CliSeq | NGS

G2M

Insight *into* Genetic Mutations

NEXT GENERATION SEQUENCING

SOLUTIONS

www.genes2me.com

Fully Automated IVD Kits Manufacturing Facility of 1,50,000 Sq. Ft. in Manesar, INDIA

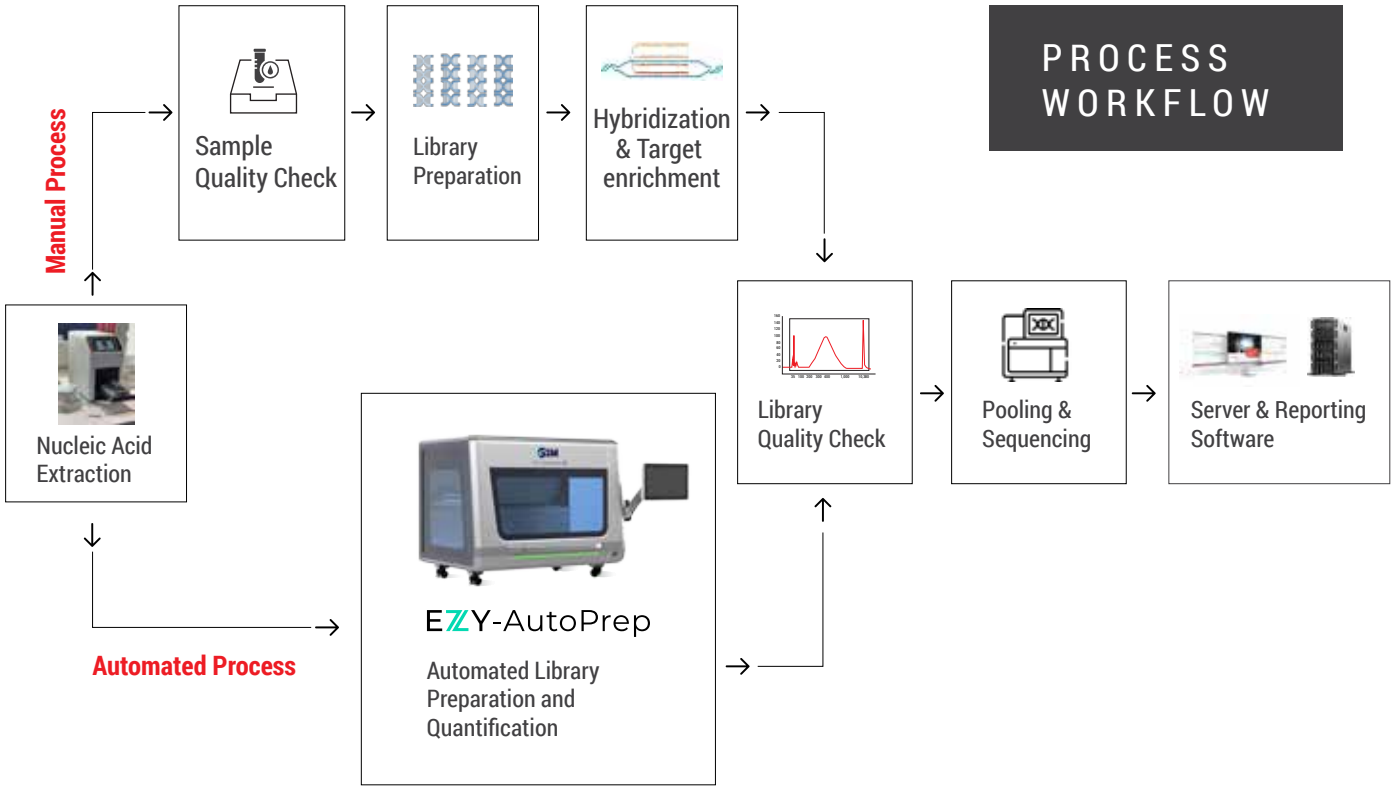
Spearheading
Innovation
in Genomics
Solutions
Manufacturing

Genes2Me developed

NGS based Clinical Panels

G2M panels are compatible with NGS platforms from Illumina, Thermo Fisher (Ion Torrent), Element Biosciences and MGI. Our target enrichment method is capable of specifically isolating your genomic loci of interest out of the whole genome & increasing the sensitivity of detecting genetic mutations by producing higher coverage & in-depth sequencing data.

PROCESS WORKFLOW



INFECTIOUS

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

ONCOLOGY PANELS

PanCan (681 genes - DNA, 105 genes- RNA)
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)

LIQUID BIOPSY PANELS

PanCan (681 genes)
CtDNA Breast (52 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

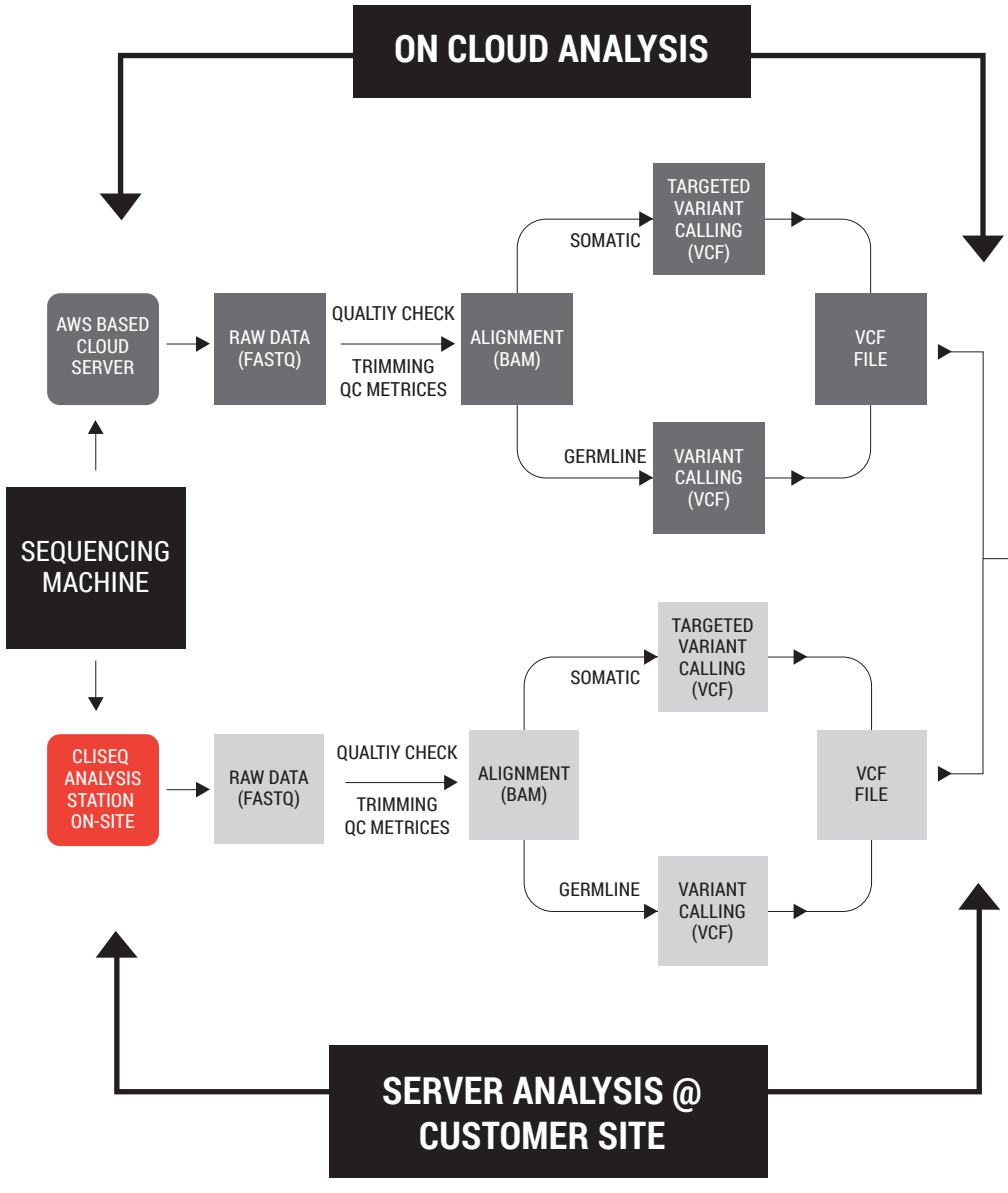
With built-in fluorometer and thermal cycler

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.

