

General dynamics of the URT microbiome and microbial signs of recovery in COVID-19 patients

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Supplementary materials S1. Case report form for COVID-19 patients

Case No.

Sex

Age

Date of admission

Diagnosis

NEWS score

MSCT score (0,1,2,3,4)

Respiratory support at the moment of enrollment:

- Oxygen inhalation;
- High-flow oxygen therapy (FiO₂, flow rate);
- Non-invasive ventilation (FiO₂, PEEP)
- Invasive ventilation (FiO₂, PEEP)

Prone positioning yes/no

Date of connecting the patient to mechanical ventilation

Date of disconnecting the patient from mechanical ventilation

Treatment:

Specific antiviral therapy:

- Plaquenil® + azithromycin;
- Kaletra® + Infibeta®;
- Hyperimmune plasma;
- Other;

Anti-cytokine therapy:

- IL-6 inhibitors;
- Janus kinase inhibitors;
- Other;

Antibiotics (except azithromycin);

Hemodiafiltration;

Cytosorption.

Outcome (date)

Lung lesions: uni-, bilateral; %

Laboratory parameters:

Parameter	Day 0	Day 5–7	Day 12–14
Complete blood count (including absolute count of neutrophils and lymphocytes)			
CRP			
Procalcitonin			
Blood gas analysis			
Acid-base balance			
Lactate			
Glucose			
Creatinine			
Fibrinogen			
D-dimer			

Table S1. ddPCR reaction mixture.

Components	Amount per one reaction (20 μ L)	Final concentration
2x ddPCR Supermix for probes	10 μ L	1x
20 μ M primer F	1 μ L	1000 nM
20 μ M primer R	1 μ L	1000 nM
10 μ M probe (FAM)	0.56 μ L	278 nM
cDNA	6 μ L	To 330 ng
diH ₂ O	1.44 μ L	-

Table S2. Amplification protocol for ddPCR.

Temperature, °C	Time	Number of cycles
95	10 min	1
94	30 sec	40
54	60 sec	
98	10 min	1
4	∞	1

Table S3. Most abundant genera in the upper respiratory tract microbiome of the COVID-19 patients and controls.

COVID-19 patients		healthy individuals	
genera	relative abundance, %	genera	relative abundance, %
<i>Prevotella</i>	26.79	<i>Prevotella</i>	29.48
<i>Streptococcus</i>	23.69	<i>Streptococcus</i>	16.00
<i>Veillonella</i>	13.44	<i>Veillonella</i>	11.72
<i>Leptotrichia</i>	2.83	<i>Haemophilus</i>	6.52
<i>Granulicatella</i>	2.54	<i>Neisseria</i>	5.84
<i>Rothia</i>	2.44	<i>Leptotrichia</i>	4.18
<i>Gemella</i>	1.85	<i>Fusobacterium</i>	3.23
<i>Neisseria</i>	1.76	<i>Limosilactobacillus</i>	3.17
<i>Staphylococcus</i>	1.74	<i>Porphyromonas</i>	2.28
<i>Haemophilus</i>	1.59	<i>Rothia</i>	1.49
<i>Fusobacterium</i>	1.59	<i>Granulicatella</i>	1.07
<i>Limosilactobacillus</i>	1.03	<i>Gemella</i>	0.80
<i>Porphyromonas</i>	1.31	<i>Staphylococcus</i>	0.40
Other	17.40	Other	13.82

Table S4. Unique representatives of the upper respiratory tract microbiome in the COVID-19 patients upon their admission to hospital (at TP0) and controls.

Bacterial genera unique for COVID-19 patients at TP0 (n = 47)			Bacterial genera unique for healthy individuals (n = 2)		
Genera	% of individuals	Mean abundance	Genera	% of individuals	Mean abundance
<i>Olsenella</i>	7.84	0.29	<i>Oblitimonas</i>	3.66	5.28
<i>Moraxella</i>	1.12	17.14	<i>Aeromonas</i>	1.22	0.17
<i>Psychrobacter</i>	2.61	0.33			
<i>Comamonas</i>	2.24	0.21			
<i>Rhodococcus</i>	2.24	0.18			
<i>Listeria</i>	0.75	0.60			
<i>Schwartzia</i>	10.07	0.15			
<i>Sphingobium</i>	1.12	0.21			
<i>Actinomarinicola</i>	1.49	0.12			
<i>Scardovia</i>	8.58	0.19			
<i>Pediococcus</i>	1.12	1.02			
<i>Paucibacter</i>	1.12	0.40			
<i>Tatumella</i>	0.75	0.47			
<i>Oryzobacter</i>	0.75	0.11			
<i>Zavarzinella</i>	0.75	0.21			
<i>Nosocomiicoccus</i>	1.87	0.21			
<i>Oscillibacter</i>	0.75	0.17			
<i>Vibrio</i>	0.37	0.11			
<i>Pantoea</i>	0.75	0.12			
<i>Serratia</i>	4.85	5.04			
<i>Rickettsia</i>	4.48	0.17			
<i>Raoultella</i>	0.75	0.43			
<i>Savagea</i>	0.37	0.22			
<i>Salmonella</i>	5.22	0.90			
<i>Ruminococcus2</i>	0.75	0.20			
<i>Ruminococcus</i>	0.37	0.93			
<i>Solibacillus</i>	0.37	0.11			
<i>Proteus</i>	0.75	1.00			
<i>Caulobacter</i>	0.75	0.41			
<i>Brochothrix</i>	1.87	0.18			
<i>Desulfobulbus</i>	2.61	0.11			
<i>Dechloromonas</i>	0.37	0.11			
<i>Dermabacter</i>	1.49	0.22			
<i>Akkermansia</i>	1.12	0.10			
<i>Acidovorax</i>	1.87	1.41			
<i>Blautia</i>	0.75	0.15			
<i>Lentilactobacillus</i>	2.24	0.18			
<i>Kosakonia</i>	1.12	0.17			
<i>Lampropedia</i>	1.12	0.12			
<i>Lactiplantibacillus</i>	10.07	0.52			
<i>Methylobacterium</i>	19.78	1.11			

<i>Melaminivora</i>	1.87	0.11			
<i>Flexilinea</i>	1.49	0.11			
<i>Flectobacillus</i>	0.37	3.21			
<i>Intestinibacter</i>	0.37	0.23			
<i>Fructilactobacillus</i>	0.75	0.24			
<i>Geobacillus</i>	1.12	0.16			

Note. TP0: time-point 0

Table S5. Unique and representatives of the upper respiratory tract microbiome in the COVID-19 patients at TP1 and controls.

Bacterial genera unique for COVID-19 patients at TP1 (n = 46)			Bacterial genera unique for healthy individuals (n = 3)		
Genera	% of individuals	Mean abundance	Genera	% of individuals	Mean abundance
<i>Facklamia</i>	1.80	0.61	<i>Oblitimonas</i>	3.66	5.28
<i>Novosphingobium</i>	4.05	0.16	<i>Dolosigranulum</i>	2.44	0.26
<i>Olsenella</i>	3.15	0.11	<i>Duncaniella</i>	1.22	0.24
<i>Moraxella</i>	0.45	11.70			
<i>Psychrobacter</i>	1.80	3.51			
<i>Rhodoferrax</i>	1.35	0.17			
<i>Fluviicola</i>	1.80	0.14			
<i>Legionella</i>	0.90	0.11			
<i>Listeria</i>	2.70	0.28			
<i>Jeotgalicoccus</i>	1.35	0.27			
<i>Schwartzia</i>	4.05	0.13			
<i>Sphingobacterium</i>	1.35	0.20			
<i>Scardovia</i>	1.80	0.28			
<i>Tepidiphilus</i>	0.90	0.17			
<i>Terrimonas</i>	1.80	0.14			
<i>Thermus</i>	0.45	0.95			
<i>Oryzobacter</i>	0.45	0.29			
<i>Xanthomonas</i>	1.80	0.12			
<i>Oscillibacter</i>	0.45	0.18			
<i>Parascardovia</i>	0.45	0.23			
<i>Serratia</i>	3.60	7.41			
<i>Rickettsia</i>	4.50	0.28			
<i>Savagea</i>	1.35	0.46			
<i>Salmonella</i>	7.66	1.02			
<i>Schleiferilactobacillus</i>	0.45	0.23			
<i>Spiroplasma</i>	1.80	0.12			
<i>Ralstonia</i>	2.25	0.25			
<i>Proteus</i>	0.45	3.93			
<i>Pseudoglutamicibacter</i>	0.90	1.20			
<i>Caulobacter</i>	0.90	0.18			

