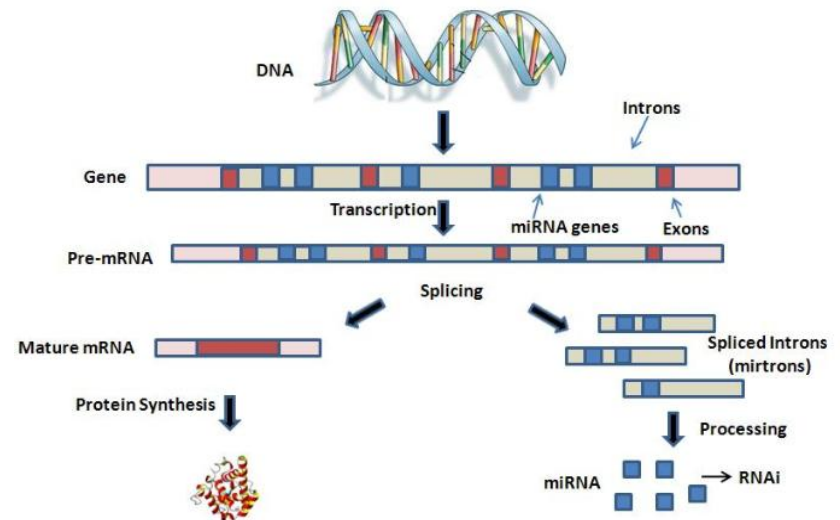
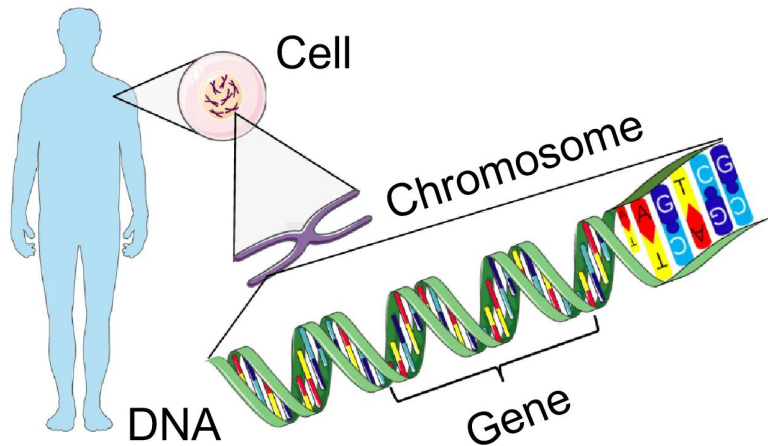


GeneMind WES Solution

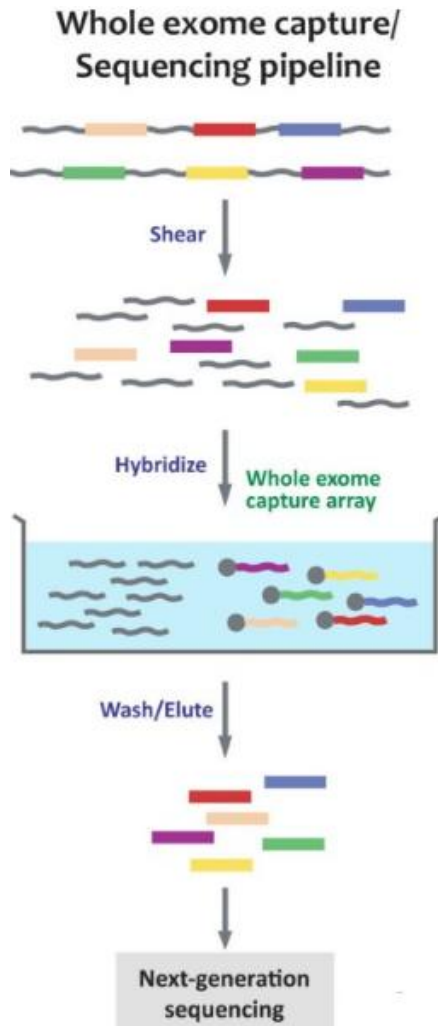


Exons and Genetic Diseases

- Whole-exome sequencing is a widely used next-generation sequencing (NGS) method that involves sequencing the protein-coding regions of the genome.
- The human exome represents less than 2% of the genome, but contains ~85% of known disease-related variants, making this method a cost-effective alternative to whole-genome sequencing.
- Exome sequencing using exome enrichment can efficiently identify coding variants across a broad range of applications, including population genetics, genetic disease, and cancer studies.



WES Principle and Advantage



Advantage of Exome Sequencing

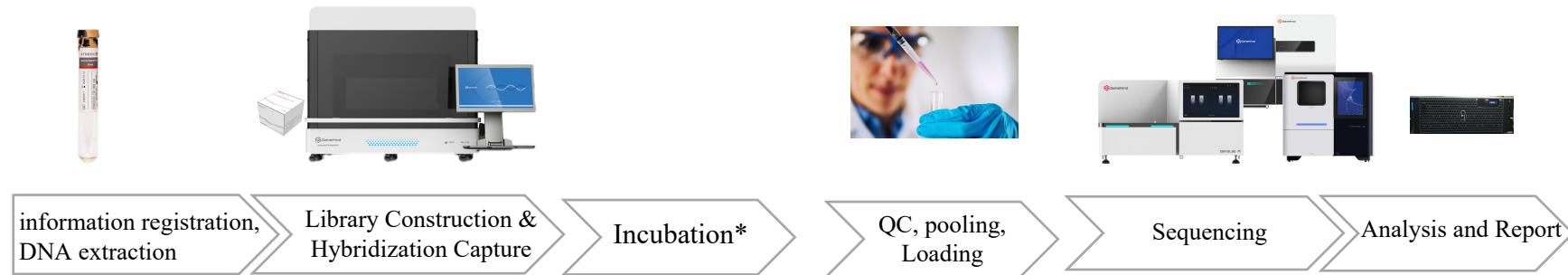
- Targeted view of the protein-coding regions of the genome
- Efficient Analysis of Coding Regions, provide reliable and sensitive detection results of coding variants (SNVs, Indels)
- Fast and cost effective sequencing compared with WGS(8–10 Gb of sequencing per exome compared to ~90 Gb per whole human genome)

