SUPPLEMENTARY MATERIAL

Supplemental Table 1. Sequence information, specificity, amplicon size, and molarity of oligonucleotide primers and probes used in the qPCR assays.

Taxon	Oligonucleotide sequence (5' -> 3') [a]	Target gene; detection limit and amplicon size	Reference	Molarity
Porphyromonas gingivalis	F: AGGATCGCTCAGCGTAGCATT	Arg-gingipain	[1]	0.10 μM
	R: CCTACGTGTACGGACAGAGCTATA	(Rgp), (10 copies/PCR), 71 bp	[1]	0.50 μM
	P: FAM-TCGCCCGGGAAGAACTTGTCTTCA-BHQ1		[1]	0.10 μM
Aggregatibacter actinomycetemcomitans	F: ACGCAGACGATTAACTGAATTTAA	Leukotoxin C	[2]	0.10 μM
	R: GATCTTCACAGCTATATGGCAGCTA	(*lktC*), (10 copies/PCR), 77 bp	[1]	0.25 μM
	P: FAM-TTACCCTTCTACCGTTGCCATGGG-BHQ1		[2]	0.10 μM
Fusobacterium nucleatum	F: TGGCATAGCTTCACCTTTGA	β-subunit of RNA polymerase	[2]	0.25 μM
	R: CAAAGACTTGGGGAAATGGA	(*rpoB*), (10 copies/PCR), 144 bp	[2]	0.50 μM
	P: FAM-TGCTCCATAAGCTTCCAATGCCCA-BHQ1		[2]	0.10 μM
Streptococcus sanguinis	F: GGCGCCTGTTAATACTGAGC	Glycosyl transferase P	[3]	0.10 μM
	R: GTTTTTCCATCCTTGAGGATAGC	(*gtfP*), (10 copies/PCR), 330 bp	[3]	0.50 μM
	P: FAM-TCGATGCAGAGACCGGAGCC-BHQ1		[2]	0.10 μM
Archaea	F: CGGTGAATAYGYCCCTGC	16S ribosomal RNA	[4]	0.25 μM
	R: AAGGAGGTGATCCRGCCGCA	(16S rRNA), (10³ copies/PCR), 173 bp	[4]	1.00 μM
	P: FAM-CTTGCACACACCGCCCGTC-BHQ1		[2]	0.10 μM
Bacteria	F: TGGAGCATGTGGTTTAATTCGA	16S ribosomal RNA	[5]	0.25 μM
	R: TGCGGGACTTAACCCAACA	(16S rRNA), (10³ copies/PCR), 159 bp	[5]	0.10 μM
	P: FAM-CACGAGCTGACGACARCCATGCA-BHQ1		[5]	0.10 μM

[a] F, forward primer; R, reverse primer; P, probe; FAM, 6-carboxyfluorescein; BHQ1, Black Hole Quencher 1.

Supplemental Table 2. Correlation of abundances between tongue scrapings and subgingival samples

	Abundances			Tongue scraping and Subgingival plaque > 0	
	Tongue scraping	Subgingival plaque	r_{SP} (95% CI)	N	r_{SP} (95% CI)
P. gingivalis	0 (0; $1.5 \cdot 10^{-5}$)	0 (0; $1.9 \cdot 10^{-4}$)	0.63 (0.55-0.70)	57	0.25 (-0.01-0.48)
A. actinomycetemcomitans	0 (0; 0)	0 (0; $8.4 \cdot 10^{-5}$)	0.16 (0.03-0.28)	15	0.03 (-0.49-0.53)
F. nucleatum	0 (0; 0)	$2.0 \cdot 10^{-3}$ (0; $1.4 \cdot 10^{-2}$)	0.21 (0.09-0.33)	44	0.06 (-0.24-0.35)
S. sanguinis	0 (0; $3.8 \cdot 10^{-6}$)	0 (0; $2.1 \cdot 10^{-3}$)	0.56 (0.46-0.64)	72	0.17 (-0.07-0.38)
Archaea	429.8 (0; 656.2)	0 (0; 0)	-0.10 (-0.23-0.03)	26	0.25 (-0.15-0.58)
% Archaea	0.01 (0; 0.02)	0 (0; 0)	-0.01 (-0.14-0.12)	26	-0.33 (-0.64-0.06)
Bacteria	$2.6 \cdot 10^{6}$ ($1.5 \cdot 10^{6}$; $4.0 \cdot 10^{6}$)	$1.7 \cdot 10^{4}$ ($9.9 \cdot 10^{3}$; $2.9 \cdot 10^{4}$)	-0.14 (-0.26-0.01)	237	-0.14 (-0.26- -0.01)

Abundances are given as Median (25% quantile, 75% quantile). r_{SP}, Spearman's correlation coefficient; CI, confidence interval

Supplemental Table 3. Median relative abundances (log10 transformed; with 25% and 75% quantiles) from subgingival pocket samples according to categories

of mesiobuccal probing depths and clinical attachment levels (categorized as ≤2, 3 and ≥4 mm).

