Blood Cancer Genomic Profiling

Next Generation Sequencing

CE IVD

www.genes2me.com

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

Hemat NGS Panel for Leukemia	No. of Genes	208* (DNA), 94 (RNA fusion genes)
	Target size	0.65 mb
	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	154 (20 DNA fusions)
	Gene count /family	~ 75
	Target size	~ 0.62 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.

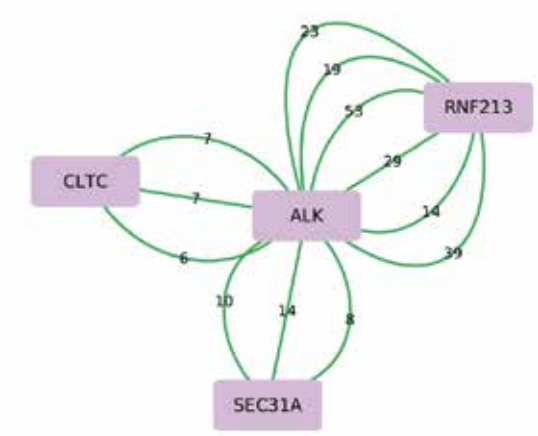

Figure 10

DNA Fusions detected by G2M Lymphoma Assay

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

Insights into Drug Recommendations

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

*Limited Cancer Types and Drug details mentioned

Streamline your NGS workflow

Nucleic Acid Extraction

EZY-AutoPrep

NGS Library Preparation (Manual/Automated)

Sequencing Platform of your choice

Data Analysis

CliSeq Interpreter

Scan for CSM Report

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

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Performance Data

Hemat NGS Assay for Leukemia

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

Scan for Gene List

Lymphoma NGS Panel

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

Scan for Gene List

: The observed values are for Illumina platform

Hemat NGS Assay

Fold 80 distribution across blood cancer samples

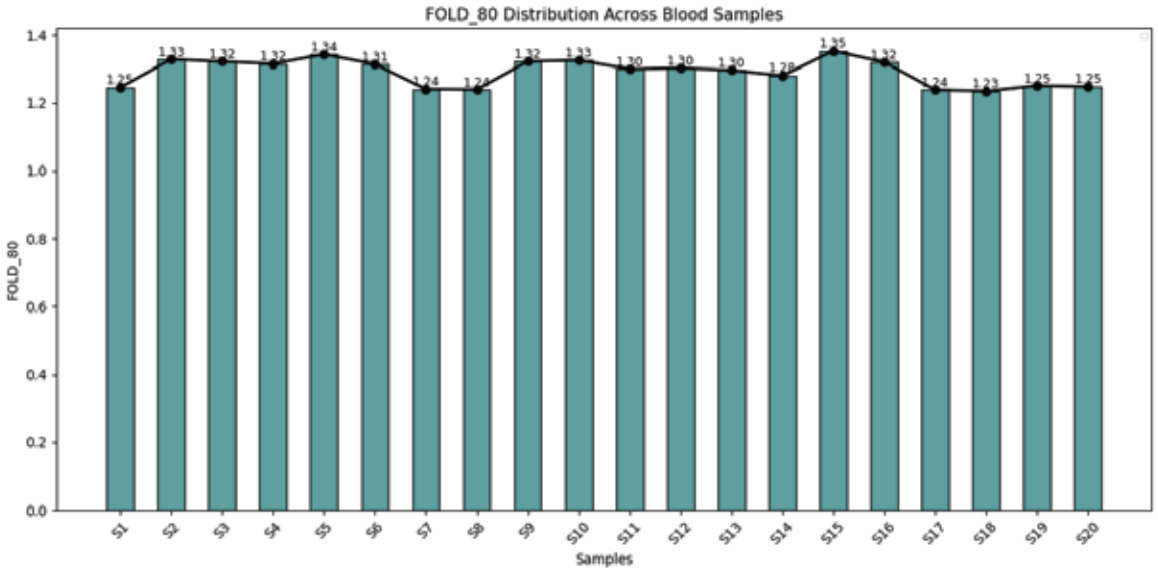

Fig 01 - Fold 80 values for blood samples ranged from 1.23–1.35, showing highly uniform coverage with minimal sequencing bias supporting accurate and dependable variant detection.

