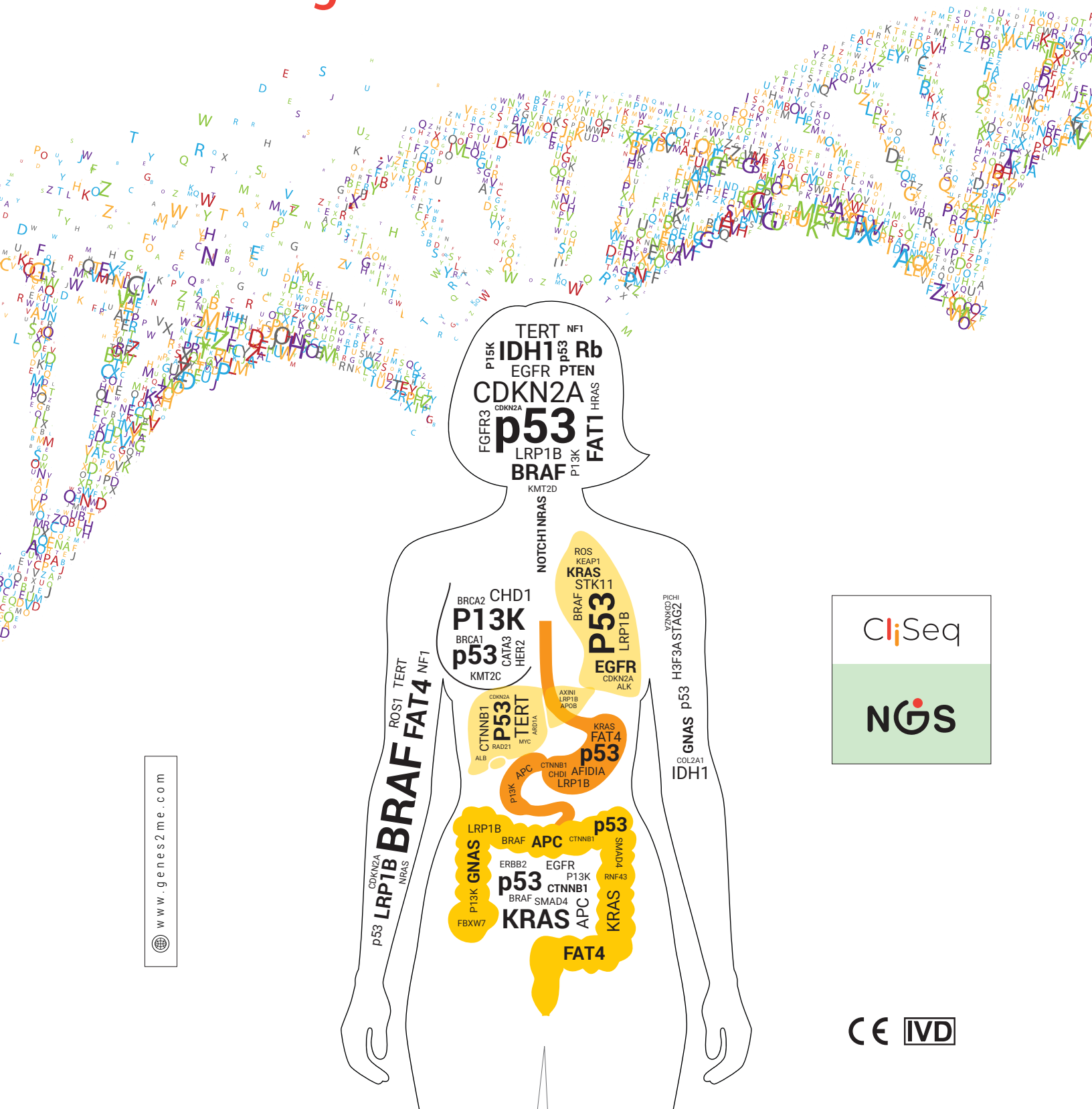
PanCan

G2M

Cancer Genomic Profiling



CliSeq

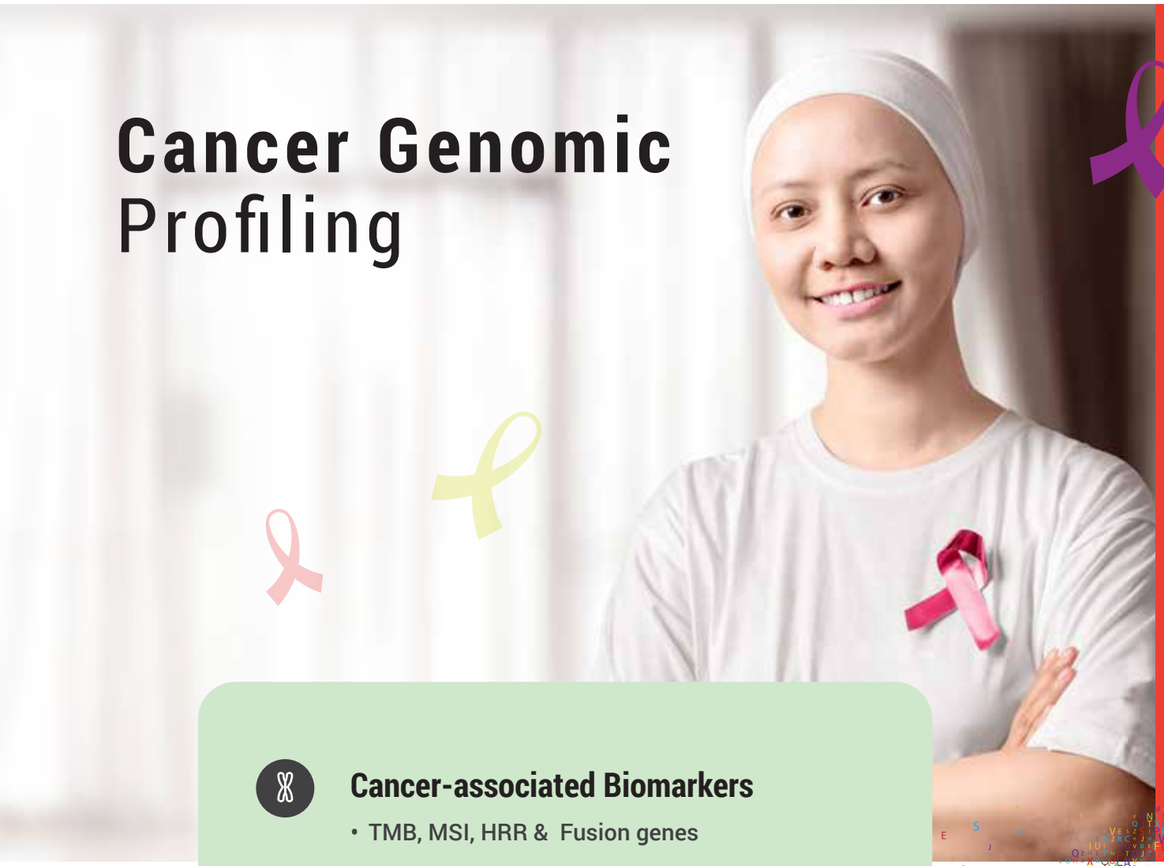
NGS

www.genes2me.com

CE IVD

PanCan | NGS

Cancer Genomic Profiling



Cancer-associated Biomarkers

- TMB, MSI, HRR & Fusion genes

- Uniform Depth Coverage
- Best On-Target Ratio
- Low Bias Base Call
- Less duplication rates
- Short Hybridization time of approx 4 hours
- Rigorously engineered to target hard to capture regions

PAN Cancer Assay

PAN Cancer Assay screens all variant types & immuno-oncology markers (MSI and TMB), which are crucial biomarkers for cancer immunotherapy

Pan Cancer Assay is an NGS Assay aimed to screen a range of cancer causing genes to identify somatic mutations in DNA- from human research samples like FFPE, fresh tissue & plasma targeting genes covering all the coding sequences enriched by Hybridization capture-based target enrichment.

