

Supplementary Materials

Supplemental Figures

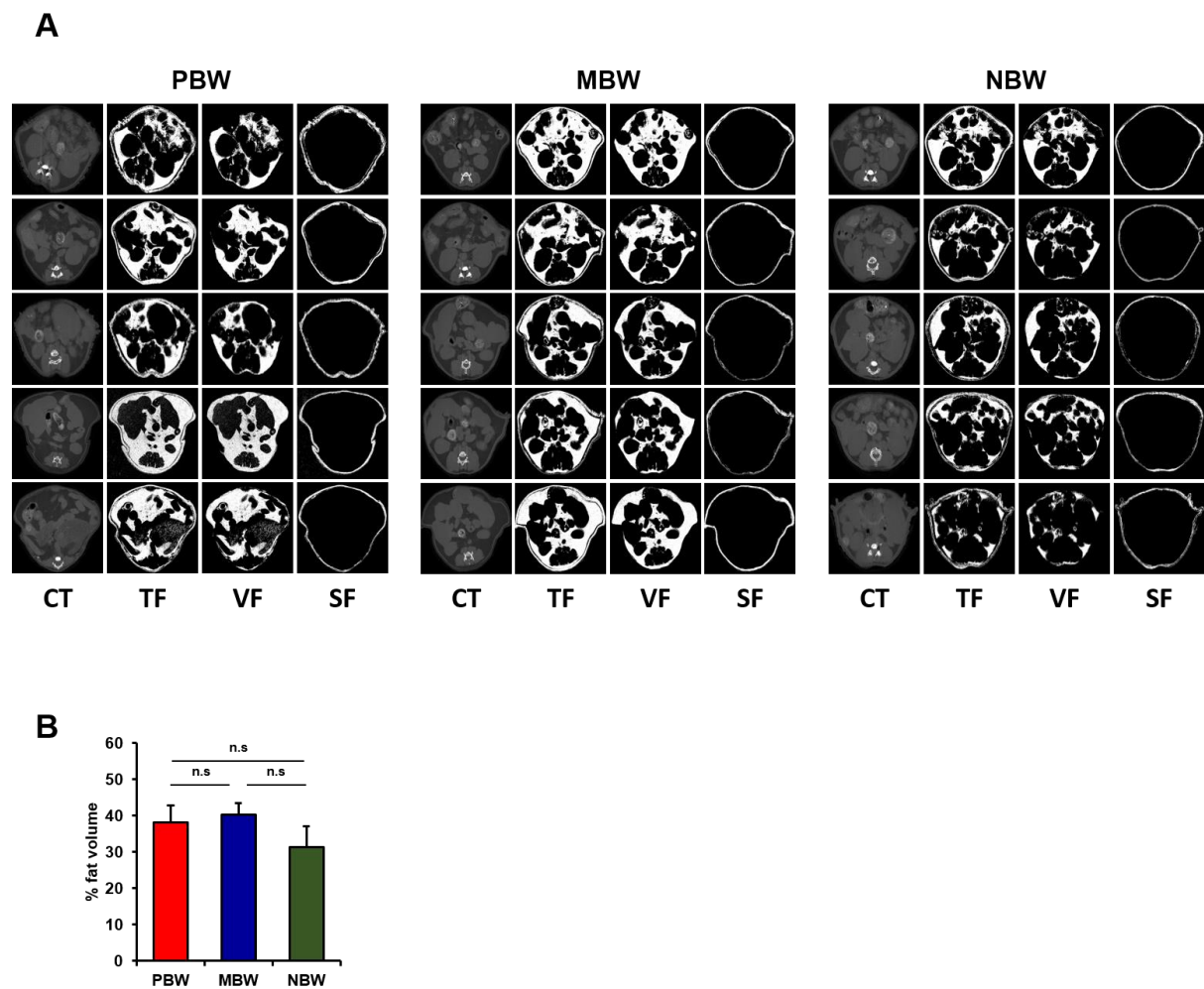


Figure S1. The representative micro-CT image of each experimental mouse of the PBW, MBW, and NBW groups three months after the gut microbiome replacement. (A) Micro-CT image, (B) The fat volume change of each group. TF, total fat; VF, visceral fat; SF, subcutaneous fat. The values are represented as mean \pm SEM. *n.s.*: not significant ($p > 0.05$).

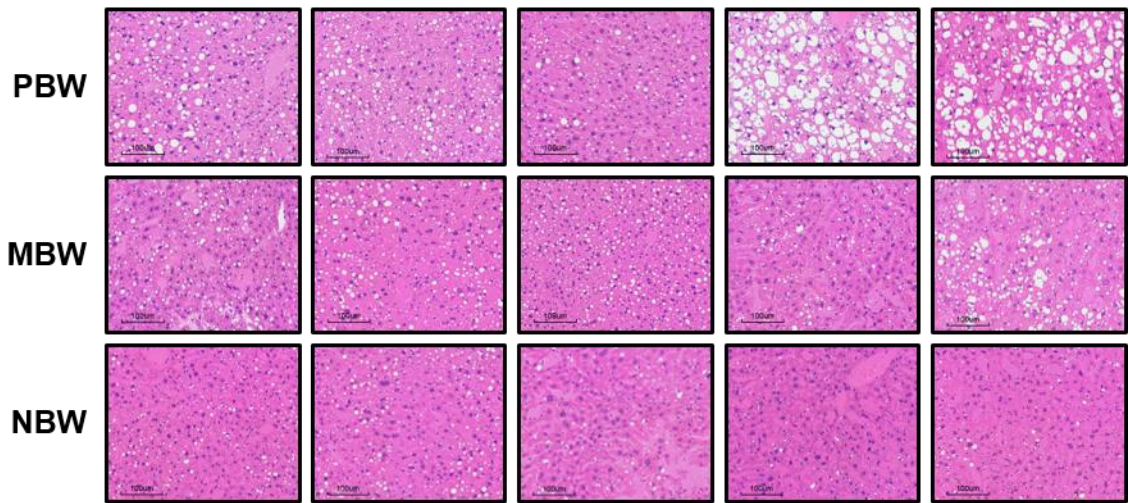
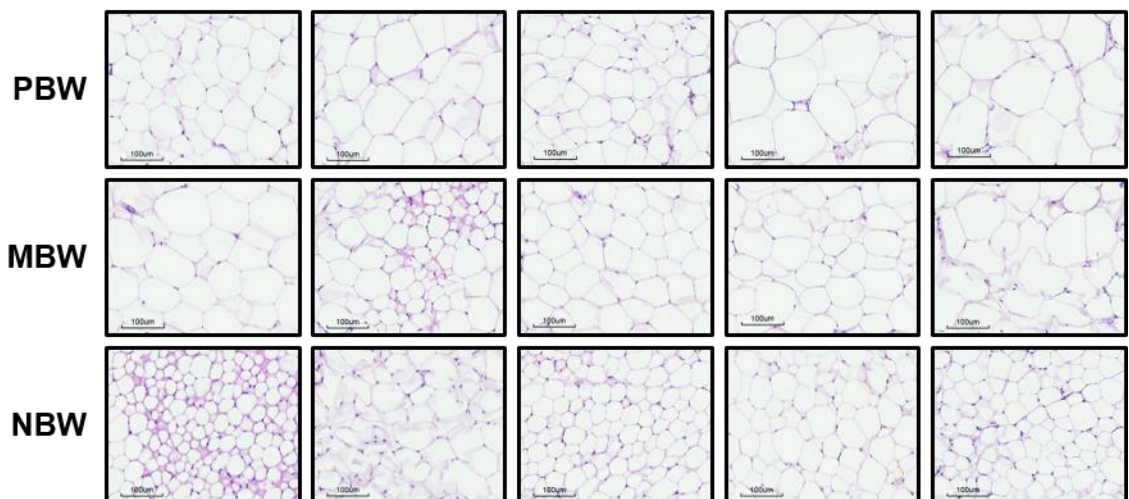
A**B**

