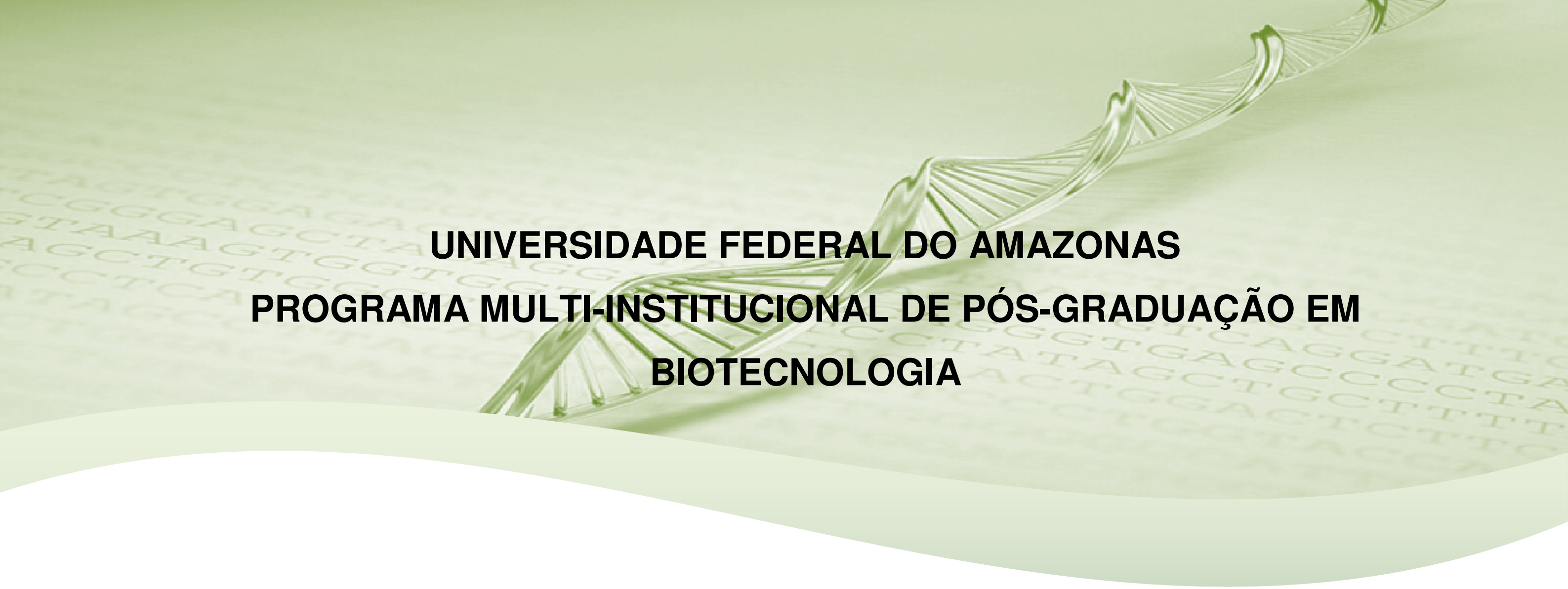

UNIVERSIDADE FEDERAL DO AMAZONAS
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Comparação por análise molecular da diversidade bacteriana da saliva de pacientes com diferentes índices de higiene bucal

JULIANA VIANNA PEREIRA

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Tese de Doutorado apresentada ao Programa de Pós-Graduação em Biotecnologia da Universidade Federal do Amazonas, como requisito parcial para a obtenção do Título de Doutor em Biotecnologia.

Orientador: Dr. Spartaco Astolfi-Filho
Co-Orientadora: Dra. Luciana Leomil

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Dedicatórias

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José Odair Pereira e

Rosa Maria Ferreira Vianna

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Lista de Abreviaturas

LISTA DE ABREVIATURAS

ABS	Absorbância
BLAST	Basic Local Alingment Search Tool
CAM	Centro de Apoio Multidisciplinar
º C	Graus Celsius
CEP	Comitê de Ética em Pesquisas
CPI	Community Periodontal Index
DNA	Ácido desoxiribonucleico
DNTP	Deoxinucleotídeos trifosfatados
DOTUR	Distance Based OUT and Richiness Determination
EDTA	Ethylenediamine tetraacetic acid - ácido etilenodiamino tetra-acético
EUA	Estados Unidos da América
g	Unidade gravitacional
GET	Tampão - Glicose, EDTA, Tris-HCl
HCl	Ácido Clorídrico
HIV	Human Immunodeficiency Virus – Vírus da imunodeficiência humana
Meio LB	Meio de cultura de células Lurian Bertani
mM	Milimolar
M	Molar
mg	Miligramas
µg	Microgramas
µL	Microlitro
MgCl2	Cloreto de Magnésio
NaOH	Hidróxido de Sódio
NCBI	National Center of Biotecnology Information
nm	Nanogramas
OMS	Organização Mundial de Saúde
OTU	Operational Taxonomic Units – Unidade Taxonômica Operacioanal
pb	Pares de bases
PCR	Polimerase Chain Reaction - Reação de Polimerase em Cadeia
pmol	Picomol
T-RFLP	Terminal Restriction Fragment Length Polymorphisms
RNA	Ácido ribonucléico
RDP	Ribossomal Database Project
rRNA	Ribosomal RNA
rpm	Rotações por minuto
SDS	Sodium Dodecyl Sulfate - Dodecil Sulfato de Sódio
Taq DNA pol	Enzima DNA polimerase extraída do Termophilus aquaticus
TE	Tampão de Tris-HCl e EDTA
TCLE	Termo de Consentimento Livre e Esclarecido
TPK	Solução composta por TE , Tween 20% e proteinase K
TEB	Tampão de Tris HCl, EDTA e ácido bórico
U	Unidade
UFAM	Universidade Federal do Amazonas

Resumo

A complexa microbiota da cavidade bucal tem sido intensivamente estudada e a saliva destaca-se por apresentar microrganismos de diferentes regiões, como a língua, biofilme subgengival e supragengival. Diante disto, o objetivo do presente estudo foi avaliar a diversidade bacteriana da saliva de pacientes com diferentes índices de higiene bucal e para isto, foram construídas duas bibliotecas genômicas da saliva, que foram constituídas por amostras de 15 pacientes cada uma, com a média de índice de biofilme de Silness; Löe diferenciado, sendo a primeira com índice de 1,0 a 3,0 (denominada alto índice) e a segunda, entre 0 a 0,5 (denominada baixo índice). O DNA da saliva foi extraído pelo método fenol/clorofórmio e o gene 16S rRNA para cada biblioteca foi amplificado e clonado. As sequências obtidas foram comparadas com aquelas armazenadas no GenBank do NCBI e RDP. A biblioteca composta pela saliva de pacientes com Alto índice de biofilme dental apresentou cinco Gêneros conhecidos: *Streptococcus*, *Granulicaella*, *Gemella*, *Veillonella* e *Peptostreptococcus* e 33,3% de bactérias não-cultivadas, agrupados em 23 OTUs. A Biblioteca, composta pela saliva de pacientes com Baixo índice de biofilme dental, foi diferente siguinificativamente da primeira (p=0,000) e foi composta de 42 OTUs, distribuídas em 11 Gêneros conhecidos: *Streptococcus*, *Granulicaella*, *Gemella*, *Veillonella*, *Oribacterium, Haemophilus, Escherichia*, *Neisseria, Prevotella, Capnocytophaga, Actinomyces,* alem de 24,87% de bactérias não-cultivadas. O Gênero Streptococcus foi o mais prevalente nas duas bibliotecas, constituindo 79,08% da primeira e 73,63% da segunda. Conclui-se que existe maior diversidade bacteriana na saliva de pacientes com Baixo índice de biofilme dental em relação à pacientes com Alto índice de biofilme dental e que apesar da maioria das espécies não-cultivadas agruparem-se com os *Streptococcus*, ainda contituem-se de microrganismos novos e desconhecidos.

Palavras-chaves: diversidade bacteriana, gene 16S rRNA, saliva

Abstract

The complex microbiota of the oral cavity has been intensively studied and saliva is characterized by microorganisms which colonize different regions of mouth, such as tongue, supragengival and subgingival biofilm. Considering this, the purpose of this study was to evaluate the bacterial diversity of the saliva of patients with different levels of oral hygiene according to the Silness, Löe index. In this research, two genomic libraries of saliva source from 15 patients each were constructed. The pooled samples differ in the average index of Silness, Löe being considered as high or low index within the rate 1.0 to 3.0 and 0 to 0.5, respectively. The DNA saliva was extracted by phenol / chloroform method and 16S rRNA gene for the microorganisms of each sample were amplified and cloned. The sequences obtained were compared to those from sequences of the GenBank – NCBI and RDP. The library resultant from saliva of patients with high level of dental biofilm showed 23 OTUs grouped as five known genus: *Streptococcus*, *Granulicaella*, *Gemella*, *Peptostreptococcus* and *Veillonella* besides 33.3% of uncultured bacteria. The Library made from saliva of patients with low level of dental biofilm, was significantly different from its counterpart (p = 0.000) and was composed by 42 OTUs, distributed among 11 known genus: *Streptococcus*, *Granulicaella*, *Gemella*, *Veillonella*, *Oribacterium*, *Haemophilus*, *Escherichia*, *Neisseria*, *Prevotella*, *Capnocytophaga*, *Actinomyces*, and 24.87% of uncultured bacteria. The genus *Streptococcus* was the more prevalent in the two libraries, constituting 79.08% of the first and 73.64% the second. In conclusion, patients with low dental biofilm index have saliva with higher bacterial diversity than patients with high dental biofilm index, and despite most uncultivated species aggregate with *Steptococcus*, they still are new and unknown microorganisms.

Key words: bacterial diversity, 16S rRNA gene, saliva

Sumário

1. Introdução

Estima-se que cerca de 700 espécies microbianas componham a microbiota da cavidade bucal, sendo que 50% delas ainda não foram cultivadas (KAZOR *et al.,* 2003). Algumas espécies compõem a microbiota comensal da boca, outras são responsáveis por diversas patologias e existem aquelas que funcionam como oportunistas de doenças sistêmicas (STARKE *et al.,* 2006).

A cavidade bucal consiste de um ambiente úmido, com temperatura relativamente constante entre 34 a 36ºC, pH neutro e abriga grande variedade de microrganismos, devido a várias estruturas anatômicas que a compõem (MARCOTTE *et al*., 1998). Esta complexa microbiota tem sido intensivamente estudada (MAGER *et al*., 2003; SAKAMOTO *et al*., 2004; HAFFAJEE *et al*., 2006; KANG *et al*., 2006), e dentre os sítios pesquisados destaca-se a saliva por apresentar uma variedade de microrganismos de diferentes regiões, como a língua, biofilme subgengival e supragengival (SAKAMOTO *et al.,* 2000).

Muitas abordagens têm sido desenvolvidas para melhor entender a diversidade de comunidades microbianas e para estabelecer relações entre organismos específicos e o potencial metabólico codificados em seus genomas (PODAR *et al.,* 2007), considerando que os métodos cultura-dependentes caracterizam apenas uma pequena porção da população bucal (KILIAN, 2005).

Com o avanço da Biologia Molecular e Bioinformática, estudos têm sido complementados para melhor descrever a microbiota bucal, como a pesquisa realizada por Tanner; Izard (2005), onde relataram que pelos métodos moleculares o número de microrganismos que colonizam a cavidade bucal é mais que o dobro do que aqueles detectados usando métodos de cultura.

A utilização de grandes bibliotecas genômicas constitui uma poderosa abordagem para isolar complexas seqüências de DNA de microrganismos não cultivados (SEBAT *et al.,* 2003), trazendo uma nova dimensão de comunidades microbianas (PODAR *et al.,* 2007).

Esses modelos caracterizam-se no isolamento do DNA, Reação da Polimerase em Cadeira (PCR), amplificação do gene 16S ou 18S rRNA, clonagem, seqüenciamento e identificação (SAKAMOTO *et al.,* 2005).

Com relação à microbiota bucal, a primeira análise de biblioteca de gene 16S rRNA foi realizada em 1994, para determinar a diversidade de espiroquetas cultiváveis e não cultivadas de pacientes com periodontite severa (SAKAMOTO *et al.,* 2005).

Apesar da cavidade bucal representar um ecossistema formado por microrganismos e os seus arredores, como dentes e mucosas, não deve ser considerada como um ambiente uniforme, pois dentes, biofilme supra e subgengival, língua e mucosas representam habitat específicos que abrigam uma microbiota variada (MARCOTTE *et al*., 1998). Por isso, várias pesquisas têm utilizado ferramentas moleculares para diferenciar pacientes saudáveis daqueles com periodontopatias (SAKAMOTO *et al.,* 2000), efeito da terapia periodontal (SAKAMOTO *et al.,* 2004; HAFFAJEE *et al.,* 2006), diferença entre sítios bucais (MAGER *et al.,* 2003) e diferença da microbiota em pacientes com idades diferentes (KANG *et al.,* 2006). Entretanto, sabe-se que hábitos de higiene bucaltambém podem influenciar qualitativamente e quantitativamente a microbiota bucal (NOGUEIRA-MOREIRA *et al.,* 2000), porém a literatura não apresenta estudos com abordagens genéticas que relacionam a microbiota da saliva de pacientes com diferentes índices de higiene bucal, sendo, portanto, um dos objetivos desta pesquisa.

A qualidade da higiene bucal pode ser avaliada por diferentes métodos. Em 1964, Silness; Löe elaboraram um índice quantitativo para mensuração do índice de biofilme dental por meio de exame clínico tátil-visual. Dessa forma, cada face dental pode ser categorizada como ausente de biofilme após sondagem da superfície (índice 0), presença de biofilme detectado após sondagem (índice 1), biofilme visível no terço cervical do dente (índice 2) e biofilme abundante que recobre a superfície dental envolvendo o terço médio da coroa dental (índice 3). Além da mensuração quantitativa do biofilme dental, as pesquisas enfocam também a avaliação qualitativa do mesmo, para conhecer a microbiota em diferentes situações, conforme descrito anteriormente.

Para a avaliação e entendimento da diversidade bacteriana da saliva em condições diferentes de higiene bucal, é importante a compreensão da colonização microbiana da estrutura dental. Logo após a limpeza da superfície dental, proteínas bacterianas se adsorvem a superfície do esmalte formando uma camada protéica denominada película adquirida. Em seguida, em um período de até quatro horas, ocorre a adesão de células bacterianas simples com posterior formação de micro-colônias distintas (24 horas). Após um dia, uma sucessão e co-agregação microbianas levam a uma alta diversidade de espécies e, ultrapassando o período de quinze dias, o biofilme atinge uma comunidade clímax e é denominado de biofilme maduro (MARSH; NYVAD, 2005).

Dessa forma, situações diferentes de acúmulo de biofilme dental podem representar comunidades microbianas distintas no ambiente bucal, o que torna a investigação da diversidade bacteriana na saliva em diferentes situações de higiene bucal de suma importância para aumentar o conhecimento desta diversidade. Além disso, estudos têm demonstrado que o biofilme dental pode interferir na saúde bucal e sistêmica da população (HAFAJJE *et al.*, 2006; GOMES *et al.*, 2008; TANWIR *et al.*, 2009). Dessa forma, o conhecimento da diversidade da saliva de acordo com a higiene bucal pode auxiliar no esclarecimento da composição da microbiota que compõe a boca e as possíveis associações com patologias.

2. Revisão da Literatura

2.1. Análise da diversidade microbiana – das técnicas de cultivo às técnicas moleculares

Tradicionalmente, a identificação e detecção de microrganismos eram baseadas em meios de obtenção de carbono e energia, nas exigências nutricionais, meios de cultivo para crescimento e observação em microscópio (KENNEDY, 1999). No entanto, Amann *et al.* (1995) já destacava que em contraste com animais e plantas, a morfologia dos microrganismos é, em geral, muito simples para servir de base para classificação e identificação, e que somente pela técnica de cultivo poderíamos ter o conhecimento sobre a diversidade microbiana incompleta e subestimada. Além disso, a diversidade das bactérias é maior que a de qualquer outro grupo de organismos (COUTINHO *et al.,* 1999).

Alternativamente, foram desenvolvidas várias técnicas para descrever a diversidade microbiana, incluindo aquelas baseadas nos ácidos nucléicos, sendo que o gene 16S rRNA mostrou-se mais adequado. Isso ocorre porque os seus genes (rDNA) são universalmente distribuídos entre os diferentes grupos de organismos, sendo considerada a molécula com o maior grau de conservação existente (LANE *et al.,* 1985). Além disso, possui a vantagem de suas informações estarem disponíveis em bases de dados, permitindo a comparação de seqüências depositadas nessas bases com àquelas recém descobertas (COUTINHO *et al.,* 1999).

Tanner; Izard, (2005) descreveram que após a introdução dos métodos moleculares, houve um rearranjo na taxonomia microbiana, com criação de novos nomes, aumentando a diversidade. No entanto, em alguns casos, esses nomes representam reagrupamentos de espécies previamente reconhecidas e não a criação de um novo grupo filogenético.

Com o advento da técnica de seqüenciamento que recentemente completou 30 anos (NOGUCHI *et al.,* 2006), estima-se que 99% das espécies microbianas não podem ser facilmente cultivadas (HUGENHOLTZ, 2002), as quais podemos denominá-las de espécies não-cultivadas.

Em 2005, Sakamoto *et al*. descreveram o impacto dos métodos cultura-independentes no conhecimento da ecologia da cavidade bucal humana. Nesta pesquisa, verificaram que a técnica de PCR em Tempo Real é um método que detecta e quantifica rapidamente bactérias periodontopatogênicas em amostras clínicas. Entretanto, esta técnica não é apropriada para o estudo de grande número de amostras ou grande número de espécies bacterianas. Outras técnicas têm sido utilizadas para o este fim, como a hibridização DNA-DNA que permite analisar a composição da microbiota sub e supra-gengival em pacientes saudáveis e com periodontite, além de níveis salivares de microbiota em relação à condição periodontal. Para estudo da diversidade da microbiota bucal, também existem trabalhos com a análise de bibliotecas de genes 16S rRNA, que são as mais utilizadas por estudar um gene conservado e por permitir comparação entre bancos de dados. Outra técnica é T-RFLP, a qual é uma alternativa molecular que permite a avaliação de comunidades complexas, permitindo rápida comparação entre a diversidade de diferentes ecossistemas.

2.2. Diversidade microbiana da cavidade bucal

A diversidade microbiana da cavidade bucal tem sido estudada por diversos pesquisadores, a fim de esclarecer o papel dos microrganismos na etiologia das doenças bucais (TANNER; IZARD, 2005).

Apesar da sua diversidade, a microbiota que habita a cavidade bucal humana não apresenta uma distribuição homogênea, devido aos diferentes micro-ambientes que a compõe (GIBBONS *et al.,* 1964a). Além disso, mesmo considerando um único ambiente, como o biofilme dental formado sobre a superfície de uma específica estrutura dental, a microbiota é única para um determinado momento, uma vez que após sua remoção, o novo biofilme que se forma em seguida é diferente qualitativamente e quantitativamente (SOCRANSKY; MANGANIELLO, 1971).

Utilizando métodos moleculares, Diaz et. al. (2006) caracterizaram a comunidade microbiana do biofilme dental no início de sua formação, ou seja, em um período de até oito horas, em três indivíduos. Os autores identificaram 97 filotipos distintos, com predominância de *Streptococcus* sp., principalmente *S. mitis* e *S. oralis*. Outros gêneros comuns foram *Actinomyces*, *Gemella*, *Granulicatella*, *Neisseria*, *Prevotella*, *Rothia*, e *Veillonella*. O estudo mostrou também que a colonização inicial do biofilme dental foi diferente entre os indivíduos estudados.

Em 2003, Mager *et al.* compararam a microbiota de vários sítios orais: dorso, lateral e ventre lingual; assoalho bucal; mucosa jugal; palato duro; mucosa vestibular anterior; mucosa labial inferior e superior; gengiva superior anterior e saliva de 225 pacientes, além do biofilme supra e subgengival de 44 indivíduos. Após análise pelo método de hibridização DNA-DNA com sonda para 40 microrganismos, os autores observaram que a proporção de *Veillonella parvula* e *Prevotella melaninogenica* foi maior na saliva e lateral da língua, enquanto que *Streptococcus mitis* e *Streptococcus oralis* foi menor na saliva e dorso lingual. Os dados permitiram a formação de dois “clusters”, com similaridade maior que 85%. O “cluster” 1 compreendia a saliva, lateral e dorso da língua, já o “cluster” 2, as demais áreas de tecido mole. As bactérias *V. parvula*, *P. melaninogenica*, *Eikenella corrodens*, *Neisseria mucosa*, *Actinomyces odontolyticus*, *Fusobacterium periodonticum*, *F. nucleatum ss vincentii* e *Porphyromonas gengivalis* estavam em maior proporção no “cluster” 1, enquanto que *S. mitis*, *S. oralis* e *S. noxia* foram mais freqüentes no “cluster” 2. O biofilme sub e supragengival apresentaram alta proporção de *Actinomyces*.

A microbiota dos canais radiculares também já foi investigada, como no trabalho descrito por Saito *et al.* (2006) onde estudaram a microbiota endodôntica de sete indivíduos, pela construção de bibliotecas 16S rRNA. As bactérias Gram-positivas do Filo Firmicutes foram as mais prevalentes (65,2%), seguido por Proteobacteria (10,9%), Spirochaetes (4,3%), Bacteroidetes (6,5%), Actinobacteria (2,2%) e Deferribacteres (2,2%). Brito (2007) avaliou a microbiota do sistema de canais radiculares, utilizando a associação das técnicas "Multiple Displacement Amplification" (MDA) e a hibridização DNA-DNA ("checkerboard") e as espécies mais comuns foram *Prevotella tannerae* e *Acinetobacter baumannii.*

Um dos nichos bucais intensivamente estudado é o biofilme dental tanto sub como supra-gengival. Gibbons *et al.* (1964b), investigaram a microbiota cultivável predominante nesse ambiente. Na época, constataram que o biofilme dental era composto de 27% de espécies de *Streptococcus* anaeróbios facultativos, 23% de espécies de *Diphtariae* facultativos, 18% de espécies de *Diphtariae* anaeróbicos, 13% de *Peptostreptococcus* sp., 6% de *Veionella* sp., 4% de *Bacteroides* sp., 4% de *Fusobaterium* sp., 3% de *Neisseria* sp., e 2% de *Vibrio* sp.

Em 1978, Campos; Zelante descreveram a ocorrência de enterobactérias, encontradas na saliva, língua e biofilme dental. Os pesquisadores isolaram *Escherichia coli*, *Klebsiella pneumoniae*, *Aerobacter aerogenes* e *Proteus rettgeri.*

Li *et al.*, (2004) elucidaram, pelo método de hibridização DNA-DNA, os primeiros colonizadores do biofilme dental para estabelecer as mudanças que ocorrem na população microbiana durante as primeiras fases do biofilme em formação. Foram coletadas amostras de biofilme dental de 15 indivíduos saudáveis, 0, 2, 4 e 6 horas após a limpeza e dentes e a composição dessas amostras foi comparada com a de toda saliva recolhida a partir do mesmo indivíduo. A composição do biofilme foi distinta da saliva, o que confirma a seletividade do processo de adesão. Na fase muito precoce, foram encontrados espécies *Actinomyces*, além de uma proporção relativa de *Streptococcus*, principalmente *S. mitis* e *S. oralis*, que aumentou em detrimento das espécies Actinomyces, entre 2 e 6 h, enquanto o nível absoluto de

Actinomyces permaneceu inalterado. Patógenos periodontais, como *Tannerella forsythensis* (*Bacteroides forsythus*), *Porphyromonas gingivalis* e *Treponema denticola*, bem como *Actinobacillus actinomycetemcomitans* estavam presentes em níveis extremamente baixos em todo o período analisado. Segundo os autores, os dados mostram que os primeiros colonizadores da superfície dental são predominantemente microrganismos benéficos.

Recentemente, Faveri *et al.* (2008) investigaram a diversidade bacteriana do biofilme sub-gengival de pacientes com periodontite agressiva, utilizando clonagem do gene 16S rRNA e a técnica de hibridização DNA-DNA. Alta taxa de patógenos periodontais, como: *T. forsythia*, *P. gingivalis* e *T. dentícola* foram encontradas nos pacientes com periodontite agressiva ($p<0{,}001$) em comparação com o grupo periodontalmente saudável. Espécies consideradas compatíveis com o hospedeiro, como *Acitnomyces* e *Streptococcus* sp. estavam em níveis elevados nos pacientes com saúde periodontal. A análise do gene 16S mostrou 120 espécies diferentes de 1094 clones.

Em outras pesquisas, em que utilizaram a metodologia da biologia molecular, há comparação de espécies microbianas do biofilme dental antes e após tratamento periodontal. Haffajee *et al.* (2006) observaram que quando se examina o efeito da terapia periodontal sobre a microbiota subgengival, os dados podem ser expressos de várias formas, como mudanças na contagem, na proporção ou na porcentagem de sítios colonizados. Acrescentaram ainda que a remoção do biofilme dental das superfícies dentais reflete em efeito benéfico nos tecidos periodontais adjacentes. Sakamoto *et al.* (2004) verificaram pela técnica T-RFLP, que três meses após a terapia peridontal, mudanças substanciais foram encontradas no biofilme de pacientes com periodontite crônica, enquanto que nos pacientes com periodontite agressiva uma pequena alteração foi observada. Com relação à proporção de bactérias, a PCR em Tempo Real mostrou que a população de *Porphyromonas gingivalis* reduziu $3{,}1\text{x}10^{-3}\%$.

A microbiota supra e subgengival também foi comparada em algumas pesquisas. Ximénez-Fyvie *et al.* (2000a, 2000b) compararam essa microbiota em dois estudos consecutivos. No primeiro, estudaram pacientes saudáveis e com periodontite, onde verificaram que *Porphyromonas gengivalis*, *Bacteroides forsythus* e *Treponema denticola* foram detectadas no biofilme supragengival de ambos os grupos. Espécies *Actinomyces* foram dominantes no biofilme sub e supragengival dos pacientes saudáveis e com periodontite. Na segunda pesquisa, compararam a microbiota supra e subgengival de pacientes com periodontite do adulto. Para análise, utilizaram 40 sondas para bactérias periodontais, utilizando a técnica de hibridização DNA-DNA. Os resultados mostraram que todas as bactérias analisadas foram encontradas em ambos os ambientes estudados. Entretanto, as amostras supragengivais apresentaram um maior número de *Actinomyces naeslundii*, *A. israelii*, *A. odontolyticus*, *Neisseria mucosa*, *Streptococcus gordonii*, *Capnocytophaga ochracea* e *C. sputigena*, mostrando que o biofilme supragengival pode ser um reservatório para espécies periodontopatogênicas.

Muitas pesquisas utilizam a saliva para estudar a diversidade da boca. Gibbons *et al.* (1964a) já afirmavam que, por banhar a cavidade bucal, na saliva estão presentes organismos do biofilme dental, do fluido sub-gengival e da língua. Posteriormente em 2008, Kulekci *et al.* complementaram que a saliva parece ter características promissoras para o diagnóstico das doenças orais, incluindo a possibilidade de examinar a microbiota bucaltotal, além de ser de fácil e rápida coleta, especialmente em crianças.

Corroborando estes dados, Sakamoto *et al.* (2000) analisando bibliotecas de 16S rDNA, compararam as bactérias orais da saliva de um paciente saudável e outros dois com doença periodontal. Após seqüenciamento do DNA das amostras, não foram encontrados clones de bactérias periodontopatogênicas na saliva do paciente periodontalmente saudável, enquanto que patógenos periodontais como *Campylobacter rectus*, *Prevotella intermédia*, *P.*

gingivalis e *T. socranskii* estavam presentes nos pacientes com periodontite, mostrando o papel desses microrganismos nas doenças periodontais.

A taxa de patógenos periodontais na saliva e sua correlação com fatores sociais também foi estudada por Könönen *et al.* (2007b). Foram examinados 1294 indivíduos com idade ≥ 30 anos que habitavam as regiões: central, norte, sul, leste e oeste da Finlândia. A análise por PCR da região 16S rRNA mostrou que 88,2% dos avaliados apresentavam pelo menos um dos seis patógenos estudados. As taxas dos microrganismos foram: *Tonnerela forsythensis* (56,9%), *Treponema denticola* (38,2%), *Porphyromonas gingivalis* (35,4%), *Campylobacter rectus* (31,3%), *Actinobacillus (Agregatibacter) actimycetemcomitans* (20,0%) e *Prevotella intermedia* (13,9%). Observaram que a idade foi associada com a presença de *P. gingivalis* (P=0,000), assim como a educação com *T. denticola* (P=0,000). Da mesma forma as associações também foram observadas entre o número de dentes e bolsas periodontais com *P. gingivalis* (P=0,000), *P. intermédia* (P=0,000), *T. denticola* (P=0,000) e *A. actimycetemcomitans* (P=0,004).

Darout *et al.* (2002) avaliaram níveis salivares de 25 bactérias e sua relação com a condição periodontal e experiência de cárie de 56 pacientes. O exame periodontal foi realizado de acordo com o “Community Periodontal Index” (CPI) e a experiência de cárie foi avaliada seguindo os critérios da Organização Mundial de Saúde (OMS). A saliva coletada foi analisada pela técnica de hibridização de DNA e os resultados mostraram uma alta porcentagem de pacientes com $\geq 10^5$ células bacterianas. Entre 12% a 16% dos avaliados apresentaram uma quantidade $\geq 10^6$ células bactérias periodontais: *Actinobacillus (Agregatibacter) actinomycetemcomitans*, *Porphyromonas melaninogenica*, *Prevotella intermedia*, *Campylobacter rectus* e *Eikenella corrodens*. Não houve diferença significativa entre idade, gênero ou condição periodontal. Já a presença de *Lactobacillus acidophilus* ($\geq 10^5$) células foi estatisticamente significativa com alto índice de cárie (p=0,02), sendo que os dados indicaram que o alto índice de bactérias periodontais na saliva pode ser um indicador de um *status* periodontal pobre.

Corroborando com os dados acima, Pratten *et al.* (2003) compararam a microbiota formada a partir da saliva utilizando cultivo tradicional, pelos meios "Fastidious Anaerobe Agar" e "Columbia Blood Agar" e por clonagem do gene 16S rRNA, pelos iniciadores 27F e 1492R. O uso do cultivo e da clonagem resultou na identificação de 35 bactérias de 16 gêneros como *Haemophilus parainfluenzae*, *Bacilus subtilis*, *Gemella haemolysans*, *Lactobacillus fermentum*, *Streptococcus parasanguis*, *S. gordonii*, *Propionibacterium acnes, Stomatococcus mucilaginosus*, entre outros. Cinco microrganismos foram encontrados utilizando-se apenas o método molecular.

Outra abordagem de pesquisa foi a realizada por Socransky; Manganiello (1971) a qual avaliaram a microbiota salivar em pacientes com idades distintas. Neste estudo, verificaram a ausência de microrganismos na cavidade bucal ao nascimento, pois nas primeiras dez horas de vida, ocorre um rápido aumento de microrganismos nesse ambiente. Entretanto, mudanças consideráveis ocorrem com a erupção dental, uma vez que fornece um novo nicho para colonização. Com a adolescência, observa-se um crescimento descontínuo, pois as lesões de cárie dental oferecem, mais uma vez, um novo habitat. Já nos adultos observa-se uma complexa microbiota que é influenciada por fatores fisiológicos e patológicos, como a perda dental.

Em outra pesquisa em que se considerou o fator idade Kulekci *et al.* (2008) estudaram a prevalência de bactérias periodontopatogênicas na saliva de crianças periodontalmente saudáveis, com dentição mista, porém neste estudo, utilizaram alíquotas de saliva de 41 crianças. Os microrganismos foram identificados utilizando iniciadores específicos para bactérias periodontais e foi detectado a presença de *Prevotella nigrescens*, *Treponema* *denticola*, *Aggregatibacter actinomycetemcomitans* e *Porphyromonas gingivalis*, indicando que existe a possibilidade de risco para doença periodontal.

Nesse sentido, Kang *et al*. (2006) investigaram as espécies bacterianas da saliva de pacientes com idades de 5, 32, 35 e 65 anos, sendo que os pacientes não apresentavam doenças periodontais e não utilizaram antibióticos por três meses. Para identificar a diversidade bacteriana, 50 clones foram selecionados de cada biblioteca, seqüenciados e comparados por identidade na base de dados “GenBank”. Trinta e sete tipos de bactérias foram identificados, classificados em 14 gêneros, duas bactérias não cultivadas e uma não identificada. Os gêneros mais comuns foram: *Streptococcus*, *Prevotella* e *Veillonella*. O gênero *Streptococcus* foi predominante, sendo contabilizadas sete diferentes espécies, destacando-se o *S. salivarius*. Os gêneros *Streptococcus* e *Prevotella* foram mais encontrados em pacientes com 32 e 35 anos, enquanto que nos pacientes com 5 e 65 anos, um maior número pertencia ao gênero *Rothia*, incluindo espécies patogênicas. Além disso, estes pacientes apresentaram uma maior diversidade bacteriana do que os adultos jovens.

Recentemente, Takeshita *et al*. (2009) analisaram a composição bacteriana na saliva de 200 indivíduos. Pela técnica de T-RFLP verificaram três agrupamentos, com predominância de espécies de *Prevotella* e *Veillonella* no primeiro, espécies de *Streptococcus* no segundo e espécies de *Neisseria*, *Haemophilus, Aggregatibacter* e *Porphyromonas* no terceiro, porém na análise do gene 16S rRNA, identificou 57 espécies bacterianas. Os parâmetros clínicos foram então comparados com agrupamentos, como a idade, sexo, fumo e o índice CPOD (dentes cariados, perdidos e obturados), sendo que não diferiram significativamente entre os três agrupamentos. No entanto, diferenças significativas foram observadas entre os parâmetros periodontais e os agrupamentos. A porcentagem de sítios com bolsas periodontais e sangramento à sondagem foi significativamente maiores no grupo I do que aqueles em grupo II e III, e as porcentagens de sítios com bolsa periodontal com mais de

4 milímetros foram significativamente maiores nos grupos I e II do que no pólo III. A proporção de indivíduos sem bolsas periodontais e aqueles com mais de 20% bolsas periodontais também diferiram significativamente entre os grupos. O montante total de bactérias na saliva dos indivíduos foi significativamente maior no grupo I do que nos grupos II e III. No entanto, a porcentagem de sítios com bolsas periodontais demonstrou uma correlação baixa com o total de bactérias em cada agrupamento (r=0,11 no grupo I; r=0,23 no grupo II; r=0,16 no grupo III), e não houve correlação significativa entre o montante total de bactérias e as porcentagens de sítios com bolsas periodontais nos grupos I e III. Dessa forma concluíram que a abundância da distribuição de bactérias comensais na saliva está correlacionada com saúde periodontal, e podem estar envolvidos na suscetibilidade de um indivíduo para doença periodontal.

