

Electronic Supplementary Information

(For raw data used to generate the experimental results)

Table S5 The weight of mice in Day 1-14

Date	Days	Average weight \pm SD (n=8, g)				
		N group	D group	MP group	MPD group	DMP group
2022.05.27	1	22.71 \pm 0.70	23.20 \pm 0.26	23.42 \pm 0.58	22.80 \pm 0.36	22.77 \pm 0.45
2022.05.28	2	22.93 \pm 1.07	23.50 \pm 0.92	23.83 \pm 0.93	22.97 \pm 1.35	22.96 \pm 0.86
2022.05.29	3	22.93 \pm 0.40	23.75 \pm 0.40	23.98 \pm 0.22	23.10 \pm 0.85	23.43 \pm 0.70
2022.05.30	4	23.02 \pm 1.13	23.87 \pm 0.23	24.13 \pm 0.41	23.21 \pm 0.50	23.58 \pm 0.44
2022.06.01	5	23.13 \pm 0.76	24.02 \pm 0.87	24.25 \pm 0.43	23.27 \pm 0.97	23.74 \pm 0.26
2022.06.02	6	23.18 \pm 1.05	24.34 \pm 1.07	24.57 \pm 0.73	23.40 \pm 1.07	24.06 \pm 0.67
2022.06.03	7	23.32 \pm 0.25	24.50 \pm 0.43	24.62 \pm 0.88	23.61 \pm 0.40	24.22 \pm 0.87
2022.06.04	8	23.41 \pm 0.56	24.57 \pm 0.27	24.73 \pm 0.68	23.70 \pm 0.48	24.33 \pm 0.59
2022.06.05	9	23.52 \pm 0.60	24.65 \pm 1.08	24.81 \pm 0.65	23.89 \pm 0.67	24.36 \pm 0.97
2022.06.06	10	23.60 \pm 0.72	24.07 \pm 0.38	24.99 \pm 0.89	23.72 \pm 1.15	24.40 \pm 0.95
2022.06.07	11	23.64 \pm 0.49	23.57 \pm 0.97	25.04 \pm 0.94	23.33 \pm 0.86	23.85 \pm 1.17
2022.06.08	12	23.79 \pm 0.35	21.03 \pm 0.83	25.07 \pm 0.37	22.95 \pm 1.35	22.83 \pm 0.90
2022.06.09	13	23.86 \pm 0.42	20.42 \pm 0.90	25.38 \pm 0.74	22.52 \pm 1.39	22.33 \pm 1.61
2022.06.10	14	24.19 \pm 0.27	20.30 \pm 0.46	25.12 \pm 0.35	22.64 \pm 0.30	22.09 \pm 0.96

Table S6 The daily food intake of mice in Day 1-14

Date	Days	Average daily food intake of mice \pm SD (n=8, g)				
		N group	D group	MP group	MPD group	DMP group
2022.05.27	1	3.42 \pm 0.31	3.62 \pm 0.11	4.02 \pm 0.25	3.75 \pm 0.16	3.95 \pm 0.20
2022.05.28	2	3.24 \pm 0.47	3.56 \pm 0.40	3.75 \pm 0.40	3.56 \pm 0.59	3.54 \pm 0.18
2022.05.29	3	3.45 \pm 0.174	3.72 \pm 0.17	4.02 \pm 0.10	3.38 \pm 0.37	3.58 \pm 0.21
2022.05.30	4	3.30 \pm 0.198	3.55 \pm 0.10	3.83 \pm 0.17	3.15 \pm 0.22	3.35 \pm 0.19
2022.06.01	5	3.45 \pm 0.336	3.28 \pm 0.38	4.23 \pm 0.18	3.58 \pm 0.13	3.68 \pm 0.11
2022.06.02	6	3.50 \pm 0.16	3.56 \pm 0.26	4.15 \pm 0.31	3.48 \pm 0.27	3.76 \pm 0.30
2022.06.03	7	3.32 \pm 0.11	3.75 \pm 0.18	3.98 \pm 0.37	3.37 \pm 0.17	3.6 \pm 0.38
2022.06.04	8	3.63 \pm 0.25	3.27 \pm 0.12	3.84 \pm 0.29	3.45 \pm 0.21	3.42 \pm 0.26
2022.06.05	9	3.68 \pm 0.26	3.39 \pm 0.26	4.24 \pm 0.276	3.37 \pm 0.30	3.35 \pm 0.23
2022.06.06	10	3.6 \pm 0.32	2.85 \pm 0.16	4.15 \pm 0.38	3.28 \pm 0.21	2.97 \pm 0.22
2022.06.07	11	3.52 \pm 0.22	2.38 \pm 0.42	4.23 \pm 0.40	2.85 \pm 0.38	2.47 \pm 0.21
2022.06.08	12	3.72 \pm 0.16	1.86 \pm 0.36	3.98 \pm 0.16	2.67 \pm 0.29	2.35 \pm 0.20
2022.06.09	13	3.32 \pm 0.19	1.53 \pm 0.39	4.34 \pm 0.32	2.4 \pm 0.61	2.58 \pm 0.21
2022.06.10	14	3.84 \pm 0.12	1.62 \pm 0.20	3.92 \pm 0.15	2.58 \pm 0.13	2.35 \pm 0.42

