PredicineHEME™

CLIA Validated NGS Assay for Hematologic Malignancies

Predicine

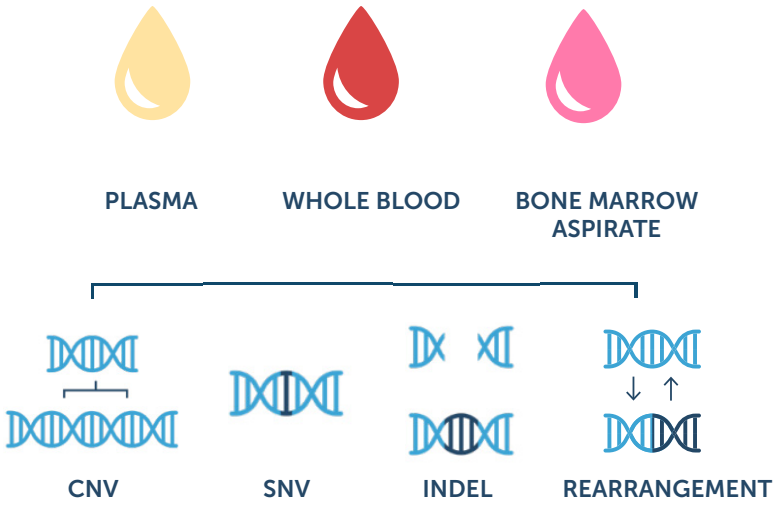
A highly sensitive heme cancer NGS assay designed for treatment selection, disease monitoring, and drug resistance detection

259

Key cancer genes interrogated

20,000x

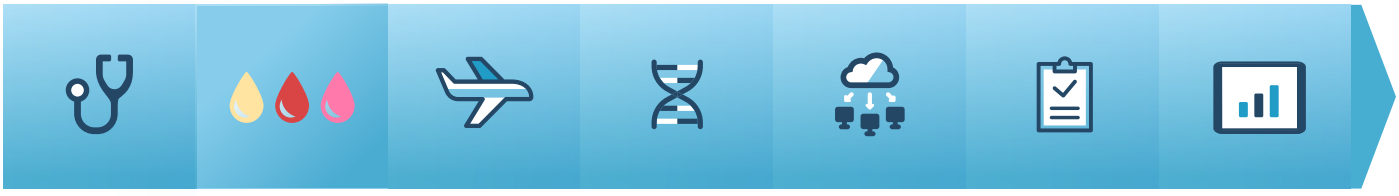
Sequencing Depth (Liquid Biopsy)



Methods and Reporting

- Detects single nucleotide variants (SNVs), insertions and/or deletions (Indels), copy number variations (CNVs), and DNA rearrangements
- Detects critical biomarkers in Multiple Myeloma (MM), Chronic lymphocytic leukemia (CLL), Diffuse large B-cell lymphoma (DLBCL), Mantle cell lymphoma (MCL), Acute Myeloid Leukemia (AML), and Acute Lymphoblastic Leukemia (ALL)
- Multiple sample types acceptable for testing, including whole blood, plasma, and bone marrow aspirate
- Comprehensive tumor profiling integrated with PredicineSCORE low-pass whole genome sequencing; no additional samples needed

Workflow



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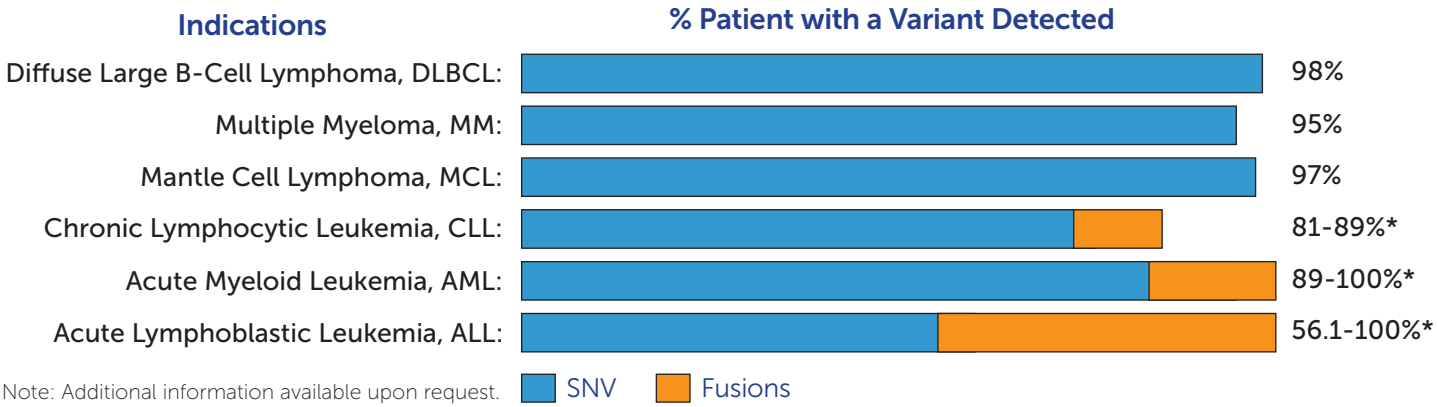
Comprehensive Gene Coverage Across Hematologic Malignancies

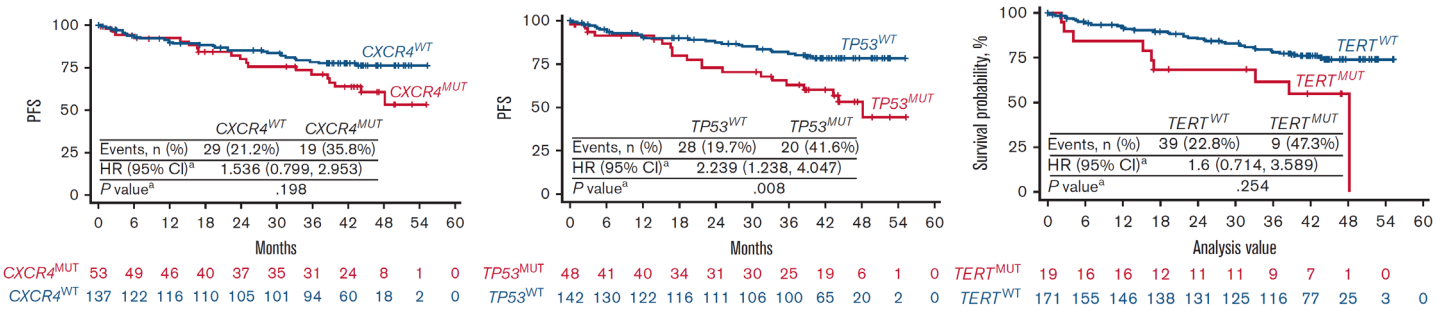


Note: Additional information available upon request.

Performance Specifications

Feature	Plasma
Detection Sensitivity	SNVs/ Indels: 0.3% AF, reportable range≥ 0.05%
Turnaround Time (TAT)	6 days
Specimen Type and Requirement (CLIA)	20 mL blood 0.2-0.4 mL bone marrow aspirate
Specimen Type and Requirement (RUO)	2-5 mL plasma 4-10 mL blood 0.2-0.4 mL bone marrow aspirate, PBMC, buffy coat, frozen blood
Target Sequence Coverage	20,000x
Regions Analyzed	259 genes
Sequencing	Illumina NGS
Clinical Validation	CLIA/CAP-accredited workflows

Case Study:
Biomarkers associated with outcomes in Waldenström Macroglobulinemia (WM)



Tam CS. et al. Blood Adv. 2024 Apr 9;8(7):1639-1650.

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