GeneMind

GenoLab M*

High-throughout Sequencing Platform

Efficient · Flexible | Explore Infinite Possibilities

*Unless otherwise informed, GeneMind sequencing platform and related sequencing reagents are not available in the USA, Canada, Australia, Japan, Singapore, Western 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

GenoLab M*

High-throughput Sequencing Platform

Flexible

Multiple throughput types available

Efficient

Single or DUAL-FLOW Cells

Compatible

Applicable to mainstream sequencing platform

Versatile

Supports sequencing and data analysis in a wide range of areas

Sequencer
1. Touch Screen
2. Dual Flowcell Compartment
3.Status Indicator
4.Refrigerated Reagent Compartment
Consumables
5.Sequencing Flowcell
6.Sequencing Reagent Cartridge

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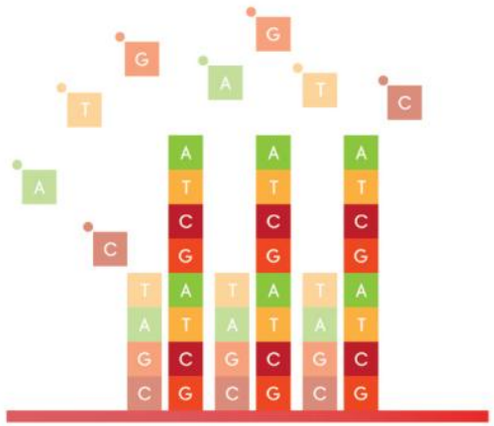
Core Technology



Surface Restricted Fluorescence Sequencing

High Integration

DNA template amplification and synthetic sequencing reactions are integrated on the surface of the flowcell. Libraries can be directly used for sequencing after preparation.

High Accuracy

Unique reversible base termination and sequencing reaction system, combined with a high-sensitivity fluorescence signal detection system to maximize sequencing accuracy.

High Compatibility

The system is compatible to mainstream NGS libraries, eliminating the need for users to redevelop samples preparation kits.

Specification

Max No. of FCs per run	Lanes/FC	Flowcell Type	Effictive reads[1]/FC	Read length	Data output/FC	Q30[2]	Run time[2]
2	4	FCM	250 M	SE75	18Gb	>85%	13h
				PE75	37Gb	>85%	22h
				PE150	75Gb	>85%	38h
		FCH	500 M	SE75	37Gb	>85%	15h
				PE75	75Gb	>85%	28h
				PE150	150Gb	>85%	50h

1. Max effective reads is determined using a standard library. Actual output may vary depending on sample type and library preparation method.
2. The percentage of bases above Q30 and run time is the average of an internal standard library over the entire run. The actual performance is affected by factors such as sample type, library quality, and insert fragment length.

Application

Application	Read length	Data/sample	FCM*1	FCM*2 or FCH*1	FCM*1+FCH*1	FCH*2
			250 M	500 M	750 M	1000 M
NIPT standard[1]	SE75	>7M average raw reads/sample	32	64	96	128
PGT-A[2]	SE75	>5M average raw reads/sample	48	96	144	192
WES[3]	PE150	7Gb/sample	10	20	30	40
RNAseq	SE50	>10M average raw reads/sample	24	48	72	96
Panel Detection[4]	SE75	5Gb/sample	12	24	36	48
mNGS	SE75	>20M average raw reads/sample	12	24	36	48

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

1. Only for T21, T18, T13
2. Detects aneuploidies, large fragment deletion/duplication CNVs(>4MB)
3. WES: average sequecning depth >200x, panel size 40Mb
4. Panel target sequencing: >95% targeted region sequencing depth >200X, panel size 2Mb

Application-NIPT

Reproductive Health—NIPT

Noninvasive prenatal testing (NIPT) performed with NGS sequencing system GenoLab M* provides reliable screening results for fetal chromosomal aneuploidies as early as 9 gestational weeks—from a single tube of 10 mL maternal blood.

Parameter		NIPT Basic	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			
No. of samples per run(1 PC +1 NC included)	GenoLab M	1 FCM : 48 2 FCM/1 FCH : 96 1 FCM+1 FCH : 144 2 FCH : 192	1 FCM : 32 2 FCM/1 FCH : 64 1 FCM+1 FCH : 96 2 FCH : 128	1 FCM : 24 2 FCM/1 FCH : 48 1 FCM+1 FCH : 72 2 FCH : 96	1 FCM : 10 2 FCM/1 FCH : 20 1 FCM+1 FCH : 30 2 FCH : 40
Read length		SE75			
Average Unique Reads / sample		⩾3.5 M	⩾5 M	⩾7 M	⩾16 M
Turn-around time		25h on GenoLab M			
Report generation		Local analysis and report system			

NIPT Basic

- Trisomies 21/18/13
- Sex identification, fetal fraction estimation

NIPT Standard

- Trisomies 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

NIPT Plus

- Trisomies 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

NIPT Pro

- Trisomies 21/18/13
- 6 Sex Chromosome Aneuploidies (SCAs) (XO/XXX/XXY/XYY/XO+XY/XXX+XY)
- Other 19 autosomal Aneuploidies
- 90 Microdeletion/duplications syndromes (Including Di-George Syndrome)
- Sex identification, fetal fraction estimation

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Application-NIPT

NIPT clinical data performance

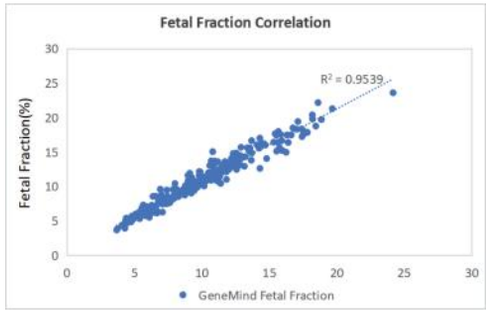
Detection Metrics	T13	T18	T21	Automoses	SCAs	Overall
Positive*	57	93	402	116	429	1097
Sensitivity	100.00%	100.00%	100.00%	98.18%	97.93%	99.21%
Specificity	99.95%	99.98%	99.94%	99.91%	99.73%	99.51%
PPV	42.11%	84.95%	90.03%	46.55%	55.24%	69.01%
NPV	100.00%	100.00%	100.00%	99.99%	99.99%	99.99%

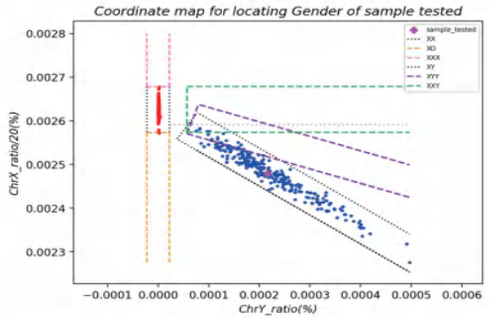
Chromosome aneuploidies	illumina			Proton		
	Sensitivity(%)	Specificity(%)	PPV(%)	Sensitivity(%)	Specificity(%)	PPV(%)
T21	98.34	99.94	88.94	98.84	99.91	82.52
T18	98.00	99.96	77.78	100.00	99.94	60.71
T13	100.00	99.97	25.00	100.00	99.91	18.18

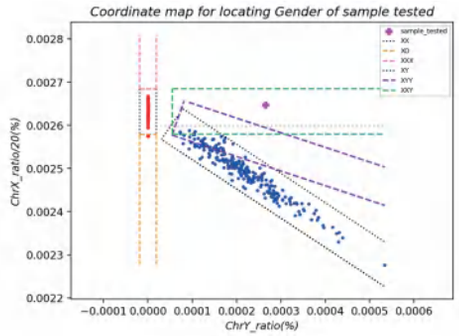
Xue et al. Molecular Cytogenetics (2019) 12:29 ,https://doi.org/10.1186/s13039-019-0441-5

Product Performance

Performance in sex identification,
fetal fraction estimation and SCAs detections







Conclusion: GeneMind NIPT products showing a highly consistent with illumina and proton on fetal chromosome aneuploidies detection.

