

***Pneumocystis jirovecii* is a potential pivotal ecological driver contributing to shifts in microbial equilibrium during the early-life lower airway microbiome assembly**

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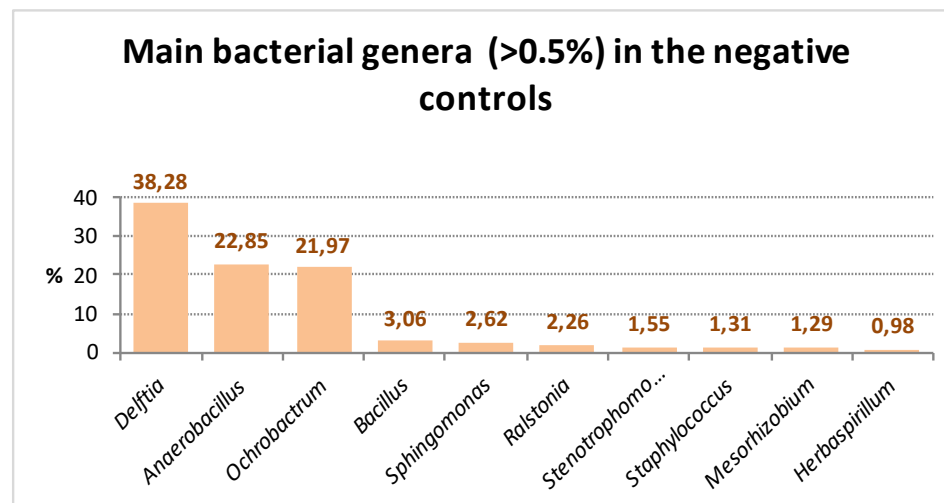
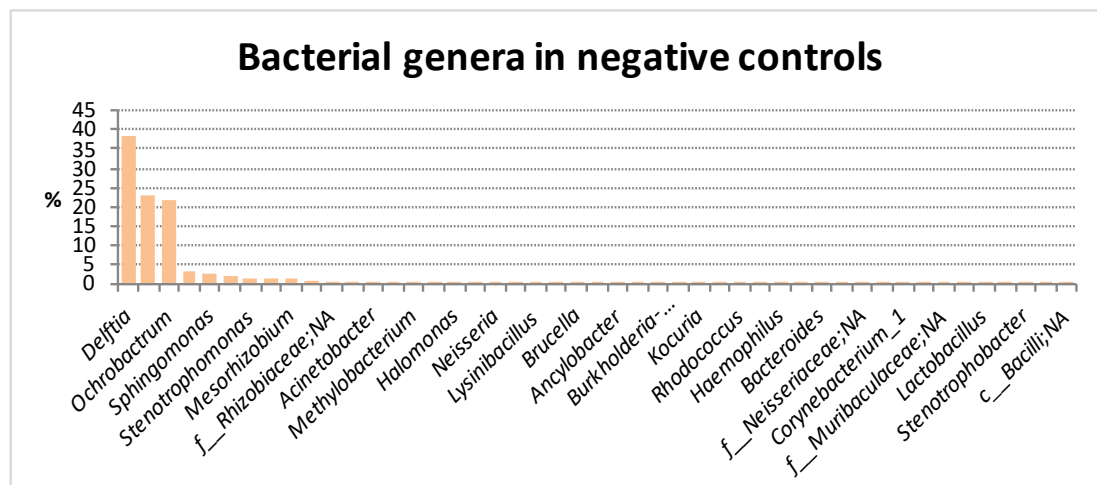
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Table S1: Fungal and bacterial diversity detected in negative controls. Relative abundance of fungal and bacterial genera identified in negative controls during the DNA extraction process.

<u>Bacterial genus</u>	<u>%</u>	<u>Number reads</u>
<i>Delftia</i>	38,2825	179.730
<i>Anaerobacillus</i>	22,8453	107.255
<i>Ochrobactrum</i>	21,9682	103.137
<i>Bacillus</i>	3,0602	14.367
<i>Sphingomonas</i>	2,6214	12.307
<i>Ralstonia</i>	2,2638	10.628
<i>Stenotrophomonas</i>	1,5494	7.274
<i>Staphylococcus</i>	1,3119	6.159
<i>Mesorhizobium</i>	1,2929	6.070
<i>Herbaspirillum</i>	0,9809	4.605
<i>f__Rhizobiaceae; NA</i>	0,4611	2.165
<i>Microbacterium</i>	0,4066	1.909
<i>Acinetobacter</i>	0,393	1.845
<i>Allorhizobium-Neorhizobium-Pararhizobium-</i>	0,3489	1.638
<i>Methylobacterium</i>	0,3284	1.542
<i>Bradyrhizobium</i>	0,2997	1.407
<i>Halomonas</i>	0,246	1.155
<i>Bosea</i>	0,2109	990
<i>Neisseria</i>	0,1649	774
<i>f__Bacillaceae; NA</i>	0,1404	659
<i>Lysinibacillus</i>	0,1402	658
<i>Curvibacter</i>	0,1282	602
<i>Brucella</i>	0,1146	538
<i>Escherichia/Shigella</i>	0,1093	513
<i>Ancylobacter</i>	0,0984	462
<i>Cutibacterium</i>	0,0469	220
<i>Burkholderia-Caballeronia-Paraburkholderia</i>	0,0447	210
<i>Serratia</i>	0,0334	157
<i>Kocuria</i>	0,0273	128
<i>Streptococcus</i>	0,0224	105
<i>Rhodococcus</i>	0,0115	54
<i>Halovibrio</i>	0,0098	46
<i>Haemophilus</i>	0,0081	38
<i>Pseudomonas</i>	0,0066	31
<i>Bacteroides</i>	0,0051	24
<i>Veillonella</i>	0,0034	16
<i>f__Neisseriaceae; NA</i>	0,0032	15
<i>Salicola</i>	0,0019	9
<i>Corynebacterium_1</i>	0,0015	7
<i>Citrobacter</i>	0,0015	7
<i>f__Muribaculaceae; NA</i>	0,0013	6
<i>Pseudochrobactrum</i>	0,0013	6
<i>Lactobacillus</i>	0,0009	4
<i>Aeromonas</i>	0,0009	4
<i>Stenotrophobacter</i>	0,0006	3
<i>Leucobacter</i>	0,0006	3
<i>c__Bacilli; NA</i>	0,0004	2



<u>Fungal genus</u>	<u>%</u>	<u>Number reads</u>
<i>Sarocladium</i>	74,4514	767.877
<i>Malassezia</i>	11,4877	118.482
<i>Aspergillus</i>	5,0368	51.949
<i>Byssochlamys</i>	3,462	35.706
<i>uncultured_fungus</i>	1,3787	14.220
<i>Filobasidium</i>	1,3212	13.627
<i>Exophiala</i>	0,9659	9.962
<i>Pseudaleuria</i>	0,9273	9.564
<i>Mycosphaerella</i>	0,5096	5.256
<i>Solicoccozyma</i>	0,2731	2.817
<i>p__Chytridiomycota;NA</i>	0,1509	1.556
<i>Penicillium</i>	0,035	361
<i>Vishniacozyma</i>	0,0003	3

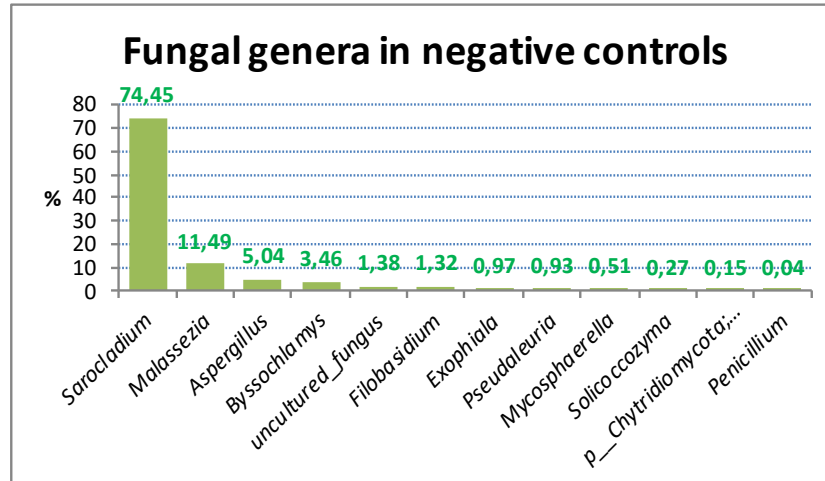


Table S2: Fungal diversity in lung tissue samples. The prevalence, mean, and standard deviations of the abundances for each taxon are reported for all lung tissue samples (labeled as "All") and for three *Pneumocystis* load categories: samples without *Pneumocystis* colonization (labeled as "Negative"), samples with low *Pneumocystis* abundance (Ct value ≥ 36 , labeled as "Low-positive"), and samples with high *Pneumocystis* abundance (Ct value < 36 , labeled as "High-positive"). NI, not identified.