GeneMind WES Total Solution

PARAMETER			
Sample type	Tissue / Blood		
Application	Genes and Inherited Disease		
Sequencing Platform	GenoLab M*	FASTASeq 300*	SURFSeq 5000*
No. of samples/run	1 FCM : 6 2 FCM/1 FCH : 12 1 FCM+1 FCH: 18 2 FCH: 24	1 FCM: 2 1 FCH: 6	1 FCM : 12 2 FCM/1 FCH : 48 1 FCM+1 FCH: 60 2 FCH: 96
Read length	PE150		
Effective throughput/sample	Around 10 Gb		
Turn-around-time	3-4 days		
Report generation	Local analysis and report system		

*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.

GeneMind WES solution Workflow(32 samples)



Automated	2.5h	4h	16h	2.5h	24-53h	10h	61-88h
-----------	------	----	-----	------	--------	-----	--------

Manually	2.5h	4h	16h	2.5h	24-53h	10h	61 - 88h
----------	------	----	-----	------	--------	-----	----------

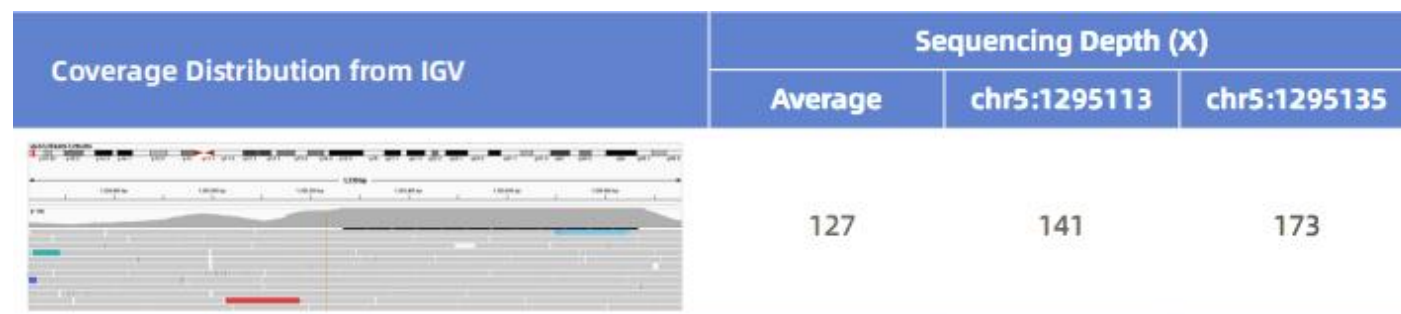
*In the incubation step of hybridization capture library preparation, the hybridization mixture is incubated to allow the probes to bind specifically to their target sequences. This step does not require human intervention once the mixture is prepared.

*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.

Library Preparation and Enrichment

Spanning 36.68 Mb target region of the human genome with efficient probe design, Genemind Universal DNA Library prep with enrichment Kit provides a more complete coverage of protein coding genes for the variant detection which could be widely used in clinical and academic research.

Database	CDS Region Coverage (%)
RefSeq	99.88
MANE	99.61
CCDS	99.92



Sequencing Platforms

Benchtop sequencer

FASTASeq 300*

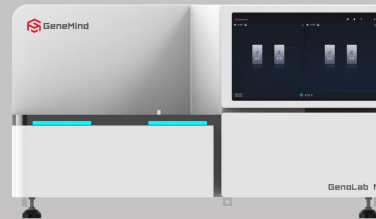


100M/250M

7.5Gb-75Gb

mNGS/tNGS/Panel/
NIPT/PGT-A

GenolabM*



250M/500M

18Gb-300Gb

NIPT/PGT-A/CNV-Seq/
mNGS/cancer panel/
WES/RNAseq

SURFSeq 5000*



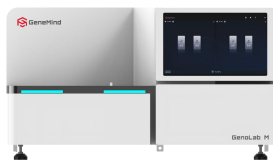
500M/2000M/3600M*

50Gb-2.2Tb (available in
Nov. 2024)

WES/WGS/cancer
panel/Single cell sequencing

*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.

