# GeneMind
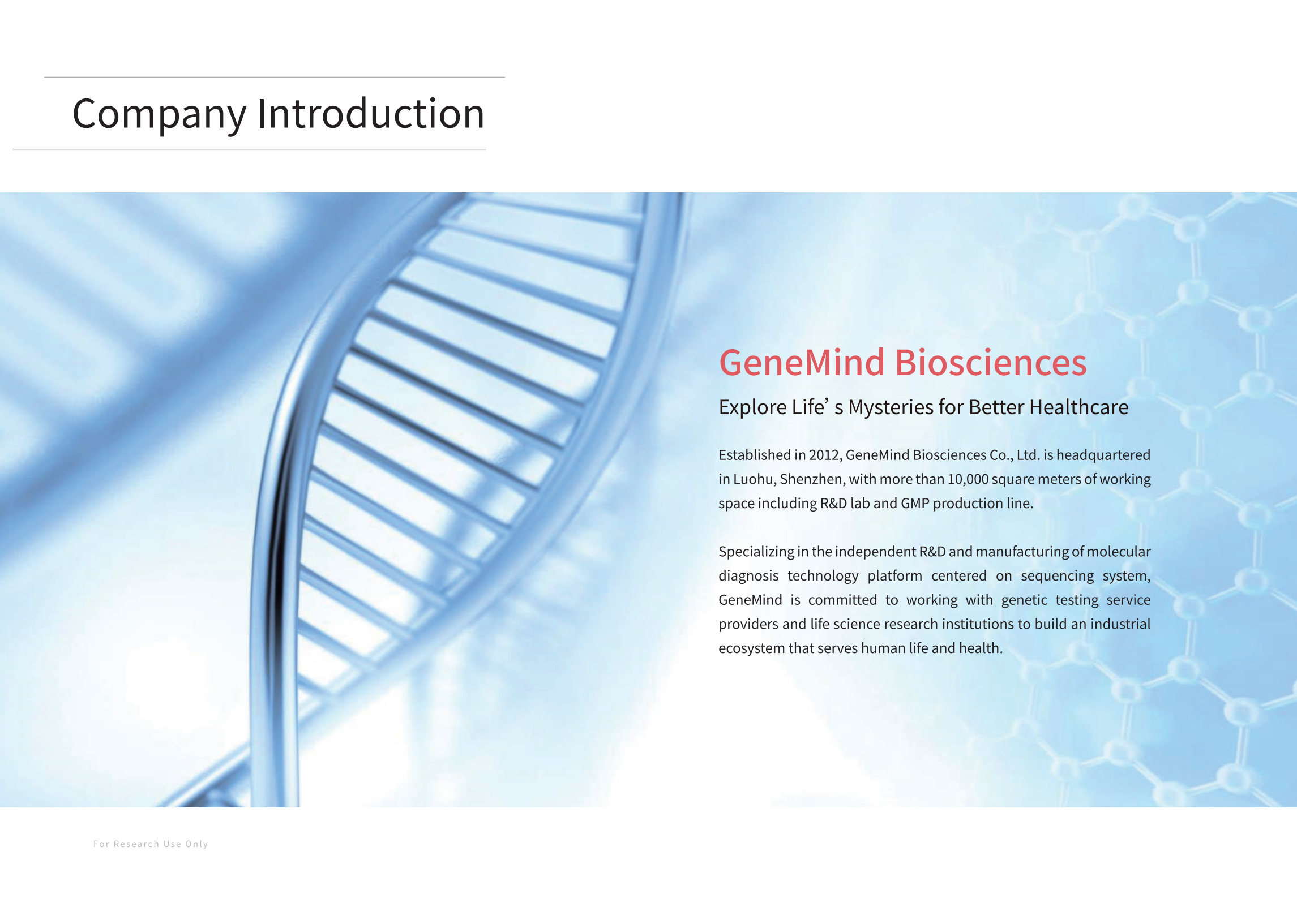
# FASTASeq 300

High-throughout sequencing platform

——Flexible · Rapid · Easy-to-use

# Company Introduction

## GeneMind Biosciences

### Explore Life's Mysteries for Better Healthcare

Established in 2012, GeneMind Biosciences Co., Ltd. is headquartered in Luohu, Shenzhen, with more than 10,000 square meters of working space including R&D lab and GMP production line.