Genus	All		Negative		Low-positive		High-positive	
	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)
<i>Yarrowia</i>	45	0.09 ($\pm$ 0.21)	15	0.06 ($\pm$ 0.14)	10	0.03 ($\pm$ 0.07)	20	0.13 ($\pm$ 0.28)
<i>Pneumocystis</i>	32	0.29 ($\pm$ 0.41)	NI	NI	8	0.004 ($\pm$ 0.006)	24	0.65 ($\pm$ 0.37)
<i>Candida</i>	31	0.13 ($\pm$ 0.3)	12	0.15 ($\pm$ 0.32)	8	0.26 ($\pm$ 0.4)	11	0.05 ($\pm$ 0.19)
<i>Byssoschlamys</i>	21	0.06 ($\pm$ 0.21)	8	0.05 ($\pm$ 0.19)	6	0.17 ($\pm$ 0.37)	7	0.03 ($\pm$ 0.06)
<i>Aspergillus</i>	20	0.15 ($\pm$ 0.31)	10	0.39 ($\pm$ 0.42)	NI	NI	10	0.03 ($\pm$ 0.08)
<i>Sarocladium</i>	12	0.04 ($\pm$ 0.18)	8	0.06 ($\pm$ 0.21)	2	0.09 ($\pm$ 0.3)	2	0.003 ($\pm$ 0.015)
<i>Rhodotorula</i>	9	0.02 ($\pm$ 0.06)	NI	NI	3	0.02 ($\pm$ 0.06)	6	0.03 ($\pm$ 0.08)
<i>Periconia</i>	9	0.003 ($\pm$ 0.017)	3	0.002 ($\pm$ 0.005)	2	0.01 ($\pm$ 0.04)	4	0.0001 ($\pm$ 0.0002)
<i>Cladosporium</i>	7	0.009 ($\pm$ 0.062)	5	0.03 ($\pm$ 0.11)	2	0.003 ($\pm$ 0.009)	NI	NI
<i>Malassezia</i>	7	0.06 ($\pm$ 0.2)	3	0.09 ($\pm$ 0.25)	1	0.09 ($\pm$ 0.28)	3	0.02 ($\pm$ 0.08)
<i>Filobasidium</i>	6	0.02 ($\pm$ 0.14)	1	0.06 ($\pm$ 0.24)	1	0.008 ($\pm$ 0.027)	4	0.003 ($\pm$ 0.011)
<i>Penicillium</i>	5	0.008 ($\pm$ 0.05)	3	0.002 ($\pm$ 0.007)	NI	NI	2	0.02 ($\pm$ 0.07)
<i>Phoma</i>	5	0.01 ($\pm$ 0.06)	NI	NI	2	0.04 ($\pm$ 0.14)	3	0.002 ($\pm$ 0.006)
<i>Saccharomyces</i>	4	0.005 ($\pm$ 0.038)	2	0.02 ($\pm$ 0.06)	2	0.0002 ($\pm$ 0.0005)	NI	NI
<i>Mucor</i>	2	0.02 ($\pm$ 0.14)	NI	NI	1	0.09 ($\pm$ 0.3)	1	0.01 ($\pm$ 0.05)
<i>Fusarium</i>	2	0.005 ($\pm$ 0.03)	1	0.002 ($\pm$ 0.007)	NI	NI	1	0.009 ($\pm$ 0.044)
<i>Apiotrichum</i>	2	0.001 ($\pm$ 0.009)	NI	NI	NI	NI	2	0.003 ($\pm$ 0.014)
<i>Diaporthe</i>	2	0.02 ($\pm$ 0.12)	1	0.05 ($\pm$ 0.2)	NI	NI	1	0.000002 ($\pm$ 0.00001)
<i>Botrytis</i>	1	0.02 ($\pm$ 0.14)	NI	NI	1	0.09 ($\pm$ 0.3)	NI	NI
<i>Pestalotiopsis</i>	1	0.02 ($\pm$ 0.13)	NI	NI	1	0.09 ($\pm$ 0.29)	NI	NI
<i>Clavispora</i>	1	0.002 ($\pm$ 0.012)	NI	NI	1	0.008 ($\pm$ 0.027)	NI	NI
<i>Meira</i>	1	0.00005 ($\pm$ 0.00037)	NI	NI	1	0.0002 ($\pm$ 0.0008)	NI	NI
<i>Pichia</i>	1	0.000004 ($\pm$ 0.00003)	NI	NI	1	0.00002 ($\pm$ 0.00007)	NI	NI
<i>Mycosphaerella</i>	1	0.008 ($\pm$ 0.055)	1	0.02 ($\pm$ 0.09)	NI	NI	NI	NI
<i>Cryptococcus</i>	1	0.004 ($\pm$ 0.03)	1	0.01 ($\pm$ 0.05)	NI	NI	NI	NI
<i>Hannaella</i>	1	0.003 ($\pm$ 0.019)	1	0.007 ($\pm$ 0.032)	NI	NI	NI	NI
<i>Epicoccum</i>	1	0.0008 ($\pm$ 0.006)	1	0.002 ($\pm$ 0.01)	NI	NI	NI	NI
<i>Kluyveromyces</i>	1	0.0003 ($\pm$ 0.0025)	1	0.001 ($\pm$ 0.004)	NI	NI	NI	NI
<i>Trichosporon</i>	1	0.0003 ($\pm$ 0.0023)	1	0.0009 ($\pm$ 0.0039)	NI	NI	NI	NI
<i>Scopuloides</i>	1	0.00004 ($\pm$ 0.00026)	1	0.0001 ($\pm$ 0.0004)	NI	NI	NI	NI

<i>Genus</i>	<i>Prevalence</i>	All	Negative		Low-positive		High-positive	
		<i>Mean (±SD)</i>	<i>Prevalence</i>	<i>Mean (±SD)</i>	<i>Prevalence</i>	<i>Mean (±SD)</i>	<i>Prevalence</i>	<i>Mean (±SD)</i>
<i>Phlebia</i>	1	0.005 (±0.035)	NI	NI	NI	NI	1	0.01 (±0.05)
<i>Bjerkandera</i>	1	0.004 (±0.029)	NI	NI	NI	NI	1	0.009 (±0.043)
<i>Rhizopus</i>	1	0.0003 (±0.0022)	NI	NI	NI	NI	1	0.0007 (±0.0033)
<i>Debaryomyces</i>	1	0.00003 (±0.00025)	NI	NI	NI	NI	1	0.0001 (±0.0004)
<i>Meyerozyma</i>	1	0.00002 (±0.00011)	NI	NI	NI	NI	1	0.00003 (±0.00017)
<i>Aureobasidium</i>	1	0.00001 (±0.0001)	NI	NI	NI	NI	1	0.00003 (±0.00015)
<i>Phanerochaete</i>	1	0.000003 (±0.000023)	NI	NI	NI	NI	1	0.00001 (±0.00003)
<i>Cryptococcus</i>	1	0.000002 (±0.000014)	NI	NI	NI	NI	1	0.000004 (±0.000021)

Table S3: Bacterial diversity in lung tissue samples. The prevalence, mean, and standard deviations of the abundances for each taxon are reported for all lung tissue samples (labeled as "All") and for three *Pneumocystis* load categories: samples without *Pneumocystis* colonization (labeled as "Negative"). samples with low *Pneumocystis* abundance (Ct value $\geq$ 36. labeled as "Low-positive"), and samples with high *Pneumocystis* abundance (Ct value < 36. labeled as "High-positive"). NI, not identified.

Phylum	Genus	All		Negative		Low-positive		High-positive	
		Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)
Firmicutes	<i>Streptococcus</i>	52	0.31 ($\pm$ 0.25)	18	0.28 ($\pm$ 0.19)	11	0.37 ($\pm$ 0.27)	23	0.31 ($\pm$ 0.29)
Firmicutes	<i>Veillonella</i>	41	0.02 ($\pm$ 0.03)	13	0.02 ($\pm$ 0.03)	10	0.03 ($\pm$ 0.04)	18	0.03 ($\pm$ 0.04)
Firmicutes	<i>Gemella</i>	39	0.06 ($\pm$ 0.10)	14	0.05 ($\pm$ 0.08)	10	0.04 ($\pm$ 0.05)	15	0.07 ($\pm$ 0.13)
Firmicutes	<i>Staphylococcus</i>	37	0.02 ($\pm$ 0.05)	14	0.01 ($\pm$ 0.03)	7	0.006 ($\pm$ 0.013)	16	0.03 ($\pm$ 0.07)
Proteobacteria	<i>Haemophilus</i>	35	0.03 ($\pm$ 0.09)	11	0.03 ($\pm$ 0.07)	10	0.01 ($\pm$ 0.02)	14	0.04 ($\pm$ 0.11)
Bacteroidetes	<i>Prevotella_7</i>	33	0.01 ($\pm$ 0.03)	12	0.01 ($\pm$ 0.02)	7	0.02 ($\pm$ 0.03)	14	0.02 ($\pm$ 0.04)
Proteobacteria	<i>Neisseria</i>	31	0.01 ($\pm$ 0.02)	12	0.010 ($\pm$ 0.016)	7	0.02 ($\pm$ 0.04)	12	0.009 ($\pm$ 0.025)
Proteobacteria	<i>Pseudomonas</i>	29	0.05 ($\pm$ 0.14)	9	0.08 ($\pm$ 0.22)	7	0.03 ($\pm$ 0.07)	13	0.04 ($\pm$ 0.08)
Firmicutes	<i>Granulicatella</i>	27	0.008 ($\pm$ 0.019)	10	0.009 ($\pm$ 0.015)	7	0.01 ($\pm$ 0.02)	10	0.006 ($\pm$ 0.020)
Proteobacteria	<i>Acinetobacter</i>	26	0.02 ($\pm$ 0.06)	10	0.02 ($\pm$ 0.05)	6	0.02 ($\pm$ 0.04)	10	0.02 ($\pm$ 0.07)
Bacteroidetes	<i>Alloprevotella</i>	26	0.01 ($\pm$ 0.04)	7	0.01 ($\pm$ 0.03)	7	0.01 ($\pm$ 0.02)	12	0.02 ($\pm$ 0.05)
Fusobacteria	<i>Fusobacterium</i>	26	0.002 ($\pm$ 0.005)	9	0.003 ($\pm$ 0.007)	5	0.002 ($\pm$ 0.006)	12	0.002 ($\pm$ 0.004)
Bacteroidetes	<i>Porphyromonas</i>	25	0.005 ($\pm$ 0.013)	10	0.009 ($\pm$ 0.017)	6	0.006 ($\pm$ 0.018)	9	0.001 ($\pm$ 0.002)
Firmicutes	<i>Anaerobacillus</i>	25	0.02 ($\pm$ 0.05)	8	0.02 ($\pm$ 0.05)	7	0.005 ($\pm$ 0.017)	10	0.02 ($\pm$ 0.06)
Bacteroidetes	<i>Prevotella</i>	24	0.006 ($\pm$ 0.019)	8	0.01 ($\pm$ 0.03)	5	0.002 ($\pm$ 0.003)	11	0.003 ($\pm$ 0.006)
Actinobacteria	<i>Actinomyces</i>	24	0.001 ($\pm$ 0.002)	9	8.9 E-04 ($\pm$ 1.9 E-03)	7	0.001 ($\pm$ 0.001)	8	0.001 ($\pm$ 0.002)
Firmicutes	<i>Lactobacillus</i>	23	0.03 ($\pm$ 0.09)	6	0.03 ($\pm$ 0.11)	6	0.03 ($\pm$ 0.05)	11	0.03 ($\pm$ 0.09)
Proteobacteria	<i>Moraxella</i>	21	0.02 ($\pm$ 0.05)	10	0.03 ($\pm$ 0.06)	6	0.006 ($\pm$ 0.020)	5	0.01 ($\pm$ 0.05)
Bacteroidetes	<i>Chryseobacterium</i>	20	0.03 ($\pm$ 0.08)	6	0.03 ($\pm$ 0.07)	5	0.02 ($\pm$ 0.06)	9	0.04 ($\pm$ 0.11)
Proteobacteria	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium</i>	19	0.006 ($\pm$ 0.021)	10	0.02 ($\pm$ 0.03)	2	3.6 E-04 ($\pm$ 1.1 E-03)	7	0.002 ($\pm$ 0.008)
Proteobacteria	<i>Klebsiella</i>	18	0.03 ($\pm$ 0.10)	9	0.05 ($\pm$ 0.14)	2	0.04 ($\pm$ 0.11)	7	0.01 ($\pm$ 0.04)
Firmicutes	<i>Enterococcus</i>	18	0.03 ($\pm$ 0.08)	9	0.04 ($\pm$ 0.10)	4	0.04 ($\pm$ 0.10)	5	0.01 ($\pm$ 0.05)
Fusobacteria	<i>Streptobacillus</i>	18	0.002 ($\pm$ 0.006)	5	0.001 ($\pm$ 0.003)	7	0.007 ($\pm$ 0.013)	6	2.3 E-04 ($\pm$ 5.5 E-04)
Firmicutes	<i>Johnsonella</i>	17	0.002 ($\pm$ 0.006)	7	0.003 ($\pm$ 0.009)	4	2.2 E-04 ($\pm$ 4.6 E-04)	6	0.001 ($\pm$ 0.005)
Actinobacteria	<i>Rothia</i>	17	5.0 E-04 ($\pm$ 3.1 E-03)	5	0.001 ($\pm$ 0.005)	4	1.1 E-04 ($\pm$ 1.6 E-04)	8	6.9 E-05 ($\pm$ 1.5 E-04)
Proteobacteria	<i>Raoultella</i>	16	0.03 ($\pm$ 0.11)	4	0.01 ($\pm$ 0.05)	4	0.07 ($\pm$ 0.15)	8	0.03 ($\pm$ 0.11)
Proteobacteria	NA	16	0.005 ($\pm$ 0.016)	4	3.5 E-05 ($\pm$ 8.5 E-05)	5	0.006 ($\pm$ 0.015)	7	0.007 ($\pm$ 0.022)
Actinobacteria	<i>Corynebacterium_1</i>	16	9.2 E-04 ($\pm$ 3.2 E-03)	6	0.001 ($\pm$ 0.004)	3	0.001 ($\pm$ 0.005)	7	2.5 E-04 ($\pm$ 6.6 E-04)
Proteobacteria	<i>Escherichia/Shigella</i>	15	0.02 ($\pm$ 0.06)	5	0.03 ($\pm$ 0.07)	3	0.03 ($\pm$ 0.11)	7	0.002 ($\pm$ 0.005)
Proteobacteria	<i>Bradyrhizobium</i>	15	0.01 ($\pm$ 0.04)	3	0.01 ($\pm$ 0.06)	1	1.4 E-04 ($\pm$ 4.6 E-04)	11	0.01 ($\pm$ 0.04)
Firmicutes	<i>Bacillus</i>	15	0.01 ($\pm$ 0.05)	5	0.003 ($\pm$ 0.008)	1	4.2 E-05 ($\pm$ 1.4 E-04)	9	0.02 ($\pm$ 0.08)
Proteobacteria	<i>Actinobacillus</i>	14	0.01 ($\pm$ 0.03)	6	0.01 ($\pm$ 0.02)	3	0.03 ($\pm$ 0.07)	5	0.001 ($\pm$ 0.004)
Proteobacteria	<i>Halomonas</i>	14	0.002 ($\pm$ 0.010)	6	0.003 ($\pm$ 0.010)	1	3.5 E-06 ($\pm$ 1.2 E-05)	7	0.003 ($\pm$ 0.012)
Actinobacteria	<i>Atopobium</i>	13	0.001 ($\pm$ 0.005)	5	0.001 ($\pm$ 0.005)	3	7.8 E-04 ($\pm$ 1.4 E-03)	5	0.002 ($\pm$ 0.007)
Firmicutes	<i>Lactococcus</i>	12	0.01 ($\pm$ 0.04)	2	3.5 E-04 ($\pm$ 1.2 E-03)	4	0.04 ($\pm$ 0.07)	6	0.008 ($\pm$ 0.037)
Proteobacteria	<i>Enterobacter</i>	12	0.01 ($\pm$ 0.04)	4	0.001 ($\pm$ 0.004)	3	0.02 ($\pm$ 0.06)	5	0.01 ($\pm$ 0.04)
Proteobacteria	<i>Herbaspirillum</i>	12	0.008 ($\pm$ 0.030)	6	0.01 ($\pm$ 0.05)	3	0.009 ($\pm$ 0.030)	3	0.002 ($\pm$ 0.012)
Bacteroidetes	<i>Bergeyella</i>	12	3.1 E-04 ($\pm$ 1.8 E-03)	4	7.5 E-04 ($\pm$ 3.0 E-03)	4	2.0 E-04 ($\pm$ 4.8 E-04)	4	3.6 E-05 ($\pm$ 8.8 E-05)
Proteobacteria	<i>Janthinobacterium</i>	11	0.002 ($\pm$ 0.009)	2	0.004 ($\pm$ 0.015)	3	0.002 ($\pm$ 0.006)	6	0.001 ($\pm$ 0.004)
Firmicutes	<i>Lachnoanaerobaculum</i>	11	4.2 E-04 ($\pm$ 1.3 E-03)	5	2.5 E-04 ($\pm$ 5.8 E-04)	3	5.0 E-04 ($\pm$ 1.2 E-03)	3	5.0 E-04 ($\pm$ 1.7 E-03)
Bacteroidetes	<i>Prevotella_6</i>	11	5.0 E-04 ($\pm$ 1.5 E-03)	4	2.4 E-04 ($\pm$ 5.4 E-04)	2	1.5 E-04 ($\pm$ 4.4 E-04)	5	8.5 E-04 ($\pm$ 2.2 E-03)
Proteobacteria	<i>Methylobacterium</i>	11	0.004 ($\pm$ 0.025)	5	0.002 ($\pm$ 0.009)	1	3.3 E-05 ($\pm$ 1.1 E-04)	5	0.008 ($\pm$ 0.037)