Genes are selected based on ACMG, AMP, NCCN and ASCO guidelines to uncover the coding region to screen a range of cancer types. The genomic DNA from the FFPE, fresh tissue or plasma is considered for library preparation and enrichment that further can be sequenced on NGS sequencer. This Assay detects all variant types and immune-oncology markers (TMB, MSI, HRR) which are crucial for cancer immunotherapy.

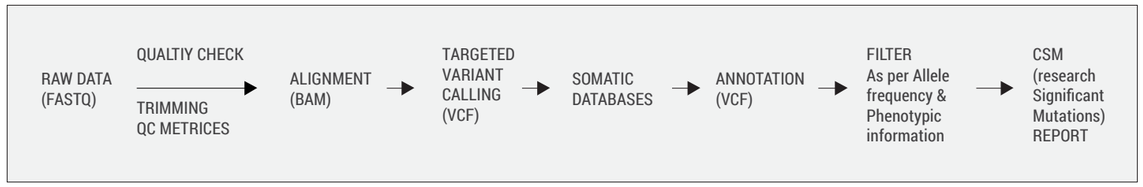
This Assay covers major mutation types like SNVs, Indels, CNV and covers the DNA and fusions as well. Results of the assay are used as an aid in identifying related cancer variants in combination with phenotypic indications.

No. of Genes	version 1 - 681 genes
	version 2 - 1157 genes
Covered region	Whole CDS, Hotspots, Fusion genes
Target size	~1.7 Mb (version 1)
	~2.8 Mb (version 2)
Mutation type	SNV/ InDels/ CNV
Biomarkers	TMB, MSI, HRR Genes
Sample type	FFPE/Fresh Frozen Tissue/Plasma

PROCESS WORKFLOW

Bioinformatics Solution

Data Analysis and Interpretation using Genes 2Me Cliseq Interpreter plaftform

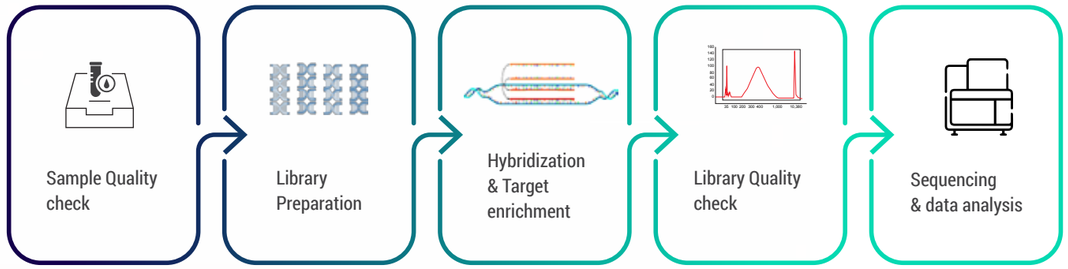


After raw data generation, we follow the GATK best practices framework for identification of variants in the sample, starting with raw data quality check using the FastQC followed by BWA read aligner for mapping/aligning to human reference genome GRCh38. After the alignment, GATK Mutect2 algorithm is used for variant calling. Annotation of the variants is performed using open-source available software SnpEff.

Further relevant mutations are annotated using published variants in literature and set of diseases databases – ClinVar, OMIM, COSMIC and HPO. The 1000Genome, gnomAD, dbSNP databases are used for annotation of variants for their minor allele frequency. The dbNSFP database is used for annotation and functional prediction of all potential non-synonymous variants.

Platform Agnostic

Compatible on multiple platforms (Illumina, Thermo Fisher, Element Biosciences, MGI)



CliSeq Interpreter

Sequencing Data Analysis Software

- Cloud based (CPU) analysis Software
- Global Software Access
- Strong customer Data Security

