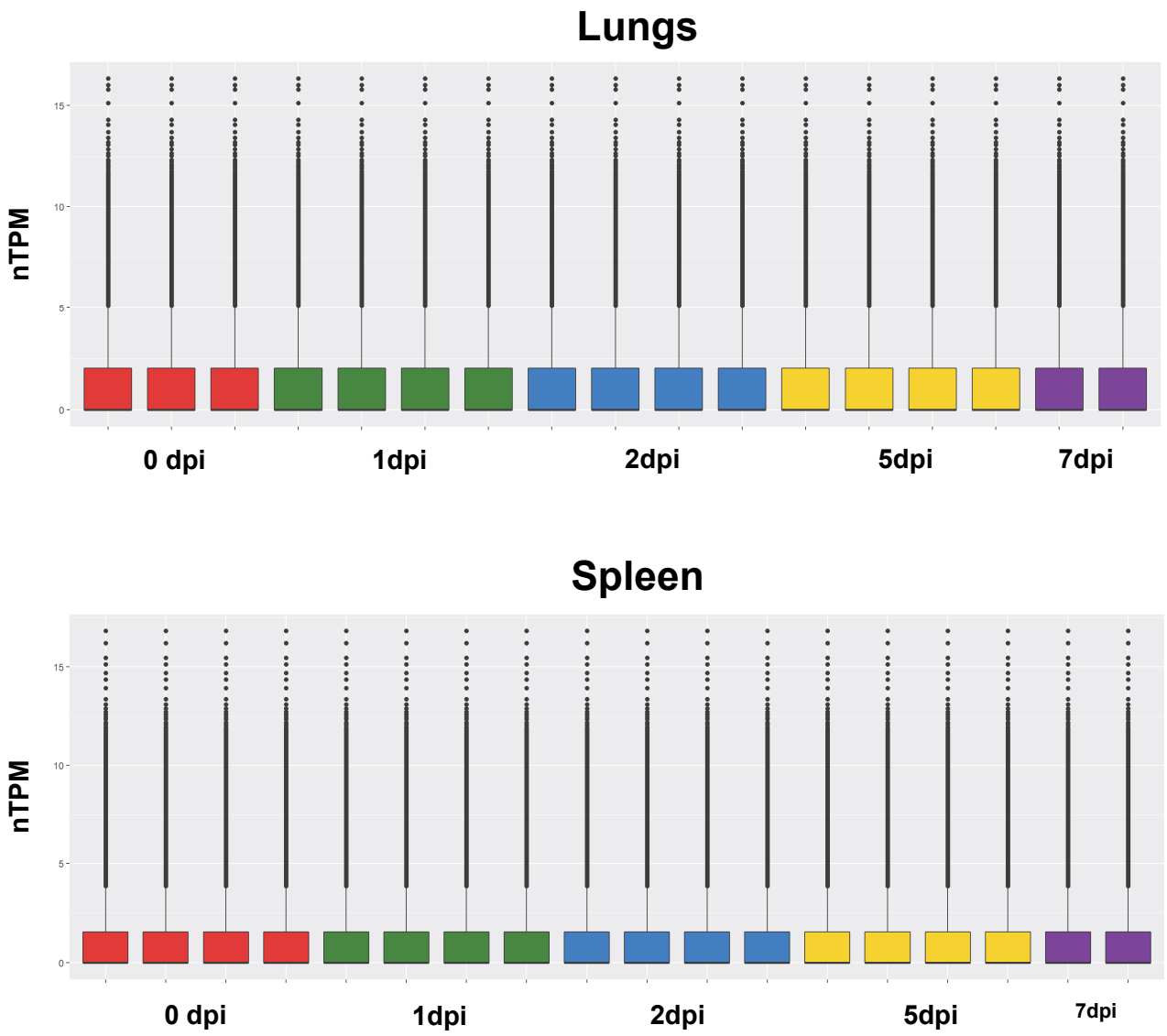
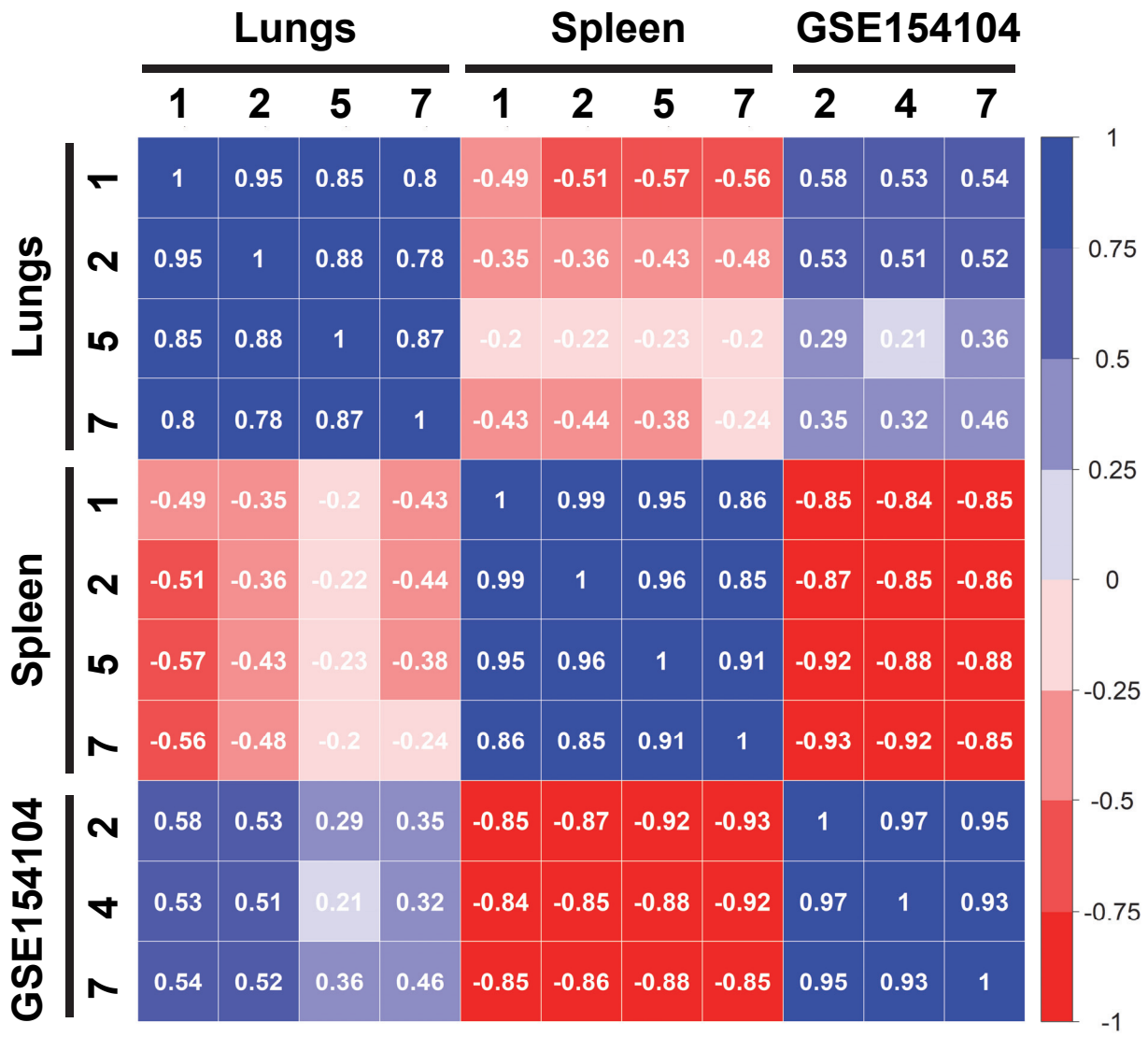
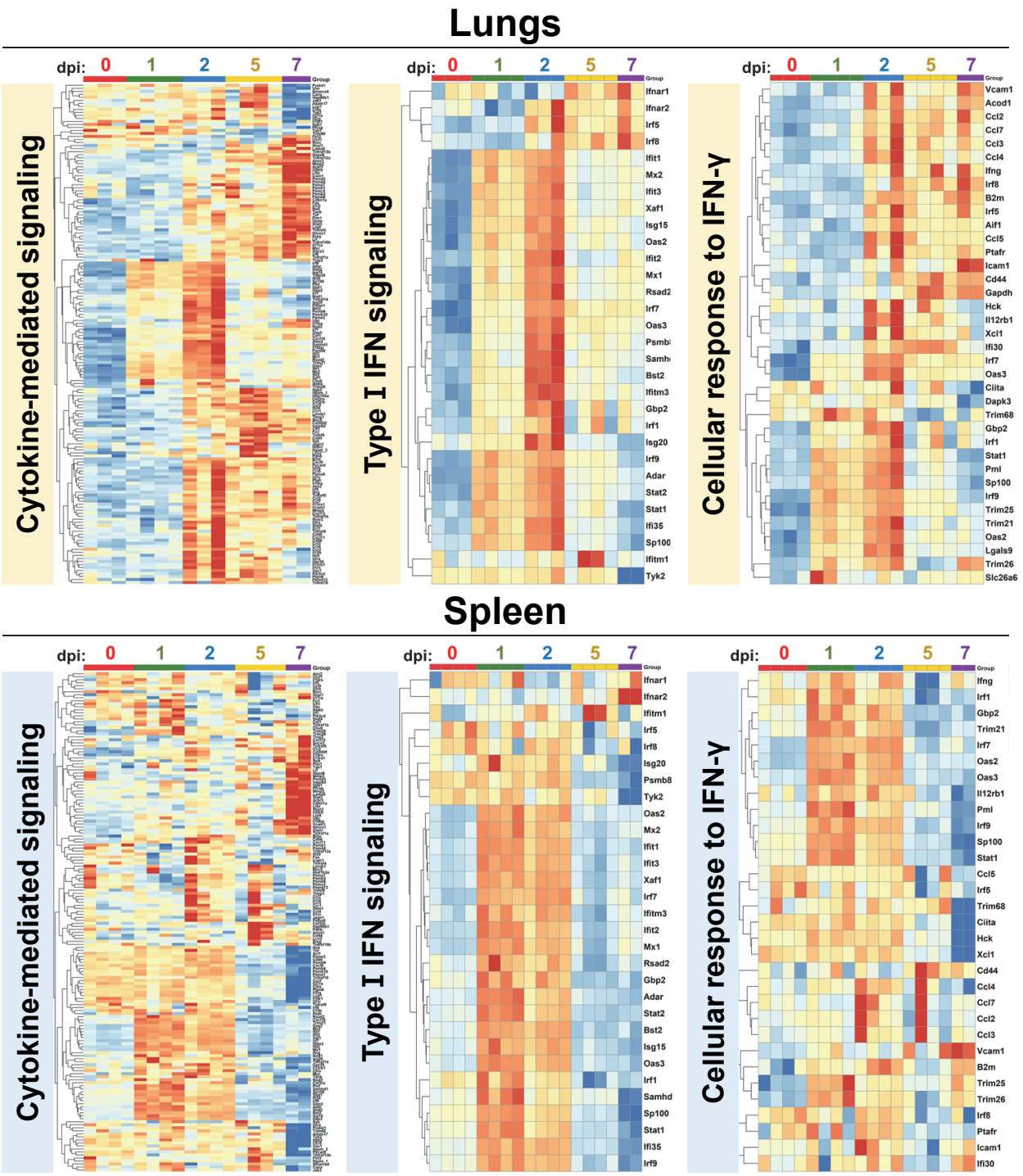


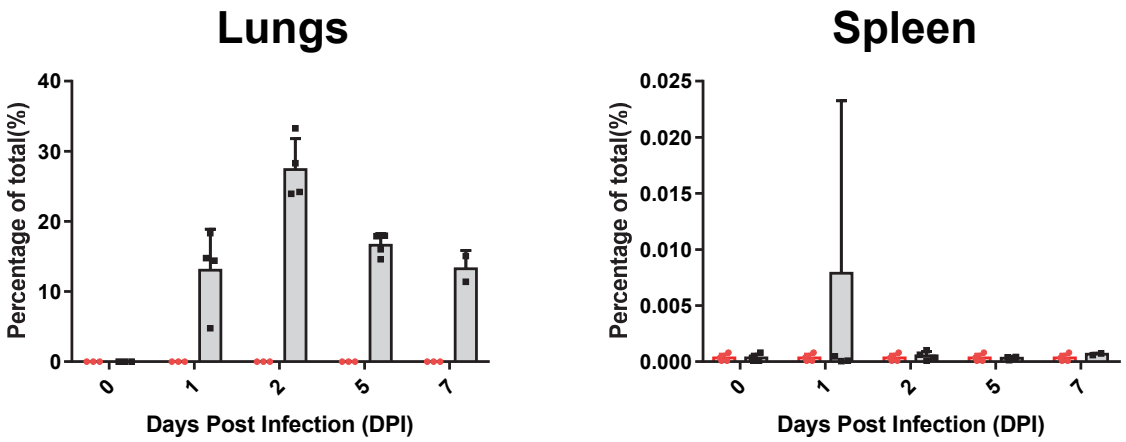
Supplementary Fig. S1. Quality assessment of gene expression in RNA-seq data. Box plots show respective distribution of gene expression across 17 lungs and 18 spleen samples of SARS-CoV-2-infected K18-hACE2 transgenic mice. The distribution was nearly consistent after normalization, showing data quality.



Supplementary Fig. S2. Correlation analysis of transcriptome of SARS-CoV-2-infected samples. Spearman correlations of expression values in lungs and spleen of this study and publicly available data from the Gene Expression Omnibus. The mRNA expression level of SARS-CoV-2 infected samples was obtained from Winkler