

Caris ChromoSeq[™]

One Comprehensive Molecular Profiling
Test for Hematologic Malignancies

Seeing the whole genome brings diagnostic clarity

From Initial Diagnosis to Treatment Selection, Myeloid Malignancies Demand Precision-Not Complexity

Myeloid malignancies are among the most genetically complex hematologic cancers, often requiring multiple assays to support accurate risk stratification and treatment decision-making

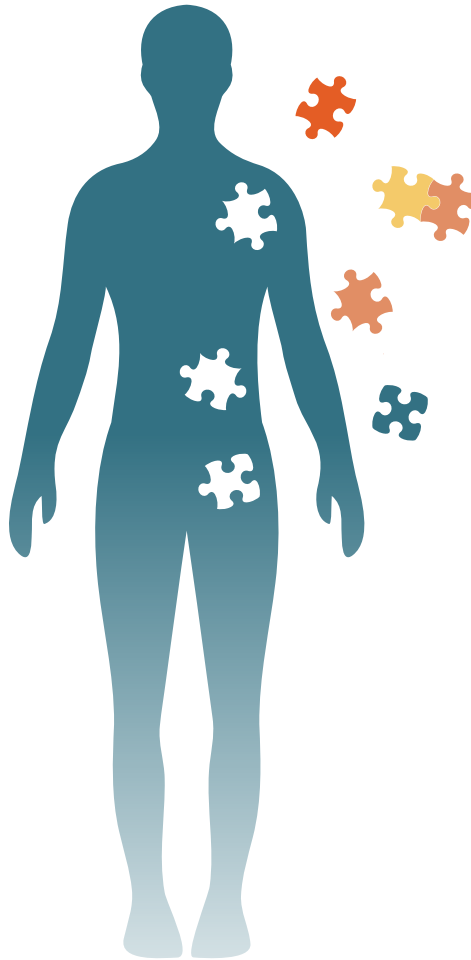


The Current Diagnostic Reality



Clinical Workup of Myeloid Cancers:

- CBC with differential
- Bone marrow aspirate & biopsy
- Morphology
- Flow cytometry
- Clinical context and symptoms



Molecular Profiling is Often Piecemeal

- Conventional cytogenetics (karyotype)
- Multiple FISH probes
- Targeted DNA NGS panels
- PCR-based single-gene tests

These tests:

- Use different methodologies
- Return results at different times
- Require multiple orders
- Can miss complex or actionable genomic events



Clinicians must often piece together fragmented data without the full genomic picture.

One Test Instead of Many

Caris ChromoSeq™ is designed to replace the genetic testing portion of traditional diagnostic workup for myeloid malignancies—complementing your clinical evaluation.

What is Caris ChromoSeq?

Caris ChromoSeq™ is a single, whole genome sequencing assay intended for the comprehensive clinical genomic evaluation of diagnosed cases of acute myeloid leukemia (AML), myelodysplastic syndromes (MDS), myeloproliferative neoplasms (MPN) and patients with suspected myeloid malignancies.



One Comprehensive Assay

- Replace fragmented genetic testing such as cytogenetics, FISH, and targeted panels with a single test



Comprehensive Whole-Genome Insights

- Deeper analysis of the entire cancer genome, ~200x mapped read depth¹ to detect structural variants, copy number alterations, and other mutations
- Average 7-day turnaround time



Diagnostic Clarity for Hematologic Malignancies

- Comprehensive genomic reporting delivers clearer diagnoses and understanding of disease risk

¹. Caris internal data

Seeing the Whole Genome Brings Diagnostic Clarity

Clinical evidence shows how whole-genome sequencing improves diagnosis and risk stratification beyond conventional testing.¹

COMPLETENESS

100%

WGS detected **all genomic features** identified by cytogenetics and FISH.

NEW INSIGHTS

25%

One in four patients in the prospective sequencing cohort had **new genetic findings** not identified by conventional testing.

