

Supplementary Materials: Oral Microbiome in Four Female Centenarians

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1. Supplementary Information

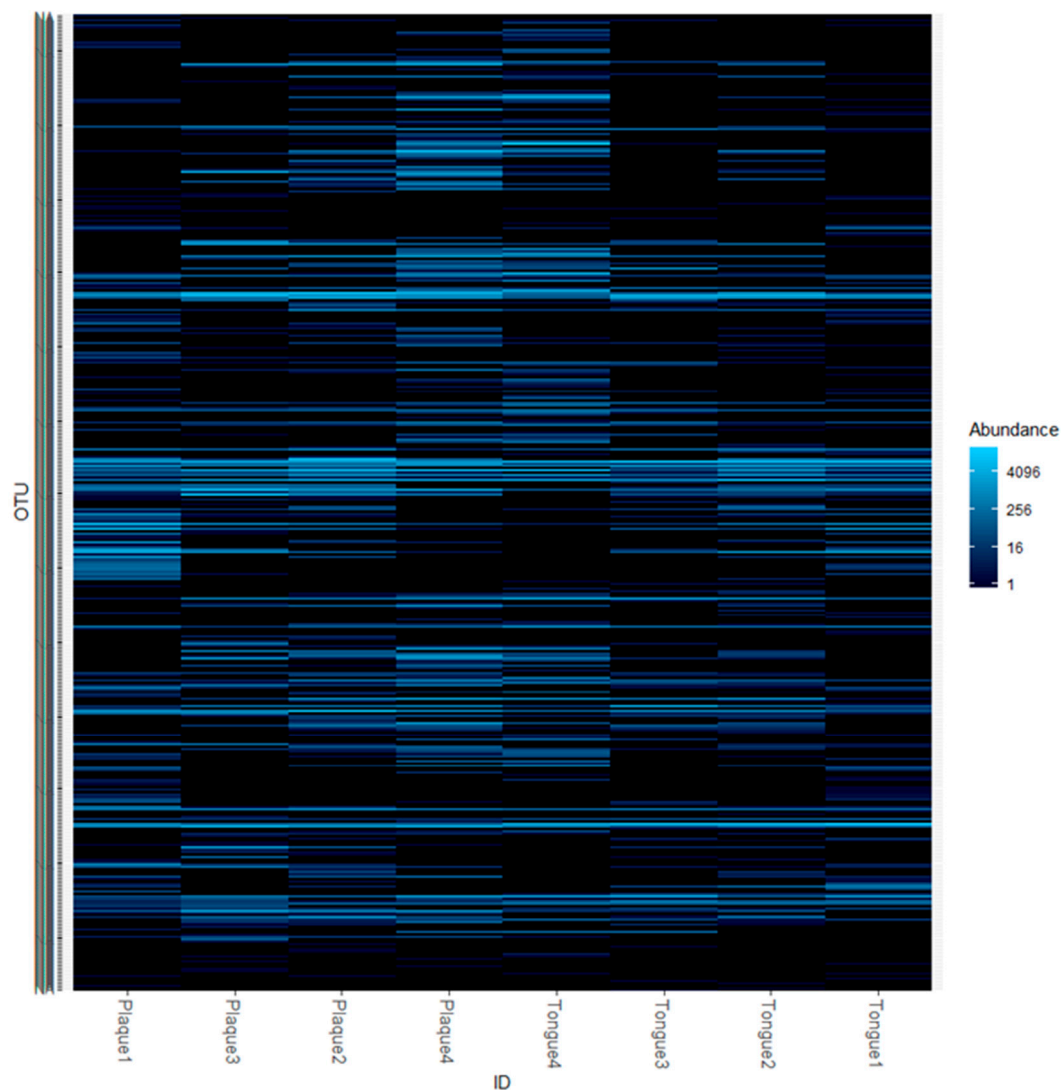


Figure S1. Heatmap of all species detected.