Table S7 The DAI score of mice in Day 1-14

Date	Days	Average DAI score of mice \pm SD (n=8, g)				
		N group	D group	MP group	MPD group	DMP group
2022.05.27	1	0	0	0	0	0
2022.05.28	2	0	0	0	0	0
2022.05.29	3	0	0	0	0	0
2022.05.30	4	0	0	0	0	0
2022.06.01	5	0	0	0	0	0
2022.06.02	6	0	0	0	0	0
2022.06.03	7	0	0.6 \pm 0.2	0	0.6 \pm 0.2	0.5 \pm 0.2
2022.06.04	8	0	0.8 \pm 0.3	0	0.8 \pm 0.2	0.8 \pm 0.3
2022.06.05	9	0	3.8 \pm 0.5	0	2.2 \pm 0.5	2.4 \pm 0.5
2022.06.06	10	0.1	5.2 \pm 1.0	0.1	2.8 \pm 0.4	3.2 \pm 0.6
2022.06.07	11	0.2 \pm 0.05	7.7 \pm 0.5	0.2 \pm 0.05	2.6 \pm 0.7	4.8 \pm 0.5
2022.06.08	12	0.1 \pm 0.05	8.0 \pm 0.7	0.1 \pm 0.05	3.0 \pm 0.8	5.0 \pm 1.0
2022.06.09	13	0	9.2 \pm 1.0	0	3.5 \pm 0.5	5.2 \pm 0.75
2022.06.10	14	0	9.5 \pm 0.5	0	3.7 \pm 0.7	5.7 \pm 0.5

Table S8 The colon length of mice in Day 14

N group	colon length(cm)	D	colon length(cm)	MP	colon length(cm)	MPD	colon length(cm)	DMP	colon length(cm)
N1	7.4	D1	6.3	MP1	7.5	MPD1	8.1	DMP1	7.3
N2	7.9	D2	7.5	MP2	8.6	MPD2	7.4	DMP2	8.3
N3	8.2	D3	7.2	MP3	9.4	MPD3	7.5	DMP3	7.3
N4	8.2	D4	6.3	MP4	7.6	MPD4	7.4	DMP4	6.7
N5	7.3	D5	7.4	MP5	7.8	MPD5	7.6	DMP5	7.2
N6	8.1	D6	7.4	MP6	7.2	MPD6	7.8	DMP6	7.5
N7	9.8	D7	6.9	MP7	7.6	MPD7	6.8	DMP7	7.2
N8	7.8	D8	7.5	MP8	7.5	MPD8	7.4	DMP8	6.7

Table S9 Histopathological score of colon in mice

Group	Inflammation	Epithelium	Glands	Depth of lesion	Extent of section affected
N1	0	0	0	0	0
N2	0	0	0	0	0
N3	0	0	0	0	0
N4	0	0	0	0	0
N5	0	0	0	0	0
N6	0	0	0	0	0
N7	0	0	0	0	0
N8	0	0	0	0	0
D1	2	1	2	2	4
D2	4	1	2	2	4
D3	2	1	2	2	4
D4	3	1	3	2	4
D5	2	1	2	2	4
D6	3	1	1	2	4
D7	3	1	2	2	4
D8	3	1	1	2	4
MP1	0	0	0	0	0
MP2	0	0	0	0	0
MP3	0	0	0	0	0
MP4	0	0	0	0	0
MP5	0	0	0	0	0
MP6	0	0	0	0	0
MP7	0	0	0	0	0
MP8	0	0	0	0	0
MPD1	0	0	0	0	0
MPD2	1	1	0	1	2
MPD3	0	0	0	0	0
MPD4	1	1	0	1	2
MPD5	0	0	0	0	0
MPD6	1	0	1	1	0
MPD7	1	0	1	0	0
MPD8	1	1	0	1	1
DMP1	2	1	1	1	2
DMP2	0	0	0	0	0
DMP3	0	0	0	0	0
DMP4	1	1	0	1	0
DMP5	0	1	0	0	1
DMP6	1	0	0	0	2
DMP7	1	0	0	0	2
DMP8	0	1	0	0	2

