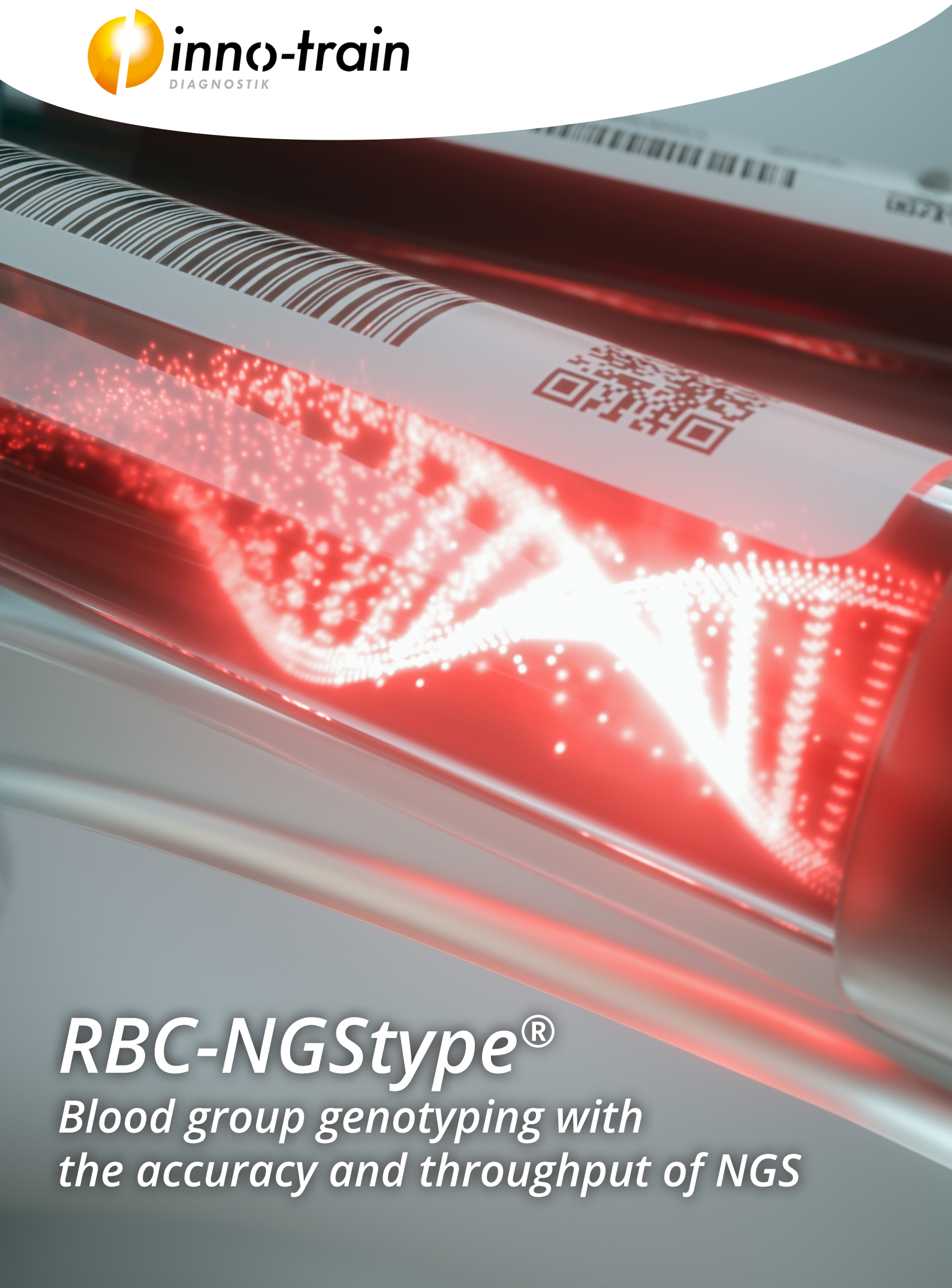
inno-train
DIAGNOSTIK



RBC-NGStype®

Blood group genotyping with the accuracy and throughput of NGS

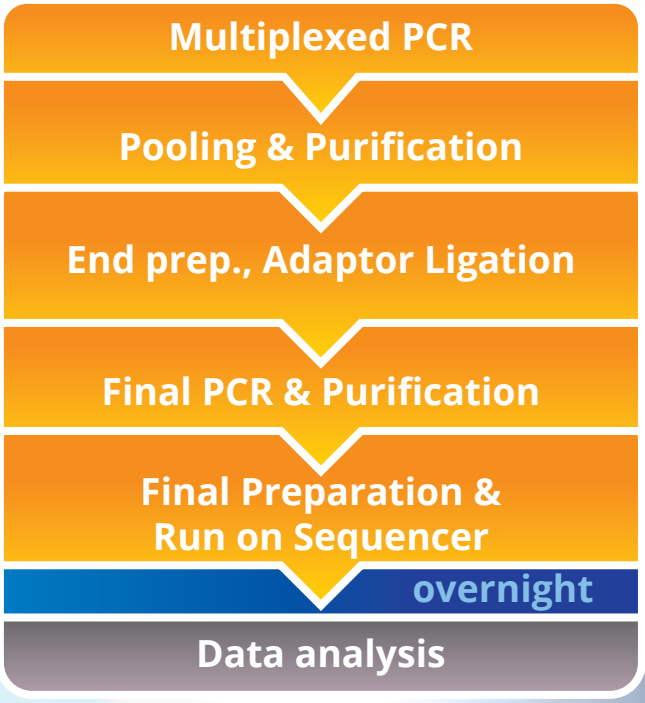
RBC-NGS*type*®

The perfect solution for your high resolution blood group genotyping

RBC-NGS*type*® uses Next-Generation-Sequencing for high resolution typing of the most important blood group systems and many samples in parallel.

It features an easy workflow which can be performed in one day and can run on any Illumina NGS system. The collected data is automatically analysed on the user-friendly and powerful NGS*type*® Software.

The Workflow



Kit Design

Initial PCR:

- Multiplexed primer mixes for initial PCR
- Reaction Mastermix, including Taq
- Control DNA

Library Preparation:

