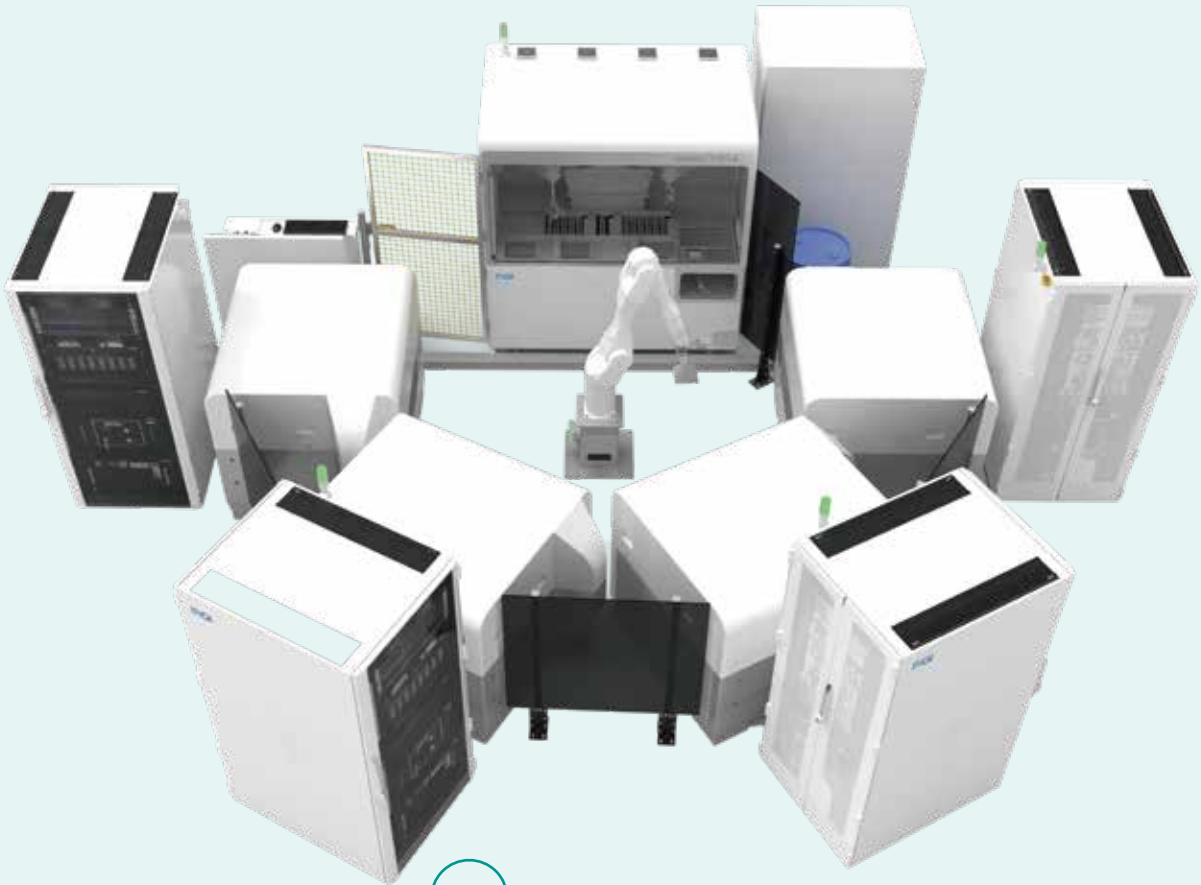
Packages for Population Genomics

Ultra-high Throughput with Flexible and Customizable Automation



Main Features

- Unique packages for population genomics
- Achievable for 50k high-depth WGS per year per set
- Flexible customization for the full workflow from 50k to 1 million genomes sequenced annually
- Automation from sample to report

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◎ DNBSEQ-T10×4RS Introduction

DNBSEQ-T10×4RS is an ultra high-throughput sequencer based on DNBSEQ™ sequencing technology. It is designed to meet the requirement of population genomics sequencing market.

Sequencing Specification

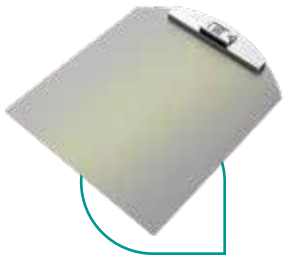
Read length	PE100	PE150
Effective reads**	360 B	256 B
Average data output	72 Tb	76.8 Tb
Run time***	96 h	108 h
Data quality****	Q30 ⩾ 85%	Q30 ⩾ 85%

One DNBSEQ-T10×4RS supports the operation of 8 sequencing slides simultaneously, producing up to 20Tb data per day(about 200 whole human genomes sequenceing data*). A single set of DNBSEQ-T10×4RS can produce more than 50,000 WGS per year.