Specializing in the independent R&D and manufacturing of molecular diagnosis technology platform centered on sequencing system, GeneMind is committed to working with genetic testing service providers and life science research institutions to build an industrial ecosystem that serves human life and health.

# Milestones



**September 2023**
SURFSeq 5000 Launched

**November 2022**
Launch of FASTASeq 300
Sequencing Platform

**September 2022**
MrLH-96 Launched

**October 2020**
GenoLab M
Sequencer Launched

**April 2020**
GenoLab M
Engineering Prototype

**September 2018**
New headquarters in
Luohu, Shenzhen

**September 2014**
Pioneering the
independent development
of sequencers

**July 2012**
GeneMind founded

# Product Introduction

## FASTASeq 300  High-throughput Sequencer

FASTASeq 300 is a desktop sequencer focused on targeted sequencing, whole-genome low-depth sequencing, with innovative breakthroughs in sequencing chemistry, high-density flowcell, fluid design and base identification algorithms, bringing users more flexibility, more consistent data quality and faster delivery.



**Flexible**
- Support two types of flow cells and multiple read lengths
- Multi-time output (MTO)
- Libraries can be loaded on each flow cell lane automatically or manually

**Easy-to-use**
- Pre-configured, plug-and-play cartridges
- Support RFID reader module
- Libraries can be directly used for sequencing after preparation
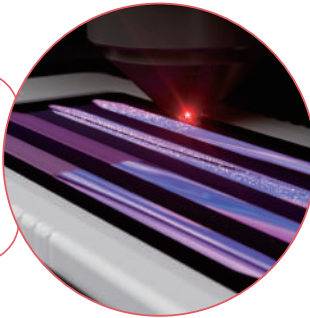- Automatic post-run wash

**Rapid**
- mNGS (SE50 4.5hrs)
- Targeted sequencing (PE75 11.5hrs)
- Targeted sequencing (PE150 19.5hrs)

# Core Technologies

**Constant temperature chemistry**
Sequencing speed increased by 1x

- Biochemical and signal acquisition processed in parallel, making sequencing more efficient

**High-density flow cell**
Signal density increased by 1x

- New high-density flow cell combined with optimized Basecall algorithm
- Accurate identification of high density signals and efficient output of high quality data
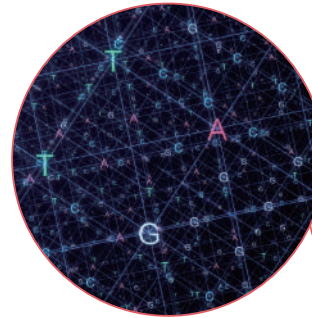
**Bi-directional sequencing**
Reagent usage reduced by 50%

- Optimized reagent formulation and fluid configuration
- Promote a significant reduction in reagent consumption per unit of data output

**Localisation**
90% of core components produced domestically

- Increased proportion of core components of sequencers made domestically
- More stable and controllable supply chain and production cycle
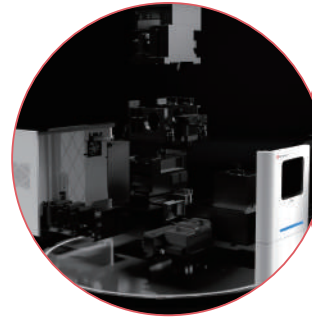
# Configuration

| Flow cell | Flowcell Type | Lane | Reads[1] | Read Length | Output | Q30[1] | index (0) Sequencing Time (index 0) | index (8+8) Sequencing Time ( index 8+8) |
|---|---|---|---|---|---|---|---|---|
| Single | FCM | 4 | 100 M | SE50[3] | 5 Gb | 85% | 4.5 hrs | 5.5 hrs |
| | | | | SE75 | 7.5 Gb | 85% | 6 hrs | 7 hrs |
| | | | | PE75 | 15 Gb | 85% | 11.5 hrs | 13 hrs |
| | | | | PE150 | 30 Gb | 80% | 19.5 hrs | 21 hrs |
| | FCH | 4 | 250 M | SE50[3] | 12.5 Gb | 85% | 5 hrs | 6.5 hrs |
| | | | | SE75 | 18.5 Gb | 85% | 6.5 hrs | 8 hrs |
| | | | | PE75 | 37.5 Gb | 85% | 12.5 hrs | 14 hrs |
| | | | | PE150 | 75 Gb | 80% | 22.5 hrs | 24 hrs |

