Supplementary Material

1 Supplementary Tables

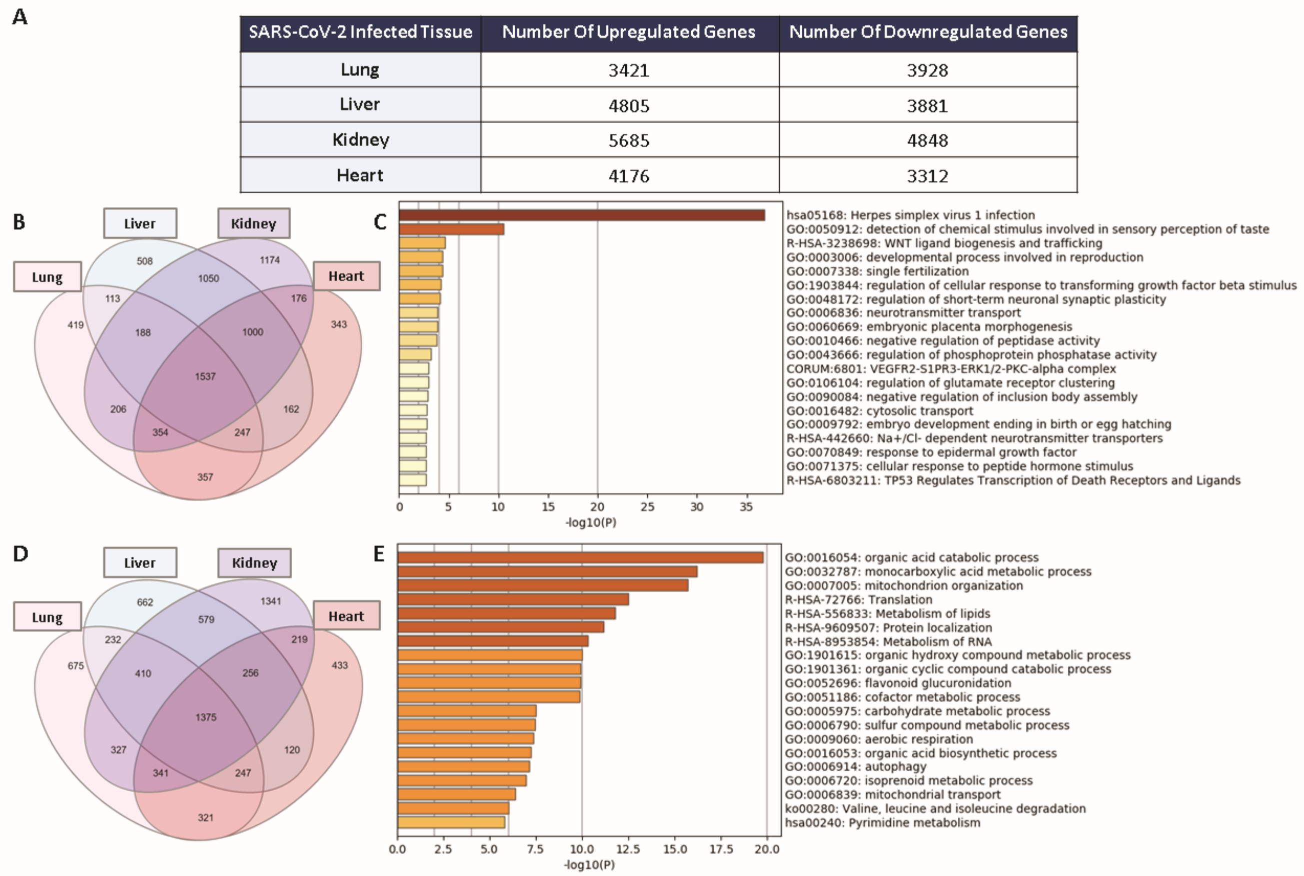
Table S1. Accession of Gene ontology sets retrieved from AmiGO 2 for the analysis of immune cell-specific gene enrichment

Accession	**Term**
GO:0042119	Neutrophil activation
GO:0030593	Neutrophil chemotaxis
GO:0043307	Eosinophil activation
GO:0048245	Eosinophil chemotaxis
GO:0042117	Monocyte activation
GO:0002548	Monocyte chemotaxis
GO:0042116	Macrophage activation
GO:0048246	Macrophage chemotaxis
GO:0045576	Mast cell activation
GO:0002551	Mast cell chemotaxis
GO:0001773	Myeloid dendritic cell activation
GO:0002407	Dendritic cell chemotaxis
GO:0030101	NK cell activation
GO:0035747	NK cell chemotaxis
GO:0051132	NK T cell activation
GO:0042110	T cell activation
GO:0010818	T cell Chemotaxis
GO:0042113	B cell activation
GO:0035754	B cell chemotaxis

Table S2. Details of primers used for qRT-PCR validation of gene expression

Gene symbol	Forward primer 5' to 3' sequence	Reverse primer 5' to 3' sequence	Amplicon Size (bp)
SOCS3	CATCTCTGTCGGAAGACCGTCA	GCATCGTACTGGTCCAGGAACT	98
TRIM56	ACCTACTGCCAAGACTGC	TGGTCTTGAAGGAGGCCAC	112
18S	TGACTCAACACGGGAAACC	TCGCTCCACCAACTAAGAAC	114

2 Supplementary Figures



SARS-CoV-2 Infected Tissue	Number Of Upregulated Genes	Number Of Downregulated Genes
Lung	3421	3928
Liver	4805	3881
Kidney	5685	4848
Heart	4176	3312

Figure S1. (A) Count of differentially expressed genes from severe COVID-19 autopsy lung, liver, kidney, and heart tissue samples. Venn diagram representation of the overlap of significantly **(B)** upregulated and **(D)** downregulated genes amongst the four types of infected tissues. Functional clustering and pathway analysis of the commonly **(C)** upregulated and **(E)** downregulated genes across lung, liver, kidney, and heart tissues in response to SARS-CoV-2 infection.