omixon NANOTYPE

Oxford NANOPORE Technologies™

APPLICATIONS

The NanoTYPE™ HLA assay: rapid, comprehensive, high-resolution HLA typing using nanopore sequencing

Nanopore long reads can be used to accurately identify SNPs, phase haplotypes and perform high-resolution genotyping within the most polymorphic region of the human genome

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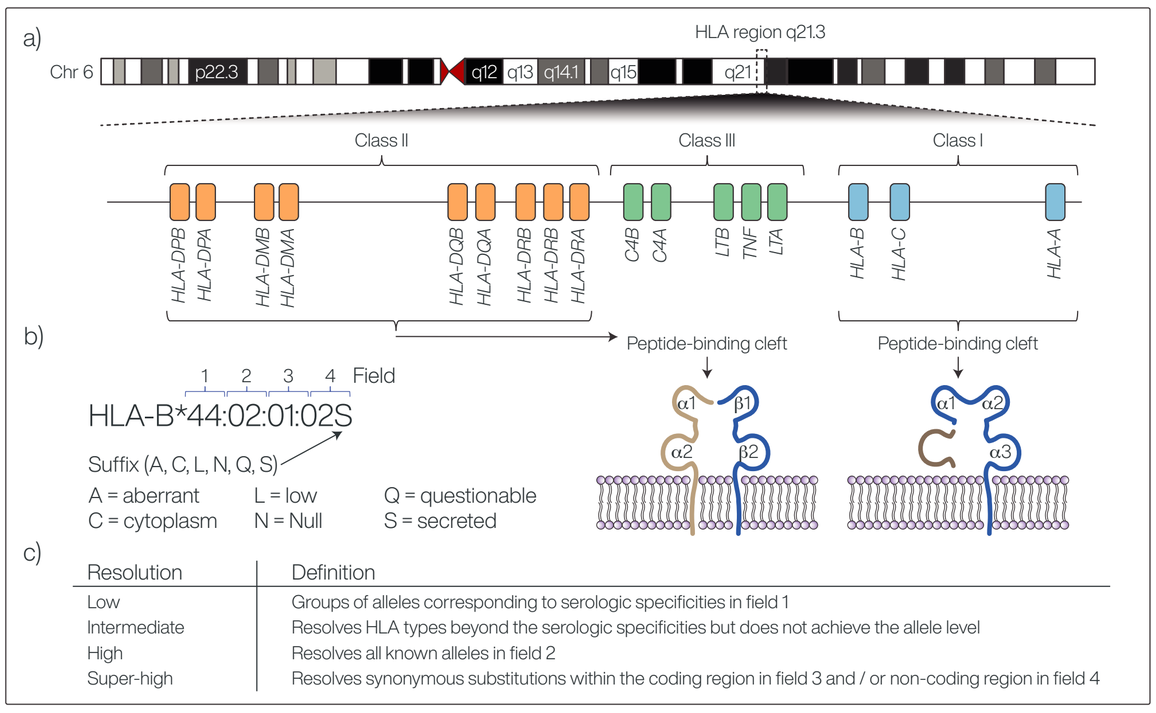


Fig. 1 Human Leukocyte Antigen (HLA) a) region b) Class I and II molecules c) nomenclature

Matching donor and recipient HLA alleles is important for tissue transplantation

The Human Leukocyte Antigen (HLA) region is a highly polymorphic region located on Chr6 (Fig. 1a). It includes Class I alpha and Class II alpha/beta chain genes, which are responsible for intracellular and extracellular antigen presentation respectively (Fig. 1b). Successful solid organ or bone marrow transplantation requires HLA matching of donors and recipients. HLA alleles are defined by the SNP and indel combinations within single phased sequences, and specific nomenclature is used to define alleles. Field 1 specifies the allele group, field 2 the specific HLA protein, field 3 captures synonymous mutations in coding regions, field 4 denotes non-coding variants, and the suffix relates to expression levels (Fig. 1c).

