

## Supplementary materials

**Table S1** Composition of three diets namely a control diet (CTL), a high-choline diet with 1% free choline (Choline), and a high-choline diet with 1% free choline plus 0.5% mangiferin (Choline + MGF).

<b>Ingredient (g)</b>	<b>CTL</b>	<b>Choline</b>	<b>Choline + MGF</b>
Corn starch	600.2	600.2	600.2
Casein	140.0	140.0	140.0
Sucrose	100.0	100.0	100.0
Powdered cellulose	50.0	50.0	50.0
Lard	40.0	40.0	40.0
AIN 93 Mineral Mix	35.0	35.0	35.0
Gelatin	20.0	20.0	20.0
AIN 93 Vitamin Mix	10.0	10.0	10.0
Choline Bitartrate	2.5	2.5	2.5
<sub>DL</sub> -Methionine	2.3	2.3	2.3
Choline chloride*	-	13.4	13.4
Mangiferin	-	-	5.0
<b>Total</b>	<b>1000.0</b>	<b>1013.4</b>	<b>1018.4</b>
<b>kcal/g</b>	<b>3.9</b>	<b>3.9</b>	<b>3.9</b>
<b>% kcal</b>			
Carbohydrate	73.8	73.8	73.8
Protein	16.9	16.9	16.9
Fat	9.4	9.4	9.4

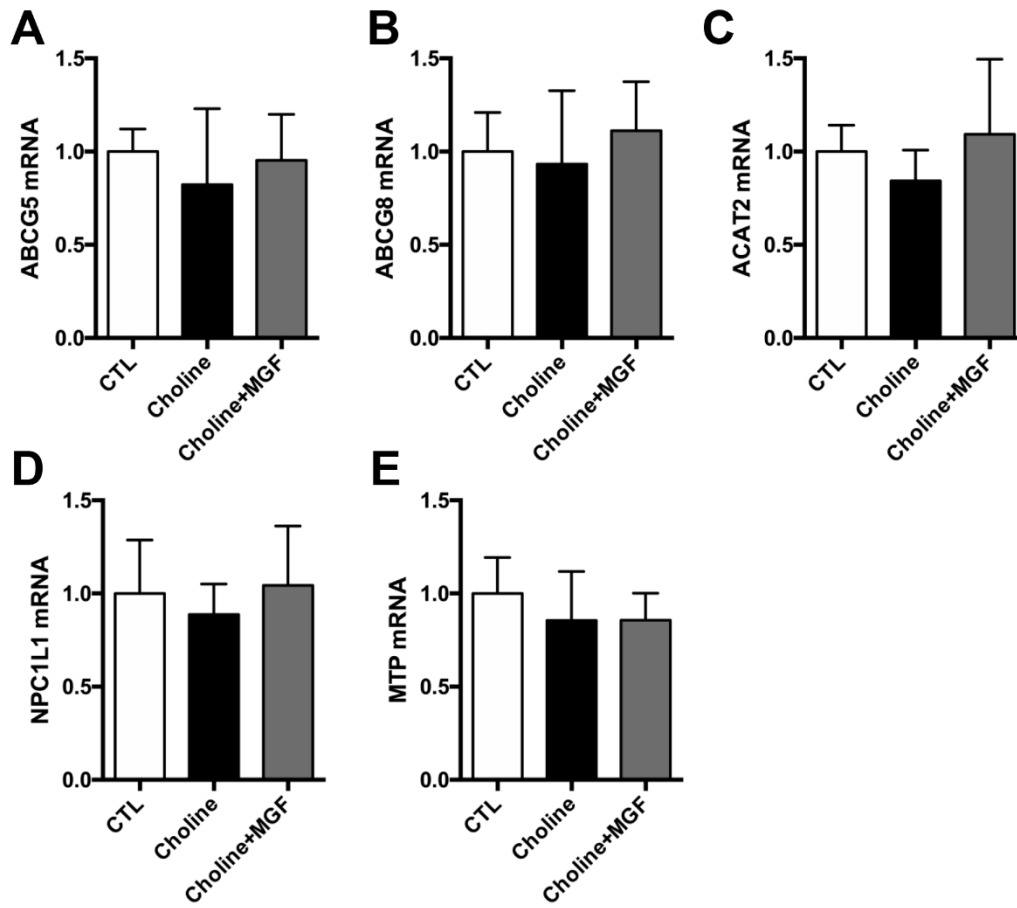
\*Choline chloride equivalent to 1% free choline was dissolved in distilled water and then mixed with the other ingredients.

**Table S2** Relative abundance (%) of 25 key genera among three groups of ApoE<sup>-/-</sup> mice fed a control diet (CTL), a high-choline diet with 1% free choline (Choline), or a high-choline diet with 1% free choline plus 0.5% mangiferin (Choline + MGF) for 15 weeks.

