{ab}, LW^b, CD36.1 ...)
	HPA Typing	HPA 1-35 Loci (7 Genes): *CD109*, *ITGA2B*, *GP1BB*, *GP9*, *ITGA2*, *ITGB3*, and *GP1BA* (Antigen: HPA-1a/b, HPA-2a/b, HPA-3a/b.....HPA-34a/b, HPA-35a/b)

Long-Read Sequencing Overcomes the Barriers to Accurate Typing



Among Long-Read Sequencing (LRS) Options, PacBio HiFi Sequencing Offers Distinct Advantages for Service Laboratories



Highest LRS Accuracy

>Q30 base-level accuracy, scaling higher with depth for precision

Batch-to-Batch Stability

Highly reproducible data ensures consistent, reliable results across all runs

Scalable and Cost-Effectiveness

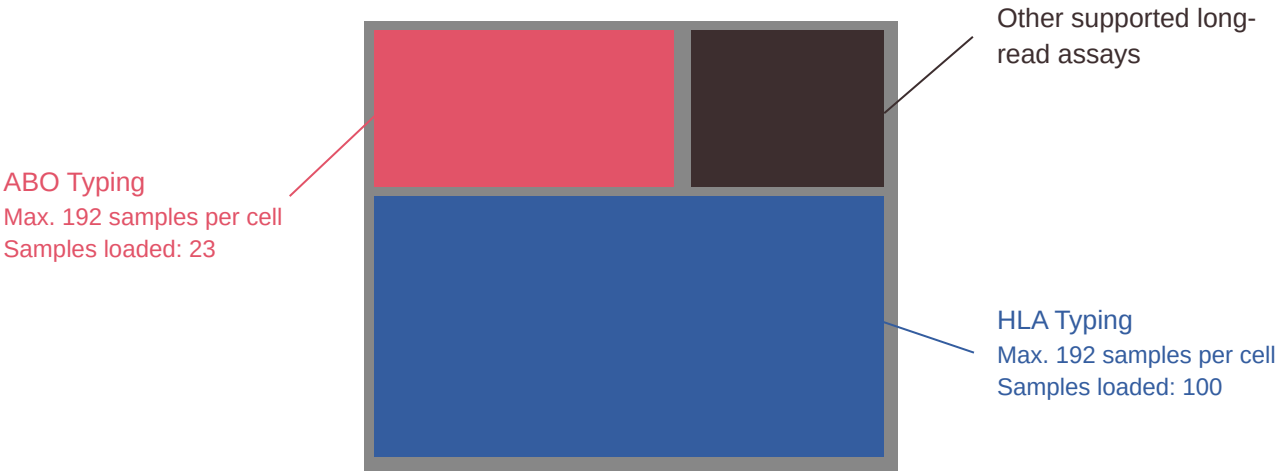
Optimized for high-throughput labs, capable of multiplexing hundreds of samples in a single run

Minimal IT Infrastructure

On-instrument primary analysis generates HiFi reads instantly, drastically lowering bioinformatics overhead and eliminating the need for expensive external compute clusters

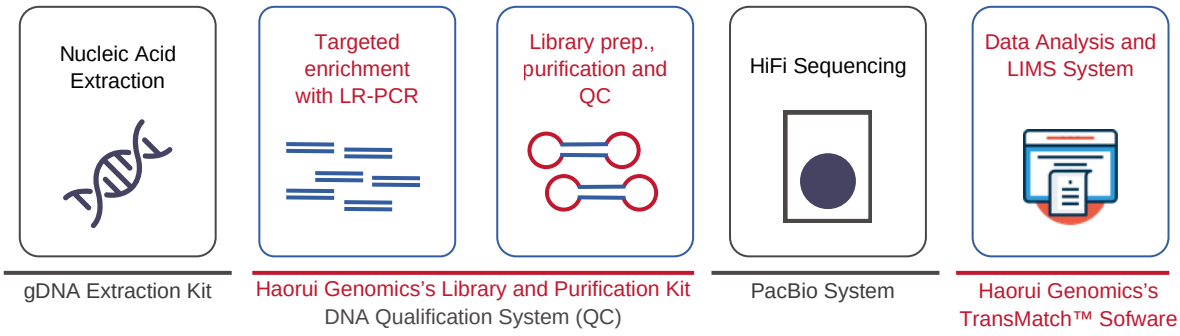
Maximize Flow Cell Utilization with Mixed Batching

Our solutions deliver complete operational flexibility by enabling you to multiplex different assay panels onto a single sequencing run. Instead of a long time to accumulate enough samples for a single-assay batch, you can combine panels on demand. This means your sequencing capacity is fully utilized, and lowering overall cost-per-sample while maintaining fast turnaround times.



Combining Multiple Assays into a Single Sequencing Run

Scalable and Unified Workflow:
Different Assays. Separate Reactions. One Universal Protocol.



	Day 1		Day 2-3		Day 4
Hand-on Time	15 minutes	15 minutes	20 minutes	15 minutes	20 minutes
Total Time	1.5 hours	8 hours	3.5 hours	~24 hours	3.5 hours

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

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.

