

Table S1. Comparison between the Relative abundance (%) in oral microbiota of Normo-weighted subjects (NWS 20<BMI<25 (n=9) and Obese subjects (OS) BMI>30 (n=10). Data as mean \pm SD, *p<0.05, **p< 0.001, *p< 0.0001 unpaired Mann-Whitney test. Significant p-values have been highlighted in bold.**

Relative abundance (%) in oral microbiota	Microbiota parameters	Normo-weighted subjects (NWS) 20<BMI<25 (n=9)	Obese subjects (OS) BMI>30 (n=10)	p-value
	α -diversity by the Shannon index	1.64 \pm 0.80	1.81 \pm 0.78	0.53
	α -diversity by the Chao 1 index	30.94 \pm 14.16	32.93 \pm 10.45	0.93
Phylum	Actinobacteria	9.77 \pm 18.70	6.41 \pm 2.83	0.15
	Bacteroidetes	15.42 \pm 16.51	18.25 \pm 12.66	0.83
	Epsilonbacteraeota	1.04 \pm 1.21	0.70 \pm 0.73	0.71
	Firmicutes	23.42 \pm 14.64	29.90 \pm 21.27	0.44
	Fusobacteria	6.50 \pm 6.16	6.28 \pm 5.88	0.90
	Patescibacteria	0.16 \pm 0.34	0.12 \pm 0.17	0.43
	Proteobacteria	43.41 \pm 37.59	38.01 \pm 32.76	0.96
	Spirochaetes	0.07 \pm 0.13	0.22 \pm 0.66	0.32
	Tenericutes	0.20 \pm 0.41	0.09 \pm 0.15	0.89
Class	Actinobacteria	9.41 \pm 18.76	6.08 \pm 3.01	0.27
	Alphaproteobacteria	1.83 \pm 5.49	0.03 \pm 0.08	0.35
	Bacilli	19.19 \pm 12.64	27.55 \pm 19.85	0.27
	Bacteroidia	15.42 \pm 16.51	18.25 \pm 12.66	0.83
	Campylobacteria	1.04 \pm 1.21	0.70 \pm 0.73	0.71
	Clostridia	3.95 \pm 4.47	2.17 \pm 2.63	0.65
	Coriobacteriia	0.36 \pm 0.81	0.33 \pm 0.40	0.30
	Fusobacteriia	6.50 \pm 6.16	6.28 \pm 5.88	0.90
	Gammaproteobacteria	41.57 \pm 36.08	37.96 \pm 32.75	0.96
	Gracilibacteria	0.15 \pm 0.34	0.11 \pm 0.16	0.42
	Mollicutes	0.20 \pm 0.41	0.09 \pm 0.15	0.89
	Negativicutes	0.28 \pm 0.60	0.19 \pm 0.21	0.71
	Spirochaetia	0.07 \pm 0.13	0.22 \pm 0.66	0.32
Order	Absconditabacteriales (SR1)	0.15 \pm 0.34	0.11 \pm 0.16	0.42
	Actinomycetales	1.14 \pm 1.67	2.05 \pm 2.02	0.23
	Bacillales	4.49 \pm 6.89	1.99 \pm 1.96	0.90
	Bacteroidales	15.06 \pm 16.26	15.62 \pm 11.84	0.90
	Betaproteobacteriales	34.48 \pm 35.85	33.26 \pm 33.83	0.84
	Campylobacteriales	1.04 \pm 1.21	0.70 \pm 0.73	0.71
	Caulobacteriales	1.63 \pm 4.89	0.01 \pm 0.02	0.35
	Clostridiales	3.95 \pm 4.47	2.17 \pm 2.63	0.65
	Coriobacteriales	0.36 \pm 0.81	0.33 \pm 0.40	0.30
	Corynebacteriales	0.05 \pm 0.07	0.30 \pm 0.43	0.17
	Flavobacteriales	0.30 \pm 0.31	2.62 \pm 3.20	*0.03
	Fusobacteriales	6.50 \pm 6.16	6.28 \pm 5.88	0.90

	Lactobacillales	14.70 ± 10.16	25.56 ± 18.42	0.18
	Micrococcales	8.21 ± 18.56	3.72 ± 2.31	0.35
