GeneMind

SURFSeq™ 5000

Tb level bench-top high-throughput sequencing platform



Research Use Only

Product Parameter

SURFSeq 5000 V2.0 Reagents

Flowcell	Lane	Throughput (Reads/FC)	Type	Read Length	Data output (FC×2)[1]	Q value	TAT[2] (h)
FCM	4	500 M	100 cycles	SE100	50 Gb×2	Q30≥90% 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	1080 Gb×2		38

SURFSeq 5000 CMS V1.0 Reagents

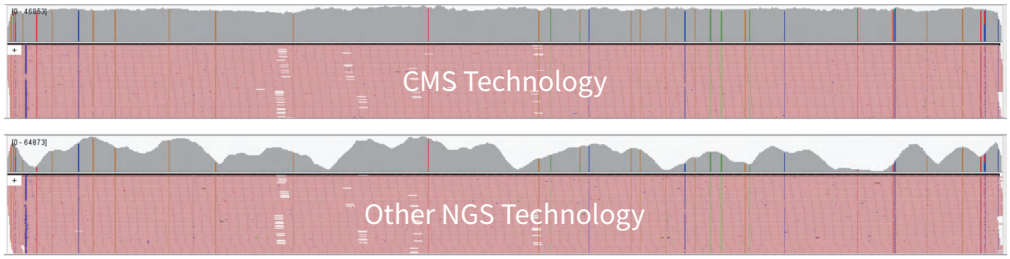
Flowcell	Lane	Throughput (Reads/FC)	Type	Read Length	Data output (FC×2)[1]	Q value	TAT[2] (h) (FC x 1)
FCM	4	500 M	100 cycles	SE100	50 Gb×2	Q30≥97% Q40≥95% Q50≥70%	9.0
				PE50	50 Gb×2		9.0
			200 cycles	PE100	100 Gb×2		12.5
			300 cycles	PE150	150 Gb×2		16.0
FCH	4	2000 M	100 cycles	SE100	200 Gb×2		12.5
				PE50	200 Gb×2		12.5
			200 cycles	PE100	400 Gb×2		18.0
			300 cycles	PE150	600 Gb×2		24.0
FCP	4	3600 M	100 cycles	SE100	360 Gb×2		14.0
				PE50	360 Gb×2		14.0
			200 cycles	PE100	720 Gb×2		21.5
			300 cycles	PE150	1080 Gb×2		29.0

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 cartaidge information	Automatical post-run wash

CMS Introduction

CMS™ (Cross Mountains and Seas) is an innovative sequencing chemistry developed by GeneMind. Through breakthroughs such as novel polymerase mutants, this technology significantly enhances sequencing capability in hard-to-sequence genomic regions, optimizes coverage uniformity across the whole genome, and delivers global unbiased Q50 -level (99.999%) precision data output.



By integrating CMS™ and Lightning Chemistry Plus™, GeneMind introduces the SURFSeq™ 5000 CMS™ Sequencing Kit V1.0 series, fully empowering users to accelerate scientific discovery and enhance testing efficiency.

Navigate the "Difficult Terrain"

Overcome limits in hard-to-sequence regions

Achieve genome-wide coverage uniformity

Achieve Q50-Level Precision

Q40＞95%
Q50＞70%

Attain Unmatched Efficiency

1500 Gb + daily output
TAT for PE150 ＜16 hrs

Lightning Chemistry Plus™ redefines sequencing efficiency with <1 minute per cycle—delivering rapid, high-quality results without compromise.

Application

Application	Reads length	Data/sample	Number of Samples / FC[3]		
			FCM	FCH	FCP
			500 M	2000 M	3600 M
NIPT Standard	SE50	7 M reads	NA[4]	160	300
NIPT Plus	SE50	12 M reads	NA[4]	96	180
NIPT Pro	SE50	20 M reads	NA[4]	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
cWES	PE150	5 Gb	16	96	164
RNAseq	PE150	10 Gb	12	48	84

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.

