

1 **Table S1.** The composition and nutrient of dam diets.

|                        | Nutrient levels at different fiber levels (%) |        |
|------------------------|---|--------|
|                        | FFD   | INU    |
| Casein                 | 20.00   | 20.00  |
| Corn starch            | 59.06   | 54.07  |
| Soybean oil            | 7.00  | 7.00   |
| Sucrose                | 10.00   | 10.00  |
| Inulin                 | 0   | 5      |
| L-cystine              | 0.3   | 0.3    |
| Choline chloride       | 0.25  | 0.25   |
| Calcium hydrophosphate | 1.00  | 1.00   |
| Potassium citrate      | 0.80  | 0.80   |
| Calcium carbonate      | 0.55  | 0.55   |
| Vitamin                | 0.03  | 0.03   |
| Mineral element        | 1   | 1      |
| Total                  | 100.00  | 100.00 |
| Nutrient levels        |   |        |
| Gross energy, MJ/kg    | 4.2   | 4.1    |
| Crude protein, %       | 17.00   | 17.00  |

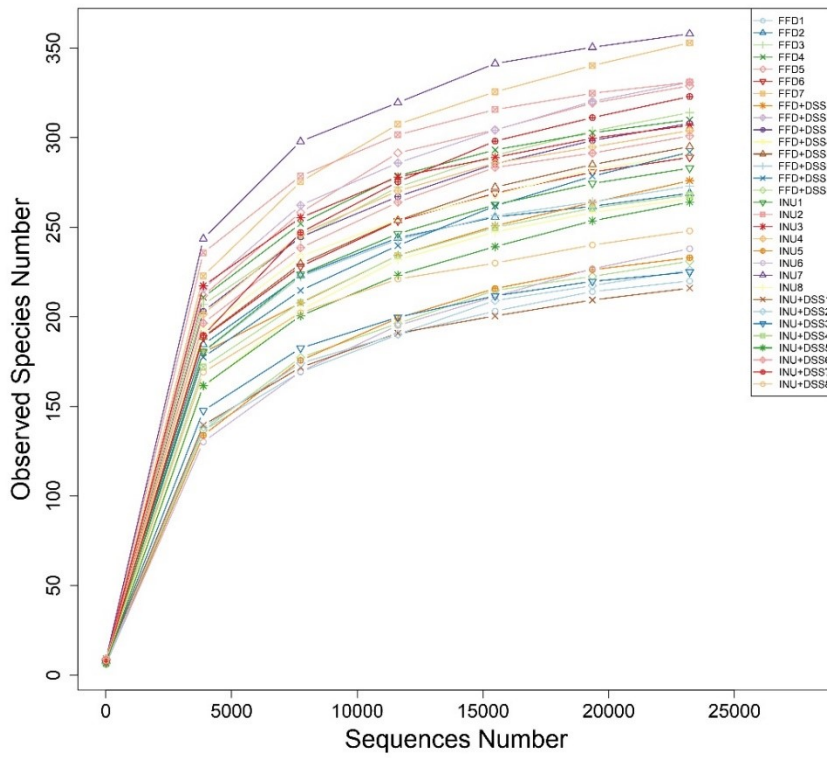
3 **Table S2.** Parameters and criteria of histological damage evaluation.

| Parameters                             | Score | Histological features  |
|--|-------|------------------------|
|  | 0     | No change              |
| (1) Loss of epithelial surface         | 1     | Localized and mild     |
|  | 2     | Localized and moderate |
| (2) Destruction of crypt               | 3     | Localized and severe   |
| (3) Infiltration of inflammatory cells | 4     | Extensive and moderate |
|  | 5     | Extensive and severe   |

