GeneMind

FASTASeq 300*

High-throughout sequencing platform

——Flexible · Rapid · Easy-to-use

For Research Use Only

*Unless otherwise informed, GeneMind sequencing platform and related sequencing reagents are not available in the USA, Canada, Australia, Japan, Singapore, Western Europe, Southern Europe and Nordic countries yet.

Company Introduction

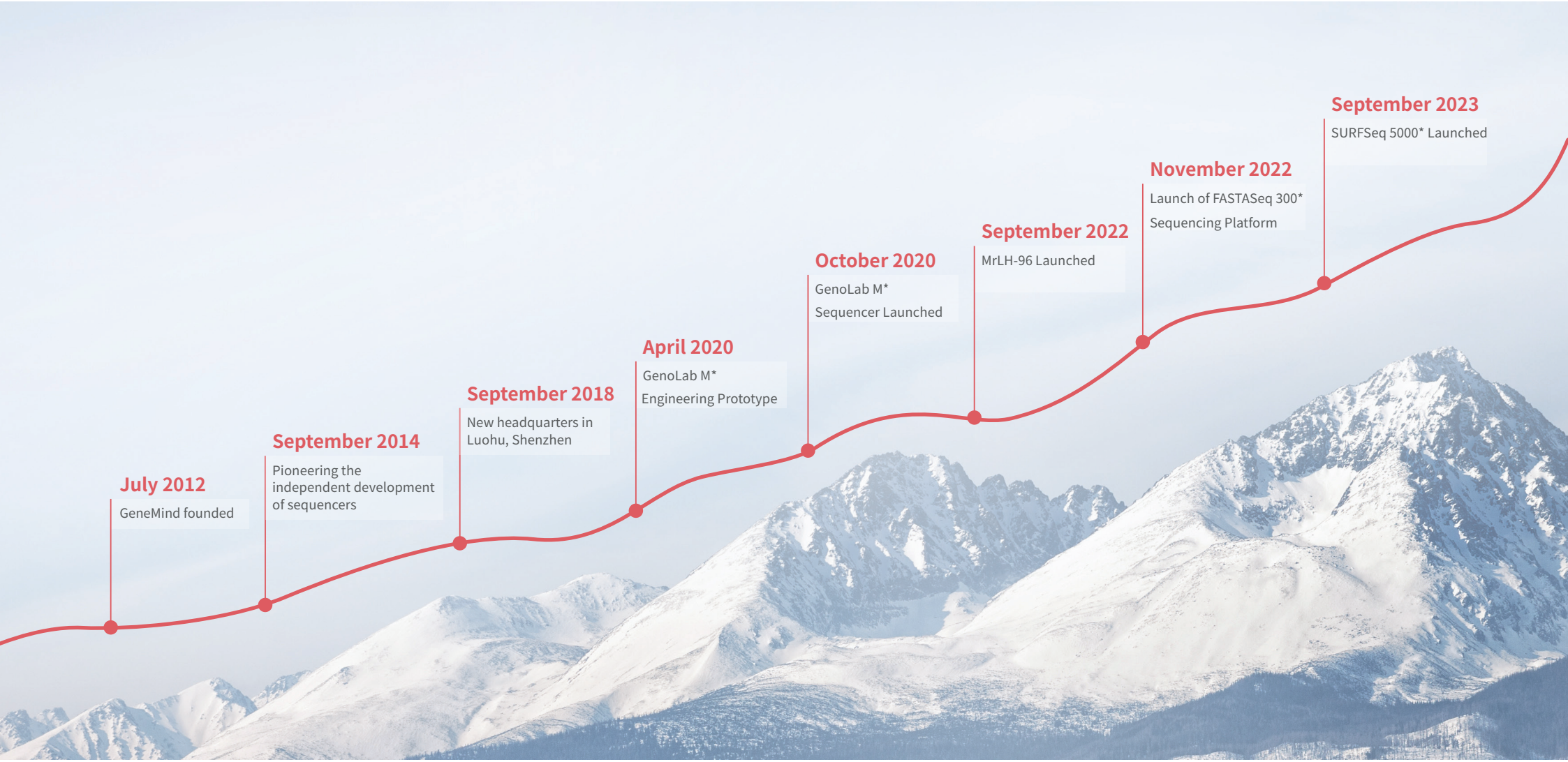
GeneMind Biosciences

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



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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)

