Intraindividual variation in core microbiota in peri-implantitis and periodontitis

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Supplementary Figures

Supplementary Figure S1. Number of taxonomic differences between peri-implantitis and periodontitis samples. Pie charts show the number of taxa that were different at the phylum (a), genus (b), and species (c) levels. The portions represent the taxa present at the peri-implantitis (red), periodontitis (blue), or both (brown) sites.

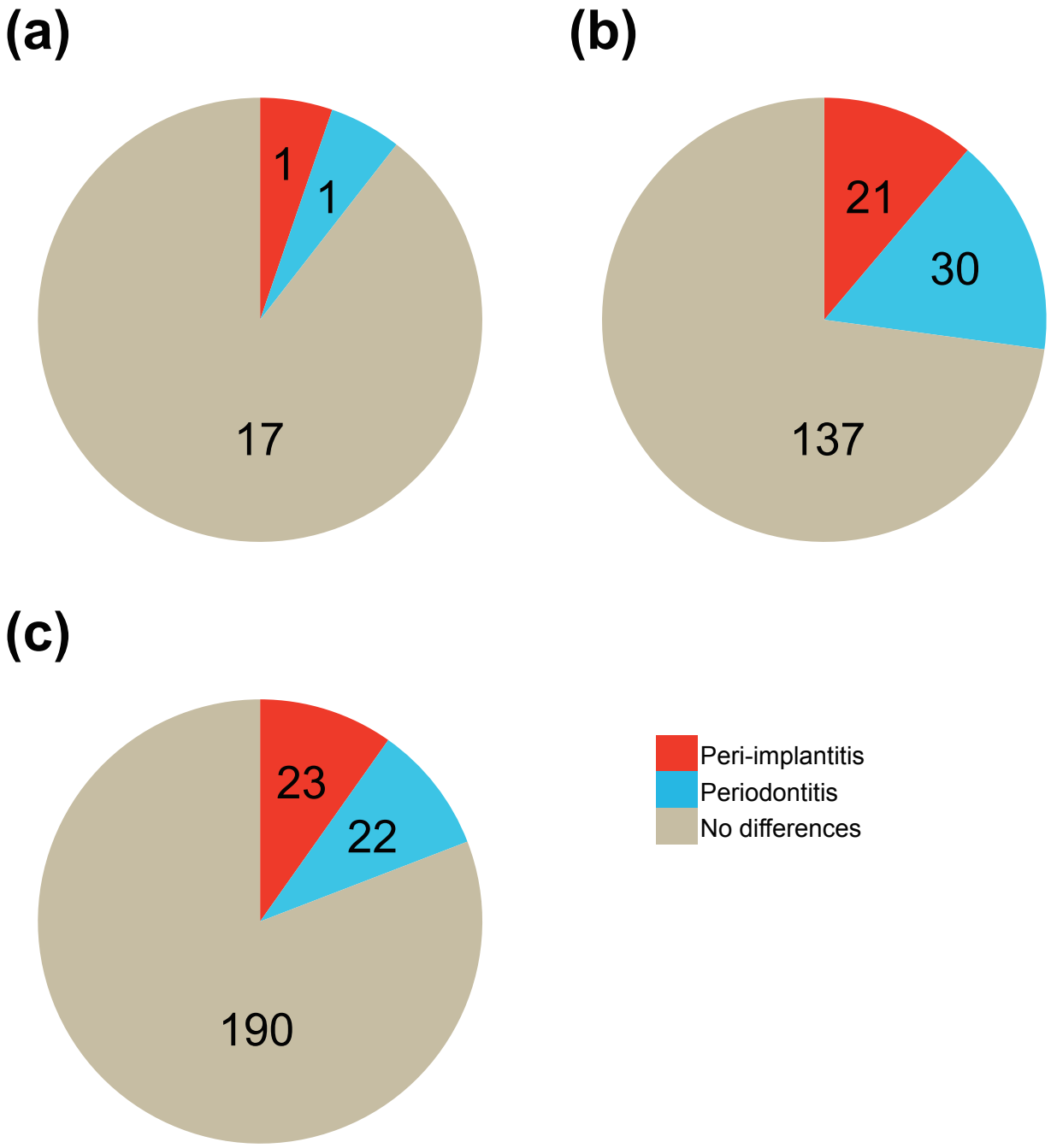
Supplementary Figure S2. The most abundant genera in peri-implantitis and periodontitis. Genera with >0.1% abundance in either peri-implantitis or periodontitis samples, which were the more abundant genera in peri-implantitis (a) and periodontitis (b). The taxonomic assignments were made using the Ribosomal Database Project (RDP) classifier. The taxonomic names were based on results from the RDP classifier. Statistical differences were calculated by Wilcoxon signed rank tests. *P <0.05 and q <0.1.

