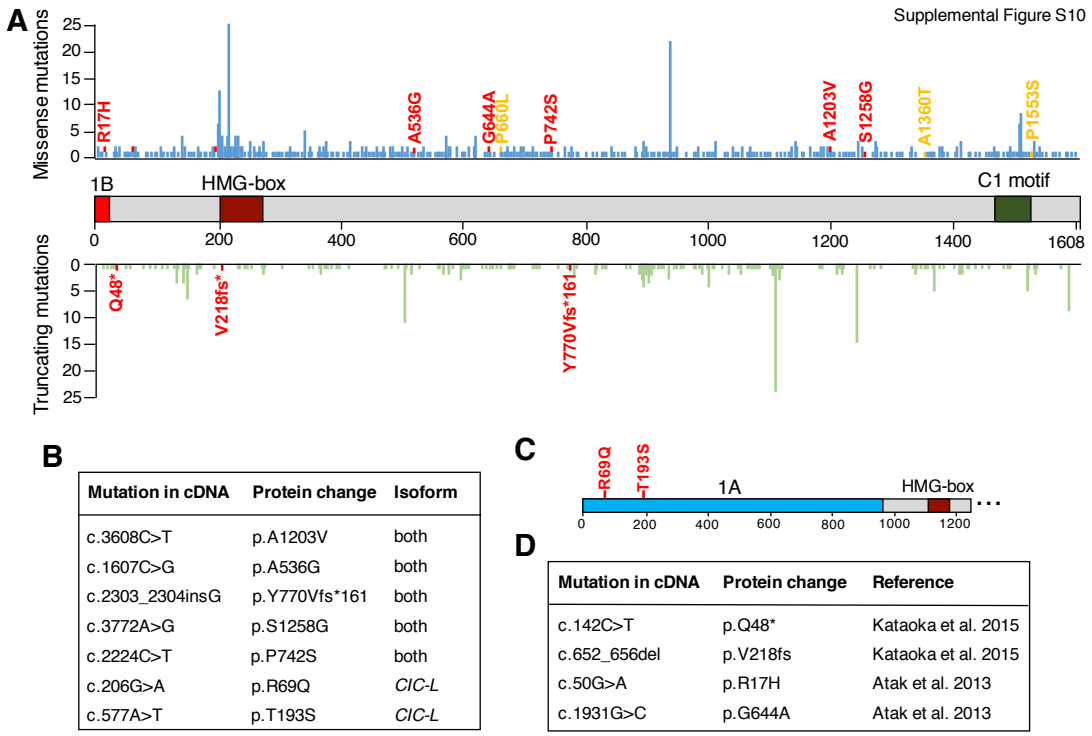

Mutation in cDNA	Protein change	Isoform
c.3608C>T	p.A1203V	both
c.1607C>G	p.A536G	both
c.2303_2304insG	p.Y770Vfs*161	both
c.3772A>G	p.S1258G	both
c.2224C>T	p.P742S	both
c.206G>A	p.R69Q	*CIC-L*
c.577A>T	p.T193S	*CIC-L*

Mutation in cDNA	Protein change	Reference
c.142C>T	p.Q48*	Kataoka et al. 2015
c.652_656del	p.V218fs	Kataoka et al. 2015
c.50G>A	p.R17H	Atak et al. 2013
c.1931G>C	p.G644A	Atak et al. 2013

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).