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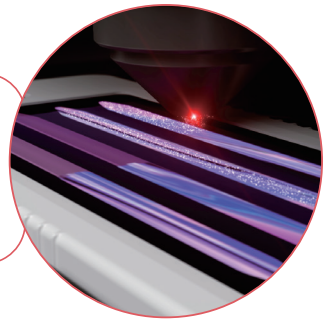
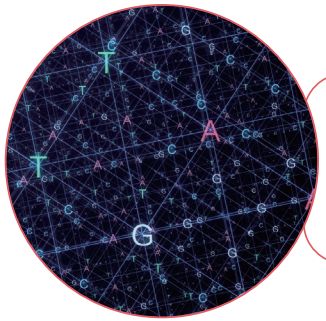
Core Technologies

Constant temperature chemistry
Sequencing speed increased by 1x

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



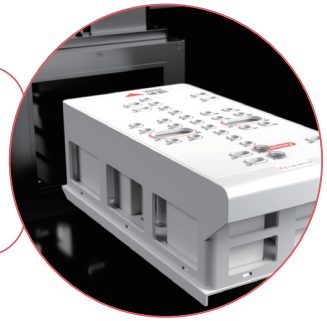


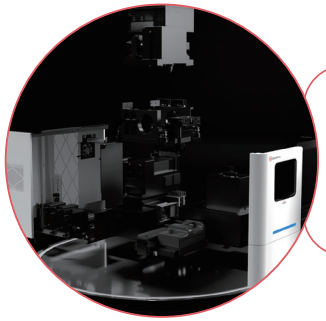
High-density flow cell
Signal density increased by 1x

- 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

System Specifications

Unit	Flow cell Type	Lane	Reads	Read Length	Output (Gb)	Q30[1]	Error rate[4]	Sequencing Time[2] (h) index (0)	Sequencing Time[2] (h) index (8+8)
1	FCM	4	100 M	SE50[3]	5.0	⩾85%	⩽1%	4.5	5.5
				SE75	7.5			6.0	7.0
				PE75	15.0			11.5	13
				PE150	30.0			19.5	21
	FCH	4	250 M	SE50[3]	12.5			5.0	6.5
				SE75	18.5			6.5	8.0
				PE75	37.5			12.5	14
				PE150	75.0			22.5	24
	FCX	4	100 M	SE400[3]	40.0			31.5	33
				PE250[3]	50.0			38.0	40
				PE300	60.0			46.0	48

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), SE400/PE250 sequencing mode is implemented based on the FASTASeq 300 sequencing kit V1.0 (FCX PE300).
4.The sequencing accuracy is obtained by comparing the sequencing data with the reference genome ATCC8739.

Application

Application	Read length	Data/sample	FCM/FCX	FCH
			100M	250M
NIPT Standard	SE75	5 M unique reads/sample	32	64
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
tNGS	PE150	0.1-1 M reads/sample	>96	>192
16S/18S/ITS	PE300	0.1 M reads/sample	>960	/
Forensic	SE400	1 M reads/sample	>96	/

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

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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:

