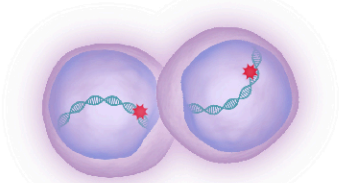
Next Generation Sequencing technology to assess risk-stratification of acute myeloid leukemia



Leukemic cells

Cytogenetic aberrations
- Hotspot mutations
- Small insertions
- Deletions
- Point mutations

Genes involved
- *NPM1*
- *TP53*
- *RUNX1*
- *ASXL1*
- *IDH1*
- *IDH2*
- *etc*

Detection methods

Next Generation Sequencing (NGS) technology

Commercially available panels
- Illumina TruSight Myeloid panel
- Illumina iSeq100
- Archer VariantPlex Core Myeloid panel
- Human Myeloid Neoplasms QIASeq DNA panel
- AmpliSeq for Illumina Myeloid panel

Contain all genes relevant for the **2017 European Leukemia Net (ELN)** classification

In-house developed NSG-based assays

RNA-based NGS (RNAseq)

Commercially available assays
Detection of AML fusion trascripts

Customized methods
AML-associated transcripts are amplified by (multiplex) PCR and subsequently sequenced by NGS

NGS-based Minimal Residual Disease (MRD) detection technology

- Whole exome sequencing (WES)
- Whole genome sequencing (WGS)

Advantages
- High value in predicting relapse and overall survival
- Measure of all mutations, including patient-specific persisten mutations in complete remission

Limitations
- Limited sensitivity and specificity
- Inability to correctly discriminate between residual leukemia and clonal hematopoiesis

Levine and Valk, Haematologica, 2019