

SUPPLEMENTAL INFORMATION TITLES AND LEGENDS

Supplemental Figures

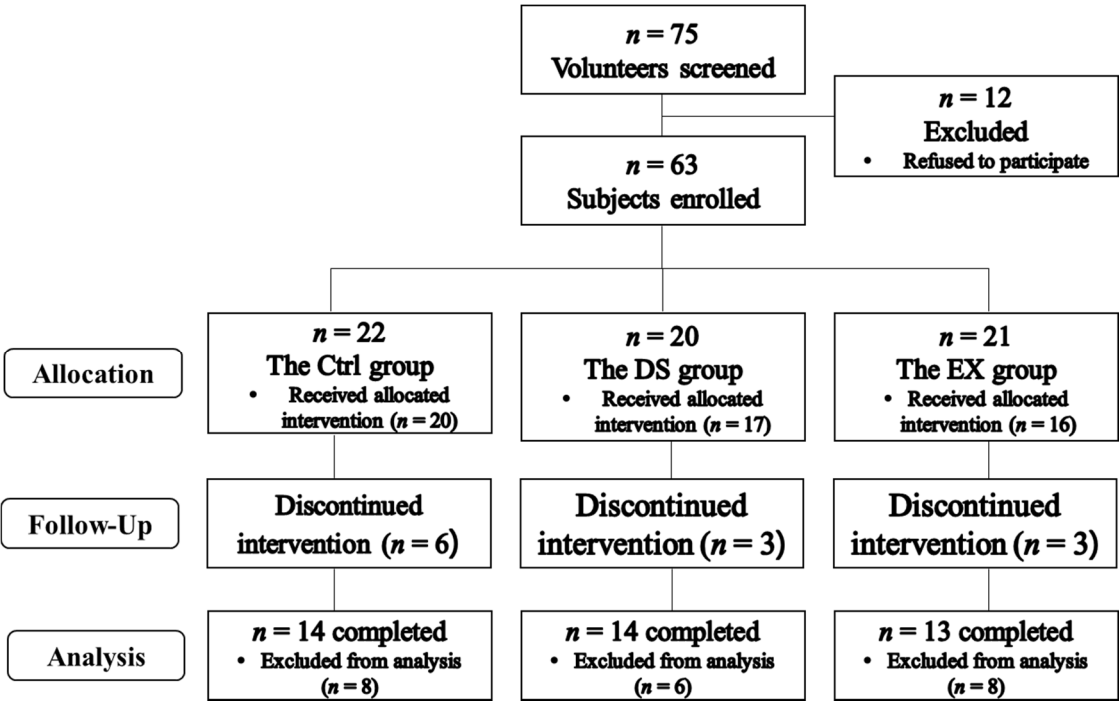


Figure S1. Flow chart for the study subjects. The Ctrl, DS, and EX represents the control, diet shift, and exercise groups each.

