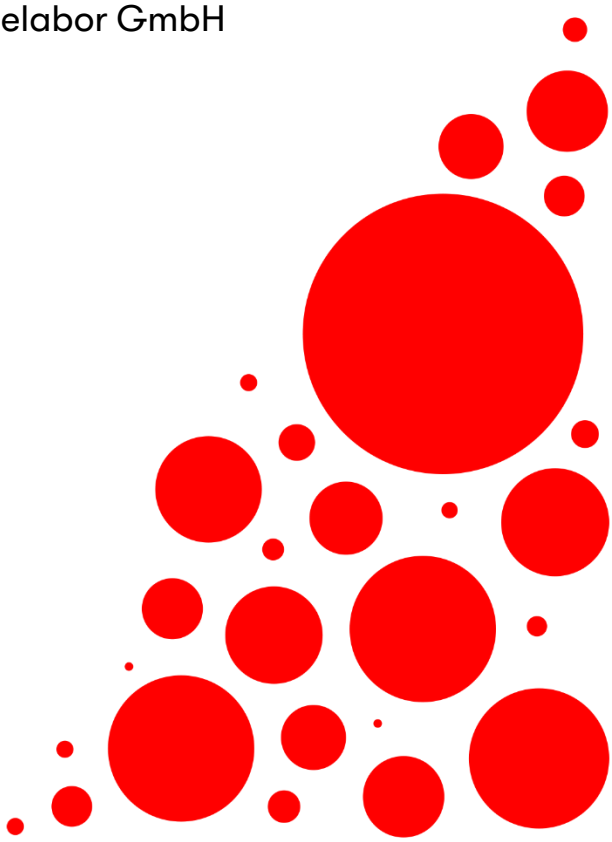
Sharing knowledge. Advancing science.

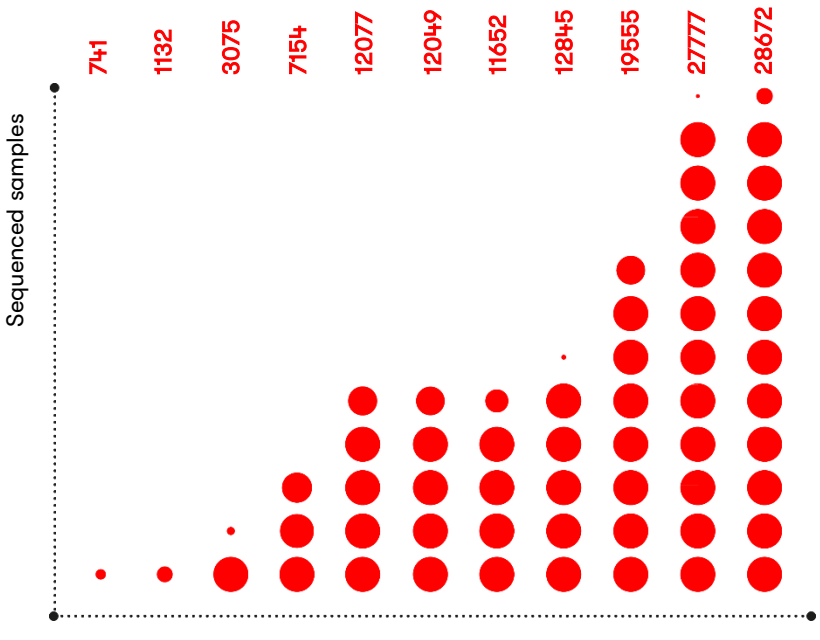
MLL Münchner Leukämielabor GmbH



Through experience and expertise

Experts in sequencing

Assisting with and enabling the diagnosis, prognosis prediction and targeted treatment of hematological diseases, molecular genetics is seen as essential for integrated diagnostics and goes hand in hand with technological progress and our growth in knowledge. There is no doubt that sequencing techniques represent a quantum leap in molecular genetics. In many cases, mutations that trigger leukemia and lymphomas and promote the development of these diseases or are associated with them can be identified by determining the precise base sequence. These mutations can act as markers for monitoring or may represent a suitable target for directed therapies. It is here where Munich Leukemia Laboratory (MLL) is right in the thick of the latest technological developments. As one example, high-throughput sequencing was already established and accredited in routine diagnostics back in 2011.



