

Supplementary Materials S1 Clinical details recorded, Sampling, DNA Extraction of Microbial DNA, 16S rRNA gene sequencing, Bioinformatic pipeline, Quantitative Polymerase Chain Reaction

Clinical details recorded

In addition to the microbial specimen, the following clinical features were also recorded for each patient: age, gender, infection type (primary or secondary, meaning initial or revision treatment), pain, tenderness to percussion, sinus tract and size of the periapical radiolucency, to determine the correlation between these features and microbial findings (Table 1). Prevalence of all clinical signs and symptoms (except periapical lesion size) were recorded on a binary scale [0 = absent, 1 = present], while the size of the radiolucency was measured in millimetres by two endodontic specialists on two-dimensional periapical radiographs (Planmeca Romexis, Coventry, UK).

Sampling

After anaesthesia, the tooth to be treated was isolated with a rubber dam (UnoDent, Essex, UK), and field decontamination was carried out before and after access opening, according to an established protocol, and shown to eliminate contaminating DNA (Data not shown). An access cavity was cut with a sterile bur under sterile saline irrigation (0.9% NaCl, Mölnlycke Health Care, Göteborg, Sweden), with contamination control samples taken. Root canal patency was assessed with a sterile K-file (Dentsply-Sirona, Ballaigues, Switzerland). For non-culture-based analysis, clinical samples were collected by inserting two paper points size 15 (Dentsply Sirona, USA) into the root canal. Each paper point was retained in the canal for 1 min with careful agitation, then was transferred to -80°C storage immediately before further analysis. Cases of secondary endodontic treatment were sampled using the same protocol, with the exception that specimens were collected after removal of the coronal gutta-percha with Gates Glidden drills (Dentsply-Sirona, Switzerland). In this process, the apical gutta-percha point was retrieved by K-files without using chemical solvents except for sterile saline. In the cases of multi-rooted teeth in both primary and secondary endodontic treatment, the sample was obtained from the canal associated with the most extensive periapical lesion.

DNA Extraction of Microbial DNA

DNA was extracted from clinical samples of both primary and secondary endodontic infections by using a commercial DNA extraction kit (Sigma GenElute bacterial DNA extraction kit, Sigma Aldrich, St. Louis, MO, USA), following the manufacturer's instruction with modifications. After incubation in 2×10^5 units of lysozyme per reaction, addition of a 1.5 mm tungsten Carbide bead and DNA-free sand (Qiagen, Venlo, Netherlands), the cells were further disrupted using a FastPrep bead beater (MpBio, Santa Ana, CA, USA) at 6 m/s for 2×30 s. For all DNA extraction procedures, positive (*Enterococcus faecalis* OMGS 3202) and negative extraction controls, non-template and negative technical controls were included. DNA extracts from clinical samples and controls were resuspended in 100 μl Tris-EDTA buffer (pH 8.6), quantified and were stored at -20°C before use. For samples subjected to 16S Next-Generation sequencing, an unbiased amplification and clean-up of the DNA was carried out using Multiple Displacement Amplification (MDA, REPLI-g Mini Kit, Qiagen) using the manufacturer's protocol. Positive amplification was confirmed by 1% horizontal agarose gel electrophoresis.

16S rRNA gene sequencing

The extracted DNA of 25 collected clinical specimens were analysed at using Illumina HiSeq Next generation sequencing was carried out at the Public Health England Genomics laboratory (Colindale, London, UK). 16S rRNA gene sequencing and samples were prepared for 16S ribosomal

RNA gene amplicons according to the Illumina protocol manual (Illumina, 2013). The hypervariable regions was amplified by using 16S Amplicon PCR with 600 cycles Forward Primer = 5' CCTACG GGNGGCWGCAG 16S Amplicon PCR Reverse Primer = 5' GACTACHVGGGTATCTAATCC [41].

Bioinformatic pipeline

Processing and taxonomic analysis of the sequence reads with matches to the GreenGenes (version 16) database was performed within dada2 using default parameters. Manually searched, non-aligned sequences were assigned by the NCBI Taxonomy (1,266,115 individual taxa) using the Lowest Common Ancestor (LCA) and the following thresholds: minimum bit-score: 80; max expectation value: 1.0×10^{-6} ; top percentage of hits considered: 10%; minimum taxon support based on all assigned reads: 0.01%. Relative abundances and extraction of species-specific binned reads were calculated.