<i>Dechloromonas</i>	0.45	0.55			
<i>Curvibacter</i>	7.66	0.20			
<i>Dermabacter</i>	1.80	0.16			
<i>Altererythrobacter</i>	0.45	0.37			
<i>Acidovorax</i>	2.70	0.34			
<i>Aerococcus</i>	1.35	0.40			
<i>Atopostipes</i>	0.90	0.16			
<i>Barnesiella</i>	0.45	0.15			
<i>Kosakonia</i>	3.15	0.10			
<i>Lactiplantibacillus</i>	4.05	0.25			
<i>Methylobacterium</i>	17.12	1.74			
<i>Melaminivora</i>	1.35	0.14			
<i>Flectobacillus</i>	0.90	0.21			
<i>Fannyhessea</i>	4.05	0.36			
<i>Glutamicibacter</i>	0.90	0.25			
<i>Geodermatophilus</i>	0.45	0.22			

Note. TP1: time-point 1 (after a median of 5.0 days since admission to hospital)

Table S6. Unique representatives of the upper respiratory tract microbiome in the COVID-19 patients at TP2 and controls.

Bacterial genera unique for COVID-19 patients at TP2 (n = 37)			Bacterial genera unique for healthy individuals (n = 1)		
Genera	% of individuals	Mean abundance	Genera	% of individuals	Mean abundance
<i>Facklamia</i>	1.14	0.10	<i>Dolosigranulum</i>	2.44	0.26
<i>Novosphingobium</i>	2.29	0.21			
<i>Psychrobacter</i>	3.43	0.15			
<i>Comamonas</i>	2.29	0.12			
<i>Rhodobacter</i>	1.14	0.50			
<i>Fluviicola</i>	4.57	0.13			
<i>Listeria</i>	4.00	0.52			
<i>Cryptomonadaceae</i>	0.57	0.11			
<i>Scardovia</i>	3.43	0.13			
<i>Pediococcus</i>	1.14	1.23			
<i>Terrimonas</i>	2.29	0.12			
<i>Wautersiella</i>	0.57	0.14			
<i>Xanthomonas</i>	1.71	0.19			
<i>Parascardovia</i>	0.57	0.60			
<i>Ureibacillus</i>	0.57	0.18			
<i>Vibrio</i>	0.57	0.20			
<i>Serratia</i>	4.00	12.53			
<i>Rickettsia</i>	20.00	0.11			
<i>Sediminibacterium</i>	0.57	0.37			
<i>Salmonella</i>	8.00	1.47			
<i>Solibacillus</i>	0.57	0.19			
<i>Ralstonia</i>	6.29	0.13			
<i>Pseudarcicella</i>	0.57	2.01			
<i>Proteus</i>	0.57	0.11			
<i>Pseudogracilibacillus</i>	1.71	0.13			
<i>Caulobacter</i>	1.71	0.14			
<i>Chlorophyta</i>	0.57	0.27			
<i>Brochothrix</i>	2.86	0.82			
<i>Aerococcus</i>	0.57	0.10			
<i>Blastocatella</i>	0.57	0.21			
<i>Asprobacter</i>	1.14	0.15			
<i>Macrococcus</i>	0.57	0.19			
<i>Kytococcus</i>	0.57	0.23			
<i>Methylobacterium</i>	12.00	1.50			
<i>Fannyhessea</i>	1.14	0.21			
<i>Herbaspirillum</i>	1.71	0.55			
<i>Intestinibacter</i>	0.57	0.14			

Note. TP2: time-point 2 (after a median of 12.0 days since admission to hospital)

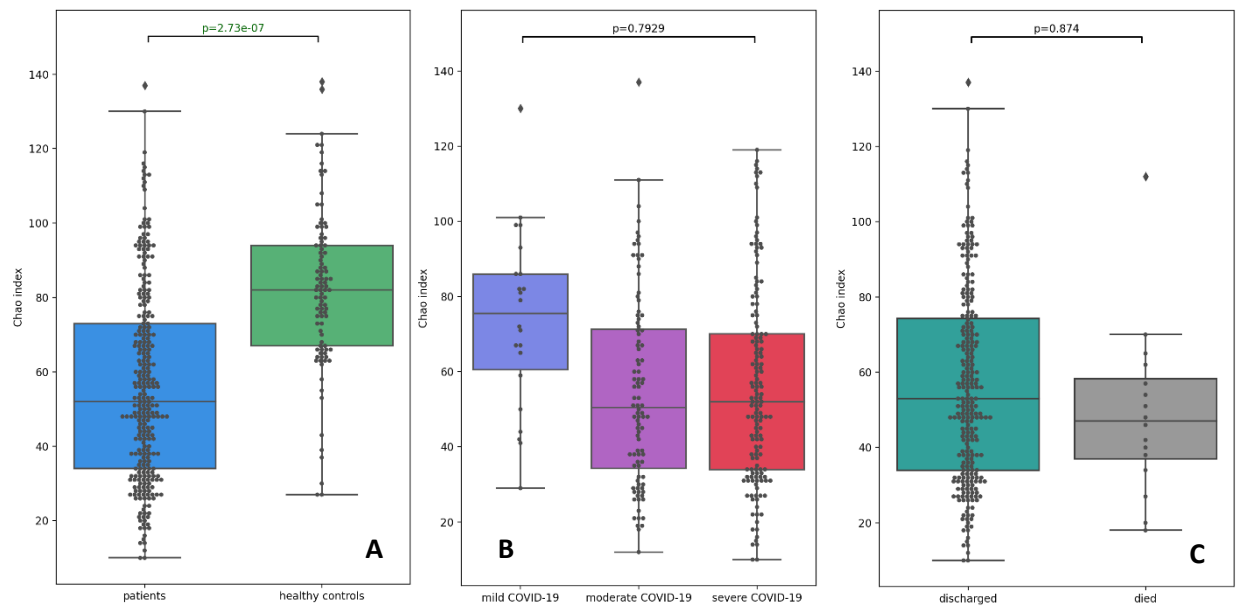


Figure S1. Comparison of the Chao indices of the upper respiratory tract microbiota between the patients and controls (A); patients with mild, moderate, and severe COVID-19 (B); discharged and deceased patients (C).

