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Supplemental Information

Heightened Innate Immune Responses in the Respiratory Tract of COVID-19 Patients

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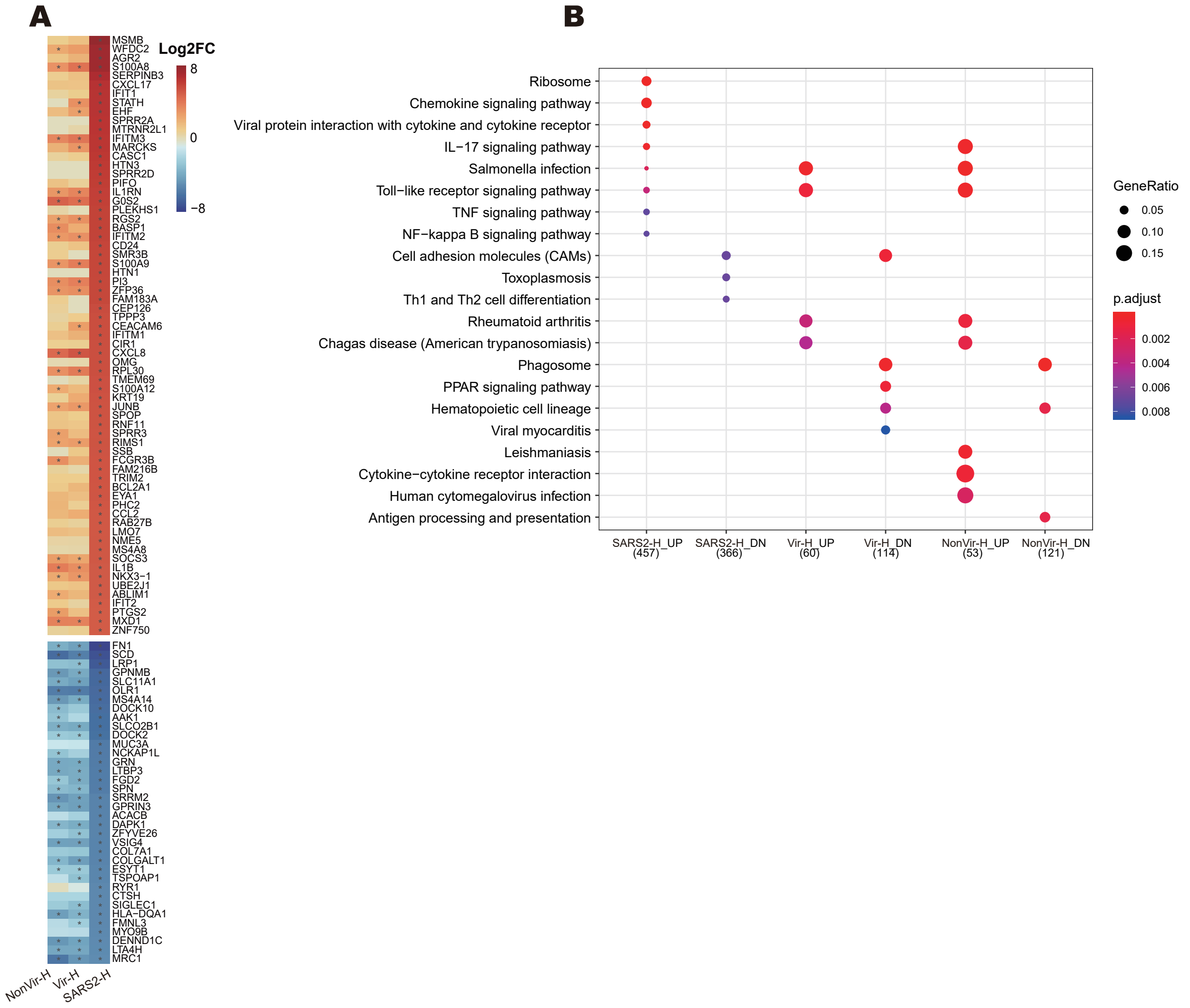
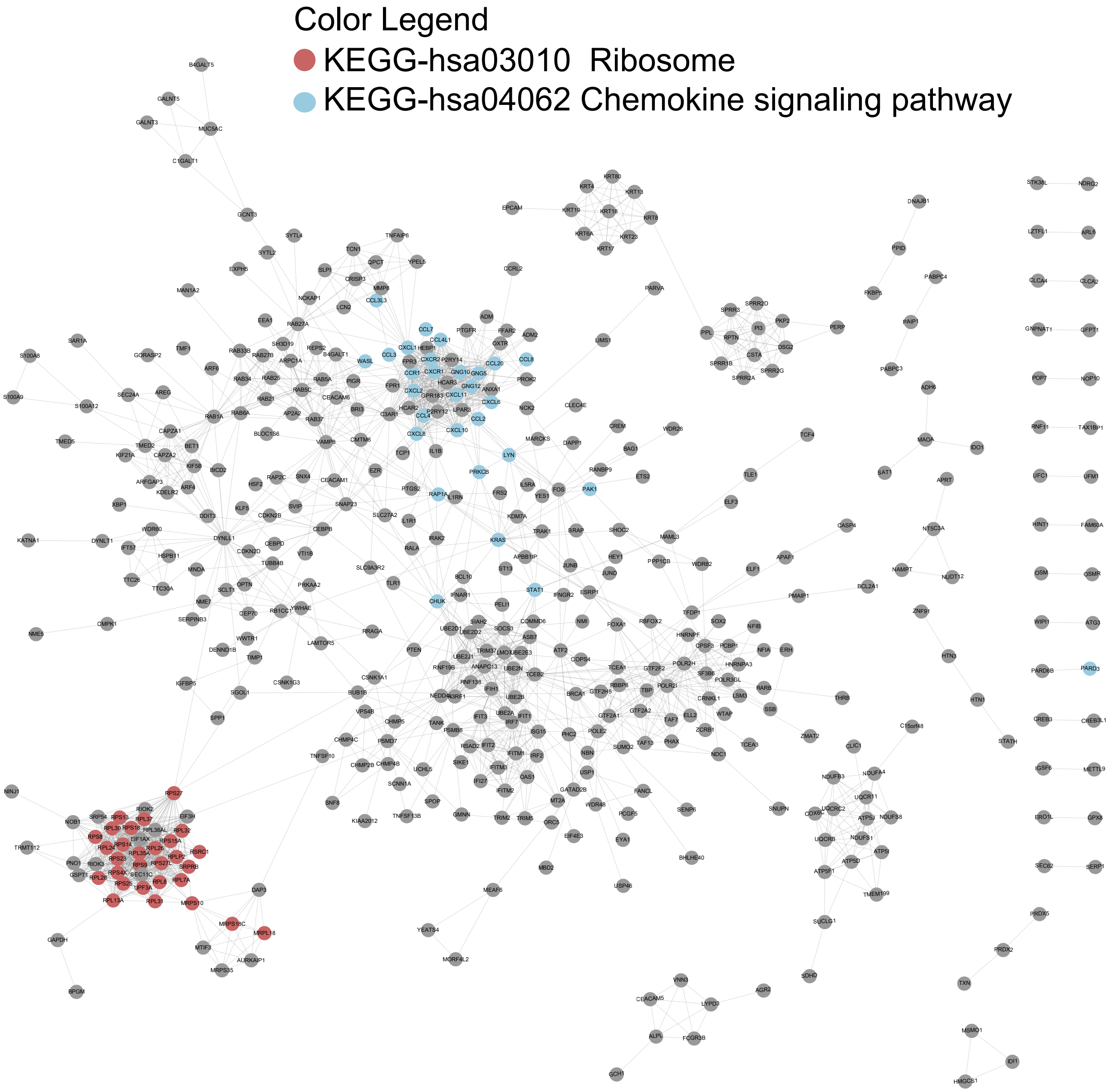


