

Table A3. Full taxonomic affiliation of microorganisms included on each cluster. Average relative abundances within their corresponding domain and the standard deviation are also shown

Taxonomic affiliation	average relative abundance (%)	Standard deviation
Cluster 1		
<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella</i>	0.25	0.22
<i>d_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Chryseobacterium</i>	0.02	0.02
<i>d_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Cloacibacterium</i>	0.12	0.12
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_vadinHB04</i>	0.09	0.08
<i>d_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_</i>	0.28	0.14
<i>d_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Comamonas</i>	0.06	0.04
<i>d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter</i>	0.12	0.07
Cluster 2		
<i>d_Archaea;p_[Parvarchaeota];c_[Parvarchaea];o_WCHD3-30;f_;g_</i>	0.05	0.16
<i>d_Bacteria;p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_</i>	0.24	1.06
<i>d_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_</i>	0.01	0.02
<i>d_Bacteria;p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_</i>	0.04	0.17
<i>d_Bacteria;p_OP11;c_WCHB1-64;o_;f_;g_</i>	0.00	0.02
<i>d_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_ASSO-13;f_;g_</i>	0.09	0.39
<i>d_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Zoogloea</i>	0.02	0.05
<i>d_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_NKB15;f_;g_</i>	0.03	0.06
<i>d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;Other</i>	0.01	0.02
<i>d_Bacteria;p_TM7;c_TM7-1;o_;f_;g_</i>	0.01	0.02
Cluster 3		
<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_</i>	0.45	0.24

<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_Paludibacter</i>	0.96	0.56
<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Blvi28</i>	0.10	0.10
<i>d_Bacteria;p_Fibrobacteres;c_Fibrobacteria;o_Fibrobacterales;f_Fibrobacteraceae;g_Fibrobacter</i>	0.02	0.02
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_</i>	3.08	6.43
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;Other</i>	0.04	0.06
<i>d_Bacteria;p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_RFN20</i>	0.14	0.27
<i>d_Bacteria;p_OD1;c_ZB2;o_f_;g_</i>	1.31	0.62
<i>d_Bacteria;p_OP3;c_PBS-25;o_f_;g_</i>	0.04	0.03
<i>d_Bacteria;p_Proteobacteria;c_o_f_;g_</i>	0.28	0.26
<i>d_Bacteria;p_Spirochaetes;c_[Brachyspirae];o_[Brachyspirales];f_Brachyspiraceae;g_</i>	0.02	0.02
<i>d_Bacteria;p_Spirochaetes;c_[Leptospirae];o_[Leptospirales];f_Sediment-4;g_</i>	0.40	0.29
<i>d_Bacteria;p_Spirochaetes;c_GN05;o_SBYZ_6080;f_;g_</i>	0.02	0.03
<i>d_Bacteria;p_Spirochaetes;c_MVP-15;o_PL-11B10;f_;g_</i>	0.06	0.06
<i>d_Bacteria;p_Spirochaetes;c_Spirochaetes;o_M2PT2-76;f_;g_</i>	0.04	0.03
<i>d_Bacteria;p_Spirochaetes;c_Spirochaetes;o_Sphaerochaetales;f_Sphaerochaetaceae;g_Sphaerochaeta</i>	0.07	0.09
<i>d_Bacteria;p_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaceae;g_Treponema</i>	1.82	1.32
<i>d_Bacteria;p_Tenericutes;c_RF3;o_ML615J-28;f_;g_</i>	0.08	0.08
<i>d_Bacteria;p_Thermotogae;c_Thermotogae;o_Thermotogales;f_Thermotogaceae;g_AUTHM297</i>	0.09	0.05
<i>d_Bacteria;p_WWE1;c_[Cloacamonae];o_[Cloacamonales];f_[Cloacamonaceae];g_W22</i>	3.41	1.42

Cluster 4

<i>d_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_WSA2;g_</i>	8.40	6.35
<i>d_Bacteria;p_[Thermi];c_Deinococci;o_Deinococcales;f_Trueperaceae;g_B-42</i>	0.02	0.03
<i>d_Bacteria;p_Acidobacteria;c_Sva0725;o_Sva0725;f_;g_</i>	0.20	0.12
<i>d_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;Other</i>	0.06	0.04
<i>d_Bacteria;p_Armatimonadetes;c_SJA-176;o_RB046;f_;g_</i>	0.05	0.02
<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_SB-1;g_</i>	9.17	3.81