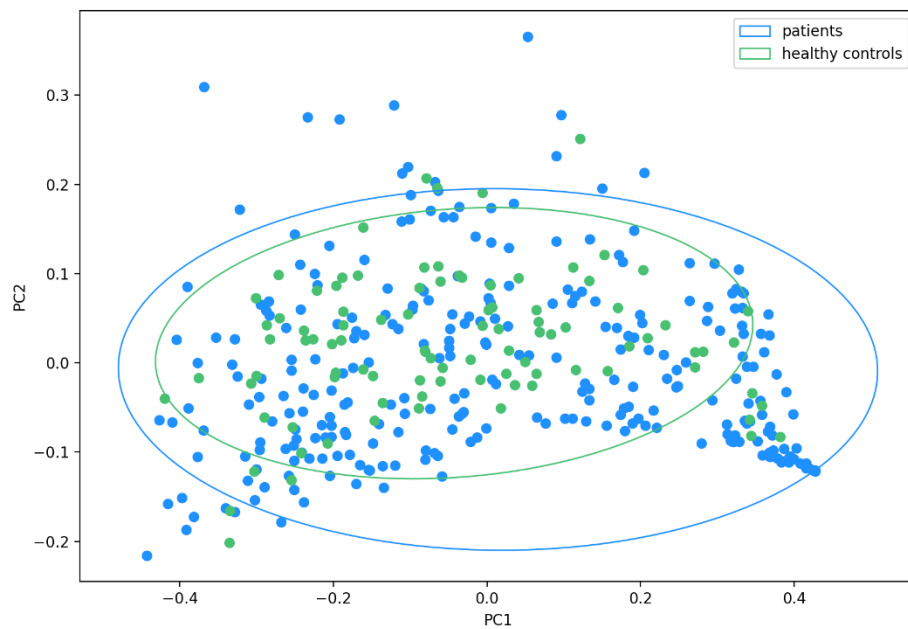


Figure S2. The Unifrac distances between the patients' and controls' upper respiratory tract microbiota. No significant difference in the microbial composition was observed between the patients and controls both along PC1 and PC2 ($P = 0.83$ and $P = 0.21$, respectively).

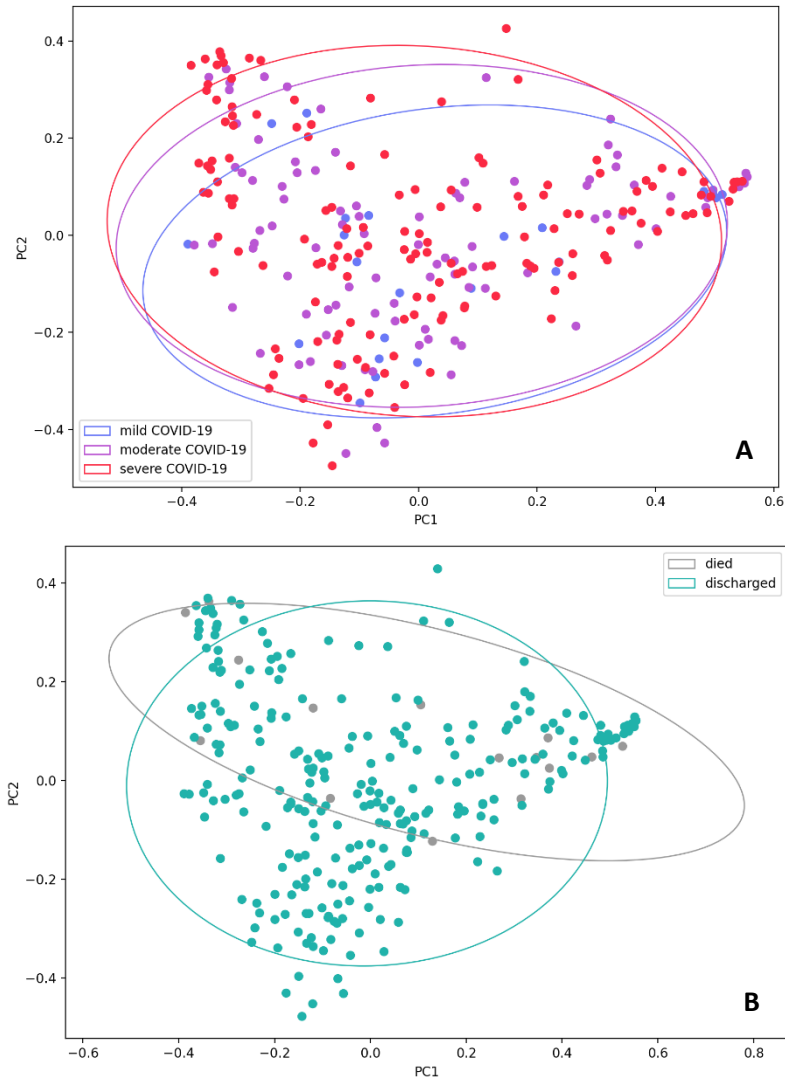


Figure S3. The Bray-Curtis dissimilarity between the upper respiratory tract microbiota of the patients with mild, moderate, and severe COVID-19 (A) and discharged or deceased patients (B). No evidence of sample clustering dependent on disease severity (PC1, $P = 0.68$; PC2, $P = 0.96$) or treatment outcome (PC1, $P = 1.00$; PC2, $P = 0.72$) was observed.

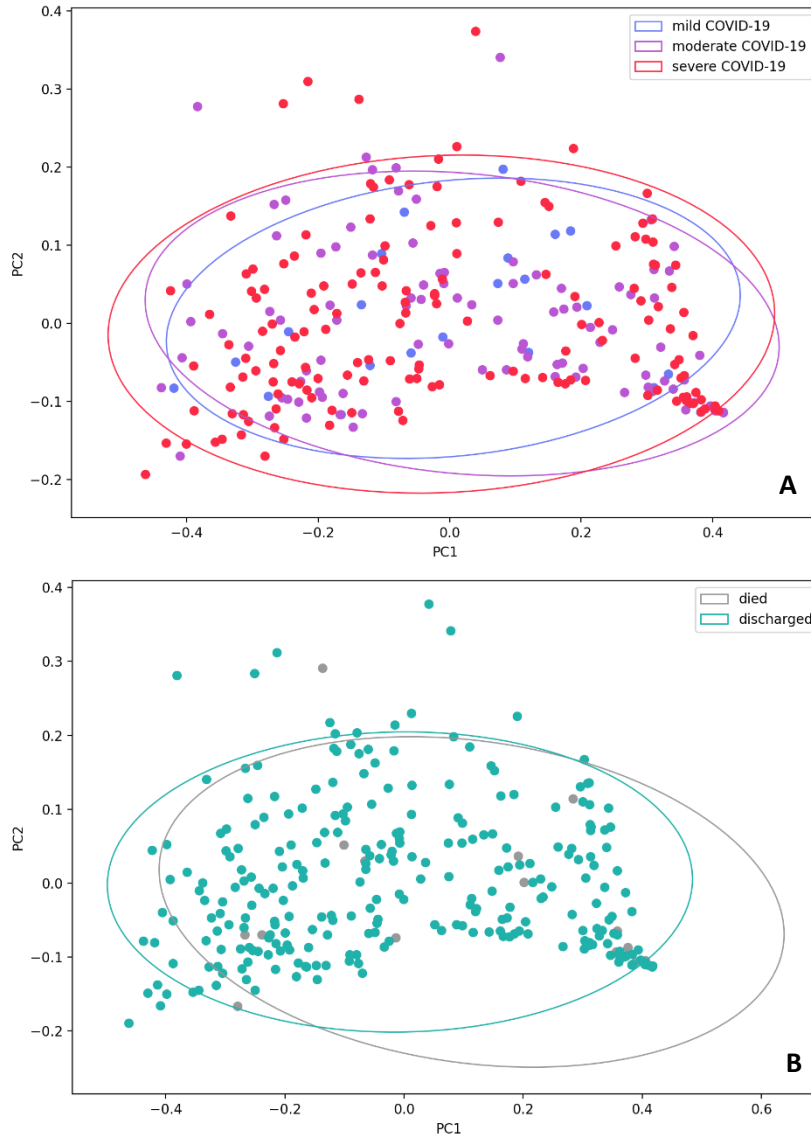


Figure S4. Unifrac distances of the upper respiratory tract microbiota in patients with mild, moderate, and severe COVID-19 pneumonia (A), and patients discharged from hospital or died (B). There was no evidence of samples' clustering by pneumonia severity ($P = 0.40$ on PC1; $P = 0.75$ on PC2) or treatment outcome ($P = 0.62$ on PC1; $P = 0.83$ on PC2).

