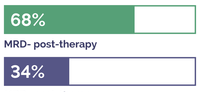
A Sysmex Group Company

The potential of NGS for MRD detection in AML

Next-generation sequencing (NGS) evaluation of measurable residual disease (MRD) has been applied in multiple ways in a clinical research settings, including assessing the scale of remission and identifying risk of relapse post-treatment.[1]

A recent meta-analysis documented the prognostic relevance of MRD in acute myeloid leukemia (AML), highlighting the difference in the 5-year survival rate of patients achieving MRD negativity post-therapy compared to those without (68% vs. 34%).[1,2]

5-year survival rate



MRD- post-therapy

MRD+ post-therapy

MRD detection is standardized and validated for certain methodologies in AML but this does not currently include NGS evaluation. However, many ongoing research studies and initiatives, such as the **FNIH Biomarkers Consortium – MRD in AML project**, are working to change this. Current work is helping to establish MRD as a surrogate endpoint in AML clinical trials to complement existing techniques, such as PCR and flow-based approaches, just as we have seen for MRD utilization in multiple myeloma.[3]

Why choose an NGS approach for MRD?

1 NGS workflows offer a convenient approach for users to incorporate a **range of existing biomarkers** into a **highly sensitive** single workflow on a **large cohort scale**

2 By streamlining multiple assays into a singular workflow you can **increase your operational efficiency**, freeing up your resources

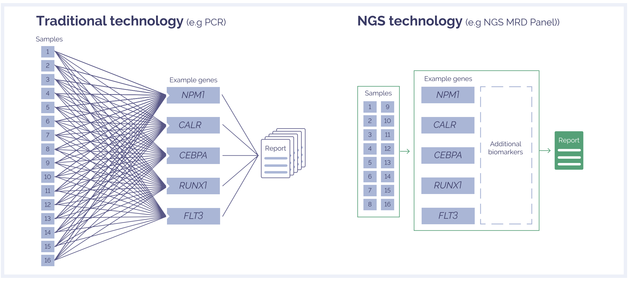


Figure 1. Consolidate existing biomarkers into a single workflow. Traditional technology (left) may be reliant on workflows where the technique is applied to every sample for every biomarker under evaluation. NGS technology (right) allows multiple biomarkers (including additional biomarkers of interest for research purposes) to be ran as a single workflow for multiple samples simultaneously.

SureSeq

Unlock ultra-low variant detection for a deeper understanding of your AML samples

Key benefits of the SureSeq™ Myeloid MRD panel

1. Clearer genetic profiles of your sample

Interrogate an expansive range of biomarkers, such as large *FLT3*-ITDs, detected at ultra low frequencies in a single assay

	Variant	Expected frequency: 0.04%		Expected frequency: 0.05%		Negative control	
Gene	**HGVSc**	**Read depth**	**Observed VAF (%)**	**Read depth**	**Observed VAF (%)**	**Read depth**	**Observed VAF (%)**
FLT3	ITD300	13119	0.05	12208	0.04	21686	0

Gene	HGVSc	Length	Position (hg38)	Read depth	Observed VAF (%)
FLT3	NM_004119.3:c.1770_1793ins	24	chr13:28034125	11340	0.81
FLT3	NM_004119.3:c.1804_1805ins	57	chr13:28034114	11844	0.71
FLT3	NM_004119.3:c.1814_1815ins	21	chr13:28034104	23831	0.03

Table 1: *FLT3*-ITDs are challenging to target and subsequently detect due to their inherent repeat content and length. Data generated using the SureSeq Myeloid MRD Panel in combination with the OGT's Universal NGS Workflow Solution V2 and OGT's Interpret NGS Analysis Software highlights the detection of a 300 bp *FLT3*-ITD as well as 3 examples of *FLT3*-ITD detection in orthogonally validated research samples.

2. Identify AML genomic evolution

Simultaneously track multiple variants within samples across timepoints

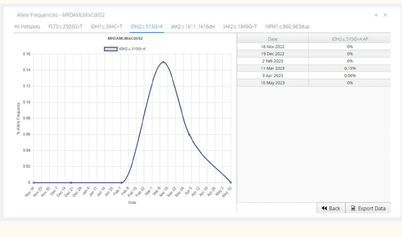


Figure 2: OGT's complimentary NGS data analysis software, Interpret, provides an 'out of the box' bioinformatic analysis pipeline as standard for MRD, including the ability to visualize a wide range of somatic variants including structural aberrations.

3. Sensitive detection of rare leukaemic clones

Discover more variants with ultra-low detection down to a possible 0.01% VAF

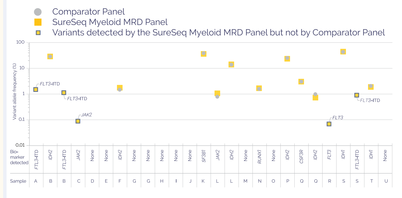


Figure 3. In a cohort of 22 AML clinical research samples OGT's SureSeq Myeloid MRD Panel (yellow) displayed 100% concordance with known variants from a comparator panel (grey) and additionally identified 5 previously undetected clinically-relevant variants.

Enhance your MRD detection capabilities with SureSeq

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References

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