CRISPR/Cas9 editing reveals IRF8 regulated gene signatures restraining plasmablast differentiation

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Supplementary Data

Supplemental Table 1. Differentially expressed genes between KO and WT cell types. Related to Fig. 5 and Fig. 6.

Supplemental Table 2. List of 66 IFN genes derived from a GSEA Leading Edge Analysis. Related to Fig. 6E.



Supplementary Figure 1. Lentiviral infection of HSCs and sorting strategy.

Related to Fig. 2. (A) Schematic of the Thy1.1 expressing lentiviral construct. (B) Histogram showing GFP expression in CD19⁺ versus CD19⁻ cells from *Rosa26*^{LSL-Cas9-GFP}*Cd19*^{CRE/+} mice. (C) Gating strategy to sort c-Kit⁺Sca-1⁺ HSCs by FACS. (D) Flow cytometry analysis of Thy1.1 transduced HSCs 24 hr post-infection. Plots for all live HSCs and c-Kit⁺Sca-1⁺ cells are shown. (E) Histogram showing the GFP expression in CD19⁺Thy1.1⁺ and CD19⁺Thy1.1⁻ B cells.



Supplementary Figure 2. Sorting and gating strategy to phenotype CRISPRgenic **B cells.** Related to **Fig. 4**. (**A**) Sorting strategy to isolate Thy1.1⁺ and Thy1.1⁻ naïve splenic B cells from IRF8 CRISPRgenic mice to perform TIDE assay. Post-sort purity of

(B) Thy1.1⁺ and (C) Thy1.1⁻ populations isolated in A. (D) Representative enrichment of Thy1.1⁺ cells prior to *ex vivo* culture. Related to Fig. 4B-H. (E) Gating strategy associated with Fig. 4C, 4D, and 4F. (F) Gating strategy associated with Fig. 4E, 4G, 4H, and 4I. (G) Bar plot showing the percentage of IRF8 positive cells in the Thy1.1⁺ and Thy1.1⁻ cell populations from sgRNA1, sgRNA2, and control CRISPRgenic mice. Data associated with Fig. 4C and 4D.