Supplementary Material

Aberrant innate immune profile associated with COVID-19 mortality in Pretoria, South Africa.

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1. Detailed information flow cytometry reagents, set up and analysis

1.1 Fluorescence Reagent Description

The following reagents were used for the monocyte panel:

Characteristic	*Analyte*	*Detector*	*Reporter*	*Manufact.*	*Clone*	*Cat#*
Monocyte lineage marker	CD14	Anti-CD14	ECD	Beckman Coulter	RMO52	B92391
Used to differentiate monocyte subsets	CD16 (FcγRIII)	Anti-CD16	Krome Orange	Beckman Coulter	3G8	B00069
Monocyte migration marker	CCR2	Anti-CCR2	FITC	Miltenyi Biotec	REA624	130-126-939
Co-receptor on monocytes for T-cell activation	CD86	Anti-CD86	PC 5.5	Beckman Coulter	HA5.2B7	B30647
Co-receptor for monocytes for T-cell activation	CD80	Anti-CD80	AF-750	Beckman Coulter	MAB104	B30643
Immune checkpoint inhibitor	PD-L1 (CD247)	Anti-PD-L1	PC7	Beckman Coulter	PD-L1	A78884

The following reagents are being used for the T-cell panel:

Characteristic	*Analyte*	*Detector*	*Reporter*	*Manufact.*	*Clone*	*Cat#*
T helper	CD4	Anti-CD4	APC	Beckman Coulter	13B8.2	B53328
T cytotoxic	CD8	Anti-CD8	AF-700	Beckman Coulter	B9.11	B53328
T lineage marker	CD3	Anti-CD3	APC-750	Beckman Coulter	UCHT-1	B53328
Common leukocyte antigen	CD45RO	Anti-CD45RO	Krome Orange	Beckman Coulter	J33	B53328
Common leukocyte antigen	CD45RA	Anti-CD45RA	FITC	Beckman Coulter	2H4	B53328
T-cell homing marker	CD197 (CCR7)	Anti-CD197	PE	Beckman Coulter	G043H7	B53328
Co-stimulatory ligand to CD80 and CD86	CD28	Anti-CD28	ECD	Beckman Coulter	CD28.2	B53328
Co-stimulatory molecule	CD27	Anti-CD27	PC7	Beckman Coulter	1A4.CD27	B53328
T-cell exhaustion marker	CD57	Anti-CD57	Pacific Blue	Beckman Coulter	NC1	B53328
T-cell activation marker	CD279 (PD1)	Anti-CD279	PC5.5	Beckman Coulter	PD1.3.5	B53328

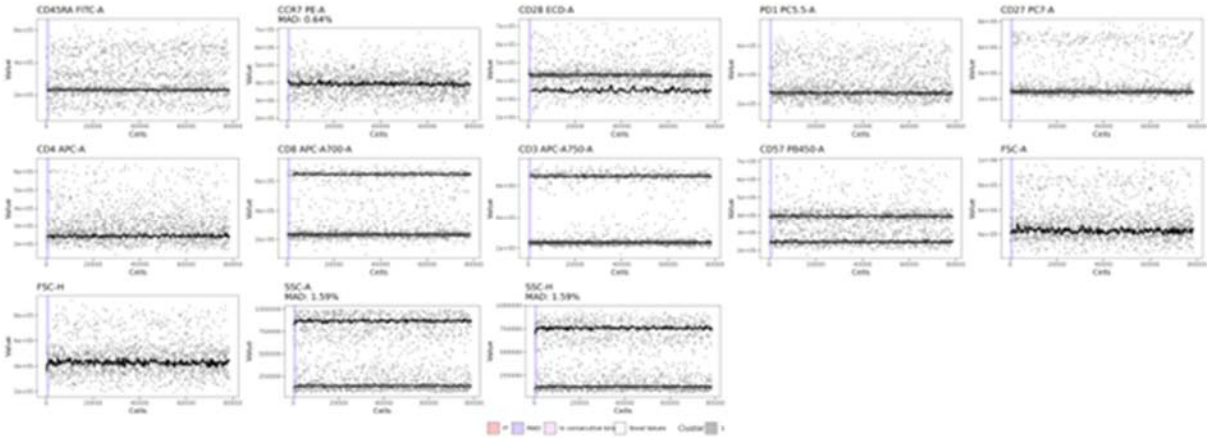
1.2 Instrument optics

The instrument has not been altered; BioSense 150 µm x 450 rectangular channel with an integral lens. The instrument has a three-laser base configuration: 488 nm blue argon iron laser, target power range 40-60 mW; 638 nm red solid-state laser, target power range 40-60 mW; 405 nm violet solid state laser, target power range 70-120 mW.