Mesmo tendo conhecimento de que o biofilme dental é o principal fator etiológico para o desenvolvimento da cárie e doença periodontal e, de que a população não apresenta índices ideais de higiene bucal (GARCIA *et al.*, 2004), há deficiência de dados a nível nacional e principalmente no Estado do Amazonas, estudando se há ou não uma relação de higiene bucal com a microbiota comensal e não comensal de pacientes com biofilme supra-gengival.

3. Objetivos

3.1. Objetivo Geral

Avaliar a diversidade bacteriana da saliva em um grupo de pacientes da cidade de Manaus – AM com diferentes índices de higiene bucal (baixo e alto índice de biofilme dental).

3.2. Objetivos Específicos

- Construir duas bibliotecas gênicas com amostras de saliva de pacientes com baixo e alto índice de biofilme dental;
- Alinhar e editar as sequências encontradas por métodos de bioinformática;
- Verificar a diversidade bacteriana das duas bibliotecas construídas;
- Comparar a diversidade bacteriana das duas bibliotecas construídas;
- Relacionar filogeneticamente as OTUs (Unidade Taxonômica Operacional) encontradas.

Material e Métodos

4.1 Desenho do estudo

Trata-se de um estudo experimental baseado na análise comparativa da diversidade bacteriana da saliva de dois grupos de pacientes com diferentes condições de higiene bucal, na cidade de Manaus-AM.

4.2 População de estudo

Para o desenvolvimento da pesquisa, foram analisadas amostras de saliva de 108 pacientes de ambos os sexos que participaram inicialmente do estudo "Prevalência de *Helicobacter pylori* detectado por PCR na cavidade bucal de pacientes dispépticos e influência do controle do biofilme dental na terapia de erradicação do *Helicobacter pylori* gástrico", provenientes do Consultório Médico de Gastroenterologia, Manaus (AM).

4.3 Procedimentos éticos

O estudo inicial foi submetido à análise pelo Comitê de Ética de Pesquisa (CEP) da Universidade Federal do Amazonas (UFAM) (Anexo 1). A cada paciente identificado como elegível a participar do estudo, foi explicado os objetivos e procedimentos da pesquisa. Após a obtenção da assinatura no Termo de Consentimento Livre e Esclarecido (TCLE) (Apêndice A) dos indivíduos que concordaram em participar da pesquisa, foi aplicado um formulário (Apêndice C) para a coleta dos dados e, posteriormente, realizado o exame clínico. Em seguida, a complementação com os objetivos de investigar a diversidade bacteriana da saliva nas amostras de saliva previamente coletadas foi novamente submetido ao CEP da UFAM (Anexo 2) com a obtenção de um novo TCLE (Apêndice B).

4.4 Critérios de inclusão

- Pacientes com faixa etária acima de 18 anos de idade;

- Portadores de pelo menos quatro dentes na cavidade bucal.

4.5 Critérios de exclusão

- Pacientes com história de imunossupressão;
- Pacientes com distúrbios sistêmicos, tais como diabetes e HIV positivos;
- Uso de medicamentos que reduzem o fluxo salivar (antidepressivos antihipertensivos);
- Gravidez;
- Tratamento com antimicrobianos nos últimos três meses.

4.6 Coleta e preparo das amostras

Os pacientes foram submetidos à anamnese e exame físico (Apêndice C). Durante o exame da cavidade bucal, foi coletada 1 mL de saliva, obtida após estímulo mastigatório de 1 grama de parafina. As amostras foram transferidas para tubos de centrífuga esterilizados, contendo solução TE (Tris HCl 10mM, EDTA 1mM) e mantidas em gelo até sua manipulação no Laboratório de Biologia Molecular do Centro de Apoio Multidisciplinar (CAM) da UFAM.

Posteriormente, foi realizado exame periodontal com avaliação do índice de biofilme dental dos pacientes (Apêndice D), segundo critérios de Silness; Löe (1964), obtendo-se uma média por indivíduo, considerando cada superfície dental de acordo com a classificação:

0 - ausência de biofilme dental

1 - superfície dental aparentemente sem biofilme, mas que pode ser removido por uma sonda

2 - biofilme visível do terço cervical do dente

3 – biofilme abundante

Os pacientes foram agrupados de acordo com a descrição abaixo:

Grupo A: pacientes com a média de índice de biofilme de Silness; Löe (1964) de 1,0 a 3,0

Grupo B: pacientes com a média de índice de biofilme de Silness; Löe (1964) entre 0 a 0,5

4.7 Extração e quantificação de DNA genômico da saliva

Alíquotas de 500 µL das amostras de saliva, contidas em TE, foram transferidas para um microtubo contendo 500 µL de TPK (TE, Tween 20 a 10%, proteinase K 10 mg/mL) para incubação em banho-maria por 56ºC, por 2 horas. Posteriormente, as células foram submetidas à fervura por 10 minutos para inativação da proteinase K. A seguir o DNA foi extraído pelo método do fenol/clorofórmio (1:1), precipitado com etanol 70% gelado e ressuspendido em 40 µL de tampão TE (SAMBROOK *et al.*, 1989).

A quantificação do DNA foi realizada por espectrofotometria (Biomate-3, Termo-Electro Corporation, EUA) medida pela absorbância (ABS) das bases a 260 nm e 280 nm. A estimativa da pureza dos ácidos nucléicos é obtida pela relação entre ABS260 nm e ABS280 nm que fornece uma estimativa da pureza dos ácidos nucléicos. A concentração de DNA equivale ao valor de ABS260nm, considerando que 1UABS260 corresponde a 50 µg/mL. Dessa forma, uma alíquota de cada amostra foi diluída e a concentração de DNA foi calculada conforme a fórmula abaixo:

Concentração de DNA da amostra = ABS260nm x 50µg/µL x 100 (fator de diluição)

Foram selecionadas para a etapa seguinte amostras com concentração superior a 50 ng/µL.

4.8 Amplificação do gene 16S rRNA pela PCR

A amplificação do gene 16S rRNA foi realizada por meio da reação de PCR e consistiu de um volume final de 25µL (50mM $MgSO_4$, 0,5 µL DNTPs 10 mM, 5pmol/µL de cada iniciador, 1,25 U/µL de Platinum *Taq* DNA polimerase Hight Fideliy, tampão 10X). Os iniciadores universais para o gene 16S rRNA foram: 530F (5' - TTG GAG AGT TTG ATC CTG GCT C - 3') e 1492R (5' - ACG TCA TCC CCA CCT TCC TC - 3'), os quais se ligam, respectivamente, às regiões 530 e 1492pb do gene 16S rRNA e amplificam 962 pb.

O ciclo de amplificação consistiu em desnaturação inicial à 94ºC por 2 minutos, seguido de 35 ciclos de desnaturação de fitas-molde à 94ºC por 30 segundos, pareamento dos iniciadores a 58ºC por 30 segundos e extensão à 68ºC por 1 minuto, com extensão final a 68ºC por 5 minutos, processado em termociclador Eppendorf-Mastercycler gradient (Alemanha).

Os amplicons foram analisados por eletroforese (Locus-Biotecnologia LHC, Brasil) em gel de agarose à 0,8% em tampão TBE (Tampão de Tris HCl, EDTA e ácido bórico), utilizando para visualização o brometo de etídio (10 mg/mL). Os resultados obtidos foram visualizados em trans-iluminador em luz ultravioleta e fotografados em seguida para serem analisados.

Após a PCR, as amostras de cada grupo (A e B) foram agrupadas para a construção das 2 bibliotecas gênicas, assim denominadas:

- Biblioteca A: biblioteca genômica de bactérias da saliva das amostras do Grupo A
- Biblioteca B: biblioteca genômica de bactérias da saliva das amostras do Grupo B

4.9 Clonagem do gene 16S rRNA

4.9.1. Sistemas de ligação

O sistema de ligação foi realizado com o kit “TOPO TA Cloning for sequencing” (Invitrogen) como segue: 1,0µL do vetor; 4µL do produto da PCR; 1,0µL da solução de sal diluída, no volume final de 10µL. Em seguida, a solução foi incubada por 30 minutos a temperatura ambiente, sendo depois armazenada à -20ºC.

4.9.2. Transformação por eletroporação

A transformação foi realizada de acordo com o fabricante do kit “Transforming One Shot Mach – T1 Competente Cell” (Invitrogen). Foi utilizado 2 µL do sistema de ligação para 50 µL de células eletro-competentes. A mistura foi levada a um Eletroporador (Eletroporator 2510, Eppendorf, EUA) com 1900 Volts. Após a eletroporação, 1 mL do meio LB (Luria-Bertani) foi colocado na cuveta para recuperação do sistema e vetor. Essas células foram incubadas sob agitação em “shaker” a 180 rpm à 37ºC por 1 hora, sendo em seguida, semeadas em placas de meio LB com Ampicilina (Novafarma) (200 µg/mL) e incubadas à 37ºC durante 18 horas.

4.10 Seleção e estoque dos clones

As colônias transformantes foram transferidas com auxílio de palitos previamente esterilizados para microplacas de 96 poços contendo 150 µL de meio “Circle Grow” (Q-BioGene) e 100 µL /mL de ampicilina (Novafarma), e depois incubadas sob agitação em “shaker” a 180 rpm a 37ºC durante 22 horas. Decorrido esse período, 100 µL da suspensão das células foram transferidas para outra placa de 96 poços, acrescidas com volume igual de glicerol a 50% e armazenada à -80ºC.

4.11 Extração plasmidial

Após o crescimento em microplacas de 96 poços, as células trasformadas foram submetidas à extração plasmidial segundo protocolo de Birnboim; Doly (1979). As placas de 96 poços foram centrifugadas à 20ºC durante 6 min a 2750 g para sedimentar as células, descartando o sobrenadante. O sedimento bacteriano foi ressuspendido em 240 µL de solução tampão GET - Glicose, EDTA, Tris (1M Tris-HCL, pH 8,0; 0,5M EDTA, pH 8,0 e 20% de glicose filtrada), agitado em “vortex” por 2 minutos e centrifugado a 20ºC durante 9 minutos à 2750 g. O sobrenadante foi descartado e a placa permaneceu invertida sobre papel absorvente por 5 minutos. Adicionou-se 80 µL de solução tampão GET, e em seguida, as células foram ressuspendidas por agitação em “vórtex” por 2 minutos. Em uma microplaca de polipropileno de 250 µL de fundo em U (tipo Elisa) foi adicionado 1,5 µL de RNAse (10 mg/mL) em cada cavidade. Em seguida, foram transferidos 60 µL de cada suspensão de células para seus respectivos poços. Adicionou-se 80 µL de NaOH/SDS (NaOH 0,2 N; SDS 10%), o conteúdo foi homogeneizado 30 vezes por inversão e, em seguida, mantido em temperatura ambiente por 10 minutos e, posteriormente centrifugado à 20ºC durante alguns segundos à 2750 g. Foram adicionados 80 µL de acetato de potássio 3M gelado. Mais uma vez, o conteúdo foi homogeneizado 30 vezes por inversão, e a placa incubada por 10 minutos em temperatura ambiente, seguido de centrifugação por tempo igual à 20ºC à 2750 g. O sobrenadante foi transferido para a microplaca com filtro (PVDF 0,2 µm - Millipore) e centrifugado à 20ºC durante 5 min a 2750 g. Ao material filtrado foi adicionado 100 µL de isopropanol absoluto (Merck), a solução foi misturada 30 vezes por inversão, e o material foi centrifugado à 20ºC durante 45 min a 2750 g. Depois de centrifugado, o sobrenadante foi descartado e o precipitado foi lavado com 200 µL de etanol 70% gelado (Merck), e posteriormente, centrifugado à 20ºC durante 5 min à 2750 g. O sobrenadante foi descartado e dado um pulso de 60 g na placa invertida sobre papel absorvente. As amostras foram deixadas por 15minutos no fluxo laminar para secagem, e ressuspendidas em 40 µL de água deionizada autoclavada, sendo mantidas por 18 horas a temperatura ambiente para solubilização do material e armazenada à -20ºC.

Para visualização da extração do DNA plasmidial, uma alíquota de 5 µL foi adicionada a 3 µL de tampão de carregamento (0,025% de azul de bromofenol e 50% de glicose), e a mistura foi submetida a eletroforese em gel de agarose à 0,8% em tampão TBE, utilizando como corante o brometo de etídio (10 mg/mL) para visualização. Os resultados obtidos foram visualizados em transiluminador em luz ultravioleta e fotografados.

4.12 Seqüenciamento do gene 16S rRNA

A reação de sequenciamento foi processada utilizando-se 2 µL de "DyEnamic Et Dye Terminador Cycle Sequencing Kit for Mega BACE" – Amersham – Biosciences®, 100 ng de DNA, 1 µL do iniciador M13R (5' – TAA TAC GAC TCA CTA TAG GG – 3') na concentração de 5 pmol/ µL; água Milli-Q autoclavada para um volume final de 10 µL.

O perfil térmico consistiu de 35 ciclos, como segue: desnaturação de fitas-molde à 95ºC por 3 minutos, pareamento do iniciador a 95ºC por 30 segundos e extensão à 60ºC por 30 segundos, com extensão final à 60ºC por 1 minuto e 20 segundos.

Após a reação, as amostras foram precipitadas para o seqüenciamento, conforme instrução do fabricante. Adicionou-se em cada poço, 10 µL de acetato de amônia e 30 µL de etanol absoluto. O material foi homogeneizado em "vórtex" e incubado em temperatura ambiente por 10 min. Em seguida, as amostras foram centrifugadas à 4ºC durante 40 minutos a 2750 g. O sobrenadante foi removido e em cada poço da placa foi adicionado 120 µL de etanol 70%, seguido de agitatação em vórtex por alguns segundos. Posteriormente, as amostras foram centrifugadas à 4ºC durante 10 minutos à 2750 g. O sobrenadante foi removido e a placa centrifugada à 60 g por alguns segundos, invertida, sob papel absorvente. As amostras foram secas no fluxo laminar por 15 minutos, até todo etanol ser evaporado, sendo ressuspendidas em 10 µL de tampão "loading buffer", agitadas em vórtex e centrifugadas a 4ºC a 60 g por alguns segundos.

O seqüenciamento foi realizado em seqüenciador capilar Mega BACE (Amersham – Biosciences®), conforme recomendações do fabricante.

4.13 Processamento e análise das seqüências

As seqüências obtidas foram processadas para remoção do vetor contaminante e de nucleotídeos de baixa qualidade utilizando-se os programas “Phred/Cross-Match”. Cada seqüência foi comparada com seqüências depositadas no “Genbank” utilizando-se o programa de busca avançada BLAST (“Basic Local Alignment Search Tool”) do “National Center of Biotecnology Information” (NCBI) (ZHANG *et al.*, 2000), utilizando-se os parâmetros “nucleotide blast”, “others database set” e “highly similar sequences”.

As seqüências foram alinhadas e editadas com o auxílio dos programas Clustal W (THOMPSOM *et al.*, 1994) e BioEdit 5.0.9 (HALL, 1999), respectivamente. Posteriormente, foi construída uma matriz de distância genética, utilizando o programa Phylip 3.67 (FELSENSTEIN; PHYLIP, 2007) para posterior análise pelo programa DOTUR (“Distance Based OTU and Richiness Determination”) (SCHLOSS; HANDELSMAN, 2005), para determinação do número de Unidades Taxonômicas Operacionais (OTU), cálculo da estimativa de riqueza pelos métodos de ACE, Chao1, Bootstrap e Jackknife; índices de diversidade de Shannon e o recíproco de Simpson.

A afiliação taxonômica das sequências alinhadas foi realizada pelo programa “Bayesian rRNA Classifier” do banco de dados do “Ribossomal Database Project II” (RDP) (WANG *et al.*, 2007) e pela ferramenta BLAST do NCBI.

Para as análises de relações filogenéticas das seqüências nucleotídicas, foi utilizado o programa Análise Genética de Evolução Molecular MEGA 4.0 (TAMURA *et al.,* 2007), usando o método da construção “neighbor-joining” (SAITOU; NEI, 1987) com algoritmos “Jukes-Cantor” (JULKES; CANTOR*.*, 1969). Os ramos das árvores geradas foram inferidos pelo índice de “bootstrap” com 1000 réplicas em cada nó, para visualização das espécies proximamente relacionadas.

A análise estatística foi realizada quanto ao grau de diferença significativa entre as seqüências nucleotídicas, pela comparação de suas curvas homólogas através do programa S-LIBSHUFF (SCHOLL *et al.,* 2004). Nessa análise, as curvas homólogas das amostras, formadas pela relação entre as distâncias evolutivas e as coberturas de amostragem, são comparadas, sendo calculadas as diferenças entre os pontos eqüidistantes da curva.

5. Resultados

5.1 Índice de biofilme dental - Silness; Löe (1964)

Foram coletadas 108 amostras de saliva, divididas em dois grandes grupos, assim denominados: Grupo A e Grupo B. No primeiro, Grupo A, foram selecionados 25 pacientes com índice de biofilme entre 1 a 3,0 e, no Grupo B, foram selecionados 25 pacientes com índice de biofilme entre 0 a 0,5. Os dados referentes ao índice de biofilme dos pacientes examinados podem ser visualizados na Figura 1.

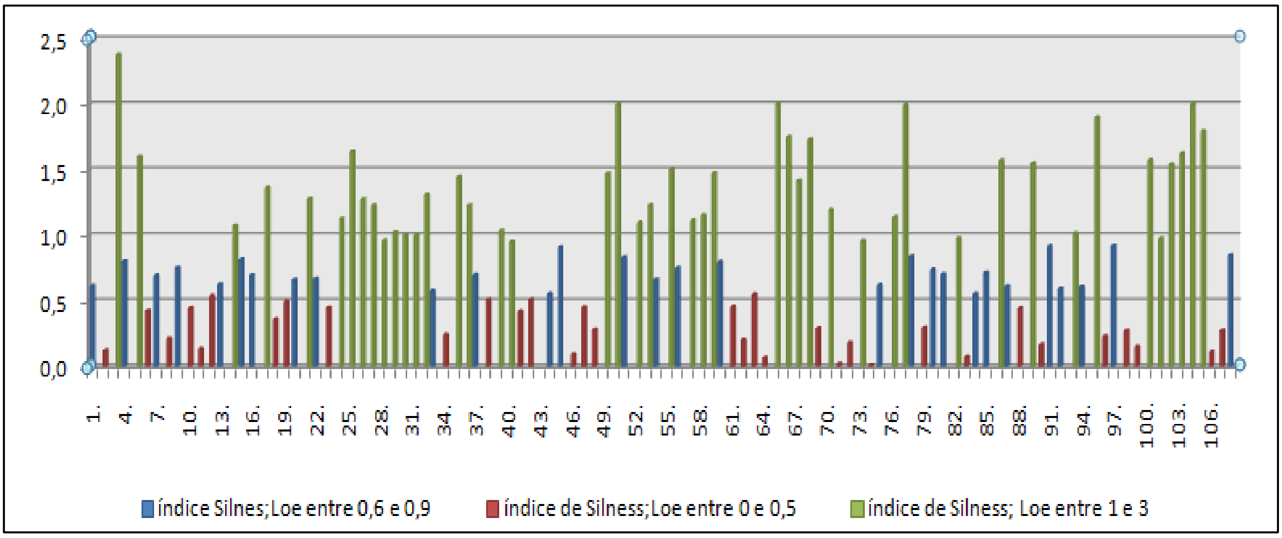

Figura 1: Índice de biofilme dental dos pacientes examinados de acordo com Silness; Löe (1964)

5.2 Quantificação do DNA genômico da saliva

Após a coleta, o material foi encaminhado ao Laboratório de Biologia Molecular, CAM (UFAM) e foi realizada a extração de DNA pelo método fenol:clorofórmio (1:1). Em seguida, quantificou-se o DNA das amostras selecionadas por espectrofotometria, e os resultados se encontram nas Tabelas 1 e 2.

Tabela 1: Quantificação de DNA dos pacientes com alto índice de biofilme dental (Grupo A). Em destaque, as amostras selecionadas para serem processadas pela PCR

Amostras	**Abs 260**	**Abs 280**	**Proporção***	**valor calculado DNA (ng/µL)**
3	0,027	0,013	2,077	135
5	0,028	0,013	2,154	140
17	0,050	0,023	2,174	250
21	0,026	0,013	2,000	130
25	0,015	0,006	2,500	75
26	0,033	0,016	2,063	165
32	0,001	0,000	****	5
35	0,046	0,022	2,091	230
49	0,020	0,009	2,222	100
50	0,013	0,006	2,167	65
55	0,042	0,021	2,000	210
59	0,026	0,013	2,000	130
65	0,020	0,010	2,000	100
66	0,014	0,006	2,333	70
67	0,016	0,008	2,000	80
68	0,055	0,028	1,964	275
77	0,027	0,013	2,077	135
86	0,001	0,000	****	5
89	0,031	0,017	1,824	155
95	0,003	0,000	****	15
100	0,005	0,002	2,500	25
102	0,001	-0,001	-1,000	5
103	0,002	0,000	****	10
104	0,001	-0,002	0,500	5
105	0,002	-0,002	1,000	10

*Estimativa de pureza dos ácidos nucléicos: relação entre ABS260 nm e ABS 280 nm

Tabela 2: Quantificação de DNA dos pacientes do Grupo B, com baixo índice de biofilme. Em destaque, as amostras selecionadas para serem processadas pela PCR

Amostras	Abs 260	Abs 280	Proporção*	valor calculado DNA (ng/μL)
2	0,010	0,005	2,000	50
6	0,020	0,009	2,222	100
8	0,020	0,009	2,222	100
11	0,012	0,006	2,000	60
18	0,015	0,007	2,143	75
23	0,010	0,005	2,000	50
34	0,004	0,002	2,000	20
41	0,015	0,007	2,143	75
46	0,009	0,007	1,286	45
48	0,008	0,004	2,000	40
62	0,007	0,003	2,333	35
64	0,000	0,002	0,000	0
69	0,011	0,005	2,200	55
71	0,003	0,001	3,000	15
72	0,014	0,006	2,333	70
74	0,017	0,007	2,429	85
79	0,027	0,012	2,250	135
83	0,004	0,000	****	20
88	0,021	0,009	2,333	105
90	0,015	0,007	2,143	75
96	0,010	0,005	2,000	50
98	0,013	0,005	2,600	65
99	0,006	0,002	3,000	30
106	-0,003	-0,003	1,000	-15
107	-0,003	-0,003	1,000	-15

*Estimativa de pureza dos ácidos nucléicos: relação entre ABS260nm e ABS 280nm

5.3 Amplificação do gene 16S rRNA pela PCR

Após a quantificação, foram selecionadas 15 amostras de cada grupo com valores ≥ a 50 ng/μL para serem processadas pela PCR, conforme destacado nas Tabelas 1 e 2. Após processamento pela PCR, as amostras de cada grupo foram reunidas para formar as bibliotecas A (Grupo A) e B (Grupo B). O perfil eletroforético em gel de agarose a 0,8% dos agrupamentos das PCRs das bibliotecas pode ser visualizado na Figura 2.

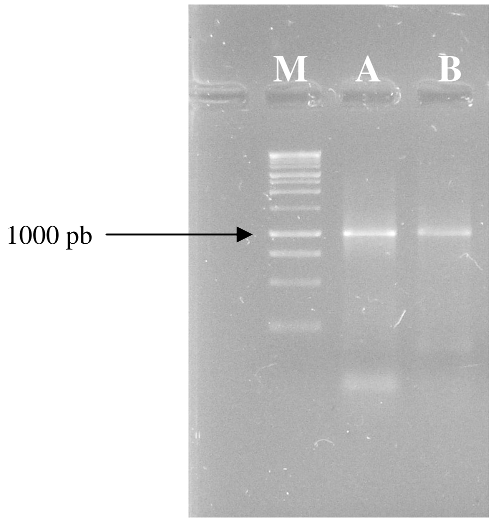

Figura 2: Perfil eletroforético em gel de agarose a 0,8% corado com brometo de etídeo (1µg/µL), evidenciando um fragmento de 962 pb resultante da amplificação da região 16S rRNA de bactérias da saliva dos pacientes com ALTO índice de biofilme dental (A) e BAIXO índice de biofilme dental (B). M - marcador de peso molecular de 1 Kb (Invitrogen Life Technologies).

5.4 Clonagem e análise das sequências

Após a PCR, foi realizada a transformação em células *E. coli* e semeadas em placas de Petri contendo meio LB com ampicilina (200 µg/mL). Para a biblioteca A, foram obtidos 1930 clones e destes foram selecionados 672 para o seqüenciamento. Para a biblioteca B, foram obtidos 4500 clones e selecionados 1032 para seqüenciamento.

Os clones selecionados tiveram o DNA plasmidial extraído (Figura 3) para subsequente preparo das reações de seqüenciamento.

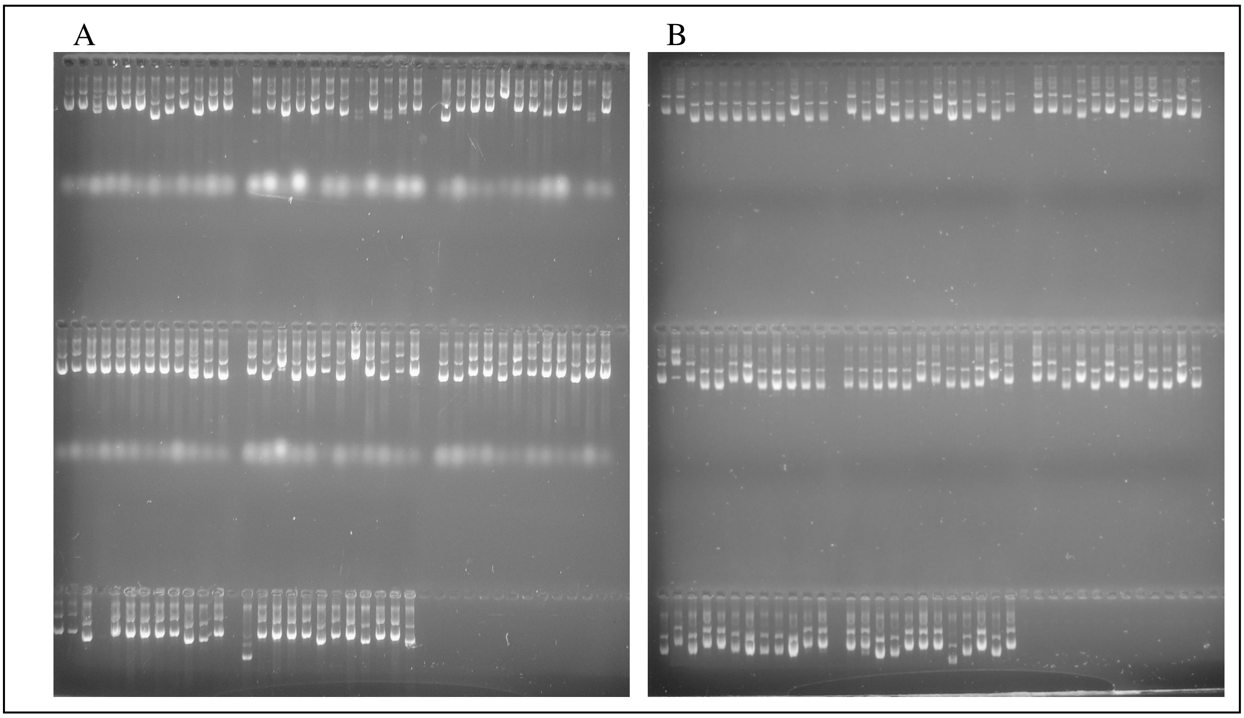

Figura 3: Perfil eletroforético em gel de agarose a 0,8% corado com brometo de etídeo (1µg/µL), evidenciando plasmídios extraídos de clones das bibliotecas A (A) e B (B).

Os plasmídios extraídos foram seqüenciados e, após a remoção do vetor e nucleotídeos de baixa qualidade, alinhamento e edição, 153 sequencias foram selecionadas e consideradas validadas para a biblioteca A e 201 sequencias para a biblioteca B.

O número de OTUs (Unidade Taxonômica Operacional) foi estimado por meio do método de rarefação ao nível de 97% de identidade, pelos métodos não-paramétricos de estimativa, considerando-se a distância evolutiva de 0,03, sendo obtidas 23 OTUs para a biblioteca A e 42 OTUs para a biblioteca B (Figura 4). O cálculo da estimativa de riqueza pelos métodos de ACE e CHAO1, índice de diversidade de Shannon e o recíproco de Simpson estão representados na Tabela 3. A análise estatística realizada quanto ao grau de diferença significativa entre as seqüências nucleotídicas, pela comparação de suas curvas homólogas através do programa S-LIBSHUFF indicou que as duas bibliotecas são diferentes entre si (p=0,000).

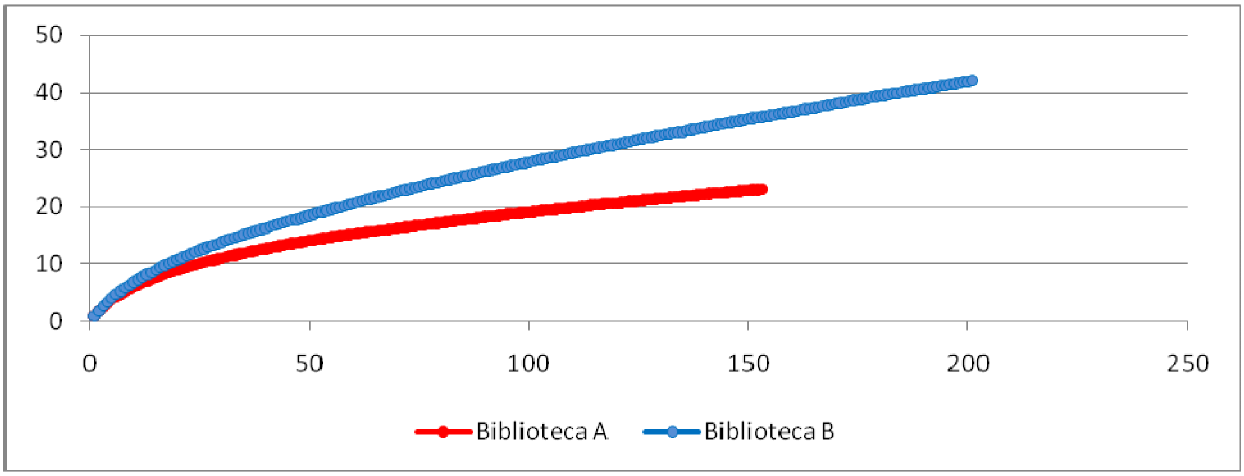

Figura 4: Curvas de rarefação das Unidades Taxonômicas Operacionais (OTUs) das bibliotecas bacterianas da saliva A (linha vermelha) e B (linha azul). Eixo X: número de sequencias; Eixo Y: número de OTUs.

Tabela 3: Estimativas de riqueza de OTUs e índices de diversidade calculados para as bibliotecas A e B

		Índice de riqueza				**Índice de diversidade**	
Biblioteca	**OTU**	**ACE**	**Chao1**	**Jackknife**	**Bootstrap**	**Simpson**	**Shannon**
A	23	39,0031	32	33	27,2235	0,159615	2,31024
B	42	103,332	102	118,502	518,886	0,100846	279,908

O número de clones obtidos pela clonagem, selecionados para o sequenciamento e validados após alinhamento, bem como o número de OTUs obtidos para cada biblioteca pode ser observado na Tabela 4.

Tabela 4: Numero de clones obtidos, selecionados, validados e número de OTUs das bibliotecas A e B

Biblioteca	**Clones obtidos**	**Clones selecionados**	**Clones válidos**	**OTUs**
A	1930	672	153	23
B	4500	1032	201	42

Cada seqüência válida foi comparada com seqüências depositadas no “Genbank” utilizando-se o programa de busca avançada BLAST do NCBI e a ferramenta “Classifier” do

RDP para detrminação da identidade entre as sequencias obtidas com aquelas depositadas nos referidos bancos de dados.

Na Biblioteca A, todas as sequencias analisadas pertenceram ao Filo Firmicutes, entretanto, na Biblioteca B, quatro Filos foram encontrados, Firmicutes, Proteobacteria, Bacteroidetes e Actinobacteria, conforme ilustra a Figura 5.

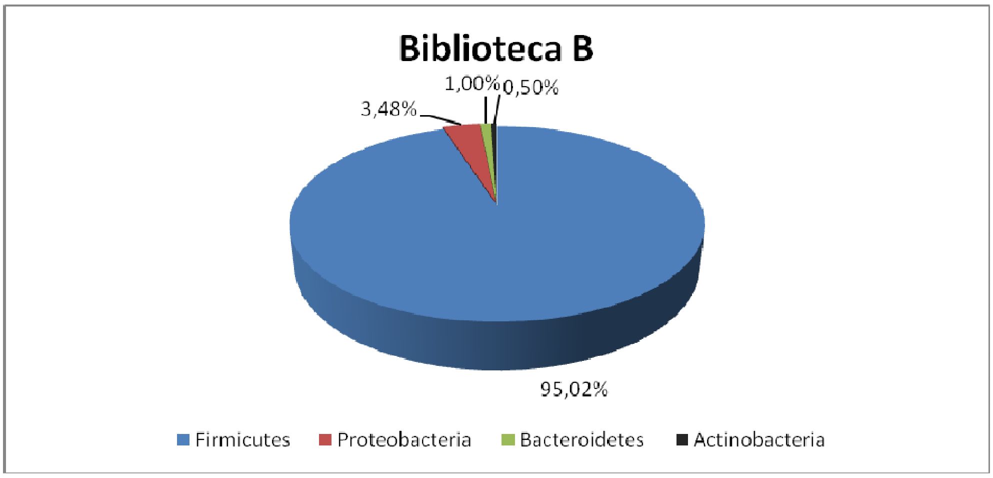

Figura 5: Distribuição dos Filos encontrados para a Biblioteca B.

Com relação à Classe, a Biblioteca B apresentou maior diversidade, com maior prevalência para a Classe Bacilli, conforme ilustrado na Figura 6. Já na Biblioteca A, apenas duas Classes foram encontradas, 90% das sequencias pertenceram à Classe Bacilli e 10% à Classe Clostridia.