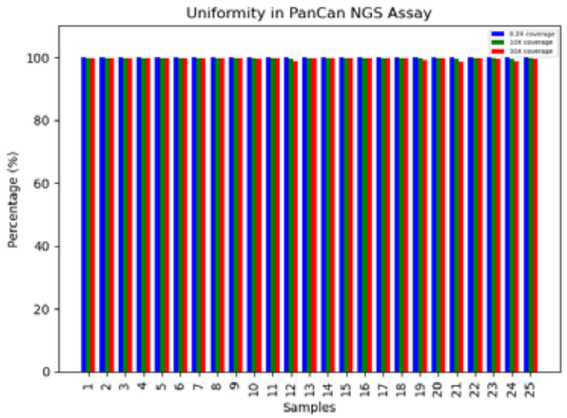
ASSAY PERFORMANCE

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 Assay

Fig-01 - The genomic DNA libraries from FFPE tissues (n=64) were enriched using the G2M Pan-Cancer NGS Assay 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

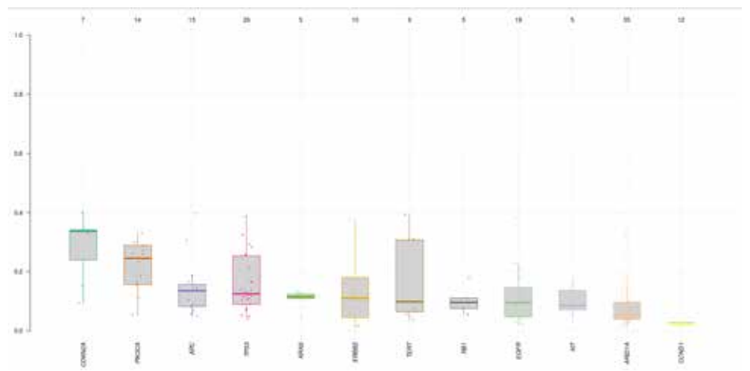


Fig-02 - This VAF plot shows distribution of some of the important genes in 44 PanCancer patient samples. Genes like CDKN2A and PIK3CA display higher median VAFs with greater variability, suggesting a higher mutation burden which may reflect a greater impact on disease progression. In contrast, genes 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

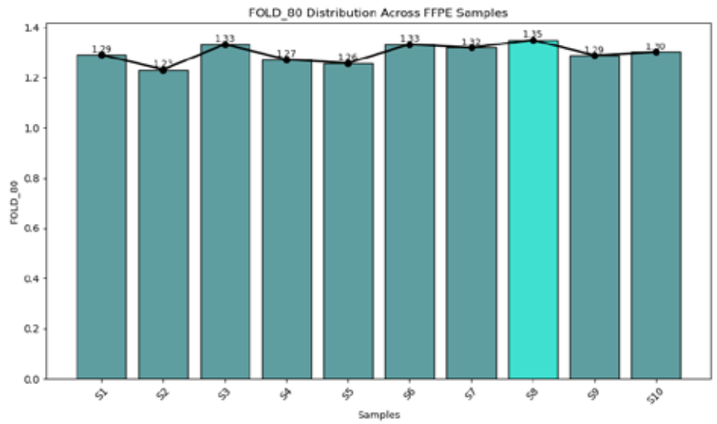


Fig-03 - Fold 80 base penalty across both FFPE (blue bar) and blood-derived (cyan bar) samples. The G2M PanCan CGP Assay demonstrates a fold 80 base penalty below 1.3, reflecting exceptional coverage uniformity across target regions. This low value indicates that only 1.3× the average sequencing depth 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

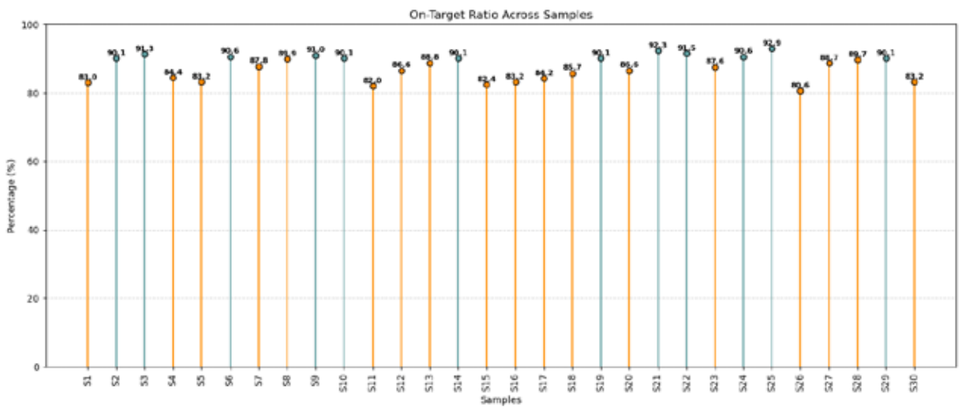


Fig-04 - Across all cancer patient samples, the on-target alignment consistently exceeded 80%, reflecting the Assay's high specificity, optimized assay conditions, and efficient target enrichment. This strong performance underscores the reliability and precision of the sequencing workflow.

