SUPPLEMENTARY MATERIAL
to the article "Transcriptomics of severe COVID-19"
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Table S1. Studies of the severe form of COVID-19 using a single-cell RNA-seq

Material and time of collecting	Severity of COVID-19 (number of patients)	Features of gene expression and cellular composition in severe COVID-19
Hadjadj et al., 2020		
Peripheral blood leukocytes; during hospitalization (median = 10 days after the onset of symptoms)	Mild or moderate form (n = 15), severe form (n = 17) and critical form (n = 18)	↑ *BATF*, *IRF4* and *CD274*; genes associated with apoptosis; genes involved in the type I interferon signaling (*IFNAR1*, *JAK1* and *TYK2*); IL-6-induced genes (*IL6R*, *SOCS3* and *STAT3*); *TNFSF10*; *IL1B*; genes of the NF-κB signaling pathway; *CXCR2*; ↓ IFN-stimulated genes (ISG) (*MX1*, *IFITM1* and *IFIT2*)
Arunachalam et al., 2020		
Peripheral blood mononuclear cells (PBMCs); at different points in time	1 cohort (n = 36, mild – 75 %, severe – 14 %, critical – 11 %); 2 cohort (n = 40, mild – 18 %, severe – 60 %, critical – 18 %)	↑ *S100A12* in myeloid cells; ↓ genes encoding TNFSF14 and OSM in monocytes; type I interferons; CD86 and HLA-DR proteins on monocytes and myeloid dendritic cells; temporary expression of IFN-stimulated genes
Silvin et al., 2020		
Peripheral blood samples; at different points in time	Mild course of the disease (n = 27), moderate (n = 16), severe (n = 43)	↑ classical monocytes expressing CD141 (THBD); immature neutrophils; ↑ *S100A8* and *S100A9*; genes involved in the production of reactive oxygen species (ROS) and nitric oxide (NO); genes involved in the induced NOS pathway, IL-1 signaling, and NF-κB activation; transcription factor RelA/p65 (P-p65) in classical monocytes; ↓ classical monocytes expressing CD169; HLA-DR protein on the surface of monocytes; nonclassical monocytes
Schulte-Schrepping et al., 2020		
Peripheral blood samples and peripheral blood mononuclear cells (PBMCs); at different points in time between the 3rd and 20th days after the onset of symptoms	1 cohort (n = 8 mild and n = 10 severe), 2 cohort (n = 8 mild and n = 9 severe)	↑ white blood cells, neutrophils; ↓ total number of lymphocytes and T cells, non-classical monocytes; ↑ expression of CD226 and CD69, *SELL* (CD62L), *MAFB*, *PLBD1*, *CD163*, *MPO*, *PLAC8* in monocytes; *CD24*, *PGLYRP1*, *DEFA3* and *DEFA4* in immature neutrophils; *FCGR3B* (CD16b), *CXCL8* and *LCN2* in neutrophils; *PADI4*, *CD24*, *OLFM4*, *LCN2*, *BPI*, *S100A8*, *S100A9*, *ISG15*, *IFITM1/3*, *RSAD2*, *FCGR1A* (CD64), *CD274* (PD-L1) and *ARG1* in low-density neutrophils (LDN); *MPO*, *ELANE* and *PRTN3* in the pro-neutrophils; *CD177* on mature activated neutrophils; ↓ expression of *HLA-DR*; *ISG15* and *IFI6* in monocytes
Lee J.S. et al., 2020		
Peripheral blood mononuclear cells (PBMCs); during hospitalization	Severe form, mild form and asymptomatic form (n = 8)	↑ proportion of classical monocytes; ↓ proportion of dendritic cells, non-classical monocytes, intermediate monocytes, NK cells, EM-like $CD8^+$ T cells and EM-like $CD4^+$ T cells; ↑ IFN-stimulated genes (ISG), including *ISG15*, *IFITM1/2/3* and *ISG20*; *TNF*, *IL1B*, *CCL3*, *CCL4* and *CXCL2* in monocytes

