Insight *into*
Genetic Mutations

Next Generation *Sequencing* Solutions

www.genes2me.com

Spearheading Innovation in Genomics Solutions Manufacturing

Genes2Me developed **NGS based Clinical Panels**

Since its inception in 2016, Genes2me has been constantly striving towards setting a benchmark in the diagnostics space by introducing premium quality (Made in India) diagnostic kits which are CE-IVD, ISO-13485 & ISO 9001:2016 certified, assuring our clients of unparalleled quality and compliance with international standards.

Our product portfolio includes molecular POC testing solutions, RT-PCR kits, rapid antigen/antibody testing kits, and molecular biology reagents. We have broadened our horizons to include Next Generation Sequencing clinical panels to cater to personalised medicine for every patient.

The company's flagship products like Rapi-Q/ Rapi-Q HT Point-of-Care (POC) RT-PCR devices are trailblazing inventions that are changing the paradigm of molecular POC testing across the world. These platforms help to detect infectious diseases with utmost sensitivity and least turnaround time thus helping in effective treatment and timely containment of the infection.

Our NGS clinical panels are designed to encompass testing solutions for oncology, liquid biopsy, cardiovascular diseases, neurological disorders, and HLA typing. These panels are compatible with the most popular sequencing platforms, Illumina, MGI, Thermo Fisher and Element Bio Sciences. We also offer cloud-based interpretation bioinformatics software with our NGS clinical panels which is designed to interpret data in a flexible and user-friendly manner. We ensure the highest standards for compliance at our lab & manufacturing site and have thus obtained all necessary accreditations and licences to run the same.

Our lab is accredited by the National Accreditation Board for Testing & Calibration Laboratories (NABL), ISO 9001, and ISO 14001. Our manufacturing site is approved by Drugs Controller General of India (DCGI) & is fortified by the prestigious IS0-13485 accreditation.

INFECTIOUS

Pan Pathogen (7000+ Organisms)
Comprehensive Respiratory Virus Panel (CRVP) (~9 virus)
TB NGS Panel (75 drug resistance genes)

ONCOLOGY PANELS

PanCan (681 genes - 104 DNA Fusions, 105 RNA Fusions)
Common Hereditary Cancer (83 genes)
BRCA 1/2 (2 genes)
Onco-Check (53 genes)
Cancer Check 50 (67 genes)
Cancer Check 100 (148 genes)
Focus Lung panel (73 genes - DNA & 18 genes RNA fusions)

BLOOD CANCERS

Myeloid Leukemia (208 genes - DNA & 94 RNA Fusions)
Lymphoma (95 genes- DNA & 94 RNA Fusions)

LIQUID BIOPSY PANELS

PanCan (681 genes)
CtDNA Breast (63 genes)
CtDNA Colorectal (25 genes)
CtDNA Lung (32 genes)

HRD PANEL

CancerCheck Core (HRD Score)

CONTENTS

NEXT GENERATION SEQUENCING PANELS

G2M panels are compatible with NGS platforms from **Illumina, Thermo Fisher (Ion Torrent), Element Biosciences & MGI.**

EXOME SEQUENCING

Whole Exome Sequencing (>21,500 genes)
Clinical Exome Sequencing (8124 genes)

TRANSPLANT IMMUNOLOGY

HLA Typing (11 loci)

MOTHER & CHILD CARE

NIPT (Non Invasive Prenatal Testing)
NBS (New Born Screening) (335 genes)

TARGETED THERAPIES

Neuromuscluar Panel (497 genes)
Cardiovascular Panel (357 genes)
Alzheimer-Parkinsons-Dementia (139 genes)

PHARMACOGENOMICS

Med4Me Standard (163 genes)

LEONEXT OFFERINGS

Whole Genome Sequencing
Transcriptomics

CliSeq Interpreter

Robust Automated Data Analytics Platform

G2M NGS Panels are supported by in-house comprehensive cloud-based (or on site server) software and tertiary clinical reporting platform

Ease of Use

Most of the G2M NGS Panels share a common workflow

Hybridization Based Enrichment

- Less duplication rates
- Covers larger target region in one run

Quality Excellence

- Best On-Target Ratio
- Uniform Depth Coverage
- Low Bias Base Call

High Performance

Quality performance with complex sample types like FFPE and CtDNA

Reduced Overall Run-time

Short Hybridisation time of approx 4 hours

G2M

NEXT GENERATION SEQUENCING PANELS

Key Features

Maintaining High Quality standards

All 29+ NGS Panels are certified with CE-IVD Certifications

Platform agnostic clinical panels

Compatible on platforms from
Illumina, Thermofisher, MGI, Element Biosciences

Wide range of Portfolio with Panels Specific to Germline & Somatic Mutations

Panels Rigorously Engineered to Target Hard to Capture Regions

Like homologous, repetitive sequences & GC rich regions

Multiple Panel Muliplexing

Adapters for upto 384 Unique Primers

Automated NGS Library Preparation Platform

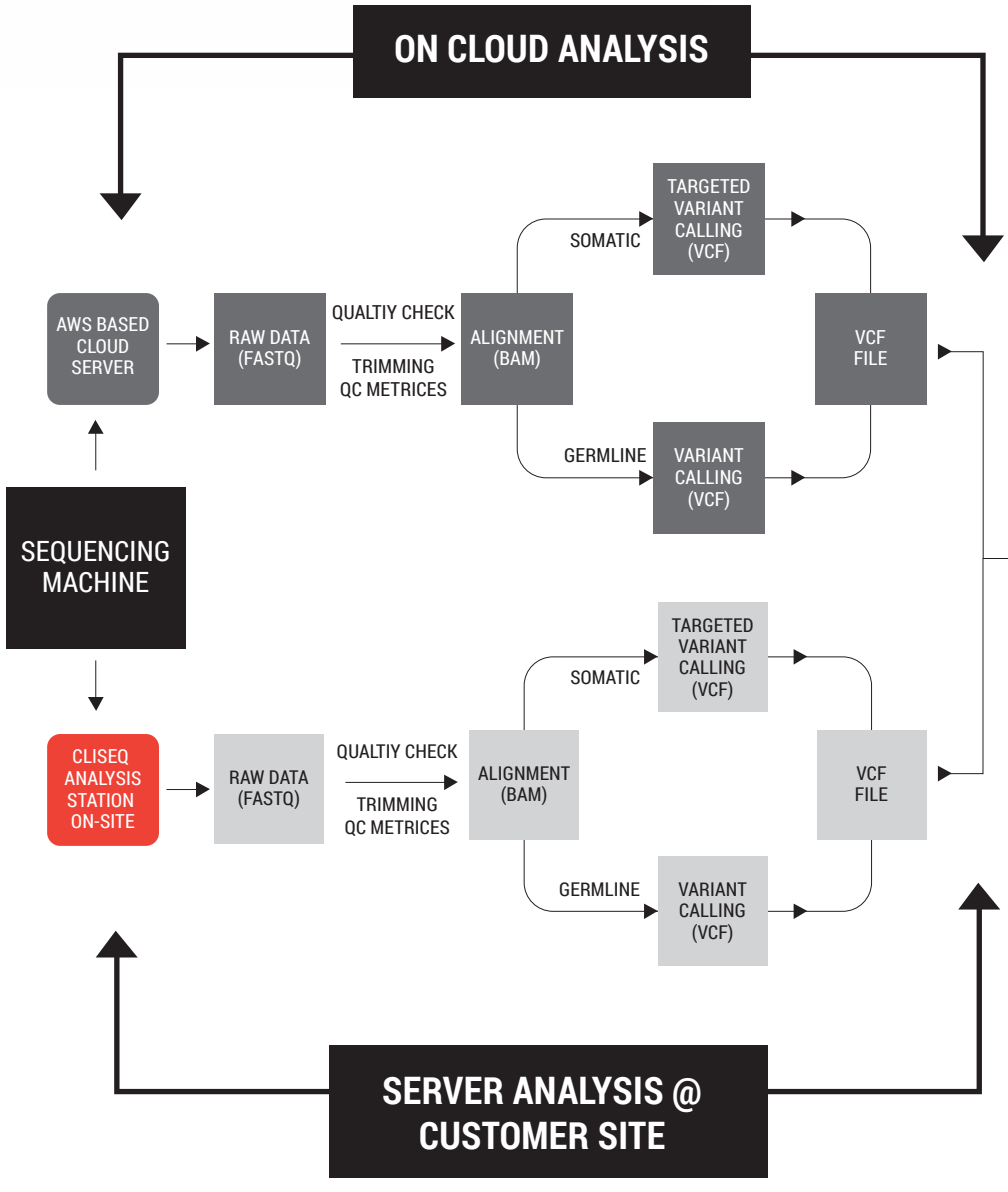
With built-in fluorometer and thermal cycler

EZY-AutoPrep

CliSeq Interpreter

Automated **Analysis Reporting Platform**

- **Clinically Relevant Mutations**
- **Abbreviated Report Time**
- **User Friendly**
- **Multiple Parameter Analysis**



- Platform Independent
- GUI Driven
- Automated Pipelines
- FASTQ to CSM Reporting
- Optimised Data Mining
- Linux Based
- Available as both cloud based as well as standalone server

Cliseq Interpreter is a cloud based NGS data analysis software which offers an unparallel platform performance designed to streamline and enhance the interpretation of complex biological data.

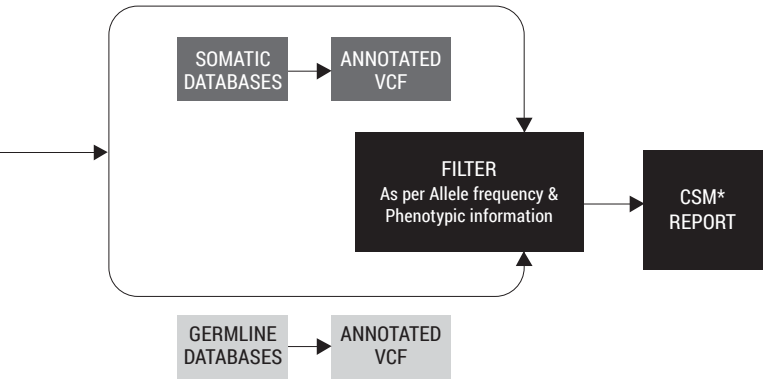
With a user-friendly interface, and advanced visualization capabilities, Cliseq empowers you to extract meaningful insights from vast genomic datasets with precision & efficiency.

Cliseq algorithms seamlessly work with G2M NGS clinical panels allowing for effortless data import/export & inter-operability with common sequencing platforms like Illumina, Thermo Fisher, MGI and Element Biosciences.

PROCESS WORKFLOW

Once Quality Check, Alignment, Variant calling, and annotations are achieved, the annotated VCF files will be available to download.

CSM reporting will be done as per ACMG, ASCO, NCCN & AMP guidelines and based on phenotypic details as provided.



KEY FEATURES

- Cancer & Rare Disease Diagnostics
- SNP, InDels, Copy Number Variation (CNV) Identification, Fusion & Gene rearrangements
- Tumor Mutation Burden (TMB), Microsatellite Instability (MSI), HRD score
- CSM Reporting according to ACMG, ASCO, NCCN & AMP Guidelines based on provided Phenotypic information
- Analysis using updated databases & automated pipeline
- Annotated VCF with MAF, Gene Name, Location etc.
- Clinically significant variants with associated diseases
- Cloud Based Data storage on regional AWS Servers: Middle East, Europe, India, US respectively

G2M

Oncology

NGS Assays

- PanCan
- HRD Panel
- Blood Cancers
- Liquid Biopsy
- Cancer Check 50
- Cancer Check 100
- Oncocheck
- Common Hereditary Cancers
- BRCA 1&2
- Focus Lung

PanCan

CGP Assay

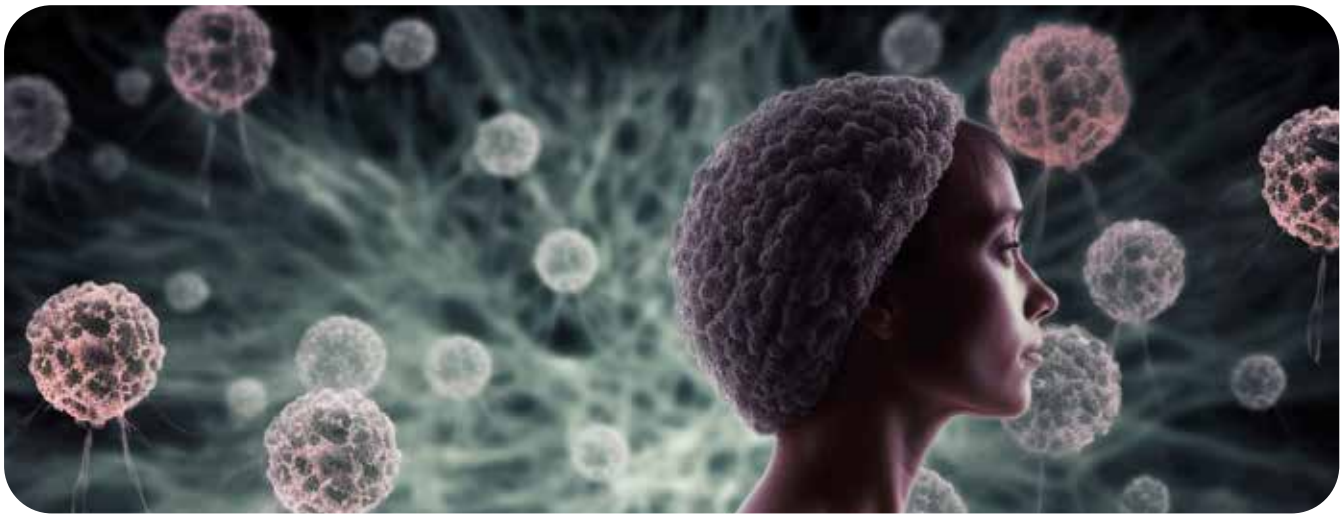
PanCan is a CGP (comprehensive genomic profiling) NGS assay aimed to screen a range of cancer causing genes to identify somatic mutations in DNA & RNA from human clinical samples like FFPE and fresh tissue targeting 681 genes (for DNA & 105 genes for RNA fusions) covering all the coding sequences enriched by Hybridization capture-based target enrichment.

The PanCan Assay detects all variant types and immuno-oncology markers (MSI and TMB), which are crucial biomarkers for cancer immunotherapy.

The panel is also designed to detect Epstein-Barr virus (EBV) and Human Papillomaviruses (HPV), allowing for the comprehensive analysis of cancer-associated genes

Cancer-Associated Biomarkers

TMB, MSI, HRR & Fusion Genes



PanCan

PanCan is aimed to screen a range of cancer causing genes to identify somatic mutations in DNA & RNA from human clinical samples like FFPE and fresh tissue. It provides comprehensive detail of the cancer and the recommendations regarding the FDA approved drugs, helping to decide the best course of treatment.

No. of Genes	681 genes (DNA)
Fusions	104 (DNA), 105 (RNA)
Gene count/ family	524
Covered region	Whole CDS, Hotspots, Fusion genes
Target size	~1.7 Mb
Mutation type	SNV/ InDels/ CNV
Biomarkers	TMB, MSI, HRR Genes
Sample type	FFPE & Fresh Frozen Tissue

Gene and Drug recommendations

TYPE OF CANCER*	GENE	DRUG
Gilioma, Acute Myeloid Leukemia	IDH1	Olutasidenib
Breast Cancer, Ovarian Cancer	BRCA1	Olaparib
NSCLC, Colorectal Cancer	EGFR	Osimertinib
Colorectal Cancer, NSCLC	KRAS	Cetuximab
NSCLC, Melanoma, Metastatic Colorectal Cancer	BRAF	Encorafenib
Follicular Lymphoma Tumor	EZH2	Tazemetostat
Medullary Thyroid Cancer, Thyroid Cancer	RET	Selpercatinib
Prostate Cancer	BRCA2	Niraparib
Breast Cancer, Gastroesophageal Cancer	ERBB2	Trastuzumab
Non-Small Cell Lung Cancer	ALK	Alectinib
Esophageal, colorectal, Lung cancer	TP53	Venetoclax
Breast Cancer, Ovary, stomach cancer	PIK3CA	Alpelisib
Gastrointestinal Stromal Tumors, glioblastoma, melanoma	PDGFRA	Avapritinib
Urothelial Cancer, multiple myeloma, bladder cancer	FGFR3	Erdafitinib
NSCLC, Metastatic cancer	MET	Capmatinib
Myeloma , lung adenocarcinoma, colon adenocarcinoma, melanoma, breast carcinoma	PDGFRB	Imatinib Mesylate
Acute Myelogenous Leukemia, Bone Marrow cancer	FLT3	Quizartinib
Aggressive Systemic Mastocytosis, lung adenocarcinoma,	KIT	Imatinib
colon adenocarcinoma	ESR1	Elacestrant
Breast Cancer, endometrial and prostate cancer Solid Tumors, lung cancer, colorectal cancer	NTRK1	Entrectinib

*Limited cancer type details mentioned

Scan for PanCan Gene List

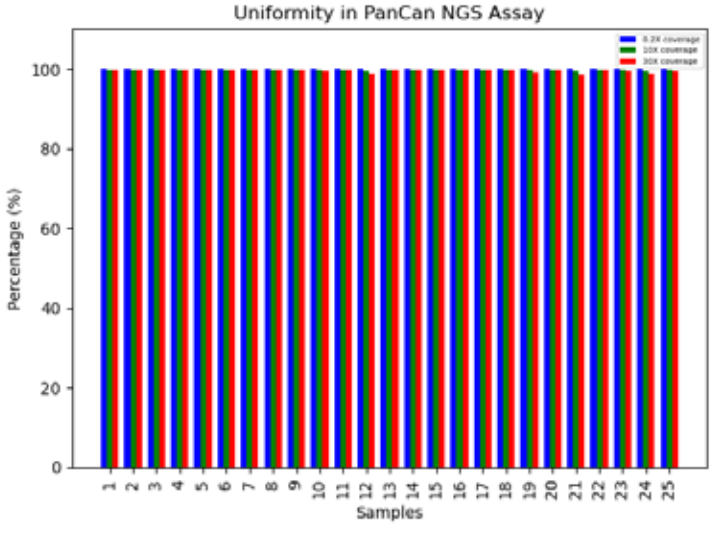
ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity (%)	>98
Precision (%)	>95
Reproducibility (%)	97
On Target Ratio (%)	86-95
Sensitivity (VAF @1%)	98.6

*Note :- This data has been calculated from a sample number size of 92 samples
: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Coverage uniformity achieved with the G2M Pan-Cancer CGP Panel

Fig-01 - The genomic DNA libraries from FFPE tissues (n=64) were enriched using the G2M Pan-Cancer NGS Panel and sequenced on a NovaSeq system using 2 x 150 paired-end reads. The data represents near-complete uniform coverage (~100%) across all samples at 0.2X, 10X, and 30X thresholds. This high level of uniformity indicates that the probe design is well optimized, enabling targeted NGS assays to consistently deliver high-confidence and reproducible results.



VAF PLOT

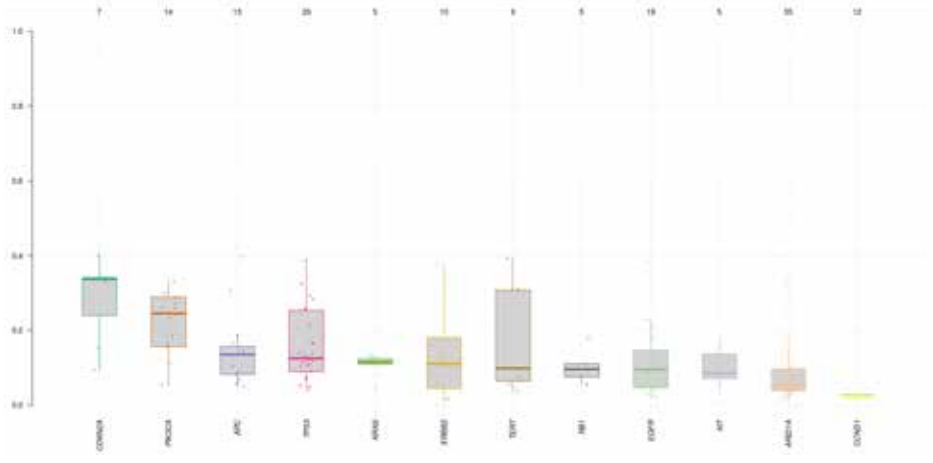


Fig-02 - This VAF plot shows distribution of some of the important genes in 44 PanCancer patient samples. Genes like CDKN2A and PIK3CA display higher median VAFs with greater variability, suggesting a higher mutation burden which may reflect a greater impact on disease progression. In contrast, genes like ARID1A and CCND1 exhibit lower and more consistent VAFs, indicating a smaller or more stable role in the overall genetic profile.

Consistent Fold 80 Value Across Sample Types

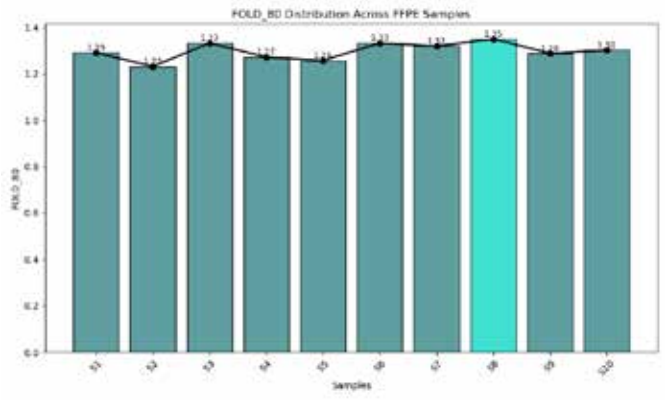


Fig-03 - Fold 80 base penalty across both FFPE (blue bar) and blood-derived (cyan bar) samples. The G2M PanCan CGP Panel demonstrates a fold 80 base penalty below 1.3, reflecting exceptional coverage uniformity across target regions. This low value indicates that only 1.3× the average sequencing depth is required to achieve 80% coverage at the desired threshold, minimizing over-sequencing and ensuring efficient, balanced read distribution affirming the robustness of the data quality.`

High On-Target Ratio Across Different Tumor Samples

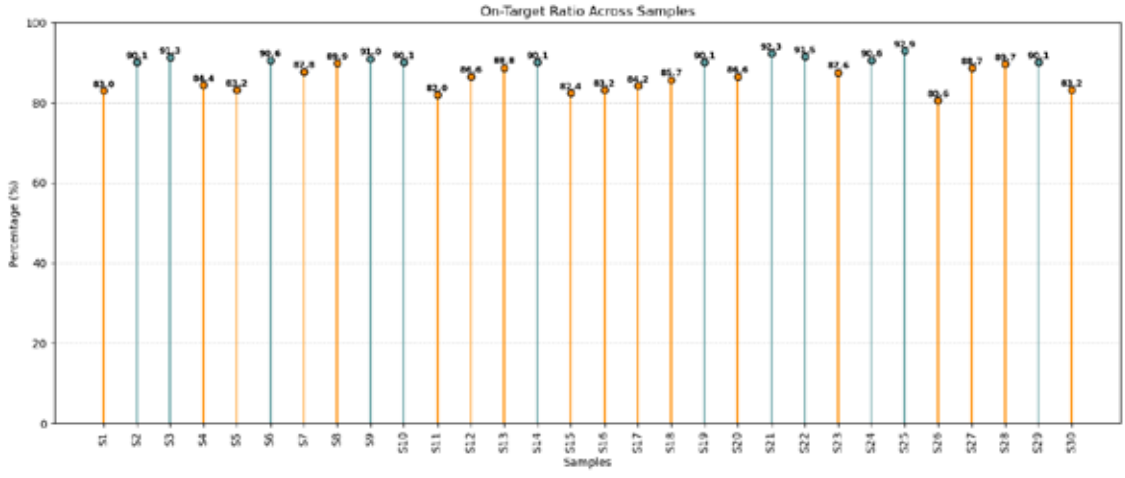
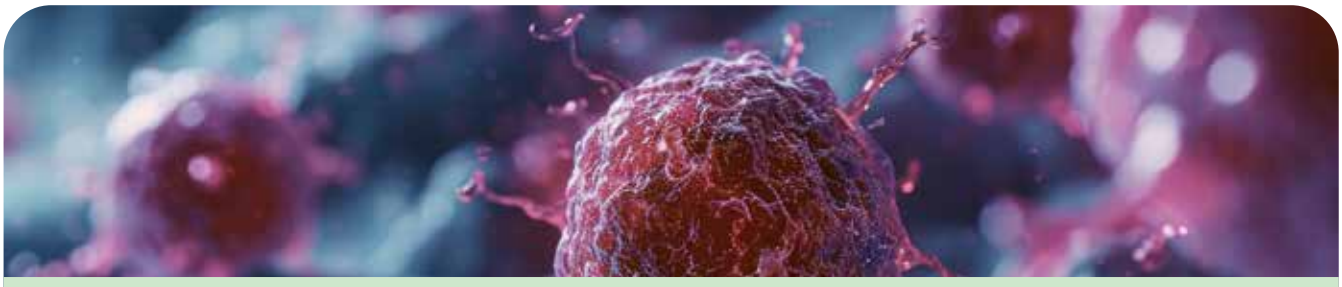


Fig-04 - Across all cancer patient samples, the on-target alignment consistently exceeded 80%, reflecting the panel's high specificity, optimized assay conditions, and efficient target enrichment. This strong performance underscores the reliability and precision of the sequencing workflow.