<i>d_Bacteria;p_BRC1;c_PRR-11;o_;</i> f_;	g_	0.15	0.07	
<i>d_Bacteria;p_Caldiserica;c_OP5;o_WCHB1-02;</i> f_;	SHBZ1169;	g_	0.16	0.12
<i>d_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;</i> f_;	Anaerolinaceae;	g_C1_B004	0.07	0.03
<i>d_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;</i> f_;	Anaerolinaceae;	g_SHD-231	0.37	0.16
<i>d_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;</i> f_;	Anaerolinaceae;	g_T78	3.75	1.44
<i>d_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;</i> f_;	Anaerolinaceae;	g_WCHB1-05	0.52	0.38
<i>d_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Caldilineales;</i> f_;	Caldilineaceae;	g_	0.02	0.03
<i>d_Bacteria;p_Chloroflexi;c_Anaerolineae;o_OPB11;</i> f_;	g_	0.05	0.03	
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;</i> f_;	Christensenellaceae;	g_	0.32	0.09
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;</i> f_;	Gracilibacteraceae;	g_Gracilibacter	0.05	0.09
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;</i> f_;	Gracilibacteraceae;	Other	0.12	0.06
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;</i> f_;	Ruminococcaceae;	g_	1.27	0.34
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;</i> f_;	Ruminococcaceae;	g_Ruminococcus	0.03	0.04
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_SHA-98;</i> f_;	g_	0.57	0.38	
<i>d_Bacteria;p_Gemmatimonadetes;c_Gemm-5;o_;</i> f_;	g_	0.12	0.29	
<i>d_Bacteria;p_Hyd24-12;c_;</i> o_;	f_;	g_	0.51	0.36
<i>d_Bacteria;p_NKB19;c_noFP_H4;o_;</i> f_;	g_	0.12	0.05	
<i>d_Bacteria;p_OD1;c_;</i> o_;	f_;	g_	0.44	0.21
<i>d_Bacteria;p_OP11;c_OP11-2;o_WCHB1-07;</i> f_;	g_	0.04	0.03	
<i>d_Bacteria;p_OP11;c_WCHB1-64;o_d153;</i> f_;	g_	0.93	0.47	
<i>d_Bacteria;p_OP8;c_OP8_1;o_;</i> f_;	g_	0.01	0.02	
<i>d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;</i> f_;	g_	0.05	0.04	
<i>d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;</i> f_;	Rhodobacteraceae;	g_Paracoccus	0.03	0.06
<i>d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;</i> f_;	Rhodobacteraceae;	g_Rhodobacter	0.01	0.01
<i>d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;</i> f_;	g_	0.08	0.05	
<i>d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;</i> f_;	Acetobacteraceae;	g_	0.10	0.13

<i>d_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;Other</i>	0.05	0.03
<i>d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_</i>	0.04	0.07
<i>d_Bacteria;p_Synergistetes;c_Synergistia;o_Synergistales;f_Synergistaceae;g_vadinCA02</i>	1.85	0.68
<i>d_Bacteria;p_Synergistetes;c_Synergistia;o_Synergistales;f_Thermovirgaceae;g_</i>	0.22	0.11
<i>d_Bacteria;p_Thermotogae;c_Thermotogae;o_Thermotogales;f_Thermotogaceae;g_SC103</i>	0.23	0.20
<i>d_Bacteria;p_Verrucomicrobia;c_Verruco-5;o_WCHB1-41;f_;g_</i>	0.13	0.04
<i>d_Bacteria;p_Verrucomicrobia;c_Verruco-5;o_WCHB1-41;f_WCHB1-25;g_</i>	0.24	0.09
<i>d_Bacteria;p_WS6;c_B142;o_;f_;g_</i>	0.02	0.03
<i>d_Bacteria;p_WS6;c_SC72;o_A-2AF;f_;g_</i>	0.41	0.22
<i>d_Bacteria;p_WS6;c_SC72;o_WCHB1-15;f_;g_</i>	1.10	0.49
<i>d_Bacteria;p_WWE1;c_[Cloacamonae];o_[Cloacamonales];f_[Cloacamonaceae];g_Candidatus Cloacamonas</i>	0.51	0.27
<i>d_Bacteria;p_WWE1;c_[Cloacamonae];o_[Cloacamonales];f_[Cloacamonaceae];g_W5</i>	1.16	2.14

