

Homgen[®] HLA Typing NGS Panel

202205V5

Product Introduction

HLA, fully known as Human Leukocyte Antigen, is the expression product of the human major histocompatibility complex (MHC), located on the short arm of chromosome 6. It is currently recognized as the most complex polymorphic system in the human body, with each gene having thousands of alleles. HLA is associated with susceptibility and resistance to many autoimmune and infectious diseases.

First-generation sequencing is currently the main method for HLA typing and has been applied in HLA tissue typing laboratories and various clinical hospitals. However, it has low throughput and is time-consuming. Second-generation sequencing based on probe hybridization capture enables high-throughput, low-cost, high-resolution HLA typing. Compared to PCR-based target sequence enrichment methods, hybrid capture has a significant advantage in tolerating high sequence polymorphism. In the face of highly polymorphic HLA sequences, Homgen Biotech Co., Ltd combines the HLA database (IPD-IMGT/HLA database) with the company's algorithmic expertise in hybrid capture probe design to create encrypted probes for polymorphic gene sequences. This has led to the development and production of an NGS Panel testing kit for high-precision HLA typing.

Intended Use

Detection for high-precision HLA typing in multiple samples with high throughput.

Product Advantages

- * **HLA-Small Panel:** Cover classic full-length HLA-I (A, B, C), HLA-II coding regions (DR, DP, DQ), non-classical HLA-I (E, F, G), and HLA-II (DO, DM), with probe regions designed for dense polymorphism detection;
- * **HLA-BIG Panel:** Includes 11 genes such as classic HLA-I (A, B, C) and HLA-II (DR, DP, DQ) ; (HLA-A, HLA-B, HLA-C, HLA-DQB1, HLA-DPB1, HLA-DQA1, HLA-DPA1, HLA-DRB1, HLA-DRB3/4/5), full-length coverage with probe regions designed for dense polymorphism detection;
- * Hybrid capture NGS sequencing method allows high sequencing depth with fewer reads, achieving stable high-resolution HLA typing;
- * DNA probes with high stability; supports hybridization of multiple samples; compatible with spike-in usage.

