Science Advances

Supplementary Materials for

Immediate myeloid depot for SARS-CoV-2 in the human lung

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Figure S1. Virus replication in infected PCLS. (A-B) PCLS were infected with SARS-CoV-2 (A) or IAV (B) and recovered at 48 and 72h post-infection. Viral replication was assessed by RT-qPCR. Individual donors color-coded and Mean +/- SD. ****p<0.0001. Confocal images were obtained from non-infected controls (scale bar = 50 μ m). Zoomed area is marked by the white rectangles. For each zoomed area, slices appear on the side (scale bar = 5 μ m in (C) and 10 μ m in (D). (C) PCLS stained for DAPI (dark blue), EpCAM (green), ACE2 (red) and spike (light blue). (D) PCLS stained for DAPI (dark blue), CD45 (orange), ACE2 (red) and spike (light blue).



Figure S2. SARS-CoV-2 infection drives dsRNA production in both epithelial and immune cells in PCLS. PCLS were infected with SARS-CoV-2 and used for confocal imaging. Alveolar spaces (Alv.) are indicated in the large image (scale bar = 50 µm). Zoomed area is marked by the white rectangle. For each zoomed area, z-stacks appear on the side (scale bar = 10 µm). (A) PCLS stained for DAPI (dark blue), EpCAM (green) and dsRNA (red). (B) PCLS stained for DAPI (dark blue), CD45 (red) and dsRNA (light blue). Autofluorescence appears in green.



Figure S3. SARS-CoV-2 infection of epithelial and immune cells occurs mainly in ACE2+ cells. SARS-CoV-2-infected PCLS were used for confocal imaging. EpCAM+ (A) or CD45+ (C) cells were analyzed for ACE2 and spike staining. (A, C) Counts are presented in pie charts. Data are pooled from three donors. (B, D) SARS-CoV-2-infected PCLS were dissociated and stained for intracellular dsRNA and spike. Epithelial (B) and myeloid (D) cell infection was assessed by flow cytometry.



Figure S4. Cell type annotations for scRNA-seq in human PCLSs. (A) A dot plot describing the expression of the top 5 genes per identified cluster in the human PCLS dataset, used to assign cell type annotations. (B) A dot plot describing the expression of the top 5 genes per identified myeloid subcluster in the human PCLS dataset, used for myeloid cell type annotations.



Figure S5. Cell type annotations for scRNA-seq in human ETA samples. A dot plot describing the expression of the top 5 genes per identified cluster in the human ETA dataset, used to assign cell type annotations.



Figure S6. ACE2 transcript is expressed in human alveolar macrophages. A) *ACE2* expression in PCLS scRNA-seq. Cells are grouped according to their SARS-CoV-2 status (positive or negative). (B) *ACE2* transcript expression was assessed by RTqPCR in Vero-TMPRSS2 cells (green), AT2 primary cells (blue), colorectal cancer (CRC) organoid (violet), Jurkat cells (orange) and AMs from human BAL (red (plated) and pink (flow-sorted), n= 3 donors). Relative mRNA expression is displayed as 2^{-/Δ/CT} relative to GAPDH for probe Hs00222343. Vero-TMPRSS2 are set at 100. Mean +/- SD. (C) Amplification curves for AT2 primary cells and sorted AMs with their corresponding negative control (no RT).



Figure S7. Human BAL cell profile. (A) Proportion of AMs (CD45+ CD15-, CD3- CD19- HLA-DR+ CD169+) amongst total, live BAL cells (n=6 donors). (B) Flow cytometry gating of human BAL cells. (C, D) Proportions of leukocytes (CD45+) and epithelial cells (CD45- EpCAM+) in total and ACE2+ BAL cells (n=6 donors).



GAPDH

- 37kDa

GAPDH

(n=4). Staining was done using 3 antibodies (A: 10108-MM36-P, B: AC18F, C: FAB933T). Results are displayed as contour plots, grey lines represent FMO staining, colored lines are the fully stained samples. Delta MFI (Stained MFI - FMO MFI) was measured for each population. (D-E) Vero-TMPRSS2 and sorted AMs (n=4 donors) were used for Western Blot using 2 ^{37kDa} monoclonal antibodies (SN0754, D and AC18F, E).