1.The number of reads and Q30 are based on sequencing using standard libraries; performance may vary depending on library type and quality, insert size, loading concentration, and other experimental factors.
2.Sequencing time includes the time from sample loading to base identification to generate the Basefile file.
3.SE50 sequencing mode is implemented based on the FASTASeq 300 sequencing kit V1.0 (FCM/FCH-D SE075-D).

# Application

| Application | Read length | Data/sample | FCM*1 | FCH*1 |
| --- | --- | --- | --- | --- |
| | | | 100M | 250M |
| NIPT/PGT-A/CNV-Seq | SE75 | 5 M reads/sample | 20 | 48 |
| Small tumor panel (tissue) | PE75 | 0.2 Gb/sample | >48 | >96 |
| Small tumor panel (ctDNA) | PE150 | 5 Gb/sample | 6 | 16 |
| Large tumor panel (tissue) | PE150 | 5 Gb/sample | 6 | 16 |
| mNGS | SE75 | 20 M reads/sample | 4 | 12 |
| tpNGS | PE150 | 0.1-1 M reads/sample | >96 | >192 |

Recommended data output and sample numbers are only for reference, actual application will require optimisation adjustments.

# Application summary

A total of 60 runs were counted（FASTASeq 300 FCH）

| Parameter | Mean |
|---|---|
| Q30 | 90% |
| Output reads | 310 M |

# Application

## Application—PGT-A/CNV-Seq/NIPT

➤ Sequencing:FASTASeq 300 Chromosomal Abnormality Detection
➤ Sample type:Construct PGT-A and CNV-seq libraries based on PGT-A reference standard and CNV-seq reference standard
➤ Read length:SE75

Table 1. Consistency assessment of CNV-Seq results

| | | | | | | CNV-Seq Reference Standard Sequencing | | |
|---|---|---|---|---|---|---|---|---|
| No. | Sample | Effective data (reads) | Average GC | Average coverag | Average depth | Results | Reference standard | Consistency |
| 1 | GM12 | 4811803 | 38.15% | 7.34% | 0.159 | +13 | T13 | Yes |
| 2 | GM15 | 5187339 | 38.46% | 7.88% | 0.173 | +16 | T16 | Yes |
| 3 | GM21 | 5394891 | 38.26% | 8.18% | 0.178 | -X | XO | Yes |
| 4 | GM27 | 5302386 | 38.18% | 8.05% | 0.177 | -22 (q11.21,~ 2.96Mb) | 22q11.21 (del,2.5Mb) | Yes |
| 5 | GM31 | 4843680 | 38.50% | 7.39% | 0.162 | -7 (q11.23, ~ 1.78Mb) | 7q11.23 (del,1.8Mb) | Yes |
| 6 | GM40 | 5845360 | 38.06% | 8.82% | 0.192 | +X—31%;-1 (p36.33-p36.22,~ 10.65Mb)—31% | XXY—30%;1p36.33-p36.22 (del,11.0Mb)—30% | Yes |
| 7 | GM42 | 4906427 | 38.23% | 7.48% | 0.162 | Normal | Regular Sample | Yes |