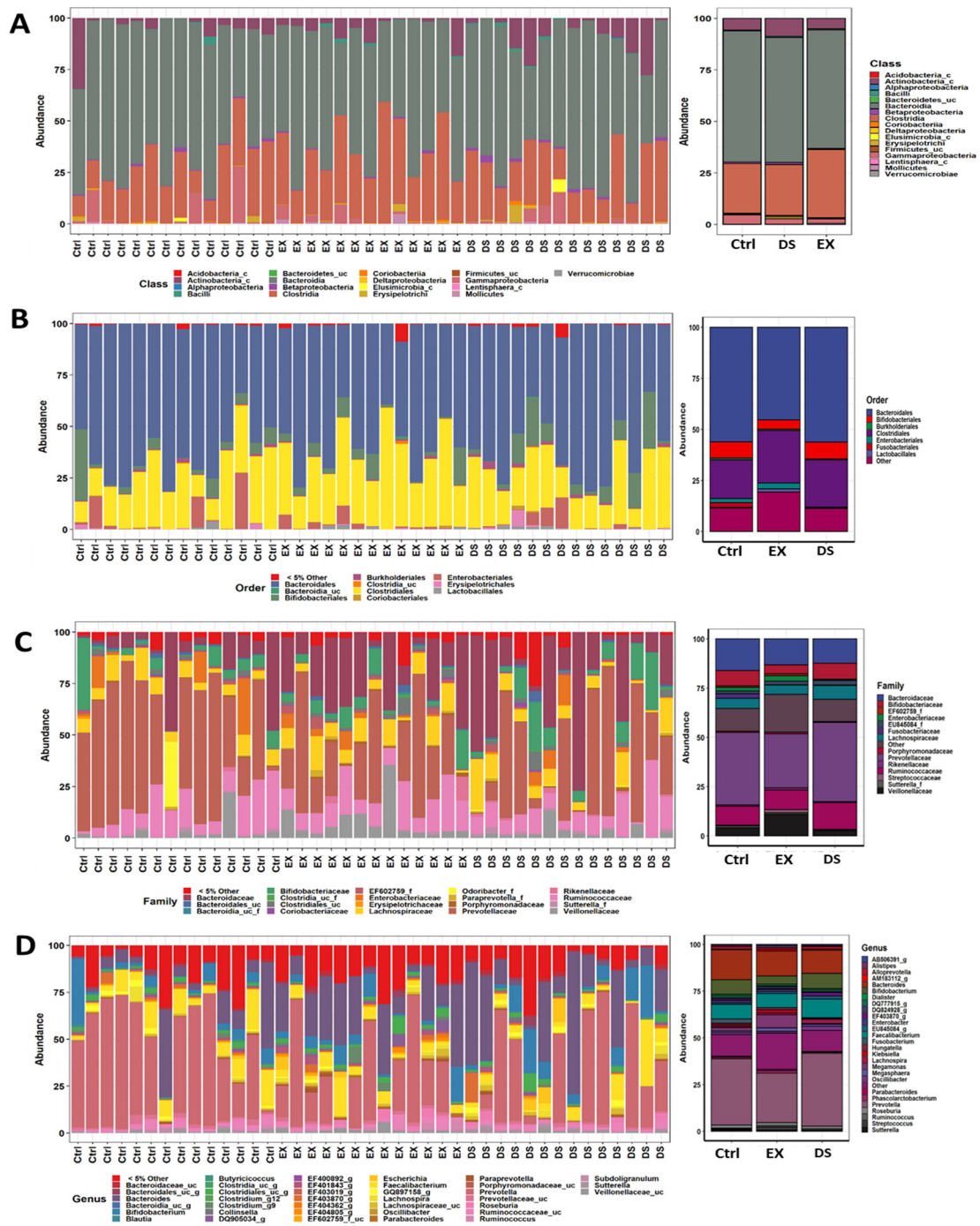
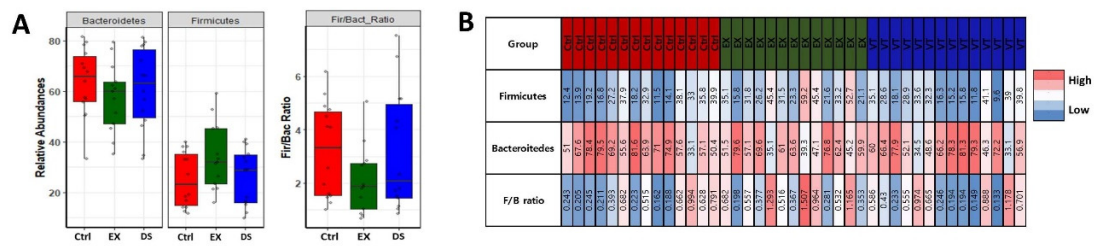
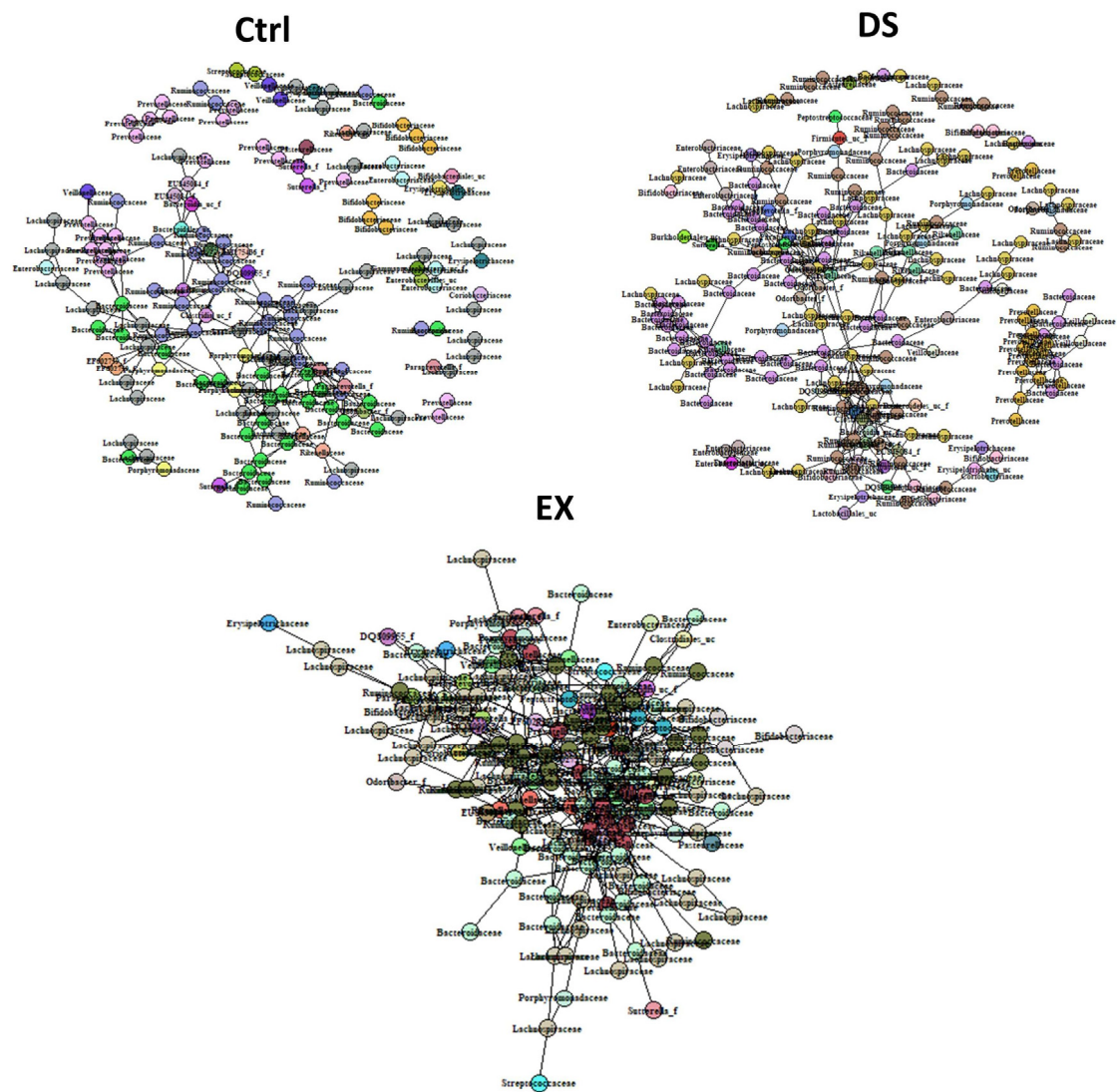


