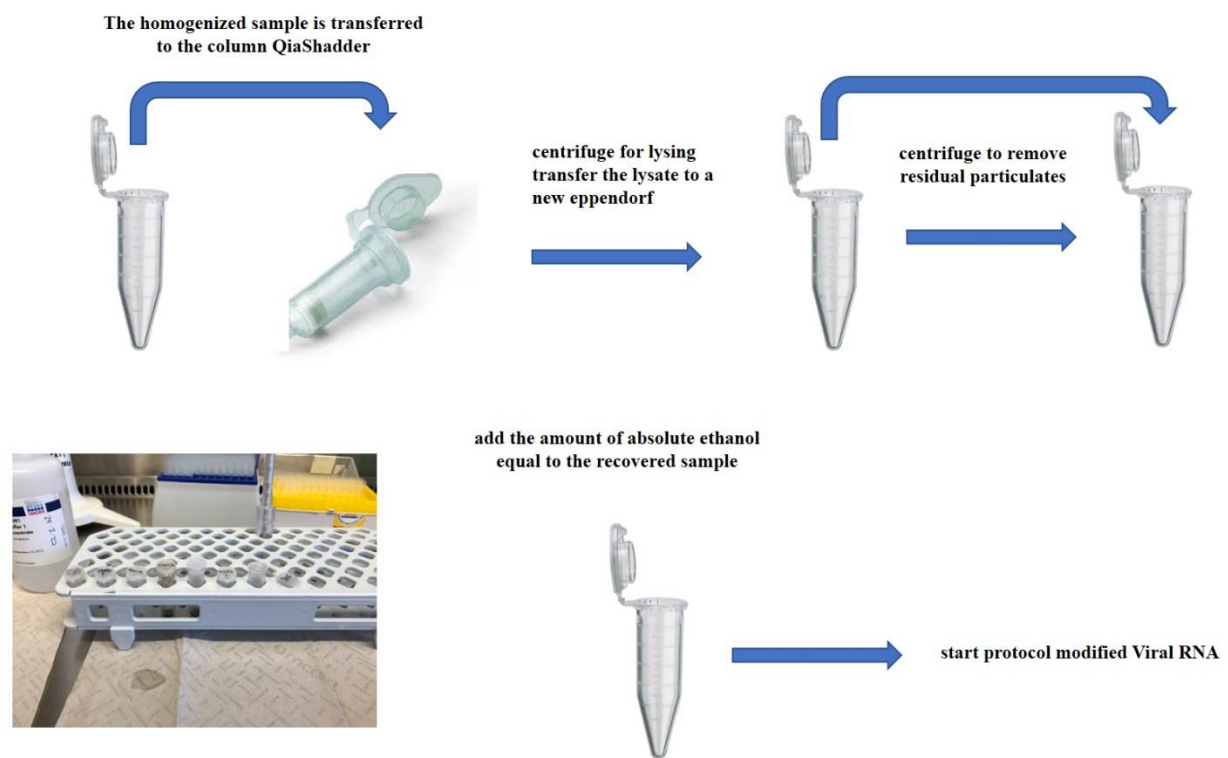


## Supplementary material

**Table S1.** Socio-demographic and clinical-pathological features of COVID-19 patients

Clinical Findings			
	Old Tissues	Fresh Tissues	
	(16 Samples)	(2 Samples)	
Age (years)	83.5	75.5	
Sex	8M, 8F	2F	
Male (%)	8 (50%)	0 (0%)	
Female (%)	8 (50%)	2 (100%)	
<b>Comorbidities</b>			
Hypertension	11 (68.75%)	2 (100%)	
Diabetes	5 (31.25%)	1 (50%)	
Chronic pulmonary diseases	2 (12.5%)	---	
Obesity (BMI > 30)	3 (18.75%)	---	
Cardiovascular diseases	11 (68.75%)	---	
Chronic renal diseases	3 (18.75%)	---	
Cancer	3 (18.75%)	---	
Alzheimer's disease	1 (6.25%)	---	
Burial time (days)	50.19 (24 – 78)	3	
Laboratory Findings (CI 95%)			
	First exams after COVID-19 positivity	Last exams before death	P-value
Redcells (x 10 <sup>6</sup> /μL)	4.49 (4.04 - 4.94)	4.12 (3.66 - 4.58)	0,219
Hemoglobin (g/dL)	12.64 (11.28 - 14.00)	11.75 (10.46 - 13.05)	0,303
Hematocrit (%)	38.85 (34.72 - 42.98)	36.17 (32.19 - 40.16)	0,308
Platelets (10 <sup>3</sup> /μL)	254.3 (175.49 - 333.11)	160.45 (96.37 - 224.52)	0,052
White Blood Cells (10 <sup>3</sup> /μL)	18.8 (2.98 - 40.57)	12.1 (6.8 - 17.34)	0,513
Neutrophils	8.2 (3.68 - 12.74)	10.8 (5.31 - 16.33)	0,415
Lymphocytes	0.99 (0.55 - 1.42)	0.82 (0.38 - 1.26)	0,549
