

**Supplementary Table 1:** Summary of characteristics from COVID-19 patients analyzed. The study included individuals Sars-CoV2 positive RT-PCR and admitted to Intensive Care Units (ICU) from Brazil between May 7 to September 17, 2020. Sample IDs were modified to preserve the patient's integrity.

Samples	CT RT-PCR - N1	CT RT-PCR - N2	Intervals (first symptom sampling) (days)	Age range (years)	Sex	Risk factor	Ventilation use	X-ray	Chest computed tomography	Hospitalization (days)	Death
Mtg-Cov_01	22.36	28.23	4	80-90	Male	Obesity; advanced age	Yes; invasive	Mixed	Not performed	28	Yes
Mtg-Cov_02	34.75	26.81	5	80-90	Female	Advanced age	Yes; invasive	Interstitial infiltrate	Not performed	6	Yes
Mtg-Cov_03	26.52	29.57	5	50-60	Male	Immunocompromised	Yes; invasive	Interstitial infiltrate	Not performed	55	No
Mtg-Cov_04	26.8	29.3	5	50-60	Female	Diabetes; obesity	Yes; invasive	Interstitial infiltrate	Not performed	23	No
Mtg-Cov_05	20.2	19.92	6	40-50	Male	Diabetes; hypertension	Yes; invasive	Interstitial infiltrate	Not performed	7	Yes
Mtg-Cov_06	33.59	37.28	6	80-90	Male	Advanced age	Yes; invasive	Interstitial infiltrate	Not performed	11	Yes
Mtg-Cov_07	33.89	37.66	7	40-50	Male	Diabetes; hypertension; ex-smoker	Yes; invasive	Interstitial infiltrate	Not performed	60	Yes
Mtg-Cov_08	29.2	30.6	7	30-40	Male	Diabetes	Yes; invasive	Normal	Not performed	3	Yes
Mtg-Cov_09	19.7	25.3	7	65-70	Male	Diabetes; obesity; hypertension; advanced age	Yes; invasive	Interstitial infiltrate	Not performed	2	Yes
Mtg-Cov_10	17.98	18.97	7	40-50	Female	Obesity	Yes; invasive	Consolidation	Not performed	7	Yes
Mtg-Cov_11	18.63	20.73	8	40-50	Female	Diabetes; chronic heart disease	Yes; invasive	Interstitial infiltrate	Not performed	10	Yes
Mtg-Cov_12	25.46	26.56	8	50-60	Male	Retocolitis	Yes; not invasive	Mixed	Not performed	17	No
Mtg-Cov_13	27.87	29.36	9	60-65	Female	COPD; diabetes; obesity; hypertension	Yes; invasive	Interstitial infiltrate	Not performed	10	Yes
Mtg-Cov_14	16.94	18.15	10	50-60	Female	Obesity; chronic heart disease	Yes; invasive	Interstitial infiltrate	Not performed	13	Yes
Mtg-Cov_15	24	26	11	50-60	Male	Obesity; hypertension	Yes; invasive	Not performed	COVID suggestive with 50%-75% damage	17	No
Mtg-Cov_16	26	29.5	12	65-70	Male	Diabetes; chronic heart disease; advanced age	Yes; invasive	Not performed	Not performed	18	Yes
Mtg-Cov_17	35.56	32.73	15	70-80	Male	Diabetes; chronic heart disease; advanced age	Yes; invasive	Not performed	Not performed	2	Yes
Mtg-Cov_18	15.9	16.3	16	65-70	Female	Hypertension; advanced age	Yes; invasive	Mixed	Not performed	6	Yes
Mtg-Cov_19	24	28	16	80-90	Female	Chronic heart disease; advanced age	Yes; invasive	Interstitial infiltrate	Not performed	10	No
Mtg-Cov_20	32	32	18	50-60	Male	None	Yes; invasive	Not performed	Ground-glass images and consolidation areas with impairment of about 25%-50% of the lung parenchyma	20	No
Mtg-Cov_21	30	32	34	70-80	Female	Diabetes; hypertension; advanced age	Yes; invasive	Not performed	Pulmonary damage>50%	37	Yes

**Supplementary Table 2:** Microbial species abundance of COVID-19 patients. Fifty most prevalent species found in bronchoalveolar lavage fluids from COVID-19 patients obtained through taxonomic inference provided on the MGRASP server. Species abundance is shown as normalized.