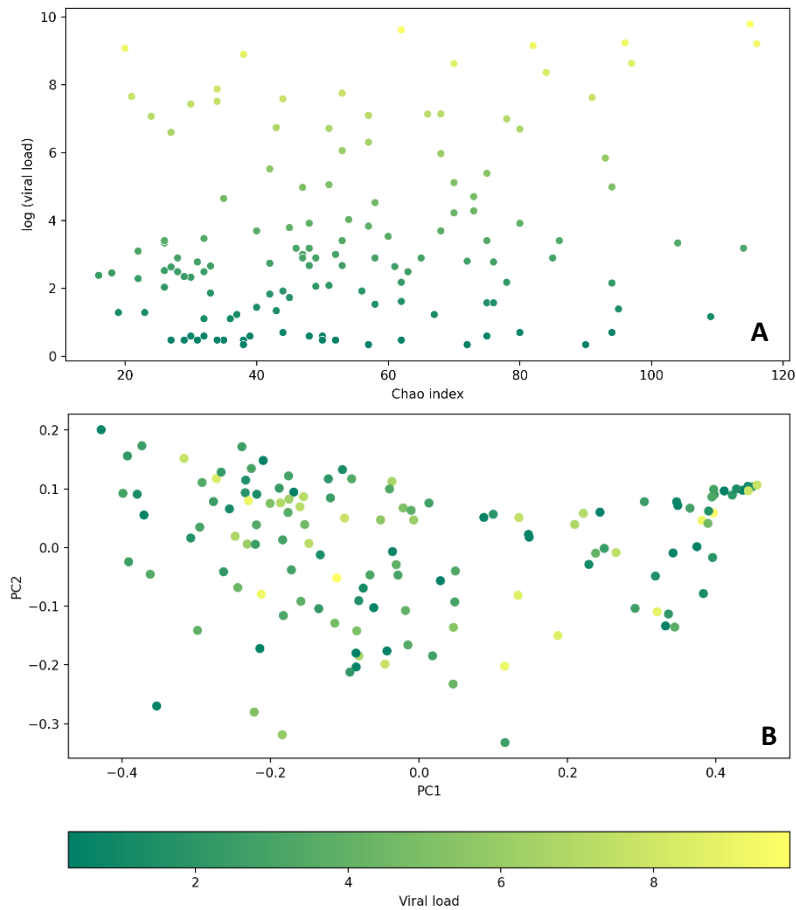


Figure S5. Relationship between SARS-CoV-2 viral load and diversity metrics of the upper respiratory tract microbiota in the COVID-19 patients. (A) The plot showing no association between the Chao α -diversity indices and the log values of SARS-CoV-2 viral load ($P = 0.25$). (B) The PCA plot of the Unifrac dissimilarity showing no SARS-CoV-2 viral load dependent clustering of the samples load (PC1, $P = 0.74$; PC2, $P = 0.86$). Each dot represents a sample, with the intensity of its color corresponding to the SARS-CoV-2 viral load in copies/mL (see the color scale under the plot).

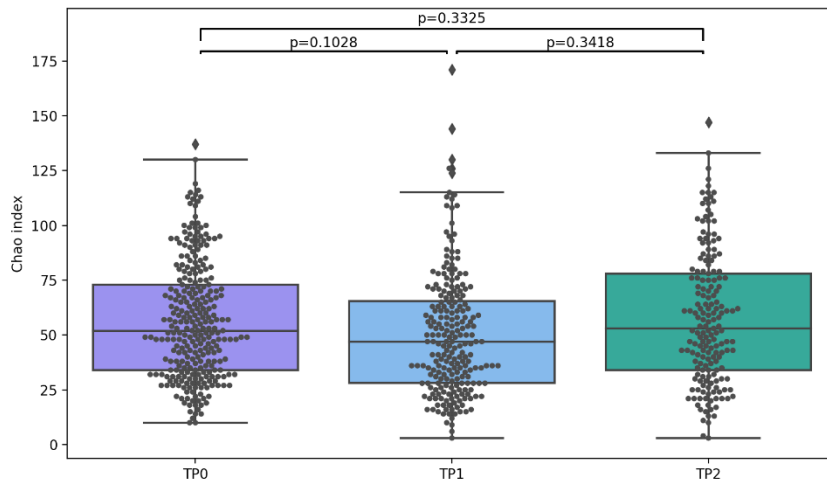


Figure S6. The dynamics of Chao indices in the COVID-19 patients during their treatment. TP0: time-point 0 (upon admission to the hospital); TP1: time-point 1 (after a median of 5.0 days); TP2: time-point 2 (after a median of 12.0 days).

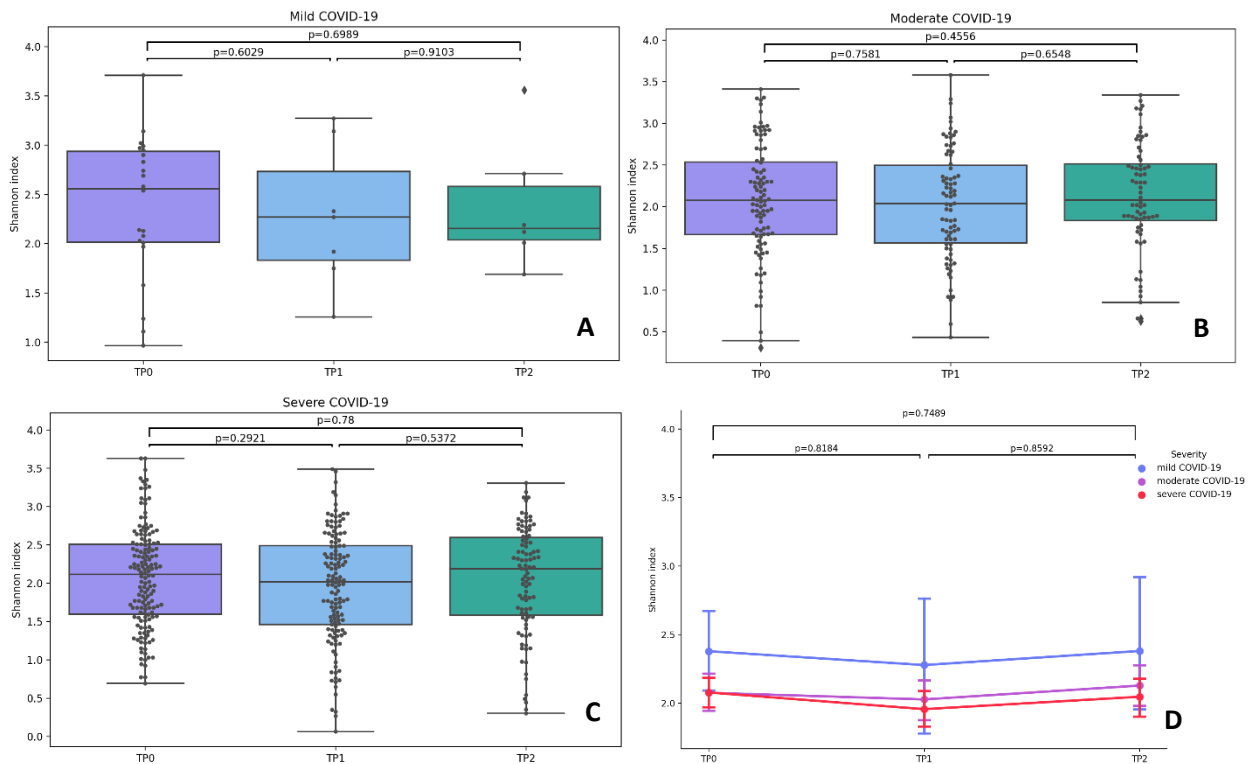


Figure S7. Changes in the Shannon indices of the upper respiratory tract microbiota in the patients with mild (A), moderate (B), and severe (C) COVID-19 throughout their treatment. TP0: time-point 0 (upon admission to the hospital); TP: time-point 1 (after a median of 5.0 days); TP2: time-point 2 (after a median of 12.0 days). (D) Comparison of the rates of change in the Shannon indices between the patients with mild, moderate, and severe COVID-19.

