Supporting information for

Different responses between soil fauna gut and plant rhizosphere microbiomes to manure applications

Running title: Comparison of gut and rhizosphere microbiomes

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This supplementary file includes 6 figures and 5 tables: Figs. S1 to S6, and Tables S1 to S5

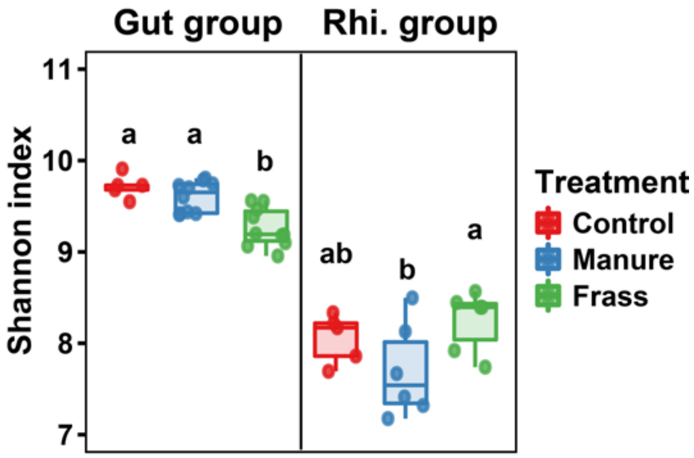

Fig. S1 Bacterial diversity (Shannon index) of the gut and rhizosphere groups in different treatments. Different letters above the boxes indicate significant differences between treatments determined by nonparametric Kruskal-Wallis test ($P < 0.01$). The gut group includes all the gut and frass samples, while the rhizosphere group includes all the rhizosphere soil samples. Abbreviation: Rhi., rhizosphere.

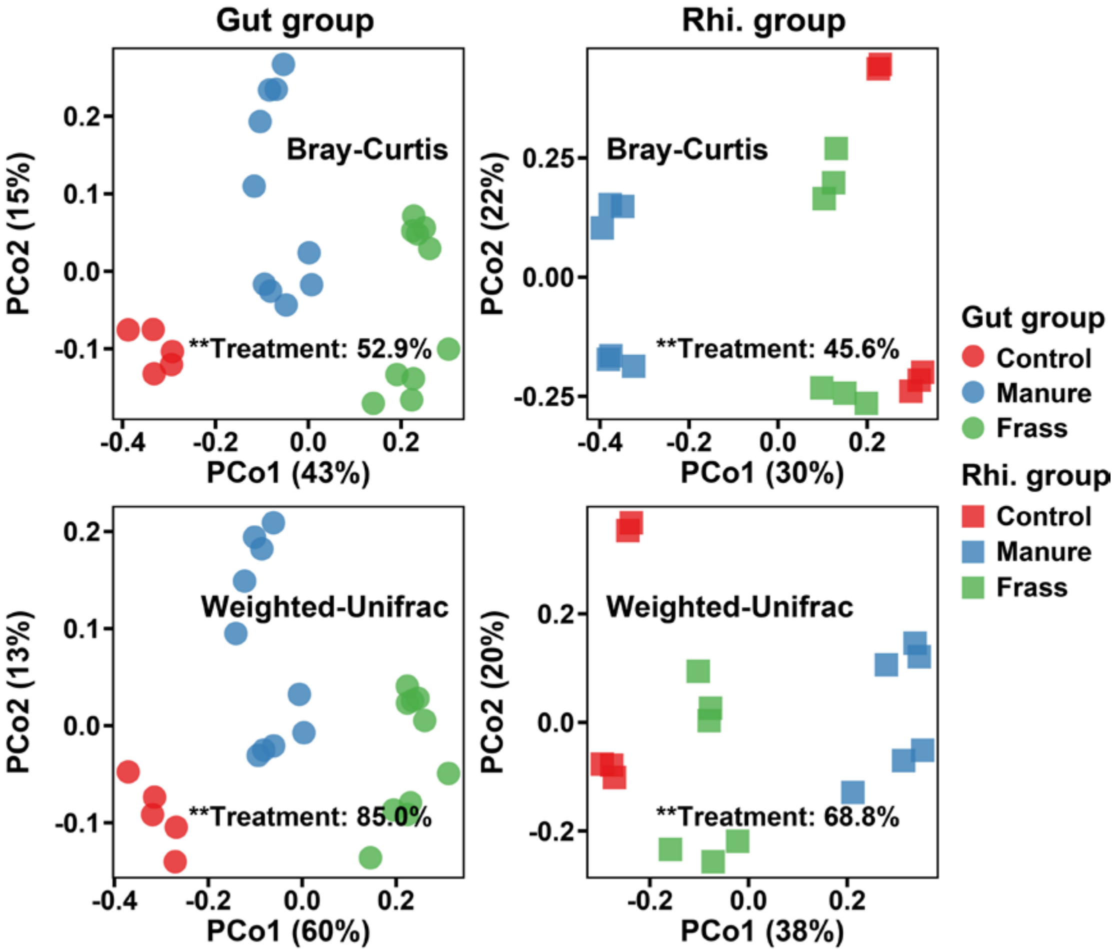

Fig. S2 Bacterial community structures of the gut and rhizosphere groups. Principal coordinate analysis (PCoA) based on Bray-Curtis dissimilarity matrices and weighted-UniFrac distance matrices depicting bacterial community structures of the gut and rhizosphere groups in different treatments, respectively. The relative contribution of treatment on community structures is tested with PERMANOVA. “Treatment” represents the effects of control/manure/frass. $^{**}P < 0.01$.

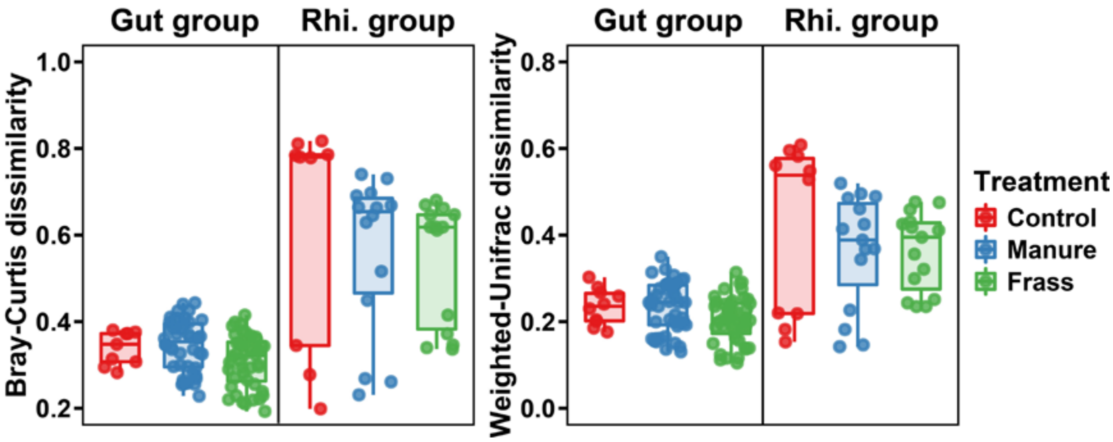

Fig. S3 Compositional variations of bacterial communities of the gut and rhizosphere groups based on Bray-Curtis dissimilarity matrices and weighted-UniFrac distance matrices. The boxplots show community dissimilarities between different treatments.

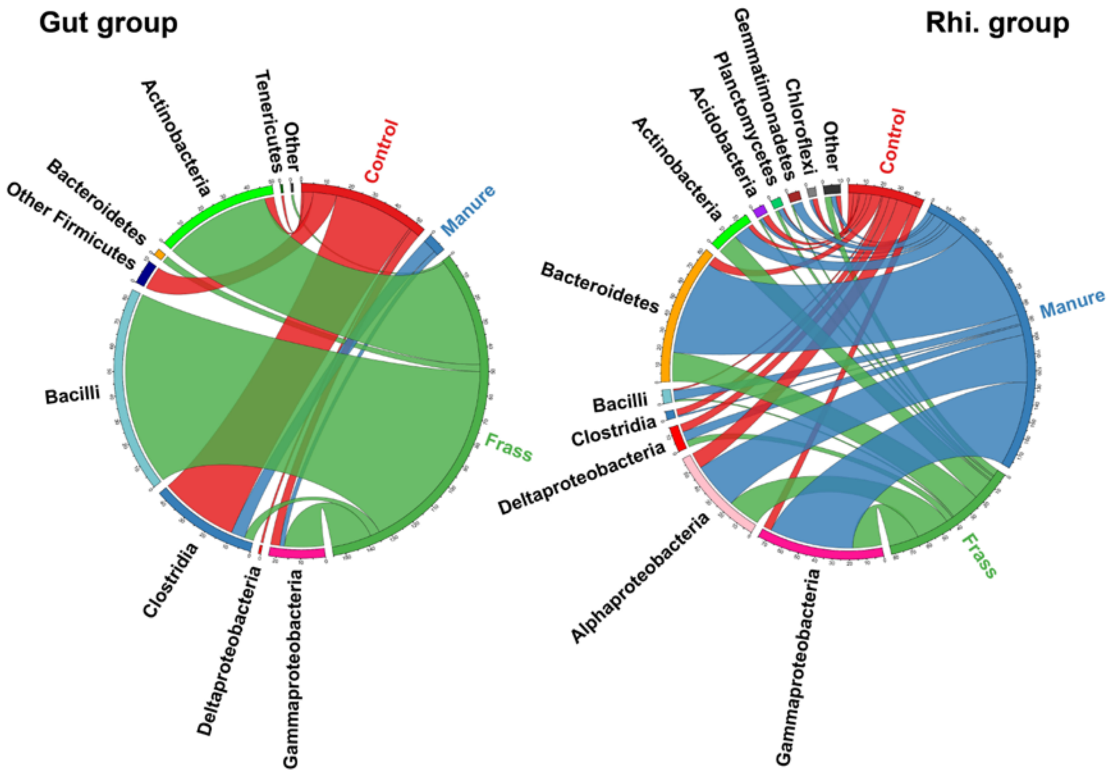

Fig. S4 Compositions of enriched bacterial ZOTUs for different treatments in the gut and rhizosphere groups. Ribbons in red, blue, and green represent bacterial ZOTUs belonged to a specific phylum enriched in the control, manure, and frass applications, respectively. Ribbon width is proportional to the numbers of bacterial ZOTUs enriched in the treatments.

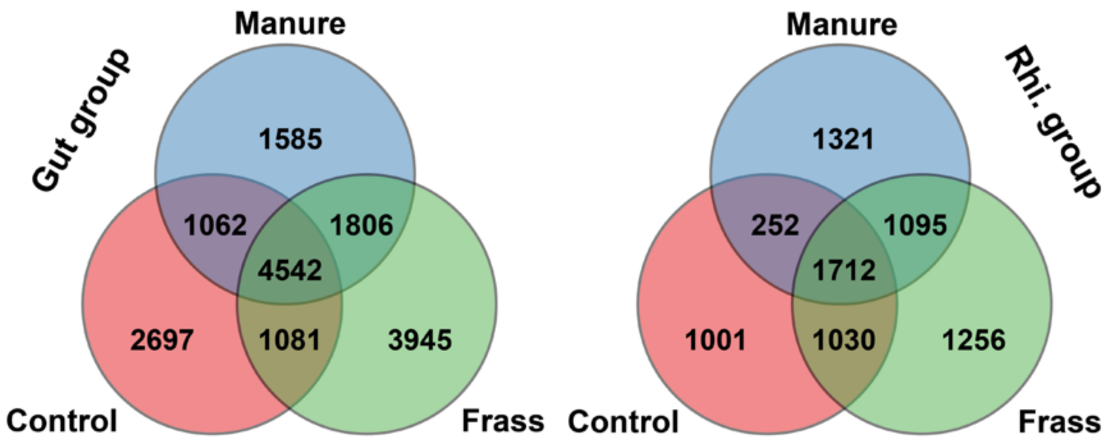

Fig. S5 Venn diagrams showing shared and specific bacterial ZOTU numbers of the gut and rhizosphere groups in different treatments.

