



Supplemental Figure S10. Investigating the transcriptomic program of B cells from *Eμ-TCL1;CXCR4^{C1013G}* mice.

- (a) GSEA of *Eμ-TCL1* vs. *WT* CD19+ B cells showing normalized enrichment scores (NES) and false discovery rates (FDR) for curated gene sets listed in MsigDB (7, 8).
- (b) Overlap of DEG with $\text{padj} < 0.05$ of *Eμ-TCL1;CXCR4^{C1013G}* vs. *Eμ-TCL1* CD19+ B cells with the Cancer Gene Census (CGC) (15).
- (c) Overlap of DEG with $\text{padj} < 0.05$ of *Eμ-TCL1;CXCR4^{C1013G}* vs. *Eμ-TCL1* CD19+ B cells with DLBCL drivers in patient datasets (16, 17).
- (d) GSEA showing enrichment of a Richter's transformation signature in *Eμ-TCL1;CXCR4^{C1013G}* vs. *WT*, *Eμ-TCL1* vs. *WT* and *CXCR4^{C1013G}* vs. *WT* CD19+ B cells showing normalized enrichment scores (NES) and false discovery rates (FDR).