

Supplementary Information

Supplemental Figures

Figure S1

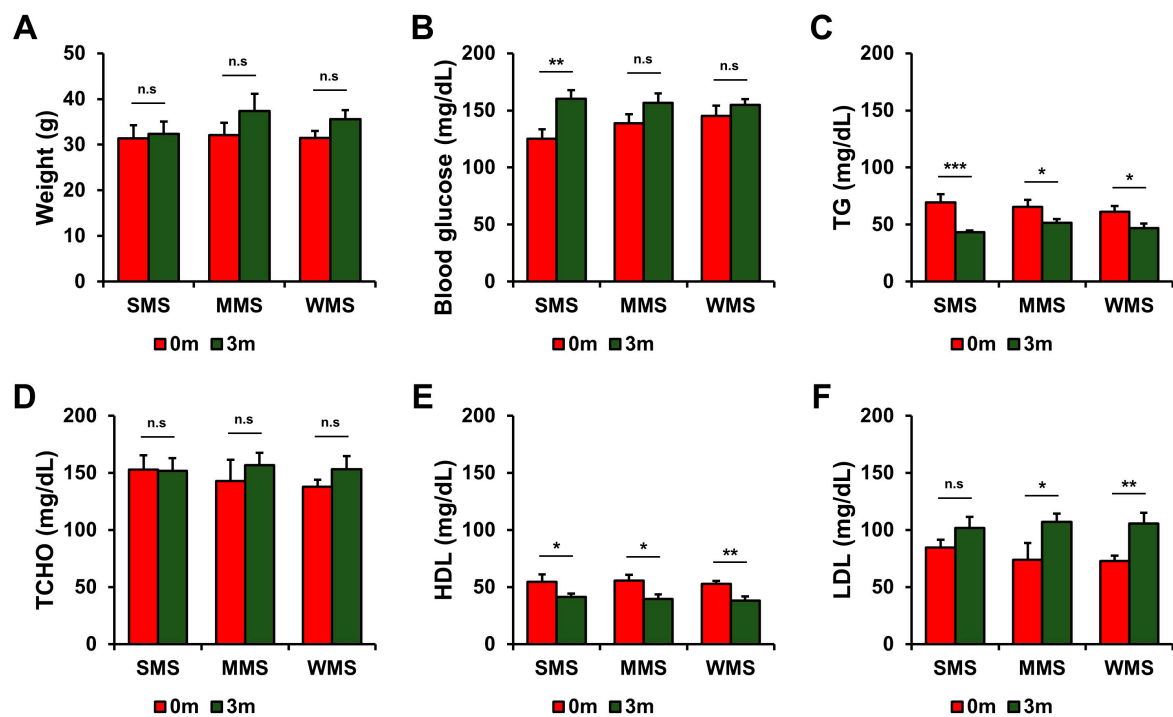


Figure S1. The effects of FMT on changes in blood glucose, blood pressure, and lipid levels.

The average values of (A) Weight, (B) Blood glucose, (C) Total glycerol (TG), (D) Total cholesterol (TCHO), (E) HDL-cholesterol (HDL-CHO), and (F) LDL-cholesterol (LDL-CHO) for each group are shown. The values are represented as mean \pm SEM. 0m represents before the FMT, and 3m represents 3 months after the FMT. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; n.s.: not significant ($p > 0.05$)