CLINICAL CONSEQUENCE

50%

Among patients with newly identified findings, **over half were assigned a different risk category.**

How WGS Improves the Experience



vs. Cytogenetics

- Not dependent on live cell culture
- More reliable turnaround
- Genome-wide resolution in a single assay



vs. FISH

- Not constrained by predefined probes
- No need to decide in advance what to look for
- Detects known and unexpected abnormalities



vs. Targeted NGS

- Not limited to a fixed gene list
- Detects mutations, CNAs, and structural variants together
- Captures broader disease biology

One Test. One Report. Diagnostic Clarity

The Caris ChromoSeq™ test results bring together easy to interpret reporting for faster insights:

Caris ChromoSeq™
Somatic Variant Detection

PATIENT

Name: [Redacted]
DOB: [Redacted]
Sex: M
Case Number: [Redacted]
Diagnosis: Acute Myeloid Leukemia (AML)

SPECIMEN INFORMATION

Specimen Type: [Redacted]
Specimen ID: [Redacted]
Specimen Collected: 03/15/2026
Test Report Date: [Redacted]

ORDERED BY

FINAL REPORT

Clinical Interpretation

Risk Category
NCCN AML Risk Category: Poor/Adverse

Comments: Duplications of chromosome 8 and 21 and a deletion of the short arm of chromosome 12 were identified, consistent with a complex karyotype. Mutations in IDH1, ASXL1, EZH2, RUNX1 and ZRSR2 were also detected. Given the patient history and associated clinical data, this case is best classified as AML with myelodysplastic-related gene mutations by International Consensus Classification (ICC) criteria. The overall constellation of mutations is consistent with poor/adverse molecular risk per NCCN guidelines.

Caris ChromoSeq Summary of Findings

Rearrangements are shown by green lines between genomic positions

- Copy Number Gains
- Copy Number Losses

Pathogenic or Likely Pathogenic Alterations

BIOMARKER	PROTEIN CHANGE	DNA CHANGE	VF (%)	INTERPRETATION
ASXL1	G669S	c.1934dupG	45	Pathogenic Variant
IDH1	R132C	c.1747C>T	29	Pathogenic Variant
RUNX1	T926	c.274dupA	54	Pathogenic Variant
EZH2	R583*	c.1747C>T	83	Pathogenic Variant
ZRSR2	c.203+1G>A	c.203+1G>A	87	Pathogenic Variant

Structural Variants

BIOMARKER	ISCN-LIKE	INTERPRETATION
None Detected		

Copy Number Alterations

CHROMOSOME	ISCN-LIKE	INTERPRETATION
chr8	seg[GRCh38] x8	Gain
chr8	seg[GRCh38] dup[8](q24.23q24.3)	Gain
chr21	seg[GRCh38] x21	Gain
chr8	seg[GRCh38] del[8](q24.23q24.23)	Loss
chr12	seg[GRCh38] del[12](p13.31p12.1)	Loss

Results continued >

The selection of any, all, or none of the matched therapies resides solely with the discretion of the treating physician. Decisions on patient care and treatment must be based on the independent medical judgment of the treating physician, taking into consideration all available information concerning the patient's condition, the FDA prescribing information for any therapeutic, and in accordance with the applicable standard of care. Whether or not a particular patient will benefit from a selected therapy is based on many factors and can vary significantly. All trademarks and registered trademarks are the property of their respective owners.

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Text summary of key findings and risk category based on disease

Comprehensive list of important gene mutations, structural variants, and copy number alterations

Circos visualization of genome structure for structural variants, and copy number alterations

Caris ChromoSeq™ | Somatic Variant Detection

PATIENT

Name: [Redacted] DOB: [Redacted] Sex: M
Diagnosis: Acute Myeloid Leukemia (AML)

FINAL REPORT

Results with Therapy Associations

BIOMARKER	RESULT	THERAPY ASSOCIATIONS	BIOMARKER LEVEL*
IDH1	Pathogenic Variant Eon 4 R132C	BENEFIT ivosidenib +/- azacitidine, olutasidenib	Level 2

Biomarker reporting classification: Level 1 - Comparison diagnostic (CD); Level 2 - Strong evidence of clinical significance or is endorsed by standard clinical guidelines; Level 3 - Potential clinical significance. Bolded benefits therapies, if present, highlight the most clinically significant findings.