Phylum	Genus	All		Negative		Low-positive		High-positive	
		Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)
Firmicutes	<i>Peptostreptococcus</i>	11	5.8 E-04 ($\pm$ 2.2 E-03)	5	0.001 ($\pm$ 0.003)	1	3.3 E-05 ($\pm$ 1.1 E-04)	5	4.9 E-04 ($\pm$ 1.8 E-03)
Firmicutes	<i>Clostridium_sensu_stricto_1</i>	10	0.01 ($\pm$ 0.05)	5	0.02 ($\pm$ 0.08)	2	0.001 ($\pm$ 0.004)	3	0.008 ($\pm$ 0.041)
Proteobacteria	<i>Brucella</i>	10	0.002 ($\pm$ 0.013)	1	0.005 ($\pm$ 0.022)	2	2.6 E-04 ($\pm$ 7.0 E-04)	7	3.3 E-04 ($\pm$ 1.1 E-03)
Fusobacteria	<i>Leptotrichia</i>	9	0.002 ($\pm$ 0.012)	4	6.0 E-04 ($\pm$ 2.2 E-03)	2	0.008 ($\pm$ 0.025)	3	0.001 ($\pm$ 0.005)
Proteobacteria	<i>Lelliottia</i>	9	7.5 E-04 ($\pm$ 2.4 E-03)	3	2.1 E-04 ($\pm$ 8.0 E-04)	1	4.8 E-04 ($\pm$ 1.6 E-03)	5	0.001 ($\pm$ 0.003)
Bacteroidetes	<i>Bacteroides</i>	9	1.7 E-04 ($\pm$ 5.5 E-04)	6	2.2 E-04 ($\pm$ 5.3 E-04)	NI	NI	3	2.1 E-04 ($\pm$ 6.8 E-04)
Proteobacteria	<i>Serratia</i>	8	0.01 ($\pm$ 0.07)	1	2.9 E-05 ($\pm$ 1.2 E-04)	2	2.4 E-04 ($\pm$ 5.4 E-04)	5	0.03 ($\pm$ 0.10)
Proteobacteria	<i>Enhydrobacter</i>	8	5.0 E-04 ($\pm$ 3.0 E-03)	3	0.001 ($\pm$ 0.005)	3	1.1 E-04 ($\pm$ 2.8 E-04)	2	1.3 E-04 ($\pm$ 5.8 E-04)
Proteobacteria	<i>Stenotrophomonas</i>	7	0.004 ($\pm$ 0.024)	1	1.7 E-04 ($\pm$ 7.3 E-04)	2	0.02 ($\pm$ 0.05)	4	0.002 ($\pm$ 0.009)
Firmicutes	<i>Paeniclostridium</i>	7	0.02 ($\pm$ 0.11)	2	3.2 E-05 ($\pm$ 1.2 E-04)	1	0.010 ($\pm$ 0.033)	4	0.04 ($\pm$ 0.16)
Proteobacteria	<i>Shewanella</i>	7	0.001 ($\pm$ 0.005)	3	0.002 ($\pm$ 0.008)	2	0.001 ($\pm$ 0.004)	2	1.8 E-04 ($\pm$ 7.3 E-04)
Firmicutes	<i>Faecalibacterium</i>	7	8.9 E-05 ($\pm$ 3.6 E-04)	5	1.3 E-04 ($\pm$ 2.5 E-04)	1	3.2 E-06 ($\pm$ 1.1 E-05)	1	9.9 E-05 ($\pm$ 4.9 E-04)
Proteobacteria	<i>Delftia</i>	7	0.004 ($\pm$ 0.018)	2	0.005 ($\pm$ 0.017)	NI	NI	5	0.006 ($\pm$ 0.022)
Firmicutes	<i>Ruminococcaceae_UCG-014</i>	7	2.4 E-04 ($\pm$ 8.3 E-04)	5	4.7 E-04 ($\pm$ 1.2 E-03)	NI	NI	2	1.7 E-04 ($\pm$ 6.6 E-04)
Proteobacteria	<i>Bosea</i>	6	0.01 ($\pm$ 0.06)	2	2.8 E-04 ($\pm$ 8.8 E-04)	1	0.009 ($\pm$ 0.029)	3	0.02 ($\pm$ 0.09)
Proteobacteria	<i>Comamonas</i>	6	4.7 E-04 ($\pm$ 2.3 E-03)	2	2.8 E-04 ($\pm$ 8.9 E-04)	3	0.002 ($\pm$ 0.005)	1	4.0 E-05 ($\pm$ 2.0 E-04)
Proteobacteria	<i>Aeromonas</i>	6	2.8 E-04 ($\pm$ 1.1 E-03)	2	2.4 E-04 ($\pm$ 9.9 E-04)	2	3.8 E-04 ($\pm$ 1.1 E-03)	2	2.6 E-04 ($\pm$ 1.2 E-03)
Proteobacteria	<i>Pantoea</i>	6	0.001 ($\pm$ 0.007)	1	0.003 ($\pm$ 0.012)	1	9.4 E-05 ($\pm$ 3.1 E-04)	4	6.5 E-04 ($\pm$ 1.9 E-03)
Proteobacteria	<i>Citrobacter</i>	6	3.1 E-04 ($\pm$ 1.2 E-03)	1	6.1 E-05 ($\pm$ 2.6 E-04)	1	6.7 E-05 ($\pm$ 2.2 E-04)	4	6.1 E-04 ($\pm$ 1.8 E-03)
Actinobacteria	<i>Bifidobacterium</i>	6	0.001 ($\pm$ 0.011)	5	0.004 ($\pm$ 0.018)	NI	NI	1	1.0 E-05 ($\pm$ 4.9 E-05)
Actinobacteria	<i>Cutibacterium</i>	6	3.0 E-04 ($\pm$ 2.0 E-03)	5	8.8 E-04 ($\pm$ 3.3 E-03)	NI	NI	1	2.8 E-06 ($\pm$ 1.4 E-05)
Firmicutes	<i>Agathobacter</i>	6	8.4 E-05 ($\pm$ 4.0 E-04)	5	2.1 E-04 ($\pm$ 6.6 E-04)	NI	NI	1	2.4 E-05 ($\pm$ 1.2 E-04)
Firmicutes	<i>Dialister</i>	6	1.6 E-05 ($\pm$ 5.9 E-05)	3	1.2 E-05 ($\pm$ 2.8 E-05)	NI	NI	3	2.5 E-05 ($\pm$ 8.4 E-05)
Proteobacteria	<i>Ralstonia</i>	5	0.003 ($\pm$ 0.014)	2	0.004 ($\pm$ 0.018)	2	0.005 ($\pm$ 0.017)	1	0.002 ($\pm$ 0.009)
Proteobacteria	NA	5	4.2 E-04 ($\pm$ 2.0 E-03)	1	1.2 E-04 ($\pm$ 5.1 E-04)	2	4.1 E-04 ($\pm$ 1.2 E-03)	2	6.4 E-04 ($\pm$ 2.9 E-03)
Proteobacteria	<i>Hafnia-Obesumbacterium</i>	5	0.01 ($\pm$ 0.06)	2	0.02 ($\pm$ 0.08)	1	3.4 E-04 ($\pm$ 1.1 E-03)	2	0.02 ($\pm$ 0.06)
Bacteroidetes	<i>Sphingobacterium</i>	5	1.3 E-04 ($\pm$ 5.7 E-04)	2	1.6 E-04 ($\pm$ 4.8 E-04)	1	3.3 E-04 ($\pm$ 1.1 E-03)	2	1.2 E-05 ($\pm$ 4.3 E-05)
Firmicutes	<i>Parvimonas</i>	5	2.6 E-04 ($\pm$ 1.2 E-03)	2	1.2 E-04 ($\pm$ 4.2 E-04)	1	1.9 E-04 ($\pm$ 6.3 E-04)	2	3.9 E-04 ($\pm$ 1.7 E-03)
Proteobacteria	<i>Rahnella</i>	5	2.9 E-04 ($\pm$ 1.6 E-03)	3	8.0 E-04 ($\pm$ 2.6 E-03)	1	3.7 E-05 ($\pm$ 1.2 E-04)	1	3.0 E-05 ($\pm$ 1.5 E-04)
Fusobacteria	<i>Oceanivirga</i>	5	1.3 E-04 ($\pm$ 4.8 E-04)	4	2.7 E-04 ($\pm$ 6.4 E-04)	NI	NI	1	8.8 E-05 ($\pm$ 4.3 E-04)
Firmicutes	<i>Ruminococcus_2</i>	5	3.8 E-05 ($\pm$ 1.6 E-04)	5	1.1 E-04 ($\pm$ 2.6 E-04)	NI	NI	NI	NI
Firmicutes	<i>Subdoligranulum</i>	5	2.8 E-05 ($\pm$ 1.0 E-04)	4	5.3 E-05 ($\pm$ 1.2 E-04)	NI	NI	1	2.2 E-05 ($\pm$ 1.1 E-04)
Firmicutes	<i>Ruminococcus_1</i>	5	2.6 E-05 ($\pm$ 1.3 E-04)	4	2.4 E-05 ($\pm$ 4.8 E-05)	NI	NI	1	4.0 E-05 ($\pm$ 2.0 E-04)
Firmicutes	<i>Dolosigranulum</i>	5	4.6 E-05 ($\pm$ 2.5 E-04)	2	2.2 E-05 ($\pm$ 7.4 E-05)	NI	NI	3	8.4 E-05 ($\pm$ 3.6 E-04)
Firmicutes	NA	5	9.6 E-06 ($\pm$ 3.7 E-05)	4	1.5 E-05 ($\pm$ 3.2 E-05)	NI	NI	1	9.6 E-06 ($\pm$ 4.7 E-05)
Bacteroidetes	<i>Parabacteroides</i>	5	1.2 E-05 ($\pm$ 5.5 E-05)	4	1.3 E-05 ($\pm$ 2.9 E-05)	NI	NI	1	1.6 E-05 ($\pm$ 7.9 E-05)
Bacteroidetes	<i>Flavobacterium</i>	4	5.1 E-04 ($\pm$ 3.1 E-03)	1	3.6 E-05 ($\pm$ 1.5 E-04)	2	0.002 ($\pm$ 0.007)	1	4.2 E-05 ($\pm$ 2.0 E-04)
Firmicutes	<i>Sarcina</i>	4	0.009 ($\pm$ 0.045)	3	0.03 ($\pm$ 0.08)	1	0.001 ($\pm$ 0.005)	NI	NI
Firmicutes	<i>Leuconostoc</i>	4	2.5 E-04 ($\pm$ 1.5 E-03)	1	4.4 E-05 ($\pm$ 1.8 E-04)	2	0.001 ($\pm$ 0.003)	1	4.6 E-06 ($\pm$ 2.3 E-05)
Firmicutes	<i>Lysinibacillus</i>	4	4.0 E-04 ($\pm$ 2.4 E-03)	NI	NI	1	3.2 E-04 ($\pm$ 1.1 E-03)	3	7.3 E-04 ($\pm$ 3.4 E-03)
Bacteroidetes	<i>Cloacibacterium</i>	4	4.4 E-05 ($\pm$ 2.0 E-04)	1	6.8 E-06 ($\pm$ 2.9 E-05)	1	8.7 E-05 ($\pm$ 2.9 E-04)	2	5.2 E-05 ($\pm$ 3.3 E-04)
Actinobacteria	<i>Kocuria</i>	4	3.2 E-05 ($\pm$ 1.3 E-04)	2	5.7 E-05 ($\pm$ 2.0 E-04)	1	4.2 E-05 ($\pm$ 1.4 E-04)	1	7.9 E-06 ($\pm$ 3.8 E-05)
Proteobacteria	NA	4	2.4 E-04 ($\pm$ 1.7 E-03)	1	7.0 E-04 ($\pm$ 3.0 E-03)	2	1.2 E-05 ($\pm$ 2.7 E-05)	1	2.8 E-06 ($\pm$ 1.4 E-05)
Firmicutes	<i>Vagococcus</i>	4	1.2 E-04 ($\pm$ 6.1 E-04)	NI	NI	1	7.2 E-06 ($\pm$ 2.4 E-05)	3	2.6 E-04 ($\pm$ 9.0 E-04)
Firmicutes	<i>Peptococcus</i>	4	6.6 E-05 ($\pm$ 3.4 E-04)	3	1.5 E-04 ($\pm$ 5.6 E-04)	NI	NI	1	3.0 E-05 ($\pm$ 1.5 E-04)
Firmicutes	<i>Roseburia</i>	4	4.9 E-05 ($\pm$ 2.2 E-04)	3	6.3 E-05 ($\pm$ 1.6 E-04)	NI	NI	1	6.1 E-05 ($\pm$ 3.0 E-04)
Firmicutes	NA	4	4.3 E-05 ($\pm$ 1.9 E-04)	2	1.7 E-05 ($\pm$ 6.2 E-05)	NI	NI	2	8.2 E-05 ($\pm$ 2.8 E-04)
Epsilonbacteraeota	<i>Campylobacter</i>	4	6.7 E-06 ($\pm$ 2.8 E-05)	2	1.2 E-05 ($\pm$ 4.2 E-05)	NI	NI	2	6.0 E-06 ($\pm$ 2.2 E-05)

