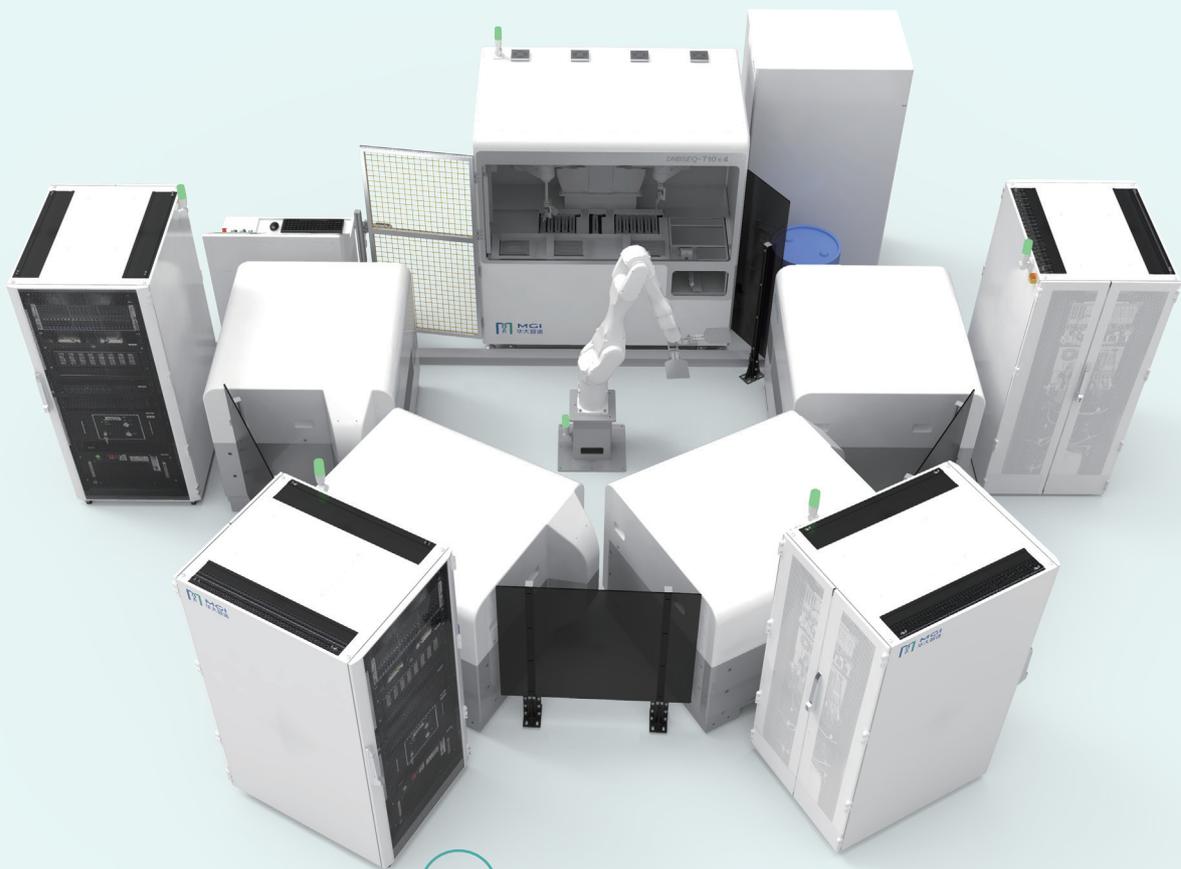


Packages for Population Genomics

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

© 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.

| | |
|---------------------|-----------|
| Read length | PE100* |
| Effective reads** | 360G |
| Average data output | 72Tb |
| Run time*** | 96h |
| Data quality**** | Q30 ≥ 85% |

Sequencing Specification

One DNBSEQ-T10 × 4RS supports the operation of 8 sequencing slides simultaneously, producing up to 20Tb data per day (about 200 whole human genomes sequenced at 30 ×). A single set of DNBSEQ-T10 × 4RS can produce more than 50,000 WGS per year.

* PE100 sequencing is recommended, PE150 will be available by 2021 Q2;

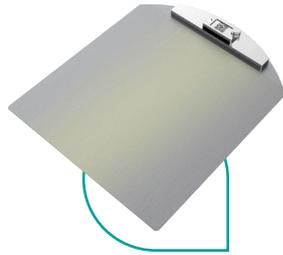
** The sequencing data was measured by running 8 sequencing slides;

*** 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.



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/mm², and one slide can load 70G DNB spots.

Innovative Sequencing Technologies

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.

