

Supplementary file

Table S1. Laboratory Data of NSCLC Patients with COVID-19 on Admission.		
Laboratory Data	Reference interval	NSCLC patients with COVID-19 (n=17)
White blood cells (WBC)	4-11 ($\times 10^3 / \text{mm}^3$)	5.3 (4.1-8.1)
Neutrophil	2-7 ($10^3 / \text{mm}^3$)	3.8 (2.7-6.9)
Lymphocyte	0.8 - 4 ($10^3 / \text{mm}^3$)	0.8 (0.3-1.1)
Monocyte	0.12 - 1.2 ($10^3 / \text{mm}^3$)	0.41 (0.2-0.6)
Platelet	150 - 450 ($10^3 / \text{mm}^3$)	191 (126-238)
Hemoglobin	14-18 (g/dL)	12.2 (9.4-13.1)
D-dimer	Up to 350 (ng/mL)	500 (360-1880)
Creatinine	0.7-1.4 (mg/dL)	1.51 (0.7-1.9)
Alanine aminotransferase	10-40 (U/liter)	32 (21-38)
Aspartate aminotransferase	10-40 (U/liter)	35 (24-43)
C-reactive protein (CRP)	1-6 (mg/dL)	38.1 (4.6–103.9)
Procalcitonin	0-0.5 ($\mu\text{g/L}$)	0.13 (0.03–0.45)

Table S2. Laboratory Data of Patients with COVID-19 on Admission.		
Laboratory Data	Reference range	patients with COVID-19 (n=40)
White blood cells ($\times 10^9$ cell/ml)	4-11 ($\times 10^3 / \text{mm}^3$)	4.9 (3.5-7.8)
Neutrophil ($\times 10^9$ cell/ml)	2-7 ($10^3 / \text{mm}^3$)	3.26 (2.39–4.67)
Lymphocyte ($\times 10^9$ cell/ml)	0.8 - 4 ($10^3 / \text{mm}^3$)	0.99 (0.3.7–1.31)
Monocyte ($\times 10^9$ cell/ml)	0.12 - 1.2 ($10^3 / \text{mm}^3$)	0.45 (0.4-0.6)
Platelet ($\times 10^9$ cell/ml)	150 - 450 ($10^3 / \text{mm}^3$)	201 (137-248)
Hemoglobin (mg/l)	14-18 (g/dL)	13.8 (11.3-15.3)
D-dimer (mg/l)	Up to 350 (ng/mL)	4 (1.8-16.7)
Creatinine (mg/dl)	0.7-1.4 (mg/dl)	1.01 (0.6-1.1)
Alanine aminotransferase (U/liter)	10-40 (U/liter)	31 (21-36)
Aspartate aminotransferase (U/liter)	10-40 (U/liter)	33 (23-39)

C-reactive protein (CRP)(mg/dL)	1-6 (mg/dL)	23.2 (2.4-54.9)
Procalcitonin	0-0.5 (µg/L)	0.06 (0.03-0.24)

