CE IVD

Myeloid Leukemia
NGS Panel

NGS Clinical Panels

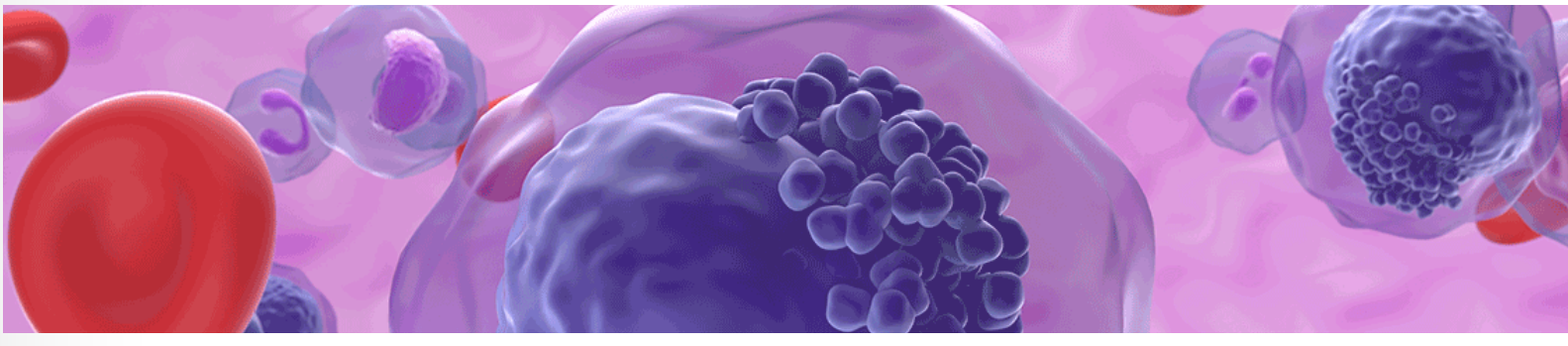
The Genes 2Me Myeloid Leukemia Panel is a hybridization based solution for targeted sequencing employing NGS. With a fast turnaround time this product provides detection of 75 clinically relevant genes spanning a region of 0.28 Mb (whole CDS and hotspots) which covers major somatic mutations (SNVs/ CNVs, InDels/Fusions) linked to Myeloid Leukemia.

Focused Comprehensive Panel: Targets genes reported for causing cancer encapturing ultra-low VAF mutations

Low Input: Process compatible with low input quality compromised samples

Robust and Rapid Workflow: Hybridization enhancer technology and enzyme based library preparation enables quick turn around time.

CliSeq Interpreter: User friendly companion software for automated & cloud based analysis and reporting.



Myeloid Leukemia
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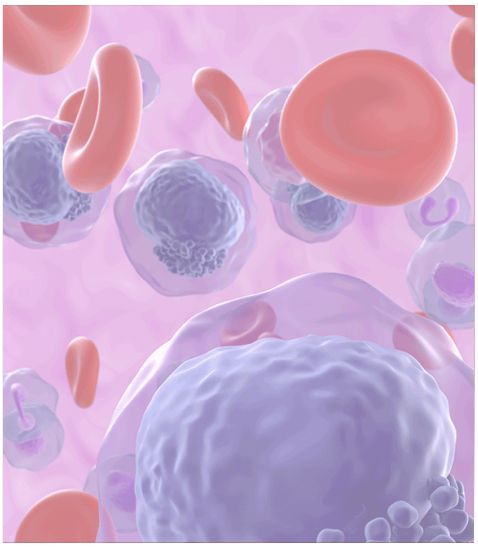


Myeloid Leukemia is a type of blood cancer where functioning of bone marrow is altered due to genetic mutations. This causes the bone marrow to produce abnormal amount of blood cells. Since it is the most common type of leukemia in adults, sequencing of clinically relevant genes to identify significant mutations proves to be an effective method for timely management of the disease.

No. of Genes	75
Gene count /family	~49
Covered region	Whole CDS, Hotspots
Target size	0.28 Mb
Mutation type	SNV/InDels/CNVs/Fusions*
Sample type	Blood, Bone marrow

The Genes 2Me Myeloid Leukemia Panel detects known, novel, and low-frequency genomic alterations. This panel can enhance clinicians decision for prescribing targeted drugs by giving a comprehensive insight on the patient's genomic profile.

