Presence of the MLL gene rearrangement at 11q23 is an important prognostic feature. Moreover, the rearrangements represent a suitable target for the minimal residual disease (MRD) monitoring in some subtypes of childhood acute leukaemias (AL). Currently more than 80 different translocations involving the MLL gene and more than 50 of those are characterised at the molecular leve\. Using multiplex-reverse transcriptase polymerase chain reaction (multiplex RT -PCR) and - in some cases - its combination with DNA analysis of the translocation breakpoint we examined a group of infants «1 year of age) diagnosed with acute lymphoblastic leukaemia (ALL), children with M4 and M5 subtypes of acute myeloid leukaemia (AML) and patients with secondary leukaemias. Moreover, we exaITÚned children with B-cell precursor fulfilling at least one of the t'ollowing criteria: proB immunophenotype, cytogenetically confirmed MLL rearrangement and/or expression ot'NG2 molecule shown by f10w cytometry. MultiplexRT PCR technique enables fast detection of the most frequent fusion partners of the :MLL gene (AF4, AF6, AF9, AFlO, ENL a ELL). We screened almost 80 patients diagnosed and treated in the Czech Republic between 1997 and 2007 and we found an MLL-fusion gene in 51 of them. Vast majority of rearrangements (92%) was detected by the multiplex-RT PCR, the rest of the cases by DNA analysis of the breakpoint regIOn. Analysis of the MLL rearrangements in childhood haematological malignancies is crucial as a prognostic marker used in current treatment stratifications and, moreover, as a suitable (and sometimes the only) target for the MRD monitoring.