Quantitative Polymerase Chain Reaction

All quantitative (Q)PCR analyses for bacteria, fungi and amoebae were performed in triplicate. All PCR reactions were carried out in a total volume of 25 μ L in SYBR PCR Mastermix (Applied Biosystems, Warrington, UK). Total bacterial density was determined using a 466-bp conserved 16S ribosomal RNA gene fragment, as described previously [42], at a concentration of 100 nM each for primers EubF (5'-TCCTACGGGAGGCAGCAGT-3') and EubR (5'-GGACTACCAGGGTATCTAAT CCTGTT-3'). The fungal universal primers ITS-1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS2 (5'-GCATCGATGAAGAACGCAGC-3') were used to amplify the ITS1 region. Quantitative PCR assays were carried out using a temperature profile of 50 °C for 2 min, 95 °C for 10 min, followed by 45 cycles at 95 °C for 15 s and 60 °C for 60 s. The primers used for *Entamoeba* and *E.gingivalis* were used as described elsewhere [40], EGHF Primer (5'-TACCATACAAGGAATAGCTTTGTGAATAA-3') and EGHF (5'-ACAATTGTAAATTTGTTCTTTTCT-3') were used to target the small subunit ribosomal 18S region of *E.gingivalis*. After thermal cycling, positive amplification and specificity of the amplicon was ascertained using Horizontal 2% Agarose gel electrophoresis. All positive bands amplified were excised, subjected to sanger sequencing (Eurofins Genomics, Cologne, Germany) and analysed using the Chromas Pro Software suite (Technelysium, Brisbane, Australia).

Results

Correlations with metadata, clinical signs and symptoms

Cases with sinus tracts yielded the largest number of bacterial associations (Figures 3 & 4), namely *Haemophilus parahaemolyticus* (which was the only species solely associated with lesion size above 5 mm in the present study), *Porphyromonas endodontalis*, *Bilophila* sp., *Catonella* sp., *Gemella* sp., *Corynebacterium* sp., *Megasphaera* sp., significantly (the sole genus found to be associated with pain), *Mogibacteriaceae*, *Porphyromonas endodontalis*, *Prevotella melaninogenica*, *Prevotella pallens*, *Streptococcus anginosus* and *Treponema* sp.

Positive associations of reads and radiolucency size were observed for the OTU *Haemophilus parahaemolyticus* ($p = 0.035$), which was not observed in radiolucencies < 5mm. The OTU *Pseudoramibacter/Eubacterium* sp. was strongly correlated with lesions smaller than 5 mm ($p = 0.021$).

The association of age yielded significant associations for *Coriobacteriaceae*. ($p = 0.028$), *Prevotella nigrescens* ($p = 0.044$), *Bifidobacterium* sp. ($p = 0.037$), *Atopobium* sp. ($p = 0.018$), and *Aggregatibacter segnis* ($p = 0.036$), *Staphylococcus* sp. ($p = 0.039$), with *Staphylococcus aureus* ($p = 0.03$), for the group above and below the mean age, respectively. Gender differences were observed for for *Bifidobacterium longum*, *Bacteroides* sp. ($p = 0.035$) and *Butyrivibrio* sp. ($p = 0.044$) enriched in females, and *Lactobacillus zeae* ($p = 0.038$) for male patients.

