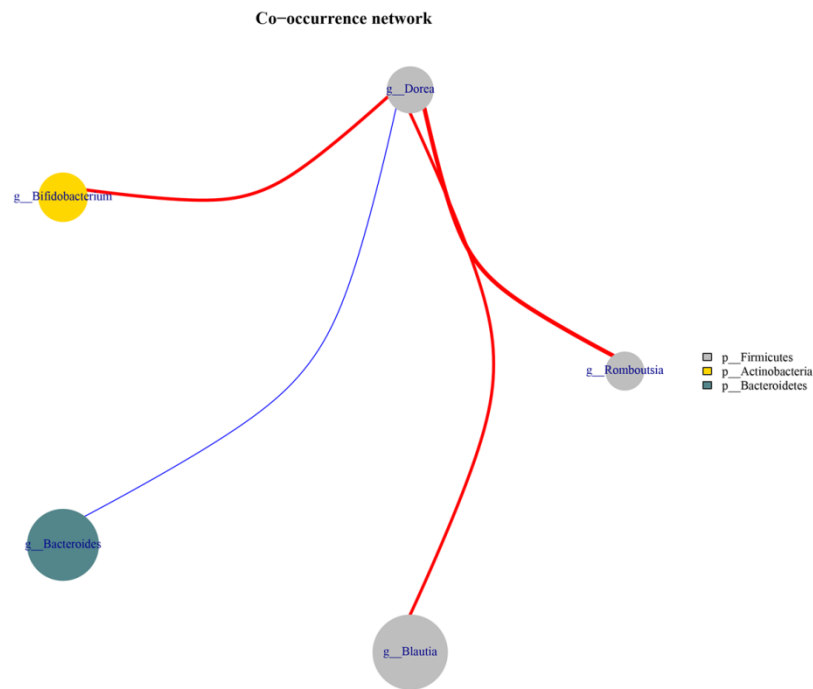




Supplementary Figure 1 The association network diagram of bacterial genera among the different groups. Network analysis was conducted through Spearman correlation ($R > 0.6$ and $P < 0.01$ indicate a positive correlation).

Supplementary Table 1 Relative

	IT	H	IA
o__Clostridiales	0.4571889	0.745091	0.7197638
o__Bacteroidales	0.3327221	0.0941596	0.1126866
o__Selenomonadales	0.1329844	0.0257525	0.0783391
o__Bifidobacteriales	0.0201254	0.0386267	0.0210984
o__Lactobacillales	0.0143873	0.0130552	0.0102322
o__Enterobacteriales	0.0116844	0.012182	0.0082021
o__Burkholderiales	0.0076374	0.0027849	0.0016823
o__Coriobacteriales	0.0066914	0.0341111	0.0214563
o__Pasteurellales	0.0063152	0.0002517	0.0009102
o__Erysipelotrichales	0.0053217	0.0279631	0.0166343
o__Desulfovibrionales	0.0024216	0.0024466	0.0031653
o__Fusobacteriales	0.0016692	0.0010817	0.003917
o__Actinomycetales	0.0002265	0.0003619	0.0002608
o__Synergistales	0.0001571	0.0002557	0.000133
o__Mollicutes_RF9	0.0001169	0.0004642	0.000133
o__unidentified	0.0001096	0.0001809	9.72E-05
o__Bacillales	8.04E-05	0.0001455	0.000179
o__Campylobacteriales	6.21E-05	0	0
o__Verrucomicrobiales	4.75E-05	0.0008142	0.0002506
o__Micrococcales	2.19E-05	8.65E-05	4.60E-05
o__Spirochaetales	1.46E-05	0	0
o__Thermoanaerobacteriales	7.31E-06	3.93E-06	0
o__Corynebacteriales	3.65E-06	1.97E-05	0
o__Methanobacteriales	3.65E-06	0	0
o__Flavobacteriales	0	2.75E-05	4.09E-05
o__Rhodospirillales	0	0.0001298	7.16E-05
o__Victivallales	0	3.93E-06	0
o__Pseudomonadales	0	0	2.05E-05
o__Aeromonadales	0	0	0.0006801

Supplementary Table 2 Difference

	IT5	IT12	IT15	IT16	IT18	IT20	IT22	IT31	IT36	IT43	IT45	IT48	IT50	IT52	H7	H8	H11	H12	H13	H14	H15	H16	H17	H18	H19	H20	H21	IA8	IA9	IA16	IA17	IA18	IA19	IA20	IA21	IA22	IA23		
g__Prevotellaceae	0.0732256	0.0393741	0.175496	5.11E-05	0	0	0	0	0.0621293	0.0034772	0	0	0.0003579	0	0	0.0002557	0	5.11E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
g__Ruminococcus	0	5.11E-05	5.11E-05	0.0024034	0	0.0001023	0	0.0012784	0	0.0070567	0.0012784	0.0023011	0	0	0.0019943	0.0063408	5.11E-05	0.0001023	0.0030681	0.0003068	0.0214256	0.0027102	0	0.0036817	0.0004602	0.024954	0.0250562	0.0007159	0.0265903	0.0002557	0.0262835	0.0039374	0.0065453	0.0012272	0.0002557	5.11E-05	0		
g__Ruminococcus	0.0014829	0	0	0.0007159	0.0003068	0.0002557	0.0004091	0.0001534	0.0002045	0.0013807	0.001892	0.0029658	0.0232665	0.000767	0.0017386	0.0009204	0.0021477	0.0015341	0.002659	0.0044488	0.003784	0.0004091	0.0266414	0.0329311	0.0052158	0.0057783	0.0004091	0.0008182	0.0002557	0.0010227	0.0033749	0.0015852	0.0002557	0.0016363	0.0042442	0.0002045	0.0002045		
g__Blautia	0.0119656	0.0015852	0.0152894	0.0062896	0.0636633	0.0210166	0.0319595	0.0187666	0.0289425	0.1097873	0.097208	0.1658826	0.3234301	0.0373798	0.2064328	0.1264574	0.2112395	0.1479853	0.0840663	0.0831458	0.3492534	0.2077623	0.0770096	0.1123952	0.0993046	0.3215381	0.0924013	0.3203109	0.303692	0.077521	0.3835651	0.1485478	0.2293414	0.1054919	0.1909388	0.1152076	0.0453569		
g__Faecalibacterium	0	0	0	0	5.11E-05	0	5.11E-05	0	0	0.0002557	0	0	0	0	0.0019943	0.0009204	0	5.11E-05	0.0001023	0	0	0.0002045	0	0	0	0.0006136	5.11E-05	0.0002557	0.0007159	0.0003579	0.0050112	0.0033749	0.0008182	0	5.11E-05	0	0		
g__Erysipelatoclostridium	0	0	0	0	0	0	0	0.0001534	0	0	0	0	0.0008182	0	0	0.0009716	0	0	5.11E-05	0	0.0001023	0	0.0001023	5.11E-05	0	0	0.0001023	0.0002557	0	0.0003068	0.0027102	0.0001023	0	0.0009204	0	5.11E-05	5.11E-05		
g__Sutterella	0.0091532	0.0039885	0.0154428	0.0331356	0.004909	0.0063408	0.0052669	0.0025568	0.0082839	0.0005625	0.0005114	0	0.0003068	0	5.11E-05	0.0001023	0.0001534	0	0.0008693	0.0003579	0	0	0.0002557	0	0.0004602	0	0	0	0	0	0	5.11E-05	0	0.0006648	0	0.0003579	0.0002557		