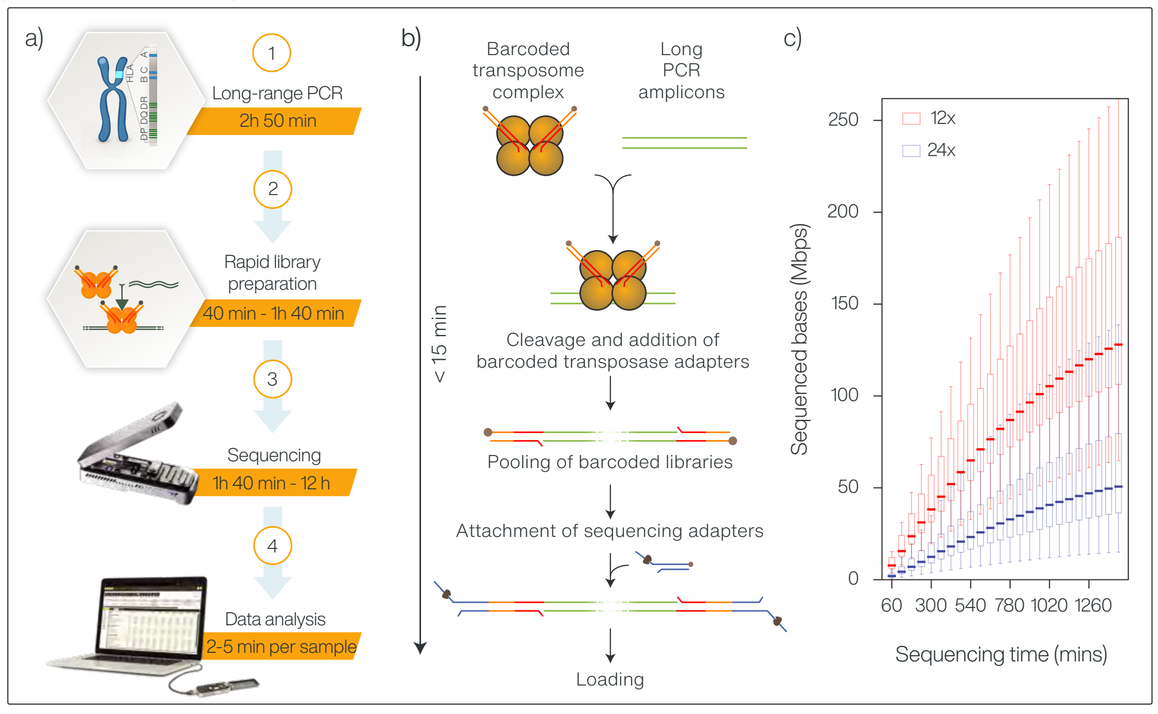
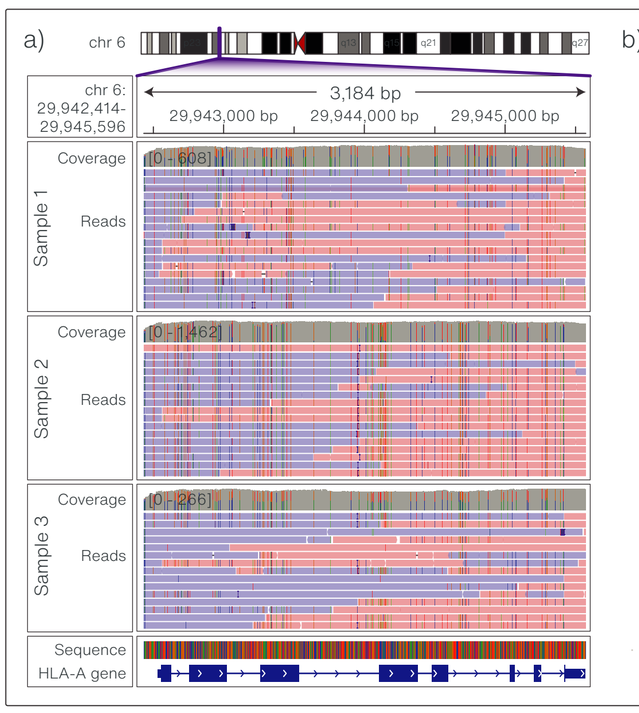