Figure S2. The representative histological images of each experimental mouse of the PBW, MBW, and NBW groups three months after gut microbiome replacement. (A) The H&E-stained liver images. (B) The H&E-stained adipose tissue images. Scale bars, 100 µm in all the images.

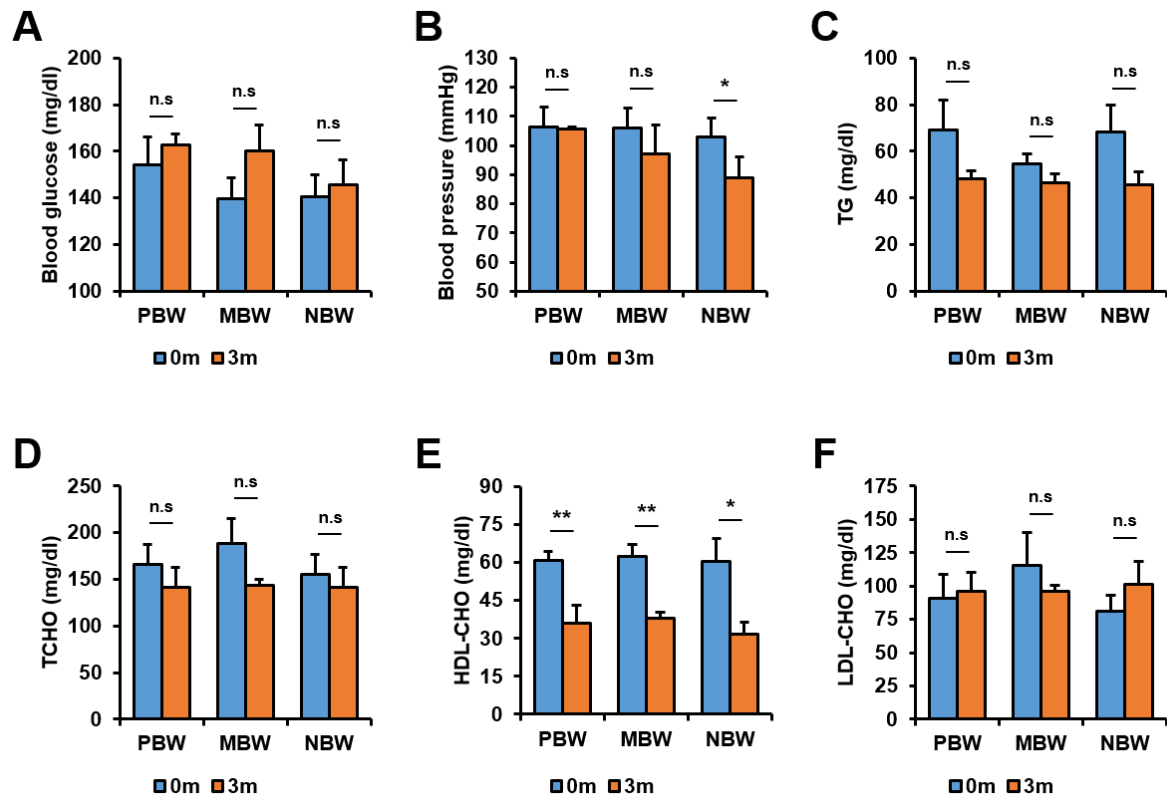
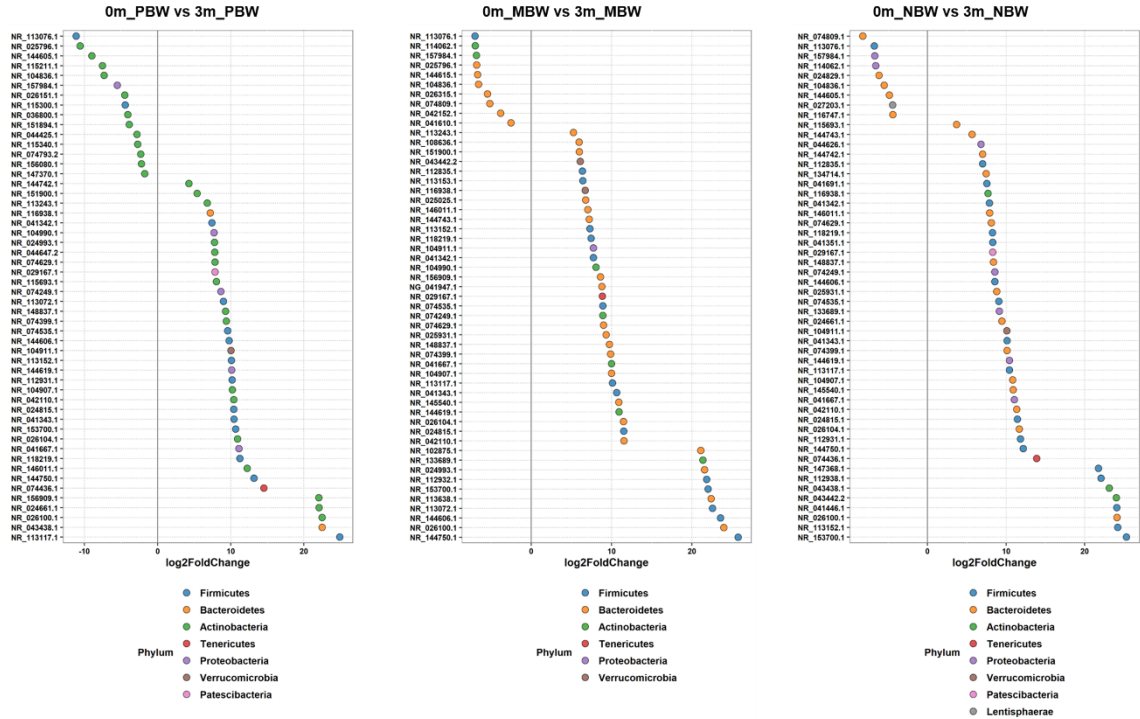


