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METAGENOMIC ANALYSIS OF MILK MICROBIOTA IN THE BOVINE SUBCLINICAL MASTITIS

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Abstract

Subclinical mastitis is one of the most widespread diseases affecting dairy herds with detrimental effects on animal health as well as on milk productivity and quality. Despite the multi-factorial nature of this intramammary infection, the presence of pathogenic bacteria is regarded one of the main drivers of subclinical mastitis, leading to a disruption of the homeostasis of the bovine milk microbial community.

However, the bovine milk microbiota alterations associated with subclinical mastitis still represents a largely unexplored research area.

In this context, the species-level milk microbiota of a total of 72 milk samples, collected from both healthy and subclinical mastitis-affected cows from two different stables, was deeply profiled through an ITS, rather than a traditional, and less informative, 16S rRNA gene microbial profiling-based sequencing.

The obtained data of the present study, not only revealed that subclinical mastitis is characterized by a reduced number of species in the bovine milk microbiota, but also that this disease does not induce standard alterations of the milk microbial community across stables.

In addition, a flow cytometry-based total bacterial cell enumeration highlighted that subclinical mastitis is accompanied by a significant increment in the number of milk microbial cells.

Furthermore, the combination of the metagenomic approach and total bacterial cell enumeration allowed to identify different potential microbial marker strictly correlated with subclinical mastitis across stables.

Importance

Although it is widely recognized that the bovine milk microbial community is directly involved in the onset of bovine subclinical mastitis, the microbial ecosystem of the bovine milk associated with this inflammatory disease is still far from being fully dissected.

Here, we investigated the microbial community of bovine milk from healthy and subclinical mastitis-affected cows down to the species-level through an ITS microbial profiling combined with a flow cytometry-based microbial cell enumeration allowing the identification of taxonomical differences in the microbial composition of milk samples from healthy and subclinical mastitis-affected cows, as well as possible microbial biomarkers associated with this silent bovine mammary gland inflammation.

1. Introduction

Bovine mastitis is a worldwide recognized disease affecting dairy cows with devastating impacts on productivity, milk quality, and animal well-being (1-3). Clinically defined as an inflammation of the mammary gland, based on the severity of the symptoms, this disease is classified into clinical or subclinical mastitis (SM), both accompanied by high milk somatic cell count (4, 5).

However, if the former is distinguished by evident physiological alterations, including swelling and inflammation of the mammary gland as well as changes in milk color, consistency, and yield, the latter is characterized by a shortage of visible clinical symptoms, yet a damage in lactation performance, immune function, and alteration of the normal metabolic activities (3, 5-7).

1.1 Subclinical Mastitis

In particular, in SM there is only a significant increase in Somatic Cells in milk that exceed the quantity of 200,000/ml (50) to define the SM in the absence of other alterations visible instead in clinical mastitis.

The Somatic Cells (SCs) of milk are a parameter that is easy and quick to determine and indicate the health status of the udder and hygienic quality of the milk.

In the absence of inflammation, they are represented by flaking cells of the mammary glandular epithelium (0-7%), neutrophilic leukocytes (10%), macrophages (60%) and B and T lymphocytes (30%).

Under normal conditions, with the mammary epithelium intact (tight junction, desmosomes, etc.) the passage of substances from the extracellular matrix to the

alveolar lumen is allowed only by transcellular transport, while in the presence of an inflammatory process the epithelium is damaged and the components present in the interstitium diffuse into the milk, especially polymorphonuclear neutrophils, thus causing an increase in SCs.

Consequently, due to the long latency period and the lack of obvious clinical signs that prevent prompt interventions to limit its spread, SM incidence is significantly higher than that of clinical mastitis, accounting for approximately 90% of bovine mastitis cases (7).

1.2 Microbial agents of mastitis

Furthermore, despite its multi-factorial nature, SM generally occurs as a result of intramammary infection induced by specific pathogenic bacteria that not only trigger inflammation, leading to detrimental effects for both mammary tissue and bovine physiology, but also disrupt the homeostasis of the bovine milk microbial community with a consequent overgrowth of these pathogenic microorganisms and potential risk of their transmission to healthy cows (5, 8-10).

The onset of bovine mastitis is therefore to be found in multi-etiological factors, including several microbial and environmental predisposing agents (3-5): we can speak of an "etiological complex".

As far as microbial agents are concerned, they can be divided into two groups: contagious pathogens and environmental pathogens which usually act separately, but can also cause mixed mastitis.

The contagious pathogens survive exclusively inside the udder or near it and the infection occurs from infected to healthy cow mainly in the milking parlor.

The pre-dipping and post-dipping phases during milking are therefore very important which, if carried out correctly, make it possible to significantly reduce the probability of contagion between infected and healthy cows, as well as having the foresight to milk infected cows last.

The main contagious aetiological agents are *Staphylococcus aureus* which can also survive on the skin and nipple, and causes subclinical but rarely clinical mastitis and is not very sensitive to antibiotic treatment, highly contagious *Streptococcus agalactiae*, which causes contagious catarrhal mastitis, *Mycoplasmas* spp, *Corynebacterium bovis* (*Actinomyces pyogenes*) commensal of the teat tip and associated with suboptimal post-dipping, which causes subclinical infections and therefore high increase of milk SCs and coagulase negative staphylococcus including *S. chromogenens* and *S. epidermidis*.

Environmental pathogens, on the other hand, survive outside the udder and the infection therefore takes place in the environment in which the cows live, especially through the bedding.

They are often associated with faecal contamination, during lactation by retrograde flow due to vacuum fluctuations during milking or by passive penetration into the teat canal immediately after milking, when the sphincter is still patent.

Furthermore, they can also arise during the dry period with infection in the first three weeks and detectable at the beginning of lactation.

The main environmental aetiological agents are *E. coli* which is responsible for clinical mastitis and is often the cause of chronic recurring infections, other Enterobacteriaceae such as *Klebsiella*, *Serratia* and *Citrobacter*, *Streptococcus uberis*

which is the frequent cause of chronic recurring mastitis with properties similar to both contagious pathogens and environmental pathogens, *Streptococcus dysgalactiae* present on skin and tonsils, which survives for a long time in the environment, *Streptococcus fecalis*, *Streptococcus mitis*, *Nocardia* spp., *Pseudomonas aeruginosa*, Yeasts and *Prototheca*.

1.3 Metagenomic approach

However, despite the relevant role played by bacteria in SM etiology, the milk microbial composition associated to this clinical status is still far from being completely dissected.

Indeed, most of publicly available metagenomic studies only employed 16S rRNA gene microbial profiling-based sequencing, thus preventing an accurate and complete characterization of the bovine milk microbiota associated to SM down to the species level (3, 6, 7, 11, 12).

At the same time, studies limited to culture-dependent investigations, despite being able to identify the presence of underrepresented pathogenic microorganisms in subclinical bovine milk whose detection can escape metagenomics due to the intrinsic limit of this molecular approach (13), do not allow to obtain an accurate overview of how the milk microbiota can change during SM (14-16).

In this context, to evaluate possible species-level alterations of bovine milk microbial composition due to SM, a total of 72 milk samples, subdivided into 38 and 34 milk samples from healthy and SM-affected cows, respectively, were collected from two different stables.

Subsequently, samples were simultaneously subjected to an Internally Transcribed Spacer (ITS) microbial profiling sequencing and to a flow cytometry-based total bacterial cell enumeration.

The analysis of the microbial profiles revealed that environmental factors play a crucial role in modulating the taxonomic composition of milk microbiota and, therefore, to avoid biases related to environmental factors, samples were analyzed separately based on their stable of origin.

In this context, the comparison of milk microbial community between healthy and diseased cows from the two stables highlighted that SM does not induce unique alterations in the bovine milk microbiota, but rather, the microbial modulation seems to be stable-dependent.

In support of this finding, diverse bacterial species have been identified to be associated to SM, and therefore as microbial marker closely associated with subclinical mastitis, including *Corynebacterium bovis*, *Corynebacterium xerosis*, and *Streptococcus uberis*, between the two considered stables.

Furthermore, total bacterial cell enumeration highlighted that SM is strictly associated with a significant increment of the total microbial cells present in the milk samples.

2. Experimental Procedures

2.1 Ethical statement

All the dairy cows involved in this study were reared in commercial private farms and were not subjected to any invasive procedures.

Milk samples used for the analyses were collected during the daily milking procedure in according to the International Committee for Animal Recording procedures (ICAR <https://www.icar.org/index.php/icar-recordingguidelines/>).

2.2 Sample collection and clinical health status screening

Raw milk samples were collected from a total of 72 Italian Fresian dairy cows, divided into 38 healthy cows and 34 cows affected by SM, from two different farms located in the North of Italy (Table S1).

Per each cow, two milk samples were sterilely collected by hand from all milking quarters during the morning milking.

One of the two milk samples of each milking quarter was collected in bronopol tubes for Somatic Cell Count (SCC) analysis.

Before collection, the teat-ends were cleaned and properly disinfected with 70% ethanol, while the first milk jets were discarded.

Furthermore, only milk samples from dairy herds that had not undergone any antibiotic treatment during the two months prior sample collection were included in this study.

Once collected, milk samples were refrigerated and immediately shipped to the laboratory where 50 ml were preserved at -20° C for DNA extraction and flow

cytometry-based cell enumeration, while the other 50 ml in bronopol tubes were stored at 4° C for SCC analysis.

The latter was performed by using the fluoro-optical electronic cell counting methods with Fossomatic7DC™ (Foss, Denmark) and the cut-off value set for the determination of SM was SCC > 200,000 cells/ml, as previously described (16, 17).

Sample collection

For the microbiological diagnosis of mastitis it is important that the sampling of a sterile milk sample is carried out in compliance with hygienic standards in order to minimize all environmental contamination that could alter or invalidate the test (51).

It is therefore necessary to carry out the sampling to be supervised with the PPE necessary for the activities to be carried out, in particular disposable gloves to avoid contaminating the sample.

The sampling was effective in the pre-milking phase.

The organic material present on the surface of the teat was first removed by applying a detergent product and transported with disposable absorbent paper.

Subsequently, the tip of each nipple was carefully disinfected with sterile gauze soaked in 70% ethyl alcohol: first the nipples furthest from the operator and then those closest to avoid contamination with the hands or the nipple sphincter.

Samples were taken in the reverse order: first the nipples closest to the operator and then those furthest away from the operator.

The first jets of milk were removed from each teat and the test tube was then filled up to about ¾ of its volume, tending it at an angle of about 45° which was then closed again without touching the inside of the cap.

Clinical health status screening

The animals to be sampled were chosen on the basis of the number of SCs resulting from the Functional Controls performed each month.

As regards the cows classified as healthy, animals with SCs < 200,000/ml (50) were selected in the functional controls and without administration of antimicrobials in the two months prior to sampling.

Cattle with SM are selected with SCs > 200,000/ml, without signs of ongoing clinical mastitis (50) and without administration of antimicrobials in the two months prior to sampling.

2.3 DNA extraction and microbial ITS profiling

DNA extraction

Raw milk samples were subjected to DNA extraction using the DNeasy PowerFood Microbial Kit (Qiagen, Germany), following the manufacturer's instructions.

The DNeasy PowerFood Microbial Kit is used to isolate high-quality genomic DNA from microorganisms cultured from food according to FDA guidelines (Bacteriological Analytical Manual, Edition 8, Revision A/1998).

The kit combines Inhibitor Removal Technology® (IRT) with reformulated buffers to provide high-quality, inhibitor-free DNA for use in applications including PCR and qPCR.

The milk is pelleted by centrifugation and resuspended in lysis buffer.

The lysed cells are transferred to a bead beating tube containing beads designed for small-cell (microbial) lysis and vortexed using a Vortex Adapter.

After protein and inhibitor-removal steps, the DNA released from the lysed cells is bound to a silica spin filter.

The spin filter is washed, and the DNA is recovered in Solution EB.

ITS microbial profiling analysis

Subsequently, the Internal Transcribed Spacer (ITS) sequences were amplified from extracted DNA.

Internal transcribed spacer (ITS) is the spacer DNA situated between the small-subunit ribosomal RNA (rRNA) and large-subunit rRNA genes in the chromosome.

In bacteria there is a single ITS, located between the 16S and 23S rRNA genes.

During rRNA maturation, ITS pieces are excised and degraded as non-functional by-products of this maturation.

It is amplified thanks to its small size associated to the availability of highly conserved flanking sequences.

It is easy to detect even from small quantities of DNA due to the high copy number of the rRNA clusters.

It has a high degree of variation even between closely related species: this can be explained by the relatively low evolutionary pressure acting on such non-coding spacer sequences.

The amplification occurs using the primer pair UNI_ITS_fw (5' - KRGGRYKAAGTCGTAACAAG-3') and UNI_ITS_rv (5' - TTTTCRYCTTTCCCTCACGG-3'), targeting the entire spacer region between the 16S rRNA and 23 rRNA genes within the rRNA locus, as previously described (18).

Illumina adapter overhang nucleotide sequences were added to the ITS amplicons, which were further processed using the 16S Metagenomic Sequencing Library Preparation Protocol (Part No. 15044223 Rev. B – Illumina).

Amplifications were carried out using a Verity Thermocycler (Applied Biosystem, USA).

The integrity of the PCR amplicons was analyzed by gel electrophoresis. DNA products obtained following PCR-mediated amplification of the ITS region sequences were purified by a magnetic purification step employing the Agencourt AMPure XP DNA purification beads (Beckman Coulter Genomics GmbH, Brea, USA), to remove primer dimers. DNA concentration of the amplified sequence library was determined by a fluorometric Qubit quantification system (Life Technologies, USA).

Amplicons were diluted to a final concentration of 4 nM, and 5 μ l of each diluted DNA amplicon sample were mixed to prepare the pooled final library.

Sequencing was performed using an Illumina MiSeq sequencer with MiSeq reagent kit v3 chemicals, using 300 cycles.

After sequencing, the obtained .fastq files were processed using the METAnnotatorX2 pipeline (19). Specifically, paired-end reads were merged, and quality control retained only sequences with a minimum length of 100 bp and a mean sequence quality score of >20.

Sequences with mismatched forward and/or reverse primers were omitted.

Furthermore, sequences were filtered to remove *Bos taurus* DNA.

2.4 Evaluation of bacterial cell density by flow cytometry

The bacterial cell density was evaluated by flow cytometry.

The flow cytometry is a technique used to detect the physico-chemical characteristics of a population of cells so that they can be distinguished and then counted.

The sample containing the cells is suspended in a fluid and the cells are labeled with fluorescent markers so light is absorbed and then emitted at specific wavelengths.

Then, the sample is injected into the flow cytometer and passed one cell at a time through a laser beam, where the light is absorbed by the cells and then emitted at wavelength characteristic of the individual cells and their components, so that they can be differentiated and then counted through computer processing.

For total bacterial cell count, each milk sample was 10,000 diluted in physiological solution (Phosphate Buffered Saline, PBS, pH 6.5).

Subsequently, 1 ml of the obtained bacterial cell suspension was stained with 1 μ l of SYBR Green I (Invitrogen, Waltham, USA) (1:100 diluted in dimethyl sulfoxide), vortex-mixed, and incubated in the dark for at least 15 min before measurement.

All count experiments were performed using an Attune NxT flow cytometry (ThermoFisher Scientific, Waltham, USA) equipped with a blue laser set at 50 mV and tuned at an excitation wavelength of 488 nm.

Multiparametric analyses were performed on both scattering signals, i.e., side scatter and forward scatter, while SYBR Green I fluorescence was detected on the BL1 530/30 nm optical detector.

Cell debris was excluded from acquisition analysis by setting a BL1 threshold.

In addition, to exclude remaining background events and obtain an accurate microbial cell count, the gated fluorescence events were evaluated on the forward-sideways density plot, as previously described (20). All data were statistically analyzed with the Attune NxT flow cytometry software.

2.5 Statistical analyses

Eigenvalue scores were retrieved from a Bray-Curtis dissimilarity matrix based on the taxonomical profiles of samples.

Two-dimensional PCoA representation of eigenvalue scores were carried out using OriginLabPro 2021b. Ellipses in the PCoA were drawn based on standard deviation of each group. The confidence limit for ellipses was set to 0.95.

PERMANOVA statistical analyses were performed using Rstudio software. Furthermore, SPSS software was used to compute the independent Student's T-test statistical analyses.

3. Results and Discussion

3.1 Microbial community of milk from healthy and SM-affected cows

To highlight possible species-level taxonomical differences in the bovine milk microbial community between healthy cows and cows affected by SM, a total of 72 milk samples were collected, divided into 38 milk samples from healthy cattle and 34 milk samples from cows with subclinical mastitis (Table S1).

	Sample	Clinical status	Number of lactation	Day of lactation	Kg of produced milk	Somatic Cell Count (cells/ml)	Diet	Litter
Stable 1	2169	Healthy	5	141	36	29000	75% crop - 25% concentrate	Straw litter
	2195	Healthy	4	117	41	29000	75% crop - 25% concentrate	Straw litter
	2197	Healthy	4	104	38	26000	75% crop - 25% concentrate	Straw litter
	2237	Healthy	4	103	50	32000	75% crop - 25% concentrate	Straw litter
	2439	Healthy	2	216	40	24000	75% crop - 25% concentrate	Straw litter
	2447	Healthy	2	231	30	26000	75% crop - 25% concentrate	Straw litter
	2448	Healthy	2	120	37	42000	75% crop - 25% concentrate	Straw litter
	2477	Healthy	2	194	27	83000	75% crop - 25% concentrate	Straw litter
	2489	Healthy	2	239	50	26000	75% crop - 25% concentrate	Straw litter
	2505	Healthy	2	175	36	43000	75% crop - 25% concentrate	Straw litter
	2509	Healthy	2	121	47	10000	75% crop - 25% concentrate	Straw litter
	2515	Healthy	2	102	38	31000	75% crop - 25% concentrate	Straw litter
	2517	Healthy	2	150	36	21000	75% crop - 25% concentrate	Straw litter
	2518	Healthy	2	152	32	19000	75% crop - 25% concentrate	Straw litter
	2530	Healthy	2	109	39	20000	75% crop - 25% concentrate	Straw litter
	1966	SM	6	26	32	671000	75% crop - 25% concentrate	Straw litter
	1982	SM	5	94	36	13133000	75% crop - 25% concentrate	Straw litter
	2223	SM	4	131	35	585000	75% crop - 25% concentrate	Straw litter
	2224	SM	4	277	22	376000	75% crop - 25% concentrate	Straw litter
	2246	SM	4	20	38	760000	75% crop - 25% concentrate	Straw litter
	2256	SM	4	142	36	435000	75% crop - 25% concentrate	Straw litter
	2362	SM	3	119	40	354000	75% crop - 25% concentrate	Straw litter
	2382	SM	3	157	35	335000	75% crop - 25% concentrate	Straw litter
	2471	SM	2	76	40	794000	75% crop - 25% concentrate	Straw litter
	2478	SM	2	234	37	386000	75% crop - 25% concentrate	Straw litter
	2496	SM	2	104	36	350000	75% crop - 25% concentrate	Straw litter
	2529	SM	2	65	34	1079000	75% crop - 25% concentrate	Straw litter
	2556	SM	2	50	37	681000	75% crop - 25% concentrate	Straw litter

Table S1: Metadata associated to the milk samples collected in Stable 1

	Sample	Clinical status	Number of lactation	Day of lactation	Kg of produced milk	Somatic Cell Count (cells/ml)	Diet	Litter
	5	Healthy	2	149	36	86000	66% crop - 34% concentrate	Bedding sand
	8	Healthy	2	124	35	27000	66% crop - 34% concentrate	Bedding sand
	22	Healthy	2	123	35	26000	66% crop - 34% concentrate	Bedding sand
	72	Healthy	1	251	28	45000	66% crop - 34% concentrate	Bedding sand
	74	Healthy	1	252	27	36000	66% crop - 34% concentrate	Bedding sand
	76	Healthy	1	236	31	27000	66% crop - 34% concentrate	Bedding sand
	77	Healthy	1	208	32	24000	66% crop - 34% concentrate	Bedding sand
	83	Healthy	1	184	33	27000	66% crop - 34% concentrate	Bedding sand
	94	Healthy	1	130	25	63000	66% crop - 34% concentrate	Bedding sand
	95	Healthy	1	150	33	20000	66% crop - 34% concentrate	Bedding sand
	104	Healthy	1	113	32	18000	66% crop - 34% concentrate	Bedding sand
	772	Healthy	4	184	31	33000	66% crop - 34% concentrate	Bedding sand
	895	Healthy	3	211	38	48000	66% crop - 34% concentrate	Bedding sand
	901	Healthy	3	191	43	54000	66% crop - 34% concentrate	Bedding sand
	919	Healthy	2	311	31	52000	66% crop - 34% concentrate	Bedding sand
	950	Healthy	2	234	29	21000	66% crop - 34% concentrate	Bedding sand
	963	Healthy	2	255	26	74000	66% crop - 34% concentrate	Bedding sand
	969	Healthy	2	224	32	45000	66% crop - 34% concentrate	Bedding sand
	972	Healthy	2	190	31	21000	66% crop - 34% concentrate	Bedding sand
	973	Healthy	2	250	30	49000	66% crop - 34% concentrate	Bedding sand
	980	Healthy	2	235	29	21000	66% crop - 34% concentrate	Bedding sand
Stable 2	991	Healthy	2	136	40	33000	66% crop - 34% concentrate	Bedding sand
	993	Healthy	2	157	30	48000	66% crop - 34% concentrate	Bedding sand
	26	SM	2	84	55	324000	66% crop - 34% concentrate	Bedding sand
	30	SM	1	447	15	1031000	66% crop - 34% concentrate	Bedding sand
	38	SM	2	88	29	1228000	66% crop - 34% concentrate	Bedding sand
	44	SM	4	386	28	247000	66% crop - 34% concentrate	Bedding sand
	64	SM	2	297	30	585000	66% crop - 34% concentrate	Bedding sand
	65	SM	2	273	34	322000	66% crop - 34% concentrate	Bedding sand
	108	SM	2	104	32	1382000	66% crop - 34% concentrate	Bedding sand
	120	SM	2	56	47	428000	66% crop - 34% concentrate	Bedding sand
	419	SM	8	44	29	901000	66% crop - 34% concentrate	Bedding sand
	658	SM	5	177	25	7440000	66% crop - 34% concentrate	Bedding sand
	709	SM	5	224	28	4698000	66% crop - 34% concentrate	Bedding sand
	739	SM	4	182	37	259000	66% crop - 34% concentrate	Bedding sand
	764	SM	4	269	21	217000	66% crop - 34% concentrate	Bedding sand
	783	SM	4	272	42	2696000	66% crop - 34% concentrate	Bedding sand
	784	SM	4	295	22	566000	66% crop - 34% concentrate	Bedding sand
	807	SM	3	331	24	1244000	66% crop - 34% concentrate	Bedding sand
	814	SM	4	172	40	276000	66% crop - 34% concentrate	Bedding sand
	840	SM	4	194	31	4107000	66% crop - 34% concentrate	Bedding sand
	877	SM	3	170	30	1807000	66% crop - 34% concentrate	Bedding sand
	924	SM	1	430	16	222000	66% crop - 34% concentrate	Bedding sand
	989	SM	2	195	38	348000	66% crop - 34% concentrate	Bedding sand

Table S1: Metadata associated to the milk samples collected in Stable 2

Sample	Number of produced reads	Number of reads after quality check	Number of reads after <i>Bos taurus</i> filtering
5	34174	26093	25878
8	53183	42109	39765
22	30807	24562	24300
26	24425	21202	20273
30	51301	22868	19542
38	26749	21649	1778
44	43054	31585	31177
64	46831	43987	43800
65	29427	26719	26523
72	30724	29032	28974
74	42798	32931	32493
76	46989	40334	40021
77	32777	23372	22635
83	3817	2825	2813
94	3938	3016	2928
95	53103	51095	51088
104	5823	4309	3770
108	26042	24203	24106
120	41649	36933	36186
419	1917	1218	1098
577	2362	1679	1640
658	2497	1870	1738
709	5902	4427	2767
739	44702	34369	34237
764	39420	35446	32657
772	45883	36770	36029
783	30839	29597	29589
784	37354	32376	32042
807	39050	28533	25017
814	54519	39278	37238
840	19776	18777	18774
895	42663	35177	34225
901	27278	26010	25990
919	17807	14310	14231
924	3525	2557	1644
950	2665	2478	2475
963	6550	5031	4720
969	30864	25024	24566
972	35240	27618	27482
973	19062	15879	14261
980	37758	35264	35160
989	28634	24403	24330
991	41705	35418	34953
993	27927	19376	18692
1966	48425	44509	43857
1982	455970	8841	2329
2169	59688	37238	36686
2195	72109	65127	63233
2197	80212	29481	28493
2223	285856	11526	7358
2224	51432	46978	45748
2237	54589	39323	38849
2246	80028	40009	39080
2256	37887	35316	35120
2362	268334	20609	15823
2382	219303	17621	14410
2439	28809	26232	26219
2447	68979	65073	64821
2448	74926	71322	71137
2471	61187	41046	40496
2477	303202	22091	15905
2478	48361	45935	45863
2489	259782	18896	13589
2496	62593	58379	58122
2505	51708	48886	48707
2509	57452	50966	50791
2515	53152	50429	50093
2517	72884	39434	38543
2518	50855	46030	45967
2529	77042	73993	73980
2530	41132	38098	38068
2556	43473	40017	38920

Table S2: Filtering report related to the milk samples sequenced.

Subsequently, the microbial DNA extracted from each milk sample was subjected to an ITS microbial profiling, as previously described (18).

Illumina sequencing generated a total of 4,342,880 reads with an average of 60,317 reads per sample, reduced to a total of 2,085,812 reads with an average of 28,969 reads per sample after filtering for quality and *Bos taurus* DNA (Table S2).

The species richness analysis revealed that the number of bacterial species present in healthy cow milk is significantly higher than that of the milk collected from cows with SM, with an average number of species of 54 and 35, respectively (Student's T-test p -value < 0.01) (Figure S1a).

Thus, suggesting that subclinical mastitis is characterized by a significant reduction of milk microbial biodiversity, a condition that is frequently encountered in microbial communities associated with various diseases (32864871, 35038617).

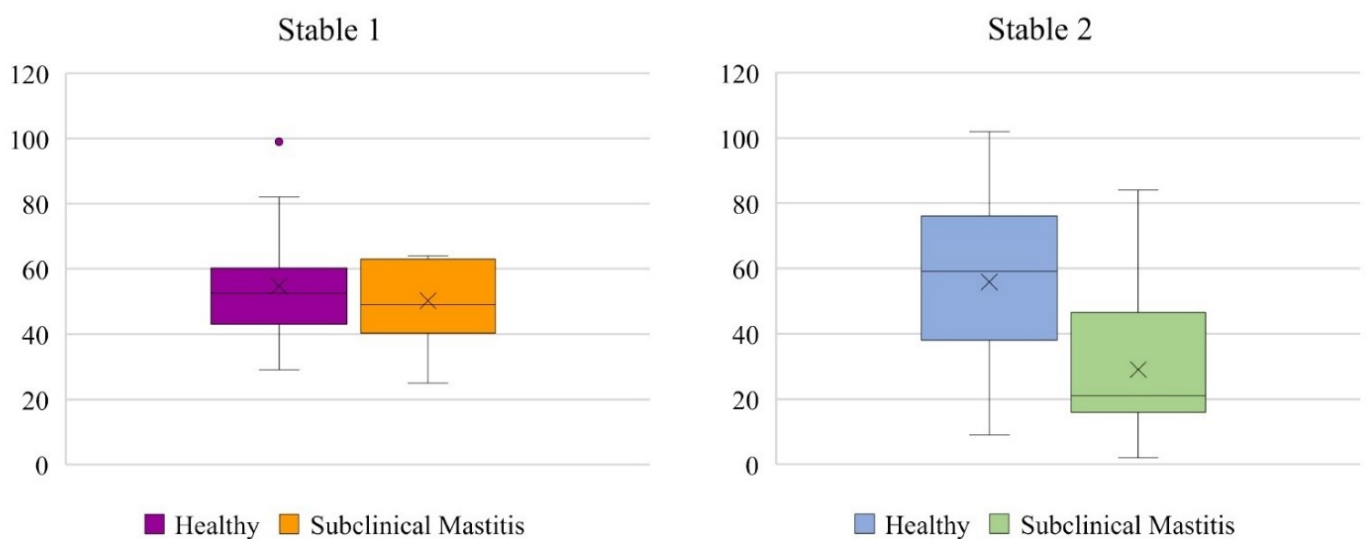


Figure 1.a : Species-level milk microbial biodiversity between healthy and SM-affected cows. Box and whisker plot of the calculated species-richness based on the number of microbial species observed between the two clinical status groups divided per stable. For each box and whisker plot, the x-axis reports the two considered clinical status-based groups, while the y-axis depicts the number of bacterial species. Boxes are determined by the 25th and 75th percentiles. The whiskers are determined by the maximum and minimum values that correspond to the box extreme values. Lines inside the boxers represent the average of the species number, while crosses correspond to the median.

However, a Bray-Curtis dissimilarity-based beta-diversity analysis, represented through a Principal Coordinate Analysis (PCoA), revealed that environmental factors ($R^2 = 0.181$ and PERMANOVA p -value = 0.001), i.e., the different stable from which samples were collected, seemed to have a higher impact on the modulation of milk microbial biodiversity than cow clinical status ($R^2 = 0.038$ and PERMANOVA p -value = 0.003), with a clear separation of samples according to their stable of origin (Figure S1b).