g__Ruminococcus	0.000767	0	0	0	0.0013295	0	0.0005625	0.0001023	0	0	0.0012272	0	0.0001023	0.0008182	0.0021988	0	0.0035795	0.0046533	0.0024034	0.0006648	0	0	0.0084373	0	0	0.0003579	0.0044999	0.0006136	0.0042954	0.0023522	0.0017897	0.0042954	0.000767	0.0019943	0.0035795	0.0031192	0.0037329		
g__Faecalibacterium	0.0616179	0.0038351	0.0497034	0.0288914	0.1049806	0.1087134	0.0798732	0.035539	0.0428513	0.0933729	0.0912252	0.1019636	0.0676519	0.0436183	0.0711291	0.1247188	0.130088	0.0332379	0.0952649	0.1287584	0.004909	0.0636633	0.1619452	0.145224	0.1025772	0.0190223	0.2082225	0.0935263	0.0608509	0.0882082	0.1369401	0.0725609	0.2107282	0.0677541	0.1992227	0.1713541	0.1667519		
g__Sellimonium	0	0	0	0	0	0	0	0	0	0	0.000767	0	0	0	0	0	0	0	0.0009204	0.0003068	0.0001023	0	0.0001534	0	0	5.11E-05	0	0.0659133	0.0001534	5.11E-05	5.11E-05	0.0029658	0.0003068	0.0003068	0.0046533	0.0006136	0	0	
g__Fusicatella	0.0021477	0.0010227	0.0042442	0.0095623	0.0166701	0.0369708	0.0142667	0.0073123	0.0024034	0.0050624	0.050675	0.2105236	0.0018409	0.013244	0.0606975	0.0070055	0.0275107	0.0323174	0.0209143	0.0199939	0.0189712	0.0402434	0.0318061	0.0554817	0.0377889	0.0183064	0.0228574	0.033647	0.0074146	0.0363571	0	0.0245449	0.0224484	0.0133463	0.0338004	0.0118122	0.0194314		
g__Butyrivibrio	0.0035795	0.0029658	0.0025568	0.0060851	0.0094089	0.0106873	0.0054715	0.0084884	0.0109941	0.0074146	0.0082328	0.0092555	0.0019943	0.0031192	0.0124259	0.0101248	0.0156985	0.0061362	0.0210677	0.0094089	0.0197893	0.0153917	0.0083862	0.0029658	0.0057783	0.0153917	0.0193291	0.004142	0.0139599	0.0042954	0.0002557	0.0047556	0.0035795	0.0096646	0.0089998	0.0054715	0.0105339		
g__Klebsiella	0	0	0	0.0009204	0	0.0003579	0.019278	0.0020454	0.0070567	0.0019431	0.026488	0.0008693	0.0004091	5.11E-05	0.0002045	0.0153406	0.0002557	0.0048067	0.0035283	0	0.0005625	0.0001534	0	0.0003579	0.0140622	0.0014829	0.0303232	0	0.0010738	0	0	0	0	0.0006648	0	0	5.11E-05		
g__Alloprevotella	0.103242	0.1383719	5.11E-05	0	0	0	0	0	0.0526693	0	0	0	0.002659	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
g__Eubacterium	0.007568	0.0009716	0.0052669	0.0014318	0.0063919	0.0206075	0.0103804	0	0.0147269	0	0.0201984	0.0503682	0.0147781	0.0288403	0.03063	0.0329311	0.0695439	0.0459194	0.0272551	0.0110452	0.0518511	0.0361015	0.0562999	0.0456637	0.0238801	0.0602884	0.0327265	0.0226018	0	0.0243915	0.0716916	0.0326243	0.0280732	0.018153	0.0179996	0.0170792	0.0121702		
g__Haemophilus	5.11E-05	0.0001534	0.0462774	0.0008693	0.0001534	0.0255676	0.0012272	0.008335	0.0003579	0.0019431	0.0023522	0.0002557	5.11E-05	0.0002557	0.0001534	0	0	0.0002045	0	0	0.0002045	0.0006136	0	0	0.0018409	5.11E-05	0.0002045	0.0041931	5.11E-05	0	0.0004091	0	0	0.0038351	0	0.0002557	0.0003579		
g__Gemellimonas	0.0001023	0	0.0005114	0	5.11E-05	0	0	0.0003068	0	0	5.11E-05	0	5.11E-05	0	5.11E-05	0.0001534	0.0001534	0.0001534	0.0001023	0	0.0001023	0.0005625	0	0.0001023	0.0001023	0	0.0003579	0.0001023	0.0003579	0.0002045	5.11E-05	0.0001534	0.0006136	0	0.0001023	5.11E-05	5.11E-05		
g__Senegalimassilia	0.0002045	0	0	5.11E-05	0	0	0	0	0	0.0007159	0.0006648	0	0	0.0020454	0	0	0	0	0	0	0	0	0	5.11E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Lachnospiraceae	0.0003068	0	0.0002557	0.0003068	0.0004091	0.0024034	5.11E-05	0	0.0016875	0	0.0003068	0.0024034	0.0018409	0.0004091	0.0061874	0.0005625	0.0026079	0.0015341	0.0031192	0.0014829	0	0.0010738	0.004909	0.0030681	0.0019943	0.001125	0.0004602	0.0020454	0	0.0004091	0.001125	0.0002557	0	0.0025568	0.0010227	0.0015341	0.0013807		
