Supplemental Figure S7. RNAseq analysis of T-ALL driven by Cic inactivation.

(*A*) Left: Heatmap displaying differentially expressed genes (log_2FC of $\geq +3$ or ≤ -3; adjusted p-value <0.05; FDR 0.05) as estimated by RNAseq from WT thymuses and T-ALLs developed in Tmx-treated $Cic^{lox/lox}$;$hUBC$-$CreERT2^{+/T}$ mice. Relative expression (log_2FC) is scaled in color code (indicated), from dark blue (-3) to dark red (+3). Right: Zoom into the top 30 highest expressed genes. Gene symbols are also indicated.

(*B*) Relative expression levels of *K-Ras, Etv1, Etv4, Etv5* and *Cic* mRNAs in thymuses from *H-Ras*$^{-/-}$;*N-Ras*$^{-/-}$;*K-Ras*$^{lox/lox}$;*hUBC-CreERT2*$^{+/T}$ mice either left untreated (n=2, open bars) or treated with Tmx diet for 7 days (n=3, closed bars). *β-Actin* expression levels were used for normalization. Data represent mean ± SD. Asterisks depict statistically significant differences, *p < 0.05, unpaired Student's t test.