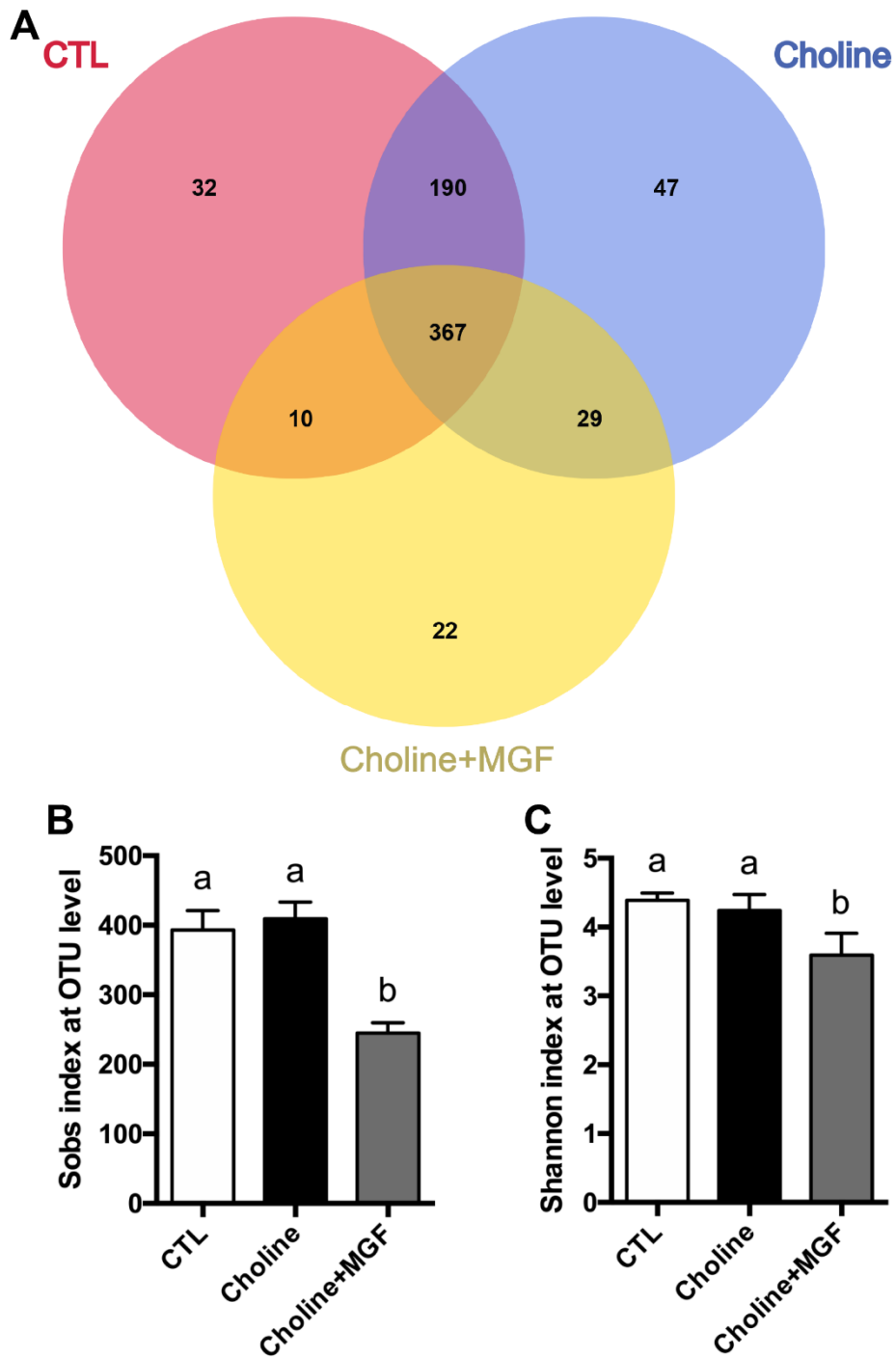
Relative abundance (%)	CTL	Choline	Choline + MGF	<i>p</i> value
<i>Acetatifactor</i>	2.94 ± 1.48 <sup>a</sup>	2.58 ± 1.41 <sup>a</sup>	0.20 ± 0.31 <sup>b</sup>	0.001
<i>Akkermansia</i>	1.67 ± 2.42 <sup>b</sup>	1.36 ± 1.79 <sup>b</sup>	19.10 ± 12.12 <sup>a</sup>	0.003
<i>Alistipes</i>	11.14 ± 5.89	11.47 ± 4.93	17.77 ± 4.84	0.065
<i>Allobaculum</i>	0.00 ± 0.00	0.00 ± 0.00	1.71 ± 3.39	0.063
<i>Bacteroides</i>	1.58 ± 1.86 <sup>b</sup>	4.28 ± 5.62 <sup>ab</sup>	6.48 ± 2.43 <sup>a</sup>	0.005
<i>Bilophila</i>	2.01 ± 1.76 <sup>a</sup>	1.23 ± 0.37 <sup>ab</sup>	0.12 ± 0.07 <sup>b</sup>	0.001
<i>Blautia</i>	3.24 ± 4.41 <sup>ab</sup>	10.66 ± 10.58 <sup>a</sup>	0.65 ± 1.11 <sup>b</sup>	0.022
<i>Desulfovibrio</i>	1.54 ± 0.66 <sup>b</sup>	1.27 ± 0.81 <sup>b</sup>	3.35 ± 1.41 <sup>a</sup>	0.005
<i>Dubosiella</i>	1.19 ± 1.85	0.48 ± 0.49	0.02 ± 0.05	0.095
<i>Faecalibaculum</i>	1.01 ± 1.55	0.71 ± 0.87	2.19 ± 2.91	0.129
<i>GCA-900066575</i>	3.07 ± 1.29 <sup>a</sup>	1.00 ± 1.03 <sup>b</sup>	0.61 ± 0.26 <sup>b</sup>	0.003
<i>Helicobacter</i>	5.50 ± 2.28 <sup>b</sup>	7.89 ± 3.12 <sup>a</sup>	2.09 ± 0.95 <sup>c</sup>	0.002
<i>Ileibacterium</i>	1.44 ± 2.28	0.11 ± 0.19	0.01 ± 0.02	0.051
<i>Lachnospiraceae_UCG-006</i>	0.25 ± 0.14 <sup>b</sup>	0.13 ± 0.08 <sup>b</sup>	1.11 ± 1.02 <sup>a</sup>	0.001
<i>Odoribacter</i>	1.61 ± 0.99 <sup>b</sup>	2.86 ± 1.17 <sup>a</sup>	0.36 ± 0.11 <sup>c</sup>	0.001
<i>Oscillibacter</i>	3.01 ± 2.17	1.95 ± 1.85	1.32 ± 0.58	0.127
<i>Parabacteroides</i>	0.50 ± 0.28 <sup>b</sup>	0.75 ± 0.30 <sup>b</sup>	2.75 ± 1.61 <sup>a</sup>	0.001