Supplementary Figure S3. Comparison of the alpha diversity indexes in peri-implantitis and periodontitis. (a–c) Scatter plots are shown with black spots and the bars show the mean and standard deviation, respectively. (a) Shannon Index representing species richness and evenness. (b) Operational taxonomic units (OTUs) generated with a minimum pairwise identity of 97%. (c) Chao1 is used to estimate species richness. (d) Rarefaction curves of the number of OTUs in each sample.

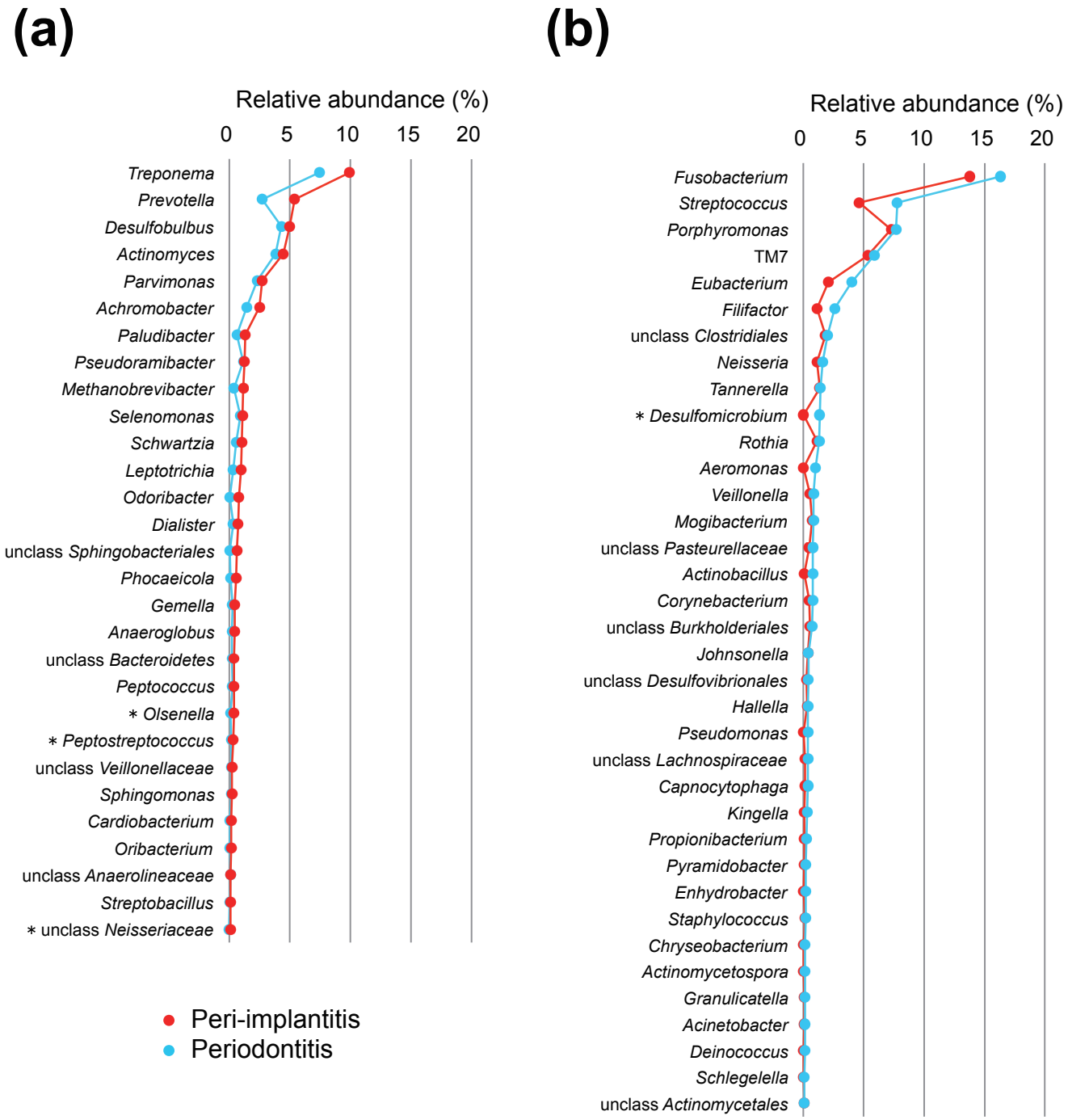
Supplementary Figure 4. **Comparison of the characteristics of constituent species in peri-implantitis and periodontitis** (a) Overall abundance of anaerobic and aerobic bacteria in the peri-implantitis and periodontitis samples. (b) Overall abundance of the gram-negative and gram-positive bacteria. (c) Percentage of cultivated species with ≥98.5% similarity by sample type. Statistical differences were calculated using paired t-tests.

