

**Table S1 Ingredient composition of the basal diet (% , as-fed basis)**

Component	Content	Nutrient composition <sup>2</sup>	Level
Corn	52.07	Metabolizable energy (MJ/kg)	12.38
Wheat	5.00	CP	21.60
Soybean meal (45% crude protein)	33.0	Ca	1.00
Corn gluten meal (52% crude protein)	3.00	Total P	0.74
Soybean oil	2.28	Available P	0.47
<i>L</i> -Lysine·HCl (98.5%)	0.25	Total Lys	1.29
<i>DL</i> -Methionine (99%)	0.17	Total Met	0.52
Limestone	1.25	Total Met+Cys	0.93
Dicalcium phosphate	1.68	Total Thr	0.86
Sodium chloride	0.30	Total Trp	0.21
Premix <sup>1</sup>	1.00	Total Ile	0.77
Total	100.00		

<sup>1</sup>The premix provided per kilogram of diet: vitamin A, 12,000 IU; vitamin D<sub>3</sub>, 600 IU; vitamin E, 45 mg; vitamin K<sub>3</sub>, 2.5 mg; vitamin B<sub>1</sub>, 2.4 mg; vitamin B<sub>2</sub>, 5.0 mg; vitamin B<sub>6</sub>, 3.5 mg; vitamin B<sub>12</sub>, 0.01 mg; choline, 1,300 mg; nicotinic acid, 42 mg; pantothenic acid, 12 mg; folic acid, 1.00 mg; biotin, 0.12 mg; Fe, 80 mg; Cu, 7.0 mg; Mn, 80 mg; Zn, 85 mg; I, 0.70 mg; Se, 0.15 mg.

<sup>2</sup>Total Lys, Met, Met+Cys, Thr, Ile, and ME were calculated values in the mixed feed. CP was measured value.

**Table S2 Primer sequences used for quantitative real-time PCR**

Genes	Direction	Primer sequence (5'-3')	NCBI References	Amplicon (bp)
<i>OCN</i>	Forward	TCATCCTGCTCTGCCTCATCT	NM_205128.1	147
	Reverse	CATCCGCCACGTTCTTCAC		
<i>ZO-1</i>	Forward	CCAAAGACAGCAGGAGGAGA	XM_015278981.1	217
	Reverse	TGGCTAGTTTCTCTCGTGCA		
<i>CLDN1</i>	Forward	CTTCATCATTGCAGGTCTGTCAG	NM_001013611.2	103
	Reverse	AAATCTGGTGTTAACGGGTG		
<i>MUC2</i>	Forward	CATTCAACGAGGAGAGCTGC	NM_001318434.1	248
	Reverse	TTCCTTGCAGCAGGAACAAC		
<i>FXR</i>	Forward	CAGAAAGAATGCAGCGGCTC	NM_204113.2	94
	Reverse	CAAACCTGCCCATTTTGCGA		
<i>GPRC6A</i>	Forward	TGAAATGCTGCAACCAGAAG	XM_040666655.2	217
	Reverse	GGACAGGAACCTCAGAGCAG		
<i>GPRC5A</i>	Forward	AGCCAGGTTACGGAGGATTT	XM_040660498.2	208
	Reverse	GATGCCAGCATAACCACACAC		
<i>GPRC5B</i>	Forward	CGAACATAATGCAGCGCTAA	XM_015294794.2	225
	Reverse	GCCAGGGAATAATTCTGCAA		
<i>GPRC5C</i>	Forward	CCATCCTGAAGGAGCAGAAG	XM_040649806.1	163
	Reverse	TTGTGCATCAGAGCCATCTC		
<i>SIRT1</i>	Forward	TAACATGGAGGCTTGGCTGA	NM_001004767.2	193
	Reverse	GACATCACTCGAAGCAGCAG		
<i>SIRT2</i>	Forward	CCACCGTTTGCCACTACTTC	NM_001017414.2	202
	Reverse	TTCTCCTTCACCCAGCTCAG		
<i>SIRT3</i>	Forward	ATCTTGTAGGACCGTTTGCC	NM_001199493.1	173
	Reverse	GCCAGCTGTCCTATTTGTCT		
<i>SIRT4</i>	Forward	GCATTTCAAACCAGAGCCCA	XM_025155741.2	179
	Reverse	CTTGGCTGAGACCCTCTTCA		
<i>SIRT5</i>	Forward	TAAACATCCCAACGCTGCAC	NM_001276364.2	191
	Reverse	TTGCAGTCACGTTTCCACAG		
<i>SIRT6</i>	Forward	GGACCGACAACAATGAGCTC	NM_001039320.2	150
	Reverse	AGCTCACACACCTTCCTCTC		
<i>SIRT7</i>	Forward	TCAAAACTGTGATGGGCTGC	NM_001291971.1	243
	Reverse	TGTGTCAGTGTCCCCTTCTC		
<i>IL17A</i>	Forward	GGAGAACTGCCTTGCCTAAC	NM_204460.2	165
	Reverse	CTCATGGAGCACGTTGGAAG		
<i>IL22</i>	Forward	AACTTCCAGCAGCCCTACAT	NM_001199614.1	192
	Reverse	CTTGGCCTCTGTGAGAAGGA		
$\beta$ -actin	Forward	AAGCCAACAGAGAGAAGATGA	NM_205518	101
	Reverse	ACCAGAGGCATACAGGGA		