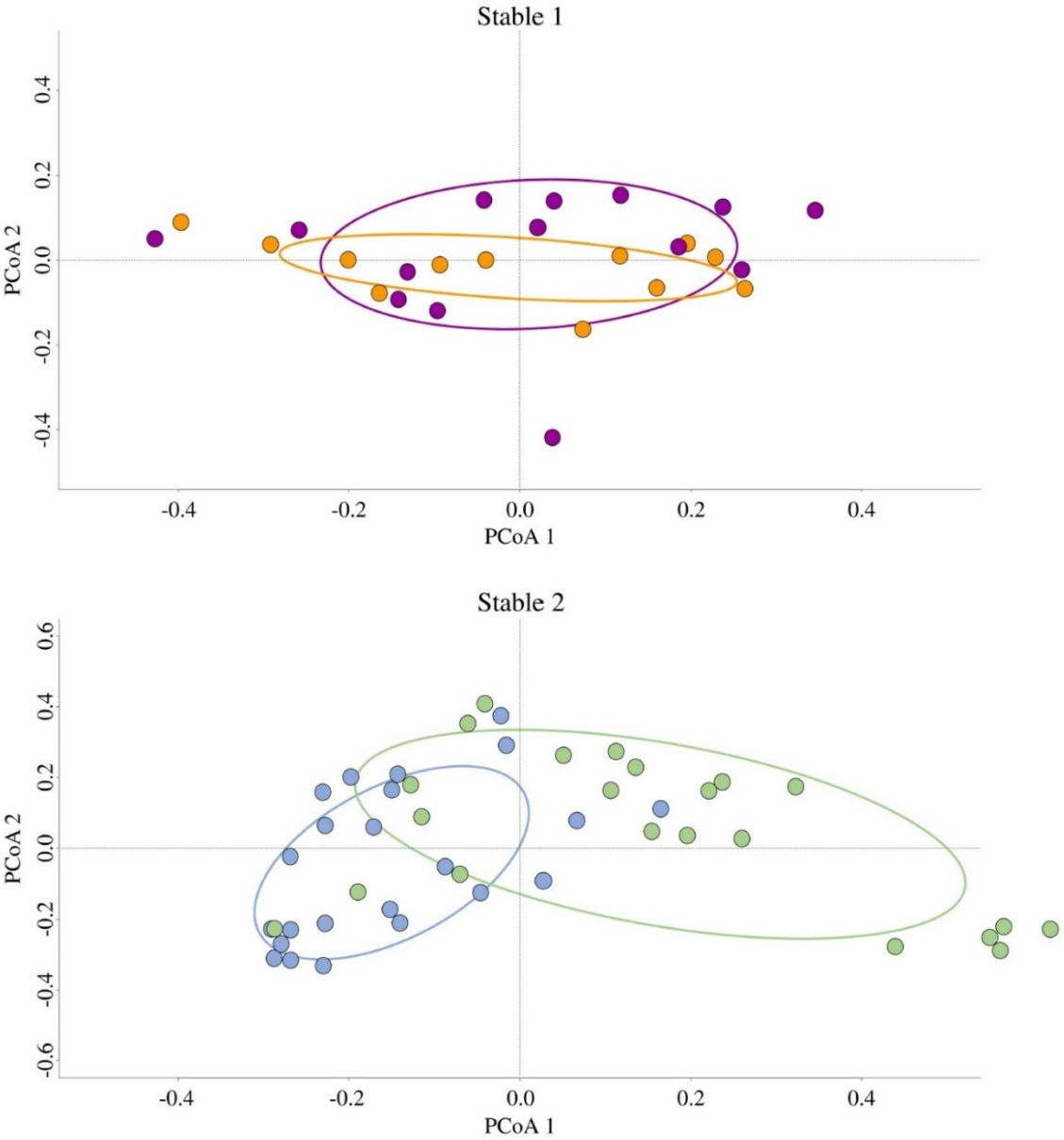


Figure 1.b Two bidimensional Bray-Curtis dissimilarity index-based PCoA of each milk sample divided per stable. The ellipses of the PCoA were drawn based on the standard.

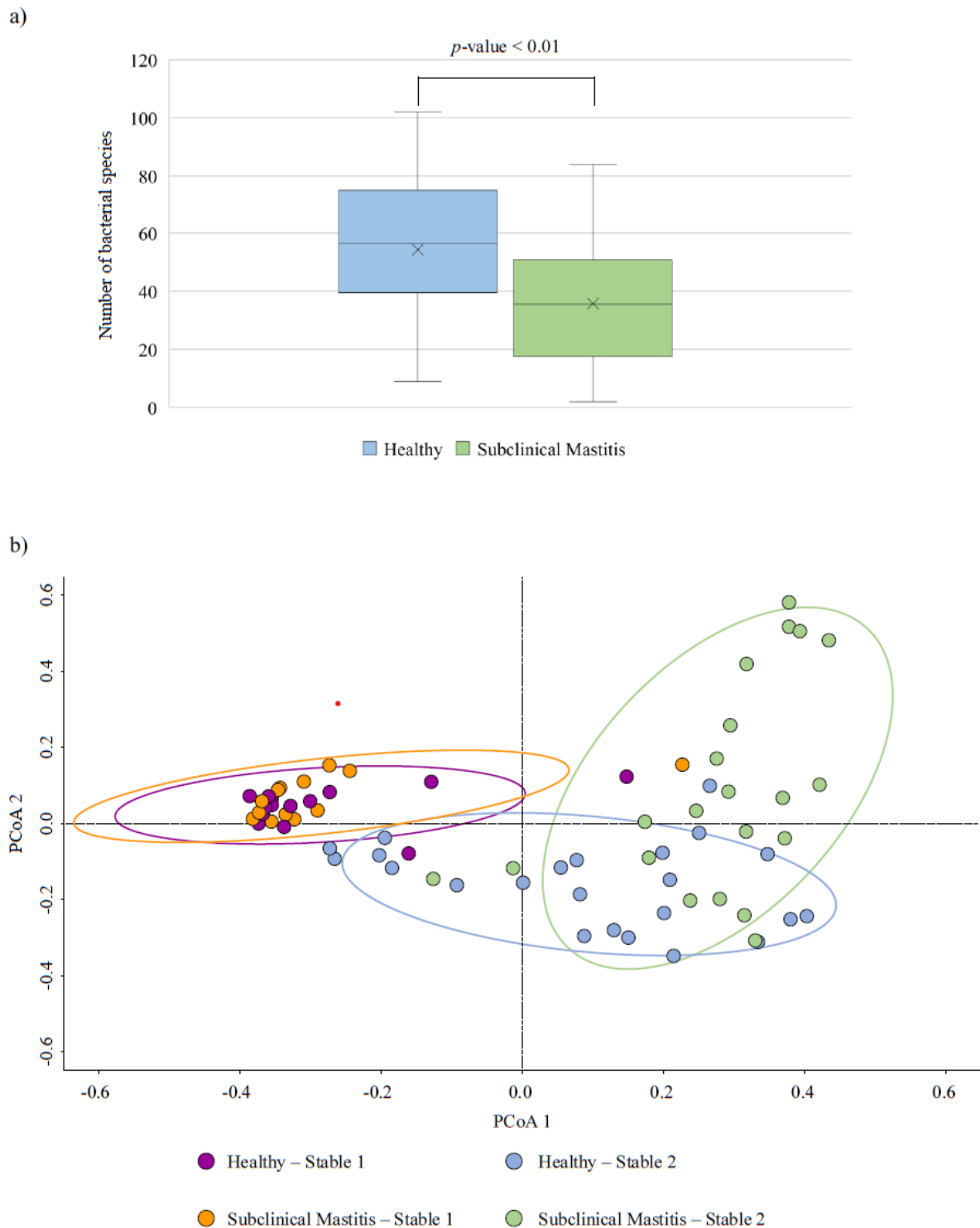


Figure S1 : Differences in milk microbial biodiversity between healthy and SM-affected dairy cows. Panel a shows the box and whisker plot of the calculated species-richness based on the number of microbial species observed between the two clinical status groups. For each box and whisker plot, the x-axis reports the two considered clinical status-based groups, while the y-axis depicts the number of bacterial species. Boxes are determined by the 25th and 75th percentiles. The whiskers are determined by the maximum and minimum values that correspond to the box extreme values. Lines inside the boxers represent the average of the species number, while crosses correspond to the median. Panel b displays the two bidimensional Bray-Curtis dissimilarity index-based PCoA of each collected milk sample. The ellipses of the PCoA were drawn based on the standard deviation of each considered group.

Thus, indicating that different diets, environments, and litters could play a crucial role in the modulation of the bovine milk microbiota regardless of the cow clinical status. Furthermore, the PCoA showed that two samples from stable 1 displayed a microbial taxonomic profile that strongly differed from that of the other samples from the same stable (Figure S1b).

Therefore, they were considered as outliers and eliminated from subsequent analysis.

3.2 Stable-related differences in the taxonomic composition of milk samples between healthy and SM-affected cows

Based on the above findings according to which the exposure to different diet, litters, and breeding management, strongly influenced the milk microbial communities, to avoid biases related to environmental factors, the collected samples were separately analyzed according to their stable of origin to evaluate possible differences in the taxonomic composition of milk samples from healthy and SM-affected cows.

A separation that was possible because, despite the small number of sampled stables, the number of milk samples is balanced between healthy and subclinical mastitis-affected cows within each stable (Table S1).

In this context, the species richness analysis highlighted that only for one of the two stables, i.e., stable 2, the number of bacterial species was significantly higher in the milk samples from healthy cows when compared to that from cows with SM (Student's t-test p-value < 0.001), counting an average number of microbial species of 55 and 29, respectively (Figure 1 and Table S3). However, even if not statistically significant (Student's T-test p-value = 0.482), a slight increase in the average number of

microbial species was observed in healthy cow milk samples from stable 1 respect to the SM-affected cows, passing from an average of 54 to 50 bacterial species, respectively (Figure 1 and Table S3).

	Samples	Number of bacterial species	Clinical Status
Stable 1	2169	49	Healthy
	2195	99	Healthy
	2197	50	Healthy
	2237	47	Healthy
	2447	61	Healthy
	2448	29	Healthy
	2477	82	Healthy
	2489	55	Healthy
	2505	60	Healthy
	2509	40	Healthy
	2515	58	Healthy
	2517	57	Healthy
	2518	35	Healthy
	2530	44	Healthy
	1966	60	Subclinical Matitis
	1982	25	Subclinical Matitis
	2223	50	Subclinical Matitis
	2224	63	Subclinical Matitis
	2246	39	Subclinical Matitis
	2256	47	Subclinical Matitis
	2362	63	Subclinical Matitis
	2382	48	Subclinical Matitis
	2471	37	Subclinical Matitis
	2478	44	Subclinical Matitis
	2496	64	Subclinical Matitis
	2556	63	Subclinical Matitis

Table S3 (Stable 1): Number of bacterial species per milk sample

	Samples	Number of bacterial species	Clinical Status
Stable 2	5	41	Healthy
	8	102	Healthy
	22	57	Healthy
	72	78	Healthy
	74	63	Healthy
	76	63	Healthy
	77	56	Healthy
	83	23	Healthy
	94	9	Healthy
	95	16	Healthy
	104	24	Healthy
	772	91	Healthy
	895	75	Healthy
	901	47	Healthy
	919	59	Healthy
	950	24	Healthy
	963	38	Healthy
	969	74	Healthy
	972	40	Healthy
	973	77	Healthy
	980	75	Healthy
	991	77	Healthy
	993	76	Healthy
	26	84	Subclincial Mastitis
	30	16	Subclincial Mastitis
	38	18	Subclincial Mastitis
	44	47	Subclincial Mastitis
	64	16	Subclincial Mastitis
	65	20	Subclincial Mastitis
	108	26	Subclincial Mastitis
	120	49	Subclincial Mastitis
	419	2	Subclincial Mastitis
	658	15	Subclincial Mastitis
	709	20	Subclincial Mastitis
	739	53	Subclincial Mastitis
764	54	Subclincial Mastitis	
783	16	Subclincial Mastitis	
784	3	Subclincial Mastitis	
807	30	Subclincial Mastitis	
814	34	Subclincial Mastitis	
840	33	Subclincial Mastitis	
877	21	Subclincial Mastitis	
924	7	Subclincial Mastitis	
989	46	Subclincial Mastitis	

Table S3 (Stable 2): Number of bacterial species per milk sample

Thus, strengthening the abovementioned notion that, even if not always statistically significant, SM is characterized by a general reduction of milk microbial biodiversity. In addition, in-depth insights into the microbial biodiversity of milk samples divided per stable and represented through a PCoA highlighted that the SM played a significant role ($R^2 = 0.0894$ and PERMANOVA p -value < 0.001) in the modulation of the taxonomic composition of milk samples 208 from stable 2 with a clear separation of samples according to their clinical status, while the microbial communities of milk samples from stable 1 did not differ in biodiversity between healthy and SM cows ($R^2 = 0.024$ and PERMANOVA p -value = 0.798) (Figure 1).

Thus, suggesting that subclinical mastitis does not always induce a drastic modulation in the taxonomic composition of the milk microbial communities.

Conversely, this finding indicates that, depending on the environmental factors, SM is characterized by a different alteration of the bovine milk-related microbial community biodiversity and species richness.

3.3 SM effects on species-level core milk microbial communities

Reconstruction of the “core” milk microbiota, i.e., the bacterial taxa that are shared across samples of a defined cohort, allows the identification of the most prevalent bacterial species that inhabits the bovine milk (21, 22). In this context, to evaluate the impact that subclinical mastitis may have on the most prevalent milk bacterial species, the “core” microbial community characterizing milk samples from healthy cows was compared to that of milk from SM-affected bovines.

Specifically, only those bacterial taxa with a prevalence $> 80\%$ were considered as part of the “core” milk community, as previously described (23).

Based on this cut-off, 23 bacterial species resulted to be shared between the “core” microbiota of healthy and SM cows from stable 1, with *Aerococcus urinaeequi*, *Jeotgalibaca porci*, *Paraclostridium bifermentans*, *Romboutsia ilealis*, *Turicibacter sanguinis*, *Weissella jogaejeotgali* as well as two not yet identified species belonging to the genera *Romboutsia* and *Turicibacter* as the most abundant “core” taxa (average relative abundance >3%) (Table S4).

Species	Healthy - Stable 1		SM - Stable 1		Healthy - Stable 2		SM - Stable 2	
	Average	Prevalence	Average	Prevalence	Average	Prevalence	Average	Prevalence
<i>Abiotrophia</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,03%	4,35%	0,00%	0,00%
<i>Absicoccus</i> unknown_species	0,02%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Acholeplasma</i> unknown_species	0,39%	35,71%	0,27%	33,33%	0,42%	43,48%	0,04%	14,29%
<i>Achromobacter</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	4,76%
<i>Acinetobacter indicus</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,01%	4,76%
<i>Acinetobacter</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	4,76%
<i>Actinotalea</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Adlercreutzia</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,16%	34,78%	0,02%	4,76%
<i>Aequorivita</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	8,70%	0,01%	4,76%
<i>Aerococcus</i> unknown_species	0,67%	78,57%	0,58%	91,67%	0,68%	56,52%	9,91%	33,33%
<i>Aerococcus urinaeequi</i>	14,72%	100,00%	17,51%	100,00%	0,58%	65,22%	0,27%	38,10%
<i>Aerococcus viridans</i>	0,40%	92,86%	0,50%	83,33%	0,01%	4,35%	0,15%	19,05%
<i>Aeromicrobium</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,03%	17,39%	0,00%	4,76%
<i>Agarilytica</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Agathobaculum</i> unknown_species	0,02%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Akkermansia muciniphila</i>	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Alistipes</i> unknown_species	0,00%	0,00%	0,01%	8,33%	0,01%	4,35%	0,00%	0,00%
<i>Alkaliphilus</i> unknown_species	0,01%	14,29%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Amedibacterium</i> unknown_species	0,00%	0,00%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Aminipila</i> unknown_species	0,06%	28,57%	0,02%	25,00%	0,02%	13,04%	0,02%	9,52%
<i>Anaerobiospirillum</i> unknown_species	0,02%	14,29%	0,00%	0,00%	0,08%	26,09%	0,01%	9,52%
<i>Anaerococcus</i> unknown_species	0,19%	21,43%	0,37%	25,00%	0,00%	0,00%	0,00%	0,00%
<i>Anaerorhabdus</i> unknown_species	0,19%	35,71%	0,05%	25,00%	0,03%	13,04%	0,01%	4,76%
<i>Arcanobacterium</i> unknown_species	0,09%	28,57%	0,02%	8,33%	0,00%	0,00%	0,01%	4,76%
<i>Aromatoleum</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,03%	4,76%
<i>Bacillus aryabhatai</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,01%	4,76%
<i>Bacillus licheniformis</i>	0,03%	7,14%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Bacillus megaterium</i>	0,01%	7,14%	0,01%	8,33%	0,01%	13,04%	0,00%	0,00%
<i>Bacillus subtilis</i>	0,00%	0,00%	0,00%	0,00%	0,04%	13,04%	0,02%	4,76%
<i>Bacillus</i> unknown_species	0,04%	28,57%	0,03%	33,33%	0,16%	69,57%	0,11%	38,10%
<i>Bacillus velezensis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	4,76%
<i>Bacteriovorax</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Beduini</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,04%	8,70%	0,00%	0,00%
<i>Beutenbergia</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Bifidobacterium merycicum</i>	0,09%	21,43%	0,06%	25,00%	0,01%	4,35%	0,00%	0,00%
<i>Bifidobacterium pseudolongum</i>	0,47%	92,86%	0,40%	75,00%	0,14%	26,09%	0,00%	0,00%

<i>Bifidobacterium scardovii</i>	0,00%	0,00%	0,00%	0,00%	0,04%	4,35%	0,00%	4,76%
<i>Bifidobacterium unknown_species</i>	0,02%	7,14%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Bilophila wadsworthia</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	4,76%
<i>Blautia unknown_species</i>	0,02%	21,43%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Brachyбактерium massiliense</i>	0,00%	0,00%	0,00%	0,00%	0,16%	52,17%	0,02%	9,52%
<i>Brachyбактерium unknown_species</i>	0,04%	28,57%	0,02%	16,67%	0,05%	26,09%	0,02%	9,52%
<i>Brevibacterium frigiditolerans</i>	0,00%	0,00%	0,01%	8,33%	1,43%	30,43%	0,31%	14,29%
<i>Brevibacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	8,70%	0,00%	0,00%
<i>Brevilactibacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Bulleidia unknown_species</i>	0,06%	14,29%	0,07%	16,67%	0,00%	0,00%	0,00%	0,00%
<i>Burkholderia stabilis</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	4,76%
<i>Butyricococcus unknown_species</i>	0,04%	21,43%	0,01%	8,33%	0,01%	4,35%	0,01%	4,76%
<i>Carnobacterium unknown_species</i>	0,08%	50,00%	0,15%	83,33%	0,01%	8,70%	0,00%	0,00%
<i>Cecembia unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,10%	52,17%	0,11%	9,52%
<i>Cellulomonas unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Clostridioides difficile</i>	1,73%	100,00%	1,80%	100,00%	1,60%	82,61%	0,38%	57,14%
<i>Clostridioides unknown_species</i>	0,50%	100,00%	0,43%	91,67%	0,50%	86,96%	0,16%	42,86%
<i>Clostridium bornimense</i>	0,00%	0,00%	0,00%	0,00%	0,02%	13,04%	0,00%	0,00%
<i>Clostridium botulinum</i>	0,00%	0,00%	0,00%	0,00%	0,03%	26,09%	0,01%	4,76%
<i>Clostridium perfringens</i>	0,00%	0,00%	0,00%	0,00%	0,03%	4,35%	0,03%	9,52%
<i>Clostridium unknown_species</i>	0,19%	100,00%	0,16%	83,33%	0,21%	65,22%	0,06%	23,81%
<i>Comamonas unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	4,76%
<i>Corynebacterium bovis</i>	0,35%	14,29%	1,60%	58,33%	7,48%	69,57%	2,82%	57,14%
<i>Corynebacterium camporealensis</i>	0,00%	0,00%	0,00%	0,00%	0,06%	13,04%	0,14%	14,29%
<i>Corynebacterium frankenforstense</i>	0,42%	57,14%	0,12%	41,67%	0,00%	0,00%	0,00%	0,00%
<i>Corynebacterium propinquum</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,01%	4,76%
<i>Corynebacterium sanguinis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Corynebacterium unknown_species</i>	1,06%	85,71%	0,79%	91,67%	2,95%	100,00%	3,35%	85,71%
<i>Corynebacterium urealyticum</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,01%	4,76%
<i>Corynebacterium xerosis</i>	0,37%	64,29%	0,44%	75,00%	0,43%	60,87%	0,49%	47,62%
<i>Cutibacterium acnes</i>	0,09%	14,29%	0,04%	16,67%	0,78%	60,87%	1,80%	52,38%
<i>Cutibacterium granulosum</i>	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Cutibacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,03%	13,04%	0,33%	14,29%
<i>Cyclobacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Cytobacillus firmus</i>	0,00%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Cytobacillus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Dehalobacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,01%	4,76%
<i>Demequina unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Dietzia aerolata</i>	0,00%	0,00%	0,00%	0,00%	0,13%	52,17%	0,03%	14,29%
<i>Dietzia unknown_species</i>	0,00%	0,00%	0,01%	8,33%	0,10%	47,83%	0,03%	19,05%
<i>Dolosigranulum unknown_species</i>	0,04%	14,29%	0,09%	16,67%	1,04%	39,13%	1,21%	28,57%
<i>Dubosiella unknown_species</i>	0,02%	7,14%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Dyadobacter unknown_species</i>	0,00%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Eggerthella unknown_species</i>	0,02%	7,14%	0,01%	8,33%	0,00%	4,35%	0,01%	4,76%
<i>Eggerthia unknown_species</i>	0,06%	21,43%	0,03%	16,67%	0,05%	8,70%	0,00%	0,00%
<i>Emergencia unknown_species</i>	0,01%	14,29%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Endozoicomonas unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,02%	8,70%	0,01%	4,76%
<i>Enterobacter asburiae</i>	0,00%	0,00%	0,00%	0,00%	0,03%	13,04%	0,00%	4,76%
<i>Enterobacter bugandensis</i>	0,00%	0,00%	0,00%	0,00%	0,46%	30,43%	0,12%	14,29%
<i>Enterobacter hormaechei</i>	0,00%	0,00%	0,00%	0,00%	0,98%	30,43%	0,26%	14,29%
<i>Enterobacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%

<i>Enterococcus aquimarinus</i>	0,12%	42,86%	0,11%	33,33%	0,33%	26,09%	0,01%	4,76%
<i>Enterococcus casseliflavus</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,02%	4,76%
<i>Enterococcus cecorum</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Enterococcus durans</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,03%	9,52%
<i>Enterococcus faecalis</i>	0,00%	0,00%	0,00%	0,00%	0,06%	8,70%	0,01%	4,76%
<i>Enterococcus faecium</i>	0,01%	7,14%	0,00%	0,00%	0,01%	4,35%	0,01%	4,76%
<i>Enterococcus gallinarum</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,06%	4,76%
<i>Enterococcus hirae</i>	0,06%	7,14%	0,00%	0,00%	0,02%	8,70%	0,00%	0,00%
<i>Enterococcus pseudoavium</i>	0,00%	0,00%	0,01%	8,33%	0,03%	13,04%	0,00%	0,00%
<i>Enterococcus saccharolyticus</i>	0,00%	0,00%	0,00%	0,00%	1,29%	69,57%	2,19%	71,43%
<i>Enterococcus unknown_species</i>	0,29%	92,86%	0,34%	91,67%	1,26%	86,96%	0,12%	33,33%
<i>Entomoplasma unknown_species</i>	0,03%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Escherichia coli</i>	0,04%	21,43%	0,00%	0,00%	0,20%	21,74%	0,51%	23,81%
<i>Escherichia marmotae</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Eubacterium unknown_species</i>	0,00%	0,00%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Exiguobacterium acetylicum</i>	0,00%	0,00%	0,00%	0,00%	0,09%	17,39%	0,01%	4,76%
<i>Exiguobacterium chiriqhucha</i>	0,00%	0,00%	0,00%	0,00%	0,09%	30,43%	0,03%	23,81%
<i>Exiguobacterium indicum</i>	0,00%	0,00%	0,00%	0,00%	0,03%	4,35%	0,00%	0,00%
<i>Exiguobacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,05%	8,70%	0,00%	0,00%
<i>Facklamia unknown_species</i>	0,19%	50,00%	0,25%	58,33%	0,53%	60,87%	0,11%	33,33%
<i>Faecalibacillus intestinalis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Faecalibacillus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,04%	21,74%	0,00%	0,00%
<i>Faecalicoccus unknown_species</i>	0,14%	35,71%	0,01%	8,33%	0,03%	13,04%	0,02%	4,76%
<i>Faecalitalea unknown_species</i>	0,02%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Fenollaria unknown_species</i>	0,00%	0,00%	0,03%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Filifactor unknown_species</i>	0,01%	7,14%	0,03%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Flavobacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,01%	4,76%
<i>Flavonifractor unknown_species</i>	0,03%	14,29%	0,00%	0,00%	0,00%	4,35%	0,00%	4,76%
<i>Frankia coriariae</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Fusobacterium necrophorum</i>	0,11%	21,43%	0,05%	16,67%	0,00%	0,00%	0,00%	0,00%
<i>Fusobacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Gemella unknown_species</i>	0,02%	7,14%	0,00%	0,00%	0,00%	0,00%	0,04%	9,52%
<i>Georgenia unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	8,70%	0,00%	0,00%
<i>Gilliamella unknown_species</i>	0,04%	14,29%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Globicatella sanguinis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Globicatella unknown_species</i>	0,97%	100,00%	1,90%	100,00%	0,53%	73,91%	0,12%	33,33%
<i>Gordonibacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Gottschalkia unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,03%	8,70%	0,00%	0,00%
<i>Gudongella unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Haloactinobacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Haloglycomyces unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Haloplasma unknown_species</i>	0,00%	0,00%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Helcococcus kunzii</i>	0,01%	7,14%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Helcococcus unknown_species</i>	0,06%	14,29%	0,12%	16,67%	0,01%	4,35%	0,87%	4,76%
<i>Holdemania unknown_species</i>	0,12%	42,86%	0,05%	25,00%	0,03%	21,74%	0,03%	14,29%
<i>Hungateiclostridium unknown_species</i>	0,01%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Ilumatobacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	8,70%	0,00%	0,00%
<i>Inediibacterium unknown_species</i>	0,01%	7,14%	0,02%	16,67%	0,00%	0,00%	0,00%	0,00%
<i>Intestinibacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,05%	8,70%	0,00%	0,00%
<i>Intestinibaculum porci</i>	0,01%	7,14%	0,01%	8,33%	0,01%	4,35%	0,00%	0,00%
<i>Intestinibaculum unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%