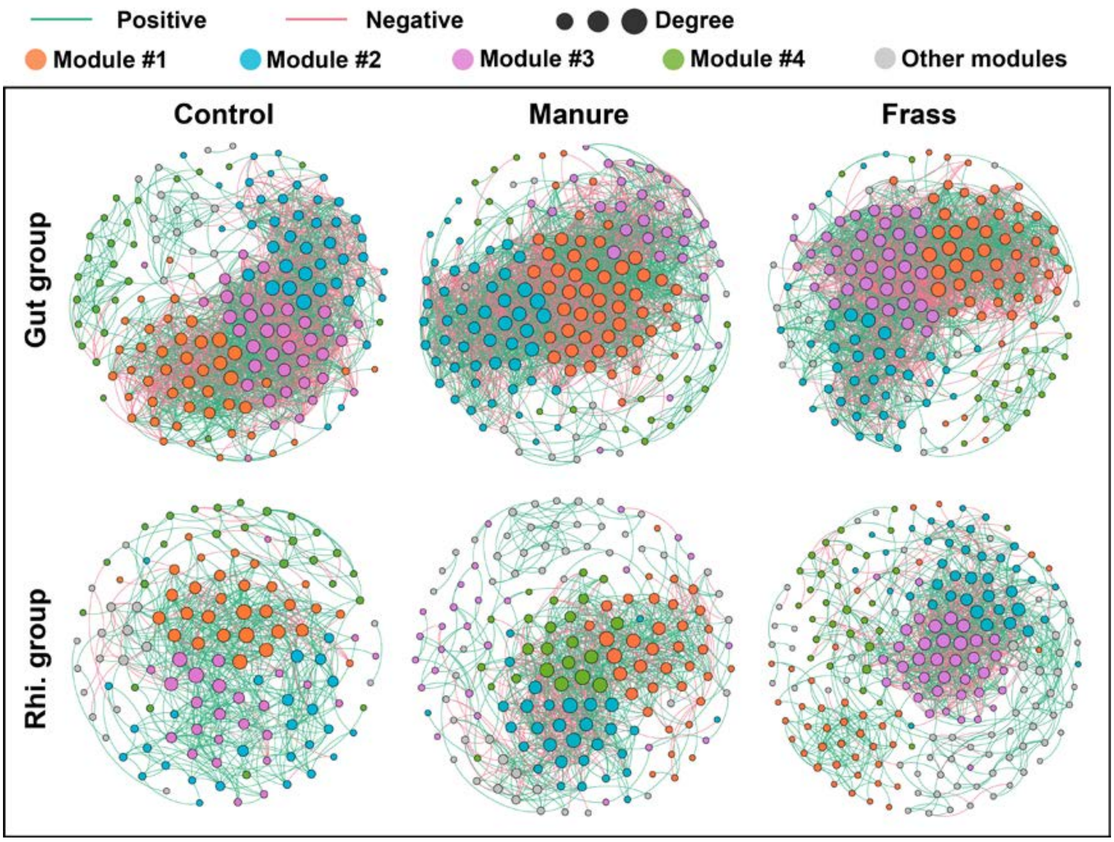

Fig. S6 Networks visualizing bacterial co-occurrence patterns of the gut and rhizosphere groups. Each node represents a special genus of bacteria; node colors represent network modules; node size is proportional to degree of connection; edges in green and red represent positive and negative connections among bacterial taxa, respectively.

Table S1 Enriched bacterial ZOTUs for three treatments in the gut group based on Fig. 2. All enriched ZOTUs were shared between three treatments.

ZOTUs	Enriched in	Relative abundance in				Taxonomy
		Control	Manure	Frass	Average	
ZOTU347	Control	0.001998	0.000224	0.000389	0.00087	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae
ZOTU422	Control	0.001359	0.000162	0.000292	0.000605	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae
ZOTU1012	Control	0.000949	7.72E-05	0.000185	0.000404	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae;g__Xylanimicrobium
ZOTU327	Control	0.0016	0.000148	0.000248	0.000666	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae;g__Xylanimicrobium
ZOTU10361	Control	0.000871	8.12E-05	0.000195	0.000383	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU10980	Control	0.002895	0.000579	0.000639	0.001371	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU12274	Control	0.000745	6.33E-05	0.000106	0.000305	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU12289	Control	0.001424	0.000158	0.000235	0.000606	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU13787	Control	0.000807	0.000245	0.000128	0.000394	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU21184	Control	0.000673	7.92E-05	5.52E-05	0.000269	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU26871	Control	0.000484	0.000105	7.88E-05	0.000223	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU27469	Control	0.001053	6.14E-05	6.51E-05	0.000393	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU6422	Control	0.001386	0.000125	0.000197	0.000569	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU7881	Control	0.002969	0.000408	0.000645	0.001341	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU8903	Control	0.001162	0.00019	0.000175	0.000509	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium;s__uncultured bacterium
ZOTU10588	Control	0.000861	8.92E-05	0.000101	0.00035	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured Clostridiales bacterium;s__uncultured Clostridiales bacterium
ZOTU16798	Control	0.000708	0.0002	0.000101	0.000336	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured Clostridiales bacterium;s__uncultured Clostridiales bacterium
ZOTU37894	Control	0.000361	4.15E-05	1.97E-06	0.000135	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
ZOTU20334	Control	0.000862	5.94E-05	3.15E-05	0.000318	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Eubacterium] xylanophilum group;s__uncultured bacterium
ZOTU2208	Control	0.008821	0.000143	3.16E-05	0.002998	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium 10;s__uncultured bacterium
ZOTU2386	Control	0.00717	8.71E-05	3.35E-05	0.00243	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium 10;s__uncultured bacterium
ZOTU2525	Control	0.017473	0.000309	9.07E-05	0.005958	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium 10;s__uncultured bacterium
ZOTU10691	Control	0.001028	0.000182	3.55E-05	0.000415	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3
ZOTU16170	Control	0.000603	7.73E-05	3.35E-05	0.000238	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3
ZOTU6469	Control	0.00179	0.000307	2.96E-05	0.000709	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3

ZOTU7246	Control	0.003528	0.000699	0.000103	0.001443	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3
ZOTU7957	Control	0.001366	0.000315	5.32E-05	0.000578	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3
ZOTU11570	Control	0.00077	0.000105	3.55E-05	0.000304	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3;s__uncultured bacterium
ZOTU7526	Control	0.001307	0.000143	3.75E-05	0.000496	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3;s__uncultured bacterium
ZOTU8722	Control	0.002295	0.000305	8.28E-05	0.000894	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3;s__uncultured bacterium
ZOTU32208	Control	0.000541	0.000125	1.97E-05	0.000228	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3;s__uncultured Clostridiales bacterium
ZOTU29428	Control	0.000669	0.000142	2.57E-05	0.000279	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella 3;s__uncultured Eubacteriaceae bacterium
ZOTU23927	Control	0.000948	2.97E-05	3.16E-05	0.000336	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__uncultured;s__uncultured bacterium
ZOTU3240	Control	0.005632	8.90E-05	2.76E-05	0.001916	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__uncultured;s__uncultured organism
ZOTU20012	Control	0.000455	4.15E-05	9.86E-06	0.000169	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 6;s__uncultured Clostridiaceae bacterium
ZOTU23373	Control	0.000887	3.95E-05	9.87E-06	0.000312	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 6;s__uncultured Clostridiaceae bacterium
ZOTU25263	Control	0.000463	2.77E-05	5.92E-06	0.000166	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 6;s__uncultured Clostridiaceae bacterium
ZOTU28100	Control	0.000328	1.78E-05	1.97E-06	0.000116	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 6;s__uncultured Clostridiaceae bacterium
ZOTU1099	Control	0.003809	0.000435	0.000199	0.001481	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU1148	Control	0.005964	0.002102	0.000971	0.003012	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU1460	Control	0.006964	0.000781	0.000229	0.002658	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU1512	Control	0.002326	0.000865	0.00038	0.00119	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU1797	Control	0.002747	0.000404	0.000171	0.001107	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU2377	Control	0.002195	0.000237	0.000136	0.000856	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU2469	Control	0.001794	0.000562	0.000343	0.0009	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU899	Control	0.002895	0.001055	0.000455	0.001468	k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter;s__uncultured bacterium
ZOTU16056	Control	0.000945	0.000309	9.87E-06	0.000421	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__uncultured;s__uncultured bacterium
ZOTU9279	Control	0.001359	0.000515	5.92E-05	0.000645	k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__uncultured;s__uncultured bacterium
ZOTU324	Control	0.00292	0.000218	0.000264	0.001134	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas
ZOTU553	Control	0.001039	7.13E-05	9.66E-05	0.000402	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas
ZOTU843	Control	0.000859	5.74E-05	8.08E-05	0.000332	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas
ZOTU297	Control	0.001433	8.52E-05	9.46E-05	0.000537	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas;s__uncultured bacterium
ZOTU5262	Control	0.00067	2.77E-05	7.89E-06	0.000235	k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales;f__Anaeroplasmataceae;g__Anaeroplasma;s__uncultured bacterium
ZOTU14590	Manure	7.17E-05	0.000669	8.47E-05	0.000275	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
ZOTU13486	Manure	0.000231	0.00089	0.00016	0.000427	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Intestinimonas
ZOTU17202	Manure	0.000291	0.000716	0.000103	0.00037	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 9;s__uncultured bacterium

ZOTU26929	Manure	0.000171	0.000562	6.70E-05	0.000267	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae NK4A214 group
ZOTU8707	Manure	0.000358	0.001007	0.000292	0.000552	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae NK4A214 group
ZOTU21079	Manure	1.19E-05	0.000295	2.96E-05	0.000112	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__uncultured;s__uncultured bacterium
ZOTU2251	Manure	0.000892	0.002535	0.000396	0.001275	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio
ZOTU4845	Manure	0.000283	0.001071	0.000311	0.000555	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Oxalobacter;s__uncultured bacterium
ZOTU5275	Manure	0.000733	0.002115	0.000721	0.00119	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Oxalobacter;s__uncultured bacterium
ZOTU4236	Frass	8.35E-05	0.000507	0.001084	0.000558	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Flaviflexus
ZOTU144	Frass	0.000159	0.002553	0.003947	0.00222	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1
ZOTU203	Frass	0.000469	0.004579	0.009112	0.00472	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1
ZOTU231	Frass	0.000131	0.002183	0.003874	0.002063	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1
ZOTU1665	Frass	0.000199	0.001109	0.003702	0.00167	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__Corynebacterium glutamicum
ZOTU2482	Frass	1.59E-05	0.00019	0.000529	0.000245	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__Corynebacterium glutamicum
ZOTU3423	Frass	2.78E-05	0.00018	0.000467	0.000225	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__Corynebacterium glutamicum
ZOTU1204	Frass	8.35E-05	0.000644	0.002225	0.000984	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__uncultured bacterium
ZOTU380	Frass	0.000103	0.001304	0.00303	0.001479	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__uncultured bacterium
ZOTU709	Frass	0.000115	0.001182	0.00336	0.001553	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__uncultured bacterium
ZOTU883	Frass	7.94E-05	0.00108	0.002972	0.001377	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__uncultured bacterium
ZOTU901	Frass	0.000279	0.001446	0.005047	0.002257	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1;s__uncultured bacterium
ZOTU14570	Frass	3.97E-05	0.000144	0.000323	0.000169	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales
ZOTU2569	Frass	0.000127	0.000899	0.001606	0.000877	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Brevibacteriaceae;g__Brevibacterium;s__uncultured bacterium
ZOTU2672	Frass	7.99E-06	0.000333	0.000627	0.000323	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Brevibacteriaceae;g__Brevibacterium;s__uncultured bacterium
ZOTU3442	Frass	3.95E-06	0.000242	0.000501	0.000249	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Brevibacteriaceae;g__Brevibacterium;s__uncultured bacterium
ZOTU4131	Frass	2.38E-05	0.000313	0.000554	0.000297	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Demequinaceae;g__uncultured;s__uncultured bacterium
ZOTU4530	Frass	2.80E-05	0.000257	0.000522	0.000269	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Demequinaceae;g__uncultured;s__uncultured bacterium
ZOTU4725	Frass	0.000103	0.00054	0.001049	0.000564	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Demequinaceae;g__uncultured;s__uncultured bacterium
ZOTU5261	Frass	6.75E-05	0.000437	0.000887	0.000464	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Demequinaceae;g__uncultured;s__uncultured bacterium
ZOTU680	Frass	9.96E-05	0.000812	0.002199	0.001037	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermabacteraceae;g__Brachybacterium
ZOTU1129	Frass	0.000104	0.000412	0.001544	0.000687	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermabacteraceae;g__Brachybacterium;s__uncultured bacterium
ZOTU770	Frass	0.000275	0.001186	0.004348	0.001936	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermabacteraceae;g__Brachybacterium;s__uncultured bacterium
ZOTU818	Frass	0.000103	0.000681	0.001855	0.00088	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermabacteraceae;g__Brachybacterium;s__uncultured bacterium
ZOTU2365	Frass	0.000227	0.000791	0.001423	0.000814	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae

ZOTU2285	Frass	9.16E-05	0.000418	0.000816	0.000442	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Gulosibacter
ZOTU2970	Frass	5.57E-05	0.000398	0.000643	0.000365	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Gulosibacter
ZOTU3556	Frass	4.78E-05	0.000212	0.000497	0.000252	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Gulosibacter;s__uncultured bacterium
ZOTU2454	Frass	0.000183	0.001079	0.002934	0.001399	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Leucobacter
ZOTU3720	Frass	3.97E-05	0.000437	0.001264	0.00058	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Leucobacter
ZOTU10244	Frass	9.54E-05	0.000439	0.00099	0.000508	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Leucobacter;s__uncultured bacterium
ZOTU2467	Frass	9.96E-05	0.000778	0.001795	0.000891	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Leucobacter;s__uncultured bacterium
ZOTU2750	Frass	8.36E-05	0.000661	0.001431	0.000725	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Leucobacter;s__uncultured bacterium
ZOTU1223	Frass	5.18E-05	0.000432	0.002015	0.000833	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Enteractinococcus
ZOTU1266	Frass	0.000263	0.0008	0.004076	0.001713	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Enteractinococcus
ZOTU1514	Frass	4.77E-05	0.000396	0.001695	0.000713	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Enteractinococcus
ZOTU1908	Frass	3.98E-05	0.000236	0.001357	0.000544	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Enteractinococcus
ZOTU6425	Frass	1.59E-05	0.000168	0.000617	0.000267	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Enteractinococcus
ZOTU8974	Frass	2.78E-05	0.00016	0.000826	0.000338	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Enteractinococcus
ZOTU359	Frass	0.000104	0.001317	0.003307	0.001576	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Glutamicibacter
ZOTU394	Frass	0.00031	0.00228	0.007279	0.00329	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Glutamicibacter
ZOTU445	Frass	4.78E-05	0.001311	0.002968	0.001442	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Glutamicibacter
ZOTU738	Frass	8.34E-05	0.000774	0.002363	0.001073	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Glutamicibacter
ZOTU3086	Frass	0.000111	0.00041	0.001555	0.000692	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Glutamicibacter;s__uncultured bacterium
ZOTU6626	Frass	1.19E-05	0.000145	0.000556	0.000238	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Nesterenkonia
ZOTU6827	Frass	3.99E-05	0.000172	0.000757	0.000323	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Yaniella
ZOTU669	Frass	0.002455	0.003307	0.003763	0.003175	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__uncultured
ZOTU335	Frass	0.000219	5.15E-05	0.000531	0.000267	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Ulvibacter;s__uncultured bacterium
ZOTU492	Frass	0.000112	3.17E-05	0.000412	0.000185	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__uncultured;s__uncultured compost bacterium
ZOTU49627	Frass	4.78E-05	0.000748	0.0015	0.000766	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae
ZOTU2105	Frass	0.000159	0.000318	0.000798	0.000425	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Amphibacillus
ZOTU2790	Frass	9.95E-05	0.000283	0.000611	0.000331	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Amphibacillus
ZOTU3133	Frass	0.000195	0.000354	0.000741	0.00043	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Amphibacillus
ZOTU136	Frass	7.17E-05	0.001032	0.002084	0.001062	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus
ZOTU208	Frass	0.000286	0.002029	0.005361	0.002559	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus
ZOTU323	Frass	7.96E-05	0.000895	0.001895	0.000956	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus

ZOTU340	Frass	4.37E-05	0.000608	0.001863	0.000838	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus
ZOTU7200	Frass	7.97E-05	0.000305	0.00056	0.000315	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Oceanobacillus
ZOTU176	Frass	9.96E-05	0.001878	0.00289	0.001623	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Oceanobacillus;s__uncultured bacterium
ZOTU197	Frass	0.000406	0.005935	0.012014	0.006118	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Oceanobacillus;s__uncultured bacterium
ZOTU245	Frass	5.17E-05	0.002341	0.004286	0.002226	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Oceanobacillus;s__uncultured bacterium
ZOTU383	Frass	7.16E-05	0.001515	0.003517	0.001701	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Oceanobacillus;s__uncultured bacterium
ZOTU239	Frass	0.000111	0.002044	0.004171	0.002109	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__uncultured;s__uncultured bacterium
ZOTU310	Frass	0.000541	0.004836	0.009586	0.004988	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__uncultured;s__uncultured bacterium
ZOTU371	Frass	9.16E-05	0.001994	0.003485	0.001857	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__uncultured;s__uncultured bacterium
ZOTU542	Frass	9.14E-05	0.001124	0.002885	0.001367	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__uncultured;s__uncultured bacterium
ZOTU3571	Frass	3.17E-05	0.000281	0.000838	0.000384	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae
ZOTU793	Frass	0.000227	0.002003	0.006211	0.002814	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae
ZOTU824	Frass	0.000135	0.001531	0.003868	0.001845	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae
ZOTU1063	Frass	8.74E-05	0.001408	0.003565	0.001687	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planococcus;s__uncultured bacterium
ZOTU1200	Frass	0.000131	0.001115	0.002631	0.001292	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina
ZOTU1406	Frass	8.75E-05	0.000863	0.002991	0.001314	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina
ZOTU2639	Frass	8.77E-05	0.000448	0.00156	0.000698	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina
ZOTU2799	Frass	0.000127	0.001859	0.003218	0.001735	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina
ZOTU2542	Frass	1.99E-05	0.000778	0.001002	0.0006	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina;s__uncultured bacterium
ZOTU3392	Frass	3.57E-05	0.000691	0.001124	0.000617	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina;s__uncultured bacterium
ZOTU4292	Frass	2.39E-05	0.00041	0.000909	0.000448	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Sporosarcina;s__uncultured bacterium
ZOTU4395	Frass	3.98E-05	0.000352	0.000621	0.000338	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Aliicoccus;s__uncultured bacterium
ZOTU18	Frass	0.000474	0.003773	0.00979	0.004679	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus
ZOTU25	Frass	0.000318	0.00344	0.009545	0.004435	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus
ZOTU20	Frass	0.001584	0.008154	0.025124	0.01162	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus;s__Jeotgalicoccus halotolerans
ZOTU36	Frass	0.00033	0.002137	0.007771	0.003413	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus;s__Jeotgalicoccus halotolerans
ZOTU4543	Frass	0.000127	0.00072	0.001243	0.000697	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus;s__uncultured bacterium
ZOTU9167	Frass	1.59E-05	0.000115	0.000497	0.000209	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Salinicoccus
ZOTU4284	Frass	1.59E-05	0.000438	0.000732	0.000395	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerococcus;s__uncultured bacterium
ZOTU1224	Frass	7.96E-05	0.00093	0.002013	0.001008	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerosphaera;s__uncultured bacterium
ZOTU645	Frass	0.000454	0.004313	0.007111	0.003959	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerosphaera;s__uncultured bacterium

ZOTU6541	Frass	5.58E-05	0.000366	0.000635	0.000352	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerosphaera;s__uncultured bacterium
ZOTU672	Frass	0.000103	0.001706	0.00265	0.001486	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerosphaera;s__uncultured bacterium
ZOTU794	Frass	6.76E-05	0.001561	0.002484	0.001371	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerosphaera;s__uncultured bacterium
ZOTU122	Frass	9.54E-05	0.002032	0.004477	0.002201	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia;s__uncultured bacterium
ZOTU50	Frass	0.000219	0.003757	0.005198	0.003058	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia;s__uncultured bacterium
ZOTU61	Frass	0.000665	0.008011	0.014231	0.007636	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia;s__uncultured bacterium
ZOTU87	Frass	0.000119	0.003245	0.005112	0.002825	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia;s__uncultured bacterium
ZOTU3303	Frass	2.00E-05	0.000546	0.000848	0.000471	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__uncultured;s__uncultured bacterium
ZOTU4340	Frass	2.38E-05	0.000471	0.00066	0.000385	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__uncultured;s__uncultured bacterium
ZOTU396	Frass	0.000147	0.002601	0.003888	0.002212	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Alkalibacterium
ZOTU562	Frass	8.37E-05	0.002362	0.003641	0.002029	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Alkalibacterium
ZOTU875	Frass	9.55E-05	0.001382	0.003056	0.001511	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Alkalibacterium
ZOTU153	Frass	0.000306	0.003699	0.006759	0.003588	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU2118	Frass	3.18E-05	0.00054	0.001173	0.000582	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU223	Frass	0.000521	0.003014	0.008477	0.004004	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU2411	Frass	9.96E-05	0.001117	0.002681	0.001299	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU2634	Frass	0.000151	0.001703	0.002858	0.001571	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU274	Frass	0.000215	0.003396	0.006289	0.0033	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU2863	Frass	2.38E-05	0.000479	0.000909	0.000471	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU308	Frass	0.000207	0.002156	0.005158	0.002507	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU3080	Frass	2.00E-05	0.000349	0.00083	0.0004	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU582	Frass	0.00049	0.003949	0.006646	0.003695	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes;s__uncultured bacterium
ZOTU1842	Frass	2.79E-05	0.000303	0.000783	0.000371	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Desemzia
ZOTU1335	Frass	6.38E-05	0.000456	0.000807	0.000442	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Desemzia;s__uncultured bacterium
ZOTU1429	Frass	0.000171	0.000927	0.002113	0.00107	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Desemzia;s__uncultured bacterium
ZOTU2507	Frass	2.79E-05	0.000238	0.000582	0.000283	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Desemzia;s__uncultured bacterium
ZOTU1218	Frass	3.97E-05	0.000871	0.002007	0.000973	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca
ZOTU1268	Frass	2.79E-05	0.000896	0.001611	0.000845	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca
ZOTU1703	Frass	3.98E-05	0.000877	0.001291	0.000736	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca
ZOTU2009	Frass	3.57E-05	0.000497	0.001049	0.000527	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca
ZOTU752	Frass	0.000597	0.007291	0.012928	0.006939	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca

ZOTU990	Frass	5.18E-05	0.001116	0.00171	0.000959	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca
ZOTU1355	Frass	5.57E-05	0.000679	0.001359	0.000698	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca;s__uncultured bacterium
ZOTU667	Frass	8.35E-05	0.001387	0.002585	0.001352	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca;s__uncultured bacterium
ZOTU789	Frass	5.17E-05	0.001196	0.00182	0.001022	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca;s__uncultured bacterium
ZOTU912	Frass	5.57E-05	0.001293	0.002287	0.001212	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Jeotgalibaca;s__uncultured bacterium
ZOTU10553	Frass	2.39E-05	0.000236	0.000708	0.000323	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Lacticigenium;s__uncultured bacterium
ZOTU431	Frass	0.000398	0.005611	0.009568	0.005192	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Marinilactibacillus
ZOTU2638	Frass	3.58E-05	0.000612	0.00083	0.000492	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__uncultured;s__uncultured bacterium
ZOTU2698	Frass	0.000115	0.001279	0.002454	0.001283	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__uncultured;s__uncultured bacterium
ZOTU2956	Frass	3.18E-05	0.000523	0.000828	0.000461	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__uncultured;s__uncultured bacterium
ZOTU4091	Frass	3.59E-05	0.000329	0.000658	0.000341	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__uncultured;s__uncultured bacterium
ZOTU180	Frass	0.000832	0.002603	0.004351	0.002595	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus
ZOTU69	Frass	0.001114	0.004048	0.005563	0.003575	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus
ZOTU35	Frass	0.003843	0.010463	0.014112	0.009473	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus;s__Enterococcus faecium
ZOTU6595	Frass	3.58E-05	0.000224	0.00073	0.00033	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;s__Lactobacillus crispatus
ZOTU11507	Frass	0.000439	0.000471	0.000531	0.00048	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__Christensenellaceae R-7 group;s__uncultured bacterium
ZOTU12970	Frass	0.000279	0.000545	0.000548	0.000457	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__Christensenellaceae R-7 group;s__uncultured bacterium
ZOTU10392	Frass	0.000188	0.00036	0.000548	0.000365	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__[Eubacterium] coprostanoligenes group;s__uncultured Firmicutes bacterium
ZOTU13556	Frass	0.000327	0.000386	0.000545	0.000419	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__[Eubacterium] coprostanoligenes group;s__uncultured organism
ZOTU22	Frass	0.000211	0.000212	0.002263	0.000895	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Oceanisphaera
ZOTU23	Frass	0.000777	0.000392	0.006998	0.002722	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Oceanisphaera
ZOTU37	Frass	0.000143	0.000147	0.001784	0.000691	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Oceanisphaera
ZOTU90	Frass	9.95E-05	8.51E-05	0.001395	0.000527	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Oceanisphaera
ZOTU2531	Frass	0.000131	1.19E-05	0.000452	0.000198	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Idiomarinaceae;g__Aliidiomarina
ZOTU6874	Frass	0.000379	0.000523	0.00084	0.00058	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Comamonas
ZOTU730	Frass	7.96E-05	3.56E-05	0.00041	0.000175	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Paenalcaligenes
ZOTU971	Frass	0.000255	7.72E-05	0.001109	0.00048	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Paenalcaligenes
ZOTU1496	Frass	0.000294	0.00019	0.000593	0.000359	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Halomonas
ZOTU21	Frass	0.000641	0.000164	0.007883	0.002896	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter
ZOTU29	Frass	0.000163	5.35E-05	0.001978	0.000732	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter

ZOTU47	Frass	0.000131	3.56E-05	0.001933	0.0007	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter
ZOTU17	Frass	0.000251	5.15E-05	0.00274	0.001014	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter;s__uncultured bacterium
ZOTU1104	Frass	2.78E-05	7.92E-06	0.000306	0.000114	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas
ZOTU550	Frass	6.37E-05	1.19E-05	0.000399	0.000158	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas
ZOTU656	Frass	0.000219	5.93E-05	0.001509	0.000596	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas
ZOTU3083	Frass	0.000147	4.55E-05	0.000519	0.000237	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__uncultured
ZOTU4912	Frass	0.000323	0.000404	0.000653	0.00046	k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia;s__uncultured Verrucomicrobia bacterium

Table S2 Enriched bacterial ZOTUs for three treatments in the rhizosphere group based on Fig. 2. Bacterial ZOTUs marked in bold were shared between three treatments.

ZOTUs	**Enriched in**	**Relative abundance in**				**Taxonomy**
		Control	**Manure**	**Frass**	**Average**	
ZOTU10938	**Control**	**0.003039**	**5.91E-05**	**0.000225**	**0.110743**	**k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__uncultured;g__uncultured Acidobacteria bacterium;s__uncultured Acidobacteria bacterium**
ZOTU39382	Control	0.001045	0	4.98E-05	0.036479	k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__uncultured;g__uncultured Acidobacteria bacterium;s__uncultured Acidobacteria bacterium
ZOTU11685	**Control**	**0.002102**	**5.58E-05**	**0.00032**	**0.082605**	**k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__uncultured;g__uncultured bacterium;s__uncultured bacterium**
ZOTU15397	**Control**	**0.001239**	**3.31E-06**	**0.000153**	**0.046487**	**k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Acidobacteriales;f__uncultured;g__uncultured bacterium;s__uncultured bacterium**
ZOTU29125	**Control**	**0.000685**	**6.27E-05**	**5.59E-05**	**0.026779**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Sinomonas**
ZOTU15113	**Control**	**0.002455**	**9.86E-06**	**0.000254**	**0.090655**	**k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__uncultured;g__uncultured bacterium;s__uncultured bacterium**
ZOTU45662	**Control**	**0.00117**	**6.92E-05**	**0.000195**	**0.047808**	**k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Gaiellales;f__uncultured;g__uncultured bacterium;s__uncultured bacterium**
ZOTU36410	Control	0.000374	0	1.32E-05	0.012912	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU31271	Control	0.000405	0	0	0.013485	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__env.OPS 17
ZOTU23730	Control	0.000615	0	3.33E-06	0.020624	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__KD3-93;g__uncultured bacterium;s__uncultured bacterium
ZOTU15959	Control	0.000971	0	0	0.032354	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__NS11-12 marine group;g__metagenome;s__metagenome
ZOTU14390	**Control**	**0.002002**	**3.27E-06**	**3.98E-05**	**0.068166**	**k__Bacteria;p__Bacteroidetes;c__Ignavibacteria;o__Ignavibacteriales;f__BSV40**
ZOTU26810	Control	0.001075	0	0	0.035824	k__Bacteria;p__Bacteroidetes;c__Ignavibacteria;o__OPB56;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU15868	**Control**	**0.00113**	**2.63E-05**	**0.000145**	**0.043391**	**k__Bacteria;p__Chloroflexi;c__Ktedonobacteria;o__Ktedonobacterales;f__JG30-KF-AS9;g__uncultured bacterium;s__uncultured bacterium**
ZOTU20037	**Control**	**0.000881**	**3.28E-06**	**7.62E-05**	**0.032003**	**k__Bacteria;p__Chloroflexi;c__Ktedonobacteria;o__Ktedonobacterales;f__JG30-KF-AS9;g__uncultured bacterium;s__uncultured bacterium**
ZOTU34447	**Control**	**0.000824**	**2.31E-05**	**9.61E-05**	**0.031438**	**k__Bacteria;p__Chloroflexi;c__Ktedonobacteria;o__Ktedonobacterales;f__JG30-KF-AS9;g__uncultured bacterium;s__uncultured bacterium**
ZOTU39634	Control	0.000529	0	0	0.017629	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Alicyclobacillaceae;g__Tumebacillus;s__uncultured bacterium
ZOTU25522	**Control**	**0.001246**	**0.000112**	**9.89E-05**	**0.048562**	**k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 1;g__Clostridium sensu stricto 10**
ZOTU13168	Control	0.001714	0	0	0.057128	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XVIII;g__uncultured;s__uncultured bacterium
ZOTU13337	Control	0.002273	0	6.65E-06	0.075995	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XVIII;g__uncultured;s__uncultured bacterium
ZOTU6273	Control	0.005296	0	6.60E-06	0.176755	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XVIII;g__uncultured;s__uncultured bacterium
ZOTU7750	**Control**	**0.004186**	**1.32E-05**	**2.98E-05**	**0.140986**	**k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira**
ZOTU32236	Control	0.000486	0	3.32E-06	0.01632	k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira;s__uncultured bacterium
ZOTU19705	Control	0.001181	0	0	0.039362	k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium

ZOTU45737	**Control**	**0.000566**	**6.63E-06**	**2.32E-05**	**0.019873**	**k__Bacteria;p__Planctomycetes;c__BD7-11;o__uncultured bacterium;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium**
ZOTU40090	Control	0.000415	0	0	0.013826	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Azospirillales;f__Azospirillaceae;g__Nitrospirillum
ZOTU32354	Control	0.000766	0	3.29E-05	0.026617	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales;f__Elsteraceae;g__uncultured;s__uncultured alpha proteobacterium
ZOTU36185	Control	0.00079	0	2.63E-05	0.027197	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales;f__uncultured
ZOTU26704	**Control**	**0.000732**	**6.56E-06**	**7.59E-05**	**0.027147**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales;f__URHD0088**
ZOTU11258	**Control**	**0.003265**	**0.000221**	**0.000648**	**0.137799**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae**
ZOTU21493	Control	0.000524	0	1.32E-05	0.017896	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Methylocella
ZOTU43801	**Control**	**0.000716**	**1.98E-05**	**4.96E-05**	**0.026182**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Roseiarcus;s__uncultured bacterium**
ZOTU3723	**Control**	**0.006653**	**6.26E-05**	**0.001337**	**0.268424**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys;s__uncultured Pseudolabrys sp.**
ZOTU39868	Control	0.000313	0	0	0.010445	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Magnetospirillaceae;g__Telmatospirillum
ZOTU38471	Control	0.000769	0	0	0.025642	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Magnetospirillaceae;g__uncultured
ZOTU16734	**Control**	**0.002187**	**8.55E-05**	**0.000208**	**0.082694**	**k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Haliangiaceae;g__Haliangium;s__uncultured bacterium**
ZOTU36236	**Control**	**0.000674**	**6.61E-06**	**4.30E-05**	**0.024107**	**k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Polyangiaceae**
ZOTU38460	**Control**	**0.000449**	**9.91E-06**	**3.97E-05**	**0.016605**	**k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Polyangiaceae;g__Pajaroellobacter**
ZOTU20261	Control	0.000789	0	9.90E-06	0.026645	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Polyangiaceae;g__Pajaroellobacter;s__uncultured bacterium
ZOTU29549	Control	0.002105	0	6.57E-06	0.070372	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Oligoflexales;f__0319-6G20;g__uncultured bacterium;s__uncultured bacterium
ZOTU28677	**Control**	**0.000962**	**9.94E-06**	**5.27E-05**	**0.034141**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Burkholderia-Caballeronia-Paraburkholderia**
ZOTU13357	**Control**	**0.001644**	**1.65E-05**	**6.60E-06**	**0.055571**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Leptothrix**
ZOTU19176	**Control**	**0.001497**	**3.32E-06**	**6.89E-05**	**0.052301**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__uncultured**
ZOTU36550	Control	0.000567	0	3.27E-06	0.019024	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__KF-JG30-C25;f__uncultured gamma proteobacterium;g__uncultured gamma proteobacterium;s__uncultured gamma proteobacterium
ZOTU18420	Control	0.001143	0	0	0.038115	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Salinisphaerales;f__Solimonadaceae;g__Nevskia
ZOTU18127	Manure	0	0.000842	7.96E-05	0.030728	k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Solibacterales;f__Solibacteraceae (Subgroup 3);g__Bryobacter;s__uncultured bacterium
ZOTU41869	Manure	0	0.000405	9.96E-06	0.013836	k__Bacteria;p__Acidobacteria;c__Blastocatellia (Subgroup 4);o__Blastocatellales;f__Blastocatellaceae;g__Stenotrophobacter
ZOTU41053	Manure	0	0.000232	0	0.007747	k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__uncultured
ZOTU36088	**Manure**	**1.19E-05**	**0.000955**	**6.28E-05**	**0.034327**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;f__Nakamurellaceae;g__Nakamurella;s__uncultured bacterium**
ZOTU21649	Manure	0	0.00127	0.000103	0.045749	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Bogoriellaceae
ZOTU15297	**Manure**	**7.88E-06**	**0.002787**	**0.000372**	**0.105589**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Cellulomonadaceae;g__Actinotalea**
ZOTU19070	Manure	0	0.000882	1.65E-05	0.029964	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Cellulomonadaceae;g__Actinotalea
ZOTU11286	Manure	0	0.004457	9.58E-05	0.151759	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Microbacterium

