**Table S1.** Composition and proximate analysis of experimental diets. Data are given in g/kg (on dry weight basis)

| | CM0 | CM0.5 | CM1 | CM2 | CM4 |
|---|---|---|---|---|---|
| Ingredients (g/kg) | | | | | |
| White fish meal | 400 | 400 | 400 | 400 | 400 |
| Soybean meal | 100 | 100 | 100 | 100 | 100 |
| Soy protein concentration | 100 | 100 | 100 | 100 | 100 |
| Yeast meal | 60 | 60 | 60 | 60 | 60 |
| Fish oil | 33 | 33 | 33 | 33 | 33 |
| Soybean oil | 33 | 33 | 33 | 33 | 33 |
| $\alpha$-starch | 200 | 200 | 200 | 200 | 200 |
| Zeolite powder | 16.5 | 16.5 | 16.5 | 16.5 | 16.5 |
| [1]Vitamin premix | 5 | 5 | 5 | 5 | 5 |
| [2]Mineral premix | 20 | 20 | 20 | 20 | 20 |
| Dicalcium phosphate | 20 | 20 | 20 | 20 | 20 |
| Choline chloride | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 |
| Cellulose | 10 | 9.5 | 9 | 8 | 6 |
| Curcumin | 0 | 0.5 | 1 | 2 | 4 |
| Proximate composition (g/kg) | | | | | |
| Moisture | 83.9 | 81.5 | 84.1 | 82.1 | 84.6 |
| Crude protein | 428.0 | 411.1 | 420.3 | 430.1 | 426.5 |
| Crude lipid | 91.9 | 93.6 | 88.8 | 87.4 | 89.1 |
| Ash | 144.6 | 150.7 | 136.7 | 145.9 | 140.9 |

[1]Vitamin mixture (mg/kg diet): thiamine hydrochloride, 5; riboflavin, 20; calcium pantothenate, 10; D-biotin, 0.6; pyridoxine hydrochloride, 10; folic acid, 1; inositol, 1000; L-ascorbyl-2-monophosphate-Mg, 60; $\alpha$-tocopheryl acetate, 60; menadione, 5; nicotinic acid 120; retinol acetate, 5000 IU; cholecaliferol, 2000 IU.

[2]Mineral mixture (mg/kg diet): calcium dihydrogen phosphate monohydrate, 6000; five water hydroxy calcium propionate, 6540; ferrous sulphate hexahydrate, 42.5; magnesium sulphate heptahydrate, 1340; sodium dihydrogen phosphate, 1744; sodium chloride, 870; aluminium chloride hexahydrate, 3; potassium iodate, 2.5; potassium chloride, 1500; copper chloride dihydrate, 20; manganese sulphate monohydrate, 16; cobalt chloride hexahydrate, 20; zinc sulphate heptahydrate, 6.

**Table S2.** Serum biochemical indices of Chinese soft-shelled turtles fed with diets containing different curcumin levels for 6 weeks

| | CM0 | CM0.5 | CM1 | CM2 | CM4 |
|---|---|---|---|---|---|
| TP (g/L) | 32.80 ± 1.57[a] | 40.82 ± 0.39[b] | 29.69 ± 2.06[a] | 30.19 ± 0.81[a] | 34.05 ± 1.04[a] |
| ALB (g/L) | 7.20 ± 1.31 | 8.13 ± 0.90 | 6.33 ± 0.31 | 6.74 ± 0.58 | 8.19 ± 0.22 |
| TG (mmol/L) | 1.50 ± 0.14[a] | 2.14 ± 0.05[ab] | 2.14 ± 0.41[ab] | 2.69 ± 0.28[b] | 3.05 ± 0.45[b] |
| TCHO (mmol/L) | 5.54 ± 0.48[a] | 6.98 ± 0.27[b] | 7.14 ± 0.24[b] | 7.11 ± 0.12[b] | 7.59 ± 0.11[b] |
| GLU (mmol/L) | 3.28 ± 1.08 | 3.67 ± 0.44 | 4.02 ± 0.63 | 4.64 ± 0.30 | 4.98 ± 0.65 |
| ALP (U/L) | 1180.33 ± 207.55[b] | 1234.33 ± 266.68[b] | 1146 ± 120.09[b] | 857.67 ± 77.12[a] | 832.33 ± 59.50[a] |
| AST (U/L) | 119.00 ± 7.51[c] | 122.67 ± 9.96[c] | 93.67 ± 4.70[b] | 63.33 ± 2.85[a] | 64.33 ± 2.40[a] |

TP, total protein; ALB, albumin; TG, triglyceride; TCHO, total cholesterol; GLU, glucose; ALP, alkaline phosphatase; AST, aspartate transaminase.

Data were presented as mean ± SD. Different letters in the same row represent a significant difference among groups ($P < 0.05$).