Figure S2

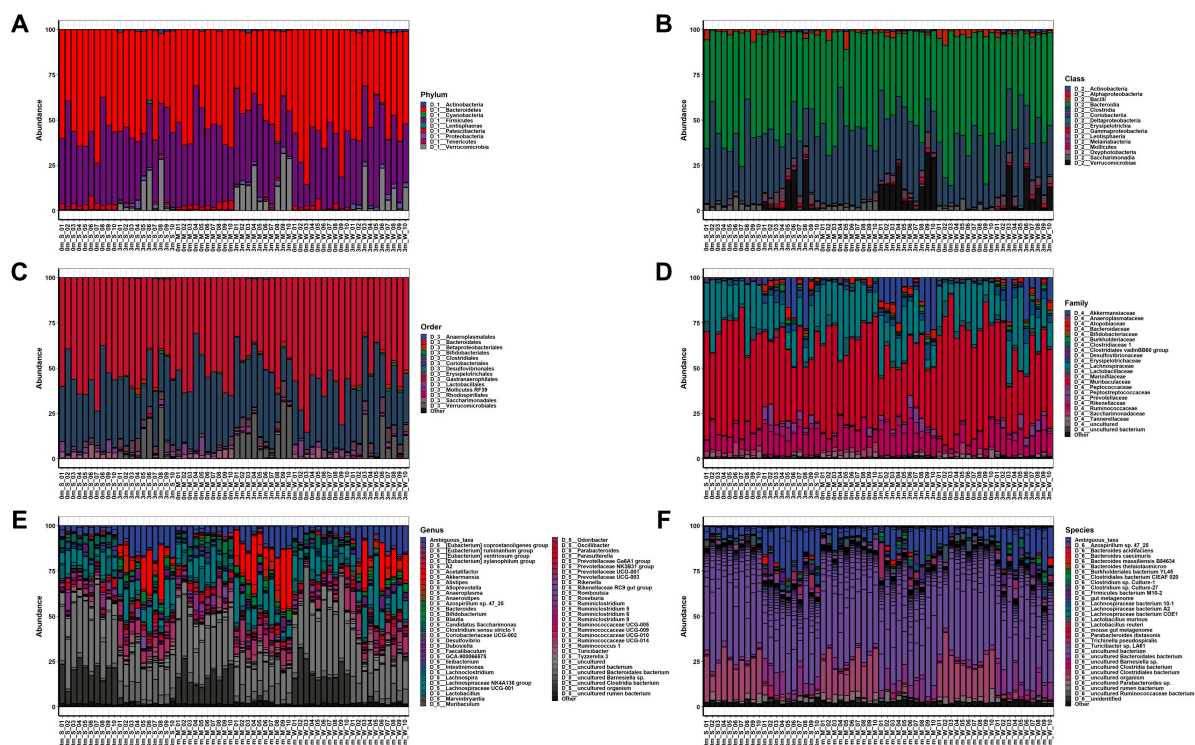


Figure S2. Changes in the composition of the gut microbiome of each mouse before and after FMT. The compositional changes of the gut microbiome at **(A)** phylum level, **(B)** class level, **(C)** order level, **(D)** family level, **(E)** genus, and **(F)** species level are shown. 0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S1. The valid reads of the 16S rRNA amplicon sequence

Group	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W
Total reads	41,550 ± 1,113	44,773 ± 2,565	46,584 ± 1,215	39,230 ± 2,515	40,207 ± 1,718	36,142 ± 2,031

All values are the mean ± SEM. 0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S2. Comparison of taxonomy abundance at the phylum level

Phylum	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W	0m	3m
D__Verrucomicrobia	0	0	0.017	7.552	14.915	8.123	0.006	10.197
D__Bacteroidetes	56.093	53.922	63.633	52.068	43.928	49.416	57.883	48.471
D__Firmicutes	40.116	42.569	33.938	36.244	37.628	38.496	38.875	37.456
D__Patescibacteria	3.240	2.791	2.030	0.510	0.373	0.129	2.687	0.337
D__Actinobacteria	0.055	0.266	0.074	0.929	0.698	1.093	0.132	0.907
D__Proteobacteria	0.336	0.335	0.253	1.835	1.671	2.264	0.308	1.924
D__Tenericutes	0.158	0.115	0.055	0.629	0.574	0.236	0.109	0.480
D__Cyanobacteria	0.003	0.001	0	0.232	0.210	0.241	0.001	0.228
D__Lentisphaerae	0	0	0	0.001	0.002	0.002	0	0.002

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S3. Comparison of taxonomy abundance at the class level

Class	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W	0m	3m
D__Verrucomicrobiae	0	0	0.017	7.552	14.915	8.123	0.006	10.197
D__Bacteroidia	56.093	53.922	63.633	52.068	43.928	49.416	57.883	48.471
D__Clostridia	36.684	38.674	29.873	30.437	32.948	32.293	35.077	31.893
D__Erysipelotrichia	0.943	1.396	0.695	4.538	3.467	4.969	1.011	4.325
D__Saccharimonadia	3.240	2.791	2.030	0.510	0.373	0.129	2.687	0.337
D__Bacilli	2.489	2.499	3.370	1.269	1.211	1.234	2.786	1.238
D__Actinobacteria	0	0.193	0.004	0.735	0.515	0.846	0.066	0.699
D__Coriobacteriia	0.055	0.074	0.070	0.194	0.183	0.247	0.066	0.208
D__Deltaproteobacteria	0.142	0.193	0.124	0.245	0.306	0.371	0.153	0.308
D__Gammaproteobacteria	0.134	0.097	0.089	1.211	1.016	1.438	0.107	1.222
D__Mollicutes	0.158	0.115	0.055	0.629	0.574	0.236	0.109	0.480
D__Alphaproteobacteria	0.060	0.045	0.039	0.379	0.349	0.455	0.048	0.394
D__Melainabacteria	0	0	0	0.230	0.206	0.239	0	0.225
D__Oxyphotobacteria	0.003	0.001	0	0.002	0.004	0.002	0.001	0.003
D__Lentisphaeria	0	0	0	0.001	0.002	0.002	0	0.002

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S4. Comparison of taxonomy abundance at the order level