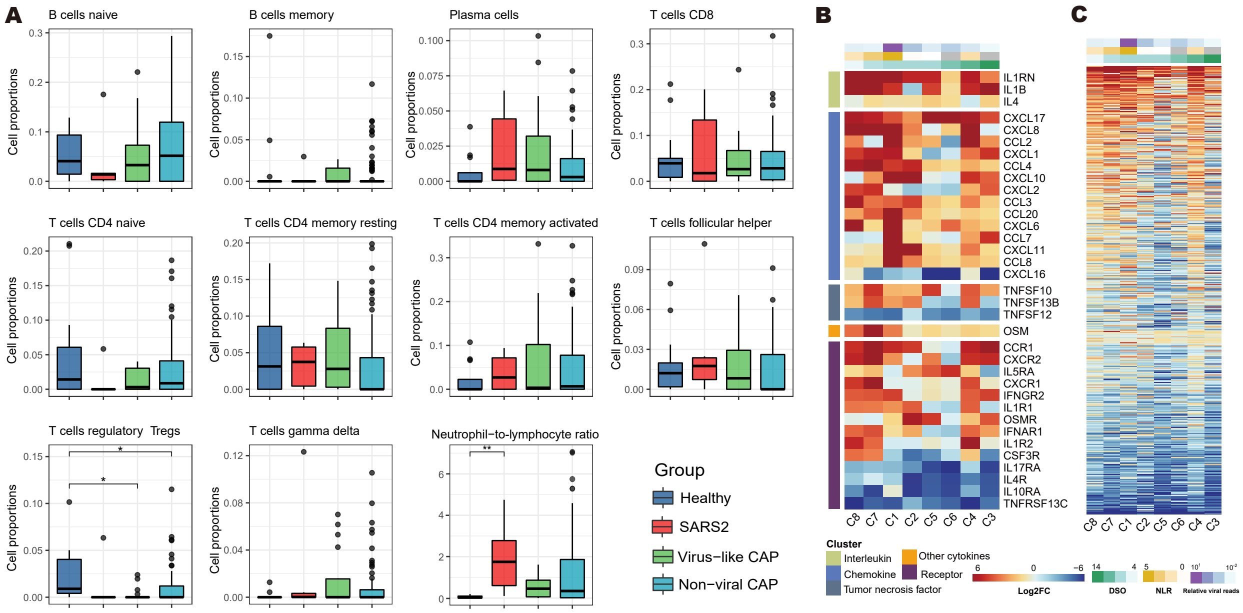
Supplementary Figure 1. KEGG pathway enrichment analysis of up-regulated and down-regulated DEGs, Related to Figure 1.