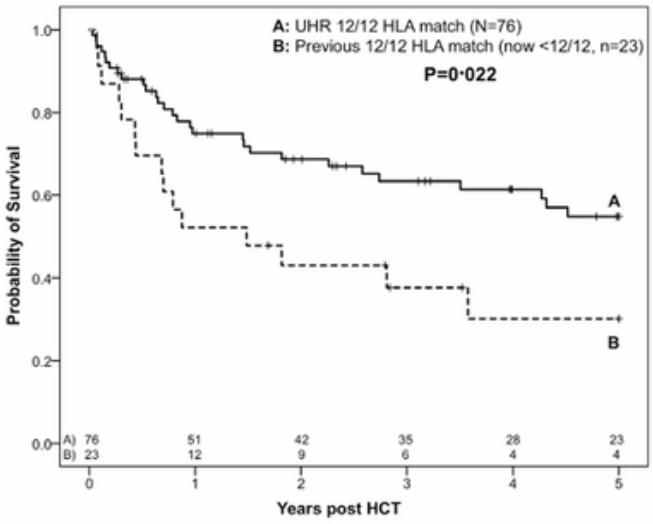
Given the critical importance of HLA molecules in immune responses, HLA genotyping is widely applied in fields such as transplantation matching, research on immune-related diseases, pharmacogenomics, and platelet transfusion compatibility. Currently, HLA genotyping is performed using a variety of techniques. However, even with high-resolution NGS, commercially available HLA-specific assays still yield ~3% ambiguous results [1].

Current Technologies	Limitations
PCR-SSP	Low resolution with detection limited to known genotypes only
PCR-SSO	Relies on a large number of probes, driving up costs while delivering low resolution and limited to detecting only known genotypes
PCR-SBT (Sanger)	Low throughput with a tendency to produce ambiguous results
NGS	High instrument costs and still yield ambiguous results

More Precise Typing Leads to Improved Patient Outcome

A study involving 891 patients with hematological malignancies across 32 UK transplant centers demonstrated that precise validation using PacBio LRS HLA typing (ultra-high resolution, UHR) corrected previous Sanger typing results in 29.1% of cases.

Furthermore, patients with a true 12/12 HLA match confirmed by LRS (UHR 12/12 HLA match) exhibited a significantly higher survival rate compared to those who appeared to be 12/12 matches but were actually mismatched stemming from previous assay errors (Previous 12/12 HLA match) (5-year Overall Survival [OS]: 54.8% vs. 30.1%; p=0.022).



Information and figure derived from reference [2]

Break the Ambiguity. Resolve with Confidence.

Powered by Long-Read Sequencing

AltruType™ Long-Read HLA Genotyping is a complete sample-to-report HLA typing solution powered by PacBio HiFi sequencing. Designed for ease of use and operational efficiency, AltruType™ delivers high-resolution results up to 8-digit with gold-standard accuracy and unambiguous allele calls, all from a single streamlined workflow.

Basic 11 loci

Class I: *HLA-A*, *HLA-B*, *HLA-C*
Class II: *HLA-DRB1*, *HLA-DRB3-5*, *HLA-DQA1*, *HLA-DQB1*, *HLA-DPA1*, *HLA-DPB1*

\+

Extended 3 loci

HLA-F, *HLA-E*, *HLA-G*

Clinical-Grade Precision

- CE-IVD Marked
- Ultra-High Resolution (8-digit): Generates intact, fully phased sequences straight from raw reads (≥200 depth) for unambiguous, high-confidence typing

Streamlined & Automated Workflow

- Pre-Mixed Reagents: Minimal transfer steps
- Automation-Ready Protocols
- Hands-off Analysis and Reporting Software

Flexibility & Scalability

- Flexible Target Options: 11/ 14 loci, with full support for further target customization
- Various Kit Configurations: 24/ 46/ 96/ 192 reactions

To Dec 2025, >20,000 AltruType™ Long-Read HLA Genotyping Test Had Completed and Identified More Than 100+ Novel Alleles

Publications with AltruType™ Long-Read HLA Genotyping

Core Technology

Single-Tube Long-Range PCR Enrichment

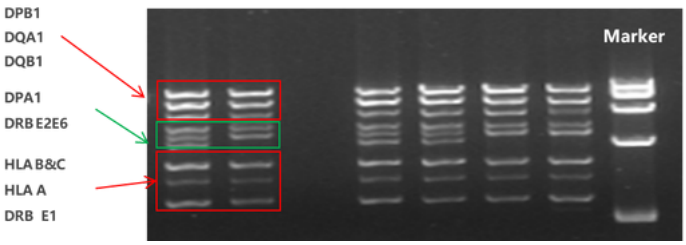
AltruType™ utilizes a streamlined, single-tube LR-PCR enrichment strategy to establish a highly stable and efficient foundation for downstream analysis. By generating ultra-long amplicons (spanning several kilobases) that cover entire genes, this approach yields fully phased alleles directly in the raw reads.

