

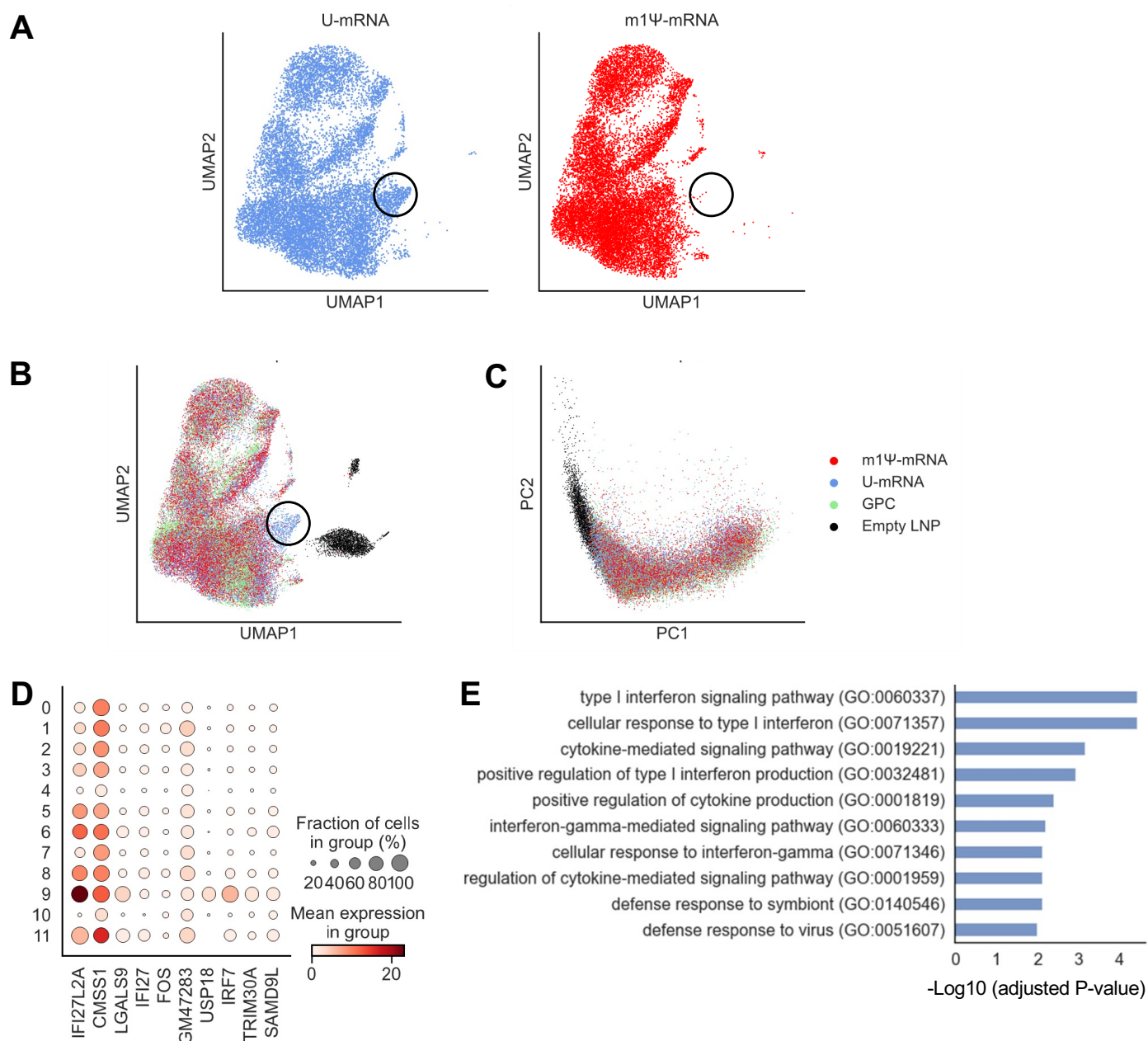


Fig. S1. Cluster 9 in lymph node B cells of mice immunized with U-mRNA vaccine demonstrates upregulation of genes involved in the innate immune response. Data from the study shown in Fig. 3. **A.** Comparison of single-cell RNA-seq data from lymph nodes isolated from immunized mice: U-mRNA (left) and m1Ψ-mRNA (right). Cluster 9 is circled. **B.** Clustering of single-cell RNA-seq data from lymph nodes isolated from immunized mice based on the U-mRNA and m1Ψ-mRNA groups combined. Cluster 9 is circled. **C.** Principal component analysis of B cells from single-cell RNA-seq. **D.** Mean expression of top 10 differentially expressed genes for mice immunized with U-mRNA across clusters. **E.** Top 10 significantly upregulated terms from the Gene Ontology Biological Processes database using the differentially expressed genes for Cluster 9.