Figure S10. Infection of BAL cells and flow-sorted AMs with SARS-CoV-2 variants. (A) BAL cells were infected with SARS-CoV-2 for 48h at MOI 0.1 and 1 (BAL). As a control, SARS-CoV-2 was incubated in cell culture media alone (Media). Cell-free supernatant was used to infect Vero-TMPRSS2 cells. At 24h after infection, Vero-TMPRSS2 were stained for intracellular spike expression. Using flow cytometry, infection rate was measured (n=8 donors, mean ± SD). Results appear in fold change compared to media incubation. (B) Similarly, IAV-Venus was used to infect BAL cells or incubated with media. Cell-free supernatant was used to infect MDCK cells. At 24h, MDCK were recovered for flow cytometry (n=5 donors, mean ± SD). Venus expressing cells percentage was measured and appears as a fold change from media incubation. (C, D, E) Viral titer was determined by plaque assay. (D, E) Results appear as fold change from media incubated virus (n=5-6 donors, mean ± SD). (F, G) BAL AMs (live, EpCAM-CD45+CD3-CD19-HLA-DR+CD169+) were flow-sorted and SARS-CoV-2 variants were incubated with either AMs (MOI 0.1 - 1) or media for 48h. Cell free supernatant was used for plaque assay. (G) Results are expressed as fold-change compared to media incubation (n=5-6 donors, mean ± SD). ns not significant, *p<0.05, **p<0.01, ***p<0.001.



Figure S11. SARS-CoV-2 induces blunted interferon responses in alveolar macrophages. (A-C) PCLS AM pathway analysis at 48h postinfection. (A) AMs from IAV-infected PCLS compared to non-infected PCLS. (B) AMs from IAV-infected PCLS compared to non-infected PCLS. (C) Within SARS-CoV-2-infected PCLS, comparison of SARS-CoV-2 positive AMs compared to SARS-CoV-2 negative AMs. (D) Log2 fold change of select ISGs in the PCLS experiment in IAV- and SARS-CoV-2-infected AMs at 48 and 72h vs control. (E-F, H-K) Plated AMs were infected with SARS-CoV-2 or IAV at MOI 0.1 or 1 for 48h (n= 3 donors). (E) *IFNa* and (F) *IFNg* gene expressions were measured by RT-qPCR. (G) IFITM3 staining in AMs after infection with SARS-CoV-2 (Ancestral, delta) at MOI 0.1 - 1 (n=7-9 donors). Results appear in fold change compared to uninfected cells. (H) *IFITM3*, (I) *ISG15*, (J) *IFI16*, and (K) *IRF7* gene expression were measured in plated AMs at 48h post-infection. *p<0.05, **p<0.01, ***p<0.001.

