

# SURFSeq™



Ultra-high Throughput Sequencing System



**Sequencing Powerhouse: Unleash the Genetic Potential**

## Superb Data Output



- Ultra-high throughput: 14 Tb/Run
- Powerful productivity: 9 Tb/day, 20,000+ WGS (30 ×)/year

## Ultra-high Data Quality



- Innovative sequencing chemistry+ AI based recognition algorithm
- Capable of producing  $\geq 90\%$  of output bases with a Q40 score

## User-friendly Design



- Automated individual lane loading for up to eight lanes per flow cell
- Allow customer to obtain data from different applications of the same sequencing run
- Support to resuming from the break-point to continue sequencing
- Post-run wash performed automatically after every sequencing run

# Product Parameter

| Flow Cell Type | Lane | Throughput <sup>1</sup> (Reads/FC) | Sequencing Reagent Type | Read Length <sup>1</sup> | Output (FC ×2) | Data Quality <sup>1</sup> |      | TAT <sup>2</sup> (Hr) |  |  |
|----------------|------|------------------------------------|-------------------------|--------------------------|----------------|---------------------------|------|-----------------------|--|--|
|                |      |                                    |                         |                          |                | Q30                       | Q40  |                       |  |  |
| FCM            | 4    | 11.7 B                             | 50 cycles               | SE50                     | 0.6 Tb ×2      | ≥90%                      | ≥90% | 10                    |  |  |
|                |      |                                    | 100 cycles              | SE100                    | 1.2 Tb ×2      |                           |      | 13                    |  |  |
|                |      |                                    | 200 cycles              | PE50                     |                |                           |      | 19                    |  |  |
|                |      |                                    | 300 cycles              | PE100                    | 2.3 Tb ×2      |                           |      | 24                    |  |  |
|                |      |                                    | 50 cycles               | PE150                    | 3.5 Tb ×2      |                           |      | 24                    |  |  |
| FCH            | 8    | 23.3 B                             | 50 cycles               | SE50                     | 1.2 Tb ×2      | ≥90%                      | ≥90% | 17                    |  |  |
|                |      |                                    | 100 cycles              | SE100                    | 2.3 Tb ×2      |                           |      | 22                    |  |  |
|                |      |                                    | 200 cycles              | PE50                     |                |                           |      | 29                    |  |  |
|                |      |                                    | 300 cycles              | PE100                    | 4.7 Tb ×2      |                           |      | 36                    |  |  |
|                |      |                                    | 50 cycles               | PE150                    | 7 Tb ×2        |                           |      | 36                    |  |  |

1. This parameter is obtained based on the average of multiple test results of GeneMind P3 standard library. The data output and the proportion of high quality data are affected by factors such as sample type, sample quality and effective flow cell utilization. The actual performance may vary.

2. The sequencing time to complete the sample read length plus the paired-end index (8+8), includes the time from sample loading to base calling, and generating basefile.

# Application<sup>3</sup>

| Applications | Reads length | Data/sample | FCM | FCH |
|--------------|--------------|-------------|-----|-----|
| WGS          | PE150        | 110 Gb      | 26  | 52  |
| Single cell  | PE150        | 120 Gb      | 24  | 48  |
| ctDNA        | PE150        | 50 Gb       | 48  | 96  |
| WES          | PE150        | 11 Gb       | 256 | 512 |

3 The above sample numbers for different applications are only for reference. Users need to adjust the sample numbers according to the actual experiment. ctDNA means 2.5 M panel.

Note: This document is based on company data of October, 2025, and is provided for reference only.

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This document does not constitute any offer, commitment, or warranty.

## Ordering Information

| Catalog NO. | Sequencer   |
|-------------|---|
| SQ00063     | SURFSeq Q Sequencing System Set                       |
| Catalog NO. | Sequencing reagent kit                                |
| S000379     | SURFSeq Q Sequencing Reagent kit V1.0 (FCM 50cycles)  |
| S000380     | SURFSeq Q Sequencing Reagent kit V1.0 (FCM 100cycles) |
| S000381     | SURFSeq Q Sequencing Reagent kit V1.0 (FCM 200cycles) |
| S000382     | SURFSeq Q Sequencing Reagent kit V1.0 (FCM 300cycles) |
| S000383     | SURFSeq Q Sequencing Reagent kit V1.0 (FCH 50cycles)  |
| S000384     | SURFSeq Q Sequencing Reagent kit V1.0 (FCH 100cycles) |
| S000385     | SURFSeq Q Sequencing Reagent kit V1.0 (FCH 200cycles) |
| S000386     | SURFSeq Q Sequencing Reagent kit V1.0 (FCH 300cycles) |

## System Specification

|                        |   |
|------------------------|---|
| Dimensions (W × D × H) | 975 mm × 921 mm × 1570 mm   |
| Net Weight             | < 500 kg  |
| Power                  | < 6000 W  |
| Power Requirements     | 200-240 V~, 50/60 Hz  |
| Operating Environment  | Temperature: 19°C-25°C<br>Realvtive humidity: 20%-80% ( non-condensing)<br>Altitude: below 2000 meter                                     |
| Computer Configuration | CPU: Intel Xeon Gold 6326 ×2<br>Memory: 2 TB<br>Solid-state drive: 3.7 TB<br>Hard disk drive: 76.3 TB<br>Operating system: Windows 10 ×64 |

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