4 Histological score was the sum of scoring from parameter (1), (2) and (3).

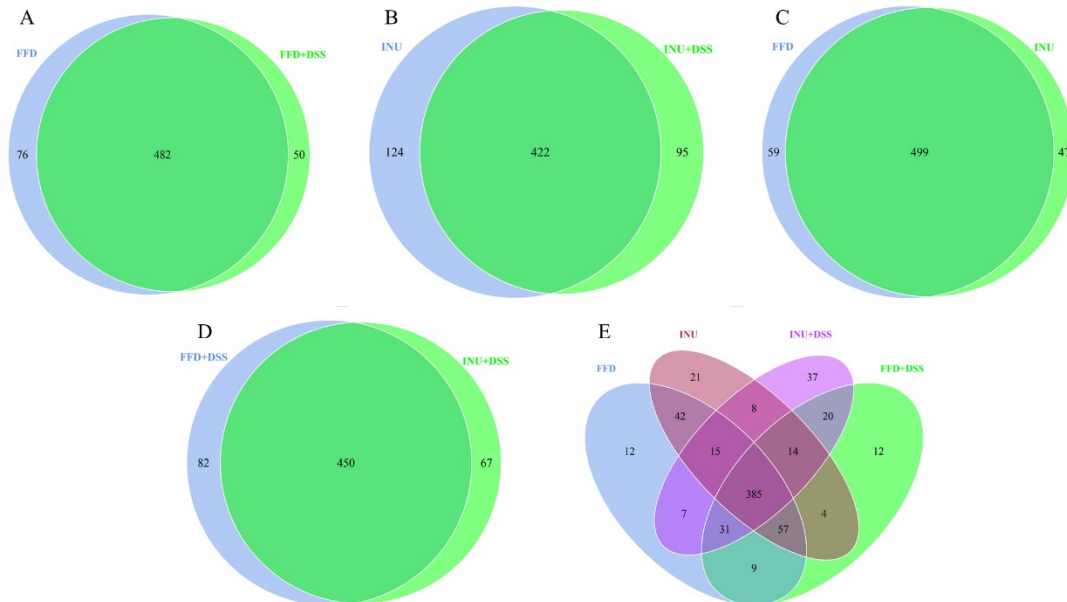
5 **Table S3.** The Primer Sequence of target gene and housekeeping gene.

| Gene           | Primer Sequence (5'-3')     | GenBank NO.    |
|----------------|-----------------------------|----------------|
| TNF- $\alpha$  | F: GCATGATCCGAGATGTGGAAGTGG | NM_012675.3    |
|                | R: CGCCACGAGCAGGAATGAGAAG   |                |
| IL-22          | F: CTGCCTGCTTCTCGTTGCTCTG   | NM_001191988.1 |
|                | R: AAGGTGCGGTTGACGATGTATGG  |                |
| IL-1 $\beta$   | F: ATCTCACAGCAGCATCTCGACAAG | NM_031512.2    |
|                | R: CACACTAGCAGGTCGTCATCATCC |                |
| IL-10          | F: CACACTAGCAGGTCGTCATCATCC | NM_012854.2    |
|                | R: CTCTCGGAGCATGTGGGTCT     |                |
| NF- $\kappa$ B | F: TGTGGTGGAGGACTTGCTGAGG   | NM_001276711.1 |
|                | R: AGTGCTGCCTTGCTGTTCTTGAG  |                |
| $\beta$ -actin | F: CAC AGC TGA GAG GGA AAT  | NM_045626.1    |
|                | R: TCA GCA ATG CCT GGG TAC  |                |



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7 **Figure S1:** Rarefaction curves of each sample. The ordinate is the number of OTU that can be  
 8 constructed based on the number of sequencing strips, which is used to reflect the sequencing depth.  
 9 Different samples are represented by curves with different colors.



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11 **Figure S2:** The Venn diagram of OTUs between the colon microbiota of (A) FFD and FFD+DSS, (B)  
 12 INU and INU+DSS, (C) FFD and INU, (D) FFD+DSS and INU+DSS groups, and among (E) FFD,  
 13 INU, INU+DSS and FFD+DSS groups.