Figure S3. The effects of the gut microbiome replacement on the changes in the blood glucose, blood pressure, and lipid levels. The average values of (A) Blood glucose, (B) Blood pressure, (C) Total glycerol (TG), (D) Total cholesterol (TCHO), (E) HDL-cholesterol (HDL-CHO) (F) LDL-cholesterol (LDL-CHO) of each group are shown. The values are represented as mean \pm SEM. 0m represents before the gut microbiome replacement, and 3m represents 3 months after the gut microbiome replacement. * $p < 0.05$; ** $p < 0.01$; n.s.: not significant ($p > 0.05$).

A



B

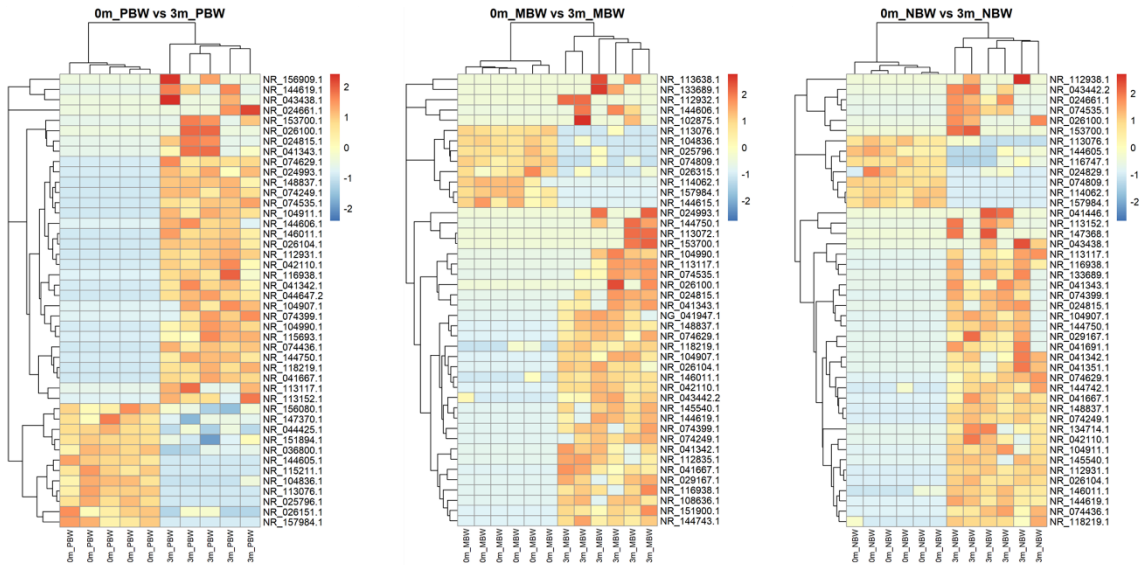


Figure S4. Differential abundance analysis of species changes of each group before and after the gut microbiome replacement. (A) Dotplots showing significantly differentially abundant OTUs, where OTUs are sorted by species along the y-axis and colored by phylum, analyzed by DESeq2 differential abundance analysis. The x-axis indicates the log2 fold-change in 3 month of each group compared to 0 month of each groups as baseline. **(B)** Heatmaps of significantly differentially abundant species in 0 month and 3 month of each group.

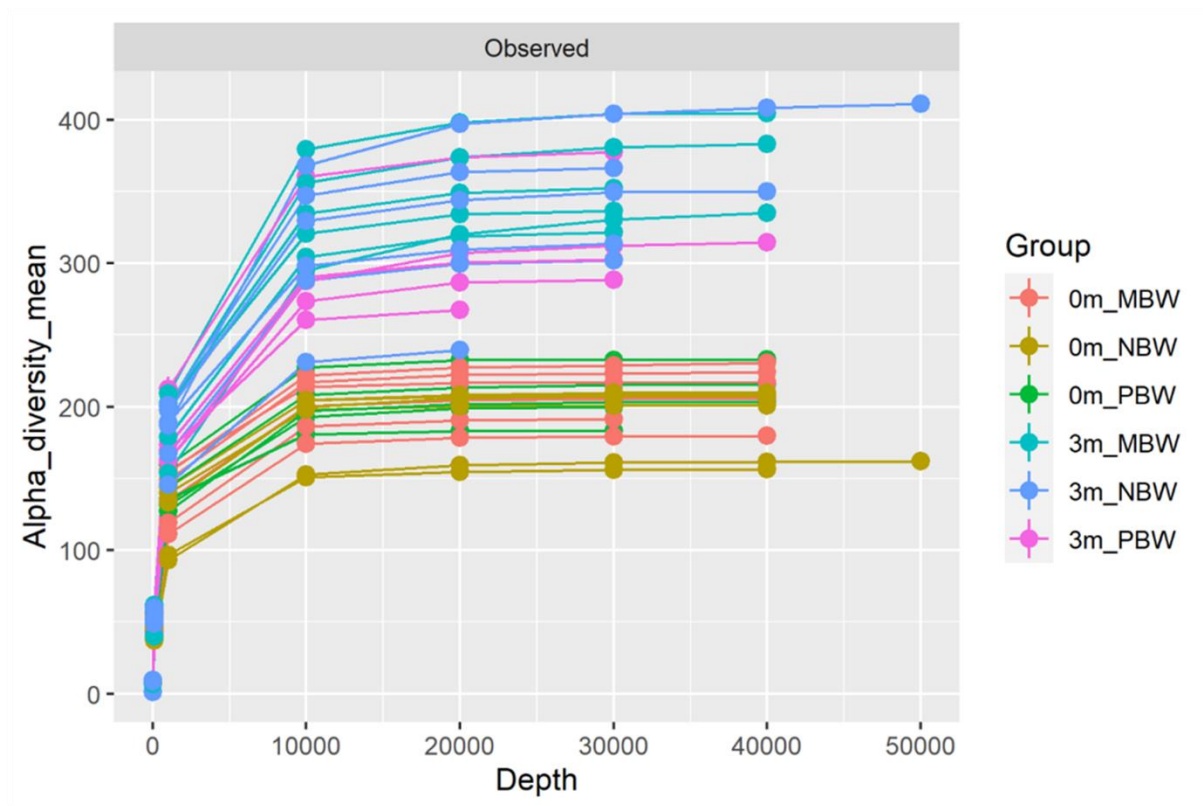


Figure S6. Rarefaction curves of each sample. Rarefaction curve constructed based on observed richness.