Phylogenetic correlations at lower phylogenetic levels

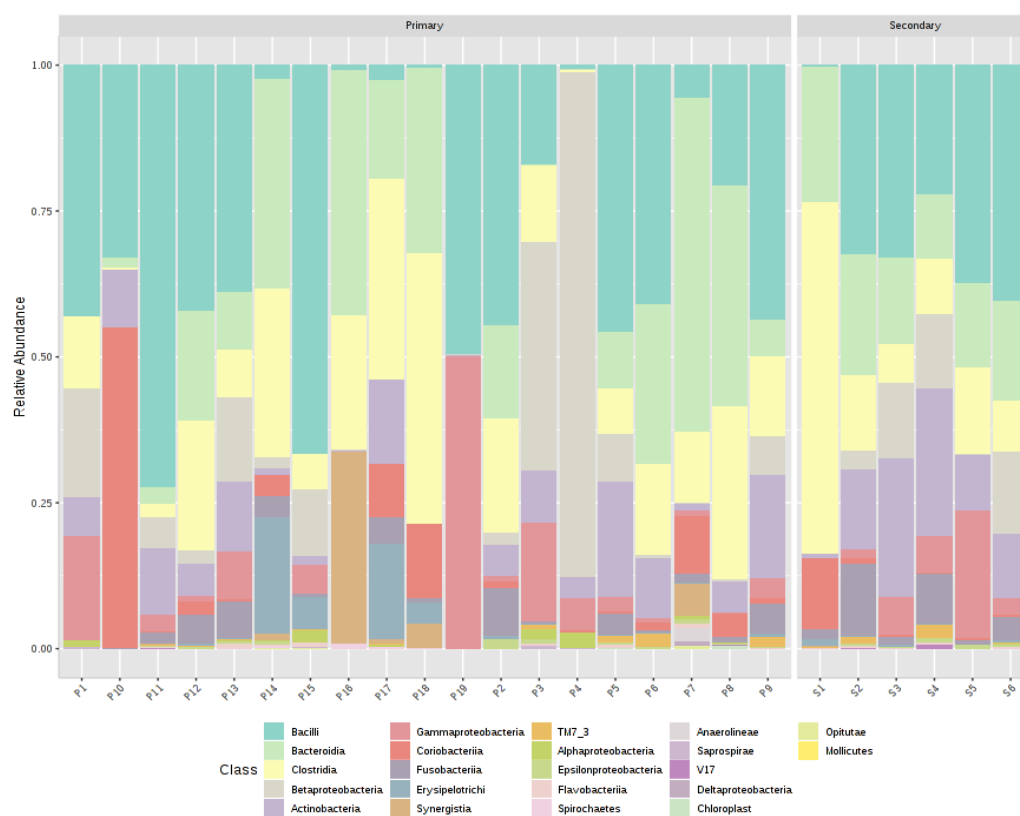
The most abundant OTU (OTU068), *Streptococcus* sp. (excluding *S. sobrinus* and *S. anginosus*, which generally did not correlate with other *Streptococcus* OTUs or their respective correlates) showed the strongest correlations with *Actinomyces* sp. ($R = 0.57$), *Rothia* sp. (0.42), and at a similar correlation strength to *R. aeria* (0.48), *R. dentocariosa* (0.39), *Scardovia* sp. (0.57), *Veillonella dispar* (0.58), *Aggregatibacter segnis* (0.458) and *Atopobium* sp. (0.359). A negative association was established for *Actinotalea* (−0.264) and *Dialister* sp. (−0.219), *Alkalibacterium transvaalinensis* (−0.26), *Treponema soncranskii* (−0.240), TG5 (−0.243), *Bacteroidales* (−0.203), *Oxalobacter* (−0.203) and *Propionibacterium acnes* (−0.174).

Species-level resolved *S. sobrinus* and *S. anginosus* did not typically follow these trends except for a correlation between *Streptococcus* sp./*S. sobrinus* and both *Veillonella dispar* (0.229 and 0.301, respectively) and *Cardiobacterium* sp. (0.357 and 0.497, respectively). An inverse correlation was observed with *Paracoccus* sp. and *Streptococcus* sp. (−0.261) and *S. anginosus* (0.447) and similarly for *Alkalimonas* sp. with −0.221 and 0.396 being the respective values obtained.

At species-unique level, a positive association of *S. anginosus* with *Megasphaera* sp. (0.98), *Campylobacter* sp. (0.98), *Actinotalea* sp. (0.64) and a negative correlation to *Atopobium* sp. (−0.115) was established. A further strong positive correlation to non-*P. acnes* *Propionibacterium* sp. (0.98) was established, the latter having a negative correlation to *S. sobrinus* (−0.16) but none to other *Streptococcus* sp. members (−0.03). *S. sobrinus* presented with a strong correlation to *Lactobacillus zeae* (0.67). *Mycoplasma* sp. displayed the strongest correlation with *Treponema* sp. (0.50), *Treponema amylovorum* (0.97), *Treponema soncranskii* (0.62) and *Desulfovibrio* sp (0.85), suggesting common niches.