1.3 Flow cytometry data analysis description

1.3.1 PeacoQC for both T-cells and monocytes

Kaluza default visualization settings were used to clean and scale data before uploading to Cytobank. After uploading the files onto the Cytobank platform an additional quality check was performed by running the PeacoQC algorithm. This algorithm detects and removes any irregularities (upregulating or down regulating signal) that occurred during the acquisition of the data. In the figure below the purple highlighted area indicates data that was removed. A new file was then generated that was labelled as a 'Cleaned file'.



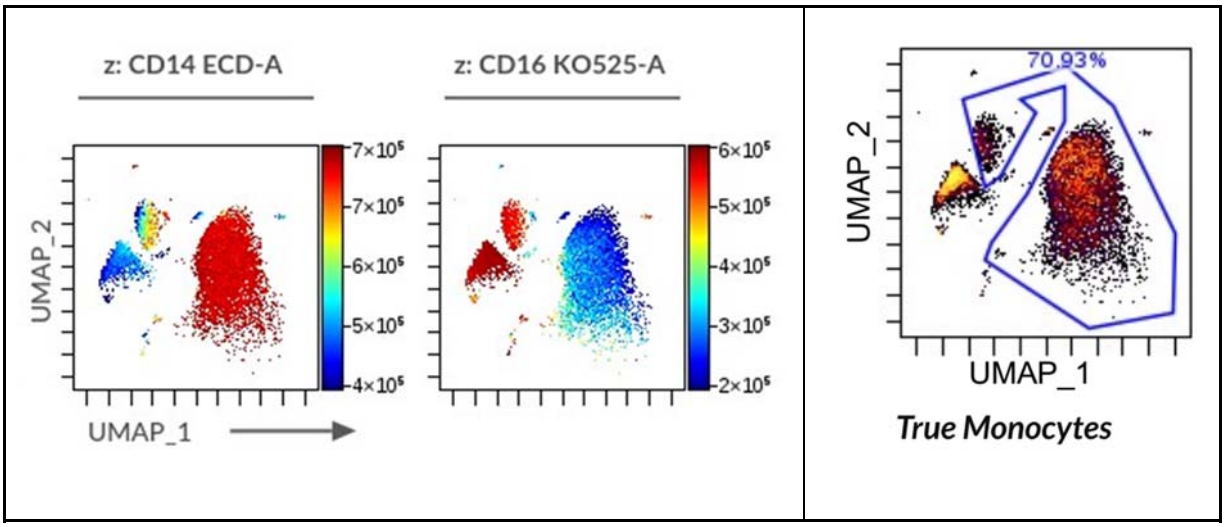
Supplementary Figure 1: Output report of a sample from the PLWH cohort as a representative example and graphs generated by the PeacoQC algorithm. The purple highlighted area on the graphs represents the irregularities in the run that were removed from the newly generated 'Cleaned file'.