	P. gingivalis	*A. actinomy-cetemcomitans*	*F. nucleatum*	*S. sanguinis*	*Archaea*	*% Archaea*	Total bacteria	Sum score
mesiobuccal PD								
≤2 mm (N=46)	0 $(0; 3.2 \cdot 10^{-5})$	0 $(0; 0)$	$3.6 \cdot 10^{-4}$ $(0; 2.6 \cdot 10^{-3})$	0 $(0; 1.2 \cdot 10^{-3})$	0.00 $(0.00; 0.00)$	0 $(0; 0)$	4.18 $(3.97; 4.36)$	$1.7 \cdot 10^{-3}$ $(1.9 \cdot 10^{-4}; 9.9 \cdot 10^{-3})$
ˉ3 mm (N=130)	0 $(0; 3.7 \cdot 10^{-5})$	0 $(0; 2.1 \cdot 10^{-5})$	$9.3 \cdot 10^{-4}$ $(0; 7.3 \cdot 10^{-3})$	0 $(0; 8.8 \cdot 10^{-4})$	0.00 $(0.00; 0.00)$	0 $(0; 0)$	4.22 $(4.00; 4.47)$	$3.0 \cdot 10^{-3}$ $(3.6 \cdot 10^{-4}; 2.7 \cdot 10^{-2})$
≥4 mm (N=56)	$6.3 \cdot 10^{-6}$ $(0; 1.3 \cdot 10^{-3})*·**$	0 $(0; 9.5 \cdot 10^{-5})$	$1.1 \cdot 10^{-3}$ $(0; 5.2 \cdot 10^{-3})$	0 $(0; 1.0 \cdot 10^{-3})$	0.00 $(0.00; 0.00)$	0 $(0; 0)$	4.28 $(3.99; 4.70)$	$3.5 \cdot 10^{-2}$ $(1.2 \cdot 10^{-2}; 3.8 \cdot 10^{-2})$ *
mesiobuccal CAL								
≤2 mm (N=100)	0 $(0; 1.4 \cdot 10^{-5})$	0 $(0; 0)$	$7.0 \cdot 10^{-4}$ $(0; 3.1 \cdot 10^{-3})$	0 $(0; 8.0 \cdot 10^{-4})$	0 $(0; 0)$	0 $(0; 0)$	4.23 $(3.99; 4.46)$	$1.0 \cdot 10^{-3}$ $(8.2 \cdot 10^{-5}; 7.2 \cdot 10^{-3})$
ˉ3 mm (N=38)	$6.5 \cdot 10^{-7}$ $(0; 7.4 \cdot 10^{-4})$ *	0 $(0; 2.6 \cdot 10^{-5})$	$6.0 \cdot 10^{-4}$ $(0; 4.8 \cdot 10^{-3})$	0 $(0; 1.3 \cdot 10^{-3})$	0 $(0; 2.34)$ *	0 $(0; 0.48)$ *	4.24 $(4.05; 4.57)$	$2.0 \cdot 10^{-3}$ $(2.6 \cdot 10^{-4}; 6.1 \cdot 10^{-3})$
≥4 mm (N=48)	$8.5 \cdot 10^{-6}$ $(0; 1.2 \cdot 10^{-3})$ *	0 $(0; 9.7 \cdot 10^{-5})$ *	$1.9 \cdot 10^{-3}$ $(3.0 \cdot 10^{-4}; 6.9 \cdot 10^{-3})$ *	0 $(0; 1.0 \cdot 10^{-3})$	0 $(0; 1.19)$ *	0 $(0; 0.25)$	4.33 $(4.09; 4.75)$ *	$3.8 \cdot 10^{-3}$ $(6.2 \cdot 10^{-4}; 3.2 \cdot 10^{-2})$ *