	Mycoplasmatales	0.16 ± 0.29	0.09 ± 0.15	0.89
	Pasteurellales	2.53 ± 2.65	4.59 ± 4.43	0.27
	Pseudomonadales	4.55 ± 13.59	0.04 ± 0.08	0.49
	Rhizobiales	0.20 ± 0.59	0 ± 0	0.34
	Selenomonadales	0.28 ± 0.60	0.19 ± 0.21	0.71
	Spirochaetales	0.07 ± 0.13	0.22 ± 0.66	0.32
Family	Actinomycetaceae	1.14 ± 1.67	2.05 ± 2.02	0.23
	Aerococcaceae	0.02 ± 0.04	0.61 ± 1.35	0.05
	Atopobiaceae	0.36 ± 0.81	0.31 ± 0.38	0.30
	Bacteroidaceae	0.15 ± 0.43	0 ± 0	0.34
	Burkholderiaceae	0.10 ± 0.16	0.85 ± 1.94	0.08
	Campylobacteraceae	1.03 ± 1.21	0.70 ± 0.73	0.71
	Caulobacteraceae	1.63 ± 4.89	0.01 ± 0.02	0.35
	Corynebacteriaceae	0.05 ± 0.07	0.29 ± 0.42	0.17
	Family XI	1.36 ± 1.30	2.18 ± 2.09	0.30
	Family XIII	0.67 ± 1.06	0.21 ± 0.35	0.77
	Flavobacteriaceae	0.27 ± 0.29	2.47 ± 3.02	*0.04
	Fusobacteriaceae	4.67 ± 3.78	3.60 ± 3.94	0.77
	Lachnospiraceae	1.32 ± 1.53	0.99 ± 1.25	0.90
	Lactobacillaceae	0.37 ± 1.07	0.02 ± 0.05	0.64
	Leptotrichiaceae	1.83 ± 3.42	2.68 ± 2.71	0.23
	Micrococcaceae	8.15 ± 18.40	3.72 ± 2.31	0.35
	Moraxellaceae	4.53 ± 13.59	0.03 ± 0.08	0.86
	Multi-affiliation	1.17 ± 0.98	2.59 ± 1.79	*0.04
	Mycoplasmataceae	0.16 ± 0.29	0.09 ± 0.15	0.89
	Neisseriaceae	34.39 ± 35.87	32.41 ± 34.11	0.96
	Pasteurellaceae	2.53 ± 2.65	4.59 ± 4.43	0.27
	Peptostreptococcaceae	0.96 ± 1.47	0.59 ± 0.92	0.77
	Porphyromonadaceae	3.99 ± 6.58	6.04 ± 5.85	0.38
	Prevotellaceae	10.13 ± 12.29	8.94 ± 9.19	0.96
	Rhizobiaceae	0.20 ± 0.59	0 ± 0	0.34
	Rikenellaceae	0.23 ± 0.58	0.04 ± 0.08	0.96
	Ruminococcaceae	0.66 ± 0.97	0.16 ± 0.20	0.30
	Spirochaetaceae	0.07 ± 0.13	0.22 ± 0.66	0.32
	Staphylococcaceae	3.35 ± 7.28	0.009 ± 0.02	0.57
	Streptococcaceae	13.14 ± 9.83	22.34 ± 17.13	0.24
	Tannerellaceae	0.22 ± 0.26	0.50 ± 1.05	0.96
	Unknown	0.24 ± 0.34	0.16 ± 0.16	0.83
	Veillonellaceae	0.28 ± 0.60	0.19 ± 0.21	0.71
Genus	<i>Abiotrophia</i>	0.02 ± 0.04	0.61 ± 1.35	0.05
	<i>Acinetobacter</i>	4.53 ± 13.59	0 ± 0	0.14
	<i>Actinobacillus</i>	0.04 ± 0.13	0.37 ± 0.69	0.18
	<i>Actinomyces</i>	1.14 ± 1.67	2.05 ± 2.02	0.23

	<i>Aggregatibacter</i>	0.14 ± 0.25	0.78 ± 1.56	0.23
	<i>Alloprevotella</i>	1.49 ± 2.43	0.66 ± 0.82	0.77
	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium</i>	0.20 ± 0.59	0 ± 0	0.34
	<i>Atopobium</i>	0.36 ± 0.82	0.31 ± 0.38	0.30
	<i>Bacteroides</i>	0.15 ± 0.44	0 ± 0	0.34
	<i>Bergeyella</i>	0.03 ± 0.03	0.15 ± 0.24	0.18
	<i>Brevundimonas</i>	1.63 ± 4.89	0 ± 0	0.34
	<i>Campylobacter</i>	1.04 ± 1.21	0.70 ± 0.73	0.71