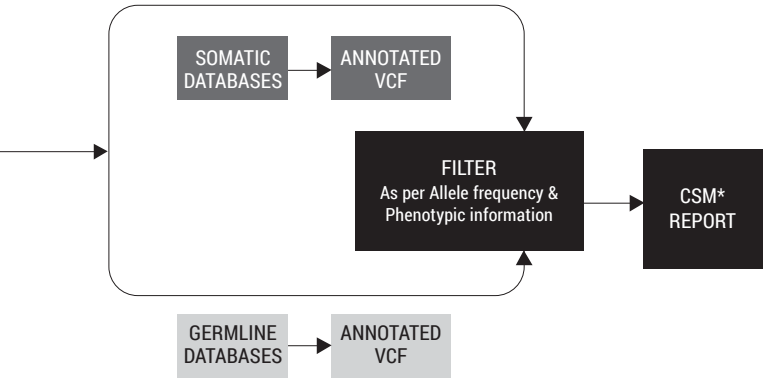
With a user-friendly interface, and advanced visualization capabilities, Cliseq empowers you to extract meaningful insights from vast genomic datasets with precision & efficiency.

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

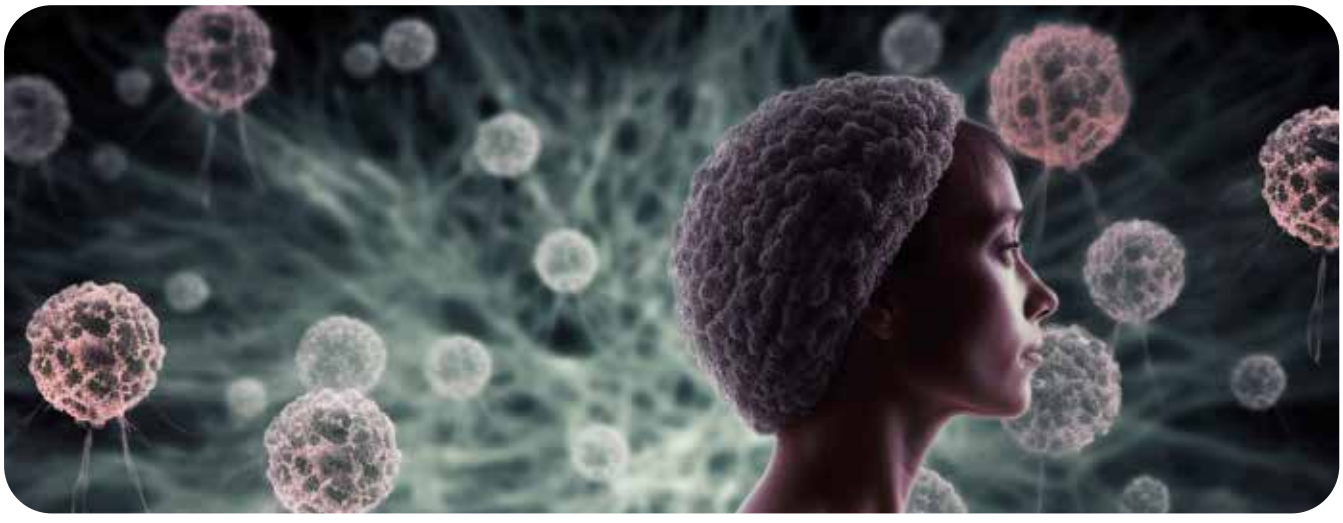
PanCan is a CGP (comprehensive genomic profiling) NGS assay aimed to screen a range of cancer causing genes to identify somatic mutations in DNA & RNA from human clinical samples like FFPE and fresh tissue targeting 681 genes (for DNA & 105 genes for RNA fusions) covering all the coding sequences enriched 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), 105 (RNA Fusions)
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	Illumina	MGI	Element (AVITI)
Coverage uniformity (%)	>98	>98	85%
Precision (%)	>95	>96	90%
Reproducibility (%)	97	97	96.5%
On Target Ratio (%)	86-95	85-95	82-90%
Sensitivity (VAF @1%)	98.6	96	95%

*Note :- This data has been calculated from a sample number size of 92 samples
VAF - Variant Allele Frequency

Number of Genes covered in G2M CGP assay vs the Competitor CGP assay

The above illustration shows a Venn diagram comparison for number of genes covered by G2M vs by other competitor companies in their CGP panels. For instance, in figure (a), G2M covers 378 unique genes when compared to 18 unique genes of the competitor company. They both have an overlap of 303 genes.

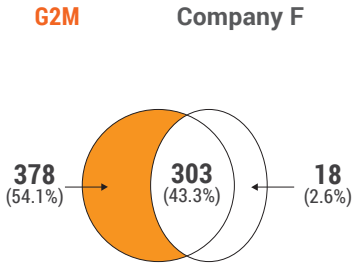


Figure A

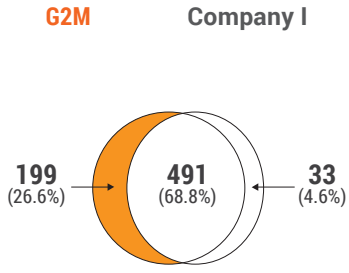
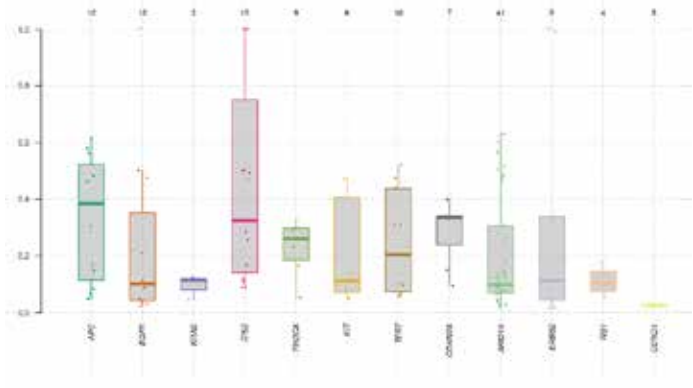


Figure B

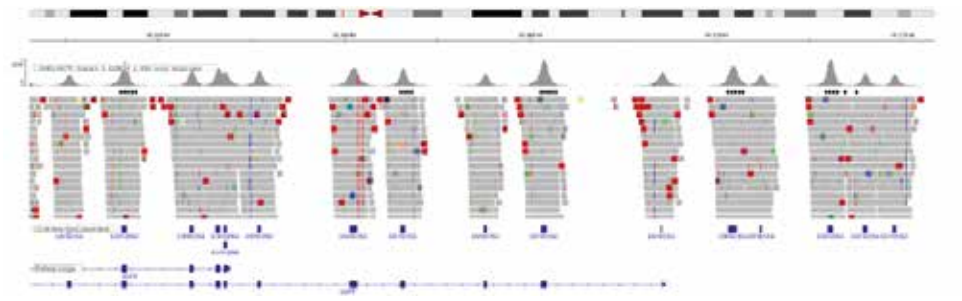
VAF PLOT

VAF is the percentage of sequence reads observed matching a specific DNA variant divided by the overall coverage at that locus. This VAF plots shows, the top 8 out of 12 genes that were detected under median value 1-20% VAF.

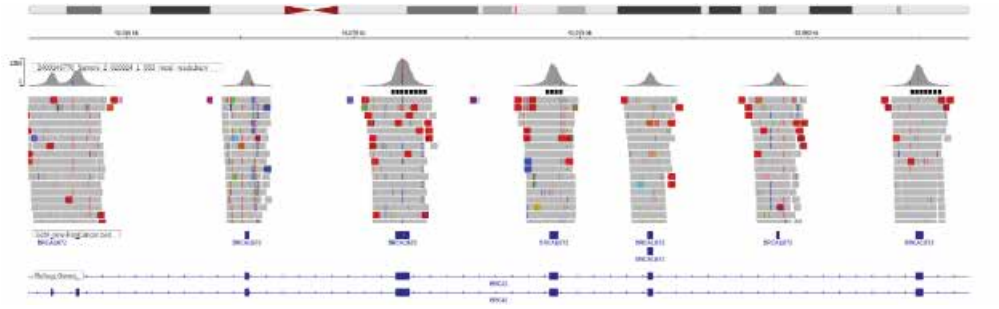


Coverage across Genes

The below mentioned plots showcase the coverage across the exonic regions of BRCA 1 and EGFR genes, two most important genes in Cancer. The plots show how uniformly our panel covers the exonic regions of the EGFR and BRCA1 gene.



