

species_name	diff	d_std	pval	mann_whitneyse	se_std	median_zerc	median_oneqval	qval_mann_whitney		
s_Ruminococcaceae_unclassified_SGB15260 _SGB15260	5.370964224	2.58401549	7.94E-20	0.054841597	0.589308498	0.331027143	0	0.489E-17	0.997857809	
s_Faecalibacterium_prausnitzii _SGB15322	4.936455009	1.08058368	0.000138239	0.559925145	1.295216404	0.26162077	0	0.007096283	0.997857809	
s_Faecalibacterium_prausnitzii _SGB15323	-4.752911955	-1.791152799	2.66E-10	0.260224785	0.752337466	0.289275352	0	0.819E-08	0.997857809	
s_Lachnospiraceae_bacterium _SGB4671	4.738046308	1.34222256	2.20E-06	0.360590381	1.00083002	0.270514518	0	0.00019361	0.997857809	
s_Collinsella_intestinalis _SGB14741	4.091692088	1.474960523	1.97E-07	0.641025649	0.786516983	0.275626523	0	2.43E-05	0.997857809	
s_Bifidobacterium_pseudocatenulatum _SGB17237	3.952812284	1.70888482	1.67E-09	0.095525666	0.655811391	0.285535413	0	3.36E-07	0.997857809	
s_Catenibacterium_sp_AM22_15 _SGB6783_group	3.750632953	0.812160853	0.004176015	0.549854487	1.309326837	0.254268167	0	0.067695394	0.997857809	
s_GGB3256_SGB4303 _SGB4303	3.595248133	1.423551779	5.14E-07	0.231516186	0.716046387	0.27360096	0	5.28E-05	0.997857809	
s_Flavobacteriales_bacterium _SGB2275	3.512725715	0.993912765	0.00455574	0.330847774	1.002031856	0.25904258	0	0.015590771	0.997857809	
s_Ruminococcus_sp_NSJ_7 _SGB4290	3.425610682	0.848335068	0.001237389	0.991282543	1.14486991	0.255148506	0	0.005048439	1	
s_Blautia_producta _SGB4791	3.352382647	0.725384579	0.010512956	0.53343045	1.313030245	0.252301751	0	0.121070812	0.997857809	
s_GGB4585_SGB6340 _SGB6340	3.301498018	0.858005759	0.002476084	0.387508065	1.090953889	0.255389819	0	0.054236689	0.997857809	
s_Neglecta_timonensis _SGB14851	3.280358604	1.030573581	0.00027808	0.801025612	0.902459819	0.260109933	0	0.012235504	0.997857809	
s_Bifidobacterium_animalis _SGB17278	3.119764056	0.716726332	0.011473198	0.506634717	1.234110214	0.252116942	0	0.123991049	0.997857809	
s_Lachnospiraceae_bacterium _SGB5060	3.107066486	0.975611975	0.000579452	0.415616342	0.902940184	0.258522642	0	0.017847100	0.997857809	
s_Eggerthellaceae_bacterium _SGB14334	3.032159915	0.915807096	0.001237389	0.811246102	0.938714777	0.25688409	0	0.033140517	0.997857809	
s_Clostridia_bacterium _SGB14929	2.870119267	1.099230906	0.00105723	0.429189365	0.740280945	0.262200115	0	0.005920487	0.997857809	
s_Lacrimispora_saccharolytica _SGB4701	-2.862869691	-0.766677453	0.00684404	0.220421153	0.508703738	0.253211696	0	0.098107376	0.997857809	
s_Candidatus_Pseudolachnospira_aviium _SGB59819	-2.836766679	-1.696470083	2.18E-09	0.022399806	0.474092373	0.284982169	0	0.36E-07	0.997857809	
s_GGB3478_SGB4643 _SGB4643	-2.801627505	-0.930549358	0.010030314	0.83570424	0.853604185	0.257279333	0	0.030222545	0.997857809	
s_GGB9632_SGB15089 _SGB15089	2.691579928	0.89967312	0.00150762	0.167593353	0.848219189	0.256458088	0.009525	0.038695584	0.997857809	
s_Bacteroides_faecis _SGB1860	2.643387918	0.719600874	0.005237785	0.487694634	0.946760635	0.253783615	0	0.080661883	0.997857809	
s_Mesosutterella_multiformis _SGB9272_group	-2.578509763	-0.761259688	0.007252582	0.02475234	0.980332255	0.253089628	0	0.099279784	0.997857809	
s_Eubacterium_sp_AM28_29 _SGB6796_group	-2.555316955	-0.725293082	0.010522717	0.757500694	0.998868005	0.252299787	0	0.121070812	0.997857809	
s_Ruminococcaceae_unclassified_SGB4425 _SGB4425_group	2.544784271	0.890235897	0.0016899	0.327216088	0.810459703	0.256212094	0	0.041639127	0.997857809	
s_Pseudoflavonifractor_SGB15156 _SGB15156_group	-2.541365101	-0.861849129	0.002367316	0.022171885	0.836029056	0.255486418	0	0.054009867	0.997857809	
s_GGB3463_SGB4621 _SGB4621	2.538935608	0.724447168	0.01061335	0.643090382	0.993643337	0.252281642	0	0.121070812	0.997857809	
s_GGB3817 _SGB72433 _SGB72433_group	2.412385406	0.729715927	0.010059965	0.514961407	0.937299583	0.252394985	0	0.121070812	0.997857809	
s_Clostridia_unclassified_SGB14844 _SGB14844	-2.393854053	-0.821684441	0.003753818	0.252793228	0.825996415	0.254496507	0	0.063112829	0.997857809	
s_Butyricimonas_faecioliformis _SGB17786	-2.389823478	-0.750958888	0.008080518	0.122631369	0.902267302	0.252859768	0	0.104257665	0.997857809	
s_Roseburia_sp_AM59_24X _SGB4654	-2.375067986	-0.712425312	0.011978535	0.118191691	0.94519684	0.252025913	0	0.124976071	0.997857809	
s_Allisonella_histaminiformans _SGB5843	2.369836598	1.004954479	0.00393287	0.474985207	0.668586447	0.259360442	0	0.014250879	0.997857809	
s_Clostridia_bacterium _SGB3989	-2.325972438	-0.614615679	0.003174338	0.07330776	1.072967299	0.250095978	0	0.0214830269	0.997857809	
s_Lachnospiraceae_bacterium _SGB4771	-2.30387824	-0.764321524	0.002071607	0.487694634	0.854612006	0.253158515	0	0.098302493	0.997857809	
s_GGB3034_SGB4030 _SGB4030	-2.294672827	-1.006989464	0.000382714	0.018740316	0.646072719	0.259419365	0	0.014250879	0.997857809	
s_Clostridium_SGB6179 _SGB6179	-2.277901721	-0.886383838	0.001769965	0.191054092	0.728616012	0.256112364	0	0.011943558	0.997857809	
s_Oscillibacter_sp_NSJ_62 _SGB79833	-2.243094166	-1.049181934	0.00021514	0.090133471	0.606153	0.260664758	0	0.010194332	0.997857809	
s_Anaerobutyricum_hallii _SGB4537	2.199307451	1.100045484	0.00104482	0.061253078	0.566840485	0.262225619	0.00385	0.048115	0.005920487	0.997857809
s_GGB9640_SGB15115 _SGB15115	2.198623354	0.809277532	0.00413208	0.156022332	0.770262776	0.254199521	0	0.068108745	0.997857809	
s_GGB6649_SGB9391 _SGB9391	-2.179907481	-0.75044478	0.008123974	0.238000085	0.823578267	0.252848372	0	0.014257665	0.997857809	
s_GGB9610_SGB15045 _SGB15045	2.155913453	0.618126465	0.029244334	0.464863308	0.988870773	0.250160568	0	0.021445844	0.997857809	
s_Escherichia_coli _SGB10068	2.138358052	0.636928956	0.024672326	0.703466547	0.951864194	0.250512461	0.01717	0.02252	0.188228139	0.997857809
s_Clostridia_bacterium _SGB4133	-2.118090825	-0.699052204	0.013678089	0.608822808	0.859054124	0.25174617	0	0.129626194	0.997857809	
s_GGB35068_SGB47850 _SGB47850	2.112087905	0.702820601	0.013178842	0.250717904	0.852026423	0.251824494	0	0.128859789	0.997857809	
s_Clostridia_bacterium _SGB15389	2.092269308	0.695118494	0.014216986	0.881823996	0.853383611	0.251664835	0	0.132691866	0.997857809	
s_GGB9524_SGB14924 _SGB14924	2.08777085	0.72828955	0.010207184	0.658609522	0.812763717	0.252364224	0	0.121070812	0.997857809	
s_GGB51510_SGB17883 _SGB17883	-2.067742562	-0.736272203	0.00940732	0.119720652	0.796239319	0.2525371	0	0.118263544	0.997857809	
s_Lachnospiraceae_bacterium _SGB4728	-2.061171393	-0.670732982	0.017994464	0.316633065	0.871264463	0.251170301	0	0.153016665	0.997857809	
s_Lachnospiraceae_bacterium _SGB4817	2.042617706	0.61397977	0.03034548	0.137202524	0.943232133	0.250084316	0	0.0214830269	0.997857809	
s_Lachnospiraceae_bacterium _SGB48024	-2.033833589	-0.706686945	0.0126857	0.158392363	0.815990243	0.251904888	0	0.128104775	0.997857809	
s_Ruminococcaceae_bacterium _SGB15272	-1.954458506	-0.636016593	0.024878962	0.306768104	0.871251594	0.250495154	0.00685	0.188228139	0.997857809	