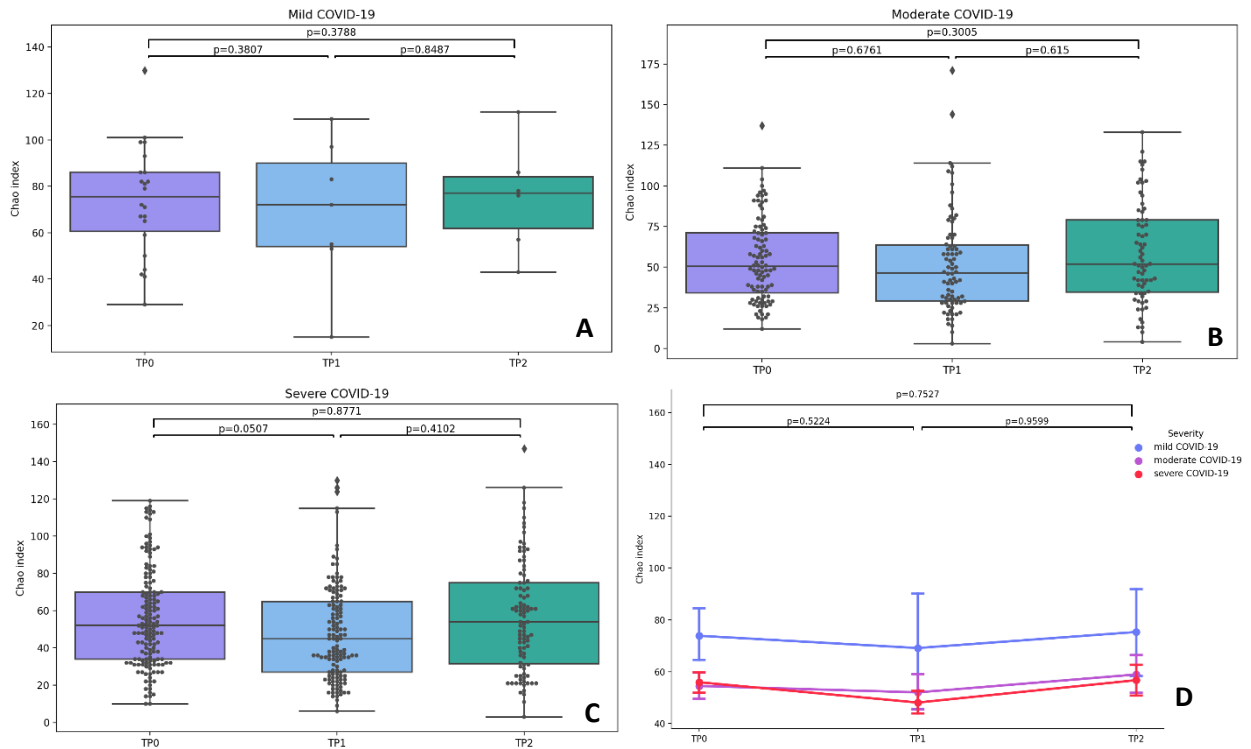


Figure S8. Changes in the Chao indices of the upper respiratory tract microbiota in the patients with mild (A), moderate (B), and severe (C) COVID-19 throughout their treatment. TP0: time-point 0 (upon admission to the hospital); TP: time-point 1 (after a median of 5.0 days); TP2: time-point 2 (after a median of 12.0 days). (D) Comparison of the rates of change in the Chao indices between the patients with mild, moderate, and severe COVID-19.

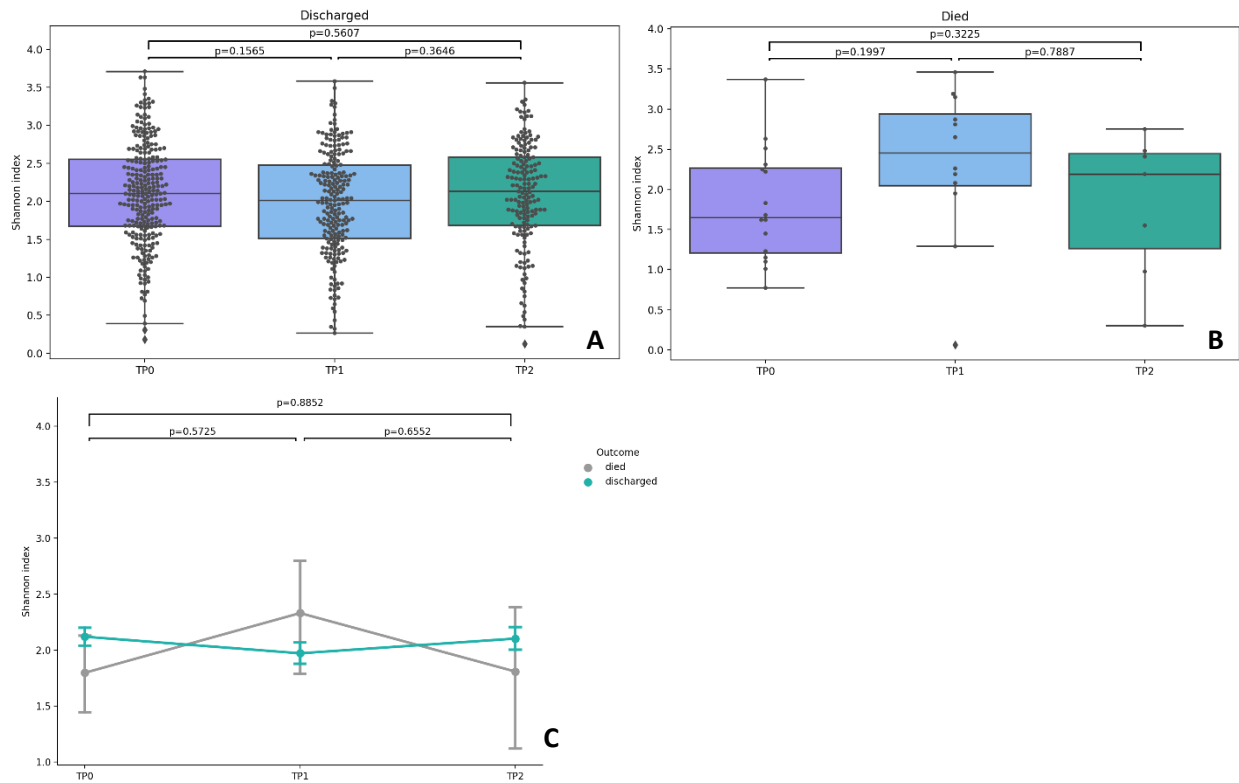


Figure S9. Changes in the Shannon indices of the upper respiratory tract microbiota in the discharged (A) and deceased (B) patients. TP0: time-point 0 (upon admission to the hospital); TP: time-point 1 (after a median of 5.0 days); TP2: time-point 2 (after a median of 12.0 days). (D) Comparison of the rates of change in the Shannon indices between the discharged and deceased patients.

