

# SURFSeq™ 5000

Tb level bench-top

high-throughput sequencing platform



## Product Parameter

| Flowcell | Lane | Throughput<br>(Reads/FC) | Type       | Read Length | Data output<br>(FC × 2) <sup>1</sup> | Q value<br>(Balanced mode) | TAT <sup>2</sup> (h) |
|----------|------|--------------------------|------------|-------------|--------------------------------------|----------------------------|----------------------|
| FCM      | 4    | 500 M                    | 100 cycles | SE100       | 50 Gb × 2                            | Q30 ≥ 90%<br>Q40 ≥ 85%     | 12                   |
|          |      |                          |            | PE50        | 50 Gb × 2                            |                            | 12                   |
|          |      |                          | 200 cycles | PE100       | 100 Gb × 2                           |                            | 18                   |
|          |      |                          | 300 cycles | PE150       | 150 Gb × 2                           |                            | 22                   |
|          |      |                          | 600 cycles | PE300       | 300 Gb × 2                           |                            | 48                   |
| FCH      | 4    | 2000 M                   | 50 cycles  | SE50        | 100 Gb × 2                           |                            | 14                   |
|          |      |                          | 100 cycles | SE100       | 200 Gb × 2                           |                            | 21                   |
|          |      |                          |            | PE50        | 200 Gb × 2                           |                            | 21                   |
|          |      |                          | 200 cycles | PE100       | 400 Gb × 2                           |                            | 26                   |
|          |      |                          | 300 cycles | PE150       | 600 Gb × 2                           |                            | 30                   |
| FCP      | 4    | 3600 M                   | 50 cycles  | SE50        | 180 Gb × 2                           |                            | 16                   |
|          |      |                          | 100 cycles | SE100       | 360 Gb × 2                           |                            | 24                   |
|          |      |                          | 200 cycles | PE100       | 720 Gb × 2                           |                            | 32                   |
|          |      |                          | 300 cycles | PE150       | 1.1 Tb × 2                           |                            | 38                   |

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 TAT (turnaround time) for a standard run (paired-end 8+8 indexing) encompasses the entire process from library loading to the generation of base-called sequence files.

### Main Features

|                                         |                                                                                       |
|-----------------------------------------|---------------------------------------------------------------------------------------|
| Provide various flow cell types         | Individually addressable flow cell lanes with manual onboard independent lane loading |
| Support one or two flow cells in a time | User-friendly interface to easily switch read/index sequence                          |
| Obtain data in real-time at high-speed  | Obtain data in batches based on different applications in one run                     |
| RFID recognize cartidge information     | Automatical post-run wash                                                             |

## Application

| Application                   | Reads length | Data/sample | Number of Samples / FC <sup>3</sup> |       |        |
|-------------------------------|--------------|-------------|-------------------------------------|-------|--------|
|                               |              |             | FCM                                 | FCH   | FCP    |
|                               |              |             | 500 M                               | 200 M | 3600 M |
| NIPT Pro                      | SE50         | 20 M reads  | NA <sup>4</sup>                     | 64    | 120    |
| WES                           | PE150        | 11 Gb       | 12                                  | 48    | 84     |
| Large Oncology Panel (Tissue) | PE150        | 6 Gb        | 16                                  | 96    | 164    |
| Large Oncology Panel (Plasma) | PE150        | 50 Gb       | 2                                   | 8     | 16     |
| WGS                           | PE150        | 110 Gb      | 1                                   | 4     | 8      |
| Single cell RNA-seq           | PE150        | 120 Gb      | 1                                   | 4     | 8      |

3. The above sample numbers for different applications are only for reference. Users need to adjust the sample numbers according to the actual experiment.
4. NA means not applicable.