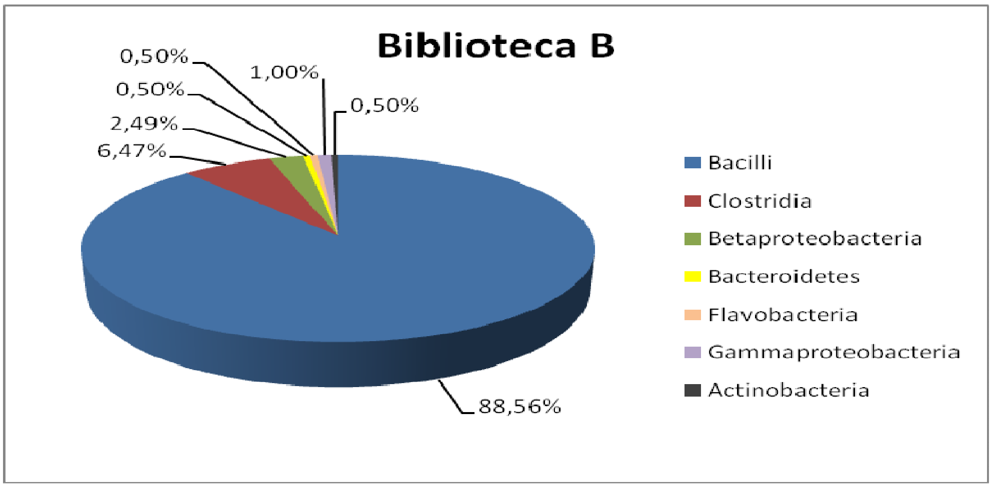

Figura 6: Distribuição das Classes encontradas para a Biblioteca B.

Quanto à Ordem taxonômica, a maior predominância para as duas bibliotecas foi para Lactobacillales, entretanto, uma maior diversidade foi observada para a biblioteca B. Verificou-se também que ambas as bibliotecas apresentaram sequências sem identidade com a Ordem. A diferenciação das sequencias em Ordem pode ser visualizada nas Figuras 7 e 8.

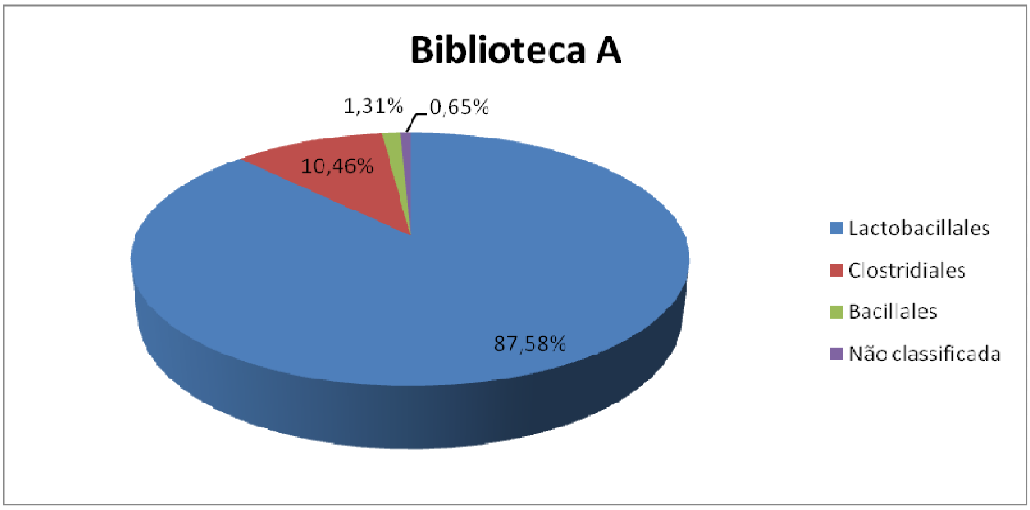

Figura 7: Distribuição das sequencias de acordo com a Ordem para a Biblioteca A.

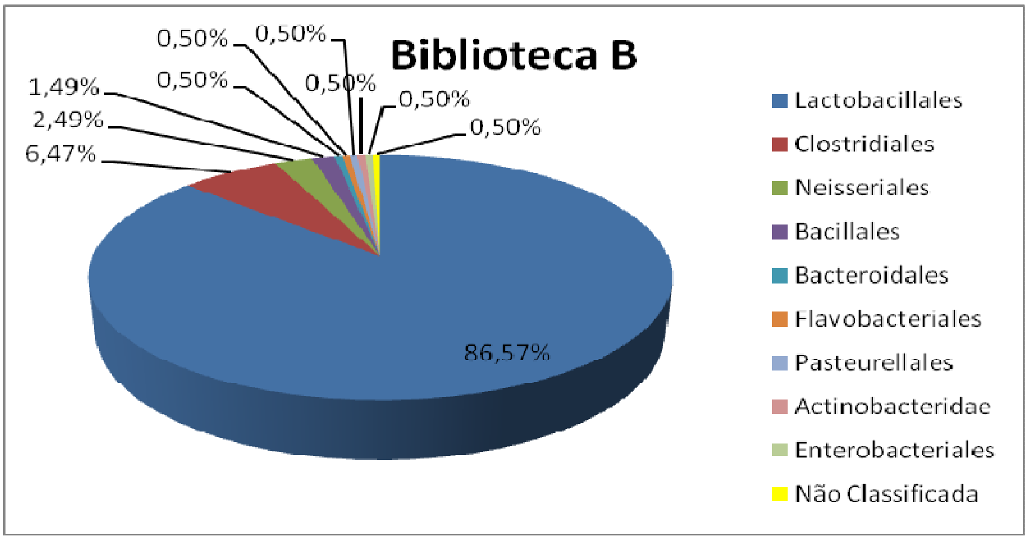

Figura 8: Distribuição das sequencias de acordo com a Ordem para a Biblioteca B.

A Distribuição para Família está representada nas Figuras 9 e 10, destacando-se a Família Streptococaceae nas duas bibliotecas estudadas. Sequências que não apresentaram identidade mínima com as Famílias dos bancos de dados utilizados também fizeram parte das duas bibliotecas.

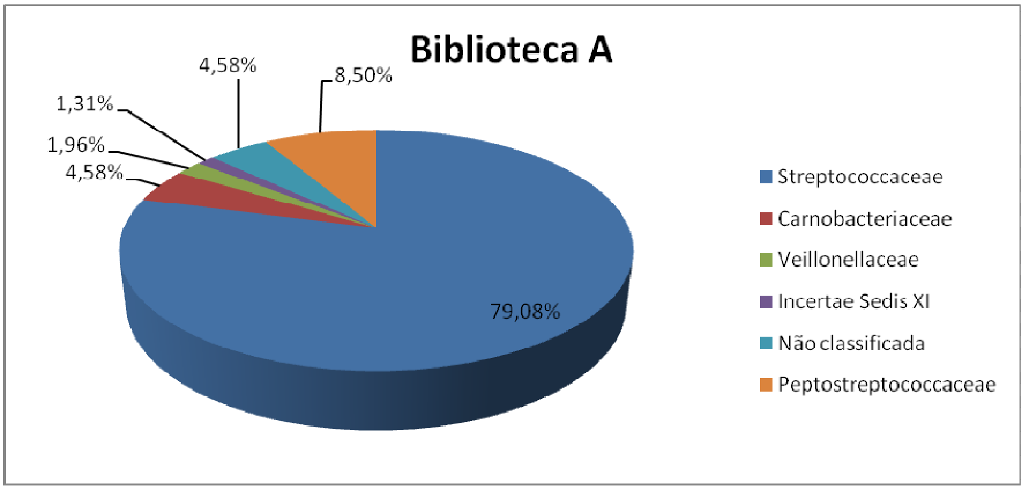

Figura 9: Distribuição das sequencias de acordo com a Família para a Biblioteca A.

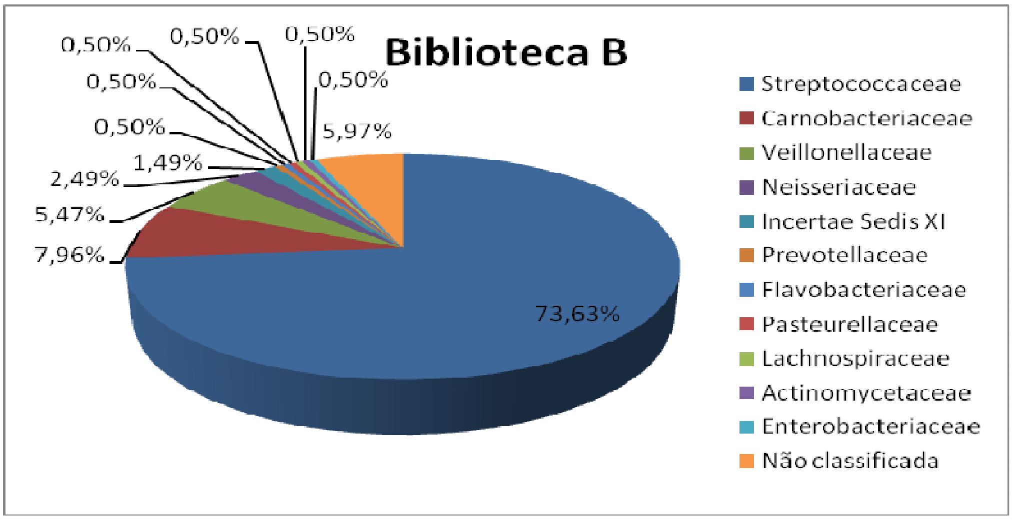

Figura 10: Distribuição das sequencias de acordo com a Família para a Biblioteca B.

O Gênero *Streptococcus* foi o mais prevalente nas duas bibliotecas. Na Biblioteca A, representou 79,08% e na Biblioteca B, 73,63% das sequencias analisadas. Com relação às espécies, maior identidade foi observada para *S. oralis*, seguido por *S. penumoniae* na

Biblioteca A e na Biblioteca B. A identidade encontrada para Gênero e Espécie, bem como a afiliação taxonômica completa das sequencias estudadas estão apresentadas nas Tabelas 5 e 6. A proporção entre bactérias cultiváveis e não cultivadas está representada na Figura 11. Em ambas as bibliotecas, os microrganismos cultiváveis representaram a maioria das sequencias estudadas. Na Biblioteca A, das 153 sequencias analisadas, 51 não apresentaram identidade com espécies conhecidas (33,3%). Para a Biblioteca B, essa proporção foi menor, das 201 sequencias analisadas, 50 foram detectadas como não cultivadas (24,87%).

Tabela 5: Classificação taxonômica das sequencias da Biblioteca A.

Filo	Classe	Ordem	Família	Gênero	Espécie	N°a
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	*Streptococcus*	*Streptococcus oralis*	24
					Streptococcus parasanguinis	8
					Streptococcus sp. **b**	34
					Streptococcus sanguinis	1
					Streptococcus pneumoniae	9
					Streptococcus mitis	4
					Streptococcus gordonii	4
					Streptococcus cristatus	2
					Streptococcus salivarius	2
					Streptococcus thermophilus	1
					Uncultured Streptococcus sp. **b**	21
					Uncultured bacterium **b**	11
			Carnobacteriaceae	*Granulicatella*	*Granulicatella para-adiacens*	3
					Uncultured *Granulicatella* sp. **b**	4
			Nào classificada	Não classificada	Uncultured bacterium **b**	6
		Bacillales	Incertae Sedis XI	*Gemella*	Uncultured *Gemella* sp. **b**	2
		Não classificada	Não classificada	Não classificada	Uncultured bacterium	1
	Clostridia	Clostridiales	Veillonellaceae	*Veillonella*	*Veillonella* sp. **b**	2
					Uncultured *Veillonella* sp.	1
			Peptostreptococcaceae	*Peptostreptococcus*	*Peptostreptococcus* sp. **b**	3
					Peptostreptococcus stomatis	5
					Uncultured *Peptostreptococcus* sp. **b**	5

a: numero de sequencias obtidas na Biblioteca A
b: clones diversos

Tabela 6: Classificação taxonômica das sequencias da Biblioteca B.

Filo	Classe	Ordem	Família	Gênero	Espécie	N° **a**
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	*Streptococcus*	*Streptococcus oralis*	40
					Streptococcus parasanguinis	8
					Streptococcus sp. **b**	23
					Streptococcus sanguinis	4
					Streptococcus pneumoniae	14
					Streptococcus infantis	1
					Streptococcus pseudopneumoniae	3
					Streptococcus genomosp	7
					Streptococcus mitis	9
					Streptococcus gordonii	3
					Streptococcus intermedius	1
					Streptococcus cristatus	2
					Streptococcus thermophilus	5
					Streptococcus oligofermentans	1
					Streptococcus peroris	1
					Streptococcus salivarius	5
					Streptococcus mutans	1
					Uncultured *Streptococcus* sp. **b**	10
					Uncultured bacterium **b**	10
			Carnobacteriaceae	*Granulicatella*	*Granulicatella adiacens*	1
					Uncultured *Granulicatella* sp. **b**	11
					Uncultured bacterium **b**	4
			Não classficada	Não classficada	Uncultured bacterium **b**	10
		Bacillales	Incertae Sedis XI	*Gemella*	*Gemella haemolysans*	1
					Uncultured *Gemella* sp.	1
					Uncultured bacterium	1
		Não classficada	Não classficada	Não classficada	Uncultured bacterium	1
	Clostridia	Clostridiales	Veillonellaceae	*Veillonella*	*Veillonella* sp. **b**	9
					Veillonella atypica	1
					Uncultured bacterium	1
			Lachnospiraceae	*Oribacterium*	*Oribacterium sinus*	1
			Não classficada	Não classficada	Uncultured *Clostridiales*	1
Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	*Haemophilus*	*Haemophilus parainfluenzae*	1
		Enterobacteriales	Enterobacteriaceae	*Escherichia*	*Escherichia coli*	1
	Betaproteobacteria	Neisseriales	Neisseriaceae	*Neisseria*	*Neisseria meningitidis*	3
					Neisseria genomosp	1
					Neisseria sp.	1
Bacteroidetes	Bacteroidetes	Bacteroidales	Prevotellaceae	*Prevotella*	*Prevotella histicola*	1
	Flavobacteria	Flavobacteriales	Flavobacteriaceae	*Capnocytophaga*	*Capnocytophaga* sp.	1
Actinobacteria	Actinobacteria	Actinobacteridae	Actinomycetaceae	*Actinomyces*	*Actinomyces graevenitzii*	1

a: numero de sequencias obtidas na Biblioteca B
b: clones diversos

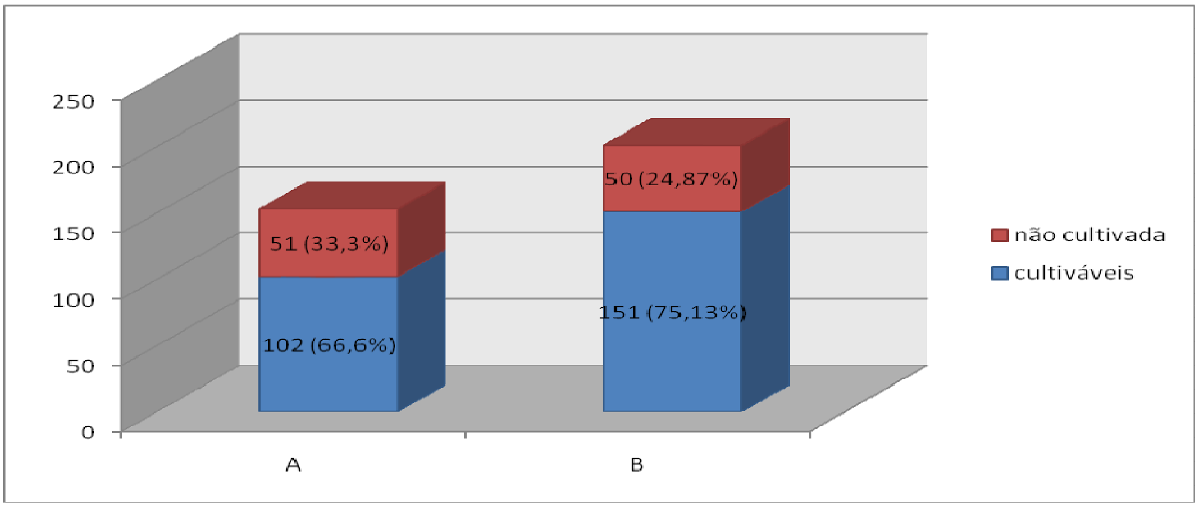

Figura 11: Proporção de bactérias cultiváveis e não cultivadas para as Bibliotecas A e B.

5.5 Análise Filogenética

Foram construídas duas árvores filogenéticas pelo método de “Neigbor-Joining”, uma para cada biblioteca. Cada árvore foi construída utilizado-se um representante de cada OTU identificadas pelo DOTUR e por um grupo externo, constituído pelo *Staphylococcus aureus* (Figuras 12 e 13).

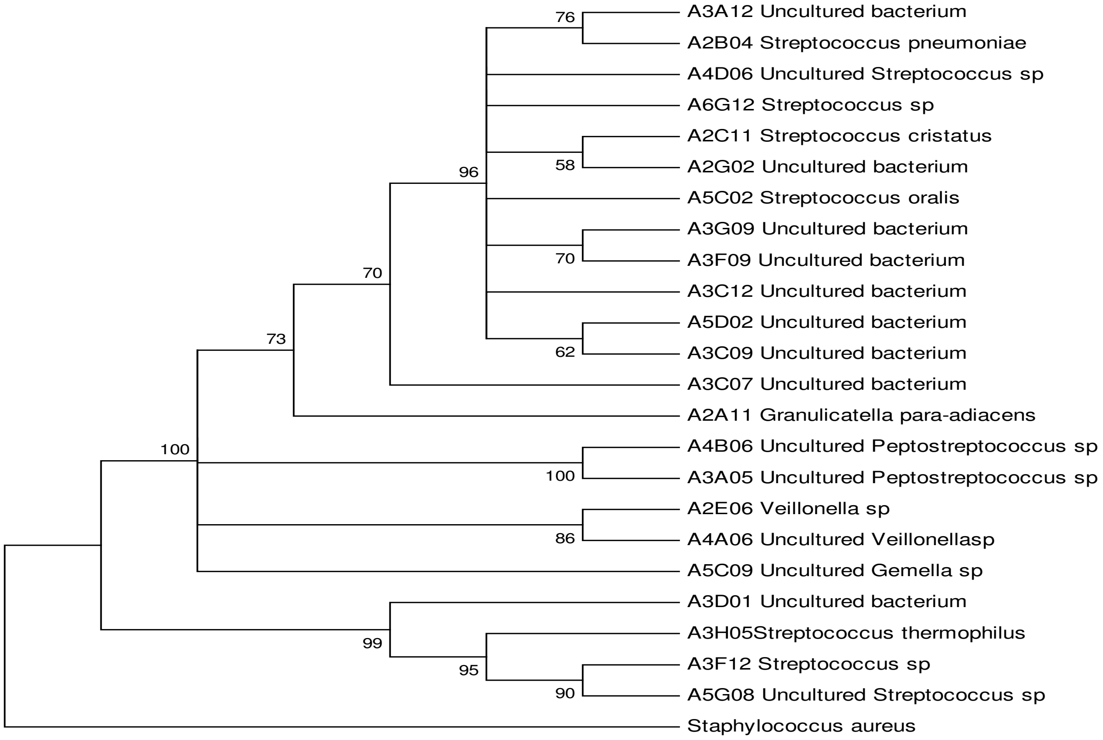

Figura 12: Dendrograma filogenético exibindo as OTUs da Biblioteca A. Método de construção “Neighbor-Joining” com algoritmos de “Jukes-Cantor” e Bootstrap de 1000 réplicas. Para identificação dos clones, observar apêndice F.

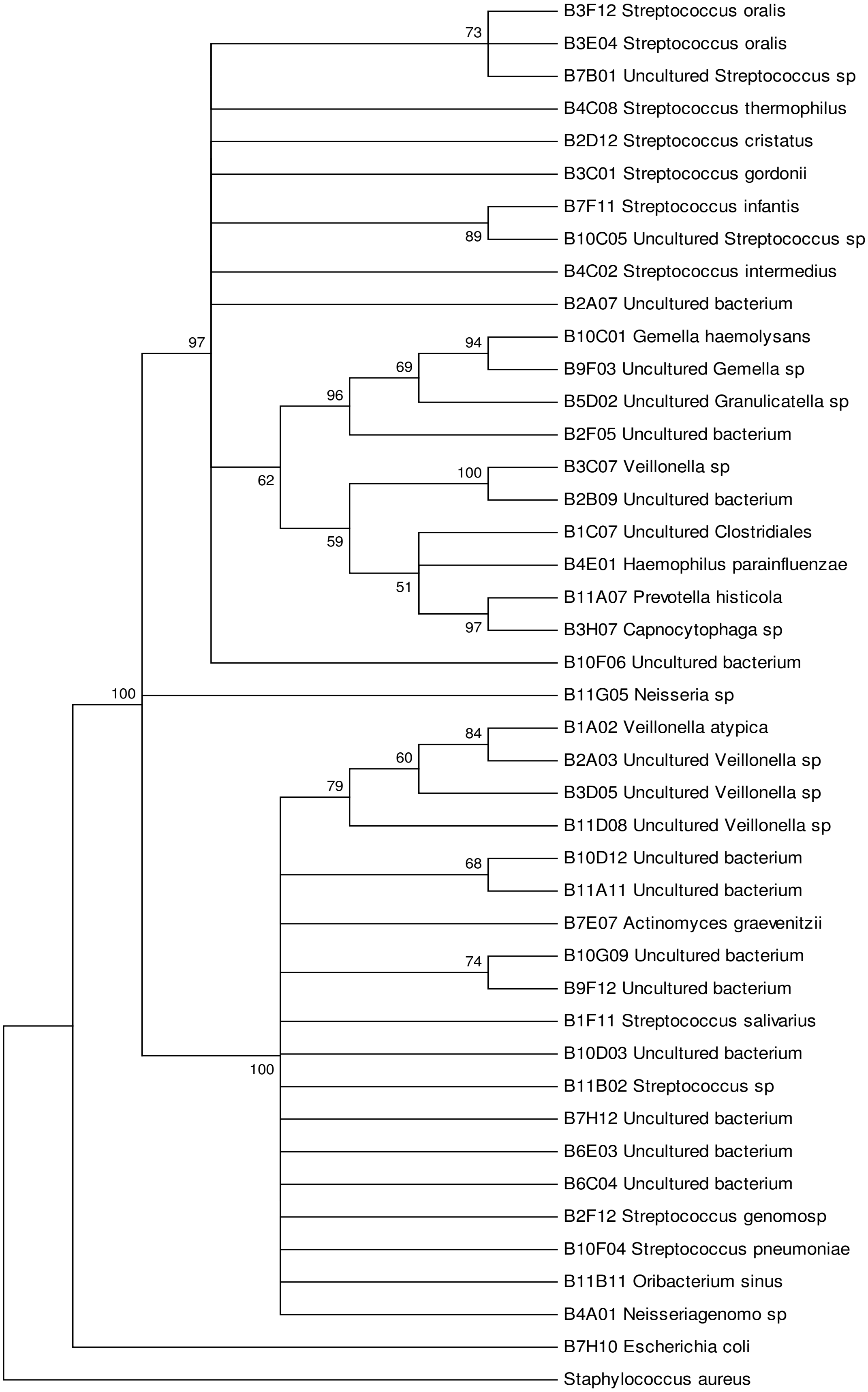

Figura 13: Dendrograma filogenético exibindo as OTUs da Biblioteca B. Método de construção “Neighbor-Joining” com algoritmos de “Jukes-Cantor” e Bootstrap de 1000 réplicas. Para identificação dos clones, observar apêndice F.

6. Discussão

A microbiota da cavidade bucal tem sido foco de diversos estudos, com a finalidade de esclarecer a etiologia das infecções que acometem a boca, principalmente a doença periodontal, cárie dental e infecções endodônticas. Apesar dos patógenos predominantes dessas patologias serem conhecidos, com o avanço das técnicas moleculares o conhecimento sobre a microbiota vem aumentando o número de espécies ou filotipos detectados em diferentes sítios bucais ou reorganizando a taxonomia microbiana (TANNER; IZARD, 2005).

Desde 1994, quando a primeira análise molecular utilizando biblioteca de gene 16S rRNA foi realizada para a cavidade bucal (SAKAMOTO *et al.,* 2005), o número estimado de microrganismos da boca praticamente dobrou, pois os resultados mostram que cerca de 50% das espécies ainda não eram cultivados (KAZOR *et al.,* 2003).

Dentre os métodos moleculares disponíveis, a construção de bibliotecas gênicas permite a análise da dimensão das comunidades microbianas, incluindo microrganismos cultiváveis ou não (PODAR *et al.*, 2007). Nesse modelo, o DNA da amostra em estudo é amplificado utilizando-se iniciadores que amplificam o gene 16S rRNA das bactérias e os “amplicons” são ligados à plasmídios artificiais e inseridos em uma célula hospedeira, em geral a *Escherichia coli*. As colônias resultantes são, então, utilizadas para seqüenciamento, podendo ser comparadas com bancos de dados internacionais de domínio público (TANNER; IZARD, 2005).

De acordo com o fabricante, o sistema TOPO® consiste em um vetor de clonagem, fornecido linearizado, que possui um “overhang” timina (T) em suas extremidades, ligado a uma enzima topoisomerase I. Esta enzima realiza ligação com o produto de PCR produzido por Taq DNA polimerase, a qual acrescenta ao produto de PCR um “overhang” adenina (A), possibilitando o pareamento das bases complementares com o vetor de clonagem.

Considerando-se que a cavidade bucal consiste de um ecossistema complexo, por apresentar distintos micro-ambientes (MARCOTTE *et al.*, 1998) e, que pesquisas recentes mostram que existem diferenças de acordo com o sítio bucal investigado (MAGER *et al.,* 2003), a idade (KANG *et al.,* 2006) e a saúde periodontal (SAKAMOTO *et al.,* 2000, SAKAMOTO *et al.,* 2004; HAFFAJEE *et al.,* 2006) e que os hábitos de higiene também interferem na microbiota da boca (NOGUEIRA-MOREIRA *et al.,* 2000), o estudo da diversidade bacteriana da saliva em pacientes com diferentes condições de higiene bucal nos chamou a atenção, já que métodos moleculares ainda não foram aplicados com esta abordagem.

Deste modo, a saliva foi escolhida como sítio de investigação, por já estar comprovado que a mesma carrega microrganismos oriundos de outros sítios bucais, da língua, do biofilme supra e sub-gengival e tecidos de revestimento da boca (SAKAMOTO *et al.,* 2000, MAGER *et al*., 2003).

Para diferenciar as condições de higiene bucal, adotoudo-se o método quantitativo de Silness; Löe (1964), que permitiu identificar a quantidade de biofilme por superfície dental, gerando uma média para cada indivíduo.

No presente estudo, das 108 amostras de saliva de pacientes com diferentes índices de higiene bucal, foram selecionadas 25 amostras, cujas médias de biofilme dental dos pacientes foram consideradas alta, por já apresentarem biofilme visível ou abundante (>1, segundo Silness; Löe, 1964) e outras 25 amostras, cujas médias de biofilme dental foram consideradas baixa, com biofilme não visível (< 0,5), já que a quantidade e qualidade do biofilme dental têm mostrado interferir nas condições de saúde bucal dos indivíduos, como demonstraram Haffajee *et al.* (2006) onde a remoção do biofilme das superfícies dentais refletiu em um efeito benéfico nos tecidos periodontais adjacentes. Da mesma forma, Gomes *et al.* (2008) verificaram que o controle do biofilme dental supra-gengival reduz a microbiota sub-gengival. Mais recentemente, Tanwir *et al.* (2009) verificaram também que uma pobre higiene bucal pode influenciar no agravamento das doenças periodontais, principalmente na presença de doenças sistêmicas, como diabetes.

Com a diferenciação quantitativa do biofilme dental foram formados dois grandes grupos, A e B, cujas amostras de saliva permitiram a construção de duas bibliotecas gênicas para investigação da diversidade bacteriana da saliva de pacientes com diferentes índices de higiene bucale, dessa forma, comparar a diversidade bacteriana das duas bibliotecas construídas.

A saliva abriga os microrganismos que, por meio de processos dinâmicos, formam o biofilme dental. Usualmente, logo após limpeza a superfície dental é recoberta por uma camada protéica acelular denominada de película, composta de glicoproteínas salivares, fosfoproteínas e lipídeos (LEVINE *et al.*, 1985). A estrutura desta camada tem papel fundamental na composição da microbiota inicial do biofilme dental, pois é seletiva, determinada pelos receptores ali presentes que permitem que componentes específicos das superfícies bacterianas, as adesinas, reconheçam esses sítios (GIBBONS, 1989). Dessa forma, os colonizadores iniciais do biofilme dental constituem uma parte altamente seletiva da microbiota bucal, principalmente o *S. sanguinis*, *S. oralis* e o *S. mitis* (NYVAD; KILIAN, 1990), que juntos representam 95% dos *Streptococcus* e 56% da microbiota total inicial. Outras bactérias encontradas nesta etapa são representadas por *Actinomyces* sp., *Haemophilus* sp. e *Neisseria* sp. A sucessão microbiana que se segue é decorrente da alteração que os colonizadores iniciais geram no ambiente, tornando-o suscetível a colonizadores secundários, principalmente anaeróbios estritos ou facultativos, em decorrência da redução na concentração de oxigênio, o que pode ser observado em biofilmes com nove dias de desenvolvimento. A comunidade clímax é caracterizada pela homeostase microbiana, que tende a expulsar espécies invasoras que não estavam presentes previamente (MARSH; NYVAD, 2005).

Apesar deste estudo não ter como foco de investigação as fases de formação do biofilme dental, os dois grupos estudados mostram-se distintos (p=0,00). A biblioteca formada pelo grupo B, que apresenta a diversidade da saliva dos pacientes com índice de biofilme dental considerado baixo, contém representantes bacterianos observados no início da formação do biofilme. Nesta biblioteca, o Gênero *Streptococcus* totalizou 148 das 201 sequencias analisadas, representando 73,63% da diversidade observada, o que está de acordo com Diaz *et al.* (2006) onde os *Streptococcus* constituem de 66% a 80% da microbiota do biofilme dental num período de 4 a 8 horas de desenvolvimento. O alto índice de *Streptococcus* observado no início da formação do biofilme dental se deve a especificidade da adesão microbiana à película adquirida. Além disso, reflete a alta proporção destes microrganismos na saliva (SCHEIE, 1994). Entretanto, diferentemente do presente estudo em que o *S. oralis* foi o mais prevalente, os autores afirmaram que o *S. salivarius* é a espécie de *Streptococcus* que mais se destaca na saliva. Segundo Li *et al.* (2004), os primeiros colonizadores do biofilme dental são de grande importância para a sucessão de fases do biofilme.

A biblioteca formada pelo grupo A, que apresenta a diversidade bacteriana da saliva dos pacientes com alto índice de biofilme dental parece banhar uma comunidade microbiana em sucessão ou madura, uma vez que a diversidade encontrada foi menor que na Biblioteca B. Além disso, apresentou maior proporção de bactérias não cultivadas. Segundo Marsh; Nyvad (2005) a proporção de microrganismos anaeróbios facultativos e estritos aumenta conforme o biofilme vai se tornando maduro, o que pode justificar o maior número de bactérias não cultivadas.

Contribuindo com o presente estudo, porém utilizando a técnica de T-RFLP, Takeshita *et al.* (2009) analisaram a composição bacteriana na saliva de 200 indivíduos e encontraram 57 espécies bacterianas. Os autores verificaram que espécies de *Prevotella* e *Veillonella* foram relacionadas à fase ativa da doença periodontal, espécies de *Streptococcus* com a fase de remissão da doença periodontal e espécies de *Neisseria*, *Haemophilus, Aggregatibacter* e *Porphyromonas* com indivíduos saudáveis, concluindo que a distribuição de bactérias comensais na saliva está correlacionada com saúde periodontal, e podem estar envolvidos na susceptibilidade de um indivíduo para doença periodontal.

As sequências obtidas na biblioteca A, apresentam cinco Gêneros bacterianos conhecidos, em sua maioria, Gram-positivos representados pelo Gênero *Streptococcus,* com 89 clones cultiváveis e 32 não cultivadas.

O Gênero *Streptococcus* representados por cocos Gram-positivos podem se apresentar isoladamente, em diplococos, cadeias pequenas ou em massa. São anaeróbios facultativos com metabolismo predominantemente fermentativo e é o Gênero mais encontrado na cavidade bucal (JORGE, 2006). A maioria das espécies faz parte da microbiota normal das vias aéreas superiores e dos diferentes nichos ecológicos da cavidade bucal. Como agentes etiológicos são associados à bacteremia, endocardite subaguda, abscessos e outras infecções. Algumas espécies de *Streptococcus* podem elaborar cápsulas de diferentes polissacarídeos extracelulares (PEC) e intracelulares a partir, exclusivamente da sacarose, podendo assim otimizar a progressão da doença cárie (LORENZO, 2004).

A abundância de espécies desse Gênero no presente estudo nas duas bibliotecas está de acordo com os dados apontados na literatura. Segundo Hoshino *et al.* (2004), a identificação das espécies desse Gênero é valiosa, pois contribui com o diagnóstico das infecções bucais e da endocardite infecciosa.

Dentre os 89 clones cultiváveis de *Streptococcus* obtidos na Biblioteca A é possível elucidar a participação de alguns como primordiais para a evolução das doenças bucais. Foram encontradas 24 amostras de *S. oralis* e 04 de *S. gordoni,* alguns das principais colonizadoras da superfície dental contribuindo assim para o desenvolvimento do biofilme dental (DIAZ, 2006). *S. oralis* se liga especificamente a resíduos terminais de ácido siálico das glicoproteínas salivares, possuindo também uma adesina que se liga à galactose. *S. gordoni*, presente nas duas bibliotecas, tem sido associado à endocardite bacteriana, uma vez que o mesmo apresenta em sua parede celular uma glicoproteína que medeia a ligação deste organismo com as plaquetas, fator importante na patogênese deste microrganismo nos casos de endocardite (XIONG *et al*., 2008).

A espécie *S. sanguinis,* mais freqüente na biblioteca B, também é pioneiro na colonização do biofilme dental, pois possui adesinas que reconhecem receptores específicos na película adquirida. Quando encontrado em altas taxas podem sugerir uma proteção contra patógenos das doenças periodontais como o *A. actinomycetemcomitans*, principalmente pela produção de peróxido de hidrogênio. Por outro lado, *S. sanguinis* pode se implantar facilmente em agregados de fibrina e plaquetas existentes nas válvulas cardíacas lesadas, sendo assim é um participante ativo da endocardite bacteriana, uma preocupação nos procedimentos odontológicos invasivos em pacientes de risco (LORENZO, 2004; DAS *et al*., 2009).