EGFR



BRCA 1

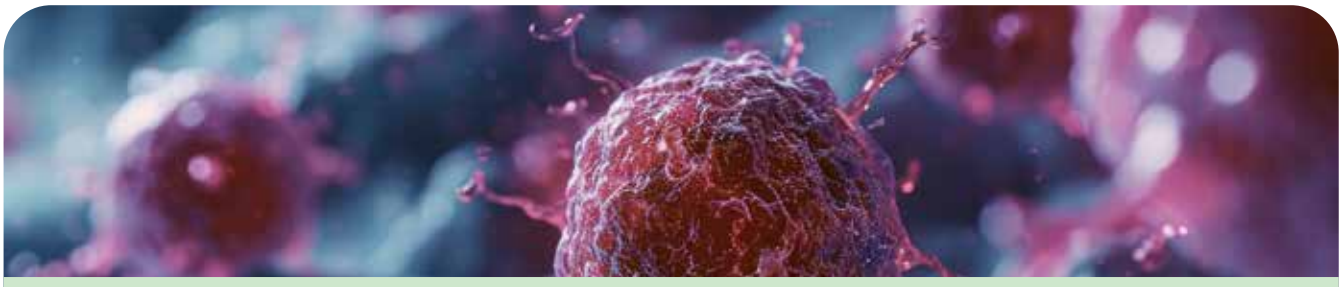
COVERS A WIDE RANGE OF CANCER

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

ORDERING INFORMATION

Commercial Name	Cat No.
PAN Cancer Panel	G2MPC06001-ill; G2MPC06001-TF; G2MPC06001-MG

Scan for PanCan sample report



CancerCheck Core (HRD Assay)

There are various DNA repair pathways, HRR (Homologous Recombination Repair) being one of them.

It is a fundamental cellular process that repairs double-strand breaks (DSBs) in DNA. This repair process ensures that the genetic information is restored correctly, thus maintaining genomic stability and preventing mutations that could lead to diseases like cancer.

There are certain genes that are responsible for HRR which if mutated, can lead to a dysfunction in the HRR process leading to chromosomal structural changes across the cells. The accumulation of these variants are also known as genomic instabilities. 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).

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.

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
- BREAST CANCER
- PROSTATE CANCER
- PANCREATIC CANCER

SNP Count	> 50,000	
Test Approach	Tumor only	Matched sample
Sample type	Tumor sample	Tumor sample
		Blood or peripheral normal tissue

ORDERING INFORMATION

Commercial Name	Cat No.
CancerCheck Core Panel	G2MCC02001-ill; G2MCC02001-TF; G2MCC02001-MG

ONCOLOGY

Blood Cancer NGS Assays

- Myeloid Leukemia
- Lymphoma

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

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

Myeloid Leukemia NGS Panel	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
Sample types	Blood, Bone marrow

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

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

Myeloid Leukemia NGS Panel

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	>98%	>96%	97.6%
Precision	>95%	>96%	96%
Reproducibility	99%	99%	98.2%
Sensitivity	5%VAF@>95%	5%VAF@>95%	5%VAF@>95%
On Target Ratio	85-95 %	83-95%	83-90%

Scan for Gene List

Lymphoma NGS Panel

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	>90%	>90%	>85%
Precision	>95%	>95%	>95%
Reproducibility	99%	99%	99%
Sensitivity	5%VAF@>95%	5%VAF@>95%	5%VAF@>95%
On Target Ratio	85-90 %	80-90%	75-85%

Observations

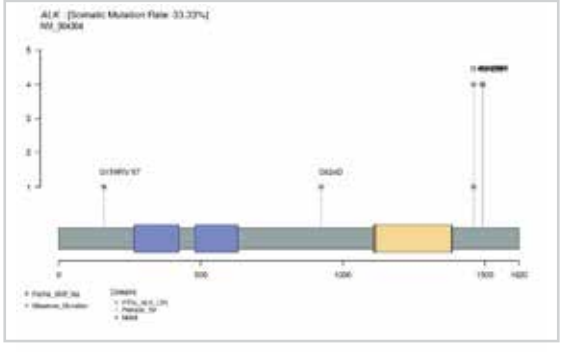


Figure 1(a)

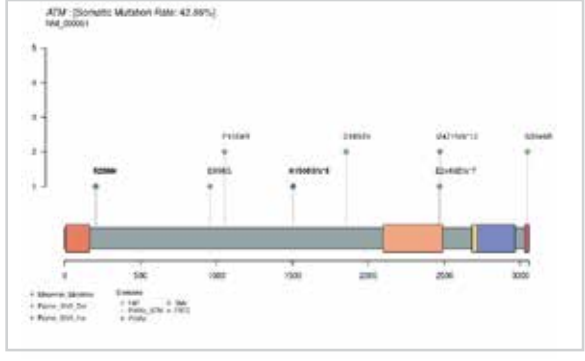


Figure 1(b)

These Lollipop plots show the distribution of hotspots in ALK and ATM Genes across Lymphoma samples.

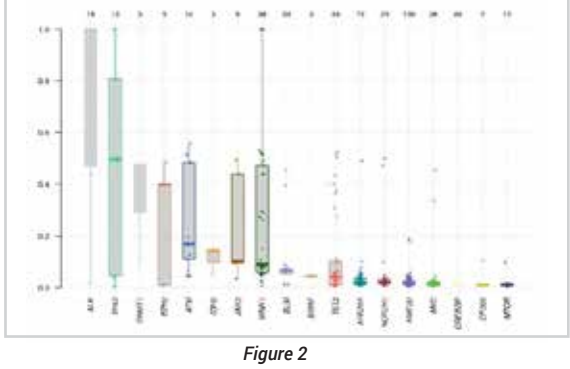


Figure 2

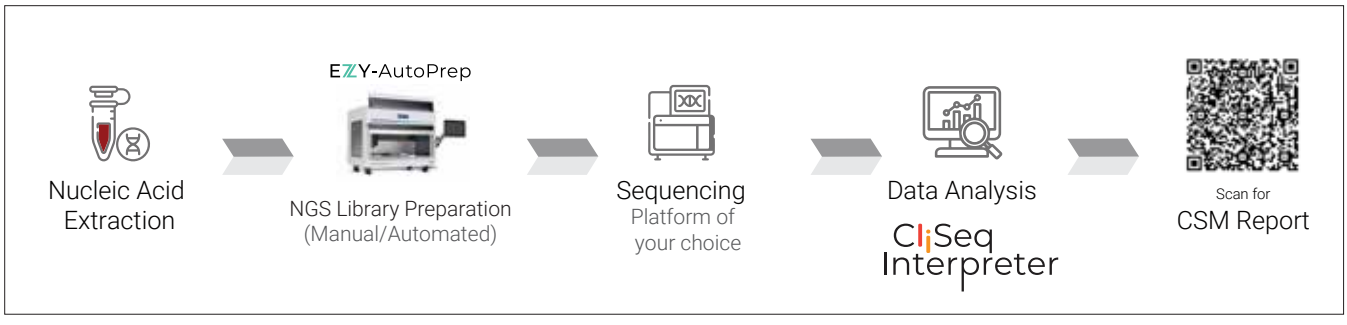
This VAF plot shows some of the important genes of Lymphoma that were detected under median value 5-10% VAF.