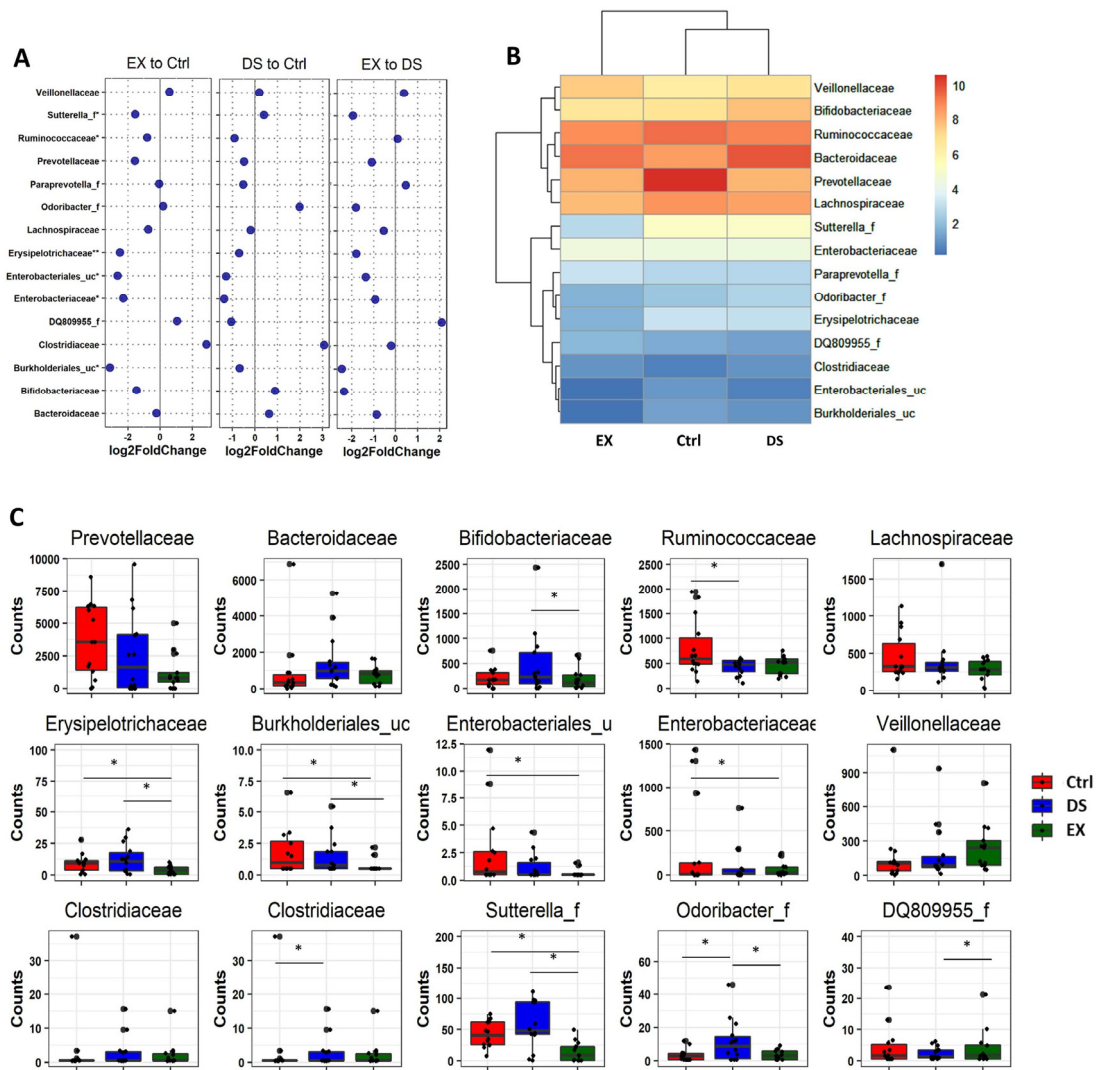
Figure S2. The composition changes of gut microbiome after diet shift or exercise. The composition changes of gut microbiome at (A) class levels (B) order levels (C) family levels and (D) genus during the 12 week experimental period are shown. The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.



**Figure S3. The abundance change of Bacteroidetes and Firmicutes in the gut microbiome in the three experimental groups.** The Ctrl, EX and DS represents the control, exercise, and diet shift groups each. .



**Figure S4. Co-occurrence network analysis by the ReBoot algorithm for the Ctrl, EX, and DS groups.** Color-coded network graph representations of the co-occurrence interactions among OTUs in family level.



**Figure S5. The most significantly changed microbes at family level by differential abundance analysis.** (A) Log2 fold change of abundance on most abundantly present families in the gut microbiome of the three experimental groups analyzed by DESeq2 differential abundance analysis. Each point represents a species comparison between two experimental groups. (B) Heatmap of most abundantly present species in the three experimental groups. (C) Normalized abundances of significantly different 15 families of interest that were identified from differential abundance analyses. Boxplot represent normalized count abundances of individual species in each group.  $p$  value  $< 0.05$  was considered as significant. The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.

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

Group	Ctrl	EX	DS
<b>Total reads</b>	7664±2045	3275±165	8928±1198

All values are the mean±SEM. OTUs, operational taxonomic units; Ctrl, the control group; Ex, the physical exercise group; DS, the vegetarian diet group.

