Electronic Supplementary Material (ESI) for Food & Function.
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Table S1. The composition of the standard maintenance diet.

Ingredients	Proportion (%)
Corn starch	28.2
Wheat bran	27.0
Fish meal	5.2
Soy bean flour	17.3
Wheat flour	16
Yeast powder	1
Bone meal	2
Salt	1
Vitamin Mix	1
Mineral Mix	1.3
Total	100

Table S2. The numbers of sequences recorded in each group.

	Ctrl-14	CiMe-14	ANP-CiMe-14	Ctrl-42	CiMe+NR-42	CiMe+ANP-42
1	50935	52052	46850	66748	65493	63455
2	57017	58643	46847	74002	67645	59882
3	55907	50208	49516	71765	64970	57616
4	49720	51157	49202	74678	67914	55667
5	49026	49676	41120	73555	68044	66218
Average	52521±3682.9	52347.2±3635.0	46707±3367.9	72149.6±3206.4	66813.2±1462.8	60567.6±4285.5
Min	49026	49676	41120	66748	64970	55667

Fig. S1. FT-IR spectrum of ANP.

Fig. S2. Body weight gains of mice were measured weekly during the experiment. Data are expressed as mean ± SD (n=8 per group), *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, and ****$p < 0.001$ by the Tukey's HSD tests.

Fig. S3. The total numbers of OTUs recorded in each group. Data are expressed as mean ± SD (n=5 per group), *$p < 0.05$, **$p < 0.01$, and ***$p < 0.001$ by the Tukey's HSD tests.

Fig. S4. The relative proportions of main phyla in different groups at the level. Ctrl-14 vs CiMe-14 (A), CiMe-14 vs ANP-CiMe-14 (B), and CiMe-14 vs CiMe+ANP-42 (C). Data are expressed as mean ± SD (n=5 per group), *$p < 0.05$ and **$p < 0.01$ by the Student t-tests.

Fig. S5. The relative proportions in different groups at the phylum (A), order (B), class (C), family (D), and genus (E) level.

Fig. S6. Difference in dominant microorganisms between groups based on LDA>3.5.

Fig. S7. The main microbiotas relative proportions in different groups at the genera level. Data are expressed as mean ± SD (n=5 per group), *$p < 0.05$, **$p < 0.01$, and ***$p < 0.001$ by Kruskal-Wallis tests.

Fig. S1.