ZOTU1436	**Manure**	**0.00046**	**0.018648**	**0.001915**	**0.700749**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Parafrigoribacterium**
ZOTU9639	Manure	3.94E-06	0.0027	0	0.090129	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Glutamicibacter
ZOTU42395	Manure	4.01E-06	0.000588	0	0.019748	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Sanguibacteraceae;g__Sanguibacter
ZOTU47953	Manure	0	0.000375	3.97E-05	0.01381	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;g__Aeromicrobium
ZOTU47610	Manure	0	0.000403	0	0.013441	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Dysgonomonadaceae;g__Fermentimonas;s__uncultured bacterium
ZOTU1235	Manure	0	0.017538	6.65E-06	0.584834	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Dysgonomonadaceae;g__Proteiniphilum
ZOTU30633	Manure	0	0.000789	0	0.026315	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Dysgonomonadaceae;g__Proteiniphilum
ZOTU6489	Manure	0	0.003121	0	0.104048	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Dysgonomonadaceae;g__Proteiniphilum
ZOTU2295	Manure	0	0.000452	0	0.015078	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Dysgonomonadaceae;g__Proteiniphilum;s__uncultured Ruminobacillus sp.
ZOTU2474	Manure	0	0.001297	0	0.043245	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Dysgonomonadaceae;g__Proteiniphilum;s__uncultured Ruminobacillus sp.
ZOTU3651	Manure	0	0.000229	0	0.007649	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Dysgonomonadaceae;g__Proteiniphilum;s__uncultured Ruminobacillus sp.
ZOTU6639	Manure	0	0.00313	0	0.104321	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prolixibacteraceae;g__WCHB1-32;s__uncultured bacterium
ZOTU17749	**Manure**	**4.01E-06**	**0.00285**	**6.62E-06**	**0.095343**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prolixibacteraceae;g__WCHB1-32;s__uncultured soil bacterium**
ZOTU28742	Manure	0	0.000593	7.93E-05	0.022426	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Flavihumibacter
ZOTU45446	Manure	0	0.000313	0	0.010422	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Niabella;s__uncultured bacterium
ZOTU4194	Manure	0	0.005889	4.63E-05	0.197835	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Taibaiella;s__uncultured bacterium
ZOTU18552	Manure	0	0.001371	0	0.0457	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured
ZOTU37453	Manure	0	0.00043	3.97E-05	0.015654	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured
ZOTU7855	**Manure**	**5.55E-05**	**0.003527**	**4.61E-05**	**0.12096**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured**
ZOTU10580	Manure	0	0.001829	0	0.060963	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU12139	Manure	0	0.001616	3.30E-06	0.053969	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU20122	Manure	0	0.000867	3.32E-06	0.029024	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU21133	Manure	0	0.00074	6.65E-06	0.024878	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU22108	Manure	0	0.001063	1.97E-05	0.036103	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU28324	Manure	0	0.000499	3.30E-06	0.016753	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU33593	**Manure**	**7.93E-06**	**0.00054**	**9.84E-06**	**0.018577**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium**
ZOTU10342	**Manure**	**2.78E-05**	**0.000427**	**3.30E-05**	**0.016271**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured soil bacterium**
ZOTU41043	Manure	0	0.000585	0	0.019484	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured soil bacterium
ZOTU4258	Manure	0	0.006418	2.29E-05	0.2147	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured soil bacterium
ZOTU45851	Manure	0	0.000478	3.30E-06	0.016037	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Cyclobacteriaceae;g__uncultured;s__uncultured Bacteroidetes bacterium
ZOTU27132	**Manure**	**8.02E-06**	**0.000795**	**0.000136**	**0.031305**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Cytophagaceae;g__Sporocytophaga;s__uncultured bacterium**

ZOTU7762	Manure	0	0.002985	3.30E-06	0.099618	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Hymenobacteraceae;g__Adhaeribacter;s__uncultured bacterium
ZOTU35136	Manure	0	0.000444	0	0.014807	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__Ohtaekwangia
ZOTU23765	Manure	0	0.000792	0	0.026392	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__Ohtaekwangia;s__uncultured Bacteroidetes bacterium
ZOTU19689	Manure	0	0.000895	0	0.029818	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured;s__uncultured bacterium
ZOTU25463	Manure	0	0.001065	0	0.035497	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured;s__uncultured bacterium
ZOTU40359	Manure	0	0.000454	0	0.01512	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured;s__uncultured bacterium
ZOTU4391	Manure	0	0.007533	0.000867	0.279999	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured;s__uncultured bacterium
ZOTU32214	Manure	0	0.000305	0	0.010162	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Arenibacter
ZOTU23038	Manure	0	0.000423	0	0.014116	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Confluentibacter;s__uncultured bacterium
ZOTU8820	Manure	0	0.002858	5.25E-05	0.097018	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium
ZOTU32126	Manure	0	0.000662	5.96E-05	0.024039	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__uncultured bacterium
ZOTU41567	Manure	0	0.000567	0	0.018903	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Chryseobacterium;s__uncultured bacterium
ZOTU22393	Manure	0	0.000713	0	0.023769	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__KD3-93
ZOTU24293	Manure	0	0.000712	0	0.023746	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__KD3-93;g__uncultured bacterium;s__uncultured bacterium
ZOTU8795	Manure	0	0.002284	0	0.076145	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__NS11-12 marine group;g__uncultured Bacteroidetes bacterium;s__uncultured Bacteroidetes bacterium
ZOTU13572	Manure	0	0.003213	4.96E-05	0.108755	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Arcticibacter
ZOTU34937	Manure	0	0.00049	0	0.016339	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Arcticibacter
ZOTU15727	Manure	0	0.00202	0.000179	0.073289	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Arcticibacter;s__uncultured bacterium
ZOTU20882	Manure	0	0.00141	0.000367	0.059238	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Parapedobacter;s__uncultured bacterium
ZOTU36970	Manure	0	0.000427	2.64E-05	0.015114	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Parapedobacter;s__uncultured bacterium
ZOTU16068	Manure	0	0.00193	8.96E-05	0.067305	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter
ZOTU19926	Manure	0	0.001306	0	0.043545	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter
ZOTU29980	Manure	0	0.000548	1.97E-05	0.018921	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter
ZOTU3248	Manure	0	0.009375	6.54E-06	0.312704	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter
ZOTU34756	Manure	0	0.000435	0	0.014489	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter
ZOTU5073	Manure	0	0.006884	0.000168	0.235045	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter
ZOTU19534	Manure	0	0.000949	3.30E-06	0.031748	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter;s__uncultured bacterium
ZOTU12435	Manure	0	0.001744	0	0.058131	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pelobium;s__uncultured bacterium
ZOTU31735	Manure	0	0.000328	0	0.010944	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pelobium;s__uncultured bacterium
ZOTU17191	Manure	0	0.000674	6.27E-05	0.024567	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium

ZOTU7294	**Manure**	**3.95E-06**	**0.003118**	**0.000257**	**0.112649**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium**
ZOTU15122	Manure	0	0.000946	3.32E-06	0.031634	k__Bacteria;p__Bacteroidetes;c__Ignavibacteria;o__OPB56;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU20655	Manure	0	0.000932	3.30E-06	0.03119	k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__SBR1031;f__A4b;g__OLB13;s__uncultured bacterium
ZOTU18143	Manure	0	0.000899	0	0.029952	k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Chloroflexales;f__Roseiflexaceae;g__uncultured;s__uncultured bacterium
ZOTU19377	Manure	0	0.000666	3.30E-06	0.022302	k__Bacteria;p__Fibrobacteres;c__Fibrobacteria;o__Fibrobacterales;f__Fibrobacteraceae;g__uncultured;s__uncultured bacterium
ZOTU31478	Manure	0	0.000645	7.24E-05	0.023925	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus
ZOTU10897	**Manure**	**0.000182**	**0.002282**	**0.000436**	**0.096657**	**k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus;s__Bacillus sp.**
ZOTU25719	**Manure**	**1.98E-05**	**0.000746**	**9.55E-05**	**0.028698**	**k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae;g__Paenibacillus**
ZOTU46934	**Manure**	**7.92E-06**	**0.000832**	**9.93E-06**	**0.028322**	**k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Lysinibacillus**
ZOTU48185	**Manure**	**3.17E-05**	**0.000734**	**0.000155**	**0.030707**	**k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Lysinibacillus**
ZOTU17516	**Manure**	**1.59E-05**	**0.001655**	**3.30E-05**	**0.056801**	**k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Solibacillus**
ZOTU10302	**Manure**	**9.13E-05**	**0.002454**	**4.62E-05**	**0.086371**	**k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Acetivibrio;s__uncultured bacterium**
ZOTU25312	Manure	0	0.00095	1.33E-05	0.032102	k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas
ZOTU7489	**Manure**	**2.37E-05**	**0.002688**	**0.00032**	**0.101065**	**k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas**
ZOTU25892	Manure	0	0.000971	0	0.03235	k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas;s__uncultured bacterium
ZOTU46305	Manure	0	0.000688	0	0.022923	k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas;s__uncultured bacterium
ZOTU22828	Manure	0	0.000831	3.30E-06	0.027798	k__Bacteria;p__Gemmatimonadetes;c__Longimicrobia;o__Longimicrobiales;f__Longimicrobiaceae;g__uncultured bacterium;s__uncultured bacterium
ZOTU27214	Manure	0	0.000859	1.98E-05	0.029279	k__Bacteria;p__Gemmatimonadetes;c__Longimicrobia;o__Longimicrobiales;f__Longimicrobiaceae;g__uncultured bacterium;s__uncultured bacterium
ZOTU44475	Manure	0	0.000457	2.31E-05	0.016014	k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Planctomycetales;f__Rubinisphaeraceae;g__Planctomicrobium;s__uncultured bacterium
ZOTU42795	Manure	0	0.000316	0	0.010523	k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Planctomycetales;f__Rubinisphaeraceae;g__SH-PL14;s__uncultured bacterium
ZOTU21995	Manure	0	0.000789	0	0.026305	k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Planctomycetales;f__uncultured;g__uncultured bacterium;s__uncultured bacterium
ZOTU18374	Manure	0	0.000814	9.95E-06	0.027458	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas
ZOTU32819	Manure	0	0.000418	3.30E-06	0.014039	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas
ZOTU39878	Manure	0	0.000532	7.61E-05	0.02028	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas
ZOTU5838	Manure	0	0.005775	0.000441	0.207207	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas
ZOTU4907	Manure	0	0.005354	1.99E-05	0.179115	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas;s__Brevundimonas diminuta
ZOTU19469	Manure	0	0.001484	1.32E-05	0.049915	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas;s__Brevundimonas olei
ZOTU4568	Manure	0	0.0057	5.62E-05	0.191885	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas;s__Brevundimonas olei
ZOTU6275	**Manure**	**5.94E-05**	**0.002933**	**0.000618**	**0.120332**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Phenylobacterium**
ZOTU8685	Manure	0	0.001997	6.65E-06	0.066782	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Phenylobacterium;s__uncultured bacterium
ZOTU13673	**Manure**	**7.91E-06**	**0.001226**	**5.95E-05**	**0.043121**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Micropepsales;f__Micropepsaceae;g__uncultured;s__metagenome**