**Table S2. The  $\alpha$ -diversity indexes for each sample.  $p$  value calculated by Kruskal-Wallis test, and Wilcoxon sum test was used for group comparison. The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.**

Group	ACE	se.ACE	Shannon	Simpson	InvSimpson	Fisher	Evenness
Ctrl	254.94	8.30	2.86	0.85	6.47	35.84	0.52
Ctrl	288.78	8.82	3.15	0.88	8.39	40.23	0.56
Ctrl	399.07	10.02	3.28	0.90	9.74	51.29	0.55
Ctrl	290.28	9.13	2.79	0.88	8.25	30.74	0.49
Ctrl	252.85	8.32	3.37	0.93	13.35	33.90	0.61
Ctrl	245.04	8.17	3.81	0.96	22.34	41.74	0.69
Ctrl	277.56	8.90	2.90	0.86	7.18	30.34	0.52
Ctrl	269.96	8.44	3.92	0.96	26.14	46.38	0.70
Ctrl	299.64	9.68	3.61	0.94	15.92	46.12	0.63
Ctrl	274.45	8.98	3.54	0.93	15.35	41.76	0.63
Ctrl	215.64	7.78	3.62	0.94	15.60	35.85	0.67
Ctrl	343.96	10.05	4.18	0.97	28.66	64.01	0.72
Ctrl	242.89	8.82	3.40	0.94	15.76	36.67	0.62
Ctrl	200.30	7.47	3.51	0.94	16.64	30.61	0.66
EX	260.31	8.31	3.96	0.96	24.44	44.25	0.71
EX	230.76	7.99	2.72	0.79	4.76	33.03	0.50
EX	297.10	8.81	4.41	0.98	49.36	58.50	0.78
EX	256.62	7.97	4.02	0.96	25.09	50.27	0.72
EX	234.80	7.82	3.91	0.96	26.89	42.36	0.72
EX	142.47	6.37	3.69	0.96	23.16	33.02	0.74
EX	244.33	8.84	3.67	0.95	19.10	37.02	0.67
EX	160.22	6.29	3.18	0.91	10.58	26.01	0.63
EX	309.78	9.48	4.18	0.97	30.11	57.79	0.73
EX	310.26	9.54	3.59	0.93	13.72	44.36	0.63
EX	282.15	9.84	3.87	0.95	21.34	43.65	0.69
EX	314.10	9.22	4.32	0.97	37.29	63.44	0.75
EX	240.73	9.00	3.15	0.91	10.59	31.20	0.57
DS	353.45	9.95	3.61	0.94	16.56	47.48	0.62
DS	350.40	9.45	4.07	0.97	29.45	53.76	0.69
DS	399.62	10.38	3.37	0.89	8.96	52.12	0.56
DS	349.99	10.12	3.80	0.95	19.08	52.27	0.65
DS	341.50	9.78	3.90	0.95	21.72	55.46	0.67
DS	311.02	9.07	3.75	0.95	19.72	40.71	0.65
DS	405.98	10.70	3.66	0.95	19.66	54.19	0.61
DS	157.14	6.57	3.08	0.90	9.89	25.21	0.61
DS	350.53	9.47	3.14	0.87	7.73	46.25	0.54
DS	223.13	7.43	3.21	0.90	10.45	31.11	0.59
DS	311.94	8.91	3.97	0.96	26.27	53.19	0.69
DS	192.07	7.62	2.77	0.84	6.20	24.17	0.53
DS	153.86	7.20	2.47	0.86	7.31	15.31	0.49
DS	406.30	10.47	3.93	0.95	19.89	60.14	0.65
Kruskal-Wallis $p$ value	0.09	0.28	0.15	0.10	0.10	0.47	<b>0.02</b>
$p$ value CvsE	0.27	0.35	0.08	0.28	0.05	0.46	<b>0.03</b>
$p$ value CvsD	0.25	0.47	0.74	0.90	0.73	0.47	0.98
$p$ value DvsE	0.06	0.18	0.17	0.34	0.09	0.97	<b>0.02</b>

**Table S3. Comparison of taxonomy abundance at Phylum level.** The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.

	<b>Phylum</b>	<b>Ctrl (%)</b>	<b>DS (%)</b>	<b>EX (%)</b>
1	Bacteroidetes	63.57	60.65	57.55
2	Firmicutes	25.02	26.02	34.02
3	Proteobacteria	5.21	3.77	2.48
4	Actinobacteria	5.91	8.92	5.3
5	Elusimicrobia	0.11	0.44	0
6	Tenericutes	0.11	0.18	0.6
7	Lentisphaerae	0.07	0.03	0.01
8	Verrucomicrobia	0	0	0.04
9	Acidobacteria	0	0	0.01



**Table S4. Co-occurrence network indices.** The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.

Network Indexes indices	Ctrl	DS	EX
Node	161	205	171
Edge	274	397	535
Network Density	0.021	0.019	0.037
Assortativity	-0.010	-0.008	-0.009
Module	28	20	8
Network Heterogeneity	0.613	0.718	0.676
Network Centralization	0.11	0.071	0.084
Clustering coefficient	0.424	0.336	0.347
Average Number of Neighbors	4.465	4.09	4.693

**Table S5. The comparison of the abundance of the phyla constituting the gut microbiome of the three experimental groups by DESeq2 differential abundance analysis. The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.**

**DS to Ctrl**

	<b>Phylum</b>	<b>baseMean</b>	<b>log2FoldChange</b>	<b>lfcSE</b>	<b>stat</b>	<b>pvalue</b>	<b>padj</b>
6	Tenericutes	13.522	-0.544	1.414	-0.385	0.700	0.909
8	Verrucomicrobia	0.637	-0.453	3.572	-0.127	0.899	0.909
4	Actinobacteria	316.759	-0.385	0.616	-0.624	0.532	0.909
3	Firmicutes	1471.933	0.187	0.267	0.700	0.484	0.909
2	Bacteroidetes	3454.093	0.347	0.295	1.173	0.241	0.909
9	Elusimicrobia	0.017	0.408	3.573	0.114	0.909	0.909
7	Acidobacteria	0.112	0.869	3.573	0.243	0.808	0.909
5	Lentisphaerae	1.018	0.966	2.410	0.401	0.689	0.909
1	Proteobacteria	152.004	1.304	0.546	2.387	0.017	0.153