<i>Intestinimonas</i> unknown_species	0,11%	50,00%	0,03%	25,00%	0,03%	13,04%	0,01%	4,76%
<i>Isoptericola</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,06%	17,39%	0,03%	4,76%
<i>Janibacter</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,37%	65,22%	0,06%	28,57%
<i>Janthinobacterium</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Jeotgalibaca arthritidis</i>	0,07%	35,71%	0,10%	33,33%	0,15%	34,78%	0,04%	19,05%
<i>Jeotgalibaca porci</i>	3,75%	100,00%	3,42%	100,00%	0,82%	73,91%	0,21%	33,33%
<i>Jeotgalibaca</i> unknown_species	0,01%	7,14%	0,03%	16,67%	0,50%	26,09%	0,10%	9,52%
<i>Jeotgalicoccus coquinae</i>	2,06%	100,00%	1,65%	100,00%	0,12%	21,74%	0,06%	19,05%
<i>Jeotgalicoccus saudimassiliensis</i>	0,01%	7,14%	0,00%	0,00%	0,09%	26,09%	0,04%	9,52%
<i>Jeotgalicoccus</i> unknown_species	0,19%	42,86%	0,28%	83,33%	0,22%	47,83%	0,29%	33,33%
<i>Kallipyga</i> unknown_species	0,01%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Klebsiella grimontii</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,02%	4,76%
<i>Klebsiella michiganensis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,38%	14,29%
<i>Klebsiella</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,04%	4,76%
<i>Knoellia sinensis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Kocuria</i> unknown_species	0,04%	35,71%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Kroppenstedtia</i> unknown_species	0,01%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Kurthia huakuii</i>	0,00%	0,00%	0,00%	0,00%	0,05%	13,04%	0,01%	4,76%
<i>Kurthia</i> unknown_species	0,06%	21,43%	0,07%	16,67%	1,72%	82,61%	0,80%	42,86%
<i>Lactobacillus acidipiscis</i>	1,48%	71,43%	1,05%	91,67%	0,00%	0,00%	0,00%	0,00%
<i>Lactobacillus amylovorus</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,13%	9,52%
<i>Lactobacillus crispatus</i>	0,00%	0,00%	0,00%	0,00%	0,10%	17,39%	0,03%	14,29%
<i>Lactobacillus delbrueckii</i>	0,07%	14,29%	0,00%	0,00%	0,14%	4,35%	0,00%	0,00%
<i>Lactobacillus farciminis</i>	0,43%	35,71%	0,40%	33,33%	0,00%	0,00%	0,00%	0,00%
<i>Lactobacillus ginsenosidimitans</i>	0,06%	21,43%	0,02%	16,67%	0,00%	0,00%	0,00%	0,00%
<i>Lactobacillus iners</i>	0,03%	14,29%	0,14%	8,33%	0,08%	8,70%	0,18%	14,29%
<i>Lactobacillus mucosae</i>	0,03%	7,14%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Lactobacillus parabuchneri</i>	0,01%	7,14%	0,00%	0,00%	0,05%	4,35%	0,00%	0,00%
<i>Lactobacillus paracasei</i>	1,05%	14,29%	0,00%	0,00%	2,18%	4,35%	0,00%	0,00%
<i>Lactobacillus reuteri</i>	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Lactobacillus</i> unknown_species	0,37%	64,29%	0,16%	41,67%	0,04%	8,70%	0,03%	4,76%
<i>Lactococcus garvieae</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,02%	4,76%
<i>Lactococcus lactis</i>	0,47%	28,57%	0,01%	8,33%	0,96%	8,70%	0,00%	0,00%
<i>Lactococcus petauri</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	2,72%	4,76%
<i>Lactococcus</i> unknown_species	0,05%	28,57%	0,00%	0,00%	0,02%	4,35%	0,11%	9,52%
<i>Lagierella massiliensis</i>	0,03%	7,14%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Lagierella</i> unknown_species	0,03%	7,14%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Lancefieldella</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Lawsonella</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,04%	4,35%	0,01%	4,76%
<i>Lentibacillus</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	8,70%	0,00%	0,00%
<i>Leptothrix</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Levyella</i> unknown_species	0,14%	42,86%	0,13%	41,67%	0,03%	13,04%	0,00%	0,00%
<i>Longibaculum</i> unknown_species	0,03%	21,43%	0,01%	8,33%	0,15%	34,78%	0,04%	9,52%
<i>Longicatena</i> unknown_species	0,22%	78,57%	0,13%	58,33%	0,12%	26,09%	0,01%	4,76%
<i>Longimicrobium</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Luteimonas arsenica</i>	0,00%	0,00%	0,00%	0,00%	0,02%	8,70%	0,01%	4,76%
<i>Luteimonas</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,03%	17,39%	0,00%	0,00%
<i>Luteococcus</i> unknown_species	0,10%	57,14%	0,12%	66,67%	0,00%	0,00%	0,00%	0,00%
<i>Lysinibacillus capsici</i>	0,00%	0,00%	0,00%	0,00%	0,02%	13,04%	0,00%	0,00%
<i>Lysinibacillus</i> unknown_species	0,00%	0,00%	0,02%	16,67%	2,95%	91,30%	1,89%	52,38%
<i>Lysobacter</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,17%	52,17%	0,02%	4,76%

<i>Macrococcus bohemicus</i>	0,00%	0,00%	0,00%	0,00%	1,06%	56,52%	2,40%	23,81%
<i>Macrococcus canis</i>	0,00%	0,00%	0,00%	0,00%	0,22%	30,43%	0,57%	19,05%
<i>Macrococcus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	1,12%	86,96%	0,17%	33,33%
<i>Mahella unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	4,76%
<i>Mailhella unknown_species</i>	0,01%	7,14%	0,00%	0,00%	0,01%	8,70%	0,00%	0,00%
<i>Marihabitans unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Marinilactibacillus unknown_species</i>	0,15%	42,86%	0,25%	58,33%	1,57%	65,22%	1,31%	38,10%
<i>Marinobacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Marinococcus halophilus</i>	0,01%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Marinospirillum unknown_species</i>	0,01%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Marmoricola unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Massilimaliae unknown_species</i>	0,04%	21,43%	0,01%	8,33%	0,00%	0,00%	0,02%	4,76%
<i>Megasphaera elsdenii</i>	0,01%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Methanobrevibacter unknown_species</i>	0,00%	0,00%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Microbacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Micrococcus lylae</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,03%	4,76%
<i>Miniphocibacter unknown_species</i>	0,03%	14,29%	0,05%	16,67%	0,09%	13,04%	0,01%	4,76%
<i>Mitsuokella unknown_species</i>	0,01%	7,14%	0,00%	0,00%	0,03%	17,39%	0,02%	4,76%
<i>Mobilibacterium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Mogibacterium unknown_species</i>	0,44%	78,57%	0,33%	83,33%	0,10%	34,78%	0,02%	4,76%
<i>Moraxella osloensis</i>	0,00%	0,00%	0,00%	0,00%	0,03%	8,70%	0,00%	0,00%
<i>Moraxella unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,05%	8,70%	0,00%	0,00%
<i>Mycoplasma unknown_species</i>	0,56%	35,71%	0,12%	25,00%	0,14%	26,09%	0,04%	4,76%
<i>Myroides unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,01%	4,76%
<i>Ndongobacter unknown_species</i>	0,03%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Neobacillus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,02%	17,39%	0,00%	4,76%
<i>Nocardioides unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,28%	65,22%	0,02%	9,52%
<i>Oceanobacillus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,20%	43,48%	0,01%	4,76%
<i>Olsenella umbonata</i>	0,07%	21,43%	0,01%	8,33%	0,02%	8,70%	0,00%	0,00%
<i>Olsenella unknown_species</i>	0,27%	92,86%	0,21%	66,67%	0,15%	43,48%	0,02%	14,29%
<i>Ornithinococcus hortensis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Ornithinococcus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Ornithinimicrobium unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,53%	69,57%	0,11%	38,10%
<i>Oscillibacter unknown_species</i>	0,02%	14,29%	0,00%	0,00%	0,00%	4,35%	0,01%	4,76%
<i>Paenarthrobacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Paeniclostridium sordellii</i>	0,83%	100,00%	0,79%	100,00%	0,33%	65,22%	0,08%	28,57%
<i>Paeniclostridium unknown_species</i>	0,77%	100,00%	0,73%	100,00%	0,86%	82,61%	0,21%	38,10%
<i>Pantoea agglomerans</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Paraclostridium bifermentans</i>	6,58%	100,00%	6,34%	100,00%	2,22%	78,26%	0,54%	47,62%
<i>Paraclostridium unknown_species</i>	1,00%	100,00%	0,94%	100,00%	0,62%	78,26%	0,19%	42,86%
<i>Parapedobacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Parvimonas unknown_species</i>	0,02%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Pediococcus pentosaceus</i>	0,17%	28,57%	0,37%	33,33%	0,00%	0,00%	0,00%	0,00%
<i>Peptacetobacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,03%	4,35%	0,01%	4,76%
<i>Peptoclostridium unknown_species</i>	0,01%	7,14%	0,00%	0,00%	0,01%	8,70%	0,01%	4,76%
<i>Peptoniphilus indolicus</i>	0,00%	0,00%	0,03%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Peptoniphilus pacaensis</i>	0,00%	0,00%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Peptoniphilus unknown_species</i>	0,08%	14,29%	0,21%	33,33%	0,03%	4,35%	0,00%	0,00%
<i>Peptoniphilus vaginalis</i>	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Peptostreptococcus russellii</i>	0,00%	0,00%	0,04%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Peptostreptococcus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,01%	4,76%

<i>Peribacillus</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,02%	17,39%	0,00%	0,00%
<i>Phascolarctobacterium</i> unknown_species	0,01%	7,14%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Phocaeicola</i> unknown_species	0,02%	14,29%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Planococcus</i> unknown_species	0,01%	7,14%	0,01%	8,33%	0,13%	39,13%	0,03%	19,05%
<i>Planomicrobium glaciei</i>	0,03%	7,14%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Plesiomonas</i> unknown_species	0,00%	0,00%	0,01%	8,33%	0,01%	4,35%	0,00%	0,00%
<i>Prevotella</i> unknown_species	0,05%	14,29%	0,00%	0,00%	0,02%	8,70%	0,00%	0,00%
<i>Pseudactinotalea</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Pseudoalteromonas translucida</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,01%	4,76%
<i>Pseudoflavonifractor</i> unknown_species	0,15%	71,43%	0,05%	41,67%	0,07%	30,43%	0,02%	4,76%
<i>Pseudohongiella</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Pseudomonas flexibilis</i>	0,00%	0,00%	0,00%	0,00%	0,03%	13,04%	0,00%	0,00%
<i>Pseudomonas saudiphocaensis</i>	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Pseudomonas stutzeri</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,02%	9,52%
<i>Pseudomonas</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,19%	14,29%
<i>Psychrobacillus</i> unknown_species	0,00%	0,00%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Psychrobacter phenylpyruvicus</i>	0,03%	14,29%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Ralstonia pickettii</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	9,52%
<i>Rhodococcus</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,06%	17,39%	0,00%	0,00%
<i>Romboutsia hominis</i>	0,02%	14,29%	0,05%	41,67%	0,01%	4,35%	0,00%	0,00%
<i>Romboutsia ilealis</i>	8,97%	100,00%	9,20%	100,00%	4,83%	82,61%	0,87%	42,86%
<i>Romboutsia timonensis</i>	1,24%	100,00%	1,15%	100,00%	1,33%	73,91%	0,22%	28,57%
<i>Romboutsia</i> unknown_species	4,33%	100,00%	4,60%	100,00%	3,40%	95,65%	0,75%	57,14%
<i>Rummeliibacillus</i> unknown_species	0,07%	14,29%	0,03%	16,67%	0,37%	65,22%	0,14%	33,33%
<i>Saccharopolyspora</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,01%	13,04%	0,00%	4,76%
<i>Salinicoccus</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,02%	8,70%	0,00%	0,00%
<i>Salipaludibacillus</i> unknown_species	0,02%	21,43%	0,00%	0,00%	0,01%	8,70%	0,00%	4,76%
<i>Selenomonas</i> unknown_species	0,01%	7,14%	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%
<i>Senegalia</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,02%	8,70%	0,00%	0,00%
<i>Serinicoccus</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,04%	13,04%	0,00%	0,00%
<i>Serratia fonticola</i>	0,00%	0,00%	0,00%	0,00%	0,07%	4,35%	0,00%	0,00%
<i>Serratia</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Serratia ureilytica</i>	0,00%	0,00%	0,00%	0,00%	0,34%	4,35%	0,00%	0,00%
<i>Slackia</i> unknown_species	0,01%	7,14%	0,01%	8,33%	0,01%	4,35%	0,00%	0,00%
<i>Sneathia</i> unknown_species	0,03%	7,14%	0,04%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Solibacillus isronensis</i>	0,00%	0,00%	0,00%	0,00%	0,04%	30,43%	0,01%	9,52%
<i>Solibacillus</i> unknown_species	0,01%	7,14%	0,01%	8,33%	0,33%	69,57%	0,16%	42,86%
<i>Spiroplasma</i> unknown_species	0,14%	21,43%	0,00%	0,00%	0,01%	4,35%	0,01%	4,76%
<i>Sporosarcina</i> unknown_species	0,00%	0,00%	0,00%	0,00%	0,12%	8,70%	0,03%	4,76%
<i>Staphylococcus arlettae</i>	1,79%	92,86%	2,17%	91,67%	0,01%	4,35%	0,01%	4,76%
<i>Staphylococcus aureus</i>	0,00%	0,00%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Staphylococcus auricularis</i>	0,00%	0,00%	0,04%	25,00%	0,19%	21,74%	0,01%	4,76%
<i>Staphylococcus capitis</i>	0,02%	7,14%	0,00%	0,00%	0,06%	17,39%	0,15%	4,76%
<i>Staphylococcus chromogenes</i>	0,80%	7,14%	0,00%	0,00%	10,03%	91,30%	8,90%	71,43%
<i>Staphylococcus cohnii</i>	2,18%	92,86%	1,32%	83,33%	0,00%	0,00%	0,00%	0,00%
<i>Staphylococcus epidermidis</i>	0,05%	21,43%	0,12%	16,67%	0,05%	21,74%	1,21%	19,05%
<i>Staphylococcus equorum</i>	0,60%	85,71%	0,87%	91,67%	0,00%	0,00%	0,00%	0,00%
<i>Staphylococcus felis</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Staphylococcus gallinarum</i>	0,00%	0,00%	0,01%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Staphylococcus haemolyticus</i>	0,00%	0,00%	0,02%	16,67%	1,28%	47,83%	2,93%	33,33%

<i>Staphylococcus hominis</i>	0,34%	71,43%	0,47%	83,33%	0,08%	30,43%	0,11%	28,57%
<i>Staphylococcus hyicus</i>	0,01%	7,14%	0,07%	16,67%	0,00%	0,00%	0,00%	0,00%
<i>Staphylococcus microti</i>	0,00%	0,00%	0,00%	0,00%	0,20%	30,43%	0,18%	19,05%
<i>Staphylococcus muscae</i>	0,00%	0,00%	0,00%	0,00%	2,41%	34,78%	0,93%	33,33%
<i>Staphylococcus petrasii</i>	0,00%	0,00%	0,00%	0,00%	0,01%	8,70%	0,01%	4,76%
<i>Staphylococcus saprophyticus</i>	0,00%	0,00%	0,02%	16,67%	0,00%	0,00%	0,00%	0,00%
<i>Staphylococcus sciuri</i>	0,00%	0,00%	0,02%	8,33%	0,21%	8,70%	0,00%	0,00%
<i>Staphylococcus simulans</i>	0,00%	0,00%	0,00%	0,00%	0,18%	26,09%	2,19%	19,05%
<i>Staphylococcus unknown_species</i>	0,79%	85,71%	0,36%	75,00%	12,49%	100,00%	6,00%	85,71%
<i>Staphylococcus xylosus</i>	0,35%	64,29%	0,66%	66,67%	0,06%	17,39%	0,07%	14,29%
<i>Stenotrophomonas ginsengisoli</i>	0,00%	0,00%	0,00%	0,00%	0,00%	0,00%	0,02%	4,76%
<i>Stenotrophomonas koreensis</i>	0,00%	0,00%	0,00%	0,00%	0,03%	13,04%	0,06%	9,52%
<i>Stenotrophomonas maltophilia</i>	0,00%	0,00%	0,00%	0,00%	0,13%	4,35%	0,03%	9,52%
<i>Streptococcus cristatus</i>	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Streptococcus dysgalactiae</i>	0,00%	0,00%	3,96%	25,00%	0,00%	0,00%	0,00%	0,00%
<i>Streptococcus equinus</i>	0,03%	21,43%	0,06%	25,00%	0,07%	17,39%	0,00%	0,00%
<i>Streptococcus gordonii</i>	0,00%	0,00%	0,00%	0,00%	0,02%	8,70%	0,00%	0,00%
<i>Streptococcus halotolerans</i>	0,00%	0,00%	0,00%	0,00%	0,03%	4,35%	0,01%	4,76%
<i>Streptococcus salivarius</i>	0,13%	14,29%	0,00%	0,00%	0,10%	4,35%	0,00%	0,00%
<i>Streptococcus thermophilus</i>	0,11%	14,29%	0,00%	0,00%	0,21%	4,35%	0,00%	0,00%
<i>Streptococcus uberis</i>	0,00%	0,00%	0,63%	8,33%	0,02%	4,35%	20,68%	47,62%
<i>Streptococcus unknown_species</i>	0,12%	21,43%	0,09%	25,00%	0,13%	21,74%	10,80%	47,62%
<i>Streptococcus vestibularis</i>	0,04%	14,29%	0,00%	0,00%	0,16%	4,35%	0,00%	0,00%
<i>Suicoccus unknown_species</i>	0,01%	7,14%	0,08%	16,67%	0,16%	43,48%	0,03%	14,29%
<i>Tessaracoccus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,14%	47,83%	0,07%	33,33%
<i>Tetragenococcus halophilus</i>	0,49%	50,00%	0,22%	41,67%	0,00%	0,00%	0,00%	0,00%
<i>Tetragenococcus unknown_species</i>	1,77%	78,57%	0,84%	83,33%	0,00%	0,00%	0,00%	0,00%
<i>Tetrasphaera elongata</i>	0,00%	0,00%	0,00%	0,00%	0,23%	56,52%	0,07%	23,81%
<i>Tetrasphaera unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,05%	4,35%	0,00%	0,00%
<i>Thalassolituus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,04%	21,74%	0,00%	0,00%
<i>Thauera phenolivorans</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,01%	9,52%
<i>Thauera unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,02%	4,35%	0,00%	0,00%
<i>Thermoanaerobacter unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,01%	4,35%	0,00%	0,00%
<i>Thermovirga unknown_species</i>	0,03%	7,14%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Tissierella unknown_species</i>	0,05%	21,43%	0,06%	16,67%	0,05%	26,09%	0,00%	0,00%
<i>Traorella unknown_species</i>	0,05%	28,57%	0,02%	8,33%	0,04%	13,04%	0,14%	14,29%
<i>Treponema unknown_species</i>	0,02%	14,29%	0,00%	0,00%	0,01%	8,70%	0,01%	4,76%
<i>Trichococcus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,03%	4,35%	0,00%	0,00%
<i>Trueperella pyogenes</i>	0,06%	14,29%	0,00%	0,00%	0,00%	0,00%	0,15%	4,76%
<i>Trueperella unknown_species</i>	0,05%	21,43%	0,12%	16,67%	0,05%	13,04%	0,02%	9,52%
<i>Tumebacillus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,00%	4,35%	0,00%	0,00%
<i>Turicibacter sanguinis</i>	11,20%	100,00%	10,45%	100,00%	5,30%	78,26%	1,11%	57,14%
<i>Turicibacter unknown_species</i>	11,29%	100,00%	9,80%	100,00%	6,78%	95,65%	1,85%	71,43%
<i>Urinococcus unknown_species</i>	0,04%	14,29%	0,02%	8,33%	0,00%	0,00%	0,00%	0,00%
<i>Vaginisenegalia unknown_species</i>	0,03%	14,29%	0,02%	8,33%	0,21%	30,43%	0,07%	9,52%
<i>Virgibacillus unknown_species</i>	0,00%	0,00%	0,00%	0,00%	0,04%	17,39%	0,00%	0,00%
<i>Weissella jogaejeotgali</i>	4,93%	92,86%	4,86%	91,67%	0,00%	0,00%	0,00%	0,00%
<i>Weissella paramesenteroides</i>	0,17%	35,71%	0,25%	25,00%	0,00%	0,00%	0,00%	0,00%
<i>Weissella unknown_species</i>	0,38%	57,14%	0,29%	50,00%	0,00%	0,00%	0,00%	0,00%

Table S4: Milk "core" microbiota for healthy and subclinical mastitis cows divided per stable. For each group, the average relative abundance and prevalence for each bacterial species are reported.

Thus, suggesting that these microbial species are typical colonizers of the bovine milk regardless of the clinical status for stable 1.

Conversely, three bacterial species, including *Bifidobacterium pseudolongum*, and two not yet characterized species belonging to the genera *Olsenella*, and *Staphylococcus* were exclusively part of the “core” microbiota of milk from healthy cows, while six microbial taxa only belonged to the “core” microbial community of subclinical mastitis milk samples, encompassing *Lactobacillus acidipiscis*, *Staphylococcus hominis*, and four unknown species of the genus *Anaerococcus*, *Jeotgalicoccus*, *Mogibacterium*, and *Tetragenococcus* (Table S4).

Interestingly, *B. pseudolongum* has been identified as one of the main bifidobacterial players of the mammalian milk in healthy subjects (24-26), thus indicating that this bacterial species may be considered as marker of a healthy status that may undergo a reduction in prevalence in case of subclinical mastitis.

Differently from stable 1, in stable 2 only two bacterial species were shared between the “core” milk microbiota of healthy and SM-affected cows, i.e., two yet unclassified species belonging to the genera *Corynebacterium* and *Staphylococcus* (Table S4). Interestingly, the latter corresponded to the only two taxa present with a prevalence > 80% in the SM milk samples.

In contrast, the “core” microbial community of milk collected from healthy cows consisted of 11 additional bacterial taxa including *Staphylococcus chromogenes*, *Clostridioides difficile*, and *R. ilealis* together with 8 not yet identified species belonging to genera *Clostridioides*, *Enterococcus*, *Kurthia*, *Lysinibacillus*,

Macrococcus, *Paeniclostridium*, *Romboutsia*, *Staphylococcus*, and *Turicibacter* (Table S4).

Thus, suggesting that, for stable 2, the inflammation of the mammary gland induced a more pronounced modulation of the “core” milk microbial community, when compared to that observed for stable 1, recording a drastic reduction in the number of bacterial species shared among the milk samples collected from cows with SM.

Overall, these results highlighted that SM does not induce standard modulation of the “core” milk bacterial composition, but rather, these microbial changes seem to depend on environmental factors.

An observation that underlines the importance of characterizing the milk microbiota of healthy cows within each stable to create a “reference standard” to be compared with the microbial community of milk samples from subclinical mastitis-affected cows from the same stable to identify those microbial species potentially involved in the onset of SM for each stable.

At the same time, the presence of yet unclassified species in the “core” microbiota of milk from both healthy and diseased cows highlighted the urgent need to apply culture-dependent approaches aimed at isolating and characterizing this milk microbial dark matter.

3.4 Prediction of putative milk microbial markers correlated with SM

To identify possible microbial biomarkers strictly associated with SM, milk samples collected from healthy cows were compared with those from SM-affected cows. Interestingly, for stable 1, only one bacterial species, i.e., a not yet characterized species of the genus *Lactococcus*, was significantly more abundant in healthy cows

when compared to the diseased ones (Student's T-test p-value = 0.042), thus indicating that this taxon may be considered as a positive microbial biomarker associated with a healthy condition.

However, the latter microbial species showed a reduced relative abundance (0.05%) as well as a low prevalence (26.67%) (Figure 2 and Table S4), thus suggesting that SM does not induce striking changes in the milk microbiota of stable 1, preventing the identification of SM-related microbial biomarkers.

However, in depth insight into taxonomic profiles of milk samples from stable 1 highlighted that *Streptococcus dysgalactiae*, one of the most prevalent pathogens causing bovine mastitis worldwide, was detected only in milk samples from SM-affected cows, and when present, this species displayed a high average relative abundance (3.96%) (10, 27-29) (Table S4 and Table S5).

At the same time, *Corynebacterium bovis*, another bacterial species listed among the pathogenic microorganisms closely associated with SM, possessed a higher average relative abundance and prevalence in milk samples from cows with SM with respect to the ones collected from healthy cows (Table S4) (30-32).

In this context, even if not statistically significant, these results strengthen the notion that both *S. dysgalactiae* and *C. bovis* may be considered as microbial biomarkers of SM.

Differently from stable 1, the comparison of taxonomic profiles between healthy and diseased cows from stable 2 highlighted that the average relative abundance of 33 bacterial species significantly differed based on the clinical status (Figure 2 and Table S5).

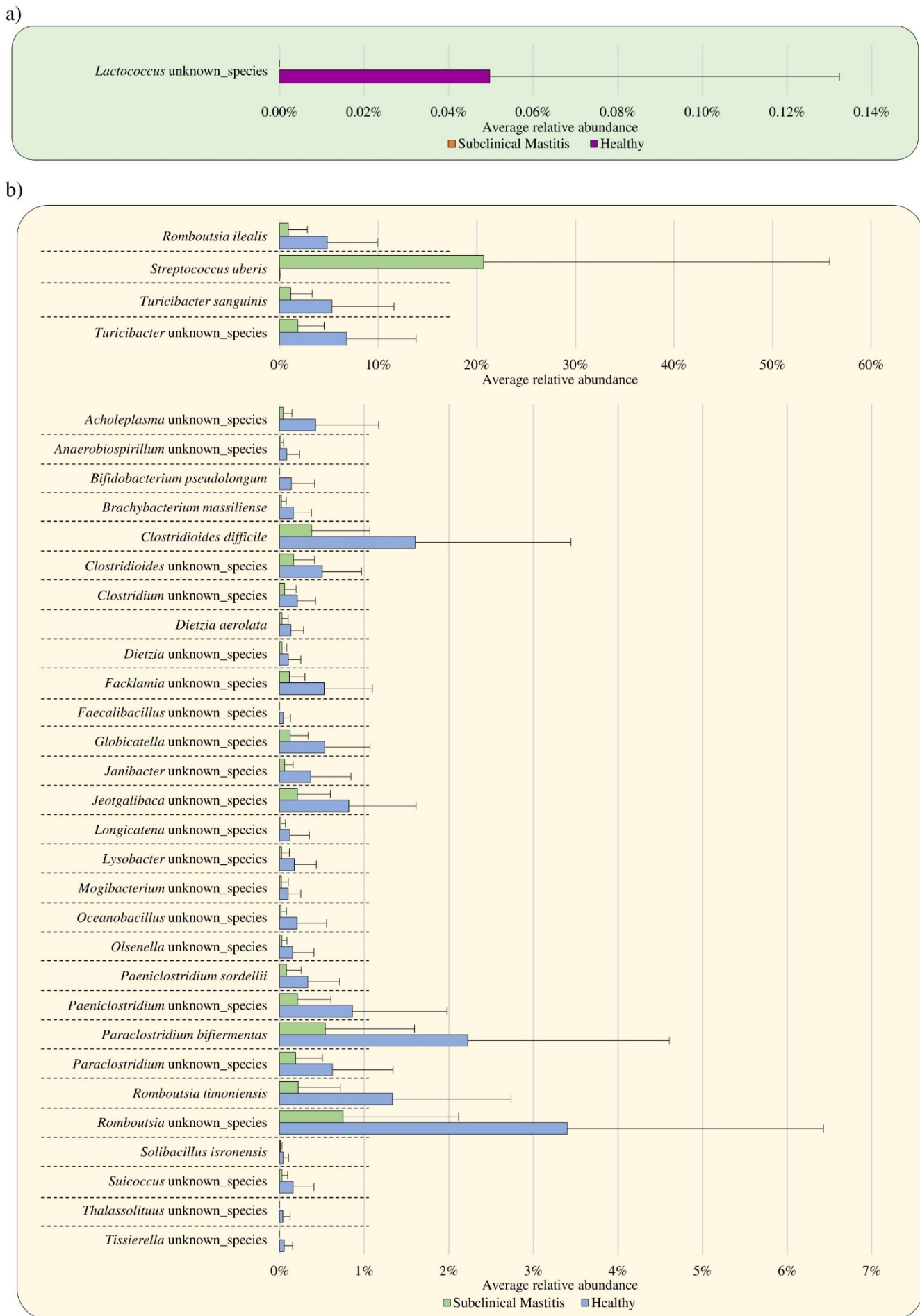


Figure 2: Species-level differences in the taxonomic composition of milk samples from healthy and SM-affected cows. Panels a and b report the average relative abundances of those bacterial species that significantly differ in the milk samples from healthy and diseases cows for stable 1 and 2, respectively.

Among the latter, *B. pseudolongum* was only found in milk samples from healthy cows (Student's T-test p-value = 0.025) (Figure 2 and Table S5).

In this context, as above reported, since *B. pseudolongum* has been identified as a commensal microorganisms of bovine milk and members of the genus *Bifidobacterium* are known to play multiple beneficial effects upon their host promoting anti-inflammatory response, providing protection against pathogen colonization, and favoring the proliferation of beneficial butyrogenic microbial players that can use the acetate produced by the bifidobacterial fermentation of complex glycans, this species can be considered as microbial biomarker of a healthy status (7, 30, 33-35).

Furthermore, *Dietzia aerolata*, as well as three yet unclassified species of the genera *Dietzia*, *Facklamia*, and *Janibacter* were not only more prevalent but also significantly more abundant in milk samples from healthy cows when compared to that of subjects with SM (Figure 3, Table S4 and Table S5).

Notably, these genera were considered as commensal microorganisms of the milk microbiota (36-38) suggesting their possible involvement as positive microbial markers of a healthy conditions.