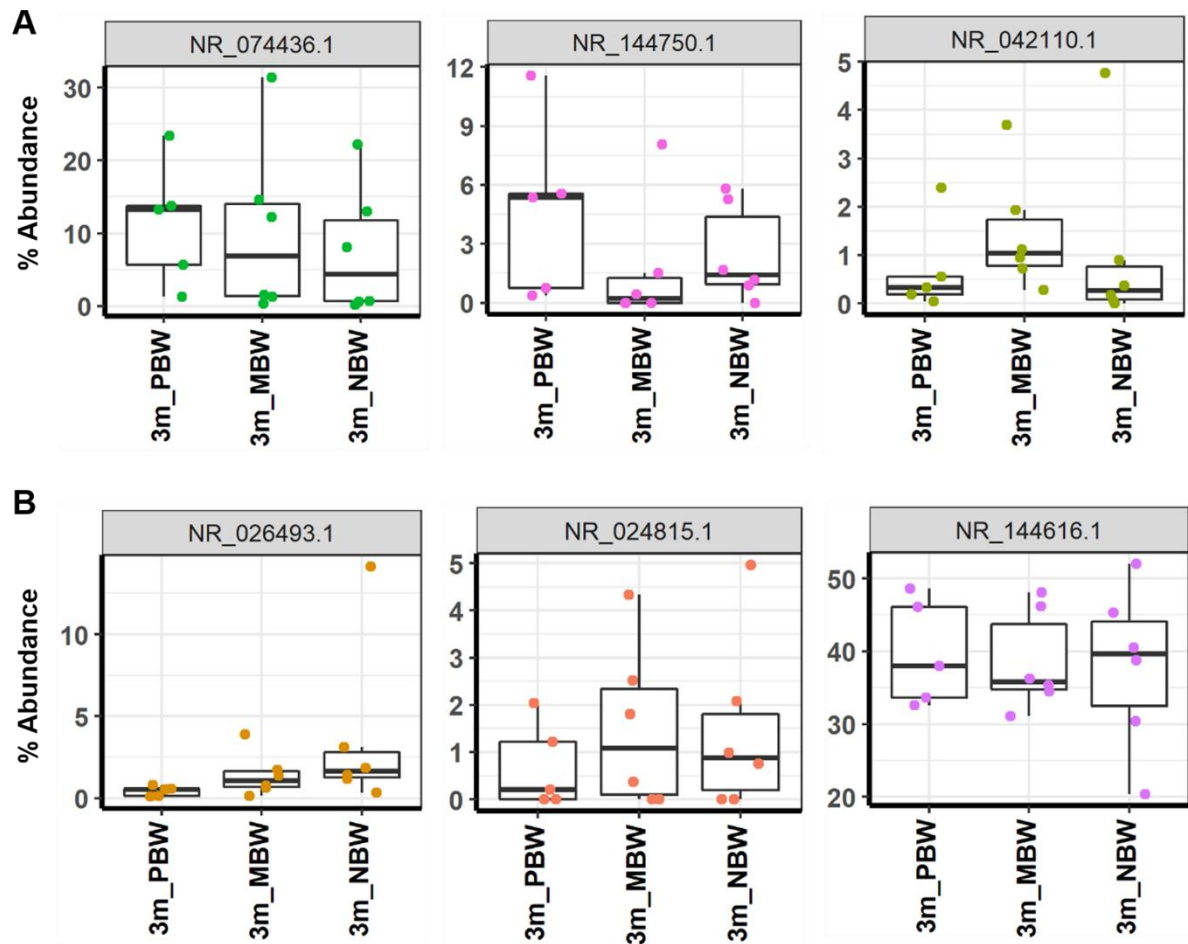


Figure S7. The relative abundance of the top 3 relatively abundant gut microbiota at the species level in PBW and NBW groups from 3 month after gut microbiome replacement. **(A)** Relative distribution by sample group of the species more abundant in the PBW group than in the NBW group. **(B)** Relative distribution by sample group of the species more abundant in the NBW group than in the PBW group.

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

Group	0m_PBW	0m_MBW	0m_NBW	3m_PBW	3m_MBW	3m_NBW
Total reads	42029 ± 3363	43137 ± 1116	44629 ± 1727	33441 ± 2994	40193 ± 2538	37144 ± 4007

All values are mean ±SEM.OTUs,operationaltaxonomic units.

Table S2. Comparison of taxonomy abundance at the phylum level.

	Phylum	0m_PBW (%)	0m_MBW (%)	0m_NBW (%)	3m_PBW (%)	3m_MBW (%)	3m_NBW (%)	Total (%)
1	D_1_Verrucomicrobia	0	0.52	0	11.48	10.23	7.44	4.94
2	D_1_Bacteroidetes	52.12	54.39	63.02	53.22	49.30	51.29	53.89
3	D_1_Firmicutes	44.99	41.44	34.23	30.73	36.61	36.85	37.47
4	D_1_Patescibacteria	2.16	2.89	2.21	0.66	0.37	0.21	1.42
5	D_1_Actinobacteria	0.23	0.07	0.08	0.81	0.66	0.84	0.450
6	D_1_Proteobacteria	0.32	0.47	0.33	2.22	2.17	2.45	1.33
7	D_1_Tenericutes	0.18	0.22	0.14	0.37	0.54	0.40	0.308
8	D_1_Cyanobacteria	0	0.002	0	0.51	0.11	0.51	0.189
9	D_1_Lentisphaerae	0	0	0	0.001	0.01	0	0.001

Table S3. Comparison of taxonomy abundance at the class level.