Fig. 2 Omixon NanoTYPE assay a) workflow b) rapid library preparation c) sequencing output

The Omixon NanoTYPE workflows combine multiplexed PCR with nanopore sequencing

The Omixon NanoTYPE assay uses multiplexed long-range PCR paired with rapid library preparation, nanopore sequencing, and specialised data-analysis methods (Fig. 2a). Library preparation can be performed in 15 minutes (Fig. 2b). Different levels of multiplexing are possible, and the typical output when 12 and 24 samples are sequenced in parallel is shown in Fig. 2c). Data analysis and HLA type calling is performed using the HLA Twin software. Data can be analysed against any version of the IPD-IMGT/HLA database, a specialist repository for sequences of the human HLA regions.



b)

		Sample 1: NA17228		Sample 2: NA17440		Sample 3: NA17283	
Locus	Allele	Published HLA type	HLA Twin	Published HLA type	HLA Twin	Published HLA type	HLA Twin
HLA-A	1	*01:01:01	HLA-A*01:01:01	*02:01:01	HLA-A*02:01:01	*02:01:01	HLA-A*02:01:01
	2	*24:02:01	HLA-A*24:02:01	*02:06:01	HLA-A*02:06:01	*03:01:01	HLA-A*03:01:01
HLA-B	1	*15:01:01	HLA-B*15:01:01	*15:15	HLA-B*15:15:01	*07:02:01	HLA-B*07:02:01
	2	*55:01:01	HLA-B*55:01:01	*35:23	HLA-B*35:23	*07:02:01	HLA-B*07:02:01
HLA-C	1	*03:03:01	HLA-C*03:03:01	*01:02:01	HLA-C*01:02:01	*07:02:01	HLA-C*07:02:01
	2	*03:03:01	HLA-C*03:03:01	*04:01:01	HLA-C*04:01:01	*07:02:01	HLA-C*07:02:01
DPA1	1	*01:03:01	HLA-DPA1*01:03:01	*01:03:01	HLA-DPA1*01:03:01	*01:03:01	HLA-DPA1*01:03:01
	2	*01:03:01	HLA-DPA1*01:03:01	*01:03:01	HLA-DPA1*01:03:01	*01:03:01	HLA-DPA1*01:03:01
DPB1	1	*04:01:01	HLA-DPB1*04:01:01	*04:01:01	HLA-DPB1*04:01:01	*04:01:01	HLA-DPB1*04:01:01
	2	*04:01:01	HLA-DPB1*04:01:01	*04:01:01	HLA-DPB1*04:01:01	*04:01:01	HLA-DPB1*04:01:01
DQA1	1	*01:03:01	HLA-DQA1*01:03:01	*04:01:01	HLA-DQA1*04:01:01	*01:02:01	HLA-DQA1*01:02:01
	2	*05:05:01	HLA-DQA1*05:05:01	*04:01:01	HLA-DQA1*04:01:01	*01:02:01	HLA-DQA1*01:02:01
DQB1	1	*03:01:01	HLA-DQB1*03:01:01	*04:02:01	HLA-DQB1*04:02:01	*06:02:01	HLA-DQB1*06:02:01
	2	*06:03:01	HLA-DQB1*06:03:01	*04:02:01	HLA-DQB1*04:02:01	*06:02:01	HLA-DQB1*06:02:01
DRB1	1	*12:01:01G	HLA-DRB1*12:01:01G	*08:02:01	HLA-DRB1*08:02:01	*15:01:01	HLA-DRB1*15:01:01
	2	*13:01:01	HLA-DRB1*13:01:01	*08:02:01	HLA-DRB1*08:02:01	*15:01:01	HLA-DRB1*15:01:01
DRB3	1	*01:01:02	HLA-DRB3*01:01:02G				
	2	*02:02:01	HLA-DRB3*02:02:01G				
DRB4	1						
	2						
DRB5	1					*01:01:01	HLA-DRB5*01:01:01
	2					*01:01:01	HLA-DRB5*01:01:01

