

Blood Cancer Genomic Profiling



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)



Easy to use assay workflows and Automation friendly



Covering Whole Coding Sequences, DNA & RNA Fusions and Hotspots



FDA Approved drug recommendations



Platform Agnostic panels; compatible with the commonly available sequencer platforms (Illumina, Element Biosciences, MGI, Thermo Fisher)



NGS data analysis with GATK workflows for variant analysis giving an access to annotated VCF and a clinically significant mutations (CSM) report



Hybridisation capture based target enrichment with a Hybridisation time of ~ 4 hours

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.

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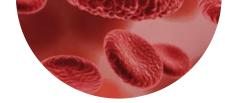
Lymphoma NGS Panel	No. of Genes Gene count /family	95 ~ 75
	Target size	~ 0.54 Mb
	Catalogue No.	G2MBR4-0228-ill, G2MBR4-0202-MG G2MBR4-0230-TF

C<mark>li</mark>Seq Interpretei

Interpret and report relevant variants with Cliseq Interpreter

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%

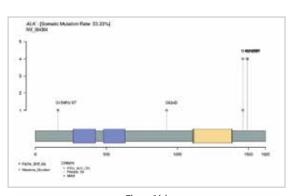
Scan for Gene List



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



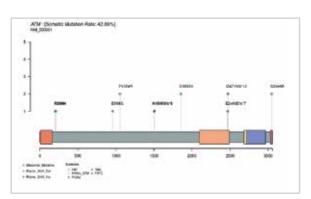


Figure 1(a) Figure 1(b)

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

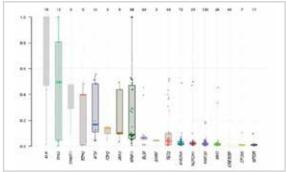


Figure 2

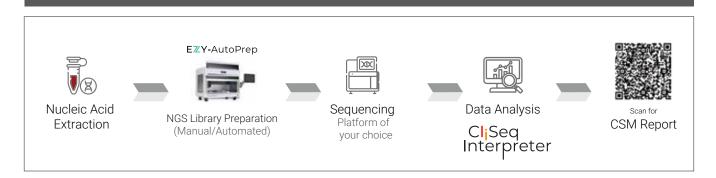
This VAF plot shows some of the important genes of Lymphoma that were detected under median value 5-10% VAF.

Insights into Drug Recommendations

Type of Cancer*	Gene	Drug
	IDH1	Tibsovo (ivosidenib)
Acute Myeloid Leukemia		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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