

## **Impact of Oral Hygiene Discontinuation on Supragingival and Salivary Microbiomes**

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### **Appendix**

**Appendix Table 1. Background and oral characteristics of the cohort**

<b>Gender (M/F)*</b>	5/24 (17%/83%)
<b>Age**</b>	24.7 (22-29)
<b>Number of teeth**</b>	27.8 (24-28)
<b>DMFT**</b>	1.7 (0-7)
<b>DT**</b>	0.0 (0-0)
<b>DMFS**</b>	2.4 (0-12)
<b>DS**</b>	0.0 (0-0)

DMFT: Decayed-missed-filled-teeth

DT: Decayed-teeth

DMFS: Decayed-missed-filled-surfaces

DS: Decayed-surfaces

\*: Gender expressed as number and percentage of the cohort

\*\*: Parameters expressed as mean and range

**Appendix Table 2. Species level abundance of supragingival microbiota.** Mean relative abundance of bacterial species in pooled supragingival sample, which were influenced by oral hygiene discontinuation. Relative abundance in baseline samples (n=29) was compared to relative abundance in samples collected at day 4 (n=29), day 7 (n=29) and day 10 (n=29) after discontinuation of oral hygiene and 14 days (n=29) after reuptake of oral hygiene. \*: relative abundance significantly different from baseline levels (adjusted p-value <0.01).

Species name	Baseline	Day 4	Day 7	Day 10	Day 24
<i>Abiotrophia_defectiva</i>	0.1245%	0.1901%	0.3412%*	0.4763%*	0.3219%*
<i>Actinobaculum_sp_HOT_183</i>	0.0516%	0.0823%	0.1543%*	0.1208%	0.1965%*
<i>Actinomyces_graevenitzii</i>	0.0187%	0.0021%	0.0001%*	0.0004%*	0.0004%*
<i>Actinomyces_johnsonii</i>	0.0060%	0.0242%*	0.0101%	0.0345%*	0.0680%*
<i>Actinomyces_lingnae</i>	0.0400%	0.0104%	0.0035%*	0.0050%*	0.0019%*
<i>Actinomyces_massiliensis</i>	0.0300%	0.1060%*	0.0449%	0.0586%	0.0744%*
<i>Actinomyces_naeslundii</i>	0.0223%	0.0028%*	0.0020%*	0.0160%	0.0010%*
<i>Actinomyces_sp_HOT_170</i>	0.0104%	0.0324%*	0.0066%	0.0396%*	0.0333%*
<i>Actinomyces_sp_HOT_171</i>	0.0143%	0.0342%	0.0138%	0.0518%*	0.0305%
<i>Actinomyces_sp_HOT_172</i>	0.0143%	0.0342%	0.0138%	0.0518%*	0.0305%
<i>Alloprevotella_sp_HOT_308</i>	0.0113%	0.0017%*	0.0008%*	0.0014%*	0.0009%*
<i>Alloprevotella_sp_HOT_914</i>	0.1887%	0.0989%	0.0505%*	0.0511%*	0.0623%*
<i>Atopobium_parvulum</i>	0.0109%	0.0012%*	0.0001%*	0.0002%*	0.0002%*
<i>Atopobium_rimae</i>	0.0052%	0.0108%*	0.0010%*	0.0045%	0.0036%
<i>Butyrivibrio_sp_HOT_455</i>	0.0082%	0.0063%	0.0002%*	0.0000%*	0.0001%*
<i>Campylobacter_gracilis</i>	0.2688%	0.4099%*	0.4535%*	0.4146%*	0.5479%*
<i>Capnocytophaga_leadbetteri</i>	0.2460%	0.7850%*	0.7656%*	0.5916%*	0.3886%