Removes Phasing Ambiguity

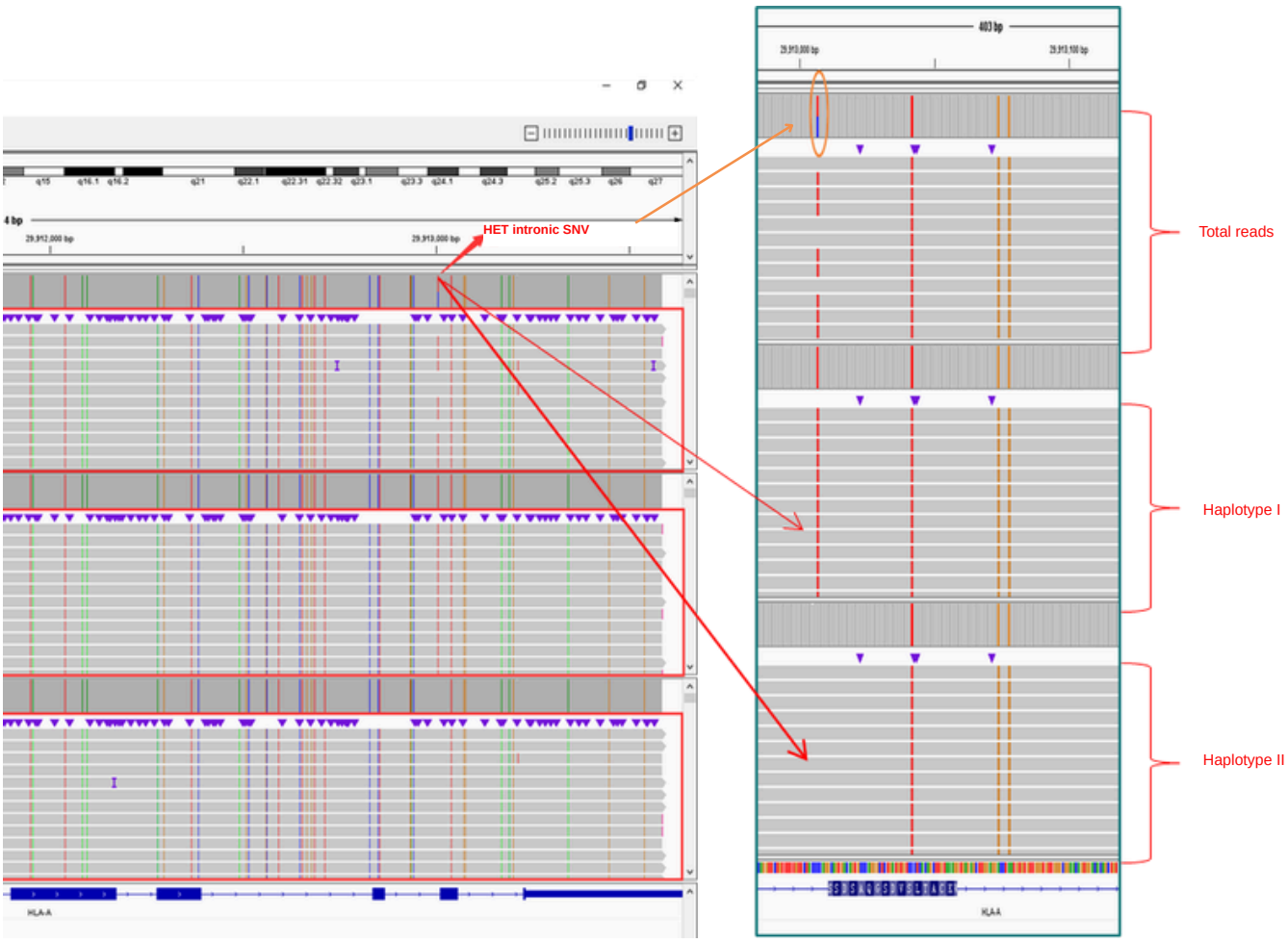
- Prevents alignment errors from fragmented raw sequence

Eliminates Amplification Imbalance

- Ensures uniform coverage across the gene
- Reliably distinguishes true homozygosity from potential allelic dropout



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



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

TransMatch™
All-In-One Software for Sample Management, Bioinformatics, and Reporting