Table 2. Consistency assessment of PGT-A results

| | | | | | | PGT-A Reference Standard Sequencing | | |
|---|---|---|---|---|---|---|---|---|
| No. | Sample | Effective data (reads) | Average GC | Average coverage | Average depth | Results | Reference standard | Consistency |
| 1 | GM02008 | 4641367 | 39.59% | 5.92% | 0.169 | -11(q23.3-q25,~ 14.7Mb) | -11(q23.3-q25,~ 14.7Mb) | Yes |
| 2 | GM06473 | 5123946 | 39.33% | 6.70% | 0.183 | -1(q43-q44,~ 9.9Mb) | -1(q43-q44,~ 9.9Mb) | Yes |
| 3 | GM06097 | 4964662 | 39.43% | 6.72% | 0.179 | -17(p13.3-p13.2,~ 4.2Mb) | -17(p13.3-p13.2,~ 4.2Mb) | Yes |
| 4 | GM13325 | 5330814 | 39.49% | 7.79% | 0.197 | -22(q11.21,~ 2.3Mb) | -22(q11.21,~ 2.3Mb) | Yes |
| 5 | GM25372 | 4115286 | 39.39% | 5.42% | 0.151 | -17(p11.2,~ 1.2Mb) | -17(p11.2,~ 1.2Mb) | Yes |
| 6 | GM01359 | 3914767 | 40.17% | 5.84% | 0.151 | +18 | +18 | Yes |
| 7 | GM02767 | 3872356 | 39.47% | 5.08% | 0.141 | +21 | +21 | Yes |

Conclusion:

FASTASeq 300 has excellent detection of chromosomal abnormalities.

# Application

## Application-Target tumor panel

➤ Sample typr:HD832 (FFPE)
➤ Library prep:TruSight Oncology 500
➤ Sequencing platform:GenoLab M，FASTASeq 300,Competitor A (NS platform) and Competitor B (NV platform)
➤ Read length:PE150
➤ Analysis:Extract 100M reads/sample to do deep analysis

| Platform | FATSASeq 300 | GenoLab M | NS Platform | NV Platform |
|---|---|---|---|---|
| Q30 | 91.33% | 88.58% | 83.45% | 91.25% |
| Total SE reads (M) | 100 | 100 | 100 | 100 |
| Fold80 | 1.41 | 1.43 | 1.41 | 1.56 |
| Unique mapping rate | 99.34% | 99.22% | 97.45% | 98.14% |
| Target region rate | 84.74% | 84.37% | 83.74% | 83.05% |
| Target mean depth | 1182 | 1551 | 1178 | 1165 |

| AF | Mut Number | FASTASeq 300 | GenoLab M | NS Platform | NV Platform |
|---|---|---|---|---|---|
| AF≤10% | 9 | 88.89% | 77.78% | 77.78% | 77.78% |
| 10%<AF≤20% | 24 | 100.00% | 100.00% | 100.00% | 100.00% |
| 20%<AF≤30% | 49 | 100.00% | 100.00% | 100.00% | 100.00% |
| AF>30% | 124 | 100.00% | 100.00% | 100.00% | 100.00% |
| NGS no value | 6 | 83.33% | 83.33% | 83.33% | 83.33% |
| Total | 212 | 99.06% | 98.58% | 98.58% | 98.58% |

TAT: 24h (FASTASeq 300 FCH PE150 Dual index)

Conclusion:

High data quality (Q30>91%, unique mapping rate>99%) for FASTASeq 300, the sequencing time only takes 24h for PE150. And the results of FASTASeq 300 mutation detection are consistent with GenoLab M and other competitors.
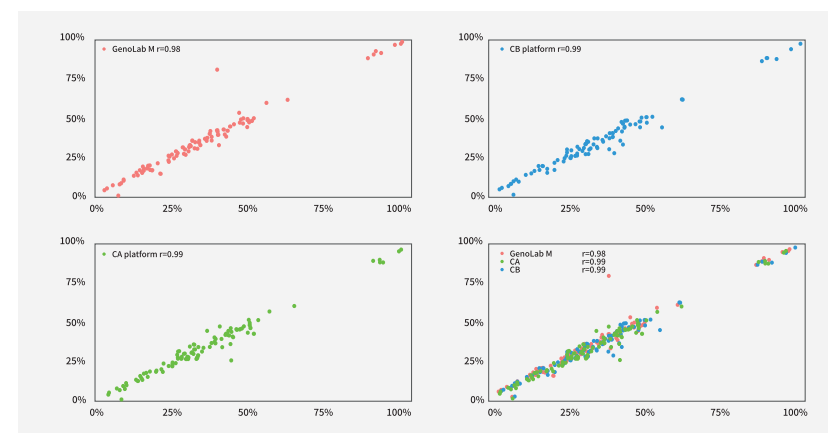
# Application