Gene List

ABL1	ANKRD26	ASXL1	ATRX	BCOR	BCORL1	BRAF	CALR	CBFB
DNMT3A	EED	ETV6	EZH2	FBXW7	FLT3	GATA1	GATA2	GNAS
LYL1	MPL	MYD88	NF1	NOTCH1	NPM1	NRAS	PDGFRA	PHF6
SMARCB1	SMC1A	SMC3	SRSF2	STAG1	STAG2	STAT3	TERC	TERT
CBL	CBLB	CBLC	CDC23	CDKN2A	CEBPA	CSF3R	CUX1	DAXX
HRAS	IDH1	IDH2	IKZF1	JAK2	JAK3	KAT6A	KDM6A	KIT
PPM1D	PRPF8	PTEN	PTPN11	RAD21	RB1	RUNX1	SAMD9L	SETBP1
TET2	TP53	U2AF1	U2AF2	WT1	ZRSR2	DDX41	DEK	KMT2A
KRAS	SF3B1	SH2B3						

* Gene family / # CNVs

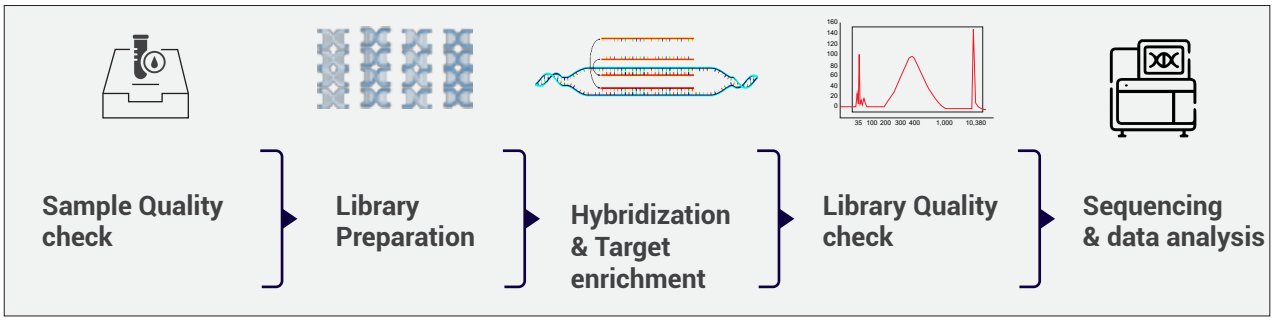
Fusion Genes (DNA & RNA)

ABL1	AML	BCR	CBFA2T3	CBFB	DEK	ETO	ETV6	EVI1
GLIS2	JAK2	KMT2A	MKL1	MLLT10	MYH11	NUP214	PDGFRB	PML
RARA	RBM15	RPN1	RUNX1	RUNX1T1	SET			

Process Workflow

A. Platform Agnostic

Sequencing on multiple platforms (Thermo Ion-Torrent, Illumina, MGI and Element Biosciences)



B. Bioinformatics Solutions

Data Analysis and Interpretation using Genes 2Me Cliseq Interpreter software

RAW DATA (FASTQ) → **QUALTIY CHECK** TRIMMING QC METRICES → **ALIGNMENT** (BAM) → **TARGETED VARIANT CALLING** (VCF) → **SOMATIC DATABASES** → **ANNOTATION** (VCF) → **FILTER** As per Allele frequency & Phenotypic information → **CSM** (Clinical Significant Mutations) **REPORT**

Panel Performance

Features	Illumina	MGI	Thermo Fisher
Coverage uniformity	>96%	>96%	>83%
Precision	>90%	>90%	>90%
Reproducibility	99%	99%	99%
Sensitivity	5% VAF @95%	5% VAF @95%	5% VAF @95%
On Target Ratio	85-95 %	85-95%	76-85%

Specifications

Starting Material (DNA)	Library preparation time	Bioinformatics analysis	Databases used for Annotation
50-500 ng	1.5 days (including Target Capture & Enrichment) for manual process With **G2M Auto EzyPrep automated NGS Library preparation system:** Minimum Hands-on required	Within 24hrs (Raw data to CSM report)	COSMIC, TCGA,ICGC, FusionDB, OncoDB, ClinVar, gnomAD, 1000Genome, dbSNP, FDA

Gene & Drug details

Type of Cancer	Gene	Drug
Acute Myelogenous Leukemia	ALK	Ivosidenib, olutasidenib
Acute Myelogenous Leukemia	ATM	Caffeine
Acute Myelogenous Leukemia	B2M	Doxycycline
Chronic Myeloid Leukemia	BCR-ABL fusion	nilotinib

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Ordering Details

Commercial Name	Cat No.	Pack Size
Myeloid Leukemia NGS Panel	G2MML28001-ill	96T
	G2MML28001-MG	96T
	G2MML28001-TF	96T

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