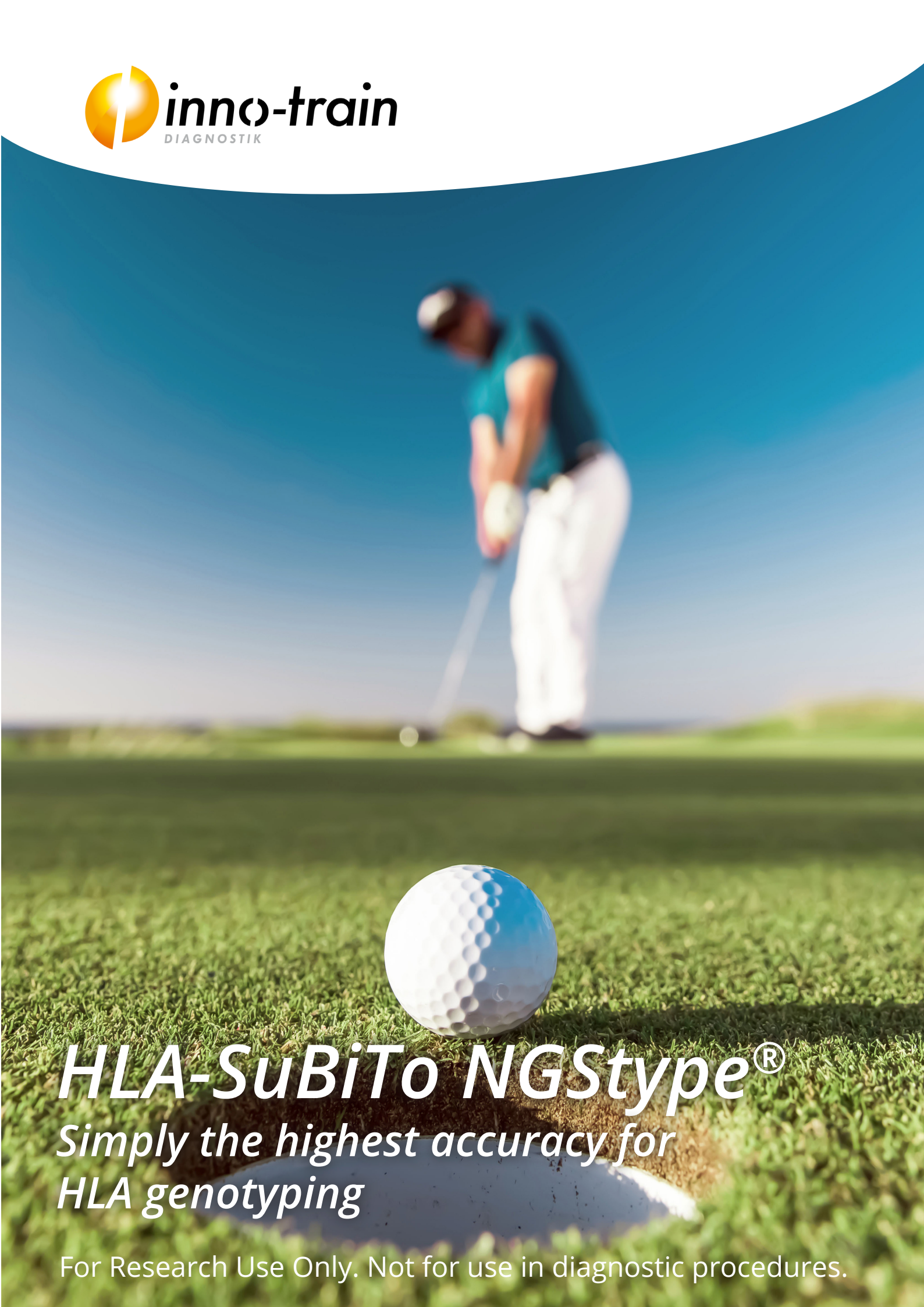
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DIAGNOSTIK



HLA-SuBiTo NGStype®

Simply the highest accuracy for HLA genotyping

For Research Use Only. Not for use in diagnostic procedures.