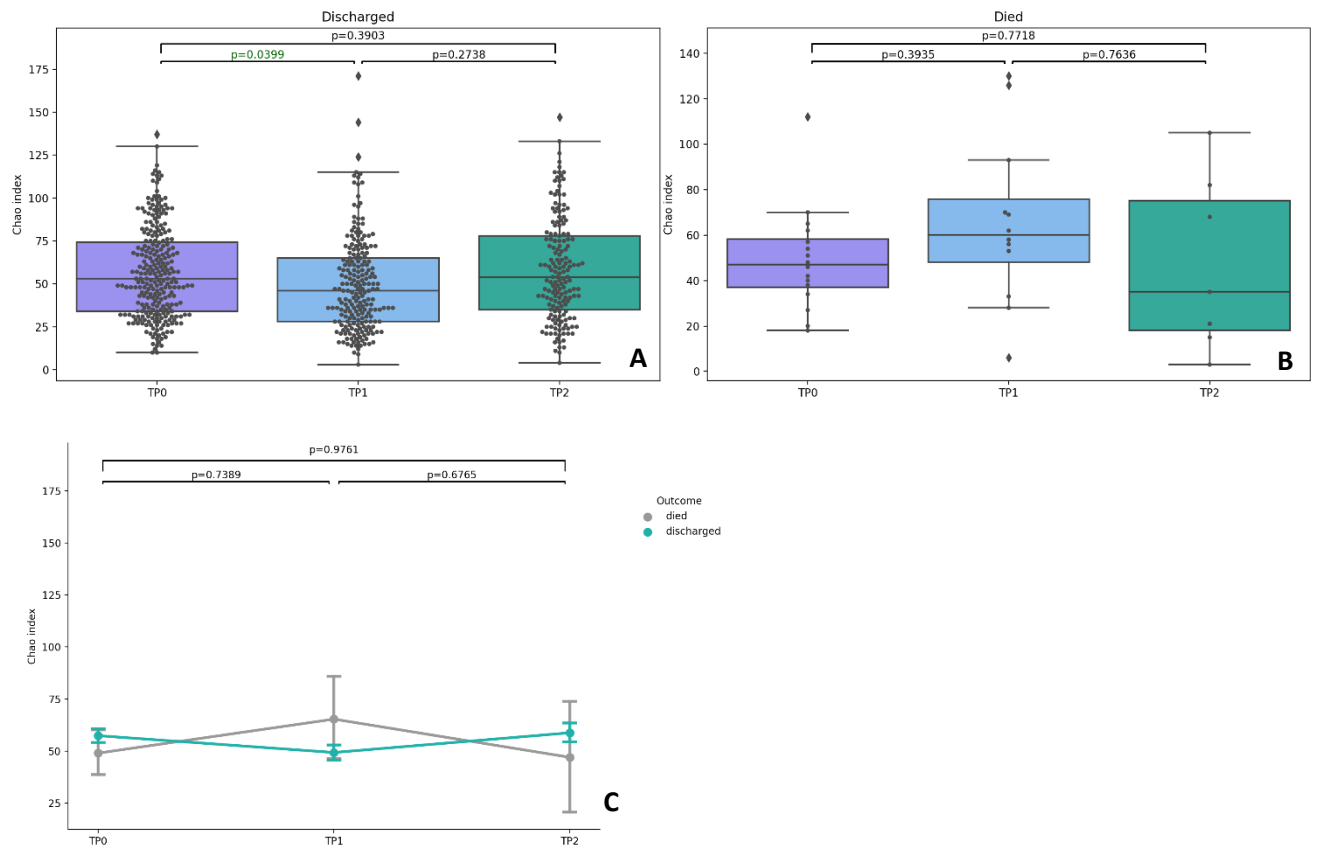


Figure S10. Changes in the Chao indices of the upper respiratory tract microbiota in the discharged (A) and deceased (B) patients. TP0: time-point 0 (upon admission to the hospital); TP: time-point 1 (after a median of 5.0 days); TP2: time-point 2 (after a median of 12.0 days). (D) Comparison of the rates of change in the Chao indices of between the discharged and deceased patients.

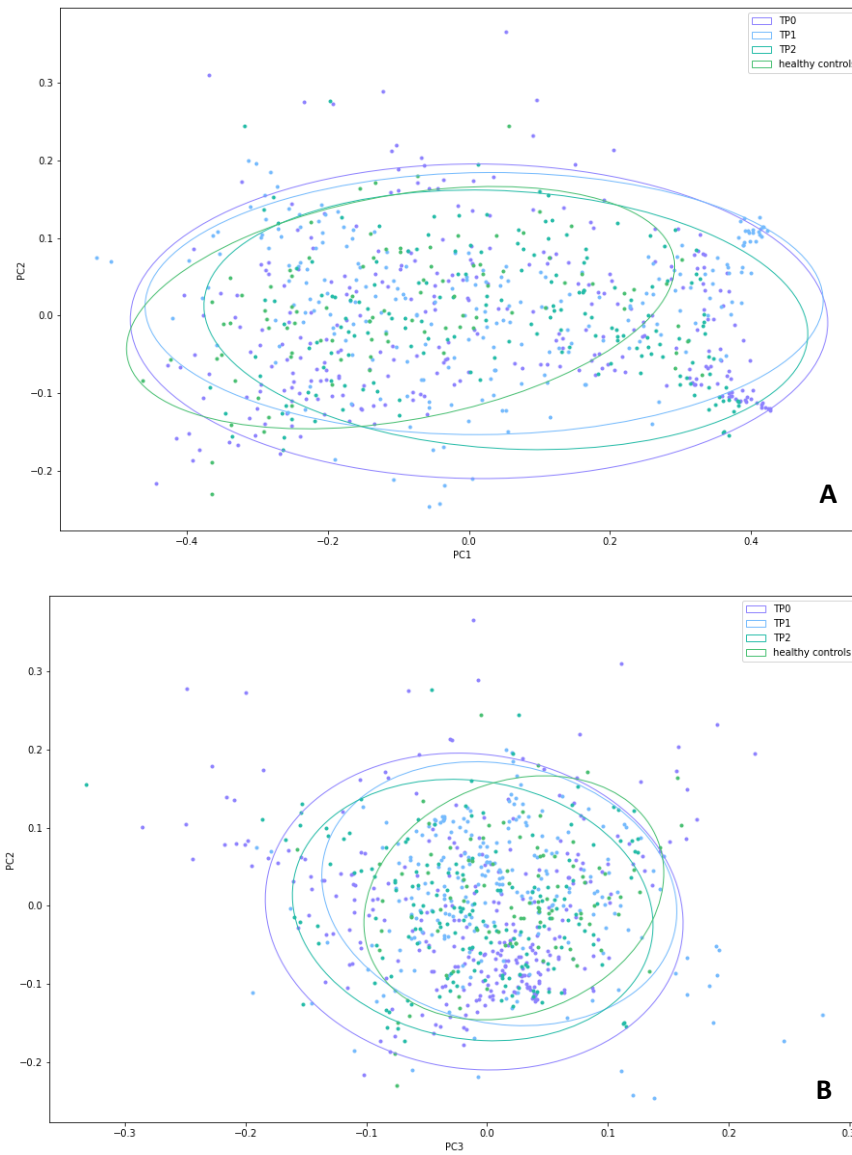


Figure S11. The Unifrac distances between the upper respiratory microbiota in the patient samples collected at different time-points during their treatment and control samples. (A) The Unifrac distances plotted along PC1 and PC2. (B) The Unifrac distances plotted along PC2 and PC3. No significant differences were observed at any TP between the patient and control samples. TP0: time-point 0 (upon admission to the hospital); TP1: time-point 1 (after a median of 5.0 days); TP2: time-point 2 (after a median of 12.0 days).