COVERS A WIDE RANGE OF CANCER

Breast	Cervix Uteri	Ovary
Prostate	Stomach	Thyroid
Lung	Liver	Oesophagus
Colorectal	Corpus Uteri	Non-Hodgkin Lymphoma
Prostate	Leukemia	Bladder

Scan for PanCan sample report



CancerCheck Core
(HRD Assay)

The HRD Assay from G2M enriches non-exonic, single-nucleotide polymorphism (SNP)-based on targeted next generation sequencing. This targets more than 50,000 SNPs enriched across whole genome making it capable of detecting the genomic instabilities and calculate the Genomic Scar Score. These biomarkers (LOH (Loss of heterozygosity), TOI (Telomeric imbalances), LSTs (Large scale transitions)), can be measured and used to evaluate the HRD Status and Genomic scar score (GSS).

This helps in maximizing diagnostics insights for clinicians to guide for PARP inhibitors or platinum drugs used in the treatment of various cancers.

- OVARIAN CANCER
- PROSTATE CANCER
- BREAST CANCER
- PANCREATIC CANCER

SNP Based	> 51,000	
Target Size	6.3 MB	
Test Approach	Tumor only	Matched sample
Sample type	Tumor sample	Tumor sample
		Blood or peripheral normal tissue

Scan for CancerCheck Core HRD sample report

Positive and Negative HRD Score from G2M HRD Assay Data

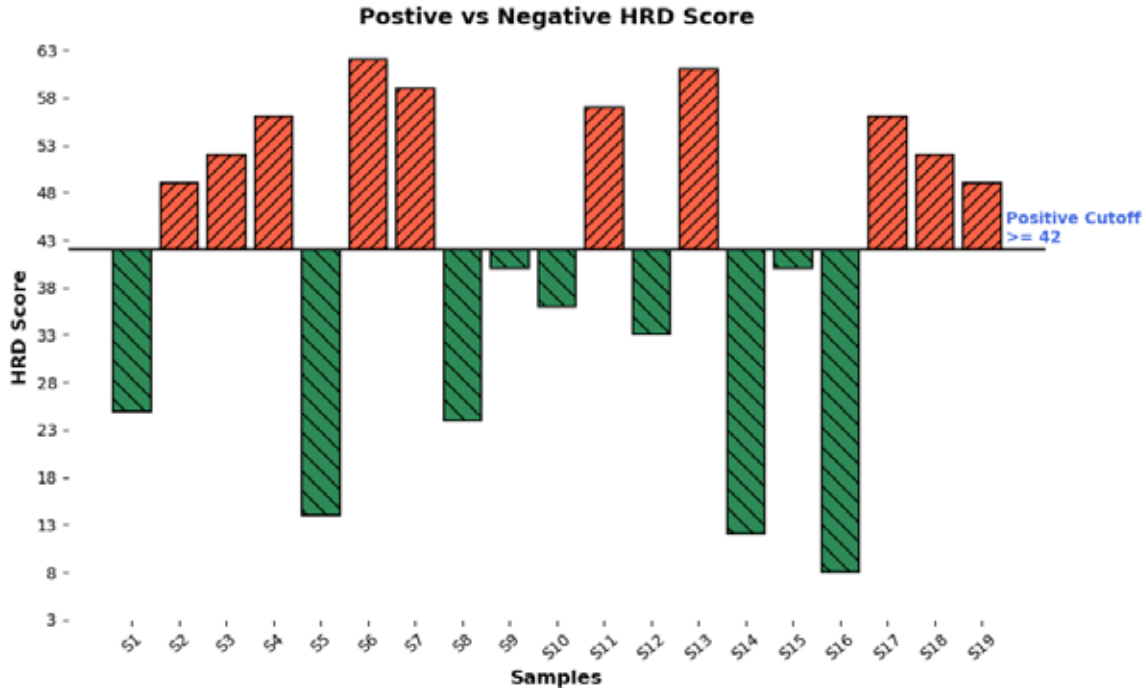


Figure 05: Comparison of Positive and Negative HRD score calculated from G2M HRD Assay data

G2M HRD Scoring Pipeline Comparison

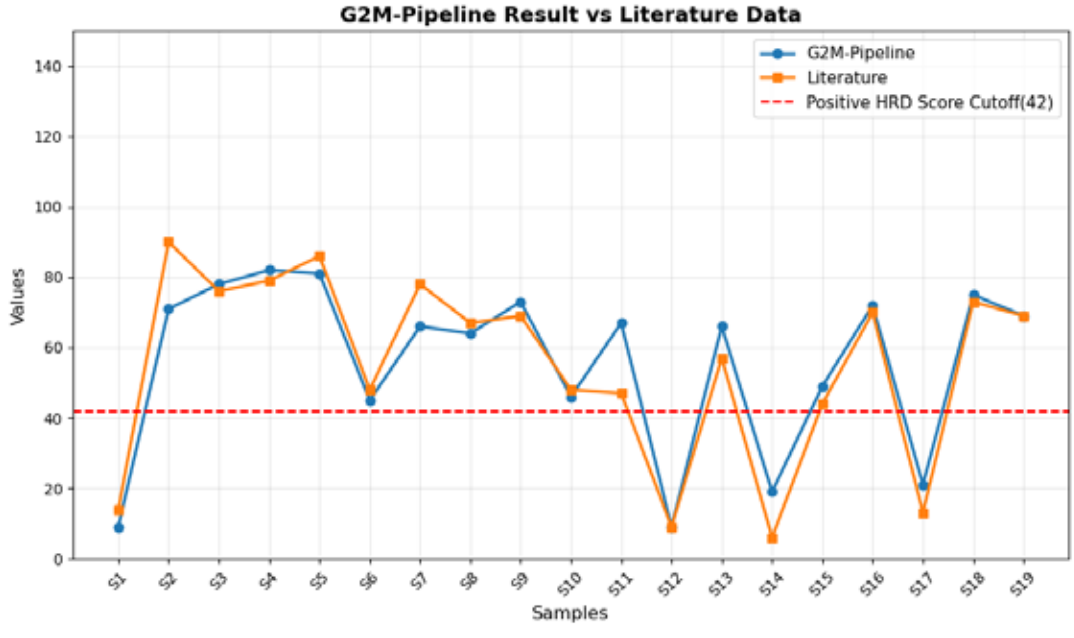


Figure 06: Comparative analysis of G2M HRD Assay pipeline on publically available Whole Exome data

G2M HRD Scoring Pipeline Comparison

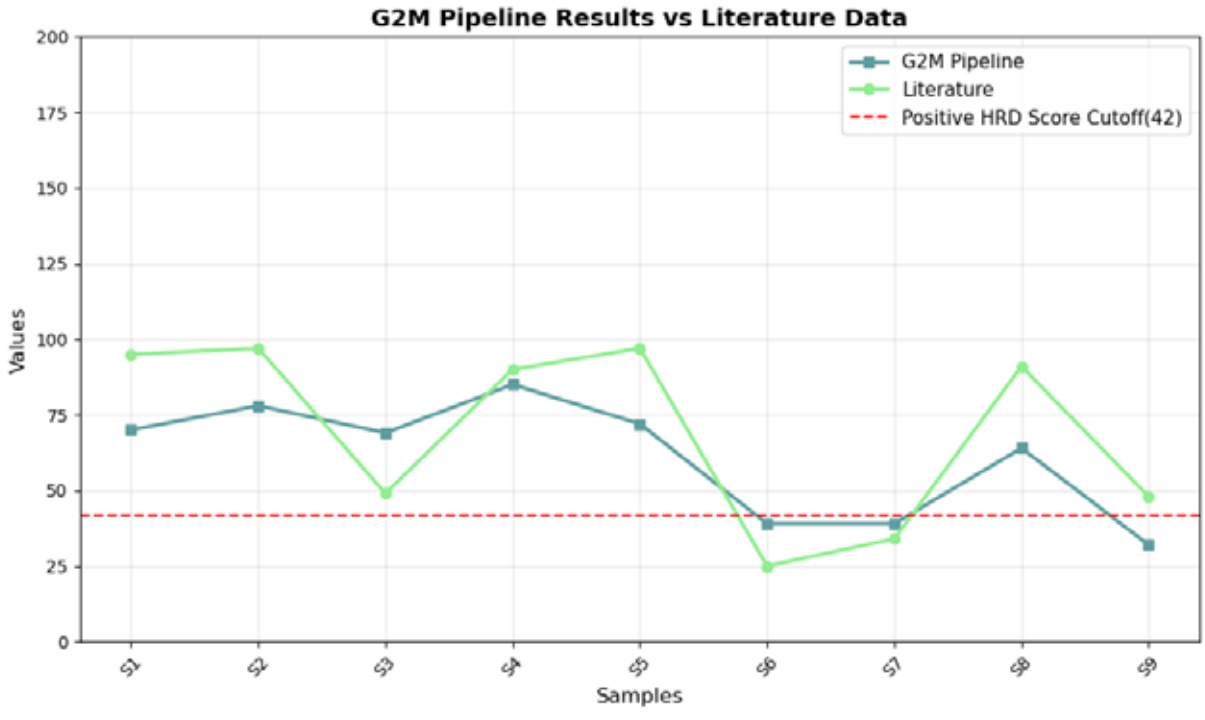


Figure 07: Comparative analysis of G2M HRD Assay pipeline on publically available HRD reference standard data

HRD Scoring Parameters

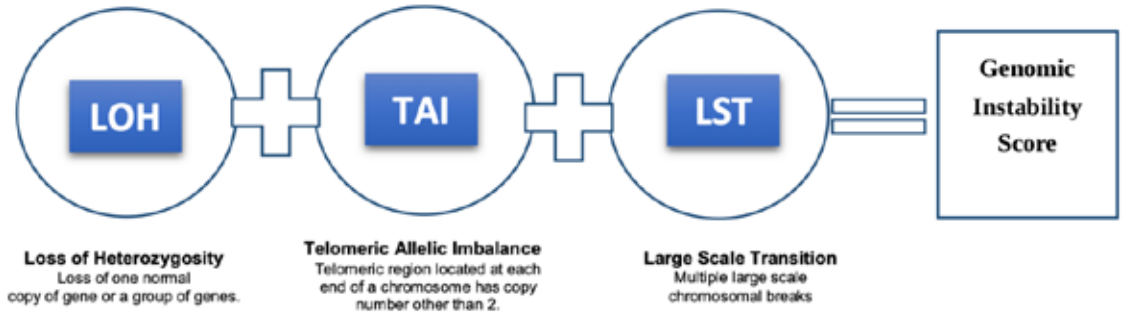
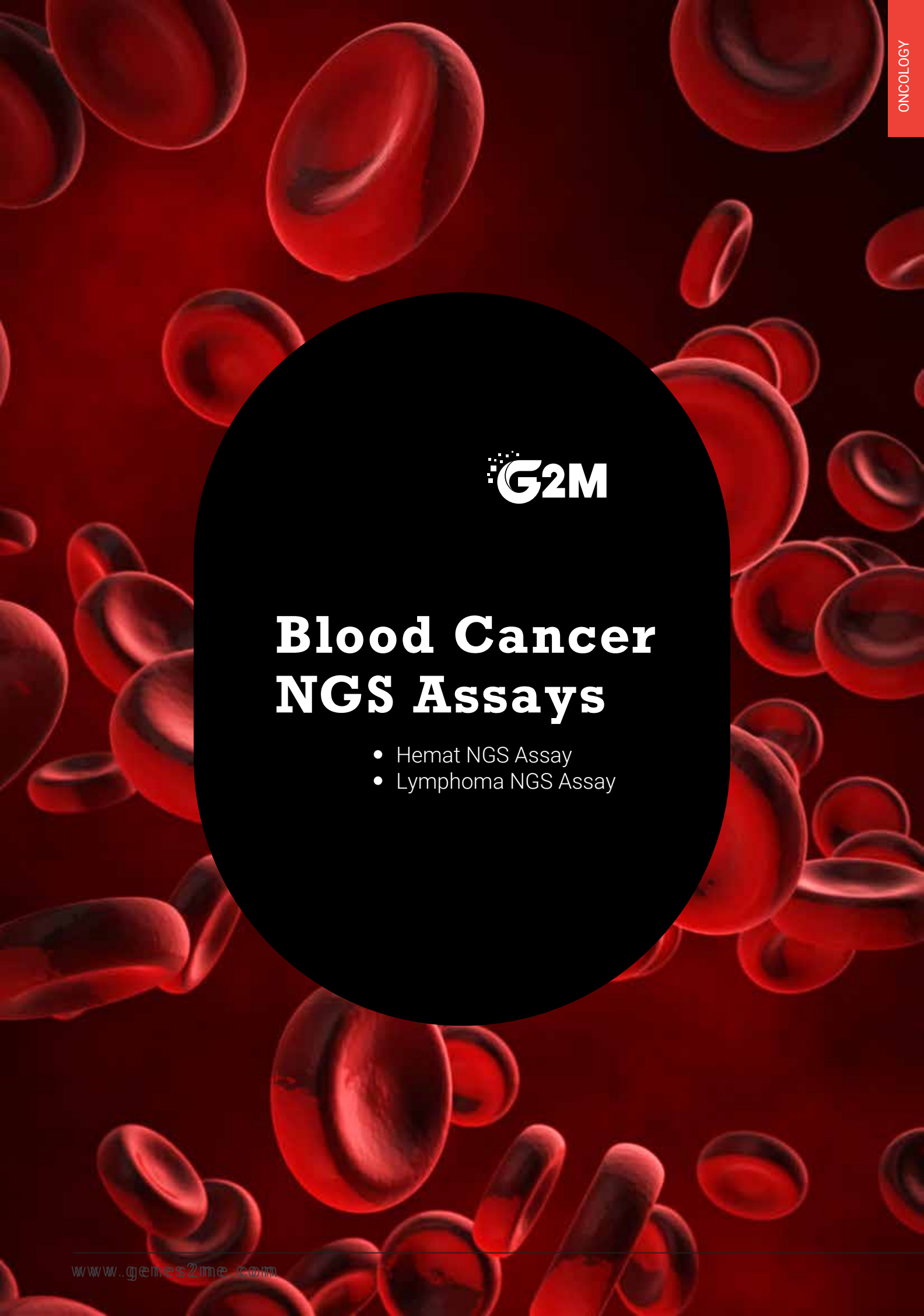


Figure 08: HRD scoring parameters for G2M HRD Assay pipeline.



ONCOLOGY

Blood Cancer NGS Assays

- Hemat NGS Assay
- Lymphoma NGS Assay

Genomic Profiling in Blood Cancers

Hematologic malignancies, encompass a diverse group of cancers that affect the blood, bone marrow, and lymphatic system. These cancers disrupt the normal production and function of blood cells, leading to a range of severe health issues and associated deaths. The primary types of blood cancers include leukemia, lymphoma, and myeloma.

Advances in technology, particularly with the advent of Next-Generation Sequencing (NGS), have evolved our understanding of these diseases. G2M offers end to end solutions for Leukemia (Myeloid & Lymphoid) and Lymphoma detection by NGS that can accelerate and streamline the detection covering a range of blood cancer causing genes with assays based on Hybridisation capture target enrichment. Genes and variants selected as per AMP/ASCO/NCCN guidelines.

Confidently detect key variants and biomarkers

- Panels rigorously engineered to target hard to capture regions (Homologous, Repetitve, GC Rich)
- Covering Whole Coding Sequences, DNA & RNA Fusions and Hotspots
- Platform Agnostic panels; compatible with the commonly available sequencer platforms (Illumina, Element Biosciences, MGI, Thermo Fisher)
- Hybridisation capture based target enrichment with a Hybridisation time of ~ 4 hours
- Easy to use assay workflows and Automation friendly
- FDA Approved drug recommendations
- NGS data analysis with GATK workflows for variant analysis giving an access to annotated VCF and a clinically significant mutations (CSM) report

Our Solutions

Hemat NGS Assay for Leukemia	No. of Genes	208* (DNA), 94 (RNA fusion genes)
	Target size	653 Kb
	Catalogue No.	G2MML28001-ill; G2MML28001-MG; G2MML28001-TF

*Note : includes 57 DNA fusion genes.

Covered regions	Whole CDS, Hotspots
Mutation types	SNV, InDels, CNV, DNA & RNA Fusions, FLT3-ITD
Sample types	Blood, Bone marrow

Lymphoma NGS Panel	No. of Genes	95 (DNA), 94 (RNA fusion genes)
	Gene count /family	~ 75
	Target size	~ 0.54 Mb
	Catalogue No.	G2MBR4-0228-ill, G2MBR4-0202-MG G2MBR4-0230-TF

Covered regions	Whole CDS, Hotspots
Mutation types	SNV, InDels, CNV, DNA & RNA Fusions
Sample types	Blood, Bone marrow

CliSeq Interpreter

Interpret and report relevant variants with Cliseq Interpreter Platform

The NGS data analysis is supported by combining guideline recommended variants with the analytical capability of G2M's Cliseq Interpeter Platform.

Cliseq Interpreter is a cloud based NGS data analysis software which offers an unparallel platform performance designed to streamline and enhance the interpretation of complex biological data. Once Quality Check, Alignment, Variant calling, and annotations are achieved, the annotated VCF files and clinically significat mutations (CSM) report will be available to download.

Performance Data

Hemat NGS Assay for Leukemia

Features	Performance#
Coverage uniformity	>98%
Precision	>95%
Reproducibility	99%
Sensitivity	5%VAF@>95%
On Target Ratio	85-95 %

Scan for Gene List

Lymphoma NGS Panel

Features	Performance#
Coverage uniformity	>90%
Precision	>95%
Reproducibility	99%
Sensitivity	5%VAF@>95%
On Target Ratio	85-90 %

Scan for Gene List

: The observed values are for Illumina platform

Hemat NGS Assay

Fold 80 distribution across blood cancer samples

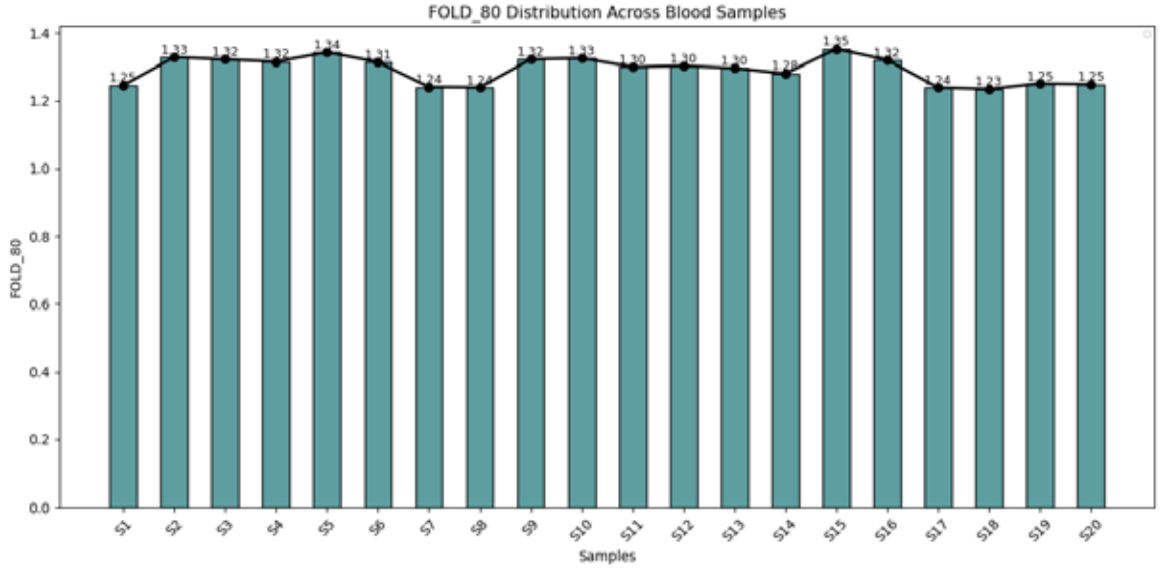


Fig 09 - Fold 80 values for blood samples ranged from 1.23–1.35, showing highly uniform coverage with minimal sequencing bias supporting accurate and dependable variant detection.

Comprehensive Mutation Profiling in Leukemia

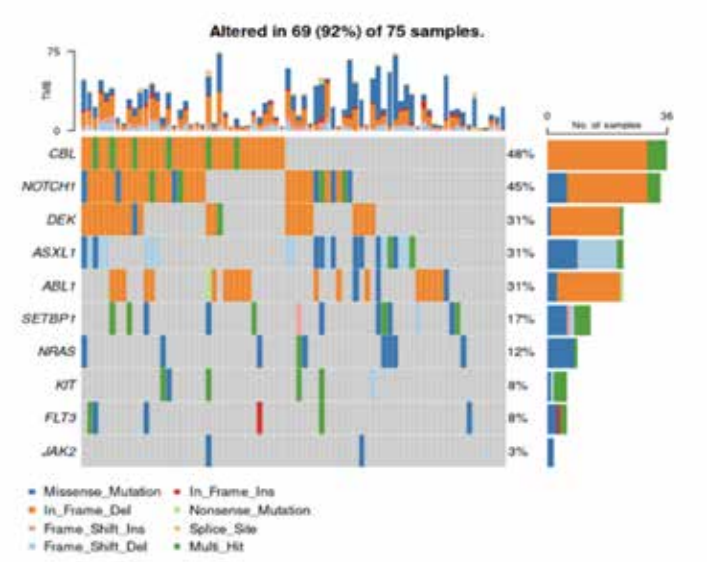


Figure 10 : Comprehensive Mutation Profiling in Leukemia - The Oncoplot shows the somatic mutations in the top 10 most frequently mutated genes in the Hemat NGS Panel. This oncoplot illustrates the distribution of all the mutations across the samples containing at least one aberration in the top 10 most frequently mutated genes. Missense mutation was the most prevalent form in almost all the top 10 mutated genes (represented with blue) followed by inframe mutation (represented with orange). The green represents the multi-hit mutations present in a single gene in all the tested samples. It contains all the types of mutations like missense, in frame shift. The right panel displays the percentage of mutations in each gene.

VAF Distribution Across Key Genes in Leukemia

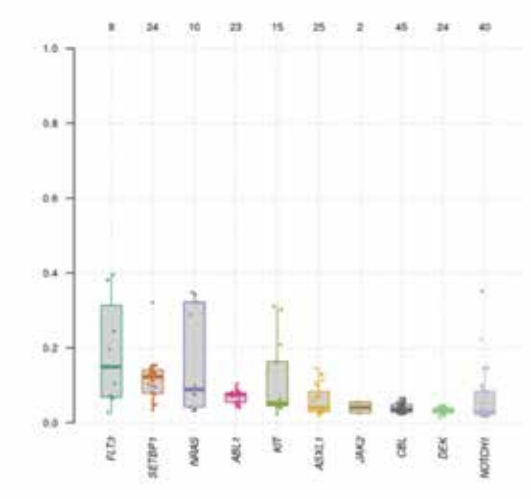


Figure 11 : The VAF plot shows distribution of some of the important genes in 75 myeloid patient samples. Genes like FLT3, SETBP1, and NRAS display higher median VAFs with greater variability, suggesting a higher mutation burden which may reflect a greater impact on disease progression. In contrast, genes like JAK2, CBL, and DEK exhibit lower and more consistent VAFs, indicating a smaller or more stable role in the overall genetic profile.

Common fusion partners in G2M Hemat RNA fusion panel

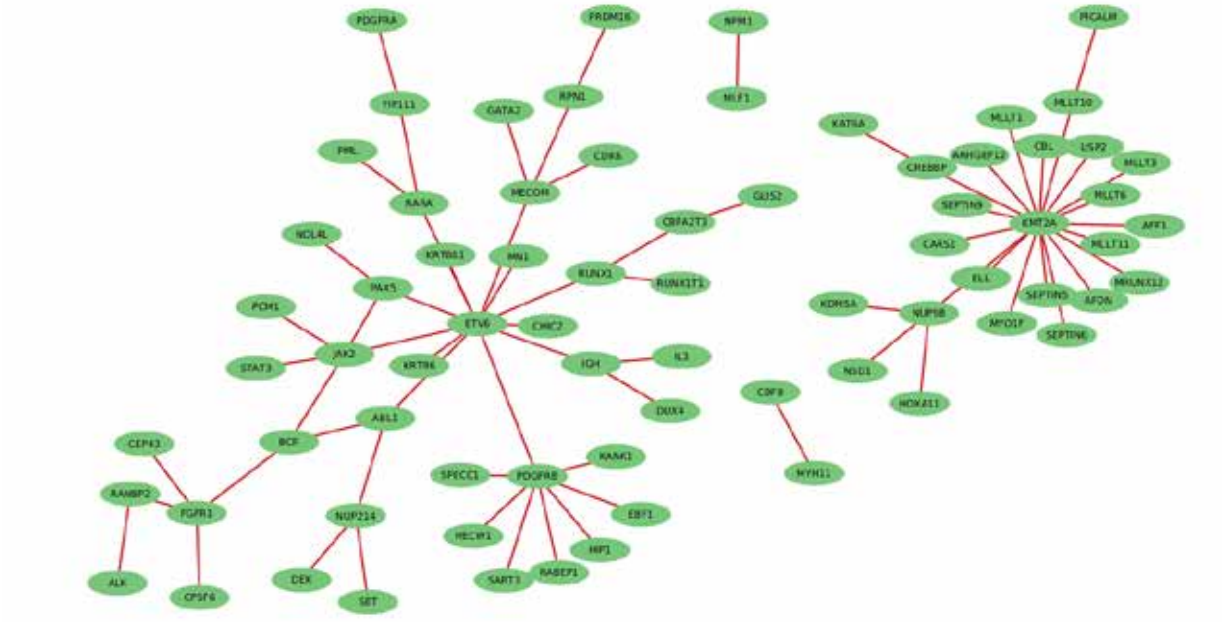


Figure 12

RNA Fusion Detection Power in Leukemia

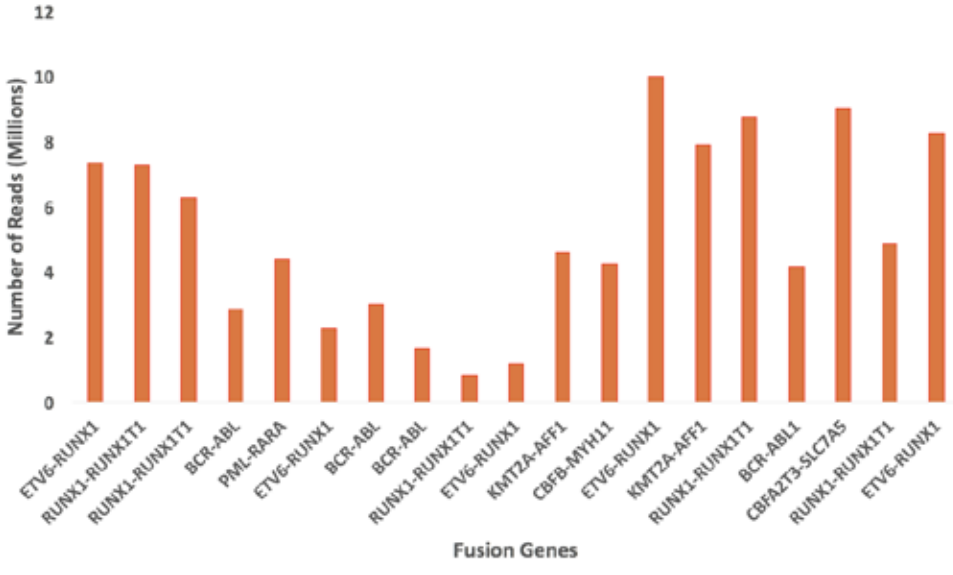


Figure 13: High-resolution profiling of RNA fusion genes in leukemia using our advanced NGS Panel, showcasing detection power across millions of sequencing reads.

