

Table S1

The result of linear discriminant analysis (LDA). The nonparametric factorial Kruskal-Wallis (KW) sum rank test was used to find species with significant differences from the phylum to genus level ($p < 0.05$), in which the value of LDA was greater than 2. p, c, o, f and g represent the taxonomic level, which were phylum, class, order, family and genus, respectively.

Species name	Group	Mean	LDA-value	p-value
<i>p_Firmicutes.c_Clostridia.o_ungrouped_c_Clostridia.f_ungrouped_c_Clostridia</i>	SSe	1.82	3.22	0.015
<i>p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae.g_Prevotellaceae_UCG-001</i>	SeMet	3.74	3.40	0.019
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Roseburia</i>	Blank	4.23	3.95	0.011
<i>p_Firmicutes.c_Clostridia.o_Peptostreptococcales-Tissierellales</i>	Control	3.44	3.08	0.001
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae_UCG-001</i>	Control	3.70	3.35	0.002
<i>p_Firmicutes.c_Clostridia.o_Christensenellales.f_Christensenellaceae.g_norank_f_Christensenellaceae</i>	SSe	1.89	2.97	0.016
<i>p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_Negativibacillus</i>	SSe	3.22	2.93	0.000
<i>p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Butyricicoccaceae.g_UCG-009</i>	Control	3.25	3.01	0.000
<i>p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae.g_ungrouped_f_Prevotellaceae</i>	SeMet	3.00	3.01	0.003
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Tuzzerella</i>	Control	3.08	2.84	0.018
<i>p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales</i>	SeMet	2.32	3.29	0.006
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae_NK4A136_group</i>	Control	4.90	4.50	0.007
<i>p_Campylobacterota.c_Campylobacteria.o_Campylobacteriales.f_Helicobacteraceae</i>	Blank	4.91	4.53	0.021
<i>p_Firmicutes.c_Clostridia.o_Oscillospirales.f_UCG-010</i>	SSe	2.96	2.71	0.008
<i>p_Actinobacteriota.c_Actinobacteria.o_Micrococcales.f_Micrococcaceae</i>	Blank	2.24	2.95	0.010
<i>p_Firmicutes.c_Bacilli.o_Erysipelotrichales.f_Erysipelotrichaceae.g_ungrouped_f_Erysipelotrichaceae</i>	SSe	2.56	2.57	0.037
<i>p_Firmicutes.c_Clostridia.o_Monoglobales.f_Monoglobaceae.g_Monoglobus</i>	Control	3.26	2.98	0.002
<i>p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_norank_o_Rhodospirillales.g_norank_f_norank_o_Rhodospirillales</i>	SSe	3.44	3.15	0.029

<i>p_Firmicutes.c_Clostridia.o_unclassified_c_Clostridia.f_unclassified_c_Clostridia.g_unclassified_c_Clostridia</i>	SSe	1.82	3.22	0.015
<i>p_Firmicutes.c_Clostridia.o_Peptostreptococcales-Tissierellales.f_Anaerovoracaceae.g_Eubacterium_no_datum_group</i>	Control	3.17	2.94	0.003
<i>p_Firmicutes.c_Clostridia.o_Christensenellales</i>	SSe	1.93	2.96	0.016
<i>p_Campylobacterota.c_Campylobacteria.o_Campylobacterales</i>	Blank	4.91	4.53	0.021
<i>p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Muribaculaceae.g_Muribaculum</i>	SeMet	2.87	2.67	0.043
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g ASF356</i>	Control	3.79	3.48	0.012
<i>p_Firmicutes.c_Clostridia.o_Peptostreptococcales-Tissierellales.f_Anaerovoracaceae.g_Family XIII AD 3011_group</i>	Control	2.94	3.02	0.000
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Lachnoclostridium</i>	Control	3.96	3.60	0.010
<i>p_Proteobacteria.c_Gammaproteobacteria.o_Burkholderiales.f_Sutterellaceae.g_Parasutterella</i>	Control	3.20	2.97	0.002
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_A2</i>	Control	3.28	2.97	0.002
<i>p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Ruminococcaceae.g_Ruminococcus</i>	SSe	3.44	3.18	0.013
<i>p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Tannerellaceae.g_Parabacteroides</i>	SeMet	3.84	3.46	0.024
<i>p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales</i>	SSe	3.44	3.15	0.029
<i>p_Proteobacteria.c_Gammaproteobacteria.o_Burkholderiales.f_Sutterellaceae</i>	Control	3.20	2.97	0.002
<i>p_Firmicutes.c_Clostridia.o_Monoglobales.f_Monoglobaceae</i>	Control	3.26	2.98	0.002
<i>p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales</i>	SeMet	2.65	2.70	0.007
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Eubacterium_xylanophilum_group</i>	Blank	3.51	3.28	0.005
<i>p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae</i>	SSe	2.65	2.56	0.008
<i>p_Campylobacterota.c_Campylobacteria</i>	Blank	4.91	4.53	0.021
<i>p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_norank_f_Rikenellaceae</i>	Blank	2.42	2.70	0.014
<i>p_Firmicutes.c_Clostridia.o_Peptostreptococcales-Tissierellales.f_Anaerovoracaceae</i>	Control	3.44	3.08	0.001

