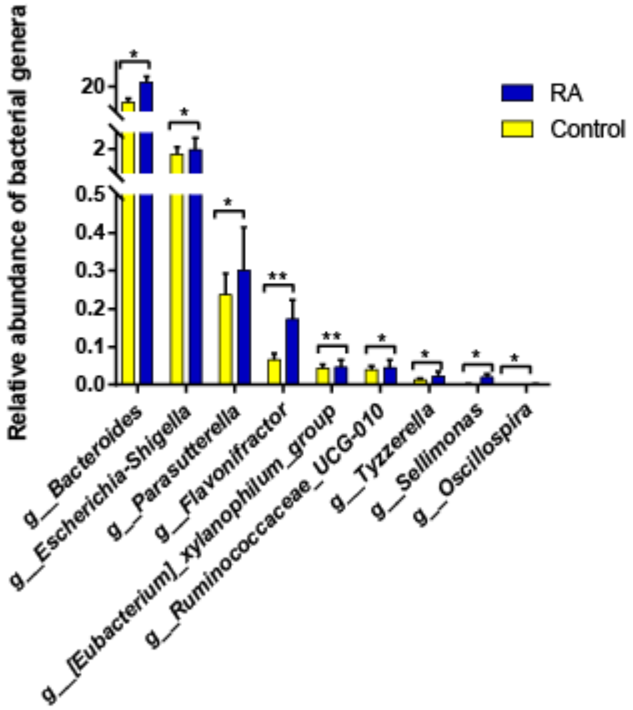
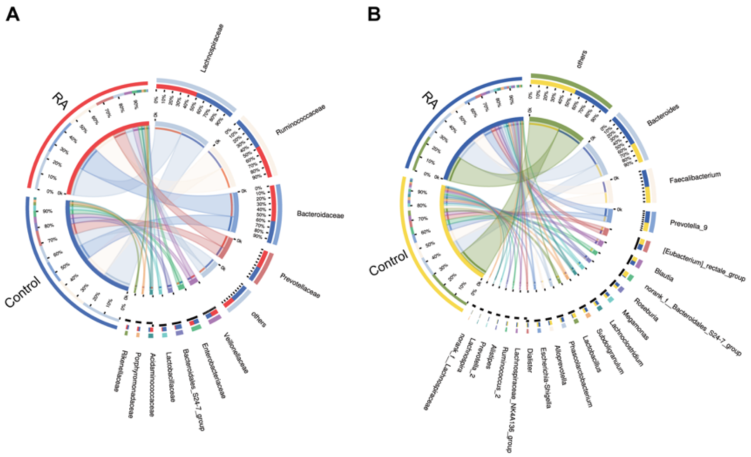
Supplementary Material

1 Supplementary Figures and Tables

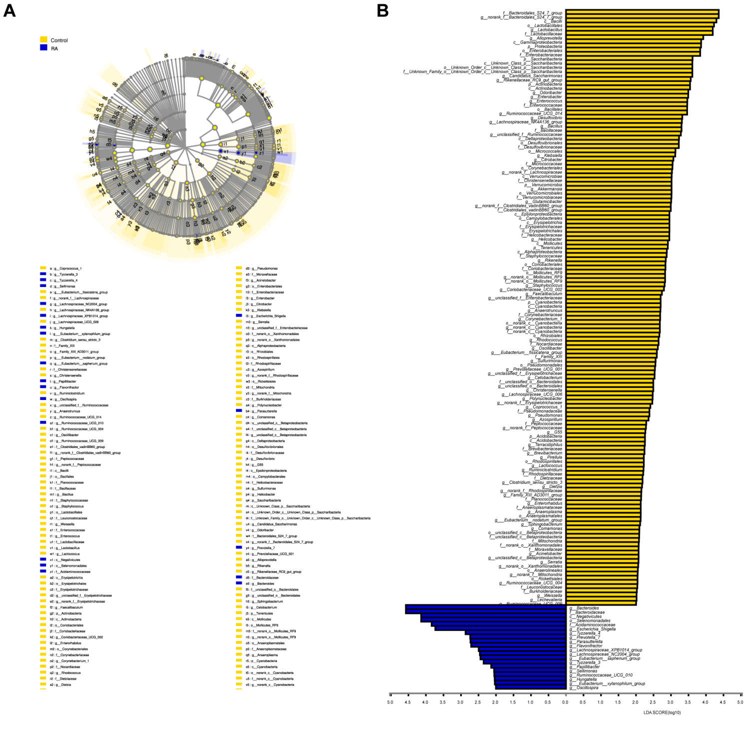
1.1 Supplementary Figures



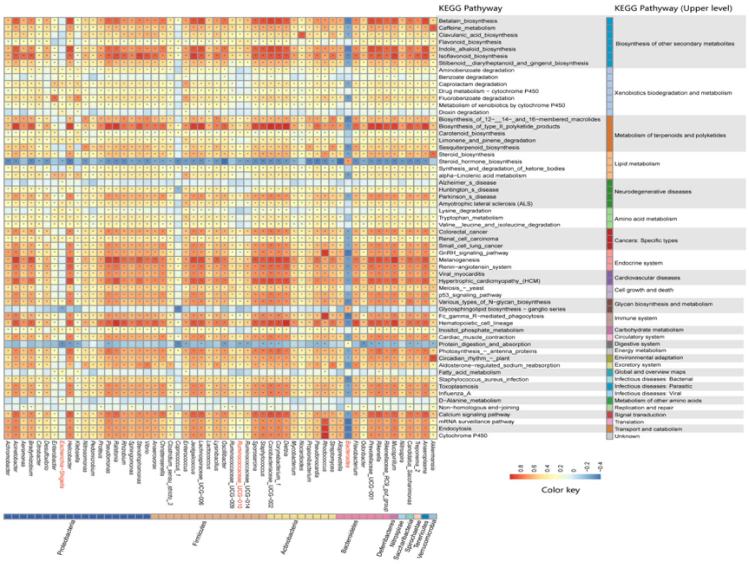
Supplementary Fig. 1 Bacterial genera with significant higher abundance in the RA group.



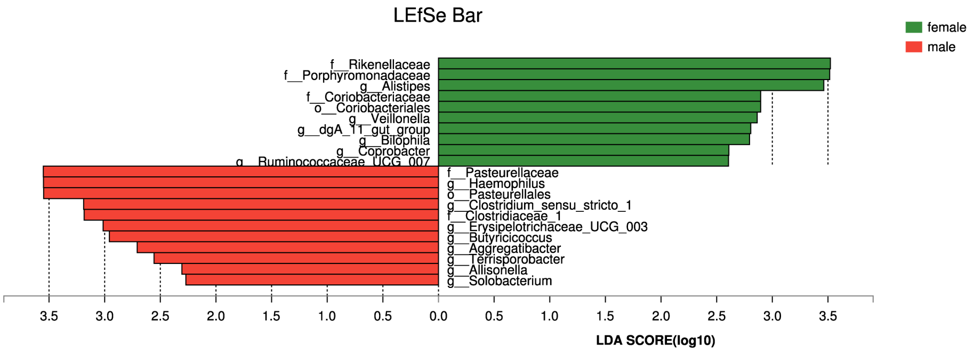
Supplementary Fig. 2 Differences in composition of the gut microbiome between the RA group and control group. (A)Circos plots were used to visualize the relationship between sample groups and specific bacterial families and (B)genera .