Table S7. Inter-time-point changes in the relative abundance of various upper respiratory tract microorganisms in the COVID-19 patients.

Microorganism	Between TP0 and TP1				Between TP1 and TP2				Between TP0 and TP2			
	RC	Log-RC	Bonferroni-unadjusted <i>p</i> -value	Bonferroni-adjusted <i>p</i> -value	RC	Log-RC	Bonferroni-unadjusted <i>p</i> -value	Bonferroni-adjusted <i>p</i> -value	RC	Log-RC	Bonferroni-unadjusted <i>p</i> -value	Bonferroni-adjusted <i>p</i> -value
<i>Acinetobacter</i>	0.95	-0.05	0.87	1.00	3.15	1.15	2.82e-03	0.80	3.59	1.28	4.96e-04	0.14
<i>Actinomarinicola</i>	0.88	-0.13	0.04	1.00	1.07	0.07	0.16	1.00	0.91	-0.10	0.30	1.00
<i>Actinomyces</i>	0.32	-1.15	6.56e-04	0.19	3.03	1.11	2.41e-03	0.68	0.82	-0.20	0.61	1.00
<i>Aggregatibacter</i>	1.17	0.15	0.46	1.00	2.10	0.74	0.01	1.00	2.58	0.95	9.33e-04	0.26
<i>Alloprevotella</i>	0.84	-0.17	0.60	1.00	2.57	0.94	0.02	1.00	1.84	0.61	0.12	1.00
<i>Anaeroglobus</i>	0.49	-0.72	9.51e-05	0.03	0.94	-0.06	0.66	1.00	0.51	-0.67	1.27e-03	0.36
<i>Aquabacterium</i>	1.12	0.11	0.25	1.00	0.74	-0.30	0.01	1.00	0.92	-0.08	0.16	1.00
<i>Bifidobacterium</i>	0.51	-0.66	1.07e-03	0.30	0.93	-0.07	0.70	1.00	0.45	-0.80	6.98e-04	0.20
<i>Bradyrhizobium</i>	0.83	-0.19	0.04	1.00	1.60	0.47	1.88e-03	0.53	1.42	0.35	0.03	1.00
<i>Bulleidia</i>	0.93	-0.07	0.30	1.00	1.45	0.37	0.01	1.00	1.42	0.35	0.01	1.00
<i>Campylobacter</i>	0.58	-0.54	0.08	1.00	2.32	0.84	0.03	1.00	0.87	-0.14	0.70	1.00
<i>Capnocytophaga</i>	0.39	-0.95	3.10e-03	0.88	1.92	0.65	0.07	1.00	0.51	-0.67	0.10	1.00
<i>Catonella</i>	1.01	0.01	0.96	1.00	2.18	0.78	0.02	1.00	1.76	0.56	0.10	1.00
<i>Chryseobacterium</i>	1.20	0.18	0.45	1.00	1.95	0.67	0.03	1.00	2.17	0.77	0.01	1.00
<i>Corynebacterium</i>	0.64	-0.45	0.17	1.00	3.44	1.24	1.72e-03	0.49	1.82	0.60	0.08	1.00
<i>Desulfobulbus</i>	0.88	-0.13	0.05	1.00	1.04	0.04	0.32	1.00	0.88	-0.12	0.14	1.00
<i>Dialister</i>	0.38	-0.96	4.97e-04	0.14	1.63	0.49	0.10	1.00	0.60	-0.50	0.12	1.00
<i>Duncaniella</i>	0.89	-0.11	0.04	1.00	1.09	0.09	0.16	1.00	0.97	-0.03	0.66	1.00
<i>Enhydrobacter</i>	0.75	-0.29	0.04	1.00	0.86	-0.16	0.16	1.00	0.78	-0.25	0.12	1.00
<i>Enterococcus</i>	2.12	0.75	1.33e-03	0.38	0.68	-0.39	0.22	1.00	1.83	0.60	0.02	1.00
<i>Eubacterium</i>	0.74	-0.31	0.26	1.00	3.05	1.12	4.80e-04	0.14	1.77	0.57	0.11	1.00
<i>Filifactor</i>	0.89	-0.12	0.40	1.00	1.83	0.60	2.84e-03	0.80	1.56	0.45	0.03	1.00
<i>Flavobacterium</i>	0.46	-0.78	4.43e-03	1.00	2.35	0.85	0.01	1.00	1.00	0.00	0.99	1.00
<i>Fretibacterium</i>	0.59	-0.53	0.01	1.00	1.29	0.25	0.21	1.00	0.83	-0.18	0.41	1.00
<i>Fusobacterium</i>	0.34	-1.06	1.75e-03	0.50	7.54	2.02	6.45e-06	1.82e-03	1.41	0.35	0.45	1.00
<i>Gemella</i>	0.61	-0.49	0.15	1.00	4.26	1.45	3.72e-04	0.11	2.43	0.89	0.06	1.00
<i>Granulicatella</i>	1.28	0.25	0.49	1.00	2.43	0.89	0.03	1.00	2.00	0.69	0.10	1.00
<i>Haemophilus</i>	0.95	-0.05	0.90	1.00	11.66	2.46	1.04e-08	2.96e-06	8.32	2.12	6.43e-06	1.82e-03
<i>Hydrogenophilus</i>	1.12	0.12	0.04	1.00	0.93	-0.08	0.14	1.00	1.04	0.04	0.32	1.00