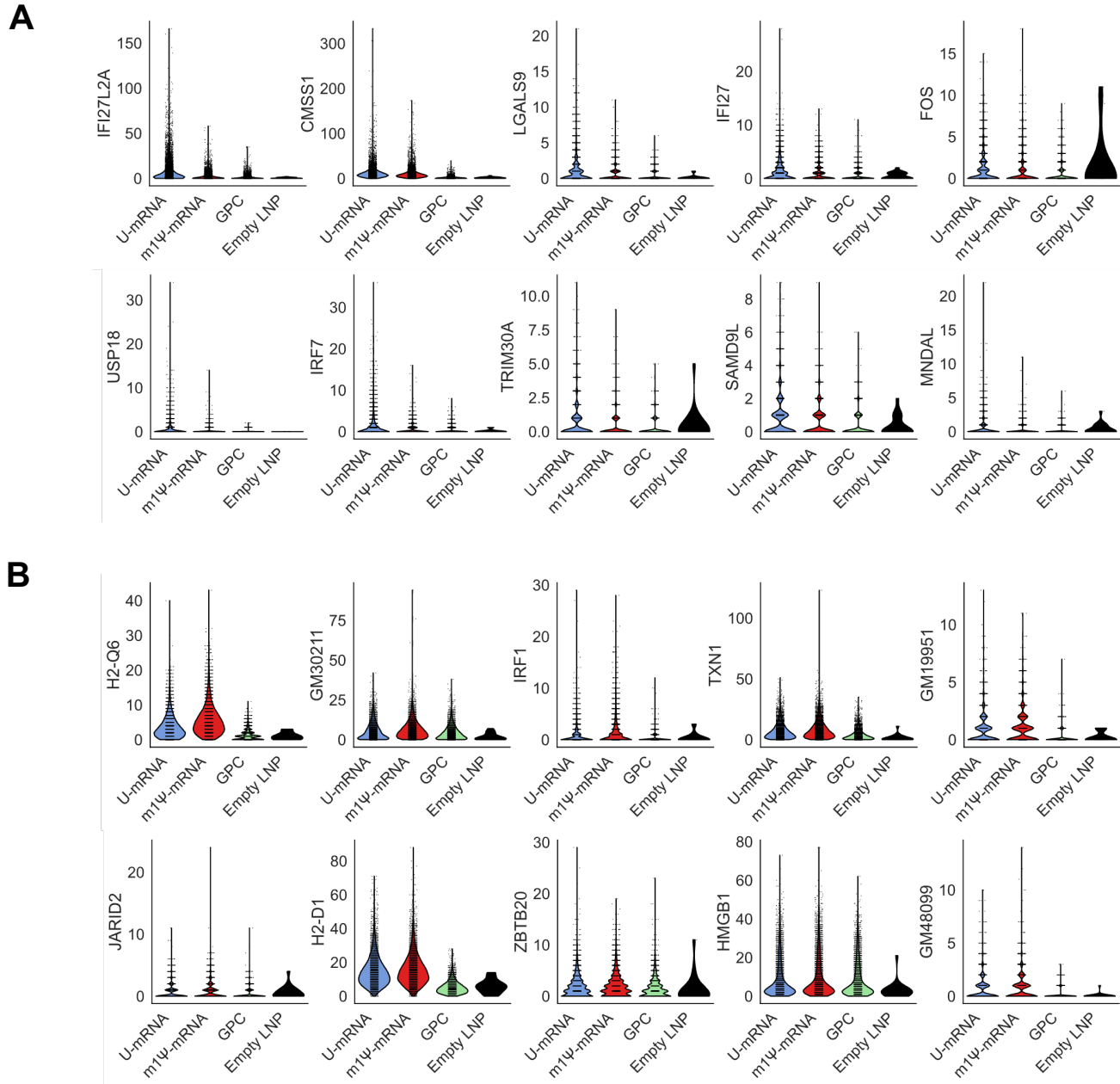


Fig. S2. Gene expression patterns in B cells of mice immunized with ANDV U-mRNA and m1Ψ-mRNA are similar. Data from the study shown in Fig. 3. Top 10 differentially expressed genes for B cells of mice immunized with U-mRNA (A) and m1Ψ-mRNA (B).