Table S10 The number of goblet cells in mice

Group	The number of goblet cells
N1	690
N2	870
N3	960
N4	810
N5	780
N6	960
N7	1180
N8	840
D1	750
D2	900
D3	600
D4	480
D5	460
D6	510
D7	470
D8	580
MP1	980
MP2	980
MP3	930
MP4	870
MP5	2580
MP6	1130
MP7	1290
MP8	1350
MPD1	660
MPD2	590
MPD3	680
MPD4	680
MPD5	780
MPD6	630
MPD7	750
MPD8	710
DMP1	650
DMP2	840
DMP3	840
DMP4	760
DMP5	950
DMP6	720
DMP7	480
DMP8	910

Table S11 The inflammatory cytokines in colon tissues and IgA concentrations of mice

Group	IL-6 (Pg/100mg tissue)	TNF- α (Pg/100mg tissue)	IL-17 (Pg/100mg tissue)	IL-10 (Pg/100mg tissue)	IgA in serum (Pg/100mL)	IgA in colon (Pg/100mg tissue)
N1	242.061	132.648	290.452	232.590	48.333	272.3333
N2	199.725	178.379	244.724	268.816	42.049	276.0486
N3	190.291	166.240	297.259	298.634	47.333	257.3333
N4	199.778	171.897	223.619	279.137	43.259	260.259
N5	218.440	207.832	230.103	265.468	45.000	255.9853
N6	223.678	200.398	227.000	263.392	46.882	266.8817
N7	218.134	209.162	160.517	292.328	41.667	261.6667
N8	266.794	201.991	175.000	259.662	46.000	256.0896
D1	446.085	522.145	764.570	190.703	19.233	209.2328
D2	455.174	518.150	796.670	182.875	21.000	221.8755
D3	568.102	560.726	822.849	158.886	23.966	213.9662
D4	520.765	590.748	883.348	166.225	23.833	203.8333
D5	354.204	539.759	717.824	162.930	23.768	196.7676
D6	381.288	512.862	728.130	129.780	17.667	191.6667
D7	569.422	598.793	789.121	175.995	16.254	206.254
D8	425.260	564.310	800.651	170.880	27.843	197.8432
MP1	178.543	205.934	272.701	290.037	52.875	262.8746
MP2	136.271	180.103	278.445	278.612	49.037	259.0366
MP3	143.181	179.671	263.507	298.295	42.167	263.1667
MP4	114.834	180.517	292.227	211.945	43.833	253.8333
MP5	138.492	202.840	234.241	289.644	42.590	262.5896
MP6	130.165	183.614	234.931	210.269	46.816	260.8165
MP7	119.793	204.201	301.207	242.452	52.667	262.6667
MP8	205.833	200.070	300.655	208.144	46.333	266.3333
MPD1	156.292	305.349	205.429	286.456	44.544	234.5445
MPD2	183.939	313.689	206.771	215.629	45.993	245.993
MPD3	147.881	326.743	203.796	232.260	44.667	244.6667
MPD4	176.713	368.446	207.146	224.810	37.500	237.5
MPD5	149.475	387.690	203.639	209.712	41.667	251.6667
MPD6	170.439	334.586	201.955	201.667	38.333	238.3333
MPD7	187.448	438.448	208.798	201.666	40.287	250.2875
MPD8	158.103	379.931	209.171	214.544	39.004	239.0037
DMP1	284.814	408.678	349.224	216.667	34.667	244.6667
DMP2	291.742	395.360	358.276	207.676	34.667	234.6667
DMP3	274.159	363.391	356.181	196.667	33.259	233.259
DMP4	267.354	376.802	350.107	183.425	37.882	237.8817
DMP5	306.937	430.303	347.843	206.667	37.167	247.1667
DMP6	294.327	435.665	357.209	207.676	41.833	241.8333

DMP7	350.617	351.517	347.233	205.993	41.454	237.4545
DMP8	251.323	378.323	358.838	197.832	40.599	240.5993

Table S12 Quantitative analysis of Short-chain fatty acid (n=8)