Species	Mtg- Cov_01	Mtg- Cov_02	Mtg- Cov_03	Mtg- Cov_04	Mtg- Cov_05	Mtg- Cov_06	Mtg- Cov_07	Mtg- Cov_08	Mtg- Cov_09	Mtg- Cov_10	Mtg- Cov_11	Mtg- Cov_12	Mtg- Cov_13	Mtg- Cov_14	Mtg- Cov_15	Mtg- Cov_16	Mtg- Cov_17	Mtg- Cov_18	Mtg- Cov_19	Mtg- Cov_20	Mtg- Cov_21
<i>Acinetobacter baumannii</i>	150	78	460	5	31	91	462	100	161	6	65	9	78	1443	23845	10	97	482	19	23949	24061
<i>Streptococcus pneumoniae</i>	425	177	357	978	14121	43	577	11	82	4212	5965	2484	67	2563	0	1925	45	154	6364	0	0
<i>Pseudomonas aeruginosa</i>	93	524	225	8	8	58	237	13750	199	389	24	8	311	54	23	41	285	303	7	44	34
<i>Staphylococcus aureus</i>	498	5520	365	152	81	4643	263	29	281	352	210	278	138	720	0	1653	181	209	142	0	0
<i>Enterococcus faecalis</i>	197	401	233	535	620	174	343	16	137	460	497	1326	78	343	0	589	128	175	778	0	0
<i>Escherichia coli</i>	85	139	161	27	41	31	165	96	232	32	167	55	216	140	74	59	206	192	65	104	102
<i>Listeria monocytogenes</i>	220	79	275	66	72	141	197	6	376	51	124	135	110	124	0	94	246	232	98	0	0
<i>Streptococcus agalactiae</i>	35	17	42	117	140	4	61	3	11	307	120	117	16	63	0	57	10	29	327	0	0
<i>Streptococcus pyogenes</i>	44	26	24	99	137	9	50	5	11	285	116	107	26	63	1	59	4	12	364	0	0
<i>Streptococcus spp.</i>	6	2	12	15	515	1	12	0	1	126	246	41	1	47	0	68	0	5	149	0	0
<i>Acinetobacter spp. ADPI</i>	3	5	32	2	3	2	39	8	20	0	3	1	11	34	350	2	9	40	1	390	394
<i>Bacillus cereus</i>	555	152	890	38	86	349	806	28	1398	72	245	79	374	372	2	107	872	900	72	1	2
<i>Bacillus anthracis</i>	481	136	728	40	72	241	630	35	1228	53	175	66	329	286	0	61	691	673	72	0	0
<i>Bacillus thuringiensis</i>	197	46	304	13	27	130	326	9	549	16	92	32	145	137	0	34	348	333	38	0	0
<i>Burkholderia pseudomallei</i>	59	168	251	4	28	39	228	25	241	16	28	10	351	154	10	50	318	316	4	9	4
<i>Streptococcus suis</i>	56	35	50	121	155	7	69	42	31	370	167	159	32	134	0	96	18	39	368	0	0
<i>Acidovorax spp.</i>	144	877	787	2	9	50	965	18	254	28	25	3	1522	89	1	160	1073	1002	5	0	6
<i>Comamonas testosteroni</i>	8	231	221	0	2	7	292	7	65	11	6	1	493	18	1	46	348	334	2	0	0
<i>Cupriavidus metallidurans</i>	33	140	129	2	4	11	146	23	75	3	16	1	239	32	1	26	193	204	3	2	1
<i>Streptococcus mitis</i>	61	17	50	145	1571	6	56	0	12	358	646	236	4	263	0	194	4	18	717	0	0
<i>Pseudomonas putida</i>	16	2727	64	3	6	15	60	124	24	4	8	6	91	12	3	15	86	80	4	12	10
<i>Stenotrophomonas maltophilia</i>	380	81	78	0	8	84	61	9	630	15	43	17	122	328	4	37	381	77	17	24	1
<i>Delftia acidovorans</i>	35	3895	3129	0	2	13	3868	2	67	101	12	1	6808	23	0	693	4336	4359	2	3	0
<i>Coprobacillus spp.</i>	3061	322	414	113	206	232	158	198	640	3	1335	24	471	829	260	42	297	103	420	2	3
<i>Enterococcus faecium</i>	271	201	167	155	241	119	227	1	196	188	276	322	65	211	0	206	146	151	327	0	0
<i>Staphylococcus epidermidis</i>	129	54	126	42	12	12147	42	2	93	328	23	439	56	200	0	4022	40	50	26	0	0