Own and established library preparation workflow can be used.

3rd party recommendations are available.

Data analysis:

- RBC-NGS*type*® Software

ISBT Database

Revolutionize Your Genotyping with our ISBT-based Database and NGS Technology

Our product utilizes Next-Generation-Sequencing technology to align data to our comprehensive database, based on the ISBT list, which includes all stated SNPs and other available sequences.

This database has been developed in collaboration with renowned expert Prof. Dr. C. Gassner, and will be continuously updated with the latest ISBT information to ensure the highest level of accuracy and reliability.

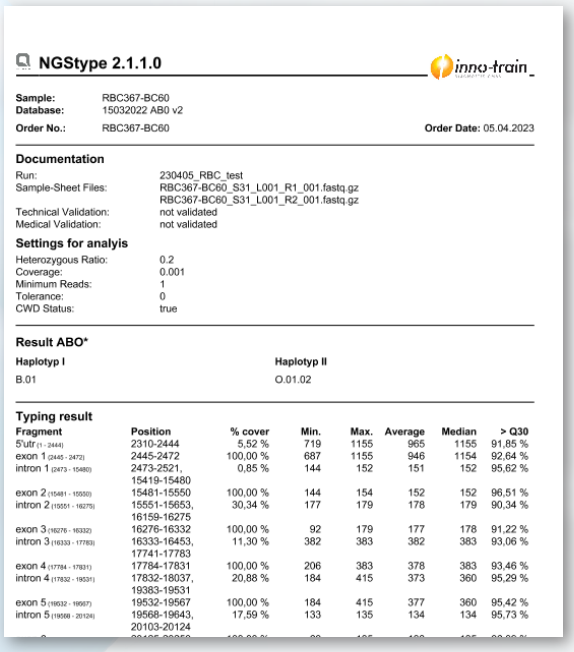
NGS*type*® Software

Sample and loci overview with color code for analysis status.