**EX to Ctrl**

	<b>Phylum</b>	<b>baseMean</b>	<b>log2FoldChange</b>	<b>lfcSE</b>	<b>stat</b>	<b>pvalue</b>	<b>padj</b>
5	Verrucomicrobia	0.637	-3.529	3.620	-0.975	0.330	0.593
3	Tenericutes	13.522	-2.393	1.441	-1.661	0.097	0.290
8	Acidobacteria	0.112	-1.357	3.641	-0.373	0.709	0.776
9	Elusimicrobia	0.017	-1.034	3.642	-0.284	0.776	0.776
2	Firmicutes	1471.933	-0.468	0.273	-1.716	0.086	0.290
7	Actinobacteria	316.759	0.270	0.629	0.429	0.668	0.776
4	Bacteroidetes	3454.093	0.369	0.301	1.225	0.220	0.496
1	Proteobacteria	152.004	1.467	0.559	2.624	0.009	0.078
6	Lentisphaerae	1.018	1.894	2.496	0.758	0.448	0.672

**EX to DS**

	<b>Phylum</b>	<b>baseMean</b>	<b>log2FoldChange</b>	<b>lfcSE</b>	<b>stat</b>	<b>pvalue</b>	<b>padj</b>
7	Lentisphaerae	1.018	-0.927	2.501	-0.371	0.711	0.866
3	Actinobacteria	316.759	-0.655	0.629	-1.041	0.298	0.866
8	Proteobacteria	152.004	-0.164	0.559	-0.292	0.770	0.866
9	Bacteroidetes	3454.093	-0.023	0.301	-0.075	0.940	0.940
1	Firmicutes	1471.933	0.655	0.273	2.402	0.016	0.147
6	Elusimicrobia	0.017	1.443	3.643	0.396	0.692	0.866
2	Tenericutes	13.522	1.849	1.435	1.288	0.198	0.866
5	Acidobacteria	0.112	2.226	3.642	0.611	0.541	0.866
4	Verrucomicrobia	0.637	3.076	3.619	0.850	0.395	0.866

**Table S6. The comparison of the abundance of the families constituting the gut microbiome of the three experimental groups by DESeq2 differential abundance analysis.** The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.

	Family	baseMean	EX to DS				DS to Ctrl				EX to Ctrl			
			log2Fold Change	lfcSE	stat	pvalue	log2Fold Change	lfcSE	stat	pvalue	log2Fold Change	lfcSE	stat	pvalue
1	Prevotellaceae	2556.55	-1.09	1.01	-1.07	0.28	-0.48	0.99	-0.48	0.63	-1.57	1.01	-1.54	0.12
2	Bacteroidaceae	1053.93	-0.86	0.59	-1.45	0.15	0.63	0.58	1.09	0.28	-0.23	0.59	-0.38	0.70
3	Bifidobacteriaceae	576.11	-2.34	0.86	-2.71	0.01	0.90	0.85	1.06	0.29	-1.45	0.86	-1.68	0.09
4	Ruminococcaceae	570.65	0.09	0.31	0.30	0.76	-0.90	0.30	-2.97	0.00	-0.80	0.31	-2.61	0.01
5	Lachnospiraceae	383.23	-0.54	0.38	-1.43	0.15	-0.19	0.37	-0.50	0.61	-0.73	0.38	-1.92	0.05
6	Veillonellaceae	199.86	0.38	0.58	0.66	0.51	0.20	0.56	0.36	0.72	0.58	0.58	1.01	0.31
7	Enterobacteriaceae	153.38	-0.93	1.07	-0.86	0.39	-1.36	1.05	-1.29	0.20	-2.29	1.07	-2.13	0.03
8	Clostridiales_uc	73.09	-0.36	0.38	-0.95	0.34	0.36	0.38	0.96	0.34	0.00	0.39	0.00	1.00
9	EU845084_f	59.22	-1.38	1.71	-0.81	0.42	0.71	1.68	0.42	0.67	-0.67	1.71	-0.39	0.69
10	Bacteroidales_uc	39.95	-0.66	0.52	-1.27	0.20	0.08	0.51	0.16	0.87	-0.58	0.52	-1.11	0.27
11	Sutterella_f	37.93	-1.94	0.57	-3.41	0.00	0.40	0.55	0.73	0.46	-1.54	0.57	-2.70	0.01
12	EF602759_f	34.15	0.95	1.10	0.87	0.38	-0.78	1.08	-0.72	0.47	0.18	1.09	0.16	0.87
13	Rikenellaceae	30.83	0.49	0.98	0.50	0.62	1.18	0.96	1.22	0.22	1.67	0.98	1.70	0.09
14	Porphyromonadaceae	28.48	-0.02	0.43	-0.05	0.96	0.58	0.42	1.37	0.17	0.56	0.43	1.29	0.20
15	Paraprevotella_f	20.07	0.47	1.00	0.47	0.64	-0.52	0.98	-0.53	0.60	-0.05	1.00	-0.05	0.96
16	Coriobacteriaceae	12.75	-1.18	0.81	-1.45	0.15	0.13	0.78	0.16	0.87	-1.05	0.81	-1.29	0.20
17	Erysipelotrichaceae	11.98	-1.79	0.75	-2.38	0.02	-0.70	0.70	-1.00	0.32	-2.49	0.75	-3.32	0.00
18	Streptococcaceae	9.63	1.09	1.16	0.93	0.35	-0.04	1.15	-0.03	0.97	1.05	1.16	0.90	0.37
19	Clostridia_uc_f	9.02	-0.30	0.43	-0.70	0.49	0.03	0.42	0.08	0.94	-0.27	0.44	-0.61	0.54
20	Odoribacter_f	5.76	-1.80	0.72	-2.49	0.01	1.99	0.71	2.82	0.00	0.19	0.75	0.26	0.80
21	Pasteurellaceae	5.60	-0.61	1.29	-0.47	0.64	-0.56	1.25	-0.44	0.66	-1.16	1.29	-0.90	0.37
22	Bacteroidia_uc_f	5.43	-0.52	0.67	-0.77	0.44	-0.02	0.64	-0.03	0.98	-0.54	0.68	-0.79	0.43
23	Erysipelotrichales_uc	4.93	0.17	1.56	0.11	0.91	-2.81	1.50	-1.87	0.06	-2.64	1.53	-1.72	0.09
24	DQ809955_f	4.54	2.11	0.91	2.31	0.02	-1.04	0.91	-1.15	0.25	1.06	0.90	1.19	0.24
25	AM275436_f	4.21	0.26	1.43	0.18	0.85	1.15	1.42	0.81	0.42	1.41	1.45	0.97	0.33
26	DQ809526_f	2.09	0.41	1.06	0.39	0.70	1.22	1.09	1.11	0.27	1.63	1.11	1.47	0.14
27	Peptostreptococcaceae	1.93	0.55	1.05	0.52	0.60	1.01	1.08	0.94	0.35	1.56	1.10	1.43	0.15
28	Lactobacillaceae	1.89	1.08	1.47	0.73	0.46	-2.30	1.41	-1.63	0.10	-1.23	1.43	-0.86	0.39
29	Burkholderiales_uc	1.67	-2.44	1.16	-2.11	0.04	-0.67	1.03	-0.65	0.51	-3.12	1.15	-2.70	0.01
30	AF371945_f	1.66	0.64	1.83	0.35	0.72	1.76	1.84	0.95	0.34	2.40	1.87	1.28	0.20
31	Clostridiaceae	1.47	-0.20	1.44	-0.14	0.89	3.08	1.47	2.09	0.04	2.88	1.51	1.91	0.06
32	Mogibacterium_f	1.29	-0.11	1.25	-0.09	0.93	0.51	1.23	0.42	0.68	0.41	1.27	0.32	0.75
33	EF445272_f	1.08	1.20	2.30	0.52	0.60	-0.23	2.27	-0.10	0.92	0.97	2.31	0.42	0.67
34	Enterobacteriales_uc	1.02	-1.36	1.28	-1.06	0.29	-1.27	1.17	-1.09	0.28	-2.63	1.26	-2.09	0.04
35	AB185535_f	1.00	-1.52	3.14	-0.49	0.63	-1.72	3.04	-0.57	0.57	-3.25	3.12	-1.04	0.30

