

**Supplementary Table S 1. Epidemiological, clinical, and microbiological characteristics of participants younger than 5 split by SARS-CoV-2 RNA detection by RT-PCR.** Values expressed as No. (%), unless otherwise stated. Continuous variables were described as median and interquartile range (IQR) values.

		All infants ≤ 5 years  (n=265)	SARS-CoV-2 RNA detection		P value  <i>Pos vs. Neg</i>
			Positive (n=24)	Negative (n=241)	
Gender, female		115 (43.4%)	8 (33.3%)	107 (44.4%)	0.41 <sup>a</sup>
Median age, years (IQR)		2.9 (1.8, 3.8)	2.5 (1.7, 3.8)	2.9 (1.8, 3.8)	0.728 <sup>b</sup>
Days since adult’s infection (IQR)		53 (43, 62)	47 (39, 59.5)	53 (44, 62)	0.057 <sup>b</sup>
Median body temperature, °C (IQR)		36.1 (35.8, 36.4)	36 (25.8, 36.2)	36.1 (35.8, 36.4)	0.622 <sup>b</sup>
Active respiratory symptoms		9 (3.4%)	1 (4.2%)	8 (3.3%)	1 <sup>a</sup>
Antibiotic use (last 3 months)		37 (n=138) (26.8%)	5 (n=15) (33.3%)	32 (n=123) (26%)	0.768 <sup>a</sup>
Probiotic use (last 3 months)		10 (n=137) (7.3%)	1 (n=15) (6.7%)	9 (n=122) (7.4%)	1 <sup>a</sup>
Other respiratory viruses	Overall	83 (31.3%)	14 (58.3%)	69 (28.6%)	0.006 <sup>a</sup>
	Rhinovirus/Enterovirus	60 (22.6%)	12 (50%)	48 (19.9%)	0.002 <sup>a</sup>
	Adenovirus	12 (4.5%)	1 (4.2%)	11 (4.6%)	1 <sup>a</sup>
	Bocavirus	28 (10.6%)	6 (25%)	22 (9.1%)	0.039 <sup>a</sup>
	Coronavirus	1 (0.38%)	0 (0%)	1 (0.42%)	1 <sup>a</sup>
	Metapneumovirus	0 (0%)	0 (0%)	0 (0%)	-
	VRS (type A and B)	1 (0.38%)	0 (0%)	1 (0.42%)*	1 <sup>a</sup>
	Influenza virus (A and B)	0 (0%)	0 (0%)	0 (0%)	-
	Parainfluenza virus 1	5 (1.9%)	3 (12.5%)	2 (0.83%)	0.006 <sup>c</sup>
	Parainfluenza virus 2	3 (1.1%)	1 (4.2%)	2 (0.83%)	0.248 <sup>c</sup>
	Parainfluenza virus 3	1 (0.38%)	0 (0%)	1 (0.42%)	1 <sup>a</sup>
	Parainfluenza virus 4	0 (0%)	0 (0%)	0 (0%)	-

<sup>a</sup>Chi-square test.

<sup>b</sup>Wilcoxon Rank Sum test.

<sup>c</sup>Fisher exact test.

Abbreviations: IQR, Interquartile Range

\*VRS Type B

(n=X) indicate the total number of subjects with available data

**Supplementary Table S 2. Epidemiological, clinical, and microbiological characteristics of participants older than 5 split by SARS-CoV-2 RNA detection by RT-PCR.** Values expressed as No. (%), unless otherwise stated. Continuous variables were described as median and interquartile range (IQR) values.