Outra bactéria, *S. salivarius,* mais abundantes na biblioteca B, são produtores de glucanos e de grande quantidade de frutanos, motivo pelo qual desenvolve colônias muito viscosas. Suas adesinas têm alta afinidade por receptores situados na superfície da mucosa bucal, seu sítio preferencial (LORENZO, 2004). Algumas cepas produzem bacteriocina, podendo gerar um efeito protetor na cavidade bucal (HORZ *et al*., 2007).

Outra espécie encontrada, *S. thermophilus,* também mais frequente na biblioteca B, é uma bactéria Gram-positiva, anaeróbica facultativa. Trata-se de um microrganismo termofílico, cuja temperatura ótima de crescimento varia entre 37 a 42 °C, não se desenvolvendo bem em temperaturas mais baixas, (18 ou 20 °C), mas é termotolerante com maior resistência a tratamentos aquecimento e pasteurização a 62°C. É um organismo encontrado no leite e produtos lácteos e geralmente é usado na produção de iogurte (FARROW; COLLINS, 1984).

A espécie *S. pneumoniae*, presente em alta proporção nas bibliotecas estudadas, é o mais freqüente agente etiológico de infecções que acometem o sistema respiratório e tem sido foco de investigações devido à alta taxa de resistência à penicilina observada em diferentes países (DOBAY *et al.*, 2003; HOBAN *et al.*, 2003; JONES *et al.*, 2003; KARLOWSKY *et al.*, 2003). O microrganismo está associado com 3 a 5 milhões de mortes por ano. Nos Estados Unidos, é responsável por 500.000 casos anuais de pneumonia, 50.000 casos de bacteremia, 3.000 casos de meningite e cerca de 7 milhões de casos de otite média aguda (ZETTLER *et al.*, 2004).

Outro Gênero encontrado em ambas as bibliotecas foi o do microrganismo *Granulicatella*, representados por Gram-positivos habitualmente aeróbios (DRANCOURT, *et al.*, 2004). Este Gênero foi descrito por Frenkel; Hirsch (1961) como um novo tipo de *Streptococcus* do grupo viridans, que exibe satelitismo em torno de colônias de outras bactérias, devido a sua necessidade nutricional fastidiosa (ROBERTS *et al.*, 1979). O mesmo faz parte da microbiota normal do homem, sendo encontrado na faringe, trato intestinal e urogenital, mas também causam septicemia e são responsáveis por alta taxa de endocardite bacteriana (COLLINS; LAWSON, 2000).

Em menor quantidade, foi evidenciado na Biblioteca A o Gênero *Gemella*, representado por dois clones detectados como não-cultivados. São anaeróbios facultativos caracterizados por cocos Gram-positivos com pequenas dimensões, geralmente dispostos aos pares. O Gênero é encontrado na cavidade bucal e se caracteriza como parasitas exclusivos dos seres humanos (JORGE, 2006). A espécie *G. haemolysans,* encontrada na Biblioteca B, originalmente denominada *Neisseria haemolysans,* já foi associada à pneumonia (EISENHUT *et al.*, 2004), endocardite sub-aguda (KHAN *et al.*, 2004), abscesso cerebral (LEE *et al.*, 2004; DIAZ-PEDROCHI *et al.*, 2005) e meningite (ANIL *et al.*, 2007)

O Gênero *Veillonella* é representado por cocos Gram-negativos, anaeróbios estritos de pequena dimensão. As bactérias deste Gênero não conseguem iniciar a fermentação de carboidratos, presentes no meio bucal, deste modo necessitam de produtos intermediários, como o lacto e piruvato produzido por outras bactérias do biofilme bucal e desta metabolização restam o ácido acético e propiônico, aumentando assim o risco à cárie (LORENZO, 2004). Assim como ocorre com os *Streptococcus*, espécies de *Veillonella* aderem-se ao biofilme dental, pois interagem metabolicamente com o ácido lático produzido pelos *Streptococcus* (CHALMERS *et al.*, 2008). Acreditamos que a maior proporção desses organismos na bilioteca B seja devido ao fato desses microrganismos fazerem parte do grupo pioneiro na colonização da superfície dental (DIAZ *et al.,* 2006), entretanto, Sakamoto *et al.* (2000) encontraram um maior número de sequências de *Veillonella* em indivíduos com periodontite.

O Gênero *Peptostreptococcus* é caracterizado por cocos Gram-positivos que se aglomeram em pares, em tétrade, cadeias ou massas irregulares, além disso, são anaeróbios estritos, metabolizam peptonas e aminoácidos formando ácidos, sendo assim proteolíticos. Estão relacionados com infecções anaeróbias mistas e presentes em sítios com gengivite, periodontite e abscessos periapicais (LORENZO, 2004). A bactéria *P. stomatis*, encontrada no presente estudo na Biblioteca A, está estritamente relacionada com *P. anaerobius* que é conhecido por ser mais resistente que outros cocos anaeróbios Gram-positivos, podendo ser encontrado, além da cavidade bucal, na faringe e em amostras gástricas (KÖNÖNEN *et al.*, 2007a). Sakamoto *et al.* (2000) ao investigar a saliva de pacientes saudáveis e com periodontite, encontraram este Gênero apenas em pacientes com doença periodontal, sugerindo possível associação. Complementando, em 2004, Sakamoto *et al.* também detectaram *Peptostreptococcus* sp. em pacientes com periodontite crônica, com redução total após a terapia periodontal. Esses autores enfatizam que apesar de espécies de *Peptostreptococcus* serem membros da microbiota bucal comensal, algumas espécies estão associadas com infecções anaeróbicas, incluindo gengivite e periodontite, sugerindo que o monitoramento dessas espécies possa ser útil no controle da doença periodontal.

As sequências obtidas na biblioteca B apresentam 11 gêneros bacterianos conhecidos, totalizando 201 clones, com um número proporcional de bactérias Gram-positivas e Gram-negativas, e maior população do Gênero *Streptococcus,* com 128 clones cultiváveis e 20 não cultivados, demonstrando assim, uma população microbiana mais diversa quando comparado com as sequências obtidas na biblioteca A, onde os indivíduos estavam com alto biofilme, levando ao crescimento demasiado de alguns microrganismos em detrimento a outros apresentando uma população bacteriana menos diversa.

Dentro do Gênero *Streptococcus*, na Biblioteca B, foram identificadas algumas espécies diferentes às encontradas na biblioteca A e que são de interesse da área Odontológica, como *S. mutans* e *S. intermedius,* além disso, são comensais da cavidade bucal humana, sendo o primeiro associado à cárie dentária, enquanto que o segundo está associado a infecções purulentas (PECHARKI et. al., 2005). *S. intermedius* é classificado como participante do grupo do *S. mutans* que são considerados como as espécies mais cariogênicas para o dente humano e de vários outros animais, pois reúnem todos os atributos da cariogenicidade, como: acidogênese intensa, aderência as estruturas dentais, produção de glucano insolúvel e aciduricidade (LORENZO, 2004).

Vale ressaltar que o sequenciamento parcial do gene 16S rRNA não distingue com clareza os *Streptococcus* orais, uma vez que algumas espécies diferem apenas em poucos pares de base umas das outras. Além disso, algumas linhagens podem se assemelhar geneticamente dos Gêneros *Abiotrophia* e *Granulicatella*. Esta semelhança genética entre as espécies estreptocócicas pode, muitas vezes, super-estimar o número de *S. mutans* detectados no biofilme dental e na saliva (AL-AHMAD *et al.*, 2006). Recentemente, Do *et al.* (2009) analisaram a estrutura populacional de 113 isolados de *S. oralis* e constataram pela análises das sequências do gene 16S rRNA uma população altamente diversificada intra e inter-espécies. A comparação com exemplos de *S. pneumoniae*, *S. mitis* e *S. pseudopneumoniae* agrupou as espécies em populações distintas, sugerindo que esta discrepância foi possível devido à natureza híbrida de *S. pseudopneumoniae*.

A espécie *Oribacterium sinus,* encontrada na biblioteca B, é representado por um bacilo anaeróbio estrito, Gram-positivo, geralmente isolado de secreções do seio maxilar de crianças com sinusite maxilar. Há relatos de resistência a eritromicina, porém, sensível às penicilinas e geralmente são encontrados na cavidade bucal pelas secreções oriundas do seio maxilar (CARLIER *et al.* 2004).

Também na biblioteca B foram identificadas bactérias do Gênero *Haemophilus*, espécie *H. parainfluenzae*, caracterizados por bacilos Gram-negativos curvos, com extremidades arredondadas, anaeróbio facultativo, fermentador e necessitando de fatores V e X do sangue para seu desenvolvimento. A espécie *H. parainfluenzae* é a mais abundante na cavidade bucal e está associada a casos de endocardite infecciosa (LORENZO, 2004, NWAOHIRI *et al.*, 2009). Ao comparar a saliva de pacientes com idades diferentes, Kang *et al.* (2006) encontraram um clone dessa espécie apenas em paciente com idade de 5 anos.

Espécies de *Neisseria* também foram encontradas a biodiversidade da Biblioteca B. São bactérias Gram-negativas, imóveis, em forma de rins, geralmente dispostas em diplococos, são aeróbios e formadores de oxidase e catalase. As espécies *N. meningitides* são participantes da meningite cérebro-espinhal epidêmica e também podem ser encontradas no trato respiratório, pois possuem fimbrias que se conectam a receptores específicos nas células epiteliais colunares ciliadas na nasofaringe, sem causar sintomas, sendo classificadas em pelo menos 13 grupos sorológicos associados às doenças humanas (JORGE, 2006).

No presente estudo, encontradas em pequena quantidade, também foram identificados bactérias dos Gêneros *Prevotela, Capnocytophaga, Escherichia* e *Actinomyces*. O Gênero *Prevotella* é representado por bacilos Gram-negativos com diferentes dimensões, anaeróbio estrito, sacarolítico, habituam o sulco gengival, participam na etiologia das gengivites no período da gestação, além disto, são encontrados também em infecções endodônticas e na microbiota perimplantar (LORENZO, 2004). Espécies de *Prevotella* também são mais prevalentes em pacientes com doença periodontal agressiva do que em pacientes saudáveis (FAVERI *et al*., 2008). Segundo Downes *et al*. (2008) a espécie *P. histicola* é sacarolítica e produz ácido acético como um dos principais produtos finais da fermentação.

As bactérias do Gênero *Capnocytophaga* classificada antigamente como *Bacteroides,* são Gram-negativas e estão relacionadas com a doença periodontal. A progressão da doença periodontal esta relacionada com vários eventos, dentre eles: colonização bacteriana inicial, defesa do hospedeiro e destruição tecidual. As principais bactérias envolvidas com os distúrbios periodontais são do Gênero *Actinobacillus (Agregatibacter)*, porém a patogenicidade destes microrganismos podem ser influenciada por outras bactérias como as do Gênero *Capnocytophaga*, pois liberam produtos que paralisam a quimiotaxia dos neutrófilos, aumentam a exsudação vascular, e possuem também a capacidade de degradar as imunoglobulinas tipo A e G (SLOTS; GENCO, 1984). Uma sequência desse Gênero também foi encontrada por Sakamoto *et al*. (2004), em paciente com periodontite crônica antes do tratamento periodontal e por Faveri *et al*. (2008) em pacientes com periodontite agressiva.

Outras bactérias que possuem papel fundamental na progressão da doença periodontal são as do Gênero *Actinomyces*, bacilos Gram-positivos, altamente pleomórficos, anaeróbios facultativos, encontrado no biofilme dental subgengival (LORENZO, 2004). Este Gênero também é um dos pioneiros na formação do biofilme dental, sendo que a espécie *A. graevenitzii* já foi encontrado em superfícies de implante dental, cujo sucesso não foi alcançado (SARKONEN *et al.*, 2005). Entretanto, foi encontrado apenas na Bilioteca B, com amostras de saliva de pacientes com baixo índice de biofilme dental, corroborando com os resultados encontrados por Ximénez-Fyvie *et al.* (2000a) que constataram que 63,2% do biofilme dental de pacientes periodontalmente saudáveis apresentavam espécies desse Gênero.

O Gênero *Escherichia*, representados por bastonetes Gram-negativos anaeróbios facultativos, já foi considerado um integrante de uma microbiota transitória que compõe a boca (CAMPOS; ZELANTE, 1978). Segundo Socransky; Manganiello (1971), estes organismos, embora presentes estejam em proporção muito baixa no sulco gengival, na língua e na saliva. Entretanto, representantes da Família *Enterobacteriaceae* foram encontrados em alta proporção (21,6%) na saliva e biofilme dental em grupos de menor idade e de condições de higiene bucal e sócio-econômicas baixas. Além disso, já foi associado à osteomielite mandibular (SCOLOZZI *et al.*, 2005).

Apesar dos microrganismos cultiváveis representarem a maioria das sequencias estudadas, a proporção de bactérias não cultivados, 33,3% para a Biblioteca A e 24,87% para a Biblioteca B, nos levou a construção de duas árvores filogenéticas para auxiliar no agrupamento das sequencias classificadas como não-cultivadas. Os valores de Bootstrap mostram, mais uma vez, que o sequenciamento parcial do gene 16S rRNA não distingue com clareza os *Streptococcus* bucais entre si e entre as demais espécies bucais, conforme relatado por Al-Ahmad *et al.*, 2006. Dessa forma, não se observa uma divisão clara entre as OTUs inferidas pelo DOTUR com os gêneros apontados pelos bancos de dados utilizados e, consequentemente, não houve formação de “Clusters” consistentes.

Entretanto, na árvore contruída com as sequências da Biblioteca A é possível notar que a maioria das sequências apontadas como não-cultivadas se agrupa com os *Streptococcus*, sendo mais próximas, porém distintas, de *S. pneumoniae*, *S. cristatus* e *S. oralis*, indicando que um grande número de espécies deve ser desse Gênero. Outro grupo de *Streptococcus* ficou mais próximo dos demais Gêneros como *Granulicatella, Veillonella, Gemella* e do *S. thermophilus*, quando o *Staphylococcus aureus* foi utilizado como grupo externo.

Para a árvore contruída com as sequências da Biblioteca B verificou-se que um grupo de bactérias detectadas como não-cultivadas ficou mais próximo de um grupo formado por *S. infantis*, *S. oralis*, *S. gordonii*, *S. intermedius*, *S. cristatus*, e *S. thermophylus*. Por outro lado, as demais sequências não-cultaváveis se aproximaram mais de *S. salivarius*, *S. pneumoniae*, *S. genomosp* e dos demais Gêneros.

A estimativa de riqueza de OTUs foi inferida com o auxílio do programa DOTUR em função da distância evolutiva entre as sequências e o número de sequências analisadas (SCHLOSS; HANDELSMAN, 2005), observando-se curvas ascendentes para as duas bibliotecas, o que mostra que a cobertura de amostragem cobriu parcialmente a diversidade dos ambientes estudados. Entretanto, observa-se tendência a atingir um platô, principalmente na Biblioteca A. Desta forma, fica claro que mesmo com um maior número de sequências analisadas para a Biblioteca B e, com maior número de OTUs observados para esta biblioteca, sua diversidade é maior que na Bibliioteca A, sendo necessário ampliar o número de sequências para alcançar a diversidade completa deste ambiente.

Os índices de estimativa de riqueza e de diversidade mostraram diferenças entre as duas bibliotecas, sendo que a Biblioteca B apresentou valores superiores quando comparada com a Biblioteca A, exceto para o índice de Simpson (Tabela 3). É importante ressaltar que esses valores são influenciados pelo número de sequências analisadas (JANSSEN, 2006, SCHOLOSS; HANDELSMAN, 2005).

O método de Chao1 utiliza o número de espécies que ocorrem uma ou poucas vezes para estimar o número de espécies desconhecidas (CHAO, 1984, CHAO *et al.*, 1993). O valor estimado para a Biblioteca B foi superior ao da Biblioteca A, já que sequências únicas representaram metade da diversidade encontrada na saliva dos pacientes com baixo índeice de biofilme dental (Tabela 6).

Já o estimador ACE, baseado na cobertura de abundância, separa as espécies observadas em grupos de espécies raras (com apenas um representante ou com menos de 10 representantes) e abundantes (com mais de 10 representantes), utilizando o grupo de espécies raras para estimar o número de espécies conhecidas (CHAO; LEE, 1992; CHAO *et al.*, 1993). Dessa forma, é esperado que seu valor fosse superior na Biblioteca B, pois esta apresenta um grande número de sequências raras ou únicas, contrabalanceando com espécies abundantes, como *Streptococcus* sp., *S. oralis*, *S. pneumoniae* (Tabela 6).

Os índices de diversidade de Simpson e Shannon empregam independentes aproximações matemáticas para medida de diversidade. O índice de Shannon considera a riqueza ou números diferentes de espécies encontradas em diferentes áreas e a equitabilidade ou igualdade da distribuição de indivíduos sendo, portanto, superior na Biblioteca B. Para o índice de Simpson, o cálculo dá maior peso às espécies mais abundantes, e a adição de espécies raras praticamente não causa mudanças significativas no valor encontrado para o mesmo (MAGURRAN, 1988), dessa forma seu valor foi superior na Biblioteca A, em que as espécies raras representam a minoria das espécies encontradas (Tabela 5), diferentemente da Biblioteca B, que contém espécies raras e abundantes distribuídas de forma mais uniforme (Tabela 6).

As estimativas realizadas pelo Bootstrap baseiam-se em sub-amostragens do conjunto de OTUs, consideando o número de OTU em função do número da amostra (SMITH; VAN

BELLE, 1984) e o estimador Jackknife mostra apenas OTUs únicas (BURNHAM; OVERTON, 1979), que é superior na Biblioteca B (Tabela 6).

O conhecimento e a descrição dos gêneros bacterianos encontrados na cavidade bucal humana são de grande importância para podermos formar um alicerce para sustentar o estudo da participação desses microrganismos na ecologia e na patologia do sistema estomatognático. A detecção de microrganismos considerados como não-cultivados na cavidade bucal indica que muitos filotipos ainda não são conhecidos, o que pode refletir na identificação incompleta dos agentes etiológicos das diversas doenças bucais, considerando que muitas delas são de origem poli-microbiana (TANNER; IZARD, 2005), ou se constituem de microrganismos comensais, sem característica patológica. Assim, a busca incansável pelo esclarecimento da microbiota da boca, em diversas condições de higiene, como aqui estudada, bem como pela interferência de outros fatores ou doenças, estudados anteriormente, ainda é necessária. Esta teoria concretiza-se ao percebermos, nesta pesquisa, que as bactérias não-cultivadas estiveram presentes em maior proporção no grupo de pacientes que apresentava os maiores índices de biofilme dental (Biblioteca A), assim como em estudos que antecederam este trabalho, onde bactérias não classificadas preenchem uma considerável proporção nas patologias estudadas, o que mostra que a investigação da microbiota da boca ainda não pode ser interrompida. Dessa forma, determinadas doenças poderão ser melhor compreendidas considerando-se a associação entre microrgansimos inclusive aqueles ainda desconhecidos da ciência.

Os dados aqui apresentados contribuem para o esclarecimento da microbiota da cavidade bucal quando as condições de higiene bucal são levadas em consideração, o que ainda não havia sido estudado com a abordagem adotada nesta pesquisa. As bibliotecas construídas constituem em um levantamento pioneiro para a microbiologia bucal no Amazonas, podendo ser utilizadas como base para investigações futuras, levando em consideração as características da região, incluindo principalmente os hábitos alimentares peculiares e tradicionais da população.

7 . Conclusões

- Existe maior diversidade bacteriana na saliva de pacientes com Baixo índice de biofilme dental em relação à pacientes com Alto índice de biofilme dental;
- Os microrganismos cultiváveis representaram a maioria das sequências encontradas para as duas bibliotecas construídas;
- A Biblioteca representada pela saliva dos pacientes com Alto índice de biofilme dental apresentou maior proporção de bactérias não cultivadas em relação à Biblioteca formada pela saliva de pacientes com Baixo índice de biofilme dental;
- A análise filogenética evidenciou que apesar da maioria das espécies não-cultivadas agruparem-se com os *Streptococcus*, ainda contituem-se de microrganismos novos e desconhecidos.

Referências

AL-AHMAD, A.; AUSCHILL, T.M.; BRAUN, G.; HELLWIG, E.; ARWEILER, N.B. Overestimation of *Streptococcus mutan* prevalence by nested PCR detection of the 16S rRNA gene. **J. Med. Microbiol**., v.55, p. 109-113, 2006.

ANIL, M.; OZKALAY, N.; HELVACI, M.; AGUS, N.; GULER, O.; DIKERTER, A.; KANAR, B. Miningitis due to *Gemella haemolysans* in a pedriatic case. **J. Clin. Microbiol**., v.45, n.7, p. 2337-2339, 2007.

AMANN, R.I.; LUDWIG, W.; SCHLEIFER, K.H. Phylogenetic identification and in situ detection of individual microbial cells without cultivation. **Microbiol. Rev.**, v.59, p.143-169, 1995.

BIRNBOIM, H.C.; DOLY, J. A rapid alkaline extraction procedure for screening recombinant plasmid DNA. **Nucleic Acids Res.**, v.24,n.7, p.1513-1523, 1979.

BRITO, L.C.N. **Análise microbiológica de infecções endodônticas utilizando a associação das técnicas do "Multiple Displacement Amplification" (MDA) e da Hibridização DNA-DNA ("Chekerboard")**. 2007, 63f. Dissertação (Mestrado) - Universidade Federal de Minas Gerais, Faculdade de Odontologia.

BURNHAM, K.P.; OVERTON, W.S. Robust estimation of population size when capture probabilities vary among animals. **Ecology**, v.60, p.927-936, 1979.

CAMPOS, C.M.; ZELANTE, F. Contribuição ao estudo da microbiota bucal humana. I. Ocorrência de enterobactérias na saliva, língua e placa dental. **Rev. Fac. Odont. S. Paulo**, v.16, n.1, p.77-86, 1978.

CARLIER, J.F.; K'OUAS, G.; BONNE, I.; LOZNIEWSKI, A.; MORY, F. *Oribacterium sinus* gen. nov., esp. non., within the family "Lachospiraceae" (phylum Firmicutes). **Int. J. Syst. Evol. Microbiol.**, v.54, p.1611-1615, 2004.

CHALMERS, N.I.; PALMER JR, R.J.; CISAR, J.O.; KOLENBRANDER, P.E. Characterization of a Streptococcus sp.-Veillonella sp. community micromanipulated from dental plaque. **J Bacteriol**., v.190, n.24, p.8145-8154, 2008.

CHAO, A. Non-parametric estimation of the number of classes in a population. **Scand. J. Stat**., v.11, p.265-270,1984.

CHAO, A;. LEE, S.M. Estimating the number of classes via sample coverage. **J. Am. Stat. Assoc**., v.87, p.210-217, 1992.

CHAO, A; MA, M.C.; YANG, M.C.K.. Stopping rules and estimation for recapture debugging with unequal failure rates. **Biometrika,** v.80, p.193-201, 1993.

COLLINS, M.D.; LAWSON, P.A. The genus Abiotrophia (Kawamura *et al.*) is not monophyletic: proposal of Granulicatella gen. nov., Granulicatella adiacens comb. nov., Granulicatella elegans comb. nov. and Granulicatella balaenopterae comb. nov. **Int. J. Syst. Evol. Microbiol.,** v.50, p.365–369, 2000.

COUTINHO, H.L.; DE OLIVEIRA, V.M.; MANFIO, G.P.; ROSADO, A.S. Evaluating the microbial diversity of soil samples: methodological innovations. **An. Acad. Bras. Cienc**., v.71, n.3, p.491-503. 1999.

DAROUT, I.A.; ALBANDAR, J.M.; SKAUG, N.; ALI, R.W. Salivary microbiota levels in relation to periodontal status, experience of caries and miswak use in Sudanese adults. **J. Clin. Periodontol**, v.29, p.41420, 2002.

DAS, S.; KANAMOTO, T.; GE, X.; XU, P.; UNOKI, T.; MUNRO, C.L.; KITTEN, T. Contribution of lipoproteins and lipoprotein processing to endocarditis virulence in *Streptococcus sanguinis*. **J. Bacteriol.,** v.191, n.13, p.4166-4179, 2009.

DIAZ, P.I.; CHALMERS, N.I.; RICKARD, A.H.; KONG, C.; MILBURN, C.L.; PALMER, R.J.; KOLENBRANDER, P.E. olecular Characterization of Subject-Specific Oral Microflora during Initial Colonization of Enamel. **Appl. Environ.Microbiol**., v.72, n.4, p.2837-2848, 2006.

DIAZ-PEDROCHE, C.; LÓPEZ-MEDRANO, F.; ARRESE, I; GARCIA-MARTINEZ, J. Cerebral abscess due to *Gemella haemolysans*. **Enferm. Infecc. Microbil. Clin**., v.23, n.6, p.385-386, 2005.

DO, T.; JOLLEY, K.A.; MAIDEN, M.C.; GILBERT, S.C.; CLARK, D.; WADE, W.G.; BEIGHTON, D. Population structure of Streptococcus oralis. **Microbiology**, v.155, p.2593-2602, 2009.

DOBAY, O.; ROZGONYI, F.; HAJDU, E.; NAGY, E.; KNAUSZ, M.; AMYES, S.G. Antibiotic susceptibility and serotypes of Streptococcus pneumoniae isolates from Hungary. **J. Antimicrob. Chemother**., v.51, p.887-893, 2003.

DOWNES, J., HOOPER, S.J.; WILSON, M.J.; WADE, W.G. *Prevotella histicola* sp. nov., isolated from the human oral cavity. **Int. J. Syst. Evol. Microbiol**., v.58,p.1788-1791, 2008.

DRANCOURT, M.; ROUX, V.; FOURNIER, P.E.; RAOULT, D. rpoB gene sequence-based identification of aerobic Gram-positive cocci of the genera *Streptococcus*, *Enterococcus*, *Gemella*, *Abiotrophia*, and *Granulicatella*. **J. Clin. Microbiol.**, v.42, n.2, p.497-504, 2004.

EISENHUT, M.; JONES, C.; HUGHES, D.; HERRINGTON, S.; KOKAI,G. Acute renal failure associated with *Gemella haemolysans* pneumonia. **Pediatr. Nephrol.**, v.19, n.4, p.448-450, 2004.

FARROW, J.A.E.; COLLINS, M.D. DNA Base Composition, DNA-DNA Homology and Long-chain Fatty Acid Studies on Streptococcus thermophilus and Streptococcus salivarius. **J. Gen. Microbiol.,** v.130, n.2, p.357-362, 1984.

FAVERI, M. ; MAYER, M.P.A. ; FERES, M. ; FIGUEIREDO, L.C. ; DEWHIRST, F. E. ; PASTER, B.J. . Microbiological diversity of generalized aggressive periodontitis by 16S rRNA clonal analysis. **Oral Microbiol. Immunol.**, v. 23, p. 112-118, 2008.

FELSENSTEIN, J. PHYLIP: **Phylogenetic inference package**. Version 3.67. Seatle. Department of Genetics, University of Washington, 2007.

FRENKEL, A.; HIRSCH, W. Spontaneous development of L forms of streptococci requiring secretions of other bacteria or thiol compounds for normal growth. **Nature**, v.191, 728–730, 1961.

GARCIA, P.P.N.S.; CAMPOS, F.P.; RODRIGUES, J.A.; SANTOS, P.A.; DOVIGO, L.N. Avaliação dos efeitos da educação e motivação sobre o conhecimento e comportamento de higiene bucal em adultos. **Cienc. Odontol. Bras.**, v.7, n.3, p.30-39, 2004.

GIBBONS, RJ. Bacterial adhesion to oral tissue: a model for infectious diseases. **J. Dent. Res**., v.68, p.750-760, 1989.

GIBBONS, R.J.; KAPSIMALIS, B.; SOCRANSKY, S.S. The source of salivary bactéria. **Arch. Oral. Biol**., v.9, p101-103, 1964a.

GIBBONS, R.J.; SOCRANSKY, S.S.; ARAUJO, W.C.; VAN HOUTE, J. Studies of the predominant cultivable microbiota of dental plaque. **Arch. Oral. Biol**., v.9, p. 365-370, 1964 b.

GOMES, S.C.; NONNENMACHER, C.; SUSIN, C.; OPPERMANN, R,V,; MUTTERS, R.; MARCANTONIO, R.A. The effect of a supragingival plaque-control regimen on the subgingival microbiota in smokers and never-smokers: evaluation by real-time polymerase chain reaction. **J. Periodontol**., v.79, n.12, p.2297-2304, 2008.

HAFFAJEE, A.D.; TELES, R.P.; SOCRANSKY, S.S. The effect of periodontal therapy on the composition of the subgingival microbiota. **Periodontol 2000**, v.42, p.219-258, 2006.

HALL, T.A. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. **Nucl. Acids. Symp. Ser.**, v.41, p.95–98, 1999.

HOBAN, D.; WAITES, K.; FELMINGHAM, D. Antimicrobial susceptibility of community-acquired respiratory tract pathogens in North America in 1999-2000: findings of the PROTEKT surveillance study. **Diagn. Microbiol. Infect. Dis**., v.45, p.251-259, 2003.

HOSHINO, T.; KAWAGUCHI, M.; SHIMIZU, N.; HOSHINO, N.; OOSHIMA, T.; FUJIWARA, T. PCR detection and identification of oral streptococci in saliva samples using gtf genes. **Diagn. Microbiol. Infect. Dis.**, v.48, n.3, p.195-199, 2004.

HORZ, H.P.; MEINELT, A.; HOUBEN, B.; CONRADS, G. Distribution and persistence of probiotic *Streptococcus salivarius* K12 in the human oral cavity as determined by real-time quantitative polymerase chain reaction. **Oral Microbiol. Immunol**., v.22, n.2, p.126-130, 2007.

HUGENHOLTZ, P. Exploring prokaryotic diversity in the genomic era. **Genome Biol.**, v.3, n.2, Reviews 0003.1-0003.8, 2002,

JANSSEN, P.H. Identifying the dominant soil bacterial taxa in 16S rRNA and 16S rRNA genes. **Appl. Environ. Microbiol**., v.72, n.3, p.1719-1728, 2006.

JONES, M.E.; BLOSSER-MIDDLETON, R.S.; CRITCHLEY, I.A.; KARLOWSKY, J.A.; THORNSBERRY, C.; SAHM, D.F. In vitro susceptibility of Streptococcus pneumoniae, Haemophilus influenzae and Moraxella catarrhalis: a European multicenter study during 2000-2001. **Clin. Microb. Infect**., v.9, p.590-599, 2003.

JORGE, AOC. **Princípios de Microbiologia e Imunologia**. São Paulo; Ed. Santo, 2006.

JUKES, T.H.; CANTOR, C.R. Evolution of protein molecules. In Munro H.N., editor, **Mammalian Protein Metabolism**, pp. 21-132, Academic Press, New York, 1969.

KANG, J.G.; KIM, S.H.; AHN T.Y. Bacterial diversity in yha human saliva from different ages. **J. Microbiol**. v.44, n.5, p.572-576, 2006.

KARLOWSKY, J.A.; THORNSBERRY, C.; JONES, M.E.; EVANGELISTA, A.T.; CRITCHLEY, I.A.; SAHM, D.F. Factors associated with relative rates of antimicrobial resistance among Streptococcus pneumoniae in the United States: results from the TRUST Surveillance Program (1998-2002). **Clin. Infect. Dis**.,v.36, p.963-970, 2003.

KAZOR, C.E.; MITCHELL, P.M.; LEE, A.M.; STOKES, L.N.; LOESCHE, W.J.; DEWHIRST, F.E.; Paster, B.J. Diversity of Bacterial Populations on the Tongue Dorsa of Patients with Halitosis and Healthy Patients. **J. Clin Microbiol**., v.41, n.2, p.558-563, 2003.

KILIAN, M. Facing facts – Making sense of oral infection. **Oral Biosci. Med**., v.2, n.2/3, p.163-165, 2005.

KENNEDY, A.C. Bacterial diversity in agroecosystems. **Agric. Ecosyst. Environ**., v.74, p.65-76, 1999

KHAN, R.; URBAN, C.; RUBIN, D.; SEGAL-MAURER, S. Subacute endocarditis caused by *Gemella haemolysans* and a review of the literature. **Scand. J. Infect. Dis**., v.36, n.11-12, p.885-888, 2004.

KÖNÖNEN, E.; BRYK, A.; NIEMI, P.; KANERVO-NORDSTRÖM, A. Antimicrobial susceptibilities of Peptostreptococcus anaerobius and the newly described Peptostreptococcus stomatis isolated from various human sources. **Antimicrob. Agents Chemother**., v.51,n.6, p.2205-2207, 2007a.

KÖNÖNEN, E.; PAJU, S.; PUSSINEN, P.J.; HYVÖNEN, M.; DI TELLA, P.; SUOMINEN-TAIPALE, L.; KNUUTTILA, M. Population-based study of salivary carriage of periodontal pathogens in adults. **J. Clin. Microbiol**. v.45, n.8, p.2446-2451, 2007b.

KULEKCI, G.; LEBLEBICIOGLU, B.; KESKIN,F.; CIFTCI, S.; BADUR, S. Salivary detection of periodontopathic bacteria in periodontally helthy children. **Anaerobe**., v.14, p.49-54, 2008.

LANE, D.L.; PACE, B.; OLSEN, G.J.; STAHL, D.A.; SOGIN, M.L.; PACE, N.R. Rapid determination of 16S ribossomal RNA sequences for phylogenetic analyses**. Proc. Natl. Acad. Sci. U.S.A.**, v.82, p.6955-6959, 1985.

LEE, M.R.; LEE, S.O.; KIM, S.Y.; YANG, S.M.; SEO, Y.H.; CHO ,Y.K. Brain abscess due to *Gemella haemolysans*. **J. Clin. Microbiol**., v.42, n.5, p.2338-2340, 2004.

LEVINE, M.J.; TABAK, L.A.; REDDY, M.; MANDEL, I.D. Nature of salivary pellicles in microbial adherence: role of salivary mucins. In: Mergenhagen, S.E.; Rosan, B. **Molecular basis of oral microbial adhesion**. Washington, DC: American Society of Microbiology. P.125-130, 1985.

LI, J.; HELMERHORST, E.J.; LEONE, C.W.; TROXLER, R.F.; YASKELL, T.; HAFFAJEE, A.D.; SOCRANSKY, S.S.; OPPENHEIM, F.G. Identification of early microbial colonizers in human dental biofilm. **J. Appl. Microbiol**., v.97, n.6, p.1311-1318, 2004.

LORENZO, J.L. **Microbiologia para o Estudante de Odontologia**. São Paulo; Atheneu, 2004.