## Targeted tumor panel

➤ Sample typr:HD832（FFPE）
➤ Library prep:TruSight Oncology 500
➤ Sequencing platform:GenoLab M，FASTASeq 300, Competitor A and Competitor B
➤ Read length:PE150
➤ Analysis:Extract 100M reads/sample to do deep analysis

| AF | Mut Number | FASTASeq 300 | GenoLab M | NS Platform | NV Platform |
|---|---|---|---|---|---|
| AF≤10% | 9 | 88.89% | 77.78% | 77.78% | 77.78% |
| 10%<AF≤20% | 24 | 100.00% | 100.00% | 100.00% | 100.00% |
| 20%<AF≤30% | 49 | 100.00% | 100.00% | 100.00% | 100.00% |
| AF>30% | 124 | 100.00% | 100.00% | 100.00% | 100.00% |
| NGS no value | 6 | 83.33% | 83.33% | 83.33% | 83.33% |
| Total | 212 | 99.06% | 98.58% | 98.58% | 98.58% |



Conclusion：

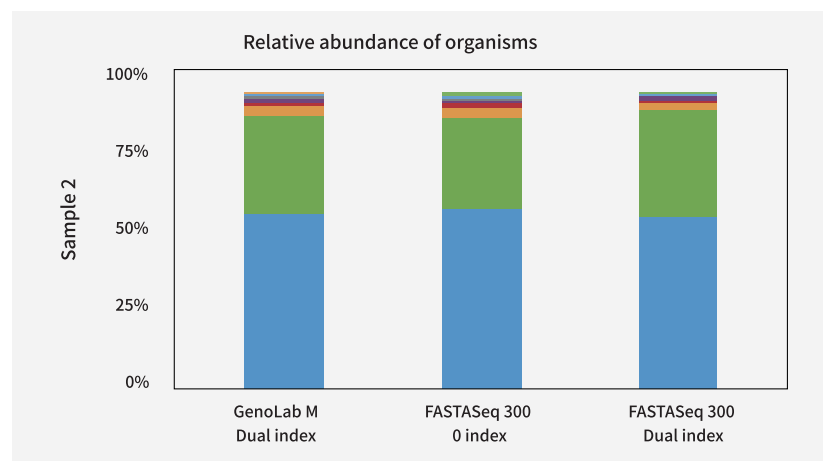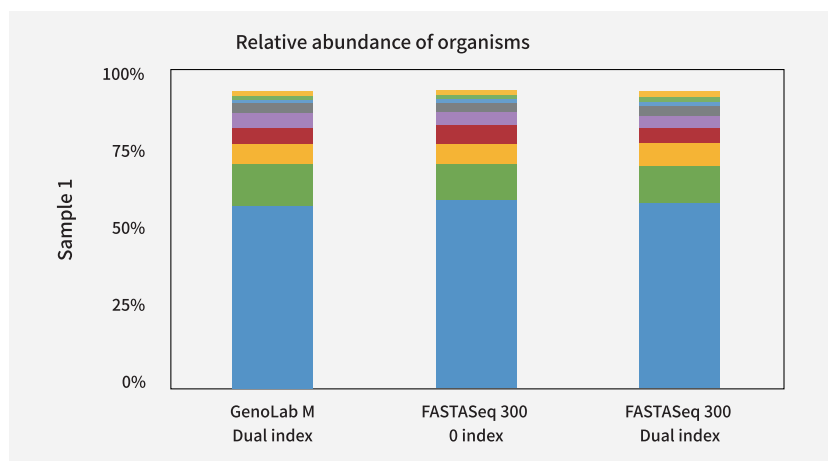The results of FASTASeq 300 mutation detection are consistent with GenoLab M and other competitors.

# Application

## Application-mNGS

➤ sample type:Clinical samples(Alveolar lavage fluid, sanies, urine, tissue, hydrothorax)
➤ Library:6 mNGS libaries
➤ Sequencing platfirm:GenoLab M, FASTASeq 300
➤ Read length:SE50
➤ Data analysis:50M reads/sample for deep anaysis



Conclusion:

The microbial detection of FASTASeq 300 are consistent with GenoLab M, and the clinical judgment results of all test samples are 100% accurate detected.