		All infants > 5 years  (n=205)	SARS-CoV-2 RNA detection		P value
			Positive (n=21)	Negative (n=184)	Pos vs. Neg
Gender, female		94 (45.9%)	14 (66.7%)	97 (52.7%)	0.325 <sup>a</sup>
Median age, years (IQR)		8.2 (6.4, 10.7)	9.4 (6.9, 12.3)	8.1 (6.4, 10.4)	0.365 <sup>b</sup>
Days since adult’s infection (IQR)		52 (41, 59)	54 (34, 59)	51 (42, 59)	0.956 <sup>b</sup>
Median body temperature, °C (IQR)		36 (35.6, 36.2)	35.8 (35.5, 36.2)	36 (35.7, 36.2)	0.373 <sup>b</sup>
Active respiratory symptoms		12 (n=203) (5.9%)	2 (n=20) (10%)	10 (n=183) (5.5%)	0.751 <sup>a</sup>
Antibiotic use (last 3 months)		19 (n=77) (24.7%)	2 (n=9) (22.2%)	17 (n=68) (25%)	1 <sup>a</sup>
Probiotic use (last 3 months)		7 (n=77) (9.1%)	0 (n=9) (0%)	7 (n=69) (10.1%)	0.703 <sup>a</sup>
Other respiratory viruses	Overall	32 (15.6%)	6 (28.6%)	26 (14.1%)	0.159 <sup>a</sup>
	Rhinovirus/Enterovirus	29 (14.1%)	6 (28.6%)	23 (12.5%)	0.094 <sup>a</sup>
	Adenovirus	1 (0.49%)	0 (0%)	1 (0.54%)	1 <sup>c</sup>
	Bocavirus	1 (0.49%)	0 (0%)	1 (0.54%)	1 <sup>c</sup>
	Coronavirus	0 (0%)	0 (0%)	0 (0%)	-
	Metapneumovirus	0 (0%)	0 (0%)	0 (0%)	-
	VRS (type A and B)	0 (0%)	0 (0%)	0 (0%)	-
	Influenza virus (A and B)	1 (0.49%)	0 (0%)	1 (0.54%)*	1 <sup>c</sup>
	Parainfluenza virus 1	1 (0.49%)	0 (0%)	1 (0.54%)	1 <sup>c</sup>
	Parainfluenza virus 2	1 (0.49%)	0 (0%)	1 (0.54%)	1 <sup>c</sup>
	Parainfluenza virus 3	0 (0%)	0 (0%)	0 (0%)	-
	Parainfluenza virus 4	0 (n=204) (0%)	0 (0%)	0 (n=183) (0%)	-

<sup>a</sup>Chi-square test.

<sup>b</sup>Wilcoxon Rank Sum test.

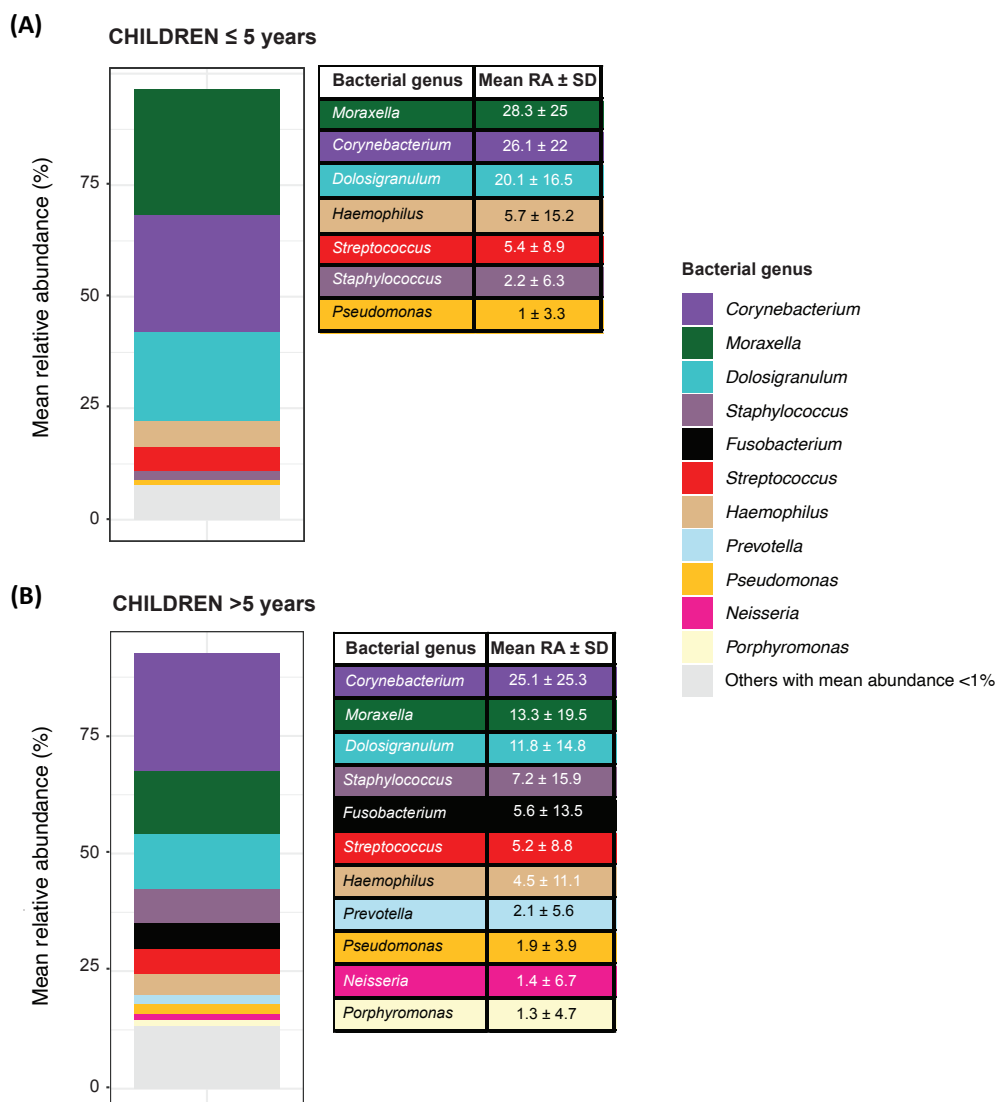
<sup>c</sup>Fisher exact test.