s_Copro bacter fastidiosus _SGB1963	1.924030601	0.855369882	0.002553303	0.159237609	0.637739883	0.255323797	0	0.054235669	0.997857809	
s_Blautia_sp_MSK_20_85 _SGB4828_group	1.912203328	0.820810748	0.003790868	0.571170798	0.660505733	0.254475456	0	0.063112829	0.997857809	
s_GGB3005_SGB3996 _SGB3996	-1.871535311	-0.825071444	0.00331328	0.501981964	0.643119397	0.254578306	0.00355	0.000295	0.063112829	0.997857809
s_Lachnospiraceae_bacterium _SGB4957	-1.869997979	-0.612708797	0.03069038	0.011072709	0.865311704	0.250061042	0	0.0214830269	0.997857809	
s_Lacrimispora_celerescens _SGB4868	1.842552404	1.223530412	1.59E-05	0.089931222	0.426963389	0.266278912	0.00405	0.121675	0.001226269	0.997857809
s_Ruminococcaceae_unclassified_SGB4191 _SGB4191	-1.83152913	-0.686307435	0.015492514	0.078291095	0.756513454	0.251484223	0	0.138626986	0.997857809	
s_Streptococcus_anginosus _SGB8028_group	-1.817979285	-0.686071419	0.015528023	0.409040837	0.751285764	0.251479415	0	0.138626986	0.997857809	
s_Eisenbergiella_tay _SGB4988	-1.814327051	-0.8238609	0.003662125	0.441845713	0.624362338	0.254549518	0.00179	0.063112829	0.997857809	
s_Phocaecola_plebeius _SGB1903_group	1.805198551	0.589220257	0.03768884	0.503816522	0.868626079	0.249639238	0	0.249198405	0.997857809	
s_Clostridia_bacterium _SGB14874	-1.742532002	-0.669927018	0.018133468	0.418974285	0.737460607	0.251154242	0	0.153016665	0.997857809	
s_Clostridia_bacterium _SGB53497	-1.736285025	-0.987617231	0.00495092	0.182165469	0.498531042	0.258862748	0.00469	0.001665	0.016051394	0.997857809
s_Lachnospiraceae_bacterium _SGB4784	1.685742387	0.6683048	0.018415321	0.360590381	0.7151583	0.251121973	0	0.153295103	0.997857809	
s_Clostridium_innocuum _SGB4037_group	-1.675295168	-0.651990121	0.021469944	0.96038805	0.728510604	0.250801569	0.00096	0.004685	0.017159551	0.997857809
s_Blautia_glucerase _SGB4816	1.65425197	0.775899327	0.006206762	0.335354253	0.604479869	0.253421329	0	0.093252821	0.997857809	
s_Clostridiaceae_bacterium_NSJ_31 _SGB14839	-1.637566388	-0.850034502	0.002716385	0.380116953	0.546195243	0.25519073	0	0.005048439	0.997857809	
s_Turicibacter_sanguinis _SGB6847	1.605896315	0.632105543	0.025781827	0.063576116	0.720300074	0.250421232	0.000475	0.013144646	0.997857809	
s_Clostridiales_bacterium_BX7 _SGB72833	-1.603030957	-0.699275379	0.013648063	0.381085587	0.649952415	0.251750798	0	0.129626194	0.997857809	
s_Dielma_fastidiosus _SGB4031	-1.588300385	-0.674525735	0.017354898	0.832037782	0.667604997	0.251246121	0.00088	0.0011	0.152723098	0.997857809
s_Clostridia_bacterium _SGB54300	-1.571024646	-1.020061331	0.000320882	0.395070575	0.436668854	0.259800375	0	0.013177568	0.997857809	
s_Cloacibacillus_eyrensis _SGB15506	1.526569472	0.71949331	0.011158187	0.56993427	0.60155504	0.252175776	0	0.123991049	0.997857809	
s_Clostridiales_bacterium_Marseille_P2846 _SGB29342	1.476378134	0.635238622	0.020506343	0.269970776	0.658940599	0.250480415	0	0.188228139	0.997857809	
s_GGB51959_SGB72479 _SGB72479	1.463546484	0.710813009	0.012172994	0.993465051	0.583763195	0.251991922	0	0.124976071	1	
s_Bifidobacterium_adollescens _SGB17244	1.439281135	0.704921215	0.0129076	0.993913235	0.57888275	0.251868325	0.27371	0.128243249	0.997857809	
s_Candidatus_Aristotelia_aviatoris _SGB63343	-1.438947672	-1.13260797	6.48E-05	0.253120493	0.360206097	0.263258626	0	0.004318891	0.997857809	
s_Bacteroides_finegoldii _SGB1862	1.38									

s_Parabacteroides_goldsteini _SGB1941	1.689820773	0.428501103	0.130698116	0.250653341	1.118083548	0.247181232	0	0	0.454858981	0.997857809
s_Mediterraneanibacter_sp_gm002 _SGB4553	1.683382752	0.473636399	0.094810569	0.926816964	1.007681671	0.247795404	0	0	0.417166502	0.997857809
s_SGB32463_SGB47515 _SGB47515	1.679921363	0.412773395	0.154452676	0.373899358	1.153885756	0.246981329	0	0	0.484226864	0.997857809
s_SGB3293_SGB4348 _SGB4348	-1.652469575	-0.405170736	0.15298505	0.081716102	1.156327777	0.246887321	0	0	0.459993636	0.997857809
s_Clostridia_bacterium _SGB15385	1.647132896	0.555973937	0.049883615	0.61525064	0.839962243	0.249069255	0	0	0.4293031089	0.997857809
s_Veillonella_atypica _SGB6936	1.641069122	0.5104396	0.071804174	0.54575056	0.911523923	0.248340408	0	0	0.348278514	0.997857809
s_Blauitia_hanseni _SGB4794_group	-1.621659379	-0.458273554	0.106015581	0.453549066	1.003275945	0.247579631	0	0	0.425976709	0.997857809
s_SGB3278_SGB4328 _SGB4328	-1.610582839	-0.383704908	0.17594218	0.106186009	1.190066607	0.246631145	0	0	0.527439835	0.997857809
s_Clostridia_bacterium _SGB14150	1.58183199	0.49295731	0.08208817	0.086717911	0.909780451	0.248076586	0	0	0.386022436	0.997857809
s_Sutterella_wadsworthensis _SGB9283	1.568093663	0.418901519	0.139542671	1	1.061318224	0.247058349	0	0	0.474907654	1
s_Faecalimonas_umblicata _SGB4583	1.559624971	0.46248044	0.102841725	0.894452248	0.956103457	0.24763814	0	0	0.425976709	0.997857809
s_Ruminococcaceae_bacterium _SGB15278	-1.503431266	-0.554666138	0.050424181	0.045560227	0.768488692	0.249047484	0	0	0.4293031089	0.997857809
s_Lachnospiraceae_bacterium_OF09_6 _SGB4966	-1.491407589	-0.53825377	0.057635471	0.048588166	0.785587972	0.248778475	0	0	0.308725652	0.997857809
s_Lachnospiraceae_bacterium_OM04_12BH _SGB4893	-1.485028133	-0.54428706	0.054890727	0.417447095	0.773556836	0.248876459	0	0	0.304618811	0.997857809
s_SGB3486_SGB4658 _SGB4658	1.475330987	0.366126862	0.196802007	0.970029303	1.142466377	0.246431565	0	0	0.55042458	0.997857809
s_Hungatella_hathewayi _SGB4739	-1.443073186	-0.407067814	0.15107125	0.036901476	1.005095084	0.246910619	0	0	0.493256053	0.997857809
s_Clostridium_sp_AF15_49 _SGB5111	1.392005801	-0.384524218	0.175021238	0.022028265	1.026367531	0.246640672	0	0	0.527439835	0.997857809
s_Eubacterium_candideri _SGB4080	1.383970849	0.362925596	0.200522258	0.91025682	1.081172277	0.246396208	0	0	0.556631043	0.997857809
s_Emergencia_timonensis _SGB3970	-1.3766839	-0.460392239	0.104410598	0.657389219	0.847907695	0.247608976	0	0	0.425976709	0.997857809
s_Clostridia_bacterium _SGB13982	1.354978722	0.50604161	0.074286352	0.232441226	0.759157353	0.2482732	0	0	0.354731726	0.997857809
s_Lachnospiraceae_bacterium _SGB4648	1.344157056	0.370267268	0.191568273	0.562077573	1.02924852	0.246477746	0	0	0.547033777	0.997857809
s_Ruminococcaceae_bacterium_AM07_15 _SGB14974	-1.328486051	-0.469589156	0.097666098	0.295969501	0.802092576	0.247737888	0	0	0.424862917	0.997857809
s_Clostridia_bacterium _SGB5180	1.306029688	0.467267097	0.099335201	0.341624559	0.792452801	0.247705106	0	0	0.425976709	0.997857809
s_Streptococcus_sanguinis _SGB8047	-1.296383966	-0.389161411	0.169876518	0.21932996	0.944472764	0.246694967	0	0	0.526303213	0.997857809
s_Lachnospiraceae_bacterium _SGB4718	-1.279733315	-0.286985155	0.131434032	0.038173112	1.28426879	0.245647333	0	0	0.690594251	0.997857809
s_Clostridiales_unclassified_SGB15145 _SGB15145	1.279561834	0.409894824	0.148263138	0.45750398	0.885065031	0.24694541	0	0	0.48839622	0.997857809
s_Clostridia_unclassified_SGB6317 _SGB6317	-1.277442003	-0.488737612	0.084741568	0.501404105	0.741231237	0.248014244	0	0	0.392487252	0.997857809