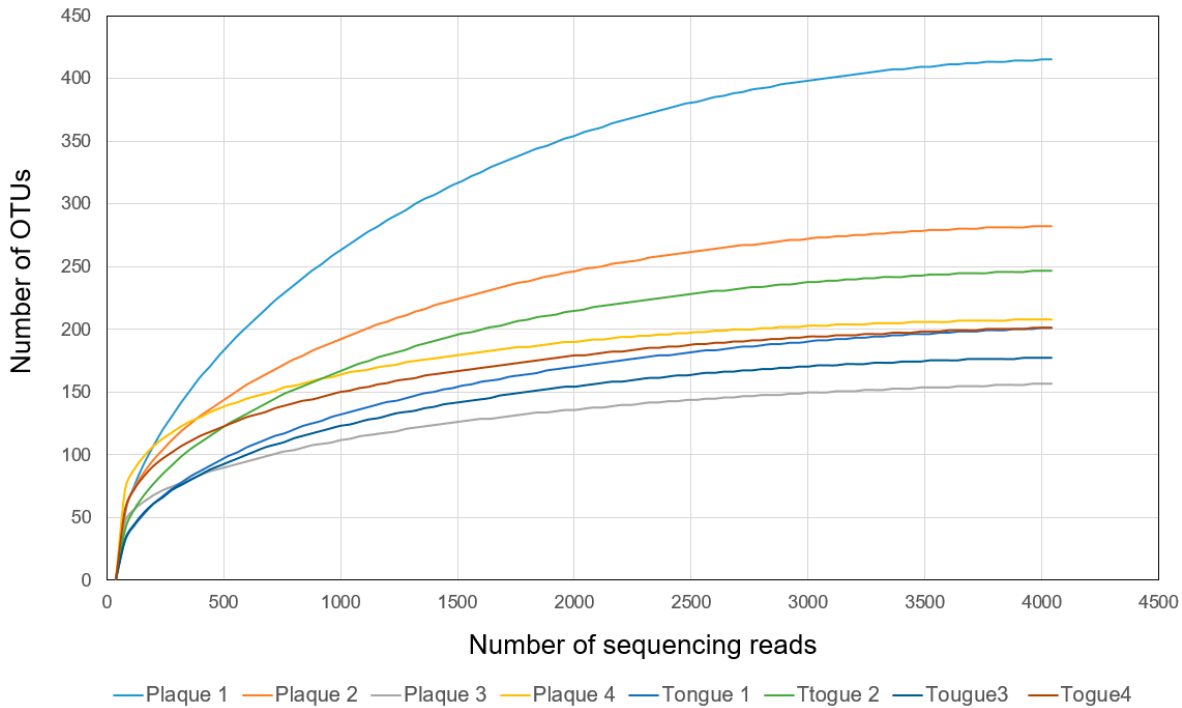


Figure S2. Rarefaction curve.