Table S1 (continued)

Material and time of collecting	Severity of COVID-19 (number of patients)	Features of gene expression and cellular composition in severe COVID-19
	Zhang J.Y. et al., 2020	
Peripheral blood mononuclear cells (PBMCs); during hospitalization	Moderate ($n = 7$), severe ($n = 4$) and convalescent ($n = 6$, of which 4 were combined with cases of moderate severity)	↓ relative % of naive T cells, mucosal-associated invariant T cells (MAIT), and dendritic cells; ↑ relative % of pro-T cells, plasma B cells, $CD14^+$ monocytes and platelets; ↑ response to IFN-α in all major cell types, with the exception of plasma B cells; metabolic and catabolic processes, cytokine secretion in monocytes; signaling NF-κB pathway and cytotoxicity in NK cells; *ITGB2*, *CCL5* and *CXCR2* in NK cells; pathways of cell death and migration; *TRAJ39* and *TRAJ43*; genes associated with IFN-α response, protein synthesis, maturation, and biological processes related to transport in B cells
	Yao et al., 2021	
Peripheral blood mononuclear cells (PBMCs); at different time points	Moderate ($n = 5$), acute respiratory distress syndrome ($n = 6$) and convalescents ($n = 6$)	↑ biological processes "response to type I IFN", "response to virus", "response to IFN-γ" and "response to IFN-β" in NK cells, CD8+ T cells, $CD4^+$ T cells; apoptosis genes in $CD8^+$ T cells, classical monocytes, and B cells; genes of metabolic and apoptotic pathways in $CD4^+$ T cells; IFN-mediated response and apoptotic signals in B cells; oxidative phosphorylation pathways in all cellular compartments; the PD-1 signaling pathway in monocytes; IRF7 in lymphocytes; ↓ genes associated with cytotoxic function in NK cells, $CD8^+$ T cells; activation genes of B cells, classical monocytes; major histocompatibility complex (MHC) class I and MHC class II in monocytes; IFN type I pathways in monocytes; signaling of sirtuins in all cellular compartments; the signaling pathway of eukaryotic translation initiation factor 2 (eIF2) in all cells except monocytes; impaired phagocytosis and altered differentiation of classical monocytes
	Wilk et al., 2021	
Peripheral blood samples and peripheral blood mononuclear cells (PBMCs); at different time points	Mild form ($n = 8$), moderate form ($n = 11$), severe form ($n = 8$), critical form ($n = 6$)	Depletion of CD16 monocytes, dendritic cells, and NK cells; ↑ plasmoblasts; the emergence of a population of developing neutrophils; ↑ genes associated with anti-inflammatory reactions (*PKM* and *CD163*); *PADI4*, *CXCR1*, *S100A8*, *S100A9*, *CD274*, *CXCL16*, *TNFSF10*, genes associated with neutrophil phagocytosis and degranulation; *DEFA1B*, *LCN2* and *MMP8* in immature neutrophils; IFN-stimulated genes (ISG), *CD163*, *PLAC8*, *MPO*, *ARG1*, *C19orf59*, *IRAK3*, *ANXA3*, *RBM47* and *TLR5* in monocytes; ↓ *FCER1A*, *CD83*, *CTSS* in type 2 dendritic cells; *CD4*, *HLA-DR*, *IL1B*, *TNF*, NF-κB pathway, level of proinflammatory cytokines in monocytes

Table S1 (end)