* The sequencing depth is 30×;
** The sequencing data was measured by running 8 sequencing slides;
*** Run time includes DNB loading and sequencing. FASTQ file generation does not take up sequencer time;
**** ⩾Q30 base ratio obtained by sequencing WGS standard library using DNBSEQ-T10×4RS

Innovative Sequencing Technologies

The dip-immersion biochemistry, which ensures more uniform biochemical reaction of sequencing slide with larger size, as well as significantly saves the cost of reagents.



Sequencing slide
DNB loading density is up to 4 million/mm^2, and one slide can load 70G DNB spots.

Different from ordinary sequencing slide and closed reaction systems used in most platforms, DNBSEQ-T10×4RS uses dip-immersion biochemistry and open systems firstly to achieve the best balance among sequencing read length, throughput, data quality and cost.

Sequencing Data Quality

	PE100		
Sample	NA12878	NA24694	NA24695
Clean data rate	99.97	99.98	99.98
Clean Q30(%)	91.565	91.625	91.62
Mapping rate(%)	99.81	99.81	99.81
Duplicate rate(%)	1.03	0.83	0.88
Mismatch rate(%)	0.3	0.3	0.3
Average sequencing depth(×)	30.66	30.76	30.71
Coverage(%)	99.2	99.89	99.21
Coverage at least 20×(%)	94.39	90.91	94.39
SNP_Precision	0.9994	0.9991	0.9992
SNP_Sensitivity	0.9908	0.9929	0.9927
INDEL_Precision	0.9901	0.9918	0.9917
INDEL_Sensitivity	0.9807	0.9803	0.9802

Human reference genomes NA12878, NA24694 and NA24695 were sequenced using DNBSEQ-T10×4RS. The bioinformatic analysis of 30×WGS data showed that the accuracy and sensitivity of SNPs exceeded 99%, and the accuracy and sensitivity of Indel also exceeded 98%, reaching industry-leading level.

- ◎ Sample —— Human Cell Line
- ◎ Library Prep Kit — MGIEasy FS PCR-Free DNA Library Prep Set
- ◎ Sequencing — PE100
- ◎ Data analysis — MegaBOLT

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◎Total Package – Customizable and Automated

Original sample

Total Package – Basic

Total Package – Advanced

1 Automated Sample Pretreatment

MGISP-960, a high-throughput automated workstation, can easily complete 192 nucleic acid extraction per day, which will be used in library construction process.

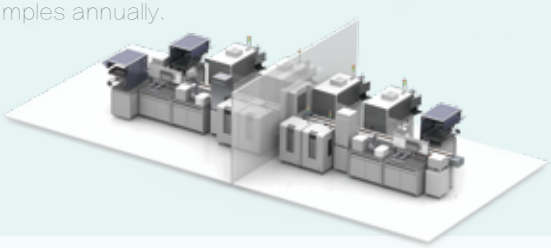
MGIGLab-S, an automated blood fractionation production line, is applied to the whole fractionation workflow and walk-away automation from blood to plasma / buffy coat, enabling annual output of 500,000 blood samples.

Nucleic acid

2 Automated Library Production Line

MGISP-96XL, a high-throughput automated workstation, is designed for fully automation of high-throughput sequencing library construction process. Three sets of MGISP-96XL are capable to realize annual preparation of 50,000 samples.

MGIGLab-L, an automated library preparation production line, integrates different MGI and third-party instruments with robot. It adopts the concept of workstation assembly line, to accomplish automated sequencing library preparation with the capability of 300,000~500,000 samples annually.



Sequencing libraries

3 High Throughput Sequencing

One DNBSEQ-T10×4RS can produce 50,000 WGS* per year.

More DNBSEQ-T10×4RS sequencing systems can be deployed for >50,000 WGS sequencing per year.

Sequencing raw data

4 Automated Data Processing and LIMS System

ZTRON: a buddy to high-throughput sequencers, is applied to automatic bioinformatics analysis, storage and governance of massive sequencing data. It also contains a software system for data management in the whole cycle, from biosample management, laboratory production, bioinformatics analysis to data governance.

ZTRON architecture – Basic

Scalability

1. Storage upgradable to 1PB, support≥100,000 WGS sequencing;
2. Three-level data analysis: Write FQ, alignment and variant detection, third-party analysis and application;
3. ZLIMS could be upgraded to ZLIMS Elite, to support larger sequencing center.

ZTRON architecture – Advanced

Report

* Calculation is based on human WGS sequenced at 30× depth.