<i>Bifidobacterium dentium</i>	20	12	456	11	3	1	10	0	0	4	9	457	17	584	0	8	2	26	7	0	0
<i>Clostridium difficile</i>	403	16	109	92	67	16	123	7	74	1802	642	141	77	133	0	151	44	39	126	1	0
<i>Granulicatella adiacens</i>	19	265	8	261	289	1	39	1	2	44	164	396	2	106	0	145	3	10	512	0	0
<i>Streptococcus salivarius</i>	8	1	10	486	111	8	46	0	1	57	137	126	22	40	0	46	0	2	1611	0	0
<i>Streptococcus anginosus</i>	37	1	36	12	12	2	80	0	1	2124	200	15	12	35	0	8	8	0	33	0	0
<i>Rothia mucilaginosa</i>	44	1	134	16	131	1	44	1	0	13	58	46	2	847	0	3963	0	6	662	0	0
<i>Atopobium parvulum</i>	156	30	58	1193	36	1	44	0	5	246	332	768	36	392	0	1009	1	271	45	0	0
<i>Actinomyces odontolyticus</i>	70	4	38	120	39	11	189	0	3	12	140	2744	14	226	0	684	0	58	43	0	0
<i>Streptococcus parasanguinis</i>	57	25	73	334	346	2	103	0	0	282	212	498	1	508	0	180	3	88	1629	0	0
<i>Parvimonas micra</i>	338	10	15	84	4	2	119	0	0	1309	747	36	284	196	0	13	6	1	21	0	0
<i>Streptococcus infantis</i>	16	6	2	14	1315	2	7	1	0	85	388	61	1	72	0	155	1	2	271	0	0
<i>Streptococcus sanguinis</i>	29	12	61	192	242	2	143	1	0	629	210	118	8	108	0	79	4	18	384	0	0
<i>Streptococcus gordonii</i>	47	17	72	94	241	3	103	0	2	684	219	124	10	159	0	66	3	15	359	0	0
<i>Leptorichia buccalis</i>	36	2	19	9	8	8	6	4	0	15	7	1202	9	6	0	64	0	1	607	0	0
<i>Veillonella parvula</i>	39	1	10	222	36	22	39	2	4	18	62	321	64	63	0	338	1	12	69	0	0
<i>Propionibacterium acnes</i>	232	26	51	14	246	189	71	2	108	13	47	199	92	206	2	104	38	133	13	0	0
<i>Bacillus subtilis</i>	730	179	963	52	77	393	872	28	1361	53	221	61	378	480	5	77	995	1103	75	0	1
<i>Streptococcus thermophilus</i>	24	15	39	704	137	6	91	2	6	150	216	223	35	106	0	66	3	12	2129	0	0
<i>Bifidobacterium longum</i>	26	37	143	68	11	7	22	0	3	17	27	181	944	196	0	127	3	513	68	0	0
<i>Lactobacillus gasseri</i>	21	10	3	1615	3	5	5	0	11	107	6	32	4	2	0	7	6	2	14	0	0
<i>Bacillus coagulans</i>	179	42	181	1	15	86	152	0	329	2	42	4	71	115	1	14	246	185	5	0	0
<i>Acidovorax ebrens</i>	46	130	142	1	5	18	146	8	84	4	12	1	232	22	0	28	160	186	3	2	1
<i>Candida albicans</i>	29580	1104202	1136	21439	53	1407860	0	14	1	248985	8	43	18	72	30	66628	6	1176	3	203	179701
<i>Candida tropicalis</i>	307	803954	6950	189	3	12343	3	2	0	2194	1	19	3	0	1	556	4	2786	0	6	1526

**Supplementary Table 3:** Overview of functional categories identified on COVID-19 patients analyzed. Functional inference provided by MG-RAST server. Metabolic categories are shown hierarchically, from Level 1 (general) up to Level 3 (more specific subpathway).

General category (level1)	Frequency (%)	Predominant category level 2	Predominant category level 3	Frequency (%)
Carbohydrates	16.62	Central carbohydrate metabolism	TCA cycle	18.04
Amino acids and derivatives	12.27	Lysine, threonine, methionine, and cysteine	Threonine anaerobic catabolism	14.16
Protein metabolism	9.78	Protein biosynthesis	Translation elongation factors bacterial	6.88
RNA metabolism	7.74	RNA processing and modification	tRNA modification yeast mitochondrial	6.95
Cofactors, Vitamins, Prosthetic Groups, Pigments	7.12	Folate and pterines	YgfZ (Fe/S cluster biogenesis)	9.68
DNA metabolism	5.68	DNA replication	DNA-replication	19.28
Cell wall and Capsule	5.34	Capsular and extracellular polysaccharides	Sialic acid metabolism	14.27
Fatty acids, Lipids, and Isoprenoids	4.57	Fatty acids	Fatty acid metabolism	40.86
Nucleosides and Nucleotides	3.83	Purines	De-novo purine biosynthesis	9.91
Membrane transport	3.79	Protein and nucleoprotein secretion system, Type IV	pVir Plasmid protein (DNA topoisomerase)	47.97
Virulence, disease and defense	3.49	Resistance to antibiotics and toxic compounds	Resistance to fluoroquinolones	17.35
Stress response	2.64	Oxidative stress	Protection from reactive oxygen species	18.29
Respiration	2.33	Electron donating reactions	Respiratory dehydrogenases 1	12.19
Phages, Prophages, Transposable elements, Plasmids	2.1	Phages, Prophages	Phage replication	14.41
Iron acquisition and metabolism	2.09	Not categorized	Iron acquisition	40.21
Regulation and Cell signaling	1.96	Not categorized	Zinc regulated enzymes	12.7
Cell division and Cell cycle	1.73	Not categorized	Bacterial cytoskeleton	12.11
Phosphorus metabolism	1.15	Not categorized	Polyphosphate kinase	13.17
Sulfur metabolism	1.09	Organic sulfur assimilation	Alkanesulfonate_assimilation	15.89
Others (frequency<1%)	7.86	n.a.	n.a.	n.a.