1.3.2 UMAP analysis monocytes

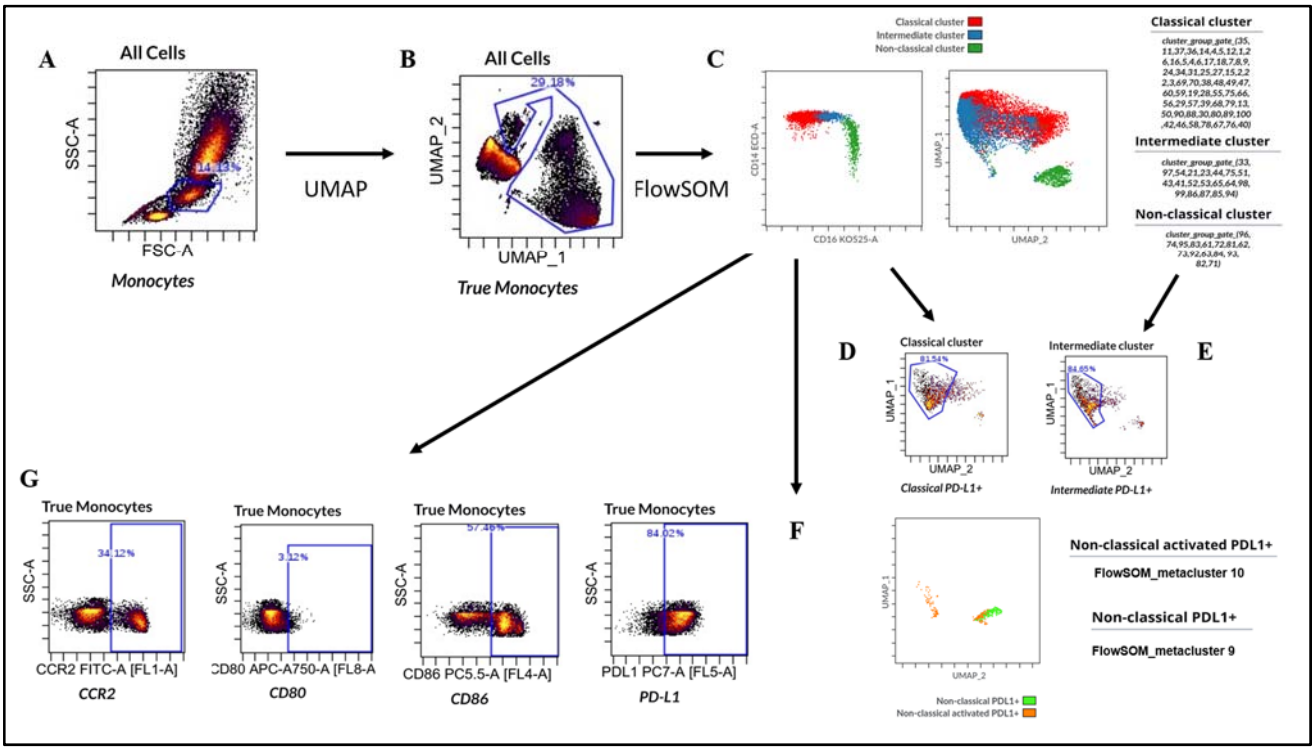
Next, the UMAP dimensionality reduction algorithm was used to visualize and gate the data in Cytobank. On the 'Cleaned files' generated by the PeacoQC algorithm, the monocyte population was gated by plotting SSC vs FSC. The monocyte population was selected as the input variable for the UMAP algorithm. The data was normalized and the internal file compensation was applied. Settings of the UMAP were as follow: Channels to be included: CCR2-FITC, CD14-ECD, CD16-KO, CD80-A750, CD86-PC5.5, PDL1-PC7; Events to be sampled: all events in monocyte gate (total of 1 551 888 across all files); Advanced settings included: number of neighbors: 25, minimum distance between clusters: 0,21 and it was selected to collapse outliers and normalize the data.

1.3.3 FlowSOM analysis monocytes

In the generated UMAP experiment, the clustering algorithm FlowSOM was used to gate the different monocyte subsets. In the UMAP experiment, the monocyte population was gated again to remove any neutrophils or lymphocytes by using the CD14-ECD and CD16-KrO Z colored channels. This population was then labelled 'True monocytes' (Supplementary Figure 2) and was used as the input variable for the FlowSOM analysis. Settings of the FlowSOM were as follow: channels to be included: CCR2-FITC, CD16-KO, CD80-A750, CD86-PC5.5, PDL1-PC7; events to be sampled: all events in selected gate (1 189 954); hierarchical consensus clustering method was used; the number of meta clusters chosen was 10, number of clusters 100 and number of iterations 10 and the seed was set to automatic (1 213 232 402). The data were normalized. The gating strategy followed for the monocytes can be seen in Supplementary Figure 3.



Supplementary Figure 2: The Z-colored channels CD14 and CD16 were used to gate out neutrophil and lymphocytes (cells not expressing CD14 but expressing CD16). The new population was labelled 'True monocytes' and used as input for downstream FlowSOM and CITRUS clustering.



Supplementary Figure 3: Gating strategy for monocyte panel. A: SSC VS FSC to determine the monocyte population that was used as the input gate for the UMAP algorithm. B: After running the UMAP, any lymphocytes and neutrophils were gated out by using the CD14 and CD16 Z-colored channels. The population was labelled as 'True monocytes' and used as the input gate to run the clustering algorithm FlowSOM. C: Monocyte subsets (Classical (CD14+CD16-), intermediate (CD14+CD16+) and non-classical (CD14dimCD16+) as determined by FlowSOM. Clusters making up each population are noted on the right. C: Classical monocytes expressing PD-L1 were gated on the Classical cluster. E: Intermediate monocytes expressing PD-L1 were gated on the Intermediate cluster. F: FlowSOM_metacluster 9 was identified as non-classical monocytes expressing PD-L1 (CD14dimCD16+PD-L1+), FlowSOM_metacluster 10 was identified as activated non-classical monocytes expressing PD-L1 (CD14dimCD16+PD-L1+CD86+CD80+). G: The overall expression of CCR2, CD80, CD86 and PD-L1 was manually gated on the 'True monocyte' population in the created FlowSOM experiment.