Species	Stable 1						
	Number of samples - Healthy	Average relative abundance - Healthy	Standard deviation - Healthy	Number of samples - Subclinical Mastitis	Average relative abundance - Subclinical Mastitis	Standard deviation - Subclinical Mastitis	p-value
<i>Abiotrophia</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Absicoccus</i> unknown_species	14	0,02%	0,08%	12	0,00%	0,00%	0,365
<i>Acholeplasma</i> unknown_species	14	0,39%	0,68%	12	0,27%	0,60%	0,645
<i>Achromobacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Acinetobacter indicus</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Acinetobacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Actinotalea</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	

<i>Adlercreutzia</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Aequorivita</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Aerococcus</i> unknown_species	14	0,67%	0,72%	12	0,58%	0,41%	0,686
<i>Aerococcus urinaeequi</i>	14	14,72%	9,39%	12	17,51%	9,66%	0,463
<i>Aerococcus viridans</i>	14	0,40%	0,34%	12	0,50%	0,37%	0,472
<i>Aeromicrobium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Agarilytica</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Agathobaculum</i> unknown_species	14	0,02%	0,08%	12	0,00%	0,00%	0,365
<i>Akkermansia muciniphila</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Alistipes</i> unknown_species	14	0,00%	0,00%	12	0,01%	0,04%	0,339
<i>Alkaliphilus</i> unknown_species	14	0,01%	0,03%	12	0,00%	0,00%	0,177
<i>Amedibacterium</i> unknown_species	14	0,00%	0,00%	12	0,01%	0,05%	0,339
<i>Aminipila</i> unknown_species	14	0,06%	0,12%	12	0,02%	0,04%	0,306
<i>Anaerobiospirillum</i> unknown_species	14	0,02%	0,06%	12	0,00%	0,00%	0,202
<i>Anaerococcus</i> unknown_species	14	0,19%	0,54%	12	0,37%	0,84%	0,520
<i>Anaerorhabdus</i> unknown_species	14	0,19%	0,35%	12	0,05%	0,11%	0,195
<i>Arcanobacterium</i> unknown_species	14	0,09%	0,19%	12	0,02%	0,06%	0,225
<i>Aromatoleum</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Bacillus aryabhatai</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Bacillus licheniformis</i>	14	0,03%	0,11%	12	0,00%	0,00%	0,365
<i>Bacillus megaterium</i>	14	0,01%	0,02%	12	0,01%	0,03%	0,864
<i>Bacillus subtilis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Bacillus</i> unknown_species	14	0,04%	0,07%	12	0,03%	0,04%	0,577
<i>Bacillus velezensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Bacteriovorax</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Beduini</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Beutenbergia</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Bifidobacterium merycicum</i>	14	0,09%	0,23%	12	0,06%	0,12%	0,678
<i>Bifidobacterium pseudolongum</i>	14	0,47%	0,30%	12	0,40%	0,45%	0,639
<i>Bifidobacterium scardovii</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Bifidobacterium</i> unknown_species	14	0,02%	0,07%	12	0,01%	0,04%	0,721
<i>Bilophila wadsworthia</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Blautia</i> unknown_species	14	0,02%	0,05%	12	0,00%	0,00%	0,084
<i>Brachybacterium massiliense</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Brachybacterium</i> unknown_species	14	0,04%	0,06%	12	0,02%	0,05%	0,518
<i>Brevibacterium frigoritolerans</i>	14	0,00%	0,00%	12	0,01%	0,02%	0,339
<i>Brevibacterium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Brevilactibacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Bulleidia</i> unknown_species	14	0,06%	0,16%	12	0,07%	0,16%	0,952
<i>Burkholderia stabilis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Butyricoccus</i> unknown_species	14	0,04%	0,07%	12	0,01%	0,04%	0,301
<i>Carnobacterium</i> unknown_species	14	0,08%	0,09%	12	0,15%	0,12%	0,131
<i>Cecembia</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Cellulomonas</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Clostridioides difficile</i>	14	1,73%	1,07%	12	1,80%	0,87%	0,851
<i>Clostridioides</i> unknown_species	14	0,50%	0,46%	12	0,43%	0,26%	0,637
<i>Clostridium bornimense</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Clostridium botulinum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	

<i>Clostridium perfringens</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Clostridium</i> unknown_species	14	0,19%	0,12%	12	0,16%	0,10%	0,488
<i>Comamonas</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Corynebacterium bovis</i>	14	0,35%	0,89%	12	1,60%	2,40%	0,110
<i>Corynebacterium camporealensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Corynebacterium frankenforstense</i>	14	0,42%	0,59%	12	0,12%	0,17%	0,086
<i>Corynebacterium propinquum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Corynebacterium sanguinis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Corynebacterium</i> unknown_species	14	1,06%	1,00%	12	0,79%	0,52%	0,390
<i>Corynebacterium urealyticum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Corynebacterium xerosis</i>	14	0,37%	0,63%	12	0,44%	0,42%	0,750
<i>Cutibacterium acnes</i>	14	0,09%	0,25%	12	0,04%	0,10%	0,510
<i>Cutibacterium granulosum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Cutibacterium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Cyclobacterium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Cytobacillus firmus</i>	14	0,00%	0,02%	12	0,00%	0,00%	0,365
<i>Cytobacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Dehalobacterium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Demequina</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Dietzia aerolata</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Dietzia</i> unknown_species	14	0,00%	0,00%	12	0,01%	0,05%	0,339
<i>Dolosigranulum</i> unknown_species	14	0,04%	0,12%	12	0,09%	0,27%	0,554
<i>Dubosiella</i> unknown_species	14	0,02%	0,07%	12	0,00%	0,00%	0,365
<i>Dyadobacter</i> unknown_species	14	0,00%	0,02%	12	0,00%	0,00%	0,365
<i>Eggerthella</i> unknown_species	14	0,02%	0,09%	12	0,01%	0,03%	0,571
<i>Eggerthia</i> unknown_species	14	0,06%	0,11%	12	0,03%	0,06%	0,397
<i>Emergencia</i> unknown_species	14	0,01%	0,03%	12	0,00%	0,00%	0,165
<i>Endozoicomonas</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterobacter asburiae</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterobacter bugandensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterobacter hormaechei</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterobacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterococcus aquimarinus</i>	14	0,12%	0,22%	12	0,11%	0,18%	0,979
<i>Enterococcus casseliflavus</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterococcus cecorum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterococcus durans</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterococcus faecalis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterococcus faecium</i>	14	0,01%	0,05%	12	0,00%	0,00%	0,365
<i>Enterococcus gallinarum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterococcus hirae</i>	14	0,06%	0,21%	12	0,00%	0,00%	0,365
<i>Enterococcus pseudoavium</i>	14	0,00%	0,00%	12	0,01%	0,03%	0,339
<i>Enterococcus saccharolyticus</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Enterococcus</i> unknown_species	14	0,29%	0,20%	12	0,34%	0,32%	0,664
<i>Entomoplasma</i> unknown_species	14	0,03%	0,12%	12	0,00%	0,00%	0,365
<i>Escherichia coli</i>	14	0,04%	0,09%	12	0,00%	0,00%	0,134
<i>Escherichia marmotae</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Eubacterium</i> unknown_species	14	0,00%	0,00%	12	0,01%	0,04%	0,339

<i>Exiguobacterium acetylicum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Exiguobacterium chiriquhucha</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Exiguobacterium indicum</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Exiguobacterium unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Facklamia unknown_species</i>	14	0,19%	0,22%	12	0,25%	0,36%	0,625
<i>Faecalibacillus intestinalis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Faecalibacillus unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Faecalicoccus unknown_species</i>	14	0,14%	0,25%	12	0,01%	0,05%	0,079
<i>Faecalitalea unknown_species</i>	14	0,02%	0,08%	12	0,00%	0,00%	0,365
<i>Fenollaria unknown_species</i>	14	0,00%	0,00%	12	0,03%	0,09%	0,339
<i>Filifactor unknown_species</i>	14	0,01%	0,05%	12	0,03%	0,10%	0,596
<i>Flavobacterium unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Flavonifractor unknown_species</i>	14	0,03%	0,08%	12	0,00%	0,00%	0,174
<i>Frankia coriariae</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Fusobacterium necrophorum</i>	14	0,11%	0,26%	12	0,05%	0,13%	0,429
<i>Fusobacterium unknown_species</i>	14	0,02%	0,07%	12	0,00%	0,00%	0,365
<i>Gemella unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Georgenia unknown_species</i>	14	0,04%	0,12%	12	0,01%	0,04%	0,426
<i>Gilliamella unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Globicatella sanguinis</i>	14	0,97%	0,63%	12	1,90%	1,90%	0,098
<i>Globicatella unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Gordonibacter unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Gottschalkia unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Gudongella unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Haloactinobacterium unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Haloglycomyces unknown_species</i>	14	0,00%	0,00%	12	0,01%	0,03%	0,339
<i>Haloplasma unknown_species</i>	14	0,01%	0,03%	12	0,02%	0,08%	0,539
<i>Helcococcus kunzii</i>	14	0,06%	0,17%	12	0,12%	0,37%	0,590
<i>Helcococcus unknown_species</i>	14	0,12%	0,20%	12	0,05%	0,10%	0,286
<i>Holdemania unknown_species</i>	14	0,01%	0,04%	12	0,00%	0,00%	0,365
<i>Hungateiclostridium unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Ilumatobacter unknown_species</i>	14	0,01%	0,03%	12	0,02%	0,04%	0,522
<i>Inediibacterium unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Intestinibacter unknown_species</i>	14	0,01%	0,04%	12	0,01%	0,04%	0,972
<i>Intestinibaculum porci</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Intestinibaculum unknown_species</i>	14	0,11%	0,16%	12	0,03%	0,05%	0,088
<i>Intestinimonas unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Isoptricola unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Janibacter unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Janthinobacterium unknown_species</i>	14	0,07%	0,11%	12	0,10%	0,17%	0,600
<i>Jeotgalibaca arthritidis</i>	14	3,75%	5,23%	12	3,42%	4,11%	0,858
<i>Jeotgalibaca porci</i>	14	0,01%	0,05%	12	0,03%	0,06%	0,495
<i>Jeotgalibaca unknown_species</i>	14	2,06%	5,67%	12	1,65%	1,48%	0,812
<i>Jeotgalicoccus coquinae</i>	14	0,01%	0,04%	12	0,00%	0,00%	0,365
<i>Jeotgalicoccus saudimassiliensis</i>	14	0,19%	0,45%	12	0,28%	0,25%	0,570
<i>Jeotgalicoccus unknown_species</i>	14	0,01%	0,05%	12	0,00%	0,00%	0,365
<i>Kallipyga unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Klebsiella grimontii</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	

<i>Klebsiella michiganensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Klebsiella</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Knoellia sinensis</i>	14	0,04%	0,06%	12	0,01%	0,03%	0,088
<i>Kocuria</i> unknown_species	14	0,01%	0,05%	12	0,00%	0,00%	0,365
<i>Kroppenstedtia</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Kurthia huakuii</i>	14	0,06%	0,11%	12	0,07%	0,21%	0,803
<i>Kurthia</i> unknown_species	14	1,48%	1,95%	12	1,05%	1,16%	0,510
<i>Lactobacillus acidipiscis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lactobacillus amylovorus</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lactobacillus crispatus</i>	14	0,07%	0,23%	12	0,00%	0,00%	0,253
<i>Lactobacillus delbrueckii</i>	14	0,43%	1,02%	12	0,40%	1,26%	0,949
<i>Lactobacillus farciminis</i>	14	0,06%	0,12%	12	0,02%	0,06%	0,407
<i>Lactobacillus ginsenosidimutans</i>	14	0,03%	0,09%	12	0,14%	0,49%	0,428
<i>Lactobacillus iners</i>	14	0,03%	0,12%	12	0,01%	0,04%	0,564
<i>Lactobacillus mucosae</i>	14	0,01%	0,04%	12	0,00%	0,00%	0,365
<i>Lactobacillus parabuchneri</i>	14	1,05%	2,84%	12	0,00%	0,00%	0,191
<i>Lactobacillus paracasei</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lactobacillus reuteri</i>	14	0,37%	0,55%	12	0,16%	0,25%	0,217
<i>Lactobacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lactococcus garvieae</i>	14	0,47%	1,18%	12	0,01%	0,04%	0,171
<i>Lactococcus lactis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lactococcus petauri</i>	14	0,05%	0,08%	12	0,00%	0,00%	0,043
<i>Lactococcus</i> unknown_species	14	0,03%	0,13%	12	0,02%	0,05%	0,643
<i>Lagierella massiliensis</i>	14	0,03%	0,10%	12	0,02%	0,07%	0,827
<i>Lagierella</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lancefieldella</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lawsonella</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lentibacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Leptothrix</i> unknown_species	14	0,14%	0,18%	12	0,13%	0,18%	0,914
<i>Levyella</i> unknown_species	14	0,03%	0,05%	12	0,01%	0,03%	0,277
<i>Longibaculum</i> unknown_species	14	0,22%	0,25%	12	0,13%	0,15%	0,279
<i>Longicatena</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Longimicrobium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Luteimonas arsenica</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Luteimonas</i> unknown_species	14	0,10%	0,11%	12	0,12%	0,11%	0,761
<i>Luteococcus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lysinibacillus capsici</i>	14	0,00%	0,00%	12	0,02%	0,06%	0,206
<i>Lysinibacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Lysobacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Macrococcus bohemicus</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Macrococcus canis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Macrococcus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Mahella</i> unknown_species	14	0,01%	0,03%	12	0,00%	0,00%	0,365
<i>Mailhella</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Marihabitans</i> unknown_species	14	0,15%	0,22%	12	0,25%	0,40%	0,431
<i>Marinilactibacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Marinobacterium</i> unknown_species	14	0,01%	0,03%	12	0,00%	0,00%	0,365
<i>Marinococcus halophilus</i>	14	0,01%	0,05%	12	0,00%	0,00%	0,365

<i>Marinospirillum</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Marmoricola</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Massilimaliae</i> unknown_species	14	0,04%	0,08%	12	0,01%	0,04%	0,324
<i>Megasphaera elsdenii</i>	14	0,01%	0,04%	12	0,00%	0,00%	0,365
<i>Methanobrevibacter</i> unknown_species	14	0,00%	0,00%	12	0,02%	0,06%	0,339
<i>Microbacterium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Micrococcus lylae</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Miniphocibacter</i> unknown_species	14	0,03%	0,08%	12	0,05%	0,11%	0,639
<i>Mitsuokella</i> unknown_species	14	0,01%	0,05%	12	0,00%	0,00%	0,365
<i>Mobilibacterium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Mogibacterium</i> unknown_species	14	0,44%	0,43%	12	0,33%	0,24%	0,431
<i>Moraxella osloensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Moraxella</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Mycoplasma</i> unknown_species	14	0,56%	1,08%	12	0,12%	0,23%	0,160
<i>Myroides</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Ndongobacter</i> unknown_species	14	0,03%	0,10%	12	0,00%	0,00%	0,365
<i>Neobacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Nocardioides</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Oceanobacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Olsenella umbonata</i>	14	0,07%	0,16%	12	0,01%	0,04%	0,178
<i>Olsenella</i> unknown_species	14	0,27%	0,20%	12	0,21%	0,17%	0,389
<i>Ornithinococcus hortensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Ornithinococcus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Ornithinimicrobium</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Oscillibacter</i> unknown_species	14	0,02%	0,06%	12	0,00%	0,00%	0,175
<i>Paenarthrobacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Paeniclostridium sordellii</i>	14	0,83%	0,50%	12	0,79%	0,34%	0,805
<i>Paeniclostridium</i> unknown_species	14	0,77%	0,68%	12	0,73%	0,35%	0,857
<i>Pantoea agglomerans</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Paraclostridium bifermentans</i>	14	6,58%	2,82%	12	6,34%	2,21%	0,812
<i>Paraclostridium</i> unknown_species	14	1,00%	0,54%	12	0,94%	0,37%	0,781
<i>Parapedobacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Parvimonas</i> unknown_species	14	0,02%	0,07%	12	0,00%	0,00%	0,365
<i>Pediococcus pentosaceus</i>	14	0,17%	0,38%	12	0,37%	0,73%	0,390
<i>Peptacetobacter</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Peptoclostridium</i> unknown_species	14	0,01%	0,02%	12	0,00%	0,00%	0,365
<i>Peptoniphilus indolicus</i>	14	0,00%	0,00%	12	0,03%	0,10%	0,339
<i>Peptoniphilus pacaensis</i>	14	0,00%	0,00%	12	0,02%	0,06%	0,339
<i>Peptoniphilus</i> unknown_species	14	0,08%	0,23%	12	0,21%	0,50%	0,421
<i>Peptoniphilus vaginalis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Peptostreptococcus russellii</i>	14	0,00%	0,00%	12	0,04%	0,15%	0,339
<i>Peptostreptococcus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Peribacillus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Phascolarctobacterium</i> unknown_species	14	0,01%	0,03%	12	0,00%	0,00%	0,365
<i>Phocaeicola</i> unknown_species	14	0,02%	0,06%	12	0,01%	0,02%	0,396
<i>Planococcus</i> unknown_species	14	0,01%	0,03%	12	0,01%	0,03%	0,994
<i>Planomicrobium glaciei</i>	14	0,03%	0,10%	12	0,00%	0,00%	0,365
<i>Plesiomonas</i> unknown_species	14	0,00%	0,00%	12	0,01%	0,05%	0,339

<i>Prevotella</i> unknown_species	14	0,05%	0,12%	12	0,00%	0,00%	0,179
<i>Pseudactinotalea</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Pseudoalteromonas translucida</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Pseudoflavonifractor</i> unknown_species	14	0,15%	0,17%	12	0,05%	0,07%	0,054
<i>Pseudohongiella</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Pseudomonas flexibilis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Pseudomonas saudiphocaensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Pseudomonas stutzeri</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Pseudomonas</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Psychrobacillus</i> unknown_species	14	0,00%	0,00%	12	0,01%	0,02%	0,339
<i>Psychrobacter phenylpyruvicus</i>	14	0,03%	0,10%	12	0,00%	0,00%	0,214
<i>Ralstonia pickettii</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Rhodococcus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Romboutsia hominis</i>	14	0,02%	0,05%	12	0,05%	0,06%	0,213
<i>Romboutsia ilealis</i>	14	8,97%	4,09%	12	9,20%	2,94%	0,868
<i>Romboutsia timonensis</i>	14	1,24%	1,33%	12	1,15%	0,97%	0,837
<i>Romboutsia</i> unknown_species	14	4,33%	2,24%	12	4,60%	1,33%	0,719
<i>Rummeliibacillus</i> unknown_species	14	0,07%	0,23%	12	0,03%	0,06%	0,538
<i>Saccharopolyspora</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Salinicoccus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Salipaludibacillus</i> unknown_species	14	0,02%	0,04%	12	0,00%	0,00%	0,112
<i>Selenomonas</i> unknown_species	14	0,01%	0,04%	12	0,00%	0,00%	0,365
<i>Senegalia</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Serinicoccus</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Serratia fonticola</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Serratia</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Serratia ureilytica</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Slackia</i> unknown_species	14	0,01%	0,03%	12	0,01%	0,04%	0,911
<i>Sneathia</i> unknown_species	14	0,03%	0,10%	12	0,04%	0,13%	0,822
<i>Solibacillus isronensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Solibacillus</i> unknown_species	14	0,01%	0,05%	12	0,01%	0,03%	0,786
<i>Spiroplasma</i> unknown_species	14	0,14%	0,36%	12	0,00%	0,00%	0,180
<i>Sporosarcina</i> unknown_species	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Staphylococcus arlettae</i>	14	1,79%	2,19%	12	2,17%	1,98%	0,647
<i>Staphylococcus aureus</i>	14	0,00%	0,00%	12	0,02%	0,07%	0,339
<i>Staphylococcus auricularis</i>	14	0,00%	0,00%	12	0,04%	0,08%	0,084
<i>Staphylococcus capitis</i>	14	0,02%	0,06%	12	0,00%	0,00%	0,365
<i>Staphylococcus chromogenes</i>	14	0,80%	3,00%	12	0,00%	0,00%	0,365
<i>Staphylococcus cohnii</i>	14	2,18%	2,76%	12	1,32%	1,53%	0,349
<i>Staphylococcus epidermidis</i>	14	0,05%	0,13%	12	0,12%	0,38%	0,530
<i>Staphylococcus equorum</i>	14	0,60%	0,83%	12	0,87%	0,93%	0,452
<i>Staphylococcus felis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Staphylococcus gallinarum</i>	14	0,00%	0,00%	12	0,01%	0,03%	0,339
<i>Staphylococcus haemolyticus</i>	14	0,00%	0,00%	12	0,02%	0,05%	0,167
<i>Staphylococcus hominis</i>	14	0,34%	0,42%	12	0,47%	0,35%	0,401
<i>Staphylococcus hyicus</i>	14	0,01%	0,05%	12	0,07%	0,20%	0,339
<i>Staphylococcus microti</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Staphylococcus muscae</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	

<i>Staphylococcus petrasii</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Staphylococcus saprophyticus</i>	14	0,00%	0,00%	12	0,02%	0,05%	0,172
<i>Staphylococcus sciuri</i>	14	0,00%	0,00%	12	0,02%	0,06%	0,339
<i>Staphylococcus simulans</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Staphylococcus unknown_species</i>	14	0,79%	2,13%	12	0,36%	0,26%	0,492
<i>Staphylococcus xylosus</i>	14	0,35%	0,46%	12	0,66%	0,82%	0,245
<i>Stenotrophomonas ginsengisli</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Stenotrophomonas koreensis</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Stenotrophomonas maltophilia</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Streptococcus cristatus</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Streptococcus dysgalactiae</i>	14	0,00%	0,00%	12	3,96%	8,94%	0,153
<i>Streptococcus equinus</i>	14	0,03%	0,07%	12	0,06%	0,11%	0,572
<i>Streptococcus gordonii</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Streptococcus halotolerans</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Streptococcus salivarius</i>	14	0,13%	0,33%	12	0,00%	0,00%	0,172
<i>Streptococcus thermophilus</i>	14	0,11%	0,28%	12	0,00%	0,00%	0,178
<i>Streptococcus uberis</i>	14	0,00%	0,00%	12	0,63%	2,17%	0,339
<i>Streptococcus unknown_species</i>	14	0,12%	0,24%	12	0,09%	0,19%	0,791
<i>Streptococcus vestibularis</i>	14	0,04%	0,11%	12	0,00%	0,00%	0,176
<i>Suicoccus unknown_species</i>	14	0,01%	0,04%	12	0,08%	0,22%	0,316
<i>Tessaracoccus unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Tetragenococcus halophilus</i>	14	0,49%	0,72%	12	0,22%	0,52%	0,296
<i>Tetragenococcus unknown_species</i>	14	1,77%	2,72%	12	0,84%	1,03%	0,250
<i>Tetrasphaera elongata</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Tetrasphaera unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Thalassolituus unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Thauera phenolivorans</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Thauera unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Thermoanaerobacter unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Thermovirga unknown_species</i>	14	0,03%	0,10%	12	0,02%	0,06%	0,810
<i>Tissierella unknown_species</i>	14	0,05%	0,11%	12	0,06%	0,16%	0,788
<i>Traorella unknown_species</i>	14	0,05%	0,11%	12	0,02%	0,06%	0,293
<i>Treponema unknown_species</i>	14	0,02%	0,06%	12	0,00%	0,00%	0,165
<i>Trichococcus unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Trueperella pyogenes</i>	14	0,06%	0,16%	12	0,00%	0,00%	0,166
<i>Trueperella unknown_species</i>	14	0,05%	0,10%	12	0,12%	0,36%	0,502
<i>Tumebacillus unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Turicibacter sanguinis</i>	14	11,20%	4,93%	12	10,45%	5,08%	0,706
<i>Turicibacter unknown_species</i>	14	11,29%	5,36%	12	9,80%	4,86%	0,469
<i>Urinococcus unknown_species</i>	14	0,04%	0,10%	12	0,02%	0,08%	0,714
<i>Vaginisenegalia unknown_species</i>	14	0,03%	0,07%	12	0,02%	0,08%	0,895
<i>Virgibacillus unknown_species</i>	14	0,00%	.00000 ^a	12	0,00%	.00000a	
<i>Weissella jogaejeotgali</i>	14	4,93%	5,96%	12	4,86%	6,60%	0,976
<i>Weissella paramesenteroides</i>	14	0,17%	0,30%	12	0,25%	0,71%	0,692
<i>Weissella unknown_species</i>	14	0,38%	0,64%	12	0,29%	0,45%	0,680

Species	Stable 2						
	Number of samples - Healthy	Average relative abundance - Healthy	Standard deviation - Healthy	Number of samples - Subclinical Mastitis	Average relative abundance - Subclinical Mastitis	Standard deviation - Subclinical Mastitis	p-value
<i>Abiotrophia</i> unknown_species	23	0,03%	0,15%	21	0,00%	0,00%	0,345
<i>Absicoccus</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Acholeplasma</i> unknown_species	23	0,42%	0,75%	21	0,04%	0,11%	0,023
<i>Achromobacter</i> unknown_species	23	0,00%	0,00%	21	0,00%	0,01%	0,329
<i>Acinetobacter indicus</i>	23	0,00%	0,00%	21	0,01%	0,03%	0,329
<i>Acinetobacter</i> unknown_species	23	0,00%	0,00%	21	0,00%	0,02%	0,329
<i>Actinotalea</i> unknown_species	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Adlercreutzia</i> unknown_species	23	0,16%	0,31%	21	0,02%	0,10%	0,056
<i>Aequorivita</i> unknown_species	23	0,01%	0,05%	21	0,01%	0,02%	0,437
<i>Aerococcus</i> unknown_species	23	0,68%	1,15%	21	9,91%	24,57%	0,101
<i>Aerococcus urinaeequi</i>	23	0,58%	0,76%	21	0,27%	0,48%	0,116
<i>Aerococcus viridans</i>	23	0,01%	0,04%	21	0,15%	0,48%	0,179
<i>Aeromicrobium</i> unknown_species	23	0,03%	0,08%	21	0,00%	0,02%	0,095
<i>Agarilytica</i> unknown_species	23	0,00%	0,01%	21	0,00%	0,00%	0,345
<i>Agathobaculum</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Akkermansia muciniphila</i>	23	0,02%	0,12%	21	0,00%	0,00%	0,345
<i>Alistipes</i> unknown_species	23	0,01%	0,05%	21	0,00%	0,00%	0,345
<i>Alkaliphilus</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Amedibacterium</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Aminipila</i> unknown_species	23	0,02%	0,07%	21	0,02%	0,06%	0,648
<i>Anaerobiospirillum</i> unknown_species	23	0,08%	0,15%	21	0,01%	0,03%	0,043
<i>Anaerococcus</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Anaerorhabdus</i> unknown_species	23	0,03%	0,08%	21	0,01%	0,05%	0,426
<i>Arcanobacterium</i> unknown_species	23	0,00%	0,00%	21	0,01%	0,04%	0,329
<i>Aromatoleum</i> unknown_species	23	0,00%	0,01%	21	0,03%	0,12%	0,359
<i>Bacillus aryabhatai</i>	23	0,00%	0,00%	21	0,01%	0,03%	0,329
<i>Bacillus licheniformis</i>	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Bacillus megaterium</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,088
<i>Bacillus subtilis</i>	23	0,04%	0,10%	21	0,02%	0,08%	0,515
<i>Bacillus</i> unknown_species	23	0,16%	0,16%	21	0,11%	0,21%	0,415
<i>Bacillus velezensis</i>	23	0,01%	0,04%	21	0,00%	0,02%	0,668
<i>Bacteriovorax</i> unknown_species	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Beduini</i> unknown_species	23	0,04%	0,14%	21	0,00%	0,00%	0,173
<i>Beutenbergia</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Bifidobacterium merycicum</i>	23	0,01%	0,04%	21	0,00%	0,00%	0,345
<i>Bifidobacterium pseudolongum</i>	23	0,14%	0,28%	21	0,00%	0,00%	0,026
<i>Bifidobacterium scardovii</i>	23	0,04%	0,21%	21	0,00%	0,02%	0,393
<i>Bifidobacterium</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Bilophila wadsworthia</i>	23	0,00%	0,00%	21	0,00%	0,02%	0,329
<i>Blautia</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Brachybacterium massiliense</i>	23	0,16%	0,21%	21	0,02%	0,06%	0,005
<i>Brachybacterium</i> unknown_species	23	0,05%	0,10%	21	0,02%	0,07%	0,303

<i>Brevibacterium frigoritolerans</i>	23	1,43%	3,26%	21	0,31%	1,02%	0,129
<i>Brevibacterium</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,162
<i>Brevilactibacter</i> unknown_species	23	0,01%	0,02%	21	0,00%	0,00%	0,345
<i>Bulleidia</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Burkholderia stabilis</i>	23	0,00%	0,00%	21	0,00%	0,02%	0,329
<i>Butyricoccus</i> unknown_species	23	0,01%	0,03%	21	0,01%	0,06%	0,569
<i>Carnobacterium</i> unknown_species	23	0,01%	0,05%	21	0,00%	0,00%	0,1765
<i>Cecembia</i> unknown_species	23	0,10%	0,13%	21	0,11%	0,48%	0,873
<i>Cellulomonas</i> unknown_species	23	0,01%	0,05%	21	0,00%	0,00%	0,345
<i>Clostridioides difficile</i>	23	1,60%	1,84%	21	0,38%	0,69%	0,006
<i>Clostridioides</i> unknown_species	23	0,50%	0,46%	21	0,16%	0,25%	0,004
<i>Clostridium bornimense</i>	23	0,02%	0,05%	21	0,00%	0,00%	0,093
<i>Clostridium botulinum</i>	23	0,03%	0,06%	21	0,01%	0,03%	0,078
<i>Clostridium perfringens</i>	23	0,03%	0,12%	21	0,03%	0,10%	0,870
<i>Clostridium</i> unknown_species	23	0,21%	0,22%	21	0,06%	0,14%	0,010
<i>Comamonas</i> unknown_species	23	0,00%	0,00%	21	0,00%	0,02%	0,329
<i>Corynebacterium bovis</i>	23	7,48%	10,31%	21	2,82%	4,55%	0,058
<i>Corynebacterium camporealensis</i>	23	0,06%	0,19%	21	0,14%	0,43%	0,442
<i>Corynebacterium frankenforstense</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Corynebacterium propinquum</i>	23	0,00%	0,00%	21	0,01%	0,05%	0,329
<i>Corynebacterium sanguinis</i>	23	0,01%	0,02%	21	0,00%	0,00%	0,345
<i>Corynebacterium</i> unknown_species	23	2,95%	2,65%	21	3,35%	4,20%	0,704
<i>Corynebacterium urealyticum</i>	23	0,00%	0,00%	21	0,01%	0,04%	0,329
<i>Corynebacterium xerosis</i>	23	0,43%	0,51%	21	0,49%	1,35%	0,832
<i>Cutibacterium acnes</i>	23	0,78%	1,73%	21	1,80%	5,16%	0,378
<i>Cutibacterium granulosum</i>	23	0,02%	0,07%	21	0,00%	0,00%	0,345
<i>Cutibacterium</i> unknown_species	23	0,03%	0,09%	21	0,33%	0,98%	0,184
<i>Cyclobacterium</i> unknown_species	23	0,01%	0,06%	21	0,00%	0,00%	0,345
<i>Cytobacillus firmus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Cytobacillus</i> unknown_species	23	0,01%	0,04%	21	0,00%	0,00%	0,345
<i>Dehalobacterium</i> unknown_species	23	0,01%	0,05%	21	0,01%	0,04%	0,908
<i>Demequina</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Dietzia aerolata</i>	23	0,13%	0,15%	21	0,03%	0,07%	0,005
<i>Dietzia</i> unknown_species	23	0,10%	0,15%	21	0,03%	0,06%	0,032
<i>Dolosigranulum</i> unknown_species	23	1,04%	4,12%	21	1,21%	5,04%	0,903
<i>Dubosiella</i> unknown_species	23	0,01%	0,07%	21	0,00%	0,00%	0,345
<i>Dyadobacter</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Eggerthella</i> unknown_species	23	0,00%	0,02%	21	0,01%	0,04%	0,650
<i>Eggerthia</i> unknown_species	23	0,05%	0,17%	21	0,00%	0,00%	0,173
<i>Emergencia</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Endozoicomonas</i> unknown_species	23	0,02%	0,08%	21	0,01%	0,03%	0,329
<i>Enterobacter asburiae</i>	23	0,03%	0,08%	21	0,00%	0,01%	0,146
<i>Enterobacter bugandensis</i>	23	0,46%	1,14%	21	0,12%	0,43%	0,193
<i>Enterobacter hormaechei</i>	23	0,98%	2,38%	21	0,26%	0,86%	0,183
<i>Enterobacter</i> unknown_species	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Enterococcus aquimarinus</i>	23	0,33%	1,25%	21	0,01%	0,05%	0,238
<i>Enterococcus casseliflavus</i>	23	0,00%	0,02%	21	0,02%	0,08%	0,428

