

The combination of exercise and konjac glucomannan synergistically restores dysbiosis in mice induced by antibiotics compared with singular intervention

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Table S1 The chemical compounds used in this work with information from NCBI PubChem compound database and the supplier sources

Compound	CAS No.	CID	MW (g/mol)	InChIKey	IUPAC name	Source
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Acetic acid	64-19-7	176	60.05	QTBSBXVTEA MEQO-UHFFFAOYSA- N	acetic acid	Aladdin® (Shanghai, China)
Propionic acid	79-09-4	1032	74.08	XBDQKXXYIPT UBI-UHFFFAOYSA-N	propanoic acid	Aladdin® (Shanghai, China)
<i>n</i> -butyric acid	107-92-6	264	88.11	FERIUCNNQQJ TOY-UHFFFAOYSA-N	butynoic acid	Aladdin® (Shanghai, China)
<i>iso</i> -butyric acid	79-31-2	6590	88.11	KQNPFQTWMS NSAP-UHFFFAOYSA- N	2-methylpropanoic acid	Aladdin® (Shanghai, China)
n-valeric acid	109-52-4	7991	102.13	NQPDZGIKBAW PEJ-UHFFFAOYSA-N	pentanoic acid	Aladdin® (Shanghai,

						China)
<i>iso</i> -valeric acid	503-74-2	10430	102.13	GWYFCOCPAB KNJV-UHFFFAOYSA-N	3-methylbutanoic acid	Aladdin® (Shanghai, China)
Ampicillin	7177-48-2	6249	349.4	RXDALBZNGVATNY- CWLIKTD RSA-N	(2S,5R,6R)-6- [[(2R)-2-amino-2-phenylacetyl]amin o]-3,3-dimethyl-7-oxo-4-thia-1-azabicyclo[3.2.0]heptane-2-carboxylic acid	Macklin® (Shanghai, China)

Clindamycin h	21462-	16051	461.4	AUODDLQVRAJAJM-	(2S,4R)-N-	Macklin®
ydrochloride	39-5	951		XJQDNNTCSA-N	[(1S,2S)-2-chloro-1-[(2R,3R,4S,5R,6R)-3,4,5-trihydroxy-6-methylsulfanyloxan-2-yl]propyl]-1-methyl-4-propylpyrrolidine-2-carboxamide;hydrochloride	(Shanghai, China)

streptomycin	57-92-1	19649	581.6	UCSJYZPVAKXKNQ- HZYVHMACSA-N	2- [(1R,2R,3S,4R,5R, 6S)-3- (diaminomethylideneamino)-4- [(2R,3R,4R,5S)-3- [(2S,3S,4S,5R,6S)- 4,5-dihydroxy-6- (hydroxymethyl)- 3- (methylamino)oxan-2-yl]oxy-4- formyl-4-hydroxy- 5-methyloxolan-2-	Macklin® (Shanghai, China)
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					yl]oxy-2,5,6- trihydroxycyclohex yl]guanidine	
Paraformaldeh yde	50-00-0	712	30.026	WSFSSNUMVMOOMR -UHFFFAOYSA-N	formaldehyde	Macklin® (Shanghai, China)

CID: PubChem compound ID; InChIKey: International Chemical Identifier

Table S2. The formula of AIN93 purified diet used in the study

Ingredient	gram	kcal
Casein, 30Mesh	200	800
L-Cystine	3	12
Corn Starch	397	1590
Maltodextrin 10	132	528

Sucrose	100	400
Cellulose	50	0
Soybean Oil	70	630
t-Butylhydroquinone	0.014	0
Mineral Mix S10022M	35	0
Vitamin Mix V10037	10	40
Choline Bitartrate	2.5	0
Total	1000	3850
Macronutrients		
Protein	20.0 (gram%)	20.3 (Kcal%)
Carbohydrate	64.0 (gram%)	63.9 (Kcal%)
Fat	7.0 (gram%)	15.8 (Kcal%)
Total		100.0 (Kcal%)
kcal/gm	3.9	

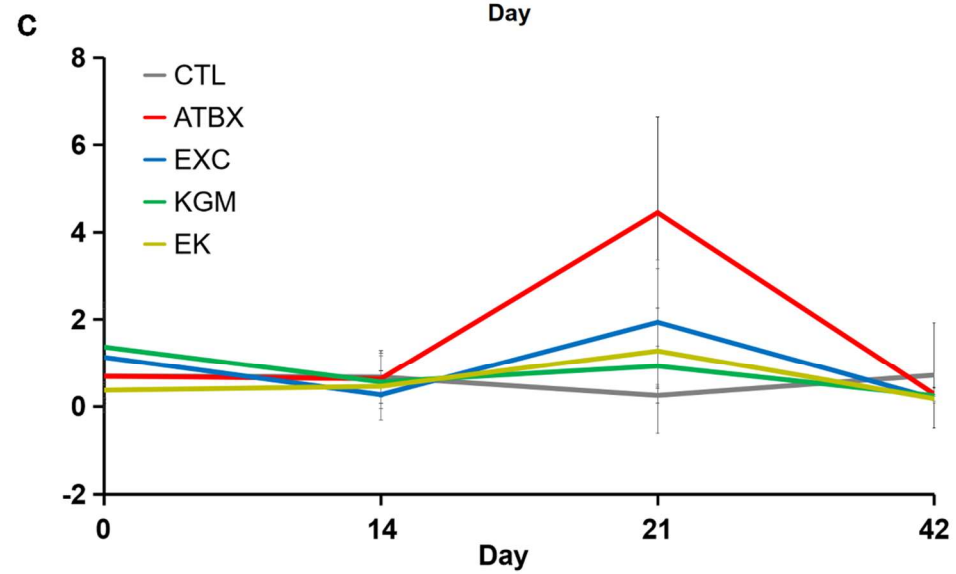
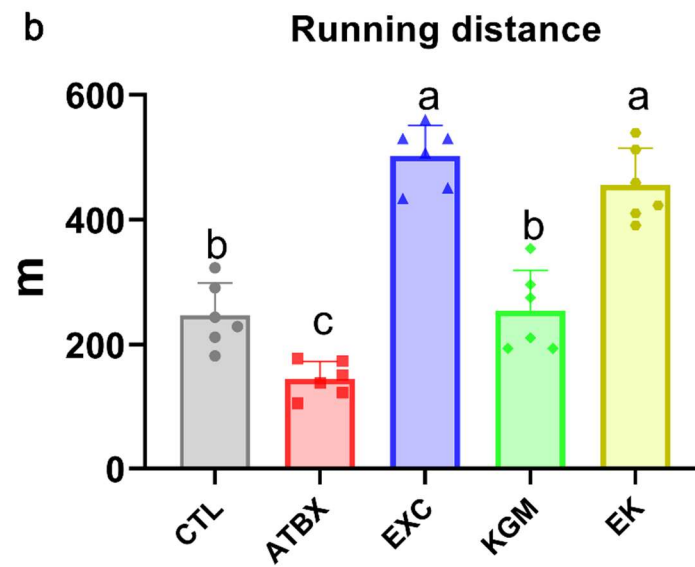
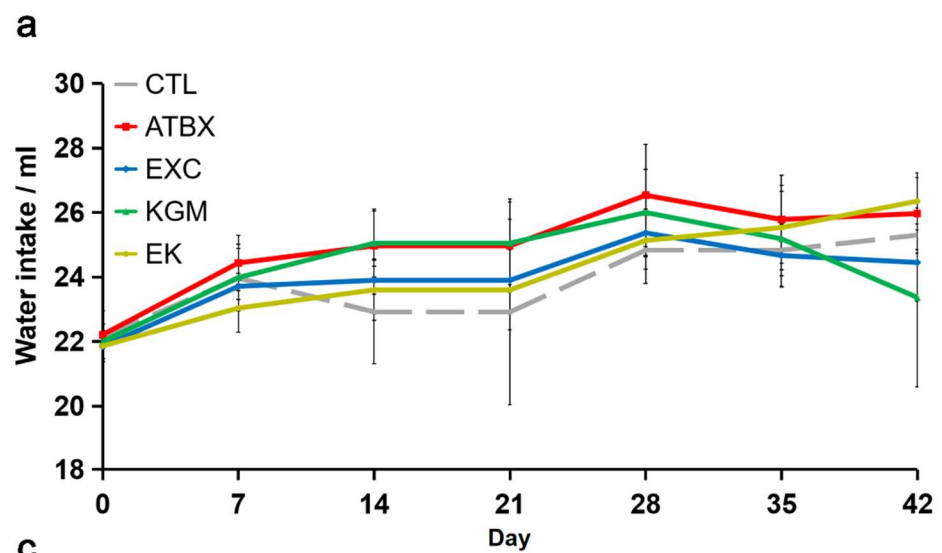