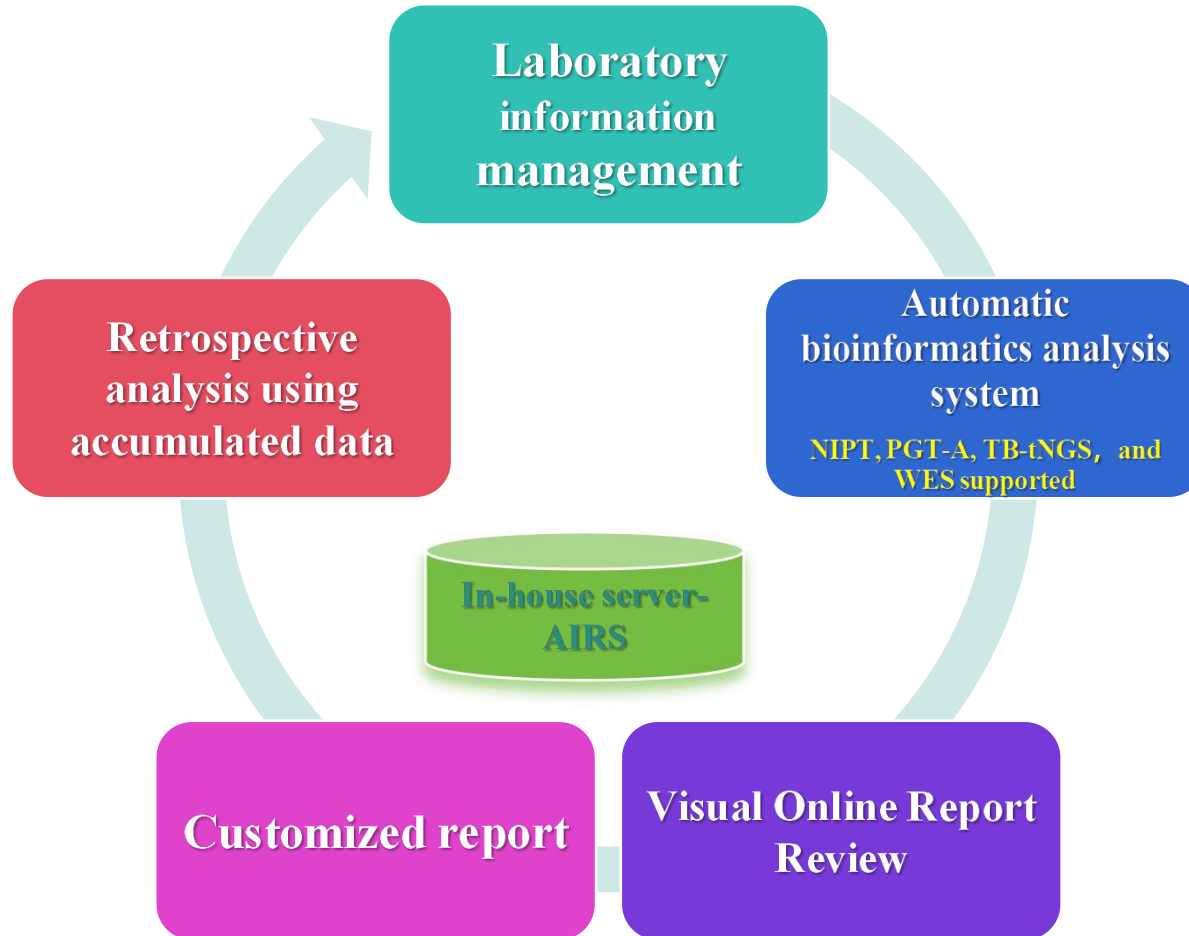
GeneMind Sequencing Platforms



Product	GenoLab M*	FASTASeq 300*	SURFSeq 5000*
Launch year	2020	2022	2023
Features	Comprehensive and flexible	Fast, flexible and simple-to-operate	Economical, efficient and all-round
Product qualification	CE IVDR	CE IVDR	CE IVDR
Applications	NIPT, PGT-A, Pathogen detection, cancer panel, and genetic disease diagnosis such as WES and WGS	NIPT, PGT-A, WES, cancer panel, pathogen detection, 16s, forensic	Scientific and technological services, MRD, Pan-cancer analysis, agricultural breeding or species identification, WES, WGS
Flow cell per run	2 Flow Cells	1 Flow Cell	2 Flow Cells
Flow cell Type	FCM: 250 M reads FCH: 500 M reads	FCM: 100 M reads FCH: 250 M reads FCX: 100 M reads (available in July 2024)	FCM: 500 M reads FCH: 2000 M reads FCP: 3600 M reads (available in November 2024)
Read length	FCM: 75/150/300 FCH: 75/150/300	FCM: 75/150/300 FCH: 75/150/300 FCX: 400/600	FCM: 100/200/300/600 FCH: 50/100/200/300 FCP: 50/100/200/300

*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.

Automatic Analysis Report System



WES Report Template

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Genetic Testing Report

SAMPLE INFORMATION

Accession ID	Specimen type
Name	Referring facility
DOB	Referring physician
Sex	Date received
Ethnicity	Date reported
Indication	Delay in motor milestones including delay in walking independently and standing up from a supine position. Progressive weakness, waddling gait and difficulty climbing stairs, running, jumping and standing up.

TEST ADMINISTERED

Targeted sequencing of whole exome as performed and data analyzed as described in methods section in appendix.

Mutations passed the filter, ordered by the weighted score calculated by the phenotype association, in silico prediction and record in database

Gene & Transcript	Chromosome location	Variant	Zygosity	Mutation location	Disease r Phenotype/ M.O.I.	ACMG (Automatic classification)
DMD NM_004006.3	ChrX: 3:25,3616-4	c.2253del(p.Lys752fs)	Het	Exon 1b	Becker muscular dystrophy (XLR) Cardiomyopathy/dilated, 3B (X1) Duchenne muscular dystrophy (XLR)	Likely pathogenic

INTERPRETATION

Variant: DMD NM_004006.3:c.2253del(p.Lys752fs)

The variant DMD:c.2253del(p.Lys752fs) is a frameshift mutation in the DMD gene. Zygosity status is heterozygous. It is expected to result in a absent or disrupted protein product. This variant is not present in population databases (Geno2MP, ExAC or frequency). This variant has not been reported in the literature in individuals with DMD-related conditions. Loss-of-function variants in DMD are reported to be pathogenic (PMID: 16770791, 25007885). For these reasons, this variant is classified as likely pathogenic.