Allele:Allele match
G group:G group match
G group:Allele match

Concordant	Allele:Allele match	49	52
	Allele:G group match	0	
	G group:G group match	1	
	G group:Allele match	2	
Discordant		0	0
No data		0	0
Total		52	52

c)

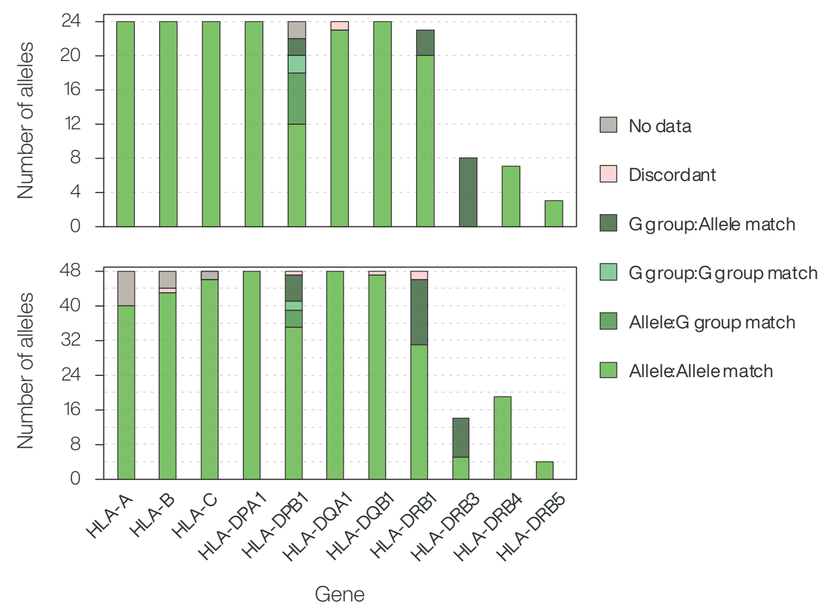


Fig. 3 NanoTYPE data a) read mapping to HLA-A b) HLA types against all loci c) 12 sample run (top), 24 sample run (bottom)

Rapid HLA typing for deceased donor typing/solid organ transplantation, and higher levels of multiplexing for potential use in registry typing/stem cell transplantation

The NanoTYPE assay has the potential to generate rapid results for deceased donor typing (used for solid organ transplantation), where time is a critical factor and a small number of samples is usually tested. We tested 3 reference samples using a 15-minute library preparation method followed by sequencing on a MinION™ Flow Cell, with analysis at multiple time points. Read mapping to the GRChH38 assembly and the large number of observable SNPs highlights the polymorphic nature of the HLA genes, with HLA-A shown as an example (Fig. 3a). Here, we can also see individual reads in sample 2 and 3 with matching SNP profiles, indicating a common allele. Determination of HLA types confirmed the HLA-A*02:01:01 allele is present in both samples. High resolution typing across all loci was possible within 30-60 minutes of sequencing per sample. Most alleles were resolved to 3-field resolution, and G-groups assigned to the remainder. The complete HLA type data is shown Fig. 3b), with HLA types classified against six possible result types and fully concordant with published data. The NanoTYPE assay also shows potential for use in routine registry typing (used to match patients for stem cell transplants), where higher levels of multiplexing are beneficial, and the most rapid turnaround time is not required. We sequenced 12 and 24 reference samples per MinION Flow Cell for 12 and 24 hours respectively and classified the resulting HLA types by gene (Fig. 3c). As previously, the majority of alleles were resolved to 3-field resolution, with some G-group assignment (equating to high-resolution typing). Concordance with published data (shown in green) was 98.6% and 95.4% respectively for the 12 and 24 sample runs.