

SUPPLEMENTAL MATERIAL

Tanaka et al., <https://doi.org/10.1084/jem.20170167>

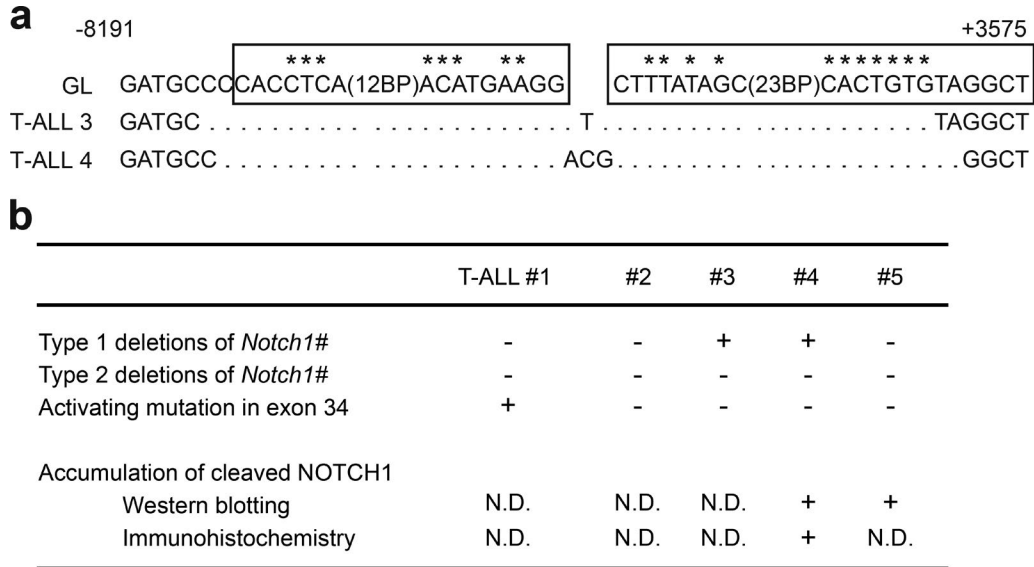


Figure S1. **Notch1 rearrangements in T-ALL nos. 3 and 4.** (a) Rearrangements in *Notch1* deduced from sequencing of PCR products generated from genomic DNA of T-ALL nos. 3 and 4 with RAG-mediated type 1 deletions (Ashworth et al., 2010). GL, sequence of the germline DNA flanking the breakpoints. Nucleotide positions are expressed relative to the ATG start codon in exon 1 of *Notch1*. Flanking sequences resembling RAG recognition sequences are boxed. Residues matching the consensus RAG signal sequence (CACATGT heptamer followed by a 12- or 23-bp spacer and the nonameric sequence ACA AAAAAC) are denoted with an asterisk. Genomic DNA was amplified using the sense primer 3'-ATGGTGAATGCCTACTTTGTA-5' and the antisense primer 3'-CGTTGGGTAGAAGAGATGCTTAC-5'. (b) Summary of Notch1-related analyses in five T-ALL samples. N.D., not done.

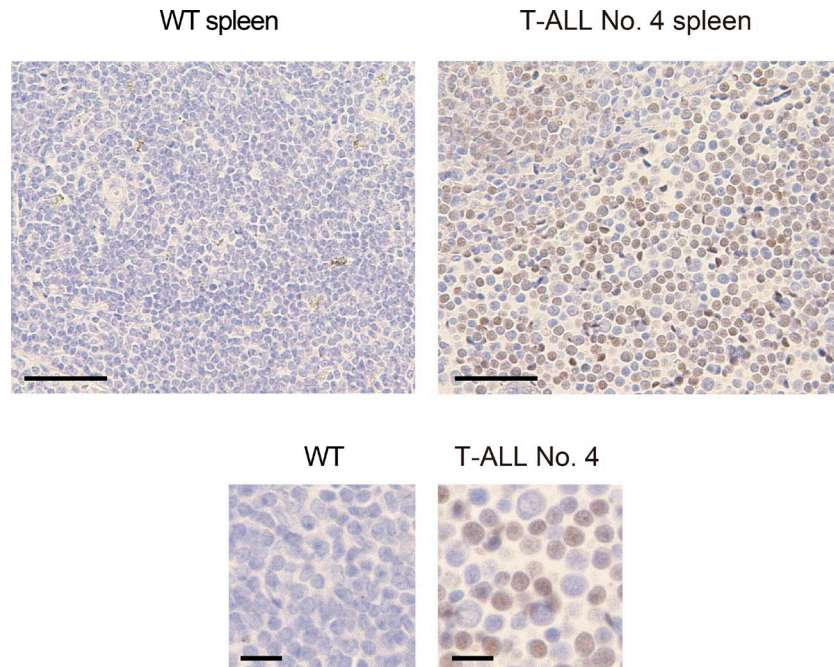


Figure S2. **Nuclear accumulation of cleaved NOTCH1 in *Bcor*^{ΔE4/y} T-ALL cells.** Immunostaining of cleaved NOTCH1 protein in CD8 SP cells from the spleens of *Bcor*^{ΔE4/y} T-ALL no. 4. Formalin-fixed, paraffin-embedded tissue sections were stained using heat-induced epitope retrieval at pH 9.0. Slides were incubated with anti-Notch1 rabbit monoclonal antibody recognizing the cytosolic domain of Notch1 (clone D1E11, 1:400 dilution; Cell Signaling Technology). Sections were visualized and counterstained with hematoxylin. Intermediate and high-power views of spleens are shown at top and bottom, respectively. Bars: (top) 50 μm; (bottom) 10 μm.

Table S1, included as a separate Excel file, lists genes up-regulated in *Bcor*^{ΔE4/y} and *Bcl6*^{Δ/Δ} DP thymocytes, Bcor ChIP-seq peaks in DP thymocytes, Notch1 ChIP-seq peaks in DP T-ALL, and Bcor^{ΔE4} ChIP-seq peaks in DP thymocytes.