DMD-associated dystrophinopathies cover a spectrum of X-linked muscle disease ranging from mild to severe that includes **Duchenne muscular dystrophy**, **Becker muscular dystrophy**, and **DMD-associated dilated cardiomyopathy (DCM)**. The mild end of the spectrum includes the phenotype of asymptomatic increase in serum concentration of creatine phosphokinase (CK) and muscle cramps with myoglobinuria. The severe end of the spectrum includes progressive muscle diseases that are classified as Duchenne/Becker muscular dystrophy when skeletal muscle is primarily affected and as DMD-associated DCM when the heart is primarily affected. For more detailed information.

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Mutations on genes in secondary findings passed the filter

Gene & Transcript	Chromosome location	Variant	Zygosity	Mutation location	Disease r Phenotype/ M.O.I.	Classification
<p>INTERPRETATION</p> <p>Notes:</p> <p>*Secondary/incidental sequence variants of genes included in ACMG SF v3.2 list are reported in this section based on the statement of ACMG (1).</p> <p>REFERENCE</p> <ol style="list-style-type: none"> Richards S, Aziz N, Bale S, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology [J]. Genetics in medicine, 2015, 17(5): 405-423. Miller D T, Lee K, Abul-Husn N, et al. ACMG SF v3.2 list for reporting of secondary findings in clinical exome and genome sequencing: A policy statement of the American College of Medical Genetics and Genomics (ACMG) [J]. Genetics in Medicine, 2021. <p>*This report is specific to the tested sample, and cannot be used for other purposes.</p> <p>*Data listed above is generated from the laboratory standard testing procedure, and is only used for clinical reference.</p> <p>*These results are obtained using Next Generation Sequencing, Sanger Sequencing on the identified variant(s) for validation is highly recommended.</p> <p>*GeneMind Clinical Laboratories reserve the right of final explanation of this report. For inquiry, please contact us within 30 days after receiving the test report.</p> <p>*The variant is named based on nomenclature recommended by HGVS (http://www.hgvs.org/nomencl).</p> <p>*Please refer to relevant guideline of American College of Medical Genetics (ACMG).</p>						

Testing approved by: _____ Date: _____

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Appendix

METHOD & LIMITATIONS

Exome sequence is generated from extracted DNA that is fragmented, adapted, barcoded, and subjected to a solution phase hybridization with the Agilent SureSelect Human All Exon V8 probe set. Next generation sequencing is performed on the GeneMind Genomab M platform. Targeted regions are sequenced to at least 100X mean base coverage with a minimum of 99% of bases at $\geq 20X$ coverage. Paired-end reads are aligned to the NCBI reference sequence (GRCh37) using the Burrows-Wheeler Aligner (BWA), and variant calls are made using the Genomic Analysis Tool Kit (GATK). Point variant, micro-insertion, deletion, and duplication (<20bp) of over 5000 genes can be simultaneously detected (including mitochondrial genome). The minimum sequence depth for all targeted exons was evaluated; further validation is recommended for exons with depth of coverage <10X. We recommend that variants of interest which do not meet the coverage minimum be confirmed clinically before treatment is undertaken.

Reported variants: Variants are specified using the numbering and nomenclature recommended by the Human Genome Variation Society (HGVS, <http://www.hgvs.org/>). Variants of uncertain significance and benign variants are not reported. Variant classification and confirmation are consistent with ACMG standards and guidelines. Detailed variant classification information is available upon request.

It should be noted that this test does not sequence all bases in a human genome, not all variants have been identified or interpreted. Mosaicism, triplet repeat expansions, high repeated and low complexity or pseudogene, translocations, copy number events, variants in the gene regulatory region and deep intron region and epigenetic effects are currently not reliably detected by the current detection. However, the overall coverage of targeted area can be over 99%. Furthermore, not all disease-associated genes have been identified and the clinical significance of variation in many genes is not well understood.

TEST STATISTIC

Accession ID	
Amount of DNA read	
Insertion size (bp)	
Average coverage	
Mean depth (X)	
Proportion (Mean Depth $\geq 10X$)	
Proportion (Mean Depth $\geq 20X$)	
Proportion (Mean Depth $\geq 30X$)	