Material and time of collecting	Severity of COVID-19 (number of patients)	Features of gene expression and cellular composition in severe COVID-19
	Saichi et al., 2021	
APC-enriched peripheral blood mononuclear cells (PBMCs); on the first and fourth days of hospitalization	Moderate form ($n = 5$) and severe form ($n = 10$)	↑ *IL1B*, *CXCR4*, *CD36*, *CD83*, *AREG*, *ITGAM*, *CTSD*, *CTSB* and *RETN*, *EREG*, *ANXA2*; hypoxia and TNF-α signaling; *AREG*, *IL1R2*, *NRGN* and *S100A12*; *CXCL8*, *NAMPT* and *G0S2* in APC; signaling pathways "TNF-α", "IL2 STAT5", "hypoxia", "IL6 JAK STAT3", "P53" and "MTORC" in plasmocytoid dendritic cells (pDC); complement system (C1GC and C1GB), VSIG4 and CD163 in monocytes; signaling pathways "complement system", "TNF-α", "KRAS" and "hypoxia" in monocytes; complement-related genes (*C1QA*, *C1QB* and *C1GC*) in $CD16^+$ monocytes; signaling pathways NFKB/STAT; ↓ *TGFB1* and *IL10RA*; IFN, MX2, ISG15, IRF7, BST2, IFITM2 and ADAR; genes in modules "innate perception", "antiviral effector molecules" and "cytotoxicity"; TLR7, DHX9, DHX36, TNFSF10 and IRF7; antiviral ISG, *BST2* and *PYCARD* in pDC; signaling "IFN-α" and "IFN-γ" in monocytes; IL10, CCL5 and TGFb, *IFNAR1* and *IFNAR2* in APC
	Ren et al., 2021	
Peripheral blood mononuclear cells (PBMCs) with further sorting into B and T cells; –	Mild and moderate forms ($n = 22$), severe form ($n = 54$), convalescents ($n = 95$), mild and moderate forms ($n = 57$), severe form ($n = 38$)	↑ B cells, plasma cells, macrophages, megakaryocytes and $CD14^+$ monocytes; plasmoblastic cells MKI67; hyperinflammatory megakaryocytes; $CD4^+$ T cells; ↓ T cells, dendritic cells, γδT cells and MAIT cells; ↑ genes encoding constant regions IgA1, IgA2, IgG1 and IgG2 in plasma cells; *MKI67* in plasmoblastic cells; *TNF*, *CCL3*, *IL1B*, *CXCL8*, *IL6*, *TGFB1*, *LTB* and *IFNG*; *ANXA1*, *FPR1*, *S100A9*, *S100A8* in T, B, NK and dendritic cells; cytokines in monocyte subtypes, T cell subtypes ($CD4^+$ and $CD8^+$) and in one subtype of megakaryocytes; *CCL3*, *IL1RN* and *TNF* in monocytes; proinflammatory cytokines (IL1B, TNF, IL-6, CCL3); *IFNG* in subtype of $CD8^+$ T cells
	Liu C. et al., 2021	
Peripheral blood mononuclear cells (PBMCs); material collected during hospitalization (median = 11 days after onset of symptoms)	Moderate form ($n = 3$), severe form ($n = 5$) and critical form ($n = 25$, 4 of whom died during hospitalization)	↑ adaptive NK cells; signs of NK cell depletion; ↓ plasmocytoid dendritic cells; ↑ signatures of apoptotic genes (*BRCA2*, *CASP3*, *CASP8*, *BID*, *BAK1* and *XBP1*) in pDC; oxidative stress genes (*FOS*, *PHC3*, *MDM4*, *CBX6* and *CDKN2D*), genes of fatty acid biosynthesis and oxidation in NK cells; NF-κB pathway in nonclassical monocytes, subgroups of NK cells, MAIT cells, memory cells and naive B cells; signals of cellular activation and proliferation (cell cycle genes) in $CD8^+$ memory T cells; IL-6, TNFRSF1B, IL-17, IL-18; cytokine-mediated signaling pathways (IL-4/13 and IL-17) in classical monocytes; ↓ TNF-β; IFN-I gene signatures; *RELA*, *NFKB1B*, *STAT1* and *IL8*, NF-κB pathway in NK cells and classical monocytes; chemokine signaling; IL-1 response; mTORC1 pathway; *IFNG* in NK cells

Note. ↑ – increase in proportion or expression. ↓ – decreased proportion or expression. "–" – the time of collection is not specified.
IL – Interleukin. APC – Antigen-presenting cells.