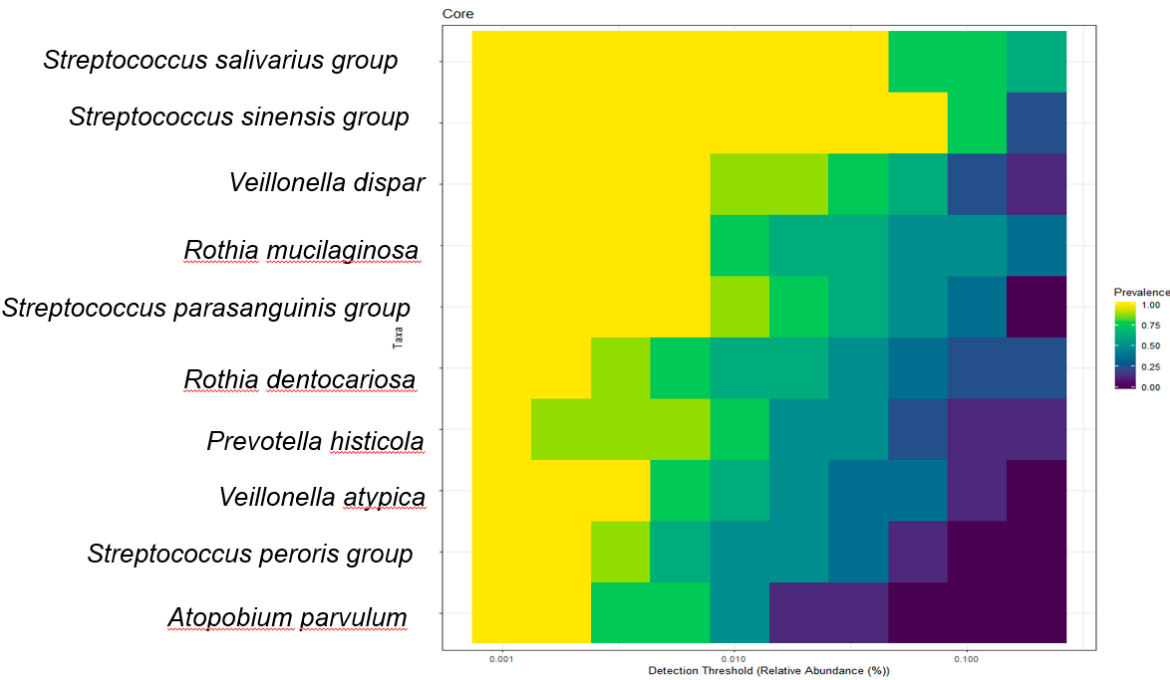


Figure S3. Core heatmap.

Table S1: Alpha diversity indices of different groups.

Sample	Plaque	Tongue	p-value
Valid reads	50398 ± 5648	52221 +/- 5433	0.658
OTUs	264 +/- 112	205 +/- 33	0.356
Ace	272 +/- 112	215 +/- 34	0.367
Chao1	266 +/- 111	209 +/- 33	0.363
Jack Knife	281 +/- 115	224 +/- 36	0.385
Shannon	3.18 +/- 0.33	2.45 +/- 0.44	0.039
Simpson	0.085 +/- 0.038	0.164 +/- 0.057	0.058

The alpha diversity indices of Ace, Chao1, Jack Knife, Shannon, and Simpson were calculated to analyze the diversity and richness of all the samples. By comparing samples of dental plaque and tongue, the indices of Ace, Chao1, Jack Knife, And Shannon were not significantly different ($P > 0.05$), proving that bacterial diversity and richness were similar in samples collected from dental plaque had higher than tongue. Data was normally distributed. P-values were calculated by t tests.

Table S2: Statistics of taxonomic assignment.