**Table S3.** Primers used for qPCR

| Gene ID | Gene symbol | Forward primer (5'-3') | Reverse primer (5'-3') |
|---|---|---|---|
| XM_006126482.3 | *SLC38A1* | TCGGCATGGTACGTGGATGGT | GGCTCCAGTCCAGGGCAGATAA |
| XM_025179876.1 | *S100B* | TGGCGATGCTGAATGCGACTTC | GGTGGCTTCTCCGATGCTTCAC |
| XM_025190937.1 | *OVCH1* | CCAGACGTGTTGTCGGAGGAGA | ACTGATGACGACGCCACCACA |
| XM_006135326.3 | *AGTR2* | GTCTCCCTGCCCGCTTCTGTAT | ACCGCCACCACCACACTGTT |
| XM_006112915 | *β-actin* | TGATGGACTCAGGTGACGGTGT | GGCTGTGGTGGTGAAGCTGTAG |

**Table S4.** Number of OTUs for each sample

| ID | domain | phylum | class | order | family | genus | species |
|---|---|---|---|---|---|---|---|
| CM0_1_1 | 9 | 2 | 10 | 28 | 87 | 110 | 45 |
| CM0_1_2 | 12 | 2 | 3 | 58 | 91 | 84 | 40 |
| CM0_1_3 | 3 | 0 | 3 | 15 | 75 | 43 | 22 |
| CM0_1_4 | 14 | 4 | 30 | 61 | 149 | 206 | 59 |
| CM0_2_1 | 8 | 3 | 10 | 44 | 102 | 123 | 58 |
| CM0_2_2 | 21 | 7 | 36 | 52 | 179 | 243 | 80 |
| CM0_3_1 | 8 | 3 | 16 | 67 | 121 | 150 | 47 |
| CM0_4_1 | 7 | 6 | 43 | 46 | 168 | 253 | 72 |
| CM1_1_1 | 16 | 3 | 9 | 59 | 152 | 132 | 58 |
| CM1_1_2 | 10 | 3 | 29 | 51 | 273 | 195 | 88 |
| CM1_2_1 | 3 | 3 | 6 | 14 | 60 | 64 | 35 |
| CM1_2_2 | 19 | 1 | 16 | 62 | 135 | 144 | 47 |
| CM1_2_3 | 12 | 3 | 5 | 46 | 75 | 89 | 26 |
| CM1_3_1 | 13 | 3 | 21 | 47 | 193 | 198 | 92 |
| CM1_3_2 | 4 | 0 | 5 | 10 | 82 | 66 | 48 |
| CM1_3_3 | 4 | 0 | 4 | 20 | 76 | 66 | 31 |
| CM1_4_1 | 1 | 5 | 13 | 27 | 104 | 138 | 63 |
| CM4_1_1 | 3 | 6 | 27 | 167 | 355 | 334 | 134 |
| CM4_2_1 | 2 | 3 | 7 | 30 | 84 | 84 | 57 |
| CM4_2_2 | 26 | 3 | 38 | 53 | 184 | 252 | 81 |
| CM4_2_3 | 30 | 5 | 41 | 47 | 144 | 234 | 88 |
| CM4_2_4 | 12 | 2 | 25 | 28 | 125 | 207 | 76 |
| CM4_3_1 | 5 | 1 | 4 | 9 | 52 | 57 | 32 |
| CM4_4_1 | 17 | 3 | 31 | 50 | 162 | 261 | 74 |
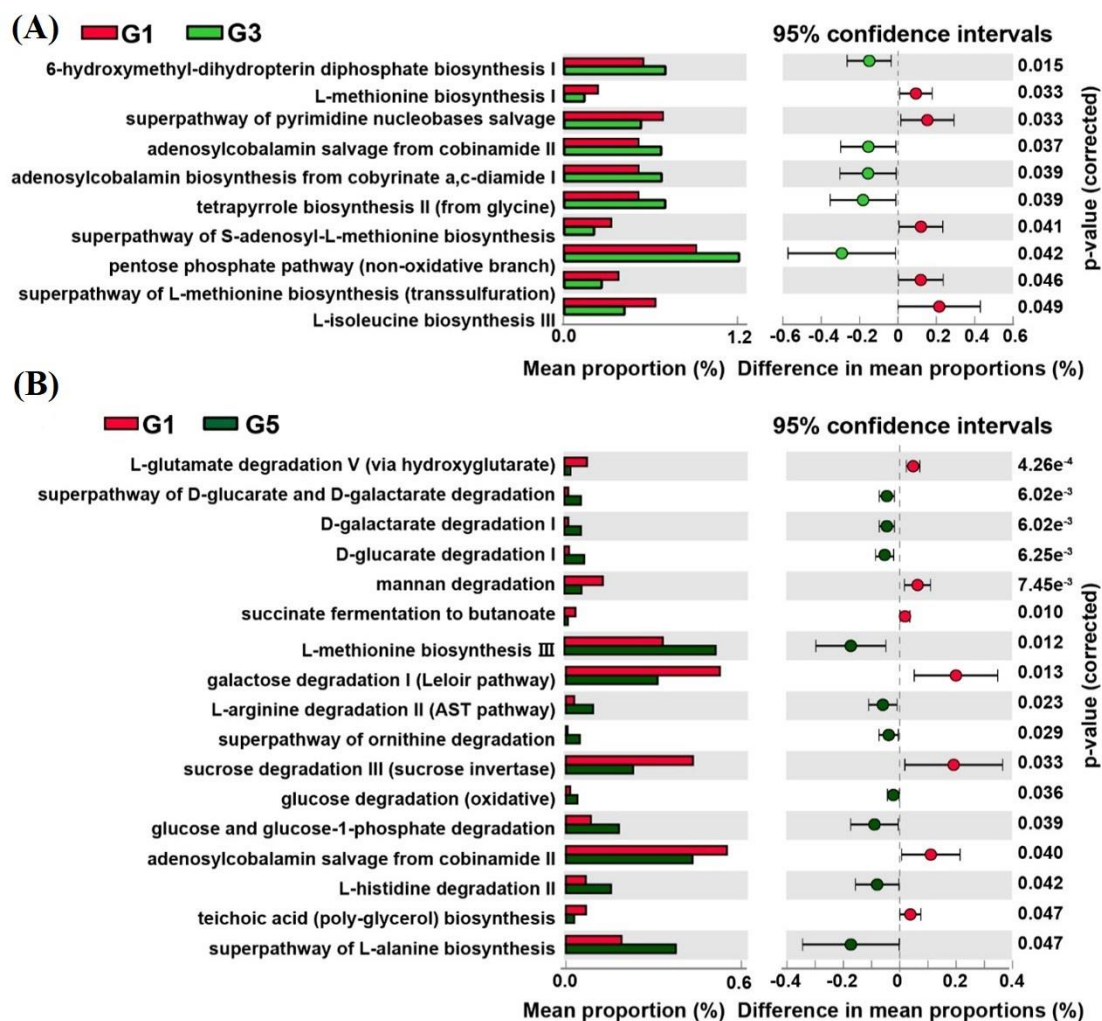
**Figure S1.** Functional prediction of changed gut microbiota by KEGG. (A) CM1 vs. CM0; (B) CM4 vs.