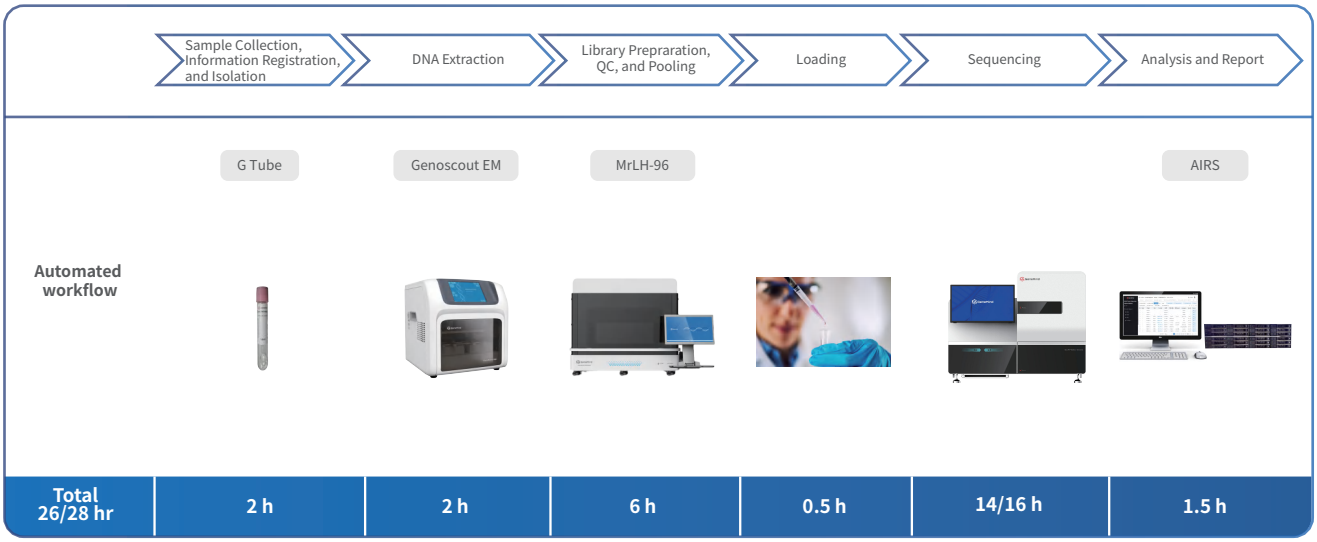
Total Solution

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
▸ Trisomy 21，18，13 ▸ 6 Sex chromosome aneuploidies (SCAs) (XO/XXX/XXY/XYY/XO+XY/XXX+XY) ▸ Other 19 autosomal aneuploidies ▸ Sex identification, fetal fraction estimation	▸ Trisomy 21，18，13 ▸ 6 Sex chromosome aneuploidies (SCAs) (XO/XXX/XXY/XYY/XO+XY/XXX+XY) ▸ Other 19 autosomal aneuploidies ▸ 60 Microdeletion/duplications syndromes ▸ Sex identification, fetal fraction estimation	▸ Trisomy 21，18，13 ▸ 6 Sex chromosome aneuploidies (SCAs) (XO/XXX/XXY/XYY/XO+XY/XXX+XY) ▸ Other 19 autosomal aneuploidies ▸ 90 Microdeletion/duplications syndromes ▸ Sex identification, fetal fraction estimation

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 1 FCP: 300	1 FCH: 96 1 FCP: 180	1 FCH: 64 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 ⩾ 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 1 FCH: 48 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



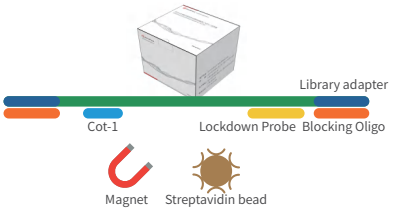
GenoScout EM

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

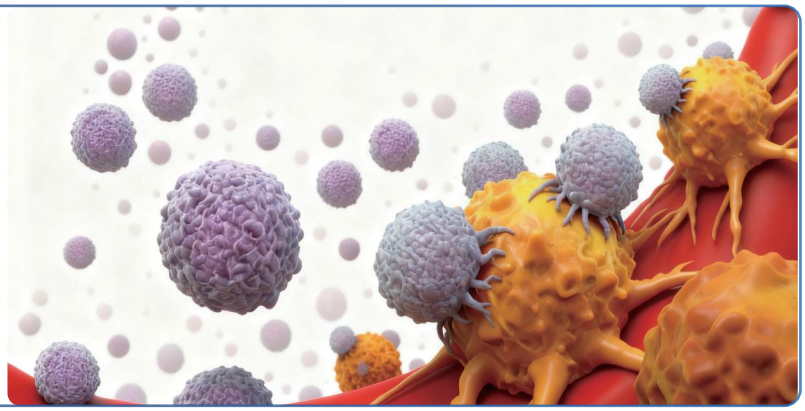
Covering targeted medication, chemotherapy, immunotherapy and hereditary tumor risk assessment
Detecting homologous recombination repair (HRR)/DNA Damage Repair (DDR)-related mutations to guide the treatment of PARP inhibitors

