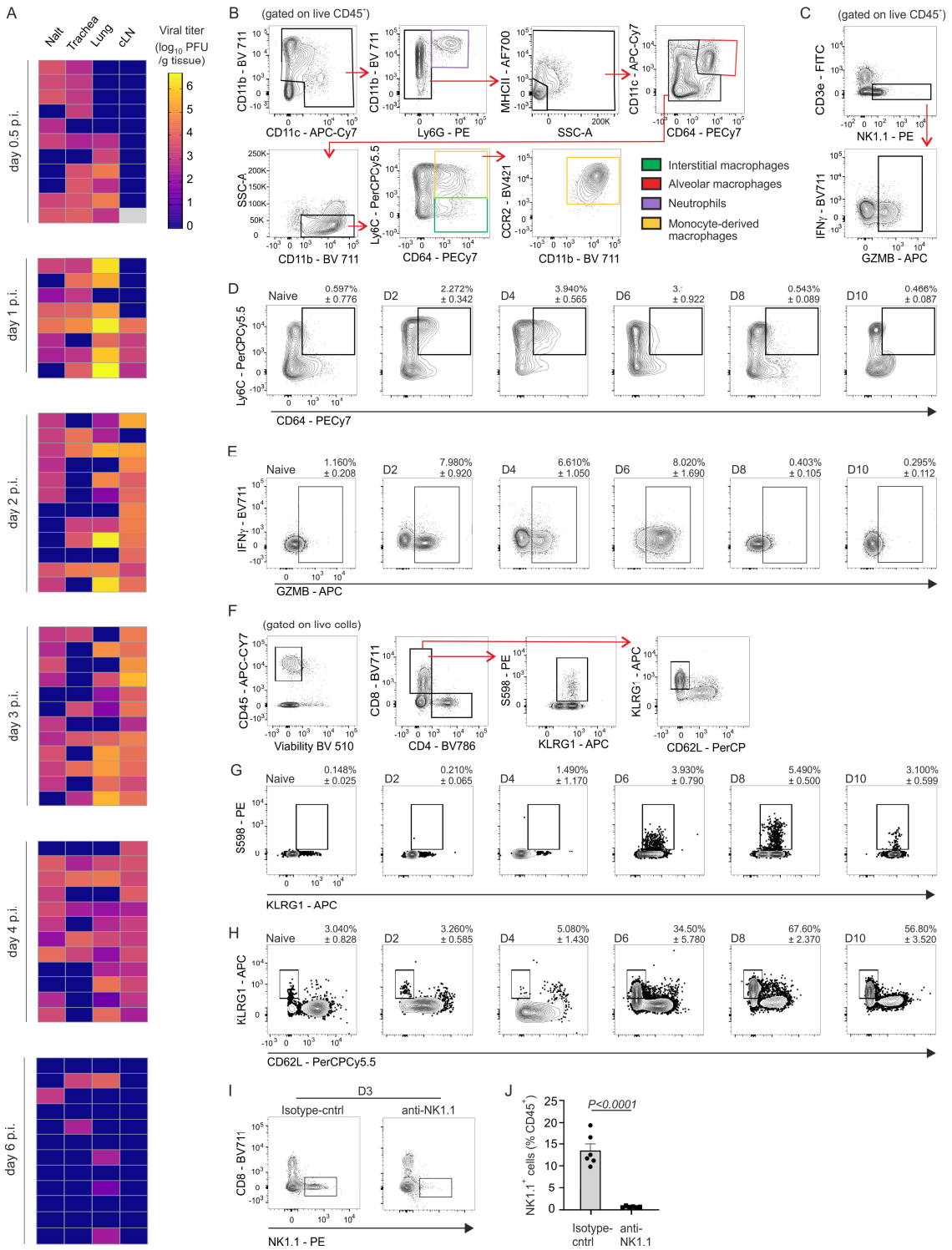
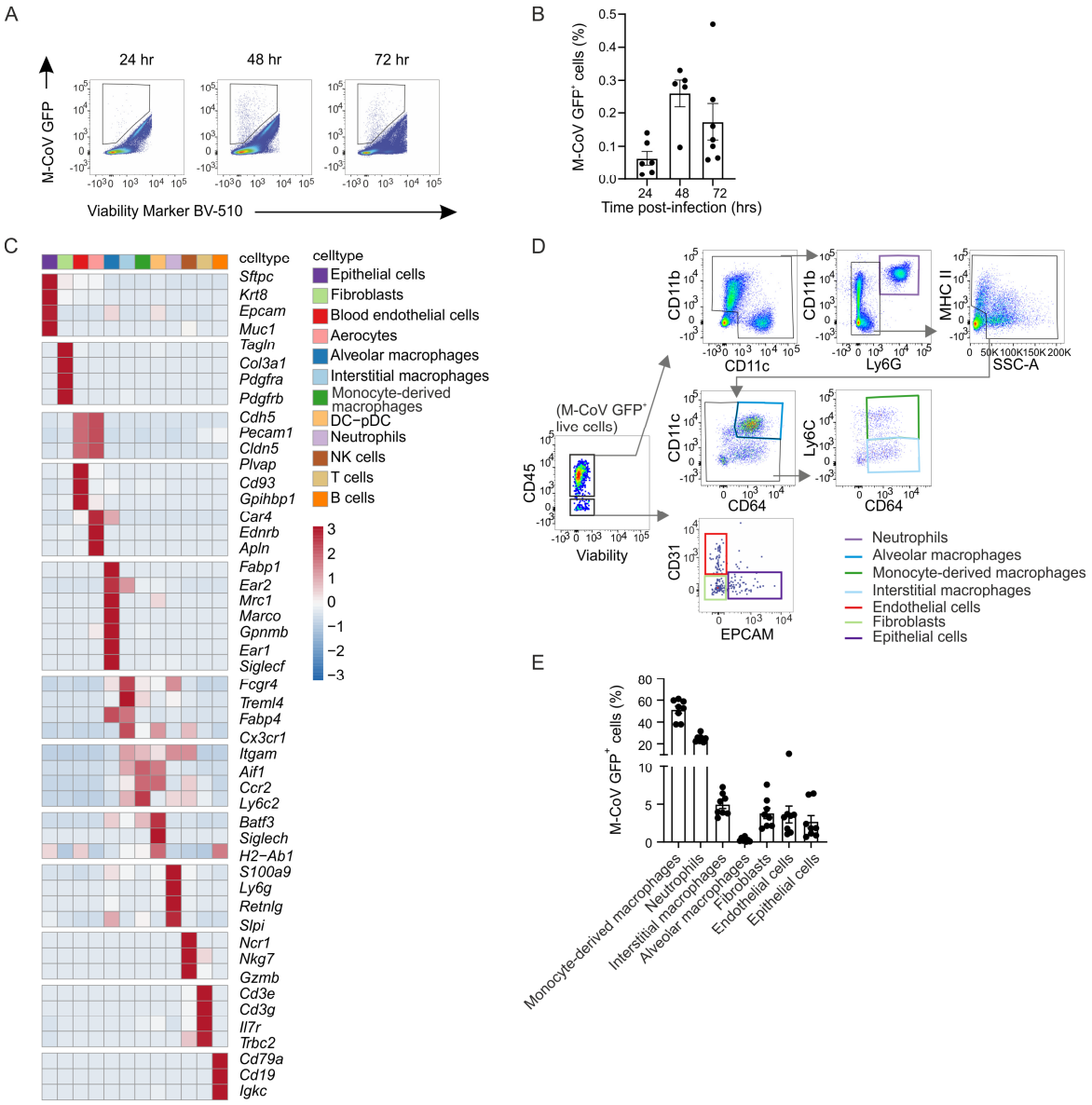


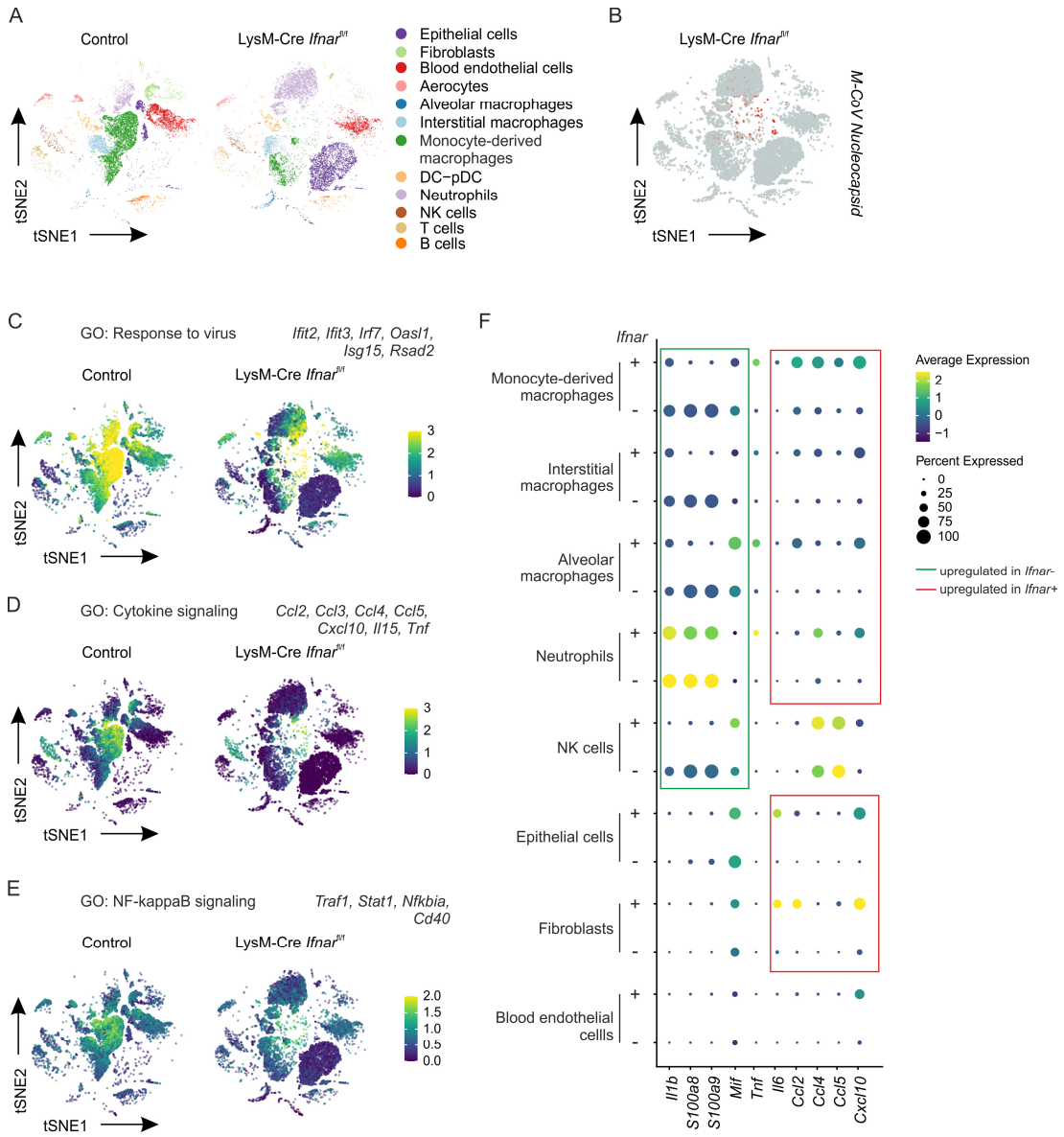
Supplementary Figure 1 Dynamics of M-CoV replication and antiviral immunity

A) Viral titers in the nasal-associated lymphoid tissue (NALT), trachea, lungs and cervical LN (cLN) over time in mice infected with M-CoV. B-C) Gating strategy of myeloid cell populations (B) and Granzyme B (GZMB)-expressing NK cells (C) in mouse lungs. D-E) Representative flow cytometric plots of monocyte-derived- and interstitial macrophages (D) and GZMB-expressing NK cells (E) at the indicated days after M-CoV infection. Mean % ± SEM relative to myeloid cells (D) or NK cells (E) are indicated. F) Gating strategy of S598^{+} CD8^{+} T cells and activated (KLRG1^{+} CD62L^{-}) CD8^{+} T cells. (G-H) Representative flow cytometric plots of S598^{+} CD8^{+} T cells (G) and activated CD8^{+} T cells (H) at the indicated days after M-CoV infection. Mean % ± SEM relative to CD8^{+} T cells is indicated. I) Representative flow cytometric plots of pulmonary NK cells after isotype control or anti-NK1.1 antibody treatment. J) Flow cytometric relative quantification of NK cells in the lungs after isotype control or anti-NK1.1 antibody treatment. Data in (A) are representative of three independent experiments. Data in (J) is representative of two independent experiments with N=6 for each group. P values as per unpaired two-tailed Student's t-test; mean ± SEM are indicated.