Application-PGT-A

The integrated GeneMind PGT-A Solution providing reagents, instruments, software, installation, and training, which is an automated, reliable solution, which detects aneuploidies, large fragment deletion/duplication CNVs (>4Mb).

Specification	
Sample volume	5-10 embryo cell
Library preparation	WGA
Method	Whole genome sequencing
Read length	SE75
Sequencing platform	GenoLab M
No. of samples/run	1 FCM : 48 2 FCM/1 FCH : 96 1 FCM+1 FCH: 144 2 FCH: 192
Turn-around-time	25 h
reads requirement/sample	average raw reads per sample⩾ 5M or effective reads per sample ⩾ 3.5M
Report generation	Local analysis and report system

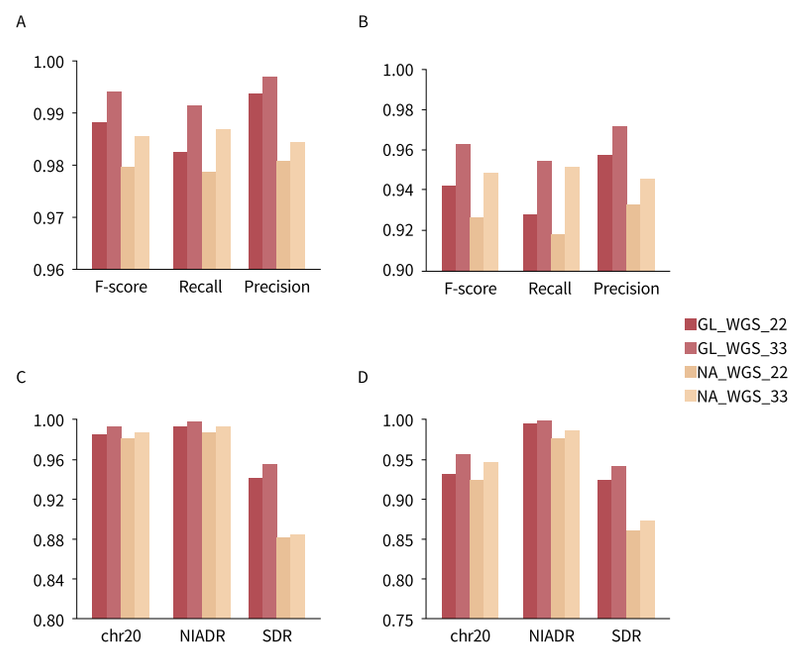
Sample ID	Karyotype validated using Array CGH	GeneMind PGT-A	Consistency
GM02906	46,XX,1q24.1q32.1(165764933-199277598)x1	-1q(q24.1~q32.1,~33.45Mb)	Yes
GM02008	46,XX,11q23.3(118170784-119064341)x-3,11q23.3q25(119078074-134449982)x1	-11q(q23.3~q25,~15.3Mb)	Yes
GM06473	46,XX,1q43q44(236343975-247190999)x-1,22q11.21(17128427-17386984)x1	-1q(q43~q44,~10.2Mb)	Yes
GM06097	46,XX,17p13.3p13.2(513-4229730)x1	-17p(p13.3~p13.2,~4.2Mb)	Yes
GM24312	46,XX,17p11.2(16662913-20256498)x1	-17p(p11.2,~3.3Mb)	Yes
GM13325	46,XX,22q11.21(17256415-19795660)x1	-22q(q11.21,~2.25Mb)	Yes
GM25372	46,XY,17p11.2(16757134-18073610)x1	-17p(p11.2,~1.2Mb)	Yes
GM01359	47,XY,+18	T18	Yes
GM02767	47,XX,+21	T21	Yes

Conclusion: Comparsion of reference standards on different platforms showing a high consistency.

Application-WGS

- Samples:NA12878 cell line
- Library:TruSeq Nano DNA library prep kit
- Sequencing Platform:GenoLab M*(GL), NA platform
- Sequencing Strategy:PE150

Samples	Sequencing platform	Bases (Gb)	Duplication rate	>Q20	>Q30	Alignment rate(%)	Mean coverage(X)
GL_WGS_22	GenoLab M	66.42	1.73%	95.35%	88.26%	99.88%	22.39
GL_WGS_33	GenoLab M	99.40	1.93%	95.22%	87.99%	99.88%	33.50
NA_WGS_22	NA	63.73	3.57%	95.92%	90.05%	99.64%	21.37
NA_WGS_33	NA	98.38	5.32%	95.92%	90.05%	99.64%	32.99



Reference Li C, Fan X, Guo X, et al. Accuracy benchmark of the GeneMind GenoLab M sequencing platform for WGS and WES analysis[J]. 2022.

Conclusion: The sensitivity and specificity of GenoLab M* sequencing data are better than those of NA platform sequencing data. GenoLab M* platform also showed significant variant detection accuracy advantage in the repeat sequence region, bringing more potential for accurate detection of disease-causing genes in this region.

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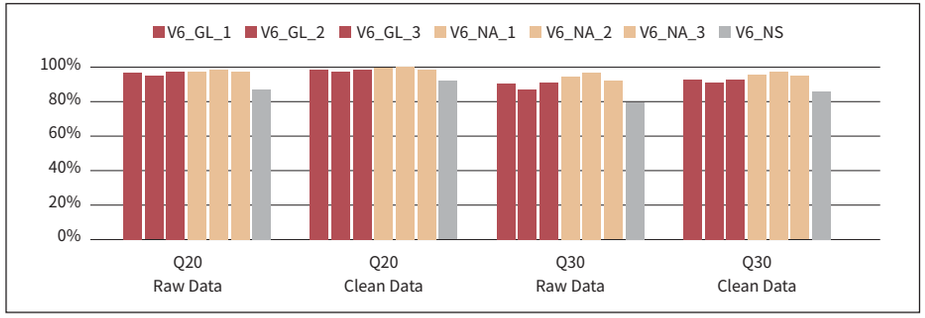
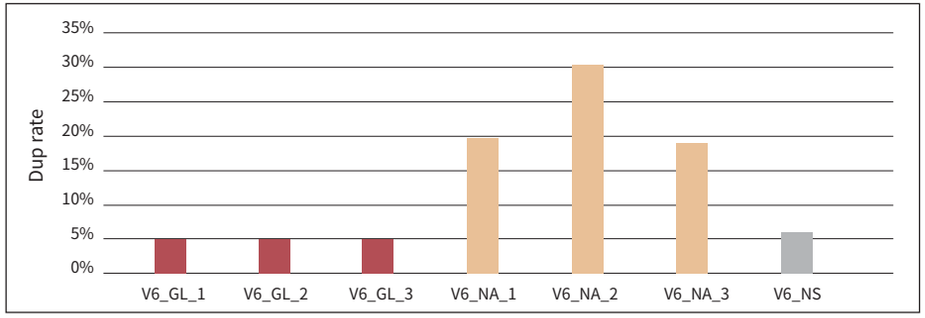
Application-WES