MAGER, D.L.; XIMENEZ-FYVIE, L.A.; HAFFAJEE, A.D.; SOCRANSKY, S.S. Distribution of selected bacterial species on intraoral surfaces. **J. Clin. Periodontol.**, v.30, n.7, p.644–654, 2003.

MAGURRAN, A.E. **Ecological diversity and its measurement**. New Jersey: Princeton, 179p, 1988.

MARCOTTE, H.; MARC, C.; LAVOIE, M.C. Oral Microbial Ecology and the Role of Salivary Immunoglobulin A. **Microbiology and molecular biology reviews**, v.62, n.1, p.71–109, 1998.

MARSH, P.D.; NYVAD, B. A microbiota oral e biofilmes formados sobre os dentes. In: Fejerskov, O. Kidd, E. **Cárie Dentária – A Doença e seu tratamento clínico**. São Paulo: Santos, p.29-48, 2005.

NYVAD, B.; KILIAN, M. Comparison of the initial streptococcal microflora on dental enamel in caries-active and in caries-inactive individuals. **Caries Res**., v.24, p. 627-672, 1990.

NOGUEIRA-MOREIRA, A.; LUNA DAVILA, G.; BIANCHINI H, A.C.; PIOVANO, S. Effect of supragingival plaque control on subgingival microflora and gingivo-periodontal tissues. **Acta Odontol. Latinoam**., v.13, n.2, p.73-86, 2000.

NOGUSHI, H.; PARK,J.; TAKAGI, T. MetaGene: prokaryotic gene finding from environmental genome shotgun sequences. **Nucleic Acids Res.**, v.34, n.19, p. 5623-5630, 2006.

NWAOHIRI, N.;, URBAN, C.; GLUCK, J.; AHLUWALIA, M.; WEHBEH W. Tricuspid valve endocarditis caused by *Haemophilus parainfluenzae*: a case report and review of the literature. **Diagn. Microbiol. Infect. Dis**.,v.64, n.2, p.216-219, 2009.

PECHARKI, D.; PETERSEN, F.C.; ASSEV, S.; SCHEIE, A.A. Involvement of antigen I/II surface proteins in *Streptococcus mutans* and *Streptococcus intermedius* biofilm formation. **Oral Microbiol. Immunol**., v.20, n.6, p.366-371, 2005.

PODAR, M.; ABULENCIA, C.B.; WALCHER, M.; HUTCHINSON, D.; ZENGLER, K.; GARCIA, J.A.; HOLLAND,T.; COTTON, D.; HAUSER, L.; KELLER, M. Targeted access to the genomes of low-abundance organisms in complex microbial communities. **App. Environ. Microbiol**., v.73, n.10, p.3205-3214, 2007.

PRATTEN, J.; WILSON, M.; SPRATT, D.A. Characterization of in vitro oral bacterial biofilms by traditional and molecular methods. **Oral Microbiol. Immunol**., v.18, p.45-49, 2003.

ROBERTS, R.B.; KRIEGER, A.G.; SCHILLER, N.L.; GROSS, K.C. Viridans streptococcal endocarditis : the role of various species, including pyridoxal-dependent streptococci. **Rev. Infect. Dis.**, v.1, p.955–966, 1979.

SAITO, D.; LEONARDO, R.T.; RODRIGUES, J.L.M.; TSAI, S.M.; HOFLING, J.F.; GONÇALES, R.B. Identification of bacteria in endodontic infections by sequence analysis of 16S rDNA clone libraries. **J. Med. Microbiol.**, v.55, p.101-107, 2006.

SAITOU, N.; NEI, M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. **Mol. Biol. Evol.,** v.4, n.4, p.406-425, 1987.

SAKAMOTO, M.; HUANG, Y.; OHNISHI, M.; UMEDA, M. ISHIKAWA, I.; BENNO, Y. Changes in oral microbial profiles after periodontal tratmente as determined by molecular analysis of 16S rRNA genes. **J. Med. Microbial**., v.53, p. 563-571, 2004.

SAKAMOTO, M.; UMEDA, M.; BENNO, Y. Molecular analysis of human oral microbiota. **J. Periodontol. Res**., v.40, p.277-285, 2005.

SAKAMOTO, M.; UMEDA, M.; ISHIKAWA, I.; BENNO, Y. Comparison of the oral bactéria flora in saliva from a healthy subject and two periodontitis patients by sequence analysis of 16S rDNA libraries. **Microbiol. Immunol**., v.44, n.8, p.643-652, 2000.

SAMBROOK, J., FRITSCH, E.F.; MANIATIS, T. **Molecular Cloning: a Laboratory Manual**, 2nd edn. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory. 1989.

SARKONEN, N.; KÖNÖNEN, E.; EEROLA, E.; KÖNÖNEN, M.; JOUSIMIES-SOMER, H.; LAINE, P. Characterization of Actinomyces species isolated from failed dental implant fixtures. **Anaerobe**, v.11, n.4, p.231-237, 2005.

SCHEIE, A.A. Mechanisms of dental plaque formation. **Adv. Dent. Res**. v.8, n.2, p.246-253, 1994.

SCHLOSS, PD; HANDELSMAN, J. Introducing DOTUR, a computer program for defining Operational Taxonomic Units and Estimating Species Richness. **Appl. Environ. Microbiol**. v.71, n.3, p.1501-1506, 2005.

SCHOLL, P.; LARGET, B.R.; HANDELSMAN, J. Integration of microbial ecology and statistics: a test to compare gene libraries. **Apll. Environ. Microbiol**., v.70, n.9, p.5485-5992, 2004.

SEBAT, J.L.; COLWELL, F.S.; CRAWFORD, R.L.; Metagenomic Profiling: Microarray Analysis of an Environmental Genomic Library. **Appl. Environ. Microbiol.**, v.69, n.8, p. 4927-4934, 2003.

SILNESS, J.; LOE, H. Periodontal disease in pregnancy II: correlation between oral hygiene and periodontal conditions. **Acta Odontol. Scand**., v.22,p.121-135, 1964.

SLOTS, J., GENCO, R.J. Black-pigmented *Bacteroides* species, *Capnocytophaga* species, and *Actinobacillus actinomicetemcomitans* in human periodontal disease: virulence factors in colonization, survival, and tissue destruction. **J. Dent. Res**, v.63, n.3, p.412-421, 1984.

SMITH, E.P.; VAN BELLE, G. Nonparametric estimation of species richness. **Biometrics** v.40, p.119-112, 1984.

SOCRANSKY, S.S.; MANGANIELLO, S.D. the oral microbiota of man from birth to senility. **J. Periodont**., v. 42, n.8, p.485-496, 1971.

STARKE, E.M.L.; SMOOT, J.C.; SMOOT, L.M.; LIU, W.T.; CHANDLER, D.P.; LEE, H.H.; STAHL, D.A. Technology development to explore the relationship between oral health and the oral microbial community. **BMC Oral Health**, v.6, Suppl 1: S10, 2006.

TAKESHITA, T.; NAKANO, Y.; KUMAGAI, T.; YASUI, M.; KAMIO, N.; SHIBATA, Y.; SHIOTA, S.; YAMASHITA, Y. The ecological proportion of indigenous bacterial populations in saliva is correlated with oral health status. **ISME J**., v.3, n.1, p.65-78, 2009.

TANNER, A.C.R.; IZARD, J. Etiology of oral disease in view of microbial complexity. **Oral Biosci. Med**., v.2, n.2/3, p.209-213, 2005.

TANWIR, F.; ALTAMASH, M.; GUSTAFSSON, A. Effect of diabetes on periodontal status of a population with poor oral health. **Acta Odontol. Scand**., v.67, n.3, p.129-133, 2009.

TAMURA, K.; DUDLEY, J.; NEI, M.; Kumar, S. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. **Mol. Biol. Evol**., v. 24, p.1596-1599, 2007.

THOMPSON, J.D.; HIGGINS, D.G.; GIBSON, T.J.; CLUSTALW: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. **Nucleic Acids Res**., v.22, p.4673-4680, 1994.

WANG,GQ.G.M.; GARRITY,J.M.; TIEDJE, J.M. COLE, J.R. Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. **Appl. Environ. Microbiol**., v.73, n.16, p.5261-5267, 2007.

XIMÉNEZ-FYVIE, L.A.; HAFFAJEE, A.D.; SOCRANSKY, S.S.Comparison of the microbiota of supra- and subgingival plaque in health and periodontitis. **J. Clin. Periodontol**., v.27, n.9, p.648-657, 2000a.

XIMÉNEZ-FYVIE, L.A.; HAFFAJEE, A.D.; SOCRANSKY, S.S. Microbial composition of supra- and subgingival plaque in subjects with adult periodontitis. **J. Clin. Periodontol**., v.27, n.10, p.722-732, 2000b.

XIONG, Y.Q.; BENSING, B.A.; BAYER, A.S.; CHAMBERS, H.F.; SULLAM, P.M. Role of the serine-rich surface glycoprotein GspB of Streptococcus gordonii in the pathogenesis of infective endocarditis. **Microb. Pathog**., v.45, n.4, p.297-301, 2008.

ZHANG, Z.; SCHWARTZ, S.; Wagner, L.; Miller, W. A greedy algorithm for aligning DNA sequences, **J. Comput. Biol.**, v.7, n.1-2, p.203-214, 2000.

ZETTLER, E.W.; SCHEIBE, R.M.; DIAS, C.A.G.; SANTAFÉ, P.; MOREIRA, J.S.; SANTOS, D.S.; FRITSCHER, C.C. A reação em cadeia da polimerase na detecção da resistência à penicilina em *Streptococcus pneumoniae*. **J. Bras. Pneumol**., v.30, n.6, 2004.

Apêndices

APÊNDICE – A

Termo de Consentimento Livre e Esclarecido de Participação em Pesquisa

Título da pesquisa: Prevalência de *Helicobacter pylori* detectado por PCR na cavidade bucal de pacientes dispépticos e influência do controle do biofilme dental na terapia de erradicação do *Helicobacter pylori* gástrico.
Pesquisadores: Cirurgiã-dentista Juliana Vianna Pereira e Médicos: Gerson Suguiyama Nakagima e Luiz Carvalho Neto

Esta pesquisa tem a justificativa de conhecer a associação da presença da bactéria *Helicobater pylori* no estômago e na boca, uma vez que a cavidade bucal pode ser reservatório dessa bactéria.
Objetivos dessa pesquisa que são:

a) Avaliar a prevalência de *Helicobacter pylori* na cavidade bucal em pacientes com diagnóstico positivo para *Helicobacter pylori* no estômago;
b) Avaliar se a complementação da terapia médica com a terapia odontológica, por meio do controle da placa dental pode contribuir para o tratamento;

Metodologia utilizada nesta pesquisa consistirá em:

a) Responder a um questionário;
b) Exame da boca pela cirurgiã-dentista com coleta de placa dental e saliva;
a) Exame pelo médico com endoscopia e biópsia do estômago;
b) Tratamento pelo médico com antibióticos, caso seja evidenciado a presença de *Helicobacter pylori* no estômago;
c) Tratamento odontológico com profilaxia, instrução de higiene oral e uso de clorexidina 0,12% por 30 dias;
d) Reavaliação do médico e do dentista.

Helicobacter pylori é uma bactéria que está associada à gastrite crônica, à formação de úlceras no estômago e duodeno. A endoscopia acompanhada de biópsia é um exame para diagnosticar o *Helicobacter pylori* na mucosa do estômago. O tratamento médico consiste em uso de antibióticos e o tratamento odontológico incluirá profilaxias profissionais, instrução de Higiene Oral e uso de bochecho de clorexidina 0,12% durante 30 dias.

A participação desta pesquisa é voluntária, podendo você deixar de participar a qualquer momento, sem qualquer prejuízo.

Confidencialidade dos dados: você terá a garantia do sigilo que assegura a sua privacidade e terá acesso aos resultados obtidos.

Desconforto, risco e benefícios esperados: vale ressaltar que a endoscopia acompanhada de biópsia é um exame realizado independentemente da pesquisa. O exame endoscópio com biópsia, apesar de desconfortável, é um excelente método para o diagnóstico da infecção de *Helicobacter pylori* no estômago. A saliva será colhida em um copo descartável e a placa dental será raspada utilizando-se instrumentos esterilizados próprios para a limpeza dos dentes, esses procedimentos não acarretarão nenhum dano ou dor, por não serem invasivos. A boca poderá ser fotografada para o fiel registro de suas características. Os tratamentos realizados terão como objetivo contribuir para a eliminação da bactéria e os benefícios esperados serão novos conhecimentos, que poderão ser úteis e proporcionar novas opções para o controle de *Helicobacter pylori*.

Compensação: não há qualquer forma de indenização decorrente da participação nesta pesquisa.

Contatos para esclarecimentos: Av. Ministro Waldemar Pedrosa, 1539, Praça 14 de Janeiro, Manaus, AM e pelos telefones (92) 3234-0593, (92) 3233-5632, (92) 8121-1347.

Tendo lido e compreendido as informações a cima, concordo com a minha participação voluntária nessa pesquisa. Tenho ciência que esta pesquisa pertence à Universidade Federal do Amazonas e concordo com a divulgação dos dados obtidos por meio de publicações científicas.

Manaus, ___ de ________________ de ________

Nome do paciente: ____

____
Assinatura do(a) participante

____
Juliana Vianna Pereira
Pesquisadora Responsável

Impressão
datiloscópica

APÊNDICE –B

Complemento do Termo de Consentimento Livre e Esclarecido de Participação em Pesquisa

Título da pesquisa: Prevalência de Helicobacter pylori detectado por PCR na cavidade bucal de pacientes dispépticos e influência do controle do biofilme dental na terapia de erradicação do Helicobacter pylori gástrico.
Pesquisador: Cirurgiã-dentista Juliana Vianna Pereira, Luiz Carvalho Neto
Justificativa: Este complemento tem a justificativa solicitar sua autorização para que seja adicionado um objetivo a ser analisado na pesquisa original, uma vez que não encontramos Helicobacter pylori na cavidade bucal. O fato da prevalência de Helicobacter pylori ter sido nula na cavidade bucal, na pesquisa nos chamou a atenção, já que este microrganismo foi identificado em alta proporção cavidade bucal em outros estudos. Por isso acreditamos que seja extremamente importante complementar esta pesquisa investigando outros microrganismos nas amostras de biofilme dental e saliva para buscar possível associação, ou seja, investigar se estes outros microrganismos estão influenciando a não sobrevivência do H. pylori na cavidade Bucal.
Objetivos dessa etapa são:
a) investigar nas amostras de saliva e biofilme dental, já coletadas, outros microrganismos presentes;
Metodologia utilizada nesta etapa consistirá em:
a) submeter as amostras de saliva e biofilme dental a análise por iniciadores (reagentes) específicos para região conservada das bactérias;
b) seqüenciar e identificar as bactérias encontradas comparando com bases de dados universais.
A participação nesta etapa da pesquisa é voluntária, podendo você deixar de participar a qualquer momento, sem qualquer prejuízo.
Confidencialidade dos dados: você terá a garantia do sigilo que assegura a sua privacidade e terá acesso aos resultados obtidos.
Desconforto, risco e benefícios esperados: vale ressaltar que esta etapa não oferece nenhum desconforto ou risco, pois consistirá na análise das amostras já coletadas. Este será o primeiro estudo no Brasil que visa justificar a não ocorrência de H. pylori na cavidade bucal, contribuindo para o entendimento do entre a relação desta bactéria com o ecossistema bucal.
Compensação: não há qualquer forma de indenização decorrente da participação nesta pesquisa.
Contatos para esclarecimentos: Av. Ministro Waldemar Pedrosa, 1539, Praça 14 de Janeiro, Manaus, AM e pelos telefones (92) 3233-5632 (Luiz Carvalho), (92) 8121-1347 (Juliana Pereira).

Tendo lido e compreendido as informações a cima, concordo com a complementação desta pesquisa e autorizo o armazenamento do material coletado para pesquisas futuras. Tenho ciência que esta pesquisa pertence à Universidade Federal do Amazonas e concordo com a divulgação dos dados obtidos por meio de publicações científicas.

Manaus, ___ de ________________ de ________
Nome do paciente: ____

________________________	_____________________
Assinatura do(a) participante	Juliana Vianna Pereira Pesquisadora Responsável

APÊNDICE – C

Ficha clínica – odontológica

Data: __/__/__ Nº ________

Identificação do paciente		
Nome:		
Data de nascimento	Idade:	Estado civil:
Nacionalidade:	Naturalidade:	Profissão:
Endereço residencial:		
Bairro:	Telefone fixo:	Celular:
Raça: 1.( ) branca 2.( ) negra 3. ( ) amarela 4. ( ) parda 5. ( ) indígena		Sexo: 1. ( )M 2. ( ) F

Anamnese		
Queixa principal:		
História da doença atual:		
História médica:		
	Sim	Não
Está tomando algum medicamento? Qual?		
Faz uso de antidepressivo?		
Faz uso de antihipertensivo?		
Tem alergia a algum medicamento? Qual?		
Tem diabetes?		
Tem AIDS?		
Está Grávida?		
Tomou antibiótico nos últimos 3 meses?		
Já fez tratamento para *Helicobacter pylori*?		
É fumante?		
Faz uso de bebida alcoólica? Qual frenquência?		
História buco-dental		
Quando foi ao dentista pela última vez?		
Quantas vezes escova os dentes por dia?		
	Sim	Não
Já recebeu instruções de higiene bucal?		
Faz uso de enxaguatório bucal? Qual?		
Utiliza fio dental diariamente?		

APÊNDICE – D

Exame físico

Índice de placa

Silness&Löe (1964): 0 - ausência de placa
1 - aparentemente sem placa, mas esta pode ser removida por sonda
2 - placa visível no terço cervical do dente
3 – placa abundante

Dente	D	V	M	L/P
18				
17				
16				
15				
14				
13				
12				
11				
21				
22				
23				
24				
25				
26				
27				
28				
38				
37				
36				
35				
34				
33				
32				
31				
41				
42				
43				
44				
45				
46				
47				
48				
Total				

Total: _____

APENDICE - E
Identidade entre as sequencias e os bancos NCBI e RDP

Tabela 4: Resultados dos clones analisados da biblioteca A, de acordo com NCBI e RDP.

Clone	Nº. acesso GenBank	NCBI	Identidade (%)	RDP	Identidade (%)
A5C09	EU071516.1	*Uncultured Gemella* sp.	97	*Gemella*	100
A3F11	EU071516.1	*Uncultured Gemella* sp.	97	*Gemella*	100
A2H02	DQ016729.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	100
A6F03	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A4H03	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3A12	FM873874.1	*Uncultured bacterium*	96	*Streptococcus*	94
A6C07	AM157421.1	*Streptococcus parasanguis*	99	*Streptococcus*	100
A4C09	AM157421.1	*Streptococcus parasanguis*	99	*Streptococcus*	100
A2H10	AM157421.1	*Streptococcus parasanguis*	99	*Streptococcus*	100
A3D03	AM157421.1	*Streptococcus parasanguis*	100	*Streptococcus*	100
A5C11	AM157421.1	*Streptococcus parasanguis*	100	*Streptococcus*	100
A5F11	AM157421.1	*Streptococcus parasanguis*	99	*Streptococcus*	100
A3E05	AM157421.1	*Streptococcus parasanguis*	99	*Streptococcus*	100
A3E09	AM157421.1	*Streptococcus parasanguis*	99	*Streptococcus*	100
A2E01	DQ232537.1	*Streptococcus oralis*	99	*Streptococcus*	100
A4C04	DQ232537.1	*Streptococcus oralis*	98	*Streptococcus*	100
A2D09	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3C02	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
A2C03	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
A6G12	FJ405281.1	*Streptococcus* sp.	98	*Streptococcus*	100
A6C05	FJ405281.1	*Streptococcus* sp.	98	*Streptococcus*	100
A2B12	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
A6H11	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
A2D04	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
A3F03	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
A6G11	FJ405281.1	*Streptococcus* sp.	98	*Streptococcus*	100
A3G02	FM873394.1	*Uncultured bacterium*	98	*Streptococcus*	94
A4D11	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
A3C05	FM873394.1	*Uncultured bacterium*	99	*Streptococcus*	99
A3D09	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
A6D08	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
A6F06	AY005040.1	*Streptococcus* sp.	99	*Streptococcus*	100
A2A05	EU341245.1	*Uncultured Streptococcus* sp.	98	*Streptococcus*	99
A2F05	AY005040.1	*Streptococcus* sp.	99	*Streptococcus*	100
A6G02	AY005040.1	*Streptococcus* sp.	99	*Streptococcus*	100
A4D06	EU341245.1	*Uncultured Streptococcus* sp.	97	*Streptococcus*	79
A4A03	EU341245.1	*Uncultured Streptococcus* sp.	98	*Streptococcus*	100
A5H06	EU341245.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	100
A3D07	EU341245.1	*Uncultured Streptococcus* sp.	100	*Streptococcus*	100
A5F07	EU341245.1	*Uncultured Streptococcus* sp.	100	*Streptococcus*	100
A6D01	EU341245.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	100
A4F02	EU341245.1	*Uncultured Streptococcus* sp.	100	*Streptococcus*	100
A3B09	EU341245.1	*Uncultured Streptococcus* sp.	100	*Streptococcus*	100
A2C11	AY584476.1	*Streptococcus cristatus*	99	*Streptococcus*	100
A2A10	AY584476.1	*Streptococcus cristatus*	99	*Streptococcus*	100
A1H07	FJ470581.1	*Uncultured bacterium*	96	*Streptococcus*	91
A2G02	FJ470581.1	*Uncultured bacterium*	97	*Streptococcus*	97
A3H08	EU373350.1	*Streptococcus salivarius*	99	*Streptococcus*	100
A1H02	EU373350.1	*Streptococcus salivarius*	99	*Streptococcus*	100
A1F02	CP000725.1	*Streptococcus gordonii*	98	*Streptococcus*	100

A6G03	CP000725.1	*Streptococcus gordonii*	100	*Streptococcus*	100
A1F03	CP000725.1	*Streptococcus gordonii*	99	*Streptococcus*	100
A3H02	AY518677.1	*Streptococcus mitis*	99	*Streptococcus*	100
A3A11	AY518677.1	*Streptococcus mitis*	99	*Streptococcus*	100
A5G03	AY518677.1	*Streptococcus mitis*	99	*Streptococcus*	100
A2B04	CP000921.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A5A08	CP000921.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A6H09	CP000921.1	*Streptococcus pneumonia*	100	*Streptococcus*	100
A4D05	DQ016726.2	*Uncultured Streptococcus* sp.	97	*Streptococcus*	98
A5E02	CP000387.1	*Streptococcus sanguinis*	99	*Streptococcus*	100
A5B07	DQ016726.2	*Uncultured Streptococcus* sp.	99	*Streptococcus*	99
A6B07	CP000921.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A5E03	CP000921.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A2E03	DQ016728.2	*Uncultured Streptococcus* sp.	98	*Streptococcus*	94
A2E02	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
A5A05	AF432135.1	*Streptococcus* sp.	100	*Streptococcus*	100
A6H03	CP000725.1	*Streptococcus gordonii*	99	*Streptococcus*	100
A5G11	DQ016728.2	*Uncultured Streptococcus* sp.	98	*Streptococcus*	99
A5H10	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
A5B11	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
A5D05	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
A4F06	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
A4H10	DQ016728.2	*Uncultured Streptococcus* sp.	98	*Streptococcus*	99
A6D04	DQ016728.2	*Uncultured Streptococcus* sp.	98	*Streptococcus*	99
A6G08	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
A3A02	AB355617.1	*Streptococcus oralis*	98	*Streptococcus*	100
A3G09	DQ532146.1	*Uncultured bacterium*	94	*Bacilli*	93
A5H09	AY485601.1	*Streptococcus mitis*	99	*Streptococcus*	100
A3F08	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3C06	FJ192922.1	*Uncultured Streptococcus* sp.	100	*Streptococcus*	100
A3C03	DQ232537.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3D06	DQ232537.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3F09	EF399017.1	*Uncultured bacterium*	96	*Streptococcus*	74
A3H03	EU341245.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	100
A3B04	DQ232536.1	*Streptococcus oralis*	98	*Streptococcus*	100
A5H05	DQ232536.	*Streptococcus oralis*	99	*Streptococcus*	100
A5A04	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A2H03	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A5C02	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A5C10	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A5D11	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A5F03	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A4C12	DQ016729.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	100
A5H03	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A2A06	DQ016729.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	100
A2B07	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3G12	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A5A07	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3C12	EF399017.1	*Uncultured bacterium*	97	*Streptococcus*	78
A6E02	EF399017.1	*Uncultured bacterium*	97	*Streptococcus*	70
A5D02	AM697564.1	*Uncultured bacterium*	98	*Streptococcus*	95
A3C09	EF510466.1	*Uncultured bacterium*	96	*Streptococcus*	89
A1F05	AM420261.1	*Uncultured Granulicatella* sp.	98	*Granulicatella*	93
A3G08	AY879301.1	*Granulicatella para-adiacens*	99	*Granulicatella*	99
A5E11	AM420261.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	92
A2A11	AY879301.1	*Granulicatella para-adiacens*	98	*Granulicatella*	98
A5F10	AY879301.1	*Granulicatella para-adiacens*	99	*Granulicatella*	98
A5B10	AM420261.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	94

A6C01	AM420261.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	98
A2F02	EF510466.1	*Uncultured bacterium*	96	*Granulicatella*	46
A3C07	EF510466.1	*Uncultured bacterium*	96	*Granulicatella*	29
A5D09	EF510466.1	*Uncultured bacterium*	97	*Granulicatella*	34
A5G06	EF510466.1	*Uncultured bacterium*	97	*Granulicatella*	33
A6A12	EF510466.1	*Uncultured bacterium*	96	*Granulicatella*	49
A3F07	EF510466.1	*Uncultured bacterium*	96	*Granulicatella*	40
A2E06	AY995756.1	*Veillonella* sp.	99	*Veillonella*	100
A3C04	AY995756.1	*Veillonella* sp.	99	*Veillonella*	100
A4A06	EU704215.1	*Uncultured Veillonella* sp.	91	*Veillonella*	75
A4B06	AM419962.1	*Uncultured Peptostreptococcus* sp.	98	*Peptostreptococcus*	100
A2B10	AM419962.1	*Uncultured Peptostreptococcus* sp.	97	*Peptostreptococcus*	100
A6H05	AM419962.1	*Uncultured Peptostreptococcus* sp.	97	*Peptostreptococcus*	100
A2F06	AF287763.1	*Peptostreptococcus* sp.	99	*Peptostreptococcus*	100
A5A10	AF287763.1	*Peptostreptococcus* sp.	99	*Peptostreptococcus*	100
A6G05	AF287763.1	*Peptostreptococcus* sp.	99	*Peptostreptococcus*	100
A2C04	DQ160208.1	*Peptostreptococcus stomatis*	99	*Peptostreptococcus*	100
A5H11	DQ160208.1	*Peptostreptococcus stomatis*	99	*Peptostreptococcus*	100
A3A09	DQ160208.1	*Peptostreptococcus stomatis*	99	*Peptostreptococcus*	100
A5B12	AF287763.1	*Peptostreptococcus* sp.	99	*Peptostreptococcus*	100
A3E06	DQ160208.1	*Peptostreptococcus stomatis*	99	*Peptostreptococcus*	100
A3A05	AM419962.1	*Uncultured Peptostreptococcus* sp.	96	*Peptostreptococcus*	100
A3D05	AM419962.1	*Uncultured Peptostreptococcus* sp.	98	*Peptostreptococcus*	100
A3F12	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A3G05	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A5F06	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A6D11	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A5G02	AF385526.1	*Streptococcus* sp.	98	*Streptococcus*	100
A4E05	AF385526.1	*Streptococcus* sp.	98	*Streptococcus*	100
A3G01	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A5H08	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A4E06	FJ823147.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A2G09	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A2F03	AF385526.1	*Streptococcus* sp.	98	*Streptococcus*	100
A2G06	AF385526.1	*Streptococcus* sp.	98	*Streptococcus*	100
A2C05	AF385526.1	*Streptococcus* sp.	98	*Streptococcus*	100
A5A09	FJ823147.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A5F04	FJ823147.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A5A12	FJ823147.1	*Streptococcus pneumonia*	99	*Streptococcus*	100
A6B11	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
A4D08	AF385526.1	*Streptococcus* sp.	98	*Streptococcus*	99
A3D01	EU670062.1	*Uncultured bacterium*	95	*Streptococcus*	93
A5G08	DQ016719.2	*Uncultured Streptococcus* sp.	98	*Streptococcus*	100
A5F02	DQ232537.1	*Streptococcus oralis*	99	*Streptococcus*	100
A3H05	FJ915699.1	*Streptococcus thermophilus*	98	*Streptococcus*	100

Tabela 5: Resultados dos clones analisados da biblioteca B, de acordo com NCBI e RDP.

Clone	Nº. acesso GenBank	NCBI	Identidade (%)	RDP	Identidade (%)
B3F12	FJ232611.1	*Streptococcus oralis*	99	*Streptococcus*	100
B11E07	FJ232611.1	*Streptococcus oralis*	100	*Streptococcus*	100
B3B11	FJ232611.1	*Streptococcus oralis*	100	*Streptococcus*	100
B11A09	FJ232611.1	*Streptococcus oralis*	99	*Streptococcus*	100
B7B01	DQ016719.2	*Uncultured Streptococcus* sp.	97	*Streptococcus*	88
B10D06	EU156771.1	*Streptococcus parasanguinis*	99	*Streptococcus*	100
B6C02	EU156771.1	*Streptococcus parasanguinis*	99	*Streptococcus*	100
B5A04	EU156771.1	*Streptococcus parasanguinis*	99	*Streptococcus*	100
B4B01	EU156771.1	*Streptococcus parasanguinis*	99	*Streptococcus*	100
B2A02	AF432139.1	*Streptococcus* sp.	99	*Streptococcus*	100
B5D06	FJ232611.1	*Streptococcus oralis*	99	*Streptococcus*	100
B7C04	AY944235.1	*Streptococcus oralis*	99	*Streptococcus*	100
B3C04	AY944235.1	*Streptococcus oralis*	100	*Streptococcus*	100
B7D06	AY281085.1	*Streptococcus sanguinis*	100	*Streptococcus*	100
B9E05	AY944235.1	*Streptococcus oralis*	99	*Streptococcus*	100
B11C02	AY944235.1	*Streptococcus oralis*	99	*Streptococcus*	100
B4F04	AY944235.1	*Streptococcus oralis*	99	*Streptococcus*	100
B8D03	AF432139.1	*Streptococcus* sp.	99	*Streptococcus*	100
B6E09	EU156789.1	*Streptococcus sanguinis*	100	*Streptococcus*	100
B3E04	FJ232611.1	*Streptococcus oralis*	98	*Streptococcus*	100
B1A01	FJ232611.1	*Streptococcus oralis*	98	*Streptococcus*	100
B10C12	EU071471.1	*Uncultured Streptococcus* sp.	98	*Streptococcus*	97
B2B11	FM873136.1	*Uncultured bacterium*	97	*Streptococcus*	97
B3B04	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B4A11	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B7D05	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B9G03	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B10G02	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B11E08	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
B7F11	FJ823146.1	*Streptococcus infantis*	99	*Streptococcus*	100
B6A08	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B6B10	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B11G10	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B9C12	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B1F06	FJ823145.1	*Streptococcus pseudopneumoniae*	99	*Streptococcus*	100
B2C12	EU156770.1	*Streptococcus oralis*	99	*Streptococcus*	100
B2C02	FJ823147.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B9G11	AF385526.1	*Streptococcus* sp.	99	*Streptococcus*	100
B2G04	FJ894993.1	*Uncultured bacterium*	97	*Streptococcus*	96
B2E04	AY278631.1	*Streptococcus genomo*sp.	100	*Streptococcus*	100
B4B02	EU156764.1	*Streptococcus mitis*	99	*Streptococcus*	100
B9G07	EU156764.1	*Streptococcus mitis*	99	*Streptococcus*	100
B3C08	EU156769.1	*Streptococcus oralis*	100	*Streptococcus*	100
B3C03	FJ823145.1	*Streptococcus pseudopneumoniae*	98	*Streptococcus*	100
B7G05	EU156769.1	*Streptococcus oralis*	99	*Streptococcus*	100
B3F01	EU156769.1	*Streptococcus oralis*	99	*Streptococcus*	100
B7C09	EU156769.1	*Streptococcus oralis*	99	*Streptococcus*	100
B1G11	FJ823145.1	*Streptococcus pseudopneumoniae*	99	*Streptococcus*	100
B2A07	EU991044.1	*Uncultured bacterium*	98	*Streptococcus*	81
B3C01	D38483.1	*Streptococcus gordonii*	99	*Streptococcus*	100
B11C07	EU156758.1	*Streptococcus gordonii*	99	*Streptococcus*	100
B9C05	EU156758.1	*Streptococcus gordonii*	98	*Streptococcus*	100
B4C02	DQ232531.1	*Streptococcus intermedius*	99	*Streptococcus*	100