Comprehensive Mutation Profiling in Leukemia

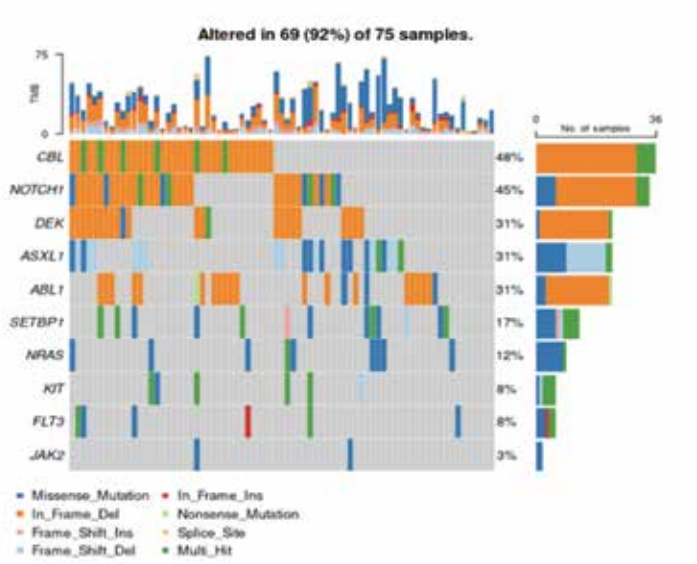

Figure 02: Comprehensive Mutation Profiling in Leukemia - The Oncoplot shows the somatic mutations in the top 10 most frequently mutated genes in the Hemat NGS Panel. This oncoplot illustrates the distribution of all the mutations across the samples containing at least one aberration in the top 10 most frequently mutated genes. Missense mutation was the most prevalent form in almost all the top 10 mutated genes (represented with blue) followed by inframe mutation (represented with orange). The green represents the multi-hit mutations present in a single gene in all the tested samples. It contains all the types of mutations like missense, in frame shift. The right panel displays the percentage of mutations in each gene.

VAF Distribution Across Key Genes in Leukemia

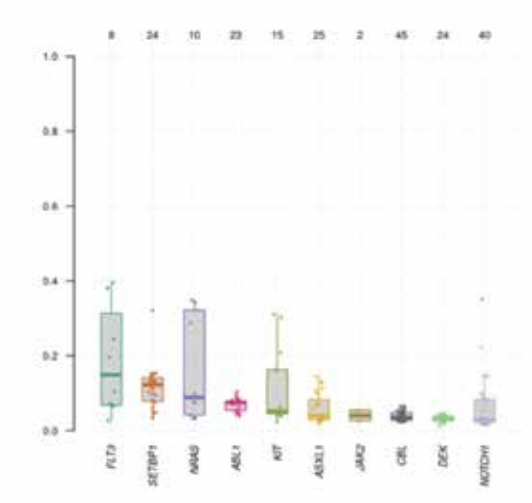

Figure 03: The VAF plot shows distribution of some of the important genes in 75 myeloid patient samples. Genes like FLT3, SETBP1, and NRAS display higher median VAFs with greater variability, suggesting a higher mutation burden which may reflect a greater impact on disease progression. In contrast, genes like JAK2, CBL, and DEK exhibit lower and more consistent VAFs, indicating a smaller or more stable role in the overall genetic profile.