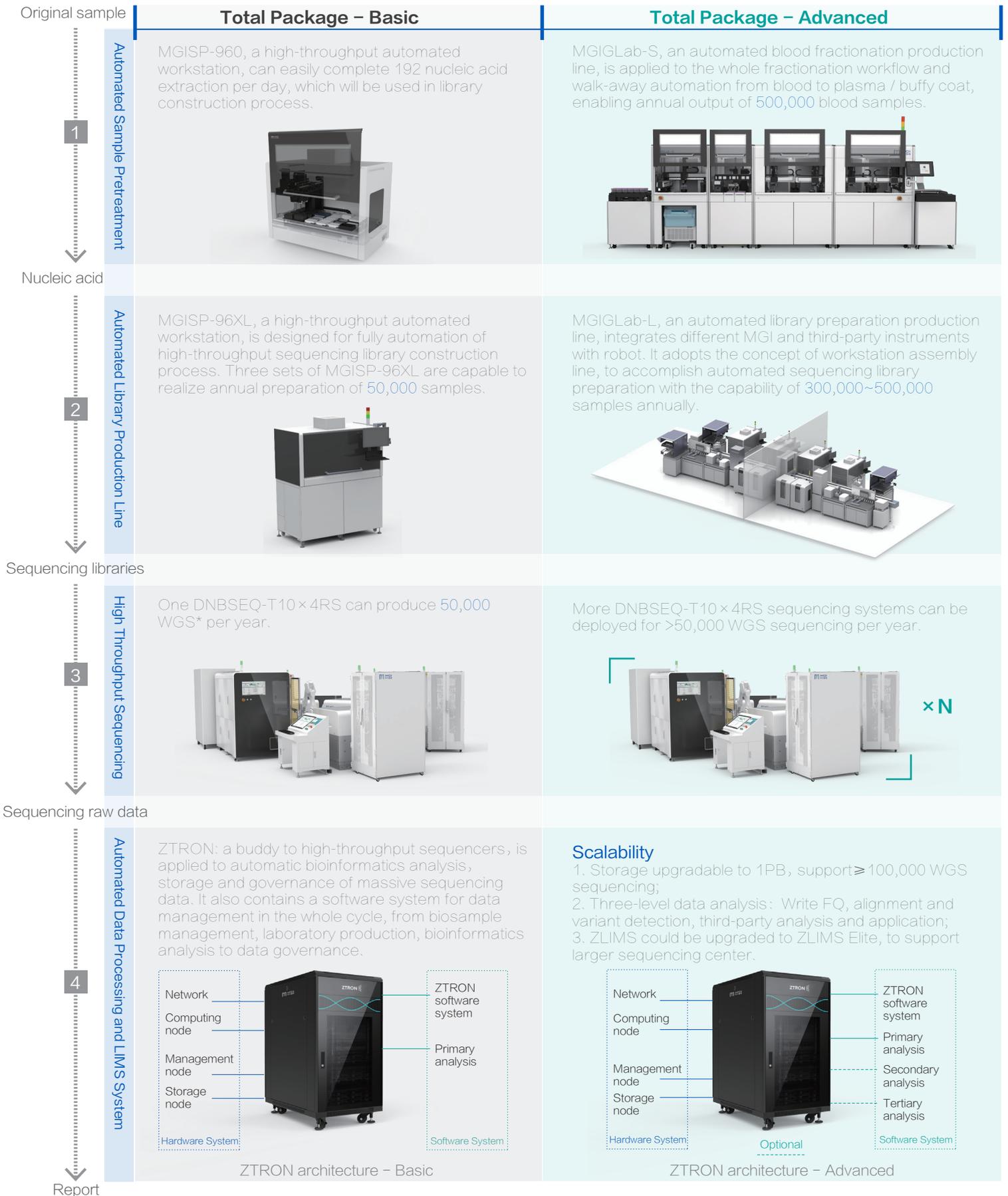
Sequencing Data Quality

| | 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(x) | 30.66 | 30.76 | 30.71 |
| Coverage(%) | 99.2 | 99.89 | 99.21 |
| Coverage at least 20x(%) | 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.