HLA-SuBiTo NGS*type*®

The perfect solution for your high resolution HLA typing

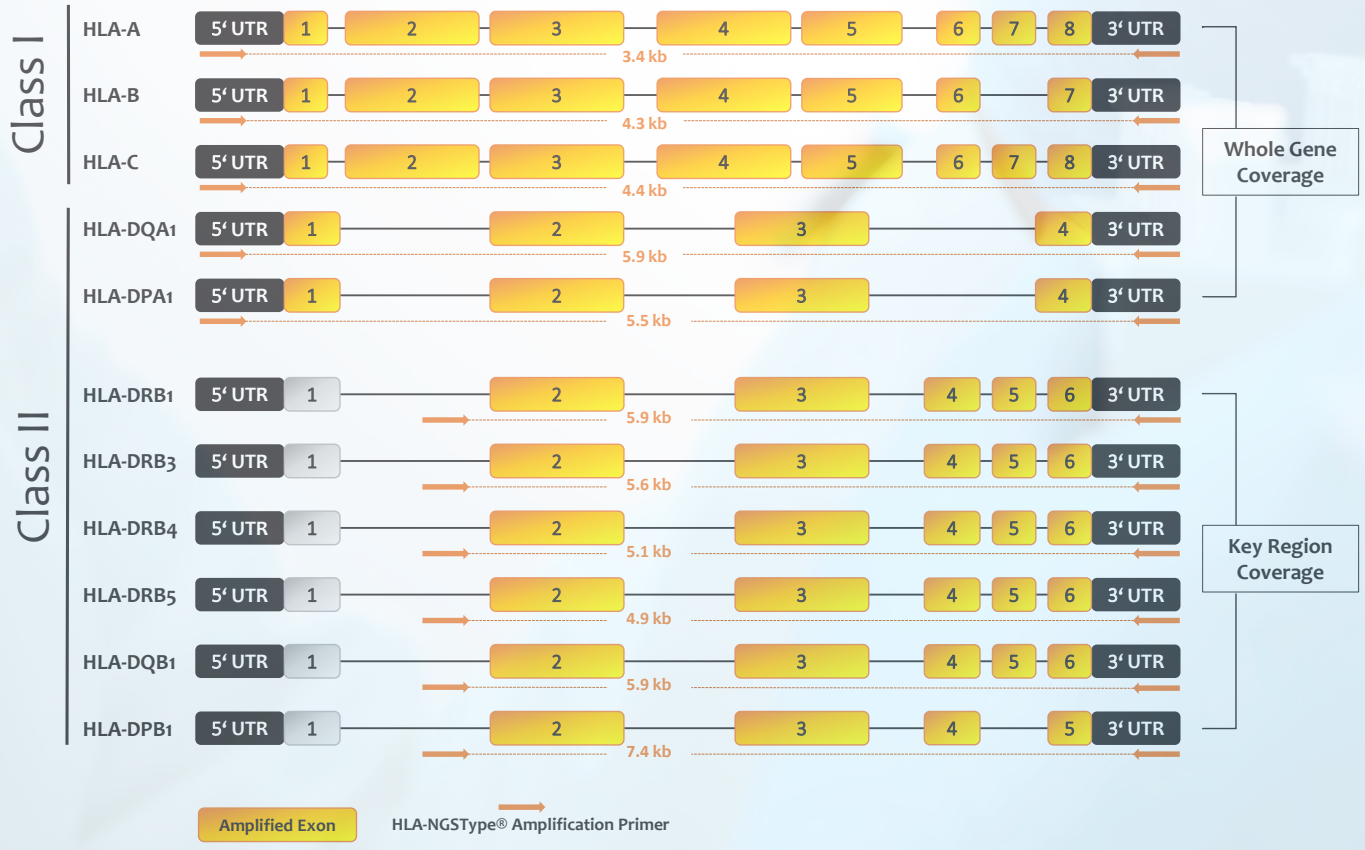
HLA-SuBiTo NGS*type*® uses Next-Generation-Sequencing for high resolution HLA typing of up to 11 loci and many samples in parallel.