For Research Use

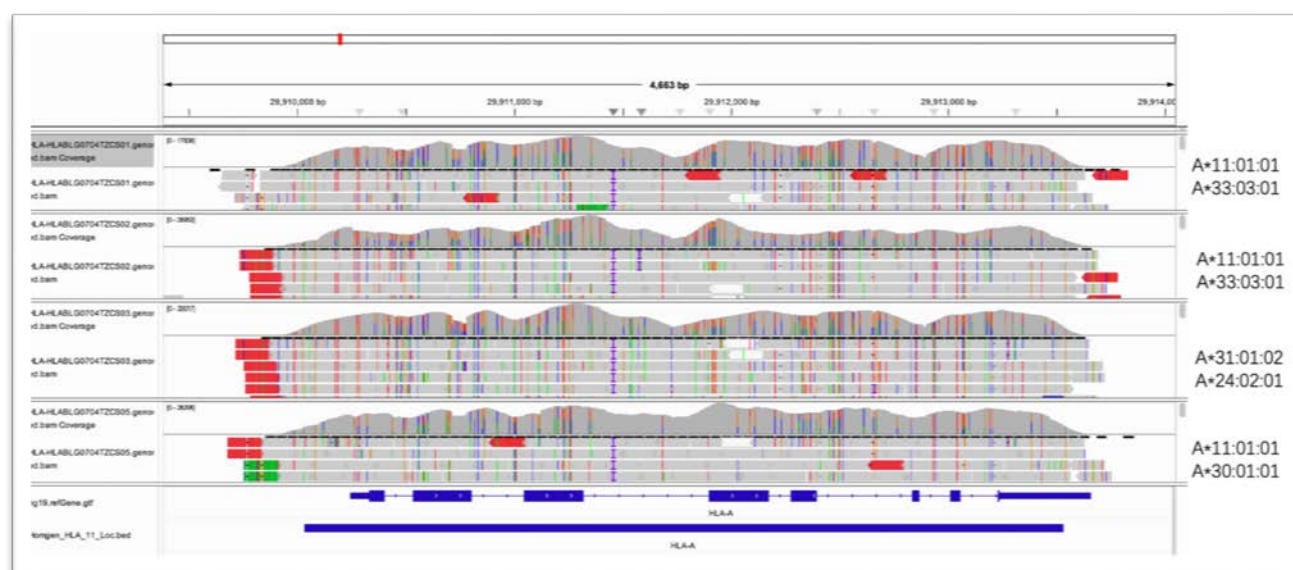
Product Specifications

Product NAME	Cat NO.	Specification	Storage	Delivery Time
HLA-Small Panel (Probe)	P10011-12	12 rxns	-20℃, 2 years,	Available in stock
HLA-Small Panel (Probe)	P10011-96	96 rxns	-20℃, 2 years,	Available in stock
HLA-BIG Panel (Probe)	P10036-12	12 rxns	-20℃, 2 years,	Available in stock
HLA-BIG Panel (Probe)	P10036-96	96 rxns	-20℃, 2 years,	Available in stock
Hybridization Reagent (10X Version) (Includes Blocker and Post-PCR)	P10006-12/96	12 / 96 rxns	-20℃/4~8℃, 2 years,	Available in stock
Hybridization Reagent (HS Version) (Includes Blocker and Post-PCR)	P10018-12/96	12 / 96 rxns	-20℃/4~8℃, 2 years,	Available in stock

HLA Probe Design and Validation

1. The HLA database (IPD-IMGT/HLA Database) is used as the basis for design.
2. DNA probes are designed for targeted full-length or coding regions of the genome, and probe types are optimized. Probes are synthesized and mixed in equal proportions.
3. Batch samples and samples with known typings are selected to perform hybrid capture experiments and next-generation sequencing (Illumina and MGI PE150), followed by statistical analysis.
4. The probes for the captured regions are further optimized and adjusted, and the samples are tested, analyzed, and statistically evaluated again.

HLA Data Presentation:



HLA Results Display: (illumina NovaSeq & MGI T7 PE150 ~0.5G Data)