* P <0.05.

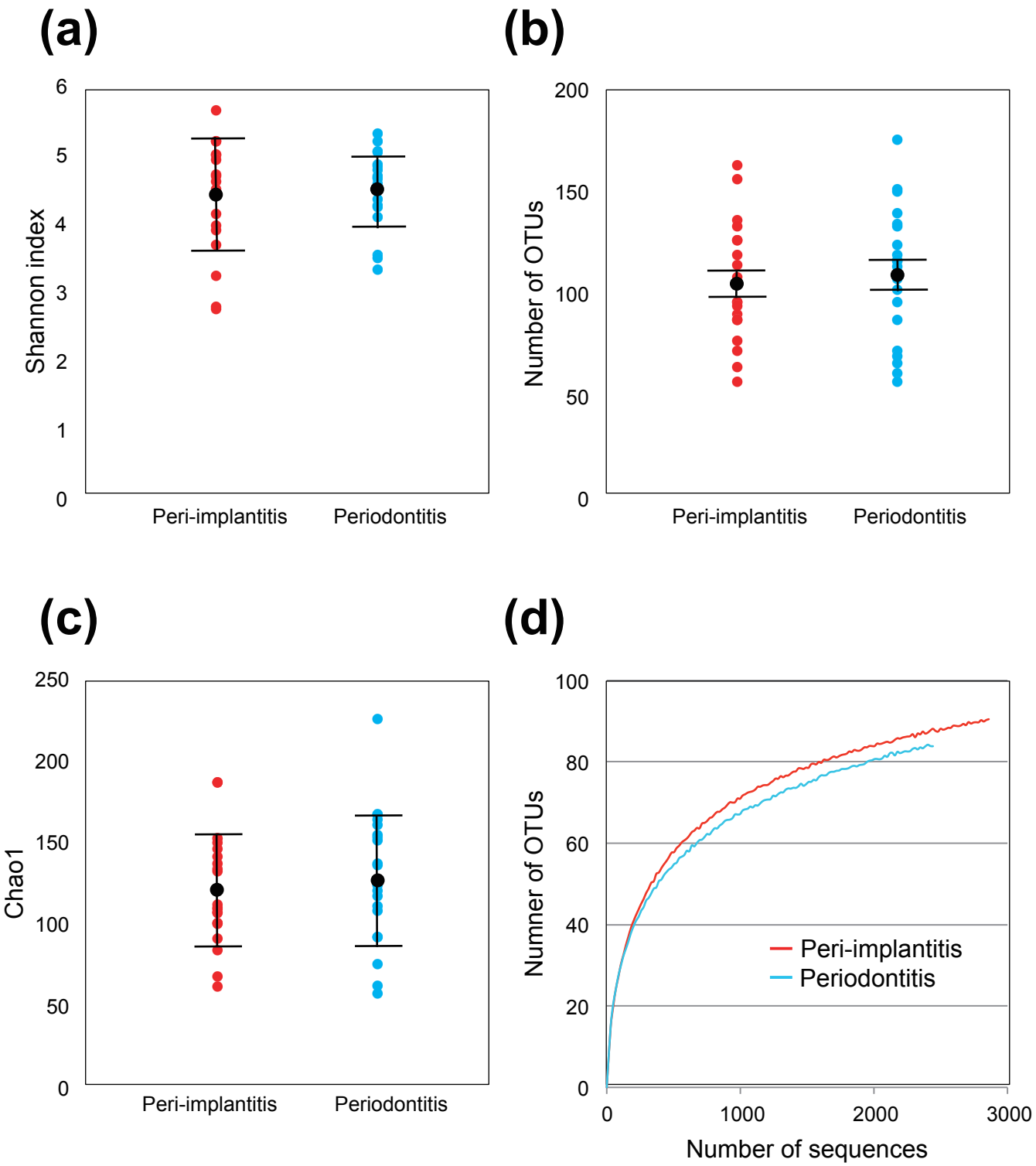
Supplementary Figure S1



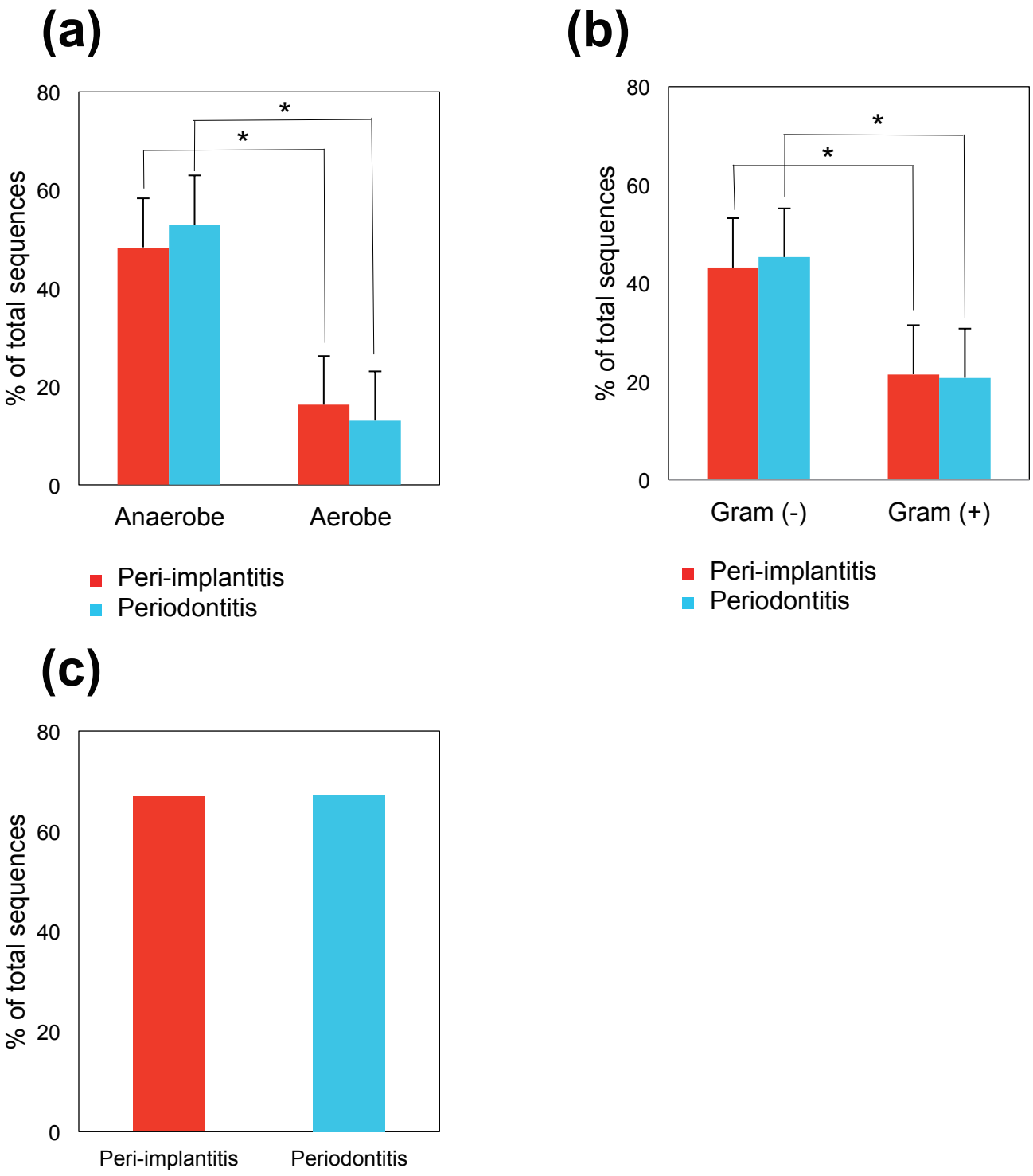
Supplementary Figure S2



Supplementary Figure S3



Supplementary Figure S4



Supplementary Table S1. Number of sequence reads and alpha diversity indexes in each sample.