*OCN*, occludin; *CLDN1*, claudin 1; *ZO-1*, Zona Occludens 1; *MUC2*, mucin 2; *FXR*, farnesoid X receptor; *GPRC6A*, G protein-coupled receptor class C group 6 member A; *GPRC5A*, G protein-coupled receptor class C group 5 member A; *GPRC5B*, G protein-coupled receptor class C group 5 member B; *GPRC5C*, G protein-coupled receptor class C group 5 member C. *SIRT1*, sirtuin 1; *SIRT2*, sirtuin 2; *SIRT3*, sirtuin 3; *SIRT4*, sirtuin 4; *SIRT5*, sirtuin 5; *SIRT6*, sirtuin 6; *SIRT7*, sirtuin 7; *IL17A*, interleukin 17A; *IL22*, interleukin 22.

**Table S3 Characteristic fragment ions of CA, CDCA, DCA, LCA standards and their optimized MS/MS conditions**

Metabolites	Q1	Q3	Declustering potential (ev)	Collision Energy (ev)
CA	406.9	289.3	-130	-59
		195.0	-130	-52
CDCA	391.2	391.2	-130	-34
DCA	391.2	343.4	-130	-53
		327.2	-130	-53
LCA	375.2	375.2	-130	-7

CA, cholic acid; CDCA, chenodexychoic acid; DCA, deoxychoic acid; LCA, lithocholic acid.

**Table S4 Effects of curcumin (CUR) supplementation on the percentages of ileal Lamina propria lymphocytes expressing cell-surface antigens for CD3<sup>+</sup>, CD4<sup>+</sup>, CD8<sup>+</sup>, and BU\_1<sup>+</sup>**

Items	Saline		LPS		SEM	P-value		
	CON	CUR	CON	CUR		CUR	LPS	CUR×LPS
CD3 <sup>+</sup> (%)	19.60 <sup>b</sup>	29.00 <sup>a</sup>	14.22 <sup>c</sup>	18.91 <sup>b</sup>	0.712	<0.001	<0.001	0.004
CD4 <sup>+</sup> (%)	4.32 <sup>b</sup>	4.61 <sup>b</sup>	3.37 <sup>c</sup>	5.39 <sup>a</sup>	0.208	<0.001	0.679	<0.001
CD8 <sup>+</sup> (%)	15.27 <sup>b</sup>	24.39 <sup>a</sup>	10.85 <sup>d</sup>	13.52 <sup>c</sup>	0.566	<0.001	<0.001	0.036
CD4: CD8 ratio	0.28	0.30	0.32	0.40	0.025	0.023	0.018	0.266
BU_1 <sup>+</sup> (%)	17.16 <sup>c</sup>	25.84 <sup>ab</sup>	31.83 <sup>a</sup>	22.93 <sup>bc</sup>	2.849	0.014	0.036	0.009

Values are mean and pooled SEM,  $n = 12$ . Means with no common superscript in the same row are significantly different ( $P < 0.05$ ).