Group	Sample volume	Isobutyric acid (µg/g)	Propionic acid(µg/g)	Acetic acid (µg/g)	Butyric acid (µg/g)	Isovaleric acid (µg/g)	Valeric acid (µg/g)	Caproic acid (µg/g)
N1	48.9mg	26.6334	620.9463	1982.0904	717.3936	25.2502	69.5377	1.6448
N2	50.5mg	26.5303	559.0251	1912.8187	965.2975	17.6600	54.0789	1.2753
N3	49.1mg	27.4537	569.0585	1803.6358	655.6755	19.8361	57.8265	1.4993
N4	48.9mg	32.6442	847.7422	2280.6832	1093.7807	18.7800	63.3593	1.9923
N5	49mg	37.5975	616.8835	1992.9668	844.0154	22.2219	60.7977	1.4431
N6	50.6mg	15.7612	648.1041	2527.9472	1296.9300	8.3364	69.7431	1.4060
N7	19.8326	583.2576	2198.5391	1017.7547	13.7931	55.7465	1.3713	19.8326
N8	35.7076	703.9956	1968.1749	839.947	23.5683	69.3673	1.7158	35.7076
D1	49.7mg	32.8674	535.3357	1484.2232	366.3216	18.7711	29.8479	0.7989
D2	49.9mg	26.2089	495.4817	1691.1621	299.9136	21.0980	5.2879	0.6939
D3	49.2mg	34.1680	624.2534	1794.0812	687.4768	26.0289	16.6934	0.7925
D4	51mg	30.2236	651.8890	2201.7533	559.2649	24.4708	35.8148	0.9157
D5	49.7mg	30.5209	774.0238	2282.1363	748.7211	23.6742	42.6795	0.9259
D6	49.4mg	32.0408	635.3607	2468.7272	750.6208	23.1691	51.3986	1.1037
D7	29.5867	679.8573	1906.5213	619.9683	20.8341	21.7836	0.8571	29.5867
D8	32.4231	558.924	2067.5163	517.4709	24.9132	38.7901	0.8852	32.4231
MP1	51.5mg	25.4098	450.3317	1552.5565	660.6501	18.3171	46.9584	1.4134
MP2	50.8mg	40.4907	637.2194	2074.3113	939.7332	22.1619	54.2969	1.4242
MP3	50.6mg	45.9246	473.9338	1407.9251	491.8563	29.7515	50.9166	1.2226
MP4	49.2mg	18.2328	614.2282	1786.9273	481.3931	13.1195	39.8712	0.9252
MP5	51.2mg	47.5492	636.4127	2732.2295	793.7704	33.8226	66.6506	1.1673
MP6	49.4mg	29.1841	608.3203	1822.5205	529.3429	22.5999	44.9241	1.6485

MP7	38.1769	593.8771	1995.7834	584.2911	25.1985	51.9775	1.1811	38.1769
MP8	30.7535	546.2711	1796.3759	714.6248	21.3926	49.2279	1.4194	30.7535
MPD1	50mg	23.5898	438.1210	1553.5077	358.9302	18.8529	27.4466	1.0120
MPD2	49.7mg	23.5502	542.8225	1457.0482	363.0033	12.3369	12.7836	0.6485
MPD3	26.9mg	31.4370	422.3513	1894.5737	526.5509	21.9951	36.3779	1.5406
MPD4	49.9mg	25.6169	491.7564	1640.4083	555.9081	16.4813	31.6210	0.9464
MPD5	51.6mg	30.5632	569.5995	2182.6851	538.2816	16.2014	49.3786	1.1216
MPD6	49.5mg	31.1839	403.3388	1995.4296	428.0203	23.2850	37.6171	1.0305
MPD7	29.8812	451.9817	2011.9313	492.6635	17.1323	34.7713	0.8775	29.8812
MPD8	25.4319	504.0143	1562.6169	430.9107	19.2518	30.3035	1.2225	25.4319
DMP1	50.4mg	41.8559	818.3570	1989.8679	471.7439	25.1756	54.4761	1.3071
DMP2	49.3mg	16.6283	670.0470	1797.0663	360.6276	14.2100	36.4306	0.7903
DMP3	51.1mg	22.1969	603.0992	2042.0559	492.5700	19.0941	41.4307	1.1046
DMP4	50.4mg	26.7154	717.5884	2082.5754	446.2313	20.1100	34.4263	1.1942
DMP5	49.2mg	40.3552	710.8701	1730.0449	496.1687	28.3738	47.4209	0.8710
DMP6	51.2mg	19.6447	611.7983	2116.3999	670.6687	12.8029	40.1439	1.3577
DMP7	21.8876	726.5546	1901.9342	513.8727	17.3397	44.9419	1.0511	21.8876
DMP8	33.9117	650.6981	2017.4057	465.4672	22.5823	39.8364	1.1563	33.9117

Table S13 Chao index

	Chao1				
	N	D	MP	MPD	DMP
1	969.11	731.923	535.881	607.443	754.315
2	560.865	488.314	821.676	421.078	641.581
3	643.501	688.68	824.842	587.628	837.066
4	710.571	443.508	667.286	559.752	628.428
5	858.504	346.38	748.014	454.952	703.883
6	868.743	741.913	618.074	680.846	1049.22
7	798.173	498.532	689.663	498.467	711.845
8	738.926	648.375	715.589	605.809	826.390

