

Online Supplementary Tables

Table S1. Eukaryotic RNA viruses identified in the URT microbiome of COVID-19 patients

Species	Occurrences	Phylum	Family	Genus
<i>Severe acute respiratory syndrome-related coronavirus</i>	1737	Pisuviricota	Coronaviridae	Betacoronavirus
<i>Adeno-associated dependoparvovirus A</i>	273	Cossaviricota	Parvoviridae	Dependoparvovirus
<i>Bat coronavirus BM48-31/BGR/2008</i>	178	Pisuviricota	Coronaviridae	Betacoronavirus
<i>Murine leukemia virus</i>	55	Artverviricota	Retroviridae	Gammaretrovirus
<i>Megavirus chiliensis</i>	20	Nucleocytoviricota	Mimiviridae	Mimivirus
<i>Tomato brown rugose fruit virus</i>	10	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Rhinovirus A</i>	7	Pisuviricota	Picornaviridae	Enterovirus
<i>Rhinovirus C</i>	6	Pisuviricota	Picornaviridae	Enterovirus
<i>Tomato mosaic virus</i>	6	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Mus musculus mobilized endogenous polytropic provirus</i>	5	Artverviricota	Retroviridae	Gammaretrovirus
<i>Tobacco mosaic virus</i>	5	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Lymphocystis disease virus 4</i>	4	Nucleocytoviricota	Iridoviridae	Lymphocystivirus
<i>Cafeteria roenbergensis virus</i>	4	Nucleocytoviricota	Mimiviridae	Cafeteriavirus
<i>Cucumber green mottle mosaic virus</i>	4	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Yacon virus A</i>	4	Kitrinoviricota	Betaflexiviridae	Capillovirus
<i>Enterovirus C</i>	4	Pisuviricota	Picornaviridae	Enterovirus
<i>Pepper mild mottle virus</i>	3	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Orf virus</i>	3	Nucleocytoviricota	Poxviridae	Parapoxvirus
<i>Human immunodeficiency virus 1</i>	2	Artverviricota	Retroviridae	Lentivirus
<i>Rhinovirus B</i>	2	Pisuviricota	Picornaviridae	Enterovirus
<i>Woodchuck hepatitis virus</i>	2	Artverviricota	Hepadnaviridae	Orthohepadnavirus
<i>Orpheovirus IHUMI-LCC2</i>	2	Nucleocytoviricota	Phycodnaviridae	Unclassified
<i>Human mastadenovirus C</i>	2	Preplasmiviricota	Adenoviridae	Mastadenovirus
<i>Clostera anastomosis granulovirus B</i>	2	Unclassified	Baculoviridae	Betabaculovirus
<i>Murine leukemia-related retroviruses</i>	2	Artverviricota	Retroviridae	Gammaretrovirus
<i>African cassava mosaic Burkina Faso virus</i>	2	Cressdnaviricota	Geminiviridae	Begomovirus
<i>Pegivirus C</i>	2	Kitrinoviricota	Flaviviridae	Pegivirus
<i>Bell pepper alphaendornavirus</i>	2	Kitrinoviricota	Endornaviridae	Alphaendornavirus
<i>Epsilonarterivirus zamalb</i>	2	Pisuviricota	Arteriviridae	Epsilonarterivirus
<i>Human coronavirus NL63</i>	2	Pisuviricota	Coronaviridae	Human coronavirus
<i>Human betaherpesvirus 6B</i>	1	Peploviricota	Herpesviridae	Roseolovirus
<i>Human alphaherpesvirus 1</i>	1	Peploviricota	Herpesviridae	Simplexvirus
<i>Human coronavirus HKU1</i>	1	Pisuviricota	Coronaviridae	Betacoronavirus
<i>Human gammaherpesvirus 4</i>	1	Peploviricota	Herpesviridae	Lymphocryptovirus
<i>Human mastadenovirus D</i>	1	Preplasmiviricota	Adenoviridae	Mastadenovirus
<i>Enterovirus D</i>	1	Pisuviricota	Picornaviridae	Enterovirus
<i>Mule deerpox virus</i>	1	Nucleocytoviricota	Poxviridae	Cervidpoxvirus
<i>Chrysochromulina ericina virus</i>	1	Nucleocytoviricota	Phycodnaviridae	Unclassified
<i>Moumouvirus</i>	1	Nucleocytoviricota	Mimiviridae	Unclassified
<i>Invertebrate iridescent virus 6</i>	1	Nucleocytoviricota	Iridoviridae	Iridovirus
<i>Enterovirus J</i>	1	Pisuviricota	Picornaviridae	Enterovirus
<i>African swine fever virus</i>	1	Nucleocytoviricota	Asfarviridae	Asfivirus
<i>Tanapox virus</i>	1	Nucleocytoviricota	Poxviridae	Yatapoxvirus
<i>Melanoplus sanguinipes entomopoxvirus</i>	1	Nucleocytoviricota	Poxviridae	Deltaentomopoxvirus
<i>Mimivirus terra2</i>	1	Nucleocytoviricota	Mimiviridae	Mimivirus
<i>Human polyomavirus 10</i>	1	Cossaviricota	Polyomaviridae	Deltapolyomavirus
<i>Betapapillomavirus 2</i>	1	Cossaviricota	Papillomaviridae	Betapapillomavirus
<i>Saimiriine gammaherpesvirus 2</i>	1	Peploviricota	Herpesviridae	Rhadovirus
<i>Rotavirus A</i>	1	Duplornaviricota	Reoviridae	Rotavirus
<i>Garlic virus A</i>	1	Kitrinoviricota	Alphaflexiviridae	Allexivirus
<i>Garlic virus X</i>	1	Kitrinoviricota	Alphaflexiviridae	Allexivirus
<i>Coleus vein necrosis virus</i>	1	Kitrinoviricota	Betaflexiviridae	Carlavirus
<i>Garlic common latent virus</i>	1	Kitrinoviricota	Betaflexiviridae	Carlavirus
<i>Mayaro virus</i>	1	Kitrinoviricota	Togaviridae	Alphavirus
<i>Brome mosaic virus</i>	1	Kitrinoviricota	Bromoviridae	Bromovirus
<i>Helianthus annuus alphaendornavirus</i>	1	Kitrinoviricota	Endornaviridae	Alphaendornavirus
<i>Oryza sativa alphaendornavirus</i>	1	Kitrinoviricota	Endornaviridae	Alphaendornavirus
<i>Ribgrass mosaic virus</i>	1	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Tobacco mild green mosaic virus</i>	1	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Rehmannia mosaic virus</i>	1	Kitrinoviricota	Virgaviridae	Tobamovirus
<i>Indiana vesiculovirus</i>	1	Negarnaviricota	Rhabdoviridae	Vesiculovirus
<i>Human metapneumovirus</i>	1	Negarnaviricota	Pneumoviridae	Metapneumovirus
<i>Sinapis alba cryptic virus 1</i>	1	Pisuviricota	Partitiviridae	Unclassified
<i>Verticillium dahliae partitivirus 1</i>	1	Pisuviricota	Partitiviridae	Unclassified
<i>Botryotinia fuckeliana partitivirus 1</i>	1	Pisuviricota	Partitiviridae	Unclassified
<i>Onion yellow dwarf virus</i>	1	Pisuviricota	Potyviridae	Potyvirus
<i>Leek yellow stripe virus</i>	1	Pisuviricota	Potyviridae	Potyvirus
<i>Squash vein yellowing virus</i>	1	Pisuviricota	Potyviridae	Ipomovirus
<i>Currant latent virus</i>	1	Pisuviricota	Secoviridae	Cheravirus
<i>Bat sapelovirus</i>	1	Pisuviricota	Picornaviridae	Sapelovirus
<i>Mischivirus D</i>	1	Pisuviricota	Picornaviridae	Mischivirus
<i>Enterovirus I</i>	1	Pisuviricota	Picornaviridae	Enterovirus