Supplementary Fig. 3 Differences in abundances of bacterial communities between the RA and healthy control groups. (A) Taxonomic cladogram obtained by LEfSe analysis revealing differences in abundances of bacterial communities. RA-enriched and healthy control-enriched taxa are depicted in blue and yellow, respectively. (B) The LDA scores of the RA group and the healthy control group. Histograms in blue and yellow indicate the enriched bacterial taxa in RA patients and healthy control individuals, respectively.



Supplementary Fig. 4 Bacterial taxa associated with RA related to gene functional pathways. Bacterial gene functions were predicted from 16S rRNA gene-based microbial compositions using the PICRUSt algorithm to make inferences from the KEGG annotated databases (Wu et al. 2016). Spearman's correlation coefficients were estimated for each pairwise comparison of genus and KEGG pathway counts. All KEGG pathways exhibiting a significant difference between the RA and control groups are included, and bacterial genera of interest are shown in the heatmap. The bacterial genera in red were enriched, while the remainder were depleted in the RA group.



Supplementary Fig. 5 Differences in abundances of bacterial communities between males and females. Linear discriminant analysis (LDA) score of males and females Histograms in green show enriched bacterial taxa in females, and those in red show enriched bacterial taxa in males.

1.2 Supplementary Tables

Supplementary Table 1. Demographic and clinical characteristics of the study cohort with RA

					Blood routine examination				Routine urine examination						
Sample ID	Gender	Age	Tender joint counts	Swell joint counts	Leukocyte $(\times 10^{9}/L)$	Hemoglobin $(\times g/L)$	Erythrocyte $(\times 10^{12}/L)$	Thrombocyte $(\times 10^{9}/L)$	Urine protein (g/L)	Urine specific gravity	PH	ketone body	Urine UGLU	Urine RBC (/ul)	LEU (/ul)
RA -001	F	60	4	4	6.93	126	4.15	242	-	1.005	8	-	normal	0-1/HP	2-3/HP
RA -002	F	35	21	11	7.79	140	4.4	194	-	1.005	8	-	normal	0-1/HP	2-3/HP
RA -003	M	65	7	6	5.39	129	4.17	242	-	1.02	6	-	normal	0-1/HP	2-3/HP
RA -004	F	44	8	4	5.86	100	3.71	266	-	1.015	8	-	normal	0-1/HP	2-3/HP
RA -005	M	61	28	3	9.61	150	4.59	325							
RA -006	F	61	22	22	5.63	133	4.1	197	-	1.025	6	-	normal	0-1/HP	2-3/HP
RA -007	F	49	3	4	7.06	122	4.44	227	-	1.01	7	-	normal	0-1/HP	2-3/HP
RA -008	F	37	2	2	9.6	145	4.64	282	-	1.015	5	+	normal	0-1/HP	2-3/HP
RA -009	F	27	6	1	9.12	121	4.57	286	-	1.01	8	-	normal	0-1/HP	2-3/HP
RA -010	F	56	4	0	3.3	85	2.6	154	-	1.03	5	-	normal	0-1/HP	4-5/HP
RA -011	F	49	6	0	9.68	126	4.22	241	-	1.025	5	-	+	0-1/HP	2-3/HP
RA -012	F	42	18	2	7.56	128	4.63	290	-	1.02	6	-	normal	0-1/HP	2-3/HP
RA -013	F	54	13	1	4.62	109	3.7	216	-	1.02	5	-	normal	0-1/HP	2-3/HP
RA -014	M	63	1	2											
RA -015	M	54	18	9	9.57	155	5.09	168	-	1.02	6	-	normal	0-1/HP	2-3/HP
RA -016	F	62	1	1											
RA -017	M	63	26	18	8.78	148	4.73	191	-	1.02	5	-	+	0-1/HP	2-3/HP
RA -018	F	61	4	2	6.91	130	4.15	205	-	1.025	7	-	normal	0-1/HP	2-3/HP
RA -019	F	34	14	12	7.35	140	4.41	265	-	1.015	6	-	normal	0-1/HP	2-3/HP
RA -020	F	73	3	1											
RA -021	F	51	11	0	4.53	143	4.57	197	-	1.015	7	-	normal	0-1/HP	2-3/HP
RA -022	F	35	20	20	3.6	121	4.13	159	-	1.015	6	-	normal	0-1/HP	2-3/HP
RA -023	F	52	15	0	8.26	110	4.2	360	-	1.02	7	-	normal	0-1/HP	2-3/HP

RA -024	F	69	4	2	6.3	152	5	243	-	1.025	5	-	normal	+	2-3/HP
RA -025	M	64	6	2	8.32	117	3.94	433	-	1.025	5	-	normal	0-1/HP	2-3/HP
RA -026	M	54	18	8					-	1.025	5	-	normal	+++	2-3/HP
RA -028	F	58	1	0	4.84	145	4.67	255	-	1.015	6	-	normal	+++	7-8/HP
RA -029	M	62	28	18	7.06	111	3.44	142	-	1.03	5	-	normal	0-1/HP	2-3/HP
RA -030	F	58	22	1	9.43	128	4.15	204	-	1.02	5	-	normal	0-1/HP	2-3/HP
RA -031	F	54	2	2	6.13	134	5.12	195	-	1.01	6	-	normal	0-1/HP	2-3/HP
RA -032	F	64	4	1	6.7	128	4.11	175	-	1.015	5	-	normal	0-1/HP	2-3/HP
RA -035	F	55	13	0	4.43	144	4.9	189	-	1.01	8	-	normal	0-1/HP	3-4/HP
RA -036	F	51	0	0											
RA -038	F	40	7	4	4.98	91	3.85	386	-	1.02	5	-	normal	0-1/HP	3-5/HP
RA -039	F	62	5	0	7.14	123	4.01	258	-	1.025	7	-	normal	1-3/HP	3-4/HP
RA -040	M	51	3	0	8.8	167	5.44	195	-	1.02	6	-	normal	0-1/HP	2-3/HP
RA -043	M	68	23	18	8.02	141	4.64	171	-	1.025	6	-	normal	0-1/HP	2-3/HP
RA -044	M	51	26	18	5.5	139	4.91	221	-	1.025	6	-	normal	0-1/HP	2-3/HP
RA -045	F	52	24	10	6.1	105	4.34	260	-	1.015	7	-	normal	0-1/HP	2-3/HP
RA -046	F	58	4	0	4.76	122	4.09	215	-	1.015	7	-	normal	0-1/HP	2-3/HP
RA -047	F	40	10	0	6.54	121	3.77	327	-	1.005	7	-	normal	0-1/HP	2-3/HP
RA -048	F	68	48	0											
RA -050	F	65	9	8	6.22	114	4.02	276	-	1.02	5	-	normal	0-1/HP	2-3/HP
RA -052	F	68	9	3											
RA -053	F	46	7	20	5.73	137	5.41	242							
RA -055	F	65	14	12	6.24	120	3.85	126							
RA -056	F	72	27	15	9.83	102	3.33	384	-			-	normal	"+++	2-3/HP
RA -058	F	58	22	20	4.18	109	3.71	299	-	1.015	6	-	normal	0-1/HP	2-3/HP
RA -064	F	63	12	4											
RA -067	M	67	9	12	8.12	120	4.45	319							
RA -077	F	33	1	1	6.92	117	4.04	305	-	1.025	5	-	normal	0-1/HP	3-4/HP
RA -078	F	64	25	20	4.68	123	4.54	169	-						