Order	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W	0m	3m
D_3_Verrucomicrobiales	0	0	0.017	7.549	14.915	8.123	0.006	10.196
D_3_Bacteroidales	56.093	53.920	63.628	52.024	43.852	49.372	57.881	48.416
D_3_Clostridiales	36.684	38.674	29.873	30.437	32.948	32.293	35.077	31.893
D_3_Erysipelotrichales	0.943	1.396	0.695	4.538	3.467	4.969	1.011	4.325
D_3_Saccharimonadales	3.240	2.791	2.030	0.510	0.373	0.129	2.687	0.337
D_3_Lactobacillales	2.489	2.499	3.370	1.267	1.211	1.234	2.786	1.237
D_3_Bifidobacteriales	0	0.193	0.004	0.733	0.515	0.846	0.066	0.698
D_3_Coriobacteriales	0.055	0.074	0.070	0.194	0.183	0.247	0.066	0.208
D_3_Desulfovibrionales	0.139	0.192	0.124	0.245	0.306	0.371	0.152	0.308
D_3_Betaproteobacteriales	0.005	0.003	0.005	1.206	1.011	1.432	0.004	1.216
D_3_Anaeroplasmatales	0	0.002	0	0.326	0.291	0.071	0.001	0.229
D_3_Mollicutes RF39	0.158	0.113	0.055	0.283	0.276	0.160	0.109	0.239
D_3_Rhodospirillales	0	0	0	0.366	0.341	0.448	0	0.385
D_3_Gastranaerophilales	0	0	0	0.230	0.206	0.239	0	0.225
Other < 0.5%	0.195	0.142	0.129	0.092	0.104	0.066	0.155	0.087

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S5. Comparison of taxonomy abundance at the family level

Family	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W	0m	3m
D_4__Akkermansiaceae	0	0	0.017	7.555	14.923	8.129	0.006	10.202
D_4__Muribaculaceae	54.598	50.660	61.670	40.613	33.303	40.784	55.642	38.233
D_4__Lachnospiraceae	24.471	24.611	19.667	16.383	18.101	19.080	22.916	17.855
D_4__Erysipelotrichaceae	0.944	1.397	0.695	4.542	3.469	4.972	1.012	4.327
D_4__Saccharimonadaceae	3.241	2.793	2.030	0.510	0.373	0.129	2.688	0.337
D_4__Tannerellaceae	1.259	2.107	1.615	0.653	0.706	0.822	1.661	0.727
D_4__Lactobacillaceae	2.466	2.476	3.360	1.249	1.205	1.232	2.767	1.228
D_4__Ruminococcaceae	9.720	10.737	7.399	12.561	13.346	11.583	9.285	12.497
D_4__Prevotellaceae	0	0	0	4.028	3.089	3.013	0	3.377
D_4__Bacteroidaceae	0	0.793	0	2.703	3.156	1.975	0.264	2.611
D_4__Clostridiales vadinBB60 group	1.670	1.526	1.391	0.852	0.859	0.798	1.529	0.836
D_4__Rikenellaceae	0.253	0.384	0.357	3.431	3.484	2.006	0.331	2.974
D_4__Bifidobacteriaceae	0	0.193	0.004	0.733	0.516	0.846	0.066	0.698
D_4__Atopobiaceae	0	0	0	0.139	0.118	0.177	0	0.145
D_4__Desulfovibrionaceae	0.139	0.193	0.124	0.246	0.306	0.371	0.152	0.308
D_4__Peptococcaceae	0.191	0.164	0.154	0.328	0.396	0.533	0.170	0.419
D_4__Burkholderiaceae	0.005	0.003	0.005	1.207	1.011	1.433	0.004	1.217
D_4__Clostridiaceae 1	0.193	0.710	0.728	0.155	0.079	0.090	0.544	0.108
D_4__Marinifilaceae	0	0	0	0.629	0.115	0.790	0	0.511
D_4__Anaeroplasmataceae	0	0.002	0	0.326	0.291	0.071	0.001	0.229
D_4__Peptostreptococcaceae	0.257	0.761	0.375	0.007	0.004	0.025	0.464	0.012
D_4__uncultured bacterium	0.094	0.068	0.038	0.162	0.194	0.083	0.067	0.146
D_4__uncultured	0	0	0	0.366	0.341	0.449	0	0.385
D_4__uncultured bacterium	0	0	0	0.193	0.183	0.178	0	0.185
Other < 0.5%	0.499	0.423	0.371	0.431	0.432	0.429	0.431	0.431

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S6. Comparison of taxonomy abundance at the genus level