<i>Hyphomicrobium</i>	1.00	0.00		1.00	1.08	0.07	0.16	1.00	1.15	0.14	0.04	1.00
<i>Lactiplantibacillus</i>	0.58	-0.55	2.27e-03	0.64	1.05	0.05	0.71	1.00	0.55	-0.59	0.01	1.00
<i>Lactobacillus</i>	0.34	-1.09	1.55e-04	0.04	1.95	0.67	0.05	1.00	0.58	-0.54	0.18	1.00
<i>Lautropia</i>	0.86	-0.15	0.57	1.00	2.51	0.92	0.01	1.00	1.75	0.56	0.11	1.00
<i>Lentilactobacillus</i>	0.90	-0.10	0.26	1.00	0.96	-0.04	0.32	1.00	0.86	-0.15	0.05	1.00
<i>Leptotrichia</i>	0.57	-0.56	0.06	1.00	0.95	-0.05	0.90	1.00	0.44	-0.82	0.04	1.00
<i>Leucobacter</i>	1.17	0.15	0.03	1.00	0.84	-0.17	0.05	1.00	1.01	0.01	0.87	1.00
<i>Limosilactobacillus</i>	0.53	-0.63	0.04	1.00	0.84	-0.18	0.62	1.00	0.41	-0.90	0.03	1.00
<i>Megasphaera</i>	1.01	0.01	0.98	1.00	2.55	0.93	0.03	1.00	2.31	0.84	0.03	1.00
<i>Metamycoplasma</i>	0.62	-0.48	0.06	1.00	2.07	0.73	0.01	1.00	1.16	0.15	0.66	1.00
<i>Methylobacterium</i>	0.83	-0.18	0.40	1.00	0.51	-0.68	0.03	1.00	0.37	-1.01	1.06e-03	0.30
<i>Neisseria</i>	0.57	-0.56	0.11	1.00	7.57	2.02	1.04e-05	2.96e-03	3.50	1.25	4.08e-03	1.00
<i>Nitrospira</i>	0.92	-0.08	0.08	1.00	1.16	0.15	0.04	1.00	1.12	0.11	0.24	1.00
<i>Nosocomiicoccus</i>	0.95	-0.05	0.37	1.00	0.96	-0.04	0.32	1.00	0.85	-0.17	0.05	1.00
<i>Olsenella</i>	0.68	-0.38	0.01	1.00	1.20	0.18	0.23	1.00	0.78	-0.25	0.13	1.00
<i>Oribacterium</i>	0.32	-1.14	7.98e-05	0.02	2.27	0.82	0.04	1.00	0.59	-0.53	0.17	1.00
<i>Parcubacteria_genera_incertae_sedis</i>	0.85	-0.16	0.44	1.00	1.64	0.49	0.04	1.00	1.37	0.32	0.23	1.00
<i>Parvimonas</i>	0.60	-0.51	0.03	1.00	2.14	0.76	5.08e-04	0.14	0.98	-0.02	0.94	1.00
<i>Peptoniphilus</i>	0.92	-0.08	0.29	1.00	1.23	0.21	0.02	1.00	1.13	0.12	0.36	1.00
<i>Peptostreptococcus</i>	0.92	-0.08	0.77	1.00	2.94	1.08	3.29e-03	0.93	1.84	0.61	0.10	1.00
<i>Phenylobacterium</i>	1.03	0.03	0.32	1.00	1.21	0.19	0.07	1.00	1.22	0.20	0.05	1.00
<i>Phocaecicola</i>	0.56	-0.59	1.12e-03	0.32	0.83	-0.18	0.31	1.00	0.48	-0.73	2.43e-04	0.07
<i>Porphyromonas</i>	0.66	-0.41	0.22	1.00	3.06	1.12	0.01	1.00	1.40	0.34	0.44	1.00
<i>Pseudoramibacter</i>	0.84	-0.17	0.03	1.00	1.09	0.08	0.28	1.00	0.90	-0.10	0.27	1.00
<i>Rhodococcus</i>	0.91	-0.09	0.32	1.00	1.08	0.08	0.46	1.00	1.22	0.20	0.05	1.00
<i>Rickettsia</i>	0.96	-0.04	0.71	1.00	2.56	0.94	9.87e-06	2.79e-03	2.44	0.89	7.49e-06	2.12e-03
<i>Romboutsia</i>	1.02	0.02	0.77	1.00	1.15	0.14	0.21	1.00	1.29	0.25	0.02	1.00
<i>Rothia</i>	0.89	-0.12	0.69	1.00	2.44	0.89	0.01	1.00	1.61	0.47	0.21	1.00
<i>Saccharibacteria_genera_incertae_sedis</i>	0.41	-0.90	0.01	1.00	3.50	1.25	0.01	1.00	1.12	0.11	0.80	1.00
<i>Scardovia</i>	0.65	-0.44	1.95e-03	0.55	1.23	0.21	0.05	1.00	0.68	-0.39	0.03	1.00
<i>Schaalia</i>	0.72	-0.33	0.28	1.00	2.14	0.76	0.04	1.00	1.25	0.22	0.54	1.00
<i>Schwartzia</i>	0.66	-0.41	0.01	1.00	0.95	-0.06	0.64	1.00	0.59	-0.52	2.27e-03	0.64
<i>Selenomonas</i>	0.31	-1.18	1.95e-04	0.06	1.86	0.62	0.12	1.00	0.46	-0.78	0.05	1.00
<i>Shuttleworthia</i>	0.68	-0.38	0.01	1.00	1.07	0.07	0.69	1.00	0.75	-0.29	0.15	1.00
<i>Sphaerochaeta</i>	0.82	-0.20	0.03	1.00	0.92	-0.08	0.16	1.00	0.70	-0.36	2.37e-03	0.67
<i>Sphingomonas</i>	0.89	-0.11	0.50	1.00	3.57	1.27	8.31e-06	2.35e-03	3.59	1.28	2.18e-06	6.18e-04
<i>Spiroplasma</i>	1.14	0.13	0.04	1.00	1.27	0.24	0.02	1.00	1.40	0.34	2.37e-03	0.67

<i>Stenotrophomonas</i>	1.35	0.30	0.01	1.00	3.05	1.11	1.13e-04	0.03	4.57	1.52	9.01e-08	2.55e-05
<i>Stomatobaculum</i>	0.42	-0.87	3.46e-03	0.98	1.42	0.35	0.31	1.00	0.55	-0.60	0.10	1.00
<i>Streptococcus</i>	1.23	0.21	0.08	1.00	1.37	0.32	0.01	1.00	1.75	0.56	2.86e-05	0.01
<i>Tannerella</i>	0.30	-1.20	7.75e-06	0.00	1.73	0.55	0.06	1.00	0.48	-0.73	0.03	1.00
<i>Treponema</i>	0.24	-1.42	2.21e-07	0.00	2.41	0.88	2.58e-03	0.73	0.51	-0.68	0.06	1.00
<i>Yersinia</i>	0.89	-0.12	0.05	1.00	1.13	0.12	0.08	1.00	0.91	-0.09	0.40	1.00
<i>Zea</i>	1.03	0.03	0.92	1.00	0.56	-0.58	0.05	1.00	0.69	-0.37	0.21	1.00
(Unassigned)	1.00	0.00	0.99	1.00	1.51	0.41	0.18	1.00	1.21	0.19	0.48	1.00
<i>Chryseobacterium</i>	1.20	0.18	0.45	1.00	1.95	0.67	0.03	1.00	2.17	0.77	0.01	1.00
<i>Corynebacterium</i>	0.64	-0.45	0.17	1.00	3.44	1.24	1.72e-03	0.49	1.82	0.60	0.08	1.00
<i>Curvibacter</i>	1.13	0.12	0.46	1.00	1.10	0.10	0.57	1.00	1.36	0.31	0.08	1.00
<i>Cutibacterium</i>	0.93	-0.08	0.70	1.00	1.17	0.15	0.49	1.00	1.05	0.05	0.85	1.00
<i>Enterococcus</i>	2.12	0.75	1.33e-03	0.38	0.68	-0.39	0.22	1.00	1.83	0.60	0.02	1.00
<i>Escherichia/Shigella</i>	1.30	0.26	0.28	1.00	0.82	-0.19	0.54	1.00	0.85	-0.16	0.59	1.00
<i>Lancefieldella</i>	1.00	0.00	0.99	1.00	1.54	0.43	0.28	1.00	1.45	0.37	0.32	1.00
<i>Micrococcus</i>	0.79	-0.24	0.30	1.00	1.16	0.14	0.51	1.00	0.93	-0.07	0.76	1.00
<i>Mogibacterium</i>	0.94	-0.06	0.76	1.00	1.06	0.06	0.77	1.00	1.07	0.07	0.73	1.00
<i>Peptostreptococcus</i>	0.92	-0.08	0.77	1.00	2.94	1.08	3.29e-03	0.93	1.84	0.61	0.10	1.00
<i>Prevotella</i>	0.94	-0.06	0.62	1.00	1.03	0.03	0.87	1.00	0.84	-0.17	0.31	1.00
<i>Selenomonas</i>	0.31	-1.18	1.95e-04	0.06	1.86	0.62	0.12	1.00	0.46	-0.78	0.05	1.00
<i>Stomatobaculum</i>	0.42	-0.87	3.46e-03	0.98	1.42	0.35	0.31	1.00	0.55	-0.60	0.10	1.00
<i>Streptophyta</i>	0.51	-0.67	0.07	1.00	0.71	-0.34	0.41	1.00	0.56	-0.58	0.16	1.00

Note. RC—regression coefficient. TP0: time-point 0 (upon admission to the hospital); TP1: time-point 1 (after a median of 5.0 days); TP2: time-point 2 (after a median of 12.0 days). This table demonstrates the genera that were differentially abundant between at least two time-points before the adjustment for multiple comparisons and after it. Genera that were differentially abundant after adjusting for multiple comparisons are indicated by red.