TP53 Mutation Landscape in Diverse Cancers

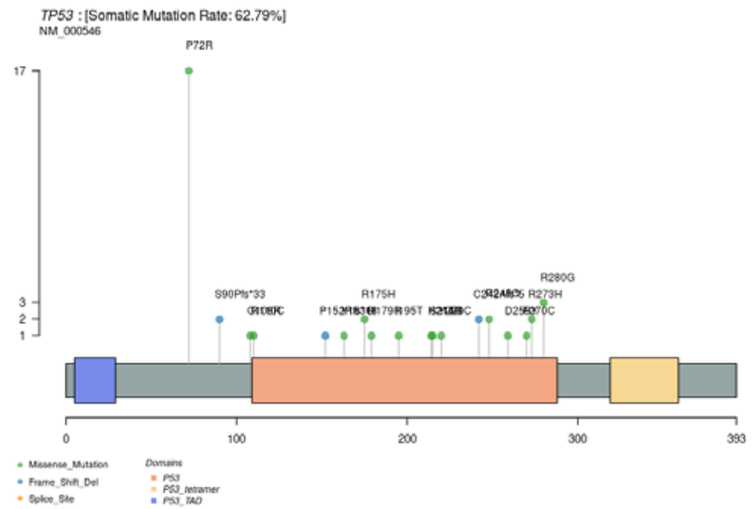


Fig-05 - Lollipop plot illustrating the spectrum and classification of TP53 mutations identified through NGS across a diverse cohort of cancer patients (N=44). The TP53 gene, a critical tumor suppressor, is frequently altered in human cancers through mechanisms such as activating point mutations, gene amplifications, and fusion events. This plot highlights the positional distribution and types of mutations, offering insights into the molecular disruption of TP53 and its potential role in tumorigenesis across multiple cancer types.

Consistent Gene Coverage Across Cancer Samples

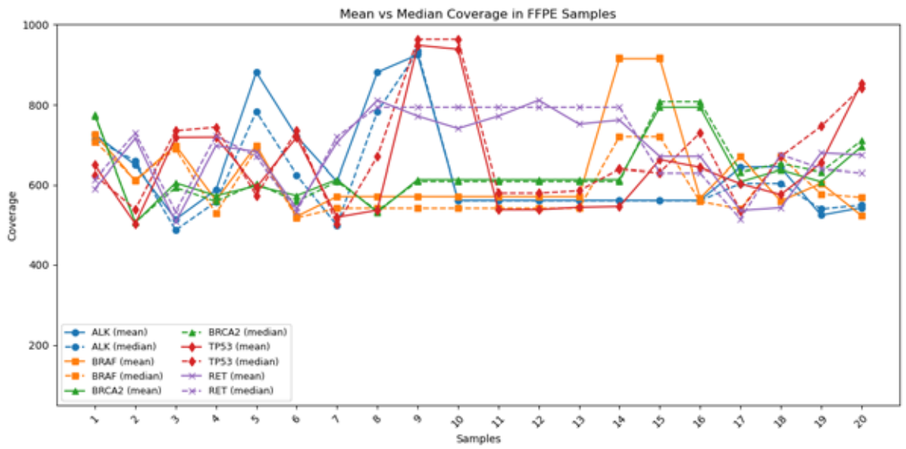


Fig-06 -Coverage of key cancer-associated genes (ALK, BRAF, BRCA2, TP53 and RET) shows strong concordance between mean (average depth) and median (central tendency), indicating minimal bias and uniform sequencing across target regions. Displaying both mean (solid line) and median (dashed line) coverage metrics offers a comprehensive view of sequencing performance. This dual metric approach enhances confidence in data quality, supporting robust variant detection across diverse FFPE samples in research-grade NGS assays.