Fig S1 The daily water intake of the mice in the experiment (a) and maximum running distance (b) and Firmicutes/Bacteroidetes at different time points (c). Average of six samples, error bars represent standard deviation at N = 6. (c) Different letters indicate the significant difference among different groups for the same index, ANOVA with Bonferroni or Tamhane T2 post-hoc test, $p < 0.05$. CTL: control; ATBX: antibiotic; EXC: exercise; KGM: the native KGM; EK: combination of exercise and KGM.

Table S3 Histological scoring system

Histological score	Degree of inflammation	Infiltration of inflammatory cells	Degree of Crypt damage to the crypt	Crypt abscesses	Degree of Reduction of submucosal edema	goblet cells	Degree of epithelial hyperplasia
0	Normal	Normal	Normal	Normal	Normal	Normal	Normal
1	Mucosa	Unifocal	Basal 1/3 of crypt	Unifocal	Unifocal	Unifocal	Unifocal

2	Submucosa	Multifocal	Basal 2/3 of crypt	Multifocal	Multifocal	Multifocal	Multifocal
3	Muscular	Suffuse	Suffuse		Suffuse	Suffuse	Suffuse
4	Serous		Damage to the crypt and ulceration				

Table S4 The relative abundance of top 20 taxa in feces at different levels on day 0

Day 0	CTL	ATBX	EXC	KGM	EK
Phylum					
Bacteroidetes	60.74 ± 19.58	59.45 ± 17.95	55.57 ± 22.94	45.81 ± 19.73	69.65 ± 9.39
	ab	ab	ab	19.73 b	a

Firmicutes	32.45 ± 18.47 ab	33.62 ± 16.93 ab	39.71 ± 24.97 ab	48.70 ± 18.02 a	24.45 ± 8.96 b
Tenericutes	4.96 ± 3.97 a	1.15 ± 0.79 b	3.16 ± 3.40 ab	2.46 ± 2.56 ab	3.58 ± 3.36 ab
Proteobacteria	0.55 ± 0.51 b	2.66 ± 1.28 a	0.61 ± 0.50 b	2.08 ± 4.18 b	1.66 ± 1.63 ab
Actinobacteria	0.60 ± 0.56	2.80 ± 5.21	0.40 ± 0.41	0.53 ± 0.73	0.26 ± 0.15
TM7	0.58 ± 0.54	0.16 ± 0.17	0.55 ± 0.60	0.34 ± 0.14	0.19 ± 0.15
Deferribacteres	0.11 ± 0.22	0.12 ± 0.14	0.00 ± 0.01	0.08 ± 0.11	0.09 ± 0.11
Crenarchaeota	0.00 ± 0.00 b	0.01 ± 0.02 ab	0.00 ± 0.00 b	0.00 ± 0.00 b	0.05 ± 0.08 a
Fusobacteria	0.00 ± 0.00 b	0.00 ± 0.01 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.02 ± 0.02 a
unclassified	0.00 ± 0.00	0.01 ± 0.01	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.01
Acidobacteria	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.01
Cyanobacteria	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.01

Chloroflexi	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Verrucomicrobia	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.01
Gemmatimonadetes	0.00 ± 0.00 b	0.00 ± 0.00 a	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 ab
Euryarchaeota	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.01	0.00 ± 0.00
Spirochaetes	0.00 ± 0.00 b	0.00 ± 0.00 ab	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 a
Nitrospirae	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Planctomycetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
SAR406	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Other	0.00 ± 0.00 b	0.00 ± 0.00 ab	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 a
Family					
S24_7	59.22 ± 19.16 ab	57.57 ± 17.40 ab	53.84 ± 22.27 ab	44.01 ± 18.70 b	66.82 ± 10.58 a
Lactobacillaceae	26.94 ± 16.14	21.83 ± 15.77	34.54 ± 28.33	37.17 ±	12.08 ± 9.58

