**Supplemental Figure S10.** Schematic representation of somatic CIC mutations in human cancer.

(A) Missense (blue) and truncating (green) mutations are plotted according to the localization in human CIC-S. Mutations identified in human T-ALL are shown in red and mutations in human T-ALL cell lines in orange. The HMG-box (brown) and the C1 motif (dark green) are indicated. Exon 1B selective for the CIC-S isoform is shown in red.

(B) CIC mutations identified in childhood T-ALL patient samples. Mutations were identified in 7 of 69 patients by targeted exon sequencing and are indicated based on the reference transcript ID ENST00000575354.2 (CIC-S) or ENST00000572681.2 (CIC-L, for the c.206G>A and c.577A>T mutations).

(C) Schematic representation of CIC mutations in exon 1A (blue, selective for CIC-L isoform).

(D) Additional CIC mutations identified in the studies by Atak et al. 2013 (2 mutations in 31 patient samples) and Kataoka et al. (2 mutations in 426 adult patient samples).