Sample	Sample ID	Rank	Similarity range	No. of reads	Ratio (%)
Plaque	1	Species	$x \geq 97\%$	42,230	97.61
		Genus	$97 > x \geq 94.5\%$	837	1.93
		Family	$94.5 > x \geq 86.5\%$	189	0.43
		Order	$86.5 > x \geq 82\%$	5	0.01
		Class	$82 > x \geq 78.5\%$	0	0.00
		Phylum	$78.5 > x \geq 75\%$	0	0.00
		Unidentified	$75\% > x$	0	0.00
		Total		43,261	100
	2	Species	$x \geq 97\%$	50,282	98.59
		Genus	$97 > x \geq 94.5\%$	641	1.25
		Family	$94.5 > x \geq 86.5\%$	77	0.15
		Order	$86.5 > x \geq 82\%$	0	0.00
		Class	$82 > x \geq 78.5\%$	0	0.00
		Phylum	$78.5 > x \geq 75\%$	0	0.00
		Unidentified	$75\% > x$	0	0.00
		Total		51,000	100
	3	Species	$x \geq 97\%$	51,176	99.62
		Genus	$97 > x \geq 94.5\%$	171	0.33
		Family	$94.5 > x \geq 86.5\%$	20	0.03
		Order	$86.5 > x \geq 82\%$	0	0.00
		Class	$82 > x \geq 78.5\%$	0	0.00
		Phylum	$78.5 > x \geq 75\%$	0	0.00
		Unidentified	$75\% > x$	0	0.00
		Total		51,367	100
	4	Species	$x \geq 97\%$	56,225	99.58
		Genus	$97 > x \geq 94.5\%$	222	0.39
		Family	$94.5 > x \geq 86.5\%$	10	0.01
		Order	$86.5 > x \geq 82\%$	0	0.00
		Class	$82 > x \geq 78.5\%$	2	0.00
		Phylum	$78.5 > x \geq 75\%$	0	0.00
		Unidentified	$75\% > x$	0	0.00
		Total		56,459	100
Tongue	1	Species	$x \geq 97\%$	50,767	99.10
		Genus	$97 > x \geq 94.5\%$	411	0.80
		Family	$94.5 > x \geq 86.5\%$	45	0.08
		Order	$86.5 > x \geq 82\%$	2	0.00
		Class	$82 > x \geq 78.5\%$	0	0.00
		Phylum	$78.5 > x \geq 75\%$	0	0.00
		Unidentified	$75\% > x$	0	0.00
		Total		51,225	100
	2	Species	$x \geq 97\%$	54,373	99.01
		Genus	$97 > x \geq 94.5\%$	469	0.85
		Family	$94.5 > x \geq 86.5\%$	69	0.12
		Order	$86.5 > x \geq 82\%$	3	0.00
		Class	$82 > x \geq 78.5\%$	0	0.00
		Phylum	$78.5 > x \geq 75\%$	0	0.00
		Unidentified	$75\% > x$	0	0.00

3	Total		54,914	100
	Species	x >= 97%	44,855	99.20
	Genus	97 > x >= 94.5%	321	0.70
	Family	94.5 > x >= 86.5%	38	0.08
	Order	86.5 > x >= 82%	0	0.00
	Class	82 > x >= 78.5%	0	0.00
	Phylum	78.5 > x >= 75%	0	0.00
	Unidentified	75% > x	0	0.00
	Total		45,214	100
4	Species	x >= 97%	57,391	99.37
	Genus	97 > x >= 94.5%	304	0.52
	Family	94.5 > x >= 86.5%	49	0.08
	Order	86.5 > x >= 82%	10	0.01
	Class	82 > x >= 78.5%	0	0.00
	Phylum	78.5 > x >= 75%	0	0.00
	Unidentified	75% > x	0	0.00
	Total		57,754	100

Table S3: Species detected in denture plaque and tongue.

Detected from all subjects in plaque.

Phylum	Genus	Species	Prevalence in plaque	Abundance (%)	
				Plaque	Tongue
Firmicutes	Streptococcus	<i>Streptococcus sobrinus</i>	50%	4.46	0.20
		<i>Streptococcus downei</i> group	75%	3.95	0.04
		<i>Streptococcus equinus</i> group	75%	0.05	0.02
		<i>Streptococcus pharyngis</i>	75%	0.05	0.01
	Lactobacillus	<i>Lactobacillus fermentum</i>	75%	2.07	1.15
		<i>Lactobacillus reuteri</i> group	75%	1.88	0.39
	<i>Selenomonas</i>	<i>Selenomonas_uc</i>	25%	0.03	0.00
	<i>Bulleidia</i>	<i>Solobacterium moorei</i>	75%	0.04	0.06
Actinobacteria	Actinomyces	<i>Actinomyces viscosus</i> group	75%	1.53	0.04
		<i>Actinomyces oris</i>	50%	0.56	0.10
		<i>Actinomyces bowdenii</i>	25%	0.03	0.00
		<i>Actinomyces timonensis</i>	0%	0.01	0.00
	<i>Parascardovia</i>	<i>Parascardovia denticolens</i>	75%	0.14	0.00
Bacteroidetes	Prevotella	<i>Prevotella oulorum</i>	50%	0.21	0.00
		<i>Prevotella_uc</i>	50%	0.04	0.01

Detected from all subjects in tongue.