Cluster 5

<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyrimonadaceae;g_</i>	0.39	0.98
<i>d_Bacteria;p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_;g_</i>	0.02	0.10
<i>d_Bacteria;p_Chlorobi;c_SJA-28;o_;f_;g_</i>	0.01	0.02
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_</i>	0.06	0.05
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Tissierella Soehngenia</i>	0.02	0.07
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_</i>	0.05	0.22
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_SHA-98;f_D2;g_</i>	0.10	0.19
<i>d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium</i>	0.02	0.03
<i>d_Bacteria;p_SRI;c_;o_;f_;g_</i>	0.06	0.27
<i>d_Bacteria;p_Verrucomicrobia;c_Verruco-5;o_LD1-PB3;f_;g_</i>	0.32	0.23

Cluster 6

<i>d_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_;g_</i>	38.08	15.03
<i>d_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanospirillaceae;g_</i>	1.25	0.44

<i>d_Archaea;p_Euryarchaeota;c_Thermoplasmata;o_E2;f_[Methanomassiliicoccaceae];g_</i>	0.85	0.52
<i>d_Archaea;p_Euryarchaeota;c_Thermoplasmata;o_E2;f_[Methanomassiliicoccaceae];g_Methanomassiliicoccus</i>	0.36	0.15
<i>d_Bacteria;p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_</i>	2.54	0.86
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_;g_</i>	1.93	0.77
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium</i>	3.90	1.14
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Syntrophomonadaceae;g_Syntrophomonas</i>	0.65	0.19
<i>d_Bacteria;p_Lentisphaerae;c_[Lentisphaeria];o_Z20;f_R4-45B;g_</i>	0.12	0.07
<i>d_Bacteria;p_NKB19;c_TSBW08;o_;f_;g_</i>	0.38	0.12
<i>d_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacteriales;f_Syntrophaceae;g_</i>	1.29	0.50
<i>d_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacteriales;f_Syntrophaceae;g_Syntrophus</i>	2.92	1.31
<i>d_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacteriales;f_Syntrophobacteraceae;g_Syntrophobacter</i>	0.26	0.14
<i>d_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacteriales;f_Syntrophorhabdaceae;g_</i>	0.77	0.24

Cluster 7

<i>d_Archaea;p_Crenarchaeota;c_MCG;o_pGrfC26;f_;g_</i>	1.33	0.71
<i>d_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_Methanobacteriaceae;g_Methanobacterium</i>	1.16	0.51
<i>d_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_Methanobacteriaceae;g_Methanobrevibacter</i>	2.11	1.35
<i>d_Archaea;p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_Methanobacteriaceae;g_Methanosphaera</i>	0.72	0.55
<i>d_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanomicrobiaceae;g_Methanoculleus</i>	3.00	4.07
<i>d_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanoregulaceae;g_Candidatus Methanoregula</i>	0.52	0.64
<i>d_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanosarcinales;f_Methanosaetaceae;g_Methanosaeta</i>	38.01	11.82
<i>d_Archaea;p_Euryarchaeota;c_Methanomicrobia;o_Methanosarcinales;f_Methanosarcinaceae;g_Methanosarcina</i>	0.28	0.17
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Acidaminobacteraceae];g_</i>	0.07	0.03

Cluster 8

<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides</i>	0.07	0.18
<i>d_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_</i>	0.01	0.03
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccoccus</i>	0.06	0.18

<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Faecalibacterium</i>	0.02	0.07
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera</i>	0.01	0.04
Cluster 9		
<i>d_Bacteria;p_Armatimonadetes;c_SJA-176;o_TP122;f_ ;g_</i>	0.04	0.02
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Acidaminobacteraceae];g_Fusibacter</i>	0.06	0.03
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_Anaerovorax</i>	1.05	0.44
<i>d_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Sedimentibacter</i>	7.84	2.73