	<i>Capnocytophaga</i>	0.27 ± 0.29	2.47 ± 3.02	*0.04
	<i>Catonella</i>	0.22 ± 0.26	0.09 ± 0.10	0.56
	<i>Corynebacterium</i>	0.05 ± 0.07	0.29 ± 0.43	0.17
	<i>Dialister</i>	0.28 ± 0.59	0.18 ± 0.20	0.80
	<i>F0058</i>	0.11 ± 0.16	0.06 ± 0.09	0.70
	<i>Filifactor</i>	0.82 ± 1.40	0.51 ± 0.94	0.90
	<i>Fusobacterium</i>	4.67 ± 3.79	3.60 ± 3.94	0.77
	<i>Gemella</i>	1.14 ± 1.20	1.98 ± 1.97	0.20
	<i>Haemophilus</i>	2.35 ± 2.43	3.45 ± 3.02	0.34
	<i>Kingella</i>	0.06 ± 0.09	0.43 ± 0.99	0.24
	<i>Lachnoanaerobaculum</i>	0.27 ± 0.50	0.17 ± 0.17	0.86
	<i>Lactobacillus</i>	0.37 ± 1.07	0.02 ± 0.05	0.64
	<i>Lautropia</i>	0.08 ± 0.14	0.78 ± 1.85	0.21
	<i>Leptotrichia</i>	1.77 ± 3.44	2.66 ± 2.72	0.26
	<i>Multi-affiliation</i>	1.17 ± 0.98	2.59 ± 1.79	*0.04
	<i>Mycoplasma</i>	0.16 ± 0.29	0.09 ± 0.15	0.89
	<i>Neisseria</i>	34.31 ± 35.90	31.90 ± 34.47	0.96
	<i>Oribacterium</i>	0.28 ± 0.38	0.31 ± 0.30	0.74
	<i>Parvimonas</i>	0.22 ± 0.26	0.20 ± 0.30	0.90
	<i>Peptostreptococcus</i>	0.12 ± 0.13	0.02 ± 0.02	0.10
	<i>Porphyromonas</i>	4.00 ± 6.58	6.04 ± 5.85	0.38
	<i>Prevotella</i>	1.61 ± 2.02	1.46 ± 1.35	0.83
	<i>Prevotella 2</i>	0.08 ± 0.12	0.15 ± 0.17	0.30
	<i>Prevotella 6</i>	0.47 ± 0.81	0.42 ± 0.53	0.96
	<i>"Prevotella 7"</i>	6.23 ± 8.71	6.25 ± 7.20	0.96
	<i>Rikenellaceae RC9 gut group</i>	0.23 ± 0.58	0.04 ± 0.08	0.96
	<i>Rothia</i>	8.15 ± 18.40	3.69 ± 2.32	0.35
	<i>Ruminococcaceae UCG-014</i>	0.66 ± 0.97	0.16 ± 0.20	0.30
	<i>Staphylococcus</i>	3.35 ± 7.28	0.009 ± 0.02	0.57
	<i>Stomatobaculum</i>	0.43 ± 0.58	0.33 ± 0.70	0.93
	<i>Streptococcus</i>	13.09 ± 9.81	22.34 ± 17.13	0.24
	<i>Tannerella</i>	0.22 ± 0.26	0.50 ± 1.05	0.96
	<i>Treponema 2</i>	0.07 ± 0.13	0.22 ± 0.66	0.32
	<i>Unknown</i>	0.63 ± 0.72	0.25 ± 0.20	0.66
	<i>[Eubacterium] brachy group</i>	0.14 ± 0.30	0.05 ± 0.09	0.74
	<i>[Eubacterium] nodatum group</i>	0.28 ± 0.53	0.08 ± 0.13	0.64

Table S2: Comparison between the Relative abundance (%) in oral microbiota of Obese males (OM) BMI>30 (n=5) and Obese females (OF) BMI>30 (n=5). Data as mean \pm SD, *p<0.05, **p< 0.001, *p< 0.0001 unpaired Mann-Whitney test. Significant p-values have been highlighted in bold.**

Relative abundance (%) in oral microbiota	Microbiota parameters	Obese males (OM) BMI>30 (n=5)	Obese females (OF) BMI>30 (n=5)	p-value
	α -diversity by the Shannon index	1.36 \pm 0.89	1.26 \pm 0.27	0.09
	α -diversity by the Chao 1 index	26.41 \pm 11.21	39.45 \pm 3.74	*0.03
Phylum	Actinobacteria	5.59 \pm 2.71	7.23 \pm 2.99	0.31