Table S2. Basic network properties of the COVID-19-URT network

Num. of Nodes	Num. of Links	Average Degree	Avg. Local Cluster Coefficient	Diameter	Average Path Length	Connected Components	Network Density	Network Modularity	Num. of Communities
1840	135105	146.853	0.781	5	2.137	1	0.080	0.152	652

Table S3. The core/periphery and nested structures in the COVID-19-URT network

ρ	Ratio of C/(C+P)	Density Matrix				P/N Ratio			Nested-ness (S)
		B11	B12(21)	B22	Whole	Core	Peri.	C-P	
0.092	0.510	0.038	0.079	0.128	0.676	1.347	0.638	0.592	0.441

Table S4. The core and periphery species in the COVID-19-URT network
(This table was listed in Excel File)**Table S5.** The strongly connected clusters in the COVID-19-URT network

Cluster	Score*	Num. of Nodes	Num. of Edges
1	103.455	277	28657
2	17.843	153	2730
3	13.521	73	987
4	7.571	70	530
5	6.464	196	1267
6	6.231	26	162
7	5.643	14	79
8	5.542	24	133
9	5.400	15	81
10	4.229	35	148
11	3	7	21
12	2.889	9	26
13	2.824	34	96
14	2.556	18	46
15	2	5	10
16	1.917	12	23
17	1.571	7	11
18	1.500	4	6
19	1.500	4	6
20	1.400	5	7
21	1.286	7	9
22	1.250	4	5
23	1.250	4	5
24	1.200	5	6
25	1.143	7	8
26	1	3	3
27	1	3	3
28	1	3	3

* Score = Density $\times$ Number of nodes**Table S6.** Species composition of the top three strongest cluster in the COVID-19-URT network
(This table was listed in Excel File)**Table S7.** Positive-to-negative links (P/N) ratios in the COVID-19-URT network

Types of correlation	Positive Links (+)	Negative Links (-)	P/N (+/-) Ratio
Whole network	54527	80578	0.677
Bacteria-Bacteria	52851	78151	0.676
Archaea-Archaea	69	3	23
Bacteria-Archaea	677	1183	0.572
Virus-Virus	8	3	2.667
Archaea-Virus	20	3	6.667
Bacteria-Virus	902	1235	0.730
EV-EV	1	0	Inf
EV-Bacteria	40	216	0.185
EV-Archaea	2	2	1