Donor	Gender	Race/ Ethnicity	Age	of death	Donation	Comorbidities	Smoking (>20PY)	Experiment Type
1	М	White	63	Anoxia	DBD	Hypertension, Pulmonary nodules	yes	BAL
2	F	White	49	Anoxia	DCD	Asthma, COPD, Sepsis pneumonia	yes	PCLS flow, PCLS imaging
3	F	White	37	Anoxia	DBD	None	no	PCLS flow, PCLS imaging
4	М	White	51	Stroke	DBD	Diabetes, CAD, Hypertension	no	PCLS flow, PCLS imaging
5	М	White	47	Stroke	DCD	None	no	PCLS flow, PCLS imaging
6	м	Asian/White	32	Head Trauma	DBD	Diabetes	no	PCLS flow
7	F	Hispanic	44	Stroke	DBD	None	no	PCLS flow, PCLS imaging
8	М	Asian	50	Stroke	DCD	Asthma, Hypertension	no	PCLS flow
9	М	White	46	Suicide	DCD	None	yes	PCLS flow, SCS
10	F	Asian	56	Stroke	DCD	Hypertension	no	PCLS imaging
11	F	White	57	Stroke	DBD	None	no	PCLS flow, PCLS imaging
12	М	Hispanic	27	Head Trauma	DBD	Asthma	no	PCLS SCS
13	М	White	43	Anoxia	DCD	None	no	BAL, PCLS flow, PCLS imaging
14	F	Hispanic	44	Stroke	DBD	None	no	PCLS imaging, PCLS SCS
15	М	White	43	Anoxia	DCD	None	no	PCLS flow
16	М	Hispanic	57	Stroke	DBD	None	no	BAL
17	М	White	50	Head Trauma	DCD	Hypertension	no	BAL
18	М	White	31	Head Trauma	DCD	None	no	BAL
19	М	Hispanic	50	Stroke	DBD	Hypertension	no	BAL
20	F	White	62	Head Trauma	DBD	Cancer	no	BAL
21	М	White	27	Anoxia	DBD	None	no	BAL
22	F	Hispanic	39	Head trauma	DBD	None	no	BAL
23	F	White	58	Anoxia	DCD	Diabetes, Hypertension	no	BAL
24	F	White	62	Anoxia	DCD	COPD, Hypertension, Hypersensitivity Lung Disease, and Diabetes	yes	BAL
25	М	White	32	Anoxia	DCD	Asthma	no	BAL
26	М	Hispanic	25	Anoxia	DCD	None	no	BAL
27	М	Hispanic	33	Head trauma	DBD	Hypertension	no	BAL
28	М	White	33	Anoxia	DBD	Diabetes	yes	BAL
29	М	White	46	Stroke	DBD	Asthma	no	BAL
30	М	Asian	51	Stroke	DBD	Diabetes, Hypertension	no	BAL
31	М	White	35	Head trauma	DBD	None	no	BAL
32	М	White	31	Anoxia	DBD	None	no	BAL

Table S1. Human lung donor demographics. Cause

33	М	White	64	Anoxia	DCD	Asthma	no	BAL
34	М	White	66	Anoxia	DBD	Hypertension	no	BAL
35	F	White	37	Stroke	DBD	Hypertension	no	BAL
36	М	White	28	Head trauma	DBD	None	no	BAL
37	М	Black	22	Head trauma	DBD	Hypertension	no	BAL
38	F	White	27	Anoxia	DBD	None	no	BAL
39	F	Hispanic	26	Head trauma	DBD	None	no	BAL
40	F	Hispanic	57	Stroke	DBD	Hypertension	yes	BAL
41	F	Black	58	stroke	DBD	Hypertension	no	BAL
42	F	White	70	Stroke	DBD	None	yes	BAL
43	М	Hispanic	36	Anoxia	DBD	None	no	BAL
44	М	Hispanic	28	Anoxia	DCD	None	yes	BAL
45	F	White	33	Anoxia	DCD	None	no	PCLS, BAL
46	М	Hispanic	63	Natural causes	DCD	Diabetes, Hypertension	no	PCLS, BAL
47	М	Hispanic	34	Anoxia	DBD	Diabetes	no	PCLS, BAL

DBD: donation after brainstem death

DCD: donation after cardiac death

COPD: chronic obstructive pulmonary disease

CAD: coronary artery disease

BAL: bronchoalveolar lavage

PCLS flow: precision cut lung slice flow cytometry

PCLS Imaging: precision cut lung slice immunofluorescence imaging

SCS: single-cell RNA sequencing

 Table S2. COVID-19 subject (endotracheal aspirate samples) demographics.

Subject	Age	Gender	Ethnicity	ARDS (Y/N) Berlin definition	ETA sampling after intubation (days)	P/F ratio at time of ETT sampling	ICU LOS (days)	Hospital LOS (days)	Death (Y/N)
1 (1)	34	F	White	Yes	0	180	12	14	No
2 (365)	55	М	White	Yes	40	110	35	60	No
3 (414)	58	М	Other / Multiple Races	Yes	1, 3	165	19	27	No
4 (415)	62	F	Black / African American	Yes	2	124	14	21	No
5 (419)	68	М	Other / Multiple Races	Yes	7	175	26	50	No
6 (476)	59	М	White	Yes	12	160	44	78	No
7 (389)	66	F	White	Yes	2	144	39	55	No