<i>Enterococcus cecorum</i>	23	0,01%	0,06%	21	0,00%	0,00%	0,345
<i>Enterococcus durans</i>	23	0,00%	0,00%	21	0,03%	0,11%	0,176
<i>Enterococcus faecalis</i>	23	0,06%	0,19%	21	0,01%	0,04%	0,263
<i>Enterococcus faecium</i>	23	0,01%	0,03%	21	0,01%	0,04%	0,828
<i>Enterococcus gallinarum</i>	23	0,00%	0,00%	21	0,06%	0,29%	0,329
<i>Enterococcus hirae</i>	23	0,02%	0,08%	21	0,00%	0,00%	0,193
<i>Enterococcus pseudoavium</i>	23	0,03%	0,09%	21	0,00%	0,00%	0,138
<i>Enterococcus saccharolyticus</i>	23	1,29%	2,69%	21	2,19%	8,63%	0,636
<i>Enterococcus unknown_species</i>	23	1,26%	3,50%	21	0,12%	0,33%	0,136
<i>Entomoplasma unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Escherichia coli</i>	23	0,20%	0,52%	21	0,51%	2,12%	0,492
<i>Escherichia marmotae</i>	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Eubacterium unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Exiguobacterium acetylicum</i>	23	0,09%	0,24%	21	0,01%	0,06%	0,162
<i>Exiguobacterium chiriqhucha</i>	23	0,09%	0,17%	21	0,03%	0,05%	0,121
<i>Exiguobacterium indicum</i>	23	0,03%	0,14%	21	0,00%	0,00%	0,345
<i>Exiguobacterium unknown_species</i>	23	0,05%	0,15%	21	0,00%	0,00%	0,162
<i>Facklamia unknown_species</i>	23	0,53%	0,57%	21	0,11%	0,19%	0,003
<i>Faecalibacillus intestinalis</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Faecalibacillus unknown_species</i>	23	0,04%	0,09%	21	0,00%	0,00%	0,033
<i>Faecalicoccus unknown_species</i>	23	0,03%	0,07%	21	0,02%	0,09%	0,820
<i>Faecalitalea unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Fenollaria unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Filifactor unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Flavobacterium unknown_species</i>	23	0,00%	0,02%	21	0,01%	0,02%	0,943
<i>Flavonifractor unknown_species</i>	23	0,00%	0,02%	21	0,00%	0,02%	0,946
<i>Frankia coriariae</i>	23	0,01%	0,05%	21	0,00%	0,00%	0,345
<i>Fusobacterium necrophorum</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Fusobacterium unknown_species</i>	23	0,00%	0,00%	21	0,04%	0,13%	0,163
<i>Gemella unknown_species</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,170
<i>Georgenia unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Gilliamella unknown_species</i>	23	0,01%	0,04%	21	0,00%	0,00%	0,345
<i>Globicatella sanguinis</i>	23	0,53%	0,54%	21	0,12%	0,21%	0,002
<i>Globicatella unknown_species</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Gordonibacter unknown_species</i>	23	0,03%	0,14%	21	0,00%	0,00%	0,256
<i>Gottschalkia unknown_species</i>	23	0,01%	0,04%	21	0,00%	0,00%	0,345
<i>Gudongella unknown_species</i>	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Haloactinobacterium unknown_species</i>	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Haloglycomyces unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Haloplasma unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Helcococcus kunzii</i>	23	0,01%	0,06%	21	0,87%	3,98%	0,337
<i>Helcococcus unknown_species</i>	23	0,03%	0,07%	21	0,03%	0,09%	0,908
<i>Holdemania unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Hungateiclostridium unknown_species</i>	23	0,01%	0,04%	21	0,00%	0,00%	0,203
<i>Ilumatobacter unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Inediibacterium unknown_species</i>	23	0,05%	0,16%	21	0,00%	0,00%	0,162
<i>Intestinibacter unknown_species</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,345

<i>Intestinibaculum porci</i>	23	0,01%	0,04%	21	0,00%	0,00%	0,345
<i>Intestinibaculum unknown_species</i>	23	0,03%	0,08%	21	0,01%	0,06%	0,479
<i>Intestinimonas unknown_species</i>	23	0,06%	0,15%	21	0,03%	0,13%	0,520
<i>Isoptericola unknown_species</i>	23	0,37%	0,48%	21	0,06%	0,10%	0,006
<i>Janibacter unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Janthinobacterium unknown_species</i>	23	0,15%	0,31%	21	0,04%	0,09%	0,110
<i>Jeotgalibaca arthritidis</i>	23	0,82%	0,79%	21	0,21%	0,39%	0,003
<i>Jeotgalibaca porci</i>	23	0,50%	2,10%	21	0,10%	0,31%	0,384
<i>Jeotgalibaca unknown_species</i>	23	0,12%	0,28%	21	0,06%	0,13%	0,379
<i>Jeotgalicoccus coquinae</i>	23	0,09%	0,19%	21	0,04%	0,14%	0,316
<i>Jeotgalicoccus saudimassiliensis</i>	23	0,22%	0,30%	21	0,29%	0,64%	0,649
<i>Jeotgalicoccus unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Kallipyga unknown_species</i>	23	0,00%	0,00%	21	0,02%	0,08%	0,329
<i>Klebsiella grimontii</i>	23	0,01%	0,04%	21	0,38%	1,56%	0,290
<i>Klebsiella michiganensis</i>	23	0,00%	0,00%	21	0,04%	0,19%	0,329
<i>Klebsiella unknown_species</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Knoellia sinensis</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Kocuria unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Kroppenstedtia unknown_species</i>	23	0,05%	0,17%	21	0,01%	0,04%	0,324
<i>Kurthia huakuii</i>	23	1,72%	1,77%	21	0,80%	1,87%	0,104
<i>Kurthia unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Lactobacillus acidipiscis</i>	23	0,01%	0,03%	21	0,13%	0,42%	0,182
<i>Lactobacillus amylovorus</i>	23	0,10%	0,33%	21	0,03%	0,09%	0,384
<i>Lactobacillus crispatus</i>	23	0,14%	0,67%	21	0,00%	0,00%	0,345
<i>Lactobacillus delbrueckii</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Lactobacillus farciminis</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Lactobacillus ginsenosidimitans</i>	23	0,08%	0,29%	21	0,18%	0,69%	0,541
<i>Lactobacillus iners</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Lactobacillus mucosae</i>	23	0,05%	0,25%	21	0,00%	0,00%	0,345
<i>Lactobacillus parabuchneri</i>	23	2,18%	10,43%	21	0,00%	0,00%	0,345
<i>Lactobacillus paracasei</i>	23	0,02%	0,08%	21	0,00%	0,00%	0,345
<i>Lactobacillus reuteri</i>	23	0,04%	0,16%	21	0,03%	0,16%	0,860
<i>Lactobacillus unknown_species</i>	23	0,00%	0,00%	21	0,02%	0,10%	0,329
<i>Lactococcus garvieae</i>	23	0,96%	4,58%	21	0,00%	0,00%	0,342
<i>Lactococcus lactis</i>	23	0,00%	0,00%	21	2,72%	12,48%	0,329
<i>Lactococcus petauri</i>	23	0,02%	0,11%	21	0,11%	0,44%	0,332
<i>Lactococcus unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Lagierella massiliensis</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Lagierella unknown_species</i>	23	0,01%	0,05%	21	0,00%	0,00%	0,345
<i>Lancefieldella unknown_species</i>	23	0,04%	0,19%	21	0,01%	0,03%	0,446
<i>Lawsonella unknown_species</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,172
<i>Lentibacillus unknown_species</i>	23	0,01%	0,06%	21	0,00%	0,00%	0,345
<i>Leptothrix unknown_species</i>	23	0,03%	0,09%	21	0,00%	0,00%	0,085
<i>Levyella unknown_species</i>	23	0,15%	0,29%	21	0,04%	0,13%	0,083
<i>Longibaculum unknown_species</i>	23	0,12%	0,23%	21	0,01%	0,06%	0,044
<i>Longicatena unknown_species</i>	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Longimicrobium unknown_species</i>	23	0,02%	0,07%	21	0,01%	0,04%	0,563
<i>Luteimonas arsenica</i>	23	0,03%	0,07%	21	0,00%	0,00%	0,064

<i>Luteimonas</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Luteococcus</i> unknown_species	23	0,02%	0,05%	21	0,00%	0,00%	0,114
<i>Lysinibacillus capsici</i>	23	2,95%	3,27%	21	1,89%	4,92%	0,404
<i>Lysinibacillus</i> unknown_species	23	0,17%	0,26%	21	0,02%	0,09%	0,015
<i>Lysobacter</i> unknown_species	23	1,06%	1,59%	21	2,40%	10,51%	0,549
<i>Macrococcus bohemicus</i>	23	0,22%	0,65%	21	0,57%	1,93%	0,414
<i>Macrococcus canis</i>	23	1,12%	2,33%	21	0,17%	0,34%	0,067
<i>Macrococcus</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,02%	0,827
<i>Mahella</i> unknown_species	23	0,01%	0,04%	21	0,00%	0,00%	0,170
<i>Mailhella</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Marihabitans</i> unknown_species	23	1,57%	5,79%	21	1,31%	5,07%	0,876
<i>Marinilactibacillus</i> unknown_species	23	0,00%	0,01%	21	0,00%	0,00%	0,345
<i>Marinobacterium</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Marinococcus halophilus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Marinospirillum</i> unknown_species	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Marmoricola</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Massilimaliae</i> unknown_species	23	0,00%	0,00%	21	0,02%	0,08%	0,329
<i>Megasphaera elsdenii</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Methanobrevibacter</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Microbacterium</i> unknown_species	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Micrococcus lylae</i>	23	0,01%	0,07%	21	0,03%	0,12%	0,670
<i>Miniphocibacter</i> unknown_species	23	0,09%	0,35%	21	0,01%	0,03%	0,256
<i>Mitsuokella</i> unknown_species	23	0,03%	0,08%	21	0,02%	0,11%	0,762
<i>Mobilibacterium</i> unknown_species	23	0,01%	0,04%	21	0,00%	0,00%	0,345
<i>Mogibacterium</i> unknown_species	23	0,10%	0,15%	21	0,02%	0,08%	0,032
<i>Moraxella osloensis</i>	23	0,03%	0,12%	21	0,00%	0,00%	0,220
<i>Moraxella</i> unknown_species	23	0,05%	0,19%	21	0,00%	0,00%	0,233
<i>Mycoplasma</i> unknown_species	23	0,14%	0,26%	21	0,04%	0,18%	0,123
<i>Myroides</i> unknown_species	23	0,00%	0,02%	21	0,01%	0,04%	0,552
<i>Ndongobacter</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Neobacillus</i> unknown_species	23	0,02%	0,04%	21	0,00%	0,02%	0,186
<i>Nocardioides</i> unknown_species	23	0,28%	0,66%	21	0,02%	0,07%	0,070
<i>Oceanobacillus</i> unknown_species	23	0,20%	0,35%	21	0,01%	0,07%	0,019
<i>Olsenella umbonata</i>	23	0,02%	0,05%	21	0,00%	0,00%	0,162
<i>Olsenella</i> unknown_species	23	0,15%	0,26%	21	0,02%	0,06%	0,033
<i>Ornithinococcus hortensis</i>	23	0,01%	0,04%	21	0,00%	0,00%	0,345
<i>Ornithinococcus</i> unknown_species	23	0,01%	0,05%	21	0,00%	0,00%	0,345
<i>Ornithinimicrobium</i> unknown_species	23	0,53%	0,97%	21	0,11%	0,19%	0,061
<i>Oscillibacter</i> unknown_species	23	0,00%	0,02%	21	0,01%	0,03%	0,689
<i>Paenarthrobacter</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Paeniclostridium sordellii</i>	23	0,33%	0,38%	21	0,08%	0,18%	0,007
<i>Paeniclostridium</i> unknown_species	23	0,86%	1,12%	21	0,21%	0,39%	0,015
<i>Pantoea agglomerans</i>	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Paraclostridium bifermentans</i>	23	2,22%	2,38%	21	0,54%	1,06%	0,004
<i>Paraclostridium</i> unknown_species	23	0,62%	0,72%	21	0,19%	0,32%	0,013
<i>Parapedobacter</i> unknown_species	23	0,00%	0,01%	21	0,00%	0,00%	0,345
<i>Parvimonas</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Pediococcus pentosaceus</i>	23	0,00%	.00000a	21	0,00%	.00000a	

<i>Peptacetobacter</i> unknown_species	23	0,03%	0,15%	21	0,01%	0,03%	0,454
<i>Peptoclostridium</i> unknown_species	23	0,01%	0,03%	21	0,01%	0,03%	0,800
<i>Peptoniphilus indolicus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Peptoniphilus pacaensis</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Peptoniphilus</i> unknown_species	23	0,03%	0,14%	21	0,00%	0,00%	0,345
<i>Peptoniphilus vaginalis</i>	23	0,02%	0,11%	21	0,00%	0,00%	0,345
<i>Peptostreptococcus russellii</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Peptostreptococcus</i> unknown_species	23	0,00%	0,00%	21	0,01%	0,03%	0,329
<i>Peribacillus</i> unknown_species	23	0,02%	0,05%	21	0,00%	0,00%	0,075
<i>Phascolarctobacterium</i> unknown_species	23	0,02%	0,08%	21	0,00%	0,00%	0,345
<i>Phocaeicola</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Planococcus</i> unknown_species	23	0,13%	0,29%	21	0,03%	0,07%	0,152
<i>Planomicrobium glaciei</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Plesiomonas</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Prevotella</i> unknown_species	23	0,02%	0,07%	21	0,00%	0,00%	0,162
<i>Pseudactinotalea</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Pseudoalteromonas translucida</i>	23	0,00%	0,00%	21	0,01%	0,03%	0,329
<i>Pseudoflavonifractor</i> unknown_species	23	0,07%	0,15%	21	0,02%	0,10%	0,180
<i>Pseudohongiella</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Pseudomonas flexibilis</i>	23	0,03%	0,07%	21	0,00%	0,00%	0,089
<i>Pseudomonas saudiphocaensis</i>	23	0,02%	0,10%	21	0,00%	0,00%	0,345
<i>Pseudomonas stutzeri</i>	23	0,00%	0,00%	21	0,02%	0,09%	0,238
<i>Pseudomonas</i> unknown_species	23	0,00%	0,02%	21	0,19%	0,51%	0,110
<i>Psychrobacillus</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Psychrobacter phenylpyruvicus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Ralstonia pickettii</i>	23	0,00%	0,00%	21	0,00%	0,01%	0,163
<i>Rhodococcus</i> unknown_species	23	0,06%	0,20%	21	0,00%	0,00%	0,186
<i>Romboutsia hominis</i>	23	0,01%	0,03%	21	0,00%	0,00%	0,345
<i>Romboutsia ilealis</i>	23	4,83%	5,11%	21	0,87%	1,95%	0,002
<i>Romboutsia timonensis</i>	23	1,33%	1,40%	21	0,22%	0,50%	0,001
<i>Romboutsia</i> unknown_species	23	3,40%	3,03%	21	0,75%	1,37%	0,001
<i>Rummeliibacillus</i> unknown_species	23	0,37%	0,82%	21	0,14%	0,36%	0,257
<i>Saccharopolyspora</i> unknown_species	23	0,01%	0,02%	21	0,00%	0,01%	0,356
<i>Salinicoccus</i> unknown_species	23	0,02%	0,06%	21	0,00%	0,00%	0,174
<i>Salipaludibacillus</i> unknown_species	23	0,01%	0,03%	21	0,00%	0,02%	0,460
<i>Selenomonas</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Senegalia</i> unknown_species	23	0,02%	0,06%	21	0,00%	0,00%	0,196
<i>Serinicoccus</i> unknown_species	23	0,04%	0,15%	21	0,00%	0,00%	0,206
<i>Serratia fonticola</i>	23	0,07%	0,33%	21	0,00%	0,00%	0,345
<i>Serratia</i> unknown_species	23	0,02%	0,09%	21	0,00%	0,00%	0,345
<i>Serratia ureilytica</i>	23	0,34%	1,64%	21	0,00%	0,00%	0,345
<i>Slackia</i> unknown_species	23	0,01%	0,06%	21	0,00%	0,00%	0,345
<i>Sneathia</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Solibacillus isronensis</i>	23	0,04%	0,07%	21	0,01%	0,02%	0,029
<i>Solibacillus</i> unknown_species	23	0,33%	0,40%	21	0,16%	0,24%	0,106
<i>Spiroplasma</i> unknown_species	23	0,01%	0,06%	21	0,01%	0,06%	0,937
<i>Sporosarcina</i> unknown_species	23	0,12%	0,48%	21	0,03%	0,12%	0,397

<i>Staphylococcus arlettae</i>	23	0,01%	0,03%	21	0,01%	0,06%	0,671
<i>Staphylococcus aureus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Staphylococcus auricularis</i>	23	0,19%	0,53%	21	0,01%	0,04%	0,118
<i>Staphylococcus capitis</i>	23	0,06%	0,19%	21	0,15%	0,71%	0,555
<i>Staphylococcus chromogenes</i>	23	10,03%	17,86%	21	8,90%	18,76%	0,839
<i>Staphylococcus cohnii</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Staphylococcus epidermidis</i>	23	0,05%	0,12%	21	1,21%	4,97%	0,297
<i>Staphylococcus equorum</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Staphylococcus felis</i>	23	0,01%	0,05%	21	0,00%	0,00%	0,345
<i>Staphylococcus gallinarum</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Staphylococcus haemolyticus</i>	23	1,28%	3,47%	21	2,93%	12,56%	0,548
<i>Staphylococcus hominis</i>	23	0,08%	0,15%	21	0,11%	0,22%	0,649
<i>Staphylococcus hyicus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Staphylococcus microti</i>	23	0,20%	0,34%	21	0,18%	0,58%	0,863
<i>Staphylococcus muscae</i>	23	2,41%	4,60%	21	0,93%	2,84%	0,204
<i>Staphylococcus petrasii</i>	23	0,01%	0,05%	21	0,01%	0,03%	0,525
<i>Staphylococcus saprophyticus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Staphylococcus sciuri</i>	23	0,21%	0,99%	21	0,00%	0,00%	0,334
<i>Staphylococcus simulans</i>	23	0,18%	0,37%	21	2,19%	8,82%	0,308
<i>Staphylococcus unknown_species</i>	23	12,49%	18,39%	21	6,00%	11,39%	0,172
<i>Staphylococcus xylosus</i>	23	0,06%	0,14%	21	0,07%	0,23%	0,754
<i>Stenotrophomonas ginsengisoli</i>	23	0,00%	0,00%	21	0,02%	0,08%	0,329
<i>Stenotrophomonas koreensis</i>	23	0,03%	0,10%	21	0,06%	0,17%	0,600
<i>Stenotrophomonas maltophilia</i>	23	0,13%	0,64%	21	0,03%	0,12%	0,491
<i>Streptococcus cristatus</i>	23	0,02%	0,08%	21	0,00%	0,00%	0,345
<i>Streptococcus dysgalactiae</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Streptococcus equinus</i>	23	0,07%	0,21%	21	0,00%	0,00%	0,123
<i>Streptococcus gordonii</i>	23	0,02%	0,08%	21	0,00%	0,00%	0,166
<i>Streptococcus halotolerans</i>	23	0,03%	0,16%	21	0,01%	0,03%	0,465
<i>Streptococcus salivarius</i>	23	0,10%	0,48%	21	0,00%	0,00%	0,345
<i>Streptococcus thermophilus</i>	23	0,21%	0,98%	21	0,00%	0,00%	0,345
<i>Streptococcus uberis</i>	23	0,02%	0,08%	21	20,68%	35,11%	0,014
<i>Streptococcus unknown_species</i>	23	0,13%	0,37%	21	10,80%	28,27%	0,099
<i>Streptococcus vestibularis</i>	23	0,16%	0,78%	21	0,00%	0,00%	0,345
<i>Suicoccus unknown_species</i>	23	0,16%	0,25%	21	0,03%	0,07%	0,023
<i>Tessaracoccus unknown_species</i>	23	0,14%	0,22%	21	0,07%	0,14%	0,224
<i>Tetragenococcus halophilus</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Tetragenococcus unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Tetrasphaera elongata</i>	23	0,23%	0,41%	21	0,07%	0,14%	0,093
<i>Tetrasphaera unknown_species</i>	23	0,05%	0,25%	21	0,00%	0,00%	0,345
<i>Thalassolituus unknown_species</i>	23	0,04%	0,09%	21	0,00%	0,00%	0,044
<i>Thauera phenolivorans</i>	23	0,01%	0,02%	21	0,01%	0,04%	0,453
<i>Thauera unknown_species</i>	23	0,02%	0,11%	21	0,00%	0,00%	0,345
<i>Thermoanaerobacter unknown_species</i>	23	0,01%	0,05%	21	0,00%	0,00%	0,345
<i>Thermovirga unknown_species</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Tissierella unknown_species</i>	23	0,05%	0,10%	21	0,00%	0,00%	0,022
<i>Traorella unknown_species</i>	23	0,04%	0,15%	21	0,14%	0,57%	0,430
<i>Treponema unknown_species</i>	23	0,01%	0,04%	21	0,01%	0,03%	0,550

<i>Trichococcus</i> unknown_species	23	0,03%	0,15%	21	0,00%	0,00%	0,345
<i>Trueperella pyogenes</i>	23	0,00%	0,00%	21	0,15%	0,67%	0,329
<i>Trueperella</i> unknown_species	23	0,05%	0,17%	21	0,02%	0,06%	0,375
<i>Tumebacillus</i> unknown_species	23	0,00%	0,02%	21	0,00%	0,00%	0,345
<i>Turicibacter sanguinis</i>	23	5,30%	6,31%	21	1,11%	2,20%	0,006
<i>Turicibacter</i> unknown_species	23	6,78%	7,05%	21	1,85%	2,68%	0,004
<i>Urinicoccus</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Vaginisenegalia</i> unknown_species	23	0,21%	0,48%	21	0,07%	0,28%	0,250
<i>Virgibacillus</i> unknown_species	23	0,04%	0,09%	21	0,00%	0,00%	0,060
<i>Weissella jogaejeotgali</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Weissella paramesenteroides</i>	23	0,00%	.00000a	21	0,00%	.00000a	
<i>Weissella</i> unknown_species	23	0,00%	.00000a	21	0,00%	.00000a	

Table S5: Student's T-test statistical analyses to compare the relative abundances of taxonomic profiles of milk samples from healthy and subclinical mastitis-affected cows, divided per stable. Significant p-value are highlighted in green.

However, the fact that these microbial species corresponded to taxa not yet isolated strengthen the notion that a culture-based research effort is required for the isolation and characterization of potential microbial markers of a healthy or SM status.

Conversely, *Streptococcus uberis* was identified as the only bacterial species, among those taxa that significantly differed between the two cow groups, with a significantly higher relative abundance in the milk samples of cows with SM when compared to the those from healthy cows (Student's T-test p-value = 0.013) (Figure 3, Table S4 and Table S5).

S. uberis has been widely described as a common pathogen strictly related with both clinical and subclinical mastitis thanks to its ability to persist under environmental stress or exposure to antibiotic treatment inducing biofilm formation when in contact with α - and β -casein milk component (39-42).

Thus, indicating *S. uberis* as the potential responsible microorganism of the bovine intramammary infection in stable 2 and electing this taxon as biomarker of subclinical mastitis.

Overall, these results not only reinforce the above-mentioned evidence that SM induces different variations in the microbial composition of bovine milk depending on the environment, but also underline that the microbial etiological agents of SM differ across stables.

Thus, suggesting that the characterization and identification of the microbial agents causing SM is essential to activate targeted strategies to limit the diffusion of the intramammary gland infection.

3.5 Bacterial cell count-dependent taxonomical differences in the milk microbiota of healthy and SM-affected cows

To evaluate whether SM may have an impact on the overall number of the bacterial cells present in bovine milk, each collected milk sample was subjected to a flow cytometry-based total bacterial cell enumeration.

Interestingly, for both stables, the average of the microbial cell number present in the milk samples collected from cows with SM was significantly higher when compared to that observed for samples from healthy cows (Student's T-test p-value of 0.002 and 0.001 for stable 1 and 2, respectively) (Figure 3 and Table S6).

Indeed, the average of the flow cytometry readouts related to milk samples from cows with SM exceeded by at least 3 times the observed average number of bacterial cells in milk samples from healthy cows for both stables, with an average of $1.84E+06$ and $1.26E+06$ cells/ml for milk from healthy cows and $6.33E+06$ and $8.34E+06$ cells/ml for milk from SM-affected cows for stable 1 and 2, respectively (Figure 3 and Table S6).

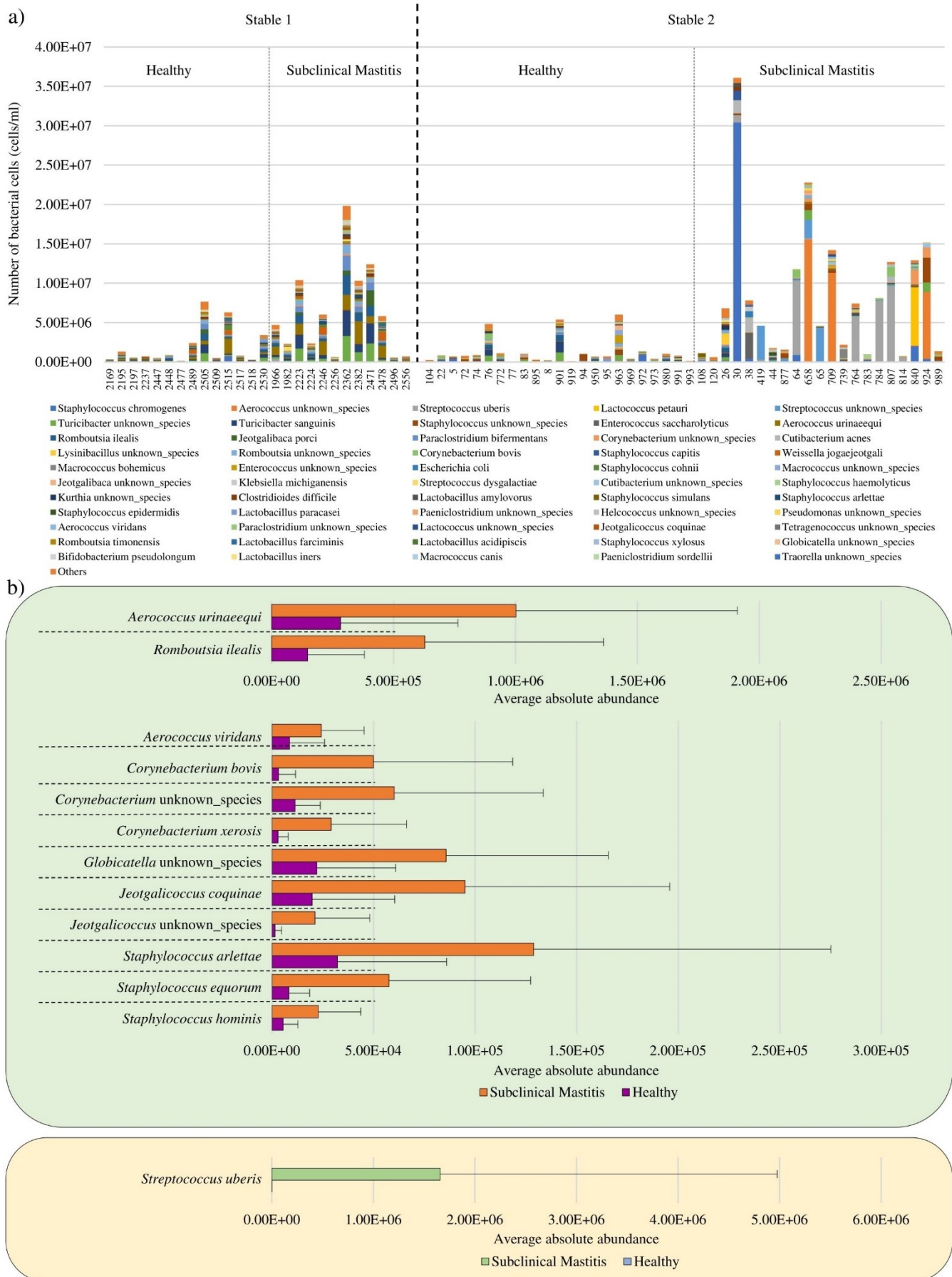


Figure 3: Evaluation of milk total bacterial counts between healthy and SM-affected cows. Panel a reports the bar plot showing the taxonomic profiles of each milk sample normalized for the flow cytometry-based bacterial cell enumeration. Panel b and c display the microbial species whose absolute abundance differed between healthy and SM-affected cows in stable 1 and 2, respectively.

