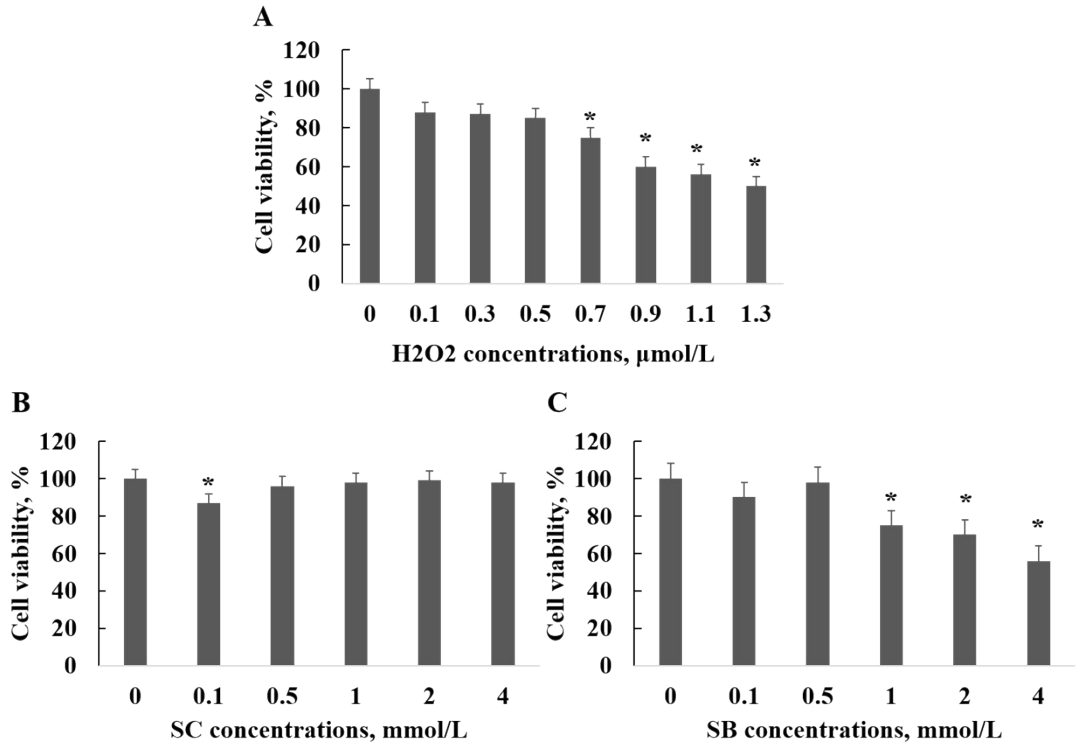
Supplementary Table 1. Nutritional composition of basal diet (g/kg, as-fed basis)[1]

Ingredients	Content
Casein, 80 Mesh	189.6
L-Cystine	2.8
Corn Starch	298.6
Maltodextrin 10	33.2
Sucrose	331.8
Cellulose, BW200	47.4
Soybean Oil	23.7
Lard	19.0
Mineral Mix M1002	9.5
Dicalcium Phosphate	12.3
Calcium Carbonate	5.2
Potassium Citrate, 1 H_2O	15.6
Vitamin Mix V10001	9.5
Choline Bitartrate	1.8
Total	1000
Nutrient levels, %[2]	
Protein	19.2
Carbohydrate	67.3
Fat	4.3
Energy, kcal/g	3.85

Note: [1]Formulated by E. A. Ulman, Ph.D., Research Diets, Inc., 8/26/98 and 3/11/99.