RA -125	M	55													
RA -126	F	68			5.3	129	4	146							
RA -127	F	58													
RA -128	F	47													
RA -130	F	67	5	3	5.87	141	4.64	236	-	1.005	6	-	normal	0-1/HP	2-3/HP
RA -131	F	52	20	0	5.19	110	6.11	122							
RA -132	M	62	1	1	5.84	118	3.82	179	-	1.025	5	-	normal	6-7/HP	4-6/HP
RA -134	F	81	10	2	6.45	109	3.42	281							
RA -135	F	40	10	6	7.69	117	4.13	206	-	1.025	7	-	normal	0-1/HP	2-3/HP
RA -136	F	39	8	8	5.63	130	4.39	172	-	1.015	7	-	normal	0-1/HP	2-3/HP
RA -138	F	62	26	14					-	1.005	6	-	normal		
RA -139	F	38	36	0	11.8	115	3.85	304							
RA -140	M	53	11	15	10.34	157	5.26	238	-	1.025	5	-	normal	0-1/HP	2-3/HP
RA -141	F	37	13	8	6.51	118	4.74	328	-	1.03	5	-	normal	0-1/HP	2-3/HP

Continued

Sample ID	Blood biochemistry						Inflammatory markers		Serological indicator			
									RF（lu/ml）			
	ALT (U/L)	AST (U/L)	ALP (U/L)	GGT (U/L)	BUN (U/L)	Cr (U/L)	ESR (mm/h)	CRP (mg/L)	RF-IgM	RF-IgA	RF-IgG	ACCP (U/ml)
RA -001	10	15				41	33	22.96	<20	0.4	2.15	<25
RA -002	13	18					4	0.44	<20	0.1	0.2	<25
RA -003	11	17				53	27	6.87	130	1.08	3.86	1600
RA -004	9	18	59	10	3	34	119	43.22	2300			
RA -005	18	18				52	14	15.63	20.4	>300	53.05	1600
RA -006	15	24				52	23	1.2	126	9.3	13.1	283.52
RA -007	13	20				41	38	0.8	67.4	36.56	59.76	1098.2
RA -008	9	12				48	2	2.96	<20	3.85	10.36	<25
RA -009	15	19				47	53	16.63	27.1	5.97	21.51	314.51
RA -010	10	22			4.8	49	109	6.6	653	25.52	83.9	<25
RA -011	16	12					21	0.69	20.6	3.64	36.03	<25
RA -012	11	17			7	53	7	3.22	<20	0.13	1.82	<25
RA -013	11	14	51	17	7.3	72	53	12.39	390	149.57	20.8	967.52
RA -014												
RA -015	9	14				55	16	9.16	123	17.1	99.97	<25
RA -016												

RA -017	17	20	54	27	7.6	72	19	6.02	621	37.61	139.11	1600
RA -018	37	33	69	30	5.6	48	22	2.75	81.3	0.48	3.55	<25
RA -019	14	18	80	16		47	14	1.64	<20	0.31	1.5	164.55
RA -020												
RA -021	17	27					8	0.54	<20	1.28	0.99	<25
RA -022	18	20				30	23	0.5	69.9	9.85	34.36	85.46
RA -023	5	16	88	16	5.3	35	77	13.44	547	104.65	90.88	77.07
RA -024	22	28			4.2	49	10	0.96	<20	0.85	2.55	<25
RA -025							68	24.19	22.4	5.33	4.86	195.39
RA -026									23.1	38.46	>300	107.88
RA -028	32	23			42	60	15	0.92	<20	3.09	1.59	<25
RA -029	50	42			10.9	55	104	83.01	148	11.81	66.49	45.58
RA -030	10	17				41	30	2.04	491	15.36	95.37	305.72
RA -031	6	17			3.4	55	26	5.77	242	211.54	85.99	192.75
RA -032	11	15			6.9	238	31	0.5	209	57.82	97.86	343.25
RA -035							10	0.5				
RA -036												
RA -038	7	9	74	14	4.8	42	110	78.4	411	9.85	94.6	
RA -039	10	16			4.2	48	30	0.4	258			1600
RA -040	14	18	60	22	7	55	4	2.64	<20	58.09	29.42	67.57
RA -043	12	17	86	14	6	72	16	2.45	263	>300	33.66	
RA -044	9	15	82	14	8.7	65	18	0.5	<20	2.24	0.6	<25
RA -045	10	12	63	12	3.3	40	37	4.77	209	1.86	15.14	1130.91
RA -046	39	33				50	9	0.33	<20	0.15	0.29	44.23
RA -047	12	20	60	10	3.4	54	48	7.9	75.9	5.02	30.49	625.64
RA -048												
RA -050	8	15	98	15	5.2	70	80	26.86				
RA -052												
RA -053	36	42	118	49	3.4	49	36	0.5	21.4	42.03	20.85	147.06

