





In the poster we demonstrate initial results of our research project focused on genetic changes associated with chronic myeloid leukemia progression.

Using exome-sequencing we have shown that *BCR-ABL1* kinase domain mutation can be acquired very rapidly and cause progression of the disease even if no other point mutations or copy number alterations are acquired concurrently.

We therefore demonstrated the power of high-throughput sequencing in studying chronic myeloid leukemia progression.