<b>Neutrophils/Lymphocyte Ratio</b>	8,28	13,17	NA
C-reactive protein (mg/L)	159.5 (56.75 - 262.3)	84.71 (17.44 - 186.9)	0,258
Prothrombin time (sec)	12.96 (9.04 - 16.87)	18.46 (6.89 - 30.02)	0,308
Prothrombin activation (%)	81.56 (61.87 - 101.2)	72.71 (41.85 - 103.6)	0,573
International Normalized Ratio (INR)	1.23 (0.98 - 1.48)	1.6 (0.59 - 2.62)	0,419
Partial thromboplastin time (sec)	28.79 (26.45 - 31.13)	37.86 (25.12 - 50.60)	0,135
D-dimer (ng/mL)	754.1 (309.4 - 1199)	845.7 (474.5 - 1217)	0,711
Erythrocyte Sedimentation Rate (ESR) (mm/h)	92.4 (50.21 - 134.6)	56 (29.44 - 141.4)	0,214
Fibrinogen (mg/dL)	595.9 (421.5 - 770.2)	435.9 (291 - 580.8)	0,12
LDH (U/L)	911.9 (561.3 - 1262)	963.9 (385.9 - 1542)	0,859

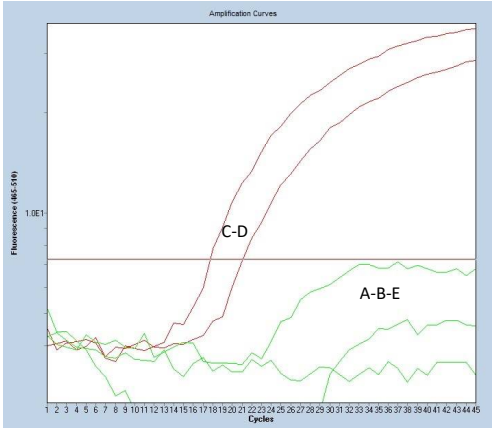
**Figure S1.** SARS-CoV 2 viral extraction from pulmonary tissues work flow.



**Figure S2.** A) RT-qPCR detection of SARS-CoV-2 N2 gene in non-infected samples. B) RT-qPCR detection of human GAPDH in control samples and lung tissues to assess the validity of the extraction protocol.

A)

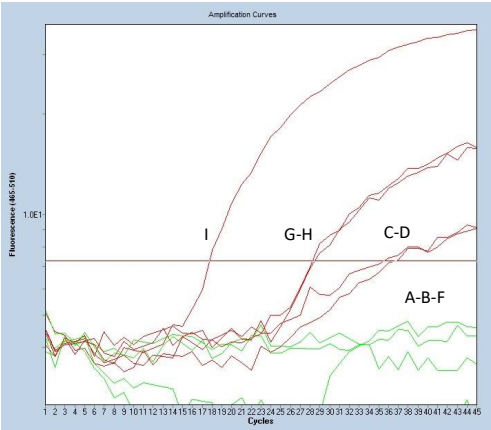
	Name	Ct
A	SARS-CoV2 N2 Lung Method 1	NA
B	SARS-CoV2 N2 Lung Method 1	NA
C	SARS-CoV2 N2 Primers CTRL Pos	20.21
D	SARS-CoV2 N2 Primers CTRL Pos	18,29
E	SARS-CoV2 N2 NTC	NA