1.3.4 UMAP analysis T-cells

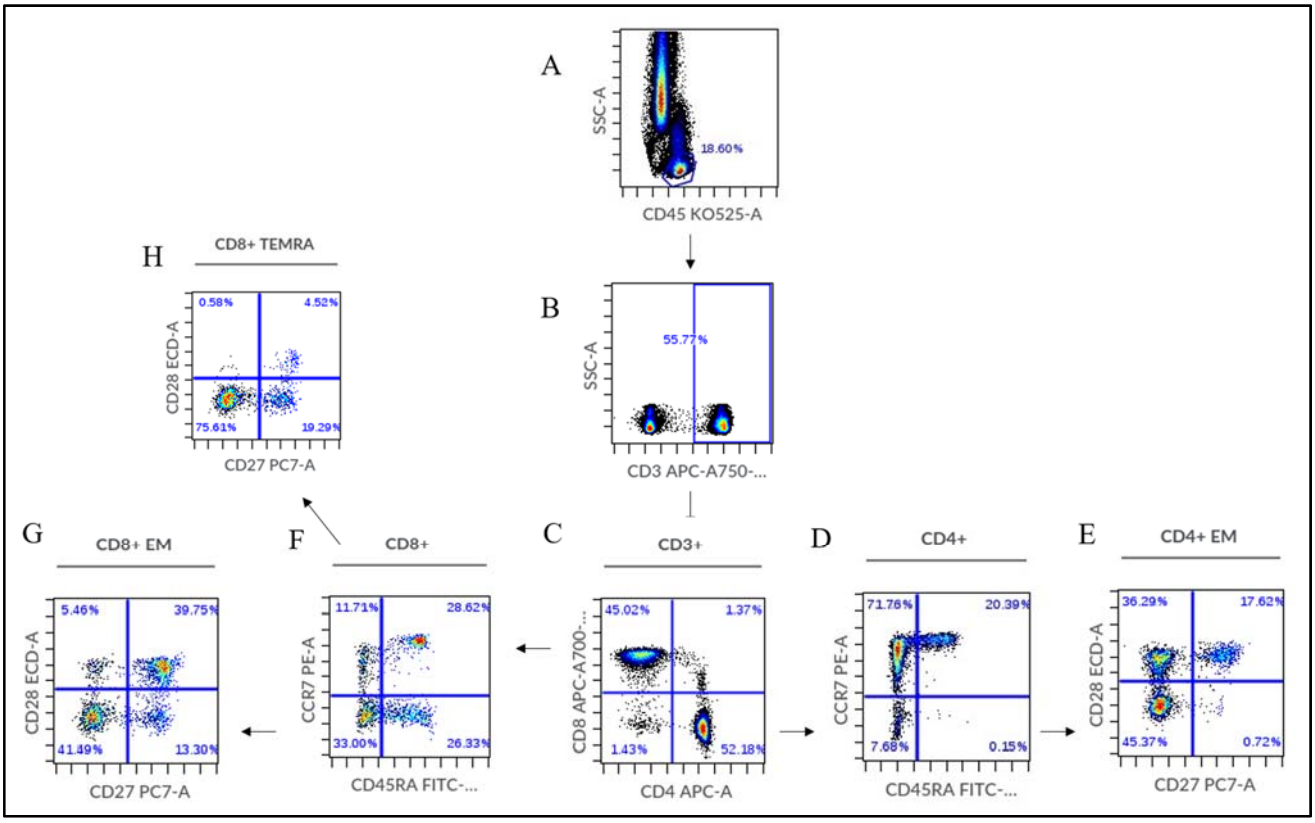
Next, the UMAP dimensionality reduction algorithm was used to visualize and gate the data in Cytobank. On the 'Cleaned files' generated by PeacoQC algorithm, the lymphocyte population was gated by plotting SSC vs CD45RO. This was followed by plotting SSC vs CD3 to gate the T-cells. The CD3 population was selected as the input parameter for the UMAP algorithm. The data were normalized and the internal file compensation was applied. Settings of the UMAP were as follow: Channels to be included: CCR7-PE, CD27-PC7, CD28-ECD, CD4-APC, CD8 APC-A700, CD45RA, CD57-Pacific Blue and PD1-PC5.5; Events to be sampled: All events in CD3 gate (total of 3 580 511 across all files); Advanced settings included: number of neighbors: 20, minimum distance between clusters: 0,01 and we selected to collapse outliers

1.3.5 CITRUS analysis T-cells

The CITRUS algorithm was used to identify significant differences of T-cell populations. After performing the UMAP analysis, CITRUS was run as downstream analysis. Two CITRUS experiments were set up, one in which the input gate was CD4 and one in which the input gate was CD8. CITRUS performs statistical analysis thus the groups and files to be compared are required to be of equal size, 27 files from both groups were selected (deceased and survived) and labelled "Deceased" and "Survived". The settings for CITRUS include; Clustering channels chosen include: CCR7-PE, CD27-PC7, CD28-ECD, CD45RA, CD57-Pacific Blue and PD1-PC5.5. Internal file compensation was used. Association model specified: Significance Analysis of Microarrays (SAM) – Correlative. Cluster characterization was set to abundance. Equal event sampling was selected. The CITRUS experiments were repeated five times for each input (CD4 and CD8) to ensure that the results generated were true results. Only populations that were shown to be significant in all five runs were back-gated onto the UMAP to include all the samples in the cohort.