Common fusion partners in G2M Hemat RNA fusion panel

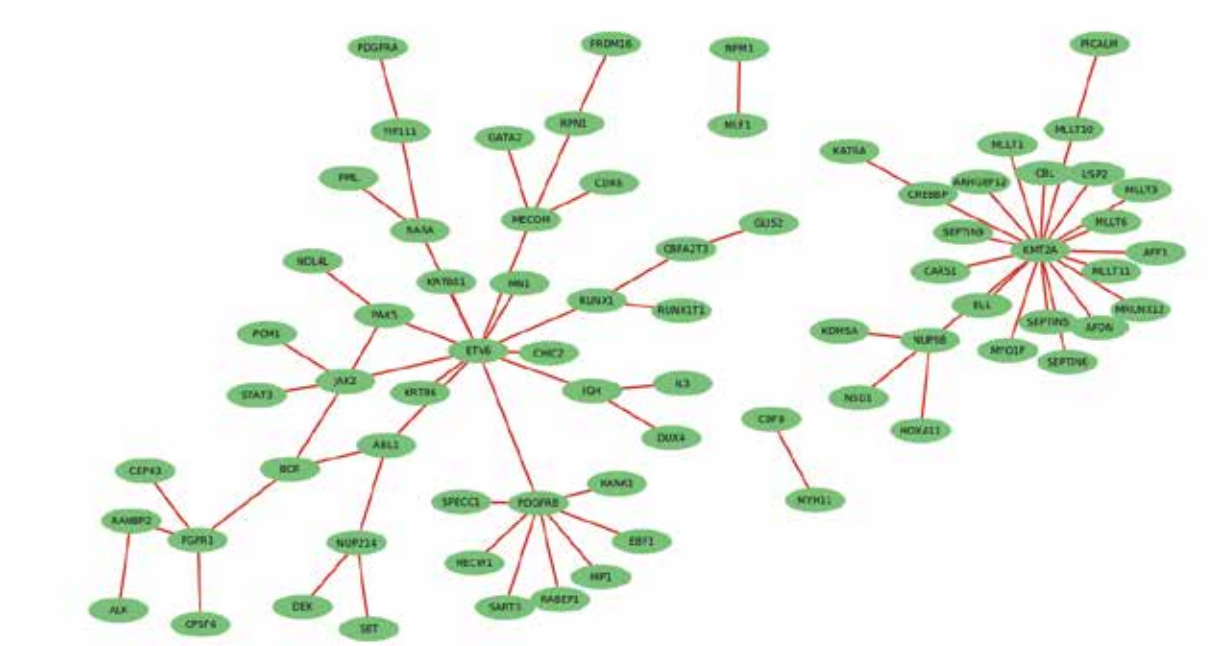

Figure 04

RNA Fusion Detection Power in Leukemia

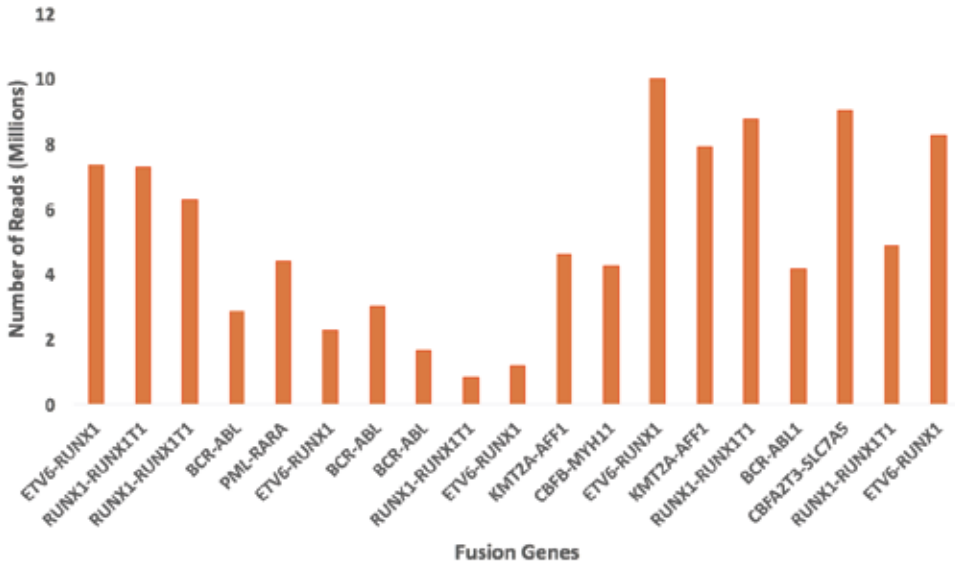

Figure 05: High-resolution profiling of RNA fusion genes in leukemia using our advanced NGS Panel, showcasing detection power across millions of sequencing reads.