CD3<sup>+</sup>, CD3<sup>+</sup> T-lymphocyte subset; CD4<sup>+</sup>, CD4<sup>+</sup> T-lymphocyte subset; CD8<sup>+</sup>, CD8<sup>+</sup> T-lymphocyte subset; BU\_1<sup>+</sup>, BU\_1<sup>+</sup> B cells.

Figure S1

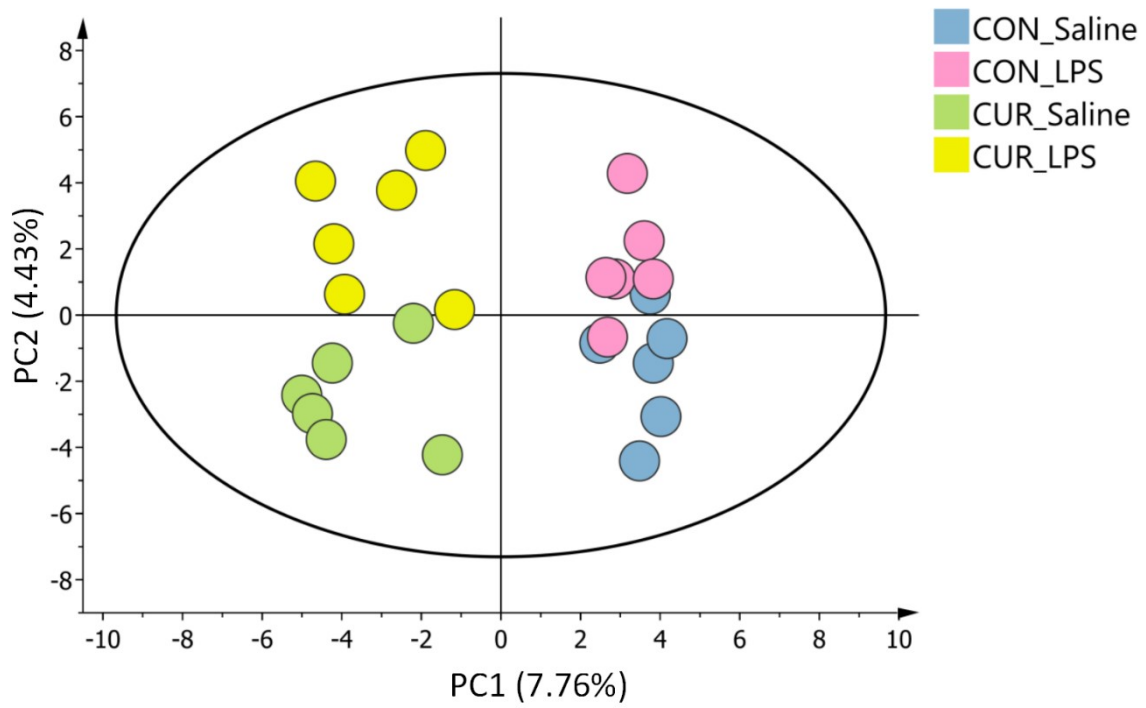


FIGURE S1. Score plots of principal component analysis derived from GC-MS data showing the metabolism differences of digesta samples among different treatment groups of chickens.