et al. (2020) (GSE154104). Only mean TPM values of 48,438 overlapping genes across samples of three studies were used. Blue indicates positive correlation and red indicates negative correlations. Non-significant values ($P > 0.05$ measured by Spearman's correlation, *t*-test) were absent. Number indicates days post infection.



Supplementary Fig. S3. Hierarchical clustering analysis of SARS-CoV-2-infected samples in enriched pathways from published data. Heatmaps of significantly upregulated genes during SARS-CoV-2 infection enriched in the cytokine-mediated signaling pathway, type I interferon, and cellular response to IFN-γ, identified through Gene Ontology analysis in the previous study (Winkler et al., 2020). Genes shown in each pathway are identical differentially expressed gene set discovered in the previous study except for few genes due to different reference genome. Columns represent samples and rows represent genes. Gene expression levels in the heat maps are z-score normalized values determined from normalized TPM values. Yellow indicates lungs and blue indicates spleen sample.



Supplementary Fig. S4. Percentage of reads mapped to corresponding SARS-CoV-2 viral genome. The bar plots show the percentage of reads mapped to SARS-CoV-2 virus genome (GenBank No. MN985325.1). Percentage of mapped reads were calculated by dividing counted fragments with total fragments aligned to the corresponding reference genome. Each dot indicates a sample. Red represents mock samples of specific organs, while black shows samples designated to days post infection.