<i>Capnocytophaga_sputigena</i>	0.1839%	0.6556%*	0.8539%*	0.7152%*	0.3751%
<i>Cardiobacterium_hominis</i>	0.1944%	0.5966%*	0.3613%	0.6466%*	0.4523%
<i>Cardiobacterium_valvarum</i>	0.0753%	0.1914%	0.2271%*	0.3107%*	0.1801%
<i>Catonella_morbi</i>	0.0879%	0.0228%	0.0008%*	0.0010%*	0.0010%*
<i>Centipeda_periodontii</i>	0.0119%	0.0435%*	0.0535%*	0.0611%*	0.0537%*
<i>Corynebacterium_matruchotii</i>	2.4006%	3.9712%	4.6308%*	4.5963%*	5.9270%*
<i>Eikenella_corrodens</i>	0.0730%	0.2121%*	0.1800%*	0.2239%*	0.1767%*
<i>Filifactor_alocis</i>	0.0011%	0.0001%*	0.0021%	0.0000%*	0.0016%
<i>Fusobacterium_periodonticum</i>	1.9247%	0.9288%*	0.6225%*	0.5221%*	0.3708%*
<i>Fusobacterium_sp_HOT_205</i>	0.0050%	0.0089%	0.0105%*	0.0109%*	0.0072%
<i>Gemella_haemolysans</i>	0.7513%	0.3571%	0.1567%*	0.1797%*	0.1844%*
<i>Gemella_morbillorum</i>	0.1236%	0.8410%*	0.3678%	0.9225%*	0.4638%
<i>Gemella_sanguinis</i>	0.5813%	0.1239%	0.0102%*	0.0078%*	0.0138%*
<i>Granulicatella_adiacens</i>	1.0356%	0.3945%*	0.3466%*	0.2933%*	0.5662%
<i>Haemophilus_parainfluenzae</i>	3.3378%	2.0639%*	1.5277%*	1.0401%*	1.5851%*
<i>Haemophilus_pittmaniae</i>	0.2362%	0.0679%	0.0039%*	0.0118%*	0.0131%*
<i>Lachnospiraceae[G-2]_sp_HOT_088</i>	0.0048%	0.0162%	0.0327%*	0.0353%*	0.0281%*
<i>Lachnospiraceae[G-3]_sp_HOT_100</i>	0.0005%	0.0016%	0.0039%*	0.0044%*	0.0029%*
<i>Lachnospiraceae[G-8]_sp_HOT_500</i>	0.0029%	0.0031%	0.0014%	0.0001%*	0.0029%
<i>Leptotrichia_goodfellowii</i>	0.0231%	0.0897%*	0.0611%	0.0469%	0.0965%*
<i>Leptotrichia_hongkongensis</i>	1.4553%	2.7461%*	3.3706%*	2.8815%*	4.0651%*
<i>Leptotrichia_shahii</i>	0.2877%	0.7174%*	1.6828%*	0.7520%*	1.7520%*
<i>Leptotrichia_sp_HOT_212</i>	0.4368%	2.0767%*	2.2239%*	2.2951%*	1.0500%
<i>Leptotrichia_sp_HOT_215</i>	0.3664%	0.5921%*	0.5370%*	0.3926%	0.1794%

<i>Leptotrichia_sp_HOT_223</i>	0.1624%	0.1005%	0.1544%	0.2972%	0.2823%
			*	*	
<i>Leptotrichia_sp_HOT_392</i>	0.1996%	0.7335%*	1.1502%	0.8745%	0.7566%
		*	*	*	*
<i>Megasphaera_micronuciformis</i>	0.0692%	0.0292%	0.0075%	0.0047%	0.0095%
		*	*	*	*
<i>Neisseria_flavescens</i>	2.3918%	0.9649%*	0.2091%	0.2003%	0.0707%
		*	*	*	*
<i>Oribacterium_asaccharolyticum</i>	0.0259%	0.0086%*	0.0018%	0.0014%	0.0017%
		*	*	*	*
<i>Oribacterium_parvum</i>	0.0724%	0.0111%	0.0002%	0.0007%	0.0001%
<i>Oribacterium_sinus</i>	0.1742%	0.0374%	0.0057%	0.0035%	0.0065%
		*	*	*	*
<i>Peptostreptococcaceae[XI][G-1][Eubacterium]_sulci</i>	0.0411%	0.0082%	0.0015%	0.0052%	0.0010%
		*	*	*	*
<i>Peptostreptococcaceae[XI][G-2]_sp_HOT_091</i>	0.0021%	0.0016%	0.0000%	0.0000%	0.0000%
		*	*	*	*
<i>Peptostreptococcus_stomatis</i>	0.0831%	0.0285%	0.0251%	0.0120%	0.0189%
			*	*	*
<i>Prevotella_melaninogenica</i>	5.0461%	1.4787%*	0.7389%	0.8553%	0.9571%
		*	*	*	*
<i>Prevotella_nanceiensis</i>	0.7485%	0.2441%	0.0605%	0.0200%	0.0223%
		*	*	*	*
<i>Prevotella_pallens</i>	0.2749%	0.2474%	0.0367%	0.2019%	0.0246%
		*		*	
<i>Prevotella_scopos</i>	0.2344%	0.0251%	0.0001%	0.0005%	0.0002%
		*	*	*	*
<i>Prevotella_shahii</i>	0.0394%	0.0085%	0.0002%	0.0003%	0.0001%
		*	*	*	*
<i>Prevotella_sp_HOT_305</i>	0.0033%	0.0038%	0.0002%	0.0002%	0.0000%
		*	*	*	*
<i>Prevotella_sp_HOT_396</i>	0.0046%	0.0021%	0.0007%	0.0032%	0.0002%
		*		*	
<i>Prevotella_sp_HOT_472</i>	0.0903%	0.3418%*	0.2770%	0.2895%	0.3087%
		*	*	*	*
<i>Prevotella_veroralis</i>	0.0431%	0.0595%	0.0068%	0.0030%	0.0074%
		*	*	*	*
<i>Propionibacterium_propionicum</i>	0.0000%	0.0007%	0.0003%	0.0013%	0.0244%
					*
<i>Propionibacterium_sp_HOT_194</i>	0.0001%	0.0003%	0.0003%	0.0004%	0.0082%
					*
<i>Rothia_dentocariosa</i>	2.2201%	0.5157%*	0.3046%	0.3484%	0.5322%
		*	*	*	*
<i>Rothia_mucilaginosa</i>	2.9438%	0.5958%*	0.0189%	0.0216%	0.0392%
		*	*	*	*
<i>Selenomonas_dianae</i>	0.0140%	0.0262%	0.0319%	0.0491%	0.0334%
				*	