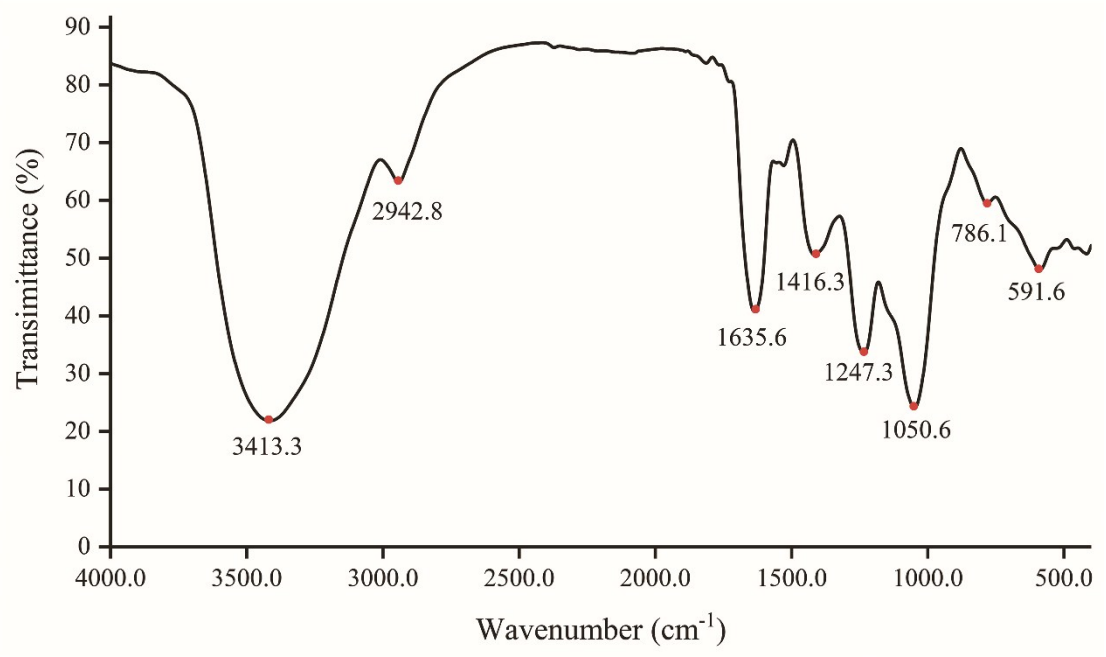

Transimittance (%)
Wavenumber (cm-1)
3413.3
2942.8
1635.6
1416.3
1247.3
1050.6
786.1
591.6

Fig. S2.

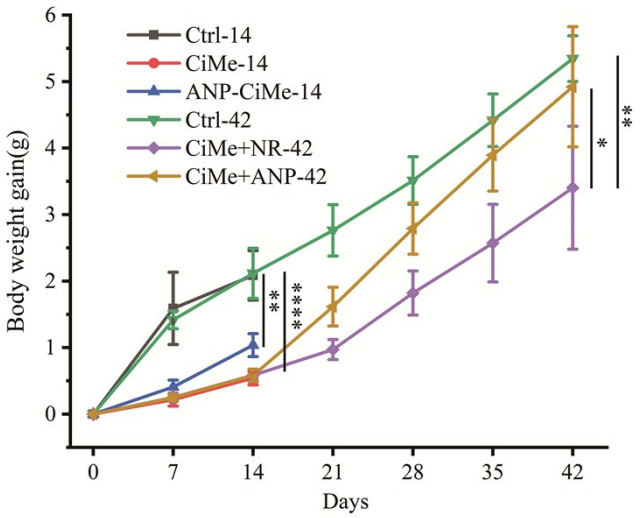

Ctrl-14
CiMe-14
ANP-CiMe-14
Ctrl-42
CiMe+NR-42
CiMe+ANP-42
Body weight gain(g)
Days
0
1
2
3
4
5
6
0
7
14
21
28
35
42
**
****
*
**

Fig. S3.