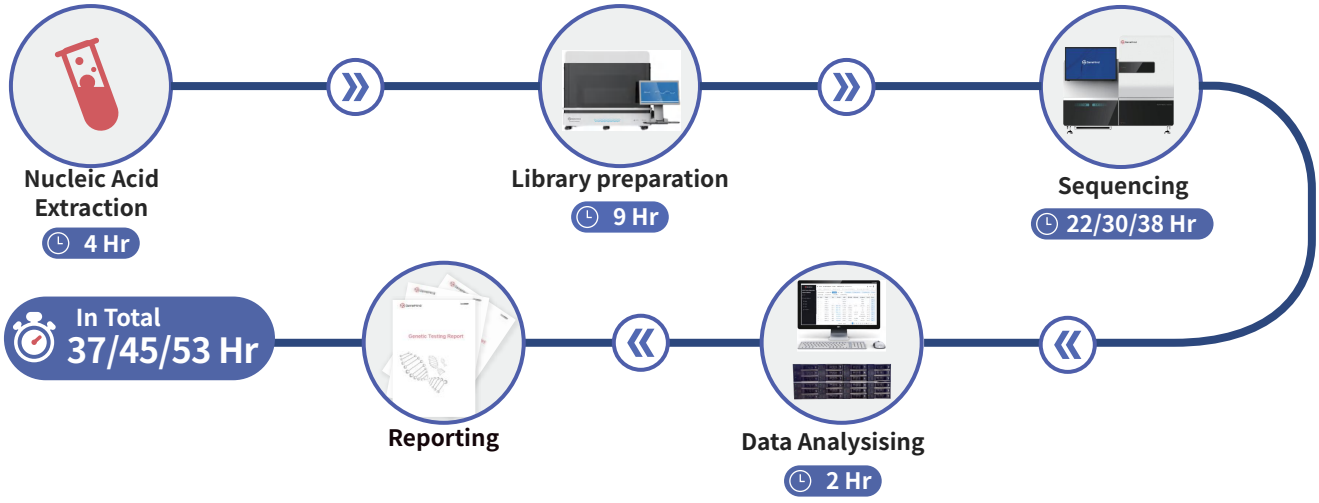
Sensitive and cost-effective

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 (⩾6 Gb PE150)	1 FCM: 16 1 FCH: 92 1 FCP: 164
	Plasma (⩾50 Gb PE150)	1 FCM: 2 1 FCH: 8 1 FCP: 16
	White blood cell (⩾2 Gb PE150)	1 FCM: 56 1 FCH: 240 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 Realvtive humidity: 20%-80% (non-condensing) Altitude: below 3000 meter
Computer Configuration	CPU：Inter Xeon Gold 6342 Memory：256 GB Hard disk1：4 TB Hard disk2：17 TB Operating system：Microsoft Windows 10 ×64

Ordring Information

PN	Product Name
S000547	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCM 100cycles)
S000552	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCM 200cycles)
S000554	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCM 300cycles)
S000556	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCH 100cycles)
S000559	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCH 200cycles)
S000561	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCH 300cycles)
S000563	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCP 100cycles)
S000566	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCP 200cycles)
S000568	SURFSeq 5000 CMS Sequencing Reagent V1.0(FCP 300cycles)
S000351	SURFSeq 5000 Sequencing Reagent V2.0(FCM 100cycles)
S000356	SURFSeq 5000 Sequencing Reagent V2.0(FCM 200cycles)
S000358	SURFSeq 5000 Sequencing Reagent V2.0(FCM 300cycles)
S000272	SURFSeq 5000 Sequencing Reagent V2.0(FCM 600cycles)
S000360	SURFSeq 5000 Sequencing Reagent V2.0(FCH 50cycles)
S000365	SURFSeq 5000 Sequencing Reagent V2.0(FCH 100cycles)
S000367	SURFSeq 5000 Sequencing Reagent V2.0(FCH 200cycles)
S000369	SURFSeq 5000 Sequencing Reagent V2.0(FCH 300cycles)
S000371	SURFSeq 5000 Sequencing Reagent V2.0(FCP 50cycles)
S000373	SURFSeq 5000 Sequencing Reagent V2.0(FCP 100cycles)
S000375	SURFSeq 5000 Sequencing Reagent V2.0(FCP 200cycles)
S000377	SURFSeq 5000 Sequencing Reagent V2.0(FCP 300cycles)

GeneMind Biosciences Co., Ltd.

Technical Support: **+86-400-822-3660**

Website: en.genemind.com Email: info@genemind.com

Address: Room 502A/502B/602, Luohu Investment Holding Building, 112 Qingshuihe 1st Road, Luohu District, Shenzhen, Guangdong, China