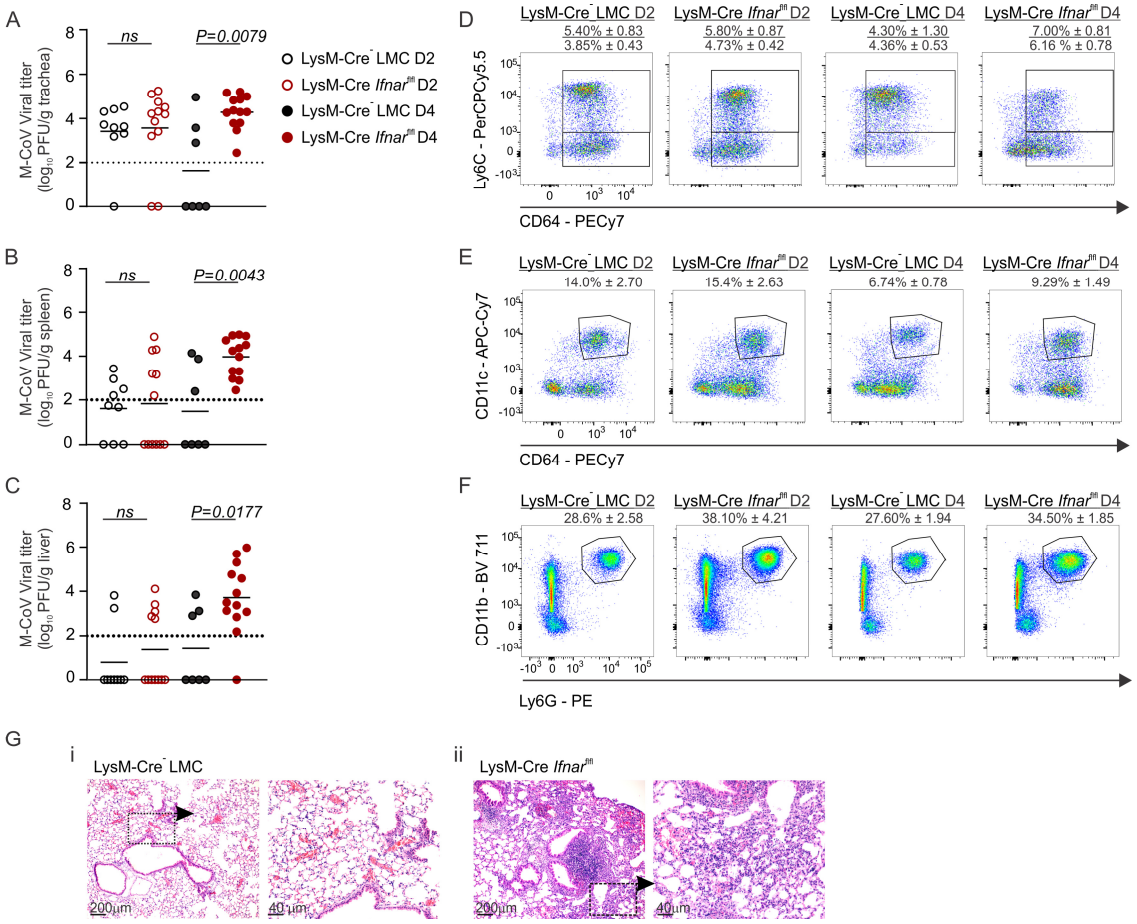
Supplementary Figure 2 M-CoV-infected cell types in the lungs

A) Representative flow cytometry plots depicting the frequency of M-CoV GFP-infected cells at 24, 48 and 72 hours post-infection. B) Relative flow cytometric quantification of M-CoV GFP$^+$ cells at the indicated time points. C) Marker genes of assigned pulmonary cell types used for scRNA-seq analysis. D) Gating strategy to identify M-CoV-GFP infected stromal and hematopoietic cell populations in the lungs of infected mice. E) Relative composition of M-CoV-GFP infected cell types within the lung at 36 hours post-infection. Data in (A-B) are representative of three independent experiments with N=6 mice at 24 hours, N=5 at 48 hours, and N=7 at 72 hours; mean ± SEM are indicated. Data in (C) are representative of 22,842 cells. Data in (E) are representative of three independent experiments with N=8 mice; mean ± SEM are indicated.