g__Clostridium	0	0	0	5.11E-05	0	0	0	0.0001023	0	5.11E-05	5.11E-05	0	0	0	0.0002557	0.0012272	5.11E-05	5.11E-05	0	5.11E-05	0.0004091	0.0003579	0	0.0004091	5.11E-05	0	0.0002557	0.0001023	5.11E-05	5.11E-05	0.0013295	0.0003579	0	0.0003068	0.0001023	5.11E-05	5.11E-05		

Supplementary Table 3 LDA score

Title	LDAscore	P value
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Tyzzerella_3	2.7737536	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Tyzzerella_4	3.7002868	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Johnsenella	0.70872	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Eubacterium_ruminantium_group	3.6315195	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Prevotellaceae.g._Prevotella	1.4656819	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Porphyromonadaceae.g._Parabacteroides	3.955113	-
k_Bacteria.p._Synergistetes.c._Synergistia.o._Synergistales	2.40769	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales	5.5220817	IT 5.1402514 0.0154638
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Leuconostocaceae.g._Leuconostoc_lactis	1.70872	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XIII.g._Eubacterium_nodatum_group.s._Eubacterium_infirmum	1.5168434	-
k_Bacteria.p._Tenericutes.c._Mollicutes.o._Mollicutes_RF9	2.6666586	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Streptococcaceae	4.074208	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Clostridiaceae_1.g._Clostridium_sensu_stricto_1	3.9881588	-
k_Bacteria.p._Actinobacteria.c._Actinobacteria.o._Corynebacteriales.f._Corynebacteriaceae	1.293746	-
k_Bacteria.p._Proteobacteria.c._Deltaproteobacteria.o._Desulfotribionales	3.5004106	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus	3.0143784	-
k_Bacteria.p._Proteobacteria.c._Deltaproteobacteria.o._Desulfotribionales.f._Desulfotribionaceae.g._Desulfotribrio	3.3351586	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Caproicoproducers	1.1646519	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Prevotellaceae.g._Paraprevotella	3.2718619	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Streptococcaceae.g._Streptococcus_s._Streptococcus_pneumoniae	3.4683878	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Dorea	4.3099663	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae	3.0143784	-
k_Bacteria.p._Spirochaetaceae.g._Spirochaetes.o._Spirochaetales.f._Brachyspiraceae.g._Brachyspiria	1.1646519	-
k_Bacteria.p._Proteobacteria	4.4490263	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Olsenella	2.2725253	-
k_Bacteria.p._Bacteroidetes.c._Flavobacteria.o._Flavobacteriales.f._Flavobacteriaceae.g._uncultured	1.6181	-
k_Bacteria.p._Fusobacteria	3.5929487	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Pasteurellales	3.8003869	IT 3.6120955 0.012908
k_Archaea.p._Euryarchaeota.c._Methanobacteria.o._Methanobacteriales	0.5625919	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Hungateella	3.1101205	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Peptostreptococcaceae.g._Intestinibacter	1.70872	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Enterorhabdus	1.8226633	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Eubacterium_eligens_group	4.1838721	-
k_Bacteria.p._Bacteroidetes.c._Flavobacteria	1.6181	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Peptostreptococcaceae	4.5296264	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Bacillales.f._Bacillaceae.g._Bacillus	3.100975	-
k_Bacteria.p._Tenericutes.c._Mollicutes	2.6666586	-
k_Bacteria.p._Actinobacteria.c._Actinobacteria.o._Micrococcales	1.9371993	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus_s._Lactobacillus_sakei	0.8958666	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Pasteurellales.f._Pasteurellaceae.g._Aggregatibacter	1.2615619	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus_s._Lactobacillus_casei	2.1510791	-
