**Supplementary Digital Content 3.** The biodiversity of nasopharyngeal and saliva microbiomes during the study, the mean number of amplicon sequence variants (ASVs) and the changes in the mean relative abundances (%) in the microbiome at the phylum level, according to HOMD (Human Oral Microbiome Database) taxonomy classification. The relative abundances do not indicate the absolute bacterial counts. None of the differences was statistically significant with a Bonferroni correction significance level adjusted for the multiple comparisons.

**Outcome *S. salivarius* K12 Control 95 % CI of the difference**

***Nasopharyngeal microbiome***

**At study entry**

Relative abundance of main phyla, Mean % (SD)

Actinobacteria 8.3 (16) 14 (23) -4.1 to 16

Bacteroidetes 9.3 (15) 3.6 (4.1) -9.9 to -1.6

Firmicutes 56 (29) 58 (27) -12 to 15

Fusobacteria 0.4 (1.1) 0.4 (0.8) -0.5 to 0.4

Proteobacteria 25 (30) 24 (22) -14 to 12

Diversity, Mean (SD)

Observed ASVs 24 (13) 21 (9.2) -9.5 to 1.4

Shannon’s index 2.6 (1.1) 2.4 (1.0) -0.7 to 0.3

Faith’s index 2.6 (1.1) 2.3 (0.8) -0.7 to 0.2

**At one month (after intervention)**

Relative abundance of main phyla, Mean % (SD)

Actinobacteria 8.3 (16) 10 (18) -7.4 to 11

Bacteroidetes 8.2 (12) 2.5 (3.4) -9.9 to -1.7

Firmicutes 56 (28) 51 (35) -22 to 11

Fusobacteria 0.5 (1.2) 0.2 (0.4) -0.8 to 0.1

Proteobacteria 25 (30) 35 (38) -7.5 to 28

Diversity, Mean (SD)

Observed ASVs 23 (12) 19 (11) -9.7 to 3.1

Shannon’s index 2.7 (1.2) 2.1 (1.2) -1.2 to 0.1

Faith’s index 2.4 (1.1) 2.2 (1.1) -0.8 to 0.4

**At two months (one month after stopping intervention)**

Relative abundance of main phyla, Mean % (SD)

Actinobacteria 9.5 (14) 3.0 (3.7) -12 to -1.4

Bacteroidetes 6.4 (10) 7.9 (15) -5.9 to 9.0

Firmicutes 54 (29) 44 (35) -29 to 9.9

Fusobacteria 0.3 (0.6) 0.7 (1.2) -0.4 to 1.1

Proteobacteria 29 (30) 44 (37) -6.1 to 35

Diversity, Mean (SD)

Observed ASVs 25 (11) 28 (12) -3.7 to 10

Shannon’s index 2.6 (1.1) 2.4 (1.3) -0.9 to 0.6

Faith’s index 2.7 (1.0) 2.7 (0.9) -0.6 to 0.7

***Saliva microbiome***

**At study entry**

Relative abundance of main phyla, Mean % (SD)

Bacteroidetes 28 (12) 26 (13) -6.9 to 3.3

Firmicutes 52 (15) 54 (15) -4.0 to 8.6

Fusobacteria 4.2 (3.7) 3.8 (2.7) -1.7 to 0.9

Proteobacteria 14 (9.9) 14 (8.4) -4.1 to 3.7

Diversity, Mean (SD)

Observed ASVs 44 (13) 48 (15) -1.2 to 9.9

Shannon’s index 4.0 (0.6) 4.2 (0.6) -0.1 to 0.4

Faith’s index 4.0 (0.8) 4.2 (0.8) -0.1 to 0.5

**At one month (after intervention)**

Relative abundance of main phyla, Mean % (SD)

Bacteroidetes 20 (12) 24 (12) -2.0 to 9.0

Firmicutes 61 (18) 58 (16) -11 to 4.6

Fusobacteria 2.8 (4.8) 2.8 (2.5) -1.8 to 1.9

Proteobacteria 13 (11) 14 (8.8) -4.1 to 5.2

Diversity, Mean (SD)

Observed ASVs 37 (14) 39 (14) -3.7 to 8.9

Shannon’s index 3.8 (0.6) 3.9 (0.5) -0.1 to 0.4

Faith’s index 3.6 (0.9) 3.7 (0.9) -0.3 to 0.5

**At two months (one month after stopping intervention)**

Relative abundance of main phyla, Mean % (SD)

Bacteroidetes 23 (12) 27 (14) -2.1 to 10

Firmicutes 57 (15) 54 (15) -11 to 3.8

Fusobacteria2.8 (2.5) 3.7 (3.2) -0.4 to 2.2

Proteobacteria 16 (14) 14 (7.3) -7.7 to 4.1

Diversity, Mean (SD)

Observed ASVs 39 (13) 43 (13) -2.0 to 10

Shannon’s index 3.8 (0.6) 3.9 (0.7) -0.2 to 0.5

Faith’s index 3.7 (0.7) 3.8 (0.7) -0.2 to 0.5

SD standard deviation