# Application

## Application- De novo WGS (single bacteria assembling)

➤ Sample type:Using Legionella pneumophila subsp. Pneumophila construct WGS library

➤ Sequencing platform:FASTASeq 300, GenoLab M, Competitor A(CA)

➤ Read length:PE150

➤ Data analysis:100×effective reads/sample for de nova analysis

| Assembling results | | | |
|---|---|---|---|
| Platform | FASTASeq 300 | GenoLab M | CA |
| Q30 | 92.10% | 91.93% | 90.60% |
| Total Length (bp) | 3387746 | 3376652 | 3377221 |
| Reference Length (bp) | 3409194 | 3409194 | 3409194 |
| Genome Fraction | 99.02% | 99.02% | 99.04% |
| GC Content | 38.22% | 38.23% | 38.23% |
| Reference GC Content | 38.33% | 38.33% | 38.33% |
| Contigs | 28 | 27 | 29 |
| Largest Contig (bp) | 989763 | 989763 | 989763 |
| Contig N50 (bp) | 363258 | 363258 | 363482 |

### Assembling result comparsion

FASTASeq 300 — C:326[S:325,D:1],F:7,M:107,n:440

GenoLab M — C:326[S:325,D:1],F:7,M:107,n:440

Competitor A — C:326[S:325,D:1],F:7,M:107,n:440

L.P(Reference) — C:326[S:325,D:1],F:7,M:107,n:440

0%  20%  40%  60%  80%  100%

■ Complete(C) and single-copy(S)
■ Complete(C) and duplicated(D)
■ Fragmented(F)
■ Missing(M)

TAT: 19.5h (FASTASeq 300 FCM PE150 0 index)

Conclusion:

Data quality and assembling results are quite comparable with GenoLab M and CA, the sequencing time only takes 19.5h for PE150.
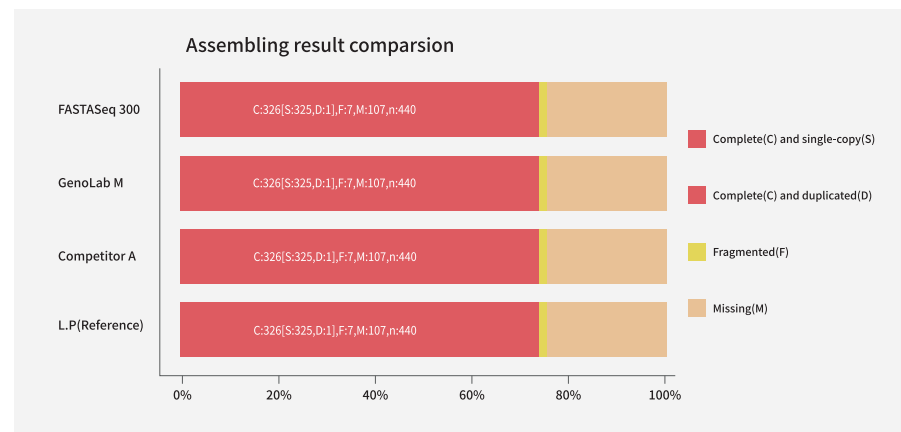
# Application

## Application-WES

➤ Sample type:HG001(NA12878), HG002(NA24835)

➤ Library prep:Agilent SureSelect Human All Exon V6

➤ Sequencing Platform:FASTASeq 300,GenoLab M, Competitor A(NV platform)