ARDS: acute respiratory distress syndrome ETA: endotracheal tube aspirate P/F ratio: PaO2/FIO2 ICU LOS: intensive care unit length of stay

Hospital LOS: hospital length of stay

Reference	Detection of ACE2 in alveolar macrophages	Method
(14)	No	Sc Seq
(25)	No	Sc Seq / WB
(29)	Yes	Flow / IHC
(36)	Yes	IHC
(37)	No	Sc Seq
(38)	Yes	IHC
(39)	Yes	IHC
(40)	Yes	IHC
(41)	No	Sc Seq
(42)	Yes	IHC
(43)	Yes	IHC
(44)	No	Sc Seq
(45)	Yes	Flow

Table S3. Published studies on ACE2 expression in alveolar macrophages.

IHC: immunohistochemistry, Sc Seq: single-cell RNA sequencing, Flow: Flow cytometry, WB: Western Blot

Staining	Antibody (clone)	Lot number	Dye	Catalog number (Supplier)
	CD169	1621398	AF594	FAB5197T (R&D Systems)
	ACE2	BJ07067522	PE	bs-1004R (BIOSS)
	EpCAM	B250368	BV650	324226 (BioLegend)
	CD31 (WM59)	8232937	BV605	562855 (BD Biosciences)
Surface	CD45 (HI30)	B333796	BV421	304032 (BioLegend)
Staining	CD14 (M5E2)	B275828	BV711	301838 (BioLegend)
	CD3 (SK7)	0314461	BB700	566575 (BD Biosciences)
	CD19 (SJ25C1)	1069967	BB700	566396 (BD Biosciences)
	Zombie (viability)	B331984	NIR	77184 (BioLegend)
	HLA-DR (G46-6)	1266420	BUV395	564040 (BD Biosciences)
Intracellular	Spike	1619059	AF647	FAB105805R (R&D Systems)
Staining	dsRNA (J2)	J2-2007	AF488	10010 (Scicons)

 Table S4. Flow cytometry panel for PCLS experiments.

Table S5.	Flow cytometry	panel for BAL	experiments.
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Staining	Antibody (Clone)	Lot number	Dye	Reference
		1621308	AE504	EAR5107T (R&D Systems)
	CD109 (#900102)	1021390	AI 334	TADJIJI (RAD Systems)
		1686194	AF647	FAB5197R (R&D Systems)
	ACE2 (#171607)	1623179	AF594	FAB9333T (R&D Systems)
	ACE2 (#36)	HR15SE2903	PE	10108-MM36-P (SinoBiological)
	ACE2 (Polyclonal)	HOK0620051	-	AF933 (R&D Systems)
	ACE2 (AC18F)	0610040-1	-	30582 (Cayman Chemical)
	CD15 (W6D3)	1089776	BV786	741013 (BD Biosciences)
Surface	CD16 (3G8)	B321940	BV605	302040 (BioLegend)
Staining	CD45 (HI30)	B333796	BV421	304032 (BioLegend)
	CD14 (M5E2)	B275828	BV711	301838 (BioLegend)
	CD3 (SK7)	0314461	BB700	566575 (BD Biosciences)
	CD19 (SJ25C1)	1069967	BB700	566396 (BD Biosciences)
	Zombie (viability)	B331984	NIR	77184 (BioLegend)
	LiveDead (viability)	2161888	PO	L34959 (Invitrogen)
	HLA-DR (G46-6)	1266420	BUV395	564040 (BD Biosciences)
	Annexin V	5190517152	FITC	130-092-52 (Miltenyi)
		51-65875X	PE	556422 (BD Biosciences)
Intracellular	Spike	1619059	AF647	FAB105805R (R&D Systems)
Staining	IFITM3 (EPR5242)	GR3416716-1	AF488	Ab198559 (Abcam)
	IAV NP	VF3017701A	D67J	MA1-7322 (Invitrogen)



Antibody: GAPDH (PLA0125-100UL)





Antibody: GAPDH (PLA0125-100UL)



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