s_Bacteroides_salysivae _SGB1857	1.27400545	0.325226501	0.251341287	0.459963551	1.110633876	0.246002853	0	0	0.638909628	0.997857809
s_SGB9608_SGB15041 _SGB15041	1.258665258	0.456450112	0.107433228	0.61325329	1.181658151	0.24755572	0	0	0.425976709	0.997857809
s_Lachnospira_SGB5077 _SGB5077	-1.256267214	-0.42391079	0.134371572	0.905299173	0.840216816	0.247122132	0	0	0.464139042	0.997857809
s_Christensenella_massiliensis _SGB29339	1.217872188	0.378985036	0.18318011	0.811927727	0.911098238	0.246576653	0	0	0.536980263	0.997857809
s_Senegalimassilia_anaerobia _SGB14824_group	-1.217465806	-0.543122866	0.055411702	0.349302888	0.635541978	0.248885747	0	0	0.304764364	0.997857809
s_Ruminococcus_SGB4421 _SGB4421	1.215325992	0.43252698	0.127120922	0.875638017	0.79664556	0.247233577	0	0	0.454858981	0.997857809
s_Bacteroides_nordii _SGB1858	1.204309053	0.479055715	0.091092166	0.70113604	0.71275042	0.247873171	0	0	0.406614308	0.997857809
s_Ruminococcus_SGB4421 _SGB4421	-1.199314399	-0.453356874	0.109674553	0.252142505	0.749731922	0.247514502	0	0	0.425976709	0.997857809
s_Massiliastercora_timonensis _SGB4628	-1.193498578	-0.437289431	0.122988145	0.179559258	0.773817384	0.247296116	0	0	0.445651162	0.997857809
s_Ruminococcaceae_bacterium _SGB14906	-1.181229338	-0.454912862	0.108601494	0.599742738	0.736193112	0.247533354	0.00017	0	0.425976709	0.997857809
s_Eubacterium_sp_AF15_50 _SGB5042	1.171217391	0.461725911	0.103410228	0.57216053	0.719182022	0.247627516	0	0	0.425976709	0.997857809
s_SGB4456_SGB6141 _SGB6141	-1.168132605	-0.446330342	0.115432049	0.443410803	0.742023988	0.247416678	0	0	0.434971322	0.997857809
s_Lachnospira_sp_NSJ_43 _SGB50587	1.166373054	0.40417664	0.153995246	0.50042006	0.818185589	0.246875156	0	0	0.496654825	0.997857809
s_Clostridium_sp_AF34_13 _SGB4659	-1.157156081	-0.410269213	0.147883075	0.742864592	0.799665888	0.246950175	0	0	0.48839622	0.997857809
s_Lachnospiraceae_bacterium _SGB4744	1.156421172	0.442484418	0.118592168	0.775235777	0.740958346	0.247365231	0	0	0.441186272	0.997857809
s_Coprococcus_eutactus _SGB5121	-1.15467323	-0.324684576	0.252171432	0.18066354	1.008253227	0.245997607	0	0	0.638909298	0.997857809
s_SGB9361_SGB14336 _SGB14336	1.145278834	0.340003086	0.230443026	0.970029303	0.955021049	0.246151979	0	0	0.607337971	0.997857809
s_Flavonifractor_sp_An _SGB15134	-1.143393188	-0.359822521	0.204398167	0.086204734	0.900933666	0.246362227	0	0	0.564615566	0.997857809
s_Candidatus_Schneewindia_gallinarum _SGB63326	1.142479897	0.462043367	0.103717235	0.804207214	0.701053858	0.247631937	0	0	0.425976709	0.997857809
s_Lachnospiraceae_unclassified_SGB4894 _SGB4894	-1.131200733	-0.430532552	0.128883432	0.093835788	0.744936478	0.247207585	0	0	0.454858981	0.997857809
s_Paraprevotella_clara _SGB1798	-1.121702373	-0.519338357	0.086995193	0.046559178	0.612368398	0.248478117	0.00233	0	0.337269617	0.997857809
s_Eubacteriaceae_bacterium _SGB3958	-1.121096267	-0.581951853	0.040112684	0.957736693	0.546187062	0.249511913	0	0	0.257622453	0.997857809
s_Faecalicatena_ortocla _SGB4616	1.107109784	0.376931886	0.18369419	0.215025968	0.832747559	0.246553156	0	0	0.541414454	0.997857809
s_Veillonella_dispar _SGB6952	-1.105556697	-0.307641049	0.277889579	0.811230223	1.018878253	0.245833914	0	0	0.661600329	0.997857809
s_SGB9237_SGB14719 _SGB14719	-1.100308382	-0.487105294	0.085786418	0.941237653	0.640438053	0.247990268	0	0	0.394361443	0.997857809
s_Clostridia_bacterium _SGB13981	-1.100253074	-0.539611056	0.05700825	0.702159118	0.578092465	0.248800426	0	0	0.380044577	0.997857809
s_Streptococcus_oralis _SGB8130	-1.098068474	-0.324040251	0.253074462	0.727561148	0.960762447	0.245991166	0	0	0.638909298	0.997857809
s_Bacteroides_intestinalis _SGB1846	1.092057183	0.368729127	0.193417829	0.42352944	0.839698721	0.24646053	0	0	0.549057062	0.997857809
s_Lachnospiraceae_bacterium _SGB48424	1.085688671	0.531684036	0.06705306	0.074254079	0.578944913	0.248672977	0	0	0.525761337	0.997857809
s_Rhodobacteriaceae_unclassified_SGB53807 _SGB53807	1.083743013	0.292287461	0.302578712	0.444849322	1.051239527	0.245694004	0	0	0.6851048	0.997857809
s_Ruminococcaceae_bacterium _SGB14869	1.083339278	0.43881452	0.121687117	0.680989189	0.699953286	0.247316284	0	0	0.443694358	0.997857809
s_Clostridia_bacterium _SGB14250	1.082548605	0.291340071	0.304148526	0.707447282	1.053495635	0.245685603	0	0	0.6851048	0.997857809
s_Eubacterium_siraum _SGB1498_group	-1.080582595	-0.481147136	0.089488899	0.945678069	0.636745112	0.247903412	0	0	0.406028556	0.997857809
s_Bacteroides_stercoris _SGB1830_group	-1.079080557	-0.541604546	0.050609333	0.717718478	0.564881203	0.248832763	0.00272	0	0.305804928	0.997857809
s_Clostridia_bacterium _SGB15411	1.065910004	0.362859667	0.060040405	0.391295881	0.832851165	0.246395483	0	0	0.556631043	0.997857809
s_SGB9635_SGB15106 _SGB15106	-1.063713273	-0.312403945	0.270517538	0.490260704	0.965369617	0.245878754	0	0	0.566058281	0.997857809
s_SGB9512_SGB14909 _SGB14909	-1.053185088	-0.388250869	0.170877667	0.522037336	0.769091163	0.246684255	0	0	0.526303213	0.997857809
s_SGB9176_SGB14114 _SGB14114	-1.052588754	-0.286474666	0.312295524	0.121252921	1.041736932	0.245642884	0	0	0.690594251	0.997857809
s_Lactococcus_lactis _SGB7984	1.049713001	0.384770478	0.174745135	0.959653109	0.773489442	0.246643539	0	0	0.527439835	0.997857809
s_Streptococcus_salivarius _SGB8007_group	-1.0455655	-0.469207087	0.097939175	0.460175965	0.631789259	0.247732483	0.0347	0.00592	0.424662917	0.997857809
s_Clostridia_bacterium_12CBH _SGB7259	-1.039586076	-0.556282498	0.049756785	0.075025695	0.529847165	0.249074399	0.00186	0	0.293031089	0.997857809
s_Alistipes_inops _SGB2286	-1.037654968	-0.30904759	0.275684933	0.784739278	0.951947867	0.245847085	0	0	0.661600329	0.997857809
s_SGB9818_SGB15459 _SGB15459	-1.035852605	-0.473707796	0.049760802	0.255509119	0.619973301	0.247796423	0	0	0.417166502	0.997857809
s_Coprococcus_eutactus _SGB5117	-1.034793867	-0.4293768	0.129913445	0.494051987	0.683283335	0.247192577	0	0	0.454858981	0.997857809
s_Ruminococcaceae_bacterium _SGB15273	1.033254436	0.544433308	0.048252571	0.826224333	0.538081608	0.248878847	0	0	0.304618811	0.997857809
s_Candidatus_Pseudoruminococcus_merdavium _SGB59562	-1.031182797	-0.436766597	0.121727835	0.011790266	0.66632738	0.247315649	0	0	0.443694358	0.997857809
s_Lachnospiraceae_bacterium _SGB4597	-1.024270423	-0.294591435	0.298783584	0.34777471	0.985780161	0.2457145				

s_Christensenellaceae_bacterium[t_SGB14127	-0.830815726	-0.513962587	0.069865213	0.711440791	0.458309394	0.248394651	0.00079	0.0013	0.344295772	0.997857809
s_GGB2983_SGB3965[t_SGB3965	-0.828221166	-0.243899368	0.389650771	0.3722458	0.962767025	0.245299488	0	0	0.750077734	0.997857809
s_Clostridia_unclassified_SGB6376[t_SGB6376	0.817778592	0.176166334	0.534368367	0.2764387	1.316143237	0.244866116	0	0	0.816043863	0.997857809
s_Cuneatibacter_caecimuris[t_SGB29380	0.816367102	0.439247614	0.211319621	0.142367979	0.526940575	0.247322024	0	0	0.546360438	0.997857809
s_Intestinimonas_butyriliproducentis[t_SGB15126	0.810210052	0.389412312	0.169601424	0.966124341	0.589893358	0.246697923	0.00763	0.00636	0.526303213	0.997857809
