Acute lymphoblastic leukemia is the most common malignancy in children. The most important examination at the time of diagnosis includes karyotype of leukemic cells which divides patients into prognostic groups according to cytogenetic finding. In up to 90 % of patients the chromosomal aberrations with well known clinical significance are designated. One of cytogenetic type is high hyperdiploid ALL (51-68 chromosomes) associated with favorable prognosis. Nevertheless, relapses of the disease occur even in these children. One possible reason why this happens could be an increased genomic instability of leukemic cells that causes cryptic structural rearrangements.

In a retrospective study, we examined a total of 232 children with newly diagnosed B-ALL using conventional cytogenetic analyses and interphase fluorescence
in situ hybridization (I-FISH) with a panel of DNA probes (Abbott Vysis) in order to detect heteroploid cells. In patients with suspect cryptic structural chromosome aberrations, we analyzed the karyotypes in detail by multicolor FISH and multicolor banding (mFISH/mBAND; MetaSystems). The extent of aberrations was determined by comparative genomic hybridization on BAC arrays (array CGH; BlueGnome).

Cell clones with high hyperdiploid karyotype were detected in a total of 102 children (44 %). In 25 of them (24,5 %), we revealed additional cryptic chromosome aberrations. Chromosomes 1, 13, 6 and 7 were most frequently structurally rearranged. The most common recurrent change found was the duplication of long arm of chromosome 1 (9 children). The minimal duplicated region in all patients was 1q31 to 1q32.3 (22.5 Mb). Further, we detected deletion of chromosome 13 long arm in 4 patients and deletion of long arm of chromosome 6 in two patients.

Patients with cryptic structural changes showed statically significant shorter EFS (Event Free Survival; p=0,038).