				28.02	
unclassified	6.70 ± 4.16	4.27 ± 1.86	5.69 ± 5.25	5.87 ± 3.64	7.49 ± 3.91
Lachnospiraceae	2.85 ± 2.45	5.16 ± 3.22	1.96 ± 2.32	6.57 ± 8.12	5.84 ± 4.72
Ruminococcaceae	0.37 ± 0.20 b	1.97 ± 1.23 a	0.39 ± 0.39 b	0.99 ± 1.48 ab	1.93 ± 1.48 b
Bacteroidaceae	0.64 ± 0.51	0.82 ± 1.02	1.34 ± 1.04	0.99 ± 0.72	1.63 ± 1.70
Enterobacteriaceae	0.37 ± 0.53	2.09 ± 0.93	0.43 ± 0.52	1.85 ± 4.16	0.27 ± 0.16
Rikenellaceae	0.61 ± 0.38	1.04 ± 1.21	0.38 ± 0.28	0.48 ± 0.49	0.92 ± 0.64
Coriobacteriaceae	0.60 ± 0.56	0.58 ± 0.53	0.40 ± 0.41	0.52 ± 0.73	0.22 ± 0.19
Micrococcaceae	0.00 ± 0.00	2.11 ± 5.17	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.01
F16	0.58 ± 0.54	0.16 ± 0.17	0.55 ± 0.60	0.34 ± 0.14	0.19 ± 0.15
Clostridiaceae	0.17 ± 0.09	0.49 ± 0.35	0.12 ± 0.21	0.21 ± 0.20	0.13 ± 0.09
Erysipelotrichaceae	0.06 ± 0.05	0.32 ± 0.42	0.15 ± 0.26	0.03 ± 0.03	0.38 ± 0.54
Porphyromonadaceae	0.27 ± 0.25 b	0.01 ± 0.01 c	0.00 ± 0.00 c	0.32 ± 0.77 a	0.23 ± 0.26

					bc
Turicibacteraceae	0.29 ± 0.21 a	0.23 ± 0.23 ab	0.02 ± 0.02 b	0.27 ± 0.34 ab	0.01 ± 0.02 b
Brucellaceae	0.02 ± 0.03 b	0.13 ± 0.16 ab	0.02 ± 0.05 b	0.04 ± 0.05 b	0.55 ± 0.70 a
Pseudomonadaceae	0.02 ± 0.02 b	0.16 ± 0.19 ab	0.03 ± 0.04 b	0.07 ± 0.07 ab	0.44 ± 0.45 a
Deferribacteraceae	0.11 ± 0.22	0.12 ± 0.14	0.00 ± 0.01	0.08 ± 0.11	0.09 ± 0.11
Alcaligenaceae	0.11 ± 0.09	0.08 ± 0.11	0.06 ± 0.06	0.03 ± 0.02	0.03 ± 0.02
Planococcaceae	0.00 ± 0.00	0.28 ± 0.68	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Other	0.07 ± 0.04	0.57 ± 0.47	0.09 ± 0.06	0.18 ± 0.14	0.75 ± 0.61
Genus					
unclassified	70.08 ± 16.55	70.89 ± 15.56	62.62 ± 27.04	$58.52 \pm$ 25.08	80.93 ± 7.40
<i>Lactobacillus</i>	26.94 ± 16.14	21.83 ± 15.78	34.54 ± 28.33	$37.17 \pm$	12.08 ± 9.58

				28.02	
<i>Bacteroides</i>	0.64 ± 0.51	0.82 ± 1.02	1.34 ± 1.04	0.99 ± 0.72	1.63 ± 1.70
<i>Anaerostipes</i>	0.27 ± 0.18	0.47 ± 0.24	0.25 ± 0.21	0.37 ± 0.26	1.10 ± 1.50
<i>Kocuria</i>	0.00 ± 0.00	2.09 ± 5.13	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
<i>Adlercreutzia</i>	0.56 ± 0.55	0.49 ± 0.45	0.32 ± 0.33	0.47 ± 0.74	0.20 ± 0.17
<i>Oscillospira</i>	0.11 ± 0.10	0.58 ± 0.50	0.09 ± 0.08	0.35 ± 0.48	0.57 ± 0.55
<i>Ruminococcaceae_Ruminococcus</i>	0.03 ± 0.03 b	0.20 ± 0.19 a	0.03 ± 0.03 b	0.35 ± 0.75 ab	0.65 ± 0.89 a
<i>Coprococcus</i>	0.09 ± 0.07	0.45 ± 0.49	0.10 ± 0.15	0.26 ± 0.42	0.36 ± 0.41
<i>Ruminococcus</i>	0.11 ± 0.09	0.25 ± 0.21	0.19 ± 0.18	0.22 ± 0.35	0.33 ± 0.26
<i>Clostridium</i>	0.17 ± 0.09	0.47 ± 0.32	0.12 ± 0.21	0.20 ± 0.20	0.13 ± 0.09
<i>Parabacteroides</i>	0.27 ± 0.25b	0.01 ± 0.01c	0.00 ± 0.00c	0.32 ± 0.77a	0.23 ± 0.26bc
<i>Turicibacter</i>	0.29 ± 0.21 a	0.23 ± 0.23 ab	0.02 ± 0.02 b	0.27 ± 0.34	0.01 ± 0.02 b

				ab	
<i>Roseburia</i>	0.11 ± 0.19	0.17 ± 0.20	0.09 ± 0.17	0.12 ± 0.25	0.28 ± 0.31
<i>Pseudomonas</i>	0.02 ± 0.02 b	0.16 ± 0.19 ab	0.03 ± 0.04 b	0.07 ± 0.07 ab	0.43 ± 0.45 a
<i>Mucispirillum</i>	0.11 ± 0.22	0.12 ± 0.14	0.00 ± 0.01	0.08 ± 0.11	0.09 ± 0.11
<i>Sutterella</i>	0.10 ± 0.09	0.07 ± 0.11	0.05 ± 0.06	0.02 ± 0.01	0.02 ± 0.02
<i>Coprobacillus</i>	0.01 ± 0.02	0.05 ± 0.04	0.11 ± 0.22	0.02 ± 0.03	0.06 ± 0.10
<i>Plesiomonas</i>	0.01 ± 0.01 b	0.07 ± 0.06 ab	0.01 ± 0.01 b	0.03 ± 0.04 b	0.11 ± 0.11 a
<i>Ralstonia</i>	0.00 ± 0.00 b	0.04 ± 0.04 ab	0.00 ± 0.01 b	0.01 ± 0.02 b	0.10 ± 0.08 a
Other	0.07 ± 0.04	0.55 ± 0.51	0.09 ± 0.05	0.17 ± 0.13	0.68 ± 0.60

Data are shown in average ± standard deviation. Different letters indicate the significant difference among different groups for the same index, ANOVA with LSD or Tamhane T2 post-hoc test, $p < 0.05$. N = 6. CTL: control; ATBX: antibiotic; EXC: exercise; KGM: the native KGM; EK: combination of exercise and KGM.