It features an easy workflow with long-range PCR, fragmentation with library preparation, and can run on any Illumina NGS system. The collected data is automatically analysed on the convienient and powerful NGS*type*® Software.

The workflow

- Long-Range PCR
- overnight
- Pooling & Purification
- Fragmentation, End prep., Adaptor Ligation
- Size selection
- Final PCR & Purification
- Final Preparation & Run on Sequencer
- overnight
- Data analysis

Coverage of all relevant 11 HLA loci

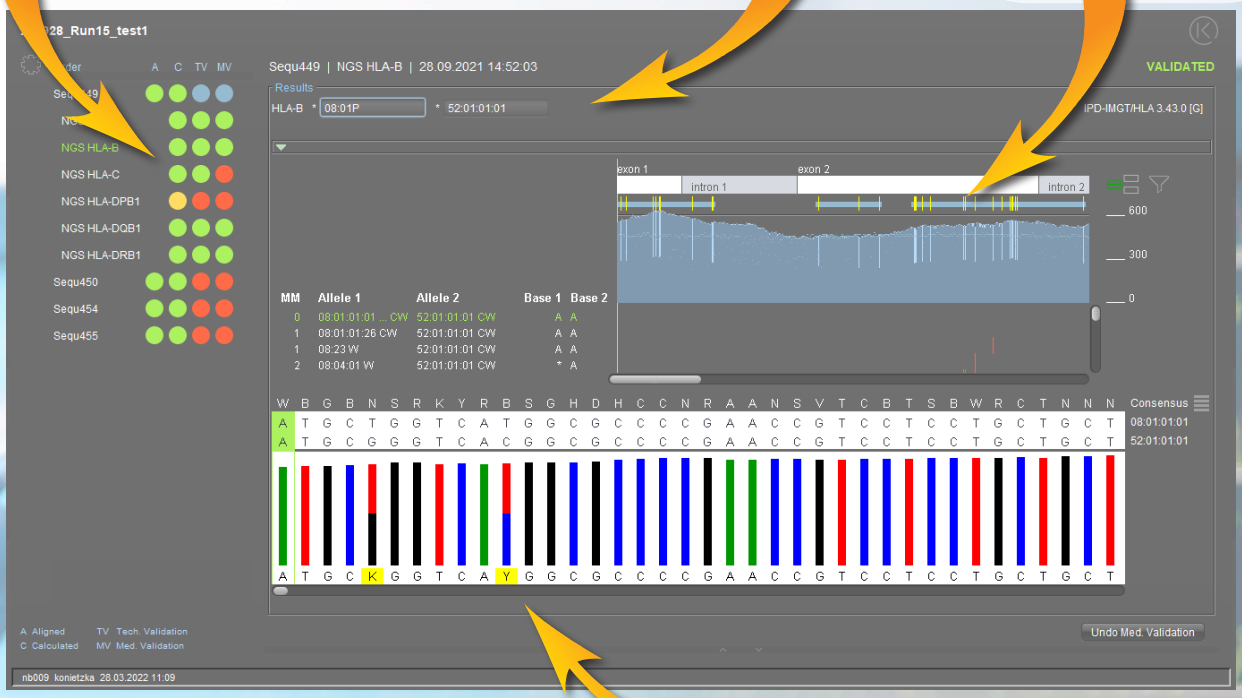


NGS*type*® Software

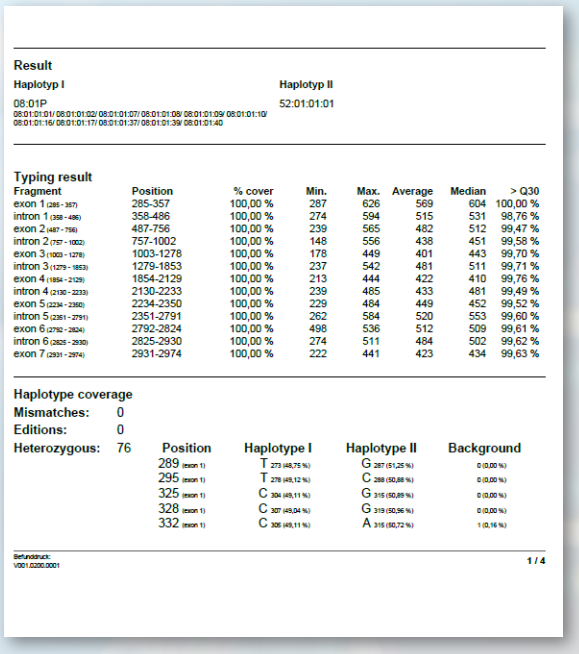
Sample and loci overview with color coding for analysis status.

High resolution results with the ability to switch ambiguities from allele strings to P-/G-groups summary with a simple double-click.

Coverage plot with indicator for heterozygous positions and contigs.



Quantitative representation of each individual base.



Result

Haplotyp I: 08:01P

Haplotyp II: 52:01:01:01

Typing result

Fragment	Position	% cover	Min.	Max.	Average	Median	> Q30
exon 1	285-357	100,00 %	287	626	569	604	100,00 %
intron 1	358-486	100,00 %	274	594	515	531	98,76 %
exon 2	487-756	100,00 %	239	565	482	512	99,47 %
intron 2	757-1002	100,00 %	148	556	438	451	99,58 %
exon 3	1003-1278	100,00 %	178	449	401	443	99,70 %
intron 3	1279-1853	100,00 %	237	542	481	511	99,71 %
exon 4	1854-2129	100,00 %	213	444	422	410	99,76 %
intron 4	2130-2233	100,00 %	239	485	433	481	99,49 %
exon 5	2234-2350	100,00 %	229	484	449	452	99,52 %
intron 5	2351-2791	100,00 %	262	584	520	553	99,60 %
exon 6	2792-2824	100,00 %	498	536	512	509	99,61 %