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



Data Analysis Platform

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CliSeq Interpreter

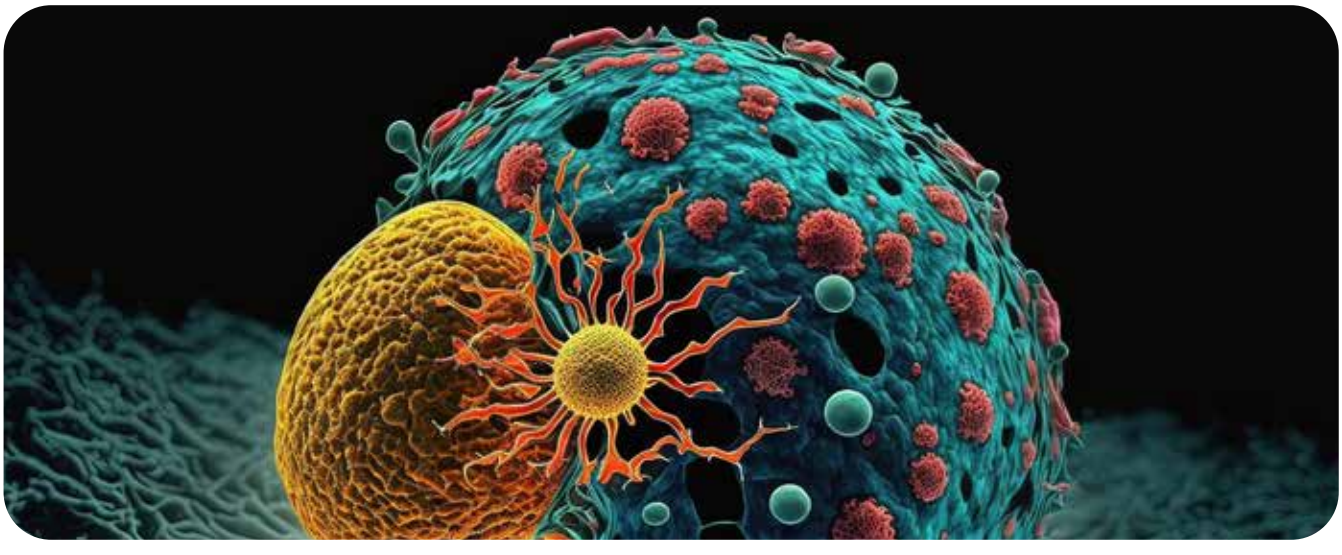
Liquid Biopsy

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	52 (13 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
CCND1	CCNE1	CDH1	CREBBP	CTNNB1	DPYD	EGFR	ERBB2	ESR1	FBXW7
FGFR1	FGFR2	FGFR3	GATA3	GNAQ	IGF1R	KIT	KPAS	KRAS	LRP2
MAP2K4	MAP3K1	MDM2	MYC	NCOR1	NCOR2	NF1	NRAS	NTRK1	NTRK2
NTRK3	PALB2	PIK3CA	PIK3R1	PTEN	RB1	RET	RNF213	SF3B1	SMAD4
TOP2A	TP53								

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

The detection sensitivity for low-frequency variants from a limited amount of sample is of great importance to ctDNA analysis kits.

ASSAY PERFORMANCE	ctDNA Lung			ctDNA Colorectal			ctDNA Breast		
Features	**Illumina**	**MGI**	**Element (AVITI)**	**Illumina**	**MGI**	**Element (AVITI)**	**Illumina**	**MGI**	**Element (AVITI)**
Coverage uniformity	98%	97%	97.5%	98%	98%	98.4%	97%	98%	96%
Precision	96%	97%	96.5%	94%	95%	95%	93%	93%	94%
Reproducibility	99%	99%	98.5%	96%	96%	96.8%	98%	98%	97.5%
Sensitivity	<1%VAF @ 95%	<1%VAF @ 95%	0.5%VAF @ 96%	<1%VAF @ 95%	<1%VAF @ 95%	0.5%VAF @ 94%	<1%VAF @ 95%	<1%VAF @ 95%	0.5%VAF @ 95.8%
On Target Ratio	86-95 %	87-95%	>80%	85-95%	86-95%	>80%	88-95%	87-95%	>80%

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

ORDERING INFORMATION

Commercial Name	Cat No.
ctDNA Colorectal Panel	G2MCTCP11001-ill; G2MCTCP11001-MG
ctDNA Breast Panel	G2MCTBP12001-ill; G2MCTBP12001-MG
ctDNA Lung Panel	G2MCTLP13001-ill; G2MCTLP13001-MG

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	AKT1	ALK	APC	ARID1A	ATM	BRAF#	BRCA*#	CDH1
CDK*	CDKN2A	CRNKL1	CSF1R	CTNNB1	DDR2	ERBB (EGFR)*#	EP300	ESR1
FGFR*	GNA*	H3-3A	RAS*	IDH*	JAK2	KDR	KIT	KNSTRN
MAP2K1	MET#	MLH1	MTOR	MYC#	MYCN	MYD88	NOTCH1	NTRK1#
PDGFRA	PIK3CA#	PIK3R1	PPP2R1A	PTCH1	PTEN#	PTPN11	RAC1	RB1
RET	ROS1	SF3B1	SMAD4	SMO	SRC	STK*	TP53 #	U2AF1

* Gene family / # CNVs

ASSAY PERFORMANCE

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	93%	94%	94.50%
Precision	90%	90%	92%
Reproducibility	98%	98%	96%
Sensitivity	1%VAF@95%	1%VAF@95%	1%VAF@94.5%
On Target Ratio	89-95 %	88-95%	80-90%

ORDERING INFORMATION

Commercial Name	Cat No.
CancerCheck 50 Panel	G2MCC03001-ill; G2MCC03001-TF; G2MCC03001-MG

CancerCheck 100 Assay

No. of Genes	148
Gene count/ family	~99
Covered region	Whole CDS
Target size	0.48 Mb
Mutation type	SNV/ InDels/ CNVs
Biomarkers	MSI, HRR Genes
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	Illumina	MGI	Element (AVITI)
Coverage uniformity	95%	95%	96%
Precision	96%	96%	97%
Reproducibility	99%	99%	98%
Sensitivity	1%VAF@95%	1%VAF@95%	1%VAF@96%
On Target Ratio	89-95 %	88-95%	80-88%

ORDERING INFORMATION

Commercial Name	Cat No.
CancerCheck 100 Panel	G2MCC04001-ill; G2MCC04001-TF; G2MCC04001-MG

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

ASSAY PERFORMANCE

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	>96%	>96%	97%
Precision	>96%	>96%	98%
Reproducibility	99%	99%	97.4%
Sensitivity	96%	97%	95.4%
On Target Ratio	86-95 %	85-95%	78-86%

ORDERING INFORMATION

Commercial Name	Cat No.
OncoCheck Panel	G2MOC01001-ill; G2MOC01001-TF; G2MOC01001-MG

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	MGI	Element (AVITI)
Coverage uniformity	98%	98%	96.5%
Precision	97%	96%	98.2%
Reproducibility	98%	98%	97.4%
Sensitivity	93%	94%	95%
On Target Ratio	85-95 %	85-95%	81-94%

ORDERING INFORMATION

Commercial Name	Cat No.
Common Hereditary Cancer NGS Panel	G2MCHC24001-ill; G2MCHC24001-MG; G2MCHC24001-TF

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	Illumina	MGI	Element (AVITI)
Coverage uniformity	97%	98%	95.4%
Precision	92%	93%	90%
Reproducibility	97%	98%	98.10%
Sensitivity	<1%VAF@95%	<1%VAF@95%	<1%VAF@93%
On Target Ratio	87-95 %	85-95%	76-85%

ORDERING INFORMATION

Commercial Name	Cat No.
BRCA 1/2 Panel	G2MBR00001-ill; G2MBR00001-TF; G2MBR00001-MG

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

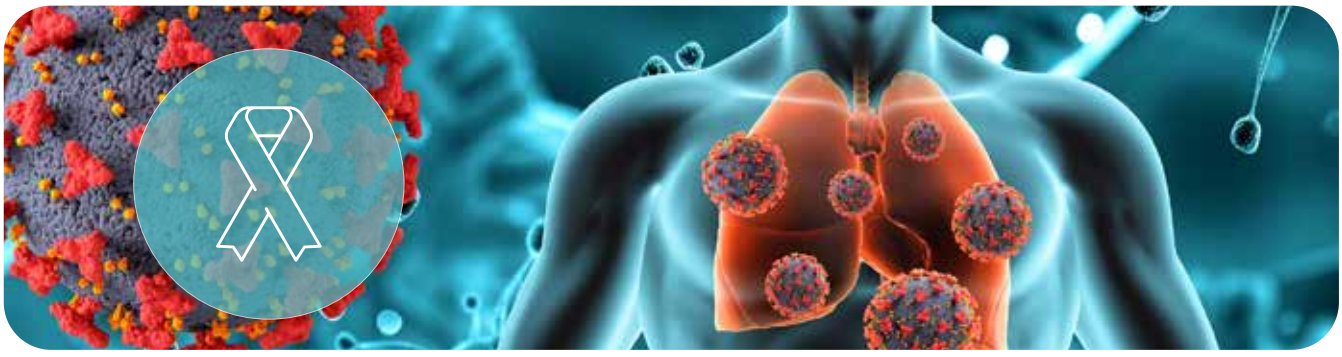
Key Features

- 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	Illumina	MGI	Element (AVITI)
Coverage uniformity	>98.5	>98	96%
Precision	>97	>96	95.75%
Reproducibility	97.2	97	96.50%
On Target Ratio	86-95	85-95	82-90%
Sensitivity (VAF@1%)	98.6	96	90%

*Note :- This data has been calculated from a sample number size of 92 samples
VAF - Variant Allele Frequency

ORDERING INFORMATION

Commercial Name	Cat No.
Lung Cancer NGS Panel	G2MBR4-0737-ill; G2MBR4-0739-TF; G2MBR4-0741-MG