Figure S2

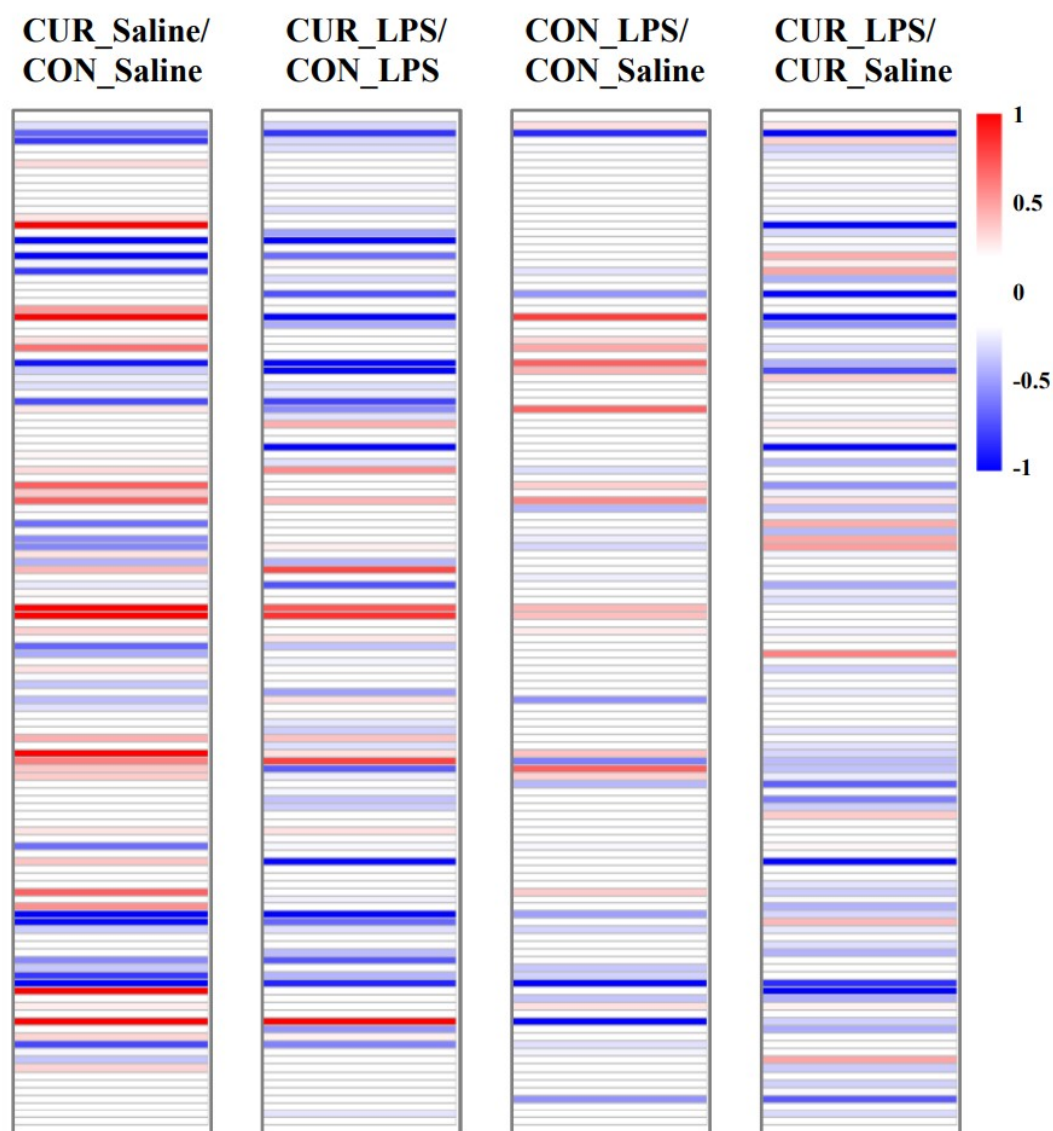


FIGURE S2. The heat map of Log<sub>2</sub> fold change (Log<sub>2</sub>FC) of all metabolites identified by GC-MS. The fold change of each metabolite between every pair-wise comparison was computed as the ratio of their mean abundance. Note that: CON\_Saline, chickens fed the control diet and injected with saline; CUR\_Saline, chickens fed the curcumin diet and injected with saline; CON\_LPS, chickens fed the control diet and challenged with LPS; CUR\_LPS, chickens fed the curcumin diet and challenged with LPS.