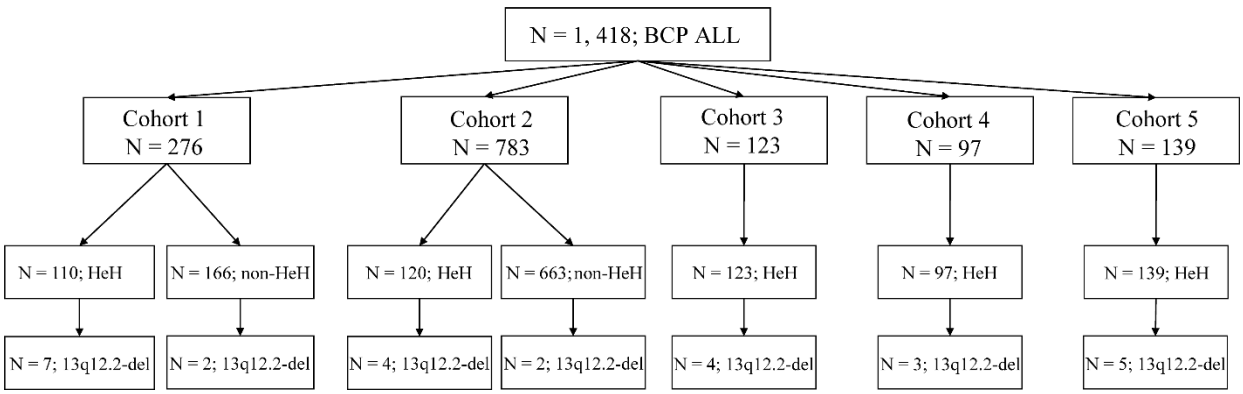
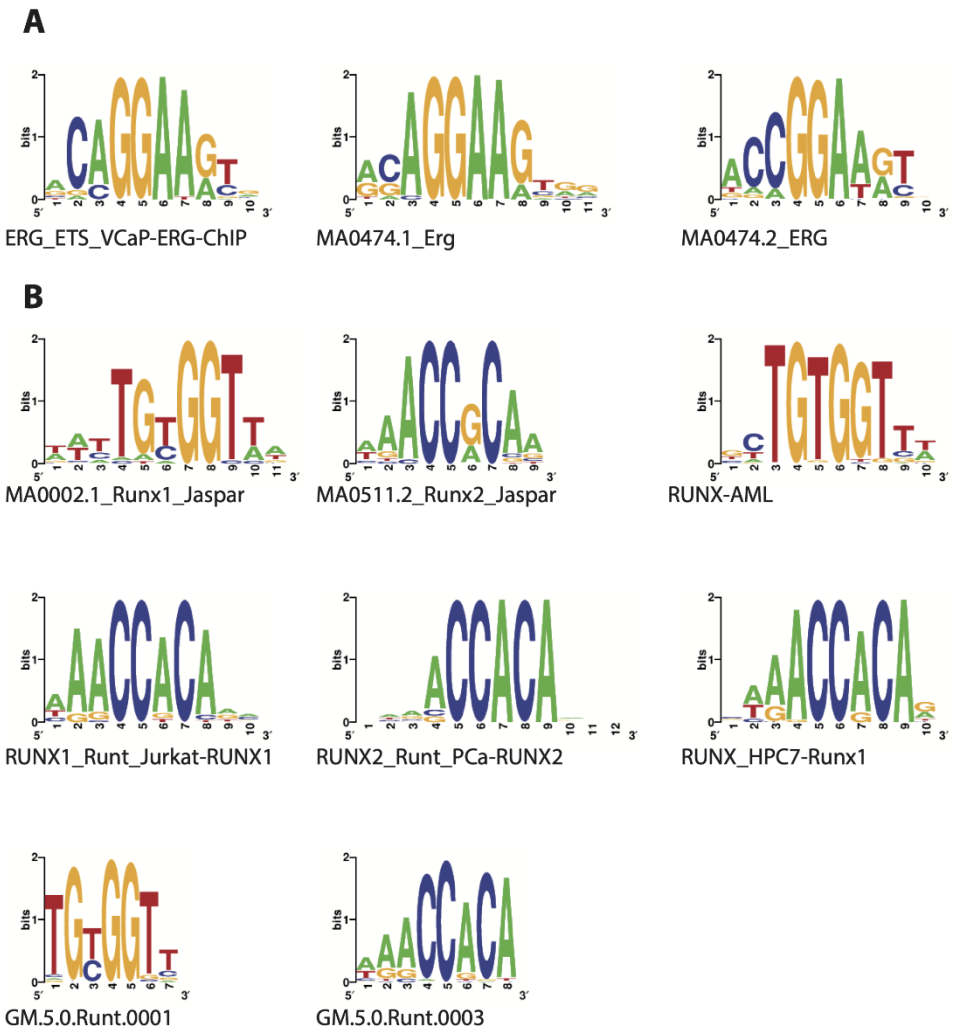
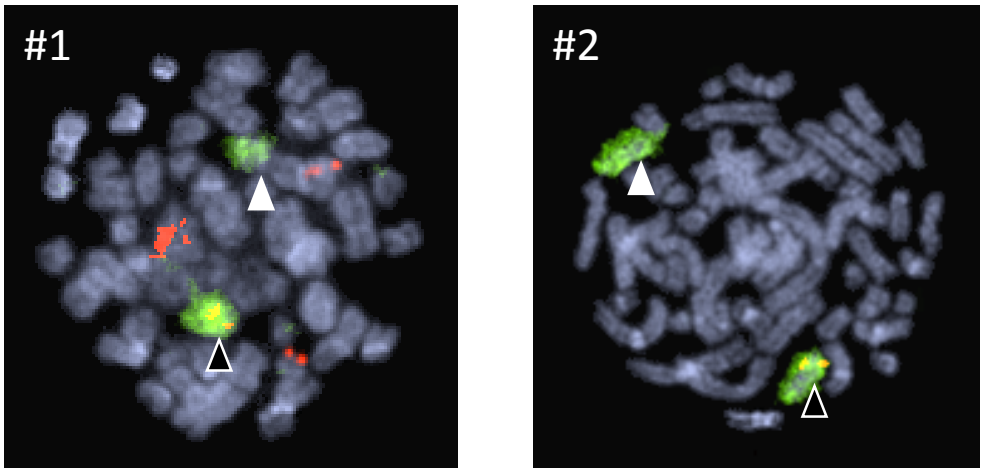