- Samples: NA12878 cell line
- Library: Agilent SureSelect Human All Exon V6 (Panel Size：60Mb)
- Sequencing Platform: GenoLab M*(GL), NA platform, NS platform
- Sequencing Strategy: PE150
- Data analysis: 13Gb raw data/sample for deep analysis





Conclusion： Q30 are higher than 86%，duplication rate is less than 5%. Showing a good data quality of GenoLab M*.

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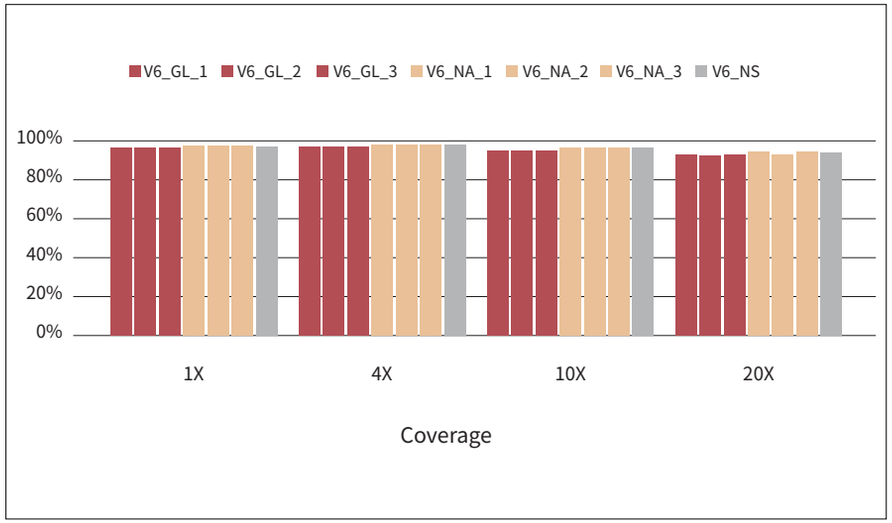
Application-WES



	V6_GL_1	V6_GL_2	V6_GL_2	V6_NA_1	V6_NA_2	V6_NA_3	V6_NS
Fold 80 base penalty	2.05	2.04	2.00	2.20	2.21	2.17	2.01
Mapping rate	99.23%	99.21%	99.22%	99.05%	98.96%	99.07%	99.50%
unique mapping rate	98.83%	98.81%	98.82%	98.70%	98.60%	98.72%	98.90%
Target resion reads (M)	53.00	51.33	53.14	46.55	41.08	46.37	48.93
Target region rate	68.98%	69.00%	68.93%	70.88%	70.66%	70.86%	71.05%
Mean sequencing depth	107.54	103.22	108.18	97.25	86.29	96.33	92.36

Conclusion: The unique mapping rate of different platform are higher than 98%. And the average coverage are quite comparable with competitors, showing a quite good uniformity performance of target region.

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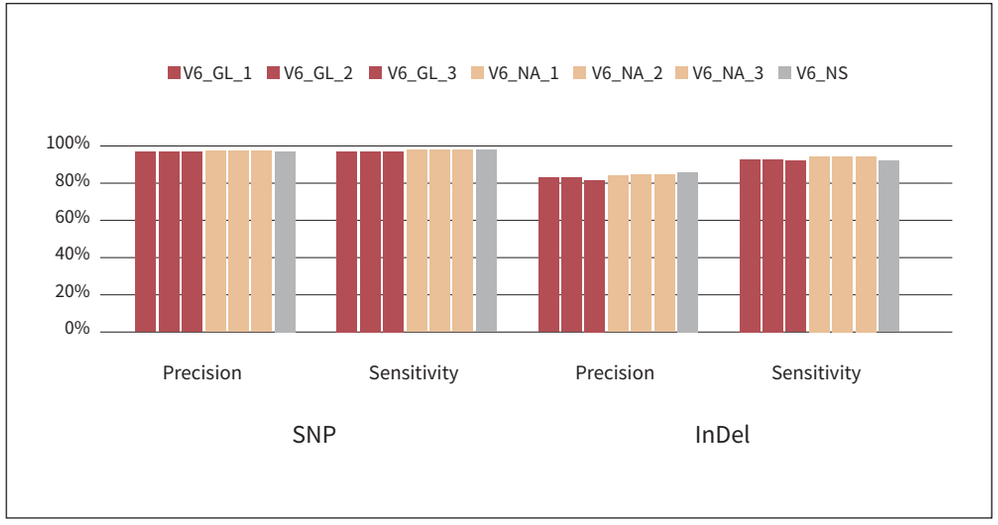
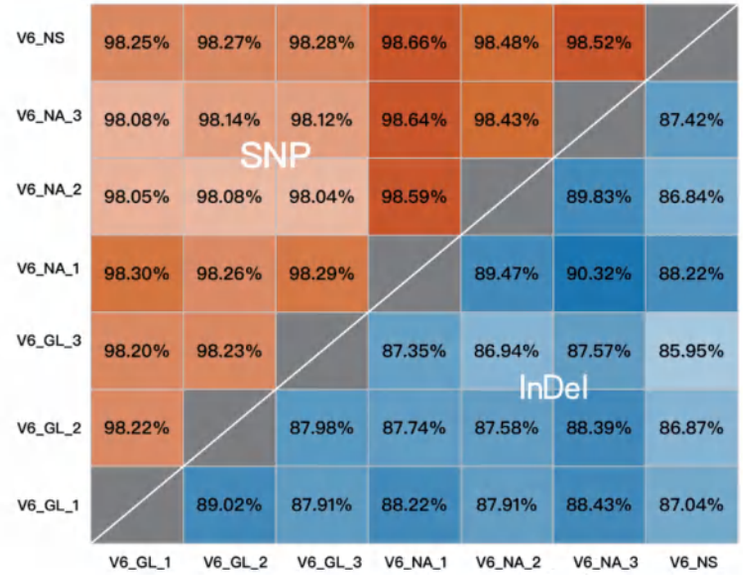
Application-WES



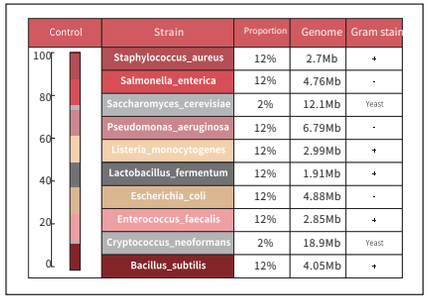


Conclusion: SNP>98%, InDel>85%.The accuracy and sensitivity of in SNP and InDel detection are quite comparable between different platforms, showing a good mutation detection performance.