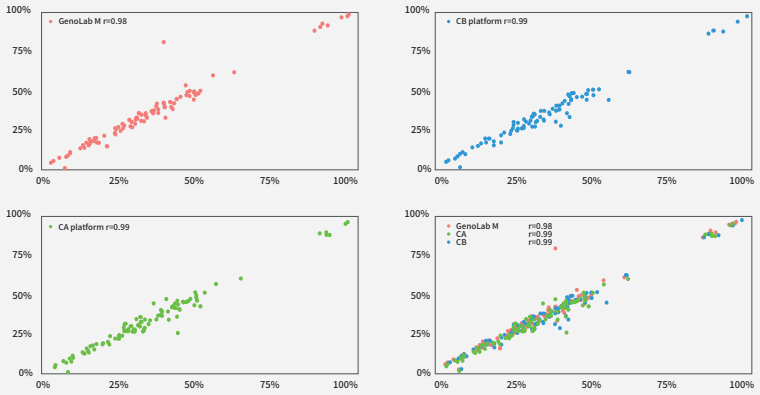
High data quality (Q30>91%, unique mapping rate>99%) for FASTASeq 300*, the sequencing time only takes 24h for PE150. And the results of FASTASeq 300* mutation detection are consistent with GenoLab M* and other competitors.

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.

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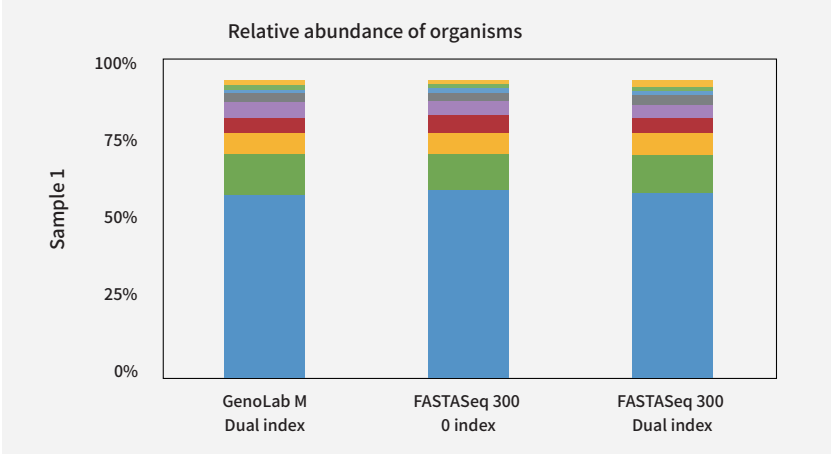
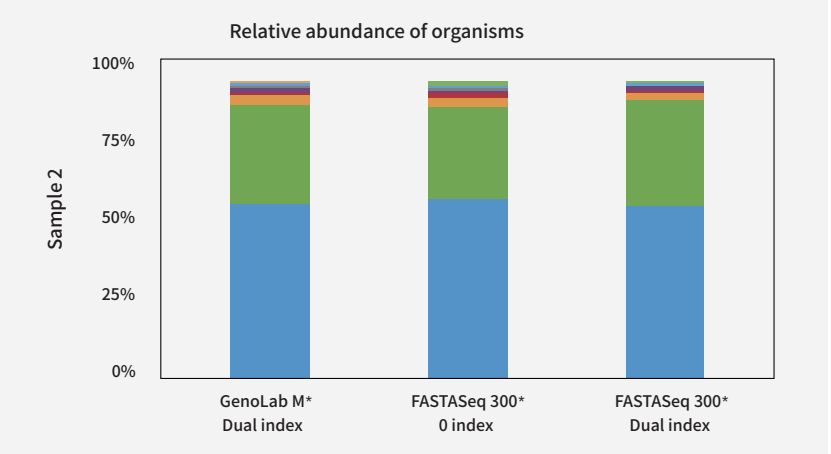
Application

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:

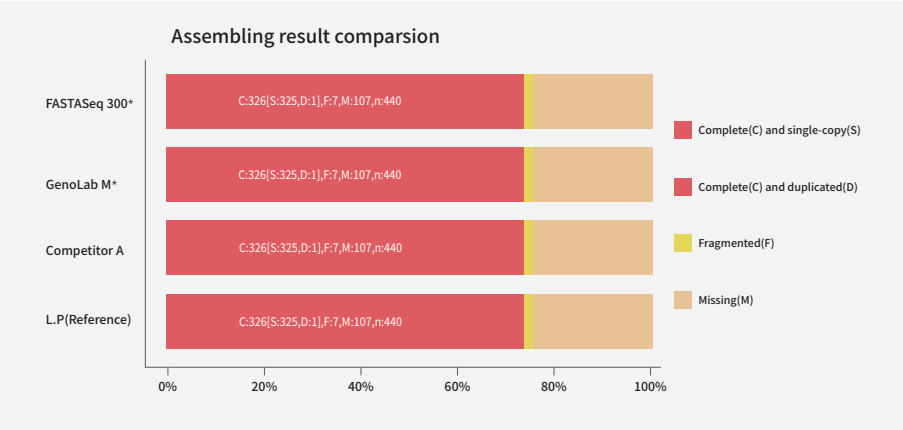
The microbial detection of FASTASeq 300* are consistent with GenoLab M*, and the clinical judgment results of all test samples are 100% accurate detected.

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



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.

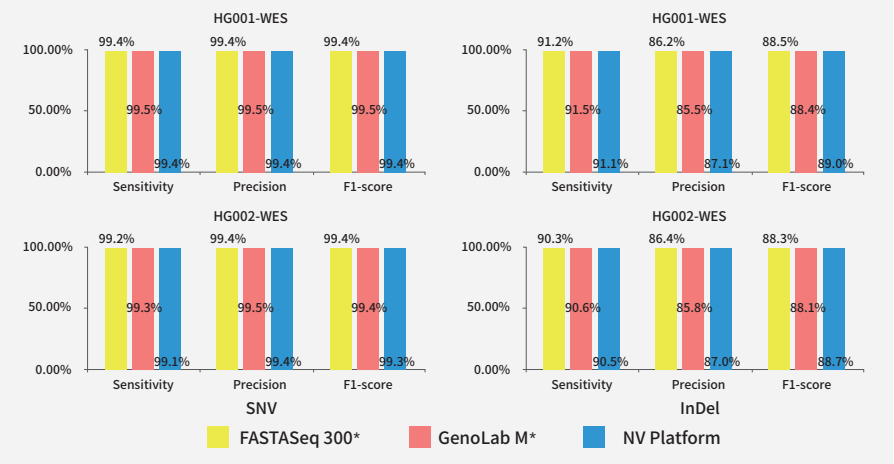
Application

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.

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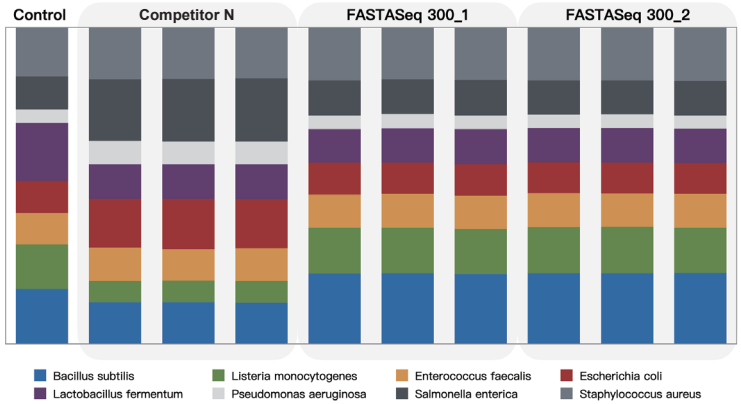
Application