Phylum	Genus	Species	Prevalence in tongue	Abundance (%)	
				Plaque	Tongue
Firmicutes	<i>Streptococcaceae_uc</i>	<i>Streptococcaceae_uc_s</i>	75%	0.06	0.04
	<i>Streptococcus</i>	<i>Streptococcus parasuis</i>	75%	0.00	0.01
	<i>Veillonellaceae_uc</i>	<i>Veillonellaceae_uc_s</i>	50%	0.00	0.00
Actinobacteria	Actinomyces	<i>Actinomyces odontolyticus</i>	75%	0.02	0.07
		<i>Actinomyces_uc</i>	75%	0.02	0.03
	<i>Actinomycetaceae_uc</i>	<i>Actinomycetaceae_uc_s</i>	0%	0.00	0.02
<i>Bacteroides</i>	<i>Prevotella</i>	<i>Prevotella melaninogenica</i>	75%	0.84	0.66
<i>Proteobacteria</i>	<i>Campylobacter</i>	<i>Campylobacter concisus</i> group	75%	0.17	0.20

Sequence data: Sequence data of the eight samples.

(A)Dental plaque

	Phylum	Genus	Species	Detection	Abundance
Cluster 1	Acidobacteri a	<i>Acidobacterium</i>	<i>HQ674949_s</i>	100%	5.63
		<i>Edaphobacter</i>	<i>JN023643_s</i>	100%	4.46
		<i>KB906767_g</i>	<i>EF516700_s</i>	100%	2.07
		<i>HM748676_g</i>	<i>EF600570_s</i>	75%	3.42
	Actinobacter ia	<i>Actinomyces</i>	<i>Actinomyces odontolyticus</i>	100%	1.53
		<i>Actinomyces</i>	<i>Actinomyces viscosus</i> group	100%	0.82
		<i>Actinobaculum</i>	<i>Actinobaculum_uc</i>	100%	0.43
		<i>Actinomyces</i>	<i>Actinomyces israelii</i>	100%	0.40
		<i>Atopobium</i>	<i>Atopobium rimae</i> group	100%	0.35
		<i>Actinomyces</i>	<i>AFQC_s</i>	75%	1.16
		<i>Actinomyces</i>	<i>Actinomyces graevenitzi</i>	75%	0.84
		<i>Olsenella</i>	<i>CP012069_s</i>	75%	0.21
	Bacteroidetes	<i>Alloprevotella</i>	<i>Alloprevotella rava</i>	100%	0.05
		<i>Flavobacteriaceae_uc</i>	<i>Flavobacteriaceae_uc_s</i>	75%	0.06
		<i>Prevotella</i>	<i>Prevotella pallens</i>	75%	0.04
		<i>Prevotella</i>	<i>KI259591_s</i>	75%	0.03
	Firmicutes	<i>Capnocytophaga</i>	<i>AM420030_s</i>	75%	0.02