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Ordering Information

GenoLab M*					
Package code	Package name	PN	Product Name	Specification	Quantity
A000095	WES package (96 reactions, for GenoLab M FCM)	L000093	GeneMind Magnetic Universal Genomic DNA Kit	96 samples/test	2
		L000092	TargetSeq One® Hyb & Wash Kit v2.0		1
		L000094	Genemind Universal DNA Library Prep Kit		1
		S000049	GenoLab M sequencing Set V1.0 (FCM 300cycles)		14
A000096	WES package (192 reactions, for GenoLab M FCH)	L000093	GeneMind Magnetic Universal Genomic DNA Kit	192 samples/test	4
		L000092	TargetSeq One® Hyb & Wash Kit v2.0		2
		L000094	Genemind Universal DNA Library Prep Kit		2
		S000044	GenoLab M sequencing Set V1.0 (FCH 300cycles)		13
FASTASeq 300*					
Package code	Package name	PN	Product Name	Specification	Quantity
A000097	WES package (96 reactions, for FASTASeq 300 FCM)	L000093	GeneMind Magnetic Universal Genomic DNA Kit	96 samples/test	2
		L000092	TargetSeq One® Hyb & Wash Kit v2.0		1
		L000094	Genemind Universal DNA Library Prep Kit		1
		S000189	FASTASeq 300 Sequencing Kit V1.0 (FCM 300cycles)		32
A000098	WES package (96 reactions, for FASTASeq 300 FCH)	L000093	GeneMind Magnetic Universal Genomic DNA Kit	96 samples/test	2
		L000092	TargetSeq One® Hyb & Wash Kit v2.0		1
		L000094	Genemind Universal DNA Library Prep Kit		1
		S000197	FASTASeq 300 Sequencing Kit V1.0 (FCH 300cycles)		14
SURFSeq 5000*					
Package code	Package name	PN	Product Name	Specification	Quantity
A000099	WES package (480 reactions, for SURFSeq 5000 FCH)	L000093	GeneMind Magnetic Universal Genomic DNA Kit	480 samples/test	10
		L000092	TargetSeq One® Hyb & Wash Kit v2.0		5
		L000094	Genemind Universal DNA Library Prep Kit		5
		S000242	SURFSeq 5000 Sequencing Kit V1.0 (FCH 300cycles)		8
A000100	WES package (192 reactions, for SURFSeq 5000 FCM)	L000093	GeneMind Magnetic Universal Genomic DNA Kit	192 samples/test	4
		L000092	TargetSeq One® Hyb & Wash Kit v2.0		2
		L000094	Genemind Universal DNA Library Prep Kit		2
		S000238	SURFSeq 5000 Sequencing Kit V1.0 (FCM 300cycles)		13

*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.

Paper Published - GeneMind NGS Platform (38+, as of June 2024)

List	Title	Application	Publication Year	IF	JCR
1	Single molecule targeted sequencing for cancer gene mutation detection	cancer	2016	4.26	Q2
2	Single molecule sequencing of the M13 virus genome without amplification	virus-genome	2017	2.77	Q2
3	Fraternal twins with Phelan-McDermid syndrome not involving the SHANK3 gene: case report and literature review	disease	2020	2.57	Q2
4	Characterizing the gene mutations associated with resistance to gatifloxacin in Mycobacterium tuberculosis through whole genome sequence	Mycobacterium-resistance	2021	12.07	Q1
5	Comparative performance of the GenoLab M and NovaSeq 6000 sequencing platforms for transcriptome and LncRNA analysis	RNA&LncRNA	2021	3.97	Q2
6	Accuracy benchmark of the GeneMind GenoLab M sequencing platform for WGS and WES analysis	WGS&WES	2022	4.55	Q2
7	Non-invasive Prenatal Screening for Common Fetal Aneuploidies by Single Molecular Sequencing	NIPT	2022	5.50	Q1
8	Systematic and benchmarking studies of pipelines for mammal WGBS data in the novel NGS platform	WGBS	2023	3.0	Q2
9	Evaluation of environmental factors and microbial community structure in an important drinking-water reservoir across seasons	metagenome	2023	5.2	Q1
10	Comparison of the Illumina NextSeq 2000 and GeneMind GenoLab M sequencing platforms for spatial transcriptomics	genomics Visium spatial transcript	2023	4.4	Q2
11	Genetic characterization of human adenoviruses in patients using metagenomic next-generation sequencing (mNGS) in Hubei, China, from 2018 to 2019	mNGS	2023	5.2	Q1
12	FWAlgaeDB, an integrated genome database of freshwater algae	metagenome	2023	4.6	Q2
13	Inhibition of Hepatitis B Virus (HBV) replication and antigen expression by Brucea javanica (L) Merr. oil emulsion	RNA-seq	2023	5.7	Q1
14	Ultra-high static magnetic fields cause immunosuppression through disrupting B-cell peripheral differentiation and negatively regulating BCR signaling	RNA-seq	2023	9.9	Q1
15	Accumulation of Endogenous Adenosine Improves Cardiomyocyte Metabolism via Epigenetic Reprogramming in an Ischemia-Reperfusion Model	RNA-seq	2023	11.4	Q1
16	Winter wheat lodging resistance characteristics as affected by nitrogen application time and the underlying mechanism	RNA-seq	2023	0.9	Q3
17	Preparation of a Single-Cell Suspension from Tumor Biopsy Samples for Single-Cell RNA Sequencing	BD scRNA-seq	2023	0.7	Q3
18	Development of Synbiotic Preparations That Restore the Properties of Cattle Feed Affected by Toxin-Forming Micromycetes	Microbe Genome	2023	3.6	Q1
19	G-Protein-Coupled Receptors Mediate Modulations of Cell Viability and Drug Sensitivity by Aberrantly Expressed Recoverin 3 within A549 Cells	RNA-seq	2023	5.6	Q1
20	3D Spheroid Configurations Are Possible Indicators for Evaluating the Pathophysiology of Melanoma Cell Lines	RNA-seq	2023	6	Q1
21	Comparative analysis of clinical and immunological profiles across Omicron BA.5.2 subvariants using next-generation sequencing in a Chinese cohort	Microbe Genome	2023	5.7	Q1
22	Case Report: Four cases of SARS-CoV-2-associated Guillain-Barré Syndrome with SARS-CoV-2-positive cerebrospinal fluid detected by metagenomic next-generation sequencing: a retrospective case series from China	mNGS	2023	7.3	Q1
23	Coinfection of SARS-CoV-2 and influenza A (H3N2) detected in bronchoalveolar lavage fluid of a patient with long COVID using metagenomic next-generation sequencing: a case report	mNGS	2023	5.7	Q1
24	Systematic evaluation of multiple NGS platforms for structural variants detection	WGS	2023	4.8	Q2
25	Draft genome sequence of perfluorinated acids C7–C9 degrading bacterium Pseudomonas mosselii 5(3), isolated from soil contaminated with pesticides	Microbe Genome	2023	0.8	Q3
26	Biodegradation Potential of C7–C10 Perfluorocarboxylic Acids and Data from the Genome of a New Strain of Pseudomonas mosselii 5(3)	Microbe Genome	2023	4.6	Q1
27	Systematic comparison of variant calling pipelines of target genome sequencing across multiple next-generation sequencers	panel	2023	3.7	Q2
28	Analysis of the transcriptional activity of model piggyBac transgenes stably integrated into different loci of the genome of CHO cells in the absence of selection pressure	RNA-seq	2023	0.9	Q4
29	Sequencing and analysis of complete chloroplast genomes of einkorn wheats Triticum sinskajae and Triticum monococcum accession k-20970	chloroplast genomes	2023	2.0	Q2
30	Transcriptome analysis reveals the underlying mechanism for over-accumulation of alkaline protease in Bacillus licheniformis	RNA-seq	2023	4	Q2
31	Expression of USP25 associates with fibrosis, inflammation and metabolism changes in IgG4-related disease	RNA-seq	2024	16.6	Q1
32	Changes in molting frequency and expression patterns of molting-related genes in Macrobrachium rosenbergii with exogenous calcium supplement in water	RNA-seq	2024	4.5	Q1
33	Ecophysiological responses of Phragmites australis populations to a tidal flat gradient in the Yangtze River Estuary, China	RNA-seq	2024	5.6	Q1
34	The complete chloroplast genome sequence of Leibnitzia anandria (Linnaeus) Turczaninow	chloroplast genomes	2024	0.5	Q4
35	Prenatal diagnosis of a trisomy 7 mosaic case: CMA, CNV-seq, karyotyping, interphase FISH, and MS-MLPA, which technique to choose?	CNV-seq	2024	3.1	Q2
36	Modulation of Epithelial–Mesenchymal Transition Is a Possible Underlying Mechanism for Inducing Chemoresistance in MIA PaCa-2 Cells against Gemcitabine and Paclitaxel	RNA-seq	2024	4.7	Q2
37	Assessing the impact of sequencing platforms and analytical pipelines on whole-exome sequencing	WES	2024	3.7	Q2
38	Nano-bio interaction of magnetic nanoparticles with cells in a tumor at the single-cell level	tumor scRNA-seq	2024	17.4	Q1