Association with epibionts

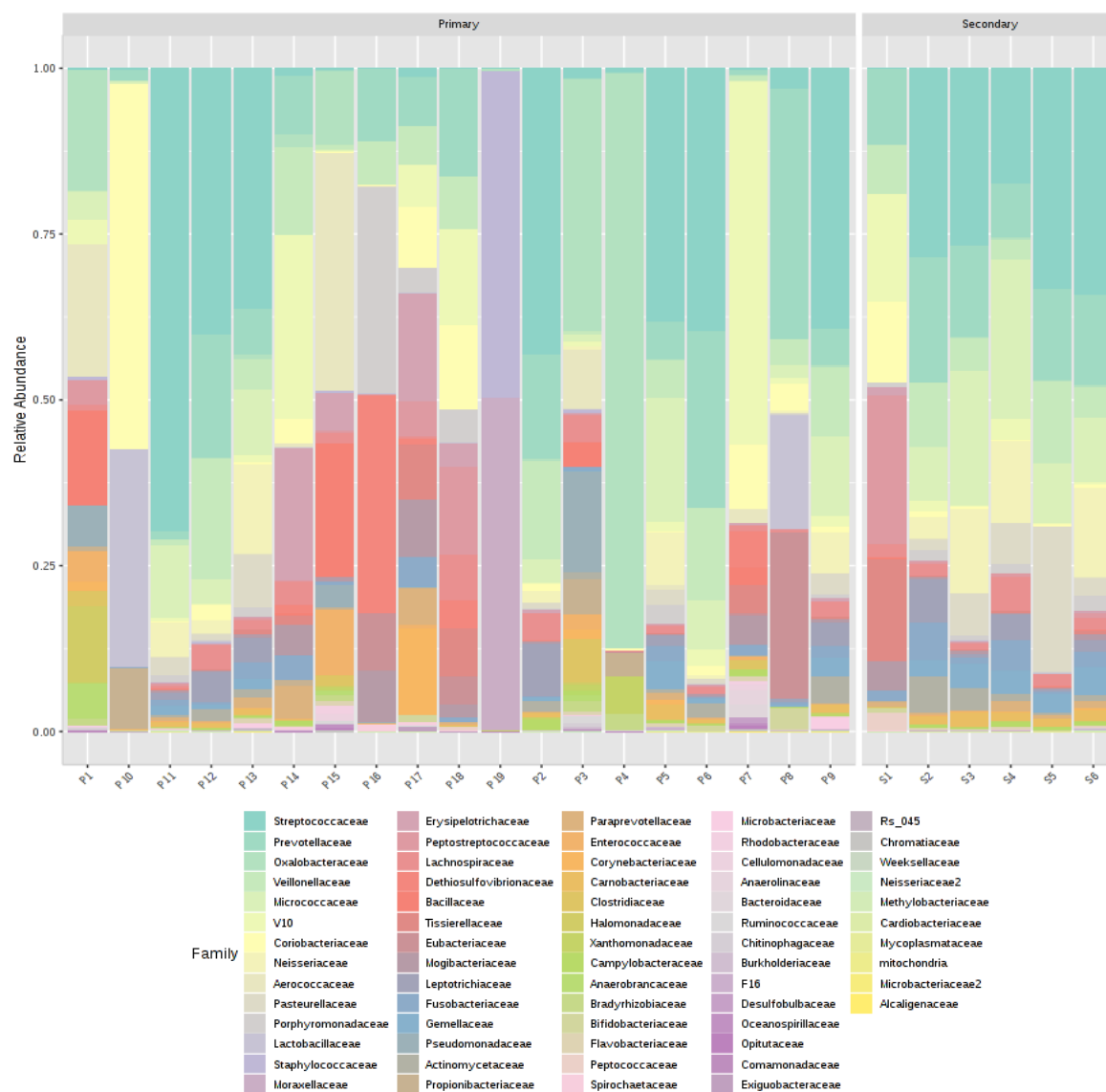
With regard to epibionts and bacterial parasites, *Candidatus Saccharibacterium* Group 3 (TM7-3), was shown to display a high species selectivity, with *Actinomyces odontolyticus* subsp. *actinosynbacter* XH001 described as the sole host to the oral clone TM7x [35], supported and potentially contributed to our data with a predominant, but specific correlation for genera within Actinomycetaceae and Clostridiaceae, as well as Veillonellaceae (*Selenomonas* sp.). For instance, the disease-specific oral clonotype I025 did not associate with *Actinomyces* sp., no association with signs or symptoms and group 3 representatives within this study could be ascertained, but with further insights into these elusive phyla, may be established for critical organisms associated with endodontic infections, and potential insights for co-culture studies established.