s_GGB9615_SGB15051[t_SGB15051	-0.809763392	-0.297431596	0.294149152	0.393201424	0.771892096	0.245740091	0	0	0.68145363	0.997857809
s_Eggerthellaceae_unclassified_SGB14341[t_SGB14341	0.80958975	0.332618643	0.240727551	0.622657725	0.690087197	0.246076634	0	0	0.621533509	0.997857809
s_Clostridia_bacterium[t_SGB3988	0.807609811	0.351731479	0.214759988	0.77087089	0.65099238	0.246274976	0	0	0.577694899	0.997857809
s_Coprobaecillus_cateniformis[t_SGB6771	-0.80359154	-0.185268481	0.513462703	0.184317504	1.229757198	0.244916265	0	0	0.80831951	0.997857809
s_Flavonifractor_plautii[t_SGB15132	-0.799738572	-0.58063069	0.04056712	0.244896759	0.390511306	0.249488932	0.11969	0.080285	0.257622453	0.997857809
s_Flavonifractor_sp_An100[t_SGB15160	0.798810421	0.415386395	0.241894149	0.130934384	0.545226569	0.247014034	0	0	0.482133325	0.997857809
s_Actinomyces_orisii[t_SGB15878	-0.797982761	-0.453183115	0.10995178	0.503816522	0.499235368	0.247509664	0	0	0.425976709	0.997857809
s_Haemophilus_parainfluenzae[t_SGB9712_group	-0.788137641	-0.298213983	0.292881006	0.285581389	0.749306713	0.245747171	0	0	0.68145363	0.997857809
s_Eubacterium_ramusii[t_SGB4960	0.787803002	0.182739244	0.5192288	0.902220094	1.222281858	0.244902077	0	0	0.80831951	0.997857809
s_Holdemania_massiliensis[t_SGB4044	-0.787553858	-0.326223978	0.249890343	0.13437863	0.684462945	0.246012714	0	0	0.638723863	0.997857809
s_Blautia_SGB4831[t_SGB4831_group	0.785584842	0.518664478	0.06734442	0.513057272	0.429429518	0.248467612	0.01597	0.018115	0.337269617	0.997857809
s_Clostridia_bacterium[t_SGB3940	-0.783686425	-0.200096946	0.480339562	0.258680917	1.110420372	0.245003347	0	0	0.797141149	0.997857809
s_GGB9623_SGB15076[t_SGB15076	-0.774526828	-0.261930474	0.355655516	0.124853109	0.838370508	0.245438248	0	0	0.726386254	0.997857809
s_Anaerofustis_stercoriformis[t_SGB4116	-0.76670938	-0.259644284	0.399780022	0.30735838	0.837216091	0.245420111	0	0	0.728015648	0.997857809
s_GGB2980_SGB3962[t_SGB3962	0.766479391	0.341639254	0.228208485	0.704128716	0.63608957	0.246168884	0	0	0.607337971	0.997857809
s_Clostridium_methylpentosum[t_SGB14962	-0.765038898	-0.457360702	0.106713104	0.377758554	0.474253154	0.247567028	0	0	0.425976709	0.997857809
s_Clostridia_unclassified_SGB15402[t_SGB15402	0.762557808	0.413296961	0.144915646	0.559937722	0.52311407	0.246987863	0	0	0.484226864	0.997857809
s_GGB42389_SGB59559[t_SGB59559	-0.762037267	-0.318561836	0.261186645	0.611758025	0.678215985	0.245937736	0	0	0.640999894	0.997857809
s_Anaerotruncus_lactatifermentans[t_SGB5193	-0.761924156	-0.306089133	0.280320919	0.975575165	0.705747565	0.245819845	0	0	0.661600329	0.997857809
s_GGB9695_SGB15209[t_SGB15209	-0.761697732	-0.450908809	0.111747472	0.046232915	0.478934936	0.247478648	0	0	0.427555546	0.997857809
s_GGB2977_SGB3950[t_SGB3950	-0.758248243	-0.322670648	0.22505858	0.567727584	0.666250439	0.245977724	0	0	0.540999894	0.997857809
s_Streptococcus_rubnerii[t_SGB8056	-0.748306247	-0.304269709	0.283189706	0.275246998	0.697278394	0.245802586	0	0	0.665820073	0.997857809
s_Peptococcaceae_bacterium[t_SGB49168	-0.746150635	-0.20596777	0.467554765	0.770022938	1.027100172	0.245039667	0	0	0.791246526	0.997857809
s_Streptococcus_infantis[t_SGB8095	-0.744857388	-0.29631536	0.295964788	0.598997546	0.712696329	0.245730023	0	0	0.681515993	0.997857809
s_Lachnospiraceae_bacterium[t_SGB4750	0.74027509	0.386081885	0.173280499	0.49489845	0.54362509	0.246658836	0.02851	0.019005	0.524733935	0.997857809
s_Erysipelotrichaceae_bacterium_3_1_53[t_SGB4036	0.7322576	0.154709707	0.58529131	0.824372684	1.341936237	0.244757861	0	0	0.844432998	0.997857809
s_Veillonella_parvula[t_SGB6939	0.732176181	0.188610899	0.50594185	0.77955427	1.100612314	0.244935311	0	0	0.80091951	0.997857809
s_Blautia_hansenii[t_SGB4798	0.722127823	0.184225346	0.51583677	0.673918689	1.111348463	0.244910309	0	0	0.80931951	0.997857809
s_Clostridia_bacterium[t_SGB5184	-0.718330246	-0.344742106	0.224011376	0.949533843	0.90765847	0.246201178	0	0	0.599960003	0.997857809
s_Clostridiales_bacterium_UBA1390[t_SGB4436	0.712175769	0.370685989	0.191088443	0.401824011	0.544740934	0.246482221	0	0	0.547033777	0.997857809
s_Clostridiales_bacterium[t_SGB15158	-0.706242593	-0.31289012	0.29772627	0.935318502	0.639952289	0.24588337	0	0.00158	0.656058281	0.997857809
s_Ruminococcus_torques[t_SGB4608	0.699353351	0.415036439	0.143231166	0.132395086	0.477744823	0.247009642	0.04622	0.108315	0.482133325	0.997857809
s_Blautia_obeum[t_SGB4811_group	0.695698894	0.566247593	0.04803833	0.539744595	0.348337717	0.249241993	0.3566	0.455315	0.297358033	0.997857809
s_Tyzzerella_nexilis[t_SGB4588_group	0.687404075	0.19961821	0.481390434	0.224570082	0.976333233	0.245000431	0	0	0.797141149	0.997857809
s_Candidatus_Saccharibacterium_unclassified_SGB19850_group	0.686345959	0.308301948	0.276858541	0.908150466	0.631177922	0.245840095	0	0	0.661600329	0.997857809
s_Roseburia_intestinalis[t_SGB4951	0.68531329	0.294656957	0.298184426	0.466937877	0.658743082	0.245717822	0.01494	0.061495	0.681669213	0.997857809
s_Clostridiales_bacterium_1_7_47FAA[t_SGB4763	0.683662633	0.306374402	0.279872917	0.128135772	0.632666624	0.245822104	0	0	0.661600329	0.997857809
s_Clostridiales_bacterium_NSJ_40[t_SGB27336	0.682135218	0.240775275	0.395752232	0.843260693	0.803237806	0.245276445	0	0	0.751223581	0.997857809
s_GGB9694_SGB15204[t_SGB15204	0.680457113	0.25239149	0.37356787	0.808435826	0.764384035	0.245363617	0	0	0.740914252	0.997857809
s_Firmicutes_bacterium_AF16_15[t_SGB4993	-0.678369537	-0.353742815	0.212149472	0.557728122	0.543706177	0.246296483	0.05427	0.026535	0.573175766	0.997857809
s_Clostridia_unclassified_SGB14951[t_SGB14951	0.678169306	0.218881586	0.440107721	0.567727584	0.878437771	0.245123234	0	0	0.781286328	0.997857809
s_Clostridia_bacterium[t_SGB3574	-0.675228262	-0.48023045	0.090301805	0.547734041	0.398645141	0.247890141	0.02153	0.01421	0.406028556	0.997857809
s_GGB9581_SGB79823[t_SGB79823	-0.674945413	-0.235430143	0.046324371	0.058423723	0.812815808	0.245237702	0	0	0.761476154	0.997857809
s_Parabacteroides_johnsonii[t_SGB1948	0.67123494	0.19802472	0.484924309	0.905299173	0.961097773	0.244990703	0	0	0.800640145	0.997857809
s_Alistipes_oderdonkii[t_SGB2303	-0.671200136	-0.427079088	0.131980145	0.319314964	0.445583691	0.247162857	0.6441	0.171615	0.456740278	0.997857809
s_Acidaminococcus_intestinalis[t_SGB5736	-0.665670395	-0.191416312	0.499587268	0.209374341	0.985974889	0.244951559	0	0	0.80931951	0.997857809
s_GGB9633_SGB15091[t_SGB15091	-0.663319359	-0.274410622	0.33111154	0.897969183	0.685341941	0.245540033	0	0	0.711765509	0.997857809
s_Longibaculum_murisii[t_SGB6769	-0.662648413	-0.208992738	0.461041694	0.849812775	0.898954111	0.245058789	0	0	0.791246526	0.997857809
s_Blautia_schinkii[t_SGB4825	0.658732072	0.295849418	0.296033711	0.729968024	0.630993352	0.24572705	0	0	0.681515993	0.997857809
s_Candidatus_Pararuminococcus_gallinarum[t_SGB63327	-0.654758149	-0.466231866	0.10006627	0.1545638	0.398166315	0.247690542	0.00549	6.00E-05	0.425976709	0.997857809
