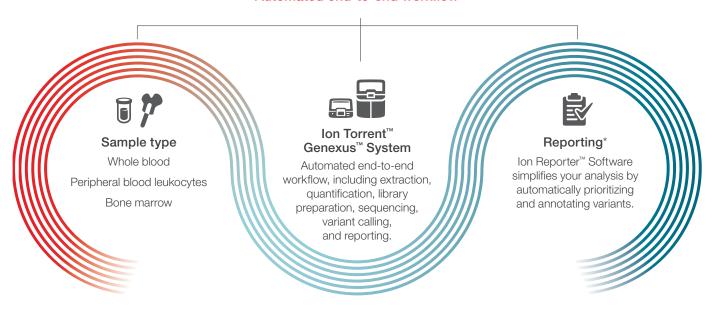
Oncomine Myeloid Assay GX v2

More rapid. More automated. More complete myeloid genomic profiling.

Automated end-to-end workflow



Simultaneously study DNA mutations and RNA fusion transcripts covering the major myeloid disorders: AML, MPN, MDS, CMML, and JMML

DNA					RNA				
Hotspot genes (28)			Full genes (17)		Fusion driver genes (34)			Expression genes (5)	Expression control genes (5)
ANKRD26 ABL1 BRAF CBL CSF3R DDX41 DNMT3A FLT3 (ITD, TKD) GATA2 HRAS	IDH1 IDH2 JAK2 KIT KRAS MPL MYD88 NPM1 NRAS	PPM1D PTPN11 SMC1A SMC3 SETBP1 SF3B1 SRSF2 U2AF1 WT1	ASXL1 BCOR CALR CEBPA ETV6 EZH2 IKZF1 NF1 PHF6 PRPF8	RB1 RUINX1 SH2B3 STAG2 TET2 TP53 ZRSR2	ABL1 ABL2 BCL2 BRAF CCND1 CREBBP EGFR ETV6 FGFR1 FGFR2 FUS	HMGA2 JAK2 KAT6A (MOZ) KAT6B KMT2A (includes PTD) MECOM MET MILLT10 MRTFA (MKL1) MYBL1 MYH11 NTRK2 NTRK3	NUP98 NUP214 PAX5 PDGFRA PDGFRB RARA RUNX1 TCF3 TFE3 ZNF384	BAALC MECOM MYC SMC1A WT1	EIF2B1 FBXW2 PSMB2 PUM1 TRIM27

*Reporting tools include Oncomine Reporter, the laboratory's own software, or other third-party software.

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Key features include:



Rapid turnaround

Results in about 1 day to help provide answers fast



Fast and simple workflow

Comprehensive panel of biomarkers



Highly automated

Approximately 20 minutes of hands-on time; minimal user intervention



Integrated reporting

Fully annotated variant report



Ability to detect a range of targets

SNVs, indels, tandem duplications, fusions



Flexible batching

Sequence 1-8 samples at once