RA -055					4.5	52.4	26	17	162.2			
RA -056	10	10	65	24	7.8	51	75	13.31	>2460	169.94	230.68	73.12
RA -058							70	62.01	<20			<25
RA -064												
RA -067	10	16	97	16	8.5	61	116	81.47	10		49	738
RA -077	6	13			268	52	36	4.87	304	>300	79.26	1213
RA -078	63	42				52	27		478	10.14	119.07	<25
RA -125												
RA -126						<5	2					<25
RA -127												
RA -128												
RA -130	22	28			40.2	0.5	14	0.7	463	6	63	1071
RA -131	19	18			47.5		7	0.85	<20	3.8	1.3	<25
RA -132	44	30				61.2	25	0.6	572	1.3	58	<25
RA -134							70	38.06	<20	1.3	4.2	<25
RA -135							37	2.3	114	66.94	79.45	170.57
RA -136	11	16					12	0.91	<20	1.4	4.1	<25
RA -138												
RA -139	24	23			4.26	46	97	111.02				
RA -140	17	18	114		4.2	51.2	5	1.84	36.2	69	8	323
RA -141	13	16	59	17	3.7	42.5	19	0.96	283	109	133	1117

ALT = alanine aminotransferase, AST= aspartate amino transferase, ALP = alkaline phosphatase, GGT = gamma-glutamyl transpeptidase, BUN = blood urea nitrogen, Cr = creatinine, ESR = erythrocyte sedimentation rate, CRP = C-reactive protein

Supplementary Table 2. Bacterial genera significantly altered between RA group and healthy control (GUT) group

Species name	GUT-Mean (%)	GUT-SD (%)	RA-Mean (%)	RA-SD (%)	P-value	Corrected p-value	Lower CI	Upper CI	Effect size
g__Rikenellaceae_RC9_gut_group	0.6708	1.1	9.46E-05	0.00054	4.55E-14	1.02E-11	-0.9557	-0.3886	-0.6708
g__Helicobacter	0.1642	0.2777	0	0	4.67E-14	1.02E-11	-0.2385	-0.0962	-0.1642
g__Rhodococcus	0.09505	0.1819	0.004259	0.01258	2.31E-13	3.38E-11	-0.1459	-0.05103	-0.09079
g__Candidatus_Saccharimonas	0.7426	1.303	0.000379	0.001287	1.88E-12	2.06E-10	-1.073	-0.4138	-0.7422
g__Coriobacteriaceae_UCG-002	0.1147	0.1953	0	0	2.38E-12	2.09E-10	-0.1648	-0.0685	-0.1147
g__Glutamicibacter	0.186	0.3246	9.46E-05	0.00054	7.38E-12	4.04E-10	-0.2707	-0.1119	-0.1859
g__Faecalibaculum	0.1014	0.1676	4.73E-05	0.000384	7.26E-12	4.04E-10	-0.1446	-0.06143	-0.1014
g__norank_f__Erysipelotrichaceae	0.05887	0.1016	0.005963	0.04767	5.86E-12	4.04E-10	-0.07939	-0.02449	-0.05291
g__Acinetobacter	0.0227	0.0383	0	0	1.55E-11	7.54E-10	-0.03269	-0.01379	-0.02269
g__Rikenella	0.13	0.2198	9.46E-05	0.00054	2.08E-11	9.12E-10	-0.1861	-0.07877	-0.1299
g__Anaeroplasma	0.02488	0.04518	0	0	3.87E-11	1.54E-09	-0.03717	-0.01437	-0.02488
g__Corynebacterium_1	0.08766	0.1587	4.73E-05	0.000384	4.82E-11	1.76E-09	-0.1335	-0.04962	-0.08761
g__Staphylococcus	0.1215	0.2101	0.000331	0.001655	6.53E-11	2.16E-09	-0.1749	-0.06763	-0.1212
g__Prevotellaceae_UCG-001	0.06731	0.1096	0.003218	0.02427	6.91E-11	2.16E-09	-0.09335	-0.03634	-0.06409
g__Acetatifactor	0.01619	0.02755	0	0	2.35E-10	6.42E-09	-0.02405	-0.00937	-0.01619
g__Jeotgalicoccus	0.009838	0.01657	0	0	2.33E-10	6.42E-09	-0.01416	-0.00552	-0.00984
g__norank_c__Cyanobacteria	0.08917	0.1476	0.001183	0.002436	4.6E-10	1.08E-08	-0.1223	-0.05186	-0.08799
g__Lachnospiraceae_UCG-006	0.05434	0.09252	0.000284	0.001311	4.99E-10	1.08E-08	-0.08023	-0.03199	-0.05406
g__Brevibacterium	0.03082	0.0563	0	0	5.65E-10	1.08E-08	-0.04628	-0.01754	-0.03082
g__Dietzia	0.02759	0.04763	0	0	5.66E-10	1.08E-08	-0.04008	-0.01614	-0.02759
g__Mucispirillum	0.01754	0.03161	0	0	5.66E-10	1.08E-08	-0.02639	-0.00999	-0.01754
g__Treponema_2	0.01671	0.02854	9.46E-05	0.00054	4.38E-10	1.08E-08	-0.02467	-0.00922	-0.01661
g__Sporosarcina	0.01411	0.02484	0	0	5.64E-10	1.08E-08	-0.0204	-0.00807	-0.01411
g__Christensenella	0.05726	0.09743	0.000899	0.002834	1.16E-09	2.11E-08	-0.08095	-0.03197	-0.05636
g__norank_c__Acidobacteria	0.01244	0.02274	4.73E-05	0.000384	2.06E-09	3.62E-08	-0.01812	-0.0072	-0.01239
g__Ralstonia	0.01478	0.02707	0	0	3.15E-09	5.3E-08	-0.02186	-0.00797	-0.01478
g__Enterorhabdus	0.02644	0.04349	0.000946	0.005849	3.33E-09	5.4E-08	-0.03606	-0.01504	-0.0255