**Table S7. The List of microbial families constituting the gut microbiome of the three experimental groups.** The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each.

	Family	Ctrl (%)	DS (%)	EX (%)
1	Prevotellaceae	46.61	30.02	28.02
2	Bacteroidaceae	11.48	25.42	23.3
3	Ruminococcaceae	12.99	11.17	13.58
4	Lachnospiraceae	6.68	8.09	8.31
5	Bifidobacteriaceae	5.63	8.59	5.08
6	Veillonellaceae	2.86	2.92	7.85
7	Enterobacteriaceae	4.31	2.41	1.92
8	Clostridiales_uc	1.15	1.83	2.13
9	EU845084_f	1.01	1.84	0.98
10	Odoribacter_f	2.3	0.23	0.08
11	Bacteroidales_uc	0.71	0.83	0.87
12	EF602759_f	0.54	0.48	1.35
13	Rikenellaceae	0.23	0.71	1.22
14	Sutterella_f	0.69	1.06	0.39
15	Porphyromonadaceae	0.33	0.61	0.91
16	Paraprevotella_f	0.25	0.38	0.68
17	Streptococcaceae	0.33	0.2	0.39
18	Erysipelotrichales_uc	0.27	0.56	0.06
19	Coriobacteriaceae	0.24	0.28	0.2
20	Clostridia_uc_f	0.16	0.19	0.25
21	Erysipelotrichaceae	0.22	0.24	0.1
22	Elusimicrobiaceae	0.11	0.44	0
23	DQ809955_f	0.1	0.05	0.26
24	AF371945_f	0.01	0.11	0.28
25	Lactobacillaceae	0.04	0.22	0.11
26	AM275436_f	0.04	0.1	0.2
27	Bacteroidia_uc_f	0.09	0.12	0.13
28	Pasteurellaceae	0.11	0.09	0.11
29	Erysipelotrichi_uc_f	0.03	0.05	0.22
30	EF445272_f	0.02	0.01	0.19
31	Peptostreptococcaceae	0.02	0.06	0.09
32	DQ809526_f	0.02	0.04	0.1
33	Clostridiaceae	0.04	0.06	0.06
34	GU112192_f	0.01	0.02	0.11
35	AM275436_o_uc	0.02	0.01	0.07
36	EU844239_f	0.01	0	0.09
37	Mogibacterium_f	0.01	0.03	0.04
38	Enterococcaceae	0	0.07	0
39	Burkholderiales_uc	0.04	0.03	0
40	AB185535_f	0.06	0.01	0

**Table S8. The comparison of the bacterial species differentially abundant in the the gut microbiome in Ctrl and EX groups by DESeq2 differential abundance analysis.  $p$  value < 0.05 is represent in the table.**

