

## **Functional and Translational Genomics for Improved Clinical Outcome in Acute Leukemias**

Recent advances in high-throughput sequencing technology have demonstrated that different cancer subtypes exhibit a far greater number of mutant tumor-relevant genes per individual tumor than initially expected, and many of the involved genes have not yet been known to be genetically altered in cancer. Thus, we are aiming to identify leukemia relevant genes by applying a novel high-throughput ultra-deep amplicon sequencing approach, which will contribute to the identification of leukemia-associated gene mutations of pathogenic, diagnostic, prognostic, and therapeutic relevance. Towards the achievement of this goal deep-coverage amplicon sequencing results will be subjected to integrative analyses combining information from gene expression, array CGH and SNP analyses, as well as from “omics” data sets available within the NGFN LeukemiaNet. Furthermore, significant findings will be validated within larger data sets, and results will be correlated with clinical data derived from prospective multicenter treatment trials of the German-Austrian AML Study Group (AMLSG). Finally, for selected candidates functional studies in cell line and murine transplantation models will be performed. Ultimately, leukemia associated mutational profiles might provide novel insights into molecular mechanisms relevant in leukemogenesis as well as novel targets for individualized patient management.