Table S14 Phylogenetic diversity (PD) whole tree analysis

	PD				
	N	D	MP	MPD	DMP
1	53.5719	33.0222	39.1488	35.5764	46.0047
2	33.3596	36.7102	44.9845	34.8607	42.4718
3	36.8179	32.9017	43.8329	39.0036	46.2499
4	40.1067	31.2071	40.8852	34.7189	40.038
5	41.7338	28.996	43.5444	33.1117	40.2079
6	46.2133	39.5243	40.22	41.0286	48.7896
7	39.0176	30.7781	43.0108	35.1787	46.0017
8	44.9161	36.6759	41.1939	37.5881	41.9186

Table S15 Venn diagram of OTUs

Venn-OUT	
N	1328
D	814
MP	999
MPD	955
DMP	1180

Table S16 Relative abundance at Phylum level (%)

Group	Firmicutes	Bacteroidetes	Actinobacteria	Proteobacteria	Verrucomicrobi a	Tenericute s	TM7	Deferribacteres	Cyanobacteria	other
N	33.226	61.977	2.134	1.894	0.00494	0.22	0.292	0.162	0.01446	0.03597
D	63.194	26.619	2.476	4.808	2.087	0.32	0.412	0.03104	0.02857	0.02504
MP	33.067	55.247	4.499	1.838	3.635	1.077	0.443	0.01234	0.06631	0.02575
MPD	46.967	47.075	3.762	1.66	0.00423	0.369	0.123	0.09452	0.05749	0.02363
DMP	47.408	48.498	1.258	1.432	0.08112	0.433	0.13	0.417	0.00282	0.03068

Table S17 Relative abundance of main bacteria at Phylum level (%)

Taxon	Abundance (yEr±, n=8)									
	N		D		MP		MPD		DMP	
Firmicutes	33.22614	2.36	63.19402	1.87	33.0675	1.09	46.9673	3.9	47.40815	4.76
Bacteroidetes	61.97674	2.43	26.61927	2.09	55.24745	3.09	47.07528	2.98	48.4981	1.87
Actinobacteria	2.13412	0.12	2.47552	0.21	4.49925	0.32	3.76213	0.14	1.25804	0.12
Proteobacteria	1.89359	0.18	4.80786	0.28	1.83786	0.15	1.65975	0.12	1.43227	0.18
Verrucomicrobia	1.00494	0.12	2.08686	0.13	3.63481	0.15	1.00423	0.57	1.08112	0.21

Table S18 Relative abundance at Family level (%)

Taxon	N	D	MP	MPD	DMP
Muribaculaceae	51.53406	10.57349	38.36479	29.1716	29.35514
Lachnospiraceae	14.19622	36.4738	12.1064	26.99622	28.98891
Ruminococcaceae	10.76865	22.77594	20.77302	7.38509	11.25748
Lactobacillaceae	4.86323	6.28527	16.33373	13.04476	12.39701
Erysipelotrichaceae	3.36642	3.3911	3.48457	5.23073	6.85592
Coriobacteriaceae	2.46459	2.83773	1.76344	1.40335	1.0958
Paraprevotellaceae	1.3582	0.71032	1.36244	1.84139	1.72276
Desulfovibrionaceae	3.58896	0.9378	0.33457	1.22242	0.75793
Bacteroidaceae	0.24582	3.23605	0.32165	1.90946	2.98022
Turicibacteraceae	0	0.59216	0.21831	4.76024	0.24794
Verrucomicrobiaceae	2.08686	3.63481	0.00494	0.00423	0.08112
Bifidobacteriaceae	0.0067	0.65693	1.35586	2.35067	1.15589
Rikenellaceae	0.76392	0.52092	0.70185	0.88737	1.02597
Clostridiaceae	0.17105	0.16823	0.19151	1.21254	0.35939
Mogibacteriaceae	0.34176	0.55549	0.36715	0.26981	0.56818
Odoribacteraceae	0.82282	1.04466	0.08147	0.07477	0.03739
unidentified_Bacteroidales	0.65283	0.94238	0.03033	0.22854	0.00917
Dehalobacteriaceae	0.40312	0.34422	0.31954	0.26134	0.48142
Helicobacteraceae	0.39783	0.56148	0.22995	0.13579	0.39854
F16	0.41194	0.44333	0.29203	0.12309	0.13049
other	1.55501	3.31386	1.36244	1.48658	0.09332

Table S19 Relative abundance of main bacteria at Family level (%)