PV-PV	6	0	Inf
PV-Bacteria	862	1019	0.846
PV-Archaea	18	1	18
EV-PV	1	3	0.333
F-F	5071	1622	3.126
P-P	28062	22637	1.240
B-B	488	98	4.980
A-A	3522	1094	3.219
F-P	4787	18647	0.257
F-B	687	1081	0.636
F-A	1030	3570	0.289
P-B	1347	6175	0.218
P-A	5119	15992	0.320
B-A	283	736	0.385

* EV: eukaryotic RNA viruses; PV: prokaryotic RNA viruses; F: Firmicutes; P: Proteobacteria; B: Bacteroidetes; A: Actinobacteria

Table S8. Species negatively correlated with *SARSr-CoV* in the COVID-19-URT network
(This table was listed in Excel File)

Table S9. Species negatively correlated with *BatCoV BM48-31* in the COVID-19-URT network
(This table was listed in Excel File)

Table S10. Links in the network of URT microbiome in the COVID-19 patients
(This table was listed in Excel File)

Online Supplementary Figures

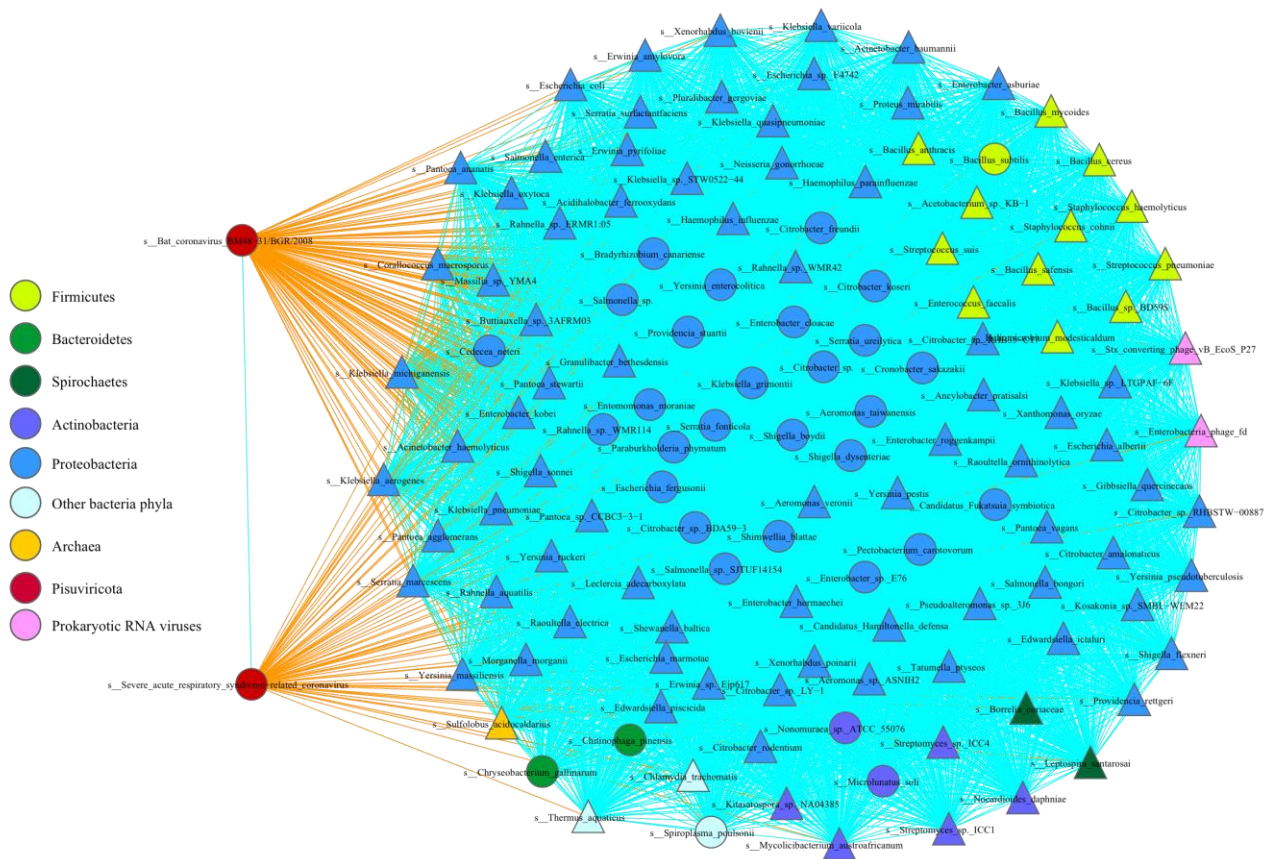


Figure S1. Sub-network associated with BatCoV BM48-31 in the COVID-19-URT microbiome network: links in cyan are positive correlation; edges in orange are negative correlations; circles represent core species; triangles represent periphery species; the color of the nodes represents the phylum to which the species belongs.

