

Supplementary document

Table S1: General physiology and tissue weight of mice

Group	Body weight (g)	Liver (mg)	Spleen (mg)
Control	39.08 ± 1.83	1922.58 ± 162.20	138.52 ± 17.77
Limonin	40.32 ± 3.89	2032.70 ± 92.36	129.70 ± 7.01
<i>p</i> value	0.62	0.61	0.74

Table S2: Taxonomy of control and limonin-treated mouse fecal microbiota at phylum level.

Averages are presented as % relative abundance of the average total bacterial population per group.

Taxon (phyla)	Control		Limonin		<i>p</i> value
	Average	±SD	Average	±SD	
Firmicutes	65.39	2.90	49.10	6.09	0.09
Bacteroidetes	19.07	4.45	48.04	5.98	0.03
Actinobacteria	13.82	4.01	1.24	0.10	0.03
Verrucomicrobioa	0.35	0.25	0.02	0.01	1.00
TM7	0.06	0.02	0.14	0.08	1.00
Proteobacteria	0.04	0.01	0.354	0.14	0.04
Deferribacteres	0.01	0.00	0.02	0.01	1.00
Tenericutes	0.01	0.01	0.01	0.01	1.00
Unassigned	1.25	0.18	1.06	0.09	1.00

Table S3: Taxonomy of control and limonin-treated mouse fecal microbiota at genus level.

Averages are presented as % relative abundance of the average total bacterial population per group. Only relative abundances >0.01% bearing significant differences between groups were presented. Order, family, and genus denoted as o_, f_, and g_ respectively. Unspecified families and genera identified as f__ and g__ respectively.

Taxon (genus)	Control		Limonin		<i>p</i> value
	Average	±SD	Average	±SD	
<i>Lactobacillus</i>	43.99	13.17	10.67	5.66	0.00
f_S24-7;g__	16.32	8.00	33.53	8.53	0.01
<i>Bifidobacterium</i>	13.03	8.96	0.04	0.02	0.01
<i>Allobaculum</i>	8.48	1.29	0.00	0.00	0.00
o_Clostridiales;f__;g__	3.29	3.93	14.38	8.76	0.03
<i>Bacteroides</i>	2.05	1.91	11.76	4.55	0.00
f_Lachnospiraceae;g__	0.53	0.50	3.22	1.91	0.02
f_Rikenellaceae;g__	0.52	0.48	2.63	0.97	0.00
<i>Streptococcus</i>	0.50	0.29	0.88	0.13	0.03
<i>Oscillospira</i>	0.33	0.05	2.95	2.48	0.05
<i>Ruminococcus</i>	0.29	0.31	4.82	0.97	0.00
f_Erysipelotrichaceae;g__	0.18	0.11	0.65	0.28	0.01
f_Peptostreptococcaceae;g__	0.12	0.13	0.00	0.00	0.02
f_Ruminococcaceae;g__	0.05	0.08	0.44	0.35	0.04
<i>Ruminococcus</i>	0.04	0.06	0.38	0.28	0.03
<i>Dehalobacterium</i>	0.03	0.05	0.18	0.13	0.04
f_Peptococcaceae;g__	0.01	0.01	0.14	0.09	0.02
<i>Burkholderia</i>	0.01	0.00	0.03	0.01	0.00
<i>Ralstonia</i>	0.01	0.00	0.02	0.00	0.01
<i>Roseburia</i>	0.00	0.01	0.12	0.06	0.00
f_Barnesiellaceae;g__	0.00	0.00	0.03	0.02	0.00
<i>Candidatus</i>	0.00	0.00	0.02	0.01	0.01