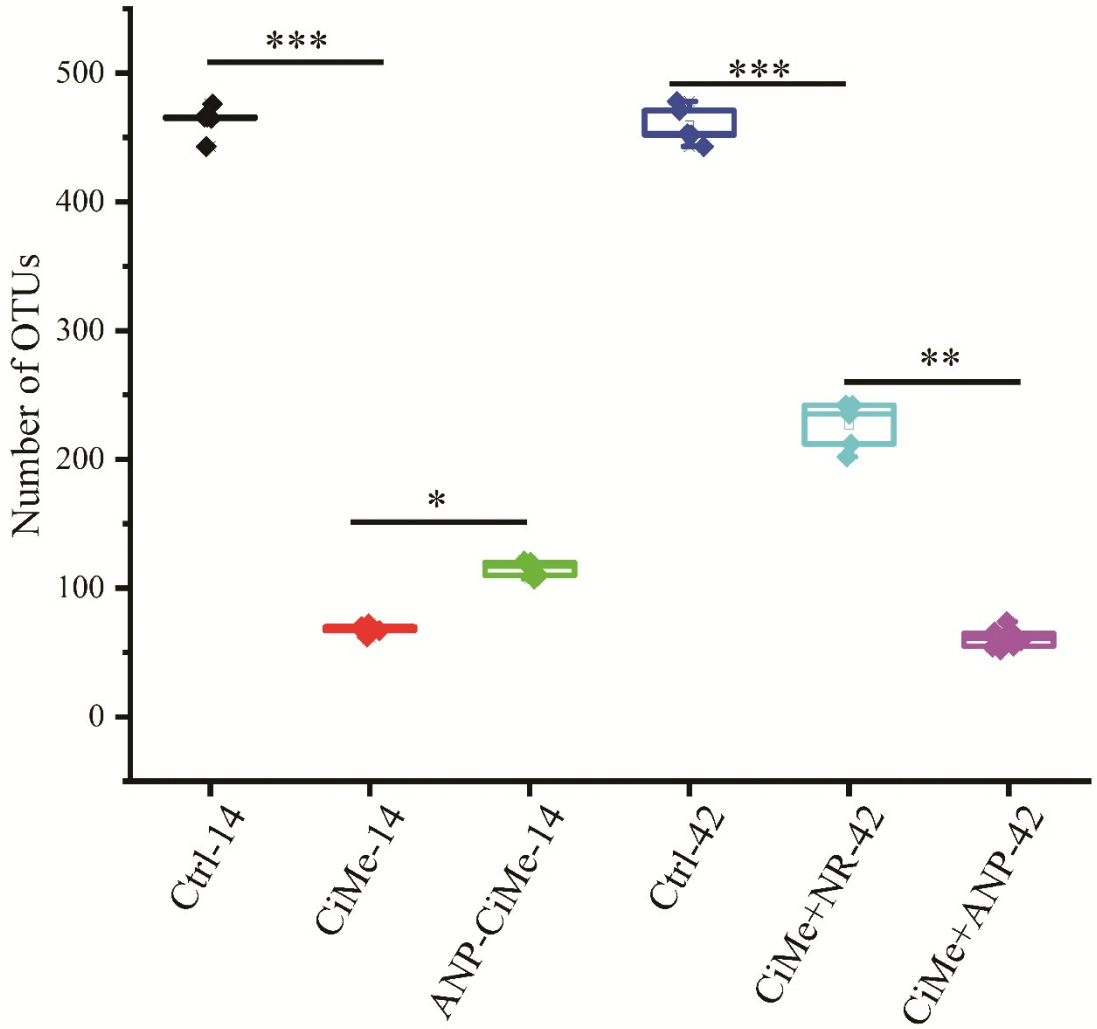

Number of OTUs
0
100
200
300
400
500
***
*
***
**
Ctrl-14
CiMe-14
ANP-CiMe-14
Ctrl-42
CiMe+NR-42
CiMe+ANP-42

Fig. S4.