s_GGB2982_SGB3964[t_SGB3964	-0.653269512	-0.450454878	0.109276636	0.993393765	0.407923015	0.247521469	0.01774	0	0.425976709	0.997857809
s_Clostridia_bacterium[t_SGB14952	-0.641278537	-0.249489614	0.378876606	0.886476628	0.728752052	0.245341459	0	0	0.740914252	0.997857809
s_Lactocaseibacillus_rhamnosus[t_SGB7144	-0.640105617	-0.259275768	0.360462293	0.497690129	0.699963294	0.245417203	0	0	0.728015648	0.997857809
s_Ruminococcus_lactaris[t_SGB4567	-0.635316886	-0.239853668	0.197563129	0.925815833	0.750982111	0.245269703	0	0	0.751223581	0.997857809
s_Anaeromassilibacillus_sp_An250[t_SGB14894	-0.63468677	-0.44983502	0.112603056	0.926105623	0.400030501	0.247464061	0.00165	0.00737	0.428169643	0.997857809
s_Ruminococcaceae_unclassified_SGB15236[t_SGB15236	-0.633693256	-0.320227688	0.258701128	0.24150246	0.56105542	0.245953888	0	0	0.640999894	0.997857809
s_GGB9623_SGB15075[t_SGB15075	-0.632387958	-0.187014338	0.509502071	0.250719042	0.958725421	0.244926171	0	0	0.80831951	0.997857809
s_Oscillibacter_sp_ER4[t_SGB15254	0.63026311	0.457690249	0.10640874	0.173904437	0.390423352	0.247571575	0	0.442275	0.425976709	0.997857809
s_Clostridia_unclassified_SGB71281[t_SGB71281	0.626250124	0.170752409	0.547003608	0.907690981	1.039840052	0.244837482	0	0	0.824353837	0.997857809
s_Lactocaseibacillus_paracasei[t_SGB7142	-0.625011803	-0.292793721	0.301742059	0.13680167	0.605218251	0.245698905	0	0	0.6851048	0.997857809
s_GGB9694_SGB15201[t_SGB15201	-0.622494493	-0.229605692	0.418034423	0.412598433	0.768667324	0.245196469	0	0	0.730044844	0.997857809
s_Blautia_wexlerae[t_SGB4837_group	0.618813493	0.448574531	0.115804053	0.262272109	0.393489063	0.247410542	0.99992	1.71139	0.434971322	0.997857809
s_Faecalibacterium_prausnitzii[t_SGB15332	0.617231248	0.268625657	0.321931847	0.652643594	0.623153834	0.245594186	0	0	0.706105128	0.997857809
s_Clostridia_bacterium[t_SGB17347	0.616110789	0.215303225	0.447619185	0.831627686	0.811323064	0.245099572	0	0	0.7900671	0.997857809
s_Lachnospiraceae_bacterium[t_SGB4594	-0.610972485	-0.249775659	0.378330285	0.126713778	0.693516977	0.245343632	0	0	0.740914252	0.997857809
s_Blautia_SGB4815[t_SGB4815_group	0.610216803	0.385257879	0.174199626	0.462885148	0.449074141	0.246649219	0.03879	0.03761	0.527439835	0.997857809
s_Ruminococcaceae_bacterium[t_SGB4181	0.609898951	0.240898561	0.381540321	0.387580805	0.696977176	0.245330927	0	0	0.743762144	0.997857809
s_Anaerococcus_obesitensis[t_SGB6661	-0.608052209	-0.166305471	0.557491508	0.312534234	1.036020732	0.244814628	0	0	0.83	

s_Clostridia_bacterium[t_SGB3993	0.513436092	0.145900558	0.606831229	0.905299173	0.997734521	0.244717469	0	0	0.84956372	0.997857809
s_Clostridium_sp_AF20_17LBJt_SGB4714	-0.50788206	-0.278745811	0.325530267	0.882018208	0.516586164	0.245576488	0	0.00094	0.708547714	0.997857809
s_Bacteroides_xylanisolvensis[t_SGB1867	0.507678431	0.225427085	0.265556629	0.972055669	0.638510693	0.245167519	0.1003	0.11595	0.772820245	0.997857809
s_Lachnospiraceae_bacterium[t_SGB4669	-0.505828594	-0.200435746	0.475956619	0.594723301	0.715506784	0.245005415	0	0	0.797141149	0.997857809
s_Streptococcus_sp_263_SSPC[t_SGB8255_group	-0.503843907	-0.211970096	0.454680954	0.241636836	0.673917867	0.245077881	0	0	0.791246526	0.997857809
s_Blautia_sp_AF19_10LBJt_SGB4810	0.493541277	0.221187034	0.435306822	0.379465991	0.632629401	0.245138684	0	0	0.777571016	0.997857809
s_GGB9633_SGB15090[t_SGB15090	0.492205467	0.207358049	0.464555037	0.835547044	0.672993846	0.245048421	0	0	0.791246526	0.997857809
s_Solobacterium_SGB6833[t_SGB6833_group	0.488407969	0.175238903	0.536522345	0.978419021	0.790201362	0.244861148	0	0	0.816043863	0.997857809
s_Phocaea_massiliensis[t_SGB14837	-0.487104628	-0.334156411	0.535259865	0.971829062	0.413292967	0.246092188	0.00251	0.00535	0.620054333	0.997857809
s_GGB9590_SGB15012[t_SGB15012	0.48206025	0.159440978	0.537807093	0.724431812	0.857209408	0.244780529	0	0	0.884685938	0.997857809
s_Sutterella_wadsworthensis[t_SGB9286	-0.480385112	-0.129934649	0.646744835	0.175011731	0.1048214391	0.244650281	0	0	0.840747304	0.997857809
s_Clostridia_bacterium[t_SGB3957	0.478686019	0.290985054	0.304738174	0.835034111	0.466407598	0.245682462	0.01018	0.011595	0.6851048	0.997857809
s_Lacrimispora_amygdalinali[t_SGB4716	0.478020022	0.319021689	0.260498867	0.637323572	0.424826325	0.245942187	0.01724	0.023005	0.640999894	0.997857809
s_GGB3537_SGB4727[t_SGB4727	-0.477420404	-0.224518503	0.428422988	0.444493308	0.602884885	0.245161295	0.00151	0	0.773925397	0.997857809
s_Clostridia_bacterium[t_SGB15374	-0.476160875	-0.195272714	0.490986202	0.462236439	0.691349579	0.244974284	0	0	0.806526667	0.997857809
s_Raoultibacter_timonensis[t_SGB33550	0.475598671	0.149498965	0.597989609	0.140200895	0.901961506	0.244733683	0	0	0.844432998	0.997857809
s_Harryflintia_acetisporal[t_SGB14838	0.474225708	0.277762618	0.327239652	0.877840096	0.484057393	0.245568171	0	0	0.799787415	0.997857809
s_Butyricococcus_sp_AM29_Z3AC[t_SGB14991	0.473078794	0.181134512	0.522904488	0.325678983	0.740487672	0.244893177	0	0	0.80931951	0.997857809
s_Bacteroides_caccae[t_SGB1877	0.471735758	0.168944162	0.551256475	0.768642114	0.791664493	0.244828116	0.01093	0.087245	0.826610239	0.997857809
s_Clostridia_bacterium[t_SGB3952	-0.468232585	-0.245834491	0.385900268	0.953006996	0.5400132	0.24531391	0	0	0.749888219	0.997857809
s_Candidatus_Allochistensenella_caecavium[t_SGB63369	-0.466203541	-0.234764638	0.407652375	0.954655431	0.563025992	0.245232939	0	0	0.761467514	0.997857809
s_Clostridium_SGB4751[t_SGB4751	0.464055423	0.16289296	0.519334626	0.800670319	0.720167629	0.24490182	0	0	0.80931951	0.997857809
s_Clostridium_sp_AF34_10BJH[t_SGB4914	-0.463501366	-0.185001717	0.514069287	0.180270032	0.710331078	0.244914759	0.10134	0.05416	0.80931951	0.997857809
s_Clostridia_bacterium[t_SGB15395	-0.450593678	-0.189501037	0.50388515	0.814489703	0.674153913	0.244940441	0	0	0.80931951	0.997857809
s_Clostridia_bacterium_UC5_1_1D1[t_SGB14995	-0.448498121	-0.288350282	0.309121199	0.442535046	0.440972707	0.245659356	0.01101	0.010695	0.689822676	0.997857809
s_Bifidobacterium_bifidum[t_SGB17256	-0.44823845	-0.110671282	0.696280045	0.957968711	1.148465234	0.244579549	0	0	0.910811009	0.997857809
s_Clostridium_symbiosum[t_SGB4699	-0.447728778	-0.22125555	0.431516407	0.812677329	0.57372974	0.245139146	0.00121	0.00373	0.777571016	0.997857809
s_Lachnospiraceae_bacterium[t_SGB5200	-0.444071007	-0.18595404	0.511905542	0.528205382	0.677068109	0.244920144	3.00E-04	7.50E-05	0.80931951	0.997857809
s_Ruminococcaceae_bacterium[t_SGB15356	-0.441862394	-0.143882895	0.61814726	0.347407349	0.870692023	0.244708549	0	0	0.852664867	0.997857809
s_Clostridiaceae_unclassified_SGB4769[t_SGB4769	-0.43876388	-0.206833874	0.465684761	0.513257888	0.601443393	0.245045114	0	0	0.791246526	0.997857809
s_Clostridium_leptum[t_SGB14853	-0.43853044	-0.234626162	0.407929025	0.262264212	0.529981801	0.245231949	0.03288	0.021765	0.761467514	0.997857809
s_Clostridia_bacterium[t_SGB14861	-0.437738148	-0.269763678	0.341362708	0.93807328	0.460062122	0.245501585	0.27786	0.135005	0.716777229	0.997857809