Table S5 The relative abundance of top 20 taxa in feces at different levels on day 14

Day 14	CTL	ATBX	EXC	KGM	EK
Phylum					
Bacteroidetes	52.70 ± 20.39 b	56.75 ± 9.44 b	77.64 ± 3.45 a	50.19 ± 22.27 b	73.57 ± 26.44 a
Firmicutes	25.95 ± 13.71	34.44 ± 5.69	20.58 ± 3.57	28.81 ± 21.51	16.92 ± 12.23
Verrucomicrobia	13.53 ± 11.20 a	7.33 ± 6.14 a	0.31 ± 0.39 b	16.67 ± 20.60 a	2.06 ± 1.81 ab
Proteobacteria	3.40 ± 2.44 a	0.62 ± 0.18 b	0.99 ± 0.38 ab	0.33 ± 0.37 b	0.53 ± 0.50 b
Actinobacteria	4.24 ± 6.22 a	0.24 ± 0.20 b	0.17 ± 0.11 b	0.20 ± 0.20 b	1.66 ± 3.34 ab
Tenericutes	0.14 ± 0.21	0.18 ± 0.21	0.24 ± 0.15	3.55 ± 8.16	0.24 ± 0.23
Deferribacteres	0.01 ± 0.02 b	0.39 ± 0.16 a	0.04 ± 0.04 b	0.09 ± 0.09 b	0.14 ± 0.21 b

Cyanobacteria	0.03 ± 0.04	0.02 ± 0.04	0.02 ± 0.03	0.05 ± 0.05	3.69 ± 8.98
TM7	0.01 ± 0.01	0.03 ± 0.07	0.02 ± 0.02	0.05 ± 0.06	0.06 ± 0.12
Acidobacteria	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.04	0.02 ± 0.41	0.17 ± 0.18
unclassified	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.02	0.02 ± 0.03
Gemmatimonadetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.02	0.00 ± 0.01
Planctomycetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.01	0.07 ± 0.17
Chloroflexi	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.01	0.02 ± 0.04
Euryarchaeota	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.02 ± 0.06
Nitrospirae	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.03 ± 0.07
Chlorobi	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.36 ± 0.88
Crenarchaeota	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.08 ± 0.21
Armatimonadetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.06 ± 0.15
Fusobacteria	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.02
Other	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.29 ± 0.72

Family					
S24_7	35.12 ± 15.21	45.82 ± 5.60	62.13 ± 3.87	41.36 ± 18.41	53.11 ± 17.83
	ab	b	a	ab	ab
Erysipelotrichaceae	10.45 ± 11.12	18.73 ± 9.90	6.10 ± 2.77	9.97 ± 12.27	7.90 ± 16.33
unclassified	3.65 ± 3.85	10.61 ± 7.89	7.59 ± 3.15	16.29 ± 25.47	6.29 ± 3.86
Verrucomicrobiaceae	13.53 ± 11.20	7.33 ± 6.14 a	0.31 ± 0.39	16.67 ± 20.60	2.01 ± 1.85 ab
	a		b	a	
Paraprevotellaceae	4.60 ± 4.84 b	7.40 ± 5.79	8.42 ± 6.26	0.71 ± 1.73 b	17.77 ± 11.24
		ab	ab		a
Bacteroidaceae	4.84 ± 2.32	1.15 ± 0.44	5.24 ± 2.93	6.49 ± 4.44	3.00 ± 2.35
Lactobacillaceae	7.90 ± 6.94	1.30 ± 1.23	4.04 ± 4.00	1.78 ± 1.37	0.27 ± 0.25
Lachnospiraceae	2.10 ± 0.97	1.55 ± 0.99	1.79 ± 1.44	2.98 ± 4.86	4.65 ± 8.54
Ruminococcaceae	1.21 ± 1.01	2.36 ± 0.77	1.23 ± 0.85	1.31 ± 0.76	1.75 ± 1.43
Rikenellaceae	3.30 ± 2.80	1.01 ± 0.45	1.65 ± 1.70	0.43 ± 0.22	0.57 ± 0.37

Porphyromonadaceae	4.14 ± 4.28	0.75 ± 0.59	0.01 ± 0.01	1.19 ± 0.91	0.04 ± 0.03
Bifidobacteriaceae	4.10 ± 6.22 a	0.14 ± 0.12 ab	0.01 ± 0.01 b	0.04 ± 0.04 b	0.02 ± 0.04 b
Helicobacteraceae	2.48 ± 2.72 a	0.00 ± 0.00 b	0.27 ± 0.29 a	0.00 ± 0.00 b	0.07 ± 0.17 b
Alcaligenaceae	0.70 ± 0.82 a	0.54 ± 0.16 a	0.64 ± 0.41 a	0.12 ± 0.07 b	0.45 ± 0.51 ab
Prevotellaceae	0.69 ± 0.88 a	0.62 ± 0.89 a	0.18 ± 0.10 a	0.00 ± 0.00 b	0.71 ± 0.83 a
Coriobacteriaceae	0.14 ± 0.08	0.10 ± 0.09	0.16 ± 0.10	0.13 ± 0.17	0.26 ± 0.21
Deferribacteraceae	0.01 ± 0.02 b	0.39 ± 0.16 a	0.04 ± 0.04 b	0.09 ± 0.09 b	0.50 ± 0.84 ab
Peptostreptococcaceae	0.29 ± 0.45 a	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.08 ± 0.21 b
Enterococcaceae	0.24 ± 0.25 a	0.01 ± 0.01 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.06 ± 0.15 b
Enterobacteriaceae	0.16 ± 0.21 a	0.00 ± 0.00 b	0.04 ± 0.02	0.02 ± 0.02 b	0.02 ± 0.03 b