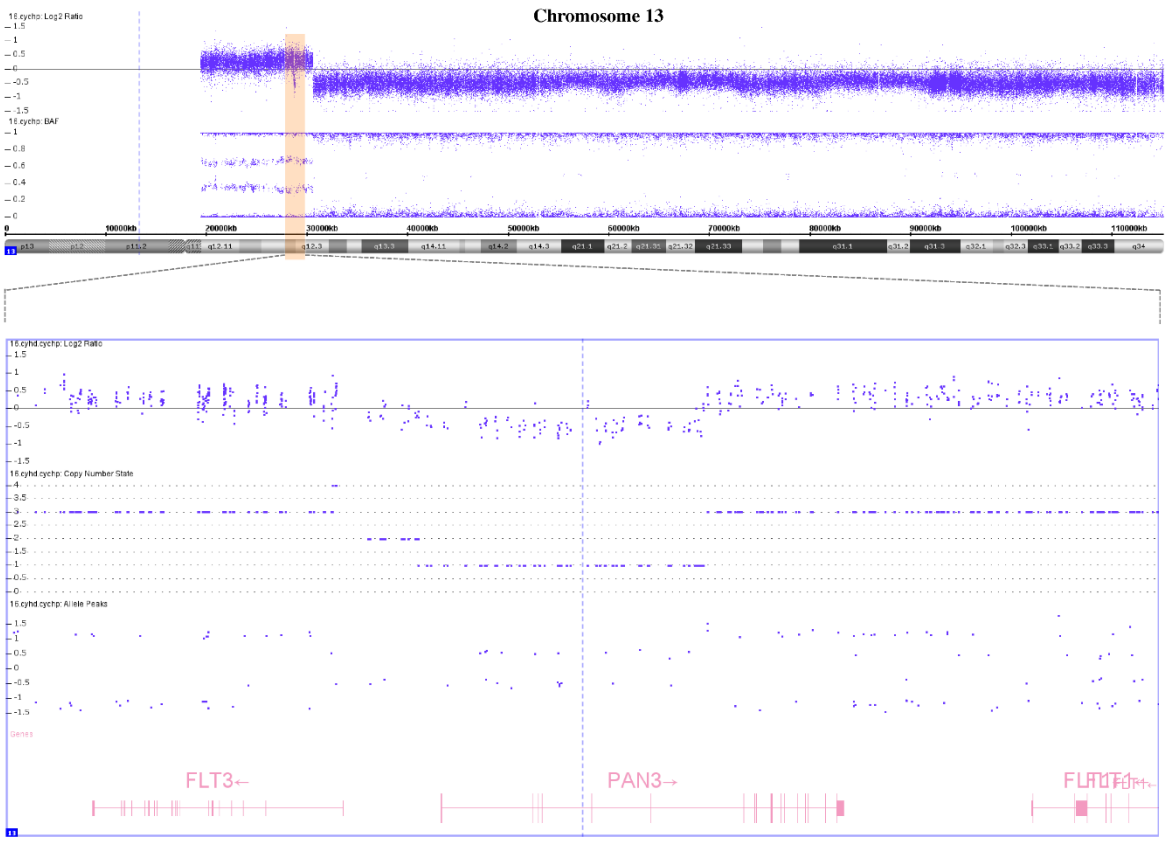

**Supplementary Figure 1.** Flowchart of the 1,418 B-cell precursor ALL (BCP ALL) cases analyzed, including five different cohorts with SNP array, whole exome sequencing and/or whole genome sequencing data. Abbreviations: HeH, high hyperdiploid.