1.3.6 The gating strategy to define T-cell subsets

The gating strategy to identify the different T-cell subsets can be seen in Supplementary Figure 4. The following gates were drawn on the UMAP1 vs UMAP2 plot by using the Z-channel coloring: CD4CM PD1+, CD4EM1 PD1+, CD4EM2 PD1+, CD4EM3 PD1+, CD4EM4 PD1+, CD4EM3 PD1+CD57+, CD8CM PD1+, CD8EM1 PD1+, CD8EM2 PD1+, CD8EM3 PD1+, CD8EM1 CD57+, CD8EM2 CD57+, CD8EM3 CD57+, CD8EM4 CD57+, CD8TEMRA pE1 PD1+, CD8TEMRA E PD1+, CD8TEMRA E PD1+CD57+.



Supplementary Figure 4: Gating strategy followed to identify T-cell populations. A: SSC vs CD45KO- lymphocyte gate to define the lymphocytes. B: SSC vs CD3-leukocyte gate applied- gate CD3 to define the T-cells. C: CD8 vs CD4-CD3 gate applied- create a quadrant gate to differentiate

between CD4, CD8, DP and DN T-cells. D: CCR7 vs CD45RA to define the different CD4 memory subsets naïve (CD4N), central memory (CD4CM), effector memory (CD4EM) and terminal effector cells re-expressing CD45RA (CD4TEMRA). E: CD28 vs CD27 to define the different effector memory subsets EM1 (CD4EM1), EM2 (CD4EM2), EM3 (CD4EM3), EM4 (CD4EM4). F: CCR7 vs CD45RA to define the different CD8 memory subsets as naïve (CD8N), central memory (CD8CM), effector memory (CD8EM), and terminal effector cells re-expressing CD45RA (CD8TEMRA). G: CD28 vs CD27 to define the different effector memory subsets as EM1 (CD8EM1), EM2 (CD8EM2), EM3 (CD8EM3), EM4 (CD8EM4). H: CD28 vs CD27 to define the different TEMRA subsets as pre-effector 1 (CD8pE1), pre-effector 2 (CD8pE2), and end-stage effectors (CD8E).

2. Supplementary Tables

Supplementary Table 1: Comorbidities by outcome.

	Deceased (n=27)	**Survived (n=134)**	**p-value**
Age	55.78 (±16.76)	50.91 (±13.42)	0.0853
Sex (male)	18/27 (66.67%)	73/144 (50.69%)	0.247
Hypertension	11/27 (40.74%)	55/144 (38.19%)	0.352
Diabetes	7/27 (25.93%)	47/144 (32.64%)	0.448
Heart disease	7/27 (25.93%)	15/144 (10.42%)	0.070
Lung disease	3/27 (11.11%)	11/143 (7.69%)	0.582
Kidney disease	5/27 (18.52%)	12/142 (8.45%)	0.553
Cancer	2/27 (7.41%)	3/142 (2.11%)	0.648
TB (Previous)	1/27 (3.70%)	6/144 (4.17%)	0.660
TB (Current)	1/27 (3.70%)	3/144 (2.08%)	0.611
HIV	5/27 (18.52%)	32/144 (22.22%)	0.603
Overweight	4/27 (14.81%)	40/143 (27.78%)	0.436

Supplementary Table 2: Routine clinical and laboratory parameters by outcome.

	Deceased	Survived	p-value
Pulse (bpm)	100	97	0.5700
	(86-108)	(88-108.5)	
Respiratory rate (breaths per minute)	26	24	0.7319
	(20-32)	(20-28)	
Temperature (°C)	36.4	36.6	0.1254
	(36-36.8)	(36.2-37.2)	
pH	7.43	7.45	0.3100
	(7.41-7.48)	(7.41-7.50)	
pCO2 (mmHg)	30.7	33.3	0.1077
	(25.7-35.1)	(29.8-37.9)	
pO2 (mmHg)	68.2	60.9	0.3590
	(46.2-82.1)	(44.7-73.1)	
ctHb (g/dL)	13.6	13.3	0.7341
	(11.6-15.6)	(12-14.7)	
sO2 (%)	92.4	89.65	0.9524
	(74.7-95.4)	(68.8-95.45)	
FO2Hb (%)	82.75	87.7	0.5978
	(73.4-93.7)	(72.1-93.5)	
FCOHb (%)	1.3	1.3	0.7573
	(0.7-1.8)	(0.9-1.6)	
FHHb (%)	15.75	10.8	0.6490
	(4.5-25.2)	(4.8-28.45)	
FMetHb (%)	0.4	0.4	0.5318
	(0.2-0.6)	(0.1-0.6)	
Glucose (mmol/L)	7.6	7.25	0.5886
	(5.9-8.9)	(6.3-9.5)	
CRP (mg/L)	156	103	0.1564