Species	Stable 1						
	Number of samples - Healthy	Average relative abundance - Healthy	Standard deviation - Healthy	Number of samples - Subclinical Mastitis	Average relative abundance - Subclinical Mastitis	Standard deviation - Subclinical Mastitis	p-value
<i>Abiotrophia</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Absicoccus</i> unknown_species	14	2,69E+02	1,01E+03	12	0,00E+00	0,00E+00	0,365
<i>Acholeplasma</i> unknown_species	14	9,64E+03	2,84E+04	12	1,95E+04	4,24E+04	0,486
<i>Achromobacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Acinetobacter indicus</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Acinetobacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Actinotalea</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Adlercreutzia</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Aequorivita</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Aerococcus</i> unknown_species	14	1,12E+04	1,85E+04	12	3,26E+04	3,34E+04	0,064
<i>Aerococcus urinaeequi</i>	14	2,82E+05	4,82E+05	12	1,00E+06	9,09E+05	0,025
<i>Aerococcus viridans</i>	14	8,57E+03	1,73E+04	12	2,43E+04	2,10E+04	0,047
<i>Aeromicrobium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Agarilytica</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Agathobaculum</i> unknown_species	14	3,04E+01	1,14E+02	12	0,00E+00	0,00E+00	0,365
<i>Akkermansia muciniphila</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Alistipes</i> unknown_species	14	0,00E+00	0,00E+00	12	1,07E+03	3,72E+03	0,339
<i>Alkaliphilus</i> unknown_species	14	7,56E+01	2,42E+02	12	0,00E+00	0,00E+00	0,263
<i>Amedibacterium</i> unknown_species	14	0,00E+00	0,00E+00	12	3,49E+02	1,21E+03	0,339
<i>Aminipila</i> unknown_species	14	8,84E+02	2,27E+03	12	1,14E+03	3,19E+03	0,812
<i>Anaerobiospirillum</i> unknown_species	14	7,33E+02	2,04E+03	12	0,00E+00	0,00E+00	0,203
<i>Anaerococcus</i> unknown_species	14	1,92E+03	4,54E+03	12	4,26E+03	8,71E+03	0,387
<i>Anaerorhabdus</i> unknown_species	14	3,41E+03	6,83E+03	12	2,86E+03	7,52E+03	0,846
<i>Arcanobacterium</i> unknown_species	14	6,72E+02	1,44E+03	12	3,38E+03	1,17E+04	0,398
<i>Aromatoleum</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Bacillus aryabhattai</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Bacillus licheniformis</i>	14	2,66E+02	9,94E+02	12	0,00E+00	0,00E+00	0,365
<i>Bacillus megaterium</i>	14	8,01E+01	3,00E+02	12	1,84E+02	6,37E+02	0,591
<i>Bacillus subtilis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Bacillus</i> unknown_species	14	7,32E+02	1,60E+03	12	1,75E+03	4,19E+03	0,408
<i>Bacillus velezensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Bacteriovorax</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Beduini</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Beutenbergia</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Bifidobacterium merycicum</i>	14	1,78E+03	6,10E+03	12	6,80E+03	1,59E+04	0,319
<i>Bifidobacterium pseudolongum</i>	14	9,10E+03	2,04E+04	12	3,41E+04	6,77E+04	0,240
<i>Bifidobacterium scardovii</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Bifidobacterium</i> unknown_species	14	2,66E+01	9,94E+01	12	6,33E+01	2,19E+02	0,578
<i>Bilophila wadsworthia</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Blautia</i> unknown_species	14	6,61E+02	2,07E+03	12	0,00E+00	0,00E+00	0,255
<i>Brachybacterium massiliense</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Brachybacterium</i> unknown_species	14	2,15E+02	4,27E+02	12	2,96E+03	6,96E+03	0,200

<i>Brevibacterium frigoritolerans</i>	14	0,00E+00	0,00E+00	12	1,32E+02	4,59E+02	0,339
<i>Brevibacterium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Brevilactibacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Bulleidia</i> unknown_species	14	3,84E+02	1,25E+03	12	8,81E+03	2,06E+04	0,184
<i>Burkholderia stabilis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Butyrivicoccus</i> unknown_species	14	8,55E+02	2,62E+03	12	2,28E+03	7,88E+03	0,530
<i>Carnobacterium</i> unknown_species	14	2,12E+03	4,71E+03	12	8,26E+03	9,13E+03	0,052
<i>Cecembia</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Cellulomonas</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Clostridioides difficile</i>	14	3,69E+04	7,08E+04	12	1,25E+05	1,53E+05	0,086
<i>Clostridioides</i> unknown_species	14	1,04E+04	1,91E+04	12	2,77E+04	3,22E+04	0,120
<i>Clostridium bornimense</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Clostridium botulinum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Clostridium perfringens</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Clostridium</i> unknown_species	14	3,93E+03	7,58E+03	12	1,17E+04	1,57E+04	0,140
<i>Comamonas</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Corynebacterium bovis</i>	14	3,14E+03	8,46E+03	12	4,99E+04	6,86E+04	0,038
<i>Corynebacterium camporealensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Corynebacterium frankenforstense</i>	14	4,14E+03	7,79E+03	12	8,90E+03	1,52E+04	0,314
<i>Corynebacterium propinquum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Corynebacterium sanguinis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Corynebacterium</i> unknown_species	14	1,13E+04	1,25E+04	12	6,01E+04	7,34E+04	0,043
<i>Corynebacterium urealyticum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Corynebacterium xerosis</i>	14	2,94E+03	5,02E+03	12	2,91E+04	3,72E+04	0,033
<i>Cutibacterium acnes</i>	14	8,55E+02	3,04E+03	12	7,28E+02	2,28E+03	0,907
<i>Cutibacterium granulosum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Cutibacterium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Cyclobacterium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Cytobacillus firmus</i>	14	6,08E+01	2,28E+02	12	0,00E+00	0,00E+00	0,365
<i>Cytobacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Dehalobacterium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Demequina</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Dietzia aerolata</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Dietzia</i> unknown_species	14	0,00E+00	0,00E+00	12	1,55E+03	5,37E+03	0,339
<i>Dolosigranulum</i> unknown_species	14	4,70E+02	1,19E+03	12	3,71E+03	1,25E+04	0,391
<i>Dubosiella</i> unknown_species	14	2,48E+02	9,29E+02	12	0,00E+00	0,00E+00	0,365
<i>Dyadobacter</i> unknown_species	14	3,87E+01	1,45E+02	12	0,00E+00	0,00E+00	0,365
<i>Eggerthella</i> unknown_species	14	3,50E+01	1,31E+02	12	5,17E+01	1,79E+02	0,786
<i>Eggerthia</i> unknown_species	14	1,56E+03	4,79E+03	12	4,11E+03	1,06E+04	0,424
<i>Emergencia</i> unknown_species	14	8,11E+01	2,71E+02	12	0,00E+00	0,00E+00	0,284
<i>Endozoicomonas</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterobacter asburiae</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterobacter bugandensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterobacter hormaechei</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterobacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterococcus aquimarinus</i>	14	5,58E+03	1,67E+04	12	6,06E+03	1,77E+04	0,944
<i>Enterococcus casseliflavus</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	

<i>Enterococcus cecorum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterococcus durans</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterococcus faecalis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterococcus faecium</i>	14	4,37E+01	1,64E+02	12	0,00E+00	0,00E+00	0,365
<i>Enterococcus gallinarum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterococcus hirae</i>	14	1,94E+03	7,24E+03	12	0,00E+00	0,00E+00	0,365
<i>Enterococcus pseudoavium</i>	14	0,00E+00	0,00E+00	12	3,46E+02	1,20E+03	0,339
<i>Enterococcus saccharolyticus</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Enterococcus unknown_species</i>	14	6,47E+03	1,19E+04	12	1,98E+04	2,52E+04	0,089
<i>Entomoplasma unknown_species</i>	14	4,26E+02	1,59E+03	12	0,00E+00	0,00E+00	0,365
<i>Escherichia coli</i>	14	7,77E+02	2,79E+03	12	0,00E+00	0,00E+00	0,346
<i>Escherichia marmotae</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Eubacterium unknown_species</i>	14	0,00E+00	0,00E+00	12	1,27E+03	4,40E+03	0,339
<i>Exiguobacterium acetylicum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Exiguobacterium chiriqhucha</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Exiguobacterium indicum</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Exiguobacterium unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Facklamia unknown_species</i>	14	4,16E+03	7,70E+03	12	9,56E+03	1,48E+04	0,271
<i>Faecalibacillus intestinalis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Faecalibacillus unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Faecalicoccus unknown_species</i>	14	3,43E+03	7,46E+03	12	8,06E+01	2,79E+02	0,117
<i>Faecalitalea unknown_species</i>	14	2,61E+02	9,75E+02	12	0,00E+00	0,00E+00	0,365
<i>Fenollaria unknown_species</i>	14	0,00E+00	0,00E+00	12	1,73E+02	5,99E+02	0,339
<i>Filifactor unknown_species</i>	14	1,01E+02	3,79E+02	12	1,98E+02	6,85E+02	0,655
<i>Flavobacterium unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Flavonifractor unknown_species</i>	14	1,75E+02	5,64E+02	12	0,00E+00	0,00E+00	0,266
<i>Frankia coriariae</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Fusobacterium necrophorum</i>	14	8,07E+02	1,62E+03	12	3,17E+02	8,67E+02	0,340
<i>Fusobacterium unknown_species</i>	14	1,59E+02	5,94E+02	12	0,00E+00	0,00E+00	0,365
<i>Gemella unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Georgenia unknown_species</i>	14	1,16E+03	3,08E+03	12	2,73E+02	9,44E+02	0,325
<i>Gilliamella unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Globicatella sanguinis</i>	14	2,20E+04	3,89E+04	12	8,57E+04	7,99E+04	0,023
<i>Globicatella unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Gordonibacter unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Gottschalkia unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Gudongella unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Haloactinobacterium unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Haloglycomyces unknown_species</i>	14	0,00E+00	0,00E+00	12	1,74E+02	6,04E+02	0,339
<i>Haloplasma unknown_species</i>	14	7,23E+01	2,70E+02	12	1,67E+02	5,79E+02	0,588
<i>Helcococcus kunzii</i>	14	3,59E+02	1,24E+03	12	1,36E+03	3,19E+03	0,325
<i>Helcococcus unknown_species</i>	14	2,48E+03	4,81E+03	12	1,25E+03	2,57E+03	0,435
<i>Holdemania unknown_species</i>	14	1,47E+01	5,52E+01	12	0,00E+00	0,00E+00	0,365
<i>Hungateiclostridium unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Ilumatobacter unknown_species</i>	14	6,68E+02	2,50E+03	12	1,09E+03	3,60E+03	0,727
<i>Inediibacterium unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Intestinibacter unknown_species</i>	14	1,49E+01	5,57E+01	12	2,21E+03	7,67E+03	0,342

<i>Intestinibaculum porci</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Intestinibaculum</i> unknown_species	14	2,02E+03	3,44E+03	12	2,44E+03	6,36E+03	0,832
<i>Intestinimonas</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Isoptericola</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Janibacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Janthinobacterium</i> unknown_species	14	2,07E+03	4,75E+03	12	4,68E+03	1,19E+04	0,457
<i>Jeotgalibaca arthritidis</i>	14	7,15E+04	1,44E+05	12	2,91E+05	5,56E+05	0,207
<i>Jeotgalibaca porci</i>	14	8,68E+01	3,25E+02	12	1,79E+03	5,90E+03	0,341
<i>Jeotgalibaca</i> unknown_species	14	1,97E+04	4,07E+04	12	9,50E+04	1,01E+05	0,029
<i>Jeotgalicoccus coquinae</i>	14	1,53E+02	5,72E+02	12	0,00E+00	0,00E+00	0,365
<i>Jeotgalicoccus saudimassiliensis</i>	14	1,42E+03	3,25E+03	12	2,11E+04	2,71E+04	0,029
<i>Jeotgalicoccus</i> unknown_species	14	6,45E+01	2,41E+02	12	0,00E+00	0,00E+00	0,365
<i>Kallipyga</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Klebsiella grimontii</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Klebsiella michiganensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Klebsiella</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Knoellia sinensis</i>	14	3,18E+02	5,43E+02	12	1,75E+03	6,07E+03	0,432
<i>Kocuria</i> unknown_species	14	1,93E+01	7,21E+01	12	0,00E+00	0,00E+00	0,365
<i>Kroppenstedtia</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Kurthia huakuii</i>	14	8,16E+02	1,80E+03	12	2,94E+03	6,89E+03	0,318
<i>Kurthia</i> unknown_species	14	2,82E+04	5,48E+04	12	4,89E+04	6,96E+04	0,403
<i>Lactobacillus acidipiscis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lactobacillus amylovorus</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lactobacillus crispatus</i>	14	2,09E+03	7,70E+03	12	0,00E+00	0,00E+00	0,357
<i>Lactobacillus delbrueckii</i>	14	1,98E+04	6,26E+04	12	2,18E+04	7,33E+04	0,942
<i>Lactobacillus farciminis</i>	14	1,46E+03	3,57E+03	12	7,12E+02	2,18E+03	0,536
<i>Lactobacillus ginsenosidimitans</i>	14	2,88E+02	7,76E+02	12	3,31E+03	1,15E+04	0,382
<i>Lactobacillus iners</i>	14	4,43E+01	1,66E+02	12	1,11E+03	3,83E+03	0,358
<i>Lactobacillus mucosae</i>	14	3,92E+02	1,47E+03	12	0,00E+00	0,00E+00	0,365
<i>Lactobacillus parabuchneri</i>	14	2,49E+04	8,94E+04	12	0,00E+00	0,00E+00	0,346
<i>Lactobacillus paracasei</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lactobacillus reuteri</i>	14	7,42E+03	1,47E+04	12	7,29E+03	1,41E+04	0,982
<i>Lactobacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lactococcus garvieae</i>	14	1,13E+04	3,88E+04	12	2,04E+03	7,07E+03	0,424
<i>Lactococcus lactis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lactococcus petauri</i>	14	8,38E+02	2,08E+03	12	0,00E+00	0,00E+00	0,155
<i>Lactococcus</i> unknown_species	14	4,89E+01	1,83E+02	12	1,09E+02	3,79E+02	0,600
<i>Lagierella massiliensis</i>	14	3,86E+01	1,45E+02	12	1,37E+02	4,74E+02	0,467
<i>Lagierella</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lancefieldella</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lawsonella</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lentibacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Leptothrix</i> unknown_species	14	3,33E+03	7,12E+03	12	4,30E+03	8,80E+03	0,759
<i>Levyella</i> unknown_species	14	6,08E+02	1,88E+03	12	1,54E+03	5,34E+03	0,546
<i>Longibaculum</i> unknown_species	14	3,91E+03	5,56E+03	12	1,21E+04	2,03E+04	0,197
<i>Longicatena</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Longimicrobium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Luteimonas arsenica</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	

<i>Luteimonas</i> unknown_species	14	2,13E+03	5,00E+03	12	1,20E+04	1,89E+04	0,104
<i>Luteococcus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lysinibacillus capsici</i>	14	0,00E+00	0,00E+00	12	4,05E+02	1,27E+03	0,293
<i>Lysinibacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Lysobacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Macrococcus bohemicus</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Macrococcus canis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Macrococcus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Mahella</i> unknown_species	14	1,03E+01	3,85E+01	12	0,00E+00	0,00E+00	0,365
<i>Mailhella</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Marihabitans</i> unknown_species	14	1,90E+03	3,60E+03	12	1,02E+04	1,82E+04	0,145
<i>Marinilactibacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Marinobacterium</i> unknown_species	14	1,68E+02	6,28E+02	12	0,00E+00	0,00E+00	0,365
<i>Marinococcus halophilus</i>	14	1,81E+02	6,77E+02	12	0,00E+00	0,00E+00	0,365
<i>Marinospirillum</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Marmoricola</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Massimaliae</i> unknown_species	14	9,87E+02	2,84E+03	12	3,02E+02	1,04E+03	0,438
<i>Megasphaera elsdenii</i>	14	1,44E+01	5,40E+01	12	0,00E+00	0,00E+00	0,365
<i>Methanobrevibacter</i> unknown_species	14	0,00E+00	0,00E+00	12	3,37E+03	1,17E+04	0,339
<i>Microbacterium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Micrococcus lylae</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Miniphocibacter</i> unknown_species	14	1,80E+02	4,60E+02	12	2,45E+03	6,33E+03	0,240
<i>Mitsuokella</i> unknown_species	14	1,78E+01	6,66E+01	12	0,00E+00	0,00E+00	0,365
<i>Mobilibacterium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Mogibacterium</i> unknown_species	14	1,01E+04	2,01E+04	12	2,08E+04	2,71E+04	0,260
<i>Moraxella osloensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Moraxella</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Mycoplasma</i> unknown_species	14	1,03E+04	2,14E+04	12	6,91E+03	1,92E+04	0,673
<i>Myroides</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Ndongobacter</i> unknown_species	14	3,34E+02	1,25E+03	12	0,00E+00	0,00E+00	0,365
<i>Neobacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Nocardioides</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Oceanobacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Olsenella umbonata</i>	14	2,91E+03	1,04E+04	12	2,71E+02	9,38E+02	0,391
<i>Olsenella</i> unknown_species	14	7,06E+03	1,54E+04	12	1,53E+04	2,79E+04	0,351
<i>Ornithinicoccus hortensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Ornithinicoccus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Ornithinimicrobium</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Oscillibacter</i> unknown_species	14	1,35E+02	4,35E+02	12	0,00E+00	0,00E+00	0,265
<i>Paenarthrobacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Paeniclostridium sordellii</i>	14	1,52E+04	2,74E+04	12	4,90E+04	5,69E+04	0,079
<i>Paeniclostridium</i> unknown_species	14	1,72E+04	3,58E+04	12	4,21E+04	4,56E+04	0,133
<i>Pantoea agglomerans</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Paraclostridium bifermentans</i>	14	1,08E+05	1,80E+05	12	4,57E+05	5,53E+05	0,057
<i>Paraclostridium</i> unknown_species	14	1,84E+04	3,36E+04	12	6,58E+04	8,27E+04	0,084
<i>Parapedobacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Parvimonas</i> unknown_species	14	2,37E+02	8,87E+02	12	0,00E+00	0,00E+00	0,365
<i>Pediococcus pentosaceus</i>	14	3,44E+03	9,10E+03	12	1,46E+04	3,53E+04	0,306

<i>Peptacetobacter</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Peptoclostridium</i> unknown_species	14	4,89E+01	1,83E+02	12	0,00E+00	0,00E+00	0,365
<i>Peptoniphilus indolicus</i>	14	0,00E+00	0,00E+00	12	2,01E+02	6,95E+02	0,339
<i>Peptoniphilus pacaensis</i>	14	0,00E+00	0,00E+00	12	1,12E+02	3,88E+02	0,339
<i>Peptoniphilus</i> unknown_species	14	8,24E+02	2,10E+03	12	1,93E+03	3,87E+03	0,365
<i>Peptoniphilus vaginalis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Peptostreptococcus russellii</i>	14	0,00E+00	0,00E+00	12	2,63E+02	9,12E+02	0,339
<i>Peptostreptococcus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Peribacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Phascolarctobacterium</i> unknown_species	14	1,10E+02	4,11E+02	12	0,00E+00	0,00E+00	0,365
<i>Phocaeicola</i> unknown_species	14	1,33E+03	4,65E+03	12	3,38E+02	1,17E+03	0,482
<i>Planococcus</i> unknown_species	14	6,46E+01	2,42E+02	12	1,80E+03	6,23E+03	0,356
<i>Planomicrobium glaciei</i>	14	1,46E+02	5,48E+02	12	0,00E+00	0,00E+00	0,365
<i>Plesiomonas</i> unknown_species	14	0,00E+00	0,00E+00	12	7,95E+02	2,75E+03	0,339
<i>Prevotella</i> unknown_species	14	2,48E+03	8,39E+03	12	0,00E+00	0,00E+00	0,318
<i>Pseudactinotalea</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Pseudoalteromonas translucida</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Pseudoflavonifractor</i> unknown_species	14	3,91E+03	6,94E+03	12	2,03E+03	4,64E+03	0,433
<i>Pseudohongiella</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Pseudomonas flexibilis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Pseudomonas saudiphocaensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Pseudomonas stutzeri</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Pseudomonas</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Psychrobacillus</i> unknown_species	14	0,00E+00	0,00E+00	12	3,78E+01	1,31E+02	0,339
<i>Psychrobacter phenylpyruvicus</i>	14	2,94E+02	7,70E+02	12	0,00E+00	0,00E+00	0,176
<i>Ralstonia pickettii</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Rhodococcus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Romboutsia hominis</i>	14	5,17E+01	1,37E+02	12	3,87E+03	7,85E+03	0,120
<i>Romboutsia ilealis</i>	14	1,48E+05	2,33E+05	12	6,28E+05	7,34E+05	0,049
<i>Romboutsia timonensis</i>	14	3,08E+04	6,93E+04	12	5,60E+04	5,20E+04	0,310
<i>Romboutsia</i> unknown_species	14	7,68E+04	1,28E+05	12	3,01E+05	3,49E+05	0,054
<i>Rummeliibacillus</i> unknown_species	14	1,02E+03	3,00E+03	12	1,80E+03	5,16E+03	0,634
<i>Saccharopolyspora</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Salinicoccus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Salipaludibacillus</i> unknown_species	14	8,08E+02	1,73E+03	12	0,00E+00	0,00E+00	0,103
<i>Selenomonas</i> unknown_species	14	3,55E+01	1,33E+02	12	0,00E+00	0,00E+00	0,365
<i>Senegalia</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Serinicoccus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Serratia fonticola</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Serratia</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Serratia ureilytica</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Slackia</i> unknown_species	14	1,29E+01	4,84E+01	12	2,14E+03	7,43E+03	0,342
<i>Sneathia</i> unknown_species	14	2,18E+02	8,16E+02	12	2,59E+02	8,99E+02	0,903
<i>Solibacillus isronensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Solibacillus</i> unknown_species	14	1,05E+02	3,93E+02	12	1,19E+03	4,12E+03	0,383
<i>Spiroplasma</i> unknown_species	14	3,17E+03	8,18E+03	12	0,00E+00	0,00E+00	0,171
<i>Sporosarcina</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Staphylococcus arlettae</i>	14	3,22E+04	5,38E+04	12	1,29E+05	1,46E+05	0,049

<i>Staphylococcus aureus</i>	14	0,00E+00	0,00E+00	12	1,97E+03	6,83E+03	0,339
<i>Staphylococcus auricularis</i>	14	0,00E+00	0,00E+00	12	2,96E+03	6,76E+03	0,158
<i>Staphylococcus capitis</i>	14	2,22E+02	8,31E+02	12	0,00E+00	0,00E+00	0,365
<i>Staphylococcus chromogenes</i>	14	5,06E+04	1,89E+05	12	0,00E+00	0,00E+00	0,365
<i>Staphylococcus cohnii</i>	14	7,01E+04	1,74E+05	12	8,03E+04	1,02E+05	0,860
<i>Staphylococcus epidermidis</i>	14	4,76E+02	1,09E+03	12	1,19E+04	3,91E+04	0,333
<i>Staphylococcus equorum</i>	14	8,30E+03	1,03E+04	12	5,76E+04	6,98E+04	0,033
<i>Staphylococcus felis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Staphylococcus gallinarum</i>	14	0,00E+00	0,00E+00	12	5,80E+01	2,01E+02	0,339
<i>Staphylococcus haemolyticus</i>	14	0,00E+00	0,00E+00	12	1,54E+03	4,45E+03	0,256
<i>Staphylococcus hominis</i>	14	5,46E+03	7,31E+03	12	2,28E+04	2,09E+04	0,017
<i>Staphylococcus hyicus</i>	14	4,10E+01	1,54E+02	12	3,88E+03	1,15E+04	0,271
<i>Staphylococcus microti</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Staphylococcus muscae</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Staphylococcus petrasii</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Staphylococcus saprophyticus</i>	14	0,00E+00	0,00E+00	12	1,33E+03	3,17E+03	0,173
<i>Staphylococcus sciuri</i>	14	0,00E+00	0,00E+00	12	4,32E+02	1,50E+03	0,339
<i>Staphylococcus simulans</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Staphylococcus unknown_species</i>	14	7,46E+03	1,55E+04	12	2,96E+04	3,62E+04	0,069
<i>Staphylococcus xylosus</i>	14	4,69E+03	6,65E+03	12	4,26E+04	7,10E+04	0,092
<i>Stenotrophomonas ginsengisoli</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Stenotrophomonas koreensis</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Stenotrophomonas maltophilia</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Streptococcus cristatus</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Streptococcus dysgalactiae</i>	14	0,00E+00	0,00E+00	12	8,06E+04	1,70E+05	0,130
<i>Streptococcus equinus</i>	14	1,06E+03	2,44E+03	12	6,66E+03	1,98E+04	0,352
<i>Streptococcus gordonii</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Streptococcus halotolerans</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Streptococcus salivarius</i>	14	2,67E+03	9,43E+03	12	0,00E+00	0,00E+00	0,339
<i>Streptococcus thermophilus</i>	14	2,40E+03	8,53E+03	12	0,00E+00	0,00E+00	0,342
<i>Streptococcus uberis</i>	14	0,00E+00	0,00E+00	12	2,95E+04	1,02E+05	0,339
<i>Streptococcus unknown_species</i>	14	1,86E+03	6,20E+03	12	3,43E+03	7,48E+03	0,565
<i>Streptococcus vestibularis</i>	14	9,16E+02	3,26E+03	12	0,00E+00	0,00E+00	0,341
<i>Suicoccus unknown_species</i>	14	1,00E+02	3,75E+02	12	2,99E+03	1,00E+04	0,339
<i>Tessaracoccus unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Tetragenococcus halophilus</i>	14	8,67E+03	1,97E+04	12	1,47E+04	3,34E+04	0,573
<i>Tetragenococcus unknown_species</i>	14	3,12E+04	7,13E+04	12	4,26E+04	6,15E+04	0,669
<i>Tetrasphaera elongata</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Tetrasphaera unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Thalassolituus unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Thauera phenolivorans</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Thauera unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Thermoanaerobacter unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Thermovirga unknown_species</i>	14	2,15E+02	8,03E+02	12	1,28E+02	4,45E+02	0,744
<i>Tissierella unknown_species</i>	14	4,26E+02	8,73E+02	12	1,09E+03	3,24E+03	0,465
<i>Traorella unknown_species</i>	14	1,63E+03	3,23E+03	12	9,61E+01	3,33E+02	0,101
<i>Treponema unknown_species</i>	14	1,02E+03	3,29E+03	12	0,00E+00	0,00E+00	0,266
<i>Trichococcus unknown_species</i>	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	

<i>Trueperella pyogenes</i>	14	3,13E+02	1,02E+03	12	0,00E+00	0,00E+00	0,269
<i>Trueperella</i> unknown_species	14	3,65E+02	7,74E+02	12	2,52E+03	8,39E+03	0,395
<i>Tumebacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Turicibacter sanguinis</i>	14	1,75E+05	2,83E+05	12	8,39E+05	1,08E+06	0,060
<i>Turicibacter</i> unknown_species	14	1,80E+05	2,90E+05	12	8,08E+05	1,06E+06	0,069
<i>Urinicoccus</i> unknown_species	14	3,62E+02	9,22E+02	12	1,64E+02	5,67E+02	0,523
<i>Vaginisenegalia</i> unknown_species	14	2,82E+02	7,82E+02	12	1,36E+02	4,70E+02	0,577
<i>Virgibacillus</i> unknown_species	14	0,00E+00	.00000 ^a	12	0,00E+00	.00000a	
<i>Weissella jogaejeotgali</i>	14	1,03E+05	1,95E+05	12	2,50E+05	3,94E+05	0,229
<i>Weissella paramesenteroides</i>	14	5,85E+03	1,77E+04	12	1,33E+04	4,14E+04	0,544
<i>Weissella</i> unknown_species	14	5,83E+03	1,46E+04	12	1,29E+04	2,48E+04	0,374