	Bacteroidetes	12.35 \pm 12.71	24.16 \pm 10.57	0.09
	Epsilonbacteraeota	0.32 \pm 0.47	1.08 \pm 0.80	0.09
	Firmicutes	13.82 \pm 11.71	45.98 \pm 15.32	**0.007
	Fusobacteria	4.42 \pm 6.43	8.14 \pm 5.27	0.29
	Patescibacteria	0.18 \pm 0.23	0.07 \pm 0.05	0.99
	Proteobacteria	63.31 \pm 25.87	12.72 \pm 12.05	**0.007
	Spirochaetes	0 \pm 0	0.45 \pm 0.93	*0.02
	Tenericutes	0.01 \pm 0.02	0.18 \pm 0.19	0.07
Class	Actinobacteria	5.44 \pm 2.73	6.72 \pm 3.46	0.42
	Bacilli	12.99 \pm 11.35	42.11 \pm 15.10	*0.03
	Bacteroidia	12.35 \pm 12.71	24.16 \pm 10.57	0.09
	Campylobacteria	0.32 \pm 0.47	1.08 \pm 0.80	0.09
	Clostridia	0.82 \pm 0.95	3.52 \pm 3.18	0.09
	Coriobacteriia	0.15 \pm 0.20	0.51 \pm 0.48	0.29
	Fusobacteriia	4.42 \pm 6.43	8.14 \pm 5.27	0.29
	Gammaproteobacteria	63.28 \pm 25.82	12.66 \pm 12.09	**0.008
	Gracilibacteria	0.17 \pm 0.22	0.06 \pm 0.05	0.83
	Mollicutes	0.01 \pm 0.02	0.18 \pm 0.19	0.06
	Negativicutes	0.02 \pm 0.02	0.36 \pm 0.16	*0.01
	Spirochaetia	0 \pm 0	0.45 \pm 0.93	*0.02
Order	Absconditabacteriales (SR1)	0.17 \pm 0.22	0.06 \pm 0.05	0.83
	Actinomycetales	0.73 \pm 0.62	3.38 \pm 2.10	*0.05
	Bacillales	0.92 \pm 0.89	3.05 \pm 2.24	0.15
	Bacteroidales	11.17 \pm 11.31	20.07 \pm 11.74	0.14
	Betaproteobacteriales	58.54 \pm 30.30	7.99 \pm 7.75	**0.008
	Campylobacteriales	0.32 \pm 0.47	1.08 \pm 0.80	0.09
	Cardiobacteriales	0.005 \pm 0.007	0.11 \pm 0.14	*0.01
	Clostridiales	0.82 \pm 0.95	3.52 \pm 3.18	0.09
	Coriobacteriales	0.15 \pm 0.20	0.51 \pm 0.48	0.20
	Corynebacteriales	0.02 \pm 0.03	0.58 \pm 0.46	*0.01
	Flavobacteriales	1.18 \pm 1.57	4.07 \pm 3.92	0.20
	Fusobacteriales	4.42 \pm 6.43	8.14 \pm 5.27	0.29
	Lactobacillales	12.07 \pm 10.48	39.05 \pm 14.09	*0.01

	Micrococcales	4.69 ± 2.57	2.74 ± 1.74	0.31
	Mycoplasmatales	0.01 ± 0.02	0.18 ± 0.19	0.06
	Pasteurellales	4.64 ± 5.08	4.55 ± 4.29	0.99
	Selenomonadales	0.02 ± 0.02	0.36 ± 0.16	*0.01
	Spirochaetales	0 ± 0	0.45 ± 0.93	*0.02
Family	Actinomycetaceae	0.73 ± 0.62	3.38 ± 2.10	*0.05
	Aerococcaceae	0.06 ± 0.06	1.15 ± 1.83	0.75
	Atopobiaceae	0.15 ± 0.20	0.47 ± 0.46	0.29
	Burkholderiaceae	0.34 ± 0.44	1.35 ± 2.77	0.99
	Campylobacteraceae	0.32 ± 0.47	1.08 ± 0.80	0.09
	Cardiobacteriaceae	0.01 ± 0.01	0.11 ± 0.14	*0.01
	Corynebacteriaceae	0.02 ± 0.03	0.57 ± 0.47	*0.01
	Family XI	0.91 ± 0.91	3.44 ± 2.24	*0.03
	Family XIII	0.02 ± 0.03	0.39 ± 0.43	*0.01
	Flavobacteriaceae	1.08 ± 1.50	3.86 ± 3.66	0.21
	Fusobacteriaceae	2.30 ± 3.95	4.89 ± 3.89	0.21