ZOTU29516	Manure	0	0.000348	1.66E-05	0.012151	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Bosea;s__uncultured bacterium
ZOTU18231	Manure	0	0.000891	5.27E-05	0.031449	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__uncultured;s__uncultured bacterium
ZOTU15499	**Manure**	**8.02E-06**	**0.00165**	**0.000294**	**0.065084**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Devosiaceae**
ZOTU16134	**Manure**	**2.79E-05**	**0.002518**	**0.000182**	**0.090936**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Devosiaceae;g__Devosia**
ZOTU28075	Manure	0	0.000937	8.93E-05	0.034222	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
ZOTU13362	Manure	0	0.002406	1.65E-05	0.080744	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Aminobacter
ZOTU7594	**Manure**	**1.20E-05**	**0.003944**	**0.000257**	**0.140451**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Aminobacter**
ZOTU13141	**Manure**	**3.97E-06**	**0.001762**	**7.62E-05**	**0.061405**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Mesorhizobium**
ZOTU23772	Manure	0	0.000847	2.31E-05	0.02901	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiales Incertae Sedis;g__uncultured;s__uncultured bacterium
ZOTU40947	Manure	0	0.000571	0	0.019042	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Afipia
ZOTU44964	**Manure**	**7.90E-06**	**0.000348**	**4.31E-05**	**0.013293**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Rhodoplanes;s__uncultured bacterium**
ZOTU8141	Manure	0	0.002458	3.00E-05	0.082937	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter;s__uncultured bacterium
ZOTU11693	Manure	0	0.001796	0.000179	0.065837	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__uncultured bacterium
ZOTU28602	Manure	0	0.000792	4.30E-05	0.027833	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__uncultured bacterium
ZOTU31046	**Manure**	**0.000107**	**0.002075**	**0.000359**	**0.084723**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium;s__uncultured bacter**
ZOTU32972	Manure	0	0.000662	9.93E-05	0.025369	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium;s__uncultured bacterium
ZOTU44682	**Manure**	**7.90E-06**	**0.000667**	**7.61E-05**	**0.025045**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium;s__uncultured bacter**
ZOTU27474	Manure	0	0.000681	0.000103	0.026134	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium;s__uncultured bacterium
ZOTU32637	Manure	0	0.000668	3.30E-06	0.02237	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium;s__uncultured bacterium
ZOTU23778	Manure	0	0.000668	0	0.022254	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Desulfuromonadaceae;g__Desulfuromonas;s__uncultured microorganism
ZOTU45245	**Manure**	**7.90E-06**	**0.000345**	**3.32E-06**	**0.011878**	**k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Nannocystaceae;g__Nannocystis**
ZOTU26835	**Manure**	**7.95E-06**	**0.000488**	**6.64E-06**	**0.01675**	**k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__P3OB-42;g__uncultured bacterium;s__uncultured bacterium**
ZOTU18392	Manure	0	0.000952	2.98E-05	0.032736	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Vulgatibacteraceae;g__Vulgatibacter
ZOTU40450	Manure	0	0.000849	0.000113	0.032073	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Vulgatibacteraceae;g__Vulgatibacter
ZOTU28570	**Manure**	**1.58E-05**	**0.000421**	**1.99E-05**	**0.015212**	**k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Oligoflexales;f__Oligoflexaceae;g__uncultured;s__uncultured bacterium**
ZOTU13611	Manure	0	0.001376	0	0.045879	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__B1-7BS;g__uncultured bacterium;s__uncultured bacterium
ZOTU11340	Manure	0	0.001696	2.97E-05	0.057524	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae
ZOTU32093	**Manure**	**3.18E-05**	**0.000552**	**3.96E-05**	**0.02077**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae**
ZOTU8097	**Manure**	**3.94E-06**	**0.005144**	**3.31E-05**	**0.17271**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Acidovorax;s__uncultured bacterium**
ZOTU16999	Manure	0	0.000951	0	0.031698	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Candidimonas
ZOTU9531	Manure	0	0.000928	8.24E-05	0.033669	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Candidimonas;s__Candidimonas sp.

ZOTU19334	Manure	0	0.003003	6.60E-06	0.100306	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Castellaniella
ZOTU46323	Manure	0	0.001166	0	0.038878	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Castellaniella
ZOTU47309	Manure	0	0.000785	0	0.026177	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Castellaniella
ZOTU5948	Manure	0	0.005676	0	0.18919	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Castellaniella
ZOTU7280	Manure	0	0.005286	3.96E-05	0.177505	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Castellaniella
ZOTU2049	Manure	0	0.022422	3.30E-06	0.747521	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Castellaniella;s__uncultured bacterium
ZOTU5633	Manure	1.20E-05	0.005033	0	0.168162	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Comamonas;s__Comamonas testosteroni
ZOTU32479	**Manure**	**0.000139**	**0.001069**	**5.92E-05**	**0.042223**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Comamonas;s__uncultured bacterium**
ZOTU12818	**Manure**	**2.77E-05**	**0.001689**	**6.28E-05**	**0.059307**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Herbaspirillum**
ZOTU38169	**Manure**	**0.000107**	**0.00114**	**0.000112**	**0.045309**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Herbaspirillum**
ZOTU20337	**Manure**	**1.20E-05**	**0.001031**	**3.30E-05**	**0.035878**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Hydrogenophaga**
ZOTU5977	**Manure**	**0.000199**	**0.006169**	**0.000374**	**0.224718**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Noviherbaspirillum;s__uncultured bacterium**
ZOTU12298	Manure	0	0.001881	3.33E-06	0.062822	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Parapusillimonas
ZOTU27890	Manure	0	0.000795	6.57E-05	0.028694	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Parapusillimonas
ZOTU38638	Manure	0	0.001289	9.90E-06	0.043293	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Parapusillimonas
ZOTU7473	Manure	0	0.000494	1.99E-05	0.017142	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Pusillimonas
ZOTU33520	Manure	0	0.000701	9.89E-05	0.026664	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Pusillimonas;s__uncultured compost bacterium
ZOTU6311	**Manure**	**0.000103**	**0.0035**	**0.000215**	**0.127279**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Methylophilaceae;g__Methylobacillus**
ZOTU16361	Manure	0	0.000844	0	0.028145	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Rhodocyclaceae;g__Azoarcus;s__uncultured bacterium
ZOTU38236	Manure	0	0.000287	1.64E-05	0.010117	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cellvibrionales;f__Cellvibrionaceae;g__Cellvibrio
ZOTU10353	**Manure**	**7.96E-05**	**0.001649**	**9.90E-05**	**0.060933**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter**
ZOTU28899	Manure	0	0.000528	4.30E-05	0.019035	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Pseudohongiellaceae;g__Pseudohongiella;s__uncultured bacterium
ZOTU20457	Manure	0	0.001308	0	0.043584	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas
ZOTU3537	Manure	0	0.008	2.31E-05	0.267443	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas
ZOTU40256	Manure	0	0.000365	0	0.012167	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas
ZOTU7012	Manure	0	0.00462	0.00033	0.165009	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas
ZOTU17672	Manure	0	0.001592	0	0.053063	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas flexibilis
ZOTU24237	Manure	0	0.001084	6.94E-05	0.038446	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas;s__Pseudomonas stutzeri
ZOTU16051	Manure	0	0.000756	0	0.025189	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__uncultured;s__uncultured bacterium
ZOTU14522	Manure	7.88E-06	0.001203	0	0.040349	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacterales;f__Steroidobacteraceae;g__uncultured;s__uncultured soil bacterium

ZOTU39594	**Manure**	**3.97E-06**	**0.000851**	**6.91E-05**	**0.030807**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Dyella**
ZOTU46483	**Manure**	**7.93E-06**	**0.000414**	**1.65E-05**	**0.014611**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Dyella**
ZOTU1869	**Manure**	**7.14E-05**	**0.02758**	**0.000187**	**0.927938**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Rhodanobacter**
ZOTU578	**Manure**	**3.97E-06**	**0.032943**	**0.000773**	**1.123986**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Rhodanobacter**
ZOTU7433	Manure	0	0.002987	0	0.099559	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Rhodanobacter
ZOTU450	**Manure**	**1.99E-05**	**0.048921**	**0.001541**	**1.682747**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Rhodanobacter;s__uncultured bacteri**
ZOTU27895	Manure	0	0.000481	3.32E-06	0.016156	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Arenimonas;s__uncultured bacterium
ZOTU9017	**Manure**	**3.95E-06**	**0.002839**	**0.000287**	**0.104334**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas**
ZOTU38174	Manure	0	0.000503	0	0.016753	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas;s__uncultured bacterium
ZOTU40224	Manure	0	0.000887	0	0.029578	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter
ZOTU33710	Manure	0	0.000463	3.27E-06	0.015541	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter;s__Lysobacter capsici
ZOTU9466	Manure	0	0.003588	9.96E-06	0.119941	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter;s__uncultured bacterium
ZOTU14232	**Manure**	**3.94E-06**	**0.001731**	**0.000298**	**0.067778**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas**
ZOTU33001	Manure	0	0.000493	3.30E-06	0.016556	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas
ZOTU906	**Manure**	**4.01E-06**	**0.027673**	**0.000258**	**0.931185**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Thermomonas**
ZOTU25049	Manure	0	0.00072	3.32E-06	0.024103	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Thermomonas;s__uncultured bacterium
ZOTU25606	**Manure**	**1.58E-05**	**0.000672**	**1.66E-05**	**0.023496**	**k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Opitutales;f__Opitutaceae;g__Opitutus;s__uncultured Verrucomicrobia bacterium**
ZOTU46431	Manure	0	0.000381	0	0.012694	k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Opitutales;f__Opitutaceae;g__uncultured
ZOTU48343	Frass	0	0	0.000292	0.00974	k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Solibacterales;f__Solibacteraceae (Subgroup 3);g__Paludibaculum;s__uncultured bacterium
ZOTU32611	Frass	0	5.92E-05	0.00056	0.020649	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Dietziaceae;g__Dietzia
ZOTU32329	**Frass**	**1.20E-05**	**4.27E-05**	**0.000476**	**0.017698**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Nocardiaceae;g__Rhodococcus**
ZOTU33562	**Frass**	**3.94E-06**	**3.27E-06**	**0.00074**	**0.024894**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Cellulomonadaceae;g__Pseudactinotalea**
ZOTU42519	Frass	0	6.63E-06	0.000408	0.013807	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Cellulomonadaceae;g__Pseudactinotalea
ZOTU12022	Frass	0	0	0.001311	0.043712	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Agromyces
ZOTU13783	**Frass**	**4.01E-06**	**5.29E-05**	**0.001905**	**0.065385**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Agromyces**
ZOTU4287	Frass	1.60E-05	0	0.00645	0.215531	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Agromyces
ZOTU2567	**Frass**	**2.37E-05**	**3.31E-06**	**0.02062**	**0.688244**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae**
ZOTU347	Frass	0	0	0.002735	0.091179	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae
ZOTU2768	**Frass**	**8.02E-06**	**0.000148**	**0.00116**	**0.043858**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae;g__Cellulosimicrobium**
ZOTU5269	**Frass**	**4.78E-05**	**0.000566**	**0.009005**	**0.320617**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Promicromonosporaceae;g__Cellulosimicrobium**
ZOTU25956	**Frass**	**0.000119**	**7.26E-05**	**0.000766**	**0.031928**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micromonosporales;f__Micromonosporaceae;g__Micromonospora**