	Class	0m_ PBW (%)	0m_ MBW (%)	0m_ NBW (%)	3m_ PBW (%)	3m_ MBW (%)	3m_ NBW (%)
1	D_2_Verrucomicrobiae	0	0.52	0	11.48	10.23	7.44
2	D_2_Bacteroidia	52.12	54.39	63.02	53.22	49.30	51.29
3	D_2_Clostridia	42.65	38.42	30.35	24.61	30.80	31.96
4	D_2_Erysipelotrichia	0.79	0.90	0.92	4.86	4.99	3.63
5	D_2_Saccharimonadia	2.16	2.89	2.21	0.66	0.37	0.21
6	D_2_Bacilli	1.55	2.12	2.96	1.26	0.82	1.26
7	D_2_Actinobacteria	0.18	0.007	0.00	0.66	0.56	0.67
8	D_2_Coriobacteriia	0.05	0.07	0.08	0.15	0.10	0.18
9	D_2_Deltaproteobacteria	0.22	0.15	0.17	0.18	0.27	0.15
10	D_2_Gammaproteobacteria	0.08	0.28	0.10	1.66	1.52	1.60
11	D_2_Mollicutes	0.18	0.22	0.14	0.37	0.54	0.40
12	D_2_Alphaproteobacteria	0.02	0.05	0.06	0.38	0.38	0.70
13	D_2_Melainabacteria	0	0	0	0.51	0.10	0.51
14	D_2_Oxyphotobacteria	0	0.002	0	0.001	0.004	0.004
15	D_2_Lentisphaeria	0	0	0	0.001	0.005	0

Table S4. Comparison of taxonomy abundance at the order level.

	Order	0m_PBW (%)	0m_MBW (%)	0m_NBW (%)	3m_PBW (%)	3m_MBW (%)	3m_NBW (%)
1	D_3_Verrucomicrobiales	0	0.52	0	11.48	10.23	7.44
2	D_3_Bacteroidales	52.12	54.38	63.02	53.21	49.28	51.25
3	D_3_Clostridiales	42.65	38.42	30.35	24.61	30.80	31.96
4	D_3_Erysipelotrichales	0.79	0.90	0.92	4.86	4.99	3.63
5	D_3_Saccharimonadales	2.16	2.89	2.21	0.66	0.37	0.21
6	D_3_Lactobacillales	1.55	2.12	2.96	1.26	0.82	1.26
7	D_3_Bifidobacteriales	0.18	0.01	0	0.66	0.56	0.67
8	D_3_Desulfovibrionales	0.22	0.15	0.17	0.18	0.27	0.15
9	D_3_Betaproteobacteriales	0	0.01	0	1.64	1.51	1.59
10	D_3_Mollicutes RF39	0.18	0.22	0.14	0.23	0.27	0.22
11	D_3_Enterobacteriales	0.04	0.22	0.05	0.007	0.009	0.008
12	D_3_Rhodospirillales	0	0	0	0.37	0.37	0.69
13	D_3_Gastranaerophilales	0	0	0	0.51	0.10	0.51
14	Other < 0.5%	0.11	0.18	0.19	0.32	0.43	0.41

Table S5. Comparison of taxonomy abundance at the family level.

	Family	0m_ PBW (%)	0m_ MBW (%)	0m_ NBW (%)	3m_ PBW (%)	3m_ MBW (%)	3m_ NBW (%)
1	D_4_Akkermansiaceae	0	0.52	0	11.48	10.23	7.45
2	D_4_Muribaculaceae	50.92	51.90	61.60	39.81	38.65	37.93
3	D_4_Lachnospiraceae	29.14	25.88	20.04	14.75	17.32	17.69
4	D_4_Erysipelotrichaceae	0.79	0.90	0.92	4.86	4.99	3.63
5	D_4_Saccharimonadaceae	2.16	2.89	2.21	0.66	0.37	0.21
6	D_4_Tannerellaceae	0.95	1.40	1.21	0.80	0.97	0.77
7	D_4_Lactobacillaceae	1.54	2.08	2.95	1.25	0.79	1.26
8	D_4_Ruminococcaceae	10.96	9.69	7.92	8.34	12.11	12.62
9	D_4_Prevotellaceae	0	0	0	7.35	3.95	5.81
10	D_4_Bacteroidaceae	0	0.78	0	1.78	2.13	2.61
11	D_4_Clostridiales vadinBB60 group	1.42	1.12	1.36	0.73	0.92	0.82
12	D_4_Rikenellaceae	0.28	0.32	0.22	2.87	2.66	3.65
13	D_4_Bifidobacteriaceae	0.19	0.01	0	0.66	0.56	0.67
14	D_4_Desulfovibrionaceae	0.22	0.15	0.17	0.18	0.27	0.15
15	D_4_Burkholderiaceae	0	0.007	0.00	1.65	1.51	1.60
16	D_4_Peptococcaceae	0.22	0.18	0.15	0.47	0.23	0.38
17	D_4_Clostridiaceae 1	0.29	0.44	0.31	0.13	0.07	0.22
18	D_4_Marinifilaceae	0	0	0	0.64	0.96	0.52
19	D_4_Peptostreptococcaceae	0.48	0.92	0.39	0.04	0	0.06
20	D_4_uncultured bacterium	0.12	0.18	0.07	0.07	0.14	0.06
21	D_4_Enterobacteriaceae	0.04	0.22	0.05	0.007	0.009	0.008
22	D_4_uncultured	0	0	0	0.37	0.37	0.69
23	D_4_uncultured bacterium	0	0	0	0.46	0.08	0.47
24	Other < 0.5%	0.29	0.41	0.45	0.63	0.70	0.72

Table S6. Comparison of taxonomy abundance at the genus level.