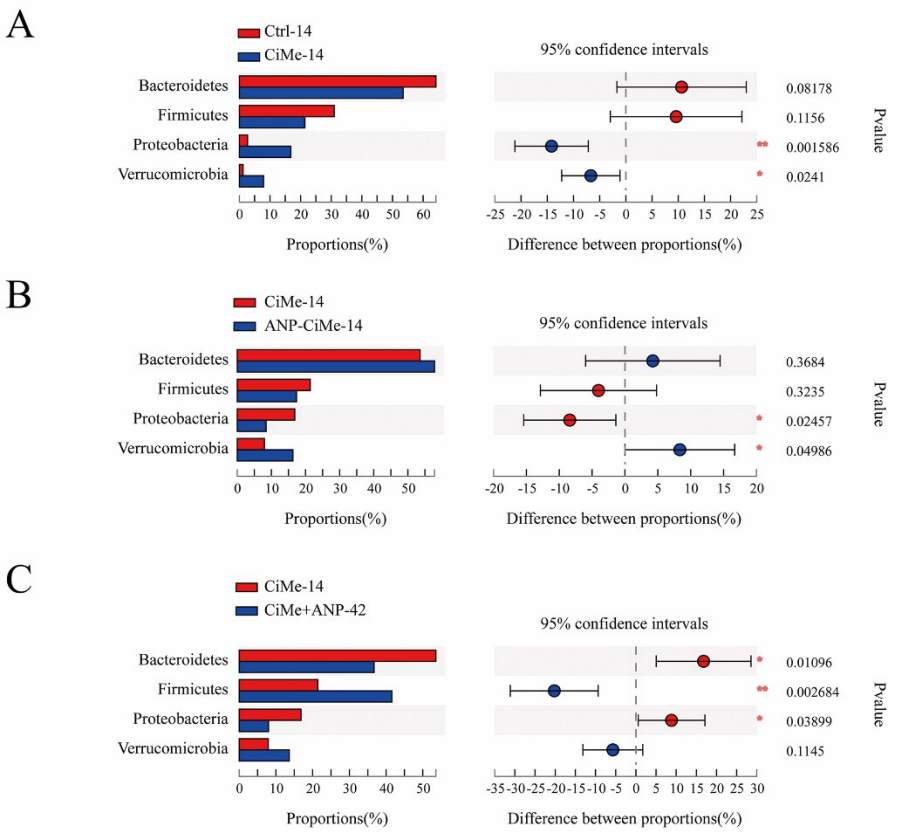

A
Ctrl-14
CiMe-14
Bacteroidetes
Firmicutes
Proteobacteria
Verrucomicrobia
0 10 20 30 40 50 60
Proportions(%)
95% confidence intervals
0.08178
0.1156
0.001586
0.0241
-25 -20 -15 -10 -5 0 5 10 15 20 25
Difference between proportions(%)
Pvalue
B
CiMe-14
ANP-CiMe-14
Bacteroidetes
Firmicutes
Proteobacteria
Verrucomicrobia
0 10 20 30 40 50
Proportions(%)
95% confidence intervals
0.3684
0.3235
0.02457
0.04986
-20 -15 -10 -5 0 5 10 15 20
Difference between proportions(%)
Pvalue
C
CiMe-14
CiMe+ANP-42
Bacteroidetes
Firmicutes
Proteobacteria
Verrucomicrobia
0 10 20 30 40 50
Proportions(%)
95% confidence intervals
0.01096
0.002684
0.03899
0.1145
-35 -30 -25 -20 -15 -10 -5 0 5 10 15 20 25 30
Difference between proportions(%)
Pvalue

Fig. S5.