Cancer-Type Relevant Biomarkers - Alterations Not Detected

VARIANTS NOT DETECTED

BCORL1	BRAF	CAR1	CBR1	CDKN2A	CEBPA	CHK2	CSF3R
DNMT3A	ETN1	ETN2	ETN3	FLT3	GATA1	GFI1B	GAB1
IDH2	KIT	KRAS	MECOM	MPL	MPC	NEF1	NPM1
NRAS	PRM1D	PRPF8	PTPN11	RAD21	RBI1	SAVMD9	SEB1
SMC1A	SMC3	SRSF2	STAT3	STAT5A	STAT5B	SLU212	TET2
TP53	UZAF1	UZAF2	UBA1	WT1			

Genes Tested with Pathogenic or Likely Pathogenic Alterations

Gene Mutations

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ASXL1	G669S	c.1934dupG	45	Pathogenic Variant
EZH2	R583*	c.1747C>T	83	Pathogenic Variant
IDH1	R132C	c.394C>T	29	Pathogenic Variant
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Copy Number Alterations

CHROMOSOME	ISCN-LIKE	INTERPRETATION
chr8	seg[GRCh38] x8	Gain
chr8	seg[GRCh38] dup[8](q24.23q24.3)	Gain
chr21	seg[GRCh38] x21	Gain
chr8	seg[GRCh38] del[8](q24.23q24.23)	Loss
chr12	seg[GRCh38] del[12](p13.31p12.1)	Loss

Genes Tested with Variants of Uncertain Significance

BIOMARKER	PROTEIN CHANGE	DNA CHANGE	VF (%)	INTERPRETATION
ORAI1	-	-	-	Rearrangement of Uncertain Significance

Results continued >

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Biomarker results with therapy associations

Cancer-type relevant biomarkers where no alterations were detected

Genes with pathogenic or likely pathogenic (PLP) alterations and variants of uncertain significance (VUS)

Genes with indeterminate results

Prospective Clinical Evidence Supporting Whole Genome Sequencing as a Single Assay Replacement in AML Management

Study Overview



255 confirmed AML patients

Patients received SOC cytogenetics and molecular results + Whole Genome Sequencing for comparison

Study Findings

Superior Detection of Hidden Abnormalities

WGS identified structural abnormalities in 47% of patients deemed cytogenetically normal AML¹

WGS identified commonly missed alterations, partial tandem duplications were discovered in KMT2A in 34 pts

Traditional Diagnostic Standards Matched

Dx-only WGS detected 93% of the prognostic and predictive genomic features reported by traditional clinical testing.¹

Refinement of Patient Risk

11 patients had their risk reclassified due to new genetic information

3 patients downgraded to "favorable risk"¹

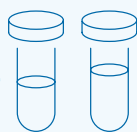
Conclusion: WGS can provide novel insights into AML disease biology, prognostication, and potential therapeutic **options**¹

¹. <https://ashpublications.org/blood/article/146/Supplement%201/455/555657/The-MEASURE-Genome-Atlas-Acute-Myeloid-Leukemia-at>



Order Caris ChromoSeq

- paper
- portal



Submit Specimen

- 2mL Bone marrow aspirate or whole blood



7-10 Day Turn-Around Time



Receive One Molecular Profiling Report

Now Covered By Medicare



Caris ChromoSeq™ is a covered benefit for Medicare beneficiaries, including Medicare and Medicare Advantage Plans.

Making the Billing Process Easier for Patients.

At Caris, we believe that cancer diagnostic testing should be accessible to everyone. We know that understanding healthcare costs can be complicated, our team is ready to support with any insurance or billing questions.

Myeloid malignancies are complex. Genetic testing shouldn't be. Get the complete molecular picture with Caris ChromoSeq.

Contact Caris

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Testing Provided by Caris Life Sciences.

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