	Genus	0m_ PBW (%)	0m_ MBW (%)	0m_ NBW (%)	3m_ PBW (%)	3m_ MBW (%)	3m_ NBW (%)
1	D_5_Akkermansia	0	0.66	0	12.66	11.50	8.15
2	Ambiguous_taxa	3.21	5.15	5.41	11.53	12.34	10.08
3	D_5_uncultured organism	13.77	13.90	22.18	0.48	0.34	0.52
4	D_5_uncultured bacterium	31.40	29.50	29.88	18.08	12.05	17.89
5	D_5_Turicibacter	0.93	1.09	1.18	1.71	1.82	1.27
6	D_5_uncultured Bacteroidales bacterium	1.97	1.65	1.95	6.43	9.07	6.19
7	D_5_Lachnospiraceae NK4A136 group	9.13	7.79	6.62	8.42	10.77	12.35
8	D_5_[Eubacterium] coprostanoligenes group	0.04	0.04	0.04	0.92	0.80	1.10
9	D_5_Candidatus Saccharimonas	3.07	3.93	2.92	0.76	0.44	0.24
10	D_5_Parabacteroides	1.28	1.86	1.60	0.94	1.16	0.85
11	D_5_Lactobacillus	2.08	2.74	3.93	1.39	0.91	1.42
12	D_5_Ruminiclostridium	3.30	3.06	2.37	0.44	0.82	0.47
13	D_5_Alloprevotella	0	0	0	5.52	1.97	2.87
14	D_5_Bacteroides	0	1.09	0	2.01	2.52	2.97
15	D_5_uncultured bacterium	1.06	0.81	0.70	0.35	0.57	0.42
16	D_5_Alistipes	0.37	0.43	0.29	2.18	2.99	2.46
17	D_5_Faecalibaculum	0	0.02	0.005	0.52	0.56	0.40
18	D_5_Prevotellaceae UCG-001	0	0	0	1.95	0.75	1.01
19	D_5_Muribaculum	0	0.08	0	1.14	0.87	1.10
20	D_5_Bifidobacterium	0.26	0.009	0	0.73	0.64	0.76
21	D_5_Intestinimonas	1.53	2.33	1.46	0.18	0.24	0.21
22	D_5_Dubosiella	0	0	0	2.80	2.92	2.09
23	D_5_Desulfovibrio	0.28	0.19	0.22	0.02	0.07	0.01
24	D_5_Ruminococcaceae UCG-014	2.73	1.35	1.78	3.82	6.00	6.08
25	D_5_uncultured	6.95	6.47	5.34	1.58	1.76	1.26
26	D_5_[Eubacterium] ventriosum group	0.26	0.23	0.26	0	0	0.006
27	D_5_Prevotellaceae NK3B31 group	0	0	0	0.52	1.72	1.62
28	D_5_[Eubacterium] ruminantium group	0	0	0	0.16	0	0.36
29	D_5_uncultured	0.57	0.53	0.41	0.32	0.86	1.07
30	Ambiguous_taxa	0.44	0.42	0.64	0.32	0.29	0.35
31	D_5_Blautia	0.34	0.69	0.40	0.20	0.36	0.26
32	D_5_Ruminiclostridium 9	1.36	1.29	1.10	0.55	1.13	1.06
33	D_5_Rikenellaceae RC9 gut group	0	0	0	1.12	0.13	1.44
34	D_5_uncultured	0	0	0	0.12	0.14	0.04
35	D_5_[Eubacterium] xylanophilum group	0.46	0.52	0.41	0.05	0.41	0.21
36	D_5_Lachnospiraceae UCG-001	1.65	1.07	0.97	0.19	0.23	0.14
37	D_5_Oscillibacter	1.41	1.07	0.95	0.48	0.61	0.67
38	D_5_uncultured Clostridia bacterium	0.11	0.06	0.21	0.006	0.01	0.009
39	D_5_Marvinbryantia	0.33	0.29	0.24	0.02	0.14	0.02
40	D_5_Parasutterella	0	0	0	1.83	1.74	1.77
41	D_5_Ruminococcaceae UCG-009	0.45	0.27	0.28	0.14	0.17	0.16
42	D_5_uncultured	0.27	0.22	0.18	0.50	0.25	0.41
43	D_5_Ruminococcus 1	1.20	0.06	0	1.02	1.23	1.12
44	D_5_Prevotellaceae Ga6A1 group	0	0	0	0.61	0.16	0.67
45	D_5_Ruminiclostridium 6	0.28	0.37	0.43	0.31	0.35	0.33
46	D_5_Clostridium sensu stricto 1	0.31	0.59	0.42	0.05	0.02	0.17
47	D_5_Roseburia	0.53	0.99	0.53	0.26	0.17	0.21
48	D_5_Lachnoclostridium	0.82	0.74	0.41	0.09	0.40	0.20
49	D_5_GCA-900066575	0.66	0.48	0.44	0.15	0.17	0.13
50	D_5_Odoribacter	0	0	0	0.68	1.06	0.45
51	D_5_Leibacterium	0	0	0	0.12	0.23	0.08
52	D_5_A2	0.97	0.63	0.46	0.02	0.20	0.06
53	D_5_Ruminiclostridium 5	0.47	0.85	0.43	0.09	0.18	0.20

54	D_5__Anaeroplasma	0	0	0	0.16	0.31	0.20
55	D_5__Lachnospira	0.39	0.36	0.27	0.003	0.004	0.004
56	D_5__Romboutsia	0.68	1.27	0.52	0.04	0	0.08
57	D_5__Anaerostipes	0	0	0	0.08	0.14	0.012
58	D_5__uncultured	0.05	0.08	0.001	0.15	0.14	0.10
59	D_5__Anaerotruncus	0.16	0.34	0.18	0.06	0.07	0.04
60	D_5__uncultured bacterium	0.16	0.25	0.09	0.08	0.17	0.07
61	D_5__Azospirillum sp. 47_25	0	0	0	0.20	0.23	0.18
62	D_5__Escherichia-Shigella	0.04	0.26	0.04	0.003	0.01	0.009
63	D_5__Ruminococcaceae UCG-010	0.10	0.03	0.04	0.27	0.21	0.28
64	D_5__Prevotellaceae UCG-003	0	0	0	0.009	0.06	0.53
65	D_5__Butyrivimonas	0	0	0	0.02	0.05	0.14
66	D_5__uncultured bacterium	0	0	0	0.51	0.09	0.51
67	D_5__uncultured rumen bacterium	0	0	0	0.12	0.05	0.14
68	D_5__uncultured bacterium	0	0	0	0.06	0.05	0.12
69	D_5__Lachnospiraceae NK4B4 group	0.20	0.11	0.14	0	0	0
70	D_5__Ruminococcaceae UCG-005	0.15	0.05	0.03	0.03	0.04	0.03
71	Other < 0.5%	1.83	1.73	1.68	1.69	2.09	2.19

Table S7. Comparison of taxonomy abundance at the species level.