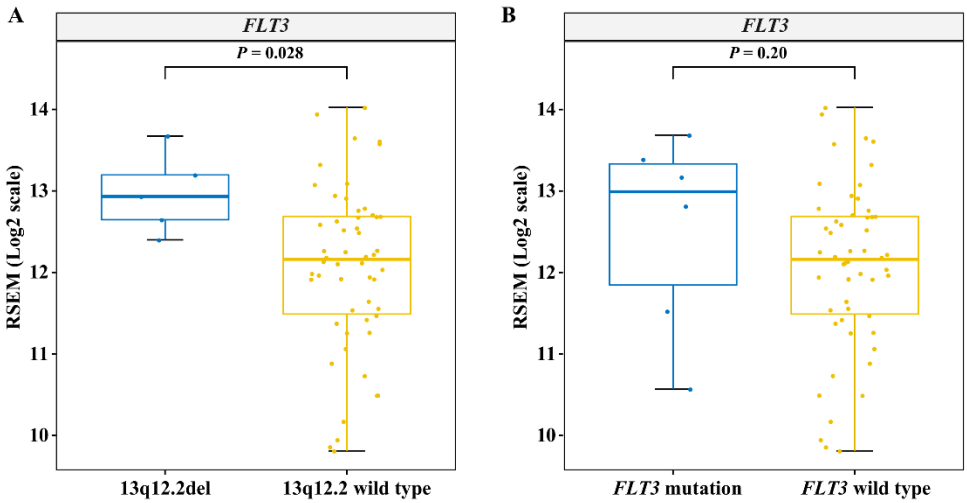

**Supplementary Figure 2. Erg and Runx position weight matrix (PWM).**
Sequence logo representation of three Erg motifs and eight Runx motifs generated from Erg and Runx PWMs from the gimme.vertebrate.v5.0, HOMER and Jaspar CORE databases.



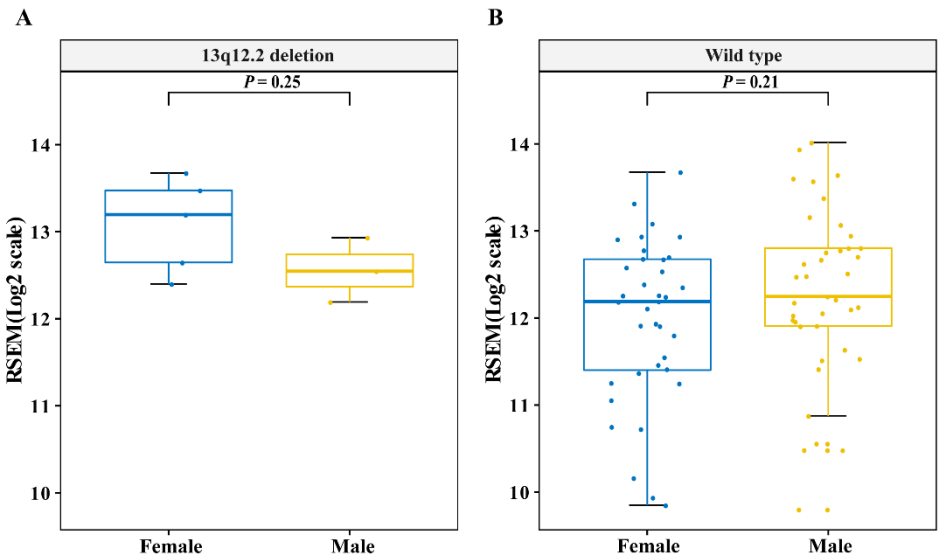

**Supplementary Figure 3.** Metaphase fluorescence in situ hybridization of the 13q12.2-deleted region in cases 1 and 2, using a whole chromosome paint probe for chromosome 13 (green) and the fosmid G248P80597D11 (red), located in the deleted region. In case 1, a probe for chromosome 21 (red) was also included to ensure that only hyperdiploid cells were analyzed. Chromosome 13 homologues with deletions are indicated with white arrow heads and those without deletions with black arrow heads. No other rearrangements were observed.