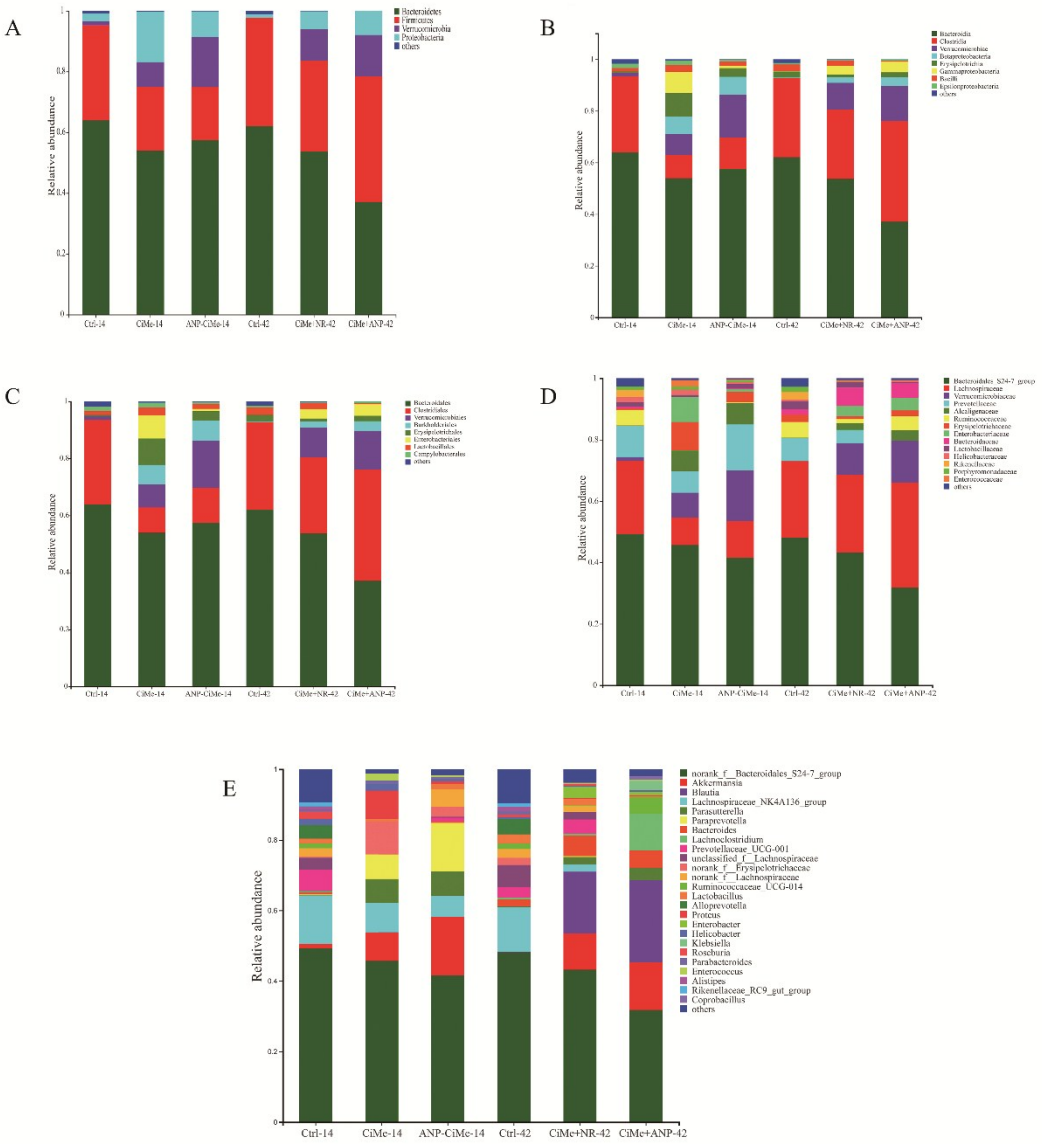
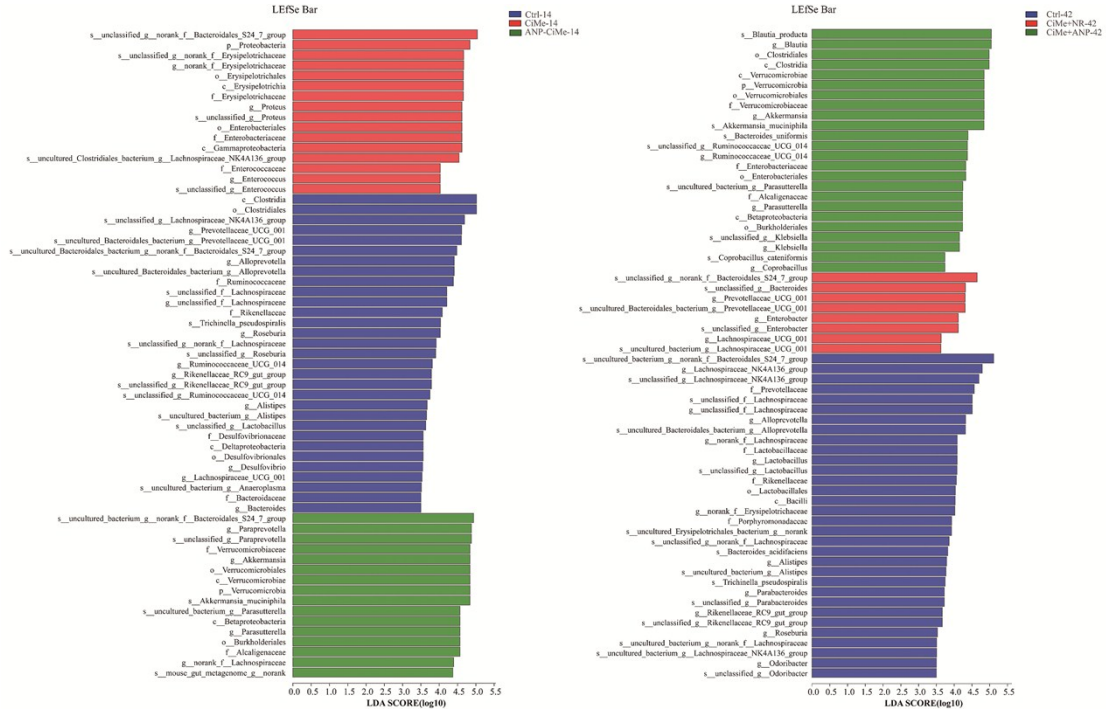