High Data Quality (Real Clinical Results)

	Flowcell-99	ZM20240510QWXZ99	ZM20240510QWXZ100	ZM20240510QWXZ101	ZM20240510QWXZ102
Raw reads	96,968,734	92,958,870	98,970,496	72,194,108	80,859,444
Raw bases	14,545,310,100	13,943,830,500	14,845,574,400	10,829,116,200	12,128,916,600
Clean reads	96,434,204	92,387,208	98,398,030	71,158,358	79,708,810
Clean bases	14,152,496,510	13,571,818,188	14,456,606,104	10,513,160,522	11,811,282,258
Q20	98.65%	98.65%	98.68%	98.56%	98.51%
Q30	95.94%	95.90%	96.01%	96.13%	95.96%
GC%	51.25%	51.15%	51.05%	52.78%	52.60%
Reads with adaptors	11,664,012	10,496,078	11,100,306	6,072,120	5,435,740
Mapping rate	99.97%	99.97%	99.97%	99.97%	99.98%
On target rate	87.14%	86.65%	87.11%	86.69%	86.43%
Insert size	213	215	217	230	241
Coverage	99.60%	99.90%	99.90%	99.60%	99.60%
Average depth	198.8X	188.4X	201.0X	142.6X	156.4X
Depth > 10X	99.10%	99.30%	99.40%	98.80%	98.70%
Depth > 20X	98.55%	98.75%	98.91%	97.35%	97.32%

- **Q30 > 95%**
- **Mapping rate > 99%**
- **On target rate > 86%**
- **Average depth > 140X**

Scientific Paper 1 (Download Link: <https://doi.org/10.1186/s12864-022-08775-3>)

- Title: Accuracy benchmark of the GeneMind GenoLab M sequencing platform for WGS and WES analysis
- Sample type: HG001 and HG002
- Library type: TruSeq Nano DNA library prep kit
- Platform: NA, NT and GenoLab M*