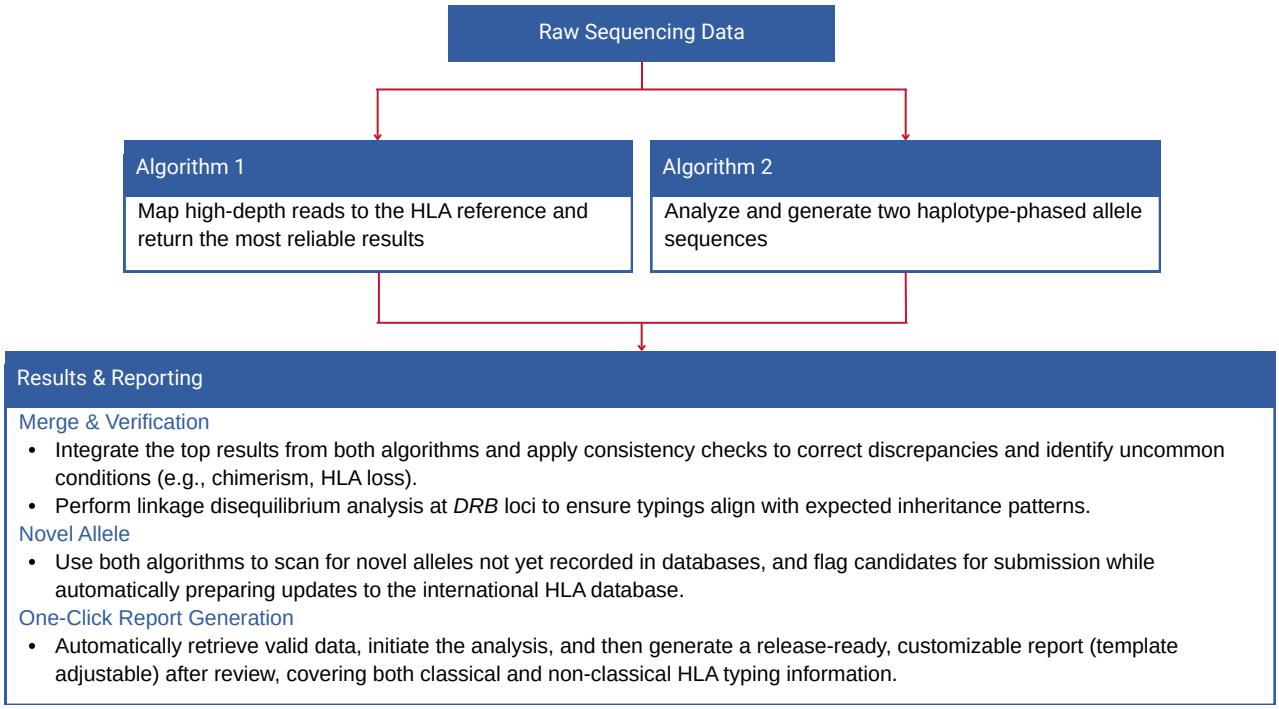
TransMatch™ is a comprehensive, user-friendly platform designed to deliver true end-to-end analytics, sample management, and results reporting for the modern service laboratory. By supporting your routine workflow from start to finish, it ensures stable, reproducible results with manual intervention in analysis.

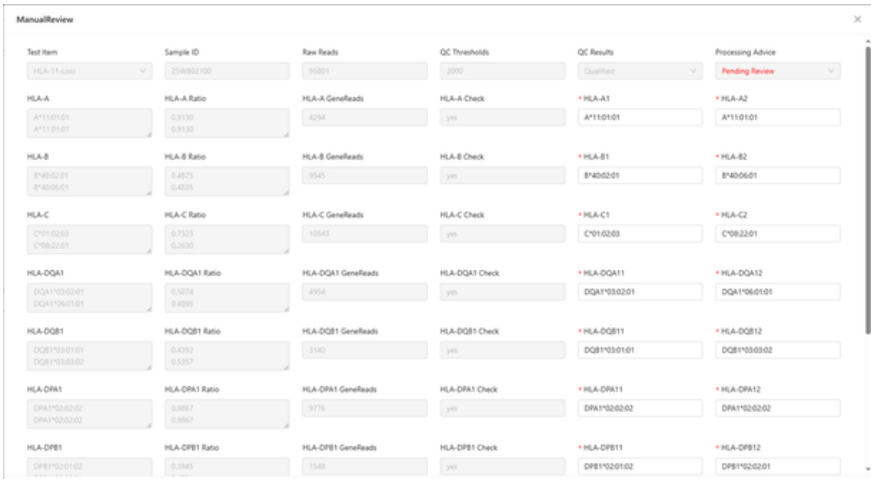
Seamless
Handles sample management, analysis, and reporting in one system

Confidence Results with Proprietary Analysis
Powered by dual-algorithm cross-validation with automated detection of novel alleles and chimeric haplotypes

One-Click Reporting
Generates customized reports instantly, streamlined for final review and sign-off

Compliant
Role-based permissions and complete activity logging ensure seamless, secure handoffs across all teams



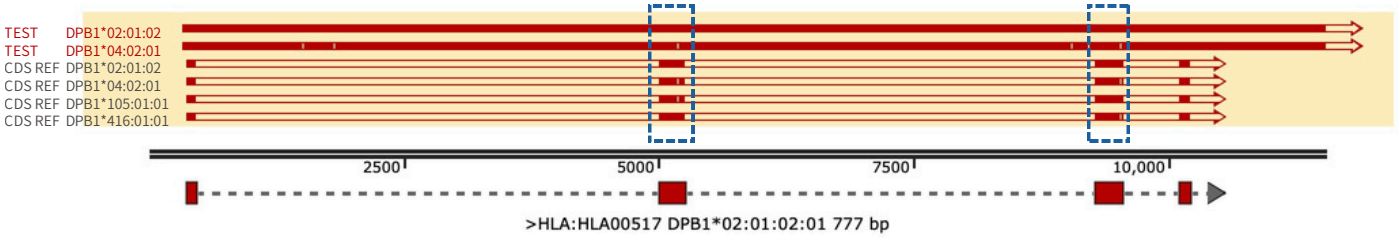


Review of HLA typing results automated called by Transmatch™

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

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.