<i>p_Actinobacteriota.c_Actinobacteria.o_Micrococcal es.f_Micrococcaceae.g_Arthrobacter</i>	Blank	2.23	2.99	0.038
<i>p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Buty ricicoccaceae</i>	Control	3.43	3.12	0.001
<i>p_Actinobacteriota.c_Coriobacteriia.o_Coriobacteri ales.f_Eggerthellaceae.g_unclassified_f_Eggerthella ceae</i>	Blank	2.30	3.25	0.015
<i>p_Firmicutes.c_Clostridia.o_Peptostreptococcales- Tissierellales.f_Anaerovoracaceae.g_Anaerovorax</i>	SSe	2.01	3.22	0.002
<i>p_Proteobacteria.c_Alphaproteobacteria.o_Rhodosp irillales.f_norank_o_Rhodospirillales</i>	SSe	3.44	3.15	0.029
<i>p_Actinobacteriota.c_Actinobacteria.o_Micrococcal es</i>	Blank	2.36	2.92	0.002
<i>p_Campylobacterota.c_Campylobacteria.o_Campylo bacteriales.f_Helicobacteraceae.g_Helicobacter</i>	Blank	4.91	4.53	0.021
<i>p_Proteobacteria.c_Gammaproteobacteria.o_Entero bacteriales.f_Enterobacteriaceae.g_Klebsiella</i>	Control	3.40	3.13	0.026
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lac hnospiraceae</i>	Control	5.24	4.78	0.020
<i>p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Rum inococcaceae.g_Harryflintia</i>	SSe	2.52	2.78	0.019
<i>p_Firmicutes.c_Clostridia.o_unclassified_c_Clostri dia</i>	SSe	1.82	3.21	0.015
<i>p_Proteobacteria.c_Gammaproteobacteria.o_Burkh olderiales.f_Burkholderiaceae.g_Burkholderia- Caballeronia-Paraburkholderia</i>	SSe	2.44	2.88	0.000
<i>p_Firmicutes.c_Clostridia.o_Clostridiales</i>	SSe	2.65	2.56	0.008
<i>p_Proteobacteria.c_Gammaproteobacteria.o_Burkh olderiales.f_Burkholderiaceae</i>	SSe	2.44	2.92	0.003
<i>p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_T annerellaceae</i>	SeMet	3.84	3.46	0.024
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lac hnospiraceae.g_Lachnospiraceae_UCG-010</i>	Control	1.96	3.27	0.013
<i>p_Firmicutes.c_Clostridia.o_Monoglobales</i>	Control	3.26	2.98	0.002
<i>p_Firmicutes.c_Clostridia.o_Lachnospirales</i>	Control	5.24	4.78	0.020
<i>p_Proteobacteria.c_Gammaproteobacteria.o_Entero bacteriales.f_Enterobacteriaceae.g_Escherichia- Shigella</i>	Blank	4.54	4.22	0.041
<i>p_Campylobacterota</i>	Blank	4.91	4.53	0.021
<i>p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Streptoc occaceae.g_Lactococcus</i>	Blank	3.86	3.63	0.010
<i>p_Firmicutes.c_Clostridia.o_Christensenellales.f_C hristensenellaceae</i>	SSe	1.93	2.95	0.016

<i>p_Firmicutes.c_Clostridia.o_Oscillospirales.f_UCG-010.g_norank_f_UCG-010</i>	SSe	2.96	2.71	0.008
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