Coverage of Key Cancer Genes in Leukemia

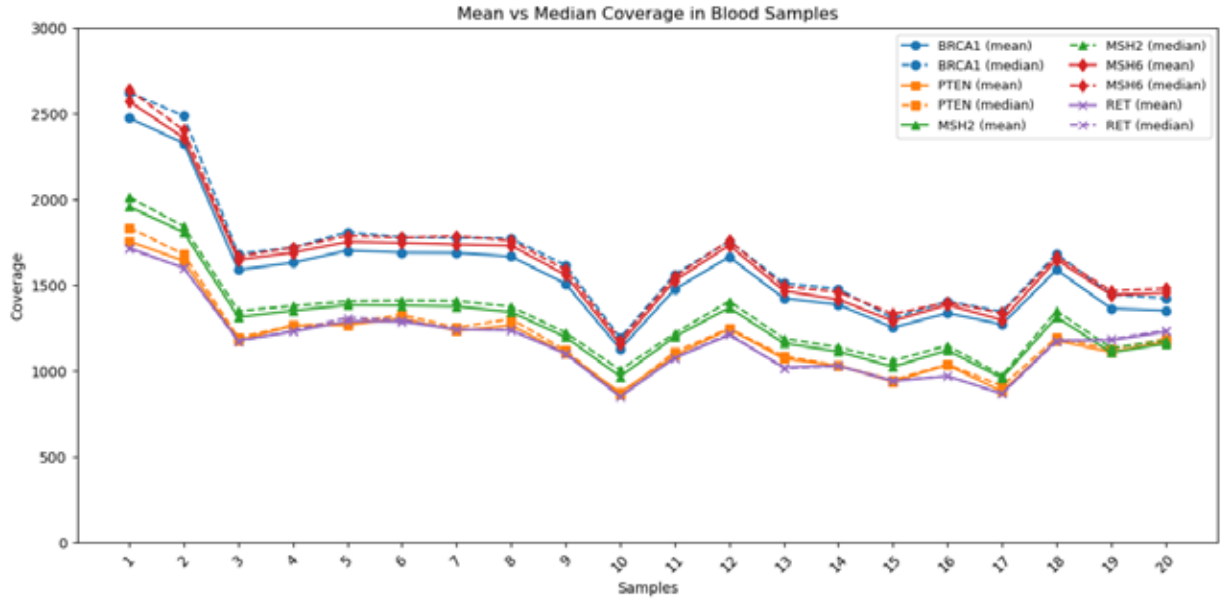


Fig 14 -Coverage patterns for key cancer genes (BRCA1, PTEN, MSH2, MSH6, RET) show strong consistency, with mean (solid) and median (dashed) values closely aligned. The consistent coverage demonstrates the workflow's robustness and reliability, ensuring dependable performance for routine clinical testing across blood and diverse sample types.

Marked On-Target Alignment Among Different Cancer Patient Samples

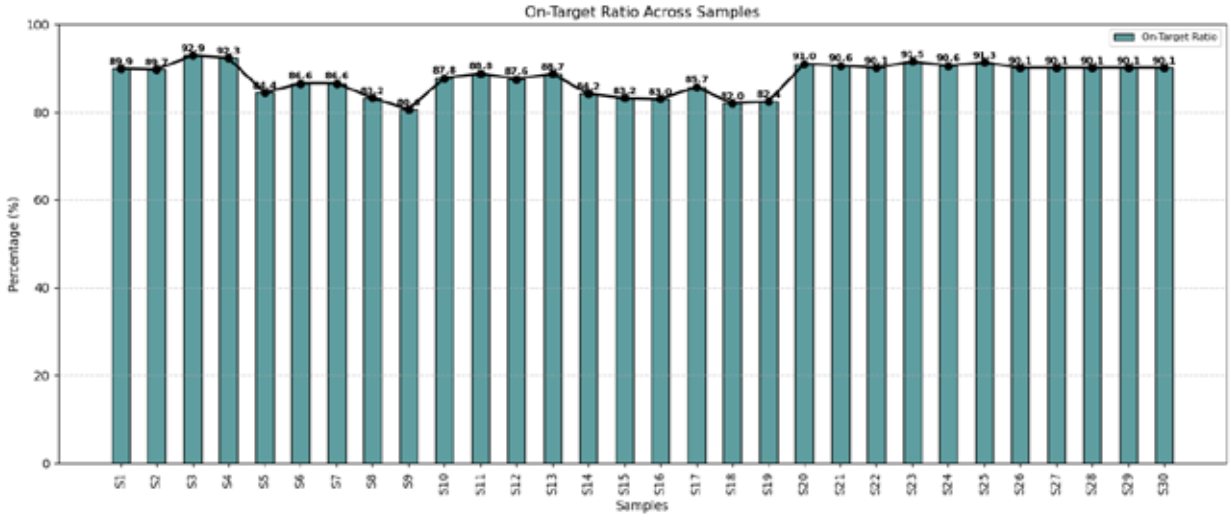


Fig 15 -On-target capture efficiency across cancer patient samples. All samples achieved >79% on-target alignment, reflecting the panel's optimized probe design, high hybridization specificity, and robust sequencing performance.

Consistent and High-Fidelity Coverage of Key Cancer Genes

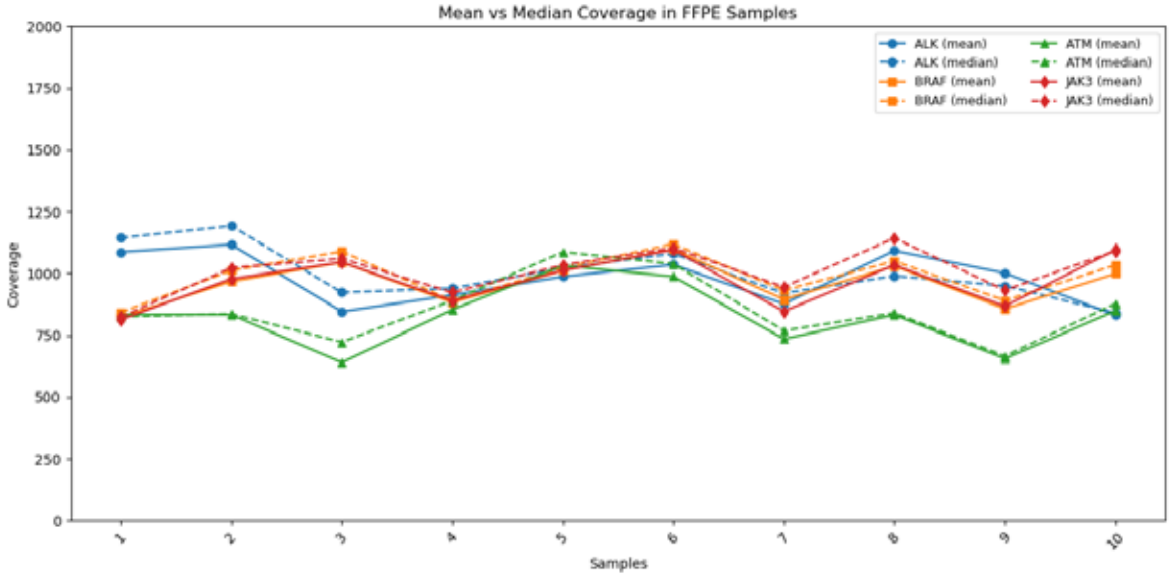


Fig 16 -The Lymphoma Assay demonstrates exceptional reliability, with coverage profiles for critical genes such as ALK, BRAF, ATM, and JAK3 showing near-perfect alignment between mean (solid line) and median (dashed line) depth. This tight concordance reflects the assay's uniform performance across all target regions, minimizing bias and ensuring robust, reproducible results. Such consistency is vital for confidently interpreting genomic data across diverse FFPE samples, reinforcing the assay's value in precision oncology.

High On - Target Enrichment for Robust Genomic Profiling

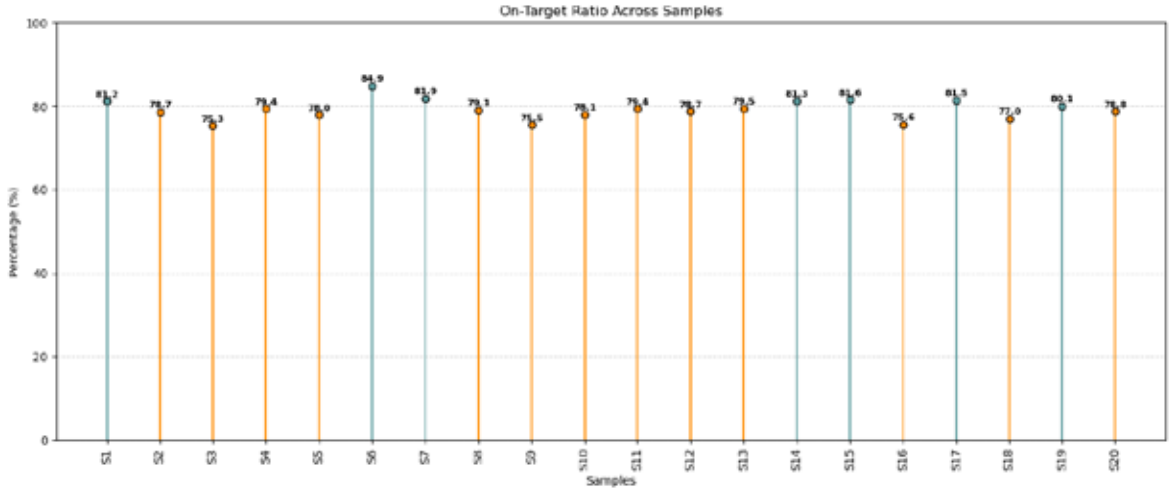


Fig 17 -All patient samples demonstrated over 80% on-target alignment reflecting the panel's precision engineered probe architecture and rigorously optimized assay chemistry. This high capture efficiency ensures uniform coverage across target regions, enabling reproducible, high confidence variant detection essential for clinical grade sequencing and scalable diagnostic workflows.

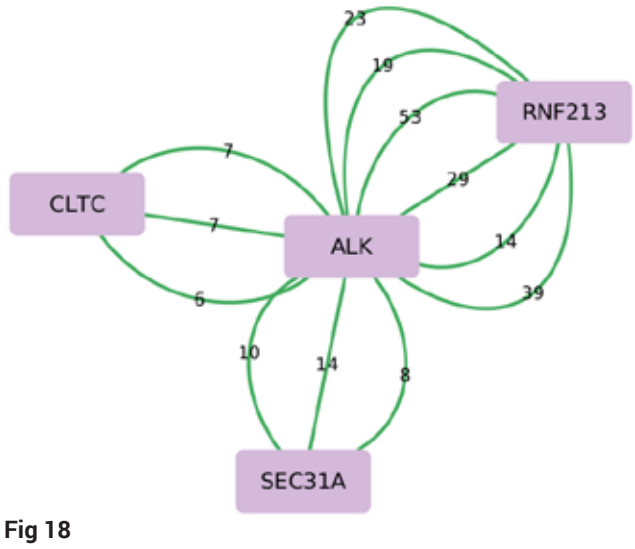


Fig 18

DNA Fusions detected by G2M Lymphoma Assay

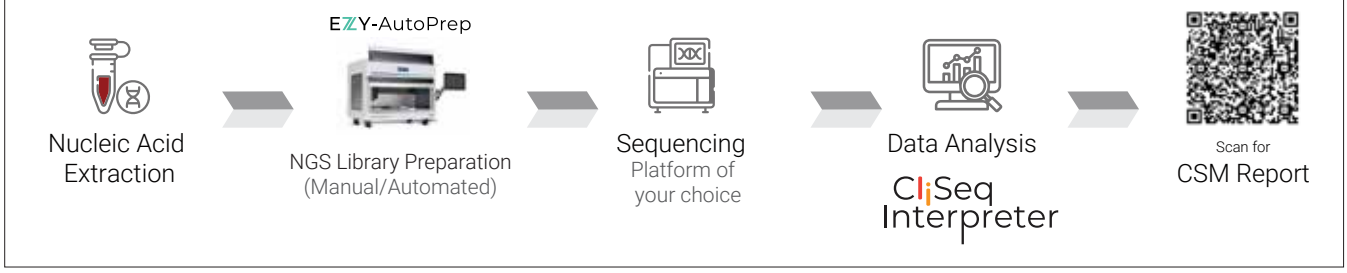
Fig 08 -DNA fusions identified with G2M Lymphoma NSG panel in plasma samples along with support reads.

Insights into Drug Recommendations

Type of Cancer*	Gene	Drug
Acute Myeloid Leukemia	IDH1	Tibsovo (ivosidenib) Rezlidhia (olutasidenib)
	IDH2	Idhifa (enasidenib)
Acute Myelogenous Leukemia	FLT3 (ITD/TDK)	Rydapt (midostaurin) Xospata (gilterinib VANFLYTA (quizartinib)
Chronic Myeloid Leukemia	BCR-ABL fusion	Tasigna (nilotinib)
DLBCL -Peripheral Blood	TP53	Rituximab
Burkitt Lymphoma	MYC	Nadroparin
Chronic Myeloid Leukemia	BCR-ABL Fusion	Tasigna (nilotinib)

*Limited Cancer Types and Drug details mentioned

Streamline your NGS workflow



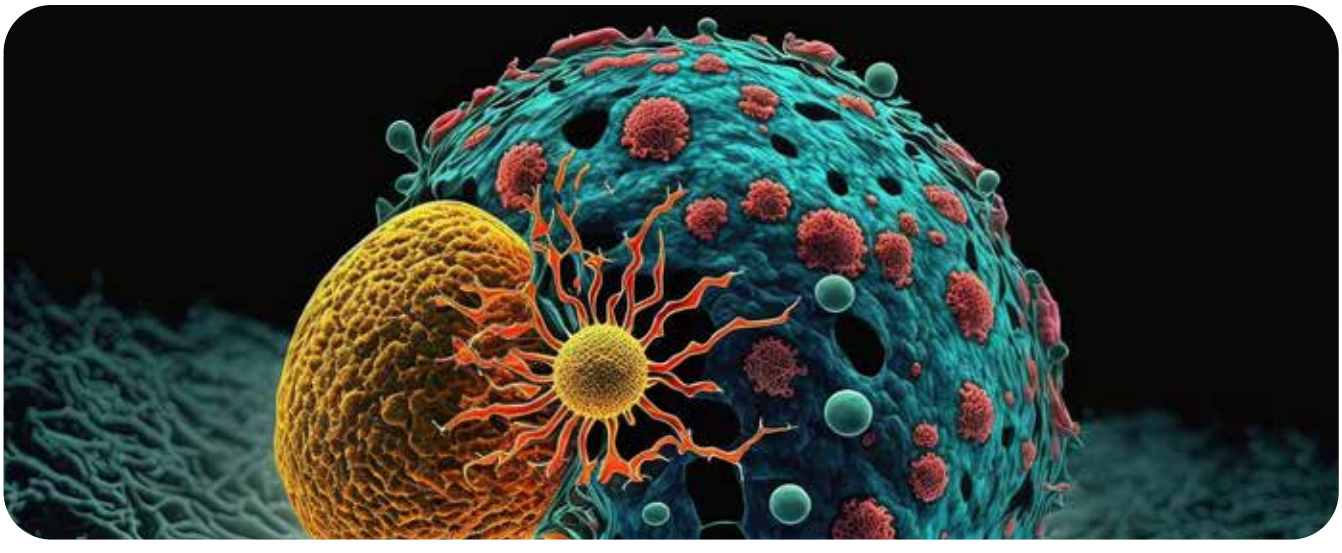
Liquid Biopsy

NGS Assays

Lung | Breast | Colorectal

The Genes2Me Liquid biopsy assays screen lung/ breast/ colorectal cancer associated genes to identify somatic mutations in DNA from blood tissue. It provides comprehensive detail of these cancers and helps to decide the best course of treatment. The screening method involves using circulating tumor cells that are used as biomarkers to detect respective cancer. Circulating tumor DNA (ctDNA) is released from apoptotic and necrotic tumor cells. Applications of ctDNA in cancer include diagnosis and detection, prognosis, response to thereopy, detecting mutations & structural alterations, minimal residual disease, tumor mutational burden, and tumor evolution tracking.

- Highly optimized panel for clinical testing with exceptional accuracy
- Receive high-quality data from our analysis software, enabling efficient duplication removal and minimizing sequencing noise



ctDNA Colorectal Assay

Gene count/ family	25
Covered region	Whole CDS
Target size	75 kb
Mutation type	SNVs/ InDels
Sample type	Blood/ Plasma

GENE LIST

APC	ASXL1	BRAF	CHEK2	CTNNB1	DNMT3A	EGFR	ERBB2	ERBB3
FBXW7	FGFR1	GNAS	HRAS	IDH1	IRS1	KRAS	MAP2K1	MET
NRAS	PDGFRB	PIK3CA	PTEN	SMAD4	TET2	TP53		

ctDNA Breast Assay

Gene count/ family	63 (14 DNA fusions)
Covered region	Whole CDS
Target size	115 kb
Mutation type	SNV/ InDels/ CNVs
Sample type	Blood/Plasma

GENE LIST

AKAP9	AKT1	APC	AR	ARAF	ARID1A	ATM	BRAF	BRCA1	BRCA2
CCDC170	CCND1	CCNE1	CD74	CDH1	CREBBP	CTNNB1	DPYD	DYRK4	EGFR
ERBB2	ESR1	ETV6	FBXW7	FGFR1	FGFR2	FGFR3	GATA3	GNAQ	IGF1R
KIT	KPAS	KRAS	LMNA	LRP2	MAP2K4	MAP3K1	MDM2	MYB	MYC
NCOR1	NCOR2	NF1	NFIB	NRAS	NRG1	NTRK1	NTRK2	NTRK3	PALB2
PIK3CA	PIK3R1	PTEN	RAD51AP1	RB1	RET	RNF213	SF3B1	SLC33A2	SMAD4
TOP2A	TP53	TPM3							

DNA FUSIONS

CCDC170	CD74	DYRK4	ESR1	ETV6	LMNA	MYB	NFIB	NRG1	NTRK1
NTRK3	RAD51AP1	SLC33A2	TPM3						

ctDNA Lung Assay

Gene count/ family	32
Covered region	Whole CDS
Target size	110 kb
Mutation type	SNV/ InDels/ CNVs
Sample type	Blood/ Plasma

GENE LIST

AKT1	ALK	ARAF	ARID1A	BRAF	CBL	CDKN2A	CTNNB1	EGFR#
ERBB2#	HRAS	KEAP1	KMT2D	KRAS	MAP2K1	MET#	MTOR	NF1
NRAS	NTRK1	NTRK2	PIK3CA#	PTEN	RB1	RET	RIT1	ROS1
SETD2	SOX2#	STK11	TP53#	U2AF1				

CNVs

Coverage of Key Cancer Genes in ct-Breast Panel

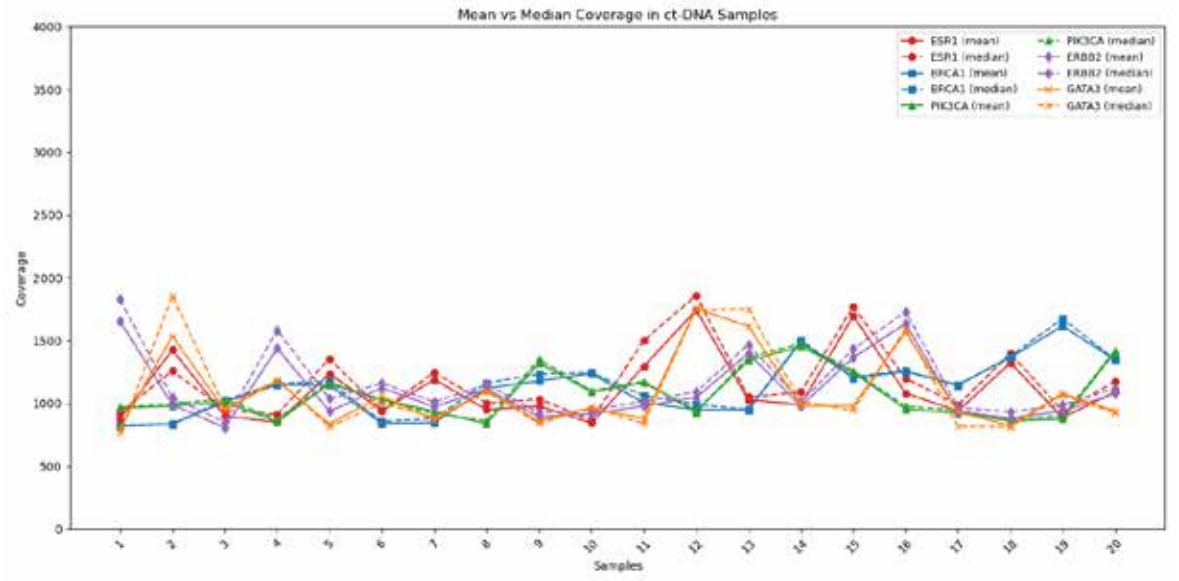


Fig 19 - Coverage profiles of critical genes (ESR1, BRCA1, PIK3CA, ERBB2, and GATA3) exhibit strong concordance between mean (solid line) and median (dashed line) depth, demonstrating uniform sequencing and minimal bias across all target regions. This alignment highlights the assay's robust performance and reliability, ensuring confident results across diverse breast cancer samples.

Reliable Target Capture for Liquid Biopsy Precision

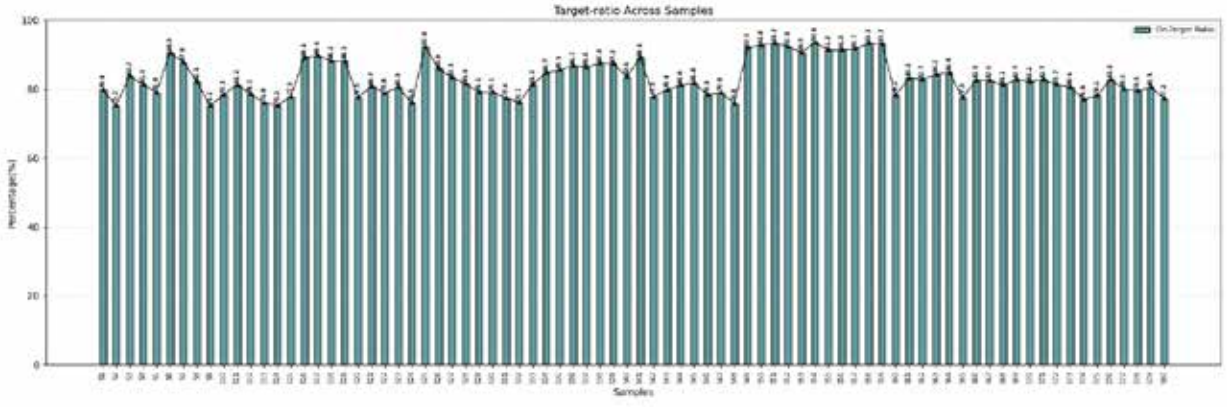


Fig 20 - The ctDNA breast cancer panel consistently delivers more than 75% on-target alignment, reflecting its smart design and efficient target capture. This ensures reliable mutation detection from low-input samples, enabling early diagnosis, treatment monitoring and scalable diagnostic utility.