Abbreviations: IQR, Interquartile Range

\*Influenza Virus Type A

(n=X) indicate the total number of subjects with available data

**Supplementary Figure S1. Bacterial genera composition in the nasopharynx of children split by age range.** Bacterial genera were filtered by a minimum of 0.01% relative abundance in at least 10% of samples within each study group (children  $\leq 5$  years in A and children  $> 5$  years in B). Only bacterial genera with a mean abundance  $> 1\%$  are shown in the table ranked from most to least abundant in each group. Same genera are properly identified by color coding as shown in the legend and kept consistent in the two groups. Bacterial genera whose mean relative abundance was  $< 1\%$  are grouped into “others”.

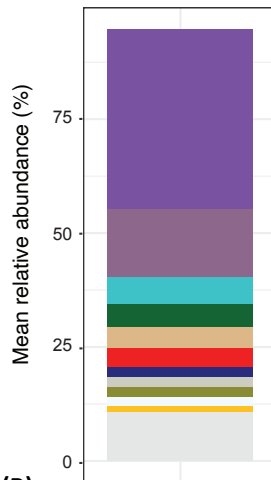


**Supplementary Figure S2. Bacterial nasopharyngeal microbiota composition in adults split by SARS-CoV-2 persistent infection and COVID-19 severity.**

Bacterial genera were filtered by a minimum of 0.01% relative abundance in at least 10% of samples within each study group (split by SARS-CoV-2 persistent RNA detection in A) and by history of COVID-19 related hospitalization in B). Only bacterial genera with a mean abundance >1% are shown in the table ranked from most to least abundant in each group. Same genera are properly identified by color coding as shown in the legend and kept consistent in the two groups. Bacterial genera whose mean relative abundance was <1% are grouped into “others”.