	Species	0m_ PBW (%)	0m_ MBW (%)	0m_ NBW (%)	3m_ PBW (%)	3m_ MBW (%)	3m_ NBW (%)
1	D_6_uncultured bacterium	0	0.90	0	14.55	13.67	7.41
2	Ambiguous_taxa	3.83	6.44	6.27	13.43	14.75	12.42
3	D_6_uncultured organism	16.44	16.27	25.67	0.58	0.41	0.62
4	D_6_uncultured bacterium	37.55	34.49	34.38	21.29	14.46	22.34
5	D_6_Turicibacter sp. LA61	1.16	1.26	1.37	2.03	2.16	1.58
6	D_6_uncultured Bacteroidales bacterium	2.34	2.01	2.25	7.49	10.94	7.70
7	D_6_Trichinella pseudospiralis	0	0	0	0.26	1.58	4.84
8	D_6_Lachnospiraceae bacterium 10-1	0	0	0	2.13	0.45	1.65
9	D_6_uncultured bacterium	3.77	4.65	3.34	0.88	0.54	0.29
10	D_6_uncultured Parabacteroides sp.	1.48	2.25	1.88	0	0.02	0.01
11	D_6_Lactobacillus murinus	2.09	1.06	2.33	0.48	0.22	0.53
12	D_6_uncultured rumen bacterium	0.37	0	0	0.60	1.01	1.43
13	D_6_uncultured bacterium	3.97	3.65	2.72	0.49	0.97	0.59
14	D_6_gut metagenome	0	0	0	6.57	2.42	3.64
15	D_6_uncultured bacterium	1.28	0.98	0.81	0.40	0.69	0.54
16	D_6_uncultured bacterium	0	0.01	0.007	1.88	2.96	2.39
17	D_6_uncultured bacterium	3.97	4.77	2.73	2.35	3.27	2.37
18	D_6_uncultured bacterium	0	0.02	0.005	0.60	0.66	0.48
19	D_6_uncultured bacterium	0	0.10	0	1.35	1.05	1.37
20	D_6_uncultured bacterium	1.84	2.88	1.67	0.09	0.13	0.09
21	D_6_uncultured bacterium	0	0	0	3.16	3.43	1.49
22	D_6_uncultured bacterium	0.35	0.24	0.26	0.03	0.08	0.01
23	D_6_Clostridiales bacterium CIEAF 020	0	0	0	0.33	0.86	1.28
24	D_6_Bacteroides caecimuris	0	0	0	0.61	0.48	0.29
25	D_6_Bacteroides acidifaciens	0	0	0	0.38	0.25	0.09
26	D_6_uncultured bacterium	0.61	0.64	0.69	0.36	0.43	0.57
27	D_6_uncultured bacterium	0	0	0	0.63	2.07	2.11
28	D_6_uncultured bacterium	3.94	3.55	2.53	0.96	1.29	1.08
29	D_6_uncultured bacterium	0	0	0	0.20	0	0.45
30	D_6_Clostridium sp. Culture-1	0.23	0.18	0.18	0.15	0.61	1.11
31	Ambiguous_taxa	0.53	0.53	0.75	0.37	0.35	0.44
32	D_6_unidentified	0.43	0.25	0.27	0.35	0.44	0.27
33	D_6_uncultured Bacteroidales bacterium	0	0	0.00	0.96	1.13	0.76
34	D_6_uncultured Clostridiales bacterium	0.81	0.49	0.36	1.18	1.80	0.14
35	Ambiguous_taxa	0	0	0	1.19	0.16	1.69
36	Ambiguous_taxa	0	0	0	0.14	0.17	0.05
37	D_6_uncultured bacterium	0.56	0.61	0.47	0.06	0.50	0.26
38	D_6_uncultured bacterium	1.94	1.25	1.13	0.23	0.25	0.18
39	D_6_uncultured organism	0	0	0	0.41	0.11	0.34
40	D_6_unidentified	0.83	0.44	0.27	0.18	0.16	0.15
41	D_6_Parabacteroides distasonis	0	0	0	0.05	0.14	0.18
42	D_6_Lachnospiraceae bacterium COE1	0.34	0.50	0.38	0.08	0.47	0.32
43	D_6_uncultured Clostridia bacterium	0.12	0.06	0.24	0.008	0.01	0.01
44	D_6_uncultured bacterium	0.32	0.28	0.21	0.00	0.15	0.00
45	D_6_Bacteroides dorei	0	0	0	0.07	0.06	0.27
46	D_6_uncultured bacterium	0	0	0	1.20	0.29	0.63
47	Ambiguous_taxa	0.54	0.32	0.33	0.16	0.20	0.19
48	D_6_uncultured bacterium	0.32	0.26	0.21	0.18	0.20	0.17
49	D_6_Firmicutes bacterium M10-2	0	0	0	0	0	1.03
50	Ambiguous_taxa	0	0	0	0.69	0.18	0.85
51	D_6_uncultured bacterium	0.12	0.23	0.43	0.39	1.11	1.11
52	D_6_uncultured bacterium	0	0	0	0.29	0.30	0.42

53	D_6_uncultured bacterium	0.69	0.55	0.50	0.37	0.78	0.85
54	D_6_uncultured bacterium	0.38	0.70	0.48	0.06	0.03	0.22
55	D_6_uncultured bacterium	0.39	0.86	0.33	0.09	0.09	0.12
56	D_6_uncultured bacterium	0.56	0.43	0.18	0.05	0.32	0.19
57	D_6_uncultured bacterium	0.56	0.43	0.35	0.08	0.17	0.15
58	D_6_uncultured bacterium	0	0	0	0.57	0.95	0.21
59	D_6_Lactobacillus reuteri	0.04	0.16	0.20	0.18	0.07	0.13
60	Ambiguous_taxa	0	0	0	0.14	0.28	0.09
61	D_6_Lachnospiraceae bacterium A2	0.75	0.51	0.37	0	0.01	0.006
62	Ambiguous_taxa	0.47	0.71	0.38	0.03	0.09	0.07
63	D_6_uncultured bacterium	0	0	0	0.19	0.38	0.24
64	D_6_uncultured bacterium	0	0	0	0.34	0.09	0.14
65	D_6_Burkholderiales bacterium YL45	0	0	0	0.69	1.27	0.87
66	D_6_mouse gut metagenome	0.16	0.28	0.17	0	0	0
67	Ambiguous_taxa	0	0	0	0.03	0.13	0.01
68	D_6_uncultured bacterium	0.07	0.11	0.002	0.17	0.17	0.13
69	D_6_uncultured bacterium	0.20	0.43	0.20	0.08	0.09	0.05
70	Ambiguous_taxa	0	0.00	0	0.24	0.27	0.33
71	D_6_Clostridium sp. Culture-27	0.46	0.24	0.38	0.02	0.05	0.01
72	D_6_uncultured bacterium	0.19	0.29	0.10	0.10	0.20	0.09
73	D_6_Azospirillum sp. 47_25	0	0	0	0.24	0.27	0.22
74	D_6_gut metagenome	0	0	0	0.35	0.24	0.38
75	D_6_uncultured bacterium	0	0	0	0.01	0.07	0.70
76	D_6_uncultured bacterium	0.42	0.28	0.16	0.03	0.05	0.07
77	D_6_uncultured bacterium	0	0	0	0	0	0.28
78	D_6_uncultured rumen bacterium	0.03	0	0.09	0.11	0.08	0.06
79	D_6_uncultured bacterium	0	0	0	0.59	0.11	0.67
80	D_6_uncultured rumen bacterium	0	0	0	0.14	0.06	0.16
81	Ambiguous_taxa	0	0	0	0	0	0.13
82	D_6_uncultured organism	0	0	0	0.13	0.04	0.02
83	D_6_uncultured bacterium	0	0	0	0.25	0.18	0.12
84	D_6_Bacteroides massiliensis B84634	0	0	0	0.03	0.30	0.20
85	D_6_uncultured bacterium	0	0	0	0.07	0.06	0.14
86	D_6_uncultured bacterium	0.23	0.14	0.16	0	0	0
87	Ambiguous_taxa	0	0	0	0	0	0.11
88	D_6_uncultured bacterium	0.02	0.15	0.02	0.02	0.00	0.009
89	D_6_uncultured bacterium	0	0	0	0.13	0	0
90	D_6_uncultured Clostridiales bacterium	0	0	0	0.07	0.02	0.15
91	D_6_Clostridium sp. Clone-44	0.02	0.12	0.11	0	0	0
92	Ambiguous_taxa	0	0	0	0	0.18	0
93	D_6_uncultured bacterium	0	0	0	0	0	0.09
94	Other < 0.5%	2.27	2.02	1.69	1.98	2.89	2.31

