

Expanded View Figures

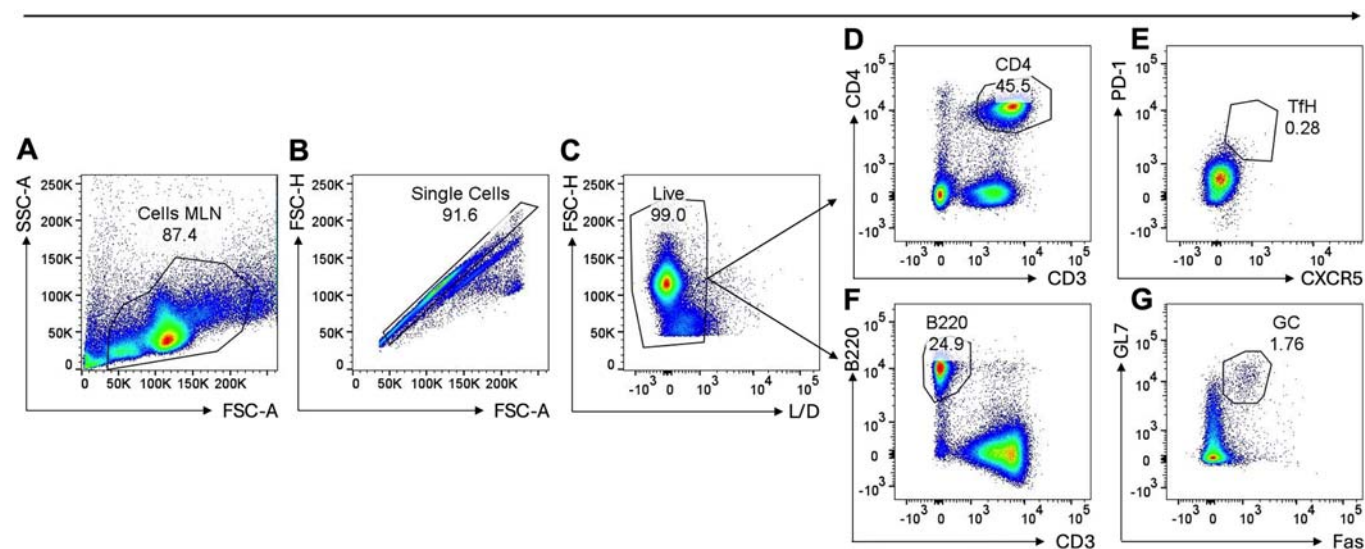


Figure EV1. Gating strategy for identification of Tfh cells and GC B cells by flow cytometry.

(A) Plot for forward versus side scatter, and mesenteric lymph node (MLN) cells gate. (B) Plot of forward scatter area as a function of forward scatter height within the MLN cells gate, and resulting single cells gate. (C) Viability dye (L/D) exclusion plot within the singlet gate, and resulting live cell gate. (D) Gating of CD4 cells, then gating of T follicular helper (Tfh) cells. (E) identified by PD-1 and CXCR5 within the CD4 gate. This panel is presented as a representative mouse in Fig. 2D. (F, G) Gating of B220+ B cells (F), then gating of germinal center (GC) B cells (G), identified by Fas and GL7 cells within the B220+ gate.