(A) Heatmap of DEGs with absolute log2FC ≥ 5 for SARS2-H. Asterisks (*) indicate significant DEGs (absolute log2FC ≥ 2, q-value < 0.05). **(B)** Pathways with q-value < 0.05 are shown, and the number of Entrez Genes was indicated in brackets.



Supplementary Figure 2. PPI network of up-regulated DEGs in SARS2 comparing to Healthy, Related to Figure 1.

Each node represents a protein, and interactions with confidence score > 0.9 are presented.



Supplementary Figure 3. The proportion of T cells, B cells, and neutrophil to lymphocyte ratio in BALF predicted from transcriptome data, Related to Figure 4.

(A) The proportion of lymphocyte was calculated as the sum of proportions of T cells, B cells, and NK cells. Asterisks represent significant differences between groups (*q-value < 0.05, **q-value < 0.01, Mann-Whitney test). **(B)** Heatmap, as described in Figure 2B, was labeled with the neutrophil-to-lymphocyte (NLR) ratio. **(C)** Heatmap, as described in Figure 3A, was labeled with the NLR ratio.

Samples	Total reads number	Number	Proportion
C1	79784870	68679727	86.08%
C2	84810261	5756943	6.79%
C3	111227521	238006	0.21%
C4	65368577	1036590	1.58%
C5	23682377	232322	0.98%
C6	52198373	2262828	4.34%
C7	79285313	15438	0.02%
C8	27703965	81393	0.29%

Table S2. The number and proportion of SARS-CoV-2 reads identified in COVID-19 cases, Related to Figure 1, Figure 2, Figure 3, and Figure S3.

In each case, the number of total reads (Total reads number) and reads that can be directly mapped to the reference genome of SARS-CoV-2 (MN908947.3) (Number) are presented. The mapping software is BWA (mem mode).