ASSAY PERFORMANCE	ctDNA Lung	ctDNA Colorectal	ctDNA Breast
Features	**Performance#**	**Performance#**	**Performance#**
Coverage uniformity	98%	98%	97%
Precision	96%	94%	93%
Reproducibility	99%	96%	98%
Sensitivity	<1%VAF @ 95%	<1%VAF @ 95%	<1%VAF @ 95%
On Target Ratio	86-95 %	85-95%	88-95%

: The observed values are for Illumina platform

Gene & Drug Details

TYPE OF CANCER*	GENE	DRUG	
Non–small cell lung cancer (NSCLC)	ALK	Alectinib, crizotinib, ceritinib, lorlatinib	**ctDNA Lung**
Non–small cell lung cancer (NSCLC)	BRAF	Dabrafenib+trametinib	
Non–small cell lung cancer (NSCLC)	EGFR	Erlotinib, Osimertinib, gefitinib, erlotinib, afatinib, mobocertinib, amivantamb	
Non–small cell lung cancer (NSCLC)	ERBB2	Fam-trastuzumab deruxtecan-nxki	
Colorectal Cancer	EGFR	Cetuximab, Panitumumab	**ctDNA Colorectal**
Gastric and Gastroesophageal Cancer	ERBB2	Trastuzumab	
Colorectal Cancer	KRAS	Cetuximab, Panitumumab	
Breast cancer, Metastatic Castrate Resistant Prostate Cancer, Ovarian Cancer	BRCA1	Olaparib, rucaparib, niraparib + abiraterone acetate	**ctDNA Breast**
Ovarian Cancer, Breast cancer	BRCA2	Talazoparib	
Breast Cancer	ERBB2	Trastuzumab, pertuzumab, ado-trastuzumab emtansine	
Breast Cancer	ESR1	Elacestrant (Orserdu)	

*Limited cancer type details mentioned

Cancercheck

NGS Assays

The changes (mutations) in the DNA within the cell may inhibit the cell to function normally and allow it to become cancerous. Most of the cancer mutations are somatic in nature as the changes in DNA occur in cell of any part of the body. These mutations can be caused by many factors such as radiations, tobacco smoking and other chemicals. Some of the cancers such as breast, ovary, colorectal etc. can also be hereditary since it can be inherited from parent.

Cancer Check NGS assays are designed to detect all types of variants associated with somatic/germline cancer. Targeting the selected genes with high sensitivity and specificity enables saving cost and effort.

The report consists of the primary, secondary, and tertiary results for the In-depth understanding and interpretation of sequencing data.

CancerCheck 50 Assay

No. of Genes	67
Gene count/ family	~54
Covered region	Whole CDS
Target size	0.2 Mb
Mutation type	SNV/ InDels/ CNVs
Sample type	Blood/FFPE

The Genes2Me CancerCheck 50 Assay screens niche set of ~67 cancer causing genes that are most prone to cancerous mutations, to identify both germline and somatic mutations in blood or tumor tissue.

GENE LIST									
ABL1	BRCA1	CSF1R	ERBB4	GNAS	KIT	MYC	PIK3CA	RB1	STK11
AKT1	BRCA2	CTNNB1	ESR1	H3-3A	KNSTRN	MYCN	PIK3R1	RET	STK19
ALK	CDH1	DDR2	FGFR1	HRAS	KRAS	MYD88	PPP2R1A	ROS1	TP53
APC	CDK4	EGFR	FGFR2	IDH1	MAP2K1	NOTCH1	PTCH1	SF3B1	U2AF1
ARID1A	CDK6	EP300	FGFR3	IDH2	MET	NRAS	PTEN	SMAD4	
ATM	CDKN2A	ERBB2	GNA11	JAK2	MLH1	NTRK1	PTPN11	SMO	
BRAF	CRNKL1	ERBB3	GNAQ	KDR	MTOR	PDGFRA	RAC1	SRC	

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity @ 0.2x	93%
Precision	99%
Reproducibility	97%
Sensitivity (VAF @ 1%)	97%
On Target Ratio	75-85 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

High Confidence and Uniform Coverage of Essential Cancer Biomarkers

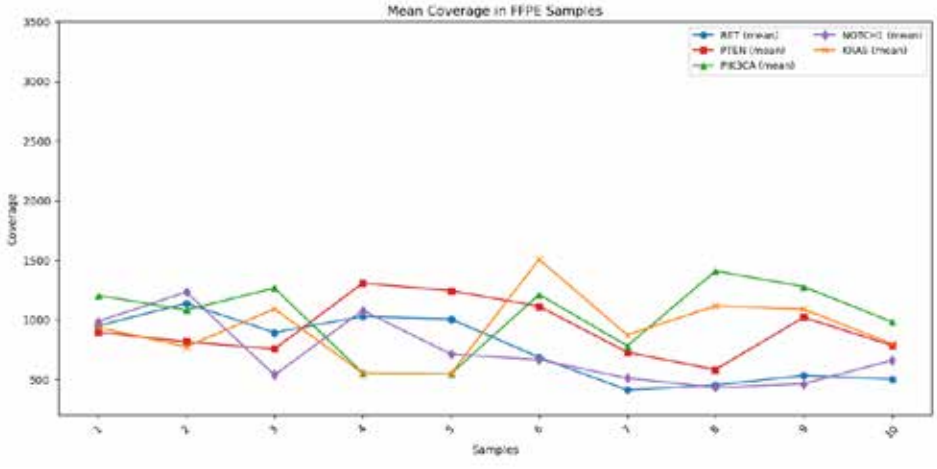


Fig 21 - Mean coverage profiles of critical cancer-associated genes (RET, PTEN, PIK3CA, NOTCH1, and KRAS) reveal remarkable consistency and uniformity across all targets. This high level of coverage stability highlights the superior robustness and precision of the Genes2Me Cancer Check 50 Assay, ensuring reliable, high-confidence results for routine clinical testing.

Efficient Target Enrichment Supports Scalable, Reliable Cancer Diagnostics

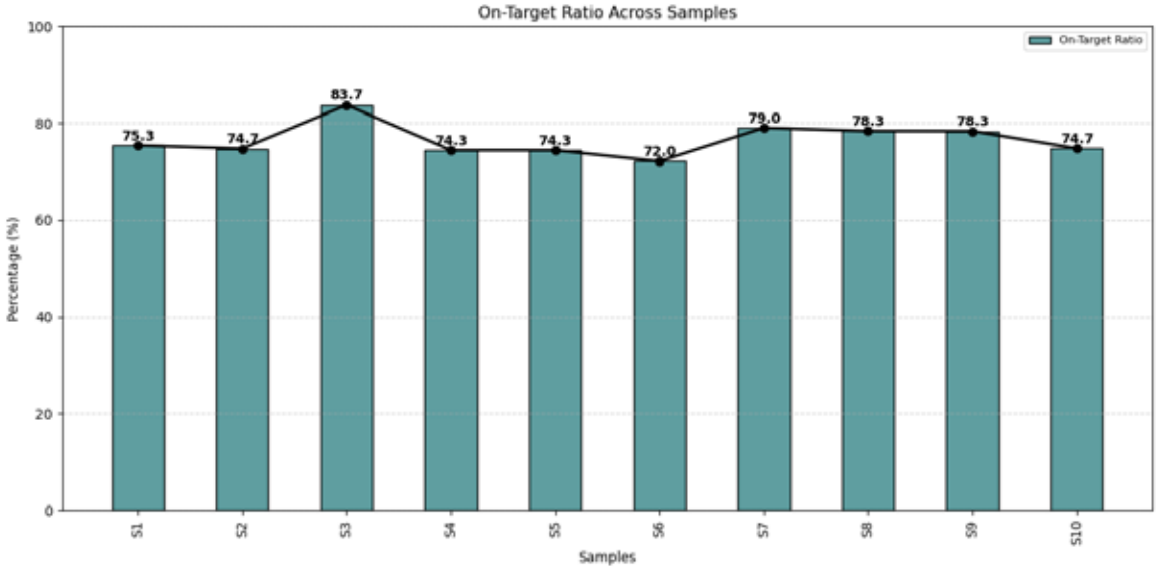


Fig 22 - Consistent with over 75% on-target alignment across all cancer patient samples, our panel exemplifies exceptional design precision, optimized assay performance, and high-efficiency target capture delivering the clinically reliable data and scalable performance for impactful oncology outcomes.

Consistent Coverage Uniformity Enables High-Confidence Cancer Profiling

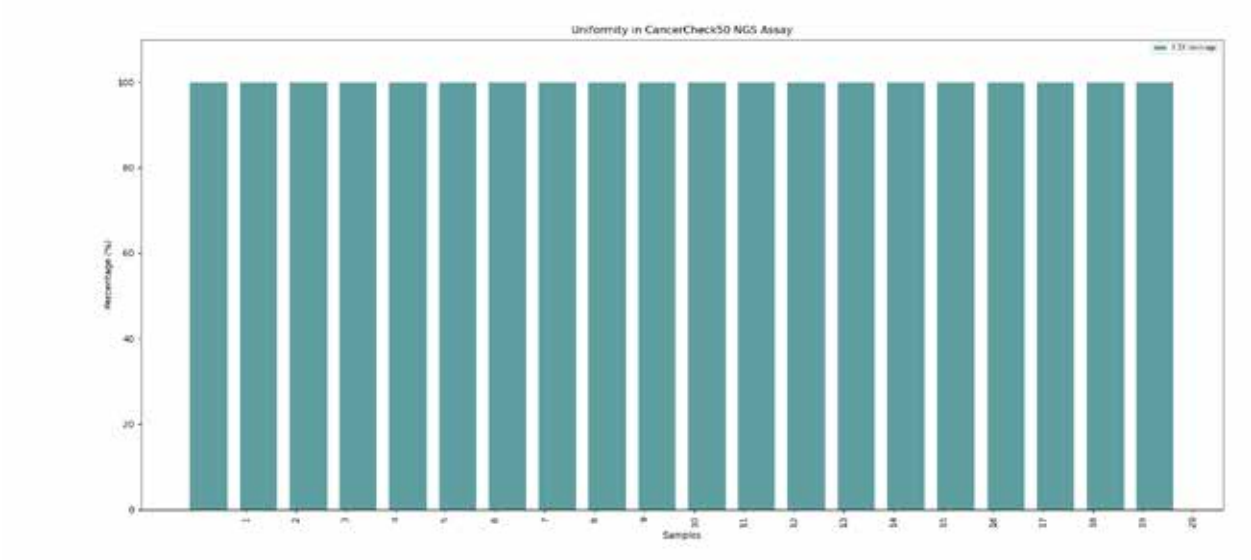


Fig 23 - Achieving ~100% coverage uniformity at 0.2X across all samples, our optimized probe design ensures consistent enrichment and reliable performance. This translates to high-confidence, reproducible results, empowering every assay with precision and efficiency.

CancerCheck 100 Assay

No. of Genes	148
Gene count/ family	~99
Covered region	Whole CDS
Target size	0.5 Mb
Mutation type	SNV/ InDels/ CNVs
Biomarkers	MSI
Sample type	Blood/ FFPE

The Genes2Me CancerCheck 100 Assay screens a set of ~148 cancer causing genes that are most prone to cancerous mutations, to identify both germline and somatic mutations in blood or tumor tissue.

It provides comprehensive detail of the biomarkers such as MSIs & HRR genes in cancer and helps to decide the best course of treatment.

GENE LIST												
ABL1	AKT1	AKT2	AKT3	ALK	#APC	ARID1A	ARID1B	ARID2	ASXL1	#ATM	ATR	ATRIP
ATRX	AURKA	AURKB	BAP1	#BARD1	BCL2	BCOR	BCR	BLM	BMPR1A	#BRAF	#BRCA1	#BRCA2
#BRIP1	CALR	#CCND1	#CCND2	CDH1	#CDK4	#CDK6	#CDKN2A	#CHEK2	CSF1R	CSF3R	CTNNB1	DAPK1
DDR2	#EGFR	EIF1AX	EP300	EPCAM	EPHB4	#ERBB2	ERBB3	ERBB4	ERCC1	ERCC2	ESR1	EWSR1
EZH2	FBXW7	FGF19	#FGF3	FGF4	FGF9	#FGFR1	FGFR2	FGFR3	FLI1	FLT3	GNA11	GNAQ
GNAS	HNF1A	HRAS	IDH1	IDH2	IGF1R	ITK	JAK1	JAK2	JAK3	KDR	KIT	KMT2C
KMT2D	#KRAS	LRP1B	LZTR1	MAP3K1	MDM2	#MET	MGMT	MLH1	MPL	MRE11	MSH2	MSH6
MTOR	MUTYH	NBN	NF1	NFE2L2	NOTCH1	NOTCH2	NOTCH3	NPM1	NRAS	NTRK1	#PALB2	PDGFRA
PDGFRB	#PIK3CA	#PIK3CB	#PIK3CD	#PIK3R1	PMS2	POLD1	POLE	PRSS1	PTCH1	PTCH2	#PTEN	PTPN11
RAD50	RAD51C	RAD51D	RASSF1	#RB1	#RET	ROS1	RUNX1	RUNX3	SEMA3B	SETBP1	SF3B1	SLX4
SMAD4	SMARCA4	SMARCB1	SMO	SRC	SRSF2	STAG2	STK11	SYK	TERT	PYCARD	TOP1	#TP53
TSC1	TSC2	U2AF1	VHL	ZMYM3								

CNVs

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity @ 0.2x	>99%
Precision	98.5%
Reproducibility	98%
Sensitivity (VAF @ 1%)	98.5%
On Target Ratio	75-85 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Coverage of Key Cancer Genes in FFPE Samples

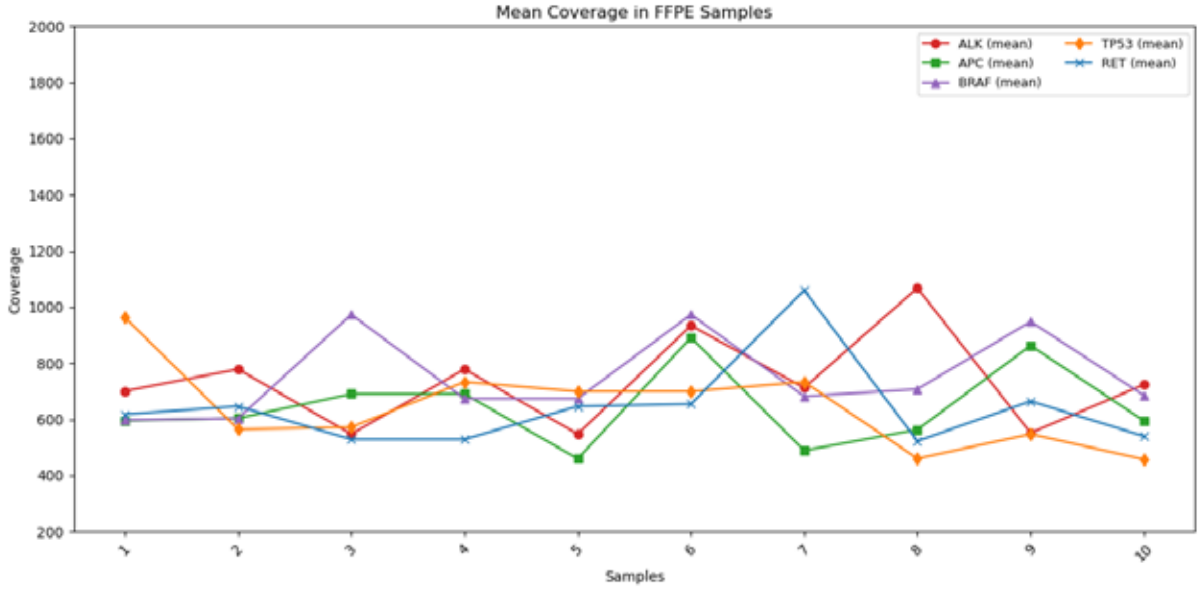


Fig 24 - Mean coverage profiles of pivotal cancer-associated genes (ALK, APC, BRAF, TP53, and RET) demonstrate uniform and consistent target representation. The plot showing consistent coverage across targets highlights the robustness and reliability of the workflow, ensuring high-quality performance and confidence in routine clinical testing across diverse FFPE samples.

On-target ratio across FFPE samples

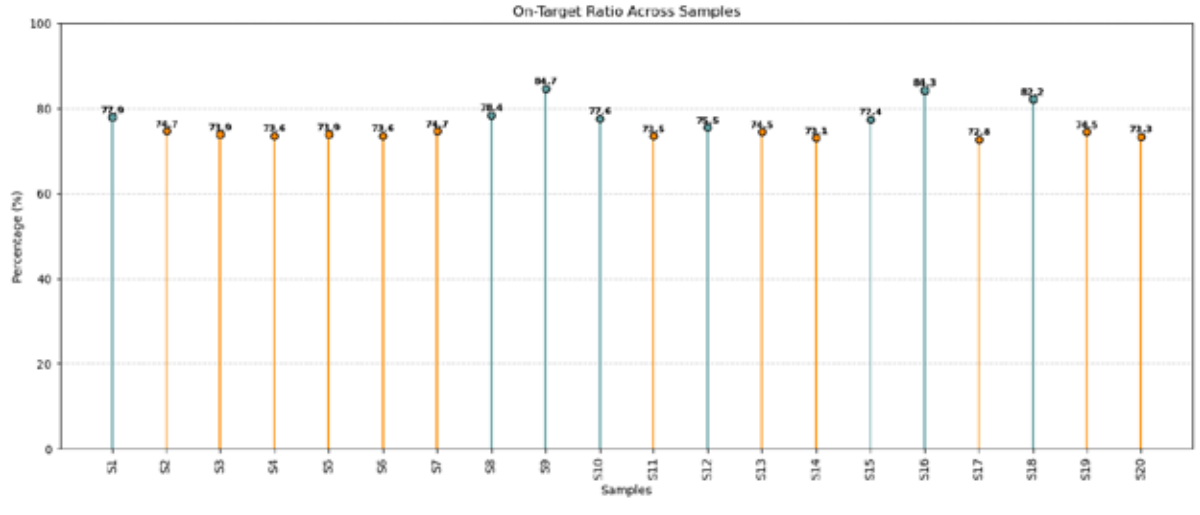


Fig 25 - All patient samples achieved more than 75% on-target alignment, reflecting the panel's exceptional design precision, optimized assay performance, and highly efficient target capture ensuring reliable, high-quality sequencing efficiency.

OncoCheck Assay

Gene count/ family	~53
Covered region	Whole CDS
Target size	0.17 Mb
Mutation type	SNV/InDels/CNV
Sample type	Blood/ FFPE

OncoCheck NGS assay is aimed to screen a range of disease causing genes to identify somatic mutations and germline mutations in DNA from FFPE and fresh tissue, blood targeting ~53 genes covering all the coding sequences enriched by hybridization capture based target enrichment methodology.

Genes are selected based on AMP/ASCO/CAP guidelines to uncover the coding region compiling to the size of ~0.17 Mb.

GENE LIST													
APC	#ATM	ATRIP	BARD1	BLM	BMPR1A	#BRCA1	#BRCA2	BRIP1	CCND1	CD274	#CDH1	CDK12	
CDK4	CDKN2A	CHEK2	EGFR	EPCAM	ERBB2	ESR1	FANCD2	FGFR1	FGFR2	GATA3	KRAS	LZTR1	
MAP3K1	MKI67	#MLH1	MLH3	MRE11	#MSH2	#MSH6	MUTYH	NBN	NF1	#PALB2	PIK3CA	#PMS2	
PPP2R2A	PRSS1	#PTEN	RAD50	RAD51B	#RAD51C	RAD51D	RAD54L	SLX4	SMAD4	#STK11	TOP2A	#TP53	VHL

CNVs

On-target ratio across Tumor samples

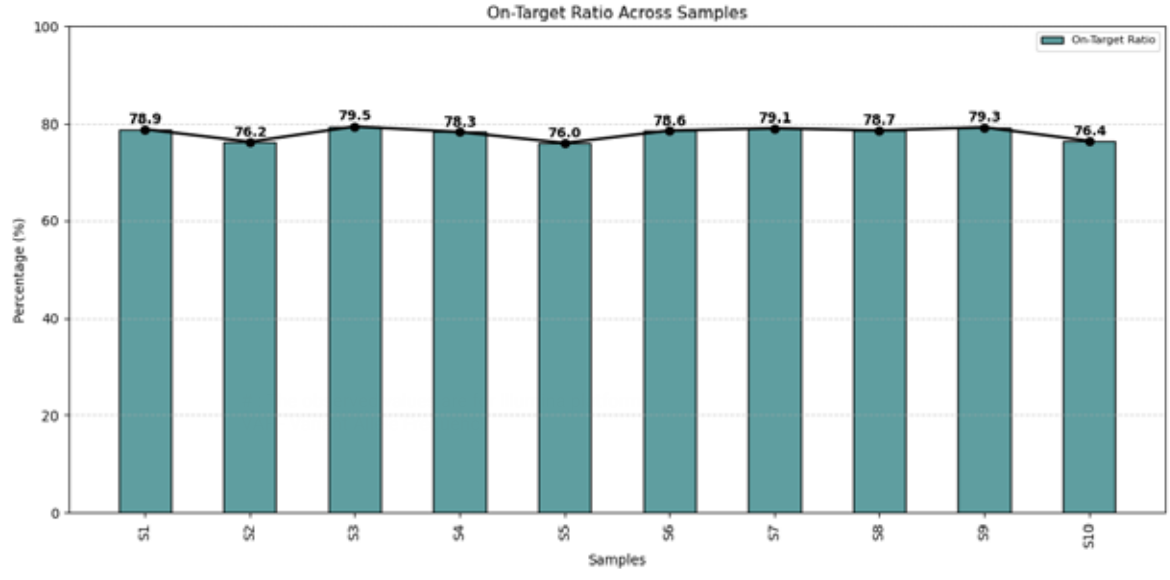


Fig 26 - Greater than 75% on-target alignment, reflecting the panel's exceptional design precision, optimized assay performance, and highly efficient target capture ensuring reliable, high-quality sequencing efficiency.

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity @ 0.2x	>96%
Precision	>96%
Reproducibility	98.2%
Sensitivity (VAF @1%)	98%
On Target Ratio	75-85 %

Common Hereditary Cancer NGS Assay

Gene count/ family	~83
Covered region	Whole CDS
Target size	0.24 Mb
Mutation type	SNV/ InDels/ CNV
Sample type	Blood

The Genes2Me Common Hereditary Assay screens a comprehensive set of genes to identify germline mutations in DNA from blood. It provides comprehensive detail of the cancer and helps physicians and geneticists to decide the best course of treatment.

GENE LIST

#APC	#ATM	ATRX	AXIN2	BAP1	BARD1	BLM	BMPR1A	BRAF	#BRCA1	#BRCA2	BRIP1	#CDH1
CDK4	CDKN1C	#CDKN2A	CHEK2	CTR9	EGLN1	EGLN2	EPAS1	#EPCAM	EXT1	EXT2	FGFR1	FH
FLCN	GREM1	H3-3A	HRAS	IDH2	KIF1B	KIT	KMT2D	MAX	MDH2	MEN1	MERTK	MET
#MLH1	MRE11	#MSH2	MSH3	#MSH6	MTAP	MUTYH	NBN	NF1	NF2	NTHL1	#PALB2	PDGFRA
#PMS2	POLD1	POLE	PRSS1	#PTEN	RAD50	#RAD51C	RAD51D	RB1	RECQL4	REST	RET	RNF43
SDHA	SDHAF2	SDHB	SDHC	SDHD	SLX4	SMAD4	SPINK1	SQSTM1	#STK11	TMEM127	#TP53	TRIM28
TSC1	#TSC2	VHL	WT1	XRCC2								

CNVs

ASSAY PERFORMANCE

Features	Illumina
Coverage uniformity @ 0.2 x	98%
Precision	98%
Reproducibility	98.2%
Sensitivity (VAF @1%)	98%
On Target Ratio	>78 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Uniform fold 80 base penalty across blood samples

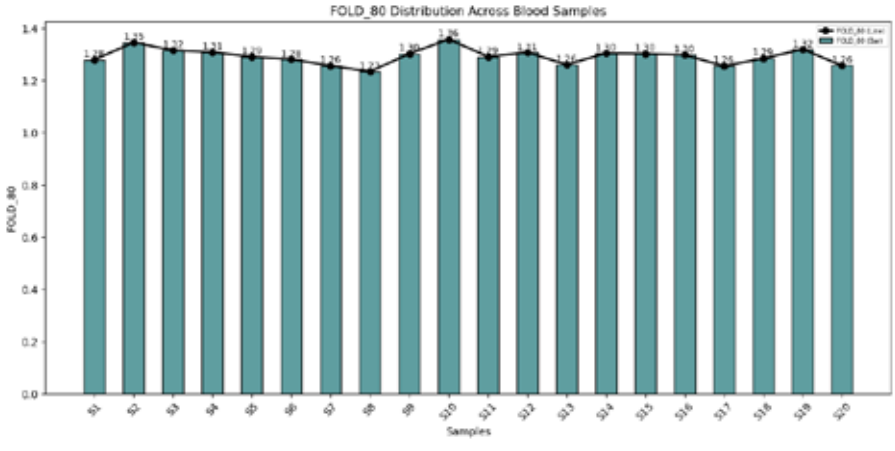


Fig 27 - Fold 80 plots were generated using genomic DNA libraries from blood samples (n=20), enriched with the G2M Common Hereditary Cancer NGS Panel and sequenced on the NovaSeq system using 2 × 150 bp paired-end reads, enabling high-depth, uniform coverage across clinically relevant targets. Fold 80 base penalty across blood-derived samples, below 1.3 demonstrates highly uniform coverage with minimal sequencing bias, reflecting the robustness of the assay design.