The Sum score was defined as the sum of relative abundances for *P. gingivalis* + *A. actinomycetemcomitans* + *F. nucleatum*. *,** P<0.05 in Mann-Whitney U tests (versus ≤2

mm or versus 3 mm, respectively); PD, probing depth; CAL, clinical attachment level
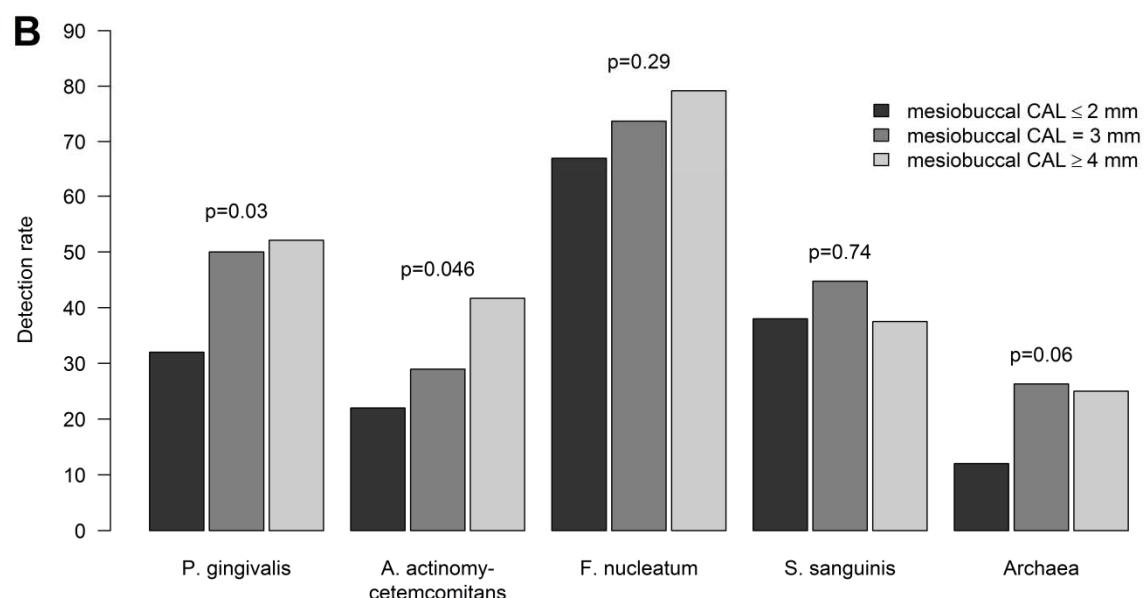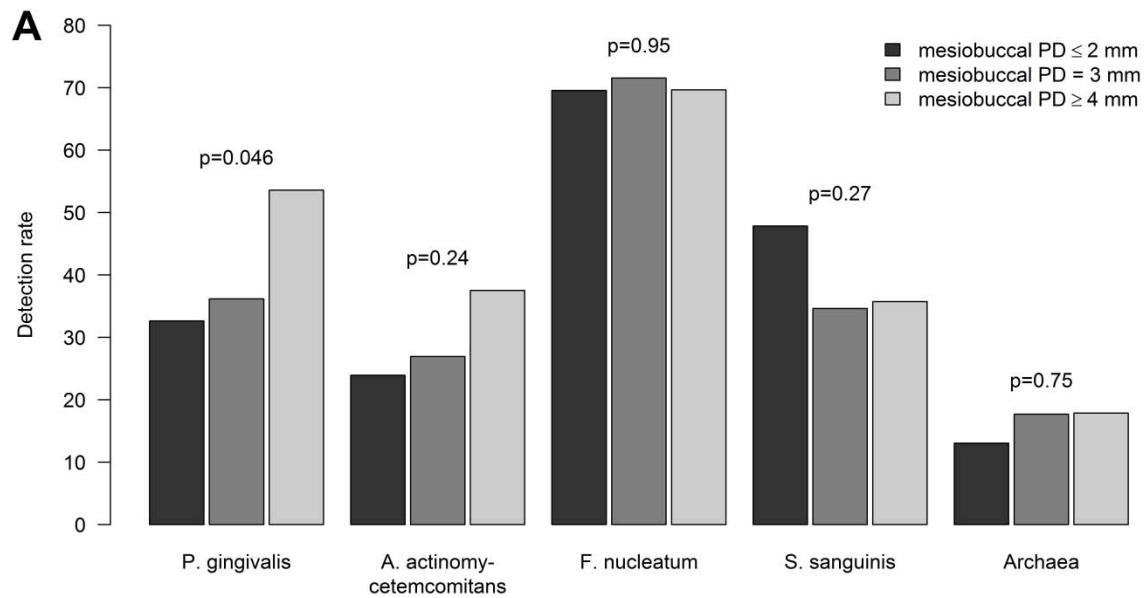
Supplemental Figure 1. Detection rates of bacteria in subgingival plaques according to (A) mesiobuccal probing depth (PD) or to (B) mesiobuccal clinical attachment level (CAL). P values were calculated from Chi squared tests evaluating differences in detection rates among groups.

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