For Research Use

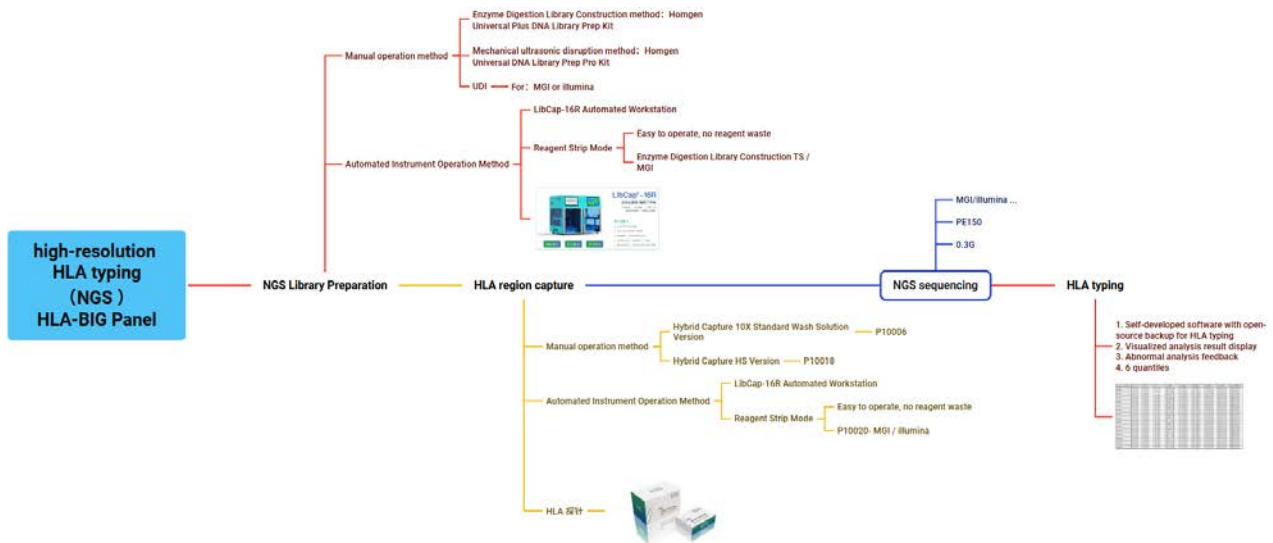
sales@homgen.com

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Homgen -HLA Panel	HLA-A	HLA-B	HLA-C	HLA-DRB1	HLA-DQA1	HLA-DQB1	HLA-DPA1	HLA-DPB1	HLA-DRB3/4/5
Sample1	A*11:01:01	B*58:01:01	C*03:02:02	DRB1*03:01:01	DQA1*05:01:01	DQB1*06:01:01	DPA1*01:03:01	DPB1*05:01:01	DRB3*02:02:01
	A*33:03:01	B*40:01:02	C*07:02:01	DRB1*08:03:02	DQA1*01:03:01	DQB1*02:01:01	DPA1*02:02:02	DPB1*04:01:01	DRB3*02:02:01
Sample2	A*11:01:01	B*56:01:01	C*01:02:01	DRB1*13:12:01	DQA1*05:03:06	DQB1*03:01:01	DPA1*01:03:01	DPB1*05:01:01	DRB3*02:02:01
	A*02:07:01	B*46:01:01	C*01:02:01	DRB1*09:01:02	DQA1*03:02:01	DQB1*03:03:02	DPA1*02:02:02	DPB1*02:01:02	DRB4*01:03:01
Sample3	A*31:01:02	B*15:07:01	C*01:02:01	DRB1*14:05:01	DQA1*03:01:01	DQB1*05:03:01	DPA1*01:03:01	DPB1*19:01:01	DRB3*02:02:01
	A*24:02:01	B*54:01:01	C*03:03:01	DRB1*04:03:01	DQA1*01:04:01	DQB1*03:02:01	DPA1*02:02:01	DPB1*02:01:02	DRB4*01:03:01
Sample4	A*30:01:01	B*13:02:01	C*06:02:01	DRB1*03:01:01	DQA1*02:01:03	DQB1*02:02:01	DPA1*02:01:01	DPB1*17:01:02	DRB3*02:02:01
	A*33:03:01	B*58:01:01	C*03:02:02	DRB1*07:01:01	DQA1*05:01:01	DQB1*02:01:01	DPA1*01:03:01	DPB1*04:01:01	DRB4*01:03:01
Sample5	A*11:01:01	B*15:01:01	C*06:02:01	DRB1*12:02:01	DQA1*06:01:01	DQB1*03:01:01	DPA1*02:02:01	DPB1*19:01:01	DRB3*02:02:01
	A*30:01:01	B*13:02:01	C*07:02:01	DRB1*07:01:01	DQA1*02:01:06	DQB1*02:02:01	DPA1*02:01:01	DPB1*17:01:02	DRB4*01:03:01
Sample6	A*11:02:01	B*15:11:01	C*03:03:01	DRB1*08:03:02	DQA1*01:04:01	DQB1*05:03:01	DPA1*02:02:02	DPB1*05:01:01	DRB3*02:02:01
	A*31:01:02	B*39:01:01	C*07:02:01	DRB1*14:05:01	DQA1*01:03:01	DQB1*06:01:01	DPA1*02:02:02	DPB1*05:01:01	DRB3*02:02:01
Sample7	A*02:01:01	B*51:01:01	C*01:02:01	DRB1*09:01:02	DQA1*03:01:01	DQB1*03:03:02	DPA1*02:02:02	DPB1*05:01:01	DRB4*01:03:01
	A*24:02:01	B*46:01:01	C*01:02:01	DRB1*04:03:01	DQA1*03:02:13	DQB1*03:02:01	DPA1*02:02:02	DPB1*05:01:01	DRB4*01:03:01
Sample8	A*30:01:01	B*13:02:01	C*08:01:01	DRB1*07:01:01	DQA1*06:01:01	DQB1*03:01:01	DPA1*02:02:02	DPB1*05:01:01	DRB3*03:01:03