High On-Target Ratio Across Different Samples

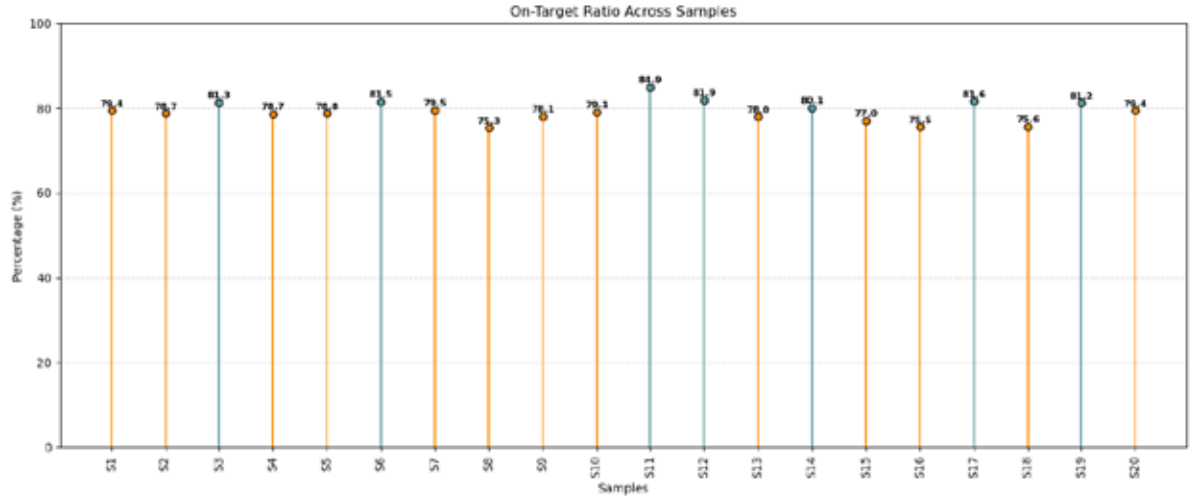


Fig 28 - On-target ratios across patient samples consistently exceeded ~80%, highlighting the panel's optimized design, efficient probe capture, and robust sequencing performance for reliable genomic profiling.

Mean vs Median Gene Coverage

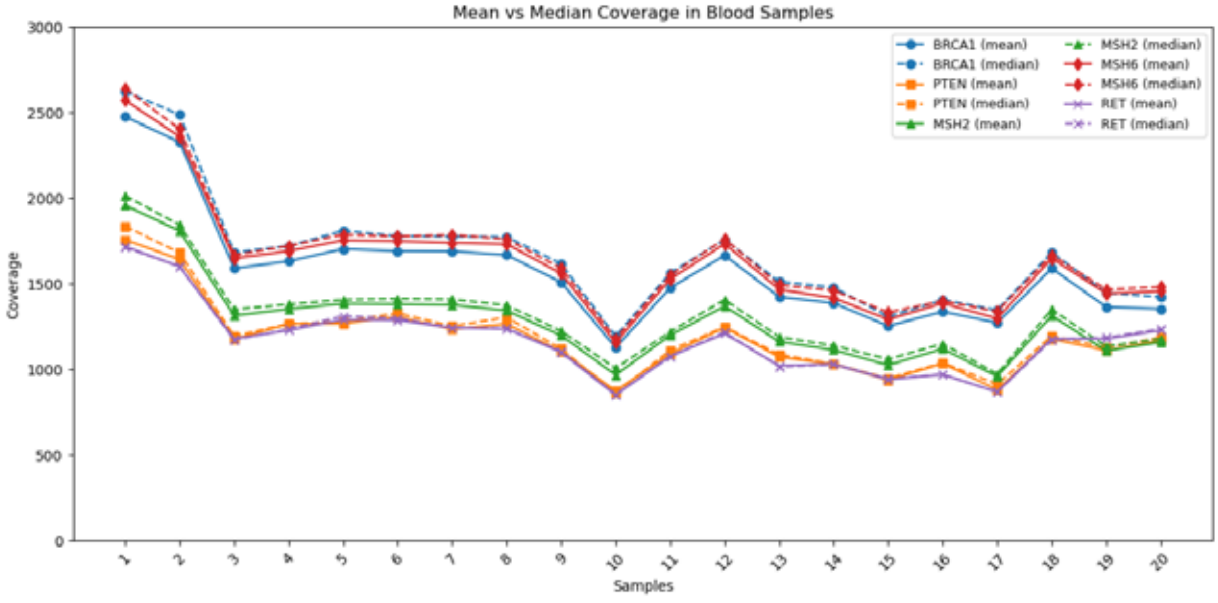


Fig 29 - Coverage profiles of key cancer-associated genes (BRCA1, PTEN, MSH2, MSH6, RET) are shown with mean (solid line) and median (dashed line) values. The plot shows a close alignment between mean and median coverage across target genes suggesting a strong indicator of uniform sequencing depth across the specified regions. This highlights the robustness of the workflow, ensuring reliability for routine clinical testing with reliable variant detection across blood sample types.

BRCA 1/2 NGS Assay

Gene count/ family	2
Covered region	Whole CDS
Target size	0.02 Mb
Mutation type	SNV/InDels/CNV/Rearrangements
Sample type	Blood/ FFPE

The Genes2Me BRCA1/2 NGS Assay is suitable for breast cancer detection and diagnosis identifying both, germline and somatic mutations in the whole CDS (+/-40bp) and promoter regions of breast cancer associated BRCA 1 & BRCA 2 genes with high specificity.

Gene & Drug Details

TYPE OF CANCER	GENE	DRUG
Breast Cancer	BRCA1	Olaparib, Talazoparib
Breast Cancer	BRCA2	Talazoparib, Olaparib

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity 0.2x	97%
Precision	96%
Reproducibility	97.3%
Sensitivity (VAF@1%)	<1%VAF@95%
On Target Ratio	>60 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Uniform Coverage in BRCA1/2 in FFPE Samples

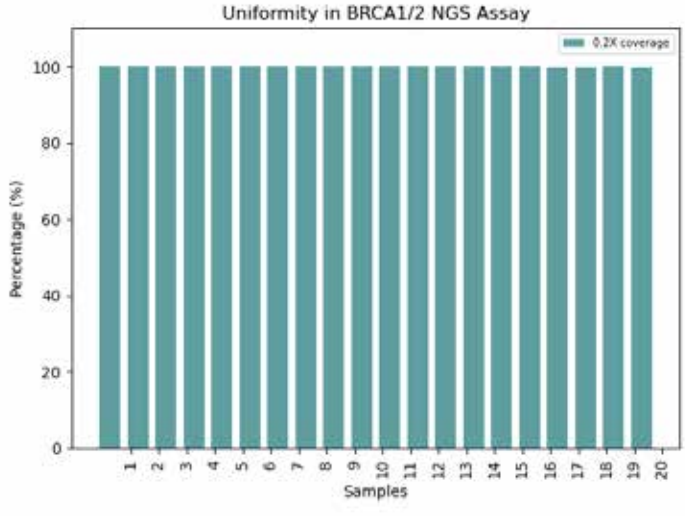


Fig 30 - Uniform coverage approaching 100% across all samples at a 0.2X threshold highlights the high efficiency of the probe design. This level of uniformity minimizes coverage bias and ensures consistent target enrichment, enabling reliable variant detection and reproducible performance delivering high confidence results for every sample, every time.

FOCUS Lung NGS Assay

Lung carcinomas are one of the most prevalent and lethal forms of cancers globally, significantly impacting public health. Early detection significantly increases the chances of survival. Next Generation Sequencing enhances the detection, and management of lung cancer by providing detailed genetic insights that inform personalized treatment approaches, improve monitoring strategies, and contribute to ongoing research efforts by allowing for the simultaneous analysis of multiple genes, providing a comprehensive view of the tumor's genetic landscape, quantify TMB, which may predict responses to immuno-therapy.

The G2M FOCUS Lung is a somatic NGS assay, aimed to screen important and guideline recommended genes and fusions (like ALK, ROS1, NRGQ, RET) associated with various lung carcinomas like Non-small cell lung cancer (ALK, ROS1, NTRK, RET etc.) and Lung adeno-carcinomas (EGFR, MET, KRAS, BRAF etc). The genes are selected based on the guidelines of the NCCN, CAP, ESMO and FDA.

Number of Genes	73 (DNA), 18 (RNA Fusions)
Target Size	261 Kb
Covered Regions	Whole coding sequence
Mutation Types	SNV / InDels / CNVs
Biomarkers	Fusions, TMB, MET exon 14 skipping
Sample Type	FFPE, Fresh Tissue
Platform Compatibility	Illumina, MGI, Thermo Fisher, Element Biosciences

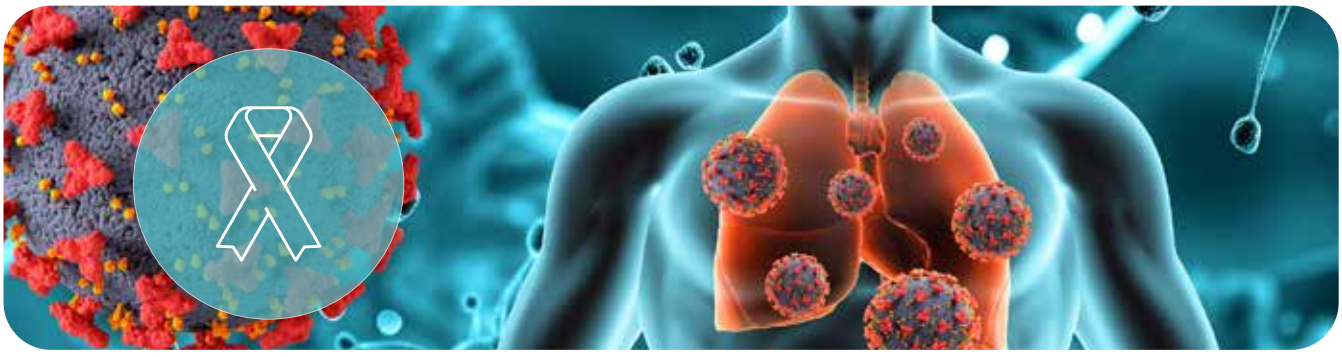
Key Features

- Cover important biomarkers like RNA fusions, TMB and MET exon 14 skipping and important fusions
- Detect SNVs and indels at allele frequency as low as 1% with >1000x sequencing coverage.
- On-target ratio of more than 80%
- Achieve sequencing-ready libraries from DNA in 12-13 hours
- Get insights into FDA approved drug recommendations
- Get compatibility with multiple sequencer platforms (Illumina, MGI, Thermo Fisher, Element Biosciences)
- Get an end-to-end solution from extraction to data analytics & tertiary reporting

FDA approved Drug recommendations for NSCL :-

Biomarkers	*FDA approved Therapies*
ALK (Fusions)	Alectinib, Brigatinib, Ceritinib, Crizotinib, Lorlatinib
RET (Fusions)	Pralsetinib, Selpercatinib
ROS1 (Fusions)	Crizotinib, Entrectinib, Repotrectinib

Limited list displayed here



GENE LIST												
AKT1	ALK	APC	ATM	BRAF	CCNE1	CDH1	CDKN2A	CSF1R	CTNNB1	DDR2	DICER1
EGFR	EIF1AX	ERBB2	ERBB4	EZH1	EZH2	FBXW7	FGFR1	FGFR2	FGFR3	FLT3	FOXL2
GNA11	GNAQ	GNAS	HNF1A	HRAS	IDH1	IDH2	JAK2	JAK3	KDR	KIT	KRAS
MAP2K1	MDM2	MET	MLH1	MPL	MYC	NOTCH1	NPM1	NRAS	NTRK1	NTRK2	NTRK3
PDGFRA	PIK3CA	POLE	PTEN	PTPN11	RAC1	RB1	RET	ROS1	SMAD4	SMARCB1	SMO
SOS1	SPOP	RC	STK11	TERT	TP53	VHL	ARAF	BRCA2	ERBB3	KEAP1	RAF1
ABL1											

RNA Fusions											
ALK	EGFR	FGFR2	MET	NTRK1	NTRK3	PPARG	RAF1	ROS1	BRAF	ERG	FGFR3
NRG1	NTRK2	PBX1	PRKACA	RET	TFE3						

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity	>98.5
Precision	>97
Reproducibility	97.2
On Target Ratio	86-95
Sensitivity (VAF@1%)	98.6

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Uniform Gene Coverage Across Tumor Samples

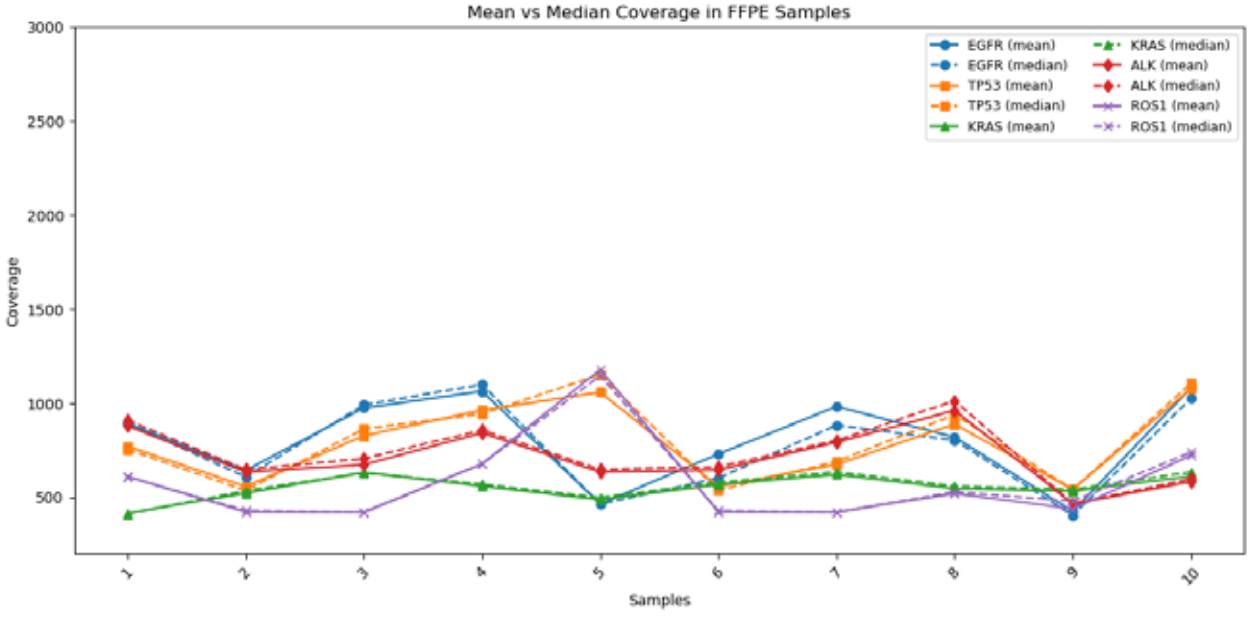


Fig 31 - Coverage of key cancer-associated genes (EGFR, TP53, KRAS, ALK and ROS1) shows strong alignment between mean (average depth) and median (central tendency), indicating minimal bias and consistent sequencing across target regions. This convergence reflects a robust, reliable assay suitable for routine clinical testing across diverse FFPE samples.

High-Efficiency Target Capture for Confident Results

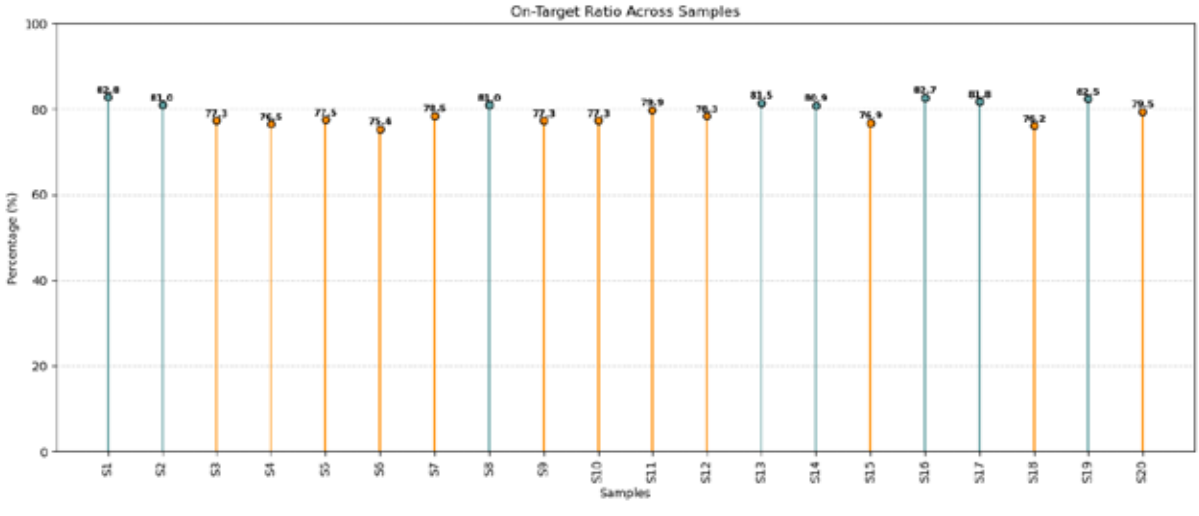


Fig 32 - All patient samples achieved over 75% on-target alignment, demonstrating the panel's advanced design, optimized assay performance, and exceptional target enrichment, delivering consistent, high-quality sequencing that supports both clinical reliability and scalable diagnostic impact.

G2M

Transplant Immunology

HLA Typing by NGS

HLA TYPiNG BY NGS

Human leukocyte antigen (HLA) typing is a test used to identify the specific proteins called HLA antigens on the surface of cells in the body. These antigens are crucial for immune system function, particularly in distinguishing between self and foreign cells. Genes2Me HLA typing NGS assay generates unambiguous, phase-resolved HLA typing results and can provide critical insight into immune disorders. It is a high-resolution allele identification and precision diagnostic assay that aids in the selection of the best donor for the recepient. DNA extracted from the blood of transplant recipients & donors is evaluated for histocompatibility antigens targeting 11 loci such as Class-1 HLA-A, B, C; Class II: HLA DPA1, DPB1, DQA1, DAQB1, DRB1/3/4/5. This panel targets the coding region compiling to the size of ~71kb. The HLA region which is the most densely polymorphic region of the genome can be sequenced accurately with our HLA typing NGS assay. The genomic DNA sample from blood is considered for library preparation and enrichment that further can be sequenced on NGS sequencer. This panel is based on Hybridization capture-based target enrichment.

Loci	11
Covered region	Whole CDS
Target size	71 kb
Mutation type	Allelic Polymorphism
Sample type	Blood

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity	97%
Precision	95%
Reproducibility	98%
Sensitivity	95%
On Target Ratio	87-95 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Key Features

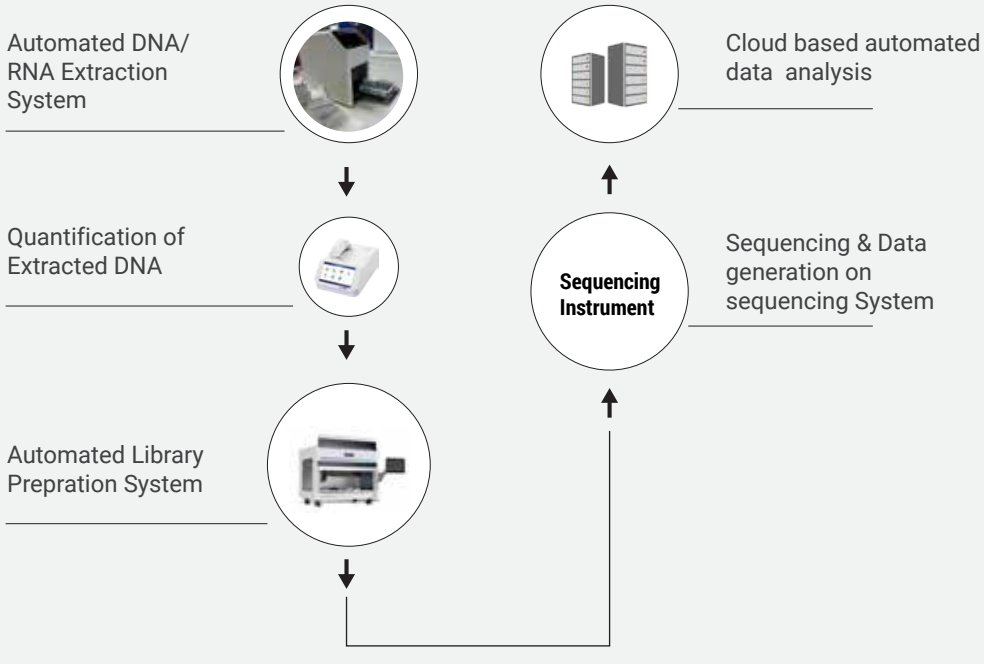
- Based on Hybridization capture target enrichment which helps increase the sensitivity upon sequencing compared to amplicon technique (which increases the chances of PCR bias such as PCR drop-outs).
- G2M HLA Workflow is simplified by reducing the number of reaction steps and hybridization time (with multiplexing/Pre capture library) resulting in shorter hands on time.
- All 11 loci covered in the G2M HLA panel are targeted by hybridization in one tube.
- G2M HLA panel produces libraries of optimal size (200-700 bp) making it compatible to run on multiple sequencing platforms.

Genes Targets

Class I: HLA-A, HLA-B, HLA-C;

Class II: HLADPA1, HLADPB1, HLADQA1, HLADAQB1, HLADRB1, HLADRB3, HLADRB4, HLADRB5.

Workflow for HLA Typing Sequencing Panel



- NIPT (Non-Invasive Prenatal Testing)
- NBS (Newborn Screening)

Reproductive Health and Pediatrics

LeoNext cfDNA Library Preparation Kit for NIPT

Discover more about your Baby's Health

LeoNext CfDNA Library Preparation Kit for NIPT is used for detection of trisomies, sex chromosomal aneuploidies, microdeletions using next generation sequencing.
NIPT is a non-invasive and accurate approach for prenatal testing of the baby to screen for chromosome abnormalities.

LeoNext cfDNA Library Preparation kit for Non-invasive Prenatal Testing (NIPT) is aimed to detect common trisomies, sex chromosomal aneuploidies and other rare aneuploidies in all 23 pairs of chromosomes employing next generation sequencing (NGS) Technology. This product is highly sensitive, robust and accurate and can additionally detect the microdeletions & duplications.

This product helps in construction of a cfDNA library which will be compatible with the commonly available sequencer platforms (Illumina, MGI, Element Biosciences (AVITI). The library preparation is performed on isolated circulating fetal DNA (cfDNA) from maternal blood sample which is A-tailed, adapter ligated and amplified to get a library that is ready to be sequenced.

NIPT Offerings by G2M

NIPT- 23 pairs of chromosomes:-

Covers all 23 pairs of chromosomes – including autosomal aneuploidies (like Common trisomies: Down Syndrome (T21) Edward Syndrome (T18) Patau Syndrome (T13) and sex chromosomal aneuploidies.

NIPT- 23 pairs of chromosomes & 90+ Micro-deletions/duplications:-

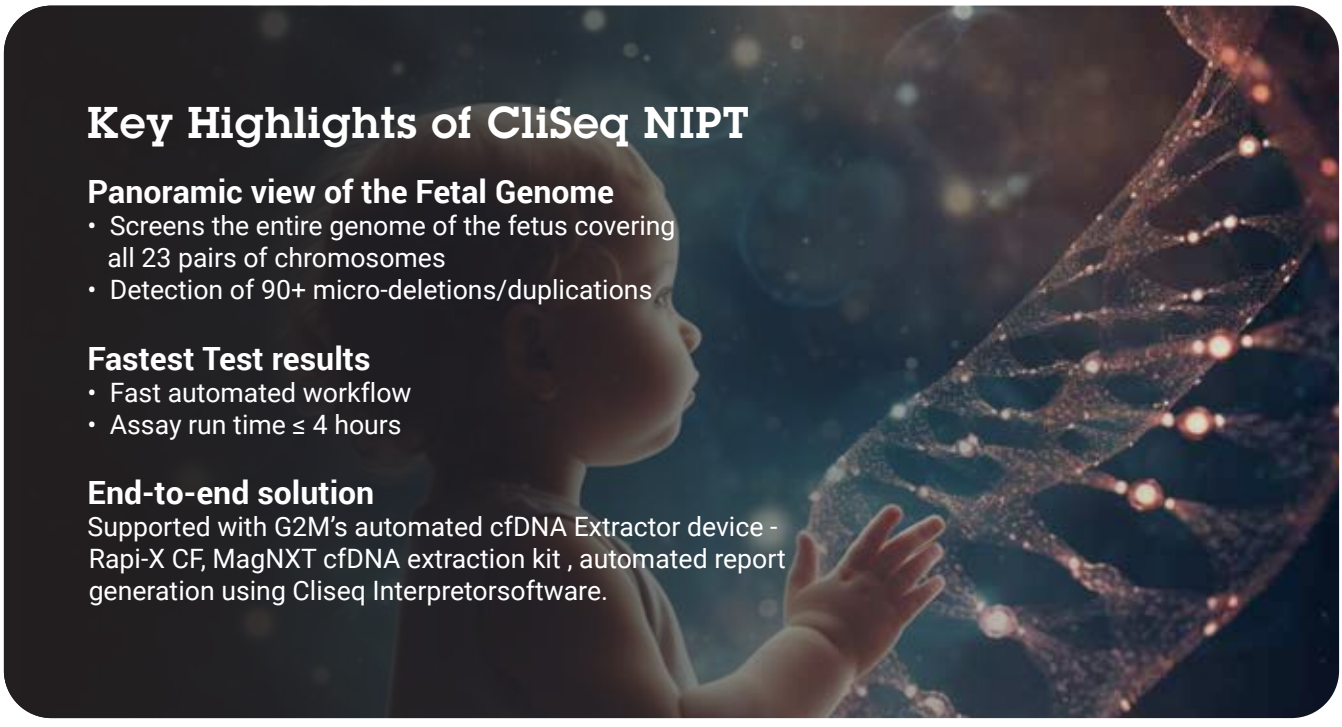
Covers all 23 pairs of chromosome – including autosomal aneuploidies (like Common trisomies: Down Syndrome (T21) Edward Syndrome (T18) Patau Syndrome (T13), sex chromosomal aneuploidies and 90+ micro-deletions and micro-duplication Syndromes.