	Species	baseMean	log2FoldChange	lfcSE	stat	pvalue
2	<i>Bacteroides fragilis</i>	7.712	-5.918	1.757	-3.368	0.001
3	<i>Phascolarctobacterium faecium</i>	6.37	-5.788	2.021	-2.865	0.004
4	<i>Megasphaera elsdenii</i>	28.748	-5.538	2.052	-2.699	0.007
5	<i>Megasphaera_uc</i>	5.9	-4.627	2.152	-2.15	0.032
6	<i>Streptococcus parasanguinis</i>	1.646	-4.411	2.185	-2.019	0.043
7	DQ793660_s	2.672	-4.134	1.687	-2.45	0.014
8	<i>Veillonella dispar</i>	4.824	-4.127	1.467	-2.813	0.005
9	<i>Bacteroides caccae</i>	7.104	-3.796	1.006	-3.773	0
10	<i>Eubacterium siraeum</i>	1.692	-3.515	1.288	-2.729	0.006
11	DQ805681_s	11.683	-3.475	0.906	-3.836	0
12	4P000072_s	4.128	-3.473	1.301	-2.669	0.008
13	DQ456272_s	2.733	-3.235	1.389	-2.33	0.02
14	EU777390_g_uc	3.142	-3.206	1.197	-2.677	0.007
15	<i>Parabacteroides distasonis</i>	2.533	-3.118	1.209	-2.58	0.01
16	DQ905718_s	0.607	-2.993	1.336	-2.24	0.025
17	EF404287_s	8.326	-2.932	1.027	-2.854	0.004
1	<i>Bacteroides vulgatus</i>	129.563	-2.799	0.699	-4.003	0
18	EF401882_g_uc	2.829	-2.603	1.277	-2.038	0.042
19	DQ804825_s	3.54	-2.538	1.055	-2.406	0.016
20	DQ905034_g_uc	5.813	-2.481	0.881	-2.814	0.005
21	<i>Odoribacter_uc</i>	0.802	-2.405	1.214	-1.981	0.048
22	EF404077_s	7.992	-2.328	0.965	-2.413	0.016
23	4P000883_s	1.147	-2.104	1.07	-1.966	0.049
24	<i>Bacteroides uniformis</i>	19.496	-1.763	0.812	-2.172	0.03
25	<i>Veillonellaceae_uc_s</i>	34.798	-1.428	0.591	-2.415	0.016
26	<i>Clostridiales_uc_s</i>	61.756	-0.857	0.345	-2.481	0.013
27	EF402172_s	59.013	1.102	0.471	2.338	0.019
28	<i>Subdoligranulum_uc</i>	6.311	1.378	0.695	1.981	0.048
29	<i>Sutterella_f_uc_s</i>	2.33	1.866	0.853	2.187	0.029
30	<i>Bifidobacterium_uc</i>	23.13	2.084	0.996	2.093	0.036
31	<i>Sutterella_uc</i>	5.672	2.348	0.88	2.668	0.008
32	GQ897158_s	48.592	2.437	0.901	2.703	0.007
33	<i>Blautia_uc</i>	3.879	2.585	0.833	3.103	0.002
34	<i>Burkholderiales_uc_s</i>	1.598	2.73	1.216	2.245	0.025
35	EU462041_s	59.173	2.788	1.294	2.155	0.031
36	EU461711_s	57.319	3.412	1.521	2.243	0.025
37	DQ795906_s	17.478	4.572	1.879	2.433	0.015
38	<i>Dialister succinatiphilus</i>	8.913	4.73	2.267	2.087	0.037
39	4P000023_s	16.634	5.145	2.473	2.081	0.037

**Table S9. The comparison of the bacterial species differentially abundant in the the gut microbiome in Ctrl and DS groups by DESeq2 differential abundance analysis. p value < 0.05 is represent in the table.**

	Species	baseMean	log2FoldChange	lfcSE	stat	pvalue
1	<i>Blautia_uc</i>	3.879	2.720	0.774	3.512	0.000
2	<i>Bacteroides vulgatus</i>	129.563	-2.361	0.686	-3.443	0.001
3	<i>DQ795906_s</i>	17.478	6.378	1.856	3.436	0.001
4	<i>Bacteroides fragilis</i>	7.712	-5.054	1.726	-2.928	0.003
5	<i>EF402172_s</i>	59.013	1.258	0.459	2.742	0.006
6	<i>4P000072_s</i>	4.128	-3.474	1.270	-2.736	0.006
7	<i>DQ805681_s</i>	11.683	-2.412	0.890	-2.710	0.007
8	<i>4P000873_s</i>	4.106	-2.904	1.177	-2.467	0.014
9	<i>Megasphaera elsdenii</i>	28.748	-4.963	2.014	-2.464	0.014
10	<i>EF401818_s</i>	1.481	2.887	1.200	2.405	0.016
11	<i>4P000883_s</i>	1.147	-2.332	1.011	-2.307	0.021
12	<i>Bacteroides_uc</i>	188.848	-0.969	0.425	-2.282	0.022
13	<i>EF401233_s</i>	2.098	2.463	1.081	2.279	0.023
14	<i>Odoribacter_uc</i>	0.802	-2.625	1.156	-2.271	0.023
15	<i>Coprococcus_uc</i>	2.296	2.470	1.097	2.252	0.024
16	<i>Phascolarctobacterium faecium</i>	6.370	-4.250	1.987	-2.139	0.032
17	<i>Odoribacter_f_uc_s</i>	1.845	-1.567	0.734	-2.134	0.033
18	<i>Bacteroidaceae_uc_s</i>	41.825	-0.661	0.333	-1.988	0.047

**Table S10. The comparison of the bacterial species differentially abundant in the the gut microbiome in EX and DS groups by DESeq2 differential abundance analysis. p value < 0.05 is represent in the table.**