			b		
Other	0.34 ± 0.11	0.21 ± 0.10	0.15 ± 0.08	0.43 ± 0.41	0.47 ± 0.64
Genus					
unclassified	43.83 ± 16.33	59.31 ± 7.91	72.45 ± 3.39	61.13 ± 18.98	60.94 ± 21.21
	b	b	a	ab	ab
<i>Allobaculum</i>	7.59 ± 8.89	18.68 ± 9.89	6.06 ± 2.77	9.83 ± 12.23	7.87 ± 16.34
<i>Akkermansia</i>	13.53 ± 11.20	7.33 ± 6.14 b	0.31 ± 0.39 c	16.67 ± 20.61	2.06 ± 1.81 bc
	a			a	
<i>Prevotella</i>	4.60 ± 4.84 ab	7.40 ± 5.79 a	8.42 ± 6.26 a	0.71 ± 1.73 b	16.43 ± 12.92
					a
<i>Bacteroides</i>	4.84 ± 2.32	1.15 ± 0.44	5.24 ± 2.93	6.49 ± 4.44	4.40 ± 2.72
<i>Lactobacillus</i>	7.90 ± 6.94	1.30 ± 1.23	4.04 ± 4.00	1.78 ± 1.37	0.27 ± 0.24
<i>Parabacteroides</i>	4.14 ± 4.28	0.75 ± 0.59	0.01 ± 0.01	1.19 ± 0.91	0.03 ± 0.03
<i>Bifidobacterium</i>	4.10 ± 6.22 a	0.14 ± 0.12 b	0.01 ± 0.01	0.04 ± 0.04 b	3.69 ± 8.98 b

			b		
<i>Oscillospira</i>	0.81 ± 0.89	0.84 ± 0.32	0.72 ± 0.56	0.33 ± 0.20	0.69 ± 0.62
<i>Helicobacter</i>	2.48 ± 2.72 a	0.00 ± 0.00 b	0.27 ± 0.29 a	0.00 ± 0.00 b	0.17 ± 0.41 b
<i>Ruminococcaceae_Ruminococcus</i>	0.21 ± 0.10	0.81 ± 0.33	0.29 ± 0.19	0.59 ± 0.42	0.76 ± 0.65
<i>Sutterella</i>	0.69 ± 0.82 a	0.54 ± 0.16 a	0.64 ± 0.41 a	0.12 ± 0.07 b	0.44 ± 0.52 ab
<i>Coprococcus</i>	0.68 ± 0.91	0.34 ± 0.27	0.86 ± 1.00	0.27 ± 0.32	0.23 ± 0.19
<i>Prevotellaceae_Prevotella</i>	0.69 ± 0.88 a	0.62 ± 0.89 a	0.18 ± 0.10 a	0.00 ± 0.00 b	0.70 ± 0.84 a
<i>Eubacterium</i>	1.26 ± 2.26 a	0.01 ± 0.01 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.02 ± 0.06 b
<i>Erysipelotrichaceae_Clostridium</i>	0.74 ± 1.35 a	0.02 ± 0.02 b	0.02 ± 0.03 b	0.08 ± 0.03 ab	0.05 ± 0.06 b
<i>Mucispirillum</i>	0.01 ± 0.02 b	0.39 ± 0.16 a	0.04 ± 0.04 b	0.09 ± 0.09 b	0.50 ± 0.84 ab
<i>Ruminococcus</i>	0.18 ± 0.22	0.13 ± 0.05	0.09 ± 0.06	0.20 ± 0.38	0.12 ± 0.19

<i>Rikenella</i>	0.54 ± 0.67 a	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.06 ± 0.15 b
<i>Adlercreutzia</i>	0.14 ± 0.07	0.07 ± 0.06	0.14 ± 0.09	0.08 ± 0.05	0.07 ± 0.03
Other	1.05 ± 0.72 a	0.19 ± 0.13 b	0.22 ± 0.21 b	0.41 ± 0.36 b	0.50 ± 0.64 b

Data are shown in average ± standard deviation. Different letters indicate the significant difference among different groups for the same index, ANOVA with LSD or Tamhane T2 post-hoc test, $p < 0.05$. N = 6. CTL: control; ATBX: antibiotic; EXC: exercise; KGM: the native KGM; EK: combination of exercise and KGM.

Table S6 The relative abundance of top 20 taxa in feces at different levels on day 21

Day 21	CTL	ATBX	EXC	KGM	EK
Phylum					
Proteobacteria	0.54 ± 0.37 b	92.72 ± 5.30	96.77 ± 2.17	70.50 ± 11.98	92.37 ± 10.95

		ab	a	b	a
Bacteroidetes	72.83 ± 7.16 a	1.54 ± 1.40 b	1.17 ± 1.04 b	15.85 ± 8.45 a	5.77 ± 8.91 b
Firmicutes	17.31 ± 9.47 a	5.08 ± 3.32 b	1.78 ± 1.17 b	11.98 ± 3.49 ab	1.36 ± 1.24 b
Verrucomicrobia	8.17 ± 4.38 a	0.05 ± 0.07 b	0.06 ± 0.06 b	0.87 ± 0.38 ab	0.00 ± 0.01 b
Actinobacteria	0.99 ± 0.63 a	0.18 ± 0.15 b	0.11 ± 0.10 b	0.54 ± 0.20 a	0.19 ± 0.39 b
unclassified	0.00 ± 0.00	0.30 ± 0.62	0.05 ± 0.05	0.09 ± 0.08	0.13 ± 0.30
Tenericutes	0.13 ± 0.12 a	0.01 ± 0.01 b	0.00 ± 0.00 b	0.02 ± 0.01 b	0.13 ± 0.30 b
Euryarchaeota	0.00 ± 0.00 b	0.07 ± 0.11 a	0.03 ± 0.02 a	0.04 ± 0.02 a	0.04 ± 0.05 a
Fusobacteria	0.00 ± 0.00 b	0.01 ± 0.02 ab	0.00 ± 0.00 b	0.02 ± 0.02 a	0.00 ± 0.00 b
Cyanobacteria	0.01 ± 0.01	0.01 ± 0.01	0.00 ± 0.00	0.01 ± 0.01	0.00 ± 0.00

Acidobacteria	0.00 ± 0.00 b	0.01 ± 0.01 ab	0.00 ± 0.01 ab	0.02 ± 0.02 a	0.00 ± 0.00 ab
Deferribacteres	0.01 ± 0.01	0.01 ± 0.01	0.00 ± 0.00	0.01 ± 0.01	0.00 ± 0.00
Gemmatimonadetes	0.00 ± 0.00	0.01 ± 0.01	0.00 ± 0.01	0.01 ± 0.01	0.00 ± 0.00
TM7	0.01 ± 0.01a	0.00 ± 0.00b	0.00 ± 0.01b	0.00 ± 0.00ab	0.00 ± 0.00b
Chloroflexi	0.00 ± 0.00	0.00 ± 0.01	0.00 ± 0.00	0.01 ± 0.01	0.00 ± 0.00
Crenarchaeota	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.01	0.00 ± 0.01
Spirochaetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.02	0.00 ± 0.00
Nitrospirae	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 a	0.00 ± 0.00 b
Planctomycetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Thermi	0.00 ± 0.00	0.00 ± 0.01	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Other	0.00 ± 0.00 ab	0.00 ± 0.00 a	0.00 ± 0.00 b	0.01 ± 0.01 a	0.00 ± 0.00 b
Family					