A
Relative abundance
Ctrl-14
CiMe-14
ANP-CiMe-14
Ctrl-42
CiMe+NR-42
CiMe+ANP-42
Bacteroidetes
Firmicutes
Verrucomicrobia
Proteobacteria
others
B
Relative abundance
Bacteroidia
Clostridia
Verrucomicrobiae
Betaproteobacteria
Erysipelotrichia
Gammaproteobacteria
Bacilli
Epsilonproteobacteria
others
C
Relative abundance
Bacteroidales
Clostridiales
Verrucomicrobiales
Burkholderiales
Erysipelotrichales
Enterobacteriales
Lactobacillales
Campylobacterales
others
D
Relative abundance
Bacteroidales_S24-7_group
Lachnospiraceae
Verrucomicrobiaceae
Prevotellaceae
Alcaligenaceae
Ruminococcaceae
Erysipelotrichaceae
Enterobacteriaceae
Bacteroidaceae
Lactobacillaceae
Helicobacteraceae
Rikenellaceae
Porphyromonadaceae
Enterococcaceae
others
E
Relative abundance
Ctrl-14
CiMe-14
ANP-CiMe-14
Ctrl-42
CiMe+NR-42
CiMe+ANP-42
norank_f__Bacteroidales_S24-7_group
Akkermansia
Blautia
Lachnospiraceae_NK4A136_group
Parasutterella
Paraprevotella
Bacteroides
Lachnoclostridium
Prevotellaceae_UCG-001
unclassified_f__Lachnospiraceae
norank_f__Erysipelotrichaceae
norank_f__Lachnospiraceae
Ruminococcaceae_UCG-014
Lactobacillus
Alloprevotella
Proteus
Enterobacter
Helicobacter
Klebsiella
Roseburia
Parabacteroides
Enterococcus
Alistipes
Rikenellaceae_RC9_gut_group
Coprobacillus
others

Fig. S6.