Product Name	No of Reads (in Millions)
NIPT-All Chromosome	7-10 Million*
NIPT-All Chromosome + Microdeletions & duplications	20-25 Million

*Note: This corresponds to unique reads generated.

Advantages of NIPT

- A Non-invasive genetic screening test, completely risk free assessment.
- Allows early accessibility of highly accurate data on all chromosomes of the fetus for informed pregnancy decisions.
- Helps to identify fetuses at risk of any serious chromosomal abnormalities.
- Completely safe and empowers expecting parents to support, manage and access early medical help if required.



Specifications

Gestational age	10 weeks onwards
Specimen type	10 ml of Maternal blood sample
Recommended extraction kits and devices	1.Genes2me – MagNXT Cell free DNA extraction kit 2.Genes2me – Rapi-X CF device
Input cfDNA	10-20 ng
Library Avg insert size	275 to 325 bp
Sequencing Methodology	Low depth whole genome sequencing
Sequencer Compatibility	2nd Generation Sequencers – Illumina, MGI, Element Biosciences
Sequencing mode	SE 50 (Single end sequencing)
Fetal Fraction	Min 3%
Pregnancy Type	Acceptable for Singleton & Twin*

*Note: "The assay can detect aneuploidy in a given sample, regardless of whether the pregnancy is singleton or twin. However, it cannot determine the type of pregnancy (e.g., twin) or distinguish between individual fetuses. It will solely report the presence or absence of aneuploidy."

Performance Characterstics

	Trisomy 13	Trisomy 18	Trisomy 21
Sensitivity (%)	100	100	100
Specificity (%)	99.96	99.95	99.96
PPV (%)	78.57	88.54	96.56
NPV (%)	100	100	100

Note : The data mentioned above is for > 3000 samples.

G2M NIPT END-TO-END Workflow

Maternal Plasma

10 ml of maternal whole blood

Cf DNA Extraction

cfDNA extraction with G2M's cell-free DNA extraction kit and extraction platform

RAPi-XCF
CELL FREE DNA EXTRACTION SYSTEM for NIPT

LeoNext cfDNA library preparation kit

Using G2M's LeoNext cfDNA library preparation kit on G2M's Ezy Autoprep - automated NGS library preparation workstation

EZY-AutoPrep

Sequencing

On the sequencing platform of your choice

Data Analysis

G2M's proprietary NIPT data analysis software

CliSeq Interpreter

Scan me for NIPT Sample Report

Newborn Screening by NGS

Genetic Analysis beyond standard New Born Screening

It covers sequencing of all exonic regions for **335 Genes** associated with metabolic and genetic diseases with a target size of 2.3 Mb. It helps in early screening for genetic and metabolic diseases that appear during the initial stages of life, providing key information for disease management and early treatment.
Early detection, intervention & management could prove essential for the infant's overall health and quality of life.

This test is indicated for :

- Neonates or infants with abnormal results of routine biochemical screening, MS/MS screening or failure on routine hearing screenings.
- Newborns who do not present symptoms of any disease but have a family history of genetic conditions
- Neonates with clinical manifestation of delayed jaundice, difficulty in feeding, vomiting, diarrhoea, anaemias
- Seeking comprehensive genetic information of the new-born

Covers more than 300 disorders

Metabolic Disorders

- Amino Acids Metabolic Disorders
- Organic Acid Metabolic Disorders
- Fatty Acid β Oxidation Metabolic Disorders
- Endocrine Disorders
- Carbohydrate Metabolic Disorders
- Metabolic Epilepsy Diseases
- Other Inborn Errors of Metabolism

Genetic Disorders

- Deafness
- Haemophilia B
- B-thalassaemia
- Noonan syndrome
- Marfan syndrome

Specimen Required

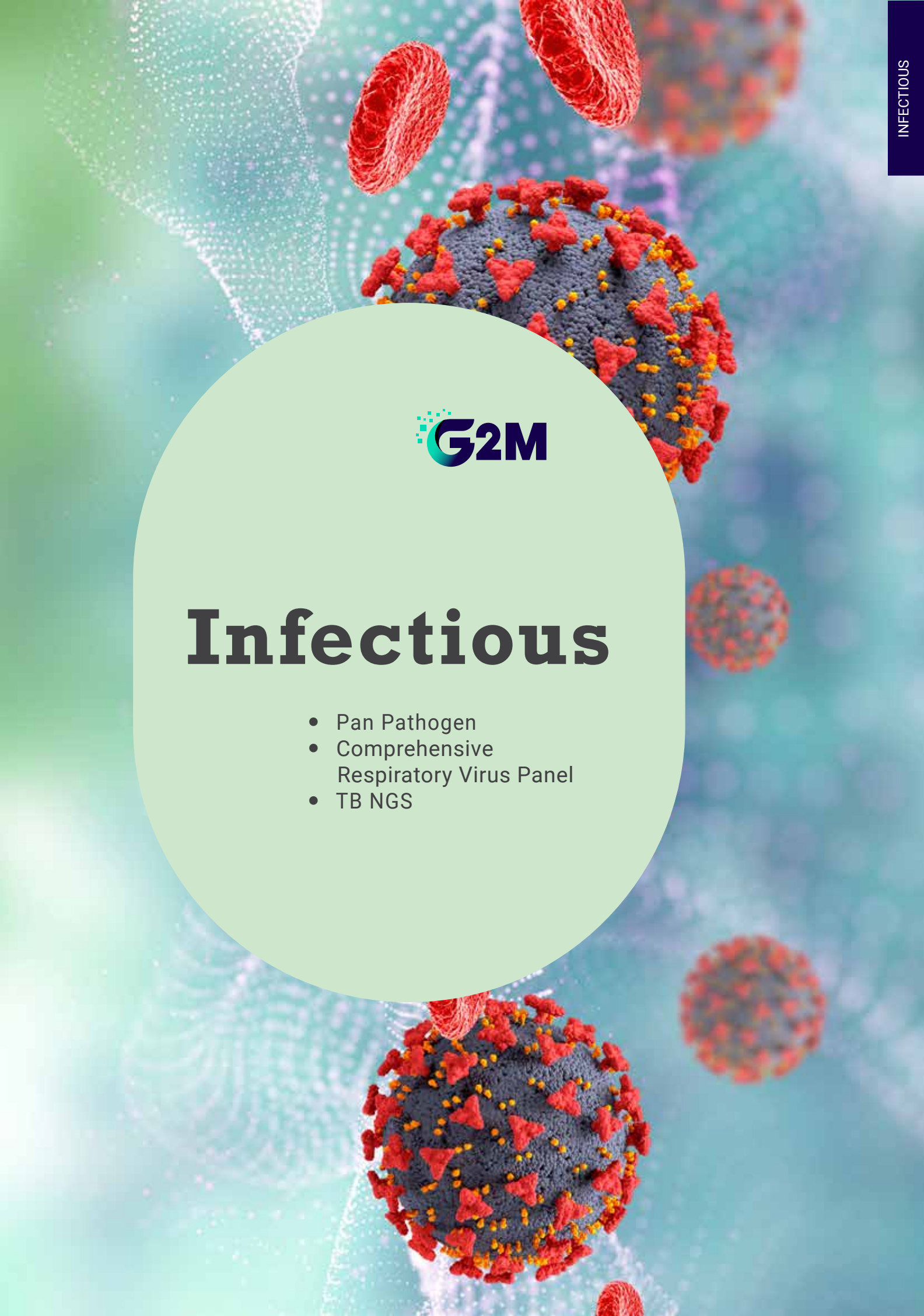
Peripheral Blood (1ml)

Dry Blood Spots (size 3.2mm, 5 pieces) by heel prick test

PANEL PERFORMANCE

Features	Performance#
Coverage uniformity	97%
Precision	95%
Reproducibility	98%
Sensitivity	91%
On Target Ratio	87-95%

: The observed values are for Illumina platform
VAF - Variant Allele Frequency



Infectious

- Pan Pathogen
- Comprehensive Respiratory Virus Panel
- TB NGS

PAN Pathogen
NGS Assay

Covering more than **7000** Pathogens

Genes2Me PAN Pathogen Assay uses hybridization based enrichment technology and second-generation high-throughput sequencing technology for high-precision detection of trace pathogenic microbial nucleic acids in samples, and can quickly identify viruses, bacteria, fungi, parasites and other pathogenic microorganisms, and also can detect multiple drug resistance genes, which can help the rapid identification and detection of pathogenic microorganisms.

Clinical Applications

- Respiratory infections
- Urinary tract infections
- Bloodstream infections
- Other infections
- Central nervous system infections
- Cardiogenic infections
- Reproductive system infections
- Skin infections

Number of Organism:- 7000 +	**Target Size**: ~8000 probes	**Target Regions**:- 16S and internal transcribed spacer (ITS)	**Sample Type**:- Blood, Sputum, Saliva, Stool, Swab, Fresh tissue, Body fluid	**Genes**:- Housekeeping genes, drug-resistant related genes	**Data Required**: 3-5 Million reads ~1 GB data
Bacteria - ~88	Fungus - ~ 31	Parasites - ~ 27	Viruses - ~ 22	Obligate Intracellular Parasite - ~8	Spirochete - ~ 3

** Minimum data output from sequencing depends on the content of pathogenic microorganism in clinical specimen. Whether a particular pathogen is detected in the report depends on the number of supporting reads detected for the pathogen, and not solely on the total amount of data obtained from sequencing.

Scan for Pathogen List

Comprehensive Respiratory Virus Panel (CRVP)

The Comprehensive Respiratory Virus Panel is an NGS assay to detect viral etiologies of respiratory diseases. The assay involves sequencing of genetic material of these viruses. The panel enables testing of ~ 9 different virus types and their 20+ strains of clinically significant and prevalent respiratory viruses. This panel consists of over 15,000 biotinylated 120 nucleotides DNA oligos that is utilized for hybridization capture-based viral sequence enrichment. This product is based on reverse transcription and cDNA library preparation followed by hybridization based viral sequence enrichment that employs probes to select viral sequences of interest in an NGS library.

List of Pathogens

Coronavirus	alpha and beta
Influenza virus	Influenza A,B,C
Respirovirus, Rubulavirus	Human parainfluenza virus 1, 2, 3, 4
Metapneumovirus, Orthopneumovirus	Human meta-pneumovirus and ortho-pneumovirus
Enterovirus	Enterovirus A, B ,C ,D Rhinovirus A, B, C
Mastadenovirus	Human adenovirus B, C, E
Bocaparvovirus	Primate bocaparvovirus 1,2

TB NGS Assay

G2M offers a rapid detection & identification platform for Mycobacterium Tuberculosis Complex and drug resistant TB, using a targeted sequencing approach directly from clinical specimens, eliminating the need for culture.

This assay is designed to map 100 kb region of the *M. tuberculosis* genome for 75 genes and associated mutation sites, as well as SNP loci. With this assay, get the drug resistance profile for all the major first and second line Anti-TB drugs (covers drug resistance, multi-drug resistance, Pre-XDR, XDR). The panel also covers the newer nitroimidazole antibiotics (Delaminid and Pretomanid), approved by WHO under the BPaL and BPaLM treatment regimen. This assay is based on Hybridization capture based Target enrichment.

- Mycobacterial species identification
- Drug resistance profile
- Lineage Identification
- Eliminate the need for culture

Drug Resistance Profiling

With G2M TB NGS assay, get the drug resistance profile for all the major first and second line Anti-TB drugs. The panel also covers the newer nitroimidazole antibiotics (Delaminid and Pretomanid), approved by WHO under the BPaL and BPaLM treatment regimen.

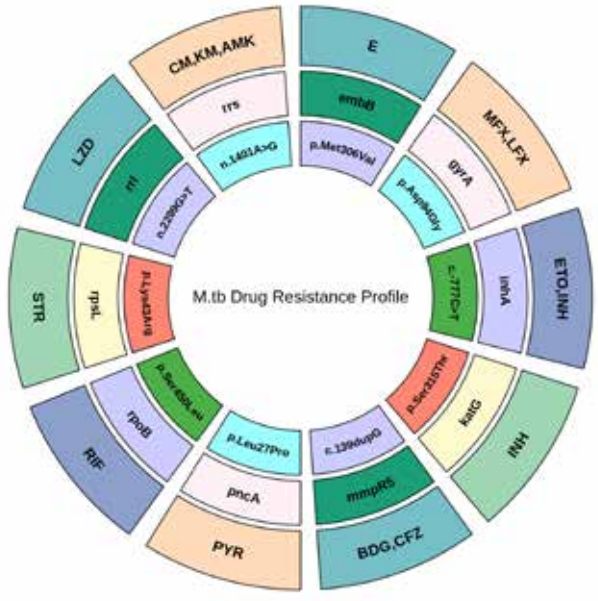
First Line		Rifampicin
		Isoniazid
		Ethambutol
		Pyrazinamide
Second Line	Group A	Bedaquiline
		Linezolid
		Moxifloxacin
		Levofloxacin
	Group B	Clofazimine
		Cycloserine
	Group C	Delamanid
		Ethionamide
		Amikacin
		Streptomycin
		Para-aminosalicylic acid
	Others	Pretomanid
		Capreomycin
		Kanamycin

Scan for TB NGS Gene List

Data Analysis and Reporting

Post sequencing, FASTQ (read) files can be uploaded to our cloud based platform – CLISEQ INTERPRETER using the coupon credentials provided along with the kit. The fully automated reporting pipeline analyses the data in under an hour, which helps in a comprehensive report with graphical representation of antibiotic resistance & spoligotyping.

Illustrative reporting



Antibiotic resistance geneprediction in MTBC : The circular map is divided into three rings. The outer rings displays the resistant anitbiotics. The middle ring display the genes responsible for resistance in antibiotics, while the inner ring shows the mutations involved in drug resistance.

CliSeq Interpreter

Species Identification and Developmental Lineage

Oraganism	Reads	Identity(%)
Mycobacterium_tuberculosis_complex	108944	99.52
Mycobacterium_tuberculosis_H37Rv	71931	65.71
Mycobacterium_canettii_CIPT_140010059	37013	33.81

Phylogenetic Lineage Based on SNPs Lineage 2.2.1.1

Panel Details

Panel name	Med4Me Tuberculosis Panel
Target region	100KB
Methodology	Hybridization capture based Target enrichment
Input Sample type	gDNA from clinical samples (sputum / culture / BAL)
DNA input quantity	50 - 100 ng
Recommended sequencers	Illumina, Element Biosciences (AVITI), MGI
Catalogue number	G2MMAP10001-ill/ele; G2MMAP10001-MG

Scan for TB NGS Sample Report

Exome Sequencing Assays

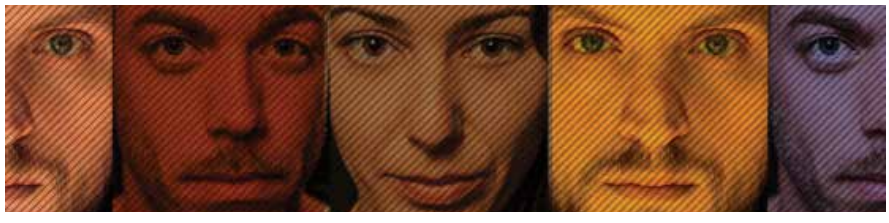
- Whole Exome Sequencing
- Clinical Exome Sequencing

Whole Exome Sequencing
Library Preparation Assay

The Genes2Me Whole Exome Sequencing (WES) Expanded NGS assay is a hybridization based solution for screening ~21500 clinically relevant genes (coding regions of the genome) for diseases associated with genetic mutations and mitochondrial genome.

It covers all major mutations like SNV, CNV, and Indels with hotspots adding up to a target size of 38.2 Mb with a hybridization-based target capture enrichment.

Gene count/ family	~21500
Covered region	Whole CDS, Mitochondrial Genome, hotspots
Target size	38.2 Mb
Mutation type	SNV/InDels/CNV
Sample type	Blood/AF/Tissue/CVS



Scan for WES Gene List

Whole eXome Sequencing

Key Features of Whole Exome Sequencing Assay

- More than 90% of bases with ≥ Q30 quality score
- Recommended sequencing depth for Mendelian disorder/rare disease: ≥ 80-100x
- Mitochondrial genome is included in the panel design.
- Databases used for Annotation : ClinVar, OMIM, gnomAD 1000Genome, dbSNP
- Complete Exome Coverage
- FASTQ to Clinical Interpretation Capability
- Flexible Integration with NGS Sequencers

Exceptional Coverage Uniformity Validated by Low Fold 80 Metric

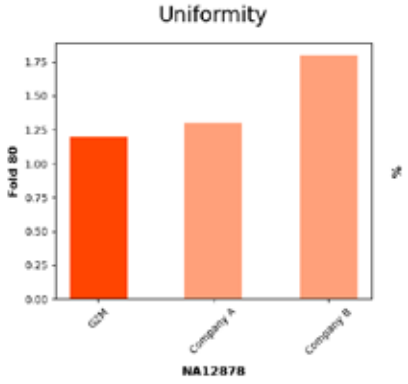


Fig 24 - Fold 80 base penalty is the fold-over-mean coverage required to ensure that 80% of targeted bases are covered at or above the mean coverage depth. It is a key metric used to evaluate the uniformity of coverage in next-generation sequencing (NGS).
A lower value indicates more uniform coverage—which means less over-sequencing is needed to achieve complete and reliable results. G2M shows <1.25 Fold 80 penalty value implying good capture design and hybridization efficiency than the competition.

Efficient Whole Exome Sequencing with Ultra-Low Depth Coverage

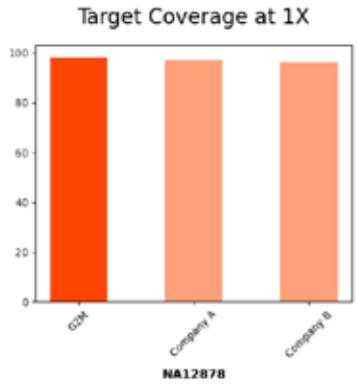


Fig 25 - G2M WES assay shows >98% coverage at a very low depth (1 X)

High On-Target Alignment Across Different Cancer Patient Samples

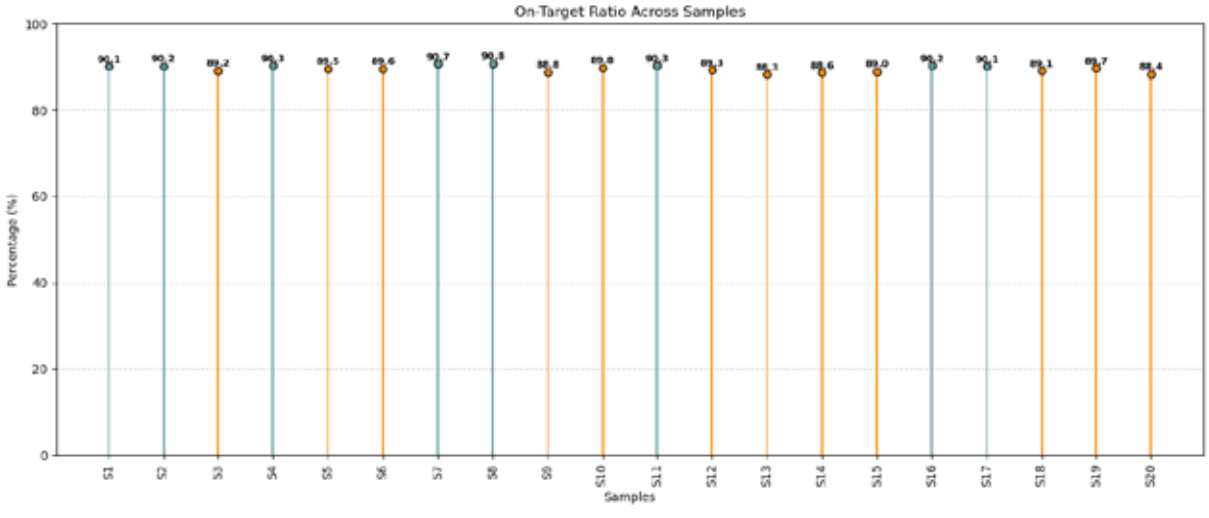


Fig 26 - On-target ratios across patient samples consistently exceeded over 85%, highlighting the panel's optimized design, efficient probe capture, and robust sequencing performance for reliable genomic profiling.

Data Analysis Platform

CliSeq Interpreter

Cliseq Interpreter is a cloud based NGS data analysis software which offers an unparallel platform performance designed to streamline and enhance the interpretation of complex biological data. Once Quality Check, Alignment, Variant calling, and annotations are achieved, the annotated VCF files and clinically significat mutations (CSM) report will be available to download.

PANEL PERFORMANCE

Features	Performance#
Coverage uniformity	96%
Precision	94%
Reproducibility	97%
Sensitivity	94%
On Target Ratio	85-95 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Scan for WES Sample Report

List of Diseases category assessed by Whole Exome Sequencing (WES) Panel*

Disease Class	List Of Diseases
Cardiac disorders	Dyslipidemia, Aortopathy, Congenital heart defect, cardiovascular diseases
Dermatological disorders	Ectodermal dysplasia, Albinism, Xeroderma pigmentosum, Ichthyosis
Endocrinological disorders	Pancreatitis, Premature ovarian failure, Adrenal hyperplasia, Hyperparathyroidism
Bone disorders	Arthrogryposis, Osteopetrosis, Cleft lip palate, Amelogenesis imperfecta
Immunological disorders	Immune dysregulation, Defects in intrinsic and innate immunity
Hepatological disorders	Polycystic liver disease, Cholestasis, Congenital hepatic fibrosis
Hematological disorders	Bleeding & Thrombotic disorder, Bone marrow failure, Anemia
Metabolic disorders	Aminoacidopathies, Purine/Pyrimidine disorders, Creatine biosynthesis disorders
Eye disorders	Ectopia lentis, Retinoblastoma, Corneal dystrophy, Optic atrophy
Pulmonological disorders	Bronchiectasis, Cystic fibrosis, Primary ciliary dyskinesia
Neurological disorders	Neuromuscular disorders, Autism, Seizures & Brain abnormalities, Neurodegenerative disorders
Oncological disorders	Hematological malignancy, Brain cancer, Colorectal cancer, Breast cancer, Ovarian cancer

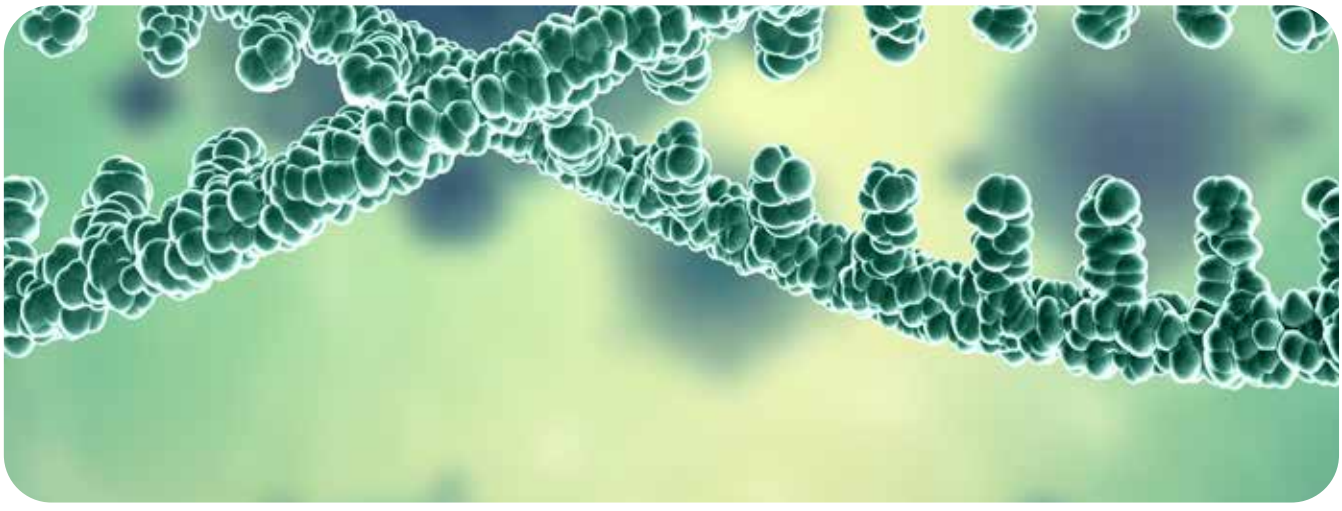
*Limited disease details mentioned

Clinical Exome Sequencing (CES) Library Preparation Assay

Exome is a subset of the genome that covers sequences of all the exons, reflecting the protein-coding region of the genome. In humans, the exome is about 1% of the genome. Clinical Exome Sequencing is a comprehensive DNA test to identify disease causing variants within the whole exome. Advances in next-generation sequencing technologies have decreased the cost of sequencing per base pair about 10-fold, improved accuracy, and greatly increased the speed of generating sequence data. This improved accuracy has enabled development of CES at a faster and cheaper rate of variant identification. It is rapidly becoming a common molecular diagnostic test for individuals with genetic disorders.

