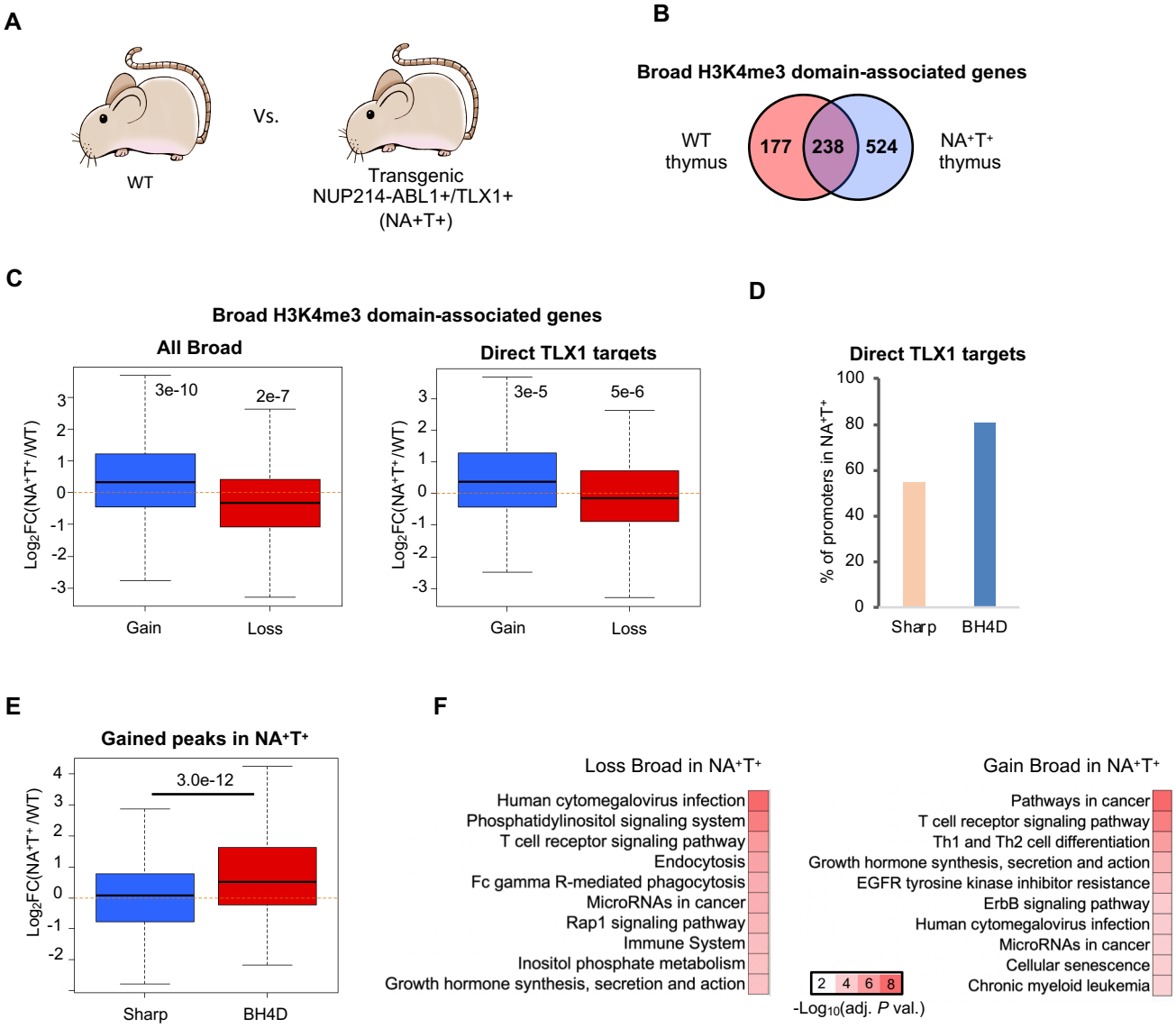

Supplemental Figure S11: Dynamics of broad H3K4me3 domains in a transgenic model of T-ALL. A) Experimental model compare ChIP-seq and RNA-seq data from thymus of wild-type (wt) and double transgenic mice expressing the fusion protein *NUP214-ABL1* (NA^+) and the *TLX1* oncogenic transcription factor (T^+). The data was obtained from Vanden Bempt *et al.* 2018 (**Supplemental Table S1**). B) Overlap between the broad H3K4 domains found in WT and NA^+T^+ thymus. C) Boxplot showing the fold change of expression of broad H3K4me3 domain-associated genes only in NA^+T^+ (gain) or WT (loss) thymi (left panel). Right panel: only the direct targets of TLX1 were analyzed. D) Percentage of broad- and sharp-associated genes in NA^+T^+ thymus that are direct targets of TLX1, based on TLX1 ChIP-seq. E) Two sets of equally expressed genes associated with broad H3K4me3 domain or sharp H3K4me3 peaks in NA^+T^+ thymus were defined. The fold change of the expression between NA^+T^+ and WT thymi was determined. F) Top 10 KEGG pathways significantly enriched for the gene-sets associated with Broad H3K4me3 domain only in NA^+T^+ (gain) or WT (loss) thymi. The inverted $\log_{10}$ of the Benjamin-corrected *P* value is shown. Significance in C and E was assessed by a Wilcoxon test.