Burkholderiaceae	0.00 ± 0.00 b	64.21 ± 35.02 ab	81.54 ± 11.62 a	21.96 ± 9.89 b	41.69 ± 31.52 ab
Enterobacteriaceae	0.04 ± 0.05 b	18.02 ± 19.95 ab	7.44 ± 6.85 b	16.48 ± 5.75 ab	38.49 ± 26.43 a
S24_7	57.04 ± 8.21 a	0.41 ± 0.44 b	0.53 ± 0.62 b	11.07 ± 6.69 a	0.19 ± 0.28 b
Halomonadaceae	0.01 ± 0.00 b	7.20 ± 6.79 b	6.16 ± 3.72 b	25.95 ± 4.84 a	1.77 ± 1.17 b
Bacteroidaceae	2.84 ± 3.41 a	0.68 ± 0.62 ab	0.30 ± 0.16 b	1.93 ± 0.86 a	5.44 ± 8.59 a
Erysipelotrichaceae	8.64 ± 5.42 a	0.98 ± 1.67 b	0.12 ± 0.09 b	1.21 ± 0.47 ab	0.07 ± 0.13 b
Verrucomicrobiaceae	8.17 ± 4.38 a	0.05 ± 0.07 b	0.06 ± 0.06 b	0.86 ± 0.38 ab	0.00 ± 0.01 b

Moraxellaceae	0.00 ± 0.00 b	0.52 ± 0.63 ab	0.20 ± 0.18 b	0.71 ± 0.58 ab	7.47 ± 9.93 a
unclassified	5.12 ± 6.00 a	0.58 ± 0.73 b	0.16 ± 0.14 b	0.88 ± 0.48 ab	0.26 ± 0.44 b
Bacillaceae	0.00 ± 0.00	2.15 ± 1.92	0.74 ± 0.47	2.90 ± 1.79	0.38 ± 0.32
Paraprevotellaceae	4.78 ± 4.43 a	0.12 ± 0.13 b	0.12 ± 0.15 b	0.71 ± 0.44 ab	0.01 ± 0.03 b
Porphyromonadaceae	3.78 ± 2.91 a	0.05 ± 0.05 b	0.05 ± 0.04 b	0.85 ± 0.53 ab	0.00 ± 0.01 b
Alcaligenaceae	0.37 ± 0.35 b	1.30 ± 1.60 ab	0.55 ± 0.27 b	1.69 ± 0.25 a	0.51 ± 0.22 b
Staphylococcaceae	0.00 ± 0.00 b	0.11 ± 0.14 b	0.06 ± 0.05 b	3.96 ± 2.67 a	0.24 ± 0.15 ab
Lactobacillaceae	2.45 ± 1.77 a	0.35 ± 0.53 b	0.11 ± 0.10 b	0.59 ± 0.26	0.11 ± 0.14 b

				ab	
Prevotellaceae	2.83 ± 2.42 a	0.16 ± 0.11 b	0.09 ± 0.07 b	0.46 ± 0.37 ab	0.03 ± 0.07 b
Pseudomonadaceae	0.00 ± 0.00 b	0.28 ± 0.25 a	0.10 ± 0.08 ab	0.78 ± 0.91 a	1.52 ± 2.55 a
Lachnospiraceae	0.50 ± 0.48 ab	0.32 ± 0.21 ab	0.20 ± 0.19 b	1.09 ± 0.82 a	0.18 ± 0.25 b
Ruminococcaceae	0.56 ± 0.56 ab	0.42 ± 0.27 ab	0.20 ± 0.17 b	0.83 ± 0.55 a	0.06 ± 0.15 b
Rikenellaceae	1.56 ± 2.09 a	0.03 ± 0.03 b	0.04 ± 0.02 b	0.43 ± 0.26 ab	0.01 ± 0.02 b
Other	1.32 ± 0.77 b	2.06 ± 2.31 b	1.23 ± 0.66 b	4.67 ± 0.64 a	1.56 ± 2.32 b
Genus					

unclassified	65.37 ± 6.99 a	19.32 ± 21.18 b	8.39 ± 7.40 c	29.56 ± 9.17 b	38.97 ± 25.77 ab
<i>Burkholderia</i>	0.00 ± 0.00 b	64.20 ± 35.02 ab	81.51 ± 11.61 a	0.19 ± 0.09 b	0.00 ± 0.00 b
<i>Pandoraea</i>	0.00 ± 0.00 b	0.00 ± 0.00 b	0.03 ± 0.02 b	21.77 ± 9.90 ab	41.69 ± 31.52 a
<i>Halomonas</i>	0.01 ± 0.00 b	7.20 ± 6.78 b	6.16 ± 3.72 b	25.94 ± 4.83 a	1.77 ± 1.17 b
<i>Bacteroides</i>	2.84 ± 3.41 a	0.68 ± 0.62 ab	0.30 ± 0.16 b	1.93 ± 0.86 a	5.44 ± 8.59 a
<i>Allobaculum</i>	7.27 ± 6.40 a	0.97 ± 1.67 b	0.10 ± 0.07 b	1.05 ± 0.41 ab	0.05 ± 0.10 b
<i>Akkermansia</i>	8.17 ± 4.38 a	0.05 ± 0.07 b	0.06 ± 0.06 b	0.86 ± 0.38 ab	0.00 ± 0.01 b