s_GGB9699_SGB15216[t_SGB15216	-0.436563619	-0.251351939	0.375328427	0.819922889	0.492437206	0.245355655	0.05162	0.054485	0.7403414252	0.997857809
s_Clostridia_bacterium[t_SGB14253	-0.43510858	-0.143127484	0.61368451	0.434518954	0.861906524	0.244705243	0	0	0.859340087	0.997857809
s_Clostridiaceae_bacterium_OM08_BBH[t_SGB4768	-0.430140136	-0.280062937	0.323249426	0.658910801	0.435451777	0.245587676	0.00707	0.0106	0.706105128	0.997857809
s_Parasuterralla_excrementihominis[t_SGB9262	-0.430115585	-0.251928434	0.372432438	0.367619047	0.484053706	0.245360064	0.02857	0.0059	0.7403414252	0.997857809
s_Eggerthellaceae_unclassified_SGB14322[t_SGB14322_group	-0.427529347	-0.189445127	0.50104371	0.87283175	0.639835084	0.244940118	0	0	0.80931951	0.997857809
s_Lachnoclostridium_undoid[t_SGB29433	-0.425510695	-0.14906537	0.599053929	0.82854922	0.809322661	0.244731705	0	0	0.844432998	0.997857809
s_Lachnospiraceae_bacterium[t_SGB4706	-0.421498867	-0.260356353	0.358463998	0.93598578	0.459000886	0.245425743	0.00114	0.002375	0.728015648	0.997857809
s_Clostridia_bacterium[t_SGB53517	-0.420537041	-0.265244492	0.349510974	0.456179484	0.449513466	0.245464822	0.00239	0.00302	0.750222146	0.997857809
s_GGB51441_SGB17759[t_SGB17759	-0.417464597	-0.250701003	0.376566277	0.366269849	0.4722116455	0.245350678	0.01437	0	0.740914252	0.997857809
s_Bacteroides_ovatus[t_SGB1871	-0.415791569	-0.206873008	0.465600365	0.710700969	0.569845871	0.24504536	0.37682	0.262515	0.791246526	0.997857809
s_Lachnoclostridium_sp_An131[t_SGB4775	-0.415625143	-0.257802028	0.363198882	0.345293511	0.457089283	0.245045611	0	0	0.730598029	0.997857809
s_GGB9615_SGB15053[t_SGB15053_group	-0.415046827	-0.273915712	0.333983788	0.379195018	0.429601423	0.245535907	0.0849	0.02945	0.711675509	0.997857809
s_Erysipelatoclostridium_amosum[t_SGB6744	-0.412247223	-0.156816989	0.58019154	0.647152065	0.745332717	0.244767873	0	0	0.844432998	0.997857809
s_Christensenella_sp_Marseille_P3954[t_SGB29301	0.406765954	0.189900192	0.502995051	1	0.607302051	0.244942749	0	0	0.80931951	1
s_Faecalibacterium_prausnitzii[t_SGB15316_group	-0.40254239	-0.288831654	0.308331015	0.97208486	0.395141268	0.24566349	0.27128	0.33656	0.689922676	0.997857809
s_Anaerofustis_stercorihominis[t_SGB49059	0.400701387	0.175807127	0.535022116	0.821276965	0.646204425	0.244864189	0	0	0.816043863	0.997857809
s_Clostridia_bacterium[t_SGB14311	-0.400520635	-0.157539804	0.578447147	0.381764121	0.720808919	0.244771338	0	0	0.844432998	0.997857809
s_GGB9602_SGB15031[t_SGB15031	-0.399187811	-0.164784376	0.561101276	0.53006096	0.686826111	0.244806948	0	0	0.831318642	0.997857809
s_Mogibacterium_diversum[t_SGB3922	0.396715882	0.207139281	0.45602635	0.741553073	0.543003565	0.24504704	0	0	0.791246526	0.997857809
s_Dorea_longicatena[t_SGB4581	0.393973537	0.336826594	0.234828693	0.855066879	0.331624214	0.246119365	0.31748	0.56588	0.615505566	0.997857809
s_Phocaeicola_vulgatus[t_SGB1814	-0.393734469	-0.319671431	0.25923768	0.414568155	0.34899548	0.245950385	3.66638	1.380975	0.640999894	0.997857809
s_Enterocloster_asparagiformis[t_SGB4724	0.392348662	0.176201618	0.534286505	0.787030305	0.631311082	0.244866306	0	0	0.816043863	0.997857809
s_Candidatus_Cibibacter_quicbialis[t_SGB15286	0.392057768	0.232168073	0.412585459	0.513528924	0.478776829	0.245214482	0.29096	0.31484	0.763004844	0.997857809
s_Clostridia_bacterium[t_SGB14845	-0.39000798	-0.123046523	0.664292752	0.314807553	0.898648144	0.24462369	0	0	0.786744978	0.997857809
s_Enterocloster_botteae[t_SGB4758_group	0.389620658	0.193826098	0.492403285	0.737908917	0.569921813	0.244965707	0.00568	0.01422	0.807504571	0.997857809
s_GGB9239_SGB14181[t_SGB14181	0.388860256	0.100905526	0.721914594	0.497956464	1.092633518	0.244548011	0	0	0.925251517	0.997857809
s_Eubacterium_rectale[t_SGB4933_group	-0.381098744	-0.264592411	0.350697751	0.399265864	0.408362347	0.245459564	2.94044	0.79638	0.750222146	0.997857809
s_Amedibacillus_dolichus[t_SGB4035	0.380989657	0.124825721	0.656971984	0.69911961	0.865355704	0.24463042	0	0	0.8287338563	0.997857809
s_Ruminococcus_birculans[t_SGB4262	0.379706409	0.182096481	0.520699464	0.169417905	0.591196604	0.244898503	0.00985	0.187935	0.80931951	0.997857809
s_GGB3677_SGB4990[t_SGB4990	0.379021911	0.146146834	0.606242448	0.830299541	0.735293054	0.244718566	0	0	0.84956372	0.997857809
s_Hydrogeniclostridium_mannosilyticum[t_SGB14890	-0.378250155	-0.127938372	0.651810837	0.608575877	0.838231255	0.244642426	0	0	0.880747304	0.997857809
s_GGB9559_SGB14969[t_SGB14969	0.373895447	0.1280618	0.651497142	0.497704084	0.827782291	0.244642908	0	0	0.880747304	0.997857809
s_Dorea_sp_AF36_15ATJ[t_SGB4552_group	0.365952923	0.244828011	0.387848189	0.712975512	0.423756973	0.245306395	0.02751	0.04038	0.750077734	0.997857809
s_Candidatus_Neoruminococcus_faecicola[t_SGB63342	-0.364672307	-0.1518468	0.595252488	0.706086044	0.680899	0.2447444475	0	0	0.844432998	0.997857809
s_Faecalibacillus_intestinalis[t_SGB6754	0.3605364	0.207223634	0.484484588	0.921387752	0.493282138	0.245047572	0.11429	0.068885	0.791246526	0.997857809
s_Candidatus_Avimicrobium_caecorum[t_SGB15350	-0.359315108	-0.239948578	0.397376407	0.627793071	0.424583696	0.245270396	0.00217	0.013115	0.751223581	0.997857809
s_Clostridium_sp_AM33_3[t_SGB4711	-0.358046302	-0.228838151	0.419592251	0.648677686	0.443604885	0.245191112	0.00177	0	0.763004844	0.997857809
s_Corynebacterium_durum[t_SGB17008	0.355088081	0.235229051	0.560725374	0.842007693	0.427987248	0.245236261	0	0	0.761467514	0.997857809
s_Dorea_sp_AF24_7LBJt_SGB4571	-0.354119548	-0.168883205	0.551520793	0.829047919	0.594676366	0.244827538	0	0	0.826610239	0.997857809
s_GGB9705_SGB15225[t_SGB15225	-0.351285795	-0.170696027	0.543733883	0.419253863	0.583771128	0.244836739	0	0	0.824353837	0

s_Etepiea_gabavorous[t_SGB15120	-0.257313182	-0.2107733905	0.457315896	0.362518489	0.346188932	0.245069921	0.34937	0.261215	0.791246526	0.997857809
s_Christensenellaceae_bacterium[t_SGB3813	-0.25844469	-0.123441131	0.66328236	0.156280002	0.587627446	0.244625175	0.00164	0	0.887644978	0.997857809
s_Clostridium_sp_AF27_2AA[t_SGB4712	-0.252991827	-0.132496166	0.640268342	0.920353170	0.541363206	0.244660538	0	0	0.880061501	0.997857809
s_GGB9787_SGB15410[t_SGB15410	0.251976315	0.111179019	0.694956907	0.390477798	0.642571964	0.244581269	0	0	0.910911009	0.997857809
s_GGB9758_SGB15368[t_SGB15368	0.249536222	0.076502023	0.787292386	0.702617247	0.92479649	0.244481915	0	0	0.945502049	0.997857809
s_Dorea_forcigenerans[t_SGB4575	0.246707771	0.18835414	0.506493809	0.977747196	0.371376099	0.244933784	0.16863	0.144475	0.80931951	0.997857809
s_Streptococcus_sp_A12[t_SGB8059_group	-0.245437922	-0.110590345	0.696492021	0.413302264	0.629235468	0.244579276	0.00047	0.000536	0.910911009	0.997857809
s_Lawsonbacter_sp_NSJ_52[t_SGB15125	0.243806813	0.051426324	0.856065865	0.544019036	1.344144355	0.244432929	0	0	0.968107698	0.997857809
s_GGB9501_SGB14898[t_SGB14898	-0.241821172	-0.083455544	0.768487572	0.950069719	0.821532382	0.244498898	0	0	0.935550088	0.997857809