The Genes2Me Clinical Exome Assay screens a range of disease causing genes to identify germline mutations in DNA.

No. of Genes	8124
Gene count/ family	~7600
Covered region	Whole CDS, Hotspots, Mitochondrial Genome
Target size	19.6 Mb
Mutation type	SNV/InDels/CNV
Sample type	Blood/ AF/ Tissue/ CVS



Key Features

- Comprehensive genomic profiling of a variety of genetic diseases
- Includes a wide range of target regions
- Cost-effective analysis : Able to provide accurate analysis with reduced sequencing costs compared to WES

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity	97%
Precision	95%
Reproducibility	98%
Sensitivity	95%
On Target Ratio	87-95 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Scan for CES Gene List

Med4Me

Pharmacogenomics Assay

The main target of Med4Me Assay is the genes associated with prescribed drugs of the corresponding diseases. The assay allows for precise selection and dosage of prescribed FDA approved drugs, and detection of genetic variants associated with drug metabolism in Oncology, Neurology, Cardiology, tuberculosis and many other diseases.

163 Genes

Covered Regions

Whole CDS + UTR (-50 bp, +10 bp)

- Assess extensive target regions associated with pharmacogenomics
- Validated assay performance: Complete validation for clinical application

Med4Me

Truly Personalized Medicine

Med4Me Panel

PHARMACOGENOMICS ASSAY

Gene count	~122
No. of genes	163
Covered region	Whole CDS + UTR (-50bp, +10 bp)
Target size	0.87 Mb
Mutation type	SNV / InDels
Sample type	Blood

PGx

PHARMACOGENOMICS INSIGHTS

500+ Drugs

Types of Drugs Covered

- Oncology
- Transplantation Biology
- Pain Management
- Cardiovascular function
- Hematology
- Urology
- Anesthesiology
- Internal Medicine
- Psychiatry
- Neurology
- Infectology
- Endocrinology
- Recreational Drugs

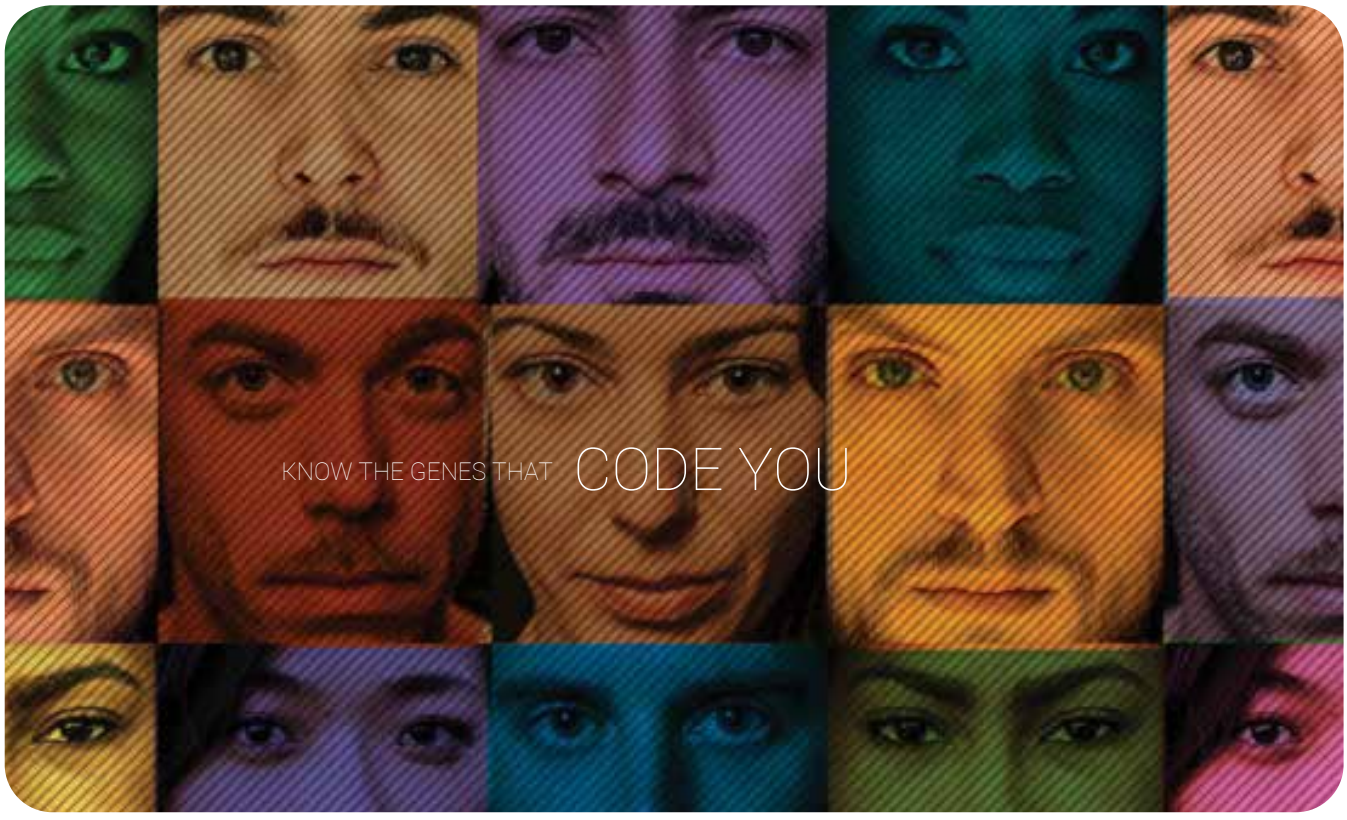
*Limited drug details mentioned

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity	94%
Precision	98%
Reproducibility	98%
Sensitivity	>90%
On Target Ratio	88-95 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Scan for Med4Me Gene List



LEONEXT | WHOLE GENOME SEQUENCING

Whole Genome Sequencing

Library Preparation Assay

Engineered to provide consistent, high-quality results for diverse applications, from basic research to complex findings. With carefully optimized protocols and high-performance reagents, the LeoNext Whole genome sequencing library preparation kit ensures reliable and time-efficient NGS library preparation protocols crucial for accurate sequencing across the entire genome and timely results.

Our user-friendly kit reduces preparation time, minimizes input requirements and works well with difficult sample types. Whether you're exploring complex genetic variations, studying rare mutations, or conducting comprehensive genomic analysis, Genes2me delivers the precision and efficiency needed to accelerate your discoveries.

Whole Genome Sequencing in Clinical & Research Use

- Provides a comprehensive view of the entire genome.
- Detects SNVs, InDels, CNV as well as large structural variants (SV)
- Can identify variants that might be missed with other targeted approaches
- Effective tools to study cancer genomics because it will capture the full spectrum of variations, from point mutation to chromosomal rearrangements in single experiments.
- Whole genome sequencing would empower pharmacogenomics and drug trials, because it captures a much broader scope of variation that might contribute to the response.
- WGS will help to look at noncoding and structural variants in linkage regions, rather than taking a gene-centric approach in family Disease Pedigrees
- Delivers large volumes of data of microbes in a short amount of time to support assembly of novel genomes.

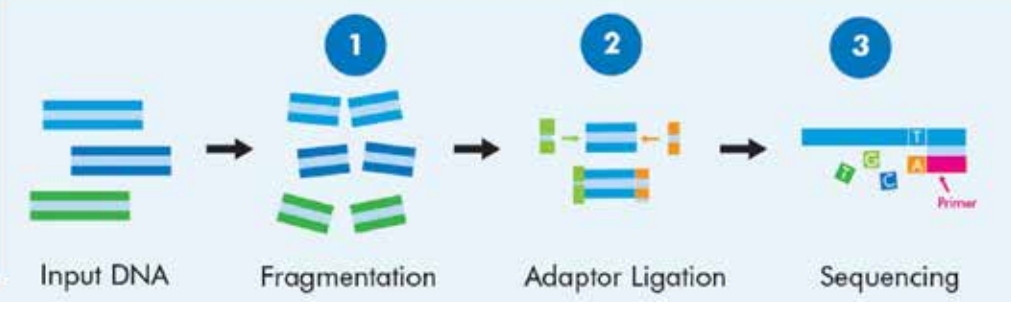
Whole Genome Sequencing Library Preparation

Our comprehensive catalog of library preparation solutions can help you no matter your research application, such as:

- DNA sequencing (whole genome and targeted sequencing)
- Methylation sequencing (whole genome and targeted bisulfite sequencing)
- Chromatin immunoprecipitation (ChIP) sequencing
- Targeted sequencing with hybridization capture
- PCR-free workflows
- Oncology research
- Metagenomics research

DNA Library Preparation

Library Preparation for Short-Read Sequencing



Time-Saving	• Library prepared within 3 to 4 hrs.
High Adaptability to Input Amount	• Effective library preparation from 100 pg - 4 µg of Input DNA.
Applicable with	• Genomic DNA, cfDNA, ctDNA, FFPE DNA, ChIP DNA, and Amplicons.
Excellent Adapter Ligation Efficiency	• Suitable for library preparation with PCR or PCR-free.

Whole Genome Sequencing Solutions is also available on Illumina, Thermofisher and MGI, Element Biosciences sequecing plafforms.

Transcriptome Sequencing

Enhance your Transcriptomics research with G2M Next Generation Sequencing Panels

A transcriptome is the complete set of RNA transcripts that are produced by the genome of an organism at a specific time or under specific conditions. It includes all types of RNA, such as messenger RNA (mRNA), ribosomal RNA (rRNA), transfer RNA (tRNA), and non-coding RNAs.

Sequencing the transcriptome provides insights into which genes are actively expressed, the levels of expression, and how these expressions can vary between different cells, tissues, or environmental conditions and offer numerous advantages when coupled with other genetic testing aids.

Diagnostics applications

- **Patient Stratification:** Helps in patient stratification in clinical environments and clinical trials which can further guide treatment strategies laying the foundation for remarkable advances in molecular diagnostics. For breast cancer, patient stratification based on expression of tumour markers (e.g., ER, PR and HER2 in breast cancer) has guided treatment strategies for over 30 years (Cardoso et al., 2016)
- **Complexity Characterization:** Gene expression profiling coupled with computational algorithms can characterise cell composition of complex tissues/cell heterogeneity
- **Improved Diagnosis:** Transcriptome sequencing improves diagnostic rates in individuals with suspected Mendelian conditions to varying degrees, primarily by directing the prioritization of candidate DNA variants identified on exome or genome sequencing.
- **Discover Novel Mutations:** For undiagnosed diseases, transcriptome sequencing can help identify mutations or expression changes that might not be captured by standard genetic testing, aiding in the diagnosis of rare genetic disorders.

G2M Transcriptomics Offerings

1. Total RNA Sequencing

This helps sequence all types of RNA present in a sample including coding and non-coding RNAs (like microRNAs and long non-coding RNAs) to provide a comprehensive view of the entire transcriptome, allowing you to study not just protein-coding genes but also regulatory and non-coding RNA species. This can be useful for understanding complex regulatory networks and cellular processes.

You can get insights for :

- ***Differential Gene expression***
- ***Alternative splicing***
- ***Presence of non-coding RNA***

Specifications	
Methodology	• Whole-transcriptome sequencing (rRNA removal)
Technology	• Next Generation Sequencing
Assay Time	• ~7 hrs
RNA input Quantity	• 50-500 ng
Sample types	• Blood, saliva, fresh tissue, FFPE, Microbiome
Biomarker	• Fusion and variants
Instrument compatibility	• Illumina, MGI, Element Biosciences (Aviti)

2. mRNA Sequencing

This specifically targets messenger RNA (mRNA), which is the RNA that gets translated into proteins, primarily on protein-coding genes, making it more suitable for studies aimed at understanding gene expression levels and changes in protein-coding genes under various conditions. It provides a detailed profile of expressed mRNAs, including quantification of transcript levels and information about alternative splicing events specific to coding genes.

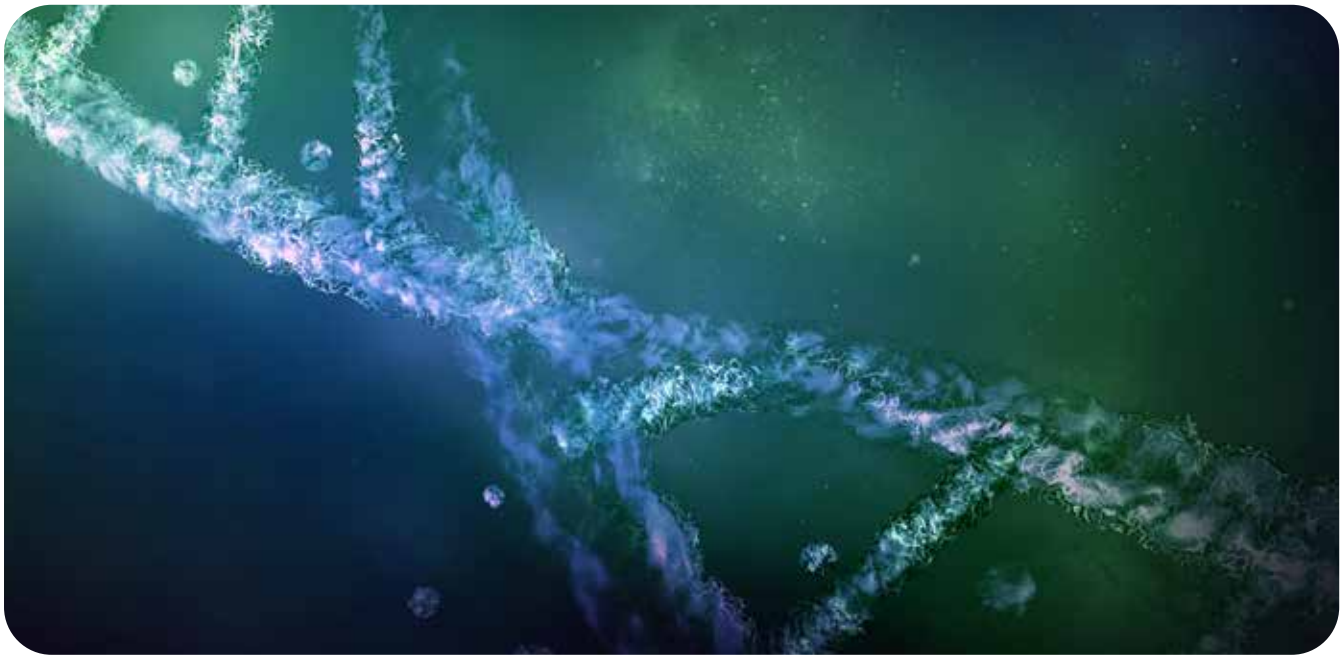
Specifications	
Methodology	• mRNA enrichment (Poly A selection)
Technology	• Next Generation Sequencing
Assay Time	• ~8 hrs
RNA input Quantity	• 1 ug
Sample types	• Blood, saliva, fresh tissue
Biomarker	• Fusion and variants
Instrument compatibility	• Illumina, MGI, Element Biosciences (Aviti)

LEONEXT

a Complete Range
for Next Generation Sequencing

NGS-based applications have considerable applicative reach across a broad spectrum of Clinical and basic research areas including **Genetics, Microbiology & Oncology**.

LeoNext Provides a complete portfolio of NGS Library preparation kits and barcodes designed to increase the flexibility and speed of library preparation for the Illumina, Ion Torrent & MGI Sequencing platforms.



Complete Range for Next Generation Sequencing - LEONEXT

DNA Library Preparation for Illumina®

Cat #	Product Name		Application	Size
NGS3104-01/02	LeoNext Universal Plus DNA Library Prep Kit for Illumina®	The LeoNext Universal Plus DNA Library Prep Kit is designed for DNA library preparation for Next Generation Sequencing (NGS) on Illumina® platforms with fast and robust workflow. The kit combines DNA fragmentation, end repair and dA tailing into one step there by reducing the time to 3 hrs. The kit is suitable for library preparation from 50 ng - 500 ng of input DNA.	DNA Lib Prep Kits for Enzymatic Fragmentation	24 rxn/96 rxn
NGS3114	LeoNext Multiplex Oligos Set 4 for Illumina®	The LeoNext Multiplex Oligos set 4 for Illumina® is designed for DNA library preparation for Illumina high throughput sequencing platform. The each kit contains LeoNext Adapter-S for Illumina, 8 LeoNext i5 PCR Primers and 12 LeoNext i7 PCR Primers. With LeoNext Universal Plus DNA Library Prep Kit for Illumina® (Genes2Me #NGS3104-01/02), it is used for generating up to 96 different combinations of double-ended Indexed libraries. Both kits together can generate up to 384 different combinations of double-ended Indexed libraries.	Dual-Indexed Adapter	192 rxn
NGS3115	LeoNext Multiplex Oligos Set 5 for Illumina®		Dual-Indexed Adapter	192 rxn
NGS3116	LeoNext Dual Index UMI DNA Adapters Set 1 for Illumina®	The LeoNext Dual Index UMI DNA Adapters for Illumina is specially designd for DNA library preparation to minimize index hopping and index misassignment. The kit contains unique and completely independent dual indexes along with 10 nt Unique Molecular Identifier (UMI) attached to adapter sequence after the i7 index, to detect low frequency mutations.	Dual-Indexed Adapter UMI Adapters	20 µl each
NGS3117	LeoNext Dual Index UMI DNA Adapters Set 2 for Illumina®		Dual-Indexed Adapter UMI Adapters	20 µl each
NGS3118	LeoNext Dual Index UMI DNA Adapters Set 3 for Illumina®		Dual-Indexed Adapter UMI Adapters	20 µl each
NGS3119	LeoNext Dual Index UMI DNA Adapters Set 4 for Illumina®		Dual-Indexed Adapter UMI Adapters	20 µl each
NGS3101-01 NGS3101-02	LeoNext Universal DNA Library Prep V3 Kit	The Genes2me LeoNext Universal DNA Library Prep Kit is specially designed for DNA library preparation for next generation sequencing (NGS) platforms. These are CE-IVD certified.	Whole genome library preparation kits	24/96 rxns

DNA Library Preparation for Ion Torrent®

Cat #	Product Name		Application	Size
NGS3136-01/02	LeoNext Universal DNA Library Prep Kit for Ion Torrent®	The LeoNext Universal Plus DNA Library Prep Kit is designed for DNA library preparation for Next Generation Sequencing (NGS) on Ion Torrent® sequencing platforms with fast and robust workflow. The kit combines end repair and dA tailing of input fragmented DNA into one step there by reducing the time to 3 hrs. The kit is suitable for library preparation from 50 ng - 100 ng of input fragmented DNA.	Universal DNA Lib Prep Kits	24 rxn/96 rxn
NGS3139-01/02	LeoNext AmpSeq Adapters 1 - 24 for Ion Torrent®	The LeoNext AmpSeq Adapters for Ion Torrent is a kit developed by AmpSeq technology for library preparation of the Ion Torrent high-throughput sequencing platform. Along with LeoNext Universal DNA Library Prep Kit for Ion Torrent®, this kit can prepare multi-sample targeted sequencing DNA libraries. The kits NGS3139-01 and NGS3139-02 contains 12 different adapter barcodes each from adapter barcode 1-12 and adapter barcode 13-24 respectively. The kits NGS3140-03, NGS3139-04 and NGS3139-05 contains 24 different adapter barcodes each from adapter barcode 25-48, adapter barcode 49-72 and adapter barcode 73-96 respectively.	Amplicon Lib Prep Adapters	12 ×10 rxn
NGS3140-03/04/05	LeoNext AmpSeq Adapters 25 - 96 for Ion Torrent®		Amplicon Lib Prep Adapters	24 ×10 rxn

Complete Range for Next Generation Sequencing - LEONEXT

DNA Library Preparation for MGI®

Cat #	Product Name		Application	Size
NGS3144-01/02	LeoNext Universal Plus DNA Library Prep Kit for MGI®	The LeoNext Universal Plus DNA Library Prep Kit is designed for DNA library preparation for Next Generation Sequencing (NGS) on MGI® platforms with fast and robust workflow. The kit combines DNA fragmentation, end repair and dA tailing into one step there by reducing the time to 3 hrs. The kit is suitable for library preparation from 50 ng - 500 ng of input DNA.	DNA Lib Prep Kits for Enzymatic Fragmentation	24 rxn/96 rxn
NGS3146-01/02	LeoNext DNA Adapters Set 8 for MGI®	The LeoNext DNA Adapters Set 8 for MGI is a kit for MGI high-throughput sequencing platform. It is suitable for preparing multi-sample DNA libraries for MGI high-throughput sequencing platform. This kit contains 96 different types of single-index adapters.	Single-Indexed Adapters	10 µl each/ 40 µl each
NGS3102-01 NGS3102-02	LeoNext Universal DNA Library Prep V3 Kit	The Genes2me LeoNext Universal DNA Library Prep Kit is specially designed for DNA library preparation for next generation sequencing (NGS) platforms. These are CE-IVD certified.	Whole genome library preparation kits	24/96 rxns

RNA Library Preparation for Illumina®

Cat #	Product Name		Application	Size
NGS3169-01/02	LeoNext Universal V8 RNA-Seq Library Prep Kit for Illumina®	The LeoNext Universal V8 RNA-seq Library Prep Kit for Illumina is designed for the preparation of RNA libraries for Illumina platform. The kit is suitable for library construction of RNA that have been obtained by mRNA enrichment or rRNA depletion. This kit combines 2nd Strand cDNA synthesis, end-repair & dA Tailing into one step that greatly simplifies the process of library construction and shortens the operation time.	Ultra Fast & Universal RNA Lib Prep Kits	24 rxn/96 rxn
NGS3170/ 3171-01/02	LeoNext RNA Adapters Set 1 / Set 2 for Illumina®	The LeoNext RNA Adapters for Illumina is a kit for high-throughput sequencing on Illumina platform. It is suitable for preparing multi-sample RNA libraries for Illumina high-throughput sequencing platform. The kit LeoNext RNA Adapters Set 1 / Set 2 for Illumina® (NGS3170/3171-01/02) contains 12 kinds of indexed adapters each. The kit LeoNext RNA Adapters Set 3 - Set 6 for Illumina® (NGS3172/3173/3174/3175) contains 24 kinds of indexed adapters each.	Single-Indexed Adapters	10 µl each/ 40 µl each
NGS3172/3173/ 3174/3175	LeoNext RNA Adapters Set 3 - Set 6 for Illumina®		Single-Indexed Adapters	20 µl each
NGS3168-01	LeoNext Universal V6 RNA-Seq Library Prep Kit	LeoNext Universal V6 RNA-seq Library Prep Kit is specially designed for the preparation of RNA libraries for Next Generation Sequencing (NGS) platforms. This is CE-IVD certified.	Transcriptome library preparation kit	48/96 rxns

Complete Range for Next Generation Sequencing - LEONEXT

RNA Library Preparation for MGI®

Cat #	Product Name		Application	Size
NGS3183-01/02	LeoNext Universal V6 RNA-Seq Library Prep Kit for MGI®	The LeoNext Universal V6 RNA-Seq Library Prep Kit for MGI® is designed for the preparation of RNA libraries for MGI platform. The kit is suitable for library construction of RNA that have been obtained by mRNA enrichment or rRNA depletion. This kit combines 2nd Strand cDNA synthesis, end-repair and dA Tailing into one step that greatly simplifies the process of library construction and shortens the operation time.	Ultra Fast & Universal RNA Lib Prep Kits	24 rxn/96 rxn
NGS3185-01/02	LeoNext RNA Adapters Set 8 for MGI®	The LeoNext RNA Adapters Set 8 for MGI® is a kit for high-throughput sequencing on MGI platform. It is suitable for preparing multi-sample RNA libraries for MGI high-throughput sequencing platform. The kit LeoNext RNA Adapters Set 8 for MGI® (NGS3185-01/02) contains 96 kinds of indexed adapters each.	Single-Indexed Adapters	10 µl each/40 µl each

Modules for RNA Library Preparation

Cat #	Product Name		Application	Size
NGS3188-01/02	LeoNext rRNA Depletion Kit (Human / Mouse / Rat)	The LeoNext rRNA Depletion Kit (Human) is designed to deplete rRNA (including cytoplasmic 28S, 18S, 5S rRNA, and mitochodrial 12S, 5.8S rRNA) from human total RNA preparations, while leaving mRNA and non-coding RNA. This kit is suitable for both intact and degraded RNA samples (i.e. FFPE RNA). The obtained rRNA-depleted RNA can be used for analysis applications of mRNA and non-coding RNA.	rRNA Depletion Kit	24 rxn / 96 rxn
NGS3186-01/02	LeoNext mRNA capture beads	LeoNext mRNA Capture Beads are paramagnetic beads coupled with Oligo d(T). The beads isolate intact mRNA from previously isolated total RNA. Magnetic separation technology permits elution of intact mRNA in small volumes that can be further used for RNA library preparation to generate transcriptome libraries for sequencing.	mRNA enrichment	24 rxn / 96 rxn

Beads

Cat #	Product Name		Application	Size
NGS3194-01/02/03	LeoNext DNA Clean Beads	The LeoNext DNA Clean Beads utilizes SPRI (Solid-Phase Reversible Immobilization) paramagnetic bead technology for High-throughput purification of nucleic acids. LeoNext DNA Clean Beads is compatible with all DNA/RNA library construction protocols.	DNA Clean-up & Size-Selection	5 ml/60 ml/ 450 ml

Additional Reagents

Cat #	Product Name		Application	Size
NGS3148-01/02	LeoNext Circularization Kit for MGI®	The LeoNext Circularization Kit for MGI is a kit optimized for the high-throughput sequencing specifically on MGI platform. This kit can convert final libraries with adapters to single-stranded circularized DNA libraries dedicated to MGI high-throughput sequencer.	Circularization Kit	16 rxn/48 rxn

Targeted Disorders

- Neuromuscular
- Cardiovascular
- Alzheimer, Parkinson, Dementia

Cardiovascular
NGS Assay

NGS has revolutionized the study of cardiovascular diseases allowing unprecedented opportunities to detect mutations in disease associated genes with high accuracy in a fast and cost-efficient manner in daily clinical practice.