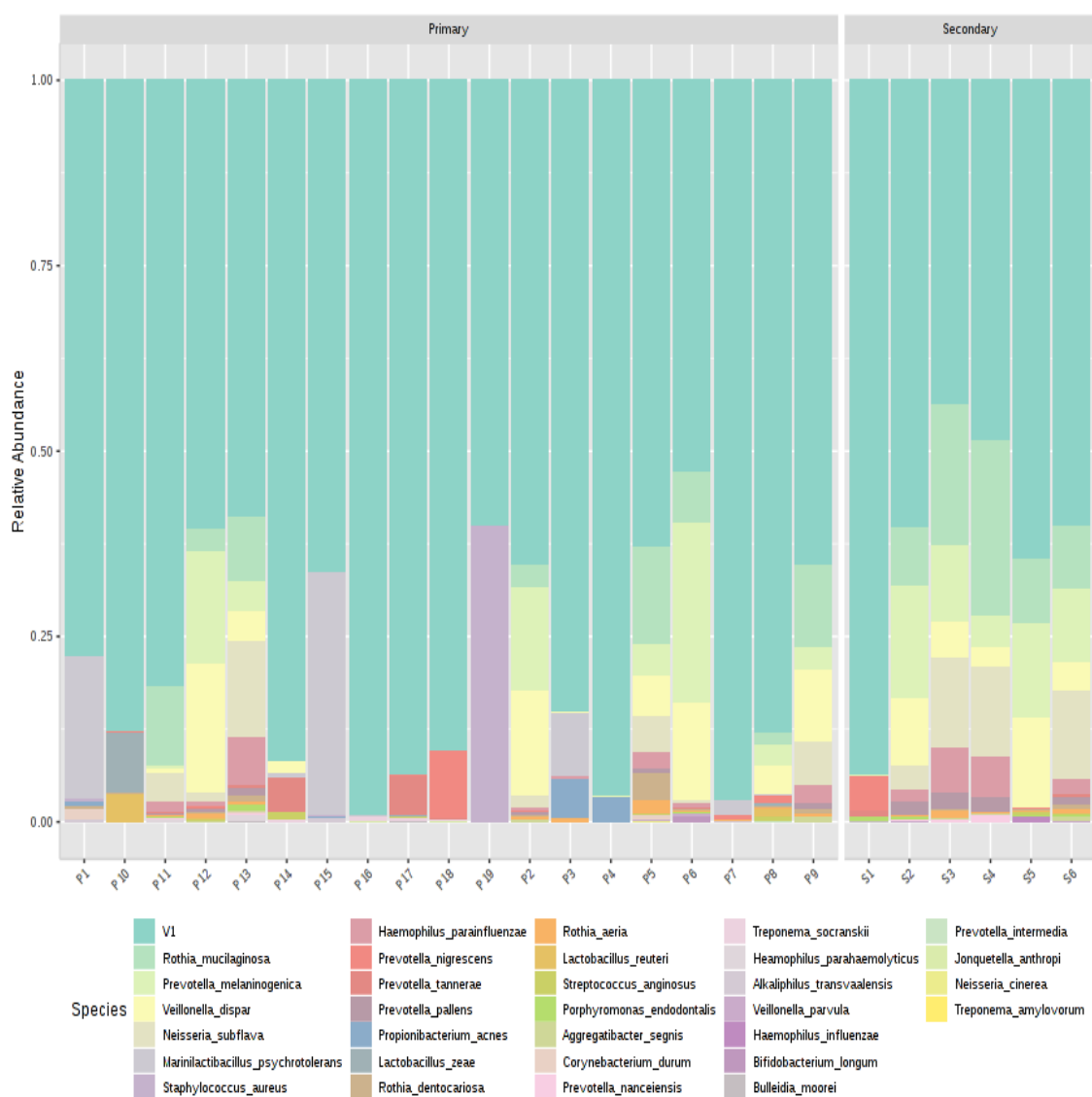
Supplementary Figure S1. Correlations across taxonomic levels and core microbiomes resolved to taxonomic levels. Correlations provided to class and treatment type (primary or secondary).



Supplementary Figure S2. Correlations across taxonomic levels and core microbiomes resolved to taxonomic levels. Correlations provided to order level and treatment type (primary or secondary).



Supplementary Figure S3. Correlations across taxonomic levels and core microbiomes resolved to taxonomic levels. Correlations provided to family level and treatment type (primary or secondary).



Supplementary Figure S4. Correlations across taxonomic levels and core microbiomes resolved to taxonomic levels. Correlations provided to species level and treatment type (primary or secondary).