	A*11:01:01	B*40:06:01	C*06:02:01	DRB1*12:02:01	DQA1*02:01:02	DQB1*02:02:01	DPA1*02:01:01	DPB1*17:01:10	DRB4*01:03:01
Sample9	A*26:01:01	B*39:01:01	C*03:03:01	DRB1*15:01:01	DQA1*03:03:01	DQB1*06:02:01	DPA1*02:02:02	DPB1*05:01:01	DRB3*02:27:11
	A*01:01:01	B*37:01:01	C*06:02:01	DRB1*04:01:01	DQA1*01:02:01	DQB1*03:01:01	DPA1*02:02:02	DPB1*05:01:01	DRB4*01:03:01
Sample10	A*02:06:01	B*51:01:01	C*16:02:01	DRB1*03:01:01	DQA1*05:01:01	DQB1*06:01:01	DPA1*01:03:01	DPB1*02:01:02	DRB3*02:02:01
	A*11:01:01	B*55:01:01	C*03:03:01	DRB1*15:02:01	DQA1*01:03:01	DQB1*02:01:01	DPA1*01:03:01	DPB1*04:01:01	DRB3*02:04:02
Sample11	A*02:01:01	B*37:01:01	C*06:02:01	DRB1*04:01:01	DQA1*03:03:01	DQB1*05:01:01	DPA1*01:03:01	DPB1*02:01:02	DRB4*01:03:01
	A*01:01:01	B*40:02:01	C*03:04:01	DRB1*10:01:01	DQA1*01:05:02	DQB1*03:01:01	DPA1*01:03:01	DPB1*04:02:01	DRB4*01:02:06
Sample12	A*11:01:01	B*13:01:01	C*03:04:01	DRB1*14:04:02	DQA1*06:01:01	DQB1*05:03:01	DPA1*02:02:02	DPB1*14:01:01	DRB3*02:02:01
	A*24:02:01	B*40:06:01	C*15:02:01	DRB1*12:02:01	DQA1*01:04:02	DQB1*03:01:01	DPA1*02:01:01	DPB1*05:01:01	DRB3*03:01:03
Sample13	A*02:03:01	B*55:02:01	C*01:02:01	DRB1*15:01:01	DQA1*03:02:11	DQB1*05:02:01	DPA1*02:01:01	DPB1*14:01:08	DRB4*01:03:02
	A*24:02:01	B*40:01:02	C*03:04:01	DRB1*09:01:02	DQA1*01:02:01	DQB1*03:03:02	DPA1*02:02:02	DPB1*13:01:01	DRB5*01:01:01
Sample14	A*02:01:01	B*18:01:01	C*07:01:01	DRB1*13:02:01	DQA1*05:01:01	DQB1*02:01:01	DPA1*02:01:01	DPB1*13:01:01	DRB3*03:01:01
	A*30:02:01	B*49:01:01	C*05:01:01	DRB1*03:01:01	DQA1*01:06:11	DQB1*06:04:01	DPA1*01:03:01	DPB1*04:01:01	DRB3*02:02:01
Sample15	A*11:01:01	B*13:01:01	C*03:04:01	DRB1*14:04:02	DQA1*06:01:01	DQB1*05:03:01	DPA1*02:02:02	DPB1*14:01:05	DRB3*02:02:01
	A*24:02:01	B*40:06:01	C*15:02:01	DRB1*12:02:01	DQA1*01:04:02	DQB1*03:01:01	DPA1*02:01:01	DPB1*05:01:01	DRB3*03:01:03

HLA High-Resolution Typing Protocol Workflow



Instructions for Use

The HLA High-Resolution Panel consists of a probe pool (HLA Probe) and a set of reagents for homogeneous hybridization capture.

For detailed experimental procedures, please refer to Homgen Biotech Co., Ltd.