High resolution results based on ISBT information.

Coverage plot with indicator for heterozygous positions and contigs.

Quantitative representation of each individual nucleotide.



NGStype 2.1.1.0

inno-train

Sample: RBC367-BC60
Database: 15032022 AB0 v2
Order No.: RBC367-BC60 **Order Date:** 05.04.2023

Documentation

Run:	230405_RBC_test
Sample-Sheet Files:	RBC367-BC60_S31_L001_R1_001.fastq.gz RBC367-BC60_S31_L001_R2_001.fastq.gz
Technical Validation:	not validated
Medical Validation:	not validated

Settings for analyis

Heterozygous Ratio:	0.2
Coverage:	0.001
Minimum Reads:	1
Tolerance:	0
CWD Status:	true

Result ABO*

Haplotyp I	Haplotyp II
B.01	O.01.02

Typing result

Fragment	Position	% cover	Min.	Max.	Average	Median	> Q30
5'utr (1 - 2444)	2310-2444	5,52 %	719	1155	965	1155	91,85 %
exon 1 (2445 - 2472)	2445-2472	100,00 %	687	1155	946	1154	92,64 %
intron 1 (2473 - 15480)	2473-2521, 15419-15480	0,85 %	144	152	151	152	95,62 %
exon 2 (15481 - 15550)	15481-15550	100,00 %	144	154	152	152	96,51 %
intron 2 (15551 - 16275)	15551-15653, 16159-16275	30,34 %	177	179	178	179	90,34 %
exon 3 (16276 - 16332)	16276-16332	100,00 %	92	179	177	178	91,22 %
intron 3 (16333 - 17783)	16333-16453, 17741-17783	11,30 %	382	383	382	383	93,06 %
exon 4 (17784 - 17831)	17784-17831	100,00 %	206	383	378	383	93,46 %
intron 4 (17832 - 19531)	17832-18037, 19383-19531	20,88 %	184	415	373	360	95,29 %
exon 5 (19532 - 19567)	19532-19567	100,00 %	184	415	377	360	95,42 %
intron 5 (19568 - 20124)	19568-19643, 20103-20124	17,59 %	133	135	134	134	95,73 %

Concise information on report

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

Valuable information like coverage and quality score 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 RBC-NGS*type*®

- High resolution blood group genotyping
- CORE kit with 48 samples on a Illumina MiSeq Nano (0.3 Gb) Flow Cell in parallel
- Exon PCR with just 2 multiplexed reactions per sample
- Paired-end reads: 2*150 bp
- Works with all Illumina platforms
- Databases based on ISBT tables
- Developed in collaboration with Prof. Dr. Christoph Gassner

	RBC-NGS*type*® CORE	RBC-NGS*type*® enCORE	RBC-NGS*type*® enCORE+
Article No.:	**001 110 024**	**001 120 024**	**001 130 024**
Multiplexes	**2**	**2**	**2**
Available	**Yes**	**Coming soon**	**Coming soon**
Blood Group Systems	ABO	Lutheran	P1PK
	Rh	Yt	Diego
	MNS	Dombrock	Scianna
	Kell	Colton	Chido/Rodgers
	Kidd	Landsteiner-Wiener	Gerbich
	Duffy	Knops	Cromer
		Vel	Indian
	All exons and relevant non-coding region amplified		John Milton Hagen
			Rh-asso. glycoprotein
	Key exons and relevant non-coding region amplified		JR
			LAN

QMS 05.23

inno-train DIAGNOSTIK

Worldwide Headquarters

inno-train Diagnostik GmbH
Niederhöchstädter Str. 62
61476 Kronberg
Deutschland

+49 (0)6173 60 79 30
info@inno-train.de

North American Division

inno-train Diagnostik

108 Utica Street
Clinton, NY 13323
USA

+1 (888) 352 2196
info@innotrain.org