Legend: A-B) Analysis of SARS-CoV-2 N2 gene expression in normal lung (performed in duplicate); C-D) Analysis of SARS-CoV-2 N2 genes in a positive control obtained for a patient with a confirmed diagnosis of COVID-19 infection (performed in duplicate); E) Non-Template Control.

B)

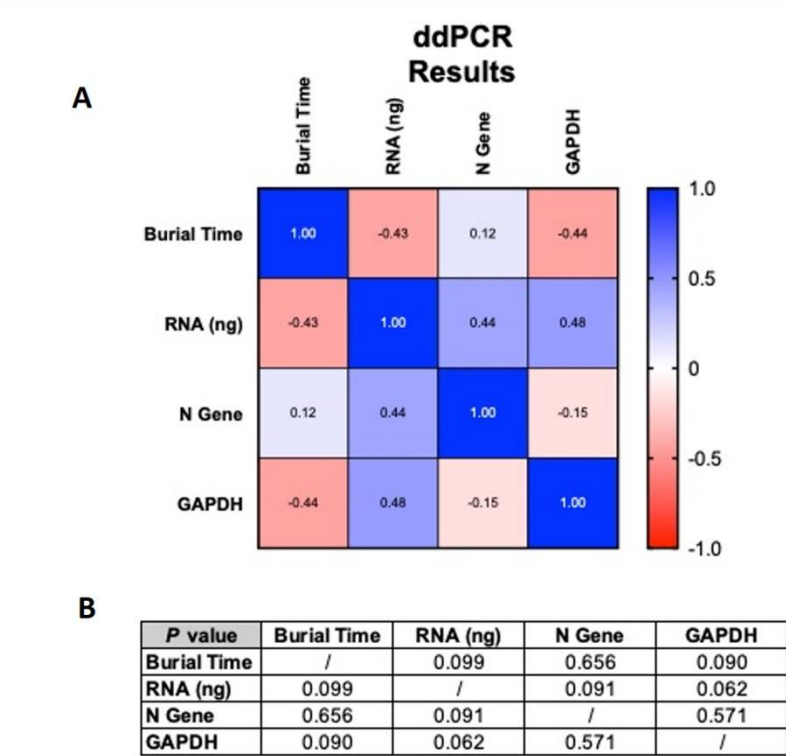
	Name	Ct
A	GAPDH Negative Sample 1	NA
B	GAPDH Negative Sample 1	NA
C	GAPDH Lung Method 2	34.80
D	GAPDH Lung Method 2	36.86
G	GAPDH Lung Method 1	27.98
H	GAPDH Lung Method 1	26.67
I	GAPDH MG-63 Human Cell Line	17.46
F	GAPDH NTC	NA



Legend: A-B) Negative samples consisting of all the buffers and components used during the extractions, tested to verify any possible cross-contamination. C-D-G-H) RNA extracted from a lung specimen obtained using two different

methods (i.e. samples kept at room temperature or in ice) and obtained from a patient negative to COVID-19 infection.

**Figure S3.** A) Pearson’s correlation matrix between the cDNA amount and the ddPCR results obtained for GAPDH and SARS-CoV-2 N2 gene, from red to blue the increasing statistical significance and B) *p*-value relative to the matrix, *p*-value ≤0.05.



**Figure S4.** Electropherograms of SARS-CoV-2 fragments. A) SARS-CoV-2 N gene sequence; B) SARS-CoV-2 Spike gene sequence; SARS-CoV-2 c) Spike/Orf3a gene sequence. N and Spike sequences were aligned with the reference genome MW041156, while the Spike/Orf3a sequence was aligned with the reference genome MT077125.