LEfSe Bar
Ctrl-14
CiMe-14
ANP-CiMe-14
s__unclassified_g__norank_f__Bacteroidales_S24_7_group
p__Proteobacteria
s__unclassified_g__norank_f__Erysipelotrichaceae
g__norank_f__Erysipelotrichaceae
o__Erysipelotrichales
c__Erysipelotrichia
f__Erysipelotrichaceae
g__Proteus
s__unclassified_g__Proteus
o__Enterobacteriales
f__Enterobacteriaceae
c__Gammaproteobacteria
s__uncultured_Clostridiales_bacterium_g__Lachnospiraceae_NK4A136_group
f__Enterococcaceae
g__Enterococcus
s__unclassified_g__Enterococcus
c__Clostridia
o__Clostridiales
s__unclassified_g__Lachnospiraceae_NK4A136_group
g__Prevotellaceae_UCG_001
s__uncultured_Bacteroidales_bacterium_g__Prevotellaceae_UCG_001
s__uncultured_Bacteroidales_bacterium_g__norank_f__Bacteroidales_S24_7_group
g__Alloprevotella
s__uncultured_Bacteroidales_bacterium_g__Alloprevotella
f__Ruminococcaceae
s__unclassified_f__Lachnospiraceae
g__unclassified_f__Lachnospiraceae
f__Rikenellaceae
s__Trichinella_pseudospiralis
g__Roseburia
s__unclassified_g__norank_f__Lachnospiraceae
s__unclassified_g__Roseburia
g__Ruminococcaceae_UCG_014
g__Rikenellaceae_RC9_gut_group
s__unclassified_g__Rikenellaceae_RC9_gut_group
s__unclassified_g__Ruminococcaceae_UCG_014
g__Alistipes
s__uncultured_bacterium_g__Alistipes
s__unclassified_g__Lactobacillus
f__Desulfovibrionaceae
c__Deltaproteobacteria
o__Desulfovibrionales
g__Desulfovibrio
g__Lachnospiraceae_UCG_001
s__uncultured_bacterium_g__Anaeroplasma
f__Bacteroidaceae
g__Bacteroides
s__uncultured_bacterium_g__norank_f__Bacteroidales_S24_7_group
g__Paraprevotella
s__unclassified_g__Paraprevotella
f__Verrucomicrobiaceae
g__Akkermansia
o__Verrucomicrobiales
c__Verrucomicrobiae
p__Verrucomicrobia
s__Akkermansia_muciniphila
s__uncultured_bacterium_g__Parasutterella
c__Betaproteobacteria
g__Parasutterella
o__Burkholderiales
f__Alcaligenaceae
g__norank_f__Lachnospiraceae
s__mouse_gut_metagenome_g__norank
0.0 0.5 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0 5.5
LDA SCORE(log10)
LEfSe Bar
Ctrl-42
CiMe+NR-42
CiMe+ANP-42
s__Blautia_producta
g__Blautia
o__Clostridiales
c__Clostridia
c__Verrucomicrobiae
p__Verrucomicrobia
o__Verrucomicrobiales
f__Verrucomicrobiaceae
g__Akkermansia
s__Akkermansia_muciniphila
s__Bacteroides_uniformis
s__unclassified_g__Ruminococcaceae_UCG_014
g__Ruminococcaceae_UCG_014
f__Enterobacteriaceae
o__Enterobacteriales
s__uncultured_bacterium_g__Parasutterella