Genus	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W	0m	3m
D_5_Akkermansia	0	0	0.027	8.155	16.339	8.986	0.009	11.160
Ambiguous_taxa	3.231	3.854	4.155	13.325	8.853	11.553	3.747	11.243
D_5_uncultured organism	18.135	15.826	18.326	0.807	0.426	0.539	17.429	0.591
D_5_uncultured bacterium	30.406	26.769	33.544	15.306	14.418	18.109	30.240	15.944
D_5_Turicibacter	0.828	1.496	0.753	1.994	1.106	1.725	1.026	1.608
D_5_uncultured Bacteroidales bacterium	1.692	1.868	2.096	7.325	6.403	7.555	1.885	7.094
D_5_Lachnospiraceae NK4A136 group	7.477	7.965	7.540	10.866	11.389	12.565	7.661	11.607
D_5_[Eubacterium] coprostanoligenes group	0.027	0.057	0.018	0.681	0.789	0.951	0.034	0.807
D_5_Candidatus Saccharimonas	4.351	3.665	2.690	0.584	0.416	0.147	3.568	0.382
D_5_Parabacteroides	1.681	2.684	2.136	0.753	0.791	0.953	2.167	0.832
D_5_Lactobacillus	3.346	3.125	4.527	1.412	1.339	1.410	3.666	1.387
D_5_Ruminiclostridium	3.731	3.249	1.929	0.624	0.701	0.508	2.970	0.611
D_5_Alloprevotella	0	0	0	1.522	1.517	1.476	0	1.505
D_5_Bacteroides	0	1.033	0	3.044	3.514	2.223	0.344	2.927
D_5_uncultured bacterium	0.987	1.066	0.947	0.475	0.476	0.497	1.000	0.483
D_5_Alistipes	0.336	0.494	0.464	2.548	3.755	1.699	0.432	2.667
D_5_Faecalibaculum	0.419	0.214	0.024	0.375	0.503	0.854	0.219	0.577
D_5_Prevotellaceae UCG-001	0	0	0	1.851	1.353	0.881	0	1.361
D_5_Muribaculum	0	0.072	0	1.069	1.094	1.180	0.024	1.114
D_5_Bifidobacterium	0	0.258	0.005	0.817	0.571	0.967	0.088	0.785
D_5_Intestinimonas	1.744	1.626	0.990	0.186	0.172	0.139	1.453	0.166
D_5_Coriobacteriaceae UCG-002	0	0	0	0.159	0.132	0.197	0	0.163
D_5_Dubosiella	0	0	0.134	2.501	1.866	2.836	0.045	2.401
D_5_Desulfovibrio	0.185	0.247	0.169	0.055	0.069	0.037	0.200	0.054
D_5_Ruminococcaceae UCG-014	1.714	2.268	2.806	7.110	6.026	5.567	2.263	6.234
D_5_uncultured	5.789	6.293	4.524	1.534	1.401	1.578	5.535	1.504
D_5_[Eubacterium] ventriosum group	0.059	0.523	0.222	0.001	0.045	0.004	0.268	0.017
D_5_Oscillibacter	1.119	1.054	0.748	0.551	0.539	0.445	0.974	0.512
D_5_Prevotellaceae NK3B31 group	0	0	0	0.878	0.236	0.662	0	0.592
D_5_[Eubacterium] ruminantium group	0	0	0	0.175	0.176	0.505	0	0.285
D_5_uncultured	0.453	0.601	0.336	0.929	1.164	1.270	0.463	1.121
Ambiguous_taxa	1.030	0.701	0.591	0.261	0.314	0.259	0.774	0.278
D_5_Blautia	0.512	0.400	0.227	0.223	0.401	0.387	0.380	0.337
D_5_Ruminiclostridium 9	1.554	1.383	1.153	1.081	1.302	1.025	1.364	1.136
D_5_Rikenellaceae RC9 gut group	0	0	0	1.256	0.142	0.480	0	0.626
D_5_uncultured	0	0	0	0.153	0.198	0.317	0	0.223
D_5_[Eubacterium] xylanophilum group	0.501	0.502	0.421	0.252	0.321	0.266	0.475	0.280
D_5_Lachnospiraceae UCG-001	1.064	1.030	0.910	0.115	0.205	0.076	1.001	0.132
D_5_uncultured	0.241	0.191	0.183	0.359	0.439	0.589	0.205	0.462
D_5_uncultured Clostridia bacterium	0.109	0.145	0.181	0.020	0.027	0.010	0.145	0.019
D_5_Marvinbryantia	0.383	0.453	0.654	0.101	0.037	0.028	0.496	0.056
D_5_Parasutterella	0	0	0	1.353	1.116	1.603	0	1.357
D_5_Ruminococcaceae UCG-009	0.283	0.345	0.277	0.151	0.192	0.129	0.302	0.157
D_5_Ruminococcus 1	0.008	0.794	0.008	1.032	1.457	1.271	0.270	1.254
D_5_Prevotellaceae Ga6A1 group	0	0	0	0.327	0.093	0.307	0	0.242