Species	Stable 2						
	Number of samples - Healthy	Average relative abundance - Healthy	Standard deviation - Healthy	Number of samples - Subclinical Mastitis	Average relative abundance - Subclinical Mastitis	Standard deviation - Subclinical Mastitis	p-value
<i>Abiotrophia</i> unknown_species	23	9,01E+01	4,32E+02	21	0,00E+00	0,00E+00	0,345
<i>Absicoccus</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Acholeplasma</i> unknown_species	23	1,03E+04	3,51E+04	21	2,40E+03	7,20E+03	0,317
<i>Achromobacter</i> unknown_species	23	0,00E+00	0,00E+00	21	1,50E+02	6,87E+02	0,329
<i>Acinetobacter indicus</i>	23	0,00E+00	0,00E+00	21	1,28E+02	5,87E+02	0,329
<i>Acinetobacter</i> unknown_species	23	0,00E+00	0,00E+00	21	3,20E+02	1,46E+03	0,329
<i>Actinotalea</i> unknown_species	23	1,05E+01	5,01E+01	21	0,00E+00	0,00E+00	0,345
<i>Adlercreutzia</i> unknown_species	23	2,92E+03	1,10E+04	21	3,77E+02	1,73E+03	0,299
<i>Aequorivita</i> unknown_species	23	8,80E+01	3,17E+02	21	3,71E+01	1,70E+02	0,516
<i>Aerococcus</i> unknown_species	23	8,03E+03	1,76E+04	21	1,69E+06	4,37E+06	0,093
<i>Aerococcus urinaequi</i>	23	5,09E+03	8,19E+03	21	3,36E+04	8,03E+04	0,120
<i>Aerococcus viridans</i>	23	3,07E+01	1,47E+02	21	2,32E+04	7,25E+04	0,159
<i>Aeromicrobium</i> unknown_species	23	2,13E+02	6,59E+02	21	3,80E+01	1,74E+02	0,231
<i>Agarilytica</i> unknown_species	23	1,68E+01	8,04E+01	21	0,00E+00	0,00E+00	0,345
<i>Agathobaculum</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Akkermansia muciniphila</i>	23	9,46E+01	4,54E+02	21	0,00E+00	0,00E+00	0,345
<i>Alistipes</i> unknown_species	23	3,73E+01	1,79E+02	21	0,00E+00	0,00E+00	0,345
<i>Alkaliphilus</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Amedibacterium</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Aminipila</i> unknown_species	23	1,44E+02	5,80E+02	21	1,28E+03	4,24E+03	0,235
<i>Anaerobiospirillum</i> unknown_species	23	6,89E+02	2,42E+03	21	4,86E+02	2,01E+03	0,765
<i>Anaerococcus</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Anaerorhabdus</i> unknown_species	23	2,19E+02	6,85E+02	21	7,73E+02	3,54E+03	0,466
<i>Arcanobacterium</i> unknown_species	23	0,00E+00	0,00E+00	21	1,66E+02	7,61E+02	0,329
<i>Aromatoleum</i> unknown_species	23	6,35E+00	3,04E+01	21	2,07E+03	9,48E+03	0,331
<i>Bacillus aryabhatai</i>	23	0,00E+00	0,00E+00	21	7,55E+02	3,46E+03	0,329
<i>Bacillus licheniformis</i>	23	3,67E+01	1,76E+02	21	0,00E+00	0,00E+00	0,345
<i>Bacillus megaterium</i>	23	2,34E+01	6,89E+01	21	0,00E+00	0,00E+00	0,118
<i>Bacillus subtilis</i>	23	1,06E+02	3,36E+02	21	1,28E+02	5,86E+02	0,878
<i>Bacillus</i> unknown_species	23	2,09E+03	3,45E+03	21	9,10E+03	2,32E+04	0,186

<i>Bacillus velezensis</i>	23	2,45E+01	1,18E+02	21	3,00E+01	1,37E+02	0,888
<i>Bacteriovorax</i> unknown_species	23	3,59E+01	1,72E+02	21	0,00E+00	0,00E+00	0,345
<i>Beduini</i> unknown_species	23	1,18E+03	4,57E+03	21	0,00E+00	0,00E+00	0,228
<i>Beutenbergia</i> unknown_species	23	5,31E+01	2,55E+02	21	0,00E+00	0,00E+00	0,345
<i>Bifidobacterium merycicum</i>	23	9,56E+01	4,59E+02	21	0,00E+00	0,00E+00	0,345
<i>Bifidobacterium pseudolongum</i>	23	2,18E+03	8,40E+03	21	0,00E+00	0,00E+00	0,226
<i>Bifidobacterium scardovii</i>	23	3,47E+02	1,66E+03	21	5,03E+02	2,31E+03	0,796
<i>Bifidobacterium</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Bilophila wadsworthia</i>	23	0,00E+00	0,00E+00	21	5,13E+02	2,35E+03	0,329
<i>Blautia</i> unknown_species	23	6,44E+00	3,09E+01	21	0,00E+00	0,00E+00	0,345
<i>Brachybacterium massiliense</i>	23	1,62E+03	2,62E+03	21	8,66E+02	2,93E+03	0,375
<i>Brachybacterium</i> unknown_species	23	3,75E+02	9,87E+02	21	7,54E+02	2,39E+03	0,489
<i>Brevibacterium frigoritolerans</i>	23	3,30E+03	8,85E+03	21	3,84E+03	1,10E+04	0,857
<i>Brevibacterium</i> unknown_species	23	7,63E+01	2,55E+02	21	0,00E+00	0,00E+00	0,165
<i>Brevilactibacter</i> unknown_species	23	5,24E+01	2,51E+02	21	0,00E+00	0,00E+00	0,345
<i>Bulleidia</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Burkholderia stabilis</i>	23	0,00E+00	0,00E+00	21	4,70E+02	2,16E+03	0,329
<i>Butyricococcus</i> unknown_species	23	5,74E+01	2,75E+02	21	8,83E+02	4,05E+03	0,362
<i>Carnobacterium</i> unknown_species	23	2,01E+01	6,68E+01	21	0,00E+00	0,00E+00	0,163
<i>Cecembia</i> unknown_species	23	7,33E+02	1,24E+03	21	8,86E+03	3,75E+04	0,333
<i>Cellulomonas</i> unknown_species	23	1,11E+02	5,30E+02	21	0,00E+00	0,00E+00	0,345
<i>Clostridioides difficile</i>	23	2,10E+04	4,36E+04	21	3,90E+04	1,17E+05	0,495
<i>Clostridioides</i> unknown_species	23	7,91E+03	1,43E+04	21	1,32E+04	3,03E+04	0,460
<i>Clostridium bornimense</i>	23	8,72E+01	3,39E+02	21	0,00E+00	0,00E+00	0,230
<i>Clostridium botulinum</i>	23	2,08E+02	4,76E+02	21	4,64E+02	2,13E+03	0,576
<i>Clostridium perfringens</i>	23	9,89E+01	4,74E+02	21	4,74E+03	2,11E+04	0,326
<i>Clostridium</i> unknown_species	23	3,42E+03	7,20E+03	21	4,34E+03	1,31E+04	0,772
<i>Comamonas</i> unknown_species	23	0,00E+00	0,00E+00	21	2,96E+02	1,36E+03	0,329
<i>Corynebacterium bovis</i>	23	7,53E+04	1,57E+05	21	1,57E+05	3,27E+05	0,291
<i>Corynebacterium camporealensis</i>	23	4,53E+02	1,57E+03	21	4,84E+03	1,53E+04	0,206
<i>Corynebacterium frankenforstense</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Corynebacterium propinquum</i>	23	0,00E+00	0,00E+00	21	1,26E+03	5,76E+03	0,329
<i>Corynebacterium sanguinis</i>	23	4,30E+01	2,06E+02	21	0,00E+00	0,00E+00	0,345
<i>Corynebacterium</i> unknown_species	23	3,86E+04	6,12E+04	21	2,28E+05	4,73E+05	0,083
<i>Corynebacterium urealyticum</i>	23	0,00E+00	0,00E+00	21	1,05E+03	4,81E+03	0,329
<i>Corynebacterium xerosis</i>	23	4,38E+03	7,81E+03	21	1,99E+04	3,67E+04	0,071
<i>Cutibacterium acnes</i>	23	3,78E+03	7,14E+03	21	2,07E+05	5,35E+05	0,098
<i>Cutibacterium granulosum</i>	23	5,90E+01	2,83E+02	21	0,00E+00	0,00E+00	0,345
<i>Cutibacterium</i> unknown_species	23	1,24E+02	3,38E+02	21	4,77E+04	1,45E+05	0,150
<i>Cyclobacterium</i> unknown_species	23	8,42E+00	4,04E+01	21	0,00E+00	0,00E+00	0,345
<i>Cytobacillus firmus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Cytobacillus</i> unknown_species	23	2,29E+01	1,10E+02	21	0,00E+00	0,00E+00	0,345
<i>Dehalobacterium</i> unknown_species	23	2,08E+01	9,95E+01	21	5,45E+02	2,50E+03	0,348
<i>Demequina</i> unknown_species	23	6,68E+01	3,20E+02	21	0,00E+00	0,00E+00	0,345
<i>Dietzia aerolata</i>	23	1,55E+03	3,38E+03	21	8,58E+02	2,48E+03	0,445
<i>Dietzia</i> unknown_species	23	1,60E+03	3,31E+03	21	7,26E+02	1,82E+03	0,293
<i>Dolosigranulum</i> unknown_species	23	3,47E+03	1,11E+04	21	9,11E+03	3,06E+04	0,413
<i>Dubosiella</i> unknown_species	23	1,50E+02	7,21E+02	21	0,00E+00	0,00E+00	0,345

<i>Dyadobacter</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Eggerthella</i> unknown_species	23	5,00E+00	2,40E+01	21	1,13E+03	5,17E+03	0,331
<i>Eggerthia</i> unknown_species	23	1,38E+03	5,16E+03	21	0,00E+00	0,00E+00	0,215
<i>Emergencia</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Endozaicomonas</i> unknown_species	23	1,94E+02	6,48E+02	21	4,74E+02	2,17E+03	0,558
<i>Enterobacter asburiae</i>	23	8,91E+01	3,00E+02	21	1,80E+01	8,24E+01	0,285
<i>Enterobacter bugandensis</i>	23	1,17E+03	3,32E+03	21	1,42E+03	4,05E+03	0,823
<i>Enterobacter hormaechei</i>	23	2,36E+03	6,72E+03	21	2,92E+03	8,22E+03	0,804
<i>Enterobacter</i> unknown_species	23	1,19E+01	5,73E+01	21	0,00E+00	0,00E+00	0,345
<i>Enterococcus aquimarinus</i>	23	3,21E+03	1,01E+04	21	7,46E+02	3,42E+03	0,295
<i>Enterococcus casseliflavus</i>	23	4,84E+01	2,32E+02	21	6,02E+03	2,76E+04	0,333
<i>Enterococcus cecorum</i>	23	4,64E+01	2,22E+02	21	0,00E+00	0,00E+00	0,345
<i>Enterococcus durans</i>	23	0,00E+00	0,00E+00	21	8,92E+03	3,42E+04	0,246
<i>Enterococcus faecalis</i>	23	1,82E+02	6,85E+02	21	6,16E+01	2,82E+02	0,458
<i>Enterococcus faecium</i>	23	2,78E+01	1,34E+02	21	1,15E+03	5,27E+03	0,341
<i>Enterococcus gallinarum</i>	23	0,00E+00	0,00E+00	21	4,96E+03	2,27E+04	0,329
<i>Enterococcus hirae</i>	23	4,06E+02	1,74E+03	21	0,00E+00	0,00E+00	0,275
<i>Enterococcus pseudoavium</i>	23	5,53E+01	1,57E+02	21	0,00E+00	0,00E+00	0,106
<i>Enterococcus saccharolyticus</i>	23	9,93E+03	1,45E+04	21	1,66E+05	6,75E+05	0,302
<i>Enterococcus</i> unknown_species	23	4,81E+04	2,09E+05	21	1,24E+04	4,73E+04	0,450
<i>Entomoplasma</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Escherichia coli</i>	23	2,64E+03	8,84E+03	21	4,01E+04	1,65E+05	0,313
<i>Escherichia marmotae</i>	23	2,05E+02	9,84E+02	21	0,00E+00	0,00E+00	0,345
<i>Eubacterium</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Exiguobacterium acetylicum</i>	23	3,33E+02	7,88E+02	21	2,37E+02	1,08E+03	0,735
<i>Exiguobacterium chiriqhucha</i>	23	7,27E+02	1,52E+03	21	1,20E+03	2,53E+03	0,449
<i>Exiguobacterium indicum</i>	23	1,18E+02	5,64E+02	21	0,00E+00	0,00E+00	0,345
<i>Exiguobacterium</i> unknown_species	23	1,59E+03	6,56E+03	21	0,00E+00	0,00E+00	0,257
<i>Facklamia</i> unknown_species	23	7,25E+03	1,47E+04	21	3,86E+03	1,05E+04	0,387
<i>Faecalibacillus intestinalis</i>	23	2,35E+01	1,13E+02	21	0,00E+00	0,00E+00	0,345
<i>Faecalibacillus</i> unknown_species	23	4,17E+02	1,30E+03	21	0,00E+00	0,00E+00	0,139
<i>Faecalicoccus</i> unknown_species	23	4,80E+02	1,85E+03	21	1,37E+03	6,28E+03	0,519
<i>Faecalitalea</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Fenollaria</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Filifactor</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Flavobacterium</i> unknown_species	23	3,79E+01	1,82E+02	21	3,66E+02	1,68E+03	0,356
<i>Flavonifractor</i> unknown_species	23	4,97E+01	2,38E+02	21	3,38E+02	1,55E+03	0,383
<i>Frankia coriariae</i>	23	1,13E+01	5,44E+01	21	0,00E+00	0,00E+00	0,345
<i>Fusobacterium necrophorum</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Fusobacterium</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Gemella</i> unknown_species	23	0,00E+00	0,00E+00	21	2,71E+03	1,18E+04	0,304
<i>Georgenia</i> unknown_species	23	7,33E+01	2,56E+02	21	0,00E+00	0,00E+00	0,183
<i>Gilliamella</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Globicatella sanguinis</i>	23	3,02E+01	1,45E+02	21	0,00E+00	0,00E+00	0,345
<i>Globicatella</i> unknown_species	23	5,09E+03	7,95E+03	21	6,35E+03	1,44E+04	0,719
<i>Gordonibacter</i> unknown_species	23	5,87E+01	2,81E+02	21	0,00E+00	0,00E+00	0,345
<i>Gottschalkia</i> unknown_species	23	1,01E+02	3,98E+02	21	0,00E+00	0,00E+00	0,237

<i>Gudongella</i> unknown_species	23	1,99E+01	9,55E+01	21	0,00E+00	0,00E+00	0,345
<i>Haloactinobacterium</i> unknown_species	23	7,28E+00	3,49E+01	21	0,00E+00	0,00E+00	0,345
<i>Haloglycomyces</i> unknown_species	23	4,48E+01	2,15E+02	21	0,00E+00	0,00E+00	0,345
<i>Haloplasma</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Helcococcus kunzii</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Helcococcus</i> unknown_species	23	1,52E+01	7,27E+01	21	1,55E+04	7,09E+04	0,330
<i>Holdemania</i> unknown_species	23	1,14E+02	2,86E+02	21	1,68E+03	6,33E+03	0,271
<i>Hungateiclostridium</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Ilumatobacter</i> unknown_species	23	8,56E+01	3,79E+02	21	0,00E+00	0,00E+00	0,290
<i>Inediibacterium</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Intestinibacter</i> unknown_species	23	1,62E+03	6,62E+03	21	0,00E+00	0,00E+00	0,253
<i>Intestinibaculum porci</i>	23	3,62E+02	1,73E+03	21	0,00E+00	0,00E+00	0,345
<i>Intestinibaculum</i> unknown_species	23	9,16E+00	4,39E+01	21	0,00E+00	0,00E+00	0,345
<i>Intestinimonas</i> unknown_species	23	1,66E+02	6,61E+02	21	9,25E+02	4,24E+03	0,401
<i>Isoptericola</i> unknown_species	23	2,55E+02	6,21E+02	21	2,23E+03	1,02E+04	0,360
<i>Janibacter</i> unknown_species	23	3,56E+03	6,50E+03	21	4,98E+03	1,41E+04	0,666
<i>Janthinobacterium</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Jeotgalibaca arthritidis</i>	23	1,34E+03	2,98E+03	21	1,85E+03	5,85E+03	0,712
<i>Jeotgalibaca porci</i>	23	1,20E+04	2,13E+04	21	1,03E+04	2,15E+04	0,797
<i>Jeotgalibaca</i> unknown_species	23	2,66E+04	1,26E+05	21	1,31E+04	5,72E+04	0,655
<i>Jeotgalicoccus coquinae</i>	23	8,35E+02	2,46E+03	21	1,34E+03	3,60E+03	0,588
<i>Jeotgalicoccus saudimassiliensis</i>	23	7,89E+02	1,79E+03	21	8,66E+02	2,81E+03	0,913
<i>Jeotgalicoccus</i> unknown_species	23	3,82E+03	1,06E+04	21	9,16E+03	2,14E+04	0,293
<i>Kallipyga</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Klebsiella grimontii</i>	23	0,00E+00	0,00E+00	21	1,43E+03	6,56E+03	0,329
<i>Klebsiella michiganensis</i>	23	7,50E+01	3,60E+02	21	3,15E+04	1,22E+05	0,252
<i>Klebsiella</i> unknown_species	23	0,00E+00	0,00E+00	21	6,00E+03	2,75E+04	0,329
<i>Knoellia sinensis</i>	23	5,40E+01	2,59E+02	21	0,00E+00	0,00E+00	0,345
<i>Kocuria</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Kroppenstedtia</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Kurthia huakuii</i>	23	3,83E+02	1,35E+03	21	4,35E+02	1,99E+03	0,919
<i>Kurthia</i> unknown_species	23	2,23E+04	3,95E+04	21	3,41E+04	1,13E+05	0,642
<i>Lactobacillus acidipiscis</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Lactobacillus amylovorus</i>	23	8,07E+01	3,87E+02	21	2,83E+04	1,06E+05	0,238
<i>Lactobacillus crispatus</i>	23	3,63E+02	1,30E+03	21	8,10E+02	2,75E+03	0,488
<i>Lactobacillus delbrueckii</i>	23	9,74E+02	4,67E+03	21	0,00E+00	0,00E+00	0,345
<i>Lactobacillus farciminis</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Lactobacillus ginsenosidimitans</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Lactobacillus iners</i>	23	2,11E+02	7,13E+02	21	1,26E+04	4,71E+04	0,243
<i>Lactobacillus mucosae</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Lactobacillus parabuchneri</i>	23	3,71E+02	1,78E+03	21	0,00E+00	0,00E+00	0,345
<i>Lactobacillus paracasei</i>	23	1,52E+04	7,30E+04	21	0,00E+00	0,00E+00	0,345
<i>Lactobacillus reuteri</i>	23	6,22E+01	2,98E+02	21	0,00E+00	0,00E+00	0,345
<i>Lactobacillus</i> unknown_species	23	2,53E+02	1,10E+03	21	7,92E+03	3,63E+04	0,345
<i>Lactococcus garvieae</i>	23	0,00E+00	0,00E+00	21	2,84E+03	1,30E+04	0,329
<i>Lactococcus lactis</i>	23	6,70E+03	3,20E+04	21	0,00E+00	0,00E+00	0,344
<i>Lactococcus petauri</i>	23	0,00E+00	0,00E+00	21	3,51E+05	1,61E+06	0,329
<i>Lactococcus</i> unknown_species	23	1,35E+03	6,49E+03	21	1,60E+04	6,18E+04	0,292

<i>Lagierella massiliensis</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Lagierella</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Lancefieldella</i> unknown_species	23	1,15E+01	5,53E+01	21	0,00E+00	0,00E+00	0,345
<i>Lawsonella</i> unknown_species	23	1,53E+02	7,32E+02	21	5,07E+01	2,32E+02	0,545
<i>Lentibacillus</i> unknown_species	23	5,05E+01	2,10E+02	21	0,00E+00	0,00E+00	0,262
<i>Leptothrix</i> unknown_species	23	2,59E+01	1,24E+02	21	0,00E+00	0,00E+00	0,345
<i>Levyella</i> unknown_species	23	1,59E+02	5,07E+02	21	0,00E+00	0,00E+00	0,148
<i>Longibaculum</i> unknown_species	23	1,49E+03	3,68E+03	21	1,87E+03	8,31E+03	0,845
<i>Longicatena</i> unknown_species	23	5,02E+02	1,43E+03	21	8,25E+02	3,78E+03	0,705
<i>Longimicrobium</i> unknown_species	23	1,70E+01	8,17E+01	21	0,00E+00	0,00E+00	0,345
<i>Luteimonas arsenica</i>	23	1,18E+02	5,10E+02	21	6,06E+02	2,78E+03	0,412
<i>Luteimonas</i> unknown_species	23	1,84E+02	5,23E+02	21	0,00E+00	0,00E+00	0,106
<i>Luteococcus</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Lysinibacillus capsici</i>	23	2,69E+02	8,95E+02	21	0,00E+00	0,00E+00	0,164
<i>Lysinibacillus</i> unknown_species	23	2,90E+04	3,99E+04	21	8,34E+04	3,01E+05	0,395
<i>Lysobacter</i> unknown_species	23	1,22E+03	2,31E+03	21	1,39E+03	6,35E+03	0,906
<i>Macrococcus bohemicus</i>	23	1,31E+04	2,43E+04	21	5,47E+04	2,28E+05	0,390
<i>Macrococcus canis</i>	23	2,53E+03	6,45E+03	21	1,91E+04	5,96E+04	0,219
<i>Macrococcus</i> unknown_species	23	3,35E+04	1,33E+05	21	6,92E+03	1,30E+04	0,365
<i>Mahella</i> unknown_species	23	5,25E+01	2,52E+02	21	9,37E+01	4,29E+02	0,696
<i>Mailhella</i> unknown_species	23	5,60E+01	2,34E+02	21	0,00E+00	0,00E+00	0,264
<i>Marihabitans</i> unknown_species	23	5,83E+01	2,79E+02	21	0,00E+00	0,00E+00	0,345
<i>Marinilactibacillus</i> unknown_species	23	6,39E+03	1,69E+04	21	1,48E+04	3,31E+04	0,287
<i>Marinobacterium</i> unknown_species	23	2,39E+01	1,15E+02	21	0,00E+00	0,00E+00	0,345
<i>Marinococcus halophilus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Marinospirillum</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Marmoricola</i> unknown_species	23	4,94E+01	2,37E+02	21	0,00E+00	0,00E+00	0,345
<i>Massilimaliae</i> unknown_species	23	0,00E+00	0,00E+00	21	1,18E+03	5,40E+03	0,329
<i>Megasphaera elsdenii</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Methanobrevibacter</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Microbacterium</i> unknown_species	23	4,75E+01	2,28E+02	21	0,00E+00	0,00E+00	0,345
<i>Micrococcus lylae</i>	23	1,53E+02	7,34E+02	21	5,73E+02	2,63E+03	0,465
<i>Miniphocibacter</i> unknown_species	23	2,53E+02	1,02E+03	21	8,01E+01	3,67E+02	0,467
<i>Mitsuokella</i> unknown_species	23	3,62E+02	1,29E+03	21	1,70E+03	7,79E+03	0,421
<i>Mobilibacterium</i> unknown_species	23	9,26E+00	4,44E+01	21	0,00E+00	0,00E+00	0,345
<i>Mogibacterium</i> unknown_species	23	1,42E+03	4,44E+03	21	1,26E+03	5,78E+03	0,920
<i>Moraxella osloensis</i>	23	5,15E+01	1,71E+02	21	0,00E+00	0,00E+00	0,163
<i>Moraxella</i> unknown_species	23	1,39E+02	5,06E+02	21	0,00E+00	0,00E+00	0,201
<i>Mycoplasma</i> unknown_species	23	1,30E+03	4,10E+03	21	2,64E+03	1,21E+04	0,619
<i>Myroides</i> unknown_species	23	2,61E+01	1,25E+02	21	6,00E+02	2,75E+03	0,351
<i>Ndongobacter</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Neobacillus</i> unknown_species	23	2,68E+02	8,43E+02	21	5,45E+02	2,50E+03	0,618
<i>Nocardioides</i> unknown_species	23	2,83E+03	6,95E+03	21	1,27E+03	4,72E+03	0,393
<i>Oceanobacillus</i> unknown_species	23	2,78E+03	8,00E+03	21	1,08E+03	4,93E+03	0,406
<i>Olsenella umbonata</i>	23	5,03E+02	2,13E+03	21	0,00E+00	0,00E+00	0,269
<i>Olsenella</i> unknown_species	23	1,86E+03	5,99E+03	21	7,89E+02	2,91E+03	0,461
<i>Ornithinococcus hortensis</i>	23	9,45E+01	4,53E+02	21	0,00E+00	0,00E+00	0,345

<i>Ornithinicoccus</i> unknown_species	23	1,00E+02	4,81E+02	21	0,00E+00	0,00E+00	0,345
<i>Ornithinimicrobium</i> unknown_species	23	5,44E+03	1,10E+04	21	4,19E+03	1,14E+04	0,716
<i>Oscillibacter</i> unknown_species	23	3,93E+01	1,88E+02	21	4,41E+02	2,02E+03	0,348
<i>Paenarthrobacter</i> unknown_species	23	5,53E+01	2,65E+02	21	0,00E+00	0,00E+00	0,345
<i>Paeniclostridium sordellii</i>	23	5,71E+03	1,31E+04	21	3,42E+03	1,05E+04	0,528
<i>Paeniclostridium</i> unknown_species	23	1,78E+04	4,24E+04	21	2,12E+04	7,36E+04	0,851
<i>Pantoea agglomerans</i>	23	1,45E+01	6,94E+01	21	0,00E+00	0,00E+00	0,345
<i>Paraclostridium bifermentans</i>	23	3,67E+04	8,65E+04	21	2,22E+04	5,77E+04	0,519
<i>Paraclostridium</i> unknown_species	23	1,39E+04	3,41E+04	21	1,66E+04	5,78E+04	0,848
<i>Parapedobacter</i> unknown_species	23	1,91E+01	9,15E+01	21	0,00E+00	0,00E+00	0,345
<i>Parvimonas</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Pediococcus pentosaceus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Peptacetobacter</i> unknown_species	23	9,07E+01	4,35E+02	21	1,32E+02	6,03E+02	0,797
<i>Peptoclostridium</i> unknown_species	23	9,44E+01	3,21E+02	21	5,17E+02	2,37E+03	0,401
<i>Peptoniphilus indolicus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Peptoniphilus pacaensis</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Peptoniphilus</i> unknown_species	23	1,16E+02	5,58E+02	21	0,00E+00	0,00E+00	0,345
<i>Peptoniphilus vaginalis</i>	23	8,78E+01	4,21E+02	21	0,00E+00	0,00E+00	0,345
<i>Peptostreptococcus russellii</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Peptostreptococcus</i> unknown_species	23	0,00E+00	0,00E+00	21	9,47E+02	4,34E+03	0,329
<i>Peribacillus</i> unknown_species	23	1,65E+02	5,04E+02	21	0,00E+00	0,00E+00	0,130
<i>Phascolarctobacterium</i> unknown_species	23	1,84E+01	8,83E+01	21	0,00E+00	0,00E+00	0,345
<i>Phocaecicola</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Planococcus</i> unknown_species	23	1,42E+03	3,85E+03	21	1,96E+03	5,82E+03	0,715
<i>Planomicrobium glaciei</i>	23	7,57E+01	3,63E+02	21	0,00E+00	0,00E+00	0,345
<i>Plesiomonas</i> unknown_species	23	6,31E+01	3,02E+02	21	0,00E+00	0,00E+00	0,345
<i>Prevotella</i> unknown_species	23	3,56E+01	1,25E+02	21	0,00E+00	0,00E+00	0,185
<i>Pseudactinotalea</i> unknown_species	23	1,15E+01	5,52E+01	21	0,00E+00	0,00E+00	0,345
<i>Pseudoalteromonas translucida</i>	23	0,00E+00	0,00E+00	21	7,25E+01	3,32E+02	0,329
<i>Pseudoflavonifractor</i> unknown_species	23	5,51E+02	1,55E+03	21	1,44E+03	6,60E+03	0,533
<i>Pseudohongiella</i> unknown_species	23	4,69E+01	2,25E+02	21	0,00E+00	0,00E+00	0,345
<i>Pseudomonas flexibilis</i>	23	1,05E+02	4,03E+02	21	0,00E+00	0,00E+00	0,224
<i>Pseudomonas saudiphocaensis</i>	23	8,32E+01	3,99E+02	21	0,00E+00	0,00E+00	0,345
<i>Pseudomonas stutzeri</i>	23	0,00E+00	0,00E+00	21	3,42E+03	1,31E+04	0,246
<i>Pseudomonas</i> unknown_species	23	3,08E+01	1,48E+02	21	3,32E+04	9,01E+04	0,107
<i>Psychrobacillus</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Psychrobacter phenylpyruvicus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Ralstonia pickettii</i>	23	0,00E+00	0,00E+00	21	1,10E+03	3,85E+03	0,203
<i>Rhodococcus</i> unknown_species	23	4,90E+02	2,00E+03	21	0,00E+00	0,00E+00	0,253
<i>Romboutsia hominis</i>	23	7,01E+00	3,36E+01	21	0,00E+00	0,00E+00	0,345
<i>Romboutsia ilealis</i>	23	7,77E+04	1,84E+05	21	3,82E+04	1,20E+05	0,408
<i>Romboutsia timonensis</i>	23	2,08E+04	4,87E+04	21	8,64E+03	2,97E+04	0,328
<i>Romboutsia</i> unknown_species	23	6,02E+04	1,12E+05	21	4,86E+04	1,18E+05	0,738
<i>Rummeliibacillus</i> unknown_species	23	5,41E+03	1,22E+04	21	3,74E+03	9,10E+03	0,613
<i>Saccharopolyspora</i> unknown_species	23	3,16E+02	9,40E+02	21	2,16E+02	9,88E+02	0,732
<i>Salinicoccus</i> unknown_species	23	1,72E+02	6,12E+02	21	0,00E+00	0,00E+00	0,191
<i>Salipaludibacillus</i> unknown_species	23	1,56E+01	5,73E+01	21	2,51E+02	1,15E+03	0,360
<i>Selenomonas</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	