# Total Solution

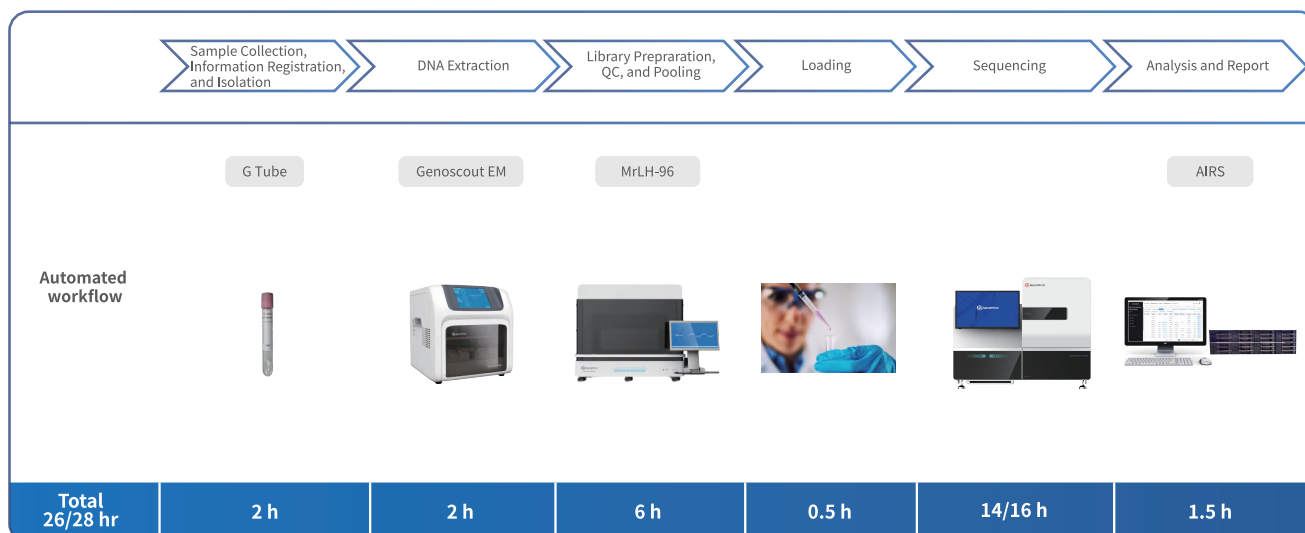
## NIGM™

## Non-invasive Prenatal Testing (NIPT) of GeneMind

- **Simple** Test from a tube of 10 ml maternal blood sample as early as 9 gestational weeks
- **Accurate** Proven >99% sensitivity based on a test of more than 100,000 pregnancies
- **Fast & Convenient** From sample to report: 26/28 hours  
Simplified operation: Automated and localized data analysis and report
- **Flexibility** Offering flexible options for both manual and automated workflows

| NIPT Standard                                                                                                                                                                                                                                                | NIPT Plus                                                                                                                                                                                                                                                                                                       | NIPT Pro                                                                                                                                                                                                                                                                                                        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <ul style="list-style-type: none"> <li>▶ Trisomy 21, 18, 13</li> <li>▶ 6 Sex Chromosome Aneuploidies (SCAs)<br/>(XO/XXX/XXY/XYX/XO+XY/XXX+XY)</li> <li>▶ Other 19 autosomal Aneuploidies</li> <li>▶ Sex identification, fetal fraction estimation</li> </ul> | <ul style="list-style-type: none"> <li>▶ Trisomy 21, 18, 13</li> <li>▶ 6 Sex Chromosome Aneuploidies (SCAs)<br/>(XO/XXX/XXY/XYX/XO+XY/XXX+XY)</li> <li>▶ Other 19 autosomal Aneuploidies</li> <li>▶ 60 Microdeletion/duplications syndromes</li> <li>▶ Sex identification, fetal fraction estimation</li> </ul> | <ul style="list-style-type: none"> <li>▶ Trisomy 21, 18, 13</li> <li>▶ 6 Sex Chromosome Aneuploidies (SCAs)<br/>(XO/XXX/XXY/XYX/XO+XY/XXX+XY)</li> <li>▶ Other 19 autosomal Aneuploidies</li> <li>▶ 90 Microdeletion/duplications syndromes</li> <li>▶ Sex identification, fetal fraction estimation</li> </ul> |

| Parameter                                                                   | NIPT Standard                            | NIPT Plus               | NIPT Pro                |
|-----------------------------------------------------------------------------|------------------------------------------|-------------------------|-------------------------|
| Sample Volume                                                               | 10 mL of a single tube of maternal blood |                         |                         |
| Library preparation                                                         | PCR                                      |                         |                         |
| Method                                                                      | Low-pass whole genome sequencing         |                         |                         |
| Number of samples per run (1 Positive Control +1 Negative Control included) | 1 FCH: 160<br>1 FCP: 300                 | 1 FCH: 96<br>1 FCP: 180 | 1 FCH: 64<br>1 FCP: 120 |
| Read length                                                                 | SE 50                                    |                         |                         |
| Average Unique Reads / sample                                               | ≥ 7 M                                    | ≥ 12 M                  | ≥ 20 M                  |
| Report generation                                                           | Local analysis and report system         |                         |                         |



## Total Solution

# GMExome V2 GeneMind Whole Exome Sequencing solution

It specifically engineered for the clinical research of hereditary diseases. Developed in accordance with the latest expert consensus and continuously updated disease and variant databases, this solution facilitates precise molecular diagnosis for patients and their families with suspected genetic disorders, thereby helping to address the diagnostic challenges posed by the heterogeneity and complexity of rare diseases.