D_5_Ruminiclostridium 6	0.358	0.331	0.211	0.167	0.395	0.174	0.300	0.245
D_5_Clostridium sensu stricto 1	0.259	0.852	0.982	0.107	0.039	0.068	0.698	0.071
D_5_Roseburia	0.683	0.584	0.427	0.338	0.350	0.251	0.565	0.313
D_5_Lachnoclostridium	0.706	0.535	0.532	0.199	0.348	0.152	0.591	0.233
D_5_GCA-900066575	0.744	0.692	0.648	0.123	0.192	0.111	0.695	0.142
D_5_Odoribacter	0	0	0	0.656	0.069	0.781	0	0.502
D_5_Ileibacterium	0	0	0	0.068	0.186	0.112	0	0.122
D_5_A2	0.531	0.410	0.473	0.115	0.086	0.044	0.471	0.082
D_5_Anaeroplasma	0	0.003	0	0.369	0.325	0.084	0.001	0.259
D_5_Lachnospira	0.268	0.328	0.309	0.010	0.002	0	0.302	0.004
D_5_Romboutsia	0.344	1.032	0.503	0.008	0.004	0.030	0.626	0.014
D_5_Ruminiclostridium 5	0.417	0.761	0.309	0.159	0.245	0.167	0.496	0.190
D_5_Anaerostipes	0	0	0	0.328	0.368	0.251	0	0.315
D_5_uncultured	0.006	0.051	0.002	0.105	0.079	0.051	0.020	0.078
D_5_Ruminococcaceae UCG-010	0.036	0.065	0.044	0.279	0.184	0.292	0.048	0.252
D_5_Tyzzereella 3	0.242	0.231	0.153	0.023	0.024	0.014	0.209	0.020
D_5_uncultured bacterium	0.126	0.091	0.053	0.186	0.218	0.099	0.090	0.167
D_5_Acetatifactor	0.165	0.148	0.131	0.075	0.122	0.098	0.148	0.098
D_5_Azospirillum sp. 47_25	0	0	0	0.250	0.112	0.183	0	0.182
D_5_Prevotellaceae UCG-003	0	0	0	0	0.206	0.044	0	0.084
D_5_uncultured bacterium	0	0	0	0.209	0.202	0.194	0	0.202
D_5_uncultured rumen bacterium	0	0	0	0.070	0.097	0.105	0	0.090
D_5_Rikenella	0	0	0	0.077	0.001	0.100	0	0.059
D_5_uncultured bacterium	0	0	0	0.078	0.076	0.035	0	0.063
D_5_Ruminococcaceae UCG-005	0.032	0.097	0.026	0.026	0.048	0.022	0.051	0.032
D_5_uncultured Barnesiella sp.	0	0	0	0.001	0.094	0.002	0	0.032
Other < 0.5%	1.686	1.540	1.480	1.674	2.109	1.776	1.569	1.853

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S7. Comparison of taxonomy abundance at the species level