HemoSure™

Long-Read Sequencing for Red Blood Cell Typing

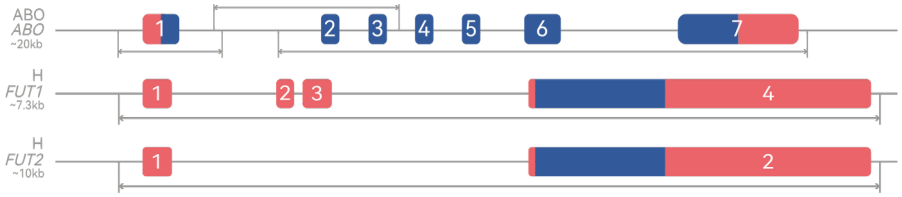
Background

Conventional serological assays frequently fail to identify weak phenotypes, subtypes, and rare types. This makes them highly prone to misinterpretation, posing significant risks to blood transfusion safety. Blood group genotyping is indicated in a wide range of scenarios where serological typing alone cannot provide a definitive answer. These include, but are not limited to:

- ABO Subtypes
- Hematological Disorders Requiring Long-Term Transfusion
- Malignancies
- Drug-Induced Interference
- Congenital or Post-Transplant Chimerism
- Autoimmune Diseases
- Leukemia

ABO Genotyping

By combining targeted amplification with long-read sequencing, we deliver high-resolution genotyping of the *ABO*, *FUT1*, and *FUT2* genes, definitively resolving complex discrepancies such as cis-AB and B(A) while accurately identifying null alleles. The result is truly precise and unambiguous genotyping (covering non-hotspot, phasing, and structural variations) of the ABO and Hh blood group systems.



Case Study: Identification of a B/O Blood Group Chimera

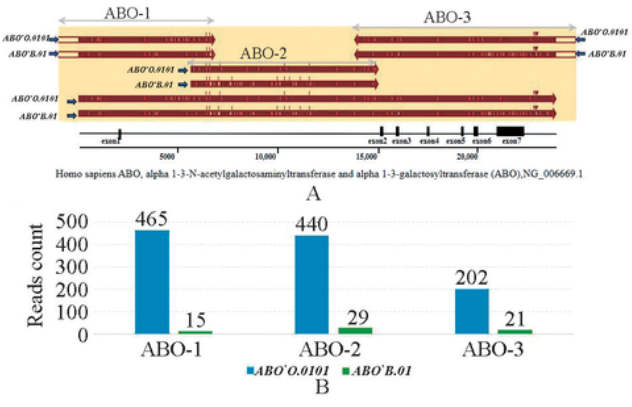
Case: 33-year-old female with no relevant medical history. ABO typing discrepancy identified during routine maternal screening.

Serology: No agglutination with anti-A, mixed-field with anti-B and anti-AB, 4+ with anti-H. Reverse typing: 3+ with A1c, no agglutination with B1c. Antibody screening was unexpectedly negative.
Sanger Sequencing: Genotyped as *ABOO.01.01/ ABOO.01.01*. No heterozygous mutation peaks at B SNP loci.

HemoSure™ ABO Genotyping:

HemoSure™ resolved two distinct haplotypes: *ABOO.01.01* and a low-read-count *ABOB.01* haplotype, with an order-of-magnitude difference in read depth between them. This read disparity indicated the presence of partial ABO*B.01 chimerism in the patient.

Information and figure derived from reference [3]

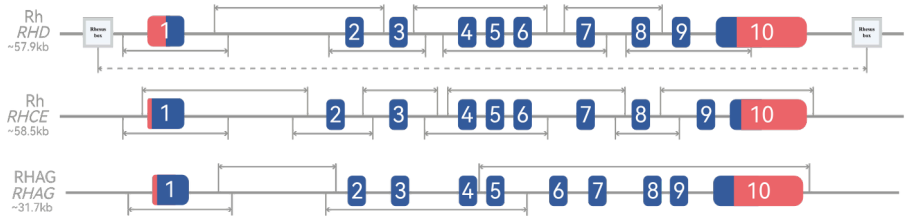


Top: Diagram of the *ABO* gene amplicon showing two distinct haplotypes detected. Bottom: Distribution of read counts for each haplotype.

Rh Genotyping

Serologic identification of RHD weak D, partial D, and DEL phenotypes is notoriously challenging. Susceptible to variable factors such as antibody reagent quality and operator technique, these groups are frequently misclassified or missed entirely. Furthermore, conventional molecular assays struggle to resolve the high sequence homology between *RHD* and *RHCE* genes, which are susceptible to structural variations. This makes complex recombinant events difficult to characterize and often requires multiple assays for definitive classification.

To overcome, our preitry assays adopted long-read sequencing to address these limitations by delivering contiguous, haplotype-resolved detection of the entire RHD locus, enabling the clear and precise detection of those blood group resulted by complex variations.