The Genes2Me Cardiovascular disorders NGS panel is a hybridization based solution for targeted sequencing. With a fast turnaround time this product provides detection and identification of ~357 clinically relevant genes spanning 1.2 Mb of genome size (whole coding sequence) that covers all major mutations like SNV, InDels, & CNV.

No. of Genes	357
Gene count/ family	~174
Covered region	Whole CDS
Target size	1.2 Mb
Mutation type	SNV/InDels/CNVs
Sample type	Blood

CARDIO

List of Diseases Assessed*

- Aortopathy & connective tissue disorders
- Arrhythmia
- Cardiomyopathy
- Congenital heart defect
- Dyslipidemia
- Other cardiovascular diseases
- Pulmonary hypertension

**Limited diseases mentioned*

Scan for Cardio Gene List

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity	90%
Precision	94%
Reproducibility	96%
Sensitivity	95%
On Target Ratio	85-95 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Neuromuscular
NGS Assay

Many neurological conditions are caused by immensely heterogeneous gene mutations. The diagnostic process is often long and complex with most patients undergoing multiple invasive and costly investigations without ever reaching a conclusive molecular diagnosis. NGS has shortened the 'Diagnostic Odyssey' for many of these patients.

The Genes2Me Neuromuscular disorders NGS assay is a hybridization based solution for targeted sequencing employing NGS. With a fast turnaround time this product provides detection and identification of 497 clinically relevant genes spanning 1.4 Mb of genome size (whole coding sequence) that covers all major mutations like SNV, InDels, & CNV.

No. of Genes	497
Gene count/ family	~293
Covered region	Whole CDS
Target size	1.4 Mb
Mutation type	SNV/InDels/CNVs
Sample type	Blood

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity	97%
Precision	95%
Reproducibility	98%
Sensitivity	>94%
On Target Ratio	87-95 %

Scan for NEURO Gene List

Alzheimer-Parkinson-Dementia NGS Assay

The Genes2Me Alzheimer Parkinson's Dementia NGS panel is a hybridization based solution for targeted sequencing employing NGS. With a fast turnaround time this product provides detection and identification of ~139 clinically relevant genes spanning 0.4 Mb of genome size (whole coding sequence) that covers all major mutations like SNV, InDels, & CNV.

No. of Genes	139
Gene count/ family	~101
Covered region	Whole-CDS
Target size	0.39 Mb
Mutation type	SNV/InDels/CNVs
Sample type	Blood

ASSAY PERFORMANCE

Features	Performance#
Coverage uniformity	92%
Precision	95%
Reproducibility	97%
Sensitivity	>90%
On Target Ratio	87-95 %

: The observed values are for Illumina platform
VAF - Variant Allele Frequency

Scan for APD Gene List

EZY-AutoPrep

AUTOMATED NGS LIBRARY PREPARATION WORKSTATION

As the demand for efficient and scalable NGS workflows increases, we are proud to introduce the EZY-AutoPrep, an automated NGS library preparation workstation that can automate the NGS sample library preparation workflow for 24/48/96 libraries in a single run.

EZY-AutoPrep is designed to streamline and automate the entire NGS library construction process. By directly loading nucleic acid samples, the system fully automates critical steps such as fragmentation, end repair, adapter ligation, PCR amplification, hybridization, and quantification. The workstation is equipped with a built-in thermal cycler and a fluorometer.

This end-to-end solution minimizes hands-on time, reduces human errors, and significantly enhances throughput, making it an ideal choice for high-throughput sequencing applications. With EZY AutoPrep, one can rely on consistent, reproducible results, allowing them to focus on their scientific discoveries and patient diagnostics with confidence.

EZY - AutoPrep
can construct 24/48/96 sample libraries in one run

Our user friendly software, robust hardware and automation processes help you provide with a good library preparation experience.

INSTRUMENT FUNCTION

Library Preparation

Fragmentation (Enzymatic Method) → End Repair → A-Tailing Addition → Adaptor Ligation → Purification → PCR Amplification → Purification

Quantitation, Pooling

Concentration Determination → Normalization → Pooling

Hybrid Capture

Probe Hybridization → Magnetic Bead Preparation → Magnetic Bead Capture → PCR Amplification → Purification

Product Features

(For 24 & 96 sample library throughput)

Precise Pipetting

- The self-developed high-precision 8/24-channel pipettor can be used as a single channel.
- A variety of liquid parameters setting ensure accurate control of liquid aspirating and dispensing process.
- Capacitive & air pressure detection function can sensitively detect the liquid level, residual liquid and blockage, ensuring accurate control of the pipetting volume.

Flexible to Match Experimental Needs

- Equipped with several temperature control modules to meet the special temperature requirements such as - for reagent and sample storage.
- High efficiency magnetic module to avoid loss or residual of magnetic beads.
- The fully automatic thermal cycling module can effectively meet the nucleic acid amplification process in the process of library construction.

Simple Operation, Get Started Quickly

- Multi-level account management system supports the different needs of new users and advanced users.
- Drag-and-drop flows simplifies program setting.
- GUI is easy to understand and use.
- New users can also quickly master the operation methods of library construction.

Intelligent & Visual

- Allows users to freely choose running part or all of the experimental processes.
- Program settings like error reporting and prompt functions ensure that users can quickly find programming errors.
- TIP area prompts the experimental demand, current available amount & whether it is sufficient to ensure the smooth progress of the experiment.
- The PC simulation operation experiment function can enable users to find problems at any time and avoid wasting samples, reagents and time.

Efficient Contamination Prevention

- Equipped with efficient purification and filter system (positive pressure HEPA system) and UV sterilization to prevent cross-contamination of the experimental cabin.
- The PCR module in EZY-AutoPrep can use disposable automatic cover or conventional sealing cover to avoid condensation on the top & reduce the risk of cross-infection.

Multiple Functional Modules

(for EZY Autoprep 96)

- The 27 plate positions, together with the gripper, 24-channel pipettor, can realize the relative simple library preparation of 96 samples, as well as the simplified type fully automated library preparation
- The software program allows flexibility for sample processing by enabling the same program to quickly execute the same experimental process by simply adjusting the number of samples.

Built in Thermal Cycler & Flourometer

(For 96 sample library throughput)

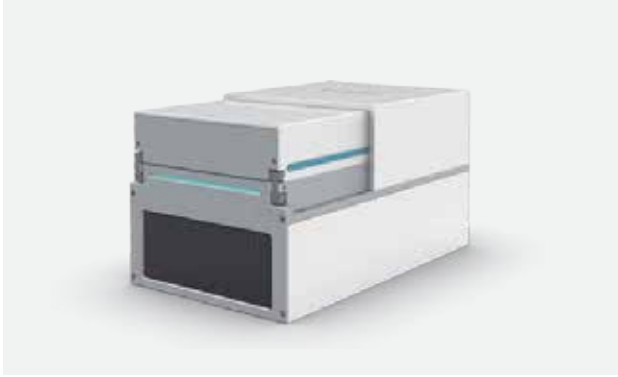
The built-in fluorometer quantitative method is sensitive and highly accurate, making it a reliable dsDNA measurement method

- Automation-specific block can test 8 / 16 / 24 samples simultaneously.
- Accurate quantitation and high accuracy with only 2-20 μl of samples
- Lowest detection limit down to 0.4 ng (dsDNA).
- Cooperates well with the automatic calculation of the software and high-precision pipetting to quickly achieve accurate sampling.

Repeatability	CV ≤ 1.5%
Linear	$R^2 \geq 0.995$
Linear range	4 orders of magnitude

SOFTWARE

The user-friendly and intuitive GUI allows you to easily initiate the library construction program right after installation, making it simple to create & run automated liquid handling protocols. To further enhance the usability of EZY-AutoPrep, we can customize the design based on customer needs for common NGS library construction methods.



PCR Amplification Block

(1) Block temperature control range: 4 °C ~ 99 °C, the max temperature of the thermo lid is 120 °C
(2) Temperature precision: ±0.3 °C @55 °C, temperature accuracy <0.3 °C @55 °C
(3) Temperature uniformity: ±0.7 °C (@55 °C, 72 °C)

Built in PCR block is safe and reliable, with extremely low cross-contamination rate

Interleave NTC (Nuclease-Free Water) between the samples for comparison, run the amplification program, & the results show that the number of reads in the control group is extremely low.

Temperature Control Module

Can be freely set at 4~105 °C. It's the standard temperature control block of NGS series. According to the usages, block adapters can be customized to meet different consumables requirements.

Temperature accuracy:	0.5°C, @55°C
Temperature uniformity:	0.5°C, @55°C

ORDERING INFORMATION

Product Description	Product Code (Old)	Product Code (New)	Variant Code	Pack Size	Platform
BRCA NGS Test Kit	**G2MBR00001**	**G710001**	**G710001-1**	**24T**	**Illumina**
			G710001-2	96T	Illumina
			G710001-3	96T-EZY	illumina-EZY
			G710001-4	24T	MGI
			G710001-5	96T	MGI
			G710001-6	96T-EZY	MGI-EZY
			G710001-7	24T	Aviti
			G710001-8	96T	Aviti
			G710001-9	96T-EZY	Aviti-EZY
			G710001-10	24T	Thermo
			G710001-11	96T	Thermo
			G710001-12	96T-EZY	Thermo-EZY
OncoCheck NGS Test Kit (HRR)	**G2MOC01001**	**G710002**	**G710002-1**	**24T**	**Illumina**
			G710002-2	96T	Illumina
			G710002-3	96T-EZY	illumina-EZY
			G710002-4	24T	MGI
			G710002-5	96T	MGI
			G710002-6	96T-EZY	MGI-EZY
			G710002-7	24T	Aviti
			G710002-8	96T	Aviti
			G710002-9	96T-EZY	Aviti-EZY
			G710002-10	24T	Thermo
			G710002-11	96T	Thermo
			G710002-12	96T-EZY	Thermo-EZY
CancerCheck Core NGS Test Kit (HRD)	**G2MCC02001**	**G710003**	**G710003-1**	**24T**	**Illumina**
			G710003-2	96T	Illumina
			G710003-3	96T-EZY	illumina-EZY
			G710003-4	24T	MGI
			G710003-5	96T	MGI
			G710003-6	96T-EZY	MGI-EZY
			G710003-7	24T	Aviti
			G710003-8	96T	Aviti
			G710003-9	96T-EZY	Aviti-EZY
			G710003-10	24T	Thermo
			G710003-11	96T	Thermo
			G710003-12	96T-EZY	Thermo-EZY
CancerCheck-50 NGS Test Kit	**G2MCC03001**	**G710004**	**G710004-1**	**24T**	**Illumina**
			G710004-2	96T	Illumina
			G710004-3	96T-EZY	illumina-EZY
			G710004-4	24T	MGI
			G710004-5	96T	MGI
			G710004-6	96T-EZY	MGI-EZY
			G710004-7	24T	Aviti
			G710004-8	96T	Aviti
			G710004-9	96T-EZY	Aviti-EZY
			G710004-10	24T	Thermo
			G710004-11	96T	Thermo
			G710004-12	96T-EZY	Thermo-EZY
CancerCheck-100 NGS Test Kit	**G2MCC04001**	**G710005**	**G710005-1**	**24T**	**Illumina**
			G710005-2	96T	Illumina
			G710005-3	96T-EZY	illumina-EZY
			G710005-4	24T	MGI
			G710005-5	96T	MGI
			G710005-6	96T-EZY	MGI-EZY
			G710005-7	24T	Aviti
			G710005-8	96T	Aviti
			G710005-9	96T-EZY	Aviti-EZY
			G710005-10	24T	Thermo
			G710005-11	96T	Thermo
			G710005-12	96T-EZY	Thermo-EZY

ORDERING INFORMATION

Product Description	Product Code (Old)	Product Code (New)	Variant Code	Pack Size	Platform
PanCan CGP NGS Test Kit	**G2MPC06001**	**G710006**	**G710006-1**	**24T**	**Illumina**
			G710006-2	96T	Illumina
			G710006-3	96T-EZY	illumina-EZY
			G710006-4	24T	MGI
			G710006-5	96T	MGI
			G710006-6	96T-EZY	MGI-EZY
			G710006-7	24T	Aviti
			G710006-8	96T	Aviti
			G710006-9	96T-EZY	Aviti-EZY
			G710006-10	24T	Thermo
			G710006-11	96T	Thermo
			G710006-12	96T-EZY	Thermo-EZY
Clinical Exome Sequencing NGS Test Kit	**G2MCES07001**	**G710007**	**G710007-1**	**24T**	**Illumina**
			G710007-2	96T	Illumina
			G710007-3	96T-EZY	illumina-EZY
			G710007-4	24T	MGI
			G710007-5	96T	MGI
			G710007-6	96T-EZY	MGI-EZY
			G710007-7	24T	Aviti
			G710007-8	96T	Aviti
			G710007-9	96T-EZY	Aviti-EZY
			G710007-10	24T	Thermo
			G710007-11	96T	Thermo
			G710007-12	96T-EZY	Thermo-EZY
Clinical Exome Sequencing NGS Test Kit	**G2MCES07001(WES)**	**G710008**	**G710008-1**	**24T**	**Illumina**
			G710008-2	96T	Illumina
			G710008-3	96T-EZY	illumina-EZY
			G710008-4	24T	MGI
			G710008-5	96T	MGI
			G710008-6	96T-EZY	MGI-EZY
			G710008-7	24T	Aviti
			G710008-8	96T	Aviti
			G710008-9	96T-EZY	Aviti-EZY
			G710008-10	24T	Thermo
			G710008-11	96T	Thermo
			G710008-12	96T-EZY	Thermo-EZY
Med4Me PGX NGS Test Kit	**G2MMSP08001**	**G710009**	**G710009-1**	**24T**	**Illumina**
			G710009-2	96T	Illumina
			G710009-3	96T-EZY	illumina-EZY
			G710009-4	24T	MGI
			G710009-5	96T	MGI
			G710009-6	96T-EZY	MGI-EZY
			G710009-7	24T	Aviti
			G710009-8	96T	Aviti
			G710009-9	96T-EZY	Aviti-EZY
			G710009-10	24T	Thermo
			G710009-11	96T	Thermo
			G710009-12	96T-EZY	Thermo-EZY
TB NGS test Kit	**G2MMAP10001**	**G710010**	**G710010-1**	**24T**	**Illumina**
			G710010-2	96T	Illumina
			G710010-3	96T-EZY	illumina-EZY
			G710010-4	24T	MGI
			G710010-5	96T	MGI
			G710010-6	96T-EZY	MGI-EZY
			G710010-7	24T	Aviti
			G710010-8	96T	Aviti
			G710010-9	96T-EZY	Aviti-EZY
			G710010-10	24T	Thermo
			G710010-11	96T	Thermo
			G710010-12	96T-EZY	Thermo-EZY
ctDNA-Breast NGS Test Kit	**G2MCTBP12001**	**G710011**	**G710011-1**	**24T**	**Illumina**
			G710011-2	96T	Illumina
			G710011-3	96T-EZY	illumina-EZY
			G710011-4	24T	MGI
			G710011-5	96T	MGI
			G710011-6	96T-EZY	MGI-EZY
			G710011-7	24T	Aviti
			G710011-8	96T	Aviti
			G710011-9	96T-EZY	Aviti-EZY

ORDERING INFORMATION

Product Description	Product Code (Old)	Product Code (New)	Variant Code	Pack Size	Platform
HLA Typing NGS Test Kit	**G2MHLA32001**	**G710014**	**G710014-1**	**24T**	**Illumina**
			G710014-2	96T	Illumina
			G710014-3	96T-EZY	illumina-EZY
			G710014-4	24T	MGI
			G710014-5	96T	MGI
			G710014-6	96T-EZY	MGI-EZY
			G710014-7	24T	Aviti
			G710014-8	96T	Aviti
			G710014-9	96T-EZY	Aviti-EZY
			G710014-10	24T	Thermo
			G710014-11	96T	Thermo
			G710014-12	96T-EZY	Thermo-EZY
Alzheimer-Parkinson- Dementia NGS Test Kit	**G2MAPD23001**	**G710015**	**G710015-1**	**24T**	**Illumina**
			G710015-2	96T	Illumina
			G710015-3	96T-EZY	illumina-EZY
			G710015-4	24T	MGI
			G710015-5	96T	MGI
			G710015-6	96T-EZY	MGI-EZY
			G710015-7	24T	Aviti
			G710015-8	96T	Aviti
			G710015-9	96T-EZY	Aviti-EZY
			G710015-10	24T	Thermo
			G710015-11	96T	Thermo
			G710015-12	96T-EZY	Thermo-EZY
Common Hereditary Cancer NGS Test Kit	**G2MCHC24001**	**G710016**	**G710016-1**	**24T**	**Illumina**
			G710016-2	96T	Illumina
			G710016-3	96T-EZY	illumina-EZY
			G710016-4	24T	MGI
			G710016-5	96T	MGI
			G710016-6	96T-EZY	MGI-EZY
			G710016-7	24T	Aviti
			G710016-8	96T	Aviti
			G710016-9	96T-EZY	Aviti-EZY
			G710016-10	24T	Thermo
			G710016-11	96T	Thermo
			G710016-12	96T-EZY	Thermo-EZY
Hemat NGS Test Kit for Leukemia	**G2MML28001**	**G710017**	**G710017-1**	**24T**	**Illumina**
			G710017-2	96T	Illumina
			G710017-3	96T-EZY	illumina-EZY
			G710017-4	24T	MGI
			G710017-5	96T	MGI
			G710017-6	96T-EZY	MGI-EZY
			G710017-7	24T	Aviti
			G710017-8	96T	Aviti
			G710017-9	96T-EZY	Aviti-EZY
			G710017-10	24T	Thermo
			G710017-11	96T	Thermo
			G710017-12	96T-EZY	Thermo-EZY
Lymhoma NGS Test Kit	**G2MLYM31001**	**G710018**	**G710018-1**	**24T**	**Illumina**
			G710018-2	96T	Illumina
			G710018-3	96T-EZY	illumina-EZY
			G710018-4	24T	MGI
			G710018-5	96T	MGI
			G710018-6	96T-EZY	MGI-EZY
			G710018-7	24T	Aviti
			G710018-8	96T	Aviti
			G710018-9	96T-EZY	Aviti-EZY
			G710018-10	24T	Thermo
			G710018-11	96T	Thermo
			G710018-12	96T-EZY	Thermo-EZY

ORDERING INFORMATION

Product Description	Product Code (Old)	Product Code (New)	Variant Code	Pack Size	Platform
GenomeKundli- New born screening NGS Test Kit	**G2MGK29001**	**G710019**	**G710019-1**	**24T**	**Illumina**
			G710019-2	96T	Illumina
			G710019-3	96T-EZY	illumina-EZY
			G710019-4	24T	MGI
			G710019-5	96T	MGI
			G710019-6	96T-EZY	MGI-EZY
			G710019-7	24T	Aviti
			G710019-8	96T	Aviti
			G710019-9	96T-EZY	Aviti-EZY
			G710019-10	24T	Thermo
			G710019-11	96T	Thermo
			G710019-12	96T-EZY	Thermo-EZY
LeoNext PanPathogen NGS Test Kit	**NGS3104-01**	**G710021**	**G710021-1**	**48T**	**Illumina**
			G710021-2	96T	Illumina
			G710021-3	96T-EZY	Illumina
			G710021-4	48T	MGI
			G710021-5	96T	MGI
			G710021-6	96T-EZY	MGI
			G710021-7	48T	Aviti
			G710021-8	96T	Aviti
			G710021-9	96T-EZY	Aviti-EZY
			G710021-10	48T	Thermo
			G710021-11	96T	Thermo
			G710021-12	96T-EZY	Thermo-EZY
LeoNext NIPT NGS Test Kit	**NGS3105-01**	**G710022**	**G710022-1**	**48T**	**Illumina**
			G710022-2	96T	Illumina
			G710022-3	96T-EZY	Illumina
			G710022-4	48T	MGI
			G710022-5	96T	MGI
			G710022-6	96T-EZY	MGI
			G710022-7	48T	Aviti
			G710022-8	96T	Aviti
			G710022-9	96T-EZY	Aviti-EZY
			G710022-10	48T	Thermo
			G710022-11	96T	Thermo
			G710022-12	96T-EZY	Thermo-EZY
Cardiovascular NGS Test Kit	**G2MCV15001**	**G710023**	**G710023-1**	**24T**	**Illumina**
			G710023-2	96T	Illumina
			G710023-3	96T-EZY	illumina-EZY
			G710023-4	24T	MGI
			G710023-5	96T	MGI
			G710023-6	96T-EZY	MGI-EZY
			G710023-7	24T	Aviti
			G710023-8	96T	Aviti
			G710023-9	96T-EZY	Aviti-EZY
			G710023-10	24T	Thermo
			G710023-11	96T	Thermo
			G710023-12	96T-EZY	Thermo-EZY
Neuromuscular NGS Test Kit	**G2MNM14001**	**G710024**	**G710024-1**	**24T**	**Illumina**
			G710024-2	96T	Illumina
			G710024-3	96T-EZY	illumina-EZY
			G710024-4	24T	MGI
			G710024-5	96T	MGI
			G710024-6	96T-EZY	MGI-EZY
			G710024-7	24T	Aviti
			G710024-8	96T	Aviti
			G710024-9	96T-EZY	Aviti-EZY
			G710024-10	24T	Thermo
			G710024-11	96T	Thermo
			G710024-12	96T-EZY	Thermo-EZY

ORDERING INFORMATION

Product Description	Product Code (Old)	Product Code (New)	Variant Code	Pack Size	Platform
LeoNext Universal RNA-Seq Library Prep Kit	**NGS3168-01**	**G710026**	**G710026-1**	**24T**	**Illumina**
			G710026-2	96T	Illumina
			G710026-3	96T-EZY	illumina-EZY
			G710026-4	24T	MGI
			G710026-5	96T	MGI
			G710026-6	96T-EZY	MGI-EZY
			G710026-7	24T	Aviti
			G710026-8	96T	Aviti
			G710026-9	96T-EZY	Aviti-EZY
LeoNext Universal DNA Library Prep Kit	**NGS3101-01**	**G710027**	**G710027-1**	**24T**	**Illumina**
			G710027-2	96T	Illumina
			G710027-3	96T-EZY	illumina-EZY
			G710027-4	24T	MGI
			G710027-5	96T	MGI
			G710027-6	96T-EZY	MGI-EZY
			G710027-7	24T	Aviti
			G710027-8	96T	Aviti
			G710027-9	96T-EZY	Aviti-EZY
ctDNA Lung NGS Test Kit	**G2MCTLP13001**	**G710028**	**G710028-1**	**24T**	**Illumina**
			G710028-2	96T	Illumina
			G710028-3	96T-EZY	illumina-EZY
			G710028-4	24T	MGI
			G710028-5	96T	MGI
			G710028-6	96T-EZY	MGI-EZY
			G710028-7	24T	Aviti
			G710028-8	96T	Aviti
			G710028-9	96T-EZY	Aviti-EZY
ctDNA Colorectal NGS Test Kit	**G2MCTCP11001**	**G710029**	**G710029-1**	**24T**	**Illumina**
			G710029-2	96T	Illumina
			G710029-3	96T-EZY	illumina-EZY
			G710029-4	24T	MGI
			G710029-5	96T	MGI
			G710029-6	96T-EZY	MGI-EZY
			G710029-7	24T	Aviti
			G710029-8	96T	Aviti
			G710029-9	96T-EZY	Aviti-EZY
Focus Lung*	**G2MBR4-0979**	**G2MBR4-0979**	**G2MBR4-0979**	**24T**	**Illumina**
			G2MBR4-0980	96T	Illumina
			G2MBR4-0981	96T-EZY	Illumina-EZY
			G2MBR4-0982	24T	MGI
			G2MBR4-0983	96T	MGI
			G2MBR4-0984	96T-EZY	MGI-EZY
			G2MBR4-0985	24T	TF
			G2MBR4-0986	96T	TF
			G2MBR4-0987	96T-EZY	TF
			G2MBR4-0988	24T	Aviti
			G2MBR4-0989	96T	Aviti
			G2MBR4-0990	96T-EZY	Aviti-EZY

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Genes2Me Pvt. Ltd.

1105, 11th Floor, Tower B, SAS Tower, Medicity,
Sector - 38, Gurgaon - 122 001, Haryana, India
Tel : + 91 18001 214030 / + 91 88000 23600
E-mail : contact@genes2me.com
www.genes2me.com