### ■ Comprehensive coverage of pathogenic variants

Almost completely covers pathogenic or likely pathogenic variants in the ClinVar and LOVD databases.

### ■ Supports CNVs detection

1. Single-exon level for key genes (e.g., DMD, Thalassemia);
2. 10 kb high-density probes for high-frequency pathogenic regions (e.g., 22q11.2, 1p36);
3. Genome-wide 200 kb spaced backbone probes (optional 50/100 kb densification);
4. Comprehensive detection of CNVs  $\geq 1$  Mb.

### ■ Mitochondria genes is incorporated

### ■ Supports gender quality control

| Parameter                   |                                               |
|-----------------------------|-----------------------------------------------|
| Covered Genes               | 20,761 genes                                  |
| Sample type                 | gDNA / Tissue / Blood                         |
| Input quantity              | 50 ng DNA                                     |
| Panel size                  | Target size: 36.79 Mb, Capture size: 53.55 Mb |
| Fold 80                     | 1.51-1.60                                     |
| On-target rate (%)          | 80-83                                         |
| Number of samples per run   | 1 FCM: 12<br>1 FCH: 48<br>1 FCP: 84           |
| Read length                 | PE150                                         |
| Effective throughput/sample | Around 11 Gb (>100× coverage)                 |
| Report generation           | Local analysis and report system              |

#### Step 1 Sample Preparation



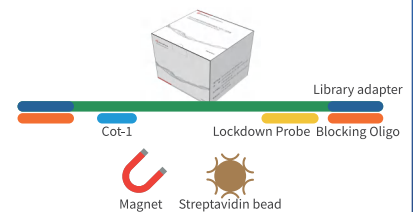
GenoScout EM

#### Step 2 Library Preparation



MrLH-96

#### Step 3 Targeted enrichment by probe hybridization



Exome Enrichment kit

#### Step 4 QC final library



Microplate reader

#### Step 5 Sequencing



SURFSeq™ 5000

#### Step 6 Data Analysis



AIRS

## Total Solution

# GeneMind™ Comprehensive Pan-Cancer (580 genes) Solution

GeneMind comprehensive pan-cancer solution using GeneMind self-developed GenoScout Onco-580 gDNA Library Preparation Kit targeted over 580 related to solid tumors based on hybrid capture technology, covering all major variant classes plus gene signatures (TMB, MSI), which are related to targeted therapy, chemotherapy, immunotherapy and hereditary tumor risk assessment. GeneMind pan-cancer solution provides a comprehensive medication guidance for patients.

### ■ Multi-dimensional evaluation of immunotherapy efficacy

Microsatellite instability (MSI) detection  
Mismatch repair (MMR) related gene detection  
Tumor mutation burden (TMB) assessment

### ■ Comprehensive guidance on targeted medication

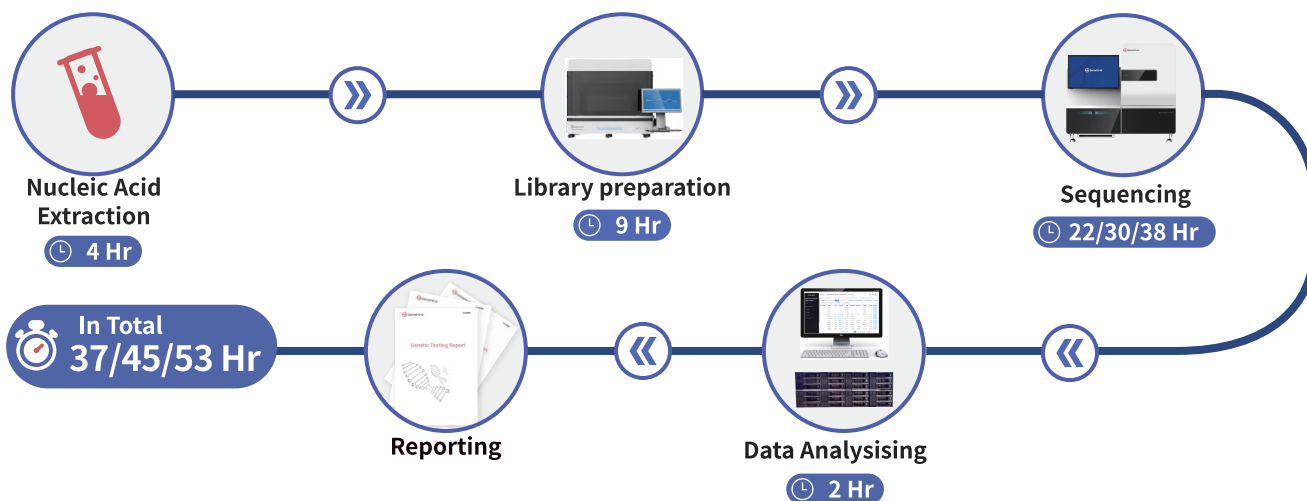
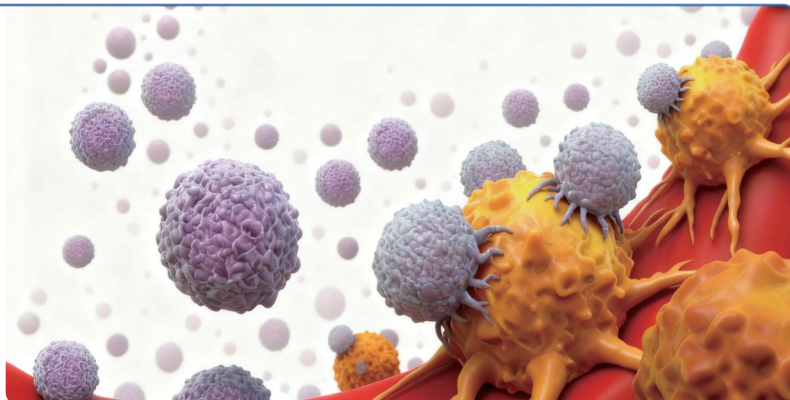
Covering targeted medication, chemotherapy, immunotherapy and hereditary tumor risk assessment  
Detecting homologous recombination repair (HRR)/DNA Damage Repair (DDR)-related mutations to guide the treatment of PARP inhibitors