Application-16S rDNA

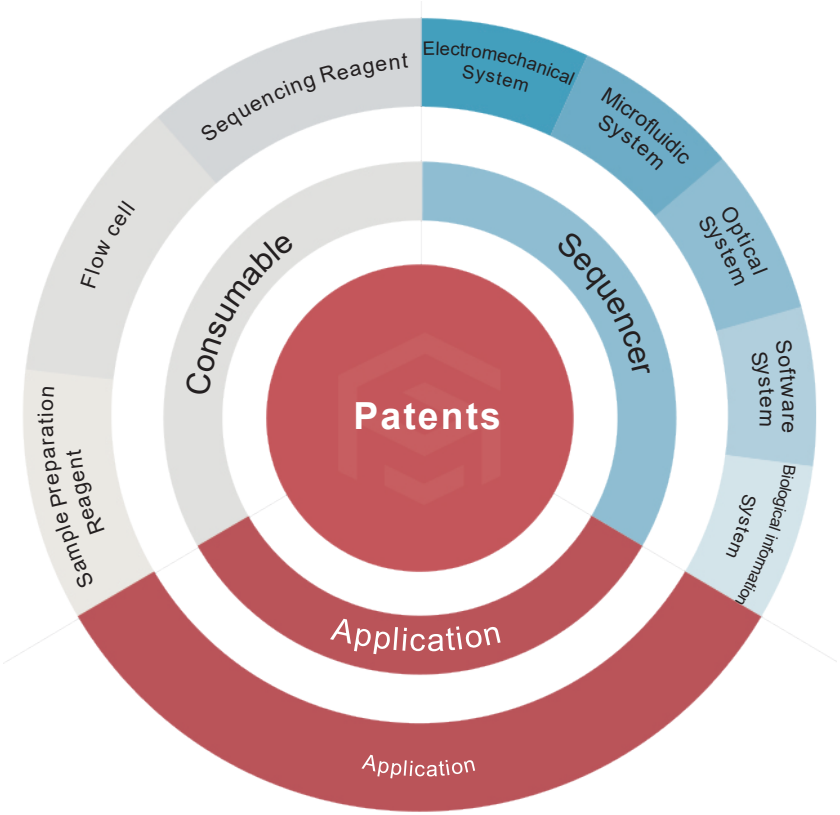
- Sample type: ZymoBIOMICS Microbial Community DNA Standard
- Library prep：Zymo_16S_1、Zymo_16S_2、Zymo_16S_3
- Sequencing platform：FASTASeq 300*，Competitor N
- Read length: PE300
- Data analysis: extract 0.1M reads/sample for deep analysis

Raw Q30%	Zymo_16S_1	Zymo_16S_2	Zymo_16S_3
FASTASeq 300_1	90.57%	90.14%	89.54%
FASTASeq 300_2	89.70%	89.39%	90.24%
Competitor N	84.55%	84.78%	84.62%



Conclusion：FASTASeq 300* has excellent result of 16s rDNA detection.

Intellectual Property & Qualifications



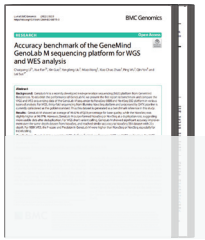
Sequencing systems are multidisciplinary specialities that combine optics, fluids, algorithms, chemistry and molecular biology. Since its establishment, GeneMind has been specializing in the independent R&D and manufacturing of molecular diagnosis technology platform centered on sequencing system. We 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

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Product Information

Product Type	Sequencer	Product Code
Sequencer	FASTASeq 300 Sequencing System Set*	SQ00019
Reagent	FASTASeq 300 Sequencing Set V1.0 (FCM-D SE075-D) *	S000181
	FASTASeq 300 Sequencing Set V1.0 (FCM 150cycles) *	S000186
	FASTASeq 300 Sequencing Set V1.0 (FCM 300cycles) *	S000189
	FASTASeq 300 Sequencing Set V1.0 (FCH-D SE075-D) *	S000191
	FASTASeq 300 Sequencing Set V1.0 (FCH 150cycles) *	S000194
	FASTASeq 300 Sequencing Set V1.0 (FCH 300cycles) *	S000197
	FASTASeq 300 Sequencing Set V1.0 (FCX 600cycles) *	S000277

Specification	
Dimensions	684 mm × 644 mm × 615 mm
Weight	145 kg
Power	2000 VA
Power Requirement	100-240 V~, 50/60 Hz
Operating Environment	Temperature:19°C-25°C Humidity: 20%-80% relative humidity (no-condensing) Altitude: below 3000 meter
Computer	CPU:Intel Xeon Silver 4216 Memory:32 GB DDR4*6 Hard Drive 1: 480 Gb Hard Drive 2: 2 TB HDD System: Windows10 x64

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GeneMind

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