Species	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W	0m	3m
D_6_uncultured bacterium	0	0	0.028	8.311	19.514	10.340	0.009	12.722
Ambiguous_taxa	3.708	4.633	4.852	16.394	10.441	13.672	4.398	13.502
D_6_uncultured organism	20.844	19.096	21.358	1.033	0.509	0.633	20.433	0.725
D_6_uncultured bacterium	34.862	32.425	39.085	18.909	17.378	21.369	35.457	19.219
D_6_Turicibacter sp. LA61	0.930	1.765	0.871	2.441	1.323	2.051	1.189	1.938
D_6_uncultured Bacteroidales bacterium	1.954	2.239	2.460	8.975	7.588	8.965	2.218	8.509
D_6_Trichinella pseudospiralis	0	0	0	2.426	3.390	1.644	0	2.487
D_6_Lachnospiraceae bacterium 10-1	0	0	0	1.214	1.071	1.447	0	1.244
D_6_uncultured bacterium	4.979	4.460	3.211	0.712	0.484	0.173	4.217	0.457
D_6_uncultured Parabacteroides sp.	1.955	3.058	2.568	0.012	0.004	0.017	2.527	0.011
D_6_Lactobacillus murinus	2.138	2.014	3.113	0.209	0.473	0.280	2.422	0.321
D_6_uncultured rumen bacterium	0	0.195	0	1.712	1.454	0.841	0.065	1.335
D_6_uncultured bacterium	4.342	3.956	2.314	0.747	0.835	0.585	3.537	0.722
D_6_gut metagenome	0	0	0	1.894	1.716	1.773	0	1.794
D_6_uncultured bacterium	1.149	1.312	1.143	0.579	0.570	0.583	1.201	0.577
D_6_uncultured bacterium	0.004	0.077	0	2.775	3.456	1.464	0.027	2.565
D_6_uncultured bacterium	4.303	4.490	2.540	3.899	4.567	6.337	3.778	4.934
D_6_uncultured bacterium	0.483	0.277	0.026	0.461	0.597	1.004	0.262	0.687
D_6_uncultured bacterium	0	0.092	0	1.326	1.328	1.396	0.031	1.350
D_6_uncultured bacterium	1.984	1.934	1.177	0.101	0.041	0.063	1.698	0.068
D_6_uncultured bacterium	0	0	0	1.784	2.074	3.050	0	2.303
D_6_uncultured bacterium	0.214	0.296	0.200	0.069	0.054	0.028	0.237	0.050
D_6_Clostridiales bacterium CIEAF 020	0	0	0	0.467	0.822	0.813	0	0.701
D_6_Bacteroides caecimuris	0	0	0	0.845	0.436	0.659	0	0.647
D_6_Bacteroides acidifaciens	0	0	0	0.315	0.095	0.078	0	0.163
D_6_uncultured bacterium	0.702	0.832	0.544	0.488	0.322	0.324	0.693	0.378
D_6_uncultured bacterium	0	0	0	1.095	0.287	0.781	0	0.721
D_6_uncultured bacterium	2.870	3.134	2.323	1.021	1.233	1.352	2.775	1.202
D_6_uncultured bacterium	0	0	0	0.229	0.213	0.588	0	0.343
D_6_Clostridium sp. Culture-1	0.176	0.252	0.103	0.870	1.158	1.163	0.177	1.064
Ambiguous_taxa	1.202	0.863	0.719	0.321	0.378	0.306	0.928	0.335
D_6_unidentified	0.242	0.406	0.555	0.320	0.192	0.160	0.401	0.224
D_6_uncultured Bacteroidales bacterium	0	0.149	0	0.639	0.401	0.900	0.050	0.647
D_6_uncultured Clostridiales bacterium	0.527	0.400	0.393	1.255	0.634	0.974	0.440	0.954
Ambiguous_taxa	0	0	0	1.535	0.155	0.543	0	0.744
Ambiguous_taxa	0	0	0	0.184	0.233	0.372	0	0.263
D_6_uncultured bacterium	0.577	0.618	0.504	0.310	0.393	0.312	0.566	0.338
D_6_uncultured bacterium	1.225	1.240	1.068	0.097	0.218	0.058	1.178	0.125
D_6_uncultured organism	0	0	0	0.275	0.332	0.539	0	0.382
D_6_unidentified	0.353	0.273	0.236	0.114	0.160	0.114	0.287	0.129
D_6_Parabacteroides distasonis	0	0	0	0.126	0.338	0.100	0	0.188
D_6_Lachnospiraceae bacterium COE1	0.396	0.331	0.263	0.245	0.239	0.320	0.330	0.268
D_6_uncultured Clostridia bacterium	0.127	0.175	0.220	0.025	0.033	0.012	0.174	0.023
D_6_uncultured bacterium	0.384	0.470	0.692	0.099	0.022	0	0.516	0.040
D_6_uncultured bacterium	0	0	0	0.545	0.357	0.338	0	0.413
Ambiguous_taxa	0.326	0.423	0.329	0.178	0.224	0.138	0.359	0.180
D_6_uncultured bacterium	0.279	0.233	0.220	0.163	0.191	0.169	0.244	0.174