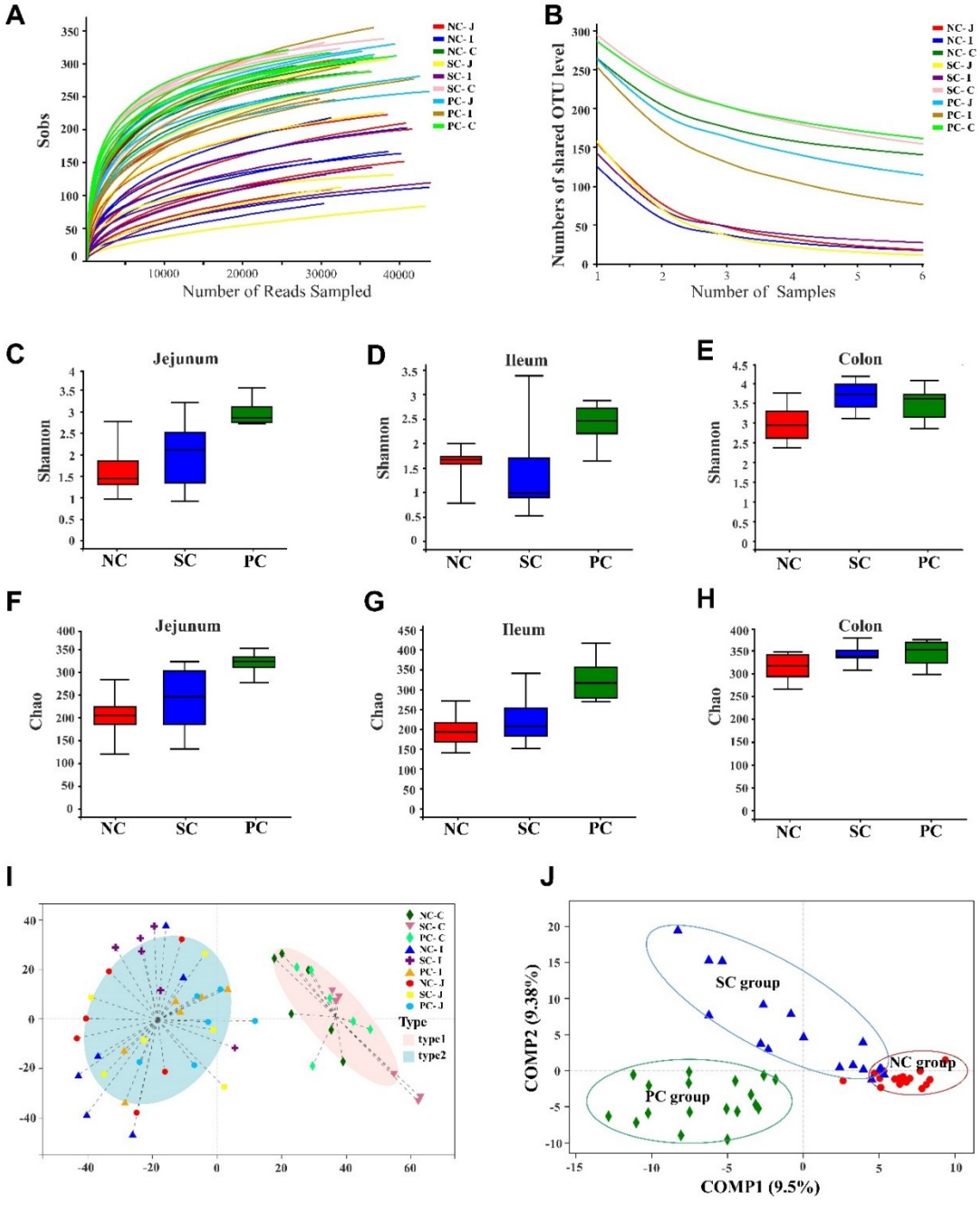
Supplementary Figure 1. Cell viability of IPEC-J2 after different incubation time with different concentrations of H_2O_2, sodium caprylate and sodium butyrate. (A) H_2O_2 treatment to IPEC-J2. **(B)** Sodium caprylate treatment to IPEC-J2. **(C)** Sodium butyrate treatment to IPEC-J2. IPEC-J2 cells were treated by different concentrations of 0.1, 0.3, 0.5, 0.7, 0.9, 1.1 and 1.3 μmol/L H_2O_2 for 4 h were used to select an optimal treatment concentration and time points. At last, IPEC-J2 cells were treated with 0.7

μmol/L H_2O_2 for 4 h to establish the oxidative damage model of the cells. Generally, 0.1, 0.5, 1, 2, and 5 mmol/L of sodium caprylate and sodium butyrate were used to select an optimal treatment concentration according to cell viability of IPEC-J2, and finally 0.5 mmol/L of sodium caprylate and 0.5 mmol/L of sodium butyrate were implemented to treatment normal IPEC-J2 for 24 h to determine expression of tight junction proteins. *P < 0.05, **P < 0.01, and ***P < 0.001, compared with untreated control cells



Supplementary Figure 2. The α-diversity and similarity of intestinal bacterial community of C57/BL6 mice fed different diets. **(A)** Sobs-Wiener curves of intestinal microbiome of mice are shown. **(B)** Core analysis on the OUT level. Chao 1 value was taken to estimate the bacterial richness in the jejunum **(C)**, ileum **(D)** and colon **(E)**. Shannon index was used to estimate the bacterial richness in the jejunum **(F)**, ileum **(G)** and colon **(H).** The Enterotype analysis **(I)** and the partial least squares discriminant analysis (PLS-DA) **(J)** were used to highlight systematic differences of bacterial

community structure among three groups. NC-J, SC-J and PC-J are jejunal content samples of mice fed with NC (basal diet), SC (basal diet with 0.5% sodium caprylate) and PC (basal diet with 0.5% sodium butyrate) diets, respectively; NC-I, SC-I and PC-I are ileal content samples of mice fed with NC, SC and PC diets, respectively; NC-C, SC-C and PC-C are colonic content samples of mice fed with NC, SC and PC diets, respectively.



Supplementary Figure 3. Effects of SC treatment on the composition of jejunal microbiota in C57/BL6 mice at the phylum, family and genus levels. **(A)** Venn of the operational taxonomic units (OTUs) among different dietary treatments in the jejunum. **(B)** Distribution of jejunal bacteria at the phylum level with proportion higher than 1%. **(C)** Distribution of jejunal bacteria at the family level with proportion higher than 1%. **(D)** The distribution of the top 15 jejunal bacteria at the genus level was shown by the heatmap plot. **(E)** Wilcoxin rank-sum test bar plot on the genus level of the top 15 jejunal bacteria with significant differences between NC (basal diet), SC (basal diet with 0.5% sodium caprylate) and PC (basal diet with 0.5% sodium butyrate) dietary treatments.