g__Bacillus	0.5491	4.068	0.002129	0.01249	6.85E-09	1.07E-07	-1.602	-0.01435	-0.5471
g__unclassified_f__Family_XIII	0.01015	0.0187	0	0	7.27E-09	1.1E-07	-0.01536	-0.00583	-0.01015
g__Pseudomonas	0.04982	0.1218	0.000189	0.000751	7.78E-09	1.14E-07	-0.08252	-0.02358	-0.04962
g__RB41	0.01228	0.02039	4.73E-05	0.000384	1.14E-08	1.61E-07	-0.01755	-0.0074	-0.01224
g__Atopostipes	0.01036	0.02109	0	0	1.67E-08	2.15E-07	-0.01661	-0.00515	-0.01036
g__norank_f__Nitrosomonadaceae	0.006611	0.01335	0	0	1.66E-08	2.15E-07	-0.01057	-0.00328	-0.00661
g__Shewanella	0.004893	0.008517	0	0	1.66E-08	2.15E-07	-0.00729	-0.00281	-0.00489
g__norank_f__Clostridiales_vadinBB60_group	0.1909	0.3197	0.007761	0.02391	2.27E-08	2.84E-07	-0.2675	-0.1116	-0.1832
g__Oscillibacter	0.08183	0.1367	0.005915	0.03308	2.92E-08	3.55E-07	-0.1132	-0.04164	-0.07591
g__unclassified_f__Erysipelotrichaceae	0.06538	0.1133	0.003691	0.02209	3.41E-08	4.04E-07	-0.09183	-0.03328	-0.06169
g__Rubrobacter	0.01202	0.02126	0	0	3.79E-08	4.25E-07	-0.01765	-0.00692	-0.01202
g__Microvirga	0.005362	0.009363	0	0	3.77E-08	4.25E-07	-0.00781	-0.00323	-0.00536
g__Nesterenkonia	0.01223	0.02255	4.73E-05	0.000384	6.35E-08	6.95E-07	-0.01785	-0.00699	-0.01219
g__Paracoccus	0.008225	0.01564	4.73E-05	0.000384	6.57E-08	7.01E-07	-0.0126	-0.00463	-0.00818
g__unclassified_o__Bacteroidales	0.05898	0.09907	0.002887	0.0102	8.14E-08	7.88E-07	-0.08353	-0.03209	-0.05609
g__Nosocomiicoccus	0.007131	0.01306	0	0	8.45E-08	7.88E-07	-0.01041	-0.0039	-0.00713
g__Micrococcus	0.00609	0.0111	0	0	8.45E-08	7.88E-07	-0.00911	-0.00333	-0.00609
g__norank_f__ODP1230B8.23	0.004008	0.007411	0	0	8.36E-08	7.88E-07	-0.00609	-0.00219	-0.00401
g__Achromobacter	0.002915	0.006969	0	0	8.22E-08	7.88E-07	-0.00495	-0.00146	-0.00292
g__Bradyrhizobium	0.002394	0.004541	0	0	8.16E-08	7.88E-07	-0.00354	-0.00125	-0.00239
g__Alloprevotella	2.616	4.159	1.127	4.466	9.44E-08	8.62E-07	-2.858	0.06179	-1.489
g__norank_f__Peptococcaceae	0.03685	0.06148	0.002934	0.0146	9.64E-08	8.62E-07	-0.05008	-0.01877	-0.03392
g__Ruminiclostridium	0.02946	0.05136	0.000852	0.003125	1.35E-07	1.18E-06	-0.042	-0.01648	-0.02861
g__Rhizobium	0.006507	0.01213	9.46E-05	0.000769	1.83E-07	1.44E-06	-0.00944	-0.00359	-0.00641
g__Brachybacterium	0.005934	0.01052	0	0	1.87E-07	1.44E-06	-0.00859	-0.00344	-0.00593
*g__norank_f__Acidobacteriaceae__Subgroup_1_*	0.004529	0.008242	0	0	1.86E-07	1.44E-06	-0.00677	-0.0026	-0.00453
g__Stenotrophomonas	0.004164	0.00749	0	0	1.86E-07	1.44E-06	-0.00604	-0.00239	-0.00416
g__Mizugakiibacter	0.00406	0.008574	0	0	1.86E-07	1.44E-06	-0.00625	-0.00219	-0.00406
g__Burkholderia-Paraburkholderia	0.0038	0.007321	0	0	1.86E-07	1.44E-06	-0.00593	-0.00208	-0.0038
g__norank_f__Xanthobacteraceae	0.00354	0.007375	0	0	1.85E-07	1.44E-06	-0.00536	-0.00193	-0.00354
g__[Eubacterium]_nodatum_group	0.02764	0.04152	0.004259	0.01344	2.16E-07	1.63E-06	-0.03385	-0.01272	-0.02338

g__Enterococcus	0.6214	1.04	0.05314	0.3338	3.14E-07	2.33E-06	-0.8427	-0.3006	-0.5682
g__norank_o__SC-I-84	0.00432	0.008114	4.73E-05	0.000384	3.34E-07	2.44E-06	-0.00662	-0.00246	-0.00427
g__norank_f__288-2	0.004737	0.008843	0	0	4.08E-07	2.75E-06	-0.00708	-0.0026	-0.00474
g__Flavobacterium	0.003384	0.006437	0	0	4.05E-07	2.75E-06	-0.0051	-0.00193	-0.00338
g__norank_c__KD4-96	0.002915	0.005359	0	0	4.07E-07	2.75E-06	-0.00427	-0.00167	-0.00292
g__unclassified_f__Xanthobacteraceae	0.002655	0.00504	0	0	4.04E-07	2.75E-06	-0.00401	-0.00146	-0.00266
g__Anaerovorax	0.00177	0.003063	0	0	3.99E-07	2.75E-06	-0.0025	-0.00104	-0.00177
g__norank_f__Rhodospirillaceae	0.03019	0.06756	0.008613	0.03954	5.78E-07	3.84E-06	-0.04562	-0.00434	-0.02158
g__Sphingomonas	0.003748	0.007246	4.73E-05	0.000384	7.49E-07	4.89E-06	-0.00563	-0.00198	-0.0037
g__unclassified_f__Comamonadaceae	0.00531	0.01064	0	0	8.83E-07	5.3E-06	-0.00812	-0.00276	-0.00531
g__Blastococcus	0.003956	0.00756	0	0	8.83E-07	5.3E-06	-0.00593	-0.00229	-0.00396
g__Vibrio	0.003956	0.008775	0	0	8.81E-07	5.3E-06	-0.00666	-0.00198	-0.00396
g__norank_p__WS6	0.00354	0.006767	0	0	8.82E-07	5.3E-06	-0.00526	-0.00198	-0.00354
g__Soonwooa	0.003071	0.005793	0	0	8.82E-07	5.3E-06	-0.00458	-0.00161	-0.00307
g__Pseudonocardia	0.001926	0.003641	0	0	8.66E-07	5.3E-06	-0.00292	-0.00109	-0.00193
g__Enterobacter	0.9451	2.834	0.8529	3.033	9.73E-07	5.76E-06	-1.151	0.9806	-0.09228
g__Ruminococcaceae_UCG-014	0.7164	1.065	0.2025	0.4618	1.44E-06	8.44E-06	-0.8068	-0.2496	-0.5139
g__norank_f__Christensenellaceae	0.01728	0.04355	0.002129	0.005645	1.73E-06	9.95E-06	-0.02696	-0.00684	-0.01515
g__Halanaerobium	0.004841	0.01025	0	0	1.89E-06	1.01E-05	-0.00755	-0.0024	-0.00484
g__norank_o__Gastranaerophilales	0.00406	0.008118	0	0	1.89E-06	1.01E-05	-0.00619	-0.00224	-0.00406
g__Aeromonas	0.003904	0.01442	0	0	1.89E-06	1.01E-05	-0.00848	-0.00141	-0.0039
g__norank_c__Actinobacteria	0.002394	0.004892	0	0	1.88E-06	1.01E-05	-0.00364	-0.0013	-0.00239
g__Arthrobacter	0.002394	0.004613	0	0	1.88E-06	1.01E-05	-0.00349	-0.0013	-0.00239
g__norank_p__Tectomicrobia	0.001666	0.00352	0	0	1.86E-06	1.01E-05	-0.00271	-0.00088	-0.00167
g__Akkermansia	0.2031	0.8314	0.05702	0.2295	1.93E-06	1.02E-05	-0.3736	0.01884	-0.1461
g__Lactobacillus	3.5	6.035	0.6953	3.346	2.69E-06	0.000014	-4.535	-0.9814	-2.805
g__Catabacter	0.004841	0.008479	0.000284	0.001311	2.85E-06	1.47E-05	-0.00693	-0.00263	-0.00456
g__Odoribacter	0.7093	0.9294	0.1544	0.251	3.26E-06	1.66E-05	-0.8042	-0.3107	-0.5549
g__Solirubrobacter	0.002967	0.006336	4.73E-05	0.000384	3.55E-06	1.79E-05	-0.00453	-0.00142	-0.00292
g__Arcobacter	0.00203	0.003674	4.73E-05	0.000384	3.74E-06	1.86E-05	-0.00287	-0.00109	-0.00198