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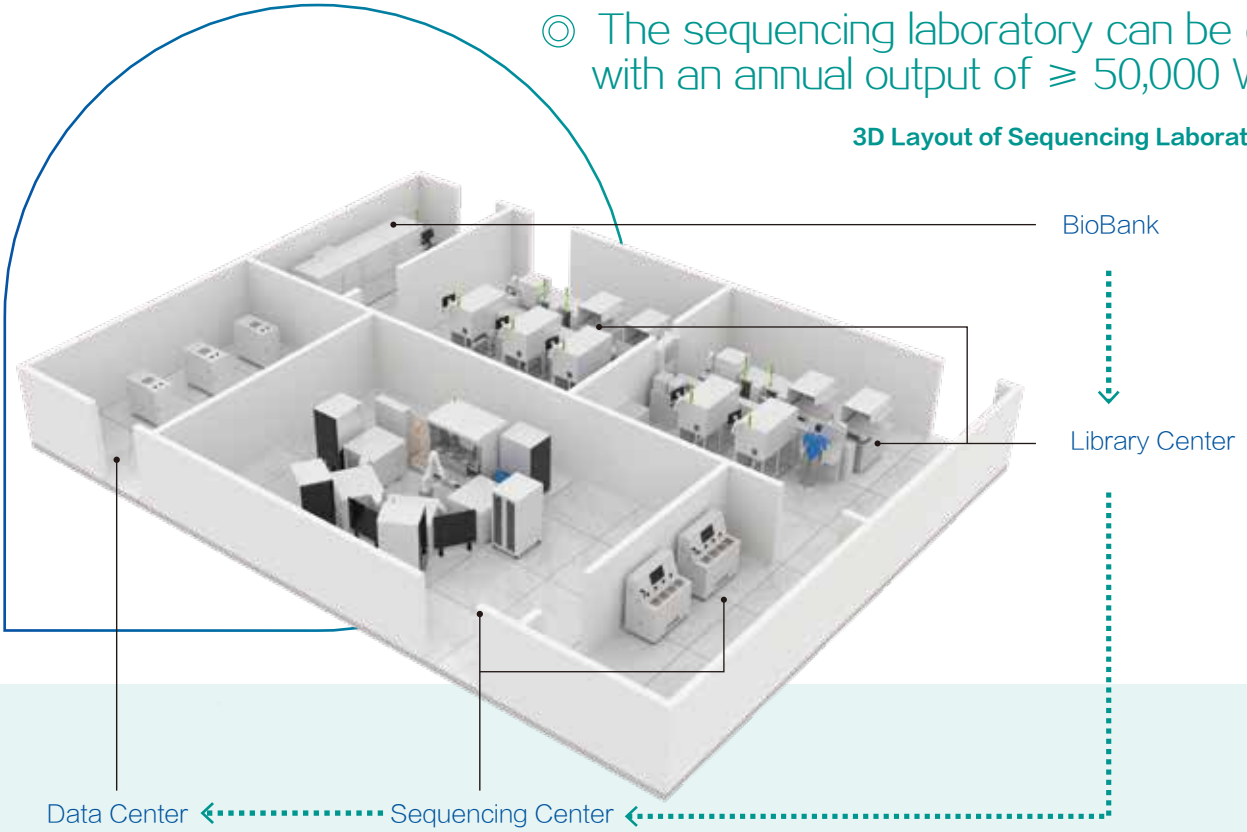
◎ The sequencing laboratory can be customized with an annual output of ⩾ 50,000 WGS

3D Layout of Sequencing Laboratory Total Package



Demo Planning for Annual Sequencing of 50,000 and 500,000 WGS*

	Zone	Biobank	Library center		Sequencing center	Data center
			Library preparation	DNB preparation		
	Main Function	Whole blood separated into plasma and buffy coat for gDNA extraction	From gDNA to library construction	From library to make DNB	DNB loading and sequencing	Write FQ, data analysis, laboratory management system
50,000 WGS per year	**Area(m²)****	50	50	50	100	20
	Key Equipment	MGISP-960	MGISP-96XL	MGISP-96XL	DNBSEQ-T10×4RS	ZLIMS/ZTRON/ MegaBOLT Pro
500,000 WGS per year	**Area(m²)**	100	150	150	500	50
	Key Equipment	MGIGLab-S MGISP-960	MGIGLab-L	MGISP-96XL	DNBSEQ-T10×4RS	ZLIMS Elite/ZTRON/ MegaBOLT Pro

* Recommended equipment quantity, configuration and site area for annual sequencing capacity of 50,000~500,000 WGS.
** The recommended area is only for core functional zone. The actual area should be determined by the on-site conditions.

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*Unless otherwise informed, this StandardMPS sequencing reagent is not available in Germany, UK, Sweden, and Switzerland.

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