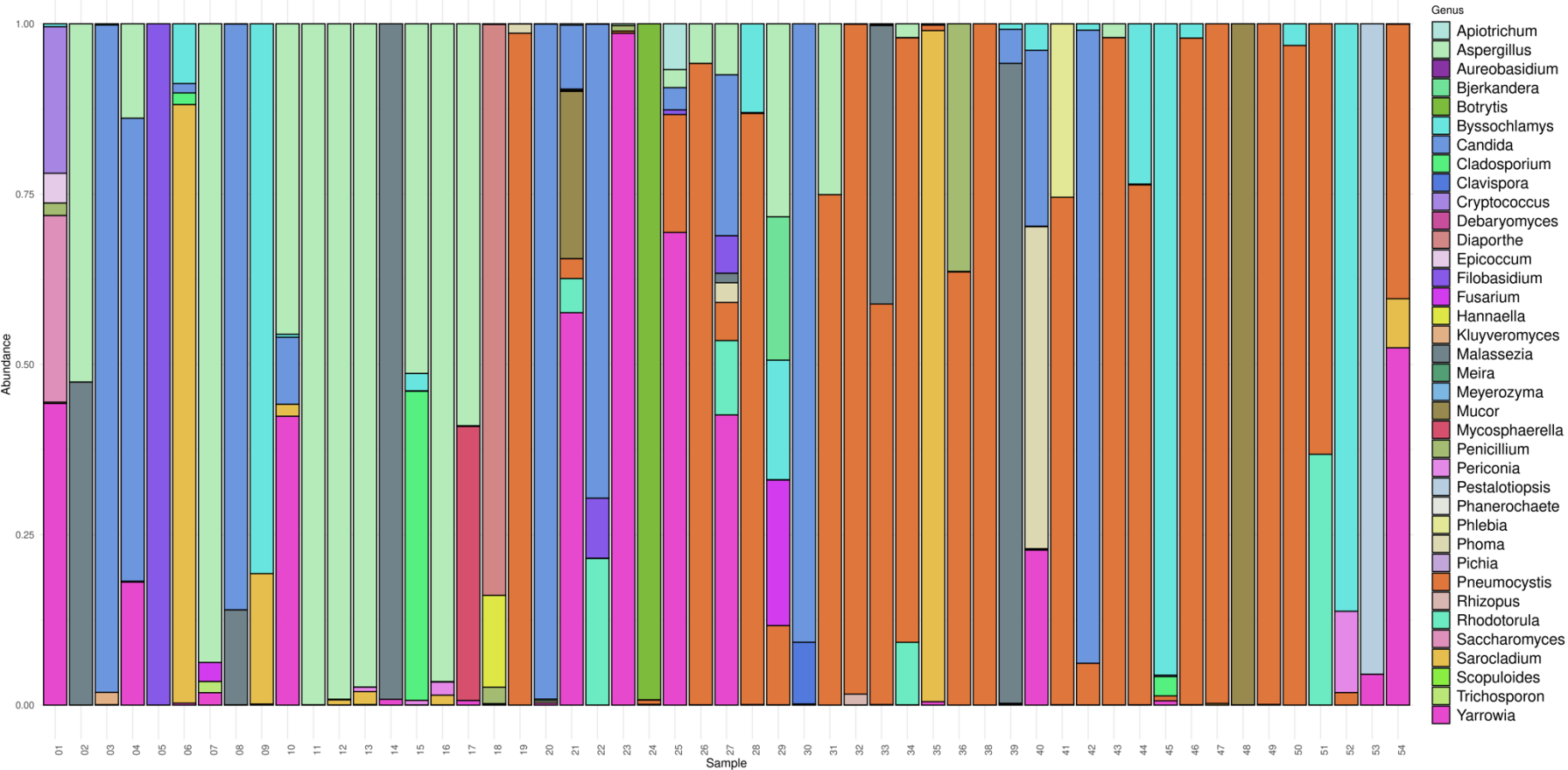
Phylum	Genus	All		Negative		Low-positive		High-positive	
		Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)
Proteobacteria	NA	3	4.3 E-04 ($\pm$ 3.0 E-03)	1	5.9 E-06 ($\pm$ 2.5 E-05)	1	0.002 ($\pm$ 0.007)	1	2.2 E-05 ($\pm$ 1.1 E-04)
Firmicutes	<i>Ruminococcaceae_UCG-002</i>	3	6.3 E-06 ($\pm$ 2.9 E-05)	1	8.0 E-06 ($\pm$ 3.4 E-05)	1	3.2 E-06 ($\pm$ 1.1 E-05)	1	6.4 E-06 ($\pm$ 3.1 E-05)
Proteobacteria	<i>Sphingomonas</i>	3	0.002 ($\pm$ 0.010)	2	0.003 ($\pm$ 0.013)	NI	NI	1	0.002 ($\pm$ 0.009)
Actinobacteria	<i>Rhodococcus</i>	3	4.4 E-04 ($\pm$ 2.7 E-03)	3	0.001 ($\pm$ 0.005)	NI	NI	NI	NI
Firmicutes	<i>Anaerococcus</i>	3	7.5 E-04 ($\pm$ 4.2 E-03)	1	2.0 E-04 ($\pm$ 8.6 E-04)	NI	NI	2	0.002 ($\pm$ 0.006)
Firmicutes	<i>Fingoldia</i>	3	1.5 E-04 ($\pm$ 7.3 E-04)	1	1.6 E-04 ($\pm$ 6.9 E-04)	NI	NI	2	2.1 E-04 ($\pm$ 9.1 E-04)
Bacteroidetes	<i>Prevotella_9</i>	3	2.4 E-05 ($\pm$ 1.1 E-04)	2	4.6 E-05 ($\pm$ 1.5 E-04)	NI	NI	1	1.8 E-05 ($\pm$ 8.6 E-05)
Actinobacteria	<i>Mycobacterium</i>	3	3.4 E-05 ($\pm$ 1.6 E-04)	1	4.4 E-05 ($\pm$ 1.9 E-04)	NI	NI	2	4.3 E-05 ($\pm$ 1.8 E-04)
Firmicutes	<i>Lachnoclostridium</i>	3	1.2 E-05 ($\pm$ 5.1 E-05)	2	2.0 E-05 ($\pm$ 6.1 E-05)	NI	NI	1	1.1 E-05 ($\pm$ 5.5 E-05)
Firmicutes	<i>Megasphaera</i>	3	2.0 E-04 ($\pm$ 1.3 E-03)	1	1.4 E-05 ($\pm$ 6.0 E-05)	NI	NI	2	4.3 E-04 ($\pm$ 1.9 E-03)
Patescibacteria	NA	3	1.1 E-05 ($\pm$ 5.5 E-05)	2	1.1 E-05 ($\pm$ 3.4 E-05)	NI	NI	1	1.6 E-05 ($\pm$ 7.7 E-05)
Firmicutes	<i>Stomatobaculum</i>	3	4.7 E-05 ($\pm$ 2.4 E-04)	1	6.7 E-06 ($\pm$ 2.8 E-05)	NI	NI	2	1.0 E-04 ($\pm$ 3.6 E-04)
Firmicutes	<i>Lachnospira</i>	3	1.5 E-05 ($\pm$ 1.0 E-04)	2	2.4 E-06 ($\pm$ 7.2 E-06)	NI	NI	1	3.0 E-05 ($\pm$ 1.5 E-04)
Firmicutes	NA	3	2.4 E-06 ($\pm$ 1.2 E-05)	NI	NI	NI	NI	3	5.3 E-06 ($\pm$ 1.7 E-05)
Proteobacteria	<i>Ochrobactrum</i>	2	0.001 ($\pm$ 0.006)	NI	NI	1	0.004 ($\pm$ 0.012)	1	6.4 E-04 ($\pm$ 3.1 E-03)
Proteobacteria	<i>Rheinheimera</i>	2	1.6 E-04 ($\pm$ 1.2 E-03)	NI	NI	1	7.7 E-04 ($\pm$ 2.6 E-03)	1	6.1 E-06 ($\pm$ 3.0 E-05)
Proteobacteria	NA	2	6.2 E-05 ($\pm$ 4.4 E-04)	1	2.5 E-06 ($\pm$ 1.1 E-05)	1	2.9 E-04 ($\pm$ 9.7 E-04)	NI	NI
Actinobacteria	<i>Corynebacterium</i>	2	7.8 E-05 ($\pm$ 4.6 E-04)	NI	NI	1	2.9 E-04 ($\pm$ 9.6 E-04)	1	4.0 E-05 ($\pm$ 1.9 E-04)
Proteobacteria	<i>Tepidimonas</i>	2	6.4 E-05 ($\pm$ 4.1 E-04)	NI	NI	1	2.7 E-04 ($\pm$ 9.0 E-04)	1	1.8 E-05 ($\pm$ 8.7 E-05)
Proteobacteria	<i>Phyllobacterium</i>	2	7.4 E-06 ($\pm$ 4.2 E-05)	NI	NI	2	3.6 E-05 ($\pm$ 9.0 E-05)	NI	NI
Actinobacteria	<i>Tropheryma</i>	2	1.3 E-05 ($\pm$ 6.6 E-05)	NI	NI	1	3.1 E-05 ($\pm$ 1.0 E-04)	1	1.5 E-05 ($\pm$ 7.2 E-05)
Fusobacteria	NA	2	4.0 E-06 ($\pm$ 2.2 E-05)	NI	NI	1	1.3 E-05 ($\pm$ 4.4 E-05)	1	2.8 E-06 ($\pm$ 1.4 E-05)
Proteobacteria	<i>Erwinia</i>	2	1.9 E-05 ($\pm$ 1.2 E-04)	NI	NI	1	7.2 E-06 ($\pm$ 2.4 E-05)	1	3.8 E-05 ($\pm$ 1.8 E-04)
Proteobacteria	<i>Brevundimonas</i>	2	4.5 E-06 ($\pm$ 2.7 E-05)	1	1.0 E-05 ($\pm$ 4.4 E-05)	1	4.8 E-06 ($\pm$ 1.6 E-05)	NI	NI
Firmicutes	<i>Melissococcus</i>	2	1.6 E-06 ($\pm$ 8.3 E-06)	1	2.5 E-06 ($\pm$ 1.1 E-05)	1	3.7 E-06 ($\pm$ 1.2 E-05)	NI	NI
Proteobacteria	NA	2	1.8 E-06 ($\pm$ 9.6 E-06)	NI	NI	1	3.5 E-06 ($\pm$ 1.2 E-05)	1	2.5 E-06 ($\pm$ 1.2 E-05)
Firmicutes	<i>Clostridium_sensu_stricto_7</i>	2	0.005 ($\pm$ 0.032)	1	4.6 E-04 ($\pm$ 2.0 E-03)	NI	NI	1	0.010 ($\pm$ 0.048)
Proteobacteria	<i>Psychrobacter</i>	2	6.7 E-05 ($\pm$ 4.8 E-04)	1	2.0 E-04 ($\pm$ 8.3 E-04)	NI	NI	1	2.0 E-06 ($\pm$ 9.7 E-06)
Firmicutes	<i>Blautia</i>	2	5.7 E-05 ($\pm$ 4.0 E-04)	2	1.7 E-04 ($\pm$ 6.9 E-04)	NI	NI	NI	NI
Firmicutes	<i>Howardella</i>	2	6.4 E-05 ($\pm$ 3.7 E-04)	1	1.5 E-04 ($\pm$ 6.2 E-04)	NI	NI	1	3.2 E-05 ($\pm$ 1.6 E-04)
Firmicutes	<i>Carnobacterium</i>	2	8.8 E-05 ($\pm$ 4.6 E-04)	1	1.1 E-04 ($\pm$ 4.6 E-04)	NI	NI	1	1.1 E-04 ($\pm$ 5.6 E-04)
Proteobacteria	<i>Legionella</i>	2	2.4 E-05 ($\pm$ 1.7 E-04)	2	7.0 E-05 ($\pm$ 2.9 E-04)	NI	NI	NI	NI
Cyanobacteria	NA	2	1.8 E-05 ($\pm$ 1.0 E-04)	2	5.3 E-05 ($\pm$ 1.8 E-04)	NI	NI	NI	NI
Patescibacteria	NA	2	1.3 E-05 ($\pm$ 7.3 E-05)	2	3.9 E-05 ($\pm$ 1.2 E-04)	NI	NI	NI	NI
Firmicutes	NA	2	9.7 E-06 ($\pm$ 6.6 E-05)	2	2.9 E-05 ($\pm$ 1.1 E-04)	NI	NI	NI	NI
Firmicutes	NA	2	1.1 E-05 ($\pm$ 6.8 E-05)	1	2.7 E-05 ($\pm$ 1.2 E-04)	NI	NI	1	3.3 E-06 ($\pm$ 1.6 E-05)
Firmicutes	<i>Phascolarctobacterium</i>	2	6.8 E-06 ($\pm$ 3.5 E-05)	2	2.0 E-05 ($\pm$ 5.9 E-05)	NI	NI	NI	NI
Firmicutes	<i>Hathewayia</i>	2	5.7 E-04 ($\pm$ 4.1 E-03)	1	1.9 E-05 ($\pm$ 7.9 E-05)	NI	NI	1	0.001 ($\pm$ 0.006)
Actinobacteria	NA	2	4.6 E-06 ($\pm$ 2.8 E-05)	2	1.4 E-05 ($\pm$ 4.8 E-05)	NI	NI	NI	NI
Patescibacteria	NA	2	4.2 E-06 ($\pm$ 2.2 E-05)	1	7.5 E-06 ($\pm$ 3.2 E-05)	NI	NI	1	3.7 E-06 ($\pm$ 1.8 E-05)
Bacteroidetes	<i>Prevotella_2</i>	2	9.8 E-06 ($\pm$ 5.6 E-05)	1	7.4 E-06 ($\pm$ 3.1 E-05)	NI	NI	1	1.6 E-05 ($\pm$ 7.9 E-05)
Bacteroidetes	<i>Alistipes</i>	2	2.2 E-06 ($\pm$ 1.2 E-05)	2	6.5 E-06 ($\pm$ 2.0 E-05)	NI	NI	NI	NI
Firmicutes	<i>Ruminococcaceae_UCG-005</i>	2	2.0 E-06 ($\pm$ 1.0 E-05)	2	5.7 E-06 ($\pm$ 1.8 E-05)	NI	NI	NI	NI
Bacteroidetes	<i>Barnesiella</i>	2	1.6 E-06 ($\pm$ 8.1 E-06)	2	4.7 E-06 ($\pm$ 1.4 E-05)	NI	NI	NI	NI
Firmicutes	<i>Lachnospiraceae_NK4A136_group</i>	2	8.1 E-06 ($\pm$ 4.9 E-05)	1	4.6 E-06 ($\pm$ 1.9 E-05)	NI	NI	1	1.4 E-05 ($\pm$ 7.1 E-05)
Proteobacteria	<i>Sutterella</i>	2	6.6 E-06 ($\pm$ 3.8 E-05)	1	4.5 E-06 ($\pm$ 1.9 E-05)	NI	NI	1	1.1 E-05 ($\pm$ 5.5 E-05)
NA	NA	2	3.4 E-06 ($\pm$ 1.8 E-05)	1	4.0 E-06 ($\pm$ 1.7 E-05)	NI	NI	1	4.6 E-06 ($\pm$ 2.3 E-05)
Firmicutes	<i>Mogibacterium</i>	2	2.7 E-06 ($\pm$ 1.4 E-05)	1	3.6 E-06 ($\pm$ 1.5 E-05)	NI	NI	1	3.3 E-06 ($\pm$ 1.6 E-05)