Taxon	Abundance (yEr±, n=8)									
	N		D		MP		MPD		DMP	
Muribaculaceae	51.53406	2.09	10.57349	0.57	38.36479	1.38	29.1716	1.76	29.35514	2.34
Lachnospiraceae	14.19622	1.56	36.4738	2.34	12.1064	1.21	26.99622	2.09	28.98891	1.17
Ruminococcaceae	10.76865	0.56	22.77594	1.04	20.77302	0.62	6.38509	0.43	11.25748	0.68
Lactobacillaceae	4.86323	0.15	6.28527	0.28	16.33373	1.23	13.04476	0.58	12.39701	2.09
Erysipelotrichaceae	3.36642	0.34	3.3911	0.57	3.48457	0.21	5.23073	0.54	6.85592	0.19
Coriobacteriaceae	2.46459	0.11	2.83773	0.23	1.76344	0.23	1.40335	0.15	1.0958	0.18
Paraprevotellaceae	1.3582	0.12	0.71032	0.13	1.36244	0.21	1.84139	0.24	1.72276	0.32
Desulfovibrionaceae	3.58896	0.27	0.9378	0.11	0.33457	0.26	1.22242	0.15	0.75793	0.08
Bacteroidaceae	0.24582	0.002	3.23605	0.21	0.32165	0.07	1.90946	0.25	2.98022	0.38
Turicibacteraceae	0	0	0.59216	0.08	0.21831	0.02	4.76024	0.51	0.24794	0.05
Verrucomicrobiaceae	2.08686	0.29	3.63481	0.23	0.00494	0.0009	0.00423	0.00012	0.08112	0.01
Bifidobacteriaceae	0.0067	0	0.65693	0.05	1.35586	0.12	2.35067	0.21	1.15589	0.13

Table S20 Relative abundance at Genus level (%)

Taxon	N	D	MP	MPD	DMP
Norank_f_Muribaculaceae	50.42499	20.95384	37.50545	35.42584	34.40022
Lachnospiraceae_NK4A136_group	12.33202	30.74304	15.82147	16.3108	10.23221
Bacteroides	12.4083	20.25559	9.08146	7.96315	15.04895
Lactobacillus	4.86146	3.28386	16.32985	10.04194	12.39067
Oscillospira	2.21489	1.75533	4.74475	4.34067	4.9219
Adlercreutzia	2.04101	1.97576	1.51445	1.22595	0.95402
unidentified_Lachnospiraceae	0.24582	2.23605	0.32165	1.90946	2.98022
Desulfovibrio	0.9379	4.59499	1.20796	1.18292	0.33682
[Ruminococcus]	0.76921	0.58287	0.54949	1.34128	1.65517
Turicibacter	0	0.59216	0.21831	4.76024	0.24794
Akkermansia	2.08686	0.63481	2.00494	3.00423	3.08112
Ruminococcus	0.59252	0.95191	0.8461	1.15294	1.82658
[Prevotella]	0.76675	3.08747	0.26157	0.62872	0.3963
Bifidobacterium	0.0067	0.65693	1.35586	2.35067	2.15589
Coprococcus	1.17481	0.21655	0.49059	1.39524	0.6687
Paraprevotella	0.59146	0.62285	0.10087	0.21267	1.32646
Clostridium	0.09558	0.98718	0.27545	0.68069	0.27404
Odoribacter	0.82282	1.04466	0.08147	0.07477	0.03739
Dehalobacterium	0.40312	0.34422	0.31954	0.26134	0.48142
Roseburia	0.04409	0	1.6915	0	0
Helicobacter	0.39783	0.56148	0.22995	0.13579	0.39854
Sutterella	0.70785	1.1908	0.13684	0.06489	0.22784
other	6.07401	2.72764	4.91049	5.5358	5.95762

Table S21 Relative abundance of main bacteria at Genus level (%)