ZOTU20723	**Frass**	**1.18E-05**	**6.62E-05**	**0.000753**	**0.027701**	**k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Pseudonocardiales;f__Pseudonocardiaceae;g__Pseudonocardia**
ZOTU11142	Frass	7.88E-06	0	0.001668	0.055875	k__Bacteria;p__Armatimonadetes;c__Fimbriimonadia;o__Fimbriimonadales;f__Fimbriimonadaceae
ZOTU28184	**Frass**	**1.97E-05**	**5.93E-05**	**0.000913**	**0.033083**	**k__Bacteria;p__Armatimonadetes;c__Fimbriimonadia;o__Fimbriimonadales;f__Fimbriimonadaceae**
ZOTU6238	**Frass**	**8.74E-05**	**6.57E-06**	**0.004426**	**0.150661**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Chitinophaga**
ZOTU7704	**Frass**	**4.01E-06**	**7.57E-05**	**0.002459**	**0.084615**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Chitinophaga;s__Chitinophaga soli**
ZOTU16377	**Frass**	**9.58E-05**	**0.000113**	**0.000984**	**0.039743**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Flavitalea;s__uncultured bacterium**
ZOTU27487	**Frass**	**0.00012**	**0.000125**	**0.001068**	**0.043768**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Flavitalea;s__uncultured bacterium**
ZOTU16789	**Frass**	**7.90E-06**	**1.32E-05**	**0.000969**	**0.033019**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Pseudoflavitalea**
ZOTU38939	Frass	0	0	0.00023	0.007657	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__uncultured;s__uncultured bacterium
ZOTU10963	Frass	0	3.31E-06	0.001759	0.058737	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured
ZOTU17057	Frass	0	0	0.001207	0.040243	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured
ZOTU20594	Frass	0	6.59E-06	0.000794	0.026691	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured
ZOTU31855	Frass	0	0	0.000337	0.011233	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Microscillaceae;g__uncultured
ZOTU14788	Frass	3.97E-05	0	0.002165	0.073487	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Spirosomaceae;g__Dyadobacter
ZOTU16866	Frass	0	4.32E-05	0.001529	0.052391	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Spirosomaceae;g__Emticicia
ZOTU20035	**Frass**	**4.01E-06**	**3.28E-06**	**0.000599**	**0.020223**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Crocinitomicaceae;g__Fluviicola;s__uncultured bacterium**
ZOTU6633	**Frass**	**2.38E-05**	**0.000161**	**0.004496**	**0.156034**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium**
ZOTU6419	Frass	4.76E-05	0	0.007476	0.250798	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__uncultured bacterium
ZOTU41379	**Frass**	**1.19E-05**	**2.62E-05**	**0.000359**	**0.013234**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Chryseobacterium**
ZOTU27222	**Frass**	**3.94E-06**	**9.60E-05**	**0.000941**	**0.034714**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Nubsella**
ZOTU30695	**Frass**	**4.01E-06**	**6.60E-06**	**0.000548**	**0.018605**	**k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Pedobacter**
ZOTU27802	**Frass**	**2.79E-05**	**2.96E-05**	**0.000369**	**0.014232**	**k__Bacteria;p__FBP;c__uncultured bacterium;o__uncultured bacterium;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacteri**
ZOTU39453	**Frass**	**1.18E-05**	**1.64E-05**	**0.000404**	**0.014403**	**k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Alicyclobacillaceae;g__Tumebacillus;s__uncultured bacterium**
ZOTU26722	Frass	0	0	0.000683	0.022772	k__Bacteria;p__Gemmatimonadetes;c__Longimicrobia;o__Longimicrobiales;f__Longimicrobiaceae;g__uncultured bacterium;s__uncultured bacterium
ZOTU23029	Frass	0	0	0.000562	0.018729	k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU38640	**Frass**	**2.37E-05**	**6.56E-06**	**0.000929**	**0.031973**	**k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Pirellulales;f__Pirellulaceae;g__uncultured;s__uncultured Planctomycetaceae bacterium**
ZOTU10933	Frass	0	6.65E-06	0.001675	0.056049	k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Planctomycetales;f__Rubinisphaeraceae;g__SH-PL14
ZOTU34790	Frass	7.95E-06	0	0.000378	0.012869	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Acetobacterales;f__Acetobacteraceae;g__Roseomonas
ZOTU4163	**Frass**	**0.000103**	**7.96E-05**	**0.005139**	**0.177407**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Caulobacter**
ZOTU8925	**Frass**	**4.77E-05**	**6.90E-05**	**0.002493**	**0.086977**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Caulobacter**
ZOTU9257	**Frass**	**3.95E-05**	**9.28E-05**	**0.001975**	**0.070252**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Phenylobacterium;s__uncultured bacterium**

ZOTU11729	**Frass**	**2.39E-05**	**0.000512**	**0.002762**	**0.109929**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Bosea**
ZOTU8249	**Frass**	**0.000104**	**0.000191**	**0.002146**	**0.081376**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Kaistiaceae;g__Kaistia**
ZOTU27317	**Frass**	**3.94E-06**	**3.32E-06**	**0.000873**	**0.029355**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium;s__uncultured bacterium**
ZOTU7290	**Frass**	**1.20E-05**	**6.26E-05**	**0.003429**	**0.116798**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Ochrobactrum**
ZOTU7737	**Frass**	**4.01E-06**	**3.29E-06**	**0.000839**	**0.028219**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Ochrobactrum;s__Ochrobactrum intermedium**
ZOTU20986	Frass	3.95E-06	0	0.000867	0.029032	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Amaricoccus
ZOTU11888	Frass	0	9.96E-06	0.00207	0.069327	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__metagenome
ZOTU28586	Frass	0	1.98E-05	0.000616	0.021178	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__metagenome
ZOTU10437	**Frass**	**3.95E-06**	**6.28E-05**	**0.001653**	**0.057339**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__uncultured bacte**
ZOTU12096	Frass	0	2.63E-05	0.001202	0.040932	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__uncultured bacterium
ZOTU37576	Frass	0	9.87E-06	0.000365	0.012486	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__uncultured bacterium
ZOTU4482	**Frass**	**0.000226**	**0.000993**	**0.011284**	**0.416766**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Altererythrobacter;s__uncultured bacte**
ZOTU14100	**Frass**	**3.16E-05**	**9.88E-05**	**0.001858**	**0.06627**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium**
ZOTU21050	**Frass**	**5.53E-05**	**2.99E-05**	**0.00085**	**0.031184**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium**
ZOTU38430	Frass	0	9.87E-06	0.000238	0.008247	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium
ZOTU26350	**Frass**	**0.000175**	**0.000189**	**0.001729**	**0.069758**	**k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas;s__uncultured marine bacterium**
ZOTU25752	Frass	0	0	0.00067	0.022317	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__BIrii41;g__uncultured bacterium;s__uncultured bacterium
ZOTU26619	Frass	0	0	0.000498	0.016595	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__BIrii41;g__uncultured bacterium;s__uncultured bacterium
ZOTU44157	Frass	0	0	0.000541	0.018017	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__BIrii41;g__uncultured bacterium;s__uncultured bacterium
ZOTU29419	**Frass**	**3.94E-06**	**5.28E-05**	**0.000464**	**0.017366**	**k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__uncultured;g__uncultured bacterium;s__uncultured bacterium**
ZOTU2954	**Frass**	**7.52E-05**	**0.000149**	**0.008177**	**0.280021**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Massilia;s__uncultured bacterium**
ZOTU12618	Frass	0	9.87E-06	0.001206	0.040529	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Methylophilaceae;g__Methylobacillus
ZOTU14716	Frass	3.97E-06	0	0.002438	0.08141	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__metagenome;g__metagenome;s__metagenome
ZOTU10982	Frass	0	0	0.003028	0.100945	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU12087	**Frass**	**3.97E-06**	**3.31E-05**	**0.002256**	**0.076427**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium**
ZOTU15802	Frass	0	0	0.00117	0.038997	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU16140	Frass	0	0	0.001426	0.047531	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU17975	Frass	0	3.28E-06	0.001391	0.046476	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU26176	Frass	0	0	0.000807	0.026891	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium

ZOTU28582	Frass	0	3.29E-06	0.000448	0.015046	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU34288	Frass	0	0	0.000388	0.012938	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU9310	Frass	0	6.65E-06	0.002845	0.095055	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__R7C24;f__uncultured bacterium;g__uncultured bacterium;s__uncultured bacterium
ZOTU324	**Frass**	**7.95E-06**	**6.62E-05**	**0.005691**	**0.192175**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas**
ZOTU989	**Frass**	**1.59E-05**	**0.000317**	**0.028188**	**0.950694**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas;s__uncultured bacterium**
ZOTU16873	**Frass**	**4.73E-05**	**5.27E-05**	**0.001256**	**0.045212**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter**
ZOTU269	**Frass**	**0.000261**	**0.000221**	**0.062093**	**2.085831**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Pseudoxanthomonas**
ZOTU352	**Frass**	**3.94E-06**	**3.63E-05**	**0.000632**	**0.0224**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Pseudoxanthomonas**
ZOTU987	**Frass**	**0.00015**	**3.27E-06**	**0.022176**	**0.744321**	**k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Pseudoxanthomonas**

Table S3 Node roles in the networks of gut group based on Fig. 4.

Node	Shared in	Role	Phylum	Class	Order	Family	Genus
Genus320	Control/Manue/Frass	Network hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Desemzia
Genus38	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium 1
Genus65	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Demequinaceae	uncultured
Genus67	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Dermabacteraceae	Brachybacterium
Genus80	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Gulosibacter
Genus83	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Leucobacter
Genus92	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Enteractinococcus
Genus93	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Glutamicibacter
Genus94	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Kocuria
Genus98	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Yaniella
Genus265	Control/Manue/Frass	Module hub	Deferribacteres	Deferribacteres	Deferribacterales	Deferribacteraceae	Mucispirillum
Genus279	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	Amphibacillus
Genus282	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	Oceanobacillus
Genus285	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	uncultured
Genus287	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	Virgibacillus
Genus296	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Lysinibacillus
Genus304	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Other
Genus298	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Planococcus
Genus302	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Sporosarcina
Genus306	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Aliicoccus
Genus307	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Jeotgalicoccus
Genus308	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Salinicoccus
Genus309	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus
Genus314	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Aerosphaera
Genus315	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Facklamia
Genus317	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Alkalibacterium
Genus318	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Atopostipes
Genus321	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Jeotgalibaca