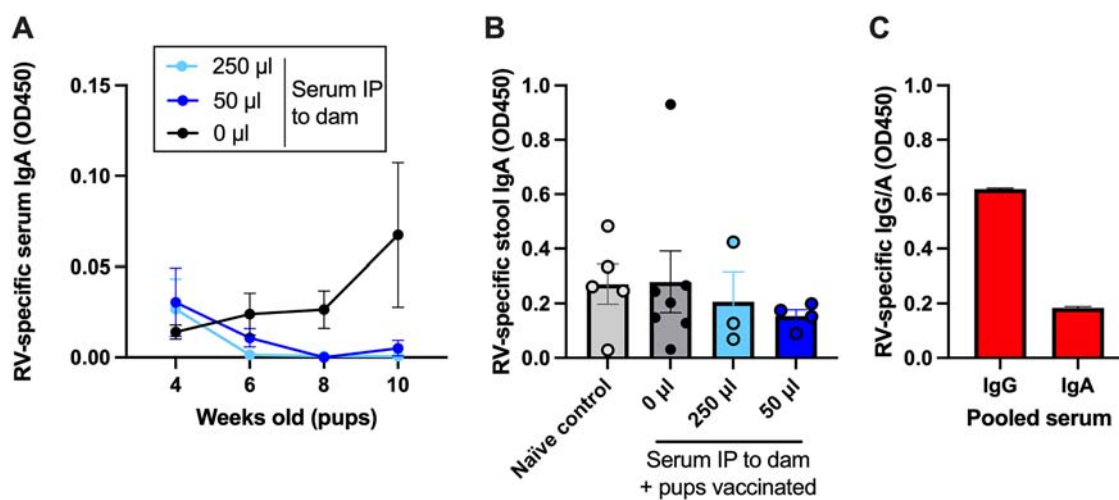


Figure EV2. Quantification of IgA in mouse stool and serum samples in the presence or absence of MatAbs.

(A) Longitudinal serum IgA titers following vaccination at 7 days old with different volumes of rotavirus-seropositive serum passively transferred to dams; $n = 3$, $n = 4$, and $n = 9$ for 250, 50, and 0 µL serum, respectively. (B) Stool IgA titers in adult mice from experiment (A) 14 days after challenge with rotavirus; $n = 5$, $n = 7$, $n = 4$, and $n = 3$ for naïve control, and 0, 50, and 250 µL, respectively. (C) Rotavirus-specific IgG and IgA ELISA of pooled serum used for passive transfer experiments, mean of $n = 2$ technical replicates shown. Data information: error bars indicate SEM. Source data are available online for this figure.

