Table S1. RNA and sequencing data quality control results.

| Sample | RIN | 28S/18S | Orientation | Raw reads | Clean reads | Q20 \(^2\) Value |
|--------|-----|---------|-------------|-----------|-------------|-----------------|
| A-7-1  | 9.9 | 2.2     | Forward/Reverse | 52,626,650 | 49,493,099  | 93.79           |
| A-7-2  | 9.4 | 1.8     | Forward/Reverse | 65,172,256 | 61,339,453  | 93.85           |
| A-7-3  | 9.4 | 1.6     | Forward/Reverse | 52,184,392 | 48,308,794  | 92.53           |
| A-21-1 | 9.8 | 2.2     | Forward/Reverse | 65,375,508 | 61,737,091  | 93.69           |
| A-21-2 | 10.0| 2.2     | Forward/Reverse | 63,130,954 | 58,822,034  | 92.76           |
| A-21-3 | 9.9 | 2.1     | Forward/Reverse | 52,378,470 | 49,102,134  | 93.30           |
| S-7-1  | 9.8 | 2.0     | Forward/Reverse | 51,769,926 | 48,551,144  | 93.68           |
| S-7-2  | 9.7 | 2.6     | Forward/Reverse | 51,973,884 | 48,915,040  | 93.93           |
| S-7-3  | 9.9 | 2.3     | Forward/Reverse | 56,478,666 | 53,034,760  | 93.55           |
| S-21-1 | 9.9 | 2.4     | Forward/Reverse | 50,999,520 | 47,905,709  | 93.60           |
| S-21-2 | 9.9 | 1.9     | Forward/Reverse | 65,885,658 | 62,039,264  | 93.48           |
| S-21-3 | 9.6 | 1.8     | Forward/Reverse | 52,273,302 | 47,750,614  | 91.71           |
| F-7-1  | 10.0| 2.3     | Forward/Reverse | 47,341,580 | 44,635,381  | 94.23           |
| F-7-2  | 9.3 | 2.3     | Forward/Reverse | 56,505,676 | 53,306,031  | 93.81           |
| F-7-3  | 9.8 | 2.3     | Forward/Reverse | 65,404,146 | 61,675,167  | 93.67           |
| F-21-1 | 9.5 | 2.4     | Forward/Reverse | 68,286,012 | 64,035,243  | 93.30           |
| F-21-2 | 9.4 | 2.3     | Forward/Reverse | 72,320,210 | 68,540,614  | 94.12           |
| F-21-3 | 9.9 | 2.4     | Forward/Reverse | 33,871,056 | 32,279,512  | 94.79           |

\(^{1}\) RIN = RNA Integrity Number  
\(^{2}\) Q20 = bases of Q≥20 / all bases of sequencing  
\(^{3}\) A = amoxicillin; S = control; F = fecal microbiota transplantation; 7 = day 7; 21 = day 21.

Table S2. Primers lists used for real-time PCR assay in this study \(^{1}\).

| Gene   | Sequence 5′−3′ |
|--------|----------------|
| CCL4   | F: CATGAAGCTCTCGTGGACTG  
R: ACGGTGTATGTGAAGCAGCA |
| CCL5   | F: CAGCATCAGCCTCCCCATA  
R: GGCGGGGAGAGGTAGGAAA |
| CXCL9  | F: TGCACTAAACCGACCGGAAAGATG  
R: TTAGGCTGACCTGTCTTCCACT |
| CD19   | F: CTTCTCCAAACGCTGAGTCT  
R: GGTCAGGAAGTCAGTCGTC |
| ICOS   | F: CGAAAGAAAGGGAAGTGGA  
R: CACTGTATGGAATAACTGAACG |
| CXCR6  | F: GTTCGTCCTCGACAGATG  
R: GCAGACACATCATGGAAGAC |
| β-actin| F: AGACCGAGAAGTACTCCGCTGT  
R: ACATCGTGTGGAAGTTGAC |

\(^{1}\) CCL4: C-C motif chemokine ligand 4; CCL5: C-C motif chemokine ligand 5; CD19: CD19 molecule; CXCL9: C-X-C motif chemokine ligand 9; CXCR6: C-X-C motif chemokine receptor 6; ICOS: inducible T cell costimulator.
**Table S3.** The regulated gene ontology (GO) terms in the ileum mucosa of piglets in the amoxicillin (AM), fecal microbiota transplantation (FMT) and control (CO) groups on days 7 and 21.

| GO term                                                                 | 7 d | 21 d | | | | |
|------------------------------------------------------------------------|-----|------|-----|-----|-----|-----|
| GO:0050853 | B cell receptor signaling pathway | DOW | NO | DOW | N | NO | NO | NO |
| GO:0030888 | regulation of B cell proliferation | DOW | N | NO | DOW | N | NO | NO |
| GO:0032729 | positive regulation of interferon-gamma production | DOW | N | NO | DOW | N | NO | NO |
| GO:0006955 | immune response | NO | UP | NO | UP | NO | NO | NO |
| GO:0006954 | inflammatory response | NO | UP | NO | UP | NO | NO | NO |
| GO:0070098 | chemokine-mediated signaling pathway | NO | UP | NO | UP | NO | NO | NO |
| GO:0048247 | lymphocyte chemotaxis | NO | NO | NO | UP | NO | NO | NO |
| GO:0045959 | negative regulation of complement activation, classical pathway | NO | NO | NO | NO | NO | UP | NO |
| GO:0030810 | positive regulation of cAMP metabolic process | NO | NO | NO | NO | NO | UP | NO |
| GO:0043950 | positive regulation of cAMP-mediated signaling | NO | NO | NO | NO | UP | NO | NO |
| GO:0006691 | leukotriene metabolic process | NO | NO | NO | NO | NO | NO | NO |
| GO:0009086 | methionine biosynthetic process | NO | DOW | N | NO | NO | NO | NO |
| GO:0055085 | transmembrane transport | NO | NO | NO | NO | NO | NO | NO |
| GO:0034219 | carbohydrate transmembrane transport | NO | NO | NO | NO | NO | NO | NO |
| GO:0071918 | urea transmembrane transport | NO | NO | NO | NO | NO | NO | NO |
| GO:0070295 | renal water absorption | NO | NO | NO | NO | NO | NO | NO |

1 UP: up-regulated; DOWN: down-regulated; NO: no significant change.

**Figure S1.** Effects of early intervention with maternal fecal microbiota and antibiotics on intestinal development gene of the ileum mucosa among the amoxicillin (AM), fecal microbiota transplantation (FMT) and control (CO) groups on days 7 and 21.
**Figure S2.** The qPCR validation of the RNA-seq. The results are displayed as the values of fold changes in the CO group on days 7 and 21, and the qPCR data are presented as the means ± SEM (n = 5). Values with different lowercase letter superscripts indicate a significant difference (P < 0.05), and those with the same letter superscripts indicate no significant difference (P > 0.05). CO: control; AM: amoxicillin; FMT: fecal microbiota transplantation. CCL4: C-C motif chemokine ligand 4; CCL5: C-C motif chemokine ligand 5; CD19: CD19 molecule; CXCL9: C-X-C motif chemokine ligand 9; CXCR6: C-X-C motif chemokine receptor 6; ICOS: inducible T cell costimulator.