	Lachnospiraceae	0.53 ± 0.61	1.45 ± 1.62	0.29
	Leptotrichiaceae	2.12 ± 2.74	3.25 ± 2.85	0.40
	Micrococcaceae	4.69 ± 2.57	2.74 ± 1.74	0.31
	Multi-affiliation	1.44 ± 1.00	3.74 ± 1.70	*0.03
	Mycoplasmataceae	0.01 ± 0.02	0.18 ± 0.19	0.06
	Neisseriaceae	58.20 ± 30.47	6.63 ± 5.27	**0.008
	Paludibacteraceae	0.007 ± 0.02	0.11 ± 0.11	*0.01
	Pasteurellaceae	464 ± 5.08	4.55 ± 4.29	0.99
	Peptostreptococcaceae	0.15 ± 0.24	1.02 ± 1.17	0.09
	Porphyromonadaceae	6.16 ± 7.61	5.91 ± 4.35	0.83
	Prevotellaceae	4.95 ± 7.28	12.93 ± 9.87	0.14
	Rikenellaceae	0.001 ± 0.001	0.08 ± 0.11	**0.009
	Ruminococcaceae	0.09 ± 0.19	0.22 ± 0.21	0.50
	Spirochaetaceae	0 ± 0	0.45 ± 0.93	*0.02
	Streptococcaceae	10.55 ± 10.42	34.12 ± 14.29	*0.05
	Tannerellaceae	0.04 ± 0.09	0.96 ± 1.40	0.06
	Unknown	0.19 ± 0.21	0.14 ± 0.12	0.99
	Veillonellaceae	0.02 ± 0.02	0.36 ± 0.16	*0.01
	Weeksellaceae	0.10 ± 0.09	0.21 ± 0.34	0.99
Genus	<i>Abiotrophia</i>	0.06 ± 0.06	1.15 ± 1.83	0.75
	<i>Actinobacillus</i>	0.72 ± 0.97	0.01 ± 0.02	0.15
	<i>Actinomyces</i>	0.73 ± 0.62	3.38 ± 2.10	*0.05
	<i>Aggregatibacter</i>	0.27 ± 0.54	1.29 ± 2.13	0.29
	<i>Alloprevotella</i>	0.84 ± 1.13	0.48 ± 0.41	0.67
	<i>Atopobium</i>	0.15 ± 0.20	0.47 ± 0.46	0.29
	<i>Bergeyella</i>	0.10 ± 0.09	0.21 ± 0.34	0.99
	<i>Campylobacter</i>	0.33 ± 0.47	1.08 ± 0.80	0.09
	<i>Capnocytophaga</i>	1.08 ± 1.50	3.86 ± 3.66	0.20
	<i>Cardiobacterium</i>	0.005 ± 0.007	0.11 ± 0.14	*0.01

	<i>Catonella</i>	0.05 ± 0.09	0.13 ± 0.10	0.29
	<i>Corynebacterium</i>	0.02 ± 0.03	0.57 ± 0.47	*0.01
	<i>Dialister</i>	0.02 ± 0.02	0.33 ± 0.15	*0.01
	<i>Eikenella</i>	0.07 ± 0.09	0.11 ± 0.13	0.52
	<i>F0058</i>	0.007 ± 0.01	0.11 ± 0.11	*0.01
	<i>Filifactor</i>	0.03 ± 0.03	0.99 ± 1.18	*0.01
	<i>Fusobacterium</i>	2.30 ± 3.95	4.89 ± 3.89	0.20
	<i>Gemella</i>	0.91 ± 0.91	3.05 ± 2.24	0.15
	<i>Haemophilus</i>	3.64 ± 3.89	3.25 ± 2.31	0.99
	<i>Kingella</i>	0.08 ± 0.10	0.77 ± 1.37	0.20
	<i>Lachnoanaerobaculum</i>	0.16 ± 0.21	0.18 ± 0.14	0.83
	<i>Lautropia</i>	0.28 ± 0.47	1.27 ± 2.62	0.83
	<i>Leptotrichia</i>	2.08 ± 2.77	3.25 ± 2.85	0.40
	<i>Moryella</i>	0 ± 0	0.14 ± 0.24	*0.02
	<i>Multi-affiliation</i>	1.44 ± 1.00	3.74 ± 1.70	*0.03
	<i>Mycoplasma</i>	0.01 ± 0.02	0.18 ± 0.19	0.06
	<i>Neisseria</i>	58.05 ± 30.64	5.75 ± 5.03	**0.008
	<i>Oribacterium</i>	0.22 ± 0.25	0.41 ± 0.34	0.67
	<i>Parvimonas</i>	0.006 ± 0.005	0.40 ± 0.33	*0.01
	<i>Porphyromonas</i>	6.16 ± 7.61	5.91 ± 4.35	0.83
