

5,000 Genome project



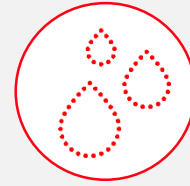
Aims



Our vision is to understand the genetic and molecular basis of the various leukemias in all their complexity and to use the acquired knowledge to further refine diagnostics in order to ensure the best possible therapy for each patient.

Material

Our biobank enables us to include rare leukemias and lymphomas and thus cover a very broad spectrum of different entities. The DNA or RNA required for the analysis is obtained from bone marrow or blood samples.



RNA-Seq
&
WGS

Methodology

Fragmentation of DNA/RNA

350bp

Sonication is used to break the DNA into fragments of 350bp in length.

Library Preparation

In the RNA-Seq workflow, cDNA synthesis and amplification by PCR are also included.

End Repair

Adapter ligation

Sequencing

Sequencing is performed at MLL using Illumina's Sequencing-By-Synthesis method on the NovaSeq 6000 system.

Nova-Seq

Data pre-processing

Base-Space

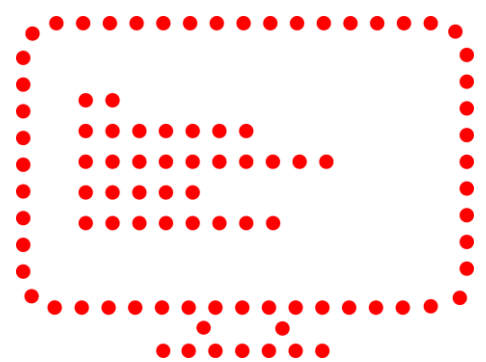
Data storage



At MLL, the data from the sequencers are transferred directly to the Amazon Cloud in Frankfurt. The WGS and RNA-Seq data of the 5K project are stored completely anonymized in a private AWS domain of the Amazon Cloud in Frankfurt.

Data processing

Data pre-processing is performed in Illumina's BaseSpace Sequencing Hub and includes alignment, variant calling and, in the case of transcriptome analysis, count estimation. Further filtering and processing is performed using in-house analysis pipelines.



Contact

MLL Münchner Leukämielabor GmbH

Max-Lebsche-Platz 31
81377 München