Coverage of Key Cancer Genes in Leukemia

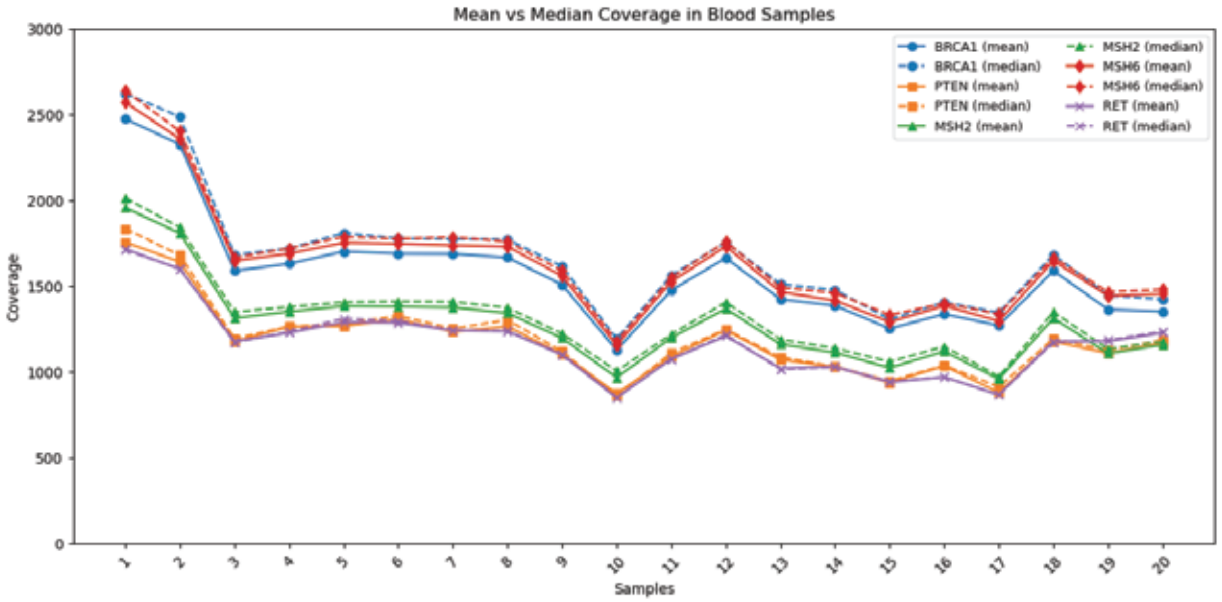

Fig 06-Coverage patterns for key cancer genes (BRCA1, PTEN, MSH2, MSH6, RET) show strong consistency, with mean (solid) and median (dashed) values closely aligned. The consistent coverage demonstrates the workflow's robustness and reliability, ensuring dependable performance for routine clinical testing across blood and diverse sample types.

Marked On-Target Alignment Among Different Cancer Patient Samples

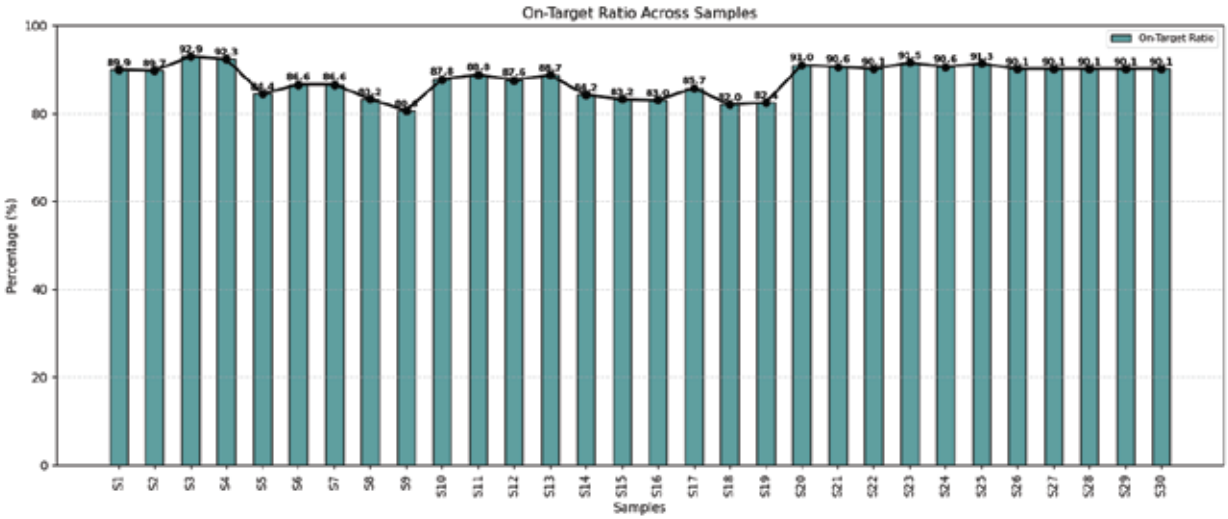

Fig 07-On-target capture efficiency across cancer patient samples. All samples achieved >79% on-target alignment, reflecting the panel's optimized probe design, high hybridization specificity, and robust sequencing performance.