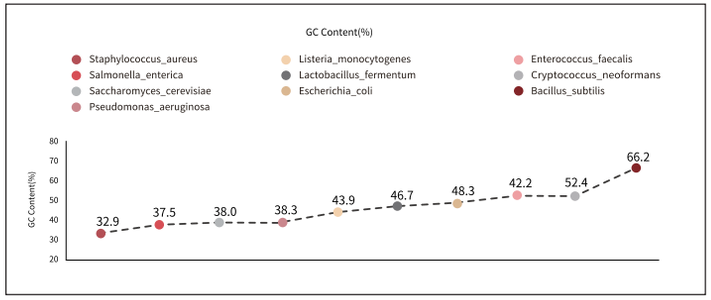
Application-mNGS

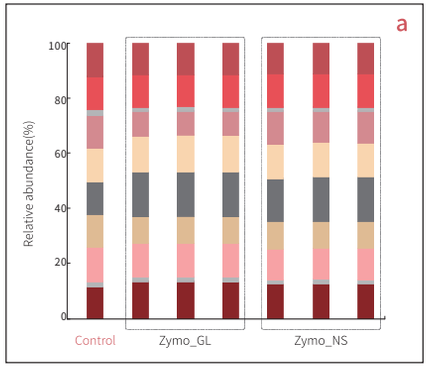
- Samples: ZymoBIOMICS Microbial Communitu DNA Standard (Zymo Research)
- Library:Hieff NGS OnePot II DNA Library Prep Kit(Yeasen)
- Sequencing Platform: GenoLab M*(GL), NS platform
- Read length: PE150

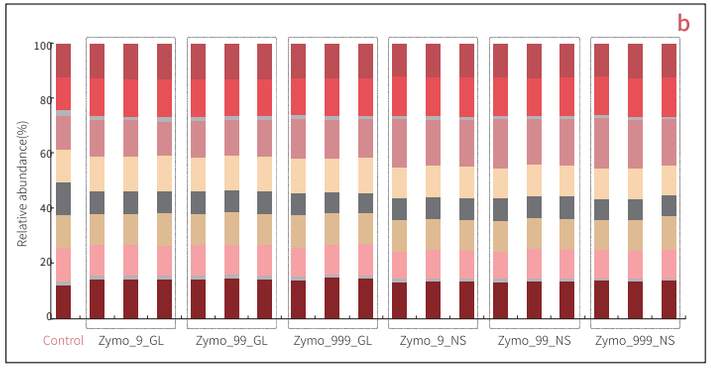
Samples	Proportion of human-derived host	No. of library	Strategy	Sequecning Platform
Zymo	0%	3	SE75, 1M reads	GenoLab M* and NS platform
Zymo-9	90%	3	SE75, 20M reads	
Zymo-99	99%	3	SE75, 20M reads	
Zymo-999	99.9%	3	SE75, 20M reads	



Control	Strain	Proportion	Genome	Gram stain
	Staphylococcus_aureus	12%	2.7Mb	+
	Salmonella_enterica	12%	4.76Mb	-
	Saccharomyces_cerevisiae	2%	12.1Mb	Yeast
	Pseudomonas_aeruginosa	12%	6.79Mb	-
	Listeria_monocytogenes	12%	2.99Mb	+
	Lactobacillus_fermentum	12%	1.91Mb	+
	Escherichia_coli	12%	4.88Mb	-
	Enterococcus_faecalis	12%	2.85Mb	+
	Cryptococcus_neoformans	2%	18.9Mb	Yeast
	Bacillus_subtilis	12%	4.05Mb	+







Conclusion: The analysis results showed that the strains and relative abundance detected by GenoLab M were in high agreement with Control and NS platforms among the metagenomic mock samples with different microbial ratios (0.1%-100%).

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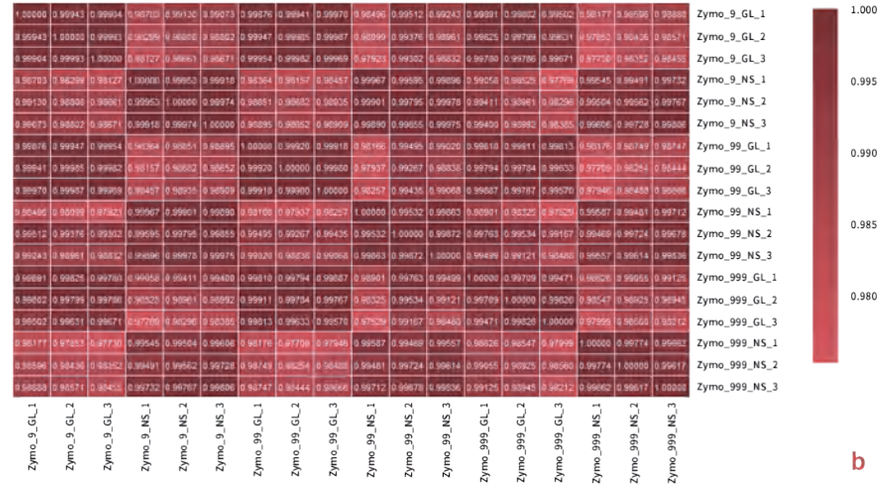
Application-mNGS

- Samples: ZymoBIOMICS Microbial Communitu DNA Standard (Zymo Research)
- Library:Hieff NGS OnePot II DNA Library Prep Kit(Yeasen)
- Sequencing Platform: GenoLab M*(GL), NS platform
- Read length: PE150



Conclusion: The analysis results showed that the strains and relative abundance detected by GenoLab M* and competitors showing a high consistency (RPKM>0.98).

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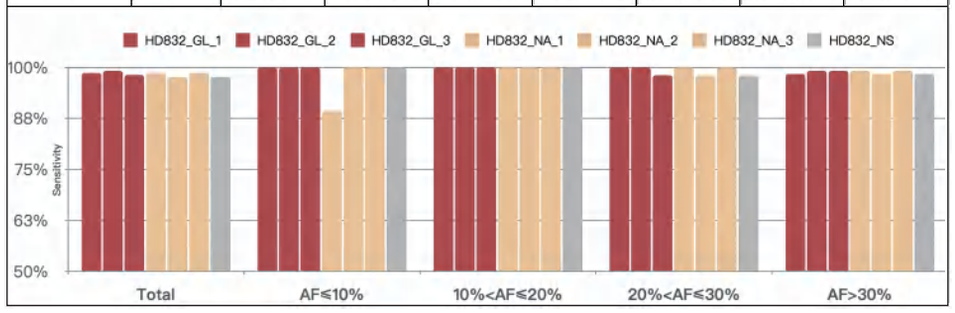
Application-Targeted commercial panel

- Sample type：FFPE (Horizon Discovery HD832)
- Target Panel：Illumina TruSight Oncology 500 (Panel size：~2Mb)
- Sequencing platform：GenoLab M*(GL), NA platform(NA), NS platform(NS)
- Sequencing strategy：PE150, 25Gb raw data/sample