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	Illumina	MGI	Element (AVITI)
Coverage uniformity	97%	97%	96.40%
Precision	95%	95%	96.80%
Reproducibility	98%	98%	98.10%
Sensitivity	95%	95%	92.90%
On Target Ratio	87-95 %	86-95%	79-85%

Key Features

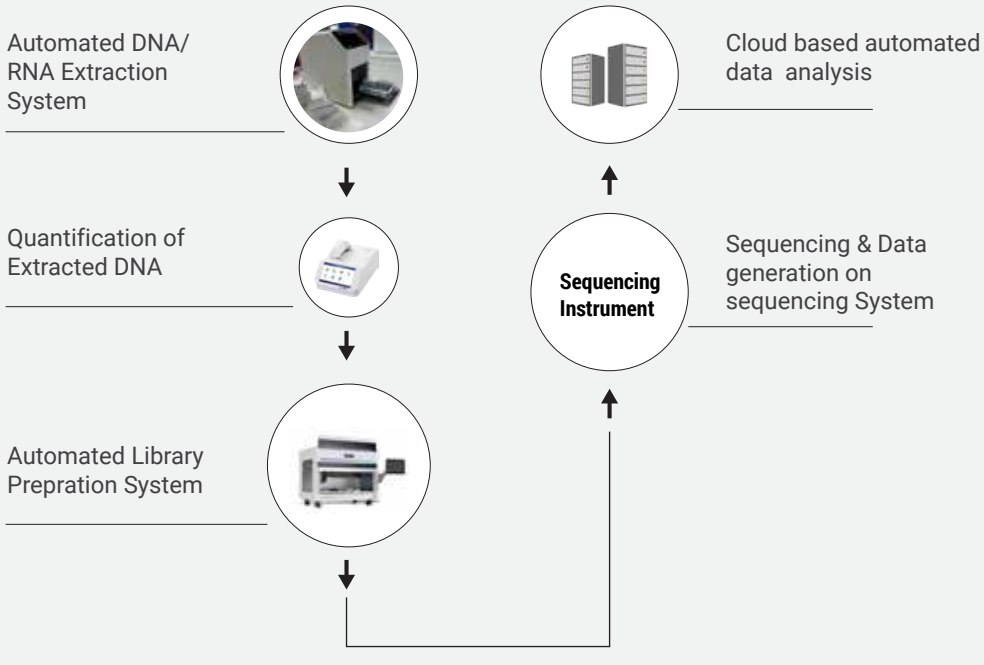
- Based on Hybridization capture target enrichment which helps increase the sensitivity upon sequencing compared to amplicon technique (which increases the chances of PCR bias such as PCR drop-outs).
- G2M HLA Workflow is simplified by reducing the number of reaction steps and hybridization time (with 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



ORDERING INFORMATION	
Commercial Name	**Cat No.**
HLA Typing NGS Panel	G2MHLA32001-ill; G2MHLA32001-MG; G2MHLA32001-TF

- 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 (Cf DNA) from maternal blood sample which is A-tailed, adapter ligated and amplified to get a library that is ready for further sequencing protocols.

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 & 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	~10 Million
NIPT-All Chromosome + Microdeletions and duplications	20-25 Million

Key Highlights of CliSeq NIPT

Panoramic view of the Fetal Genome

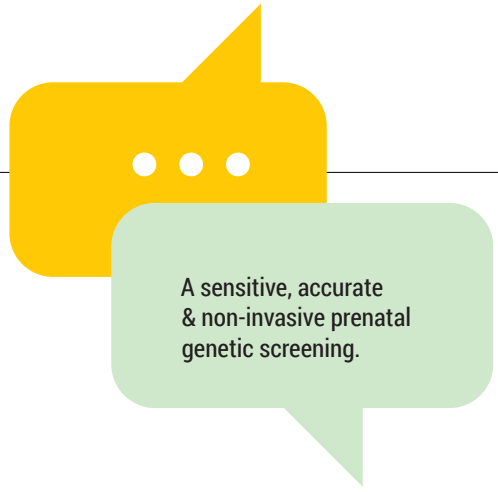
- Screens the entire genome of the fetus covering all 23 pairs of chromosomes
- Detection of 90+ micro-deletions/ duplications

Fastest Test results

- Fast automated workflow
- Assay run time ≤ 4 hours

End-to-end solution

Supported with G2M's automated cfDNA Extractor device - Rapi-X CF, MagNXT cfDNA extraction kit, automated report generation using Cliseq Interpretor software.



LeoNext cfDNA Library Preparation Kit for **NIPT**

with analysis report using
our proprietary Cliseq platform

CliSeq Interpreter

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-X CF
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 for NIPT Sample Report

ORDERING INFORMATION

Commercial Name	Cat No.
LeoNext cfDNA LibraryPrep Kit for NIPT	NGS3105-01 ; NGS3105-02 ; NGS3105-03
RAPi-X CF - Cell free DNA Extraction System for NIPT	G2M910002

Scan me for NIPT Sample Report

genomekundli

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)

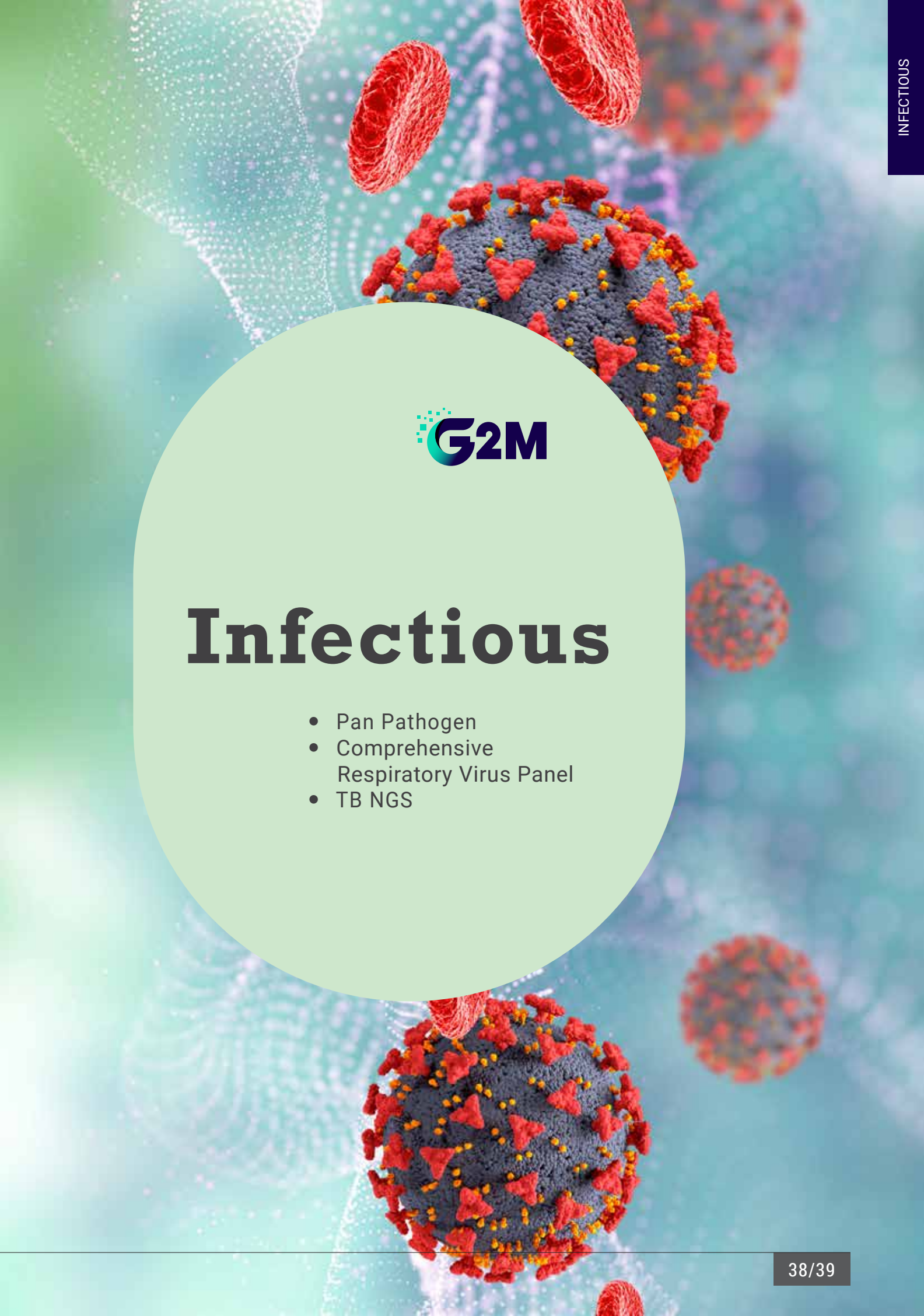
Dry Blood Spots (size 3.2mm, 5 pieces) by heel prick test

PANEL PERFORMANCE

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	97%	97%	95.4%
Precision	95%	95%	94.65%
Reproducibility	98%	98%	97%
Sensitivity	91%	92%	90.50%
On Target Ratio	87-95%	86-95%	85-92%

ORDERING INFORMATION

Commercial Name	Cat No.
Genome Kundli NGS Panel (New Born Screening)	G2MGK29001-ill, G2MGK29001-MG, G2MGK29001-TF



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**: 1 Million reads
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.