**Supplementary Table 4:** Proportion of predominant enzymes related to bacterial evasion and virulence. Relative abundance of predominant enzymes within each one of metabolic pathways related to bacterial evasion and virulence: Secretion systems; toxins and superantigens, invasion and intracellular resistance, adhesion and capsular and extracellular polysaccharides pathways.

Metabolic pathway	Enzyme	Relative abundance (%)
Secretion system Type I	T1SS secreted agglutinin (RTX)	57.51
Secretion system Type I	Hemophore HasA	13.39
Secretion system Type I	Hemophore HasA outer membrane receptor HasR	5.36
Secretion system Type II	Cell division transporter, ATP-binding protein FtsE	23.42
Secretion system Type II	Cell division protein FtsX	15.11
Secretion system Type II	General secretion pathway protein D	10.85
Secretion system Type III	Type III effector	22.96
Secretion system Type III	Inner membrane channel protein (LcrD, HrcV, EscV, SsaV)	6.81
Secretion system Type III	Virulence protein (YopE)	6.63
Secretion system Type IV	DNA topoisomerase I	47.98
Secretion system Type IV	Single-stranded DNA-binding protein	19.85
Secretion system Type IV	IncF plasmid conjugative transfer pilus assembly protein TraH	7.31
Secretion system Type V	Exoprotein involved in heme utilization or adhesion of ShlA/HecA/FhaA family	50.66
Secretion system Type V	Channel-forming transporter/cytolysins activator of TpsB family	26.58
Secretion system Type V	Fimbrial adhesin	19.7
Secretion system Type VI	Uncharacterized protein ImpC	68.97
Secretion system Type VI	IcmF-related protein	11.61

Secretion system Type VI	Sigma-54 dependent transcriptional regulator	10.23
Secretion system Type VII	Sigma-fimbriae usher protein	52.31
Secretion system Type VII	Sigma-fimbriae chaperone protein	17.91
Secretion system Type VII	Sigma-fimbriae tip adhesin	15.58
Secretion system Type VIII	Fap amyloid fiber secretin	23.03
Secretion system Type VIII	Fap amyloid fibril major component	19.66
Secretion system Type VIII	Fap system putative outer membrane protein	14.04
Toxins and superantigens	Export ABC transporter ATP-binding protein	61.74
Toxins and superantigens	Streptolysin S export transmembrane permease (SagI)	5.76
Toxins and superantigens	Streptolysin S biosynthesis protein D (SagD)	5.54
Toxins and superantigens	Streptolysin S export transmembrane permease (SagH)	5.54
Invasion and intracellular resistance	Sortase	46.1
Invasion and intracellular resistance	Lipase precursor	22.31
Invasion and intracellular resistance	Internalin	14.03
Adhesion	Signal peptidase I	23.56
Adhesion	Fibronectin/fibrinogen-binding protein	20.01
Adhesion	Predicted cell-wall-anchored protein SasA	14.72
Iron acquisition	Ferrichrome-iron receptor	21.76
Iron acquisition	TonB-dependent receptor	19.73
Iron acquisition	Non-ribosomal peptide synthetase modules, siderophore biosynthesis	1.43
TCA cycle	Dihydrolipoamide dehydrogenase	26.65
TCA cycle	Succinate dehydrogenase flavoprotein subunit	14.98
TCA cycle	Isocitrate dehydrogenase [NADP]	14.52
Capsular and extracellular polysaccharides	UDP-N-acetylglucosamine 2-epimerase	29.99
Capsular and extracellular polysaccharides	Glucosamine-1-phosphate N-acetyltransferase	26.01
Capsular and extracellular polysaccharides	Phosphoglucosamine mutase	13.51