g__Lysinibacillus	0.01431	0.09297	0	0	4E-06	1.87E-05	-0.04893	-0.00141	-0.01432
g__unclassified_f__Micromonosporaceae	0.005205	0.01119	0	0	4.01E-06	1.87E-05	-0.00797	-0.00271	-0.00521
g__norank_o__Gaiellales	0.004945	0.009747	0	0	4.01E-06	1.87E-05	-0.0076	-0.00281	-0.00495
g__norank_o__JG30-KF-CM45	0.003279	0.007006	0	0	4E-06	1.87E-05	-0.00526	-0.00161	-0.00328
g__norank_o__AKYG1722	0.002238	0.004383	0	0	3.99E-06	1.87E-05	-0.00349	-0.00115	-0.00224
g__norank_f__Gemmatimonadaceae	0.002082	0.004093	0	0	3.99E-06	1.87E-05	-0.00318	-0.00115	-0.00208
g__norank_f__Flavobacteriaceae	0.00229	0.004909	9.46E-05	0.000769	4.93E-06	2.27E-05	-0.0037	-0.00109	-0.0022
g__Morganella	0.001978	0.005269	9.46E-05	0.000769	5.42E-06	2.48E-05	-0.00345	-0.00081	-0.00188
g__norank_c__Gitt-GS-136	0.002915	0.006502	0	0	8.39E-06	3.68E-05	-0.00468	-0.00135	-0.00292
g__Nitrospira	0.002707	0.006232	0	0	8.37E-06	3.68E-05	-0.00427	-0.0013	-0.00271
g__Sphingobium	0.00229	0.004523	0	0	8.4E-06	3.68E-05	-0.00338	-0.0012	-0.00229
g__Acidibacter	0.001458	0.002786	0	0	8.34E-06	3.68E-05	-0.00219	-0.00083	-0.00146
g__Mycobacterium	0.002499	0.004409	0.000142	0.000656	9.95E-06	4.32E-05	-0.00351	-0.00131	-0.00236
g__Citrobacter	0.3332	1.795	0.02896	0.08211	1.32E-05	5.67E-05	-0.7937	-0.02906	-0.3042
g__Lactococcus	0.03352	0.09106	0.001514	0.006156	1.65E-05	7.02E-05	-0.05708	-0.0114	-0.03201
g__Caulobacter	0.002915	0.0111	0	0	1.74E-05	7.07E-05	-0.00599	-0.00094	-0.00292
g__Geodermatophilus	0.002447	0.005518	0	0	1.74E-05	7.07E-05	-0.00396	-0.0013	-0.00245
g__Thermus	0.001822	0.00374	0	0	1.74E-05	7.07E-05	-0.00292	-0.00094	-0.00182
g__norank_f__Rhodobiaceae	0.00177	0.00404	0	0	1.74E-05	7.07E-05	-0.00292	-0.00088	-0.00177
g__Streptomyces	0.001562	0.003227	0	0	1.74E-05	7.07E-05	-0.00245	-0.00083	-0.00156
g__Proteus	0.002863	0.00512	0.000189	0.000751	2.35E-05	9.42E-05	-0.00413	-0.00142	-0.00267
g__Alcaligenes	0.007496	0.04669	0	0	3.59E-05	0.000134	-0.02488	-0.00088	-0.0075
g__Dongia	0.002394	0.007028	0	0	3.58E-05	0.000134	-0.00432	-0.00078	-0.00239
g__H16	0.001874	0.004424	0	0	3.59E-05	0.000134	-0.00307	-0.00088	-0.00187
g__Microlunatus	0.001614	0.003792	0	0	3.57E-05	0.000134	-0.00266	-0.00078	-0.00161
g__Elizabethkingia	0.001353	0.002953	0	0	3.58E-05	0.000134	-0.00213	-0.00068	-0.00135
g__Truepera	0.001249	0.002648	0	0	3.57E-05	0.000134	-0.00193	-0.00057	-0.00125
g__norank_f__P-102	0.001197	0.002703	0	0	3.57E-05	0.000134	-0.00198	-0.00057	-0.0012
g__Roseiflexus	0.001093	0.00256	0	0	3.53E-05	0.000134	-0.00172	-0.00052	-0.00109
g__Parvibacter	0.002603	0.00446	0.000142	0.000656	3.65E-05	0.000135	-0.00377	-0.00134	-0.00246
g__Klebsiella	0.5667	1.063	0.3449	1.053	3.78E-05	0.000139	-0.5928	0.1807	-0.2218