Phylum	Genus	All		Negative		Low-positive		High-positive	
		Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)
Firmicutes	<i>Solobacterium</i>	2	2.2 E-06 ($\pm$ 1.1 E-05)	1	2.7 E-06 ($\pm$ 1.1 E-05)	NI	NI	1	2.8 E-06 ($\pm$ 1.4 E-05)
Actinobacteria	NA	2	1.3 E-06 ($\pm$ 7.5 E-06)	1	8.9 E-07 ($\pm$ 3.8 E-06)	NI	NI	1	2.2 E-06 ($\pm$ 1.1 E-05)
Proteobacteria	<i>Atlantibacter</i>	2	7.8 E-07 ($\pm$ 4.1 E-06)	1	8.9 E-07 ($\pm$ 3.8 E-06)	NI	NI	1	1.1 E-06 ($\pm$ 5.2 E-06)
Proteobacteria	<i>Mesorhizobium</i>	2	0.003 ($\pm$ 0.024)	NI	NI	NI	NI	2	0.007 ($\pm$ 0.036)
Firmicutes	<i>Oribacterium</i>	2	2.0 E-05 ($\pm$ 1.0 E-04)	NI	NI	NI	NI	2	4.4 E-05 ($\pm$ 1.5 E-04)
Firmicutes	<i>Weissella</i>	2	5.7 E-06 ($\pm$ 3.3 E-05)	NI	NI	NI	NI	2	1.3 E-05 ($\pm$ 4.9 E-05)
Proteobacteria	<i>Cellvibrio</i>	1	5.9 E-04 ($\pm$ 4.3 E-03)	NI	NI	1	0.003 ($\pm$ 0.009)	NI	NI
Proteobacteria	<i>Bacteriovorax</i>	1	1.2 E-04 ($\pm$ 8.4 E-04)	NI	NI	1	5.6 E-04 ($\pm$ 1.8 E-03)	NI	NI
Proteobacteria	<i>Shinella</i>	1	8.3 E-05 ($\pm$ 6.1 E-04)	NI	NI	1	4.0 E-04 ($\pm$ 1.3 E-03)	NI	NI
Bacteroidetes	NA	1	6.5 E-05 ($\pm$ 4.7 E-04)	NI	NI	1	3.1 E-04 ($\pm$ 1.0 E-03)	NI	NI
Proteobacteria	NA	1	4.9 E-05 ($\pm$ 3.6 E-04)	NI	NI	1	2.4 E-04 ($\pm$ 7.9 E-04)	NI	NI
Proteobacteria	NA	1	3.8 E-05 ($\pm$ 2.7 E-04)	NI	NI	1	1.8 E-04 ($\pm$ 6.0 E-04)	NI	NI
Proteobacteria	<i>Aquaspirillum</i>	1	3.7 E-05 ($\pm$ 2.7 E-04)	NI	NI	1	1.8 E-04 ($\pm$ 5.9 E-04)	NI	NI
Bacteroidetes	NA	1	2.8 E-05 ($\pm$ 2.0 E-04)	NI	NI	1	1.3 E-04 ($\pm$ 4.5 E-04)	NI	NI
Proteobacteria	<i>Pseudochrobactrum</i>	1	2.4 E-05 ($\pm$ 1.7 E-04)	NI	NI	1	1.1 E-04 ($\pm$ 3.8 E-04)	NI	NI
Proteobacteria	<i>Aquabacterium</i>	1	1.6 E-05 ($\pm$ 1.1 E-04)	NI	NI	1	7.6 E-05 ($\pm$ 2.5 E-04)	NI	NI
Bacteroidetes	<i>Tannerella</i>	1	1.5 E-05 ($\pm$ 1.1 E-04)	NI	NI	1	7.1 E-05 ($\pm$ 2.3 E-04)	NI	NI
Verrucomicrobia	<i>Prostheobacter</i>	1	8.2 E-06 ($\pm$ 6.0 E-05)	NI	NI	1	3.9 E-05 ($\pm$ 1.3 E-04)	NI	NI
Firmicutes	<i>Asaccharospora</i>	1	2.7 E-06 ($\pm$ 2.0 E-05)	NI	NI	1	1.3 E-05 ($\pm$ 4.4 E-05)	NI	NI
Proteobacteria	<i>Bdellovibrio</i>	1	2.7 E-06 ($\pm$ 2.0 E-05)	NI	NI	1	1.3 E-05 ($\pm$ 4.4 E-05)	NI	NI
Actinobacteria	<i>Luteococcus</i>	1	1.5 E-06 ($\pm$ 1.1 E-05)	NI	NI	1	7.1 E-06 ($\pm$ 2.3 E-05)	NI	NI
Bacteroidetes	<i>Soonwooa</i>	1	1.4 E-06 ($\pm$ 9.9 E-06)	NI	NI	1	6.6 E-06 ($\pm$ 2.2 E-05)	NI	NI
Firmicutes	<i>Lachnospiraceae_ND3007_group</i>	1	1.3 E-06 ($\pm$ 9.6 E-06)	NI	NI	1	6.3 E-06 ($\pm$ 2.1 E-05)	NI	NI
Proteobacteria	NA	1	1.2 E-06 ($\pm$ 8.8 E-06)	NI	NI	1	5.8 E-06 ($\pm$ 1.9 E-05)	NI	NI
Firmicutes	<i>Helcococcus</i>	1	7.7 E-07 ($\pm$ 5.6 E-06)	NI	NI	1	3.7 E-06 ($\pm$ 1.2 E-05)	NI	NI
Actinobacteria	NA	1	7.5 E-07 ($\pm$ 5.5 E-06)	NI	NI	1	3.6 E-06 ($\pm$ 1.2 E-05)	NI	NI
Bacteroidetes	<i>Prevotellaceae_YAB2003_group</i>	1	6.6 E-07 ($\pm$ 4.8 E-06)	NI	NI	1	3.2 E-06 ($\pm$ 1.1 E-05)	NI	NI
Proteobacteria	NA	1	6.6 E-07 ($\pm$ 4.8 E-06)	NI	NI	1	3.2 E-06 ($\pm$ 1.1 E-05)	NI	NI
Cyanobacteria	<i>Leptolyngbya_Es-Yyy1000</i>	1	0.004 ($\pm$ 0.030)	1	0.01 ($\pm$ 0.05)	NI	NI	NI	NI
Armatimonadetes	NA	1	4.7 E-04 ($\pm$ 3.4 E-03)	1	0.001 ($\pm$ 0.006)	NI	NI	NI	NI
Actinobacteria	<i>Micrococcus</i>	1	4.5 E-04 ($\pm$ 3.3 E-03)	1	0.001 ($\pm$ 0.006)	NI	NI	NI	NI
Proteobacteria	<i>Aggregatibacter</i>	1	7.3 E-05 ($\pm$ 5.3 E-04)	1	2.1 E-04 ($\pm$ 9.1 E-04)	NI	NI	NI	NI
Proteobacteria	<i>Burkholderia-Caballeronia-Paraburkholderia</i>	1	5.9 E-05 ($\pm$ 4.3 E-04)	1	1.7 E-04 ($\pm$ 7.4 E-04)	NI	NI	NI	NI
Firmicutes	<i>Aeribacillus</i>	1	4.9 E-05 ($\pm$ 3.5 E-04)	1	1.4 E-04 ($\pm$ 6.1 E-04)	NI	NI	NI	NI
Firmicutes	<i>Anoxybacillus</i>	1	3.6 E-05 ($\pm$ 2.6 E-04)	1	1.1 E-04 ($\pm$ 4.5 E-04)	NI	NI	NI	NI
Firmicutes	<i>Faecalitalea</i>	1	2.0 E-05 ($\pm$ 1.4 E-04)	1	5.8 E-05 ($\pm$ 2.5 E-04)	NI	NI	NI	NI
Proteobacteria	<i>Massilia</i>	1	1.9 E-05 ($\pm$ 1.4 E-04)	1	5.6 E-05 ($\pm$ 2.4 E-04)	NI	NI	NI	NI
Actinobacteria	<i>Blastococcus</i>	1	1.2 E-05 ($\pm$ 9.1 E-05)	1	3.7 E-05 ($\pm$ 1.6 E-04)	NI	NI	NI	NI
Firmicutes	<i>Abiotrophia</i>	1	9.1 E-06 ($\pm$ 6.6 E-05)	1	2.7 E-05 ($\pm$ 1.1 E-04)	NI	NI	NI	NI
Proteobacteria	<i>Sandaracinus</i>	1	8.6 E-06 ($\pm$ 6.3 E-05)	1	2.5 E-05 ($\pm$ 1.1 E-04)	NI	NI	NI	NI
Proteobacteria	<i>Parvibaculum</i>	1	7.6 E-06 ($\pm$ 5.6 E-05)	1	2.2 E-05 ($\pm$ 9.5 E-05)	NI	NI	NI	NI
Bacteroidetes	<i>Capnocytophaga</i>	1	7.1 E-06 ($\pm$ 5.2 E-05)	1	2.1 E-05 ($\pm$ 8.9 E-05)	NI	NI	NI	NI
Bacteroidetes	NA	1	6.7 E-06 ($\pm$ 4.9 E-05)	1	2.0 E-05 ($\pm$ 8.4 E-05)	NI	NI	NI	NI
Proteobacteria	NA	1	5.1 E-06 ($\pm$ 3.7 E-05)	1	1.5 E-05 ($\pm$ 6.4 E-05)	NI	NI	NI	NI
Proteobacteria	<i>Kluyvera</i>	1	5.1 E-06 ($\pm$ 3.7 E-05)	1	1.5 E-05 ($\pm$ 6.4 E-05)	NI	NI	NI	NI
Planctomycetes	<i>Pir4_lineage</i>	1	4.8 E-06 ($\pm$ 3.5 E-05)	1	1.4 E-05 ($\pm$ 5.9 E-05)	NI	NI	NI	NI
Proteobacteria	<i>Caulobacter</i>	1	3.5 E-06 ($\pm$ 2.6 E-05)	1	1.0 E-05 ($\pm$ 4.4 E-05)	NI	NI	NI	NI
Firmicutes	<i>Brochothrix</i>	1	1.8 E-06 ($\pm$ 1.3 E-05)	1	5.2 E-06 ($\pm$ 2.2 E-05)	NI	NI	NI	NI