	(90-207)	(51-193)	
Hb (g/dL)	12.6	13.25	0.5144
	(9.7-15.4)	(11.8-14.9)	
Cl (mmol/L)	100	100	0.6490
	(95-104)	(97-104)	
HbA1c	6.7	72	0.4771
	(6-8.4)	(6.15-10.75)	
Pro-BNP	1139.5	449	0.1164
	(927.5-2963)	(84-1343)	
LDH (U/L)	724.5	558	0.1698
	(568-1025)	(444-799)	
ALT	27	29..5	0.8069
	(20-45)	(20-50)	
GGT	57	61	0.9625
	(40-126)	(41-103)	
ALP	75	75.5	0.9941
	(64-102)	(63.5-100)	
TSH	0.94	1.03	0.4300
	(0.29-1.54)	(0.58-2.02)	
FT4	12.75	13.25	0.8489
	(11.6-15.5)	(11.6-14.5)	
Mg (mmol/L)	0.79	0.86	0.3157
	(0.71-1.02)	(0.76-0.94)	
PO4 (mmol/L)	1.2	0.89	**0.0002**
	(0.97-1.51)	(0.71-1.08)	
Tchol	5.07	3.97	0.3278
	(3.1-5.86)	(3.09-4.9)	
SARS 2 PCR Ct value	28.2	30.6	0.1693
	(23.65-32.35)	(26.6-34.85)	
WCC ($x10^9$/L)	8.56	8.97	0.8515
	(6.88-12.11)	(6.28-11.4)	

Neutrophil count ($x10^9$/L)	8.1	6.8	0.2695
	(5.97-10.41)	(4.66-9.13)	
Lymphocyte count ($x10^9$/L)	0.75	1.22	**0.0021**
	(0.68-0.93)	(0.81-1.84)	
Monocytes ($x10^9$/L)	0.46	0.02	0.8114
	(0.35-0.57)	(0.01-0.04)	
Basophils ($x10^9$/L)	0.02	0.07	0.3758
	(0.01-0.03)	(0.04-0.17)	
Immature cells ($x10^9$/L)	0.13	0.9	0.4145
	(0.05-0.18)	(0.6-1.8)	
Neutrophil (%)	82.8	77.7	0.2144
	(74.9-86.4)	(65.6-83.6)	
Lymphocytes (%)	7.5	14.1	0.0736
	(6.8-15.6)	(9.5-19.6)	
Monocytes (%)	5	4.7	0.5311
	(4.1-6.8)	(3.3-7.6)	
Basophils (%)	0.2	0.2	0.5414
	(0.1-0.3)	(0.1-0.4)	
Immature cells (%)	1.25	0.9	0.9066
	(0.5-1.5)	(0.6-1.8)	
Systolic blood pressure (mmHg)	1.25	123.79 (±1.88)	0.7083
Diastolic blood pressure(mmHg)	(0.5-1.5)	78.76 (±1.22)	0.1442
Ca (mmol/L)	2.05 (±0.04)	2.11 (±0.02)	0.1169

All variables are shown as median (interquartile range) except for Hb, SBP, DBP and Ca which are shown as mean (± standard deviation).

Abbreviations: Alanine alkaline phosphatase (ALP), alanine transaminase (ALT), chloride (Cl), concentration of total hemoglobin (ctHb), C-reactive protein (CRP), fraction of carboxyhemoglobin (FCOHb), fraction of deoxyhemoglobin (FhHb), fraction of methemoglobin (fMetHb), fraction of oxygenated hemoglobin (FO2Hb), free circulating thyroxine (fT4), gamma-glutamyl transferase (GGT), hemoglobin (Hb), hemoglobin A1c (HbA1c), lactate dehydrogenase (LDH), magnesium (Mg), oxygen saturation (s02), partial pressure of carbon dioxide (pCO2), partial pressure of oxygen (pO2), phosphate (PO4), potential of hydrogen (pH), pro-brain natriuretic peptide (Pro-BNP), severe acute respiratory syndrome polymerase chain reaction cycle threshold (SARS 2 PCR Ct value), thyroid stimulating hormone (TSH), total cholesterol (Tchol), white cell count (WCC).

Values in bold indicate significance.

Supplementary Table 3: Monocyte populations by COVID-19 outcome.