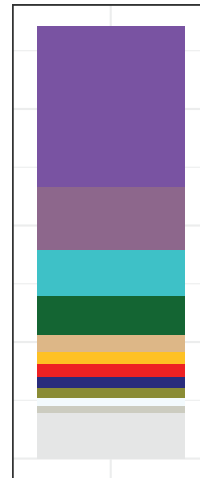
(A)

SARS-CoV-2-RT-PCR +



Bacterial genus	Mean RA $\pm$ SD
<i>Corynebacterium</i>	39.5 $\pm$ 29.5
<i>Staphylococcus</i>	15 $\pm$ 19.1
<i>Dolosigranulum</i>	6.0 $\pm$ 8.7
<i>Moraxella</i>	4.9 $\pm$ 13
<i>Haemophilus</i>	4.6 $\pm$ 13.4
<i>Streptococcus</i>	4.1 $\pm$ 9.1
<i>Anaerococcus</i>	2.4 $\pm$ 3.4
Actinomycetales	2.2 $\pm$ 3.5
<i>Propionibacterium</i>	2.0 $\pm$ 2.5
<i>Peptoniphilus</i>	2.0 $\pm$ 4.8
<i>Pseudomonas</i>	1.5 $\pm$ 3.6

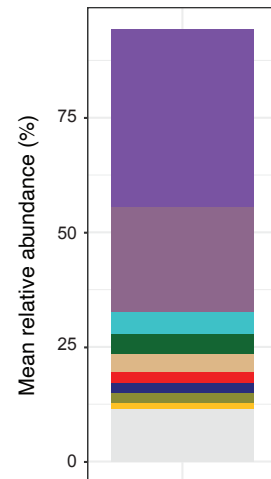
SARS-CoV-2-RT-PCR -



Bacterial genus	Mean RA $\pm$ SD
<i>Corynebacterium</i>	34.5 $\pm$ 9.1
<i>Staphylococcus</i>	13.6 $\pm$ 18.2
<i>Dolosigranulum</i>	9.9 $\pm$ 14.2
<i>Moraxella</i>	8.2 $\pm$ 13.8
<i>Haemophilus</i>	3.6 $\pm$ 12.2
<i>Pseudomonas</i>	2.8 $\pm$ 9.1
<i>Streptococcus</i>	2.7 $\pm$ 5.9
<i>Anaerococcus</i>	2.4 $\pm$ 4.0
<i>Propionibacterium</i>	2.0 $\pm$ 2.7
<i>Peptoniphilus</i>	1.8 $\pm$ 2.6
Actinomycetales	1.4 $\pm$ 3.4

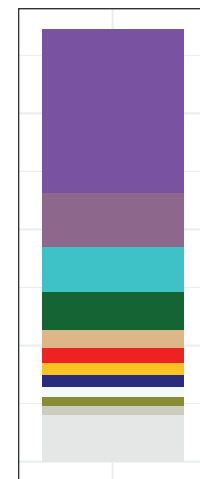
(B)

Past COVID-19 hospitalization



Bacterial genus	Mean RA $\pm$ SD
<i>Corynebacterium</i>	38.8 $\pm$ 27.7
<i>Staphylococcus</i>	23.1 $\pm$ 23.5
<i>Dolosigranulum</i>	4.9 $\pm$ 9.6
<i>Moraxella</i>	4.2 $\pm$ 9.2
<i>Haemophilus</i>	3.9 $\pm$ 13.3
<i>Streptococcus</i>	2.5 $\pm$ 3.9
<i>Anaerococcus</i>	2.3 $\pm$ 3.7
<i>Propionibacterium</i>	2.0 $\pm$ 2.5
<i>Pseudomonas</i>	1.4 $\pm$ 2.2

No hospitalization



Bacterial genus	Mean RA $\pm$ SD
<i>Corynebacterium</i>	35.1 $\pm$ 25.6
<i>Staphylococcus</i>	11.6 $\pm$ 16.1
<i>Dolosigranulum</i>	9.9 $\pm$ 13.6
<i>Moraxella</i>	8.1 $\pm$ 14.5
<i>Haemophilus</i>	3.9 $\pm$ 12.3
<i>Streptococcus</i>	3.3 $\pm$ 7.5
<i>Pseudomonas</i>	2.7 $\pm$ 8.9
<i>Anaerococcus</i>	2.4 $\pm$ 3.9
<i>Peptoniphilus</i>	2.1 $\pm$ 4.3
<i>Propionibacterium</i>	2.0 $\pm$ 2.6
Actinomycetales	1.9 $\pm$ 3.7

Bacterial genus