Library	HD832		TSO500 Theoretical SNPs (Overlap)		Verified SNPs	
HD832	386 (AF:1~100%)	SNV:356	SNV:194	212 (AF:1~100%)	NGS validation	206
		InDel:30	InDel:18		ddPCR validation	25

NGS AF	Mut Number	HD832_GL_1	HD832_GL_2	HD832_GL_3	HD832_NA_1	HD832_NA_2	HD832_NA_3	HD832_NS
AF≤10%	9	9 (100.00%)	9 (100.00%)	9 (100.00%)	8 (88.89%)	9 (100.00%)	9 (100.00%)	9 (100.00%)
10%<AF≤20%	24	24 (100.00%)	24 (100.00%)	24 (100.00%)	24 (100.00%)	24 (100.00%)	24 (100.00%)	24 (100.00%)
20%<AF≤30%	49	49 (100.00%)	49 (100.00%)	48 (97.96%)	49 (100.00%)	48 (97.96%)	49 (100.00%)	48 (97.96%)
AF>30%	124	122 (98.39%)	123 (99.19%)	123 (99.19%)	123 (99.19%)	122 (98.39%)	123 (99.10%)	122 (98.39%)
NGS (no value)	6	5 (83.333%)	5 (83.33%)	4 (66.67%)	5 (83.33%)	4 (66.67%)	4 (66.67%)	4 (66.67%)
Total	212	209 (98.58%)	210 (99.06%)	208 (98.11%)	209 (98.58%)	207 (97.64%)	209 (98.58%)	207 (97.64%)



Conclusion： GenoLab M* showing a relative high sensitivity detection rate on the commercial targeted panel (208/212, 98%) and the sensitivity of different different mutation samples are higher than 99%.

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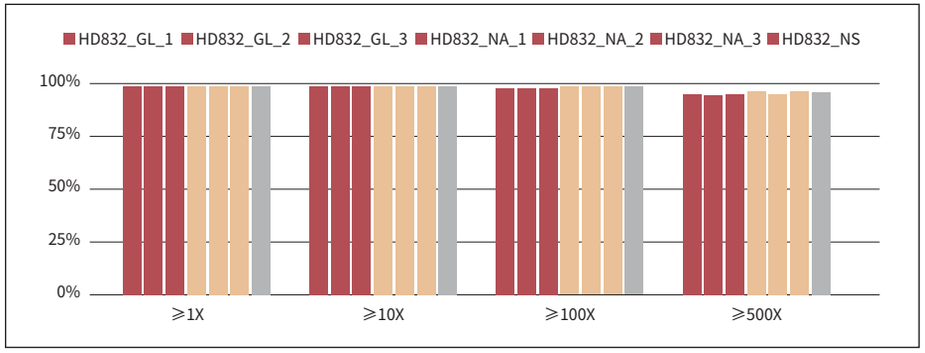
Application-Targeted commercial panel

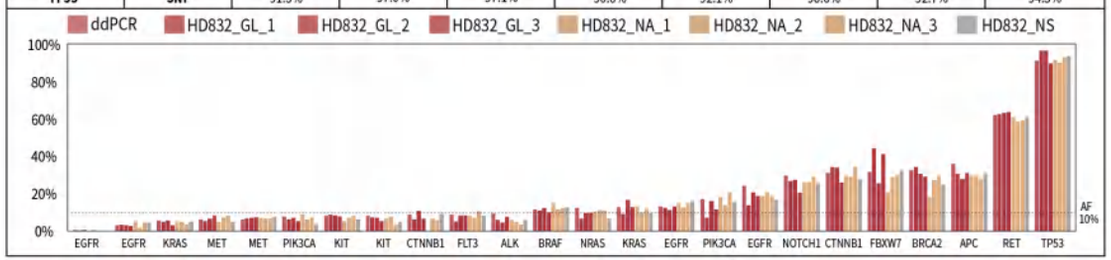
HD832	HD832_GL_1	HD832_GL_2	HD832_GL_3	HD832_NA_1	HD832_NA_2	HD832_NA_3	HD832_NS
Clean reads(M)	148.00	155.00	148.00	151.00	146.00	155.00	136.00
Mapping rate	99.49%	99.48%	99.48%	99.09%	99.15%	99.12%	99.67%
Unique mapping rate	99.07%	99.06%	99.06%	98.56%	98.66%	98.58%	99.10%
Duplicato rato	67.83%	69.09%	68.03%	71.60%	70.32%	71.69%	67.31%
Target region reads (M)	25.90	25.90	25.50	23.30	23.03	23.02	24.50
Target region rate	54.87%	54.30%	54.56%	54.71%	53.67%	53.01%	55.11%
Target region +150bp rate	71.82%	71.26%	71.54%	72.24%	71.07%	70.46%	72.37%
Target mean depth	1389	1402	1371	1283	1248	1281	1261

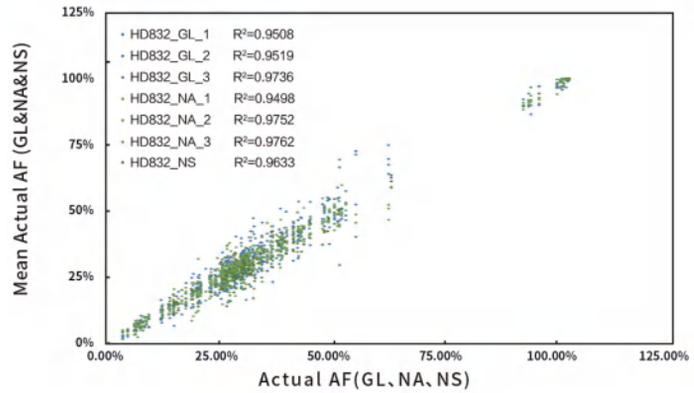


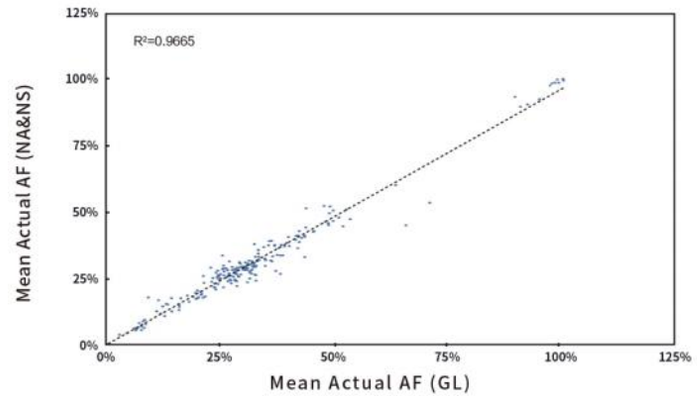
Conclusion: Mapping rate, average coverage rate and target region rate among different platforms are quite samiliar, showing a quite good data quality.