➤ Read length:PE150

➤ Analysis:12Gb/sample for deep analysis

| Platform | HG001-WES | | | HG002-WES | | |
|---|---|---|---|---|---|---|
| | FASTASeq 300 | GenoLab M | Competitor A | FASTASeq 300 | GenoLab M | Competitor A |
| Raw data(Gb) | 12 | 12 | 12 | 12 | 12 | 12 |
| Clean data(Gb) | 11.99 | 11.99 | 11.95 | 11.99 | 11.99 | 11.96 |
| Properly paired reads | 99.49% | 99.62% | 98.81% | 99.60% | 99.65% | 98.92% |
| Capture efficiency | 77.91% | 77.93% | 78.29% | 78.78% | 78.49% | 78.91% |
| Mean sequencing depth | 124.59 | 124.64 | 124.78 | 125.95 | 125.75 | 126.05 |
| Duplication ratio | 3.46% | 5.48% | 21.03% | 5.79% | 5.22% | 19.60% |
| Coverage at lease 0× | 99.64% | 99.64% | 99.65% | 99.87% | 99.87% | 99.85% |
| Coverage at lease 4× | 99.52% | 99.52% | 99.55% | 99.65% | 99.67% | 99.56% |
| Coverage at lease 10× | 99.06% | 99.05% | 99.19% | 98.57% | 98.68% | 98.16% |
| Coverage at lease 30× | 94.95% | 95.16% | 94.67% | 89.56% | 90.32% | 87.33% |

Conclusion：High data quality( Q30>91%, low duplication rate<5%)
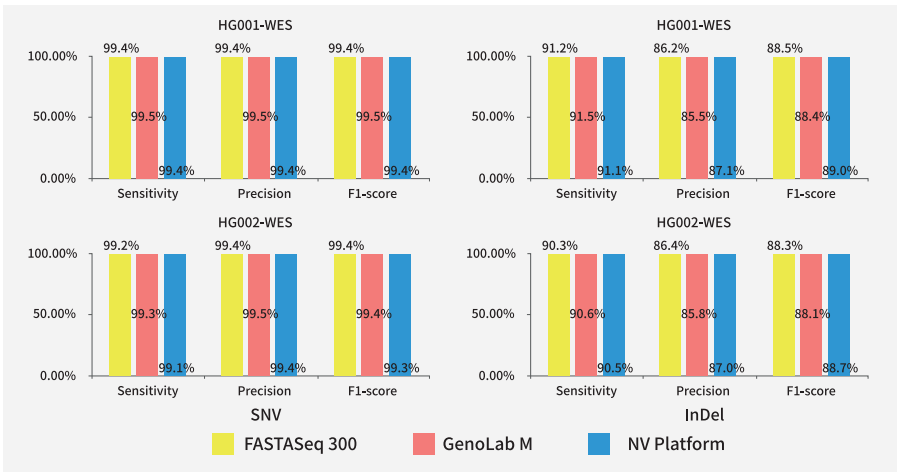


Conclusion：FASTASeq 300 excels in sensitivity and precision for germline mutation (SNV and InDel) detection.