Table S3. Primers Used in this Study for SYBR Green qPCR Reactions.				
Species	Primer sequences 5'-3'	Annealing temperature(°C)	Amplified fragment(bp)	References
<i>Bacteroidetes</i>	F- GTTTAATTTCGATGATACGCGAG R- TTAASCCGACACCTCACGG	60	122	25
<i>Firmicutes</i>	F - TGAAACTYAAGGAATTGACG R - ACCATGCACCTGTC	55	126	25
<i>Actinobacteria</i>	F- TGTAGCGGTGGAATGCGC R- AATTAAGCCACATGCTCCGCT	60	277	26
<i>Enterococcus</i> spp.	F-CCC TTA ATT GTT AGT TGC CAT CAT T R-ACT CGT TGT ACT TCC CAT TGT	56	144	27
<i>Streptococcus</i> spp.	F-CTWACCAGAAAGGGACGGCT R- AAGGRYCYAACACCTAGC	60	170	28
<i>Enterobacteriaceae</i>	F- GTGCCAGCMGCCGCGGTAA R- GCCTCAAGGGCACAACCTCCAAG	67	124	29
<i>Prevotella</i> spp.	F-CAG CAG CCG CGG TAATA R-GGC ATC CAT CGT TTA CCG T	54	309	27
<i>Lactobacillus</i> spp.	F-AGC AGT AGG GAA TCT TCC A R-CAC CGC TAC ACA TGGAG	50	341	30
<i>Clostridium</i> spp.	F-CGG TAC CTG ACT AAG AAG C R-AGT TTY ATT CTT GCG AAC G	50	429	30
<i>Bifidobacterium</i> spp.	F-GGG TGG TAA TGC CGG ATG R-TAA GCG ATG GAC TTT CAC ACC	55	442	30
<i>F. prausnitzii</i>	F-GAT GGC CTC GCG TCC GAT TAG R-CCG AAG ACC TTC TTC CTC C	58	198	31
<i>Fusobacterium</i> spp.	F-C(A/T)AACGCGATAAGTAATC R- TGGTAACATACGA(A/T)AGGG	54	273	32
<i>A. muciniphila</i>	F-CAG CAC GTG AAG GTG GGG AC R-CCT TGC GGT TGG CTT CAG AT	65	329	31
<i>Veillonella</i>	F-A(C/T)CAACCTGCCCTTCAGA R-CGTCCCGATTAACAGAGCTT	62	343	32
<i>Staphylococcus aureus</i>	F- GAGGTATTAGTGATATCGATTTAA R- GCTTTAATGTCACCTGTATTGAT	75	139	33
<i>Streptococcus pneumoniae</i>	F- ACGCAACTG ACGAGTGTGAC R- GATCGCGACACCGAACTAAT	65	264	24
<i>Pseudomonas aeruginosa</i>	F- CCAGCCATGCCGCGTGTGTGA R- GTTGGTAACGTCAAAACAGCAAGG	55	102	24

<i>Moraxella catarrhalis</i>	F-CTGCCCAAGCTGCCCTAAGT R-CAAAAGCCACAAAACCC	57	134	34
<i>Haemophilus influenza</i>	F- TTGGTGGTCAGCGTTTCGGTGAGA R- CAAGTGAGCGGATTTCTTCATAAT	65	112	35

Table S4. Bacterial strains used for formation of standard curves, efficiency, correlation coefficients and melting temperatures of quantitative PCR.

Target bacterial	Bacterial standard strain	Efficiency (%)	Correlation coefficient (R ²)	Melting temperature
Bacteroidetes	<i>B. fragilis</i> ATCC* 25285	98.7	0.999	87.5
Firmicutes	<i>C. difficile</i> ATCC 9689	102.4	0.998	84.5
Actinobacteria	<i>Mycobacterium avium</i> ATCC 15769	100	0.997	87.4
<i>Enterococcus</i> spp.	<i>E. faecalis</i> ATCC 19433	89.9	0.999	89.5
<i>Streptococcus</i> spp.	<i>S. pneumoniae</i> ATCC 49619	98	0.998	88.6
<i>Enterobacteriaceae</i>	<i>E. coli</i> ATCC 25922	88.4	0.999	89
<i>Prevotella</i> spp.	<i>P. intermedia</i> ATCC 25611D-5	90.5	0.999	87.5
<i>Lactobacillus</i> spp.	<i>L. acidophilus</i> ATCC 4356	100.5	0.999	87
<i>Clostridium</i> spp.	<i>C. perfringens</i> ATCC 13124	99.5	0.999	88
<i>Bifidobacterium</i> spp.	<i>B. bifidum</i> ATCC 29521	101	0.999	90.8
<i>F. prausnitzii</i>	<i>F. prausnitzii</i> ATCC 27766	99.8	0.997	89.5
<i>Fusobacterium</i> spp.	<i>F. nucleatum</i> ATCC 25586	99	0.998	89
<i>A. muciniphila</i>	<i>A. muciniphila</i> ATCC BAA-835	104.6	0.997	90
<i>Veillonella</i>	<i>V. parvula</i> ATCC 17745	106.2	0.998	88.8

*American Type Culture Collection.