k_Bacteria.p._Proteobacteria.c._Deltaproteobacteria	3.5004106	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Anaerostipes	4.4595842	-
k_Bacteria.p._Firmicutes.c._Negativicutes.o._Selenomonadales	5.1238007	-
k_Bacteria.p._Bacteroidetes.c._Flavobacteria.o._Flavobacteriales	1.6181	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus_s._Lactobacillus_acidophilus	1.40769	-
k_Bacteria.p._Proteobacteria.c._Epsilonproteobacteria.o._Campylobacteriales.f._Campylobacteriaceae.g._Campylobacter	1.7930409	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Gordonibacter_sp._Marseille_PT275	1.3101078	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Porphyromonadaceae.g._Odoribacter_s._Odoribacter_sp._Marseille_PT2698	2.471077	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Aeromonadales	2.8325716	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._FDJ1_392	1.9749879	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Adlercreutzia	3.3641539	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._uncultured	2.4812673	-
k_Bacteria.p._Bacteroidetes	5.5220817	IT 5.1402011 0.0154638
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales	4.5328959	H 4.1332003 0.0048106
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus_s._Lactobacillus_alimentarius	0.5947766	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Eubacterium_fissicatena_group	2.3989161	-
k_Bacteria.p._Verrucomicrobia.c._Verrucomicrobiae.o._Verrucomicrobiales	2.910747	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Lachnospiraceae_FCS020_group	3.3351393	H 3.7018513 0.0313746
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Parvibacter	1.0718979	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XI.g._Finegoldia	0.70872	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Christensenellaceae.g._Christensenellaceae_R_7_group	3.70872	-
k_Archaea.p._Euryarchaeota	0.5625919	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XIII.g._Family_XIII_AD3011_group	2.95914	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Streptococcaceae.g._Streptococcus_s._Streptococcus_mutans	2.155878	-
k_Bacteria.p._Spirochaetaceae.g._Spirochaetes.o._Spirochaetales.f._Brachyspiraceae	1.1646519	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XIII	3.1755876	-
k_Bacteria.p._Bacteroidetes.c._Flavobacteria.o._Flavobacteriales.f._Flavobacteriaceae	1.6181	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Streptococcaceae.g._Lactococcus_s._Lactococcus_garvieae	2.2575345	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Peptostreptococcaceae.g._Peptoclostridium	3.7036797	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Coprothacillus	1.7501127	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcaceae_NK4A214_group	3.2789593	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Bacillales.f._Family_XI	2.2272339	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Pseudomonadales	1.3101078	-
k_Bacteria.p._Spirochaetaceae.g._Spirochaetes.o._Spirochaetales	1.1646519	-
k_Bacteria.p._Firmicutes.c._Negativicutes.o._Selenomonadales.f._Veillonellaceae.g._Mitsuokella	1.0397132	-
k_Bacteria.p._Firmicutes.c._Negativicutes.o._Selenomonadales.f._Veillonellaceae.g._Meganomas	4.8839625	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Faecalibacillus	0.5947766	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Bacteroidaceae	5.2093582	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Bacteroidales.f._Bacteroides_s._Bacteroides_fragilis	2.2769127	-
k_Bacteria.p._Verrucomicrobia.c._Verrucomicrobiae.o._Verrucomicrobiales.f._Verrucomicrobiaceae	3.8588239	-