Genus323	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Marinilactibacillus
Genus324	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	uncultured
Genus328	Control/Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus
Genus331	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	uncultured
Genus344	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Family XIII	Anaerovorax
Genus347	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Family XIII	Other
Genus359	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia
Genus360	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Eisenbergiella
Genus362	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Hungatella
Genus369	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae NK4A136 group
Genus371	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnospiraceae UCG-001
Genus384	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Other
Genus380	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Tyzzerella 3
Genus382	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	uncultured
Genus386	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	uncultured
Genus394	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Candidatus Soleaferrea
Genus403	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminiclostridium 6
Genus408	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-009
Genus409	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-010
Genus410	Control/Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-013
Genus429	Control/Manue/Frass	Module hub	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	uncultured
Genus471	Control/Manue/Frass	Module hub	Planctomycetes	vadinHA49	uncultured bacterium	uncultured bacterium	uncultured bacterium
Genus594	Control/Manue/Frass	Module hub	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	Desulfovibrio
Genus595	Control/Manue/Frass	Module hub	Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	uncultured
Genus629	Control/Manue/Frass	Module hub	Proteobacteria	Deltaproteobacteria	Rs-K70 termite group	Other	Other
Genus632	Control/Manue/Frass	Module hub	Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	Oceanisphaera
Genus663	Control/Manue/Frass	Module hub	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Paenalcaligenes
Genus708	Control/Manue/Frass	Module hub	Proteobacteria	Gammaproteobacteria	Coxiellales	Coxiellaceae	Coxiella
Genus64	Control/Manue	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Demequinaceae	Lysinimicrobium
Genus159	Control/Manue	Module hub	Bacteroidetes	Bacteroidia	Bacteroidales	PeH15	uncultured Bacteroidetes bacterium
Genus343	Control/Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Family XIII	[Eubacterium] nodatum group

Genus375	Control/Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Natranaerovirga
Genus473	Control/Manue	Module hub	Planctomycetes	vadinHA49	Other	Other	Other
Genus575	Control/Manue	Module hub	Proteobacteria	Alphaproteobacteria	Rickettsiales	uncultured	uncultured alpha proteobacterium
Genus591	Control/Manue	Module hub	Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	uncultured
Genus761	Control/Manue	Module hub	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	Sediminispirochaeta
Genus759	Control/Frass	Module hub	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	uncultured
Genus34	Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Flaviflexus
Genus53	Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Bogoriellaceae	Bogoriella
Genus95	Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Nesterenkonia
Genus280	Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
Genus288	Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	Other
Genus283	Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	Paraliobacillus
Genus284	Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	Pseudogracilibacillus
Genus294	Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Bhargavaea
Genus295	Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Kurthia
Genus300	Manue/Frass	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Rummeliibacillus
Genus313	Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	Aerococcus
Genus319	Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Carnobacterium
Genus322	Manue/Frass	Module hub	Firmicutes	Bacilli	Lactobacillales	Carnobacteriaceae	Lacticigenium
Genus365	Manue/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Lachnoclostridium 10
Genus427	Manue/Frass	Module hub	Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	Dendrosporobacter
Genus39	Manue	Module hub	Actinobacteria	Actinobacteria	Corynebacteriales	Dietziaceae	Dietzia
Genus57	Manue	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Brevibacteriaceae	Brevibacterium
Genus90	Manue	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Other
Genus109	Manue	Module hub	Actinobacteria	Actinobacteria	Micrococcales	Other	Other
Genus301	Manue	Module hub	Firmicutes	Bacilli	Bacillales	Planococcaceae	Solibacillus
Genus316	Manue	Module hub	Firmicutes	Bacilli	Lactobacillales	Aerococcaceae	uncultured
Genus346	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Family XIII	uncultured
Genus354	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	[Eubacterium] xylanophilum group
Genus361	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Herbinix
Genus379	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Tyzzerella

Genus383	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	XBB1006
Genus388	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	Romboutsia
Genus416	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Other
Genus404	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminiclostridium 9
Genus405	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae NK4A214 group
Genus407	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcaceae UCG-005
Genus415	Manue	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	uncultured
Genus423	Manue	Module hub	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Turicibacter
Genus472	Manue	Module hub	Planctomycetes	vadinHA49	uncultured planctomycete	uncultured planctomycete	uncultured planctomycete
Genus593	Manue	Module hub	Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	Other
Genus628	Manue	Module hub	Proteobacteria	Deltaproteobacteria	Rs-K70 termite group	uncultured proteobacterium	uncultured proteobacterium
Genus645	Manue	Module hub	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Comamonas
Genus724	Manue	Module hub	Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	Halomonas
Genus733	Manue	Module hub	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Psychrobacter
Genus148	Control/Manue/Frass	Connector	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides

Table S4 Node roles in the networks of rhizosphere group based on Fig. 4.

Node	Shared in	Role	Phylum	Class	Order	Family	Genus
Genus40	Control/Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Corynebacteriales	Mycobacteriaceae	Mycobacterium
Genus521	Control/Manue/Frass	Module hub	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium
Genus416	Control/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Other
Genus401	Control/Frass	Module hub	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminiclostridium 1
Genus127	Manue/Frass	Module hub	Actinobacteria	Actinobacteria	Streptosporangiales	Streptosporangiaceae	Microbispora
Genus8	Control	Module hub	Acidobacteria	Acidobacteriia	Acidobacteriales	Acidobacteriaceae (Subgroup 1)	uncultured
Genus10	Control	Module hub	Acidobacteria	Acidobacteriia	Acidobacteriales	Koribacteraceae	Candidatus Koribacter
Genus16	Control	Module hub	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	Candidatus Solibacter
Genus139	Control	Module hub	Actinobacteria	Thermoleophilia	Gaiellales	uncultured	uncultured bacterium
Genus446	Control	Module hub	Planctomycetes	BD7-11	uncultured bacterium	uncultured bacterium	uncultured bacterium
Genus456	Control	Module hub	Planctomycetes	Planctomycetacia	Isosphaerales	Isosphaeraceae	Aquisphaera
Genus648	Control	Module hub	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Diaphorobacter
Genus709	Control	Module hub	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	Aquicella
Genus32	Frass	Module hub	Actinobacteria	Acidimicrobiia	uncultured	uncultured bacterium	uncultured bacterium
Genus215	Frass	Module hub	Bacteroidetes	Bacteroidia	Sphingobacteriales	env.OPS 17	uncultured Bacteroidetes bacterium
Genus500	Frass	Module hub	Proteobacteria	Alphaproteobacteria	Paracaedibacterales	Paracaedibacteraceae	Candidatus Odyssella
Genus646	Frass	Module hub	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Cupriavidus
Genus710	Frass	Module hub	Proteobacteria	Gammaproteobacteria	Diplorickettsiales	Diplorickettsiaceae	uncultured
Genus772	Frass	Module hub	Verrucomicrobia	Verrucomicrobiae	Opitutales	Opitutaceae	Opitutus
Genus29	Control/Manue	Connector	Actinobacteria	Acidimicrobiia	IMCC26256	uncultured bacterium	uncultured bacterium
Genus250	Control	Connector	Chloroflexi	KD4-96	uncultured bacterium	uncultured bacterium	uncultured bacterium
Genus476	Manue	Connector	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseococcus
Genus585	Manue	Connector	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis
Genus630	Manue	Connector	Proteobacteria	Gammaproteobacteria	211ds20	uncultured bacterium	uncultured bacterium
Genus248	Frass	Connector	Chloroflexi	Chloroflexia	Thermomicrobiales	JG30-KF-CM45	Other
Genus460	Frass	Connector	Planctomycetes	Planctomycetacia	Isosphaerales	Isosphaeraceae	uncultured

Table S5 Potential microbial functions of the gut and rhizosphere groups based on Fig. 5.

Type	Function	Matched ZOTUs	Relative abundance in gut group			Relative abundance in rhizosphere group		
			Control	Manure	Frass	Control	Manure	Frass
Carbon cycling	Aliphatic non methane hydrocarbon degradation	29	0.000107504	0.00011672	0.000169484	0.000981133	0.000726943	0.00149445
Carbon cycling	Aromatic compound degradation	176	0.00131369	0.000669226	0.001293852	0.002318929	0.007648522	0.004743846
Carbon cycling	Aromatic hydrocarbon degradation	42	0.000115444	0.00011672	0.000171459	0.001016913	0.006079746	0.001646862
Carbon cycling	Cellulolysis	182	0.000482002	7.32055E-05	0.000130139	0.004564908	0.003709383	0.021295474
Carbon cycling	Chitinolysis	64	7.16952E-05	5.15017E-05	0.000112362	0.001556887	0.006974378	0.01044131
Carbon cycling	Hydrocarbon degradation	165	0.000775894	0.000520582	0.001669632	0.004077337	0.006744544	0.002366336
Carbon cycling	Methanol oxidation	112	0.000398423	0.000225421	0.000329001	0.004207958	0.004569017	0.004265474
Carbon cycling	Methylotrophy	139	0.000398423	0.000225421	0.000329001	0.007268383	0.005233815	0.004942064
Nitrogen cycling	Denitrification	93	0.000402327	0.000229378	0.000336887	1.97897E-05	0.005657986	0.003432468
Nitrogen cycling	Nitrate denitrification	93	0.000402327	0.000229378	0.000336887	1.97897E-05	0.005657986	0.003432468
Nitrogen cycling	Nitrate reduction	473	0.001645681	0.002935204	0.00763145	0.012118417	0.024072896	0.014645554
Nitrogen cycling	Nitrate respiration	233	0.001068202	0.000932809	0.001590654	0.0010046	0.014450882	0.006350904
Nitrogen cycling	Nitrite denitrification	93	0.000402327	0.000229378	0.000336887	1.97897E-05	0.005657986	0.003432468
Nitrogen cycling	Nitrite respiration	123	0.000789138	0.000750747	0.00117078	0.000237875	0.006093321	0.003525414
Nitrogen cycling	Nitrogen respiration	233	0.001068202	0.000932809	0.001590654	0.0010046	0.014450882	0.006350904
Nitrogen cycling	Nitrous oxide denitrification	93	0.000402327	0.000229378	0.000336887	1.97897E-05	0.005657986	0.003432468
Sulfur cycling	Respiration of sulfur compounds	488	0.038347728	0.044074965	0.013822293	0.000392309	0.000713968	0.000146137
Sulfur cycling	Sulfate respiration	467	0.037646246	0.043633151	0.013317695	0.000392309	3.64539E-05	0.000146137
Metabolism	Aerobic chemoheterotrophy	4371	0.042338299	0.043144829	0.081511738	0.128451309	0.345381606	0.26129039
Metabolism	Chemoheterotrophy	8078	0.232789009	0.249715723	0.321166683	0.143968248	0.37499333	0.279693308
Metabolism	Dark hydrogen oxidation	91	0.000390388	0.000225421	0.000327028	0.000861635	0.002687637	0.001637265
Metabolism	Fermentation	3701	0.192327661	0.20844079	0.243446984	0.005515138	0.017249638	0.016595596
Metabolism	Nonphotosynthetic cyanobacteria	82	0.005735874	0.000625623	0.002240008	0.001515995	3.28504E-06	0.000288233
Metabolism	Ureolysis	618	0.000815736	0.000869194	0.001898833	0.073456738	0.087898211	0.054998155
Metabolism	Xylanolysis	85	0.004679293	0.001214474	0.00066845	1.5838E-05	0.000866165	0.001035216
Metal	Manganese oxidation	791	0.006744933	0.032640914	0.061179139	0.014273048	0.001903241	0.012356392
Human	Human associated	195	0.005010654	0.012713882	0.017049075	0.000788557	0.012243051	0.0056572

Human	Human gut	116	0.004492043	0.012254495	0.016185261	8.35715E-05	0.001738339	0.000118776
Human	Human pathogens all	129	0.004688061	0.011262462	0.015658742	0.000700977	0.010507858	0.005538425
Animal	Animal parasites or symbionts	218	0.00613458	0.013216363	0.01669989	0.000784548	0.012282262	0.00574294
Animal	Mammal gut	116	0.004492043	0.012254495	0.016185261	8.35715E-05	0.001738339	0.000118776
Plant	Plant pathogen	47	0.00010752	1.78115E-05	6.30759E-05	0.000544272	0.007607577	0.003463089