Table S5. Demographic Data of Samples Used in this Study.

Characteristics	NSCLC patients with COVID-19 (n=17)	NSCLC patients without COVID-19 (n=20)	Healthy control	Patients with COVID-19
Subjects	17	20	40	40
Sex ratio (male/female)	14/3	19/1	25/15	29/11
Age, y, mean(SD) ^a	58.7±5.37	56.3±2.48	52.3±16.1	55.9±8.14
BMI(Kg/m ²), mean(SD) ^a	24.52±4.3	26.31±21	26.61±4.3	27.13±1.18

^aNo significant difference between groups.

Table S6. Comparison of Population Numbers of Selected Microbial Groups in COVID-19 Patients and Healthy Individuals.

Bacterial species	Copies/gr of faecal		Levene's Test Equal variances assumed		t-test for equality of means	
	Healthy (N=40)	COVID19 (N=40)	F	Sig.	T	Sig.(2-tailed)
Bacteroidetes	3140±768.54	3317.5±591.34	2.71	0.104	-1.158	0.251
Firmicutes	4540.5±1001.74	4192.5±846.22	0.875	0.357	1.676	0.098
Actinobacteria	130±37.96	135±44.02	2.089	0.152	-0.571	0.570
<i>Prevotella</i> spp.	141.7±49.60	171.7±76.89	11.96	0.001	-2.074	0.041
<i>Veillonella</i>	114.2±43.37	125.2±36.01	0.002	0.965	-1.234	0.221
<i>Streptococcus</i> spp.	126±34.71	138±39.25	1.169	0.283	-1.507	0.136

Table S7. Comparison of Population Numbers of Selected Microbial Ggroups in COVID-19 Patients and Healthy Individuals.						
Target bacterial	Copies/gr of faecal		Levene`s Test Equal variances assumed		t-test for equality of means	
	Healthy(N=40)	COVID19(N=40)	F	Sig.	T	Sig.(2-tailed)
Bacterial Phyla						
Bacteroidetes	1.6E10±1.01E10	1.9E12±2.3E12	58.6	0.000	-5.17	0.000
Firmicutes	2.66E11±4.10E11	3.25E9±2.89E10	22.3	0.000	7.94	0.000
Actinobacteria	6.38E8±2.24E8	3.74E8±4.21E9	3.21	0.077	-0.872	0.389
Bacterial species						
<i>Enterococcus</i> spp.	5.11E5±3.2E6	9.95E6±1.80E7	11.89	0.001	-3.31	0.001
<i>Streptococcus</i> spp.	5.41E7±1.77E8	1.53E8±2.02E8	5.50	0.001	-2.33	0.021
<i>Enterobacteriaceae</i>	6.34E7±4.59E7	1.20E8±3.90E8	18.60	0.000	-1.90	0.060
<i>Prevotella</i> spp.	9.10E7±1.34E8	4.25E8±8.44E8	17.14	0.000	-2.47	0.015
<i>Lactobacillus</i> spp.	3.04E7±1.91E7	1.82E7±4.09E7	1.01	0.317	1.70	0.092
<i>Clostridium</i> spp.	8.68E8±1.86E9	1.27E9±2.30E9	0.27	0.871	-0.86	0.391
<i>Bifidobacterium</i> spp.	8.73E8±1.56E9	4.16E8±2.97E8	7.009	0.010	1.81	0.074
<i>F. prausnitzii</i>	1.83E9±1.17E9	1.06E9±6.01E8	0.580	0.449	2.54	0.013
<i>Fusobacterium</i> spp.	9.12E6±1.30E7	3.13E7±9.67E7	4.15	0.045	-1.44	0.154
<i>A. muciniphila</i>	7.04E8±8.84E8	4.08E8±5.82E8	0.603	0.440	1.76	0.081
<i>Veillonella</i>	9.48E6±1.99E7	1.00E7±1.21E7	1.45	0.231	-0.158	0.875