### ■ Sensitive and cost-effective

One test covers all major variant classes and gene signatures (TMB, MSI)  
High sensitivity: can detect SNV/InDel with AF as low as 1% for tissue and 0.2 % for ctDNA

### Applicable Population

- ✓ Patients with solid tumors
- ✓ Individuals with a high risk of familial cancer
- ✓ Patients with recurrent or metastatic cancer
- ✓ Patients receiving specific targeted therapy
- ✓ Individuals eligible for clinical trial



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

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| Parameter           |                                                                       |                                       |
|---------------------|-----------------------------------------------------------------------|---------------------------------------|
| Method              | Hybrid capture                                                        |                                       |
| Panel size          | 2419 kb                                                               |                                       |
| Variants type       | SNVs, InDels, Amplifications, Fusions, and MSIs                       |                                       |
| Input quantity      | 20 ng - 500 ng DNA                                                    |                                       |
| Sample types        | FFPE, Fresh tissue, Plasma, White blood cell, Hydrothorax, and ascite |                                       |
| Mapping rate        | 98%                                                                   |                                       |
| On-target rate      | >70%                                                                  |                                       |
| Coverage uniformity | 96%                                                                   |                                       |
| Number of sample/FC | Tissue/FFPE<br>(≥6 Gb PE150)                                          | 1 FCM: 16<br>1 FCH: 92<br>1 FCP: 164  |
|                     | Plasma<br>(≥50 Gb PE150)                                              | 1 FCM: 2<br>1 FCH: 8<br>1 FCP: 16     |
|                     | White blood cell<br>(≥2 Gb PE150)                                     | 1 FCM: 56<br>1 FCH: 240<br>1 FCP: 432 |
| Report generation   | Local analysis and report system                                      |                                       |

White blood cells should be used as a control sample—this is standard practice to eliminate germline mutation interference. For tissue or FFPE samples, a white blood cell sample from the same patient should be included as a matched control pair. For plasma samples, white blood cells must be isolated from the same plasma specimen for sequencing and analysis.

## System Specification

|                        |                                                                                                                                     |
|------------------------|-------------------------------------------------------------------------------------------------------------------------------------|
| Dimensions (W × D × H) | 1100 mm × 750 mm × 850 mm                                                                                                           |
| Net Weight             | < 300 kg                                                                                                                            |
| Power                  | 2000 VA                                                                                                                             |
| Power Requirements     | 100-240 V~, 50/60 Hz                                                                                                                |
| Operating Environment  | Temperature: 19°C-25°C<br>Realvtive humidity: 20%-80% ( non-condensing)<br>Altitude: below 3000 meter                               |
| Computer Configuration | CPU: Inter Xeon Gold 6342<br>Memory: 256 GB<br>Hard disk1: 4 TB<br>Hard disk2: 17 TB<br>Operating system: Microsoft Windows 10 × 64 |

## GeneMind Biosciences Co., Ltd.

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