Application-Targeted commercial panel

Gene	Type	Expected AF				Actual AF			
		ddPCR	HD832_GL_1	HD832_GL_2	HD832_GL_3	HD832_NA_1	HD832_NA_2	HD832_NA_3	HD832_NS
EGFR	SNP	1.0%	0.7%	0.9%		0.9%			
EGFR	DEL	1.5%							
EGFR	SNP	3.5%	3.7%	3.5%	2.7%	5.6%	2.2%	5.0%	4.8%
KRAS	SNP	6.0%	5.3%	6.0%	3.2%	5.6%	5.0%	4.0%	5.3%
MET	DEL	6.5%	5.7%	6.8%	8.5%	5.1%	7.5%	8.5%	5.4%
MET	SNP	6.5%	7.0%	7.3%	7.8%	7.4%	6.6%	6.8%	8.0%
PIK3CA	SNP	8.0%	6.5%	7.2%	5.7%	9.2%	6.5%	7.5%	4.1%
KIT	SNP	8.5%	9.1%	8.7%	8.2%	5.6%	7.2%	8.3%	6.5%
KIT	SNP	8.5%	7.6%	7.2%	5.6%	6.9%	8.0%	3.9%	5.3%
CTNNB1	DEL	9.0%	6.5%	11.0%	6.9%		6.8%	6.4%	9.4%
FLT3	DEL	9.0%	5.5%	8.4%	8.7%	8.4%	7.3%	10.7%	8.5%
ALK	INS	9.5%	6.2%	5.0%	7.9%	6.3%	5.2%	3.6%	6.2%
BRAF	SNP	12.0%	11.1%	12.7%	10.3%	15.1%	11.7%	12.7%	13.2%
NRAS	SNP	12.5%	6.7%	9.9%	9.8%	10.5%	11.5%	11.2%	6.9%
KRAS	SNP	13.0%	9.4%	16.9%	13.0%	13.4%	10.0%	12.2%	9.9%
EGFR	SNP	13.5%	12.8%	11.7%	13.5%	15.3%	13.2%	15.1%	16.4%
PIK3CA	SNP	17.5%	7.2%	16.3%	11.7%	18.5%	14.1%	20.9%	15.8%
EGFR	SNP	24.5%	14.0%	21.1%	19.1%	19.1%	21.0%	19.0%	17.0%
NOTCH1	SNP	30.0%	27.2%	27.7%	20.9%	26.5%	26.6%	29.4%	25.8%
CTNNB1	SNP	31.5%	34.8%	34.3%	26.4%	30.0%	29.6%	34.7%	28.2%
FBXW7	DEL	32.0%	44.4%	25.8%	41.6%	21.1%	28.9%	30.2%	32.7%
BRCA2	DEL	32.5%	34.5%	30.9%	29.4%	18.4%	27.7%	30.0%	25.6%
APC	SNP	36.5%	30.7%	27.8%	31.4%	29.9%	29.6%	28.6%	31.4%
RET	SNP	62.5%	62.8%	63.6%	63.8%	61.4%	59.0%	59.4%	61.4%
TP53	SNP	91.5%	97.0%	97.1%	90.0%	92.1%	90.6%	92.7%	94.3%







Conclusion: The actual detected muation calling rate is quite consistent with expection. There is no much big difference for the mutation detection result among GenoLab M* and NA, NS platforms.

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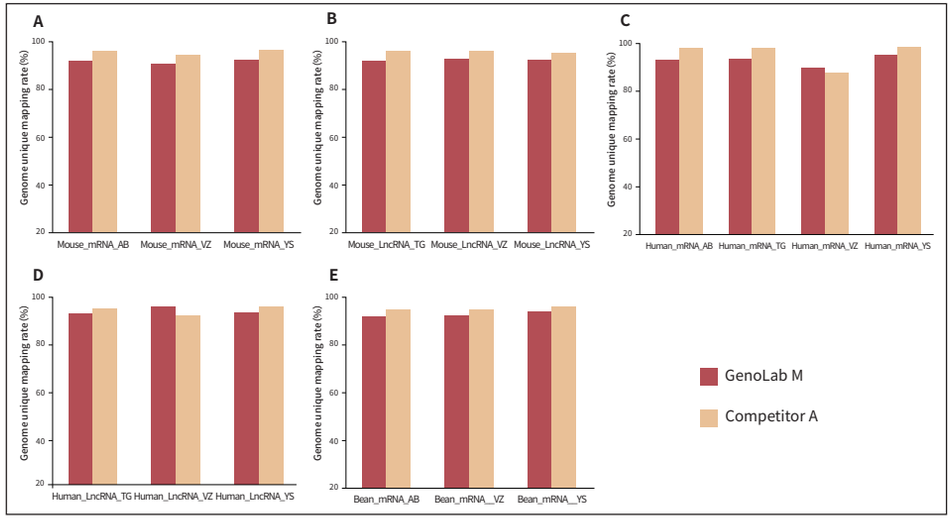
Application-RNAseq

- SSample type：Human liver stellate cells,Mouse testicular tissue, Hairy root of soybean mRNA and LncRNA library prep：Commercial RNA library prep kit
- Sequencing platform：GenoLab M *(GM) and Competitor A(NA)
- Read length: PE100/PE150
- Data analysis: >5Gb clean data/sample



Library type	Sample type	Sample name	Brand	Library prep kit
mRNA (10)	Mouse testicular tissue	Eb-T1-C1-AB	ABclonal	Fast RNA-Seq Lib Prep Module
	Human liver stellate cells	Eb-T1-TGF-AB		
	Hairy root of soybean	Eb-T1-3301.2-AB		
	Mouse testicular tissue	Eb-T1-C1-YS	Yeasen	Hieff NGS Ultima Dual-mode mRNA Library Prep Kit
	Human liver stellate cells	Eb-T1-TGF-YS		
	Hairy root of soybean	Eb-T1-3301.2-YS		
	Human liver stellate cells	Eb-T1-TGF-TG	Qiagen	TIANSeq Stranded RNA-Seg Kit
	Mouse testicular tissue	Eb-T1-C1-VZ	Vazyme	VAHTS Universal V6 RNA-Seq Library Prep Kit
	Human liver stellate cells	Eb-T1-TGF-VZ		
	Hairy root of soybean	Eb-T1-3301.2-VZ		
LncRNA (6)	Mouse testicular tissue	Eb-T1-C1-YS	Yeasen	Hieff NGS MaxUp rRNA Depletion Kit(Human/Mouse/Rat) + Hieff NGS Ultima Dual-mode RNA Library Prep Kit
	Human liver stellate cells	Eb-T1-TGF-TG		
	Mouse testicular tissue	Eb-T1-C1-TG	Qiagen	TIANSea rRNA Depletion Kit(H/M/R)+TIANSeq Stranded RNA-Seg Kit
	Human liver stellate cells	Eb-T1-TGF-YS		
	Mouse testicular tissue	Eb-T1-C1-VZ	Vazyme	Ribo-off rRNA Depletion Kit(Human/-Mouse/Rat)+VAHTS UniversalV6 RNA-Seq Library Prep Kit
	Human liver stellate cells	Eb-T1-TGF-VZ		

Conclusion: Genome unique mapping rate is quite comparable between two platforms.