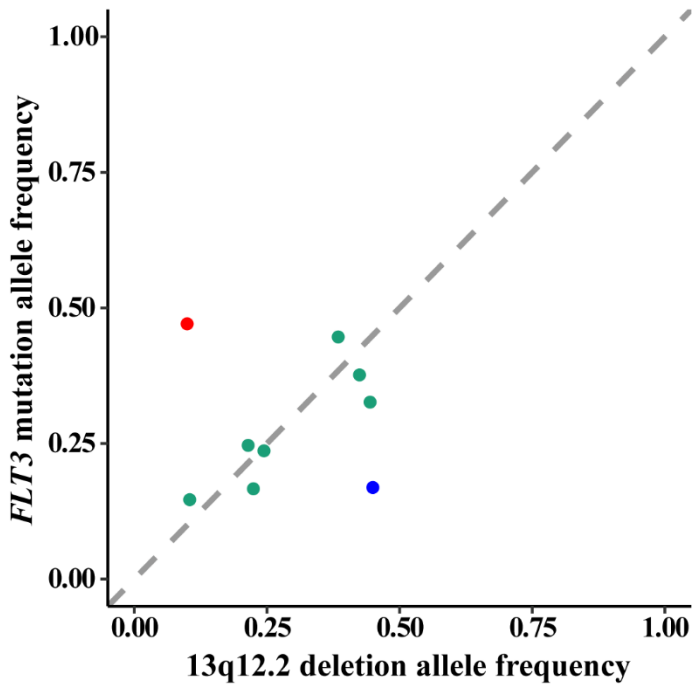

**Supplementary Figure 4.** Chromosomal view of the 13q12.2 deletion in case 16. Log R ratio, predicted copy number and B allele frequency signals are shown. Trisomy 13 is seen together with two different 13q12.2 deletions, leaving two copies of part of the chromosome and one copy of the most deleted segment.



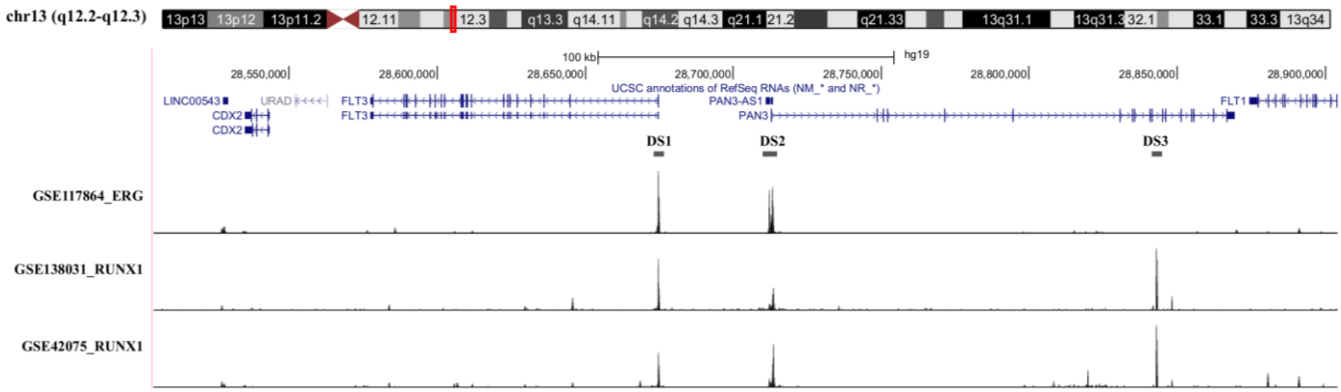

**Supplementary Figure 5. *FLT3* expression in high hyperdiploid acute lymphoblastic leukemia cases in relation to 13q12.2. deletions and *FLT3* mutations.** (A) Expression of the *FLT3* gene in cases with and without 13q12.2 deletion in cases without *FLT3* mutation (n = 59). (B) Expression of the *FLT3* gene in cases with and without *FLT3* gene mutations in cases without 13q12.2 deletion (n = 67).




**Supplementary Figure 6. *FLT3* expression in high hyperdiploid acute lymphoblastic leukemia cases in relation to gender.** (A) Expression of the *FLT3* gene in female and male cases with 13q12.2 deletion (n = 8). (B) Expression of the *FLT3* gene in female and male cases without 13q12.2 deletion (n = 75).




**Supplementary Figure 7. Comparison of the allele frequencies for *FLT3* mutations and 13q12.2 deletions in diagnostic samples from 9 acute lymphoblastic leukemia cases with both.** Seven of the cases had similar allele frequencies for the mutation and deletion, indicating that they were present in the same clone. One case (#7, red) had a higher allele frequency for the mutation, indicating that it arose first or that the mutation and the deletion were in separate subclones. One case (#22, blue) had a higher allele frequency for the deletion, indicating that it arose first or that the mutation and the deletion were present in separate subclones.




**Supplementary Figure 8.** Chromatin immunoprecipitation sequencing signals (ChIP-seq) of transcription factors RUNX1 and ERG based on the SEM cell line (GSE42075_RUNX1, GSE117864_ERG) and 697 cell line (GSE138031_RUNX1)