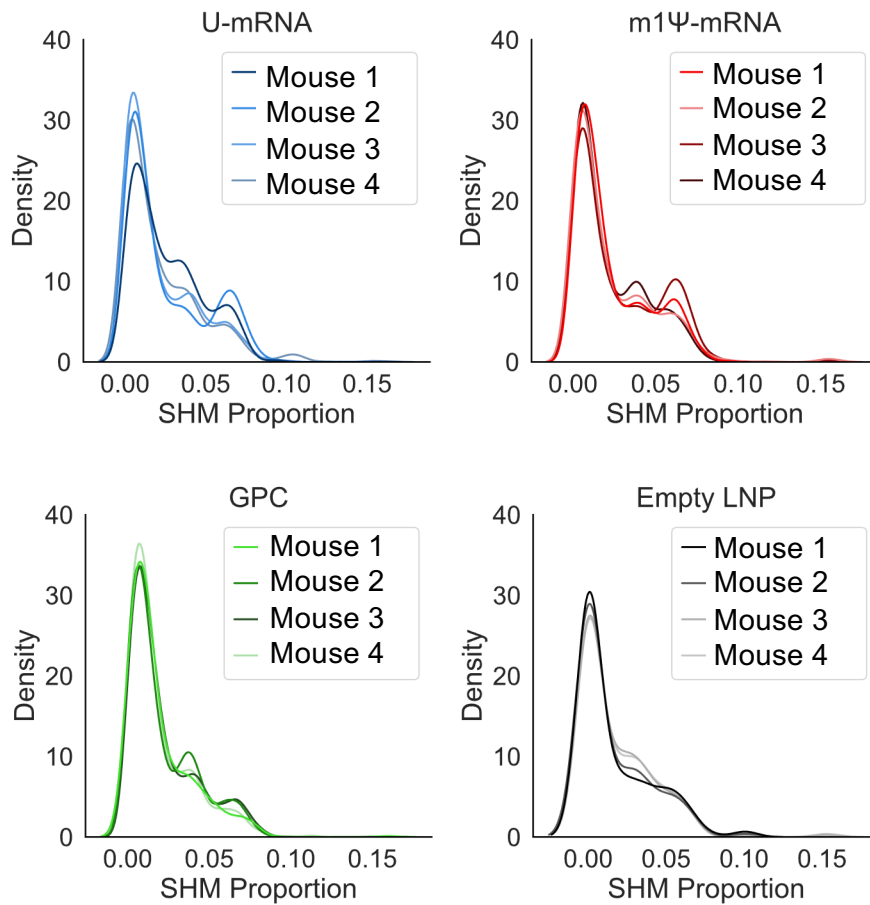


Fig. S3. Distributions of somatic hypermutations in heavy chain variable regions. Proportion of SHM is shown for the heavy chain variable region across all cells for each mouse in the four treatment groups. Distributions are represented by a kernel density estimation.

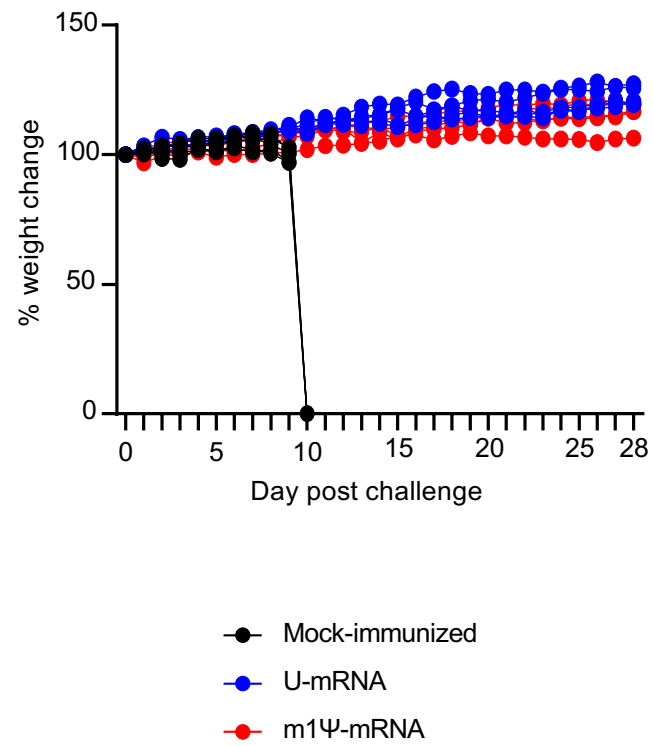


Fig. S4. Change in hamster weights in individual animals after ANDV challenge.