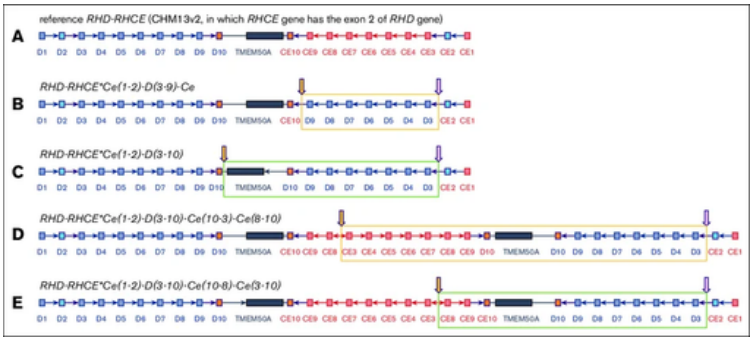


The Key to Resolving Complex Structural Variations

To date, the most frequently reported mechanism underlying the D-- phenotype is gene rearrangement. While the short-read lengths inherent to NGS limit its ability to detect these structural variations, long-read based assays play a central role in resolving them.

A study investigated a proband with the D-- phenotype and her family. Using the HemoSure™ assay and data from 29 heterozygous SNV loci, researchers manually assembled distinct *RHCE* and *RHD* gene haplotypes. By combining Bionano Optical Genome Mapping (OGM) with heterozygosity data and pedigree analysis, RHCE haplotypes carrying structural variations were definitively identified and their inheritance patterns within the family were successfully traced.

Information and figure derived from reference [4]

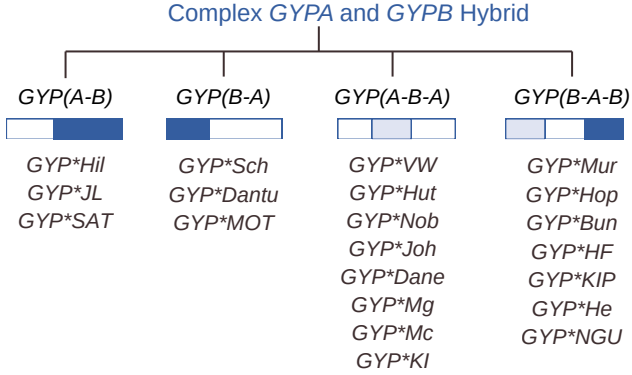


RH and SV haplotype: (A) Reference RH haplotype. (B-C) The SV haplotype of father. (D-E) The SV haplotype of mother.