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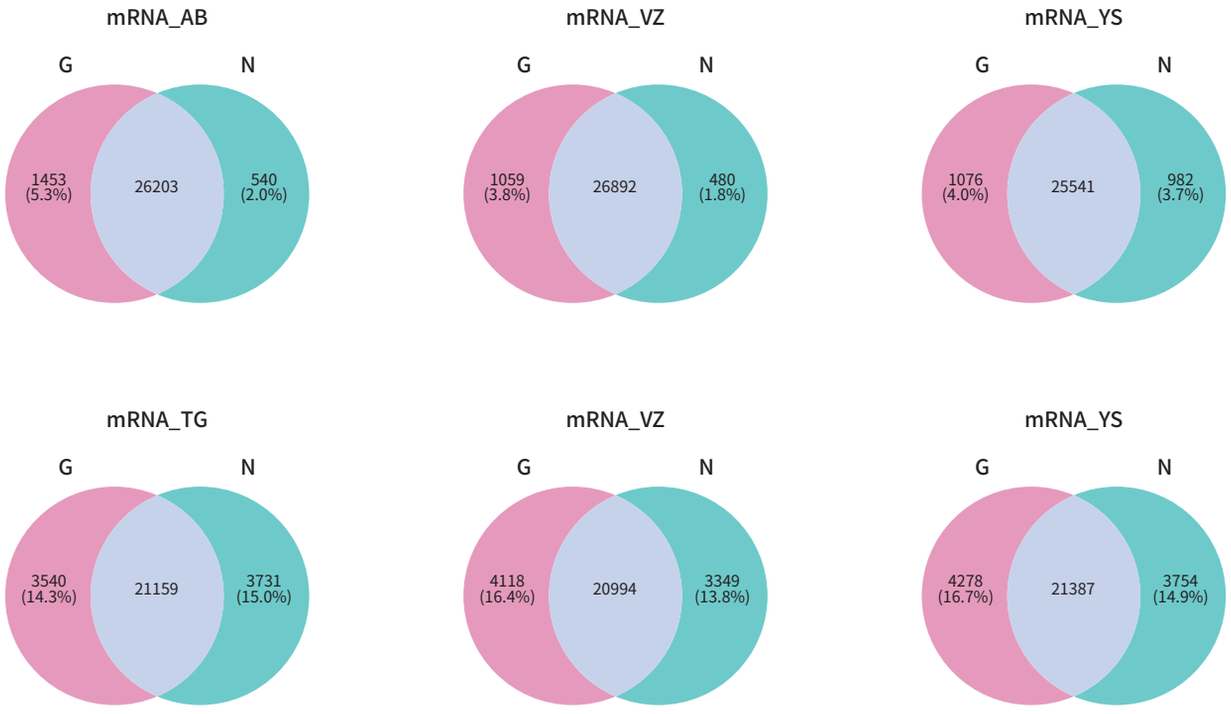
Application-RNAseq



Conclusion: The actual detected muation calling rate is quite consistent with expection. There is no much big difference for the mutation detection result among GenoLab M* and NA, NS platforms.

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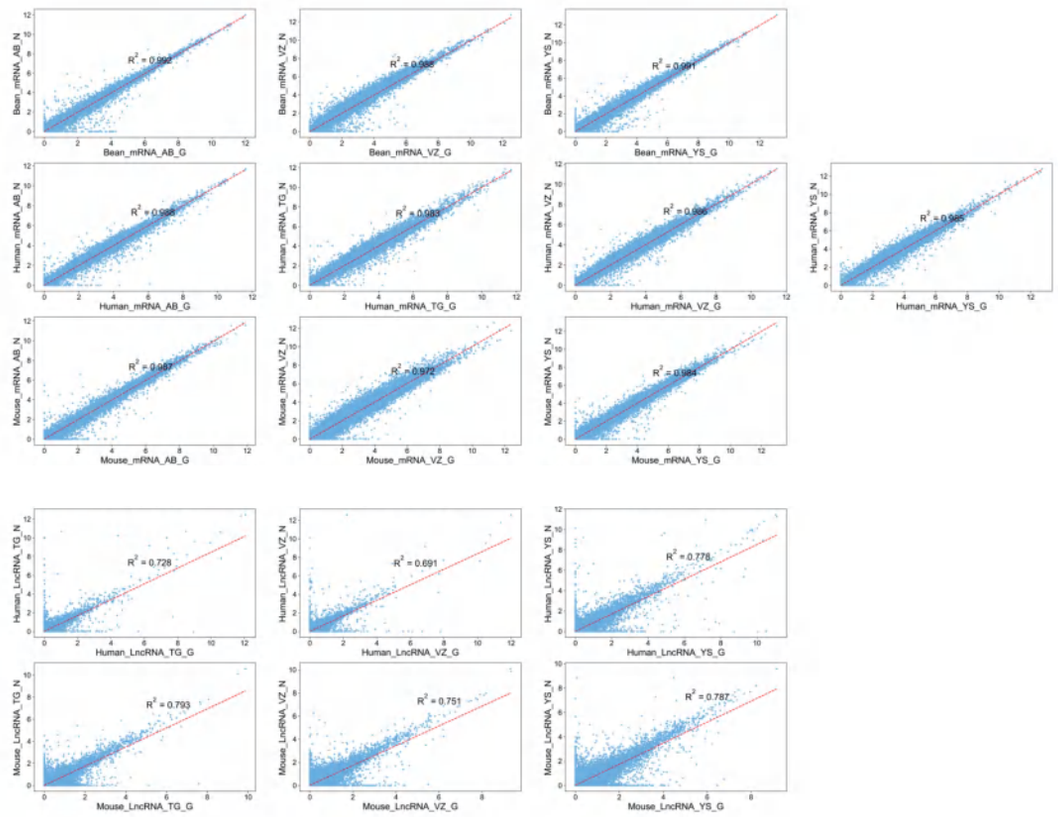
Application-RNAseq

mRNA

LncRNA



Conclusion: As for the gene quantitative correlation, the R^2 among 10 mRNA libraries between GenoLab M* and NA are higher than 97%. The R^2 among 6 LncRNA libraries between GenoLab M* and NA are higher than 70%. Showing a quite high consistency result.