<i>Rikenella</i>	1.24 ± 0.56 <sup>a</sup>	1.20 ± 0.39 <sup>a</sup>	0.37 ± 0.45 <sup>b</sup>	0.007
<i>Roseburia</i>	1.43 ± 0.98 <sup>a</sup>	1.44 ± 0.94 <sup>a</sup>	0.29 ± 0.14 <sup>b</sup>	0.005
<i>Ruminiclostridium</i>	3.37 ± 1.29 <sup>a</sup>	2.60 ± 1.35 <sup>a</sup>	0.38 ± 0.30 <sup>b</sup>	0.001
<i>norank_f__Erysipelotrichaceae</i>	0.36 ± 0.64	0.07 ± 0.07	0.97 ± 1.44	0.115
<i>norank_f__Lachnospiraceae</i>	4.33 ± 1.09 <sup>a</sup>	3.09 ± 1.09 <sup>b</sup>	1.54 ± 0.73 <sup>c</sup>	0.001
<i>norank_o__Gastranaerophilales</i>	0.16 ± 0.14	0.89 ± 1.00	0.55 ± 0.77	0.072
<i>unclassified_f__Lachnospiraceae</i>	5.09 ± 2.04 <sup>a</sup>	2.96 ± 0.98 <sup>b</sup>	2.21 ± 1.24 <sup>b</sup>	0.004
<i>unclassified_f__Ruminococcaceae</i>	1.82 ± 0.73 <sup>a</sup>	1.77 ± 1.72 <sup>ab</sup>	0.94 ± 0.39 <sup>b</sup>	0.020