		<i>Gemella</i>	<i>Gemella haemolysans</i> group	75%	0.02
		<i>Anaerovorax</i>	<i>HQ798989_s</i>	75%	0.01
		<i>Lactobacillales_uc_g</i>	<i>Lactobacillales_uc_s</i>	75%	0.01
Cluster 2	Acidobacteri a	<i>EU445199_g</i>	<i>HM748661_s</i>	100%	4.80
		<i>HM748676_g</i>	<i>JX025749_s</i>	100%	3.95
		<i>EU881125_g</i>	<i>FJ466097_s</i>	100%	3.95
		<i>HM748739_g</i>	<i>HM748739_s</i>	100%	1.90
	Actinobacter ia	<i>Actinomyces</i>	<i>KE952139_s</i>	100%	1.88
		<i>Actinomyces</i>	<i>Actinomyces radidentis</i> group	100%	0.76
		<i>Alloscardovia</i>	<i>Alloscardovia omnicoles</i>	100%	0.56
		<i>Actinomyces</i>	<i>Actinomyces naeslundii</i>	100%	0.32
		<i>Coriobacteriaceae_uc</i>	<i>Coriobacteriaceae_uc_s</i>	100%	0.29
		<i>Mycobacterium</i>	<i>Mycobacterium tuberculosis</i> group	100%	0.21
		<i>Mycobacterium</i>	<i>CP003078_s</i>	100%	0.13
		<i>Conexibacter</i>	<i>PAC000298_s</i>	100%	0.02
		<i>Actinobaculum</i>	<i>GG703879_s</i>	75%	2.12
		<i>Actinomyces</i>	<i>Actinomyces timonensis</i>	75%	1.07
		<i>Actinomyces</i>	<i>Actinomyces bowdenii</i>	75%	0.97
		<i>Aeriscardovia</i>	<i>AY278612_s</i>	75%	0.60
		<i>Bifidobacterium</i>	<i>Bifidobacterium longum</i> group	75%	0.46
		<i>Cryptobacterium</i>	<i>Cryptobacterium curtum</i>	75%	0.37
		<i>Corynebacterium</i>	<i>Corynebacterium pseudodiphtheriticum</i> group	75%	0.35
		<i>Corynebacterium</i>	<i>Corynebacterium_uc</i>	75%	0.31
		<i>Micrococcaceae_uc</i>	<i>Micrococcaceae_uc_s</i>	75%	0.23
		<i>Bifidobacterium</i>	<i>Bifidobacterium_uc</i>	75%	0.17
	Bacteroidetes	<i>Scardovia</i>	<i>Scardovia wiggisiae</i>	75%	0.14
		<i>Alloprevotella</i>	<i>FM996479_s</i>	100%	0.14
		<i>Prevotella</i>	<i>FJ976203_s</i>	100%	0.05
		<i>Bacteroides</i>	<i>Bacteroides uniformis</i>	100%	0.02