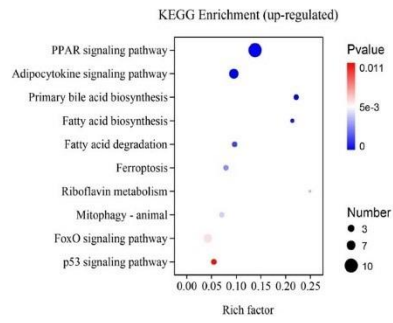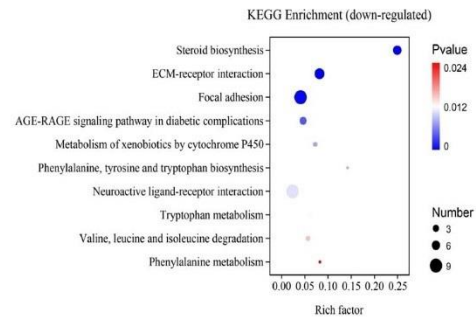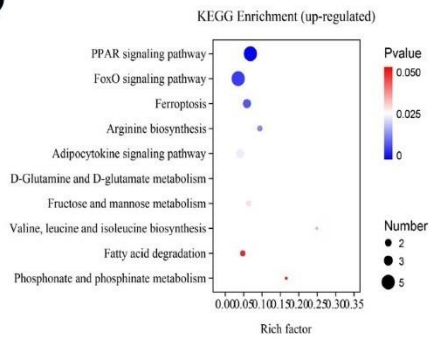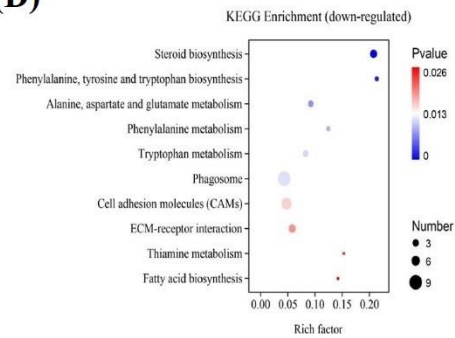CM0. Differences were considered significant at *P* < 0.05 using t-test.

**Figure S2.** (A) Top 10 significant KEGG pathways of up-regulated genes in CM0 vs CM1 group ($P < 0.05$).

(B) Top 10 significant KEGG pathways of down-regulated genes in CM0 vs CM1 group ($P < 0.05$). (C) Top

10 significant KEGG pathways of up-regulated genes in CM0 vs CM4 group ($P < 0.05$). (D) Top 10

significant KEGG pathways of down-regulated genes in CM0 vs CM4 group ($P < 0.05$)