Gene Involvement Across Cancer Types in the G2M PanCan CGP Assay

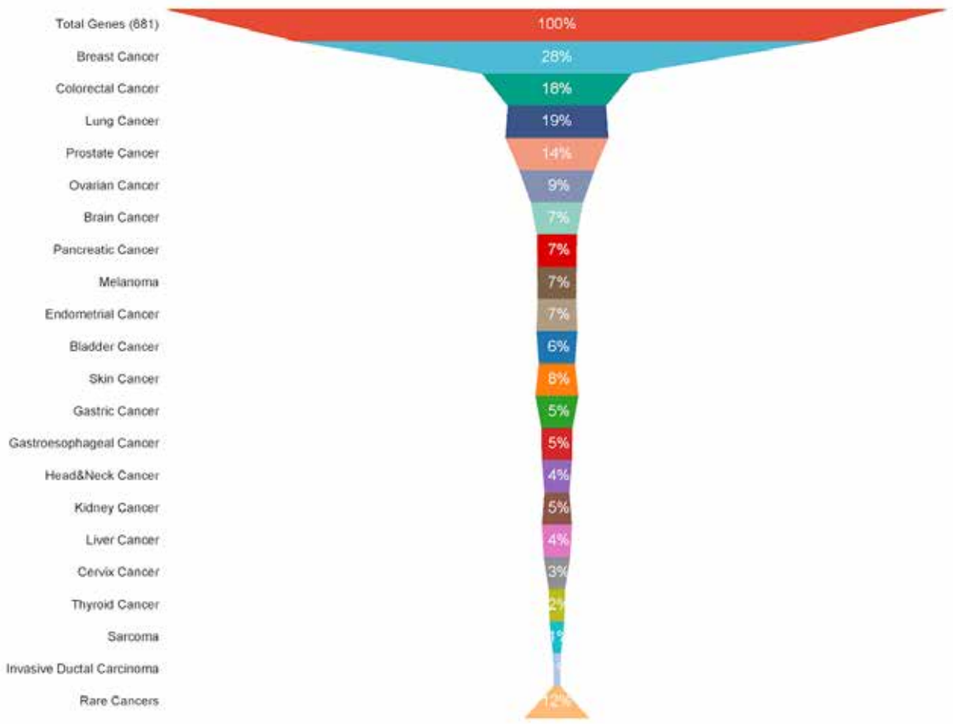


Fig-07 -Distribution of gene involvement across cancer types as profiled by the G2M PanCan CGP NGS Assay. The schematic illustrates the percentage of genes implicated in each cancer type, highlighting the assay's comprehensive coverage and its utility in pan-cancer genomic profiling.