k_Bacteria.p._Verrucomicrobia.c._Verrucomicrobiae	2.910747	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Faecalitalea	2.910747	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Holdemanella	3.0240493	IA 3.7626329 0.0165143
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Heldmanella	3.2640395	-
k_Bacteria.p._Actinobacteria.c._Actinobacteria.o._Corynebacteriales.f._Corynebacteriaceae.g._Corynebacterium_1	0.8958666	-
k_Bacteria.p._Actinobacteria.c._Actinobacteria.o._Micrococcales.f._Micrococaceae	1.9371993	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Ruminococcus_gauvreui_group	3.6145159	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria	4.5328959	H 4.1332003 0.0048106
k_Bacteria.p._Proteobacteria.c._Alphaproteobacteria.o._Rhodospirillales.f._Rhodospirillaceae	2.1132906	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Aeromonadales.f._Succinivibrionaceae	2.8325716	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus_s._Lactobacillus_gasseri	1.3407432	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XI.g._Anaerococcus	0.70872	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcaceae_UCG_009	2.7904786	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcaceae_UCG_008	3.0663826	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcaceae_UCG_005	3.310728	-
k_Bacteria.p._Proteobacteria.c._Betaproteobacteria.o._Burkholderiales.f._Alcaligenaceae	3.8918062	IT 3.6460552 0.097184
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcaceae_UCG_007	0.5947766	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcaceae_UCG_003	2.9822657	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcaceae_UCG_002	3.8911754	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Subdoligranulum	4.2597341	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Leuconostocaceae	3.1152602	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Collinsella	4.4527721	-
k_Bacteria.p._Spirochaetaceae.g._Spirochaetes	1.1646519	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Eubacterium_rectale_group	4.8249956	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Eubacterium_oxidoreducens_group	0.5947766	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Lachnospiraceae_NK4A136_group	3.9251498	-
k_Bacteria.p._Cyanobacteria.c._Chloroplast	1.553818	-
k_Bacteria.p._Actinobacteria	4.8645463	H 4.4078398 0.01346
k_Bacteria.p._Firmicutes.c._Negativicutes.o._Selenomonadales.f._Acidaminococcaceae	4.3624403	-
k_Archaea.p._Euryarchaeota.c._Methanobacteriales.f._Methanobacteriaceae	0.5625919	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Porphyromonadaceae.g._Odoribacter	2.9891032	-
k_Bacteria.p._Proteobacteria.c._Betaproteobacteria.o._Burkholderiales.f._Comamonadaceae.g._Comamonas	1.293746	-
k_Bacteria.p._Actinobacteria.c._Actinobacteria.o._Actinomycetales.f._Actinomycetaceae.g._Variabaculum	1.0397132	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Fusicatibacter	4.4814365	-
k_Bacteria.p._Firmicutes.c._Negativicutes.o._Selenomonadales.f._Veillonellaceae	5.401041	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Thermoanaerobacterales.f._Thermoanaerobacteraceae.g._Gedria	0.8636219	-
k_Bacteria.p._Firmicutes.c._Bacilli	4.1603968	-
k_Bacteria.p._Firmicutes	5.916532	IA 5.0728299 0.0185036
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Streptococcaceae.g._Streptococcus_s._Streptococcus_equinus	2.802147	-
k_Bacteria	6	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Eisenbergiella	2.21387	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Christensenellaceae.g._Christensenellaceae_R_7_group.s._iron_reducing_bacterium_enrichment_culture_clone_HN70	4.1398747	-