	Species	baseMean	log2FoldChange	lfcSE	stat	pvalue
1	<i>Veillonella dispar</i>	4.820	-4.720	1.460	-3.230	0.000
2	<i>EF401233_s</i>	2.100	-3.970	1.080	-3.690	0.000
3	<i>EF404193_s</i>	0.660	-3.470	1.740	-2.000	0.050
4	<i>Veillonella_uc</i>	0.770	-3.360	1.610	-2.090	0.040
5	<i>Bacteroides caccae</i>	7.100	-3.310	0.980	-3.370	0.000
6	<i>Parabacteroides distasonis</i>	2.530	-3.180	1.190	-2.670	0.010
7	<i>EF404287_s</i>	8.330	-2.990	1.020	-2.930	0.000
8	<i>EF404077_s</i>	7.990	-2.830	0.970	-2.920	0.000
9	<i>EF401818_s</i>	1.480	-2.600	1.240	-2.100	0.040
10	<i>Coprococcus_uc</i>	2.300	-2.420	1.130	-2.150	0.030
11	<i>EU777390_g_uc</i>	3.140	-2.390	1.160	-2.060	0.040
12	<i>Roseburia hominis</i>	1.550	-2.320	1.080	-2.150	0.030
13	<i>Eubacterium hallii</i>	1.010	-2.200	0.920	-2.400	0.020
14	<i>EF404388_s</i>	121.030	1.820	0.850	2.140	0.030
15	<i>GQ897158_s</i>	48.590	1.910	0.900	2.120	0.030
16	<i>Sutterella_f_uc_s</i>	2.330	2.180	0.840	2.600	0.010
17	<i>Bifidobacterium_uc</i>	23.130	2.190	1.000	2.200	0.030
18	<i>Sutterella_uc</i>	5.670	2.290	0.880	2.610	0.010
19	<i>4P000873_s</i>	4.110	2.800	1.210	2.300	0.020
20	<i>4P000023_s</i>	16.630	5.150	2.470	2.080	0.040
21	<i>Dialister succinatiphilus</i>	8.910	5.660	2.260	2.500	0.010

**Table S11. The List of microbial species constituting more than 0.5 % in the gut microbiome of the three experimental groups.** The Ctrl, EX, and DS represents the control, exercise, and diet shift groups each. The species has below 0.5% relative abundance after combining all three groups are not included.

	Species	Ctrl (%)	DS (%)	EX (%)
1	<i>Prevotella copri</i>	15.63	16.47	11.94
2	<i>Prevotella_uc</i>	5.96	5.93	3.6
3	<i>EU461603_s</i>	5.94	2.88	3.55
4	<i>Bifidobacterium pseudocatenulatum</i>	6.44	3.81	0.33
5	<i>Bacteroides_uc</i>	1.8	3.96	4.42
6	<i>Bacteroides vulgatus</i>	0.42	2.45	4.86
7	<i>EU462076_s</i>	4.48	1.35	1.76
8	<i>4P000745_s</i>	3.04	2.36	2.13
9	<i>EU475206_s</i>	5.18	0.83	1.34
10	<i>EF404388_s</i>	1.91	2.77	1.14
11	<i>Prevotella stercora</i>	1.37	2.24	1.55
12	<i>Bifidobacterium adolescentis</i>	0.53	1.91	2.64
13	<i>Ruminococcaceae_uc_s</i>	1.27	1.36	2.23
14	<i>Clostridiales_uc_s</i>	1.02	1.39	1.95
15	<i>FJ363527_s</i>	1.67	1.04	1.44
16	<i>Bacteroides plebeius</i>	0.65	2.45	0.77
17	<i>Faecalibacterium_uc</i>	1.07	1.28	1.24
18	<i>Prevotellaceae_uc_s</i>	1.43	1.04	1.03
19	<i>Bacteroides coprocola</i>	0.29	2.21	0.86
20	<i>BAAX01003885_s</i>	0.61	2.19	0.39
21	<i>EF402172_s</i>	1.32	0.62	1.01
22	<i>Faecalibacterium prausnitzii</i>	0.86	0.67	1.32
23	<i>DQ797252_s</i>	1.62	0.63	0.52
24	<i>EU462041_s</i>	1.64	0.68	0.39
25	<i>Klebsiella pneumoniae</i>	2.02	0.08	0.48
26	<i>EU461711_s</i>	1.83	0.44	0.29
27	<i>Megamonas rupellensis</i>	0.87	0.08	1.53
28	<i>GQ897158_s</i>	1.09	0.84	0.32
29	<i>Bacteroidaceae_uc_s</i>	0.46	0.81	0.98
30	<i>Bacteroidales_uc_s</i>	0.65	0.77	0.82
31	<i>Lachnospiraceae_uc_s</i>	0.47	0.71	0.94
32	<i>Odoribacter_uc</i>	2	0.02	0.02
33	<i>Veillonellaceae_uc_s</i>	0.28	0.51	1.24
34	<i>Escherichia coli group</i>	0.14	1.31	0.53
35	<i>Megasphaera elsdenii</i>	0.2	0.55	1.2
36	<i>DQ801259_s</i>	0.52	1.1	0.31
37	<i>EF403870_s</i>	0.5	0.79	0.44
38	<i>GQ047204_s</i>	0.43	0.98	0.33
39	<i>Bacteroides eggerthii</i>	0	0.01	1.69
40	<i>DQ795058_s</i>	0.69	0.53	0.46
41	<i>Dialister succinatiphilus</i>	0.13	1.12	0.36
42	<i>Bifidobacterium stercoris</i>	0.26	1.07	0.3
43	<i>EU531928_s</i>	0.38	0.17	0.96