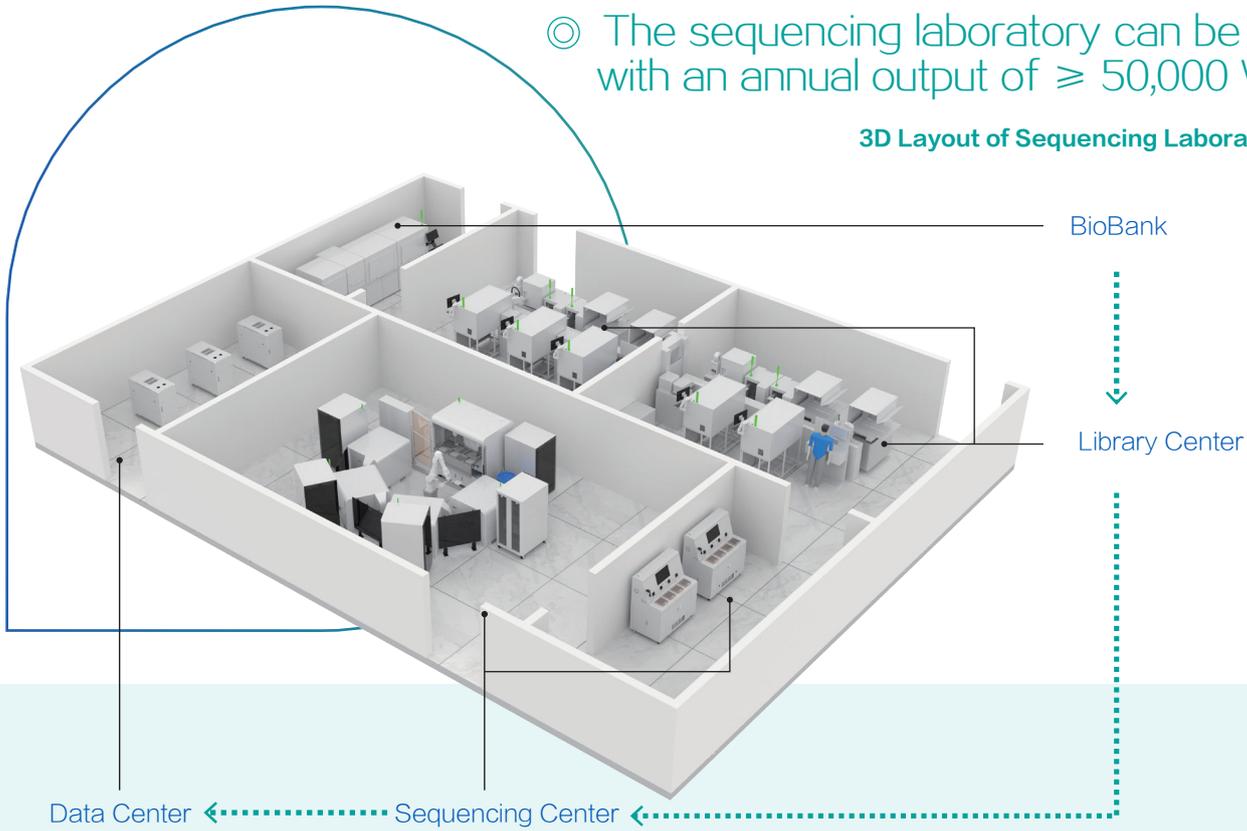
- © Sample — Human Cell Line
- © Library Prep Kit — MGIEasy FS PCR-Free DNA Library Prep Set
- © Sequencing — PE100
- © Data analysis — MegaBOLT

©Total Package – Customizable and Automated



© The sequencing laboratory can be customized with an annual output of $\geq 50,000$ 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 | MGI Lab-S MGISP-960 | MGI Lab-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.

MGI Tech Co., Ltd.

Building 11, Beishan Industrial Zone, Yantian District, Shenzhen, CHINA

www.mgi-tech.com

MGI-service@mgi-tech.com

Twitter: https://twitter.com/MGI_BGI

LinkedIn: <https://www.linkedin.com/company/mgi-bgi>

4000-966-988

FOR RESEARCH USE ONLY.

Copyright Disclaimer: The copyright of this brochure is solely owned by MGI Tech Co., Ltd. The information included in this brochure or part of, including but not limited to interior design, cover design and icons, is strictly forbidden to be reproduced or transmitted in any form, by any means (e.g. electronic, photocopying, recording, translating or otherwise) without the prior written permission by MGI Tech Co., Ltd. All the trademarks or icons in the brochure are the intellectual property of MGI Tech Co., Ltd. and their respective producers.

*Unless otherwise informed, all sequencers and sequencing reagents are not available in Germany, USA, Spain, UK, Hong Kong, Sweden, Belgium and Italy.

Version: February 2022 | MGPA0402202

Information in this brochure is updated to [22/2/2022] and only for your reference. In no event shall the brochure be regarded as warranty or commitment made by MGI Tech Co., Ltd. All rights and obligations shall subject to final executed agreement.

Website