D_6__Firmicutes bacterium M10-2	0	0	0.142	1.235	0.062	0.183	0.047	0.493
Ambiguous_taxa	0	0	0	0.411	0.107	0.345	0	0.288
D_6__uncultured bacterium	0.806	0.720	0.645	0.888	1.143	0.783	0.724	0.938
D_6__uncultured bacterium	0.386	0.204	0.317	1.482	1.093	1.099	0.302	1.225
D_6__uncultured bacterium	0	0	0	0.164	0.428	0.102	0	0.231
D_6__uncultured bacterium	0.296	1.022	1.163	0.129	0.048	0.079	0.827	0.086
D_6__uncultured bacterium	0.425	0.363	0.337	0.113	0.101	0.060	0.375	0.091
D_6__uncultured bacterium	0.414	0.266	0.362	0.138	0.360	0.106	0.347	0.201
D_6__uncultured bacterium	0.452	0.378	0.446	0.114	0.166	0.072	0.425	0.117
D_6__uncultured bacterium	0	0	0	0.572	0	0.538	0	0.370
D_6__Lactobacillus reuteri	0.207	0.138	0.175	0.144	0.081	0.145	0.173	0.123
Ambiguous_taxa	0	0	0	0.080	0.228	0.128	0	0.145
D_6__Lachnospiraceae bacterium A2	0.412	0.311	0.360	0	0.003	0	0.361	0.001
Ambiguous_taxa	0.238	0.460	0.198	0.102	0.070	0.077	0.298	0.083
D_6__uncultured bacterium	0	0.004	0	0.441	0.395	0.100	0.001	0.312
D_6__uncultured bacterium	0	0	0	0.165	0.728	0.566	0	0.486
D_6__Burkholderiales bacterium YL45	0	0	0	0.794	0.614	1.217	0	0.875
D_6__uncultured organism	0	0.324	0.090	0	0	0	0.138	0.000
D_6__mouse gut metagenome	0.352	0.264	0.169	0	0	0	0.261	0.000
Ambiguous_taxa	0	0	0	0.320	0.310	0.199	0	0.276
D_6__uncultured bacterium	0.007	0.064	0.003	0.128	0.093	0.059	0.024	0.093
D_6__unidentified	0.212	0.282	0.211	0.038	0.041	0.035	0.235	0.038
D_6__Bacteroides thetaiotaomicron	0	0	0	0.085	0.101	0.041	0	0.076
Ambiguous_taxa	0	0	0	0.161	0.073	0.372	0	0.202
D_6__Clostridium sp. Culture-27	0.140	0.321	0.231	0.026	0.023	0.041	0.231	0.030
D_6__uncultured bacterium	0.147	0.107	0.060	0.231	0.252	0.118	0.105	0.200
Ambiguous_taxa	0.192	0.181	0.159	0.005	0.001	0	0.178	0.002
D_6__Azospirillum sp. 47_25	0	0	0	0.317	0.137	0.216	0	0.223
D_6__gut metagenome	0	0	0	0.062	0.382	0.315	0	0.253
D_6__uncultured Ruminococcaceae bacterium	0	0.215	0.003	0.058	0.019	0.045	0.073	0.041
D_6__uncultured bacterium	0	0	0	0	0.251	0.052	0	0.101
D_6__uncultured bacterium	0.203	0.194	0.195	0.032	0.103	0.046	0.197	0.060
D_6__uncultured bacterium	0	0	0	0.205	0.219	0.131	0	0.185
D_6__uncultured rumen bacterium	0.056	0.017	0	0.054	0.040	0.043	0.025	0.045
D_6__uncultured bacterium	0	0	0	0.286	0.231	0.225	0	0.248
D_6__Bacteroides massiliensis B84634	0	0	0	0.137	0.519	0.187	0	0.281
D_6__uncultured rumen bacterium	0	0	0	0.085	0.115	0.123	0	0.108
Ambiguous_taxa	0	0	0	0.099	0	0.117	0	0.072
D_6__uncultured bacterium	0	0.040	0	0.084	0.227	0.431	0.013	0.247
D_6__uncultured bacterium	0	0	0	0.094	0.091	0.041	0	0.075
D_6__uncultured bacterium	0.012	0.026	0.127	0	0	0	0.055	0.000
D_6__gut metagenome	0	0	0	0.062	0.101	0.060	0	0.075
Ambiguous_taxa	0	0	0	0.015	0.063	0	0	0.026
Ambiguous_taxa	0	0	0	0.011	0.259	0.084	0	0.118
D_6__uncultured Barnesiella sp.	0	0	0	0.002	0.116	0.002	0	0.040
D_6__uncultured Clostridiales bacterium	0	0	0	0.124	0.050	0.009	0	0.061
Ambiguous_taxa	0	0	0	0.110	0	0.006	0	0.039
Other < 0.5%	1.806	1.983	1.497	2.454	2.625	2.574	1.762	2.551

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S8. The α -diversity indexes for each sample and group