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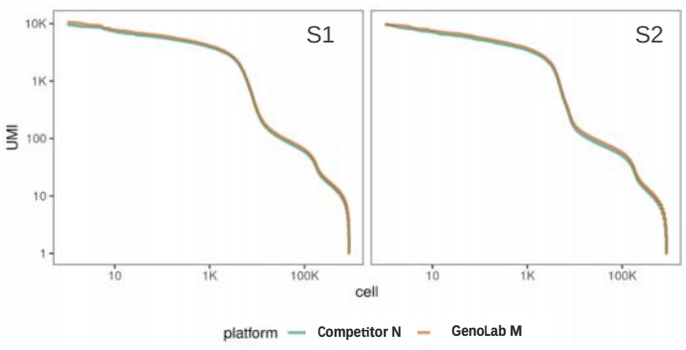
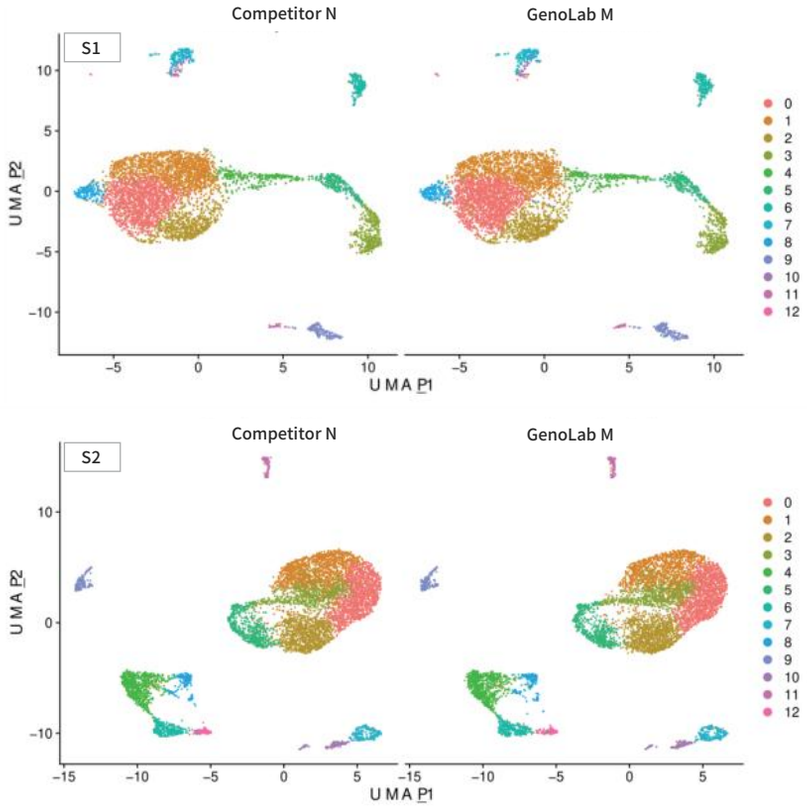
Application-Single cell

- Sample type: Single cell suspension from two different tumor tissue
- Library preparation: Galaxy Single Cell 3' mRNA Kit v1.0
- Sequencing platform: GenoLab M*, competitor N
- Read length: PE150
- Data analysis:100M reads/sample





Conclusion: The results of data analysis showed that UMI level, cell clustering and isogene expression are consistent with the comparison platform.

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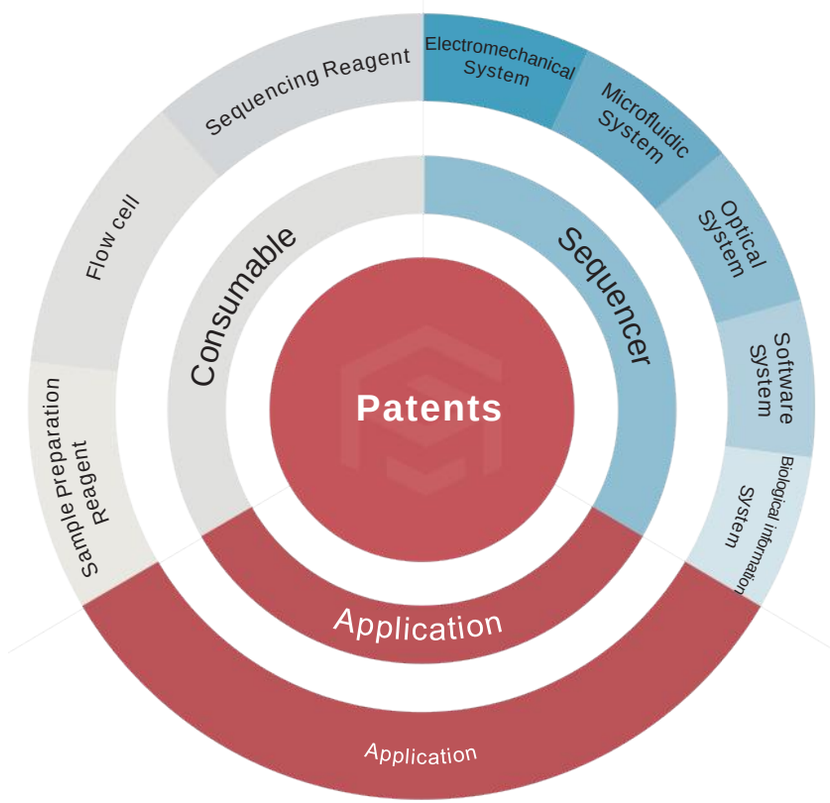
Intellectual Property & Qualifications



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 April2025, GeneMind has more than 5 00 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.

500+

Patents granted

ISO 13485:2016

Quality Management System Certification

80+

NMPA approval/ CE IVD registration

80+

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

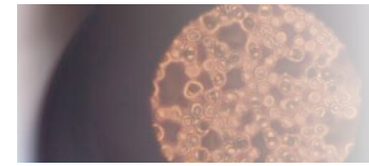
- Enzyme Engineering Lab
  Independent research and development of core enzyme

Partners

- Reproductive Health

- Genetic & Rare Diseases

- Pathogen Detection



- Oncology

- Animal Genomics

- Agrigenomics

Configuration

Instrument Control Computer
Operating System: Windows 10 CPU: Intel Xeon Silver 4216 2.1GHz Memory: 32GB*6 DDR4 Hard Drive 1: 1TB SSD Hard Drive 2: 10TB HDD

Specification	Operating Environment
Dimensions: ≤1170mm(L) *690mm(W)*600mm(H)	Temperature: 19°C-25°C Humidity: 20%-80% relative humidity, non-condensing Altitude: below 3000m

Product Type	Product Code	Product Name	Specification
Sequencer	SQ00010	GenoLab M sequencing system	GenoLab M
	SQ00011	GenoLab M Dx sequencing system	GenoLab M Dx
Reagents	S000243	GenoLab M Sequencing Set V4.0 (FCM-D SE075-D)	FCM-D SE075-D
	S000244	GenoLab M Sequencing Set V4.0 (FCM 150cycles)	FCM 150cycles
	S000245	GenoLab M Sequencing Set V4.0 (FCM 300cycles)	FCM 300cycles
	S000246	GenoLab M Sequencing Set V4.0 (FCH-D SE075-D)	FCH-D SE075-D
	S000247	GenoLab M Sequencing Set V4.0 (FCH 150cycles)	FCH 150cycles
	S000248	GenoLab M Sequencing Set V4.0 (FCH 300cycles)	FCH 300cycles
	S000402	Universal Reaction Kit for Sequencing (Reversible Terminator Sequencing)	GenoLab FCM-D SE075-D
	S000400	Universal Reaction Kit for Sequencing (Reversible Terminator Sequencing)	GenoLab FCM 150cycles
	S000401	Universal Reaction Kit for Sequencing (Reversible Terminator Sequencing)	GenoLab FCM 300cycles
	S000405	Universal Reaction Kit for Sequencing (Reversible Terminator Sequencing)	GenoLab FCH-D SE075-D
	S000403	Universal Reaction Kit for Sequencing (Reversible Terminator Sequencing)	GenoLab FCH 150cycles
	S000404	Universal Reaction Kit for Sequencing (Reversible Terminator Sequencing)	GenoLab FCH 300cycles

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GeneMind

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