"Probe Hybridization Capture Protocol 10X Standard Wash Solution Version for NGS DNA Library" or

"Probe Hybridization Capture Protocol HS/HE Version for NGS DNA Library" or

"LibCap Automated Library Workstation - Hybridization Capture Manual."

Before use, allow the probe pool (HLA Probe) to thaw naturally on ice and mix well. Use 2 µL of probe per reaction according to the instructions.

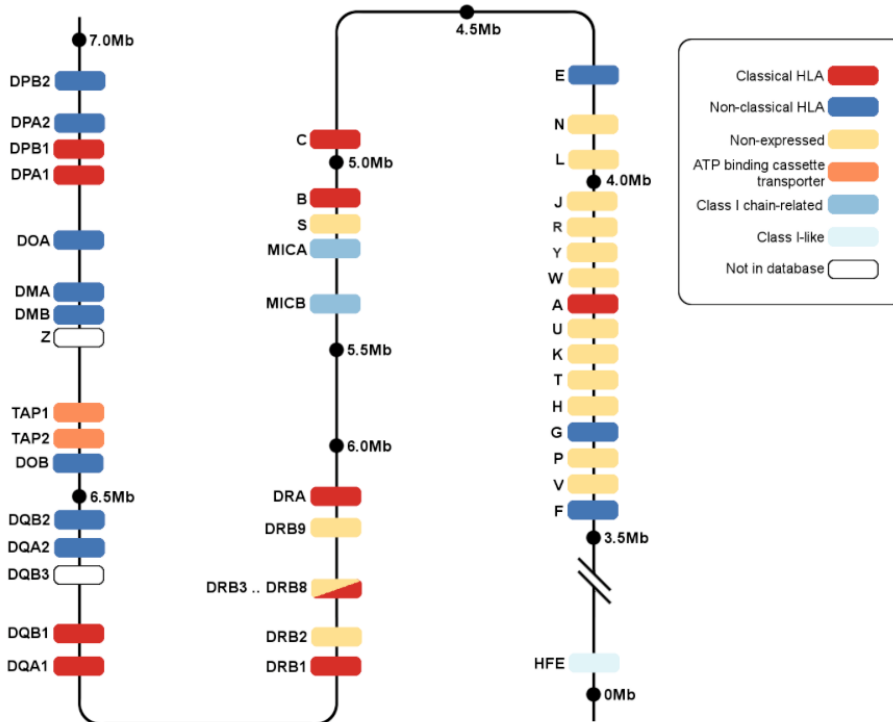
Post-PCR baseline cycle number: 15

* For adding additional regions and analysis BED files, please contact Homgen Biotech Co., Ltd.