Sample	Observed	ACE	Shannon	Simpson	InvSimpson	Fisher
0m_S_01	189	189	4.00	0.959	24.51	26.03
0m_S_02	217	217	4.44	0.978	44.45	29.98
0m_S_03	206	206.15	4.10	0.965	28.67	28.21
0m_S_04	208	208	4.02	0.958	23.63	28.25
0m_S_05	200	200.19	4.02	0.965	28.61	27.12
0m_S_06	210	210	4.26	0.973	37.50	28.51
0m_S_07	181	181.21	3.83	0.957	23.27	23.87
0m_S_08	236	236.59	4.52	0.979	48.27	33.16
0m_S_09	193	193	4.10	0.966	29.60	26.73
0m_S_10	199	199.93	4.19	0.967	30.16	27.52
0m_M_01	212	212.47	4.29	0.972	36.12	29.26
0m_M_02	224	224.25	3.86	0.944	17.86	30.20
0m_M_03	197	197.22	4.06	0.969	32.29	27.13
0m_M_04	245	245	4.54	0.977	42.60	34.12
0m_M_05	265	268.24	4.64	0.983	58.74	37.88
0m_M_06	245	245	4.44	0.975	40.33	32.49
0m_M_07	223	223.35	4.03	0.958	24.01	29.70
0m_M_08	201	201	4.19	0.973	36.42	28.32
0m_M_09	194	194.64	4.03	0.966	29.34	26.57
0m_M_10	177	177.21	3.85	0.956	22.68	23.57
0m_W_01	208	209.31	4.23	0.973	36.46	28.80
0m_W_02	171	171	3.61	0.943	17.47	22.31
0m_W_03	152	152	3.51	0.949	19.79	19.27
0m_W_04	213	213.30	4.29	0.972	35.45	29.21
0m_W_05	202	202.51	4.22	0.973	37.19	27.28
0m_W_06	204	204.15	3.99	0.961	25.94	27.52
0m_W_07	217	217.43	4.16	0.967	29.92	29.26
0m_W_08	232	232.76	4.36	0.974	38.29	31.95
0m_W_09	162	162	3.64	0.952	20.98	20.68
0m_W_10	217	217	4.08	0.964	27.88	29.32
3m_S_01	303	303.81	4.46	0.976	41.91	45.01
3m_S_02	339	339.73	4.76	0.981	52.98	52.19
3m_S_03	410	411.15	4.66	0.972	35.20	62.43
3m_S_04	246	249.46	4.28	0.970	33.60	38.53
3m_S_05	249	250.11	3.83	0.938	16.08	36.56
3m_S_06	418	420.38	4.27	0.957	23.18	61.94
3m_S_07	386	386.31	4.61	0.969	32.24	59.04
3m_S_08	295	295.16	3.88	0.911	11.21	42.96
3m_S_09	377	377.16	4.69	0.977	44.18	56.91
3m_S_10	391	396.47	4.74	0.976	42.23	59.53
3m_M_01	307	309.10	4.23	0.955	22.34	46.82
3m_M_02	291	291.39	4.35	0.964	27.96	43.98
3m_M_03	389	389.74	4.54	0.964	27.55	58.11
3m_M_04	320	320.16	4.14	0.933	14.87	46.79
3m_M_05	402	402.56	5.00	0.987	79.86	62.24
3m_M_06	380	380.68	4.81	0.983	58.74	58.89
3m_M_07	352	352.17	4.32	0.964	28.07	53.30
3m_M_08	318	319.11	3.97	0.946	18.43	47.03
3m_M_09	343	344.93	3.58	0.882	8.49	49.63
3m_M_10	292	292.94	3.76	0.905	10.55	42.81
3m_W_01	313	313.32	4.37	0.969	31.94	47.09
3m_W_02	317	318.29	4.32	0.963	26.85	49.32
3m_W_03	389	392.35	4.23	0.931	14.54	58.76
3m_W_04	388	388.16	4.70	0.975	39.81	58.82
3m_W_05	334	334.40	4.07	0.924	13.23	50.21

3m_W_06	270	270.76	4.12	0.935	15.28	43.19
3m_W_07	291	291.31	4.34	0.969	32.71	43.50
3m_W_08	326	326.56	4.43	0.967	29.89	50.19
3m_W_09	352	352.16	4.63	0.973	36.62	53.01
3m_W_10	294	294.92	4.13	0.956	22.53	43.41

Group	Observed	ACE	Shannon	Simpson	InvSimpson	Fisher
0m_S	203.9 ± 4.9	204.1 ± 4.9	4.15 ± 0.07	0.967 ± 0.002	31.9 ± 2.8	27.9 ± 0.8
0m_M	218.3 ± 8.7	218.8 ± 8.8	4.19 ± 0.09	0.967 ± 0.004	34 ± 3.7	29.9 ± 1.3
0m_W	197.8 ± 8.4	198.1 ± 8.5	4.01 ± 0.1	0.963 ± 0.004	28.9 ± 2.5	26.6 ± 1.3
3m_S	341.4 ± 20.4	343 ± 20.5	4.42 ± 0.11	0.963 ± 0.007	33.3 ± 4.2	51.5 ± 3.1
3m_M	339.4 ± 12.8	340.3 ± 12.7	4.27 ± 0.14	0.948 ± 0.011	29.7 ± 7.1	51 ± 2.1
3m_W	327.4 ± 12.5	328.2 ± 12.7	4.33 ± 0.07	0.956 ± 0.006	26.3 ± 3	49.8 ± 1.8

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.

Table S9. PERMANOVA result tables for group before and after FMT.

Factor	<i>df</i>	SS	MS	F	<i>P</i>(perm)
Group (0m)	2	0.002865	0.0014326	1.1565	0.322
Residuals	27	0.033444	0.0012387		

Factor	<i>df</i>	SS	MS	F	<i>P</i>(perm)
Group (3m)	2	0.0017165	0.0008583	0.99	0.369
Residuals	27	0.0234057	0.0008669		

0m represents before the FMT, and 3m represents 3 months after the FMT. *df*: degrees of freedom; SS: sum of squares; MS: mean sum of squares; F: F value by permutation, *P*(perm): *p*-values based on more than 9000 permutations.

Table S10. Co-occurrence network indices

Network indexes indices	0m_S	0m_M	0m_W	3m_S	3m_M	3m_W
Node	73	101	98	204	173	168
Edge	65	99	75	158	149	136
Network Density	0.025	0.020	0.02	0.008	0.010	0.010
Assortativity	-0.019	-0.014	-0.013	-0.007	-0.008	-0.008
Module	21	28	31	74	60	58
Modularity (lc)	0.879	0.861	0.905	0.961	0.956	0.969

0m represents before the FMT, and 3m represents 3 months after the FMT. S, M, and W represent the SMS group, MMS group, and WMS group respectively.