ORDERING INFORMATION

Commercial Name	Cat No.
LeoNext PP LibraryPrep Kit for PAN Pathogen	NGS3104-01; NGS3104-02

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**

ORDERING INFORMATION

Commercial Name	Cat No.
Comprehensive Respiratory Virus Panel (CRVP)	G2MCRVP17001-ill; G2MCRVP17001-TF

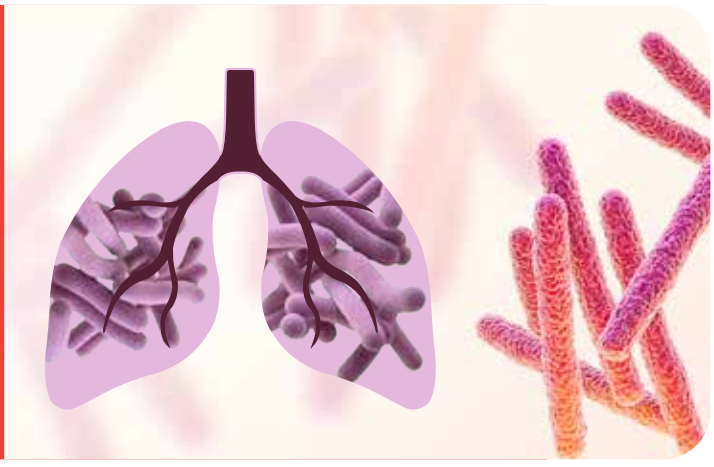
TB NGS Assay

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.

Key Features:

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



Sequencer platforms compatible : Illumina, MGI, Element Biosciences

Methodology : Targeted Gene Sequencing

Drug Resistance Prediction	**1st Line**		• Isoniazid • Rifampicin • Pyrazinamide • Ethambutol
	2nd Line	**Group A**	• Bedaquiline • Linezolid • Moxifloxacin • Levofloxacin
		Group B	• Clofazimine • Cycloserine
		Group C	• Delamanid • Ethionamide • Amikacin • Streptomycin • P-aminosalicyclic acid
		Others	• Pretomanid • Capreomycin • Kanamycin

Workflow

DNA Isolation

Purification of DNA directly from the sample

Library Preparation

Construction of target enriched libraries for sequencer compatibility

Sequencing

Sequencer of your choice
Illumina
MGI
Element Biosciences (AVITI)

Data Analysis

G2M's data analysis platform

CliSeq Interpreter

ORDERING INFORMATION

Commercial Name	Cat No.
TB NGS Panel	G2MBR4-0731 -ill; G2MBR4-0733 -TF; G2MBR4-0735 -MG

Exome Sequencing Assays

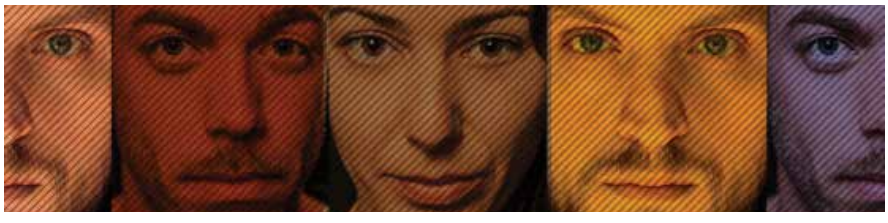
- Whole Exome Sequencing
- Clinical Exome Sequencing

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

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.

Scan for WES Sample Report

PANEL PERFORMANCE

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	96%	96%	95.80%
Precision	94%	94%	95.60%
Reproducibility	97%	97%	95%
Sensitivity	94%	94%	92%
On Target Ratio	85-95 %	85-95%	80-85%

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

ORDERING INFORMATION

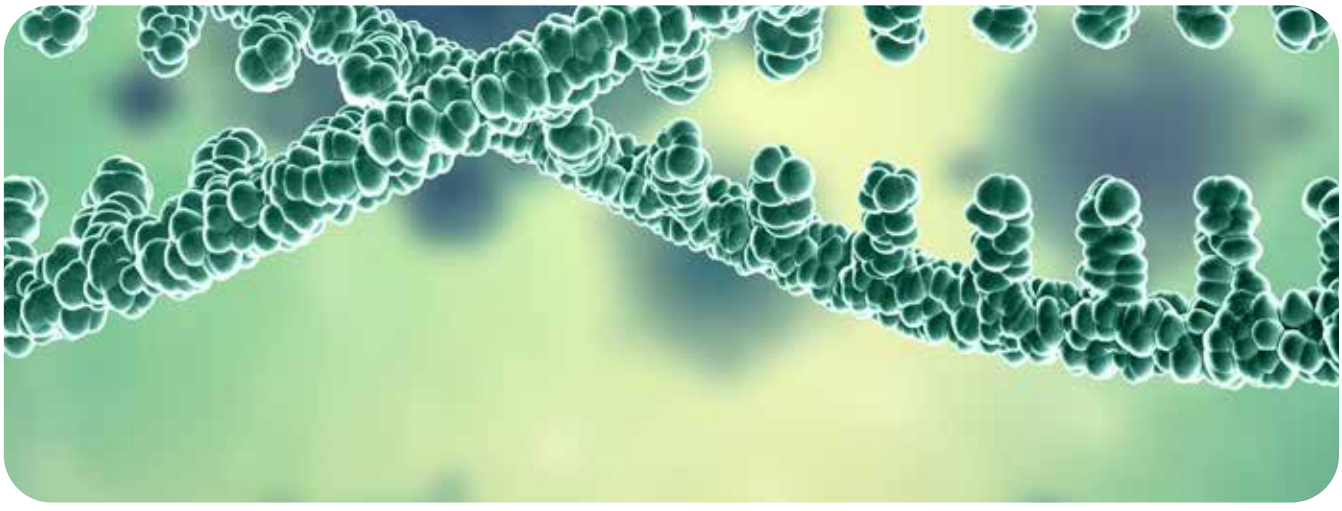
Commercial Name	Cat No.
Clinical Exome Sequencing Expanded Panel (Whole Exome Sequencing)	G2MCES07001(WES)-ill; G2MCES07001(WES)-MG, G2MCES07001(WES)-TF

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	Illumina	MGI	Element (AVITI)
Coverage uniformity	97%	97%	96.5%
Precision	95%	95%	94%
Reproducibility	98%	98%	96%
Sensitivity	95%	95%	96.5%
On Target Ratio	87-95 %	86-95%	79-85%

Cross Platform Performance

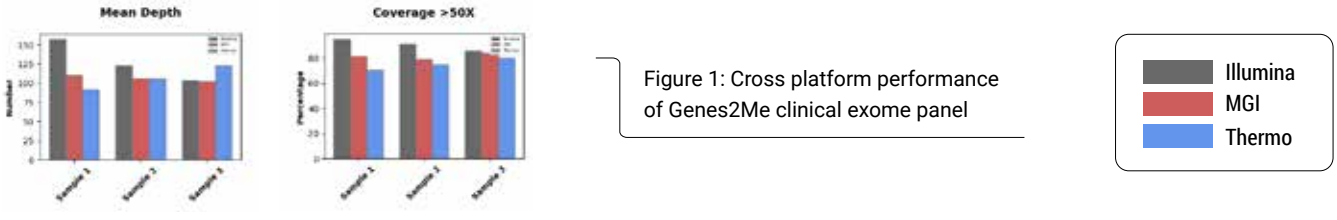


Figure 1: Cross platform performance of Genes2Me clinical exome panel

Scan for CES Gene List

ORDERING INFORMATION

Commercial Name	Cat No.
Clinical Exome Sequencing (CES) Expanded Panel	G2MCES07001-ill; G2MCES07001-MG; G2MCES07001-TF