Monocyte population (%)	Deceased	Survived	p-value
Non-classical	3.91	5.61	0.1365
	(2.05-6.60)	(2.39-11.73)	
Classical	72.07	74.35	0.7581
	(62.06-84.99)	(59.00-81.46)	
Intermediate	13.84	16.25	0.9338
	(941-28.31)	(9.28-27.47)	
Non-classical activated PD-L1	32.31	29.04	0.3417
	(23.08-44.83)	(21.15-41.32)	
Non-classical PD-L1	27.78	26.32	0.4746
	(10.88-38.46)	(17.61-40.27)	
Classical PD-L1	72.48	78.77	0.5083
	(55.88-84.03)	(53.72-88.55)	
Intermediate PDL1	76.05	81.13	0.5830
	(61.76-88.69)	(65.97-89.71)	
Classical Activated	0.27	0.41	0.6052
	(0.11-1.18)	(0.15-1.07)	
CCR2	94.05	93.08	0.4517
	(90.69-97.07)	(86.72-96.93)	
CD80	1.49	1.52	0.9020
	(0.56-3.12)	(0.72-2.93)	
PD-L1	69.69	71.14	0.8492
	(55.10-84.02)	(51.69-86.05)	
CD86	99.74	99.90	**0.0205**
	(95.63-99.93)	(99.57-99.97)	

Abbreviations: C-C chemokine receptor type 2 (CCR2), programmed cell death ligand-1 (PD-L1).

Statistically significant p-values are in bold.

Supplementary Table 4: T-cells populations by COVID-19 outcome.

T-cells (%)	Deceased	Survived	p-value
CD4+	61.35	61.18	0.5614
	(48.63-71.96)	(50.17-73.64)	
CD8+	30.57	33.47	0.8296
	(23.86-40.76)	(20.64-44.08)	
DP	0.54	0.76	0.8335
	(0.36-1.7)	(0.38-1.4)	
DN	3.32	3.60	0.6272
	(2.22-6.36)	(2.20-4.94)	
CD8+N	18.25	22.44	0.8609
	(9.99-44.43)	(11.54-38.40)	
CD8+TEMRA	31.20	32.03	0.4174
	(14.56-46.95)	(20.25-49.30)	
CD8+EM	25.34	26.55	0.9004
	(17.99-40.14)	(16.68-37.96)	
CD8+CM	4.92	8.203	0.4060
	(3.18-14.04)	(4.70-11.71)	
CD8+PD1+	40.87	34.77	0.2621
	(22.49-57.39)	(23.53-44.92)	
CD4+TEMRA	0.35	0.34	0.9880
	(0.13-0.99)	(0.09-1.32)	
CD4+EM	12.77	11.85	0.5315
	(7.31-30.59)	(7.36-21.13)	
CD4+N	30.37	26.88	0.8570
	(10.61-42.35)	(19.09-39.03)	
CD4+CM	53.01	52.95	0.3265
	(42.59-56.33)	(44.96-65.02)	
CD4+EM4	24.62	23.18	0.4407
	(19.61-42.70)	(16.60-34.23)	
CD4+EM1	37.99	47.75	0.5347
	(27.33-62.75)	(29.02-64.86)	
CD4+EM3	20.81	20.83	0.9362
	(7.92-33.67)	(6.90-38.73)	
CD4+EM2	0.31	0.46	0.6953
	(0.12-0.77)	(0.21-0.72)	
CD4+EM3 PD1+	20.82	20.83	0.9362
	(7.92-33.67)	(6.90-38.73)	
CD4+EM3 PD1+CD57+	11.60	11.81	0.9900
	(6.05-18.65)	(4.79-22.81)	

CD4+EM4 PD1+	13.26	10.73	0.1059
	(9.23-19.61)	(6.20-16.63)	
CD4+CM PD1+	41.05	42.80	0.9004
	(29.31-64.81)	(32.93-53.44)	
CD8+EM1	36.18	40.59	0.4557
	(17.60-60.71)	(27.42-56.47)	
CD8+EM2	13.68	14.96	0.3001
	(5.37-19.46)	(10.99-24.50)	
CD8+EM4	3.51	3.93	0.7148
	(1.95-7.87	(2.40-6.93)	
CD8+EM3	25.68	32.79	0.9461
	(13.31-67.61)	(16.33-48.89)	
CD8+EM1 PD1+	30.37	31.79	0.3167
	(14.03-47.47)	(22.19-45.24)	
CD8+EM2 PD1+	9.10	10.36	0.3729
	(3.66-15.79)	(6.06-18.52)	
CD8+EM3 PD1+	12.38	10.73	0.7260
	(5.07-26.40)	(5.15-21.75)	
CD8+EM4 CD57+	0.28	0.41	0.0936
	(0-0.66)	(0.20-1.06)	
CD8+EM3 CD57+	15.31	23.16	0.3441
	(7.05-37.20)	(11.22-36.64)	
CD8+EM2 CD57+	3.56	3.90	0.2475
	(1.33-6.15)	(2.26-7.05)	
CD8+EM1 CD57+	2.26	2.47	0.1494
	(0.49-3.23)	(1.30-4.17)	
CD8+TEMRA E CD57+	46.58	49.24	0.2638
	(25.32-59.35)	(36.89-61.74)	
CD8+TEMRA E CD57+PD1+	12.75	11.22	0.389
	(6.99-19.96)	(6.30-16.31)	
CD8+TEMRA pE1	4.69	5.14	0.5351
	(2.31-9.21)	(3.01-9.22)	
CD8+TEMRA pE1 PD1+	3.00	4.03	0.5150
	(1.78-7.26)	(2.24-7.36)	
CD8+CM PD1+	41.94	51.30	0.3961
	(31.94-67.00)	(40.88-59.53)	