Supplementary Table S1. OTUs identified in this study

#TAXONOMY	Kingdom	Phylum	Class	Order	Family	Genus	Species
OTU002	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae		
OTU003	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	
OTU004	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Cellulomonadaceae	Actinotalea	
OTU005	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	
OTU006	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Corynebacteriaceae	Corynebacterium	Corynebacterium durum
OTU007	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae		
OTU008	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae2		
OTU009	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Nesterenkonia	
OTU010	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	
OTU011	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	Rothia aeria
OTU012	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	Rothia dentocariosa
OTU013	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Rothia	Rothia mucilaginoso
OTU014	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae		
OTU015	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae	Propionibacterium	Propionibacterium acnes
OTU016	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae		
OTU017	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium	
OTU018	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium	Bifidobacterium longum
OTU019	Bacteria	Actinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Scardovia	
OTU020	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae		
OTU021	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Atopobium	
OTU022	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Slackia	
OTU023	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales			
OTU024	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	
OTU025	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides uniformis

Table S1. Cont.

OTU026	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Porphyromonadaceae</i>	<i>Dysgonomonas</i>	
OTU027	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Porphyromonadaceae</i>	<i>Paludibacter</i>	
OTU028	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Porphyromonadaceae</i>	<i>Porphyromonas</i>	
OTU029	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Porphyromonadaceae</i>	<i>Porphyromonas</i>	<i>Porphyromonas endodontalis</i>
OTU030	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Porphyromonadaceae</i>	<i>Tannerella</i>	
OTU031	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotella</i>	
OTU032	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotella</i>	<i>Prevotella intermedia</i>
OTU033	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotella</i>	<i>Prevotella melaninogenica</i>
OTU034	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotella</i>	<i>Prevotella nanceiensis</i>
OTU035	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotella</i>	<i>Prevotella nigrescens</i>
OTU036	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotella</i>	<i>Prevotella pallens</i>
OTU037	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	[<i>Paraprevotellaceae</i>]	[<i>Prevotella</i>]	
OTU038	Bacteria	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>	[<i>Paraprevotellaceae</i>]	[<i>Prevotella</i>]	[<i>Prevotella tanneriae</i>]
OTU039	Bacteria	<i>Bacteroidetes</i>	<i>Flavobacteriia</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Capnocytophaga</i>	
OTU040	Bacteria	<i>Bacteroidetes</i>	<i>Flavobacteriia</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>	
OTU041	Bacteria	<i>Bacteroidetes</i>	<i>Flavobacteriia</i>	<i>Flavobacteriales</i>	[<i>Weeksellaceae</i>]		
OTU042	Bacteria	<i>Bacteroidetes</i>	[<i>Saprospirae</i>]	[<i>Saprospirales</i>]	<i>Chitinophagaceae</i>	<i>Sediminibacterium</i>	
OTU043	Bacteria	<i>Chloroflexi</i>	<i>Anaerolineae</i>	<i>Anaerolineales</i>	<i>Anaerolinaceae</i>	SHD-231	
OTU044	Bacteria	<i>Cyanobacteria</i>	<i>Chloroplast</i>	<i>Streptophyta</i>			
OTU045	Bacteria	<i>Firmicutes</i>	<i>Bacilli</i>				
OTU046	Bacteria	<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>			
OTU047	Bacteria	<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Bacillaceae</i>		
OTU048	Bacteria	<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Bacillaceae</i>		
OTU049	Bacteria	<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Bacillaceae</i>	<i>Anaerobacillus</i>	
OTU050	Bacteria	<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Staphylococcaceae</i>	<i>Staphylococcus</i>	

Table S1. Cont.

OTU051	Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	Staphylococcus aureus
OTU052	Bacteria	Firmicutes	Bacilli	Bacillales	[Exiguobacteraceae]	Exiguobacterium	
OTU053	Bacteria	Firmicutes	Bacilli	Gemellales	Gemellaceae		
OTU054	Bacteria	Firmicutes	Bacilli	Gemellales	Gemellaceae	Gemella	
OTU055	Bacteria	Firmicutes	Bacilli	Lactobacillales			
OTU056	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae		
OTU057	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Alkalibacterium	
OTU058	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Alloiococcus	
OTU059	Bacteria	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Marinilactibacillus	Marinilactibacillus psychrotolerans
OTU060	Bacteria	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Granulicatella	
OTU061	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae		
OTU062	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	
OTU063	Bacteria	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Vagococcus	
OTU064	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae		
OTU065	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	
OTU066	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Lactobacillus reuteri
OTU067	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Lactobacillus zeae
OTU068	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	
OTU069	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus anginosus
OTU070	Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	Streptococcus sobrinus
OTU071	Bacteria	Firmicutes	Clostridia	Clostridiales2			
OTU072	Bacteria	Firmicutes	Clostridia	Clostridiales			
OTU073	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae		
OTU074	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Alkaliphilus	Alkaliphilus transvaalensis

Table S1. Cont.