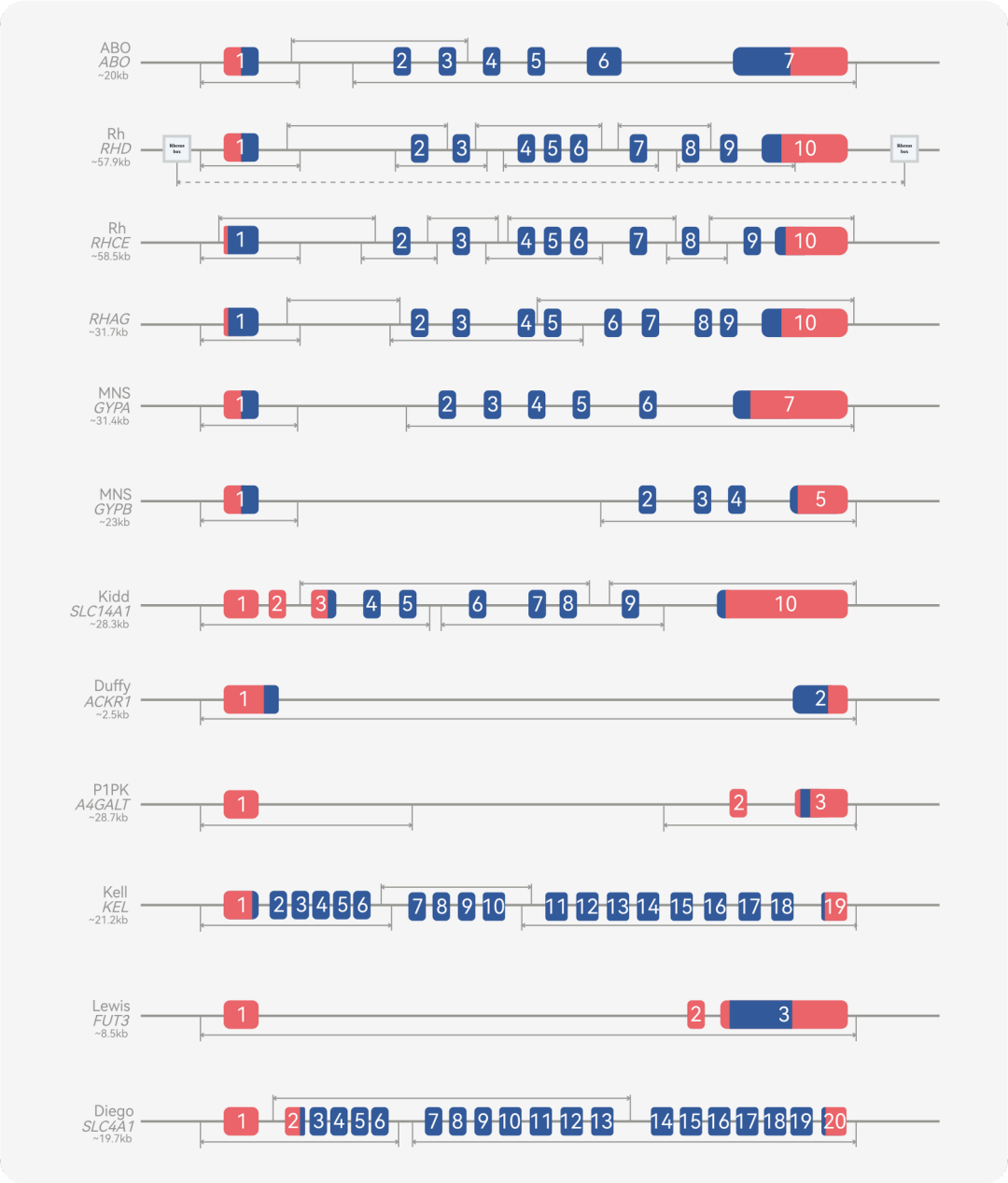
Red Blood Cell (RBC) Typing

Typing for the Highly Homologous *GYPA* and *GYPB* Genes

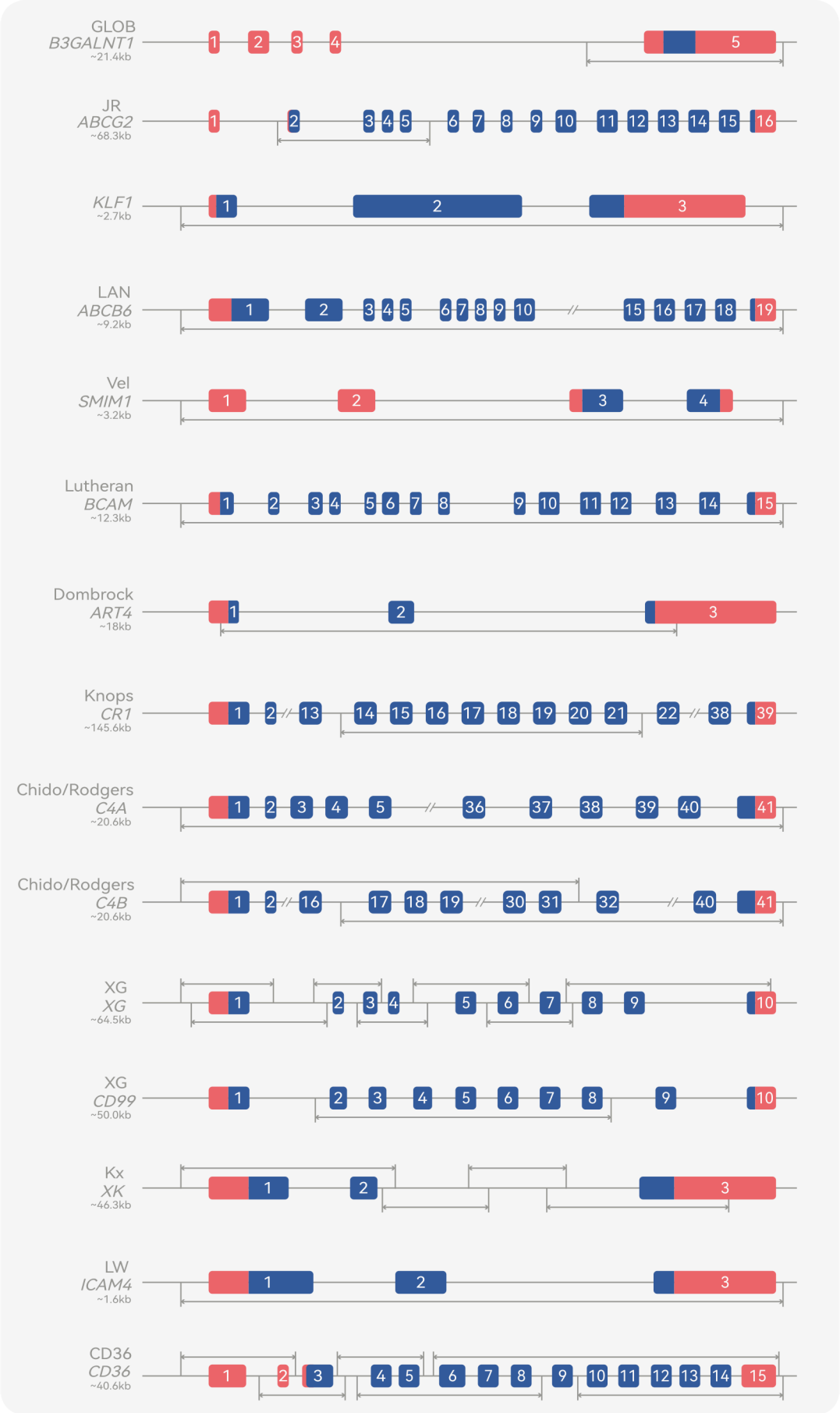
The high sequence homology between *GYPA* and *GYPB* makes precise MNS blood group genotyping exceedingly difficult with conventional assays. HemoSure™ RBC Typing Panel leverages LRS to deliver full-length coverage of both genes, definitively differentiating approximately 50 MNS variants and capturing complex hybrid variants including GYP(A-B-A), GYP(B-A), GYP(B-A-B), and GYP(A-E-A).