<i>Selenomonas_flueggei</i>	0.0016%	0.0273%*	0.0380%*	0.0301%*	0.0163%*
<i>Selenomonas_sp_HOT_137</i>	0.0008%	0.0007%	0.0017%*	0.0008%	0.0018%*
<i>Stomatobaculum_sp_HOT_097</i>	0.0911%	0.0348%	0.0074%	0.0179%*	0.0066%
<i>Tannerella_sp_HOT_286</i>	0.2752%	0.7475%*	0.6919%*	0.8474%*	0.7057%*
<i>TM7[G-1]_sp_HOT_352</i>	0.1115%	0.0514%	0.0074%*	0.0133%	0.0041%*
<i>TM7[G-1]_sp_HOT_952</i>	0.0276%	0.2077%*	0.2556%*	0.2450%*	0.3219%*
<i>Treponema_denticola</i>	0.0013%	0.0003%*	0.0018%	0.0000%*	0.0107%*
<i>Veillonella_atypica</i>	0.2874%	0.0862%	0.0175%*	0.0074%*	0.0200%*
<i>Veillonella_denticariosi</i>	0.0578%	0.0060%*	0.0022%*	0.0001%*	0.0011%*
<i>Veillonella_rogosae</i>	0.4170%	0.0854%*	0.0103%*	0.0083%*	0.0120%*

**Appendix Table 3. Species level abundance of salivary microbiota.** Mean relative abundance of bacterial species in saliva samples, which were influenced by oral hygiene discontinuation. Relative abundance in baseline samples (n=29) was compared to relative abundance in samples collected at day 4 (n=29), day 7 (n=29) and day 10 (n=29) after discontinuation of oral hygiene and 14 days (n=29) after reuptake of oral hygiene. \*: relative abundance significantly different from baseline levels (adjusted p-value <0.01).

Species name	Baseline	Day 4	Day 7	Day 10	Day 24
<i>Atopobium_parvulum</i>	0.06%	0.03%	0.01%*	0.05%	0.07%
<i>Bacteroidetes[G-5]_sp_HOT_507</i>	0.00%	0.00%	0.00%	0.39%*	0.11%*
<i>Capnocytophaga_gingivalis</i>	0.01%	0.06%*	0.07%*	0.06%*	0.01%
<i>Capnocytophaga_granulosa</i>	0.00%	0.03%	0.07%*	0.04%	0.01%
<i>Capnocytophaga_leadbetteri</i>	0.02%	0.09%*	0.15%*	0.08%	0.03%
<i>Capnocytophaga_sputigena</i>	0.02%	0.19%*	0.13%*	0.17%*	0.02%
<i>Cardiobacterium_hominis</i>	0.04%	0.14%*	0.30%*	0.13%*	0.03%
<i>Cardiobacterium_valvarum</i>	0.01%	0.03%	0.16%*	0.06%	0.01%
<i>Eikenella_corrodens</i>	0.02%	0.08%*	0.08%*	0.05%	0.02%
<i>Kingella_oralis</i>	0.03%	0.13%	0.64%*	0.12%	0.03%
<i>Leptotrichia_sp_HOT_212</i>	0.07%	0.17%	0.72%*	0.38%*	0.13%
<i>Rothia_mucilaginosa</i>	6.54%	4.52%	2.43%*	4.66%	5.14%