

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

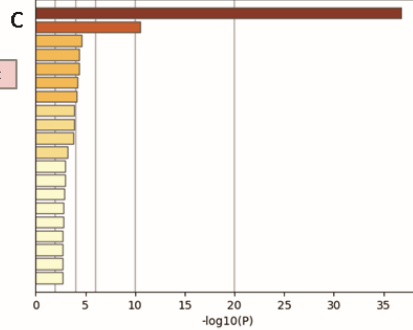
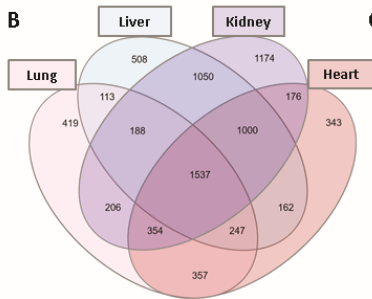
Gene symbol	Forward primer 5' to 3' sequence	Reverse primer 5' to 3' sequence	Amplicon Size (bp)
SOCS3	CATCTCTGTCGGAAGACCGTCA	GCATCGTACTGGTCCAGGAACT	98
TRIM56	ACCTACTGCCAAGACTGC	TGGTCTTGAAGGAGGCCAC	112
18S	TGACTCAACACGGGAAACC	TCGCTCCACCAACTAAGAAC	114

2 Supplementary Figures

A

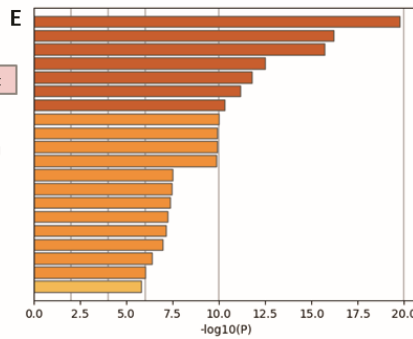
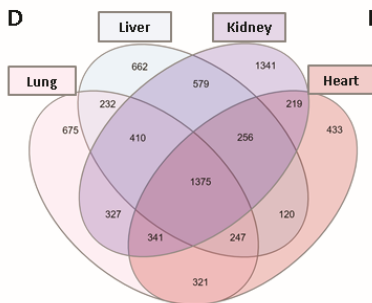
SARS-CoV-2 Infected Tissue	Number Of Upregulated Genes	Number Of Downregulated Genes
Lung	3421	3928
Liver	4805	3881
Kidney	5685	4848
Heart	4176	3312

B



hsa05168: Herpes simplex virus 1 infection
 GO:0050912: detection of chemical stimulus involved in sensory perception of taste
 R-HSA-3238698: WNT ligand biogenesis and trafficking
 GO:0003006: developmental process involved in reproduction
 GO:0007338: single fertilization
 GO:1903844: regulation of cellular response to transforming growth factor beta stimulus
 GO:0048172: regulation of short-term neuronal synaptic plasticity
 GO:0006836: neurotransmitter transport
 GO:0060669: embryonic placenta morphogenesis
 GO:0010466: negative regulation of peptidase activity
 GO:0043666: regulation of phosphoprotein phosphatase activity
 CORUM:6801: VEGFR2-51PR3-ERK12-PKC-alpha complex
 GO:0106104: regulation of glutamate receptor clustering
 GO:0090084: negative regulation of inclusion body assembly
 GO:0016482: cytosolic transport
 GO:0009792: embryo development ending in birth or egg hatching
 R-HSA-442660: Na⁺/Cl⁻ dependent neurotransmitter transporters
 GO:0070849: response to epidermal growth factor
 GO:0071375: cellular response to peptide hormone stimulus
 R-HSA-6803211: TP53 Regulates Transcription of Death Receptors and Ligands

D



GO:0016054: organic acid catabolic process
 GO:0032787: monocarboxylic acid metabolic process
 GO:0007005: mitochondrion organization
 R-HSA-72766: Translation
 R-HSA-556833: Metabolism of lipids
 R-HSA-9609507: Protein localization
 R-HSA-8953854: Metabolism of RNA
 GO:1901615: organic hydroxy compound metabolic process
 GO:1901361: organic cyclic compound catabolic process
 GO:0052696: flavonoid glucuronidation
 GO:0051186: cofactor metabolic process
 GO:0005975: carbohydrate metabolic process
 GO:0006790: sulfur compound metabolic process
 GO:0009060: aerobic respiration
 GO:0016053: organic acid biosynthetic process
 GO:0006914: autophagy
 GO:0006720: isoprenoid metabolic process
 GO:0006839: mitochondrial transport
 ko00280: Valine, leucine and isoleucine degradation
 hsa00240: Pyrimidine metabolism

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.