s_Odoribacter_splanchnicus[t_SGB1790	0.240112364	0.221098677	0.435490261	0.425720968	0.307903013	0.245138089	0.09038	0.134775	0.777571016	0.997857809
s_Roseburia_inulinivorans[t_SGB4940	0.238685527	0.113398872	0.68918149	0.289457849	0.596764514	0.244588878	0.20871	0.0416	0.910911009	0.997857809
s_Blautia_caecimuris[t_SGB4862	-0.238188445	-0.077088061	0.78570259	0.652686115	0.876030293	0.24448329	0	0	0.945502049	0.997857809
s_Faecalibacterium_prausnitzii[t_SGB15318_group	-0.233105034	-0.187541082	0.80310255	0.365478687	0.352403969	0.244929178	1.4347	0.57179	0.80331951	0.997857809
s_Marvinbryantia_SGB4691[t_SGB4691	-0.231570019	-0.115366326	0.684077434	0.715355951	0.569100315	0.244595747	0	0	0.9308171765	0.997857809
s_Ruminococcus_torques[t_SGB4563_group	0.231249459	0.150587815	0.595325779	0.697050742	0.435387995	0.244738667	0.22211	0.24553	0.844432998	0.997857809
s_Holdemania_sp_Marseille_P284[t_SGB4045	-0.22944254	-0.107123173	0.70555596	0.227217441	0.60726195	0.244567755	0.00071	0	0.912097436	0.997857809
s_Massilimalliae_massiliensis[t_SGB29347	-0.228003833	-0.149374332	0.598294864	0.161647993	0.432764599	0.244733115	0.00029	0	0.844432998	0.997857809
s_Hungateia_hathewayi[t_SGB4742	-0.224121778	-0.073891186	0.794358569	0.945678061	0.859957477	0.24447592	0	0	0.945928746	0.997857809
s_Mediterraneibacter_massiliensis[t_SGB4595	0.223627939	0.10204644	0.718903058	0.703668077	0.621317784	0.244551546	0	0	0.924518338	0.997857809
s_Pseudoflavifractor_sp_AF19_9AC[t_SGB23477	0.222912097	0.123821138	0.862309934	0.532263164	0.510416144	0.244626609	0	0	0.887644978	0.997857809
s_Slackia_isolavonicumconvertens[t_SGB14773_group	-0.222362574	-0.06908936	0.807451572	0.348416462	0.912387801	0.244465455	0	0	0.954696064	0.997857809
s_Clostridium_fessum[t_SGB4705	-0.220464237	-0.15103403	0.594234721	0.199521767	0.413854561	0.244740722	0.13825	0.08291	0.844432998	0.997857809
s_Blautia_sp_OF03_15H[t_SGB4779	0.220013276	0.134478424	0.63575145	0.655117918	0.463854564	0.244688612	0	0	0.76982716	0.997857809
s_Enterocloster_aldensis[t_SGB4762	0.218683921	0.085921316	0.761851186	0.721683921	0.721605937	0.244505274	0.00042	0	0.930811623	0.997857809
s_Candidatus_Borifalkia_oeffranzophila[t_SGB14027	0.218361531	0.081772755	0.773026429	0.932468965	0.757096666	0.244494653	0	0	0.939219469	0.997857809
s_Agathobaculum_hutvyniproductum[t_SGB14993_group	0.213272177	-0.197409952	0.486253352	0.276132106	0.306302624	0.244987072	0.29944	0.19192	0.800988829	0.997857809
s_Candidatus_Pseudobutyricoccus_lithianensis[t_SGB14975	0.211657089	-0.060283125	0.831621045	0.904757199	0.996397932	0.244448039	0	0	0.966563328	0.997857809
s_Clostridia_bacterium[t_SGB3969	0.203288664	0.091252503	0.74763125	0.364727813	0.63161718	0.244519695	0	0	0.929943513	0.997857809
s_Bacteroides_cellulosilyticus[t_SGB1844	0.201474884	0.074208109	0.793523894	0.506341551	0.769759587	0.244476637	0	0.00062	0.945928746	0.997857809
s_Clostridium_sp_NSJ_42[t_SGB6174_group	-0.200417824	-0.062882442	0.824476618	0.553398534	0.903633873	0.244452928	0	0	0.961889387	0.997857809
s_Lachnospiraceae_bacterium[t_SGB4782	-0.199164326	-0.130344926	0.645705679	0.515801386	0.433214493	0.24465191	0.01271	0.003105	0.880747304	0.997857809
s_Christensenella_minutula[t_SGB14142	0.194944102	0.088391943	0.755219252	0.738659111	0.625292146	0.244511849	0	0	0.929943513	0.997857809
s_Firmicutes_bacterium[t_SGB49188	-0.194659276	-0.09891849	0.727179401	0.173461926	0.558058004	0.244541939	0	0	0.925251517	0.997857809
s_Neobutirella_massiliensis[t_SGB7264	0.193399575	0.085462898	0.763084204	0.7516527	0.641600774	0.244504074	0	0	0.930811623	0.997857809
s_Coprococcus_catus[t_SGB4670	0.192710073	0.155682009	0.582983996	0.754272521	0.351001494	0.244762369	0.11933	0.08465	0.844432998	0.997857809
s_Actinomyces_SGB17154[t_SGB17154	0.190930074	0.05108865	0.807000742	0.790417825	0.105984184	0.244432401	0	0	0.968107698	0.997857809
s_Anaerotruncus_rubifantus[t_SGB25416	-0.189848311	-0.122031879	0.66893539	0.709613611	0.441081656	0.244619896	0.00024	0.000525	0.889191385	0.997857809
s_GGB3510_SGB4687[t_SGB4687	-0.187748008	-0.087976223	0.756333929	0.828569608	0.605056015	0.24451073	0.00028	0	0.929943513	0.997857809
s_Intestinibacillus_sp_Marseille_P656[t_SGB29313	-0.185847288	-0.094649477	0.73850361	0.592396372	0.556703007	0.244529335	0	0	0.929943513	0.997857809
s_Clostridia_unclassified_SGB6276[t_SGB6276	-0.183217794	-0.054800777	0.84634722	0.393201424	0.947908643	0.244438404	0	0	0.968107698	0.997857809
s_GGB6612_SGB9346[t_SGB9346	0.179252609	0.055399039	0.842082593	0.559925145	0.917379032	0.24443941	0	0	0.968107698	0.997857809
s_Ruminococcaceae_unclassified_SGB15265[t_SGB15265_group	-0.177435667	-0.093167606	0.74451286	0.772273786	0.539959943	0.244525087	0.00156	0.013595	0.929943513	0.997857809
s_Ruminococcus_sp_AF41_9[t_SGB25497	0.174563518	0.063024643	0.82408618	0.878170173	0.785287436	0.244453201	0	0	0.961889387	0.997857809
s_Streptococcus_mitis[t_SGB8163	0.173252322	0.076456471	0.787416029	0.918896444	0.642466329	0.244481809	0	0	0.945502049	0.997857809
s_Alistipes_shahii[t_SGB2295	0.172189808	0.132018741	0.641473399	0.657550155	0.369791915	0.244658611	0.35494	0.24713	0.880061501	0.997857809
s_Clostridium_sp_AM22_11AC[t_SGB4749	-0.1706733	-0.090918902	0.74454722	0.341180568	0.532114804	0.244518767	0.04157	0.023995	0.929943513	0.997857809
s_Actinomyces_naeslundii[t_SGB15888	0.168944305	0.046134398	0.870739382	0.85241523	1.038255542	0.244425044	0	0	0.968107698	0.997857809
s_Butyricimonas_paravosai[t_SGB1785	0.166028183	0.06682743	0.813661418	0.411903565	0.704389076	0.244460742	0	0	0.954696064	0.997857809
s_Actinomyces_SGB17168[t_SGB17168	0.159939874	0.080831443	0.775568758	0.652366866	0.560988853	0.244492316	0	0	0.940453455	0.997857809
s_Ruminococcaceae_unclassified_SGB53515	-0.156540633	-0.078621537	0.81546767	0.544022472	0.564509315	0.244486935	0	0	0.944594291	0.997857809
s_Lachnospira_eligens[t_SGB5082_group	-0.15556839	-0.09854966	0.728146734	0.59630866	0.447612318	0.244540838	0.04846	0.124005	0.925251517	0.997857809
s_Blautia_faecis[t_SGB4820	0.155511337	0.100256894	0.723628646	0.326130535	0.439777866	0.244546019	0.24995	0.424575	0.925251517	0.997857809
s_Prevotella_copri_clade_A[t_SGB1626	0.154699572	0.045829627	0.81758586	0.758671935	0.957037263	0.244424616	0	0	0.968107698	0.997857809
s_Granulicatella_adiacens[t_SGB8249	0.154375464	0.078325517	0.78234852	0.697839025	0.558805358	0.244486226	0	0	0.944594291	0.997857809
s_GGB58158_SGB79798[t_SGB79798	-0.152862392	-0.118246175	0.67663241	0.856439199	0.366521205	0.244606014	0.00173	0.000825	0.900228002	0.997857809
s_GGB1420_SGB1957[t_SGB1957	-0.150879809	-0.050925752	0.857451811	0.30734297	0.839999893	0.244432147	0	0	0.968107698	0.997857809
s_Faecalibacterium_prausnitzii[t_SGB15342	0.150767395	0.10065014	0.724135968	0.602668636	0.427179818	0.244545433	0.44136	0.537355	0.925251517	0.997857809
s_Lachnospiraceae_bacterium_WCA3_601_WT_6H[t_SGB4910	0.14778606	0.059019351	0.8305997	0.823837806	0.709918881	0.244445736	0.02003	0.006225	0.966957548	0.997857809