Samples	Library Type	Sequencing Platform	Read (M)	Bases (Gb)	Duplication rate (%)	>Q20	>Q30	Alignment rate (%)	Mean coverage (X)	%_bases_above_15x
GL_WGS_22	WGS	GenoLab M	442.77	66.42	1.73%	95.35%	88.26%	99.88%	22.39	81.30%
GL_WGS_33	WGS	GenoLab M	662.66	99.40	1.93%	95.22%	87.99%	99.88%	33.50	93.90%
NA_WGS_22	WGS	NS	424.9	63.73	3.57%	95.92%	90.05%	99.64%	21.37	87.30%
NA_WGS_33	WGS	NS	655.83	98.38	5.32%	95.92%	90.05%	99.64%	32.99	97.70%
GL_WES_100	WES Agilent V8	GenoLab M	41.87	6.28	6.00%	93.95%	84.71%	99.95%	112.42	98.00%
GL_WES_raw	WES Agilent V8	GenoLab M	70.36	10.55	9.71%	93.95%	84.71%	99.95%	188.90	99.00%
NA_WES_100	WES Agilent V8	NS	39.35	5.90	14.85%	98.01%	94.05%	99.95%	107.72	99.30%
NA_WES_raw	WES Agilent V8	NS	81.16	12.17	26.78%	98.01%	94.05%	99.95%	222.19	99.60%
NT_WES_100	WES Agilent V8	NT	37.54	5.56	5.67%	86.62%	79.06%	99.83%	101.13	99.30%
NT_WES_raw	WES Agilent V8	NT	131.76	19.50	17.54%	86.61%	79.06%	99.83%	354.92	99.60%

High performance over other product:

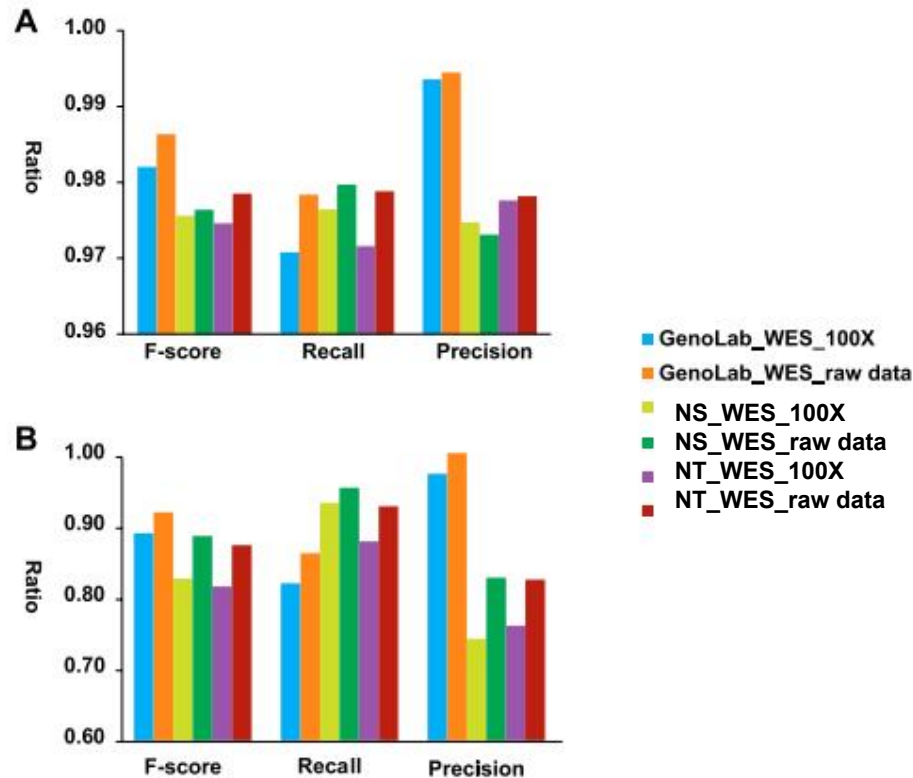
Q30 > 84%

Alignment rate > 99.95%

Low duplication rate < 10%

*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.

Data Comparison with Other Platforms (Download Link: <https://doi.org/10.1186/s12864-022-08775-3>)



- At 100X, the F-score and Precision in GenoLab M* were higher than NovaSeq or NextSeq, while the Recall in GenoLab M was slightly lower. GenoLab M* showed similar or superior performance to Illumina platforms at the WES application.

*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.

Scientific Paper 2 (Download Link: <https://doi.org/10.3389/fgene.2024.1334075>)

- Title: Assessing the impact of sequencing platforms and analytical pipelines on whole-exome sequencing
- Sample type: Tumor reference standard HD832 and standard HG001
- Library type: SureSelect Human All Exon V8 kit and SureSelect Human All Exon V6 kit
- Platform: NX, FASTASeq 300, NS, GenoLab M*, and SURFSeq 5000*