<i>Senegalia</i> unknown_species	23	6,99E+02	3,17E+03	21	0,00E+00	0,00E+00	0,302
<i>Serinicoccus</i> unknown_species	23	3,93E+02	1,48E+03	21	0,00E+00	0,00E+00	0,215
<i>Serratia fonticola</i>	23	2,71E+02	1,30E+03	21	0,00E+00	0,00E+00	0,345
<i>Serratia</i> unknown_species	23	7,32E+01	3,51E+02	21	0,00E+00	0,00E+00	0,345
<i>Serratia ureilytica</i>	23	1,33E+03	6,39E+03	21	0,00E+00	0,00E+00	0,345
<i>Slackia</i> unknown_species	23	1,30E+01	6,25E+01	21	0,00E+00	0,00E+00	0,345
<i>Sneathia</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Solibacillus isronensis</i>	23	5,69E+02	1,34E+03	21	2,23E+02	9,20E+02	0,328
<i>Solibacillus</i> unknown_species	23	7,68E+03	2,13E+04	21	7,33E+03	1,57E+04	0,952
<i>Spiroplasma</i> unknown_species	23	1,36E+02	6,52E+02	21	9,40E+02	4,31E+03	0,381
<i>Sporosarcina</i> unknown_species	23	1,49E+03	6,00E+03	21	4,17E+02	1,91E+03	0,438
<i>Staphylococcus arlettae</i>	23	7,64E+00	3,66E+01	21	1,67E+03	7,64E+03	0,331
<i>Staphylococcus aureus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Staphylococcus auricularis</i>	23	7,30E+02	2,37E+03	21	1,14E+02	5,23E+02	0,236
<i>Staphylococcus capitis</i>	23	2,85E+02	8,73E+02	21	5,57E+04	2,55E+05	0,332
<i>Staphylococcus chromogenes</i>	23	8,90E+04	2,00E+05	21	1,67E+06	6,60E+06	0,286
<i>Staphylococcus cohnii</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Staphylococcus epidermidis</i>	23	2,79E+02	6,65E+02	21	2,30E+04	8,85E+04	0,254
<i>Staphylococcus equorum</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Staphylococcus felis</i>	23	4,39E+01	2,10E+02	21	0,00E+00	0,00E+00	0,345
<i>Staphylococcus gallinarum</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Staphylococcus haemolyticus</i>	23	6,60E+03	1,40E+04	21	4,12E+04	1,28E+05	0,231
<i>Staphylococcus hominis</i>	23	3,08E+02	7,08E+02	21	3,49E+03	9,26E+03	0,132
<i>Staphylococcus hyicus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Staphylococcus microti</i>	23	1,91E+03	5,84E+03	21	2,52E+03	8,95E+03	0,791
<i>Staphylococcus muscae</i>	23	1,18E+04	2,69E+04	21	1,29E+04	3,72E+04	0,911
<i>Staphylococcus petrasii</i>	23	3,62E+01	1,52E+02	21	6,14E+01	2,82E+02	0,710
<i>Staphylococcus saprophyticus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Staphylococcus sciuri</i>	23	8,64E+02	3,94E+03	21	0,00E+00	0,00E+00	0,321
<i>Staphylococcus simulans</i>	23	1,33E+03	3,00E+03	21	2,33E+04	9,86E+04	0,319
<i>Staphylococcus</i> unknown_species	23	1,12E+05	2,00E+05	21	2,91E+05	6,88E+05	0,237
<i>Staphylococcus xylosus</i>	23	2,92E+02	7,22E+02	21	6,23E+03	2,74E+04	0,333
<i>Stenotrophomonas ginsengisoli</i>	23	0,00E+00	0,00E+00	21	1,21E+03	5,57E+03	0,329
<i>Stenotrophomonas koreensis</i>	23	2,30E+02	7,90E+02	21	2,56E+03	9,40E+03	0,270
<i>Stenotrophomonas maltophilia</i>	23	5,24E+02	2,51E+03	21	5,32E+03	1,74E+04	0,224
<i>Streptococcus cristatus</i>	23	6,33E+01	3,04E+02	21	0,00E+00	0,00E+00	0,345
<i>Streptococcus dysgalactiae</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Streptococcus equinus</i>	23	2,47E+03	1,10E+04	21	0,00E+00	0,00E+00	0,311
<i>Streptococcus gordonii</i>	23	7,37E+01	2,65E+02	21	0,00E+00	0,00E+00	0,196
<i>Streptococcus halotolerans</i>	23	1,35E+02	6,50E+02	21	1,29E+02	5,93E+02	0,975
<i>Streptococcus salivarius</i>	23	6,94E+02	3,33E+03	21	0,00E+00	0,00E+00	0,345
<i>Streptococcus thermophilus</i>	23	1,44E+03	6,89E+03	21	0,00E+00	0,00E+00	0,345
<i>Streptococcus uberis</i>	23	3,59E+01	1,72E+02	21	1,66E+06	3,32E+06	0,033
<i>Streptococcus</i> unknown_species	23	3,27E+03	1,30E+04	21	5,60E+05	1,35E+06	0,074
<i>Streptococcus vestibularis</i>	23	1,14E+03	5,47E+03	21	0,00E+00	0,00E+00	0,345
<i>Suicoccus</i> unknown_species	23	1,13E+03	1,99E+03	21	1,30E+03	4,07E+03	0,859
<i>Tessaracoccus</i> unknown_species	23	1,30E+03	2,30E+03	21	3,84E+03	8,68E+03	0,206
<i>Tetragenococcus halophilus</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	

<i>Tetragenococcus</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Tetrasphaera elongata</i>	23	1,89E+03	4,08E+03	21	3,89E+03	9,01E+03	0,359
<i>Tetrasphaera</i> unknown_species	23	5,30E+02	2,54E+03	21	0,00E+00	0,00E+00	0,345
<i>Thalassolituus</i> unknown_species	23	2,61E+02	6,64E+02	21	0,00E+00	0,00E+00	0,073
<i>Thauera phenolivorans</i>	23	5,24E+01	2,51E+02	21	1,20E+03	3,82E+03	0,187
<i>Thauera</i> unknown_species	23	2,22E+02	1,07E+03	21	0,00E+00	0,00E+00	0,345
<i>Thermoanaerobacter</i> unknown_species	23	3,81E+01	1,83E+02	21	0,00E+00	0,00E+00	0,345
<i>Thermovirga</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Tissierella</i> unknown_species	23	1,04E+03	4,17E+03	21	0,00E+00	0,00E+00	0,261
<i>Traorella</i> unknown_species	23	3,85E+02	1,56E+03	21	1,05E+04	4,42E+04	0,307
<i>Treponema</i> unknown_species	23	8,35E+01	3,32E+02	21	8,07E+02	3,70E+03	0,355
<i>Trichococcus</i> unknown_species	23	1,87E+03	8,97E+03	21	0,00E+00	0,00E+00	0,345
<i>Trueperella pyogenes</i>	23	0,00E+00	0,00E+00	21	2,60E+03	1,19E+04	0,329
<i>Trueperella</i> unknown_species	23	3,54E+02	1,18E+03	21	6,81E+02	2,18E+03	0,535
<i>Tumebacillus</i> unknown_species	23	1,50E+01	7,21E+01	21	0,00E+00	0,00E+00	0,345
<i>Turicibacter sanguinis</i>	23	1,11E+05	3,00E+05	21	4,28E+04	1,04E+05	0,328
<i>Turicibacter</i> unknown_species	23	1,46E+05	2,92E+05	21	1,59E+05	3,67E+05	0,894
<i>Urinicoccus</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Vaginisenegalia</i> unknown_species	23	4,23E+03	1,37E+04	21	2,18E+03	7,03E+03	0,541
<i>Virgibacillus</i> unknown_species	23	5,69E+02	1,72E+03	21	0,00E+00	0,00E+00	0,128
<i>Weissella jogaejeotgali</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Weissella paramesenteroides</i>	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	
<i>Weissella</i> unknown_species	23	0,00E+00	.00000 ^a	21	0,00E+00	.00000a	

Table S6: Student's T-test statistical analyses to compare the absolute abundances of taxonomic profiles of milk samples from healthy and subclinical mastitis-affected cows, divided per stable. Significant p-value are highlighted in green.

An observation that leads to suggest that this inflammatory disease affecting the bovine mammary glands is not only characterized by an alteration of the milk microbial community, but also by a significant increase in the number of microbial cells present in the milk.

Furthermore, differently from milk taxonomic composition that undergoes different alterations among stables, an increase in the number of bacterial cells in SM cow-derived milk samples seemed to be a common feature of the two different stables regardless of environmental factors.

Based on these observations, to obtain a comprehensive biological interpretation of the analyzed milk microbial community complexity and to identify further differences in the taxonomic composition of milk samples between healthy and SM-affected cows based on the number of bacterial cells, the assessed cell counts were subsequently employed to normalize ITS microbial profiling sequencing data transforming relative metagenomic data into absolute abundances, as previously described (20).

Insights into the latter revealed that the number of cells of 12 bacterial species significantly differed between milk samples from healthy and SM-affected cows in stable 1 (Figure 3).

Interestingly, *C. bovis*, whose relative abundance was not significant between the two groups as above reported, displayed a significantly higher absolute abundance in milk samples from cows with mammary gland inflammation (average absolute abundance of $4.99\text{E}+04$ cells/ml) when compared to the healthy ones (average absolute abundance of $3.14\text{E}+03$ cells/ml) (Student's T-test p-value = 0.038) (Figure 3 and Table S6).

Furthermore, *Corynebacterium xerosis*, another bacterial species frequently associated with bovine subclinical mastitis (43-45), showed a significant average absolute abundance increment of almost 10 times, moving from $2.94\text{E}+03$ to $2.91\text{E}+04$ cells/ml in milk samples from cows with intramammary infection when compared to the healthy ones (Student's T-test p-value = 0.033) (Figure 3 and Table S6).

In this context, the evaluation of the absolute abundances allowed to identify two species of the genus *Corynebacterium*, i.e., *C. bovis* and *C. xerosis*, as the potential aetiological agents of SM for stable 1.

Moreover, since the two bacterial species are not exclusively present in the microbial community of milk from cows with inflammation of the mammary gland, it is possible to assume that a certain cell number of these two species is necessary to induce the inflammatory condition typical of SM.

Conversely, the assessment of the absolute abundance-based taxonomic profiles for stable 2 revealed that only a single species significantly differed between milk samples of healthy and diseased cows, i.e., *S. uberis* (Student's T-test p-value = 0.033) (Figure 3 and Table S6).

Specifically, this microbial species displayed an increment of the cell number of almost 5-fold in the milk samples from cows with SM when compared to that of the healthy cows (Figure 3 and Table S6).

Thus, confirming the role of this species in the onset of subclinical mastitis in stable 2.

Overall, these results highlighted how the comparison of absolute abundances, obtained through the combination of a sequencing approach with a flow cytometry-based total cell count, may provide more accurate information about the alteration that the milk microbial composition may undergo in case of SM.

4. Conclusions

Bovine intramammary inflammation represents a worldwide burden causing serious repercussions not only on the health of dairy herds, but also on milk productivity and quality (15, 46).

To limit the spread of this disease, and especially of its silent form, i.e., subclinical mastitis, whose containment is difficult due to the lack of evident symptoms and its high incidence rate, the identification of SM microbial causative agents is of crucial significance (12, 47-49).

However, the impact of bovine milk microbial composition that may have on SM has not yet been fully investigated.

In this context, the application of an ITS microbial profiling to milk samples collected from healthy and SM-affected cows from two different stables highlighted that environmental factors play a predominant role in the modulation of the milk microbial community regardless of the clinical status, thus suggesting the need to separately analyze samples according to their stable of origin to avoid environmental factor-related biases.

The subsequent comparison of milk samples divided per stable showed that, in general, SM is associated to a reduced number of species in the milk microbial community.

On the contrary, the analyses of the impact that SM may have on the “core” milk microbiota between healthy and diseased bovines showed that this silent intramammary inflammation induces stable-related alteration of the “core” milk bacterial composition.

Thus, emphasizing that, despite being characterized by a lack of obvious symptoms, subclinical mastitis is accompanied by an alteration of the bovine milk microbiota. Furthermore, the enumeration of the bacterial cells presents in each collected milk sample through flow cytometry evidenced that, in general, SM is associated with a significant increase of milk bacterial cells.

Furthermore, the normalization of the metagenomic taxonomic profiles with the obtained total cell counts allowed to obtain absolute abundance-based compositional profiles that not only identified *Corynebacterium bovis* together with *Corynebacterium xerosis* and *Streptococcus uberis* as potential microbial markers of SM for stable 1 and 2, respectively, but also lead to suggest that the intramammary inflammation typical of SM may not only be associated with the presence of a certain bacterial taxon, but also with the total number of cells of that species in the bovine milk.

Thus, suggesting the importance of the combination of a sequencing approach with a bacterial cell enumeration to obtain a more accurate overview of the milk microbial composition associated with subclinical mastitis.

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References

1. Ruegg PL. 2022. The bovine milk microbiome - an evolving science. *Domest Anim Endocrinol* 79:106708.
2. Sharun K, Dhama K, Tiwari R, Gugjoo MB, Iqbal Yatoo M, Patel SK, Pathak M, Karthik K, Khurana SK, Singh R, Puvvala B, Amarpal, Singh R, Singh KP, Chaicumpa W. 2021. Advances in therapeutic and managemental approaches of bovine mastitis: a comprehensive review. *Vet Q* 41:107-136.
3. Wang Y, Nan X, Zhao Y, Jiang L, Wang H, Zhang F, Hua D, Liu J, Yao J, Yang L, Xiong B. 2022. Consumption of Supplementary Inulin Modulates Milk Microbiota and Metabolites in Dairy Cows with Subclinical Mastitis. *Appl Environ Microbiol* 88:e0205921.
4. Abebe R, Hatiya H, Abera M, Megersa B, Asmare K. 2016. Bovine mastitis: prevalence, risk factors and isolation of *Staphylococcus aureus* in dairy herds at Hawassa milk shed, South Ethiopia. *BMC Vet Res* 12:270.
5. Abed AH, Menshawy AMS, Zeinhom MMA, Hossain D, Khalifa E, Wareth G, Awad MF. 2021. Subclinical Mastitis in Selected Bovine Dairy Herds in North Upper Egypt: Assessment of Prevalence, Causative Bacterial Pathogens, Antimicrobial Resistance and Virulence-Associated Genes. *Microorganisms* 9.
6. Kaczorowski L, Powierska-Czarny J, Wolko L, Piotrowska-Cyplik A, Cyplik P, Czarny J. 2022. The Influence of Bacteria Causing Subclinical Mastitis on the Structure of the Cow's Milk Microbiome. *Molecules* 27.
7. Wang Y, Nan X, Zhao Y, Jiang L, Wang H, Zhang F, Hua D, Liu J, Yao J, Yang L, Luo Q, Xiong B. 2021. Dietary Supplementation of Inulin Ameliorates Subclinical Mastitis

via Regulation of Rumen Microbial Community and Metabolites in Dairy Cows. *Microbiol Spectr* 9:e0010521.

8. Zhang H, Wang Z, Yao H, Jiang L, Tong J. 2022. Intramammary infusion of matrine-chitosan hydrogels for treating subclinical bovine mastitis -effects on milk microbiome and metabolites. *Front Microbiol* 13:950231.

9. El-Sayed A, Kamel M. 2021. Bovine mastitis prevention and control in the post-antibiotic era. *Trop Anim Health Prod* 53:236.

10. Addis MF, Tanca A, Uzzau S, Oikonomou G, Bicalho RC, Moroni P. 2016. The bovine milk microbiota: insights and perspectives from -omics studies. *Mol Biosyst* 12:2359-72.

11. Wang Y, Nan X, Zhao Y, Jiang L, Wang H, Zhang F, Hua D, Liu J, Yang L, Yao J, Xiong B. 2022. Changes in the Profile of Fecal Microbiota and Metabolites as Well as Serum Metabolites and Proteome After Dietary Inulin Supplementation in Dairy Cows With Subclinical Mastitis. *Front Microbiol* 13:809139.

12. Steinberg RS, Silva ESLC, de Souza MR, Reis RB, da Silva PCL, Lacorte GA, Nicoli JR, Neumann E, Nunes AC. 2022. Changes in bovine milk bacterial microbiome from healthy and subclinical mastitis affected animals of the Girolando, Gyr, Guzera, and Holstein breeds. *Int Microbiol* 25:803-815.

13. Alessandri G, Argentini C, Milani C, Turrone F, Cristina Ossiprandi M, van Sinderen D, Ventura M. 2020. Catching a glimpse of the bacterial gut community of companion animals: a canine and feline perspective. *Microb Biotechnol* 13:1708-1732.

14. Polveiro RC, Vidigal PMP, de Oliveira Mendes TA, Yamatogi RS, da Silva LS, Fujikura JM, Da Costa MM, Moreira MAS. 2022. Distinguishing the milk microbiota of

healthy goats and goats diagnosed with subclinical mastitis, clinical mastitis, and gangrenous mastitis. *Front Microbiol* 13:918706.

15. Khasapane NG, Nkhebenyane JS, Kwenda S, Khumalo ZTH, Mtshali PS, Taioe MO, Thekisoie OMM. 2021. Application of culture, PCR, and PacBio sequencing for determination of microbial composition of milk from subclinical mastitis dairy cows of smallholder farms. *Open Life Sci* 16:800-808.

16. Pang M, Xie X, Bao H, Sun L, He T, Zhao H, Zhou Y, Zhang L, Zhang H, Wei R, Xie K, Wang R. 2018. Insights Into the Bovine Milk Microbiota in Dairy Farms With Different Incidence Rates of Subclinical Mastitis. *Front Microbiol* 9:2379.

17. Zhang J, Li W, Tang Y, Liu X, Zhang H, Zhou Y, Wang Y, Xiao W, Yu Y. 2022. Testing Two Somatic Cell Count Cutoff Values for Bovine Subclinical Mastitis Detection Based on Milk Microbiota and Peripheral Blood Leukocyte Transcriptome Profile. *Animals (Basel)* 12.

18. Milani C, Alessandri G, Mangifesta M, Mancabelli L, Lugli GA, Fontana F, Longhi G, Anzalone R, Viappiani A, Duranti S, Turrone F, Costi R, Annicchiarico A, Morini A, Sarli L, Ossiprandi MC, van Sinderen D, Ventura M. 2020. Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. *mSystems* 5.

19. Milani C, Lugli GA, Fontana F, Mancabelli L, Alessandri G, Longhi G, Anzalone R, Viappiani A, Turrone F, van Sinderen D, Ventura M. 2021. METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. *mSystems* doi:10.1128/mSystems.00583-21:e0058321.

20. Vandeputte D, Kathagen G, D'Hoe K, Vieira-Silva S, Valles-Colomer M, Sabino J, Wang J, Tito RY, De Commer L, Darzi Y, Vermeire S, Falony G, Raes J. 2017. Quantitative microbiome profiling links gut community variation to microbial load. *Nature* 551:507- 511.
21. Salonen A, Salojarvi J, Lahti L, de Vos WM. 2012. The adult intestinal core microbiota is determined by analysis depth and health status. *Clin Microbiol Infect* 18 Suppl 4:16-20.
22. Tap J, Mondot S, Levenez F, Pelletier E, Caron C, Furet JP, Ugarte E, Munoz-Tamayo R, Paslier DL, Nalin R, Dore J, Leclerc M. 2009. Towards the human intestinal microbiota phylogenetic core. *Environ Microbiol* 11:2574-84.
23. Alessandri G, Milani C, Mancabelli L, Mangifesta M, Lugli GA, Viappiani A, Duranti S, Turrone F, Ossiprandi MC, van Sinderen D, Ventura M. 2019. Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. *Environ Microbiol* 21:1331-1343.
24. Lugli GA, Duranti S, Milani C, Mancabelli L, Turrone F, Alessandri G, Longhi G, Anzalone R, Viappiani A, Tarracchini C, Bernasconi S, Yonemitsu C, Bode L, Goran MI, Ossiprandi MC, van Sinderen D, Ventura M. 2020. Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. *FEMS Microbiol Ecol* 96.
25. Lugli GA, Duranti S, Albert K, Mancabelli L, Napoli S, Viappiani A, Anzalone R, Longhi G, Milani C, Turrone F, Alessandri G, Sela DA, van Sinderen D, Ventura M. 2019. Unveiling Genomic Diversity among Members of the Species *Bifidobacterium*

pseudolongum, a Widely Distributed Gut Commensal of the Animal Kingdom. *Appl Environ Microbiol* 85.

26. Milani C, Duranti S, Napoli S, Alessandri G, Mancabelli L, Anzalone R, Longhi G, Viappiani A, Mangifesta M, Lugli GA, Bernasconi S, Ossiprandi MC, van Sinderen D, Ventura M, Turrone F. 2019. Colonization of the human gut by bovine bacteria present in Parmesan cheese. *Nat Commun* 10:1286.

27. Xu S, Liu Y, Gao J, Zhou M, Yang J, He F, Kastelic JP, Deng Z, Han B. 2021. Comparative Genomic Analysis of *Streptococcus dysgalactiae* subspecies *dysgalactiae* Isolated From Bovine Mastitis in China. *Front Microbiol* 12:751863.

28. Bennett S, Ben Said L, Lacasse P, Malouin F, Fliss I. 2021. Susceptibility to Nisin, Bactofencin, Pediocin and Reuterin of Multidrug Resistant *Staphylococcus aureus*, *Streptococcus dysgalactiae* and *Streptococcus uberis* Causing Bovine Mastitis. *Antibiotics (Basel)* 10.

29. Zhang S, Piepers S, Shan R, Cai L, Mao S, Zou J, Ali T, De Vliegher S, Han B. 2018. Phenotypic and genotypic characterization of antimicrobial resistance profiles in *Streptococcus dysgalactiae* isolated from bovine clinical mastitis in 5 provinces of China. *J Dairy Sci* 101:3344-3355.

30. Nagahata H, Mukai T, Natsume Y, Okuda M, Ando T, Hisaeda K, Gondaira S, Higuchi H. 2020. Effects of intramammary infusion of *Bifidobacterium breve* on mastitis pathogens and somatic cell response in quarters from dairy cows with chronic subclinical mastitis. *Anim Sci J* 91:e13406.

31. Heikkilä AM, Liski E, Pyörälä S, Taponen S. 2018. Pathogen-specific production losses in bovine mastitis. *J Dairy Sci* 101:9493-9504.

32. Taponen S, Liski E, Heikkilä AM, Pyörälä S. 2017. Factors associated with intramammary infection in dairy cows caused by coagulase-negative staphylococci, *Staphylococcus aureus*, *Streptococcus uberis*, *Streptococcus dysgalactiae*, *Corynebacterium bovis*, or *Escherichia coli*. *J Dairy Sci* 100:493-503.
33. Alessandri G, Ossiprandi MC, MacSharry J, van Sinderen D, Ventura M. 2019. Bifidobacterial Dialogue With Its Human Host and Consequent Modulation of the Immune System. *Front Immunol* 10:2348.
34. Turroni F, Milani C, Duranti S, Mahony J, van Sinderen D, Ventura M. 2018. Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. *Trends Microbiol* 26:339-350.
35. Falentin H, Rault L, Nicolas A, Bouchard DS, Lassalas J, Lambertson P, Aubry JM, Marnet PG, Le Loir Y, Even S. 2016. Bovine Teat Microbiome Analysis Revealed Reduced Alpha Diversity and Significant Changes in Taxonomic Profiles in Quarters with a History of Mastitis. *Front Microbiol* 7:480.
36. Catozzi C, Sanchez Bonastre A, Francino O, Lecchi C, De Carlo E, Vecchio D, Martucciello A, Fraulo P, Bronzo V, Cusco A, D'Andreano S, Cecilianì F. 2017. The microbiota of water buffalo milk during mastitis. *PLoS One* 12:e0184710.
37. Doll EV, Staib L, Huptas C, Scherer S, Wenning M. 2021. *Facklamia lactis* sp. nov., isolated from raw milk. *Int J Syst Evol Microbiol* 71.
38. Wang Y, Nan X, Zhao Y, Wang H, Wang M, Jiang L, Zhang F, Xue F, Hua D, Li K, Liu J, Yao J, Xiong B. 2020. Coupling 16S rDNA Sequencing and Untargeted Mass Spectrometry for Milk Microbial Composition and Metabolites from Dairy Cows with Clinical and Subclinical Mastitis. *J Agric Food Chem* 68:8496-8508.

39. Gomes F, Henriques M. 2016. Control of Bovine Mastitis: Old and Recent Therapeutic Approaches. *Curr Microbiol* 72:377-82.
40. Varhimo E, Varmanen P, Fallarero A, Skogman M, Pyorala S, Iivanainen A, Sukura A, Vuorela P, Savijoki K. 2011. Alpha- and beta-casein components of host milk induce biofilm formation in the mastitis bacterium *Streptococcus uberis*. *Vet Microbiol* 149:381- 9.
41. Cheng WN, Han SG. 2020. Bovine mastitis: risk factors, therapeutic strategies, and alternative treatments - A review. *Asian-Australas J Anim Sci* 33:1699-1713.
42. Kurban D, Roy JP, Kabera F, Frechette A, Um MM, Albaaj A, Rowe S, Godden S, Adkins PRF, Middleton JR, Gauthier ML, Keefe GP, DeVries TJ, Kelton DF, Moroni P, Veiga Dos Santos M, Barkema HW, Dufour S. 2022. Diagnosing Intramammary Infection: Meta-Analysis and Mapping Review on Frequency and Udder Health Relevance of Microorganism Species Isolated from Bovine Milk Samples. *Animals (Basel)* 12.
43. Lucken A, Woudstra S, Wente N, Zhang Y, Kromker V. 2022. Intramammary infections with *Corynebacterium* spp. in bovine lactating udder quarters. *PLoS One* 17:e0270867.
44. Goncalves JL, Tomazi T, Barreiro JR, Beuron DC, Arcari MA, Lee SH, Martins CM, Araujo Junior JP, dos Santos MV. 2016. Effects of bovine subclinical mastitis caused by *Corynebacterium* spp. on somatic cell count, milk yield and composition by comparing contralateral quarters. *Vet J* 209:87-92.
45. Goncalves JL, Tomazi T, Barreiro JR, Braga PA, Ferreira CR, Araujo Junior JP, Eberlin MN, dos Santos MV. 2014. Identification of *Corynebacterium* spp. isolated

from bovine intramammary infections by matrix-assisted laser desorption ionization-time of flight mass spectrometry. *Vet Microbiol* 173:147-51.

46. Antanaitis R, Juozaitiene V, Jonike V, Baumgartner W, Paulauskas A. 2021. Milk Lactose as a Biomarker of Subclinical Mastitis in Dairy Cows. *Animals (Basel)* 11.

47. Bari MS, Rahman MM, Persson Y, Derks M, Sayeed MA, Hossain D, Singha S, Hoque MA, Sivaraman S, Fernando P, Ahmad I, Samad A, Koop G. 2022. Subclinical mastitis in dairy cows in south-Asian countries: a review of risk factors and etiology to prioritize control measures. *Vet Res Commun* 46:621-640.

48. Fernandez L, Arroyo R, Espinosa I, Marin M, Jimenez E, Rodriguez JM. 2014. Probiotics for human lactational mastitis. *Benef Microbes* 5:169-83.

49. Hoque MN, Istiaq A, Clement RA, Sultana M, Crandall KA, Siddiki AZ, Hossain MA. 2019. Metagenomic deep sequencing reveals association of microbiome signature with functional biases in bovine mastitis. *Sci Rep* 9:13536.

50. S. **Pyörälä**, «Indicators of inflammation in the diagnosis of mastitis,» *Veterinary Research*, vol. 34, n. 5, pp. 564-578, 2003.

51. *Microbiological Procedures for the Diagnosis of Bovine Udder Infection and Determination of Milk Quality - National Mastitis Council a Global Organization for Mastitis Control and Milk Quality. Fourth Edition. Chapter Sample Collection and Handling page 1.*