g__norank_f__Bacteroidales_S24-7_group	4.856	7.436	0.6246	1.416	3.83E-05	0.00014	-6.239	-2.455	-4.231
g__unclassified_f__Prevotellaceae	0.00203	0.005138	9.46E-05	0.00054	6.52E-05	0.000236	-0.00339	-0.00085	-0.00194
g__Cloacibacterium	0.003071	0.01241	0	0	7.33E-05	0.000253	-0.00661	-0.00083	-0.00307
g__Gaiella	0.00229	0.005359	4.73E-05	0.000384	7.2E-05	0.000253	-0.0037	-0.00095	-0.00224
g__Psychroglaciecola	0.001718	0.004083	0	0	7.32E-05	0.000253	-0.00292	-0.00078	-0.00172
g__unclassified_f__Archangiaceae	0.001301	0.003059	0	0	7.31E-05	0.000253	-0.00213	-0.00057	-0.0013
g__Modestobacter	0.001093	0.002359	0	0	7.3E-05	0.000253	-0.00177	-0.00052	-0.00109
g__norank_f__DA101_soil_group	0.001041	0.002276	0	0	7.29E-05	0.000253	-0.00161	-0.00052	-0.00104
g__unclassified_f__Ruminococcaceae	0.4013	0.6113	0.0566	0.07884	7.46E-05	0.000255	-0.5108	-0.191	-0.3448
g__unclassified_f__Enterobacteriaceae	0.1591	0.8805	0.02262	0.1006	1E-04	0.00034	-0.3823	0.01005	-0.1365
g__Brevundimonas	0.006507	0.03949	0	0	0.000148	0.000475	-0.01697	-0.00078	-0.00651
g__norank_f__JG34-KF-361	0.001562	0.00366	0	0	0.000148	0.000475	-0.00255	-0.00068	-0.00156
g__Leucobacter	0.001405	0.003325	0	0	0.000148	0.000475	-0.00234	-0.00057	-0.00141
g__Arenimonas	0.001353	0.003371	0	0	0.000148	0.000475	-0.00229	-0.00057	-0.00135
g__norank_f__Planctomycetaceae	0.001353	0.003271	0	0	0.000148	0.000475	-0.00224	-0.00057	-0.00135
g__Gemmatimonas	0.001145	0.002504	0	0	0.000148	0.000475	-0.00177	-0.00057	-0.00115
g__norank_o__Xanthomonadales	0.000833	0.001896	0	0	0.000147	0.000475	-0.00135	-0.00036	-0.00083
g__Bryobacter	0.000781	0.001689	0	0	0.000147	0.000475	-0.00125	-0.00036	-0.00078
g__norank_o__Mollicutes_RF9	0.1368	0.4176	0.03805	0.1002	0.000155	0.000491	-0.2364	-0.01591	-0.09875
g__Massilia	0.001353	0.003008	4.73E-05	0.000384	0.000157	0.000495	-0.00219	-0.00058	-0.00131
g__[Eubacterium]_fissicatena_group	0.08349	0.1296	0.01287	0.02467	0.000231	0.000724	-0.1072	-0.03874	-0.07063
g__Conexibacter	0.001614	0.00599	0	0	0.000297	0.000887	-0.00333	-0.00042	-0.00161
g__Steroidobacter	0.001145	0.003041	0	0	0.000298	0.000887	-0.00198	-0.00047	-0.00115
g__Virgisporangium	0.001145	0.002815	0	0	0.000298	0.000887	-0.00187	-0.00047	-0.00115
g__Blastocatella	0.000885	0.002081	0	0	0.000297	0.000887	-0.00146	-0.00036	-0.00088
g__norank_f__Elev-16S-1332	0.000885	0.002081	0	0	0.000297	0.000887	-0.00146	-0.00042	-0.00088
g__Rhodoplanes	0.000885	0.002081	0	0	0.000297	0.000887	-0.00141	-0.00042	-0.00088
g__Skermanella	0.000833	0.001896	0	0	0.000297	0.000887	-0.00135	-0.00036	-0.00083
g__unclassified_o__Clostridiales	0.01869	0.02562	0.006862	0.01443	0.000373	0.001102	-0.01941	-0.0041	-0.01183
g__Family_XIII_AD3011_group	0.0393	0.04509	0.01547	0.0229	0.000544	0.001598	-0.03636	-0.01212	-0.02383

g__Pseudoalteromonas	0.001718	0.004433	0	0	0.000594	0.001658	-0.00292	-0.00062	-0.00172
g__norank_o__C0119	0.000989	0.002603	0	0	0.000594	0.001658	-0.00167	-0.00036	-0.00099
*g__unclassified_f__Acidobacteriaceae__Subgroup_1_*	0.000989	0.002666	0	0	0.000594	0.001658	-0.00172	-0.00036	-0.00099
g__Nitrosomonas	0.000937	0.002654	0	0	0.000593	0.001658	-0.00167	-0.00036	-0.00094
g__Chryseobacterium	0.000885	0.002159	0	0	0.000594	0.001658	-0.00146	-0.00036	-0.00088
g__Sulfurimonas	0.000781	0.001961	0	0	0.000593	0.001658	-0.00135	-0.00031	-0.00078
g__norank_f__Acidimicrobiaceae	0.000781	0.002043	0	0	0.000592	0.001658	-0.0013	-0.00031	-0.00078
g__Pelomonas	0.000729	0.001851	0	0	0.000592	0.001658	-0.00125	-0.00026	-0.00073
g__Desulfovibrio	0.5013	0.7871	0.1393	0.3278	0.000624	0.00173	-0.5794	-0.156	-0.362
g__Flavonifractor	0.06611	0.125	0.1725	0.3951	0.000628	0.00173	0.01691	0.2147	0.1064
g__[Eubacterium]_xylanophilum_group	0.0431	0.09006	0.04604	0.1468	0.00098	0.002683	-0.03574	0.0507	0.002945
g__Eisenbergiella	0.01228	0.02171	0.01126	0.04366	0.001009	0.002745	-0.01178	0.01252	-0.00102
g__[Eubacterium]_brachy_group	0.01994	0.03171	0.01169	0.06651	0.001105	0.002987	-0.02279	0.01266	-0.00825
g__Tissierella	0.01145	0.08502	0	0	0.001174	0.003102	-0.03363	-0.00026	-0.01145
g__unclassified_f__Xanthomonadaceae	0.000729	0.002102	0	0	0.001176	0.003102	-0.00135	-0.00026	-0.00073
g__unclassified_c__Betaproteobacteria	0.000677	0.001915	0	0	0.001174	0.003102	-0.0012	-0.00026	-0.00068
g__Kurthia	0.000573	0.001465	0	0	0.001174	0.003102	-0.00094	-0.00021	-0.00057
g__Weissella	0.01994	0.06107	0.000473	0.002139	0.001267	0.003303	-0.03699	-0.00609	-0.01946
g__Propionibacterium	0.001093	0.002624	4.73E-05	0.000384	0.001267	0.003303	-0.00177	-0.00043	-0.00105
g__norank_f__Lachnospiraceae	1.022	0.9018	0.7916	1.435	0.001629	0.004221	-0.6233	0.217	-0.2307
g__Comamonas	0.001405	0.003833	9.46E-05	0.00054	0.002286	0.005682	-0.00231	-0.00048	-0.00131
g__norank_c__S085	0.000677	0.001915	0	0	0.002322	0.005682	-0.0012	-0.00026	-0.00068
g__Azospirillum	0.000677	0.002578	0	0	0.002314	0.005682	-0.00141	-0.00021	-0.00068
g__Aquabacterium	0.000625	0.0018	0	0	0.002321	0.005682	-0.00109	-0.00026	-0.00062
g__Sphingobacterium	0.000573	0.001863	0	0	0.002314	0.005682	-0.00109	-0.00021	-0.00057
g__Actinophytocola	0.000573	0.001676	0	0	0.002318	0.005682	-0.00104	-0.00021	-0.00057
g__Taibaiella	0.000573	0.001676	0	0	0.002318	0.005682	-0.00104	-0.00021	-0.00057
g__Venenivibrio	0.000573	0.001574	0	0	0.00232	0.005682	-0.00099	-0.00021	-0.00057
g__unclassified_f__Intrasporangiaceae	0.000521	0.001539	0	0	0.002314	0.005682	-0.00094	-0.00021	-0.00052
g__Nordella	0.000469	0.001263	0	0	0.002314	0.005682	-0.00083	-0.00016	-0.00047
g__Ruminococcaceae_UCG-009	0.02868	0.03656	0.01358	0.0245	0.003183	0.007744	-0.02584	-0.00496	-0.0151