	<i>Prevotella</i>	0.86 ± 1.10	2.07 ± 1.40	0.14
	<i>Prevotella 2</i>	0.10 ± 0.19	0.19 ± 0.16	0.29
	<i>Prevotella 6</i>	0.13 ± 0.28	0.70 ± 0.59	0.10
	<i>Prevotella 7</i>	3.02 ± 5.70	9.47 ± 7.62	0.14
	<i>Rikenellaceae RC9 gut group</i>	0.001 ± 0.002	0.08 ± 0.11	*0.009
	<i>Rothia</i>	4.65 ± 2.61	2.74 ± 1.74	0.31
	<i>Ruminococcaceae UCG-014</i>	0.09 ± 0.19	0.22 ± 0.21	0.50
	<i>Stomatobaculum</i>	0.09 ± 0.11	0.56 ± 0.98	0.39
	<i>Streptococcus</i>	10.55 ± 10.42	34.12 ± 14.29	*0.05
	<i>Tannerella</i>	0.04 ± 0.09	0.96 ± 1.40	0.06
	<i>Treponema 2</i>	0 ± 0	0.45 ± 0.93	*0.02
	<i>Unknown</i>	0.24 ± 0.21	0.26 ± 0.22	0.99
	<i>Veillonella</i>	0.001 ± 0.002	0.02 ± 0.02	**0.009

Table S3: Comparison between the Relative abundance (%) in oral microbiota of Normo-weighted females (NWF) 20<BMI<25 (n=4) and Obese females (OF) BMI>30 (n=5). Data as mean \pm SD, *p<0.05, **p< 0.001, *p< 0.0001 unpaired Mann-Whitney test. Significant p-values have been highlighted in bold.**

Relative abundance (%) in oral microbiota	Microbiota parameters	Normo-weighted females (NWF) 20<BMI<25 (n=4)	Obese females (OF) BMI>30 (n=5)	p-value
	α -diversity by the Shannon index	1.47 \pm 0.96	2.26 \pm 0.27	0.11
	α -diversity by the Chao 1 index	31.69 \pm 15.28	39.45 \pm 3.74	0.55
Phylum	Actinobacteria	2.06 \pm 2.03	7.23 \pm 2.99	*0.03
	Bacteroidetes	11.75 \pm 16.89	24.16 \pm 10.57	0.19
	Epsilonbacteraeota	0.54 \pm 0.42	1.08 \pm 0.80	0.55
	Firmicutes	21.67 \pm 20.34	45.98 \pm 15.32	0.11
	Fusobacteria	4.57 \pm 3.17	8.14 \pm 5.27	0.55
	Proteobacteria	58.83 \pm 41.57	12.72 \pm 12.05	0.28
	Spirochaetes	0.12 \pm 0.20	0.45 \pm 0.93	0.80
	Tenericutes	0.37 \pm 0.61	0.18 \pm 0.19	0.90
Class	Actinobacteria	1.95 \pm 1.87	6.72 \pm 3.46	0.11
	Alphaproteobacteria	4.12 \pm 8.23	0.06 \pm 0.11	0.53
	Bacilli	17.65 \pm 15.45	42.11 \pm 15.10	0.06
	Bacteroidia	11.75 \pm 16.89	24.16 \pm 10.57	0.19
	Campylobacteria	0.54 \pm 0.43	1.08 \pm 0.80	0.55
	Clostridia	3.88 \pm 5.24	3.52 \pm 3.18	0.90
	Coriobacteriia	0.11 \pm 0.19	0.51 \pm 0.48	0.11
	Fusobacteriia	4.57 \pm 3.17	8.14 \pm 5.27	0.55
	Gammaproteobacteria	54.72 \pm 39.86	12.66 \pm 12.09	0.28
	Mollicutes	0.37 \pm 0.61	0.18 \pm 0.19	0.90
	Negativicutes	0.14 \pm 0.19	0.36 \pm 0.16	0.19
	Spirochaetia	0.12 \pm 0.20	0.45 \pm 0.93	0.80
Order	Actinomycetales	0.49 \pm 0.62	3.38 \pm 2.10	*0.03
	Bacillales	1.03 \pm 0.93	3.05 \pm 2.24	0.11
	Bacteroidales	11.46 \pm 16.81	20.07 \pm 11.74	0.55
	Betaproteobacteriales	43.60 \pm 42.64	7.99 \pm 7.75	0.28