Cluster 3	Firmicutes	<i>Alloprevotella</i>	<i>FJ976422_s</i>	75%	0.12	
		<i>Capnocytophaga</i>	<i>Capnocytophaga_uc</i>	75%	0.09	
		<i>Porphyromonas</i>	<i>Porphyromonas catoniae</i>	75%	0.07	
		<i>Prevotella</i>	<i>AF385554_s</i>	75%	0.06	
		<i>AB009176_g</i>	<i>EU762139_s</i>	100%	0.03	
		<i>Bulleidia</i>	<i>Solobacterium moorei</i>	75%	0.03	
		<i>Eubacterium_g10</i>	<i>Eubacterium sulci</i>	75%	0.02	
		<i>EU381776_g</i>	<i>FJ983022_s</i>	75%	0.01	
		<i>KE159538_g</i>	<i>EF605065_s</i>	75%	0.01	
		<i>Lactobacillus</i>	<i>FJ976024_s</i>	75%	0.01	
	<i>Lactobacillus</i>	<i>Lactobacillus plantarum group</i>	75%	0.00		
	Acidobacteri a	<i>Acidipila</i>	<i>FJ466282_s</i>	100%	9.72	
		<i>AF498705_g</i>	<i>AF498705_s</i>	100%	7.40	
		<i>EU445199_g</i>	<i>EU335427_s</i>	100%	4.34	
		<i>Acidipila</i>	<i>FJ870383_s</i>	100%	4.12	
		<i>Acidipila</i>	<i>EU445230_s</i>	100%	0.65	
		<i>Actinobacter ia</i>	<i>Corynebacterium</i>	<i>JQ463704_s</i>	75%	0.31
			<i>Mycobacterium</i>	<i>Mycobacterium cookii</i>	75%	0.14
			<i>Actinomyces</i>	<i>JRMV_s</i>	75%	0.10
		<i>Bacteroidetes</i>	<i>Capnocytophaga</i>	<i>Capnocytophaga ochracea</i>	75%	0.08
<i>Prevotella</i>			<i>AM420032_s</i>	75%	0.05	
<i>Bacteroides</i>	<i>Bacteroides heparinolyticus</i>		75%	0.03		
Cluster 4	<i>Actinobacter ia</i>	<i>Actinomyces</i>	<i>Actinomyces_uc</i>	75%	0.98	
		<i>Bifidobacterium</i>	<i>Bifidobacterium dentium</i>	100%	0.11	
		<i>Slackia</i>	<i>Slackia exigua</i>	75%	0.01	
	<i>Bacteroidetes</i>	<i>Capnocytophaga</i>	<i>GU561335_s</i>	100%	0.04	
	<i>Firmicutes</i>	<i>Veillonella</i>	<i>Veillonella parvula group</i>	75%	0.00	
		<i>Edaphobacter</i>	<i>Edaphobacter aggregans group</i>	100%	2.30	
	<i>Acidobacteri a</i>	<i>EU445199_g</i>	<i>AY673350_s</i>	100%	4.46	
		<i>KB906767_g</i>	<i>FJ466080_s</i>	100%	3.95	
		<i>KB906767_g</i>	<i>HQ598192_s</i>	100%	0.71	
		<i>Actinomyces</i>	<i>Actinomyces meyeri</i>	100%	0.87	
<i>Actinobacter ia</i>	<i>Actinomyces</i>	<i>Actinomyces massiliensis</i>	100%	0.23		
	<i>Bifidobacterium</i>	<i>Bifidobacterium scardovii</i>	100%	0.37		
	<i>Bifidobacterium</i>	<i>Bifidobacterium aquikefiri</i>	100%	0.17		
	<i>Bacteroidetes</i>	<i>Bacteroides</i>	<i>Phocaeicola abscessus</i>	75%	0.15	
<i>Bacteroides</i>		<i>Bacteroides plebeius</i>	75%	0.03		
<i>Capnocytophaga</i>		<i>Capnocytophaga leadbetteri</i>	75%	0.06		
<i>Prevotella</i>		<i>Prevotella jejuni</i>	100%	0.05		
<i>Prevotella</i>		<i>Prevotella intermedia</i>	100%	0.04		
<i>Prevotella</i>		<i>JQ460218_s</i>	75%	0.02		
<i>Prevotella</i>		<i>Prevotella multiformis</i>	100%	0.03		
<i>Firmicutes</i>	<i>Abiotrophia</i>	<i>Abiotrophia_uc</i>	75%	0.02		
	<i>Enterococcus</i>	<i>Enterococcus diestrammenae</i>	75%	0.02		
	<i>Gemella</i>	<i>Gemella palaticanis</i>	75%	0.01		
	<i>Lachnospiraceae_u c</i>	<i>Lachnospiraceae_uc_s</i>	100%	0.01		
	<i>Lactobacillus</i>	<i>Lactobacillus helveticus group</i>	75%	0.00		