Taxon	Abundance (yEr±, n=8)									
	N		D		MP		MPD		DMP	
Norank_f_Muribaculaceae	50.42499	3.75	20.95384	2.18	37.50545	3.98	35.42584	2.09	34.40022	1.55
Lachnospiraceae_NK4A136_group	12.33202	1.55	30.74304	2.88	15.82147	1.21	16.3108	1.85	10.23221	0.59
Bacteroides	12.4083	0.99	20.25559	2.32	9.08146	1.09	7.96315	0.58	15.04895	1.22
Lactobacillus	4.86146	0.28	3.28386	0.33	16.32985	1.34	10.04194	1.34	12.39067	2.09
Oscillospira	2.21489	0.15	1.75533	0.12	4.74475	0.56	4.34067	0.38	4.9219	0.54
Adlercreutzia	2.04101	0.22	1.97576	0.34	1.51445	0.18	1.22595	0.18	0.95402	0.09
unidentified_Lachnospiraceae	0.24582	0.05	2.23605	0.22	0.32165	0.04	1.90946	0.18	2.98022	0.32
Desulfovibrio	0.9379	0.05	4.59499	0.58	1.20796	0.21	1.18292	0.28	0.33682	0.08
[Ruminococcus]	0.76921	0.08	0.58287	0.04	0.54949	0.09	1.34128	0.18	1.65517	0.23
Turicibacter	0	0	0.59216	0.07	0.21831	0.01	4.76024	0.48	0.24794	0.07
Akkermansia	2.08686	0.32	0.63481	0.05	2.00494	0.34	3.00423	0.18	3.08112	0.28
Ruminococcus	0.59252	0.02	0.95191	0.05	0.8461	0.04	1.15294	0.12	1.82658	0.28
[Prevotella]	0.76675	0.06	3.08747	0.08	0.26157	0.06	0.62872	0.02	0.3963	0.09
Bifidobacterium	0.0067	0	0.65693	0.06	1.35586	0.15	2.35067	0.13	2.15589	0.22
Coprococcus	1.17481	0.11	0.21655	0.01	0.49059	0.09	1.39524	0.09	0.6687	0.07
Paraprevotella	0.59146	0.09	0.62285	0.02	0.10087	0.01	0.21267	0.03	1.32646	0.21
Clostridium	0.09558	0	0.98718	0.08	0.27545	0.02	0.68069	0.08	0.27404	0.07
Odoribacter	0.82282	0.02	1.04466	0.04	0.08147	0.0021	0.07477	0.0023	0.03739	0.0012
Dehalobacterium	0.40312	0.03	0.34422	0.04	0.31954	0.019	0.26134	0.06	0.48142	0.04
Roseburia	0.04409	0	0	0	1.6915	0.23	0	0	0	0
Helicobacter	0.39783	0.09	0.56148	0.06	0.22995	0.02	0.13579	0.01	0.39854	0.04
Sutterella	0.70785	0.07	1.1908	0.11	0.13684	0.02	0.06489	0	0.22784	0.04

Table S22 The relative expression of related factors by image j software

Factors	IntDen			
	N	D	MPD	DMP
Foxp3/ β -actin	306697	122764	170371	191662
ROR γ t	141472	361345	257560	227644
JAK2	119506	289395	208853	166887
STAT3	171966	358949	246717	195183
p-STAT3	117193	388877	196600	137106
GPR41	268055	170336	349705	202707
GPR43	65358	61208	165825	190347
HDAC1	88793	106361	162583	176949
β -actin	306174	306635	305260	278700

Table S23 Correlation analysis of the 22 most dominant genera with colitis index, inflammatory factors, IgA and SCFA by R Studio software

ID	N	D	MP	MPD	DMP
Norank_f_Muribaculaceae	50.42499	20.95384	37.50545	35.42584	34.40022
Lachnospiraceae_NK4A136_group	12.33202	30.74304	15.82147	16.3108	10.23221
Bacteroides	12.4083	20.25559	9.08146	7.96315	15.04895
Lactobacillus	4.86146	3.28386	16.32985	10.04194	12.39067
Oscillospira	2.21489	1.75533	4.74475	4.34067	4.9219
Adlercreutzia	2.04101	1.97576	1.51445	1.22595	0.95402
unidentified_Lachnospiraceae	0.24582	2.23605	0.32165	1.90946	2.98022
Desulfovibrio	0.9379	4.59499	1.20796	1.18292	0.33682
[Ruminococcus]	0.76921	0.58287	0.54949	1.34128	1.65517
Turicibacter	0	0.59216	0.21831	4.76024	0.24794
Akkermansia	2.08686	0.63481	2.00494	3.00423	3.08112
Ruminococcus	0.59252	0.95191	0.8461	1.15294	1.82658
[Prevotella]	0.76675	3.08747	0.26157	0.62872	0.3963
Bifidobacterium	0.0067	0.65693	1.35586	2.35067	2.15589
Coprococcus	1.17481	0.21655	0.49059	1.39524	0.6687
Paraprevotella	0.59146	0.62285	0.10087	0.21267	1.32646
Clostridium	0.09558	0.98718	0.27545	0.68069	0.27404
Odoribacter	0.82282	1.04466	0.08147	0.07477	0.03739
Dehalobacterium	0.40312	0.34422	0.31954	0.26134	0.48142
Roseburia	0.04409	0	1.6915	0	0
Helicobacter	0.39783	0.56148	0.22995	0.13579	0.39854
Sutterella	0.70785	1.1908	0.13684	0.06489	0.22784
ID	N	D	MP	MPD	DMP