Phylum	Genus	All		Negative		Low-positive		High-positive	
		Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)	Prevalence	Mean ($\pm$ SD)
Firmicutes	<i>Pediococcus</i>	1	1.3 E-06 ($\pm$ 9.1 E-06)	1	3.7 E-06 ($\pm$ 1.6 E-05)	NI	NI	NI	NI
Actinobacteria	<i>Galbitalea</i>	1	1.2 E-06 ($\pm$ 8.8 E-06)	1	3.6 E-06 ($\pm$ 1.5 E-05)	NI	NI	NI	NI
Proteobacteria	<i>Variovorax</i>	1	1.2 E-06 ($\pm$ 8.6 E-06)	1	3.5 E-06 ($\pm$ 1.5 E-05)	NI	NI	NI	NI
Actinobacteria	NA	1	1.1 E-06 ($\pm$ 8.0 E-06)	1	3.2 E-06 ($\pm$ 1.4 E-05)	NI	NI	NI	NI
Firmicutes	<i>Oscillibacter</i>	1	8.4 E-07 ($\pm$ 6.1 E-06)	1	2.5 E-06 ($\pm$ 1.1 E-05)	NI	NI	NI	NI
Proteobacteria	<i>Enterobacillus</i>	1	7.7 E-07 ($\pm$ 5.6 E-06)	1	2.3 E-06 ($\pm$ 9.6 E-06)	NI	NI	NI	NI
Firmicutes	<i>Centipeda</i>	1	6.0 E-07 ($\pm$ 4.4 E-06)	1	1.8 E-06 ($\pm$ 7.5 E-06)	NI	NI	NI	NI
Verrucomicrobia	<i>Akkermansia</i>	1	5.0 E-07 ($\pm$ 3.7 E-06)	1	1.5 E-06 ($\pm$ 6.3 E-06)	NI	NI	NI	NI
Actinobacteria	<i>Actinomadura</i>	1	4.5 E-07 ($\pm$ 3.3 E-06)	1	1.3 E-06 ($\pm$ 5.7 E-06)	NI	NI	NI	NI
Bacteroidetes	<i>Butyrlicimonas</i>	1	3.5 E-07 ($\pm$ 2.5 E-06)	1	1.0 E-06 ($\pm$ 4.3 E-06)	NI	NI	NI	NI
Bacteroidetes	NA	1	3.0 E-07 ($\pm$ 2.2 E-06)	1	8.9 E-07 ($\pm$ 3.8 E-06)	NI	NI	NI	NI
Bacteroidetes	NA	1	3.0 E-07 ($\pm$ 2.2 E-06)	1	8.9 E-07 ($\pm$ 3.8 E-06)	NI	NI	NI	NI
Proteobacteria	<i>Bordetella</i>	1	0.002 ($\pm$ 0.012)	NI	NI	NI	NI	1	0.004 ($\pm$ 0.017)
Actinobacteria	<i>Microbacterium</i>	1	3.5 E-04 ($\pm$ 2.5 E-03)	NI	NI	NI	NI	1	7.6 E-04 ($\pm$ 3.7 E-03)
Proteobacteria	<i>Diaphorobacter</i>	1	7.0 E-05 ($\pm$ 5.1 E-04)	NI	NI	NI	NI	1	1.5 E-04 ($\pm$ 7.5 E-04)
Proteobacteria	<i>Sphingobium</i>	1	3.1 E-05 ($\pm$ 2.2 E-04)	NI	NI	NI	NI	1	6.7 E-05 ($\pm$ 3.3 E-04)
Firmicutes	<i>Selenomonas_3</i>	1	2.0 E-05 ($\pm$ 1.4 E-04)	NI	NI	NI	NI	1	4.3 E-05 ($\pm$ 2.1 E-04)
Firmicutes	<i>Erysipelotrichaceae_UCG-003</i>	1	1.6 E-05 ($\pm$ 1.2 E-04)	NI	NI	NI	NI	1	3.5 E-05 ($\pm$ 1.7 E-04)
Firmicutes	<i>Coprococcus_2</i>	1	1.5 E-05 ($\pm$ 1.1 E-04)	NI	NI	NI	NI	1	3.2 E-05 ($\pm$ 1.6 E-04)
Actinobacteria	<i>Renibacterium</i>	1	9.9 E-06 ($\pm$ 7.2 E-05)	NI	NI	NI	NI	1	2.2 E-05 ($\pm$ 1.1 E-04)
Firmicutes	<i>Fusicatenibacter</i>	1	9.4 E-06 ($\pm$ 6.9 E-05)	NI	NI	NI	NI	1	2.1 E-05 ($\pm$ 1.0 E-04)
Firmicutes	<i>Lachnospiraceae_UCG-004</i>	1	8.7 E-06 ($\pm$ 6.3 E-05)	NI	NI	NI	NI	1	1.9 E-05 ($\pm$ 9.4 E-05)
Bacteroidetes	<i>Fluviicola</i>	1	7.1 E-06 ($\pm$ 5.1 E-05)	NI	NI	NI	NI	1	1.6 E-05 ($\pm$ 7.6 E-05)
Actinobacteria	<i>Collinsella</i>	1	6.5 E-06 ($\pm$ 4.8 E-05)	NI	NI	NI	NI	1	1.4 E-05 ($\pm$ 7.1 E-05)
Firmicutes	<i>Acidaminococcus</i>	1	5.8 E-06 ($\pm$ 4.2 E-05)	NI	NI	NI	NI	1	1.3 E-05 ($\pm$ 6.3 E-05)
Firmicutes	<i>Christensenellaceae_R-7_group</i>	1	5.1 E-06 ($\pm$ 3.7 E-05)	NI	NI	NI	NI	1	1.1 E-05 ($\pm$ 5.5 E-05)
Firmicutes	<i>Anthococcus</i>	1	4.7 E-06 ($\pm$ 3.4 E-05)	NI	NI	NI	NI	1	1.0 E-05 ($\pm$ 5.1 E-05)
Firmicutes	<i>Ruminococcaceae_NK4A214_group</i>	1	2.9 E-06 ($\pm$ 2.1 E-05)	NI	NI	NI	NI	1	6.4 E-06 ($\pm$ 3.1 E-05)
Proteobacteria	<i>Paracoccus</i>	1	2.7 E-06 ($\pm$ 2.0 E-05)	NI	NI	NI	NI	1	5.9 E-06 ($\pm$ 2.9 E-05)
Firmicutes	NA	1	2.5 E-06 ($\pm$ 1.8 E-05)	NI	NI	NI	NI	1	5.5 E-06 ($\pm$ 2.7 E-05)
Bacteroidetes	NA	1	2.5 E-06 ($\pm$ 1.8 E-05)	NI	NI	NI	NI	1	5.5 E-06 ($\pm$ 2.7 E-05)
Bacteroidetes	<i>Paraprevotella</i>	1	2.2 E-06 ($\pm$ 1.6 E-05)	NI	NI	NI	NI	1	4.8 E-06 ($\pm$ 2.4 E-05)
Firmicutes	<i>Selenomonas</i>	1	2.0 E-06 ($\pm$ 1.4 E-05)	NI	NI	NI	NI	1	4.4 E-06 ($\pm$ 2.1 E-05)
Firmicutes	<i>Clostridium_sensu_stricto_14</i>	1	1.8 E-06 ($\pm$ 1.3 E-05)	NI	NI	NI	NI	1	4.0 E-06 ($\pm$ 2.0 E-05)
Tenericutes	<i>Ureaplasma</i>	1	1.7 E-06 ($\pm$ 1.2 E-05)	NI	NI	NI	NI	1	3.7 E-06 ($\pm$ 1.8 E-05)
Firmicutes	<i>Holdemanella</i>	1	1.5 E-06 ($\pm$ 1.1 E-05)	NI	NI	NI	NI	1	3.2 E-06 ($\pm$ 1.6 E-05)
Firmicutes	NA	1	1.2 E-06 ($\pm$ 8.8 E-06)	NI	NI	NI	NI	1	2.7 E-06 ($\pm$ 1.3 E-05)
Proteobacteria	<i>Nissabacter</i>	1	1.1 E-06 ($\pm$ 8.1 E-06)	NI	NI	NI	NI	1	2.5 E-06 ($\pm$ 1.2 E-05)
Firmicutes	NA	1	9.9 E-07 ($\pm$ 7.2 E-06)	NI	NI	NI	NI	1	2.2 E-06 ($\pm$ 1.1 E-05)
Proteobacteria	NA	1	8.9 E-07 ($\pm$ 6.5 E-06)	NI	NI	NI	NI	1	2.0 E-06 ($\pm$ 9.7 E-06)
Firmicutes	NA	1	7.2 E-07 ($\pm$ 5.3 E-06)	NI	NI	NI	NI	1	1.6 E-06 ($\pm$ 7.8 E-06)
Proteobacteria	NA	1	6.0 E-07 ($\pm$ 4.3 E-06)	NI	NI	NI	NI	1	1.3 E-06 ($\pm$ 6.4 E-06)
Proteobacteria	<i>Curvibacter</i>	1	3.2 E-07 ($\pm$ 2.3 E-06)	NI	NI	NI	NI	1	7.1 E-07 ($\pm$ 3.5 E-06)