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

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

Types of Drugs Covered

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

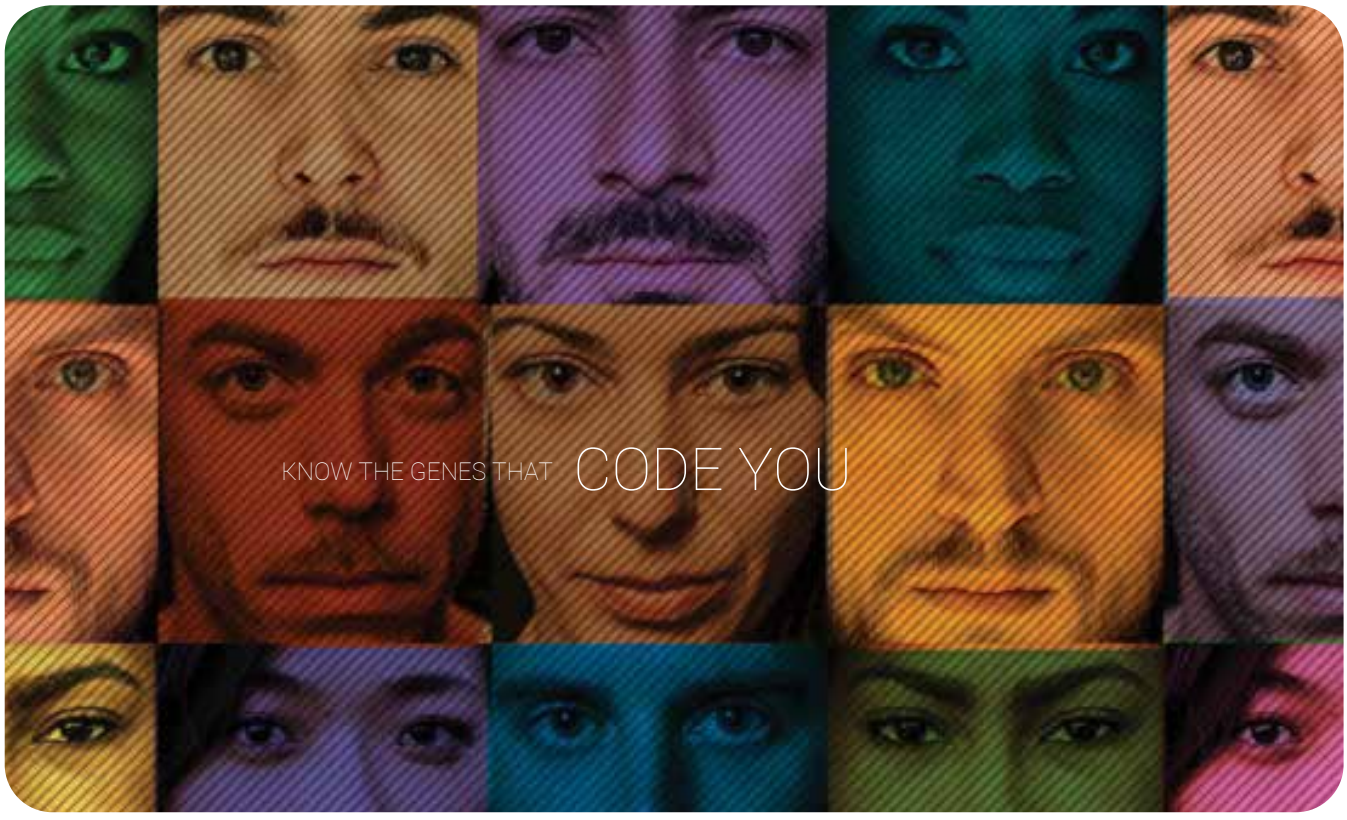
*Limited drug details mentioned

ASSAY PERFORMANCE

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	94%	93%	95%
Precision	98%	98%	96.5%
Reproducibility	98%	98%	95.4%
Sensitivity	>90%	>91%	94%
On Target Ratio	88-95 %	87-95%	85-90%

ORDERING INFORMATION

Commercial Name	Cat No.
Med4Me Standard Panel	G2MMSP08001-ill; G2MMSP08001-TF; G2MMSP08001-MG



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.

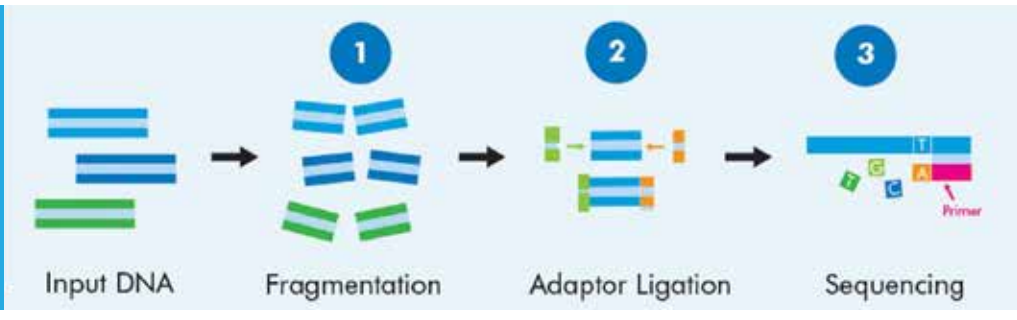
Whole Genome Sequencing Library Preparation

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.

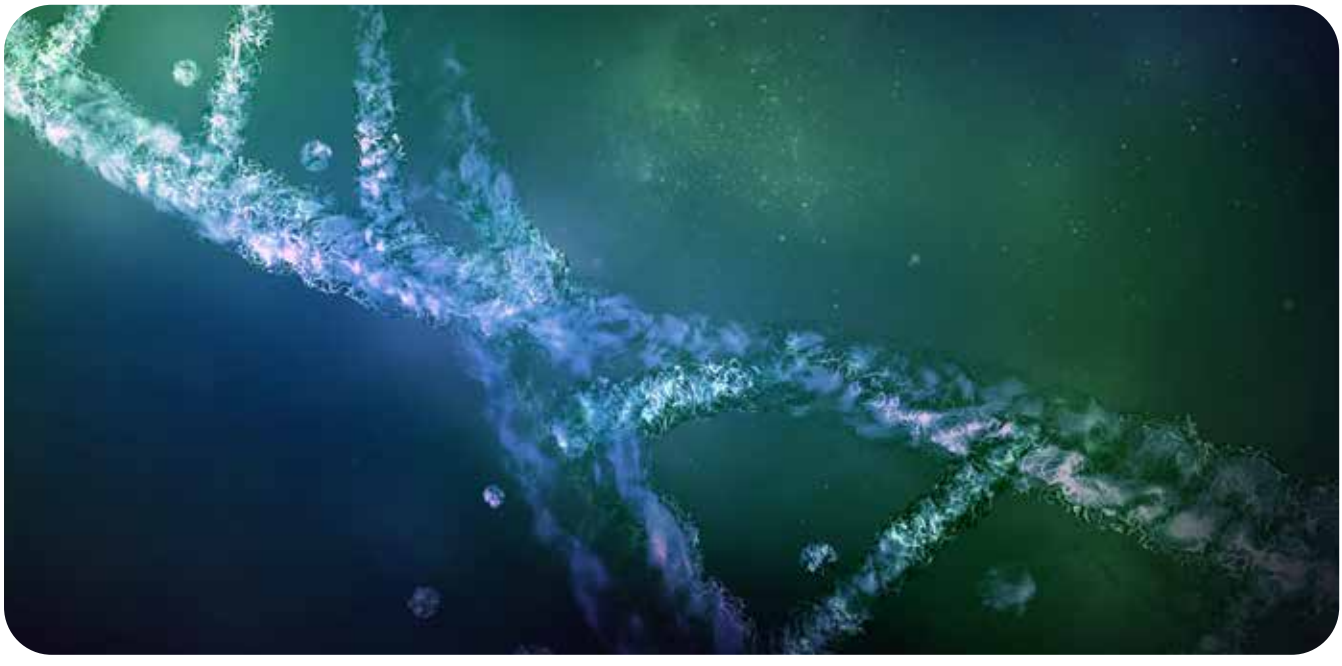
Specifications	
Methodology	• mRNA enrichment (Poly A selection)
Technology	• Next Generation Sequencing
Assay Time	• ~8 hrs
RNA input Quantity	• 1 ug
Sample types	• Blood, saliva, fresh tissue
Biomarker	• Fusion and variants
Instrument compatibility	• Illumina, MGI, Element Biosciences (Aviti)

LE NEXT

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	Illumina	MGI	Element (AVITI)
Coverage uniformity	90%	90%	92%
Precision	94%	95%	93%
Reproducibility	96%	96%	97%
Sensitivity	95%	95%	94%
On Target Ratio	85-95 %	86-95%	78-90%

ORDERING INFORMATION

Commercial Name	Cat No.
Cardiovascular NGS Panel	G2MCV15001-ill; G2MCV15001-TF; G2MCV15001-MG

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

Scan for NEURO Gene List

ASSAY PERFORMANCE

Features	Illumina	MGI	Element (AVITI)
Coverage uniformity	97%	97%	94.5%
Precision	95%	95%	96.3%
Reproducibility	98%	98%	92.5%
Sensitivity	>94%	>95%	96%
On Target Ratio	87-95 %	86-95%	76-89%

ORDERING INFORMATION

Commercial Name	Cat No.
Neuromuscular NGS Panel	G2MNM14001-ill; G2MNM14001-MG; G2MNM14001-TF

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	Illumina	MGI	Element (AVITI)
Coverage uniformity	92%	92%	90%
Precision	95%	94%	91.5%
Reproducibility	97%	96%	98.7%
Sensitivity	>90%	>91%	92%
On Target Ratio	87-95 %	86-95%	85-90%

Scan for APD Gene List

ORDERING INFORMATION

Commercial Name	Cat No.
Alzheimer-Parkinson-Dementia NGS Panel	G2MAPD23001-ill; G2MAPD23001-MG;G2MAPD23001-TF

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.