OTU075	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Geosporobacter_Thermotalea	
OTU076	Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Pseudoramibacter_Eubacterium	
OTU077	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae		
OTU078	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Butyrivibrio	
OTU079	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Catonella	
OTU080	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Moryella1	
OTU081	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Moryella2	
OTU082	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Oribacterium	
OTU083	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Peptococcus	
OTU084	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae		
OTU085	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Filifactor	
OTU086	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Peptostreptococcus	
OTU087	Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ethanoligenens	
OTU088	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae		
OTU089	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Dialister	
OTU090	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Megasphaera	
OTU091	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Schwartzia	
OTU092	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Selenomonas	
OTU093	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Veillonella2	
OTU094	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Veillonella	Veillonella dispar
OTU095	Bacteria	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	Veillonella	Veillonella parvula
OTU096	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]		
OTU097	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Anaerovorax	
OTU098	Bacteria	Firmicutes	Clostridia	Clostridiales	[Mogibacteriaceae]	Mogibacterium	
OTU099	Bacteria	Firmicutes	Clostridia	Clostridiales	[Tissierellaceae]		

Table S1. Cont.

OTU100	Bacteria	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>[Tissierellaceae]</i>	<i>Parvimonas</i>	
OTU101	Bacteria	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>[Tissierellaceae]</i>	<i>Peptoniphilus</i>	
OTU102	Bacteria	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Natranaerobiales</i>	<i>Anaerobrancaceae</i>		
OTU103	Bacteria	<i>Firmicutes</i>	<i>Erysipelotrichi</i>	<i>Erysipelotrichales</i>	<i>Erysipelotrichaceae</i>	<i>Bulleidia</i>	
OTU104	Bacteria	<i>Firmicutes</i>	<i>Erysipelotrichi</i>	<i>Erysipelotrichales</i>	<i>Erysipelotrichaceae</i>	<i>Bulleidia</i>	<i>Bulleidia moorei</i>
OTU105	Bacteria	<i>Firmicutes</i>	<i>Erysipelotrichi</i>	<i>Erysipelotrichales</i>	<i>Erysipelotrichaceae</i>	<i>PSB-M-3</i>	
OTU106	Bacteria	<i>Firmicutes</i>	<i>Erysipelotrichi</i>	<i>Erysipelotrichales</i>	<i>Erysipelotrichaceae</i>	<i>[Eubacterium]</i>	<i>[Eubacterium] dolichum</i>
OTU107	Bacteria	<i>Fusobacteria</i>	<i>Fusobacteriia</i>	<i>Fusobacteriales</i>	<i>Fusobacteriaceae</i>	<i>Fusobacterium</i>	
OTU108	Bacteria	<i>Fusobacteria</i>	<i>Fusobacteriia</i>	<i>Fusobacteriales</i>	<i>Leptotrichiaceae</i>		
OTU109	Bacteria	<i>Fusobacteria</i>	<i>Fusobacteriia</i>	<i>Fusobacteriales</i>	<i>Leptotrichiaceae</i>	<i>Leptotrichia</i>	
OTU110	Bacteria	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Bradyrhizobiaceae</i>		
OTU111	Bacteria	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Methylobacteriaceae</i>	<i>Methylobacterium</i>	
OTU112	Bacteria	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodobacterales</i>	<i>Rhodobacteraceae</i>		
OTU113	Bacteria	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodobacterales</i>	<i>Rhodobacteraceae</i>	<i>Paracoccus</i>	
OTU114	Bacteria	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rickettsiales</i>	<i>mitochondria</i>		
OTU115	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Alcaligenaceae</i>	<i>Sutterella</i>	
OTU116	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Lautropia</i>	
OTU117	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>		
OTU118	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>		
OTU119	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Neisseriales</i>	<i>Neisseriaceae</i> 2		
OTU120	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Neisseriales</i>	<i>Neisseriaceae</i>		
OTU121	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Neisseriales</i>	<i>Neisseriaceae</i>	<i>Kingella</i>	
OTU122	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Neisseriales</i>	<i>Neisseriaceae</i>	<i>Neisseria</i>	
OTU123	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Neisseriales</i>	<i>Neisseriaceae</i>	<i>Neisseria</i> 2	
OTU124	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Neisseriales</i>	<i>Neisseriaceae</i>	<i>Neisseria</i>	<i>Neisseria cinerea</i>

Table S1. Cont.