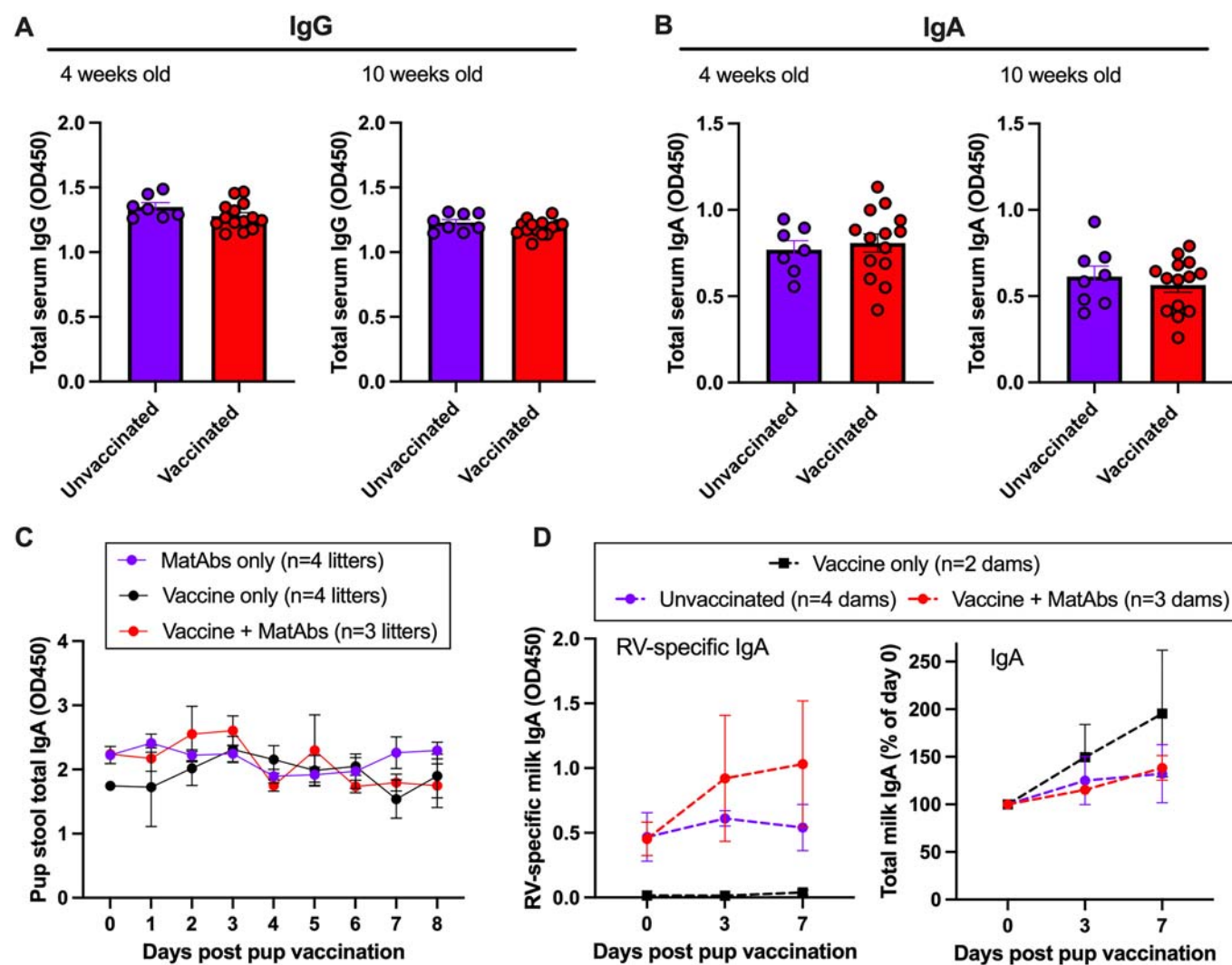


Figure EV3. Total IgG and IgA in serum, stool, and milk samples.

(A) Total IgG quantified by ELISA in serum samples from 4-week- and 10-week-old pups with MatAbs +/- rotavirus vaccination; $n = 7$ and $n = 14$ in unvaccinated and vaccinated pups at 4 wk and $n = 8$ and $n = 14$ in unvaccinated and vaccinated pups at 10 wk. (B) Total IgA quantified by ELISA in the same serum samples as in (A); $n = 7$ and $n = 14$ in unvaccinated and vaccinated pups at 4 wk and $n = 8$ and $n = 14$ in unvaccinated and vaccinated pups at 10 wk. (C) Total IgA ELISA in stool samples collected from pups 0 to 8 days after rotavirus vaccination. (D) Rotavirus-specific IgA and total IgA were quantified by ELISA in milk samples collected from dams at 0, 3, and 7 days after pup vaccination. Data information: error bars indicate SEM. Source data are available online for this figure.