s_Clostridia_bacterium[t_SGB14937	-0.147256965	-0.086749793	0.759625319	0.551212778	0.481283536	0.244507458	0.00769	0.002335	0.930811623	0.997857809
s_Phascolorctobacterium_faecium[t_SGB5792	0.145230174	0.096392237	0.733869742	0.354263366	0.427169616	0.244534418	0	0	0.929943513	0.997857809
s_Parabacteroides_merdae[t_SGB1949	0.144378089	0.096221411	0.749248146	0.746584769	0.451702537	0.244517944	0.33837	0.147805	0.929943513	0.997857809
s_GGB45432_SGB63101[t_SGB63101	0.1442628	0.089613873	0.751945833	0.802818531	0.456419996	0.24451517	0.00865	0.007525	0.929943513	0.997857809
s_Lactococcus_lactis[t_SGB7985	0.143355613	0.048520151	0.86418315	0.435285388	0.83767732	0.244428493	0	0	0.968107698	0.997857809
s_GGB9730_SGB15291[t_SGB15291	0.143167366	0.088347637	0.83338028	0.550108456	0.459446189	0.24451173	0	0.02402	0.929943513	0.997857809
s_Turicibacter_sanguinis[t_SGB8646	0.142584398	0.046398451	0.870060112	0.261821314	0.871272642	0.244425418	0	0	0.968107698	0.997857809
s_Lachnospiraceae_bacterium[t_SGB4964	0.142293724	0.058079045	0.837690708	0.663996746	0.694627277	0.244444055	0.06091	0.03867	0.968107698	0.997857809
s_Bacteroides_uniformis[t_SGB1836_group	-0.141873728	-0.127308925	0.653411555	0.46467395	0.315957513	0.244639974	3.54438	2.74805	0.880747304	0.997857809
s_Clostridiaceae_bacterium[t_SGB4269	0.138077174	0.092813427	0.743395795	0.983236091	0.423714792	0.244524081	0.38261	0.265265	0.929943513	1
s_Clostridia_bacterium[t_SGB15413	-0.13155359	-0.057387342	0.839596726	0.599764549	0.649938336	0.244442835	0	0	0.968107698	0.997857809
s_Dorea_longicatena[t_SGB4582_group	-0.131513441	-0.067955049	0.751674657	0.511697522	0.548698744	0.244463062	0.11133	0.018445	0.954696064	0.997857809
s_Ruminococcus_gnavus[t_SGB4584	0.127192344	0.050469875	0.85871439	0.733774826	0.714519851	0.244431441	0.00297	0.013065	0.968107698	0.997857809
s_GGB9694_SGB15203[t_SGB15203	0.123223294	0.043632629	0.87769216							

s_Catabacter_hongkongensis t_SGB14143	0.059835418	0.025521233	0.928275096	0.259490204	0.664725336	0.244402485	0	0	0.988245031	0.997857809
s_Bifidobacterium_longum t_SGB17248	-0.058702622	-0.029417714	0.917361062	0.847683647	0.565762473	0.244405755	0.29015	0.286925	0.986703035	0.997857809
s_Lachnospiraceae_bacterium t_SGB4832	0.055375478	0.030353604	0.914741874	0.905490049	0.517240805	0.244406609	0	0.004095	0.986703035	0.997857809
s_GGB3571_SGB4778 t_SGB4778	-0.05537382	-0.037998829	0.893383089	0.875400301	0.413161481	0.244414591	0	0.00293	0.977484871	0.997857809
s_Akkermansia_muciniphila t_SGB9228	-0.054151664	-0.013970901	0.960699038	0.009836704	1.098937423	0.244395518	0	0	0.992059111	0.997857809
s_Butyricimonas_virosa t_SGB1784	0.049380601	0.02290771	0.935603262	0.750141832	0.611167488	0.244400552	0	0	0.988561937	0.997857809
s_GGB9634_SGB15093 t_SGB15093	-0.048913245	-0.013937887	0.960791832	0.28390555	0.994981703	0.244395504	0	0	0.992059111	0.997857809
s_Clostridia_unclassified_SGB4121 t_SGB4121	-0.047475724	-0.045594183	0.87223989	0.988789639	0.295221319	0.244424288	0.02716	0.042325	0.968107698	1
s_Anaerostipes_caccae t_SGB4529	0.04480198	0.016113047	0.954679109	0.920663996	0.788324633	0.244396502	0	0	0.992059111	0.997857809
s_Anaerofilum_sp_BX8 t_SGB79822	-0.041806159	-0.018121782	0.949036436	0.343887933	0.654071028	0.244397553	0	0	0.992059111	0.997857809
s_Faecalicatena_fissicatena t_SGB4871_group	0.041411161	0.021414042	0.939793912	0.78241821	0.548282397	0.244399541	0.05526	0.056745	0.989594957	0.997857809
s_Clostridia_bacterium t_SGB3991	0.040528609	0.012715545	0.964227944	0.831892048	0.90367503	0.244395006	0	0	0.992059111	0.997857809
s_Bacilli_unclassified_SGB6571 t_SGB6571	-0.040360262	-0.011981638	0.966291342	0.801584985	0.955043868	0.244394729	0	0	0.992059111	0.997857809
s_Lachnospiraceae_unclassified_SGB4882 t_SGB4882	-0.039598729	-0.012516017	0.964788898	0.655617383	0.897016952	0.244394929	0	0	0.992059111	0.997857809
s_Eubacterium_sulci t_SGB3934	0.038903717	0.018641923	0.947575732	1	0.591678709	0.244397845	0	0	0.992059111	1
s_Clostridia_bacterium t_SGB14892	0.035152411	0.01208687	0.965995465	0.990007678	0.824568638	0.244394768	0	0	0.992059111	1
s_Trueperella_pyogenes t_SGB17137	0.034783567	0.014439705	0.959381384	0.277345374	0.682969543	0.244395721	0	0	0.992059111	0.997857809
s_Mediterraneibacter_glycyrrhizini t_SGB4606	-0.033379568	-0.013946648	0.960767206	0.588807222	0.678572759	0.244395508	0.00147	0.002975	0.992059111	0.997857809
s_Lachnospiraceae_bacterium t_SGB4767	0.030471469	0.022114434	0.937828671	0.528716943	0.390663757	0.244400006	0.00456	0.018835	0.989216543	0.997857809
s_Candidatus_Geddesella_stercoravicola t_SGB14262	0.028760258	0.010164339	0.971401672	1	0.802230513	0.244394115	0	0	0.993547566	1
s_Clostridium_sp_AM49_4BH t_SGB4652	-0.028065833	-0.012171968	0.965756204	0.88475402	0.653736458	0.2443948	0	0	0.992059111	0.997857809
s_Lachnospiraceae_bacterium t_SGB4861	0.027096543	0.008205082	0.976912505	0.970029303	0.936303234	0.244393565	0	0	0.993547566	0.997857809
s_Clostridia_bacterium t_SGB13979	-0.026491332	-0.006917487	0.960534759	0.049219674	1.06577784	0.244393267	0	0	0.993547566	0.997857809
s_GGB9712_SGB15244 t_SGB15244	0.022449813	0.007693329	0.978352113	0.758671935	0.827339942	0.244393441	0	0	0.993547566	0.997857809
s_Ruminococcaceae_unclassified_SGB15233 t_SGB15233	0.019682759	0.00528155	0.985137536	0.271303989	1.05659876	0.244392963	0	0	0.993547566	0.997857809
s_Alistipes_putredinis t_SGB2316	0.019505929	0.017902795	0.949651468	0.960926459	0.308909574	0.244397432	2.63366	1.983105	0.992059111	0.997857809
s_Actinomyces_sp_ICM47 t_SGB17167	0.016904828	0.006039778	0.977377517	0.618493373	0.596145609	0.244393524	0	0	0.993547566	0.997857809
s_GGB9621_SGB15073 t_SGB15073	0.015371069	0.006744361	0.981021828	0.882796696	0.646173011	0.244393231	0	0	0.993547566	0.997857809
s_Christensenellaceae_bacterium_NSJ_53 t_SGB82545	0.014513147	0.011349565	0.988068615	0.215415331	0.362550013	0.244394504	0	0	0.992230061	0.997857809
s_Alistipes_ijumii t_SGB2328	-0.011167467	-0.004945293	0.986083677	0.830850338	0.640247988	0.24439291	0	0	0.993547566	0.997857809
s_Dialister_invisus t_SGB5825_group	0.010927183	0.004638687	0.986946402	0.909825685	0.6678804	0.244392865	0	0	0.993547566	0.997857809
s_Ruminococcaceae_bacterium t_SGB14177	0.010268452	0.00401234	0.988708861	0.145270785	0.725592484	0.244392782	0	0	0.993547566	0.997857809
s_Streptococcus_gordonii t_SGB8053	-0.009741025	-0.003073081	0.991351915	0.761283055	0.898703202	0.244392681	0	0	0.994581075	0.997857809
s_Lachnospiraceae_bacterium t_SGB4781	0.008140902	0.005678645	0.984020242	0.88183485	0.406455818	0.244393029	0.02301	0.03402	0.993547566	0.997857809
s_Clostridiales_bacterium_KLE1615 t_SGB5090_group	-0.005640902	-0.004216154	0.988135349	0.215874018	0.379330299	0.244392808	0.2786	0.136005	0.993547566	0.997857809
s_Intestinibacillus_massiliensis t_SGB29304	-0.00225892	-0.002147973	0.993955238	0.638487236	0.298165576	0.244392607	0	0	0.995496096	0.997857809
s_Fusicatenibacter_saccharivorans t_SGB4874	-0.001835924	-0.001600431	0.995496096	0.828977322	0.325239547	0.244392576	0.69766	0.755195	0.995496096	0.997857809