<i>Acinetobacter</i>	0.00 ± 0.00 b	0.51 ± 0.61 ab	0.20 ± 0.18 b	0.70 ± 0.58 ab	7.44 ± 9.89 a
<i>Bacillus</i>	0.00 ± 0.00	2.14 ± 1.90	0.73 ± 0.46	2.89 ± 1.80	0.38 ± 0.32
<i>Prevotella</i>	4.78 ± 4.43 a	0.09 ± 0.13 b	0.11 ± 0.15 b	0.70 ± 0.43 ab	0.01 ± 0.03 b
<i>Parabacteroides</i>	3.78 ± 2.91 a	0.04 ± 0.04 b	0.05 ± 0.04 b	0.85 ± 0.53 ab	0.00 ± 0.01 b
<i>Staphylococcaceae_Staphylococcus</i>	0.00 ± 0.00 b	0.11 ± 0.13 b	0.06 ± 0.05 b	3.96 ± 2.67 a	0.24 ± 0.15 ab
<i>Achromobacter</i>	0.00 ± 0.00 c	1.28 ± 1.60 ab	0.55 ± 0.27 b	1.56 ± 0.26 a	0.51 ± 0.22 b
<i>Lactobacillus</i>	2.45 ± 1.77 a	0.35 ± 0.53 b	0.11 ± 0.10 b	0.57 ± 0.26 ab	0.11 ± 0.14 b
<i>Prevotellaceae_Prevotella</i>	2.83 ± 2.42 a	0.16 ± 0.11 b	0.09 ± 0.07 b	0.46 ± 0.37	0.03 ± 0.07 b

				ab	
<i>Pseudomonadaceae_Pseudomonas</i>	0.00 ± 0.00 b	0.28 ± 0.25 a	0.10 ± 0.08 a	0.78 ± 0.91 a	1.47 ± 2.44 a
<i>Serratia</i>	0.00 ± 0.00	0.54 ± 0.58	0.25 ± 0.17	1.26 ± 0.87	0.53 ± 0.33
<i>Chelativorans</i>	0.00 ± 0.00 b	0.25 ± 0.31 ab	0.18 ± 0.10 ab	0.83 ± 0.24 a	0.08 ± 0.15 b
<i>Bifidobacterium</i>	0.64 ± 0.51 a	0.06 ± 0.07 b	0.02 ± 0.04 b	0.27 ± 0.21 ab	0.01 ± 0.03 b
<i>Faecalibacterium</i>	0.00 ± 0.00 b	0.25 ± 0.19 a	0.12 ± 0.09 ab	0.38 ± 0.28 a	0.03 ± 0.08 b
Other	1.88 ± 0.80 ab	1.50 ± 1.39 b	0.87 ± 0.57 b	3.49 ± 1.27 a	1.22 ± 1.77 b

Data are shown in average ± standard deviation. Different letters indicate the significant difference among different groups for the same index, ANOVA with LSD or Tamhane T2 post-hoc test, $p < 0.05$. N = 6. CTL: control; ATBX: antibiotic; EXC: exercise; KGM: the native KGM; EK: combination of exercise and KGM.

Table S7 The relative abundance of top 20 taxa in feces at different levels on day 42

Day 42	CTL	ATBX	EXC	KGM	EK
Phylum					
Bacteroidetes	70.27 ± 27.36	77.95 ± 9.21	68.01 ± 8.69	70.02 ± 20.78	78.30 ± 11.06
Firmicutes	25.32 ± 26.48	20.50 ± 9.38	11.83 ± 6.13	14.31 ± 6.76	13.38 ± 3.58
Actinobacteria	0.40 ± 0.58 b	0.33 ± 0.35 b	16.25 ± 10.14 a	2.50 ± 2.62 ab	6.54 ± 10.84 ab
Proteobacteria	3.38 ± 6.04 b	0.89 ± 0.55 b	3.90 ± 1.11 a	7.34 ± 10.72 ab	1.32 ± 0.72 ab
Verrucomicrobia	0.00 ± 0.00 b	0.32 ± 0.56 ab	0.00 ± 0.01 b	5.67 ± 6.86 a	0.02 ± 0.02 b
Tenericutes	0.45 ± 0.55 a	0.00 ± 0.01 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.05 ± 0.05 a
Deferribacteres	0.02 ± 0.03 ab	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.35 ± 0.50 a

unclassified	0.06 ± 0.12	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.03 ± 0.08
TM7	0.08 ± 0.14 a	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b
Chloroflexi	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.05 ± 0.12	0.00 ± 0.00
Gemmatimonadetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.04 ± 0.10	0.00 ± 0.00
Planctomycetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.02 ± 0.06	0.00 ± 0.00
Armatimonadetes	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.02 ± 0.05	0.00 ± 0.00
Fusobacteria	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.03	0.00 ± 0.00
Nitrospirae	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.01 ± 0.03	0.00 ± 0.00
Cyanobacteria	0.00 ± 0.00 ab	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.01 ± 0.01 a
Acidobacteria	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.01	0.00 ± 0.00
Crenarchaeota	0.01 ± 0.01 a	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b	0.00 ± 0.00 b
Euryarchaeota	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
WS3	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
Other	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00

Family					
S24_7	54.55 ± 21.82 ab	32.67 ± 11.60 b	44.26 ± 8.41 ab	44.44 ± 16.80 ab	59.28 ± 9.73 a
Paraprevotellaceae	8.46 ± 4.92 a	25.39 ± 11.92 a	8.12 ± 4.72 a	0.00 ± 0.00 b	8.33 ± 2.03 a
Bacteroidaceae	3.73 ± 2.66 b	14.23 ± 9.03 a	7.30 ± 5.52 ab	18.15 ± 18.33 a	4.46 ± 2.00 b
unclassified	20.93 ± 26.97 a	9.81 ± 9.26 a	1.04 ± 0.69 b	2.46 ± 3.89 b	4.08 ± 2.63 ab
Porphyromonadaceae	1.13 ± 0.75 b	5.56 ± 2.96 ab	6.27 ± 2.74 a	5.44 ± 3.49 ab	3.93 ± 1.52 a
Lactobacillaceae	1.84 ± 1.82	3.52 ± 5.58	2.24 ± 2.55	3.01 ± 2.44	5.82 ± 2.69
Bifidobacteriaceae	0.00 ± 0.00 b	0.01 ± 0.02 b	6.41 ± 3.96 a	2.23 ± 2.48 ab	5.91 ± 10.73 ab