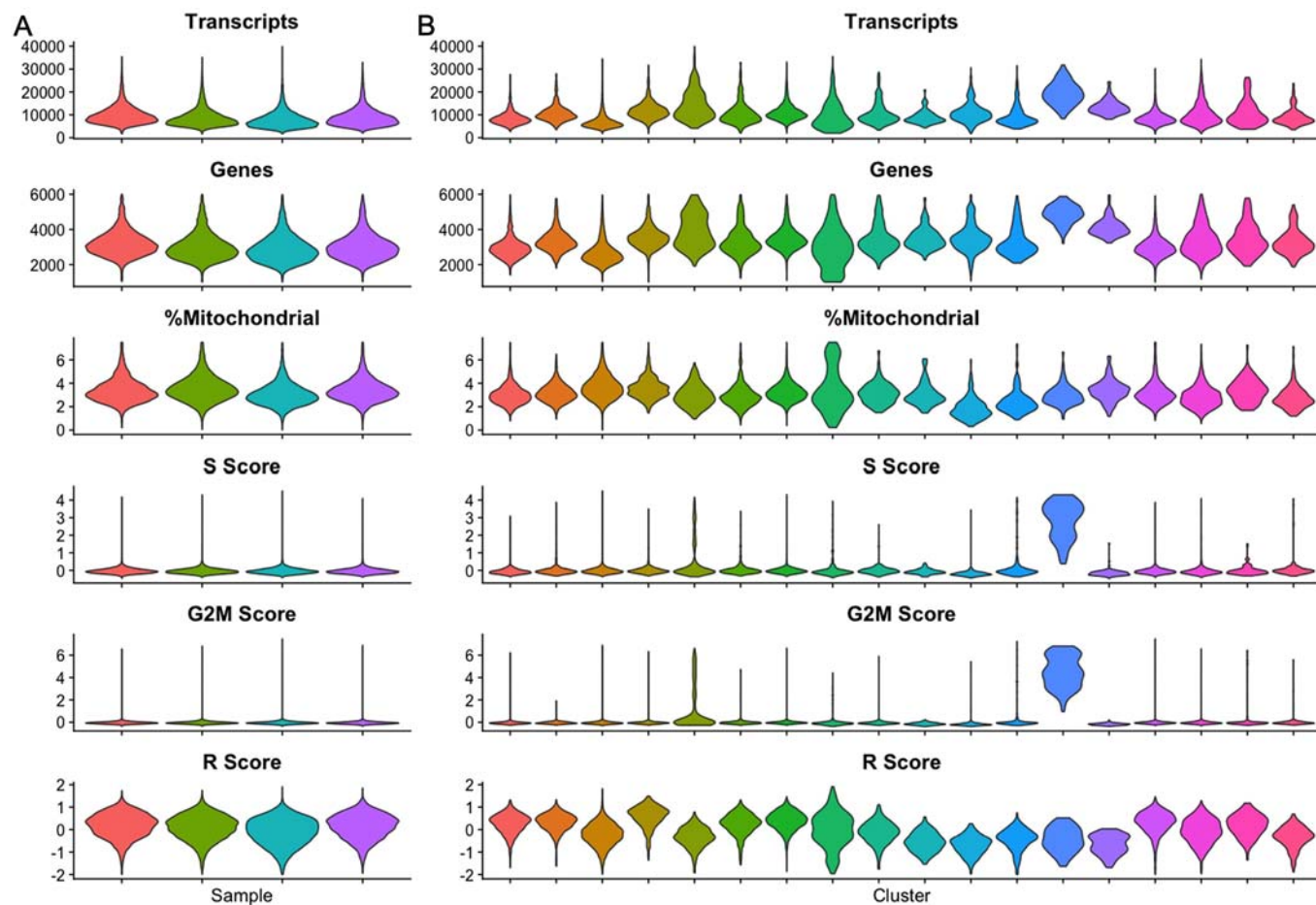
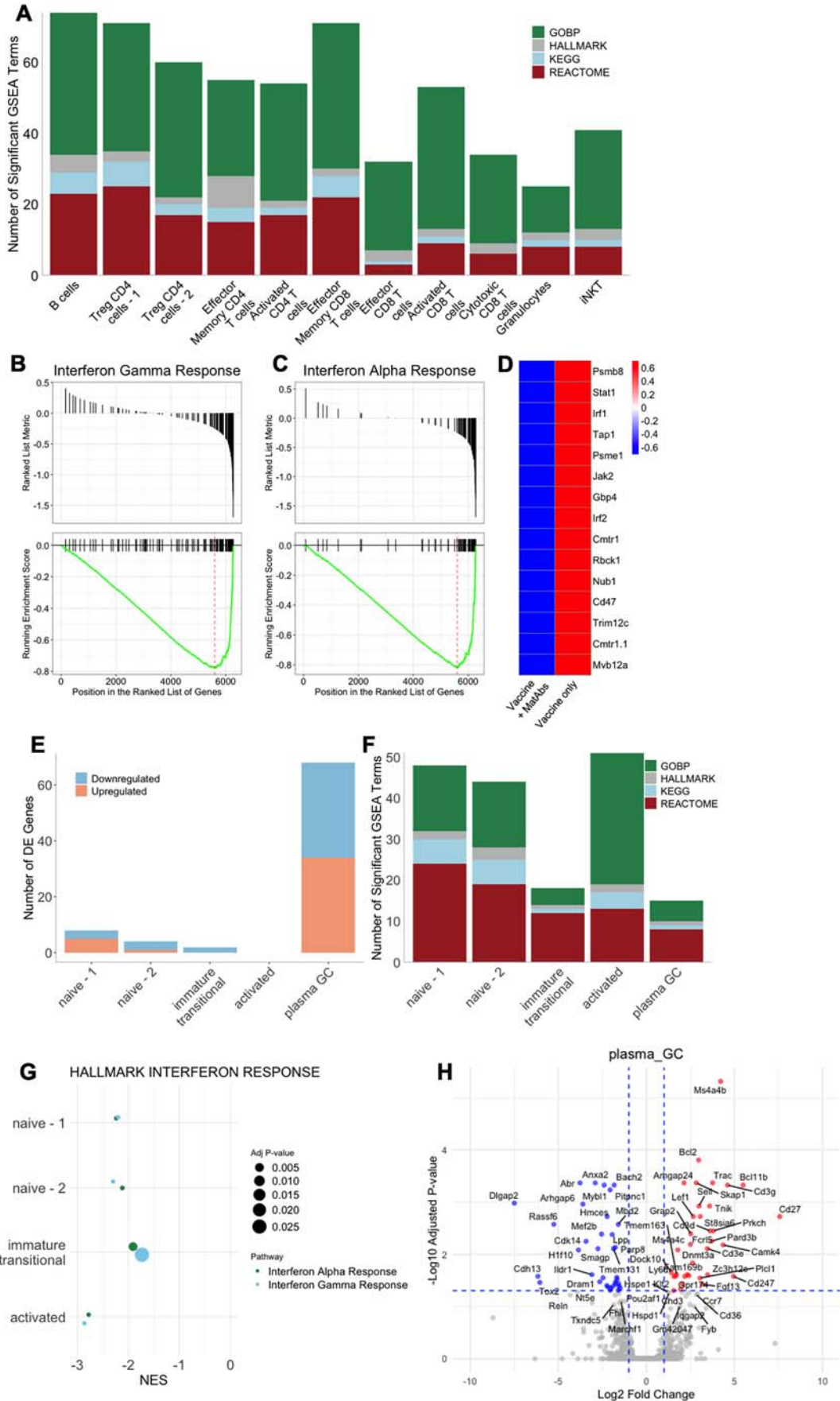