Panel 1: ABO, Rh, MNS, Kidd, Duffy Blood Group Systems (7 Genes)
Panel 2: ABO, Rh, MNS, Kidd, Duffy, P1PK, Kell, Lewis, Diego Blood Group Systems (13 Genes)



Extended Panel: 13 Blood Group Systems (17 Genes)
H, GLOB, JR, LAN, Vel, Lutheran, Dombrock, Knops, Chido/Rodgers, XG, Kx, LW, CD36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JR
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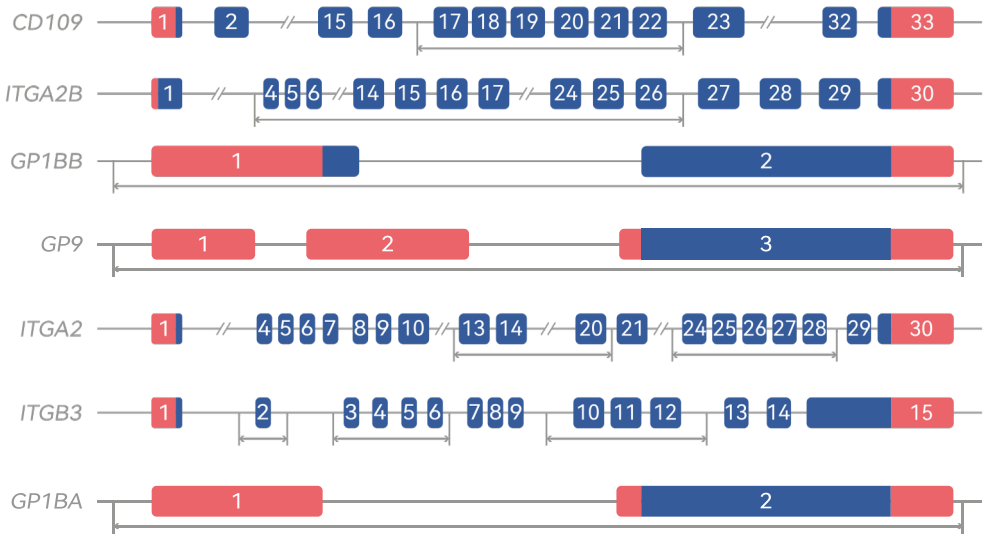
KLF1
~2.7kb
LAN
ABCB6
~9.2kb
Vel
SMIM1
~3.2kb
Lutheran
BCAM
~12.3kb
Dombrock
ART4
~18kb
Knops
CR1
~145.6kb
Chido/Rodgers
C4A
~20.6kb
Chido/Rodgers
C4B
~20.6kb
XG
XG
~64.5kb
XG
CD99
~50.0kb
Kx
XK
~46.3kb
LW
ICAM4
~1.6kb
CD36
CD36
~40.6kb

Human Platelet Antigen (HPA) Genotyping

Mismatched platelet transfusions can lead to serious adverse events including platelet transfusion refractoriness (PTR) and alloimmune thrombocytopenia. Beyond transfusion, HPA polymorphisms are closely linked to disease susceptibility, platelet-pathogen interactions, platelet-malignant cell interactions, and cardiovascular disease risk.

HemoSure™ HPA genotyping delivers comprehensive coverage across all HPA-1 to HPA-35 loci. Combined with AltruType™ HLA genotyping and HemoSure™ RBC genotyping, this creates a complete genotyping ecosystem for transplant medicine, bone marrow registries, and blood banking.



To Dec 2025, >20,000 HemoSure™ Typing Had Completed and Cited in Over 40 Publications

Publications with HemoSure™ Typing

References:
[1] Weimer ET, Montgomery M, Petraroia 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.
[2] Mayor NP, Hayhurst JD, Turner TR, et al. Recipients Receiving Better HLA-Matched Hematopoietic Cell Transplantation Grafts, Uncovered by a Novel HLA Typing Method, Have Superior Survival: A Retrospective Study. *Biol Blood Marrow Transplant*. 2019;25(3):443-450.
[3] Li R, Cui C, Hao X. B/O blood group chimera identified by PacBio third-generation sequencing: a case report. *Zhongguo shuxue zazhi*. 2025;38(3).
[4] Li M, Wang L, Li A, et al. Integrated analyses reveal unexpected complex inversion and recombination in *RH* genes. *Blood Adv*. 2024;8(12):3154-3165.

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