B2D12	EU156757.1	*Streptococcus cristatus*	98	*Streptococcus*	100
B10G01	EU156757.1	*Streptococcus cristatus*	99	*Streptococcus*	100
B9F11	AY099095.1	*Streptococcus oligofermentans*	99	*Streptococcus*	100
B4C08	FJ915699.1	*Streptococcus thermophilus*	100	*Streptococcus*	100
B1A05	FJ915699.1	*Streptococcus thermophilus*	99	*Streptococcus*	100
B7D09	FJ915699.1	*Streptococcus thermophilus*	99	*Streptococcus*	100
B9E01	FJ915699.1	*Streptococcus thermophilus*	99	*Streptococcus*	100
B7C07	FJ915699.1	*Streptococcus thermophilus*	99	*Streptococcus*	100
B6C05	EU156772.1	*Streptococcus peroris*	98	*Streptococcus*	100
B10F06	EU990723.1	*Uncultured bacterium*	97	*Streptococcus*	96
B10C05	EU705464.1	*Uncultured Streptococcus* sp.	96	*Streptococcus*	98
B7G06	EU499689.1	*Uncultured bacterium*	97	*Granulicatella*	75
B1A07	EU499689.1	*Uncultured bacterium*	97	*Carnobacteriaceae*	86
B7A02	EU499689.1	*Uncultured bacterium*	96	*Granulicatella*	73
B2G05	FJ192554.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	99
B4H07	FJ192554.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	100
B5D02	FJ192554.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	97
B7G09	FJ192554.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	84
B7D11	FJ192554.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	99
B1F12	AY879305.1	*Granulicatella adiacens*	98	*Granulicatella*	100
B2F05	EF511159.1	*Uncultured bacterium*	98	*Lactobacillales*	95
B10C01	AM157450.1	*Gemella haemolysans*	99	*Gemella*	100
B9F03	EU071516.1	*Uncultured Gemella* sp.	99	*Gemella*	98
B3C07	EF108448.1	*Veillonella* sp.	99	*Veillonella*	100
B9C07	EF108448.1	*Veillonella* sp.	100	*Veillonella*	100
B2B09	EU987243.1	*Uncultured bacterium*	98	*Veillonella*	100
B1C07	AM420048.1	*Uncultured Clostridiales*	97	*Clostridiales*	83
B11A07	EU126662.1	*Prevotella histicola*	99	*Prevotella*	100
B3H07	U42010.1	*Capnocytophaga* sp.	99	*Capnocytophaga*	100
B4E01	EU083530.1	*Haemophilus parainfluenzae*	99	*Haemophilus*	78
B2F12	AY278629.1	*Streptococcus genomo*sp.	99	*Streptococcus*	100
B6B11	AY278629.1	*Streptococcus genomo*sp.	99	*Streptococcus*	100
B10D03	FM874156.1	*Uncultured bacterium*	95	*Streptococcus*	64
B7H12	FJ894993.1	*Uncultured bacterium*	97	*Lactobacillales*	71
B8A01	AF543299.1	*Streptococcus parasanguinis*	99	*Streptococcus*	100
B4D02	EU071497.1	*Uncultured Streptococcus* sp.	98	*Streptococcus*	99
B1B11	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
B4F06	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B4D10	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B3G01	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B3H06	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B4G06	AF432135.1	*Streptococcus* sp.	98	*Streptococcus*	99
B1H03	AM697471.1	*Uncultured bacterium*	97	*Streptococcus*	89
B4A06	AY485601.1	*Streptococcus mitis*	99	*Streptococcus*	100
B11B06	AF432135.1	*Streptococcus* sp.	100	*Streptococcus*	100
B4A09	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
B4D11	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
B11D03	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
B6B06	AY518677.1	*Streptococcus mitis*	99	*Streptococcus*	100
B1D12	AY518677.1	*Streptococcus mitis*	98	*Streptococcus*	100
B7E05	AY518677.1	*Streptococcus mitis*	99	*Streptococcus*	100
B7C10	AY518677.1	*Streptococcus mitis*	99	*Streptococcus*	100
B6B03	AF543299.1	*Streptococcus parasanguinis*	99	*Streptococcus*	100
B10G06	AY278629.1	*Streptococcus genomosp*	99	*Streptococcus*	100
B10F08	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B9A02	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B11D06	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B8F06	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100

B11E06	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B9B11	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B7B04	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B9B05	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B11B02	AF432137.1	*Streptococcus* sp.	99	*Streptococcus*	100
B11E04	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B11H08	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B2C04	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B9B07	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B7E09	DQ232535.1	*Streptococcus oralis*	99	*Streptococcus*	100
B6C04	AM697471.1	*Uncultured bacterium*	95	*Lactobacillales*	95
B6C09	DQ016729.1	*Uncultured Streptococcus* sp.	97	*Streptococcus*	98
B6D02	FM873691.1	*Uncultured bacterium*	98	*Streptococcus*	100
B6E03	FM873691.1	*Uncultured bacterium*	97	*Streptococcus*	100
B6C11	EU341274.1	*Uncultured Streptococcus* sp.	98	*Streptococcus*	100
B3C02	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B11E02	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B1B03	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B6A05	FJ470575.1	*Uncultured bacterium*	98	*Streptococcus*	98
B9A03	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B11E05	FJ405281.1	*Streptococcus* sp.	100	*Streptococcus*	100
B7B03	FJ405281.1	*Streptococcus* sp.	98	*Streptococcus*	100
B10E11	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B7H02	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B7F07	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B6F08	FJ405281.1	*Streptococcus* sp.	99	*Streptococcus*	100
B1E09	FM873691.1	*Uncultured bacterium*	99	*Streptococcus*	100
B10E01	FM873691.1	*Uncultured bacterium*	98	*Streptococcus*	100
B3C05	FM873691.1	*Uncultured bacterium*	99	*Streptococcus*	100
B2E07	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B11D05	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B3C12	AB355617.1	*Streptococcus oralis*	99	*Streptococcus*	100
B8H01	EU341274.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	99
B7D04	AF003929.1	*Streptococcus mitis*	99	*Streptococcus*	100
B11B07	AF003929.1	*Streptococcus mitis*	99	*Streptococcus*	100
B10F04	CP000919.1	*Streptococcus pneumoniae*	99	*Streptococcus*	92
B9B06	CP000919.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B11F03	CP000919.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B7E11	EU189961.1	*Streptococcus sanguinis*	99	*Streptococcus*	100
B2A04	CP000387.1	*Streptococcus sanguinis*	99	*Streptococcus*	100
B3D09	CP000921.1	*Streptococcus pneumoniae*	99	*Streptococcus*	100
B8H12	DQ016723.2	*Uncultured Streptococcus* sp.	98	*Streptococcus*	98
B7A07	DQ232536.1	*Streptococcus oralis*	99	*Streptococcus*	100
B6B08	EU341245.1	*Uncultured Streptococcus* sp.	100	*Streptococcus*	100
B4G08	EU341245.1	*Uncultured Streptococcus* sp.	99	*Streptococcus*	100
B9E12	AY278629.1	*Streptococcus genomosp*	99	*Streptococcus*	100
B11G03	AY278629.1	*Streptococcus genomosp*	98	*Streptococcus*	100
B9C03	DQ232537.1	*Streptococcus oralis*	99	*Streptococcus*	100
B7D02	DQ232537.1	*Streptococcus oralis*	99	*Streptococcus*	100
B3C06	AY278629.1	*Streptococcus genomosp*	99	*Streptococcus*	100
B2D03	AF432135.1	*Streptococcus* sp.	99	*Streptococcus*	100
B1E07	DQ303191.1	*Streptococcus parasanguinis*	99	*Streptococcus*	100
B11F12	DQ303191.1	*Streptococcus parasanguinis*	98	*Streptococcus*	98
B4F07	DQ232537.1	*Streptococcus oralis*	98	*Streptococcus*	100
B1F11	AB355616.1	*Streptococcus salivarius*	99	*Streptococcus*	100
B9C04	AB355616.1	*Streptococcus salivarius*	99	*Streptococcus*	100
B9E06	AB355616.1	*Streptococcus salivarius*	99	*Streptococcus*	100
B3F06	AB355616.1	*Streptococcus salivarius*	99	*Streptococcus*	100

B4G12	AB355616.1	*Streptococcus salivarius*	99	*Streptococcus*	100
B11C01	DQ303189.1	*Streptococcus mutans*	99	*Streptococcus*	100
B10G09	FJ470583.1	*Uncultured bacterium*	97	*Granulicatella*	45
B10D12	AM696889.1	*Uncultured bacterium*	94	*Gemella*	100
B11A11	FJ470583.1	*Uncultured bacterium*	96	*Granulicatella*	96
B9F12	FJ470583.1	*Uncultured bacterium*	99	*Granulicatella*	94
B6D05	AM420261.1	*Uncultured Granulicatella* sp.	98	*Granulicatella*	98
B9E03	AM420261.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	95
B1F01	AM420261.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	82
B3E09	AM420261.1	*Uncultured Granulicatella* sp.	99	*Granulicatella*	96
B9C01	AM420261.1	*Uncultured Granulicatella* sp.	98	*Granulicatella*	78
B2C11	FJ470583.1	*Uncultured bacterium*	99	*Granulicatella*	98
B6H10	FM873530.1	*Uncultured bacterium*	99	*Granulicatella*	82
B7F04	AM420236.1	*Uncultured Granulicatella* sp.	98	*Granulicatella*	94
B6F07	AY307994.1	*Uncultured bacterium*	98	*Granulicatella*	88
B9G04	FJ470583.1	*Uncultured bacterium*	98	*Granulicatella*	81
B1A02	AY995768.1	*Veillonella atypica*	99	*Veillonella*	100
B7E01	AY995766.1	*Veillonella* sp.	100	*Veillonella*	100
B4B06	AY995766.1	*Veillonella* sp.	99	*Veillonella*	100
B11E03	AY995766.1	*Veillonella* sp.	99	*Veillonella*	100
B6A10	AY995756.1	*Veillonella* sp.	99	*Veillonella*	100
B2A03	EU704242.1	*Veillonella* sp.	95	*Veillonella*	100
B3D05	DQ677557.1	*Uncultured Veillonella* sp.	95	*Veillonella*	100
B11D08	EU071478.1	*Uncultured Veillonella* sp.	95	*Veillonella*	100
B11B11	AY323228.1	*Oribacterium sinus*	99	*Oribacterium*	100
B5F01	FJ932762.1	*Neisseria meningitidis*	99	*Neisseria*	98
B11C08	AJ786809.1	*Neisseria* sp.	100	*Neisseria*	100
B7F05	FJ932762.1	*Neisseria meningitidis*	99	*Neisseria*	97
B4A01	AY341823.1	*Neisseria genomosp*	99	*Neisseria*	86
B7E07	AJ540309.1	*Actinomyces graevenitzii*	99	*Actinomyces*	100
B11G05	AL157959.1	*Neisseria meningitidis*	99	*Neisseria*	100
B7H10	CP000948.1	*Escherichia coli*	100	*Escherichia*	100

APÊNDICE – F
Sequências nuleotídicas das Bibliotecas

Bliblioteca A

A5C09- Uncultured Gemella sp. clone EHFS1_S13g
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGG
GAACGTATTCACCGCGACATTCTGATTCGCGATTACTAGCGATTCCAGCCTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAATAGTTTTGTGAGG
TTTGCTTACTCTCGCGAGCTCGCTTCTCTTTGTTCCTATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCAGTTTATCACTGGCAGTCTATCTAGAGTCCCCATCTTACTGCTGGCAACTAGATATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTATCTGTGTCTAACCAAAGGTCAGAACAACACAATCTCTTGTGTCCTCACAGTATGTCCAGACTTGGTAAG
GTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGTGCGGGTCCCG

A3F11- Uncultured Gemella sp. clone EHFS1_S13g
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGG
GAACGTATTCACCGCGACATTCTGATTCGCGATTACTAGCGATTCCAGCCTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAATAGTTTTGTGAGG
TTTGCTTACTCTCGCGAGCTCGCTTCTCTTTGTTCCTATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCAGTTTATCACTGGCAGTCTATCTAAAGTCCCCATCTTACTGCTGGCAACTAGATATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTATCTGTGTCTAACCAAAGGTCAGAACAACACAATCTCTTGTGTCCTCACAGTATGTCAAGACTTGGTAAG
GTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTCGGGTCCCCGTCA

A2H02- Uncultured Streptococcus sp. clone 1.23
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTAGCTTCGAATTAAACCACATGCTCCACCGTTGTGCGGGCCCCCGTC

A6F03- Streptococcus oralis strain CIP 104985
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A4H03- Streptococcus oralis strain CIP 104985
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3A12- Uncultured bacterium clone MB02C05
CGCCAATCCCACCTTAGACGGCTCCCTCCCAAAAGGGTTAGGCCACCGGCTTTGGGTGTACCAACTTTCGTGACTTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTCAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGTGCGGGCCCCCGTC

A6C07- Streptococcus parasanguis 16S rRNA gene, clone 5C3
CCCACCTTAGGCGGCTGGCTCCTTACGGTTCCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTC
ACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGC
CGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTT
TATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGC
TGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTG
CTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCA

A4C09- Streptococcus parasanguis 16S rRNA gene, clone 5C3
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAAACTCTATCTCTTAGAGCGGTCAGAGGGATGTCAAGACCTGTTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2H10- Streptococcus parasanguis 16S rRNA gene, clone 5C3
TCATCTATCCCACCTTAGGCGGTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAANCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3D03- Streptococcus parasanguis 16S rRNA gene, clone 5C3
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5C11- Streptococcus parasanguis 16S rRNA gene, clone 5C3
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5F11- Streptococcus parasanguis 16S rRNA gene, clone 5C3
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC

A3E05- Streptococcus parasanguis 16S rRNA gene, clone 5C3
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCAACTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3E09- Streptococcus parasanguis 16S rRNA gene, clone 5C3
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCCAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2E01- Streptococcus oralis strain CIP 105158
AATCATCTATCCCACTTAGGCGGTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A4C04- Streptococcus oralis strain CIP 105158
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTAGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCANCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGCAGAGGGATGTCCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2D09- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TCATCTATCCCACTTAGGCGGTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTCGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3C02- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTCGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTAGAGGGATGTCAAGACCTGGTAAGGTTCTT
CGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2C03- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTCGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6G12- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTACCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGTGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTC

A6C05- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACTTAGGCGGTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTAACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAGATT
AGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGA
CACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTATAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTT
CGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2B12- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAGTGGTTACCTCACCGACTTCGGGTGTTACAAGCTCTCCTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6H11- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2D04- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3F03- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6G11- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAGCTCTCGTGGTGTGACGGGCGGTGTTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGA
GATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGTTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGTTCCACCGCTTGTGCGGGCCCCCGTC

A3G02-1 Uncultured bacterium partial 16S rRNA gene, clone FD02H05
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTTACCCACCATTGTAGCACGTTGTGTAGCCCAAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCA
CCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCT
CACGAAACGAGCTGACGACAACCATGCACCANCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCCAGACCTGGTAAG
GTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGTGCGGGCCCCCGTC

A4D11- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCANCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCAGCGATTGTGCGGGCCCCCGTC

A3C05- Uncultured bacterium partial 16S rRNA gene, clone FD02 H05
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAACT
TCCTCCGGTTTATTTACCGGCAGTCTCGCTAGAGTGGCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGG
TTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCCGTC

A3D09- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAGCTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAACT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCGTC

A6D08- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCACAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6F06- Streptococcus sp. oral strain 7A 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2A05- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGTGGCTCCAAGTGGTTACCTCACGACTTCGGGTGTTACAAATCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAA
CGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTA
GCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCT
CCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGAC
ACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTC
GCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTC

A2F05- Streptococcus sp. oral strain 7A 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGTGGCTCCAAGTGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6G02- Streptococcus sp. oral strain 7A 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAGTGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAATGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTAACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A4D06- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAGTGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAAAATGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAACT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAAAATCTCA
GAAACGAGCTTGACGACAACCATGCACCAACTGGTCACCTCTGTCCCGAAGGAAAAATCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGG
TTCTTCGCGTTGCTTCGAATTTAAACCACATGCTCCACCGGTTGTGCGGGCCCCCGTC

A4A03- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAGTGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAACTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCCGAGGGATGTCCAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAACCCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5H06- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAGTGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTC
TTCGCGTTGCTTCGAATTAAANCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3D07- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCC

A5F07- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6D01- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTATGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A4F02- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3B09- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2C11- Streptococcus cristatus strain ATCC 51100 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCGGTGTGCCGAAGCAAAATCCTATCTCTAGGACGGGCACCGGGATGTCAAGACCTGGTAAGGGTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2A10- Streptococcus cristatus strain ATCC 51100 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTTGCAACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCGGTGTGCCGAAGCAAAATCCTATCTCTAGGACGGGCACCGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A1H07- Uncultured bacterium clone A_S_01_47 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACTTAGGCGGGGGCTCCAAAAGGTTACTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAA
CGTATCACCGCGGCGTGCTGATCCGCGATTATAGCGATTCCGACTTCATGTAGGCGAGTGGGAGGGGGTACCAATCCCGAAACTGAGATTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCAANTGAATGATGGCAATTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCTGAAGGTTCTT
CGCGTTGCTTCGACTTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCA

A2G02- Uncultured bacterium clone A_S_01_47 16S ribosomal RNA gene, partial sequence
TCATCTATCACCTTAGGCGGTGGCTCCAAAAGGTTACCTCACCGACTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAAC
GTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAGATTAG
CCTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTC
CGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCCCGTAGCGGGACTTAACCCAACATCTCACGACA
CGAACTGACGACAACCATGCACCAACTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCTGGTAAGGTTCTTCG
CGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTTGCGGGCCCCCGTC

A3H08- Streptococcus salivarius strain HNL13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A1H02- Streptococcus salivarius strain HNL13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGGCTAGGATCCGAACTGAGATTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGTTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A1F02- Streptococcus gordonii str. Challis substr.
CH1TCATCTATCCCACCTTAGGCGGCGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAATGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCGGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAC
CTTCCTCCGGTTTATTACCTGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCT
CACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAAAGCTCTATCTCTAGAGCGGGCATCGGGATGTCAAGACCTGGTAAG
GTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTCA

A6G03- Streptococcus gordonii str. Challis substr.
CH1TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGC
CCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTA
AGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCC
CACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACAT
CTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAAAACTCTATCTCTAGAGCGGGCATCGGGATGTCAAGACCTGGTAA
GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A1F03- Streptococcus gordonii str. Challis substr.
CH1TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGC
CCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCGACAATCCGAACTGAGACTGGCTTTAA
GAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCC
ACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATC
TCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAAAACTCTATCTCTAGAGCGGGCATCGGGATGTCAAGACCTGGTAA
GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3H02- Streptococcus mitis strain Sm91 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATTCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGTGCGGGCCCCCGTC

A3A11- Streptococcus mitis strain Sm91 16S ribosomal RNA gene, partial sequence
CATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATTCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANCTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGG
TTCTTCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5G03- Streptococcus mitis strain Sm91 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2B04- Streptococcus pneumoniae Taiwan19F-14
TCATCTATCCCACCTTAGGCGGTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGANAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5A08- Streptococcus pneumoniae Taiwan19F-14
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAC
CTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGG
TTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6H09- Streptococcus pneumoniae Taiwan19F-14
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A4D05- Uncultured Streptococcus sp. clone 2.7 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTCAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAACT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAAAATGGCCAAATTCACTGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGGCACACCTGTCACCTCTGTCCCGAAGGCAAACTCTATCTCTAGAGCGGCCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCAGCGCTTGTGCGGGCCCCCGTC

A5E02- Streptococcus sanguinis SK36
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTTGCAGCCTACAATCCGAACTGAGACTGGCTTTCAGA
GATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCCTGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGCCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCG

A5B07- Uncultured Streptococcus sp. clone 2.7 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTCAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTACAGCGGCCAGAGGGATGTCCAAGACCTGGTAAGGTT
CTTCCCGTTGCTTCCAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6B07- Streptococcus pneumoniae Taiwan19F-14
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTTCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTCCGAATTAAACCACATGCTCCAC

A5E03-1 Streptococcus pneumoniae Taiwan19F-14
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCCGTC

A2E03- Uncultured Streptococcus sp. clone 1.24 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAGAAGGTTACCTCACCGACTTCGTTGTTACAAACTCTCGTGGTGTGACGGGCGGGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCCGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAACTGGCTTTAAAAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCGCCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2E02- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5A05- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6H03- Streptococcus gordonii str. Challis substr. CH1
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAAAACTCTATCTCTAGAGGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGNTTGTGCGGGCCCCCCGT

A5G11- Uncultured Streptococcus sp. clone 1.24 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTCCTCACCGACTTCGGGTGTTACAAATTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGTGCGGGCCCCCGTC

A5H10- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5B11- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5D05- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGNTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A4F06- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TCATCTACCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A4H10- Uncultured Streptococcus sp. clone 1.24 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCGGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAATTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACAACTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTCA

A6D04- Uncultured Streptococcus sp. clone 1.24 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGCTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6G08-treptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTAACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3A02- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCCTGATGATTTGACGTCATCCCCAAC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGGCCAANTGAATGATGGCAACTAACAATAGGGGTCGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGAAACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGG
TTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGNTTGTGCGGGCCCCCGTC

A3G09- Uncultured bacterium clone JPL1_88 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTATGCGACTTGTAGCCTACAATCCGAACTGAGACTGGCGTTAAGAGA
ATATCTTGCCGTCAGCCGACTTGCTTACTCAGTTGTACAACCATCGTATGACGTGTGTATGTCACCCAATTCATGGGGGGCCATGATGATTTGACGTCATCC
CCATCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACA
TCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAACCTCTATCCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAA
GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5H09- Streptococcus mitis strain GCSS 1303 16S small subunit ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAC
CTTCCTCCGGTTTATTACCGGCAGCCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTACTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC

A3F08- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAA
CTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3C06- Uncultured Streptococcus sp. clone GI5-006-B08 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCG
GGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGA
GATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3C03- Streptococcus oralis strain CIP 105158 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAACTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAGCCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3D06- Streptococcus oralis strain CIP 105158 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAACTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAGCCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3F09- Uncultured bacterium clone SJTU_F_10_28 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGAATCGTTGTAACAGCCATTGGAACACGTGTGTTACCCACAGTCTCATAAGGGCGCATGAAGATGTGACGTCATCCC
CATCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACA
TCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAA
GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCAACGGTTGTGCGGGCCCCCGTCA

A3H03- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCANCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCTGCACCACCTGTCACCTCTGTCCCGAAGGAAACCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGTGCGGGCCCCCGTCA

A3B04- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCANCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTCA

A5H05- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5A04- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGA
TTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGTTTGTGCGGGCCCCCGTC

A2H03- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGTGCGGGCCCCCGTC

A5C02- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCCAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCC

A5C10- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTCGCGTTGCTTCCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5D11- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC

A5F03- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGNTTGTGCGGGCCCCCGTC

A4C12- Uncultured Streptococcus sp. clone 1.23 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCAACGGTTGTGCGGGCCCCCGTC

A5H03- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGGGTCAGAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2A06- Uncultured Streptococcus sp. clone 1.23 16S ribosomal RNA gene, partial sequence
TCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAAC
GTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAG
CTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTC
CGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACA
CGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGCTAAGGTTCTTCG
CGTTGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCCGTC

A2B07- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGAT
TAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGCTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3G12-1 Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5A07- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAG
ATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3C12- Uncultured bacterium clone SJTU_F_10_28 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAATTGCAGCCTAAAATCCGAACTGGAAATGGCTTTAAAAA
AATAACTTGGCCGTCACCGATTCGCAATTCGTGGTACCAGCCATGTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCA
CCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCT
CACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAG
GTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6E02- Uncultured bacterium clone SJTU_F_10_28 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAATTGAGACTGGCTTTAGAAGA
TTAGCTTGCCGTCACCGATTCGCGATTCGTGGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATACTGGGCATGATGATTTGACGTCATCCCCACCTT
TCCTCCGGTTAATAACCGGCAGTCTCGCTAGAGTGCCCAATTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCAACTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A5D02- Uncultured bacterium partial 16S rRNA gene, isolate BF0002D075
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCCAATTGGAAGCTTACATCCCGAACTGAAACGGGCTTTAAAA
GATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCGGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCAC
CTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGG
TTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3C09- Uncultured bacterium clone P2D1-730 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGGGAATAATAACGAATCCGAGATTCCAGGTAGGCAGATTGGCACTCTACAATCCGAACTGAGAGTGGCTTTA
AGAGATTAGCTTTGCCGTCCAGCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC
CCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTTGCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCCGTC

A1F05- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
TCATCTATCCCACTTAGGCGGTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTATGCGAGTGGCGGGCTACAATCCGAACTGAGAATGGCTTTAAGAGAT
TCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTTCT
TCGCGTTGCTCGAATTAAACCACATGCTCC

A3G08- Granulicatella para-adiacens strain 03476079 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGA
TTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTTCT
TCGCGTTGCTTCGATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTC

A5E11- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
TCATCTATCCCACCTTAGCGGTGGCTCCAAAAGGTTACTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAA
CGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGATT
CGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
TCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGA
CACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTTCTT
CGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTC

A2A11- Granulicatella para-adiacens strain 03476079 16S ribosomal RNA gene, partial sequence
TATCCCACTTAGGCGGTGGTCCAAAAGGTACTCACGACTTTGGGTGTAAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATCACC
GCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGATTCGCTTACCCT
CGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTGT
CACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGA
CGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTTCTTCGCGTTGCTTC
GAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTC

A5F10- Granulicatella para-adiacens strain 03476079 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGAATCCGGGTTCCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAG
ATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTC

A5B10- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGAT
TCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTC

A6C01- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
TCATCTATCCCACCTTAGGCGGCTGGCCCAAAAGGTTACCTCACCGACTTTGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGA
ACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGAT
TCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGTACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGTCCCCGTC

A2F02- Uncultured bacterium clone P2D1-730 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGA
TTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACACCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCCAGACCGGTAAGGTTCTT
CGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCGTC

A3C07- Uncultured bacterium clone P2D1-730 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGA
TTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACACCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCCGTC

A5D09- Uncultured bacterium clone P2D1-730 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAG
ATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACACCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCCGTC

A5G06- Uncultured bacterium clone P2D1-730 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGG
GAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAG
ATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCT
TCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACACCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A6A12- Uncultured bacterium clone P2D1-730 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGTATCACCGCGGCGTGCTGATCCGCGATTACTACCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGAT
TCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACACCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGCTAAGGTTCT
TCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A3F07- Uncultured bacterium clone P2D1-730 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGAGA
TTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCANCTT
CCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACACCTCAC
GAAACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCGTC

A2E06- Veillonella sp. oral clone VeillH4 16S ribosomal RNA gene, partial sequence
TCATCGACTTTACCTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAGTGTTTCTCGG
GTTTGCTCCATCTCGCGATCTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCT
TCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCATTACGTGCCGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACTATCTCTAGTTCTGTCCATCAATGTCAAGACCTGGTAAGGT
TCTTCGCTTGCGTCGAATTAAACCACATACTCCACCGCTTGTGCGGGCCCCCGTC

A3C04- Veillonella sp. oral clone VeillH4 16S ribosomal RNA gene, partial sequence
TCATCGACTTTACCTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGCTTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAGTGTTTCTCGG
GTTTGCTCCATCTCGCGATCTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCT
TCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCATTACGTGCCGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTC
ACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACTATCTCTAGTTCTGTCCATCAATGTCAAGACCTGGTAAGGT
TCTTCGCGTTGCGTCGAATTAAACCACATACTCCACCGCTTGTGCGGGCCCCCGTC

A4A06- Uncultured Veillonella sp. clone KLOND02 16S ribosomal RNA gene, partial sequence
TCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGG
GAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAGTGTNTCTCGG
GTTTGCTCCATCTCGCGATCTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCT
TCCTCCGCATTGTCTGCGGCAGTCTCGCTAGAGTGCCCAATTGAATGATGGCAATTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCAC
GACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGACGGTCAGAGGGATGTCAAGACCTGTTAAGGTTCT
TCGCGTAGCTTCGAATTAAACCACATGCTCCAACGCTTGTGCGGGCCCCCGTC

A4B06- Uncultured Peptostreptococcus sp. partial 16S rRNA gene, clone 101D05(oral)
TATCGACGCCACTTCGACGATCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAAC
GCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGATTGG
CTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCC
AGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACAC
GAGCTGACTACAAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTCTTCG
CGTTGCTTCGAATTAAACCAATGCTCCGCTACTTGTGCGGGTCCCCGTCA

A2B10- Uncultured Peptostreptococcus sp. partial 16S rRNA gene, clone 101D05(oral)
ACTTCGACGATTCCTCCTTGCGGTTGGATAATCGGCTCGGGTGTTCGACTCCCGTGGTGTGACGGGGGTGTGTACAAGACCGGGAACGCATCACGCAGCA
TTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTCAGCCTACAATCCGAACTGAGAATGCTTAAGGGATTGGTCCACCTCACGGTTTGGC
AACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCAGGTTATCCCTGGCAGTC
TCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATG
CACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACC
ACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A6H05- Uncultured Peptostreptococcus sp. partial 16S rRNA gene, clone 101D05(oral)
TATCGACGCCACTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGTTCGGGTGTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAAC
GCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGATTGG
CTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCC
AGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACAC
GAGCTGACGACAACCATNGCACCACCGTGTCACCTCAGTCCCCCGAAGGAAAAGGGGTTGTTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAA
GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCGGTAACTTGTGCGGGTCCCGTC

A2F06- Peptostreptococcus sp. oral clone CK035 16S ribosomal RNA gene, partial sequence
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTATCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGAT
TGGCTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A5A10- Peptostreptococcus sp. oral clone CK035 16S ribosomal RNA gene, partial sequence
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTATCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGAT
TGGCTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A6G05-1 Peptostreptococcus sp. oral clone CK035 16S ribosomal RNA gene, partial sequence
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTCTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGAT
TGGCTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAGGTTCTT
CGCGTAGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A2C04- Peptostreptococcus stomatis strain W2278 16S ribosomal RNA gene, partial sequence
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGAT
TGGCTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A5H11- Peptostreptococcus stomatis strain W2278 16S ribosomal RNA gene, partial sequence
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGAT
TGGCTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCCAGCTTAGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A3A09- Peptostreptococcus stomatis strain W2278 16S ribosomal RNA gene, partial sequence
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGAT
TGGCTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAATTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCANCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTC
TTCGCGTAGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A5B12- Peptostreptococcus sp. oral clone CK035 16S ribosomal RNA gene, partial sequence
ATCGACGCCACCTTCGACGACTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAA
CGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGATTG
GCTCCACCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCT
CCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGAC
ACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGACGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTCTTC
GCGTTGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A3E06- Peptostreptococcus stomatis strain W2278 16S ribosomal RNA gene, partial sequence
TATCGACGCCACCTTCGACGACTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGA
ACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGATT
GGCTCCACCTCACGGTTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A3A05- Uncultured Peptostreptococcus sp. partial 16S rRNA gene, clone 101D05(oral)
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGGAGCATTCTGATCTGCGATAACTCATTATCTCTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGGAAATTGGTTCTAAG
GGATTGGCTCCANCTCACGGTTTGGCAACCCTCTGTACCACCCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCA
CCTTCCTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTGCCCAACTAAATGCTGGCAACTAAAGACCAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCT
CACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCCACCTTAGGTAAG
GTTCCTCGCGTTGCTTCCAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A3D05- Uncultured Peptostreptococcus sp. partial 16S rRNA gene, clone 101D05(oral)
TATCGACGCCACCTTCGACGACTTCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTTCCGACTCCCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGG
AACGCATTCACCGCAGCATTCTGATCTGCGATTACTAGTAACTCCAGCTTCATGTAGGCGAGTTTCAGCCTACAATCCGAACTGAGAATGGCTTTAAGGGAT
TGGCTCCACCTCACGGTTTGGCAACCCTCTGTACCAACCATTGTAGCACGTGTGTAGCCCTAAGCATAAGGGGCATGATGATTTGACGTCATCCCCAACTTC
CTCCAGGTTATCCCTGGCAGTCTCTCTAGAGTTGCCAACTAAATGCTGGCAACTAAAGACCAGGGTTGCGCTCGTTGCGGGACTTAAACCAACATCTCACG
ACACGAGCTGACGACAACCATGCACCANCTGTCACCTCAGTCCCGAAGGAAGGGTGTGATTAAACACCTGTCCGAGGGATGTCAAGCTTAGGTAAGGTTC
TTCGCGTTGCTTCGAATTAAACCACATGCTCCGCTACTTGTGCGGGTCCCCGTC

A3F12- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTATACGTAGGTCCCGAGCGTTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTG
GCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAAC
ACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
CGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAA
GGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGA
GATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC

A3G05- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTATACGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTG
GCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAAC
ACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
CGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAA
GGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGA
GATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAANCCC
TATTGTTA

A5F06- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTATAGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGG
CTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACA
CCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
GATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG

GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAG
ATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA

A6D11- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTAATACGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGT
GGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAA
CACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
ACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAA
AGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAG
AGATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTC

A5G02- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTAATACGTAGGTCCCGAGCGTTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTG
GCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAAC
ACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGGTAGTCCACGCCGTAA
ACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAA
AGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAG
AGATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTCGGTTAAGTCCCGCAACGAGCGCAACCCT
ATTGTTAG

A4E05- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCCGGTAATACGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTG
GCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAAC
ACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
CGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAA
GGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGGTCTAGA
GATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGAGGGTTAAGTCCCGCAACGAGCGCAAACCCTATT
GTTA

A3G01- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCAGCCGCGCGGTAATACGTAGGTCCCGAGCGTTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGG
CTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACA
CCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
GATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG
GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAG
ATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG

A5H08- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCAGCAGCCGCGGTATAGTAGGTCCCGAGCGTTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGC
TTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACAC
CGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG
ATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGG
AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGA
TAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTCGGGTTAAGTCCCGCAACG

A4E06- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTAATACGTAGGTCCCGAGCGTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTG
GCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAAC
ACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
CGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTCGAAACTCAAA
GGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTCAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGA
GATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTCGGGTTAAGTCCCGCAACGAGCGCAACCCC
TATTGTTA

A2G09- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
GGTAATACGTAGGTCCCGAGCGTAATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAG
TACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATTTGGAGGAACACCGGTGGCGA
AAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTA
GGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGG
GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCC
TTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTNGGGTTAAGTCCCGCAACGAGCGCAACCCCTATTGTTAG

A2F03- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCAGCCGCGGGTATACGTAGGTCCCGAGCGTATCCGGATTATTGGGCGTAAGCGAGCGCAGGCGGTAGATAAGTCTGAAGTAAGGCTGTGGCTTACCA
TAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGC
GAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTG
CTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGAC
GGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTT
TTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAANCCCTATTGTTA

A2G06- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCAGCCGCGGGTAATACGTAGGTCCGAGCGTATCCGGATATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTAAAGGCTGTGGCTTAC
CATAGTACGCTTTGGAAACTGTTTACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTG
GCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAG
TGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTG
ACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAG
TTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAANCCCTATTGTTA

A2C05- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCAGCGCGCGGTAATACGTAGGTCCCGAGCGTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAATAAGTCTGAAGTAAAGGCTGTGGCTTA
ACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCG
GTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGAT
GAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAA
TTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATA
GAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAANCCCTATT
GTTA

A5A09- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
TGCAGCCGCGCGGTATACGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGG
CTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACAC
CGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG
ATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGG
AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGA
TAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAATCCCTAT
TGTTA

A5F04- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
TGCAGCCGCGCGGTATACGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGC
TTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACAC
CGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG
ATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGG
AATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGA
TAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGC

A5A12- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
GCCGCGGTATAGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCAT
AGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGC
GAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTG
CTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGAC
GGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTT
TTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTCGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCGTTA

A6B11- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
CCGGTATAGTAGGTCCCGAGCGTAATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGT
ACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAA
AGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAG
GTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGG
GCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCT
TCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGC

A4D08- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTATACGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTG
GCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAAC
ACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAA
CGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTATAGTGCCGTGGCTAACGCATTAAGCACTCCGNCTGGGGAGTACGACCGCAAGGTTGAAACTCAAA
GGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTACTTCGAAGCAACGCGAAGAACCTTACCAGCTCTTGACATCCCTCTGACCGGTCTACA
GATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATTGGTTGTCGTCAGCTCGTGTCGTGAGATGTCGGGTTAAGTCCCGCAACGAGCGCAACCC
CTATCGTAA

A3D01- Uncultured bacterium clone FIU_KM_MD_010 16S ribosomal RNA gene, complete sequence
TGCCAGCCGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGT
GGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAA
CACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAA
ACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAACTAACGCCATTAAGCACTCCGCCTGGGGAGCACGAACGCAAGGTTAAAACTCA
AAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATTGATGGACAGAACTA
GAGATAGTTCCTCTTCTTCGGAAGCCAGAAAACAGGTGGTGCACGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAA
CCCTATCTTAT

A5G08- Uncultured Streptococcus sp. clone 4.8 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGTATAGTAGGTCCCGAGCGTTATCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGG
CTTAACCATAGTACGCTTTGGAAACTGTTTAGCTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACA

CCGGTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
GATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG
GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAG
ATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAGC

A5F02- Streptococcus oralis strain CIP 105158 16S ribosomal RNA gene, partial sequence
TGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGT
GGTCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGA
ACACCGGTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTA
AACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCA
AAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTA
GAGATACAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTCGGGTTAAGTCCCGCAACGAGCGCAACC
CT

A3H05- Streptococcus thermophilus strain IMAU40162 16S ribosomal RNA gene, partial sequence
TGCCAGCCGCCGCGGTATACGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTTAAAGGCTGTGG
CTCAACCATAGTTCGCTTTGGAAACTGTCAAACCTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACA
CCGGTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
GATGAGTGCTAGGTGTTGGATCCTTTCCGGGATTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAG
GAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTAGAG
ATAGAAAGTTACTTCGGTACATCGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGCGAGATGTTGGTTAAGTCCCGCAACGAGCGC

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B3F12- Streptococcus oralis 16S ribosomal RNA gene, partial sequence
GGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGA
AACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTC
TGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTAGGGT
CCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACA
AGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACAG
AGGTGACAGGTGGTGCATGGTTGTC

B11E07- Streptococcus oralis 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B3B11- Streptococcus oralis 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B11A09- Streptococcus oralis 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B7B01- Uncultured Streptococcus sp. clone 4.8 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCTGGAGCGTATCCGGATTACTTGGGCGTAAAGCGAGCGCAGGCGGTAGATAAGTCTGAAGTAAAGGCTGTGGCTTAACCATAGCACGCTTT
GGAAACTGTTTAACTTGAGTGAGAAGGGGAGAGTTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGATGGAAACACCTGGTGGCGAAAGCG
GCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTTGCTAGGTG
TTGGGTCCTTTCCGGGACTCCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGAC
CCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTC
GGGACAGAGGTGACAGGTGGTGCATGGTTGTC

B10D06- Streptococcus parasanguinis strain ATCC 15912 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGCCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGG
GTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B6C02- Streptococcus parasanguinis strain ATCC 15912 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B5A04- Streptococcus parasanguinis strain ATCC 15912 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGA
CAGAGGTGACAGGTGGTG

B4B01- Streptococcus parasanguinis strain ATCC 15912 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTACCTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGGACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B2A02- Streptococcus sp. oral clone FP064 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCTGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCTGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGC
TTTGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCG
GCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGT
TGGGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGG
GACAGAGGTGACAGGTGGTGCATGG

B5D06- Streptococcus oralis 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGACACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGCAGCATGTGGTTTACTTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGG

B7C04- Streptococcus oralis strain VS2971R 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B3C04- Streptococcus oralis strain VS2971R 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGG
GTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B7D06- Streptococcus sanguinis ATCC 29667 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGA
CAGAGGTGACAGGTG

B9E05- Streptococcus oralis strain VS2971R 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGG
GTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCGAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGGGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B11C02- Streptococcus oralis strain VS2971R 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGAGTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTACATGGTTGTC

B4F04- Streptococcus oralis strain VS2971R 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGG
GTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTGAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCACGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGNTCTAGAGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B8D03- Streptococcus sp. oral clone FP064 16S ribosomal RNA gene, partial sequence
GGTCCCGAGCGTTGTCCGGATTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTATGCTTTGGAA
ACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCT
GGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGTC
CTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATGGACGGGGGCCCGCACA
AGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACAG
AGGTGACAGGTGGTGCATGGTTGTC

B6E09- Streptococcus sanguinis strain CCRI-282 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTATGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GGCCCTTTCCGGGGCTTAGTGCCGCAACTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGNTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B3E04- Streptococcus oralis 16S ribosomal RNA gene, partial sequence
TCCCGAGCGTTATCCGGATTATTGGGCTGTAAAGCGAGCGCAGGCTGGTTAGATAAGTCTGAAGTTAAAGTGCTGTGGCTTAACCATAGTACGCTTTGGAA
ACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATAAATGGAGGAACACTGGTGGCGAAAGCGGCTCTCT
GGTCTGTAACTGACGCTGAGTGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGT
CCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAATGTTGAAACTCAAAGGAATTGACGGTGGCCCGCACA
AGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACAG
AGGTGACAGGTGGTGCATGGTTGTC

B1A01- Streptococcus oralis 16S ribosomal RNA gene, partial sequence
TAGTAGGTCCGAGCGTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTG
GAAACTGTTTAACTTGAGTGCAGAAGGAGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTC
TCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGAGTTAAATACCCTGCTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGG
GTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAATGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCAGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B10C12- Uncultured Streptococcus sp. clone EHFS1_S01g 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGACAAAGTGACAGGTGGTGCATGGTTGTC

B2B11- Uncultured bacterium partial 16S rRNA gene, clone FC02C08
TATCCTGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACTGTAGTACGCTTTGGAAACTGTTTAACTTGAATGGCAAAAGGGGAGAGTGGAATCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTATTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGAACGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTTCTGACCGATCTAGAGATAGAGCTTTCCTTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGT

B3B04- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
CGTAGGTCCGAGCGTTGCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGTAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTC

B4A11- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTAAGCTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCTGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCTGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTC

B7D05- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGCGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGT

B9G03- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTC

B10G02- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCGACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGAGTTTTCCTTCGGGACAGAGGTGACCGGTGGTGCATGGTTGTC

B11E08- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAGTTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACAGAGGTGACAGGTGGTGCATGGTTGTC

B7F11- Streptococcus infantis strain ToTI 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAG
ACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAG

B6A08- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACCGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGG
CTCTCTGGCTTGTAACTGACGCAGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTT
AGACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGG
ACAGAGGTGACAGGTGGTGCATGGTTGTC

B6B10- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAG
ACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B11G10- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTG
GAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTC
TCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGA
CCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCAC
AAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACA
GAGGTGACAGGTGGTGCATGGTTGTC

B9C12- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTG
GAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTGGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTC
TCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGA
CCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCAC
AAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACA
GAGGTGACAGGTGGTGCATGGTTGTC

B1F06- Streptococcus pseudopneumoniae strain ToTG 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAGACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B2C12- Streptococcus oralis strain CCRI-15027 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAG
ACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B2C02- Streptococcus pneumoniae strain ToTT 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAG
ACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGAACGGTCCTAAAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGC

B9G11- Streptococcus sp. oral strain T4-E3 16S ribosomal RNA gene, partial sequence
TACTAGTCCCGAGCGTTATCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTG
GAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTC
TCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGA
CCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCAC
AAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACA
GAGGTGACAGGTGGTGCACGGTTGTC

B2G04- Uncultured bacterium clone nbt188e12 16S ribosomal RNA gene, partial sequence
CCTGAGCTGTTGTCCTGGATTATTGGGCTGTAAAGCGAGCTGCAGGCTGTGTTAGATAAGTCTTGAAGTTAAATGTGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGTGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTT
AGACCCTTTCCGGGGTTTAGTTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAATCAACTGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCG
GGACAGAGGTGACAGGTGGTGCATGGTTGTC

B2E04- Streptococcus genomosp. C3 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGATCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B4B02- Streptococcus mitis strain CCRI-15034 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTTG
GAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTC
TCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGA
CCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCAC
AAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGACA
GAGGTGACAGGTGGTGCATGGTTGTC

B9G07- Streptococcus mitis strain CCRI-15034 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCT
TTGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGG
CTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTT
AGACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCTTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGG
ACCGAGGTGACAGGTGGTGCATGGTTGTC

B3C08- Streptococcus oralis strain CCRI-15017 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B3C03- Streptococcus pseudopneumoniae strain ToTG 16S ribosomal RNA gene, partial sequence
CGTAGGTCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAG
ACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B7G05- Streptococcus oralis strain CCRI-15027 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCTTAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGTTGTC

B3F01- Streptococcus oralis strain CCRI-15027 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAG
ACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTCAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCGGGAC
AGAGGTGACAGGTGGTGCATGGTTGTC

B7C09- Streptococcus oralis strain CCRI-15027 16S ribosomal RNA gene, partial sequence
CGTAGGTCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GACACTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTCCCTTCGGGA
CAGAGGTGACAGGTGGTGCATGGT

B1G11- Streptococcus pseudopneumoniae strain ToTG 16S ribosomal RNA gene, partial sequence
AGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GACACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAAACTCAAAGGAATTGACGGGGGCC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCG
GGACAGAGGTGACAGGTGGTGCATGGTTGTC

B2A07- Uncultured bacterium clone Lou_f30 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGGTAAGTCTGAAGTTAAAGGCTGTGGGTTAACCAATATTAGGCT
TGGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCG
GCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGT
TAGACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGG
GGACAAAGTGACAGGTGGTGCATGGTTGTC

B3C01- Streptococcus gordonii 16S rRNA gene
CGTAGGTCCCGAGCGTTGCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAG
ACCCTTTCCGGGGTTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGTGGAGTACGACCGCAAGTGTTGAAACTCAAAGGAATTGACGGGGGCCCG
CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCCCGCTCTAGAGATAGAGCTTTACTTCGGT
ACATCGGTGACAGGTGGTGCATGGTTGTC

B11C07- Streptococcus gordonii strain ATCC 10558 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAGCACCGGTGGCGAAAGCGG
CTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTT
AGGCCCTTTCCGGGGCTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCCCGCTCTAGAGATAGAGTTTTACTTCGG
TACATCGGTGACAGGTGGTGCA

B9C05- Streptococcus gordonii strain ATCC 10558 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTAACCATAGTACGCTTTG
GAAACTGTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCGGTGGCGAAAGCGGCTCT
CTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATCAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTAGG
CCCTTTCCGGGGCTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCAC
AAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGGCATCCCGATGCCCGCTCTAGAGGTAGAGTTTTACTTCGGTACA
TCGGTGACAGGTGGTGCATGGTTGTC

B4C02- Streptococcus intermedius strain CIP 105039 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCTGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCAGTGGCTCAACCATTGTAGGCT
TTGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGG
CTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCCAGGTGTT
AGGTCCTTTCCGGGACTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCCCGCTCTAGAGATAGAGCTTTTACTTCGG
TACATCGGTGACAGGTGGTGCATGGTTGTC

B2D12- Streptococcus cristatus strain ATCC 51100 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCTGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGTCTGTAACTTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCATAAACGATGAGTGCTAGGTGTTA
GGCCCTTTCCGGGGCTTAGTGCCGCGGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTTGACGGGGGCCCG
CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGGTGCCCGTCCTAGAGATAGGATTTTGCTTCGGC
ACACCGGTGACAGGTGGTGCATGGTTGTC

B10G01- Streptococcus cristatus strain ATCC 51100 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGGTGCCCGTCCTAGAGATAGGATTTGGCTTCGGC
ACACCGGTGACAGGTGGTGCATGGTTGTC

B9F11- Streptococcus oligofermentans 16S ribosomal RNA, partial sequence
GGTAAGTAGTCCGAGCGTTGCCGGATTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTACCATAGTACGCTTT
GGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCT
CTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGG
GTCCTTTCCGGGACTCAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCA
CAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGGTGCCCGTCCTAGAGATAGGATTTTGCTTCGGCAC
ACCGGTGACAGGTGGTGCATGGTTGTC

B4C08- Streptococcus thermophilus strain IMAU40162 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTTAAAGGCTGTGGCTCAACCATAGTTCGCTTT
GGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GATCCTTTCCGGGATTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTAGAGATAGAAAGTTACTTCGGTA
CATCGGTGACAGGTGGTGCATGGTTGTC

B1A05- Streptococcus thermophilus strain IMAU40162 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTTGATGAGTCTGAAGTTAAAGGCTGTGGCTCAACCATAGTTCGCTTT
GGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GATCCTTTCCGGGATTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTGGAGATAGAAAGTTACTTCGGTA
CATCGGTGACAGGTGGTGCATGGTTGTC

B7D09- Streptococcus thermophilus strain IMAU40162 16S ribosomal RNA gene, partial sequence
GTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTTAAAGGCTGTGGCTCAACCATAGTTCGCTTT
GGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GATCCTTTCCGGGATTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTAGAGATAGAAAGTTACTTCGGTA
CATCGGTGACAGGTGGTGCATGGTTGTC

B9E01- Streptococcus thermophilus strain IMAU40162 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTTAAAGGCTGTGGCTCAACCATAGTTCGCTTT
GGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GATCCTTTCCGGGATTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTAGAGATAGAAAGTTACTTCGGTA
CATCGGTGACAGGTGGTGCATGGTTGTC

B7C07- Streptococcus thermophilus strain IMAU40162 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTTAAAGGCTGTGGCTCAACCATAGTTCGCTTT
GGAAACTGTCAAGCTTGAGTGCAGAAGGGGAGAATGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GATCCTTTCCGGGATTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTAGAGATAGAAAGTTACTTCGGTA
CATCGGTGACAGGTGGTGCATGGTTGTC

B6C05- Streptococcus peroris strain CCUG 39814 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTATCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GATCCTTTCCGGGATTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTAGAGATAGAAAGTTACTTCGGTA
CATCGGTGACAGGTGGTGCATGGTTGTC

B10F06- Uncultured bacterium clone Lou_c57 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTAATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTG
GGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAGCTCAAAGGAATTGACGGGGGCCCGC
ACAAGCGGTGGAGTATGTGGTTTAATTCGACGCAACGCGAAGAACCTTACCAGGTCTTGACATTGATGGACAGAACCAGAGATGGTTCCTCTTCTTCGGAA
GCCAGAAAACAGGTGGTGCACGGTTGTC

B10C05- Uncultured Streptococcus sp. clone 2P-4-1-J02 16S ribosomal RNA gene, partial sequence
CGTAGGTCCCGAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAGGCTGTGGCTTAACCATAGTACGCTT
TGGAAACTGTTTAACTTGAGTGCAAGAGGGGAGAGTGGAATTCCATGTGTAGCGGTAAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGC
TCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTA
GACCCTTTCCGGGGTTTAGTGCCGTAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGAACGCAAGGGTGAAACTCCAAGGAATTGACGGGGGCCCG
GACAAACGCGGGAACCAGGGGGTTAAATCCAGAAGCAAGGCAGAAAACCTTACCAGGTCTTGATATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCG
GGACAGAGGTGACAGGTGGTGCATGGTTGTC

B7G06- Uncultured bacterium clone AerLab-63 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATTTATGGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGC
GACTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TGGGAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCG
GGACAGAGGTGACAGGTGGTGCATGGTTGTC

B1A07 Uncultured bacterium clone AerLab-63 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGC
GACTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TTGGAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACC
CGCACAAGCGGTGGAGCATGAGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCG
GGACAGAGGTGACAGGTGGTGCATGGTTGTC

B7A02- Uncultured bacterium clone AerLab-63 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCCTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCA
TTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCG
ACTCTCTGGTCTGTAACTTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TTGGAGGGTTCCGCCCTTCAGTGCGGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCG
GGACAGAGGTGACAGGTGGTGCATG

B2G05- Uncultured Granulicatella sp. clone GI5-008-A08 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCTGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGC
GACTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TTGGAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCG
GGGACAAAGTGACAGGTGGTGCATGGTTGTC

B4H07- Uncultured Granulicatella sp. clone GI5-008-A08 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGC
GACTCTCTGGTCTGTAACTGACGCCGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TTGGAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCG
GGGACAAAGTGACAGGTGGTGCATGGTTGTC

B5D02- Uncultured Granulicatella sp. clone GI5-008-A08 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGC
GACTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TTGGAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCATTCG
GGGACAAAGTGACAGGTGGTGCATGGTTGTC

B7G09- Uncultured Granulicatella sp. clone GI5-008-A08 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGC
GACTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TTGGAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCG
GGGACAAAGTGACAGGTGGTGCATGGTTGTC

B7D11- Uncultured Granulicatella sp. clone GI5-008-A08 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATATATGGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGC
GACTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTG
TTGGAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCG
GGGACAAAGTGACAGGTGGTGCATGGTTGTC

B1F12- Granulicatella adiacens strain 04424062 16S ribosomal RNA gene, partial sequence
GTAGGTGGAAGCGTTGTCCGGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATT
GGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGAC
TCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTG
GAGGGTTTCCGCCCTTCAGTGCTGCAGTTAACGCATTAACGCACTCCCGCCTGCGGAGTACGACCGCAAGGTTGAAACTCAACGGAATTGACGGGGACCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGG
GGACAAAGTGACAGGTGGTGCATGGTTGTC

B2F05- Uncultured bacterium clone P5D1-392 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
ATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGC
GGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTG
TTGGGTCCTTTCCGGGACTCAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCC
CGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGTTTTCCTTCG
GGACAGAGGTGACAGGTGGTGCATGGTTGTC

B10C01- Gemella haemolysans 16S rRNA gene, clone 12V4
CGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGTGGTTTAATAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTC
ATTGGAAACTGTTAAACTTGAGTGCAGGAGAGAAAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAGGAACACCAGTGGCGAAGGCG
GCTTTTTGGCCTGTAACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGTTAGTCCACGCCGTAAACGATGAGTGCTAAGTGT
TGGTCCCATAAGAGATCAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATACTGTGAGGACACAAGAGATTGTGTTGTTCTGACCTTT
GGTTAGACACAGATACAGGTGGTGCATGGTTGTC

B9F03- Uncultured Gemella sp. clone EHFS1_S13g 16S ribosomal RNA gene, partial sequence
GTAGGTGGCAAGCGTTGTCCGGAATTATGGGGCGTAAAGCGCGCGCAGGTGGTTTAATAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCA
TTGGAAACTGTTAAACTTGAGTGCAGGAGAGAAAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAGGAACACCAGTGGCGAAGGCG
GCTTTTTGGCCTGTAACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGT
TGGTCTCATAAGAGATCAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGCTCTAGAGATAGAGCTTTCCTTCGGGA
CAGAGGTGACCGGTGGTGCATGGTTGTC

B3C07- Veillonella sp. NVG 24cf 16S ribosomal RNA gene, partial sequence
CGTAGGTGGAAGCGTTGTCGGAATTATTGGGCGTAAAGCGCGCACAGGCGGATCAGTCAGTCTGTCTTAAAAGTTCGGGGCTTAACCCCGTGATGGGATG
GAAACTTGCTGATCTAGAGTATCGGAGAGGAAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGACT
TTCTGGACGAAAACTGACGCTGAGGCGCGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTCCTGTCCGTAAACGATGGGTACTAGGTGTAG
GAGGTATCGACCCCTTCTGTGCCGGAGTTAACGCAATAAGTACCCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
CACAAGCGGTGGAGTATGTGGTTTAATTCGACGCAACGCGAAGAACCTTACCAGGTCTTGACATTGATGGACAGAACTAGAGATAGTTCCTCTTCTTCGGA
AGCCAGAAAACAGGTGGTGCACGGTTGTC

B9C07- Veillonella sp. NVG 24cf 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGATCAGTCAGTCTGTCTTAAAAGTTCGGGGCTTAACCCCGTGATGGGA
TGGAAACTGCTGATCTAGAGTATCGGAGAGGAAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGAC
TTTCTGGACGAAAACTGACGCTGAGGCGCGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTCCTGGCCGTAAACGATGGGTACTAGGTGTA
GGAGGTATCGACCCCTTCTGTGCCGGAGTTAACGCAATAAGTACCCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCC
GCACAAGCGGTGGAGTATGTGGTTTAATTCGACGCAACGCGAAGAACCTTACCAGGTCTTGACATTGATGGACAGAACTAGAGATAGTTCCTCTTCTTCGG
AAGCCAGAAAACAGGTGGTGCACGGTTGTC

B2B09- Uncultured bacterium clone Pol_c8 16S ribosomal RNA gene, partial sequence
CGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGATCAGTCAGTCTGCCTTAAAAGTTCGGGGCTTAACCCCGTGATGGGA
TGGAAACTGCTGATCTAGAGTATCGGAGAGGAAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGAC
TTTCTGGACGAAAACTGACGCTGAGGCGCGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTCCTGGCCGTAAACGATGGGTACTAGGTGTA
GGAGGTATCGACCCCTTCTGTGCCGGAGTTAACGCAATAAGTACCCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCC
GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGCTATTTCTACAGATAGAAAGTTACTTCGG
TACATCGGTGACAG

B1C07- Uncultured Clostridiales bacterium partial 16S rRNA gene, clone 202F04(oral)
CATATGGGGCGAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGTGCGGGAAAATAAGTCAGTATGTGAAATCCCTCGGCTCAACTGAGTGAACT
GCAACTGAAACTATTTTTCTTGAGTGTTGAAGTGGGAAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAGGAACACCAGTGGCGAAG
GCGACTTTCTGGGCAACAACTGACGCTGAGGCACGAAAGTGTGGGGAGCAAACAGGATTAAATACCCTGGTAATCCACACCCGTAAACCCAAGTGGATCC
TAGGATTGTGGCAAAAATATGTGTCGGTTCCGCAGTTAACGCATTAAGTATCCCACCTGGGGAGTACGACCGCAAGGTTAAAACTCAAAGGAATTGACGG
GGGCCCGCACAAGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGGCTTGACATATACAGGAATATATAAGAGATTATATAGC
TCTACGGAGTCTGTATACAGGTGGTGCATGGTTGTC

B11A07- Prevotella histicola strain N12-20 16S ribosomal RNA gene, partial sequence
CGGAAGGTCCGGGCGTACCGGATTATTGGGTTAAAGGGAGCGTAGGCTGGAGATTAAGTGTGTTGTGAAATGTAGACGCTCAACGTCTGACTTGCAGCG
CATACTGGTTTCCTTGAGTACGCACAACGTTGGCGGAATTCGTCGTGTAGCGGTGAAATGCTTAGATATGACGAAGAACTCCGATTGCGAAGGCAGCTGA
CGGGAGCGCAACTGACGCTGAAGCTCGAAGGTGCGGGTATCGAACAGGATTAGATACCCTGGTAGTCCGCACAGTAAACGATGGATGCCCGCTGTTGGT
ACCTGGTATCAGCGGCTAAGCGAAAGCATTAAGCATCCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC
GGAGGAACATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCCGGGCTTGAATTGCAGAGGAAGGATTTAGAGATAATGACGCCCTTCGGGGTCTCT
GTGAAGGTGCTGCATGGTTGTC

B3H07- Capnocytophaga sp. 16S ribosomal RNA gene, partial sequence
CGGAGGATGCGAGCGTTATTCGGAATCATTGGGTTTAAAGGGTCTGTAGGCGGGCTATTAAGTCAGAGGTGAAAGGTTTCAGCTTAACTGAGAAATTGCT
TTGATACTGGTAGTCTTGAATATCTGTGAAGTTCTTGGAATGTGTAGTGTAGCGGTGAAATGCTTAGATATTACACAGAACACCGATTGCGAAGGCAGGGG
ACTAACAGACAATTGACGCTGAGAGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGGATACTAGCTGTTTGA
TGATAAGTTGAGTGGCTAAGCGAAAGTGATAAGTATCCCACCTGGGGAGTACGCACGCAAGTGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGC
GGTGGAGCATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCAAGGTTTAAATGGGGACTGACAGGTGTACAGATACGCCCTTCTTCGGACAGTTTTC
AAGGTGCTGCATGGTCGTC

B4E01- Haemophilus parainfluenzae strain CIP 102513 16S ribosomal RNA gene, partial sequence
TACGGAGGATGCGAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGTGACTTAAGTGAGGTGTGAAAGCCCCGGGCTTAACCTGGGAATT
GCATTTCATACTGGGTCGCTAGAGTACTTTAGGGAGGGGTAGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGG
CAGCCCCTTGGGAATGTACTGACGCTCATGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAAACGATGTCGATTTGGG
GGTTGAGCTTTAAGCTTGGCGCCCGTAGCTAACGTGATAAATCGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCG
CACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACATTCCAGAGATGGATTGGTGCCTTCGGG
AACTCTGAGACAGGTGCTGCATGGCTGTC

B2F12- Streptococcus genomosp. C1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTAAGAGATTAGCTTGTCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GNTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6B11- Streptococcus genomosp. C1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGN
CTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B10D03- Uncultured bacterium partial 16S rRNA gene, clone MC02D04
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGATGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATCCCCGGGGGGGTTGTGGAATCCGCGAATAACTACCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAG
ACTGGCTTTAAGAAATTAACTTGCCGTCACCGACTTGCGAATCGTTGTACCAGCCATTGTAGCACGTTGTGGTAGCCCAAGTCATTAAGGGGGCATGGAAT
GAATTGGAACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTG
CGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGG
GATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTTAACCACATGCTCCACCGCTTGT

B7H12- Uncultured bacterium clone nbt188e12 16S ribosomal RNA gene, partial sequence
TCACCCCAATCATCTATCCCACCTTAGGCGGCGTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGCGTACAAACTCTCGTGTGTGACGGGCGGGTGTGTA
CAAGGCCCGGGAACGTATCACCGCGGCGGCTGGCACTCAGATCAGTCAAAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTAATTACCGG
GAGTCTCGCTAAAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGTACTTAACCCAACATCTCACGACACTAGCTGACGACAA
CCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCATGACCTGGTAAGGTTCTTCGCGTTGCTTCAAATTA
AACCACATGCTCCACCGCTTGT

B8A01- Streptococcus parasanguinis 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGCTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGTCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGATCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4D02- Uncultured Streptococcus sp. clone EHFS1_S09c 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACTTAGGCGGTGGTCCTAAAAGGTTACTCACCTGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCTGGTGTGTACAA
GGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTT
TAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTGGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC
CCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B1B11- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTCGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCTGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4F06- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4D10- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
CTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B3G01- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCCCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B3H06- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557

CTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGCTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4G06- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence

CCAATCATCTATCCCACTTAGGCGGCTGGCTCCTAAAAGGTTACTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCTGGCAGTCTCGCTAGAGTTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCACAGGGATGTCAAGACCTGGTAAGGTCCTTCGCGTTGCTTCGAATTAAACCACATGCTCCATCGCTTGT

B1H03- Uncultured bacterium partial 16S rRNA gene, isolate BF0001D086

CCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGAGGGGGGGGGTGTACAAGGCCCTGGGAACTGTATTCACCCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGCCTGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTTCCGTCCGGATTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGCTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4A06- Streptococcus mitis strain GCSS 1303 16S small subunit ribosomal RNA gene, partial sequence

CCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGTGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAANCAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11B06 Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence

CCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4A09- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence

TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4D11- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence

TTCACCCCAATCATCAATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGTCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11D03- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence

TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATAATTTGACGTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6B06- Streptococcus mitis strain Sm91 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCCCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B1D12- Streptococcus mitis strain Sm91 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGNTTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCT
TTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGG
TAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7E05- Streptococcus mitis strain Sm91 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCT
TTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGG
TAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7C10- Streptococcus mitis strain Sm91 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACCGAGACTGGC
TTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTG
GTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6B03- Streptococcus parasanguinis 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGAAAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTGGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B10G06- Streptococcus genomosp. C1 16S ribosomal RNA gene, partial sequence
CCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGG
CCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTT
AAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCC
CCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B10F08- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
CTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGGGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9A02- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
CTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC

B11D06- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B8F06- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTTCACCCCAATCATCTATCCCACCTTAAGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGT
ACAAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACT
GGCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGTCTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11E06 Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
ACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATCACCGCAGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTT
TAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC
CCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9B11- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGTGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGNTTGT

B7B04- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
CTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGT
ACAAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACT
GGCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9B05- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
CTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGT
ACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACT
GGCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11B02- Streptococcus sp. oral clone FP015 16S ribosomal RNA gene, partial sequence
TCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGACCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGC
TTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTG
GTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11E04- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCCCAAAAGGTTACCTCACCGACTTTGGGTGTTACGAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTCAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11H08- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCCCAAAAGGTTACCTCACCGACTTTGGGTGTTACGAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTCAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B2C04- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9B07- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
CTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCAGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGT
ACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACT
GGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGGCAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCCAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACC

B7E09- Streptococcus oralis strain CIP 103216 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCANCGCTTGT

B6C04- Uncultured bacterium partial 16S rRNA gene, isolate BF0001D086
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCT
TTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCAACTTCCTCCGGTTTAATACCGGGCAGTCTCGCTAAAGTTGGCCAAATGAATGGATGGGAAATAACAATAGGGGTTGGGCCCCTAGCGGGACTTAA
ACCAAAATCTCACGGAAACGAGCTGACGAAAAACCATGCACCACTGTCACCTCTGTCCCGAAGGAAAAATCTATCTCTAGAGCGGTCAGAGGGATGTCAA
GACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6C09- Uncultured Streptococcus sp. clone 1.23 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCT
TTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCAACTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTTGCCAAATGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ANATCTCACGACACGAGCTGACGAAAACCATGCACCAACTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGNTTGT

B6D02 Uncultured bacterium partial 16S rRNA gene, clone MA02H05
ATTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCAACTTCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGGCCAANTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGAAACGAGCTGAAGACAACCATGCACCAACTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGNTTGT

B6E03- Uncultured bacterium partial 16S rRNA gene, clone MA02H05
TTCACCCCAATCATCTATCCCACCTTAGGCGGTTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCAACTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCAANTGAATGATGGCAACTAAACATAGGGGTTGCGCTCGTTGCGGGACTTAAAC
CAAATATCTCACGACACGAGCTGACGACAACCATGCACCACCTTGTCACTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6C11- Uncultured Streptococcus sp. clone AV_7R-N-C10 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCT
TTCAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCAACTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGG
TAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCANCGCTTGT

B3C02- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
CTTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACCAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11E02- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGC
TTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGAGGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B1B03- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGC
TTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTG
GTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6A05- Uncultured bacterium clone A_S_01_21 16S ribosomal RNA gene, partial sequence
CAATCATCTATCCCACTTAGGCGGTGGTCCAAATGGTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGA
ACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTTTAAGAGATT
AGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCCCCTTCC
TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCGCGA
CACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTT
CGCGTTGCTTCGAATTAAACCACATGCTCCACCGNTTGT

B9A03- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGCGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGGACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCCCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11E05- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7B03- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCACCTTAGGCGGCTGGCTCAAATGGTTACCTCACCGACTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAG
GCCTGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCAGGGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCTT
TAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATC
CCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B10E11- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
ATTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGGTTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7H02- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCTCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7F07- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCT
TTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGG
TAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6F08- Streptococcus sp. F1 16S ribosomal RNA gene, partial sequence
ATTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGC
TTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCANCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTG
GTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B1E09- Uncultured bacterium partial 16S rRNA gene, clone MA02H05
ATTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCGCCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCACTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTTGAATTAAACCACATGCTCCACCGCTTGT

B10E01- Uncultured bacterium partial 16S rRNA gene, clone MA02H05
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAATGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTTGCCCAAGTCCTAAGGGGGCTTGATGATTGGACG
TCATCCCCACCTTCCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAA
CCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGA
CCTGCTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B3C05- Uncultured bacterium partial 16S rRNA gene, clone MA02H05
CTCACCCCAATCATCTATCCCACTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGC
TTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCACCTTCCTCCGGCTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTG
GTAAGGTTCTTCACGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B2E07- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
ACTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTG
TACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAT
TGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGAC
GTCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAA
CCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGA
CCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11D05- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B3C12- Streptococcus oralis gene for 16S ribosomal RNA, partial sequence, strain: ATCC 10557
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGTGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B8H01 Uncultured Streptococcus sp. clone AV_7R-N-C10 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTCGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7D04- Streptococcus mitis 16S ribosomal RNA gene, complete sequence
CTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGT
ACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACT
GGCTTTAAGAGATTAGCTTGCCGTCACCGGCTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11B07- Streptococcus mitis 16S ribosomal RNA gene, complete sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGT

B10F04- Streptococcus pneumoniae JJA, complete genome
CTTCACCCCAATCGCTAATCACACCCTCGGAGCATCCCTCCTTGCGGTTAGGCCTGCTACTTCAGGTGCAACCAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9B06- Streptococcus pneumoniae JJA, complete genome
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11F03- Streptococcus pneumoniae JJA, complete genome
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTACAAACTCTCNTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7E11- Streptococcus sanguinis 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTCAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCAAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B2A04- Streptococcus sanguinis SK36, complete genome
CCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTTGCGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCC
CGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTTCAG
AGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCA
CCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCT
CACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAG
GTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B3D09- Streptococcus pneumoniae Taiwan19F-14, complete genome
ATCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTACTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B8H12- Uncultured Streptococcus sp. clone 2.29 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTTACGGTTACCTCACCGACTTCGGGTGTTACAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCT
TTAAGAGATTAGCTTGCCGTCACCGACTCGCGACCCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACAGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACCTG
GTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7A07- Streptococcus oralis strain CIP 104985 16S ribosomal RNA gene, partial sequence
CTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAGACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAATCTCTATCTCTAGAGAGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6B08- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4G08- Uncultured Streptococcus sp. clone AV_6J-G13 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAG
GCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTT
AAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCC
CCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACA
TCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTA
AGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9E12- Streptococcus genomosp. C1 16S ribosomal RNA gene, partial sequence
GCTTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTA
CAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCCCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAAACCACATGCTCCACCGCTTGT

B11G03- Streptococcus genomosp. C1 16S ribosomal RNA gene, partial sequence
ACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTCAAG
GCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGGCTTT
AAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCC
CCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9C03- Streptococcus oralis strain CIP 105158 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAAAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7D02- Streptococcus oralis strain CIP 105158 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGTGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCC

B3C06- Streptococcus genomosp. C1 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGCCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B2D03- Streptococcus sp. oral clone FN051 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAGCTGAGACTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B1E07- Streptococcus parasanguinis strain ATCC 15912 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGACTGG
CTTTAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCAACTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11F12- Streptococcus parasanguinis strain ATCC 15912 16S ribosomal RNA gene, partial sequence
GTTTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGT
ACAAGGCCGGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATT
GGCTTCAAGAGATTAGCTTGCCGTCACCGACTCGCGACTCGTCGTACCAGCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACG
TCATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTAAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTTGCTTCGAATTATACCACATGCTGCACCGCTTGT