Figure EV4. Single-cell transcriptomics of the draining mesenteric lymph node.

(A) Violin plot showing quality control metrics (from top to bottom: transcripts per cell, genes per cell, percent mitochondrial reads per cell, S score, G2M score, and R score) for each sample ($n = 4$, x-axis) processed on the 10x Genomics Chromium instrument. (B) Violin plot showing quality control metrics for each cell type (x-axis) from MLN from pups vaccinated in the absence ($n = 2$) or presence ($n = 2$) of MatAbs.



◀ **Figure EV5. Differential gene expression in the draining mesenteric lymph node.**

(A) Counts of the strongest significantly enriched gene sets with an absolute normalized enrichment score (NES) >2 across the largest cell clusters. (B) GSEA plot of hallmark interferon gamma response in activated CD4 T cells. (C) GSEA plot of hallmark interferon alpha response in activated CD4 T cells. (D) Heatmap of top ten core enrichment genes taken from the gene set Hallmark Interferon Gamma and Hallmark Interferon Alpha Response between vaccine + MatAb and vaccine only; expression values row-normalized; unique genes from both pathways plotted. (E) Counts of differentially expressed (DE) genes (y-axis) per B cell cluster, comparing vaccine + MatAb to vaccine only with absolute log2 fold change >1 and adjusted *p*-value ≤0.05. (F) Counts of the strongest significantly enriched gene sets with an absolute normalized enrichment score (NES) >2 across B cell clusters. (G) GSEA results showing downregulation of hallmark interferon alpha response and hallmark interferon gamma response in B cell clusters. Dots are sized to denote significance; the x-axis indicates NES. (H) Volcano plot for differentially expressed genes in vaccine + MatAb (*n* = 2) compared to vaccine only (*n* = 2) (MatAb/naïve) in plasma and GC cells. Up (red) and downregulated (blue) genes with absolute log2 fold change >1 and adjusted *p* value >0.05 shown; $-\log_{10}$ adjusted *p*-value shown. Data information: The Wald (default in DESeq2, version 1.44.0) test was used to generate *p*-values before Benjamini-Hochberg correction for multiple testing to generate adjusted *p*-values (H).