Landscape of Somatic Alterations in Key Cancer-Associated Genes

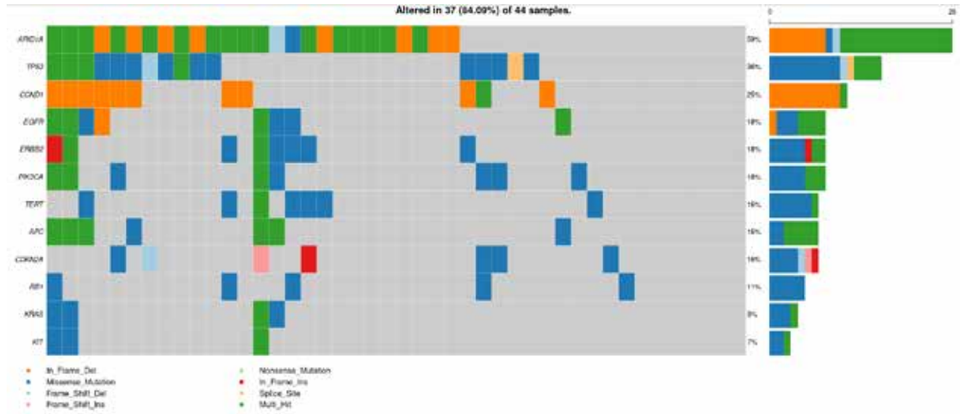
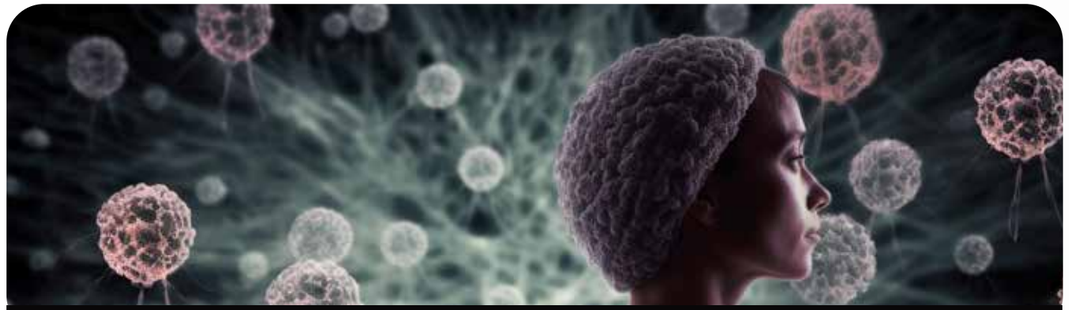


Fig-08 -The OncoPlot presents a concise overview of somatic mutations in the 12 most frequently altered genes within our Pan-Cancer Assay, highlighting mutation patterns across samples with at least one aberration in these key genes. Missense mutations (blue) dominate the landscape, while the green represents multi-hit mutations present in a single gene in all the tested samples and contains all the types of mutations-like missense, in frame shift. The right Assay quantifies the mutation frequency per gene, offering a clear snapshot of their relative contribution to the overall mutational burden.

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



COVERS WIDE RANGE OF CANCERS*

Colorectal Cancer
- →RAS
- →EGFR
- →TGF
- →ATM
- →BRAF
- →CHEK2
- →NRAS
- →PIK3CA
- →PTEN
- →TP53

Breast Cancer
- →BRCA 1
- →BRCA 2
- →PTEN
- →TP53
- →CHEK2
- →BRIP1
- →ATM
- →PALB2
- →PIK3CA
- →PMS2
- →ESR1
- →FGFR1

Ovarian Cancer
- →CHEK2
- →TP53
- →BARD1
- →KRAS
- →RAD51
- →BRIP1
- →PALB2
- →BRAF
- →ERBB2
- →PTEN
- →PIK3CA
- →BRCA1

Bladder Cancer
- →TP53
- →RB1
- →HRAS
- →PIK3CA
- →FGFR3
- →ATM
- →MTOR

Lung Cancer
- →EGFR
- →KRAS
- →ALK
- →RET
- →PIK3CA
- →EGFR
- →KRAS
- →MET
- →PTEN
- →RET
- →BRAF
- →ERBB2
- →ALK

Oesophagus Cancer
- →ERBB2
- →EGFR
- →RB1

Prostate Cancer
- →BRCA 1
- →HOXB13
- →AR
- →ATM
- →MYC
- →PTEN
- →RAF1
- →BRCA2

Pancreatic Cancer
- →BRCA 1
- →BRCA 2
- →EGFR
- →HRAS
- →KRAS
- →PALB2
- →PIK3CA
- →TP53

Thyroid Cancer
- →BRAF
- →RAS
- →RET
- →TP53
- →PTEN

Cervical Cancer
- →DICER1
- →MED1
- →HLA-A
- →PI3K
- →MAPK

Liver Cancer
- →TP53
- →CDKN2A

Gastric Cancer
- →APC
- →MLH1
- →MSH2
- →MSH6
- →EPCAM

**Limited Cancer Gene list presented here*

The Genes2Me Pan Cancer Assay screens broad range of cancer causing genes to identify somatic mutations in the tumor tissue.

It provides comprehensive detail of the cancer and recommendations regarding the FDA approved drugs, helps to decide the best course of treatment.

Scan for PanCan version 1 Gene List

Gene & 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*

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