SUPPLEMENTAL FIGURES



Representative flow cytometry showing the percentage of (A) FAS^+GL7^+ germinal center (GC) B cells and (B) CD138⁺ PCs for the dLN (left) and spleen (SPL, right) for the indicated day in naïve or memory mice. (C) Quantitation of the absolute number of GC B cells and PCs from A for the indicated day. Significance determined by two-tailed Student's *t*-test. Data related to Fig. 1.

Supplemental Figure 2



Supplemental Figure 2. FACS isolation of influenza-specific MBC and nBs.

Gating strategy showing the FACS isolation of **(A)** nBs from the mediastinal LN and **(B)** IgM and IgG MBCs from pooled spleens and mediastinal LNs from 4 mice per sample. Data related to Fig. 2 and Fig. 3.



Supplemental Figure 3. MBCs harbor unique gene expression and accessibility programs. (A) Example bar plots of genes that are differentially expressed in MBCs compared to nBs. **(B)** Genome plots (left) and gene expression (right) for select DEG containing corresponding DAR between MBC subsets and nBs. DAR are indicated by a black horizontal bar and regions of interest by a yellow-shaded box. **(C)** Genome plots (left) and gene expression (right) for PC signature genes or genes regulated by BLIMP-1 in PC. *#* denotes genes not detected by RNA-seq for the indicated cell type. DAR are indicated as above. PC RNA-seq (22), ATAC-seq (49), and BLIMP-1 ChIP-seq (50) datasets were described previously. **(D)** Quantitative RT-PCR time course for the indicated gene in nB or MBC stimulated with CD40L, IL4, and IL5. Data are plotted as a percentage of 18S rRNA with error bars representing SD. Each time point represents cells from 6-9 mice from two independent experiments. Statistical difference was determined by two-way ANOVA with Tukey's post-hoc correction with * indicating P < 0.05. Data related to Fig. 2 and Fig. 3.