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

Sample	Observed	ACE	Shannon	Simpson	InvSimpson	Fisher
0m_PBW_1	204	204.15	3.99	0.961	25.94	27.52
0m_PBW_2	234	234.00	4.52	0.980	49.80	31.97
0m_PBW_3	217	217.43	4.16	0.967	29.92	29.26
0m_PBW_4	201	201.00	4.19	0.973	36.42	28.32
0m_PBW_5	184	184.25	4.18	0.969	32.40	25.63
0m_MBW_1	225	225.48	4.30	0.973	37.32	31.04
0m_MBW_2	206	206.15	4.10	0.965	28.67	28.21
0m_MBW_3	217	217.00	4.44	0.978	44.45	29.98
0m_MBW_4	181	181.21	3.83	0.957	23.27	23.87
0m_MBW_5	232	232.76	4.36	0.974	38.29	31.95
0m_MBW_6	194	194.64	4.03	0.966	29.34	26.57
0m_NBW_1	158	158.32	3.57	0.935	15.30	20.55
0m_NBW_2	212	212.47	4.29	0.972	36.12	29.26
0m_NBW_3	201	201.00	4.03	0.960	25.02	27.58
0m_NBW_4	162	162.00	3.64	0.952	20.98	20.68
0m_NBW_5	208	208.00	4.02	0.958	23.63	28.25
0m_NBW_6	210	210.00	4.26	0.973	37.50	28.51
3m_PBW_1	270	270.76	4.12	0.935	15.28	43.19
3m_PBW_2	305	305.46	4.39	0.969	32.70	46.08
3m_PBW_3	291	291.31	4.34	0.969	32.71	43.50
3m_PBW_4	318	319.11	3.97	0.946	18.43	47.03
3m_PBW_5	383	384.08	4.66	0.969	31.93	60.19
3m_MBW_1	356	356.61	4.62	0.968	31.15	54.17
3m_MBW_2	410	411.15	4.66	0.972	35.20	62.43
3m_MBW_3	339	339.73	4.76	0.981	52.98	52.19
3m_MBW_4	386	386.31	4.61	0.969	32.24	59.04
3m_MBW_5	326	326.56	4.43	0.967	29.89	50.19
3m_MBW_6	343	344.93	3.58	0.882	8.49	49.63
3m_NBW_1	318	320.19	4.71	0.983	58.02	48.07
3m_NBW_2	307	309.10	4.23	0.955	22.34	46.82
3m_NBW_3	371	371.48	4.68	0.976	41.95	57.05
3m_NBW_4	352	352.16	4.63	0.973	36.62	53.01
3m_NBW_5	246	249.46	4.28	0.970	33.60	38.53
3m_NBW_6	418	420.38	4.27	0.957	23.18	61.94

Group	Observed	ACE	Shannon	Simpson	InvSimpson	Fisher
0m_PBW	208	208.17	4.21	0.970	34.89	28.54
0m_MBW	209.17	209.54	4.18	0.969	33.56	28.60
0m_NBW	191.83	191.97	3.97	0.958	26.43	25.81
3m_PBW	313.40	314.14	4.30	0.958	26.21	48.00
3m_MBW	360	360.88	4.44	0.956	31.66	54.61
3m_NBW	335.33	337.13	4.47	0.969	35.95	50.90

Table S9. The co-occurrence network indices.

Network indexes indices	0m_ PBW	0m_ MBW	0m_ NBW	3m_ PBW	3m_ MBW	3m_ NBW
Node	120	120	113	150	157	158
Edge	133	123	129	138	153	149
Network Density	0.019	0.017	0.020	0.012	0.012	0.012
Assortativity	-0.013	-0.013	-0.015	-0.009	-0.009	-0.008
Module	34	37	33	45	30	47
Modularity	0.894	0.895	0.817	0.929	0.951	0.957

Table S10. The taxonomic classification of the intestinal microbes most different between PBW and NBW groups.

Most abundant in PBW			
Rank	1	2	3
OUT	OTU0001	OTU0039	OTU0083
Kingdom	D_0__Bacteria	D_0__Bacteria	D_0__Bacteria
Phylum	D_1__Verrucomicrobia	D_1__Bacteroidetes	D_1__Firmicutes
Class	D_2__Verrucomicrobiae	D_2__Bacteroidia	D_2__Erysipelotrichia
Order	D_3__Verrucomicrobiales	D_3__Bacteroidales	D_3__Erysipelotrichales
Family	D_4__Akkermansiaceae	D_4__Prevotellaceae	D_4__Erysipelotrichaceae
Genus	D_5__Akkermansia	D_5__Alloprevotella	D_5__Dubosiella
Species	D_6__uncultured bacterium	D_6__uncultured bacterium	D_6__uncultured bacterium
sseqid	NR_074436.1	NR_144750.1	NR_042110.1

Most abundant in NBW			
Rank	1	2	3
OUT	OTU0024	OTU0108	OTU0004
Kingdom	D_0__Bacteria	D_0__Bacteria	D_0__Bacteria
Phylum	D_1__Firmicutes	D_1__Bacteroidetes	D_1__Bacteroidetes
Class	D_2__Clostridia	D_2__Bacteroidia	D_2__Bacteroidia
Order	D_3__Clostridiales	D_3__Bacteroidales	D_3__Bacteroidales
Family	D_4__Lachnospiraceae	D_4__Prevotellaceae	D_4__Muribaculaceae
Genus	D_5__Lachnospiraceae NK4A136 group	D_5__Prevotellaceae NK3B31 group	D_5__uncultured bacterium
Species	D_6__Trichinella pseudospiralis	D_6__uncultured bacterium	D_6__uncultured bacterium
sseqid	NR_026493.1	NR_024815.1	NR_144616.1