



Supplemental Figure S8. Activation of the Notch pathway in T-ALL driven by *Cic* inactivation and classification of mouse T-ALLs based on expression profiling.

(A) Cleaved Notch1 (NICD) IHC staining in thymus sections from WT mice or in T-ALL sections obtained from 3 different Tmx-treated $Cic^{lox/lox};hUBC-CreERT2^{+/T}$ mice at humane endpoint. Scale bar represents 25 μ m.

(B) Hes1 IHC staining in thymus sections from WT mice or in T-ALL sections obtained from 3 different Tmx-treated $Cic^{lox/lox};hUBC-CreERT2^{+/T}$ mice at humane endpoint. Scale bar represents 25 μ m.

(C) Enrichment plot showing significant enrichment (FDR < 25%) of the NOTCH1 hallmark gene set in T-ALL from $Cic^{lox/lox};hUBC-CreERT2^{+/T}$ mice treated with Tmx diet. NES, normalized enrichment score.

(D) Enrichment plot showing significant enrichment (FDR < 25%) of the TLX1⁺ (HOX11⁺) gene signature in T-ALL from $Cic^{lox/lox};hUBC-CreERT2^{+/T}$ and K^{H-}

$Ras^{G12V};hUBC-CreERT2^{+/T}$ treated with Tmx diet or $p53^{-/-}$ mice. NES, normalized enrichment score.