Consistent and High-Fidelity Coverage of Key Cancer Genes

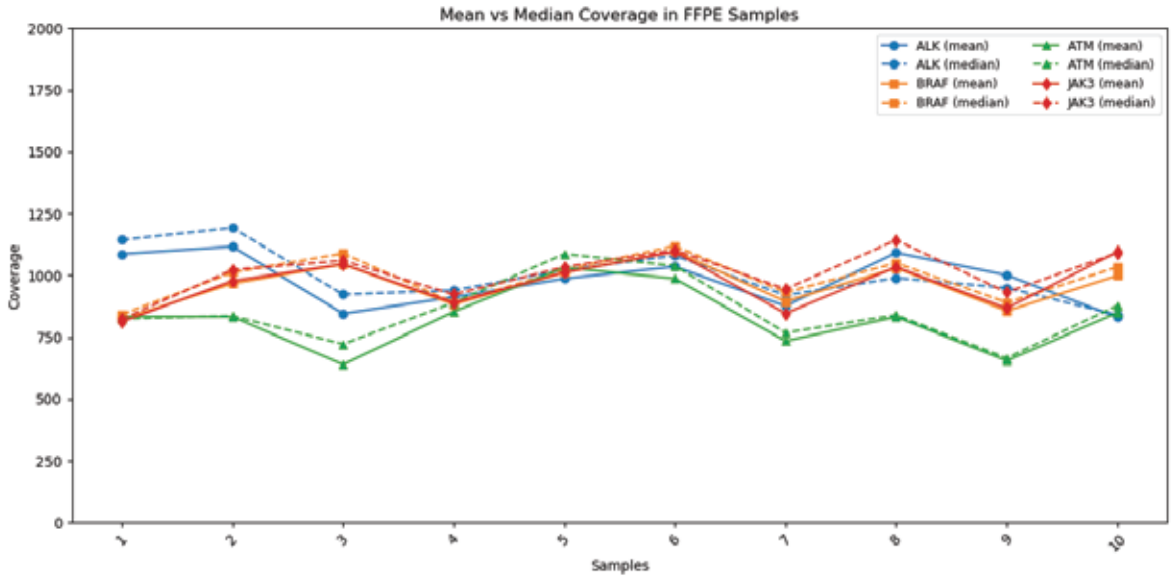

Fig 08-The Lymphoma Assay demonstrates exceptional reliability, with coverage profiles for critical genes such as ALK, BRAF, ATM, and JAK3 showing near-perfect alignment between mean (solid line) and median (dashed line) depth. This tight concordance reflects the assay's uniform performance across all target regions, minimizing bias and ensuring robust, reproducible results. Such consistency is vital for confidently interpreting genomic data across diverse FFPE samples, reinforcing the assay's value in precision oncology.

High On - Target Enrichment for Robust Genomic Profiling

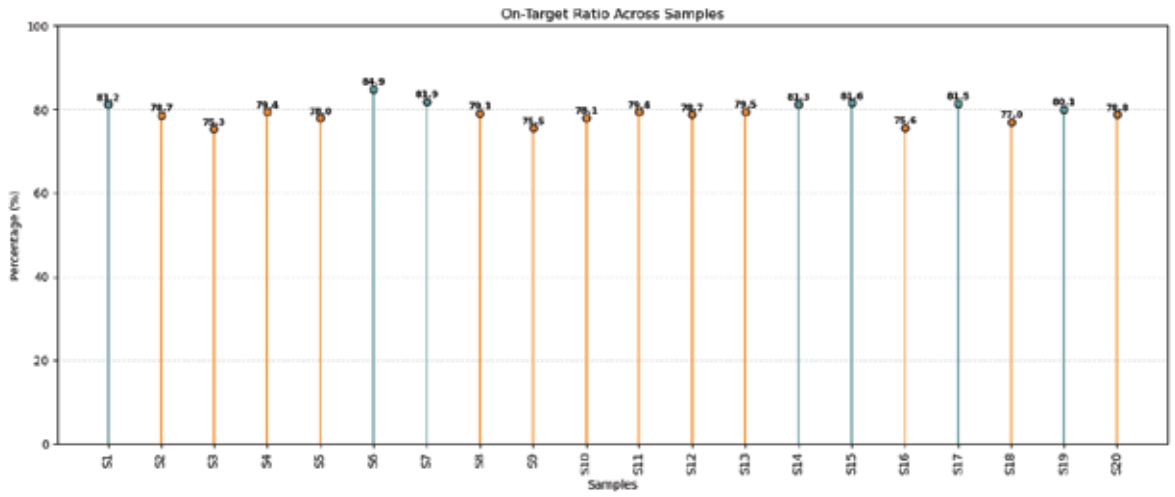

Fig 09-All patient samples demonstrated over 80% on-target alignment reflecting the panel's precision engineered probe architecture and rigorously optimized assay chemistry. This high capture efficiency ensures uniform coverage across target regions, enabling reproducible, high confidence variant detection essential for clinical grade sequencing and scalable diagnostic workflows.