Supporting Information

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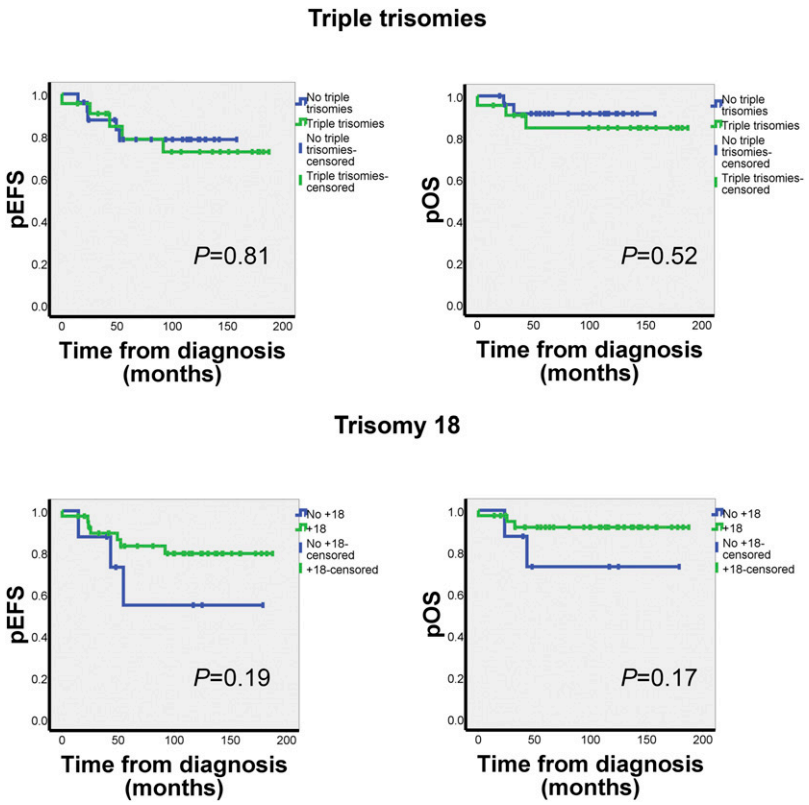

Fig. S1. Event-free and overall survival of 47 high hyperdiploid childhood acute lymphoblastic leukemia cases, treated according to the Nordic Society of Pediatric Hematology (NOPHO) 1992/2000 protocols, with and without the "triple trisomies" (i.e., concurrent +4, +10, and +17) and trisomy 18, respectively. There were no statistically significant differences in survival between the groups. pEFS, probability of event-free survival; pOS, probability of overall survival.

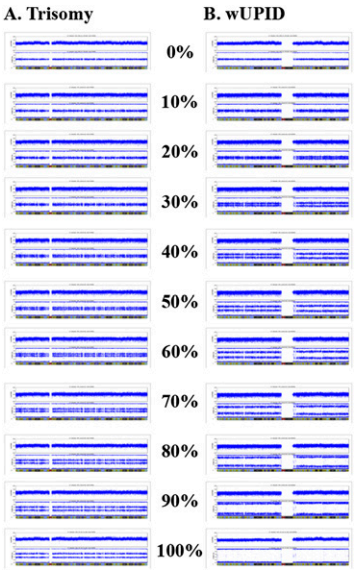

Fig. S2. To determine the extent to which subclonal trisomies and whole-chromosome uniparental isodisomies (UPIDs) were detectable by the Illumina system, a dilution series was made of a sample known to have such aberrations in 100% of the leukemic cells mixed with the corresponding remission sample in the concentrations of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, and 90%, and was subjected to SNP array analysis. Top panels show log2 ratios along the chromosomes. Each dot represents the log2 ratio of one marker. A log2 ratio of zero corresponds to a normal, diploid copy number. Increased and decreased log2 ratios correspond to gained and deleted regions, respectively. Lower panels show B allele frequencies (BAFs), which are calculated as (signal intensity for allele B)/(signal intensities for allele A + allele B). Homozygous SNPs have a value of 0 or 1, and heterozygous SNPs a value of 0.5 in a diploid chromosome segment. (*A*) Trisomy. When the extra chromosome is present in 100% of the cells, SNPs display an average log2 ratio >0.5 and BAF values of 0, ~0.33, ~0.67, and 1.0, where the middle values correspond to the heterozygous SNPs. The trisomy was detectable when it was present in 20% or more of the cells. (*B*) Whole-chromosome UPID. When the UPID is present in 100% of the cells, SNPs display a normal diploid log2 ratio of zero and BAF values of 0 and 1, corresponding to loss of heterozygosity. The UPID was detectable when it was present in 10% or more of the cells. The panels were extracted from the BeadStudio 3.1.2.0 software with Illumina Genome Viewer 3.2.9.

Other Supporting Information Files

Table S1 (DOC)
Table S2 (DOC)
Table S3 (DOC)
Table S4 (DOC)
Table S5 (DOC)