k_Bacteria.p._Firmicutes.c._Negativicutes	5.1238007	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Prevotellaceae	5.1700684	IT 4.9031204 0.026615
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Eggerthella	4.239147	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Lachnospiraceae_ND3007_group	3.7965014	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XI.g._Peptoniphilus	1.1968366	-
k_Bacteria.p._Proteobacteria.c._Epsilonproteobacteria.o._Campylobacteriales	1.7930409	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Erysipelotrichaceae_UCG_003.s._human_gut_metagenome	0.8958666	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Porphyromonadaceae.g._Butyrivibrio	3.090737	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Blautia	3.0212879	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Lachnospiraceae	5.2832952	IA 4.7838293 0.0019671
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Deffluvitellaceae	1.7708679	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Leuconostocaceae.g._Leuconostoc	1.70872	-
k_Bacteria.p._Proteobacteria.c._Betaproteobacteria.o._Burkholderiales.f._Alcaligenaceae.g._Sutterella	3.8013198	IT 3.6690976 0.0006898
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Moryella_s._human_gut_metagenome	2.0571746	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus_s._Lactobacillus_plantarum	1.70872	-
k_Bacteria.p._Actinobacteria.c._Actinobacteria.o._Corynebacteriales.f._Corynebacteriaceae.g._Corynebacterium	0.5625919	-
k_Bacteria.p._Verrucomicrobia.c._Verrucomicrobiales.f._Verrucomicrobiales.f._Verrucomicrobiaceae.g._Akkermansia	2.910747	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XIII.g._Eubacterium_brachy_group	2.2668745	-
k_Bacteria.p._Firmicutes.c._Negativicutes.o._Selenomonadales.f._Acidaminococcaceae.g._Acidaminococcus	2.3886667	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Oscillospira	1.4868712	-
k_Bacteria.p._Synergistetes.c._Synergistia.o._Synergistales.f._Synergistaceae	2.40769	-
k_Archaea.p._Euryarchaeota.c._Methanobacteria.o._Methanobacteriales.f._Methanobacteriaceae.g._Methanobrevibacter	0.5625919	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Lactobacillaceae.g._Lactobacillus_mucosae	2.252788	-
k_Bacteria.p._Proteobacteria.c._Betaproteobacteria.o._Burkholderiales.f._Alcaligenaceae.g._Sutterella_s._Burkholderia_sp._K4410_MG5_135	3.4120114	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Leuconostocaceae.g._Weissella	3.1078991	-
k_Bacteria.p._Spirochaetaceae	1.1646519	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Thermoanaerobacterales.f._Thermoanaerobacteraceae	0.8636219	-
k_Bacteria.p._Synergistetes.c._Synergistia.o._Synergistales.f._Synergistaceae.g._Pyramidobacter	1.7708679	-
k_Bacteria.p._Proteobacteria.c._Epsilonproteobacteria.o._Campylobacteriales.f._Campylobacteriaceae	1.7930409	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Sellimonas	3.7150214	H 3.7877206 0.0035134
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._uncultured.s._Eggerthellaceae_bacterium_Marseille_PT2849	2.1510791	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Eubacterium_coprostanoligenes_group	3.8016012	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Erysipelotrichaceae_UCG_003	4.4232116	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Ruminococcus_torques_group	4.2262204	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Erysipelotrichaceae_UCG_007	1.5490191	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Bacteroidaceae.g._Bacteroides_s._bacterium_NLAf_ZI_G202	4.647061	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Prevotellaceae.g._Alloprevotella	4.4266185	IT 4.0994348 0.0101577