ORDERING INFORMATION

Commercial Name	Cat No.
EZY AutoPrep Automated NGS Library Preparation Workstation	G2MBR4-0712 48 Prep
EZY AutoPrep Automated NGS Library Preparation Workstation	G2MBR4-0713 96 Prep

Built in Thermal Cycler & Flourometer

(For 96 sample library throughput)

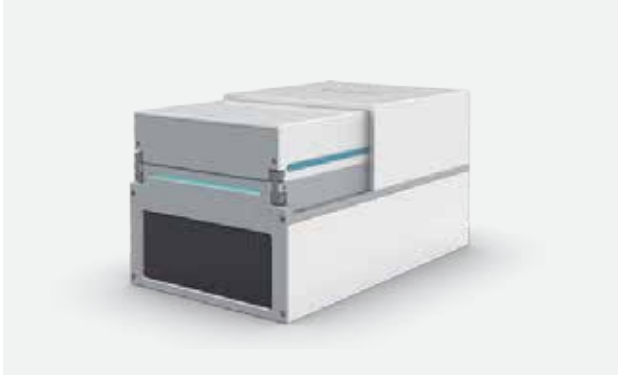
The built-in fluorometer quantitative method is sensitive and highly accurate, making it a reliable dsDNA measurement method

- 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

Specification - EZY Autoprep 96

Model		EZY-AutoPrep 96				
Throughput		1 - 96				
Deck locations		27				
Available well plate		SBS standard 24/96/384 deep and shallow well plates				
Consumable		Matching TIP				
Magnetic plate		96-well annular magnetic plate				
UV sterilization		Equipped with UV sterilization lamp, high-efficiency purification filter device				
Instrument port		USB port, CAN communication				
Ambient condition		Temperature requirement: 20±5°C, humidity: ≤80 %				
Power input		100~240 V, 50~60 Hz, rated power 1200 W				
Dimension (W×D×H)		1420 × 790 × 800 mm				
Pipettor	Pipettor type	24-channel fixed spacing pipettors, can be used as a single channel				
	Pipetting principle	Air displacement pipetting technology				
	Pipetting range	0.5 - 200 µL (20 µL tip: 0.5-20 µL; 50 µL tip: 1-200 µL; 200 µL tip: 2-200 µL)				
	Precision(CV)	0.5 µL: ≤12%	1 µL: ≤5%	20 µL: ≤2%	100 µL: ≤1%	200 µL: ≤1%
	Accuracy	0.5 µL: ±20%	1 µL: ±12%	20 µL: ±2%	100 µL: ±1%	200 µL: ±1%
Gripper		1 Gripper for automated consumable transfer and handling				
Temperature control module		Including 2 temperature control blocks. Temperature control range: 4~105 °C, Temperature control accuracy: ±0.5 °C, Temperature control uniformity: ±0.5 °C				

Specification - EZY Autoprep 24

Model		EZY-AutoPrep				
Throughput		1-24				
Deck locations		12				
Available well plate		SBS standard 24/96/384 deep and shallow well plates				
Consumable		Matching TIP				
Magnetic plate		96-well annular magnetic plate				
UV sterilization		Equipped with UV sterilization lamp, high-efficiency purification filter device				
Instrument port		USB port, CAN communication				
Ambient condition		Temperature requirement: 18~25°C, humidity: ≤80 %				
Power input		100~240 V, 50~60 Hz, power 1000 W				
Dimension (W×D×H)		800×774×775 mm				
Pipettor	Pipettor type	8-channel fixed spacing pipettors, can be used as a single channel				
	Pipetting principle	Air displacement pipetting technology				
	Pipetting range	1-200 µL				
	Precision(CV)	1 µL: ≤5%	2 µL: ≤5%	20 µL: ≤2%	100 µL: ≤1%	200 µL: ≤1%
	Accuracy	1 µL: ±12%	2 µL: ±10%	20 µL: ±2%	100 µL: ±1%	200 µL: ±1%
Temperature control module		The reagent area is equipped with a temperature control module; temperature control range: 0~105°C, temperature accuracy: 0.5°C @ 55°C, temperature uniformity: 0.5°C @ 55°C				

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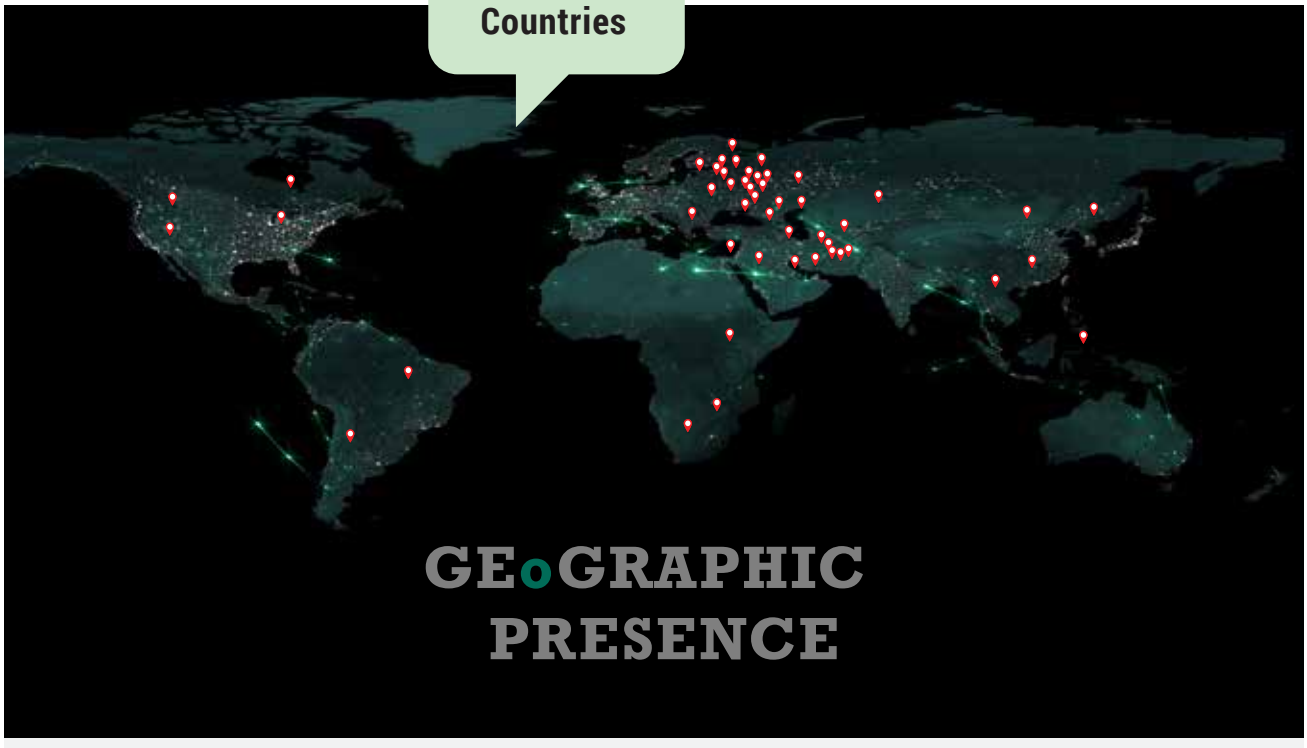

CE IVD | ISO 13485:2016 | ISO 9001:2015 | GMP Quality

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