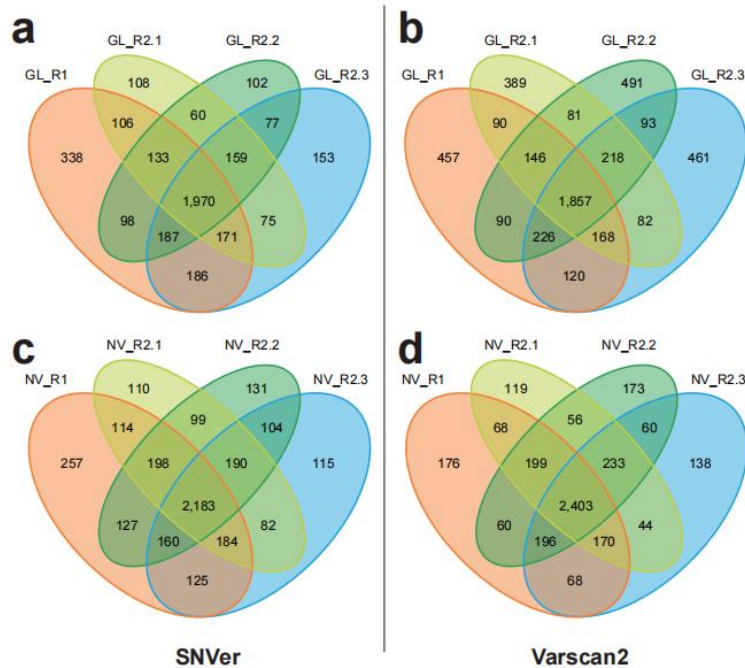
Sample	Dataset	Reads (M)	Bases (Gb)	Q20 (%)	Q30 (%)	GC (%)	Mapped Rate (%)	Capture efficiency (%)	Duplicate Rate (%)	Average depth (x)	Coverage (≥1x) (%)	Coverage (≥4x) (%)	Coverage (≥10x) (%)	Coverage (≥30x) (%)
HD832	GL_R1	31.38	8.41	96.79	92.10	47.50	99.76	58.68	8.55	128.92	99.04	98.87	98.48	96.46
	GL_R2.1	29.43	8.61	97.17	91.48	45.03	99.91	51.65	8.17	123.37	98.98	98.61	97.61	92.08
	GL_R2.2	31.50	9.21	97.85	92.87	45.01	99.91	51.57	8.60	131.87	98.98	98.60	97.62	92.41
	GL_R2.3	31.50	9.21	97.10	91.40	46.44	99.90	51.84	7.78	132.54	99.03	98.81	98.33	95.42
	NX_R1	32.95	9.75	95.77	92.26	49.24	99.93	56.14	11.29	143.04	98.92	98.67	98.23	96.40
	NS_R1	32.81	9.06	98.03	94.85	50.57	99.70	57.49	28.07	118.36	99.07	98.95	98.77	97.81
	NS_R2.1	32.95	9.75	97.45	93.15	50.19	99.87	50.75	21.31	136.42	99.07	98.94	98.76	97.75
	NS_R2.2	32.63	9.65	97.61	93.25	50.28	99.87	51.02	20.28	138.36	99.07	98.94	98.77	97.79
	NS_R2.3	32.20	9.54	97.73	93.48	50.26	99.87	50.67	23.02	134.45	99.07	98.94	98.75	97.73
HG001	HG001_FA	39.14	11.10	97.32	92.45	50.65	99.94	66.52	3.45	116.68	99.63	99.41	98.72	94.01
	HG001_GL	39.20	11.15	97.59	91.28	50.03	99.94	66.16	5.46	116.53	99.63	99.41	98.68	94.14
	HG001_NS	39.23	11.27	96.87	92.57	52.03	99.92	66.14	20.79	117.91	99.67	99.52	99.02	94.09
	HG001_SF	39.05	11.28	96.30	90.89	51.32	99.99	64.61	24.53	115.28	99.69	99.44	98.81	93.81
	HG001_NX	39.23	11.00	96.80	93.90	50.47	99.97	67.25	6.71	117.12	99.43	98.98	97.88	92.47

- **GeneMind NGS platforms showed similar or superior data quality with Illumina platforms at WES application.**

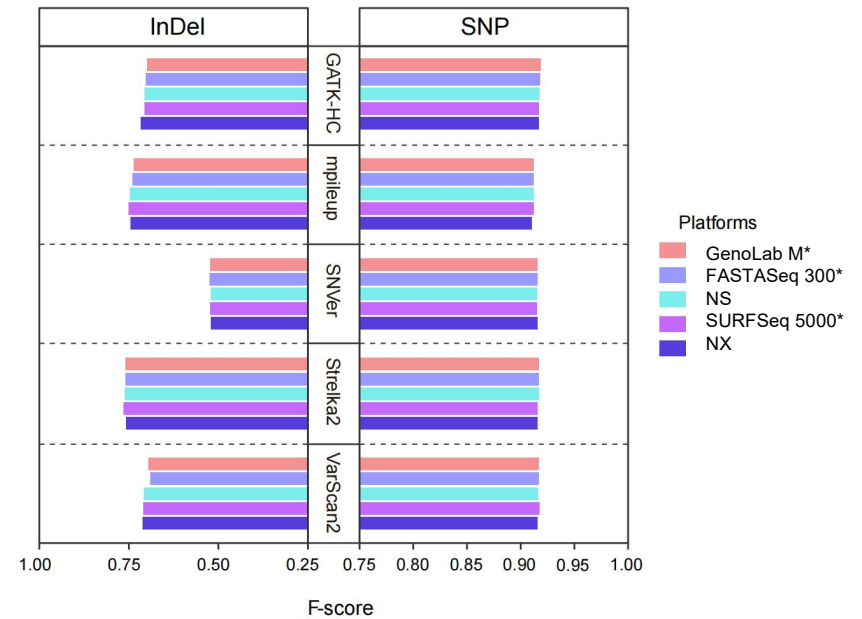
*Unless otherwise informed, GeneMind sequencing platform and related sequencing reagents are not available in the USA, Canada, Australia, Japan, Singapore, Western Europe, Southern Europe and Nordic countries yet.

Data Comparison with Other Platforms

(Download Link: <https://doi.org/10.3389/fgene.2024.1334075>)



Venn diagram of variants calling performances in GenoLab M* and NS platforms.



Comparison of F-score for SNPs (Right) and InDels (Left) detected across five callers and five platforms.

- The results underscore that under the identical analysis pipeline, the disparity in SNP detection among various sequencing platforms is minimal.

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Welcome to be our partner!