OTU125	Bacteria	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Neisseriales</i>	<i>Neisseriaceae</i>	<i>Neisseria</i>	<i>Neisseria subflava</i>
OTU126	Bacteria	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfobacterales</i>	<i>Desulfobulbaceae</i>	<i>Desulfobulbus</i>	
OTU127	Bacteria	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfovibrionales</i>	<i>Desulfovibrionaceae</i>	<i>Bilophila</i>	
OTU128	Bacteria	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfovibrionales</i>	<i>Desulfovibrionaceae</i>	<i>Desulfovibrio</i>	
OTU129	Bacteria	<i>Proteobacteria</i>	<i>Epsilonproteobacteria</i>	<i>Campylobacterales</i>	<i>Campylobacteraceae</i>	<i>Campylobacter</i>	
OTU130	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Alteromonadales</i>	<i>[Chromatiaceae]</i>	<i>Alkalimonas</i>	
OTU131	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Cardiobacteriales</i>	<i>Cardiobacteriaceae</i>	<i>Cardiobacterium</i>	
OTU132	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Oceanospirillales</i>	<i>Halomonadaceae</i>	<i>Halomonas</i>	
OTU133	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Oceanospirillales</i>	<i>Oceanospirillaceae</i>	<i>Nitrincola</i>	
OTU134	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pasteurellales</i>	<i>Pasteurellaceae</i>	<i>Haemophilus</i>	<i>Haemophilus</i> <i>parahaemolyticus</i>
OTU135	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pasteurellales</i>	<i>Pasteurellaceae</i>	<i>Aggregatibacter</i>	<i>Aggregatibacter segnis</i>
OTU136	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pasteurellales</i>	<i>Pasteurellaceae</i>	<i>Haemophilus</i>	
OTU137	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pasteurellales</i>	<i>Pasteurellaceae</i>	<i>Haemophilus</i> 2	
OTU138	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pasteurellales</i>	<i>Pasteurellaceae</i>	<i>Haemophilus</i>	<i>Haemophilus influenzae</i>
OTU139	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pasteurellales</i>	<i>Pasteurellaceae</i>	<i>Haemophilus</i>	<i>Haemophilus parainfluenzae</i>
OTU140	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonadales</i>	<i>Moraxellaceae</i>	<i>Moraxella</i>	
OTU141	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonadales</i>	<i>Pseudomonadaceae</i>	<i>Pseudomonas</i>	
OTU142	Bacteria	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>		
OTU143	Bacteria	<i>SR1</i>					
OTU144	Bacteria	<i>Spirochaetes</i>	<i>Spirochaetes</i>	<i>Spirochaetales</i>	<i>Spirochaetaceae</i>	<i>Treponema</i>	
OTU145	Bacteria	<i>Spirochaetes</i>	<i>Spirochaetes</i>	<i>Spirochaetales</i>	<i>Spirochaetaceae</i>	<i>Treponema</i>	<i>Treponema amylovorum</i>
OTU146	Bacteria	<i>Spirochaetes</i>	<i>Spirochaetes</i>	<i>Spirochaetales</i>	<i>Spirochaetaceae</i>	<i>Treponema</i>	<i>Treponema socranskii</i>
OTU147	Bacteria	<i>Synergistetes</i>	<i>Synergistia</i>	<i>Synergistales</i>	<i>Dethiosulfovibrionaceae</i>		
OTU148	Bacteria	<i>Synergistetes</i>	<i>Synergistia</i>	<i>Synergistales</i>	<i>Dethiosulfovibrionaceae</i>	<i>Jonquetella</i>	<i>Jonquetella anthropi</i>

Table S1. *Cont.*

OTU149	Bacteria	<i>Synergistetes</i>	<i>Synergistia</i>	<i>Synergistales</i>	<i>Dethiosulfovibrionaceae</i>	TG5
OTU150	Bacteria	TM7	TM7-3			
OTU151	Bacteria	TM7	TM7-3	CW040		
OTU152	Bacteria	TM7	TM7-3	CW040	F16	
OTU153	Bacteria	TM7	TM7-3	I025	Rs-045	
OTU154	Bacteria	<i>Tenericutes</i>	<i>Mollicutes</i>	<i>Mycoplasmatales</i>	<i>Mycoplasmataceae</i>	<i>Mycoplasma</i>
OTU155	Bacteria	<i>Verrucomicrobia</i>	<i>Opitutae</i>	<i>Opitutales</i>	<i>Opitutaceae</i>	<i>Opitutus</i>