DAI scores	0	9.5	0	3.7	5.7
Colon Length	8.09	7.06	7.93	7.5	7.28
Histological score	0	11.66667	0	2.333333	2.666667
Globet cells	887.5	595	1262.5	685	767.5
IL-6	219.312	465.696	145.992	166.704	290.236
TNF- α	183.264	550.536	192.124	356.704	392.924
IL-17	231.696	787.356	272.064	205.736	353.176
IL-10	270.444	167.82	253.188	223.5	202.86
IgA	45.06	21.66	47.016	41.58	37.536
Total SCFAs	3118.788	2309.58	4639.991	3601.312	3362.874
Acetic acid	1803.636	1484.223	2732.23	2182.685	2116.4
Propionic acid	559.0251	405.4817	818.357	637.2194	569.5995
Butyric acid	655.6755	299.9136	939.7332	670.6687	555.9081
Valeric acid	54.0789	16.2879	66.6506	54.4761	49.3786
Caproic acid	1.2753	0.6939	1.6485	1.5406	1.3577
Isovaleric acid	18.3364	8.7711	33.8226	23.285	28.3738
Isobutyric acid	26.7612	15.2089	47.5492	31.437	41.8559

Table S24 The quality check data for 16S rDNA sequencing

Serial Number	sample number	Sample Name	Pre primer number	Qualified or Not	Actual fragment size (bp)	Recovery concentration (ng/ul)	Amplification remarks
1	ZTPSN22GG215	N1	P061	Qualified	500bp	6.10	/
2	ZTPSN22GG216	N2	P062	Qualified	500bp	3.58	/
3	ZTPSN22GG217	N3	P063	Qualified	500bp	4.41	/
4	ZTPSN22GG218	N4	P064	Qualified	500bp	4.07	/
5	ZTPSN22GG219	N5	P065	Qualified	500bp	4.22	/
6	ZTPSN22GG220	N6	P066	Qualified	500bp	5.55	/
7	ZTPSN22GG221	N7	P067	Qualified	500bp	4.76	/
8	ZTPSN22GG222	N8	P068	Qualified	500bp	5.01	/
9	ZTPSN22GG223	D1	P069	Qualified	500bp	4.68	/
10	ZTPSN22GG224	D2	P070	Qualified	500bp	3.01	/
11	ZTPSN22GG225	D3	P071	Qualified	500bp	4.70	/
12	ZTPSN22GG226	D4	P072	Qualified	500bp	4.63	/
13	ZTPSN22GG227	D5	P073	Qualified	500bp	4.64	/
14	ZTPSN22GG228	D6	P074	Qualified	500bp	5.26	/
15	ZTPSN22GG229	D7	P075	Qualified	500bp	4.98	/
16	ZTPSN22GG230	D8	P076	Qualified	500bp	5.29	/
17	ZTPSN22GG231	MP1	P077	Qualified	500bp	3.56	/
18	ZTPSN22GG232	MP2	P078	Qualified	500bp	5.43	/
19	ZTPSN22GG233	MP3	P079	Qualified	500bp	6.16	/
20	ZTPSN22GG234	MP4	P080	Qualified	500bp	3.60	/
21	ZTPSN22GG235	MP5	P081	Qualified	500bp	6.23	/
22	ZTPSN22GG236	MP6	P082	Qualified	500bp	4.50	/

23	ZTPSN22GG237	MP7	P083	Qualified	500bp	3.98	/
24	ZTPSN22GG238	MP8	P084	Qualified	500bp	4.54	/
25	ZTPSN22GG239	MPD1	P085	Qualified	500bp	4.87	/
26	ZTPSN22GG240	MPD2	P086	Qualified	500bp	3.40	/
27	ZTPSN22GG241	MPD3	P087	Qualified	500bp	4.55	/
28	ZTPSN22GG242	MPD4	P088	Qualified	500bp	3.32	/
29	ZTPSN22GG243	MPD5	P089	Qualified	500bp	2.30	/
30	ZTPSN22GG244	MPD6	P090	Qualified	500bp	5.70	/
31	ZTPSN22GG245	MPD7	P091	Qualified	500bp	3.98	/
32	ZTPSN22GG246	MPD8	P092	Qualified	500bp	3.45	/
33	ZTPSN22GG247	DMP1	P093	Qualified	500bp	9.32	/
34	ZTPSN22GG248	DMP2	P094	Qualified	500bp	6.40	/
35	ZTPSN22GG249	DMP3	P095	Qualified	500bp	7.40	/
36	ZTPSN22GG250	DMP4	P096	Qualified	500bp	5.49	/
37	ZTPSN22GG251	DMP5	P097	Qualified	500bp	6.64	/
38	ZTPSN22GG252	DMP6	P098	Qualified	500bp	7.24	/
39	ZTPSN22GG253	DMP7	P099	Qualified	500bp	4.09	/
40	ZTPSN22GG254	DMP8	P100	Qualified	500bp	3.97	/

Remarks:

1. The amplification regions are all standard bacteria 16S V3V4 (a), and the sequencing platform is Novaseq-PE250.
2. Amplification remarks: A: completely without bands; B: A very dispersed fragment; C: Non specific bands, no target fragments; Fill in "/" without special circumstances.
3. Description of recovery concentration: If the recovery concentration is not less than 0.5ng/ul, it meets the requirements for library construction.