	Peri-implantitis	Periodontitis	*P* value [a]
Raw reads	12183.5 ± 2408.68	15315.3 ± 1976.41	0.30
Analyzed reads	9508.3 ± 1966.71	12307.7 ± 1688.73	0.26
OTUs	104.8 ± 6.49	109 ± 7.40	0.70
Shannon index	4.41 ± 0.82	4.49 ± 0.54	0.67
Chao1	120.55 ± 34.18	126.40 ± 40.27	0.65

Numbers shown are mean ± s.d.

[a] Statistical differences were calculated using paired t-tests.

Supplementary Table S2. The cultivated status, gram staining and oxygen requirements of the species in each sample.

Microbial characteristics	Peri-implantitis	Periodontitis	*P* value [c]
Cultivated [a]	66.87 ± 3.99	67.25 ± 3.58	0.90
Gram negative [b]	43.16 ± 3.75	45.27 ± 3.48	0.58
Gram positive [b]	21.46 ± 6.49	20.75 ± 2.52	0.79
Anaerobe [b]	48.34 ± 3.27	52.93 ± 3.43	0.28
Aerobe [b]	16.28 ± 3.39	13.09 ± 2.57	0.46

Numbers shown are mean ± s.d.

[a] Bacterial cultivated status are based on HOMD.

[b] Gram stain and oxygen requirement were based on NCBI Entrez Genome Project database.

[c] Statistical differences were calculated using paired t-tests.

Supplementary Table S3. The correlations between clinical parameters and alpha biodiversity indexes or microbial characteristics.

	Peri-implantitis						Periodontitis			
	Smoking	Years [c]	PPD [d]	CAL [e]	Pus	Bone loss	Smoking	PPD [d]	CAL [e]	Bone loss
OTUs	-0.009	-0.089	-0.015	-0.071	-0.044	0.113	-0.057	0.074	0.099	-0.217
Shannon index	0.057	-0.059	-0.046	-0.069	-0.026	0.029	-0.265	-0.197	-0.002	-0.208
Chao 1	0.076	0.041	0.006	-0.023	-0.026	0.115	0.000	0.039	0.039	-0.272
Cultivated [a]	0.246	-0.377	-0.014	-0.012	-0.026	-0.005	0.265	-0.050	-0.065	0.041
Gram negative [b]	0.170	-0.187	0.229	0.191	0.061	0.268	0.000	-0.176	-0.105	-0.009
Gram positive [b]	0.057	-0.217	-0.443	-0.432	-0.218	-0.546	0.170	-0.020	-0.058	0.050
Anaerobe [b]	0.114	0.029	-0.074	-0.144	-0.113	-0.063	0.114	0.074	-0.047	-0.008
Aerobe [b]	0.170	-0.470	-0.201	-0.193	-0.113	-0.250	0.076	-0.400	-0.179	-0.148

Correlations were given as Spearman's rank correlations.

[a] Bacterial cultivated status are based on HOMD.

[b] Gram stain and oxygen requirement are based on NCBI Entrez Genome Project database.

[c] The years of implant placement.

[d] Probing pocket depth.

[e] Clinical attachment loss.

Supplementary Table S4. The species correlated to smoking or years of implant placement.

Species [a]	Peri-implantitis		Periodontitis
	Smoking	Years [b]	Smoking
Actinomyces sp. | HOT-848 |	0.508	0.051	0.508*
Lachnospiraceae [G-1] sp. | HOT-496 |	0.501*	-0.517*	
Oribacterium sp. | HOT-372 |	-0.541*	0.181	-0.021
Peptostreptococcaceae [XI][G-3] sp. | HOT-495 |	-0.269	0.551*	0.238
Selenomonas sp. | HOT-134 |	0.095	0.166	-0.513*
Streptococcus salivarius	0.155	-0.644*	0.099
Streptococcus sanguinis	0.104	-0.588*	0.000

Correlations were given as Spearman's rank correlations.

*P <0.05 and q <0.1.

Blank means no detection of the bacteria.

[a] Species name and HOT (Oral Taxon ID) are based on HOMD.

[b] The years of implant placement.

Supplementary Table S5. The species positively correlated to progression of peri-implantitis or periodontitis.