Erysipelotrichaceae	0.62 ± 0.38 b	0.89 ± 1.03 b	3.29 ± 2.16 a	4.55 ± 4.22 a	2.44 ± 1.39 ab
Lachnospiraceae	0.68 ± 0.45	4.00 ± 2.91	2.51 ± 1.24	2.26 ± 2.30	1.77 ± 1.25
Coriobacteriaceae	0.20 ± 0.11 b	0.31 ± 0.33 b	9.84 ± 8.54 a	0.22 ± 0.22 b	0.63 ± 0.35 ab
Ruminococcaceae	1.28 ± 1.50	2.26 ± 1.23	2.83 ± 4.65	1.11 ± 1.76	1.20 ± 0.78
Enterobacteriaceae	1.24 ± 2.21 ab	0.05 ± 0.04 b	0.22 ± 0.47 b	6.66 ± 10.74 a	0.31 ± 0.30 ab
Verrucomicrobiaceae	0.00 ± 0.00 b	0.32 ± 0.56 ab	0.00 ± 0.01 b	5.67 ± 6.86 a	0.02 ± 0.02 b
Prevotellaceae	0.33 ± 0.25 ab	0.00 ± 0.00 b	1.56 ± 0.59 a	1.97 ± 1.95 a	0.30 ± 0.20 ab
Alcaligenaceae	0.20 ± 0.28 b	0.17 ± 0.08 b	2.18 ± 1.05 a	0.06 ± 0.06 b	0.38 ± 0.28 ab
Rikenellaceae	1.96 ± 1.40 a	0.09 ± 0.06 b	0.49 ± 0.47 ab	0.00 ± 0.00 bc	0.00 ± 0.00 c
Helicobacteraceae	0.11 ± 0.08 b	0.61 ± 0.58 a	1.18 ± 1.22 a	0.12 ± 0.17 b	0.00 ± 0.00 b
Turicibacteraceae	0.00 ± 0.00 b	0.00 ± 0.00 b	0.06 ± 0.06 ab	0.11 ± 0.27 a	0.00 ± 0.00 b

Pseudomonadaceae	0.77 ± 1.65 a	0.00 ± 0.00 b	0.00 ± 0.00 b	0.87 ± 0.93 b	0.00 ± 0.00 b
Moraxellaceae	0.46 ± 1.12	0.00 ± 0.00	0.00 ± 0.00	0.05 ± 0.12	0.00 ± 0.01
Other	1.51 ± 2.92 a	0.09 ± 0.04 b	0.22 ± 0.13 ab	0.62 ± 0.66 a	1.12 ± 0.62 a
Genus					
unclassified	79.72 ± 10.12 a	45.27 ± 18.28 b	58.09 ± 11.77 b	54.39 ± 12.65 b	65.07 ± 10.22 ab
<i>Prevotella</i>	8.46 ± 4.92 a	25.39 ± 11.92 a	8.09 ± 4.70 a	0.00 ± 0.00 b	7.63 ± 2.19 a
<i>Bacteroides</i>	3.73 ± 2.66 b	14.23 ± 9.03 a	7.30 ± 5.52 ab	18.15 ± 18.33 a	4.46 ± 2.00 b
<i>Parabacteroides</i>	1.13 ± 0.75 b	5.56 ± 2.96 ab	6.27 ± 2.74 a	5.44 ± 3.49 ab	3.93 ± 1.52 a
<i>Lactobacillus</i>	1.84 ± 1.82 b	3.52 ± 5.58	2.24 ± 2.55	3.01 ± 2.44 ab	5.82 ± 2.69 a

		ab	ab		
<i>Bifidobacterium</i>	0.00 ± 0.00 b	0.01 ± 0.02 b	6.41 ± 3.96 a	2.23 ± 2.48 ab	5.91 ± 10.73 ab
<i>Allobaculum</i>	0.45 ± 0.36	0.78 ± 1.01	2.08 ± 2.21	2.91 ± 4.33	2.04 ± 1.39
<i>Akkermansia</i>	0.00 ± 0.00 b	0.32 ± 0.56 ab	0.00 ± 0.01 b	5.67 ± 6.86 a	0.02 ± 0.02 b
<i>Oscillospira</i>	0.89 ± 1.30 a	1.72 ± 1.02 a	0.95 ± 0.67 a	0.23 ± 0.23 b	0.82 ± 0.71 a
<i>Prevotellaceae_Prevotella</i>	0.33 ± 0.25 a	0.00 ± 0.00 b	1.55 ± 0.59 a	1.97 ± 1.95 a	0.30 ± 0.20 ab
<i>Ruminococcaceae_Ruminococcus</i>	0.26 ± 0.28	0.31 ± 0.24	1.70 ± 3.90	0.79 ± 1.42	0.15 ± 0.08
<i>Sutterella</i>	0.20 ± 0.28 b	0.16 ± 0.08 b	2.18 ± 1.05 a	0.05 ± 0.06 b	0.36 ± 0.28 ab
<i>Ruminococcus</i>	0.06 ± 0.05	0.41 ± 0.11	0.88 ± 0.88	0.94 ± 1.22	0.44 ± 0.82
<i>Coprococcus</i>	0.15 ± 0.16	0.72 ± 0.93	0.17 ± 0.24	0.16 ± 0.25	0.53 ± 0.44
<i>Adlercreutzia</i>	0.17 ± 0.11 b	0.14 ± 0.12 b	0.28 ± 0.12 ab	0.15 ± 0.22 b	0.59 ± 0.35 a

<i>Lachnospiraceae_Clostridium</i>	0.01 ± 0.01 b	0.45 ± 0.62 a	0.22 ± 0.20 a	0.30 ± 0.22 a	0.14 ± 0.20 ab
<i>Erysipelotrichaceae_Clostridium</i>	0.01 ± 0.01 b	0.04 ± 0.05 b	0.09 ± 0.08 b	0.83 ± 0.89 a	0.11 ± 0.14 b
<i>Coprobacillus</i>	0.00 ± 0.00 b	0.00 ± 0.00 b	0.52 ± 0.96 a	0.41 ± 0.73 a	0.02 ± 0.02 ab
<i>Turicibacter</i>	0.00 ± 0.00 b	0.00 ± 0.00 b	0.06 ± 0.06 ab	0.87 ± 0.93 a	0.00 ± 0.00 b
<i>Pseudomonas</i>	0.77 ± 1.65 a	0.00 ± 0.00 b	0.00 ± 0.00 b	0.11 ± 0.27 b	0.00 ± 0.00 b
Other	1.83 ± 3.48	0.97 ± 0.71	0.91 ± 0.96	1.68 ± 1.84	1.68 ± 0.84

Data are shown in average ± standard deviation. Different letters indicate the significant difference among different groups for the same index, ANOVA with LSD or Tamhane T2 post-hoc test, $p < 0.05$. N = 6. CTL: control; ATBX: antibiotic; EXC: exercise; KGM: the native KGM; EK: combination of exercise and KGM.