# Intellectual Property & Qualifications
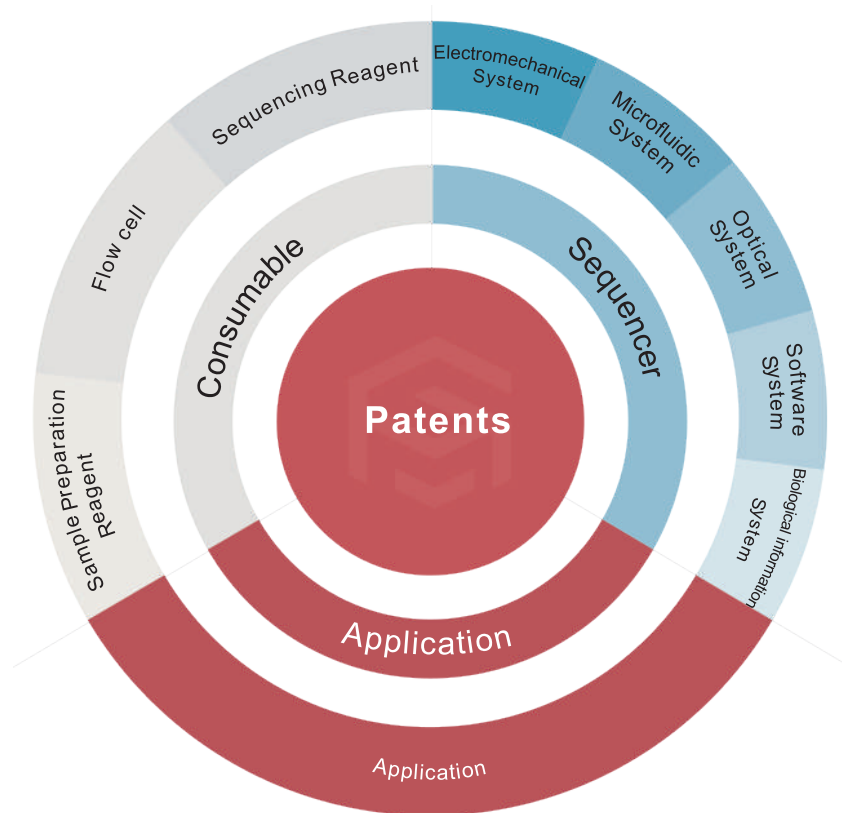


Sequencing systems are multidisciplinary specialities that combine optics, fluids, algorithms, chemistry and molecular biology. Since its establishment, GeneMind has been specializing in the independent R&D and manufacturing of molecular diagnosis technology platform centered on sequencing system. We have continuously innovated and accumulated a lot of intellectual property rights in the underlying technologies such as instrument hardware, reagent, flowcell and software algorithms.

As of October 2023, GeneMind has more than 300 granted domestic and foreign patents, and has successfully obtained ISO 13485 medical device quality management system certification. The sequencer, reagent kits and other products have also received CE certification, NMPA medical device approval.

**300+**
Patents granted

**ISO** 13485:2016
Quality Management System Certification

**34**
NMPA approval/ CE IVD registration

**10+**
Academic papers

# Independent Research & Development

In addition to the innovative breakthroughs in sequencer development, GeneMind has also realized the independent R&D and production of core materials such as enzymes, nucleotide analogues, fluorochrome and flowcell. The company has the ability to develop and manufacture the total solution of "instrument-reagent-flow cell-software" independently, and are able to provide customers total solution with good quality, low cost and short delivery time.

The total area of R&D and production in use is nearly 10,000 square meters, with sequencer production factory, GMP reagent kit production line, flow cell laboratory, organic synthesis laboratory and enzyme engineering laboratory. The designed annual capacity of sequencer is 1000 units and the annual capacity of kits is 2.4 million tests.

● **Sequencer Production Line**
Designed with annual production capacity of 1000 sequencers

● **Flow cell Lab**
In-house production of sequencing flowcell

● **Organic Synthesis Lab**
Able to synthesize our own nucleic acid and fluorochrome

● **Reagent Kits Production Line**
Designed as a GMP workshop to produce kits for 2.4 million tests annually

● **Enzyme Engineering Lab**
Independent research and development of core enzyme

# Partners



For Research Use Only

# Product Information and Specification

## Product Information

| Sequencer | |
|---|---|
| SQ00019 | FASTASeq 300 Sequencing Platform |
| **Reagent Kit** | |
| S000181 | FASTASeq 300 Sequencing Set V1.0 (FCM-D SE075-D) |
| S000186 | FASTASeq 300 Sequencing Set V1.0 (FCM 150cycles) |
| S000189 | FASTASeq 300 Sequencing Set V1.0 (FCM 300cycles) |
| S000191 | FASTASeq 300 Sequencing Set V1.0 (FCH-D SE075-D) |
| S000194 | FASTASeq 300 Sequencing Set V1.0 (FCH 150cycles) |
| S000197 | FASTASeq 300 Sequencing Set V1.0 (FCH 300cycles) |

## Product Specification

| Specification | |
|---|---|
| Dimensions | 684 mm × 644 mm × 615 mm |
| Weight | 145 kg |
| Power Requirements | 2000 VA |
| Power Requirements | 100-240 V~, 50 /60 Hz |
| Operating Environment | Temperature:19℃-25℃<br>Humidity: 20%-80% Relative Humidity, non-condensing<br>Altitude:0-3000m |
| Instrument Control Computer | CPU:Intel XeonSilver 4216<br>Memory: 32GB DDR4*6<br>Solid-state drive: 480GB<br>Hard drive: 2TB<br>Operating system: window10x64 |

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