k_Bacteria.p._Actinobacteria.c._Actinobacteria.o._Actinomycetales.f._Actinomycetaceae	2.5342959	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XIII.g._Mogibacterium	2.10666	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._uncultured.s._Intestinimonas_sp._GM5	4.2413206	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Pasteurellales.f._Pasteurellaceae.g._Actinobacillus	1.3407432	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae	5.7172448	H 5.1229714 0.0039759
k_Bacteria.p._Firmicutes.c._Bacilli.o._Bacillales.f._Staphylococcaceae	0.5947766	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Rikenellaceae.g._Alistipes	3.9967636	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Christensenellaceae.g._Christensenellaceae_R_7_group.s._metagenome	1.5490191	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Ruminococcus_1	4.1897324	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Bacteroidales_S24_7_group	3.219265	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Oribacterium	1.0397132	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia	4.465851	H 4.0977744 0.0203363
k_Bacteria.p._Fusobacteria.c._Fusobacteria.o._Fusobacteriales.f._Fusobacteriaceae.g._Fusobacterium	3.9294827	-
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Porphyromonadaceae.g._Coprothacium	2.6772029	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Howardella	1.9428032	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Aeromonadales.f._Succinivibrionaceae.g._Succinivibrio	2.8325716	-
k_Bacteria.p._Lentisphaerae.c._Lentisphaeria	0.5947766	-
k_Bacteria.p._Firmicutes.c._Erysipelotrichia.o._Erysipelotrichales.f._Erysipelotrichaceae.g._Erysipelatoclostridium	2.6432184	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Clostridiales_vadinB60_group	0.8636219	-
k_Bacteria.p._Proteobacteria.c._Alphaproteobacteria.o._Rhodospirillales	2.1132906	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XI.g._Murdochella	1.1646519	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Streptococcaceae.g._Streptococcus_s._Streptococcus_anginosus_subsp._anginosus	2.1646519	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Epulopiscium	0.5947766	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Senegalimassilia	2.4199244	IT 4.374566 0.0342053
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Ruminococcaceae.g._Faecalibacterium	5.1030841	IA 4.5065374 0.0364895
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XI.g._Parvimonas	1.70872	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Family_XI	1.8733502	-
k_Bacteria.p._Synergistetes.c._Synergistia.o._Synergistales	2.40769	-
k_Bacteria.p._Firmicutes.c._Bacilli.o._Lactobacillales.f._Streptococcaceae.g._Streptococcus_s._Streptococcus_parvuberis	0.70872	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Enterobacteriales.f._Enterobacteriaceae.g._Klebsiella	3.7377914	H 3.4818271 0.0230289
k_Bacteria.p._Bacteroidetes.c._Bacteroidia.o._Bacteroidales.f._Prevotellaceae.g._Prevotella_g_Ga6A1_group	3.8773016	-
k_Bacteria.p._Lentisphaerae.c._Lentisphaeria.o._Victivallales.f._Victivallaceae.g._Victivallis	0.5947766	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Lachnospiraceae.g._Moryella	2.0571746	-
k_Bacteria.p._Proteobacteria.c._Gammaproteobacteria.o._Enterobacteriales.f._Enterobacteriaceae.g._Escherichia_Shigella_s._Escherichia_coli	3.9894909	-
k_Bacteria.p._Actinobacteria.c._Coriobacteria.o._Coriobacteriales.f._Coriobacteriaceae.g._Enorma	1.7930409	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Christensenellaceae	3.7189547	-
k_Bacteria.p._Firmicutes.c._Clostridia.o._Clostridiales.f._Eubacteriaceae.g._Anaer		