B4F07- Streptococcus oralis strain CIP 105158 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCT
TTAAGAGATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTCAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGG
TAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGT

B1F11- Streptococcus salivarius gene for 16S ribosomal RNA, partial sequence, strain: HT9R
TTCACCCAATCATCTATCCCACTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGCT
TTAAGAGATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9C04- Streptococcus salivarius gene for 16S ribosomal RNA, partial sequence, strain: HT9R
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGC
TTTAAGAGATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGT

B9E06- Streptococcus salivarius gene for 16S ribosomal RNA, partial sequence, strain: HT9R
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAAAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B3F06- Streptococcus salivarius gene for 16S ribosomal RNA, partial sequence, strain: HT9R
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTGGC
TTTAAGAGATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAA
CATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACCTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B4G12- Streptococcus salivarius gene for 16S ribosomal RNA, partial sequence, strain: HT9R
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGATTG
GCTTTAAGAGATTAGCTTGCCGTCACCGACTCGCAACTCGTTGTACCAACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCANCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAANTGAATGATGGCAACTAACAATAGGGGTTGCGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAACTTTCTATCTCTAGAAATAGCATCGGGATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11C01- Streptococcus mutans strain ATCC 25175 16S ribosomal RNA gene, partial sequence
CTCACCCAATCATCCATCCCACCTTAGGCGGCTGGCCCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGGAGGCGAGTTGCAGCCTCCAATCCGAACTGAGATCG
GCTTTCAGAGATTAGCTTGCCGTCACCGGCTCGCAACTCGTTGTACCGACCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGT
CATCCCCACCTTCCTCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATAAGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCTCCGATGTACCGAAGTAACTTCCTATCTCTAAGAATAGCATCGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B10G09- Uncultured bacterium clone A_S_01_49 16S ribosomal RNA gene, partial sequence
TCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACA
AGACCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGG
CTTTAAGAGATTAGCTTGCCGTCACCGACTTGCGACTCGTTGTACCAGCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGGTTGT

B10D12- Uncultured bacterium partial 16S rRNA gene, isolate BF0002A074
TTCACCCAATCATCTGTCCCACCGTGACCGGCTCCCTCCTTAAAGGTTAGGCCACCGTCTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGACCCGGGAACGTATTCACCGCGACATTCTGATTCGCGATTACTAGCGATTCCAGCTTCATGTAGTCGAGTTGCAGACTACAATCCGAACTGAGAATAG
TTTNATGAGGTTTGCTTACTCTCGCGAGCTCGCTTCTCTTTGTTCCTATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCGNCTTCCTCCAGTTTATCACTGGCAGTCTGTCTAGAGTCCCCATCTTACTTGCTGGCAACTAGACATAGGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCGATGTACCGAAGTAAAGCTCTATCTCTAGAGCGGGCATCGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11A11- Uncultured bacterium clone A_S_01_49 16S ribosomal RNA gene, partial sequence
TCACCCCTACCATCTGTCCCACCGTGACCGGCTCCCTCCTTAAAGGTTAGGCCACCGTCTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGACCCGGGAACGTATTCACCGCGACATTCTGATTCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGG
CTTTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCACAGGATGTCACGACTTG
GTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9F12- Uncultured bacterium clone A_S_01_49 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGCGTACA
AGACCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGG
CTTTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCA
TCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTG
GTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6D05- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
CCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTACCTCACCGACTTTGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCC
GGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAG
AGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCAA
CTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGAACTTAACCCAAAATTC
TCACGACACGAGCTGACGAAAAACATGCACCANCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAA
GGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCA

B9E03- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGACCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATG
GCTTTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTGTCATCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B1F01- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGACCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATG
GCTTTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCCCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B3E09- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTTGGGTGTTAAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGACCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATG
GCTTTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACT
TGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9C01- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 701G07(oral)
CCCCAATCATCTATCCCACCTTAGGCGGTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGA
CCCGGGAACGTATCACCGCGGCGTGCTGATCCGGATTACTAGCGATCCGGCTTCATGTAGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAAGA
GATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCACC
TTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAATTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCA
CGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAGGTT
CTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B2C11- Uncultured bacterium clone A_S_01_49 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTAGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTAC
AAGACCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATG
GCTTTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCC
AACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTT
GGTAAGGTTCTTCGCGTTGCTTCGATTTAAACCACATGCTCCACCGCTTGT

B6H10- Uncultured bacterium partial 16S rRNA gene, clone MA01F01
CCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACTCACCGACTTTGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGACC
CGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGCTTTAA
GAGATTCGCTTACTCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCA
CCTTCCTCCGGTTTGTCACCGGCAGTCTCACTAAAGTGCCCAACTGAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCT
CACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGTAAG
GTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B7F04- Uncultured Granulicatella sp. partial 16S rRNA gene, clone 602F12(oral)
TTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAATGGTTACCTCACCGACTTTGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAA
GACCCGGGGACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGAGAATGGC
TTTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCACCTTCCTCCGGTTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B6F07- Uncultured bacterium clone UB652 16S ribosomal RNA gene, partial sequence
CTCACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTCGGGTGTACAAACTCTCGTGGTGTGACGGGCGGTGTGTCAA
GGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGGACTGAGATTGGCT
TTAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATC
CCCAACTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTGAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACTTTGTCCCCGAAGGGAAAGCTCTATCTCTAGAGTGGTCAAAGGATGTCAAGACTTGGT
AAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B9G04- Uncultured bacterium clone A_S_01_49 16S ribosomal RNA gene, partial sequence
ACCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAAGGTTACCTCACCGACTTTGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAG
ACCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGGCTTCATGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAATGGCTT
TAAGAGATTCGCTTACCCTCGCGAGTTCGCTGCTCGTTGTACCATCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCC
CCACCTTCCTCCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTCAATGCTGGCAACTAGTAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACA
TCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTA
AGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B1A02- Veillonella atypica strain ATCC 17744 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCGACTTTACCTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAG
TGTTTCTCGGGTTTGCTCCACCTCGCGGTTTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCCGAAGTGCTGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACCATCTCTGGTTCTGTCCATCAATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGTGTCGAATTAAACCACATACTCCACCGCTTGT

B7E01- Veillonella sp. oral clone VeillG1 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCGACTTTACCTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAG
TGTTTCTCGGGTTTGCTCCACCTCGCGGTTTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCCGAAGTGCTGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACTATCTCTAGTTCTGTCCATCAATGTCAAGACCT
GGTAAGGTTCTTCGCGTTGCGTCGAATTAAACCACATACTCCACCGCTTGT

B4B06- Veillonella sp. oral clone VeillG1 16S ribosomal RNA gene, partial sequence
TCACCCAATCATCGACTTTACCTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTACAA
GGCCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAGTG
TTTCTCGGGTTTGCTCCACCTCGCGGTATCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCAT
CCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCCGAAGTGCTGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACCCA
ACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACTATCTCTAGTTCTGTCCATCAATGTCAAGACCTGG
TAAGGTTCTTCGCGTTGCGTCGAATTAAACCACATACTCCACCGCTTGT

B11E03- Veillonella sp. oral clone VeillH4 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCGACTTTACCTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTAC
AAGGCCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAG
TGTTTCTCGGGTTTGCTCCATCTCGCGATCTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTC
ATCCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCATTACGTGCTGGCAACATAAGATAGGGGTTGTGCTCGTTGCGGGACTTAAC
CCAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACTATCTCTGGTCCTGTCCATCAATGTCAAGACC
TGGTAAGGTTCTTCGCGTTGCGTCGAATTAAACCACATACTCCACCGCTTGT

B6A10- Veillonella sp. oral clone VeillH4 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCGACTTTACCTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAGTGTTTCTCGGGTTTGCTCCATCTCGCGATCTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCATTACGTGCTTGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACTATCTCTAGTTCTGTCCATCAATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCGTCGAATTAAACCACATACTCCACCGCTTGT

B2A03- Uncultured Veillonella sp. clone KLONG06 16S ribosomal RNA gene, partial sequence
TTCACCCAATCATCGACTTTACCTTAGACGGCTGACTCCCGAAGGTTACCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTAATTCAACCGGAATATTGGTTGAGACTTGCAATAATAACCAATCCCAATTCCACTTAGCGCAATTGGCAGCCTACGATCCGAACTGAGAGAGTGTTTCTCGGGTTTGCTCCATCTCGCGATCTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCCGAAGTGCTGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTCTTCTGGCTTCCGAAGAAGAGGAACTATCTCTAGTTCTGTCCATCAATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCGTCGAATTAAACCACATACTCCACCGCTTGT

B3D05- Uncultured Veillonella sp. clone B01 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCGACTTTACTTAGACGGCTGGCTCCCGAAGGTTACCCCACCGGCTTTGGGCACTTCCGACTTTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCACGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAGTGTTTCTCGGGTTTGCTCCACCTCGCGGTATTGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCCGAAGTGCTGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACTACACGAGCTGACGACAACCGTGCACCACCTGTCACCTCTGTCCCGAAGGAAAACTCTATCTCTAGAGCGGTCAGAGGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B11D08- Uncultured Veillonella sp. clone EHFS1_S03d 16S ribosomal RNA gene, partial sequence
TTCACCCCAATCATCTATCCCACCTTAGGCGGCTGGCTCCAAAGTGGTTACCTCACCGACTTCGGGTGTTACAAACTCTCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGATCCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACGATCCGAACTGAGAGAGTGTTTCTCGGGTTTGCTCCATCTCGCGATCTCGCTTCCGTCTATTAACTCCCATTGTAGTACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCTTCCTCCGCATTGTCTGCGGCAGTCTCTCATGAGTTCCCACCATTACGTGCTGGCAACATAAGATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCGTGCACCACCTGTTTTCTGGCTTCCGAAGAAGAGGAACTATCTCTAGTTCTGTCCATCAATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCGTCGAATTAAACCACATACTCCACCGCTTGT

B11B11- Oribacterium sinus 16S ribosomal RNA gene, partial sequence
TTCACCCCAGTCATCAGTCCTGCCTTCGGCAGCTTCCTCTTTTGGAACACTGACTTCGGGCATTACCAACTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCAGCATGCTGATCTGCGATTACTAGCGATTCCAGCTTCGTGTAGTCGGGTTGCAGACTACAGTCCGAACTGAGACGTTATTTTTGAGATTTGCTTAAGGTCACCCTCTTGCTTCCCTTTGTTTACGCCATTGTAGCACGTGTGTAGCCCAAGTCATAAGGGGCATGATGATTTGACGTCATCCCCGCCTTCCTCCAGGTTATCCCTGGCAGTCTAGTTAGAGTGCCCATCTTACTGCTGGCTACTAACTATAGGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTCACCATTGCCCCGAAGGGAAAGTACATTACATACTCTGTCAATGGGATCTCAAGACTTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTGT

B5F01- Neisseria meningitidis strain 31015 16S ribosomal RNA gene, partial sequence
TTCACCCCAGTCATGAAGCATACCGTGGTAAGCGGGCTCCTTGCGGTTACCCTACCTACTTCTGGTATCCCCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCATGCACTCGAGTTGCAGAGTGCAATCCGGACTACGATCGGTTTTGTGAGATTGGCTCCACCTCGCGGCTTGGCTACCCTCTGTACCGACCATTGTATGACGTGTGAAGCCCTGGTCATAAGGGCCATGAGGACTTGACGTCATCCCCACCTTCCTCTGGCTTGTCACCGGCAGTCTCATTAAAGTGCCCAACTTAATGATGGCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTGTTACGGCTCCCGAAGGCACTCCTCCGTCTCTGGAGGATTCCGTACATGTCAACACCAGGTAAGGTTCTTCGCGTTGCATCGAATTAATCCACATCATC

B11C08- Neisseria sp. R-22841 partial 16S rRNA gene, isolate R-22841
TTCACCCCAGTCATGAAGCATACCGTGGTAAGCGGGCTCCTTGCGGTTACCCTACCTACTTCTGGTATCCCCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACTAGCGATTCCGACTTCATGCACTCGAGTTGCAGAGTGCAATCCGGACTACGATCGGTTTTGTGAGATTGGCTCCACCTCGCGGCTTGGCTACCCTCTGTACCGACCATTGTATGACGTGTGAAGCCCTGGTCATAAGGGCCATGAGGACTTGACGTCATCCCCACCTTCCTCCGGCTTGTCACCGGCAGTCTCATTAGAGTGCCCAACTAAATGATGGCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTGTTACGGTTCCCGAAGGCACTCCTCCGTCTCTGGAGGATTCCGTACATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCGAATTAATCCACATCATCCACCGCTTGT

B7F05- Neisseria meningitidis strain 31015 16S ribosomal RNA gene, partial sequence
TTCACCCCAGTCATGAAGCATACCGTGGTAAGCGGGCTCCTTGCGGTTACCCTACCTACTTCTGGTATCCCCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCAGCATGCTGACCTGCGATTACTAGCGATTCCGACTTCATGCACTCGAGTTGCAGAGTGCAATCCGGACTACGATCGGTTTGGTGAGATTGGCTCCACCTCGCGGCTTGGCTACCCTCTGTACCGACCATTGTATGACGTGTGAAGCCCTGGTCATAAGGGCCATGAGGACTTGACGTCATCCCCACCTTCCTCCGGCTTGTCACCGGCAGTCTCATTGGAGTGCCCAACTAAATGATGGCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTGTTACGGCTCCCGAAGGCACTCCTCCGTCTCTGGAGGATTCCGTACATGTCAAGACCAGGTAAGGTTCTTCGCGTTGCATCGAATTAATCCACATCATCCACCGCTTGT

B4A01- Neisseria genomosp. P1 clone P4PC_20 16S ribosomal RNA gene, partial sequence
TTCACCCCAGTCATGAAGCATACCGTGGTAAGCGGGCTCCTTGCGGTTACCCTACCTACTTCTGGTATCCCCCACTCCCATGGTGTGACGGGCGGTGTGTAC
AAGACCCGGGAACGTATTCACCGCAGTATGCTGACCTGCGATTACCAGCGATTCCGACTTCATGCACTCGAGTTGCAGAGTGCAATCCCGGACTACGATCG
GTTTTATGAGATTGGCTCCGCCTCGCGGCTTGGCTACCCTTTGTACCGACCATTGTATGACGTGTGAAGCCCTGGTCATAAGGGCCATGAGGACTTGACGT
CATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTGCCCAACTGAATGATGGCAACTAATGACAAGGGTTGCGCTCGTTGCGGGACTTAACC
CAACATCTCACGACACGAGCTGACGACAGCCATGCAGCACCTGTGTTACGGTTCCCGAAGGCACCCTTCCGTCTCTGGAAGGTTCCGTACATGTCAAGACC
AGGTAAGGTTCTTCGCGTTGCATCGAATTAATCCACATCATCCTCCGCTTGT

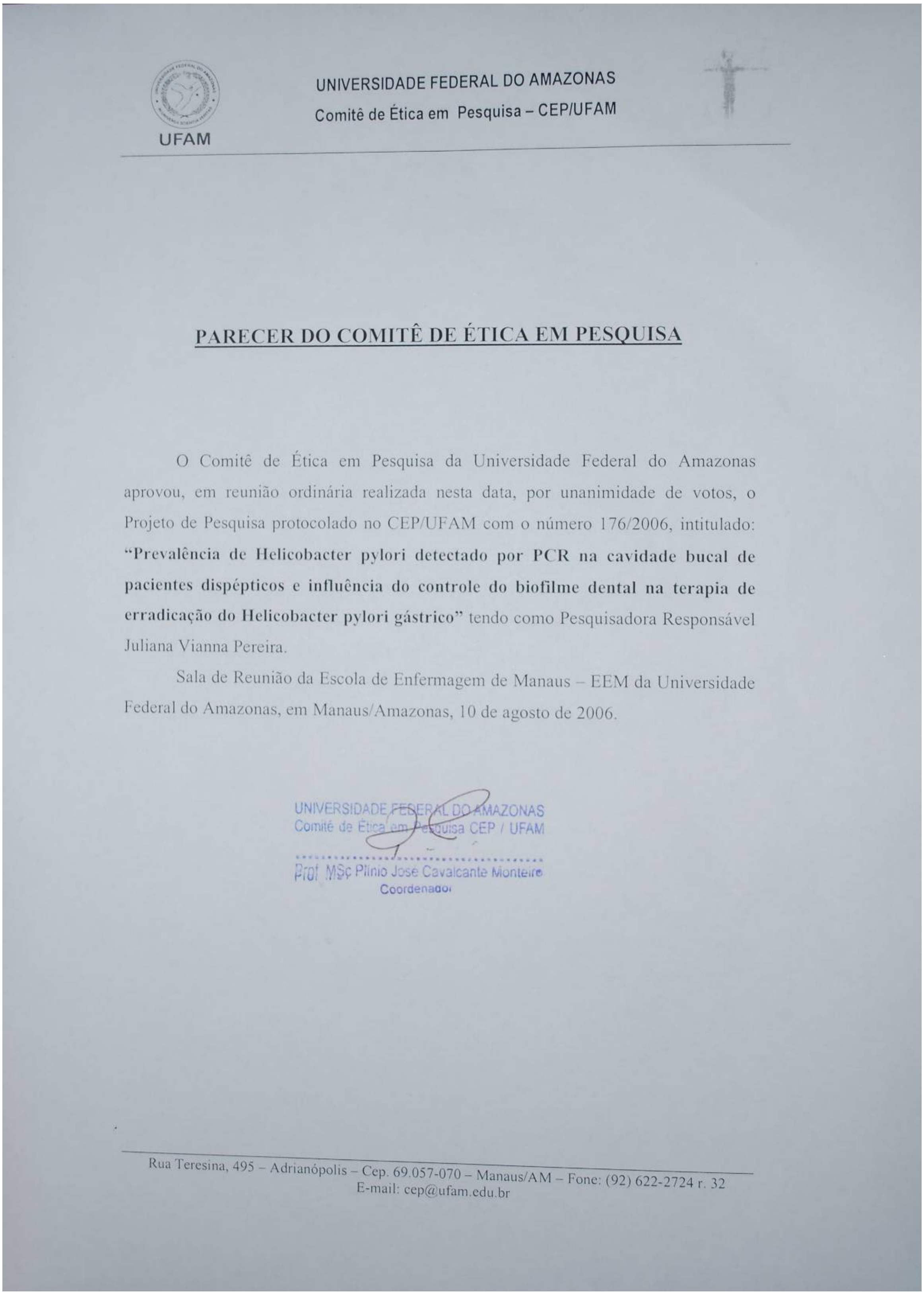
B7E07- Actinomyces graevenitzii 16S rRNA gene, strain CCUG 27294T
TTCGTCCCAATCGCTAGCCCCACCTTTAACCGCTCCCCGTAGAGCCACGGGCTTGGGGTGTGGCCAACTTTCGTGACGTGACGGGCGGTGTGTACAAGGCC
CGAGAACGTATCACCGCAGCGTGGCTGATCTGCGATTACTAGCGACTCCACCTTCATGGTGTCGAGTTGCAGACACCAATCCGAACTGAGACCAGCTTTAA
GGGATTAGCTCCACCTCACAGTATCGCAACCCTCTGTACCGGCCATTGTAGCATGCGTGAAGCCCAAGACATAAGGGGCATGATGATTTGACGTCATCCCC
ACCTTCCTCCGAGTTGACCCCGGCAGTCTCCCGCGAGTCCCCACCACAACGTGCTGGCAACACGGGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAAC
ATCTCACGACACGAGCTGACGACAACCATGCACCACCTGTGAAAACCACCCAAAAGGGTAAACCCTATCTCTAGAGCCACGGTTAACATGTCAAGCCTTGG
TAAGGTTCTTCGCGTTGCATCGAATTAATCCGCATGCTCCGCCGCTTGT

B11G05- Neisseria meningitidis serogroup A strain Z2491 complete genome
CCGAAACGCGCAAGCGTTTTTAGAAAACGACAAGGCGCGCGAATTGTCTGACGGCATTTTGGCGCAGTTGCAGGACACGCGGCAGATTCCGTTTTGTCAG
GAACACCGTGCGCGGATGTACCATTTTCATCAGGATGCGGAATATCCGAAGGGCGTGTACCGCGTATGTACCGCGGCGACTTACCGTTCCGGCTATCCCGA
GTGGAAAATCCTGTTTTCAATGGCGGATTTCGATGAATTGCTCGGCGACGATGTATATTTGGGCGGCGTGTCGCACTTGGTGGAAAAGCCCAACCGCGCGT
TGTTAACACTGAGCAAATCGGGCGGCGATACGGCGTACACGCTGGAAGTGGATTTGGAAGCAGGGGAGTTGGTAGAAGGCGGTTTTCACTTTCCGGCAG
GCAAAAACCATGTGTCGTGGCGCGATGAAAACAGCGTGTGGGTGTGTCCGGCTTGGGACGAACGCCAGTTGACCGAATCGGGCTATCCGCGCGAAGTAT
GGCTAGTGGAACGCGGCAAGAGTTTCGAGGAAAGCCTGCCGGTGTATCAAATTGCCAAAGACGGCATGATGGTAAACGCGTGGCGTTACCTCGATCCGC
AGGGTTCGCCGATTGA

B7H10-
TCCCTTGCTCCCCTCCTTGCTCTAGTAAGAGAGTCCCGACAGCCGGGCCGCGGCTGCTGGCACTCAGTCAGTCAAAGGGCGAATTCCCTACCGGGATAATG
CTTGAGCAGCACGCTATTGCAATACCGCATTGTGAGGCGATTCATGCTAAGTCGTCAGCCATTTATCTGTTAAGGCCAACAAATAAAGTTCATTTTCAGCAA
GCGGATGATGATAACGACGTGGCGGTATCGTTGGTTATTGCGTTGATTGTGGAAAATCCGCAGCAGCAATTGAAACTTTTACGCTGTTTATTTGGCAAGTT
ACAACAGCCCGATATCGTCGAGACACTAATCACTCTTCCTGAAACCCAGTTAAAGGAATACTTCACAAAGTATGTTTTAGATTCAGACGAATAAATCCCTCT
GTAACAATAAAAAGGACTATTTATGAAACGCAAGATTATTGTCGCTTGCGGAGGCGCGGTTGCGACCTCTACGATGGCGGCGGAAGAAATTAAAGAGTTG
TGTCAGAATCATAATATTCCTGTTGAATTAATCCAGTGTCGGGTTAATGAAATAGAAACCTATATGGATGGTGTGCA

Anexos

ANEXO – 1



UFAM

UNIVERSIDADE FEDERAL DO AMAZONAS
Comitê de Ética em Pesquisa – CEP/UFAM

PARECER DO COMITÊ DE ÉTICA EM PESQUISA

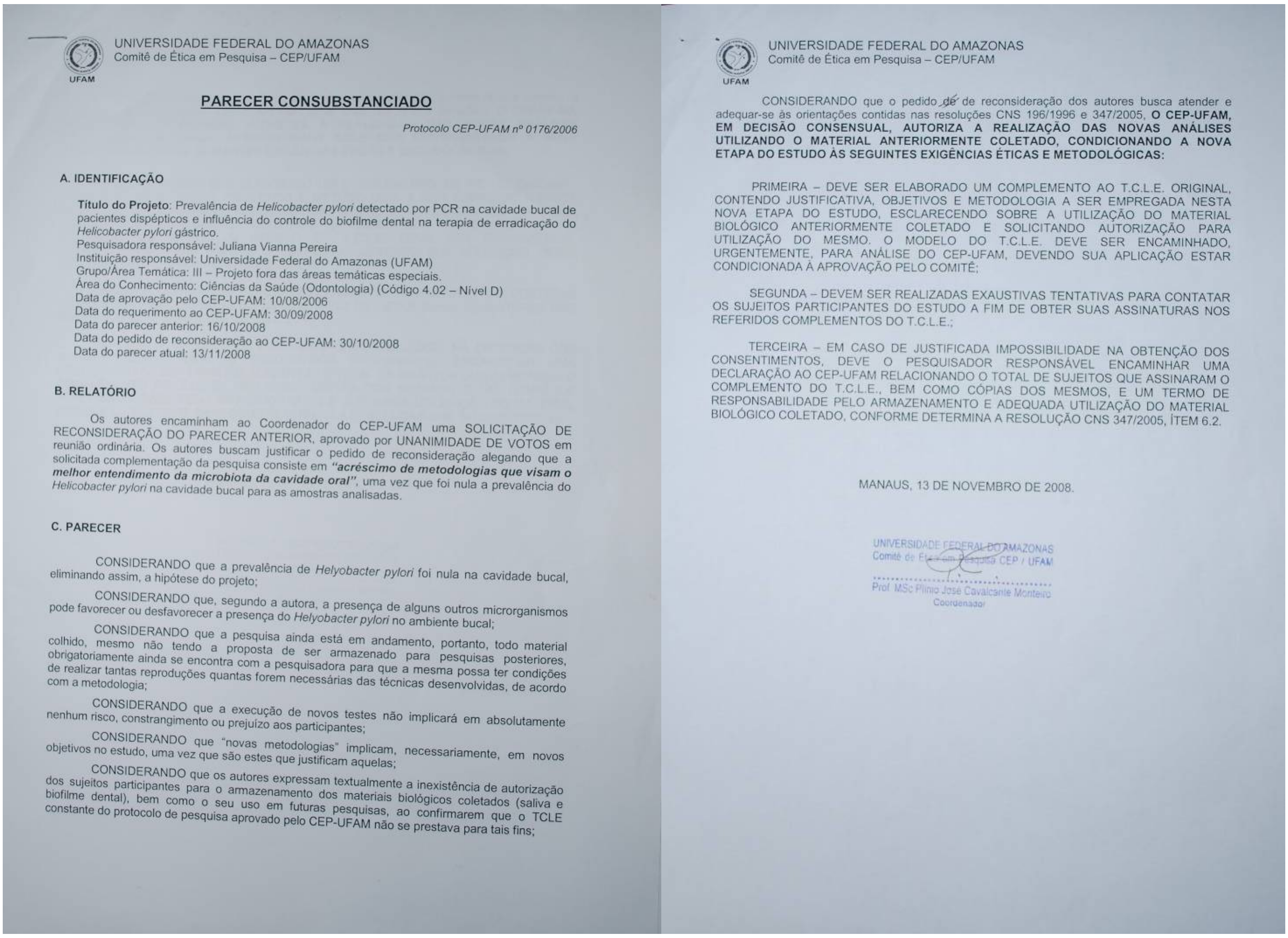
O Comitê de Ética em Pesquisa da Universidade Federal do Amazonas aprovou, em reunião ordinária realizada nesta data, por unanimidade de votos, o Projeto de Pesquisa protocolado no CEP/UFAM com o número 176/2006, intitulado: **"Prevalência de Helicobacter pylori detectado por PCR na cavidade bucal de pacientes dispépticos e influência do controle do biofilme dental na terapia de erradicação do Helicobacter pylori gástrico"** tendo como Pesquisadora Responsável Juliana Vianna Pereira.

Sala de Reunião da Escola de Enfermagem de Manaus – EEM da Universidade Federal do Amazonas, em Manaus/Amazonas, 10 de agosto de 2006.

UNIVERSIDADE FEDERAL DO AMAZONAS
Comitê de Ética em Pesquisa CEP / UFAM
Prof MSç Plínio José Cavalcante Monteiro
Coordenador

Rua Teresina, 495 – Adrianópolis – Cep. 69.057-070 – Manaus/AM – Fone: (92) 622-2724 r. 32
E-mail: cep@ufam.edu.br

ANEXO – 2



UNIVERSIDADE FEDERAL DO AMAZONAS
Comitê de Ética em Pesquisa – CEP/UFAM
UFAM

PARECER CONSUBSTANCIADO

Protocolo CEP-UFAM nº 0176/2006

A. IDENTIFICAÇÃO

Título do Projeto: Prevalência de *Helicobacter pylori* detectado por PCR na cavidade bucal de pacientes dispépticos e influência do controle do biofilme dental na terapia de erradicação do *Helicobacter pylori* gástrico.
Pesquisadora responsável: Juliana Vianna Pereira
Instituição responsável: Universidade Federal do Amazonas (UFAM)
Grupo/Área Temática: III – Projeto fora das áreas temáticas especiais.
Área do Conhecimento: Ciências da Saúde (Odontologia) (Código 4.02 – Nível D)
Data de aprovação pelo CEP-UFAM: 10/08/2006
Data do requerimento ao CEP-UFAM: 30/09/2008
Data do parecer anterior: 16/10/2008
Data do pedido de reconsideração ao CEP-UFAM: 30/10/2008
Data do parecer atual: 13/11/2008

B. RELATÓRIO

Os autores encaminham ao Coordenador do CEP-UFAM uma SOLICITAÇÃO DE RECONSIDERAÇÃO DO PARECER ANTERIOR, aprovado por UNANIMIDADE DE VOTOS em reunião ordinária. Os autores buscam justificar o pedido de reconsideração alegando que a solicitada complementação da pesquisa consiste em ***"acréscimo de metodologias que visam o melhor entendimento da microbiota da cavidade oral"***, uma vez que foi nula a prevalência do *Helicobacter pylori* na cavidade bucal para as amostras analisadas.

C. PARECER

CONSIDERANDO que a prevalência de *Helyobacter pylori* foi nula na cavidade bucal, eliminando assim, a hipótese do projeto;

CONSIDERANDO que, segundo a autora, a presença de alguns outros microrganismos pode favorecer ou desfavorecer a presença do *Helyobacter pylori* no ambiente bucal;

CONSIDERANDO que a pesquisa ainda está em andamento, portanto, todo material colhido, mesmo não tendo a proposta de ser armazenado para pesquisas posteriores, obrigatoriamente ainda se encontra com a pesquisadora para que a mesma possa ter condições de realizar tantas reproduções quantas forem necessárias das técnicas desenvolvidas, de acordo com a metodologia;

CONSIDERANDO que a execução de novos testes não implicará em absolutamente nenhum risco, constrangimento ou prejuízo aos participantes;

CONSIDERANDO que "novas metodologias" implicam, necessariamente, em novos objetivos no estudo, uma vez que são estes que justificam aquelas;

CONSIDERANDO que os autores expressam textualmente a inexistência de autorização dos sujeitos participantes para o armazenamento dos materiais biológicos coletados (saliva e biofilme dental), bem como o seu uso em futuras pesquisas, ao confirmarem que o TCLE constante do protocolo de pesquisa aprovado pelo CEP-UFAM não se prestava para tais fins;

CONSIDERANDO que o pedido ~~de~~ de reconsideração dos autores busca atender e adequar-se às orientações contidas nas resoluções CNS 196/1996 e 347/2005, **O CEP-UFAM, EM DECISÃO CONSENSUAL, AUTORIZA A REALIZAÇÃO DAS NOVAS ANÁLISES UTILIZANDO O MATERIAL ANTERIORMENTE COLETADO, CONDICIONANDO A NOVA ETAPA DO ESTUDO ÀS SEGUINTES EXIGÊNCIAS ÉTICAS E METODOLÓGICAS:**

PRIMEIRA – DEVE SER ELABORADO UM COMPLEMENTO AO T.C.L.E. ORIGINAL, CONTENDO JUSTIFICATIVA, OBJETIVOS E METODOLOGIA A SER EMPREGADA NESTA NOVA ETAPA DO ESTUDO, ESCLARECENDO SOBRE A UTILIZAÇÃO DO MATERIAL BIOLÓGICO ANTERIORMENTE COLETADO E SOLICITANDO AUTORIZAÇÃO PARA UTILIZAÇÃO DO MESMO. O MODELO DO T.C.L.E. DEVE SER ENCAMINHADO, URGENTEMENTE, PARA ANÁLISE DO CEP-UFAM, DEVENDO SUA APLICAÇÃO ESTAR CONDICIONADA À APROVAÇÃO PELO COMITÊ;

SEGUNDA – DEVEM SER REALIZADAS EXAUSTIVAS TENTATIVAS PARA CONTATAR OS SUJEITOS PARTICIPANTES DO ESTUDO A FIM DE OBTER SUAS ASSINATURAS NOS REFERIDOS COMPLEMENTOS DO T.C.L.E.;

TERCEIRA – EM CASO DE JUSTIFICADA IMPOSSIBILIDADE NA OBTENÇÃO DOS CONSENTIMENTOS, DEVE O PESQUISADOR RESPONSÁVEL ENCAMINHAR UMA DECLARAÇÃO AO CEP-UFAM RELACIONANDO O TOTAL DE SUJEITOS QUE ASSINARAM O COMPLEMENTO DO T.C.L.E., BEM COMO CÓPIAS DOS MESMOS, E UM TERMO DE RESPONSABILIDADE PELO ARMAZENAMENTO E ADEQUADA UTILIZAÇÃO DO MATERIAL BIOLÓGICO COLETADO, CONFORME DETERMINA A RESOLUÇÃO CNS 347/2005, ÍTEM 6.2.

MANAUS, 13 DE NOVEMBRO DE 2008.

UNIVERSIDADE FEDERAL DO AMAZONAS
Comitê de Ética em Pesquisa CEP / UFAM
....
Prof. MSc Plinio José Cavalcante Monteiro
Coordenador

ANEXO – 3

Tampões, soluções e meios de cultura

TE

- 10mM, Tris-HCl pH 7,6
- 0,1mM EDTA
- H_2O – para completar 1L

TPK

- Tris-HCl 50 mM, pH 8,0
- 1 mM EDTA
- proteinase K 10 µg/mL

TBE 10X

- 0,89M Tris-base
- 0,89M Ácido bórico
- 0,5 M EDTA, pH 8,0
- H_2O– para completar 1L

TAE (50x)

- 2M Tris Base
- 1M Ácido acético glacial
- 0,5M EDTA
- H_2O – para completar 1L

GET

- 20% glicose filtrada
- 0,5M EDTA
- 1M Tris-HCl
- H_2O – para completar 1L

Gel de agarose

- agarose na concentração desejada (%)
- tampão TBE 1X

Tampão de corrida – Azul de bromofenol – 5X

- Glicerol 30%
- TAE 5X
- Azul de bromofenol

Meio LB (líquido)

- 1% NaCl
- 1% Peptona
- 0,5% Extrato de levedura

Meio LB Agar (sólido)

- 1% NaCl
- 1% Peptona

- 0,5% Extrato de levedura
- Agar – 1,5%

Meio Cicle Grow

- Comercial (Q BioGene: 40g/L