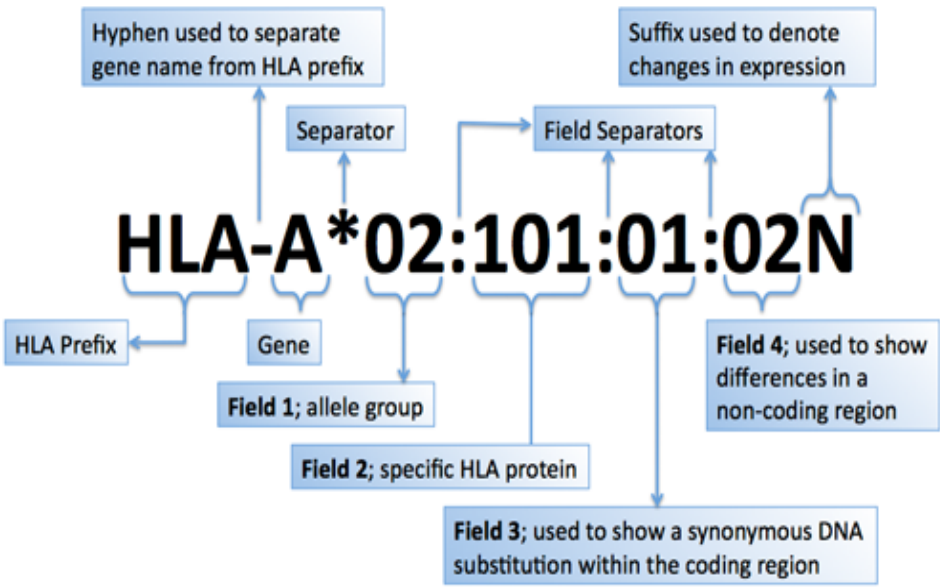
HLA Gene Chromosomal Distribution

Authoritative HLA Website: <https://www.ebi.ac.uk/ipd/imgt/hla/>

HLA Gene Classification: Class I genes, Class II genes, and Class III genes. Details are as follows:



HLA Gene Typing Nomenclature Rules



HLA Gene Mutation Statistics (Release 3.59 | 2025-01)

Numbers of HLA Alleles						
HLA class I alleles						28409
HLA class II alleles						12594
HLA alleles						41003
Other non-HLA alleles						1023
Number of confidential alleles						4
HLA class I						
Gene	A	B	C	E	F	G
Alleles	8556	10346	8657	376	115	176
Proteins	5004	6172	4776	141	22	52
Nulls	449	370	388	10	3	6

HLA class I - Pseudogenes													
Gene	<i>H</i>	<i>J</i>	<i>K</i>	<i>L</i>	<i>N</i>	<i>P</i>	<i>R</i>	<i>S</i>	<i>T</i>	<i>U</i>	<i>V</i>	<i>W</i>	<i>Y</i>
Alleles	82	33	7	6	5	5	2	7	9	7	4	13	3
Proteins	0	0	0	0	0	0	0	0	0	0	0	0	0
Nulls	0	0	0	0	0	0	0	0	0	0	0	0	0

HLA class II														
Gene	<i>DRA</i>	<i>DRB</i>	<i>DQA1</i>	<i>DQA2</i>	<i>DQB1</i>	<i>DQB2</i>	<i>DPA1</i>	<i>DPA2</i>	<i>DPB1</i>	<i>DPB2</i>	<i>DMA</i>	<i>DMB</i>	<i>DOA</i>	<i>DOB</i>
Alleles	78	4812	872	42	2813	41	765	6	2795	7	62	100	121	80
Proteins	17	3168	448	11	1682	9	373	0	1611	0	9	9	16	17
Nulls	0	215	21	0	122	1	33	0	145	0	0	0	1	1

HLA class II - DRB Alleles									
Gene	<i>DRB1</i>	<i>DRB2</i>	<i>DRB3</i>	<i>DRB4</i>	<i>DRB5</i>	<i>DRB6</i>	<i>DRB7</i>	<i>DRB8</i>	<i>DRB9</i>
Alleles	3787	1	523	273	215	4	2	1	6
Proteins	2443	0	399	169	157	0	0	0	0
Nulls	135	0	28	27	25	0	0	0	0

Other non-HLA Genes					
Gene	<i>HFE</i>	<i>MICA</i>	<i>MICB</i>	<i>TAP1</i>	<i>TAP2</i>
Alleles	6	585	307	19	106
Proteins	4	278	49	11	13
Nulls	0	9	25	1	0

HLA Typing Related Bioinformatics Analysis Software

The analytical principles of HLA typing software can be divided into two major categories: the read alignment method and the read assembly method. The read alignment method maps sequencing sample reads to reference sequences of all known HLA genotypes in the database and determines the typing based on the alignment results. The assembly method first constructs larger fragments (contigs) from the reads and then aligns them to all known HLA genotype reference sequences in the database. The assembly method allows reads to be mapped more accurately to the reference sequences, but it requires a higher sequencing depth. Relevant software examples include Athlates, xHLA, HLA-HD, HLA-scan, HISAT-genotype, HLAreporter, Optitype, HLAminer, and others.

Note: Due to the complexity of HLA variation, different analysis software and different database versions may yield different typing results and accuracy. In practical scenarios, some genotypes and 8-digit typing may require further verification by experienced experts, integrating bioinformatics analysis results and population variant frequencies.