Figure S1: Composition of microbial communities in lung tissue samples of autopsied infants. Relative abundance of genus-level taxa for fungal (A) and bacterial (B) communities.

A)



B)

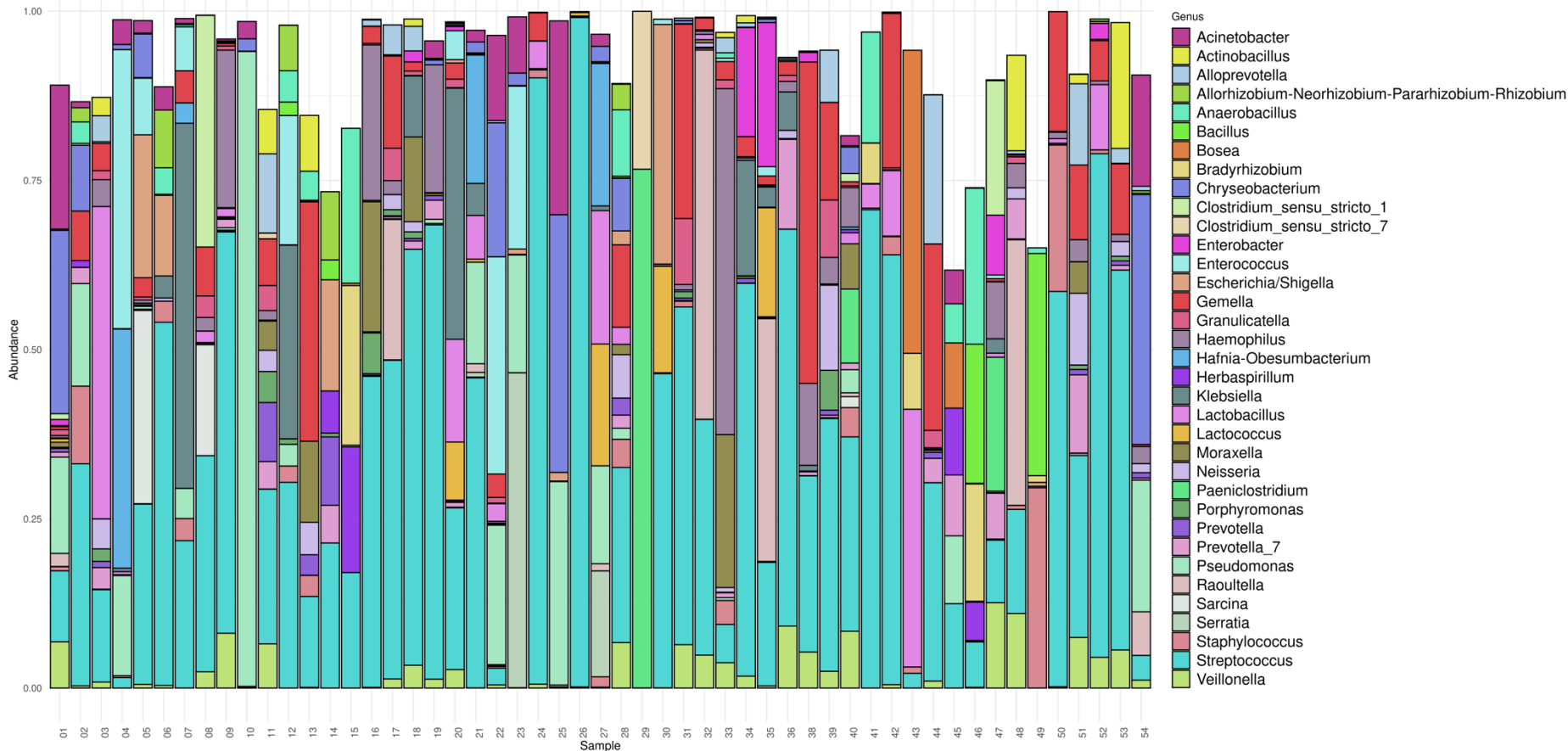


Figure S3: Silhouette plot of the PAM clustering algorithm for $k=1$ to 10, showing results for fungal (A) and bacterial (B) communities. The optimal clustering approach is indicated by the highest silhouette coefficient, which we considered as the best clustering solution.

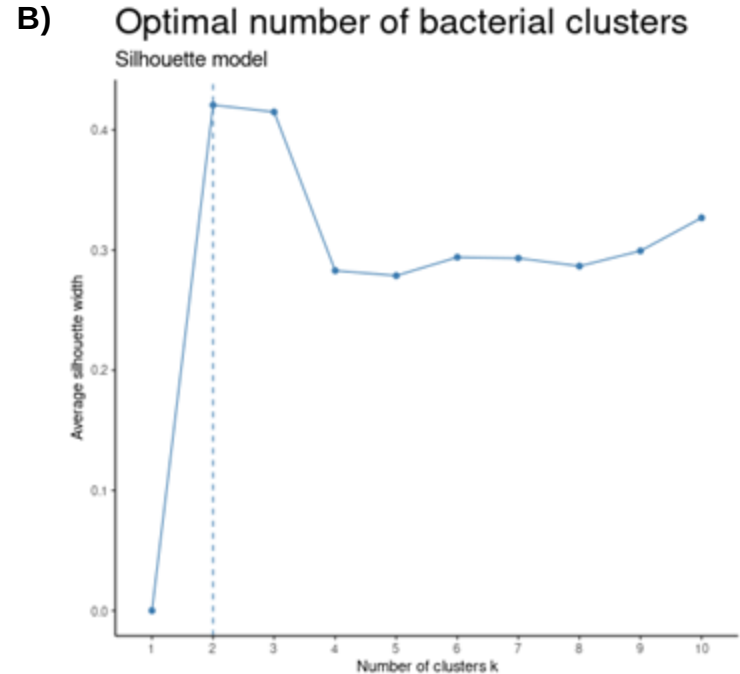
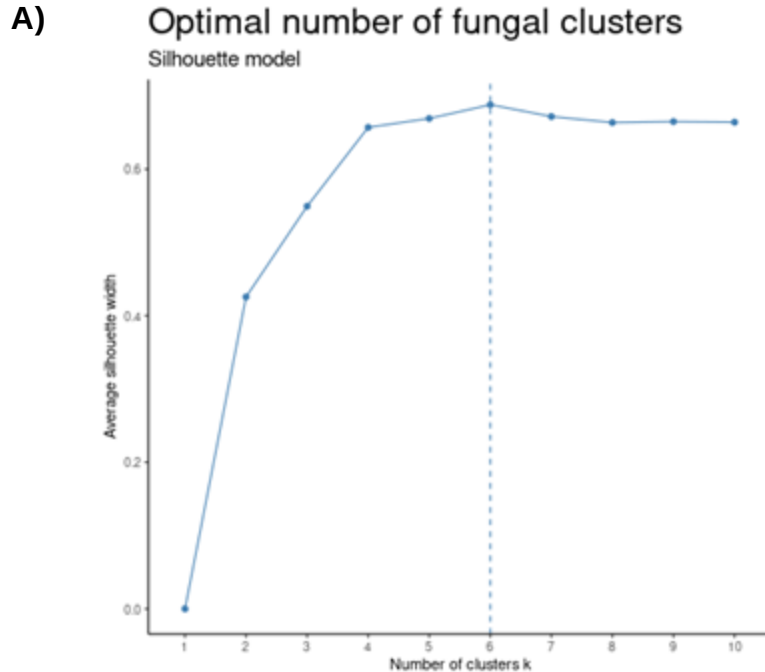


Figure S2: Distribution of individuals across age groups. Children were grouped by age, with infants over 6 months included in the same age class.