intron 6	2825-2930	100,00 %	274	511	484	502	99,62 %
exon 7	2931-2974	100,00 %	222	441	423	434	99,63 %

Haplotype coverage

Mismatches: 0

Editions: 0

Heterozygous: 76

Position	Haplotype I	Haplotype II	Background
289 (exon 1)	T 273 (48,75 %)	G 287 (51,25 %)	0 (0,00 %)
295 (exon 1)	T 278 (49,12 %)	C 288 (50,88 %)	0 (0,00 %)
325 (exon 1)	C 304 (49,11 %)	G 315 (50,89 %)	0 (0,00 %)
328 (exon 1)	C 307 (49,04 %)	G 319 (50,96 %)	0 (0,00 %)
332 (exon 1)	C 305 (49,11 %)	A 315 (50,72 %)	1 (0,16 %)

Befundnruck: V001.0200.0001

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Concise information on report

The locus specific report of the NGS*type*® Software contains all necessary information.

Results are displayed as a string of alleles and P-/G-group summary. Valuable information about each exon and intron are listed as well as the ratios for each heterozygous position.

Additionally, a summary report with all analyzed loci for a sample can be exported.

Advantages of HLA-SuBiTo NGS*type*®

- High resolution HLA typing
- 11 loci, 7 loci, and 6 loci versions
- Many samples in parallel
- Long-Range PCR with multiplexed reactions
- Fragmentation: ~400 bp per fragment
- Paired-end reads: 2*150 bp
- Works with all Illumina platforms

	HLA-SuBiTo NGS*type*® 6 loci	HLA-SuBiTo NGS*type*® 7 loci	HLA-SuBiTo NGS*type*® 11 loci
Article No.:	**002 097 024**	**002 098 024**	**002 099 024**
Sample/Kit	24	24	24
Multiplexes	2	2	3
HLA-A	•	•	•
HLA-B	•	•	•
HLA-C	•	•	•
HLA-DPA1			•
HLA-DPB1	•	•	•
HLA-DQA1		•	•
HLA-DQB1	•	•	•
HLA-DRB1	•	•	•
HLA-DRB3			•
HLA-DRB4			•
HLA-DRB5			•

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