Abbreviations: Central memory (CM), double negative (DN), double positive (DP), End-stage effector (E), Effector memory (EM), Naive (N), Terminally differentiated effector memory T-cells re-expressing CD45RA (TEMRA), pre-effector 1 (pE1), pre-effector 2 (pE2), programmed cell death 1 (PD1).

Values in bold indicate significance.

Supplementary Table 5: Cytokine analysis by outcome.

	Deceased	Survived	p value
ICAM-1	159.32	144.61	0.0918
	(133.96-194.40)	(177.47-180.88)	
TGF-β1	6.44	8.54	0.0506
	(5.07-9.63)	(5.92-12.24)	
RANTES	122.96	78.78	**0.0137**
	(66.31-269.04)	(41.91-150.50)	
IL-1β	2.86	1.95	**0.0177**
	(1.84-3.68)	(1.46-2.66)	
IL-1ra	1089.68	823.25	**0.0075**
	(707.11-1603.61)	(606.29-1046.00)	
IL-2	5.16	6.28	0.8884
	(2.29-11.55)	(1.63-10.98)	
IL-4	4.7	4.14	0.0638
	(3.67-6.73)	(3.07-5.39)	
Hu IL-5	5.34	5.34	0.4150
	(5.34-5.34)	(5.34-5.34)	
IL-6	8.19	4.055	**0.0034**
	(2.86-31.69)	(1.36-9.51)	
IL-7	43.82	44.9	0.5033
	(28.52-64.79)	(27.44-70.14)	
IL-8	27.4	17.335	**<0.0001**
	(16.68-45.03)	(9.70-22.96)	
IL-9	404.55	408.35	0.7443
	(352.09-443.2)	(367.4-440.74)	
IL-10	11.43	10.01	0.9022
	(3.14-23.17)	(3.92-19.42)	
IL-12p70	8.16	11.09	0.6487
	(3.52-16.99)	(5.13-17.19)	
IL-13	3.27	3.5	0.8554
	(2.08-5.1)	(2.18-5.5)	
IL-15	18.02	18.02	0.4254
	(18.02-18.02)	(18.02-18.02)	
IL-17	24.48	23.06	0.5703
	(17.42-35.82)	(17.39-33.86)	
Eotaxin	34.16	22.03	**<0.0001**
	(24.37-42.57)	(15.68-30.6)	
FGF basic	35.71	37.56	0.5196
	(25.21-42.28)	(29.38-46.34)	

G-CSF	200.93	147.73	**0.0124**
	(146.42-291.77)	(100.88-220.33)	
GM-CSF	1.29	1.78	0.6150
	(0.51-3.1)	(0.76-3.29)	
IFN-γ	16.93	15.725	0.5531
	(12.37-23.85)	(10.685-23.85)	
MCP-1	50.91	25.57	**0.0002**
	(27.77-142.83)	(14.47-38.68)	
MIP-1α	4.41	3.265	**0.0047**
	(3.04-5.98)	(2.36-4.61)	
PDF-bb	406.08	517.78	0.9140
	(182.19-2299.24)	(254.66-978.37)	
MIP-1β	171	168.12	0.8108
	(152.6-184.9)	(152.15-186.31)	
TNF-α	95.47	83.87	**0.0223**
	(78.66-134.25)	(67.76-102.39)	
VEGF	4.22	4.22	0.7719
	(4.22-110.27)	(4.22-91.82)	

Abbreviations: fibroblast growth factor (FGF), granulocyte colony-stimulating factor (G-CSF), granulocyte-macrophage colony-stimulating factor (GM-CSF), interferon gamma (IFN-γ), interleukin (IL) (IL-1Ra), interferon gamma-induced protein 10 (IP-10), macrophage inflammatory protein-1 alpha (MIP-1α), monocyte chemoattractant protein 1 (MCP-1), platelet-derived growth factor-BB (PDGF-BB), tumor necrosis factor (TNF)-α, vascular endothelial growth factor (VEGF).

Values in bold indicate significance.