## Bacterial diversity in saliva and oral health-related conditions: the Hisayama Study

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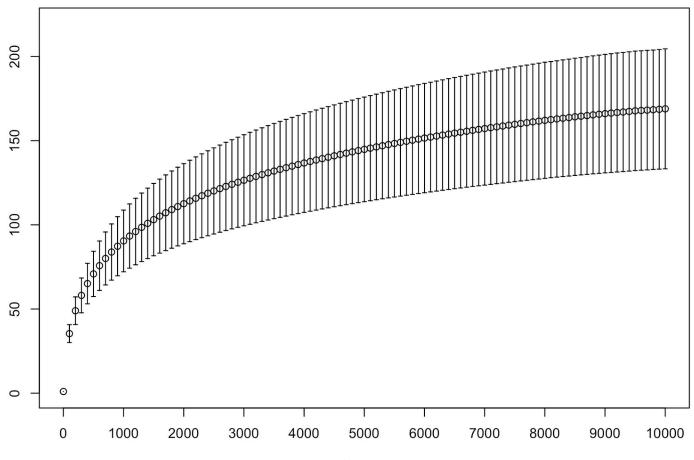
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## Supplemental Figure Legend

Supplemental Figure 1. Rarefaction curves for a number of observed operational taxonomic units (OTUs) per sample. Mean number of observed OTUs almost reached a plateau by 5,000 sequence reads. The error bars indicate the standard deviation.

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Number of observed OTUs per sample



Number of sequence reads

## Supplemental Table

	Community type			core operation	Bacterial phylum	Bacterial species
		Type I	Type II	P value <sup>a</sup>	corresponding to each OTU	corresponding to each OTU
5	OTU1	<b>2.9</b> ± <b>1.7</b>	$1.5 \pm 0.9$	< 0.001	Firmicutes	Veillonella parvula (161)
	OTU2	$0.7 \pm 1.1$	$4.3 \pm 3.6$	< 0.001	Bacteroidetes	Porphyromonas sp. (279)
	OTU3	$2.2 \pm 2.4$	$0.4 \pm 0.6$	< 0.001	Bacteroidetes	Prevotella histicola (298)
	OTU4	$1.0 \pm 1.2$	$0.9 \pm 1.1$	0.009	Bacteroidetes	Alloprevotella sp. (308)
	OTU5	$10.5 \pm 6.7$	$7.1 \pm 4.7$	< 0.001	Bacteroidetes	Prevotella melaninogenica (469)
10	OTU6	$3.2 \pm 1.8$	$1.6 \pm 1.0$	< 0.001	Firmicutes	Veillonella atypica (524)
	OTU7	$3.0 \pm 2.0$	$3.1 \pm 1.9$	0.055	Firmicutes	Granlicatella adiacens (534)
	OTU8	$1.9 \pm 2.9$	$1.0 \pm 1.4$	< 0.001	Actinobacteria	Rothia dentocariosa (587)
	OTU9	$2.7 \pm 3.1$	$15.7 \pm 8.7$	< 0.001	Proteobacteria	Neisseria flavescens (610)
	OTU10	$4.1 \pm 3.2$	$4.7 \pm 3.1$	< 0.001	Firmicutes	Streptococcus mitis (677)
15	OTU11	$10.4\pm8.3$	$7.5 \pm 5.5$	< 0.001	Actinobacteria	Rothia mucilaginosa (681)
	OTU12	$0.9 \pm 1.4$	$\boldsymbol{1.8 \pm 1.8}$	< 0.001	Proteobacteria	Haemophilus parainfluenzae (718)
	OTU13	$\textbf{2.7} \pm \textbf{2.2}$	$0.9\pm0.9$	< 0.001	Firmicutes	Streptococcus parasanguinis (721)
	OTU14	$5.1 \pm 4.3$	$1.6 \pm 1.9$	< 0.001	Firmicutes	Streptococcus salivarius (755)
	OTU15	$1.4 \pm 1.3$	$2.1 \pm 1.5$	< 0.001	Firmicutes	Gemella sanguinis (757)
20	OTU16	$1.8\pm2.6$	$1.0 \pm 1.6$	< 0.001	Actinobacteria	Actinomyces graevenitzii (866)
	OTU17	$0.8 \pm 1.0$	$1.3 \pm 1.1$	< 0.001	Firmicutes	Genus Streptococcus
	OTU18	$1.0 \pm 1.3$	$2.1 \pm 1.6$	< 0.001	Firmicutes	Genus Streptococcus
	OTU19	$\textbf{3.7} \pm \textbf{3.3}$	$3.0 \pm 2.8$	< 0.001	Actinobacteria	Genus Actinomyces
	OTU20	$\textbf{2.0} \pm \textbf{2.4}$	$0.3 \pm 0.5$	< 0.001	Bacteroidetes	Genus Prevotella
25	OTU21	$3.5 \pm 3.1$	$\textbf{3.8} \pm \textbf{3.0}$	0.020	Firmicutes	Genus Streptococcus
	OTU22	$\textbf{2.6} \pm \textbf{2.4}$	$0.9 \pm 1.0$	< 0.001	Firmicutes	Genus Streptococcus

Table S1. Relative abundances of 22 dominant core operational taxonomic units (OTUs) in each community type.

<sup>a</sup>Significant differences between two community types were evaluated by using Student's t-test. The values that were significantly higher than the other community are shown in boldface.