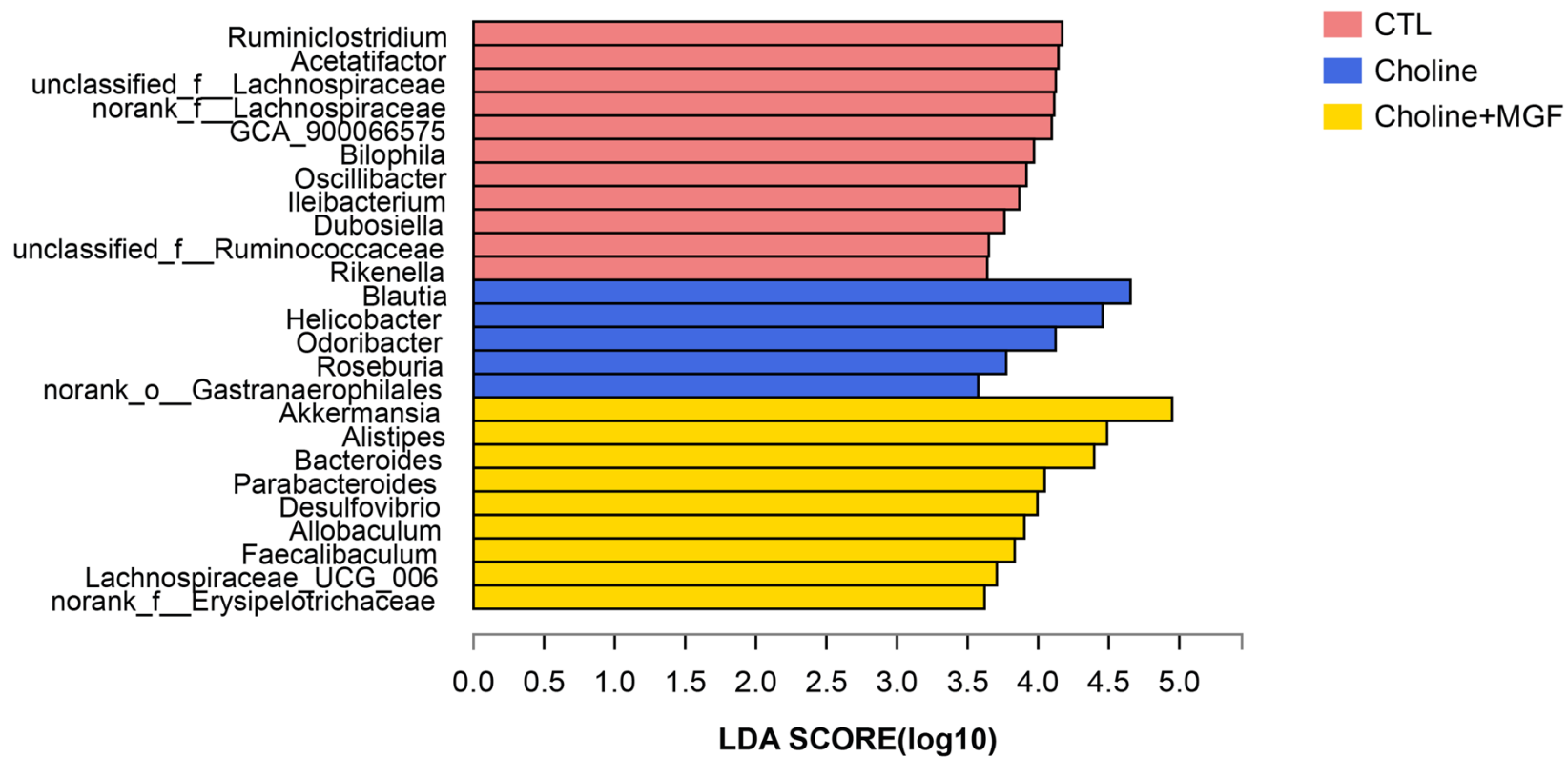
N = 9. Data are expressed as mean ± SD. Means with different superscript letters differ significantly at  $p < 0.05$ .



**Fig. S1** Relative expression of intestinal mRNA of (A) ATP-binding cassette sub-family G member 5 (ABCG5) and (B) member 8 (ABCG8), (C) acyl-coenzyme A:cholesterol acyltransferase 2 (ACAT2), (D) Niemann-Pick C1 like 1 (NPC1L1), and (E) microsomal-triacylglycerol-transport protein (MTP) in ApoE<sup>-/-</sup> mice fed a control diet (CTL), a high-choline diet with 1% free choline (Choline), or a high-choline diet with 1% free choline plus 0.5% mangiferin (Choline + MGF) for 15 weeks (n= 8). Data are expressed as mean with SD. Means with different superscript letters differ significantly at  $p < 0.05$ .



**Fig. S2 (A)** Venn diagram of the number of operational taxonomic units (OTUs) in the gut microbiota of ApoE<sup>-/-</sup> mice fed a control diet (CTL), a high-choline diet with 1% free choline (Choline), or a high-choline diet with 1% free choline plus 0.5% mangiferin (Choline + MGF) for 15 weeks (n = 9). **(B)**  $\alpha$ -Diversity evaluated by Sobs index and **(C)** Shannon index. Data are expressed as mean with SD. Means with different superscript letters differ significantly at  $p < 0.05$ .



**Fig. S3** 25 key genera were identified through linear discriminant analysis (LDA) effect size (LEfSe) with LDA score at 3.5 as a threshold.