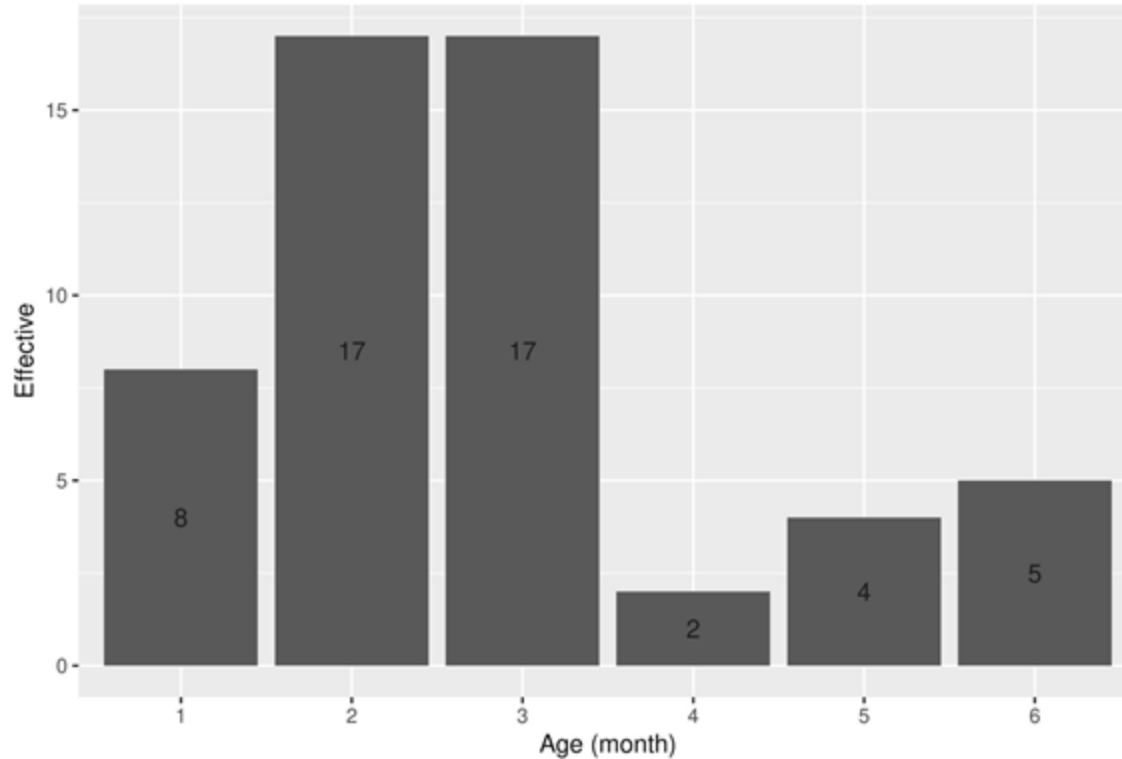
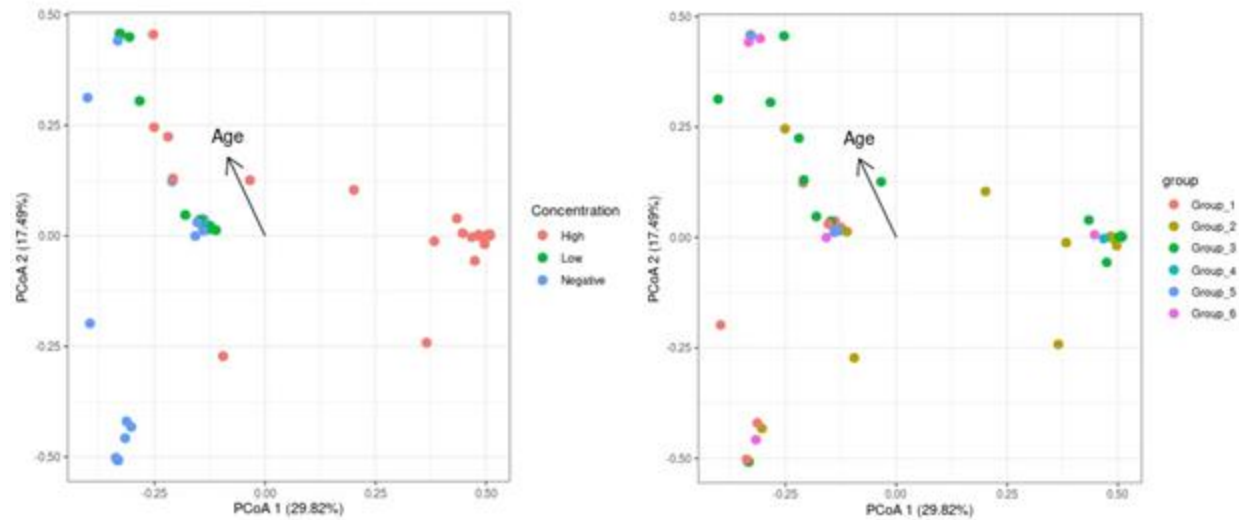


Figure S4: Effect of *Pneumocystis* load and age on fungal communities. The effects of co-variables "*Pneumocystis* load category," "Age category," and "Age" were tested using Principal Coordinates Analysis (PCoA) with the envfit() function from the vegan package (999 permutations). Analyses were performed on the full fungal communities (**A**) and on fungal communities depleted of *Pneumocystis* reads (**B**). Results from each envfit() analysis are presented in the tables. P-values < 0.05 (after Bonferroni correction) were considered statistically significant. Arrows indicate the contribution of continuous age values to the differences observed in the fungal communities. Color-coded symbols represent either the "Age category" or the "*Pneumocystis* load category." For "Age category," "Group_1" corresponds to infants aged 1 month, "Group_2" to those aged 2 months, "Group_3" to those aged 3 months, "Group_4" to those aged 4 months, "Group_5" to those aged 5 months, and "Group_6" to infants to infants aged 6 months and older (See the **Supplementary Figure S2** for the sample size at each age). For "*Pneumocystis* load category," "High" corresponds to lung tissue samples with a Ct value < 36 (High-PositiveCt), "Low" to samples with a Ct value $\geq$ 36 (Low-PositiveCt), and "Negative" to samples without *Pneumocystis* colonization.

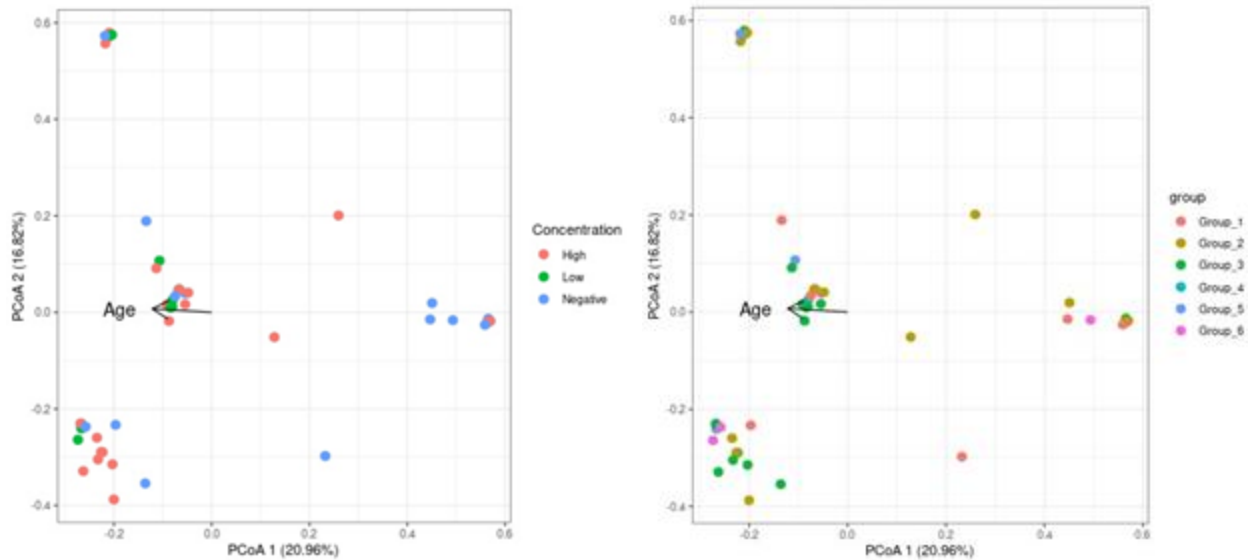
A) PCoA analysis of the effect of co-variables on fungal community



Co-variables		PCoA1 ^a	PCoA2 ^a	R ²	p-value
Pneumocystis load	H-Pc	0.301	0.031	0.480	0.003*
	M-Pc	-0.202	0.170		
	No-Pc	-0.277	-0.145		
Age categories	Group_1	-0.251	-0.177	0.156	0.252
	Group_2	0.071	-0.040		
	Group_3	0.110	0.066		
	Group_4	0.164	0.017		
	Group_5	-0.185	0.127		
	Group_6	-0.133	0.88		
Age		-0.426	0.905	0.039	1.0

^aPCoA, principal coordinate analysis.
*Considered as significant co-variable influencing the microbial community (p < 0.05).

B) PCoA analysis of the effect of co-variables on fungal community structures depleted in Pneumocystis reads



Co-variables		PCoA1 ^a	PCoA2 ^a	R ²	p-value
Pneumocystis load	H-Pc	-0.048	0.008	0.110	0.039*
	M-Pc	-0.173	0.034		
	No-Pc	0.169	-0.032		
Age categories	Group_1	0.167	-0.040	0.139	0.432
	Group_2	0.077	-0.003		
	Group_3	-0.082	-0.048		
	Group_4	-0.146	0.299		
	Group_5	-0.200	0.253		
	Group_6	-0.032	-0.086		
Age		-0.998	0.060	0.015	1.0

^aPCoA, principal coordinate analysis.
*Considered as significant co-variable influencing the microbial community (p < 0.05).