Supplementary Figure 3 Transcriptional changes to the pulmonary landscape in M-CoV-infected conditionally *Ifnar*-deficient and *Ifnar*-sufficient mice

A) Dimensional reduction t-SNE plot of lung cell types represented in scRNA-seq data from *Ifnar*-sufficient control and LysM-Cre *Ifnar*$^{fl/fl}$ mice 36 hours following M-CoV infection. B) Feature plot representing the expression of the M-CoV nucleocapsid transcript in the lungs of infected LysM-Cre *Ifnar*$^{fl/fl}$ mice. ScRNA-seq data are representative of 27,420 cells, corresponding to 14,646 cells from lungs of infected control mice and 12,774 cells from lungs of LysM-Cre *Ifnar*$^{fl/fl}$ mice. C-E) Gene expression profiles of selected genes from gene sets enriched in M-CoV-infected *Ifnar*-sufficient control mice compared to LysM-Cre *Ifnar*$^{fl/fl}$ mice projected onto t-SNE plots of transcriptomes from the respective genotypes. F) Average expression of inflammatory cytokines and chemokines in infected lungs from control or LysM-Cre *Ifnar*$^{fl/fl}$ mice. ScRNA-seq data are representative of 27,420 cells, corresponding to 14,646 cells from lungs of infected control mice and 12,774 cells from lungs of LysM-Cre *Ifnar*$^{fl/fl}$ mice.



Supplementary Figure 4 Changes in innate immune cell composition accompanying lung pathology and viral dissemination in LysM-Cre *Ifnar*$^{fl/fl}$ mice

A-C) Viral titers in the trachea (A), spleen (B) and liver (C) of LysM-Cre$^-$ LMC and LysM-Cre *Ifnar*$^{fl/fl}$ mice at days 2 and 4 after intranasal M-CoV infection. D-F) Representative flow cytometric plots of monocyte-derived and interstitial macrophages (D), alveolar macrophages (E), and neutrophils (F) in infected LysM-Cre$^-$ LMC and LysM-Cre *Ifnar*$^{fl/fl}$ mice at 2 and 4 days p.i. Mean % ± SEM relative to CD11b$^+$ CD11c$^+$ myeloid cells are indicated. G) Representative bright field image of lung lobes from LysM-Cre$^-$ LMC and LysM-Cre *Ifnar*$^{fl/fl}$ mice infected 2 days earlier with M-CoV, and stained with hematoxylin and eosin. (A-C) Data are representative of three independent experiments with N= 9 LysM-Cre$^-$ LMC mice on day 2 p.i., N=7 LysM-Cre$^-$ LMC mice on day 4 p.i., N= 12 LysM-Cre *Ifnar*$^{fl/fl}$ for day 2 p.i. and N= 13 LysM-Cre *Ifnar*$^{fl/fl}$ for day 4 p.i.. Statistical analysis was performed using unpaired two-tailed Student's t-test; mean is indicated. Data in (G) are representative of N=4 mice per genotype.