	Campylobacteriales	0.54 \pm 0.43	1.08 \pm 0.80	0.55
	Cardiobacteriales	0.004 \pm 0.003	0.11 \pm 0.14	*0.01
	Caulobacteriales	3.67 \pm 7.34	0.02 \pm 0.03	0.89
	Clostridiales	3.88 \pm 5.24	3.52 \pm 3.18	0.90
	Coriobacteriales	0.11 \pm 0.19	0.51 \pm 0.48	0.11
	Corynebacteriales	0.04 \pm 0.06	0.58 \pm 0.46	*0.03
	Flavobacteriales	0.24 \pm 0.17	4.07 \pm 3.92	*0.01
	Fusobacteriales	4.57 \pm 3.17	8.14 \pm 5.27	0.55
	Lactobacillales	16.62 \pm 14.59	39.05 \pm 14.09	0.06
	Micrococcales	1.40 \pm 1.20	2.74 \pm 1.74	0.28

	Mycoplasmatales	0.27 ± 0.42	0.18 ± 0.19	0.90
	Pasteurellales	0.91 ± 1.37	4.55 ± 4.29	0.06
	Pseudomonadales	10.21 ± 20.39	0.01 ± 0.008	0.90
	Rhizobiales	0.44 ± 0.89	0 ± 0	0.37
	Selenomonadales	0.14 ± 0.19	0.36 ± 0.16	0.19
	Spirochaetales	0.12 ± 0.20	0.45 ± 0.93	0.80
Family	Acholeplasmataceae	0.10 ± 0.19	0 ± 0	0.37
	Actinomycetaceae	0.49 ± 0.62	3.38 ± 2.10	*0.03
	Aerococcaceae	0.02 ± 0.04	1.15 ± 1.83	0.20
	Atopobiaceae	0.11 ± 0.19	0.48 ± 0.46	0.11
	Burkholderiaceae	0.03 ± 0.06	1.35 ± 2.77	0.11
	Campylobacteraceae	0.54 ± 0.43	1.08 ± 0.80	0.55
	Cardiobacteriaceae	0.004 ± 0.003	0.11 ± 0.14	*0.01
	Caulobacteraceae	3.67 ± 7.34	0.02 ± 0.03	0.89
	Clostridiales vadinBB60 group	0.17 ± 0.33	0.01 ± 0.02	0.89
	Corynebacteriaceae	0.04 ± 0.06	0.57 ± 0.47	*0.03
	Family XI	1.39 ± 1.13	3.44 ± 2.24	0.19
	Family XIII	0.76 ± 1.31	0.39 ± 0.43	0.73
	Flavobacteriaceae	0.22 ± 0.15	3.86 ± 3.66	*0.01
	Fusobacteriaceae	4.19 ± 2.92	4.89 ± 3.89	0.99
	Lachnospiraceae	0.99 ± 1.17	1.45 ± 1.62	0.41
	Leptotrichiaceae	0.38 ± 0.42	3.25 ± 2.85	*0.01
	Micrococcaceae	1.39 ± 1.20	2.74 ± 1.74	0.28
	Moraxellaceae	10.20 ± 20.39	0.0006 ± 0.001	0.86
	Multi-affiliation	0.73 ± 0.52	3.74 ± 1.70	*0.01
	Mycoplasmataceae	0.27 ± 0.42	0.18 ± 0.19	0.91
	Neisseriaceae	43.57 ± 42.67	6.63 ± 5.27	0.19
	Paludibacteraceae	0.19 ± 0.23	0.11 ± 0.11	0.90
	Pasteurellaceae	0.91 ± 1.37	4.55 ± 4.30	0.06
	Peptostreptococcaceae	1.37 ± 1.99	1.02 ± 1.17	0.99
	Porphyromonadaceae	5.13 ± 9.33	5.91 ± 4.35	0.28
	Prevotellaceae	5.09 ± 5.81	12.93 ± 9.87	0.28
	Rhizobiaceae	0.44 ± 0.89	0 ± 0	0.37
	Rikenellaceae	0.46 ± 0.88	0.08 ± 0.11	0.90
	Ruminococcaceae	0.18 ± 0.31	0.22 ± 0.21	0.90
	Spirochaetaceae	0.12 ± 0.20	0.45 ± 0.93	0.80
	Streptococcaceae	15.86 ± 14.21	34.12 ± 14.29	0.11
	Tannerellaceae	0.18 ± 0.20	0.96 ± 1.40	0.35
	Unknown	0.19 ± 0.21	0.14 ± 0.12	0.99
	Veillonellaceae	0.14 ± 0.19	0.36 ± 0.16	0.19
	Weeksellaceae	0.02 ± 0.01	0.21 ± 0.37	0.14