Overview of sequenced samples by year (2008 - 2018)

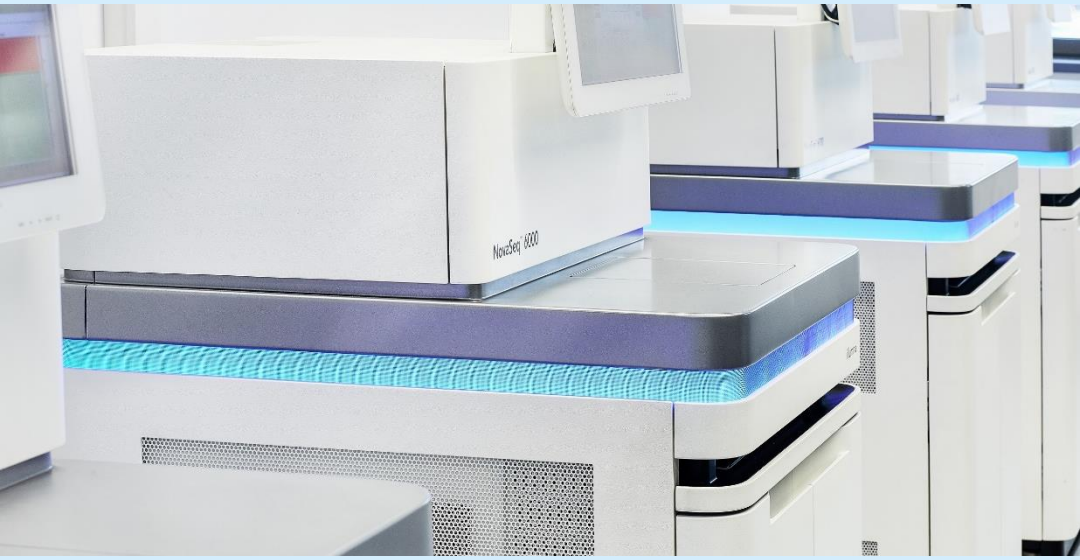
- Expertise in high-throughput sequencing, given that NGS had already been established as a test method in routine diagnostics in an accredited setting (ISO 15189, ISO 17025) back in 2011
- Industry-leading quality standards
- Rapid turnaround
- State-of-the-art laboratory equipment and devices for extracting DNA and RNA and preparing the libraries
- Needs-based data analysis:
  - Raw NGS data available for downloading
  - Prepared NGS data (VCF files) available for downloading
  - Manual interpretation via MLLi:ir

Right down to the individual base

Our sequencing methods

Next-generation sequencing (NGS)

Thanks to the introduction of modern high-throughput sequencing methods – also called *next-generation sequencing* (NGS) – it is now possible to conduct high-sensitivity analyses of hundreds of thousands of genome regions within a very short time at mutational loads of 1-3%. *Panel testing* permits the analysis of several hundred genes or genetic hotspots in one test cycle in less than a week. Several modern NGS platforms are available at MLL for routine diagnostics.



In addition to high-throughput sequencing in routine diagnostics, diagnostic procedures of the future are being tested and implemented at MLL within the context of the 5000 genome research project. Sequencing is performed on the latest generation of sequencing devices using the Illumina *sequencing by synthesis* method.

Whole-genome / whole-exome sequencing

Whole-genome sequencing (WGS) is aimed at reading a person's entire genome – or the entire coding region, also referred to as the exome (whole-exome sequencing). WGS and WES enable polymorphisms and somatic mutations to be identified. What is more, it is also possible to detect additions to and the loss of chromosomal material (*copy number variations*, CNV) as well as translocations (*structural variation*, SV).

RNA sequencing

RNA sequencing (RNA-Seq) permits the analysis of the transcriptome. With leukemia and lymphomas, the transcriptome of the affected cells is significantly altered. Along with changes in the genetic expression, it is also possible to demonstrate fusion genes using this technique.