g__unclassified_f__Christensenellaceae	0.002082	0.004173	0.000994	0.004319	0.003444	0.008333	-0.00248	0.000516	-0.00109
g__Coprococcus_1	0.121	0.1397	0.07169	0.08931	0.004159	0.01001	-0.09582	-0.01011	-0.04933
g__Pedobacter	0.000677	0.002234	0	0	0.00456	0.01057	-0.0013	-0.00016	-0.00068
g__Lechevalieria	0.000625	0.002057	0	0	0.00456	0.01057	-0.0012	-0.00021	-0.00062
g__Ureaplasma	0.000573	0.001772	0	0	0.00456	0.01057	-0.00104	-0.00021	-0.00057
g__Luteibacter	0.000469	0.001388	0	0	0.004556	0.01057	-0.00083	-0.00016	-0.00047
g__Reyranella	0.000469	0.001502	0	0	0.00455	0.01057	-0.00088	-0.00016	-0.00047
g__Tumebacillus	0.000469	0.001388	0	0	0.004556	0.01057	-0.00083	-0.00016	-0.00047
g__unclassified_f__Erythrobacteraceae	0.000364	0.001011	0	0	0.004542	0.01057	-0.00062	-0.00016	-0.00036
g__Ruminococcaceae_UCG-010	0.04039	0.07559	0.04519	0.1507	0.005119	0.0118	-0.03301	0.05252	0.004802
g__norank_p__Saccharibacteria	0.02499	0.04291	0.0151	0.02981	0.005453	0.01251	-0.02326	0.002943	-0.00989
g__Clostridium_sensu_stricto_3	0.000573	0.001574	9.46E-05	0.000769	0.0061	0.01392	-0.00094	-6.2E-05	-0.00048
g__unclassified_f__Coriobacteriaceae	0.001874	0.004535	0.000615	0.002206	0.007476	0.01697	-0.0027	-9E-05	-0.00126
g__Tyzzerella	0.01291	0.02781	0.02238	0.09932	0.007977	0.01801	-0.01162	0.03959	0.009472
g__Sellimonas	0.001093	0.003629	0.01978	0.06932	0.008081	0.01815	0.005309	0.03754	0.01869
g__Nocardioides	0.001041	0.005353	0	0	0.008935	0.01938	-0.0026	-0.0001	-0.00104
g__norank_f__Caulobacteraceae	0.000677	0.002513	0	0	0.008936	0.01938	-0.00141	-0.00016	-0.00068
g__norank_f__Mitochondria	0.000416	0.001344	0	0	0.00893	0.01938	-0.00078	-0.0001	-0.00042
g__Mycoplasma	0.000416	0.001344	0	0	0.00893	0.01938	-0.00083	-0.00016	-0.00042
g__norank_o__JG30-KF-AS9	0.000416	0.001344	0	0	0.00893	0.01938	-0.00078	-0.0001	-0.00042
g__Vitreoscilla	0.000364	0.001163	0	0	0.008924	0.01938	-0.00068	-0.0001	-0.00036
g__Rhizomicrobium	0.000364	0.001163	0	0	0.008924	0.01938	-0.00073	-0.0001	-0.00036
g__Parasutterella	0.2367	0.4548	0.3006	0.8893	0.009103	0.01964	-0.1663	0.3284	0.0639
g__Solobacterium	0.004633	0.01242	0.001893	0.005018	0.01003	0.02152	-0.00663	0.000142	-0.00274
g__Candidatus_Solibacter	0.000625	0.0018	4.73E-05	0.000384	0.01012	0.02152	-0.00109	-0.00016	-0.00058
g__Pedomicrobium	0.000625	0.0018	4.73E-05	0.000384	0.01012	0.02152	-0.00105	-0.00018	-0.00058
g__Bacteroides	13.68	11.73	21.89	17.64	0.01041	0.02202	2.895	13.08	8.208
g__Peptococcus	0.006975	0.01105	0.006909	0.02533	0.01194	0.02515	-0.00599	0.007545	-6.7E-05
g__Escherichia-Shigella	1.686	3.634	1.949	5.607	0.01497	0.03137	-1.291	2.003	0.2625
g__unclassified_f__Rhodobacteraceae	0.000416	0.001571	0	0	0.0175	0.03501	-0.00083	-0.0001	-0.00042

g__norank_d__Bacteria	0.000364	0.001419	0	0	0.0175	0.03501	-0.00078	-5.2E-05	-0.00036
g__Craurococcus	0.000364	0.001419	0	0	0.0175	0.03501	-0.00078	-5.2E-05	-0.00036
g__norank_f__Chitinophagaceae	0.000364	0.001298	0	0	0.0175	0.03501	-0.00073	-5.2E-05	-0.00036
g__unclassified_o__Acidimicrobiales	0.000312	0.001106	0	0	0.0175	0.03501	-0.00062	-5.2E-05	-0.00031
g__norank_f__KF-JG30-B3	0.000312	0.001106	0	0	0.0175	0.03501	-0.00062	-5.2E-05	-0.00031
g__norank_c__JG30-KF-CM66	0.00026	0.000871	0	0	0.01748	0.03501	-0.00052	-5.2E-05	-0.00026
g__norank_f__FFCH7168	0.00026	0.000871	0	0	0.01748	0.03501	-0.00052	-5.2E-05	-0.00026
g__Candidatus_Arthromitus	0.00026	0.000871	0	0	0.01748	0.03501	-0.00052	-5.2E-05	-0.00026
g__Pirellula	0.00026	0.000871	0	0	0.01748	0.03501	-0.00047	-5.2E-05	-0.00026
g__Oscillospira	0.000364	0.001734	0.001514	0.003883	0.01839	0.0366	0.00018	0.002224	0.00115
g__Gordonibacter	0.002447	0.005114	0.001514	0.005485	0.02231	0.04422	-0.00272	0.001135	-0.00093