Genus	<i>Abiotrophia</i>	0.02 ± 0.04	1.15 ± 1.83	0.20
	<i>Acinetobacter</i>	10.20 ± 20.39	0 ± 0	0.37
	<i>Actinomyces</i>	0.49 ± 0.62	3.38 ± 2.10	*0.03
	<i>Aggregatibacter</i>	0.03 ± 0.05	1.29 ± 2.13	0.10

	<i>Alloprevotella</i>	1.17 ± 1.84	0.48 ± 0.41	0.90
	<i>Atopobium</i>	0.11 ± 0.19	0.47 ± 0.46	0.11
	<i>Bergeyella</i>	0.02 ± 0.01	0.21 ± 0.34	0.14
	<i>Brevundimonas</i>	3.67 ± 7.34	0 ± 0	0.37
	<i>Campylobacter</i>	0.54 ± 0.43	1.08 ± 0.80	0.55
	<i>Capnocytophaga</i>	0.22 ± 0.15	3.86 ± 3.66	*0.01
	<i>Cardiobacterium</i>	0.004 ± 0.003	0.11 ± 0.14	*0.01
	<i>Catonella</i>	0.31 ± 0.27	0.13 ± 0.10	0.32
	<i>Corynebacterium</i>	0.04 ± 0.06	0.57 ± 0.47	*0.03
	<i>Dialister</i>	0.14 ± 0.19	0.33 ± 0.15	0.19
	<i>Eikenella</i>	0.03 ± 0.04	0.11 ± 0.13	0.38
	<i>F0058</i>	0.19 ± 0.23	0.11 ± 0.11	0.90
	<i>Filifactor</i>	1.21 ± 1.94	0.99 ± 1.18	0.73
	<i>Fusobacterium</i>	4.19 ± 2.92	4.89 ± 3.89	0.99
	<i>Gemella</i>	1.03 ± 0.93	3.05 ± 2.24	0.11
	<i>Haemophilus</i>	0.87 ± 1.31	3.25 ± 2.31	0.11
	<i>Kingella</i>	0.05 ± 0.04	0.77 ± 1.37	0.21
	<i>Lachnoanaerobaculum</i>	0.18 ± 0.29	0.19 ± 0.14	0.80
	<i>Lautropia</i>	0.03 ± 0.06	1.27 ± 2.62	0.20
	<i>Leptotrichia</i>	0.26 ± 0.35	3.25 ± 2.85	*0.01
	<i>Moryella</i>	0.02 ± 0.03	0.14 ± 0.24	0.53
	<i>Multi-affiliation</i>	0.73 ± 0.52	3.74 ± 1.70	*0.01
	<i>Mycoplasma</i>	0.27 ± 0.42	0.18 ± 0.19	0.90
	<i>Neisseria</i>	43.50 ± 42.70	5.75 ± 5.03	0.19
	<i>Oribacterium</i>	0.17 ± 0.30	0.41 ± 0.34	0.46
	<i>Parvimonas</i>	0.37 ± 0.31	0.40 ± 0.33	0.90
	<i>Peptostreptococcus</i>	0.16 ± 0.14	0.02 ± 0.02	0.21
	<i>Porphyromonas</i>	5.13 ± 9.33	5.91 ± 4.35	0.28
	<i>Prevotella</i>	0.61 ± 0.53	2.07 ± 1.40	0.11
	<i>Prevotella 2</i>	0.07 ± 0.10	0.19 ± 0.16	0.19
	<i>Prevotella 6</i>	0.06 ± 0.09	0.70 ± 0.59	0.14
	<i>Prevotella 7</i>	2.63 ± 4.30	9.47 ± 7.62	0.19
	<i>Rikenellaceae RC9 gut group</i>	0.46 ± 0.88	0.08 ± 0.11	0.90
	<i>Rothia</i>	1.39 ± 1.20	2.74 ± 1.74	0.28
	<i>Ruminococcaceae UCG-014</i>	0.18 ± 0.31	0.22 ± 0.21	0.90
	<i>Stomatobaculum</i>	0.29 ± 0.54	0.56 ± 0.98	0.46
	<i>Streptococcus</i>	15.86 ± 14.21	34.12 ± 14.29	0.11
	<i>Tannerella</i>	0.18 ± 0.20	0.96 ± 1.40	0.32
	<i>Treponema 2</i>	0.12 ± 0.20	0.45 ± 0.93	0.80
	<i>Unknown</i>	0.82 ± 1.00	0.26 ± 0.22	0.99
	<i>[Eubacterium] brachy group</i>	0.23 ± 0.45	0.10 ± 0.11	0.62
	<i>[Eubacterium] nodatum group</i>	0.10 ± 0.19	0.15 ± 0.16	0.53
	<i>[Eubacterium] saphenum group</i>	0.25 ± 0.37	0.08 ± 0.16	0.68