Taxonomic name [a]	Peri-implantitis				Periodontitis		
	PPD [b]	CAL [c]	Pus	Bone loss	PPD [b]	CAL [c]	Bone loss
Catonella morbi	0.673*	0.597*	0.335	0.546*	0.201	0.203	0.099
Clostridiales [F-1][G-1] sp. | HOT-093 |	0.504*	0.421	0.447*	0.562*	0.048	0.310	-0.078
Eubacterium nodatum	0.441	0.585*	0.549*	0.487*	0.301	0.219	-0.038
Peptococcus sp. | HOT-168 |	0.311	0.529*	0.571*	0.547*	0.179	0.062	-0.207
Treponema sp. | HOT-257 |	0.611*	0.646*	0.447*	0.644*	0.081	0.107	-0.147

Correlations were given as Spearman's rank correlations.

**P* <0.05 and q <0.1.

[a] Species name and HOT (Oral Taxon ID) are based on HOMD.

[b] Probing pocket depth.

[c] Clinical attachment loss.

Supplementary Table S6. The species negatively correlated to progression of peri-implantitis or periodontitis.

Taxonomic name [a]	Peri-implantitis				Periodontitis		
	PPD [b]	CAL [c]	Pus	Bone loss	PPD [b]	CAL [c]	Bone loss
Capnocytophaga gingivalis	-0.551*	-0.471	-0.168	-0.238	0.269	0.362	0.040
Corynebacterium matruchotii	-0.407	-0.502*	-0.413	-0.576*	-0.228	0.021	-0.031
Eubacterium saburreum	-0.696*	-0.758*	-0.644*	-0.661*	0.211	0.065	-0.026
Filifactor alocis	0.364	0.360	0.235	0.336	-0.263	-0.161	-0.560*
Granulicatella adiacens	-0.529*	-0.535*	-0.411	-0.430	-0.043	-0.055	0.119
Leptotrichia wadei	-0.452*	-0.516*	-0.503*	-0.422*	0.141	0.028	0.057
Porphyromonas sp. | HOT-279 |	-0.197	-0.200	-0.086	-0.423	-0.122	-0.176	-0.594*
Propionibacterium acnes	-0.100	-0.161	-0.093	-0.121	-0.531*	-0.464*	-0.338
Selenomonas noxia	-0.624*	-0.619*	-0.395	-0.604*	0.214	0.034	0.014
Solobacterium moorei	-0.488*	-0.502*	-0.449*	-0.337	0.101	-0.070	-0.065
Streptococcus oralis	-0.525*	-0.633*	-0.566*	-0.651*	-0.340	-0.135	0.053
Veillonella parvula	-0.460*	-0.537*	-0.497*	-0.550*	-0.387	-0.436	-0.249

Correlations were given as Spearman's rank correlations.

**P* <0.05 and q <0.1.

[a] Species name and HOT (Oral Taxon ID) are based on HOMD.

Aerobic/facultative bacteria are indicated in bold.

[b] Probing pocket depth

[c] Clinical attachment loss.

Supplementary Table S7. Significantly different bacteria of peri-implantitis compared to those of periodontitis from another studies.

Kumar,P.S. *et al.* 2012 (Periodontitis/Peri-implantitis)			
Low	*P* value [a]	High	*P* value [a]
Prevotella	<0.05	*Treponema*	<0.001
Lactobacillus	<0.05	*Streptococcus mutans*	<0.001
Leptotrichia	<0.01	*Butyrivibrio*	<0.001
Actinomyces	<0.01	*Campylobacter*	<0.05
		Eubacterium	<0.01
		Peptococcus	<0.01
Dabdoub,S.M. *et al.* 2013 (Diseased tooth/Diseased implant)			
Low	*P* value [a]	High	*P* value [a]
Actinomyces meyeri	<0.05	*Staphylococcus pettenkoferi*	<0.05
		Hylemonella spp.	<0.05
		Staphylococcus hominis	<0.05
		Prevotella baroniaer	<0.05
		Streptococcus agalactiae	<0.05
		Atopobium rimaes	<0.05
		Prevotella oralis	<0.05
		Megasphaera elsdenii	<0.05
		Prevotella loescheii	<0.05
		Aggregatibacteraphrophilus	<0.05
		Arthrobacter spp.	<0.05
		Campylobacter sputorum	<0.05
		Streptococcus parasanguinis	<0.05
		Clostridium botulinum	<0.05
		Unclassified Methylobacteriaceae	<0.05
		Neisseria elongata	<0.05

[a] Statistical differences were calculated using paired t-tests.