MLLi and MLL Dx

Shaping progress

MLLi - Advancing innovation

MLLi (i = innovation), a subsidiary of MLL Munich Leukemia Laboratory, is specialized in the digital processing of data from leukemia diagnostics. Among other things, MLLi offers web-based tools to provide interpretations of data for the diagnosis of hematological neoplasias.

MLLi:db

Classification and annotation of variants

Comparison with additional databases

Use of MLL Artificial Intelligence (AI) for classifying variants

Interactive search

Variant-specific report

MLLi:ir

Manual curation by experts

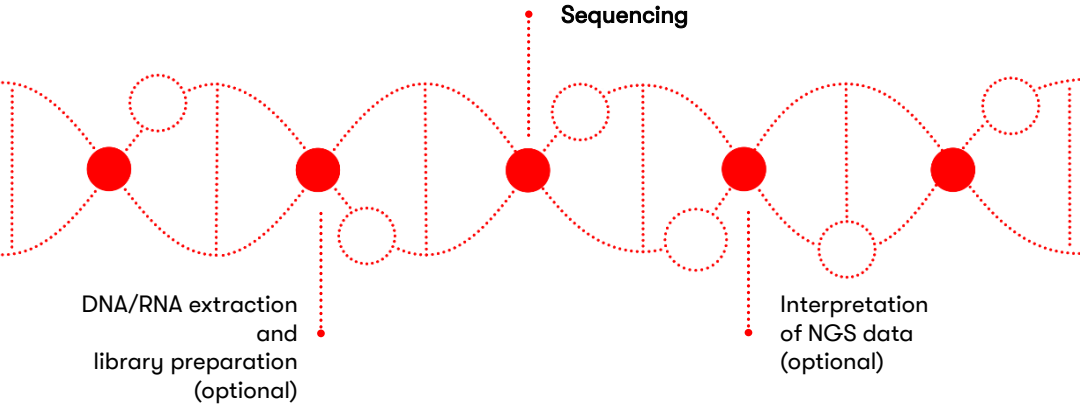
From raw NGS data to diagnostic conclusions

Personalized medical report

Classification and annotation of variants

MLL Dx - International laboratory expertise

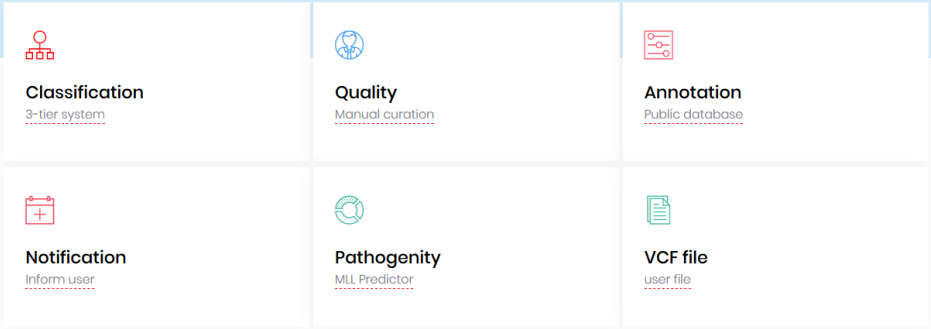
MLL Dx (Dx = diagnostics) provides expertise for diagnostic laboratories internationally and conducts the following laboratory analyses, especially for its industrial and international business partners in the medical field:



Our bioinformatics service

For clear findings

MLLi Benefits & offers



MLLi offers physicians and medical staff assistance with interpreting data from high-throughput sequencing.

Users well versed in bioinformatics will profit from MLLi:db and its clear classification of variants based on anonymized patient data.

And users without (extensive) bioinformatics knowledge who need to interpret data from high-throughput sequencing will benefit from the interpretation report service of MLLi (MLLi:ir). The raw NGS data is curated by NGS and bioinformatics experts at MLL, who handle its classification (mutated, variant of unknown significance, or wild type). The decisions made are never based solely on the in-house, well-managed variant database of ML, but also include databases as well: COSMIC, dbSNP, gnomAD, ClinVar, and dbNSFP. This makes it possible to achieve clarity despite the difficulty of interpreting the variants and the complexity of the annotations. The user will receive a report with a clear and conclusive statement based on the variants identified and will then be in a position to provide the patient with accurate and unequivocal findings.

Contact us!

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