f__Alcaligenaceae
g__Parasutterella
c__Betaproteobacteria
o__Burkholderiales
s__unclassified_g__Klebsiella
g__Klebsiella
s__Coprobacillus_cateniformis
g__Coprobacillus
s__unclassified_g__norank_f__Bacteroidales_S24_7_group
s__unclassified_p__Bacteroides
g__Prevotellaceae_UCG_001
s__uncultured_Bacteroidales_bacterium_g__Prevotellaceae_UCG_001
g__Enterobacter
s__unclassified_g__Enterobacter
g__Lachnospiraceae_UCG_001
s__uncultured_bacterium_g__Lachnospiraceae_UCG_001
s__uncultured_bacterium_g__norank_f__Bacteroidales_S24_7_group
g__Lachnospiraceae_NK4A136_group
s__unclassified_g__Lachnospiraceae_NK4A136_group
f__Prevotellaceae
s__unclassified_f__Lachnospiraceae
g__unclassified_f__Lachnospiraceae
g__Alloprevotella
s__uncultured_Bacteroidales_bacterium_g__Alloprevotella
g__norank_f__Lachnospiraceae
f__Lactobacillaceae
g__Lactobacillus
s__unclassified_g__Lactobacillus
f__Rikenellaceae
o__Lactobacillales
c__Bacilli
g__norank_f__Erysipelotrichaceae
f__Porphyromonadaceae
s__uncultured_Erysipelotrichales_bacterium_g__norank
s__unclassified_g__norank_f__Lachnospiraceae
s__Bacteroides_acidifaciens
g__Alistipes
s__uncultured_bacterium_g__Alistipes
s__Trichinella_pseudospiralis
g__Parabacteroides
s__unclassified_g__Parabacteroides
g__Rikenellaceae_RC9_gut_group
s__unclassified_g__Rikenellaceae_RC9_gut_group
g__Roseburia
s__uncultured_bacterium_g__norank_f__Lachnospiraceae
s__uncultured_bacterium_g__Lachnospiraceae_NK4A136_group
g__Odoribacter
s__unclassified_g__Odoribacter
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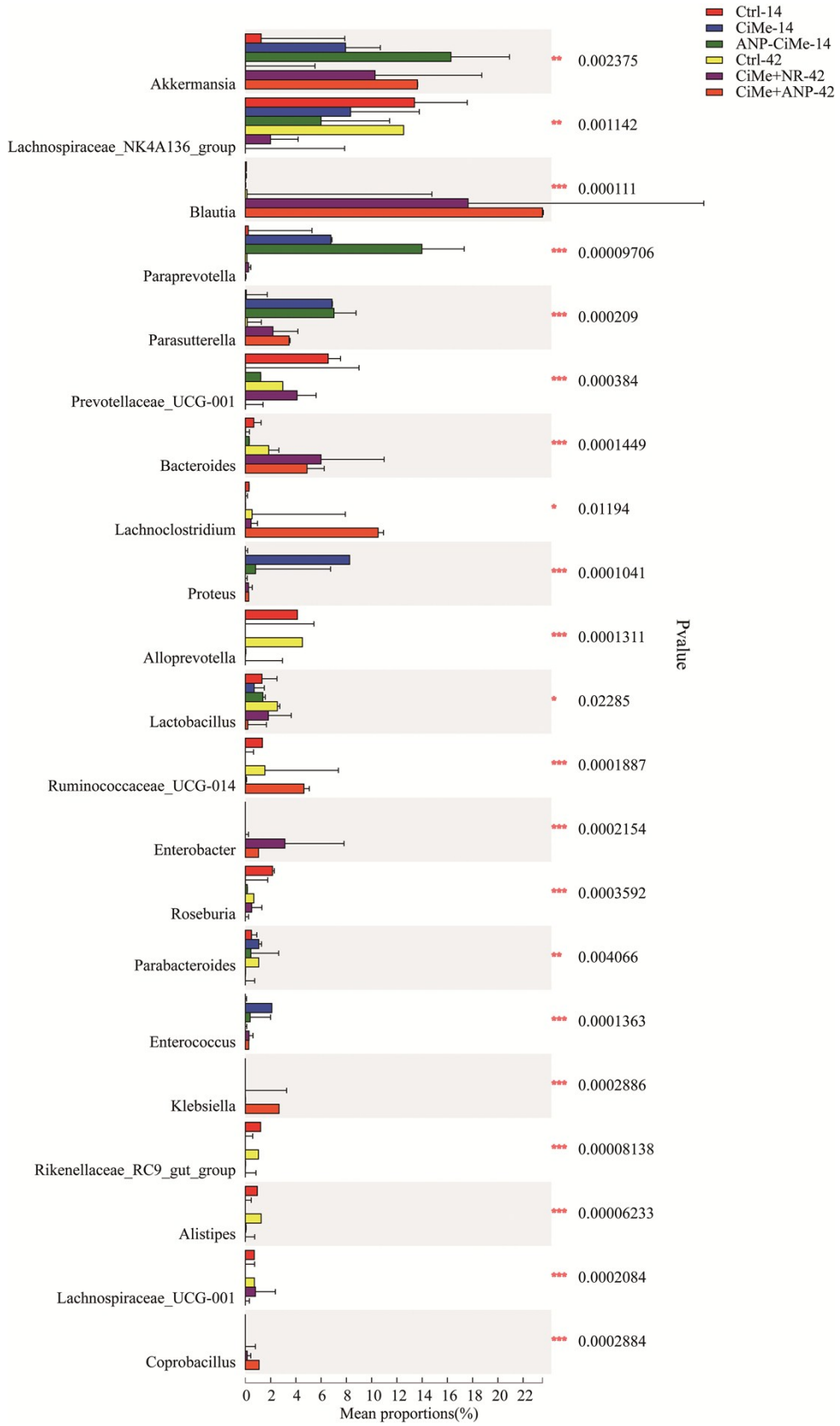
LDA SCORE(log10)

Fig. S7.


Ctrl-14
CiMe-14
ANP-CiMe-14
Ctrl-42
CiMe+NR-42
CiMe+ANP-42
Akkermansia
Lachnospiraceae_NK4A136_group
Blautia
Paraprevotella
Parasutterella
Prevotellaceae_UCG-001
Bacteroides
Lachnoclostridium
Proteus
Alloprevotella
Lactobacillus
Ruminococcaceae_UCG-014
Enterobacter
Roseburia
Parabacteroides
Enterococcus
Klebsiella
Rikenellaceae_RC9_gut_group
Alistipes
Lachnospiraceae_UCG-001
Coprobacillus
** 0.002375
** 0.001142
*** 0.000111
*** 0.00009706
*** 0.000209
*** 0.000384
*** 0.0001449
* 0.01194
*** 0.0001041
*** 0.0001311
* 0.02285
*** 0.0001887
*** 0.0002154
*** 0.0003592
** 0.004066
*** 0.0001363
*** 0.0002886
*** 0.00008138
*** 0.00006233
*** 0.0002084
*** 0.0002884
Pvalue
0 2 4 6 8 10 12 14 16 18 20 22
Mean proportions(%)