(B)Tongue

	Phylum	Genus	Species	Prevalenc e	Abundanc e	
Cluster 1	Acidobacteria	HM748676_g	JX025749_s	75%	0.04	
	Actinobacteri a	Actinomyces	Actinomyces radidentis group	100%	0.27	
		Mycobacterium	CP003078_s	100%	0.08	
		Actinomyces	Actinomyces odontolyticus	75%	0.04	
	Bacteroidetes	Alloprevotella	FM996479_s	75%	0.00	
	Firmicutes	Lactobacillus	GQ156344_s	100%	0.00	
		AF287775_g	AM420052_s	75%	0.01	
Selenomonas		Selenomonas sputigena	75%	0.00		
Cluster 2	Actinobacteri a	Actinomyces	Actinomyces naeslundii	100%	1.06	
		Actinomyces	Actinomyces israelii	100%	0.32	
		Slackia	Slackia exigua	75%	0.13	
	Bacteroidetes	Capnocytophaga	GU561335_s	75%	0.06	
		Prevotella	FJ976203_s	75%	0.01	
Cluster 3	Acidobacteria	HM748739_g	HM748739_s	100%	1.95	
		EU445199_g	HM748661_s	100%	0.62	
		Actinomyces	Actinomyces viscosus group	100%	1.03	
		Actinomyces	Actinomyces graevenitzii	100%	0.66	
		Bifidobacterium	Bifidobacterium aquikefiri	100%	0.22	
		Bifidobacterium	Bifidobacterium scardovii	100%	0.04	
		Actinomyces	Actinomyces bowdenii	75%	0.16	
		Actinomyces	Actinomyces timonensis	75%	0.08	
	Bacteroidetes	Capnocytophaga	Capnocytophaga leadbetteri	100%	0.04	
		Prevotella	FM995711_s	75%	0.04	
		Prevotella	Prevotella jejuni	75%	0.02	
	Firmicutes	Bulleidia	Solobacterium moorei	75%	0.00	
		Selenomonas	AF385503_s	75%	0.00	
		Megasphaera	Megasphaera micronuciformis	75%	0.00	
	Cluster 4	Acidobacteria	Acidipila	EU445230_s	100%	17.17
			Acidipila	FJ870383_s	100%	13.22
Acidobacterium			HQ674949_s	100%	4.89	
Edaphobacter			JN023643_s	100%	1.92	
Actinobaculum			Actinobaculum_uc	100%	1.67	
Bifidobacterium			Bifidobacterium dentium	100%	0.30	
Actinobacteri a		Atopobium	Atopobium rimae group	100%	0.08	
		Actinomyces	Actinomyces meyeri	100%	0.08	
		Coriobacteriaceae_u c	Coriobacteriaceae_uc_s	100%	0.07	
		Actinomyces	KE952139_s	75%	0.39	
Bacteroidetes		HQ674860_g	FJ625356_s	75%	0.29	
		Bacteroides	Bacteroides uniformis	100%	0.10	
		Alloprevotella	Alloprevotella rava	100%	0.09	
		Bacteroides	Bacteroides heparinolyticus	75%	0.10	
		Prevotella	KI259591_s	75%	0.02	
		Prevotella	Prevotella pallens	75%	0.01	
	Firmicutes	Lactobacillus	Lactobacillus helveticus group	100%	0.01	
Cluster 5	Acidobacteria	KB906767_g	EF516700_s	75%	1.15	
		Edaphobacter	Edaphobacter aggregans group	100%	3.83	
		Actinomyces	Actinomyces massiliensis	100%	0.54	
Bacteroidetes	Prevotella	AM420032_s	75%	0.00		
Cluster 6	Acidobacteria	Acidipila	FJ466282_s	100%	25.06	
		KB906767_g	HQ598192_s	100%	2.39	

Cluster 7	<i>Actinobacteria</i> <i>a</i>	<i>Actinomyces</i>	<i>CAGY_s</i>	75%	1.29
		<i>Rothia</i>	<i>Rothia aerea</i>	75%	0.06
		<i>Rothia</i>	<i>Rothia mucilaginosa</i>	75%	0.01
		<i>Corynebacterium</i>	<i>Corynebacterium kroppenstedtii</i> group	75%	0.01
	<i>Acidobacteria</i>	<i>EU881125_g</i>	<i>FJ466097_s</i>	100%	0.54
		<i>EU445199_g</i>	<i>EU335427_s</i>	100%	0.52
		<i>AF498705_g</i>	<i>AF498705_s</i>	100%	0.51
		<i>KB906767_g</i>	<i>FJ466080_s</i>	100%	0.33
		<i>Conexibacter</i>	<i>PAC000298_s</i>	100%	0.37
		<i>Bifidobacterium</i>	<i>Bifidobacterium_uc</i>	100%	0.20
		<i>Actinomyces</i>	<i>Actinomyces_uc</i>	75%	0.17
	<i>Bacteroidetes</i>	<i>Corynebacterium</i>	<i>Corynebacterium_uc</i>	75%	0.05
		<i>Capnocytophaga</i>	<i>AM420030_s</i>	100%	0.07
		<i>Bacteroides</i>	<i>Bacteroides plebeius</i>	75%	0.09