Supplemental Information

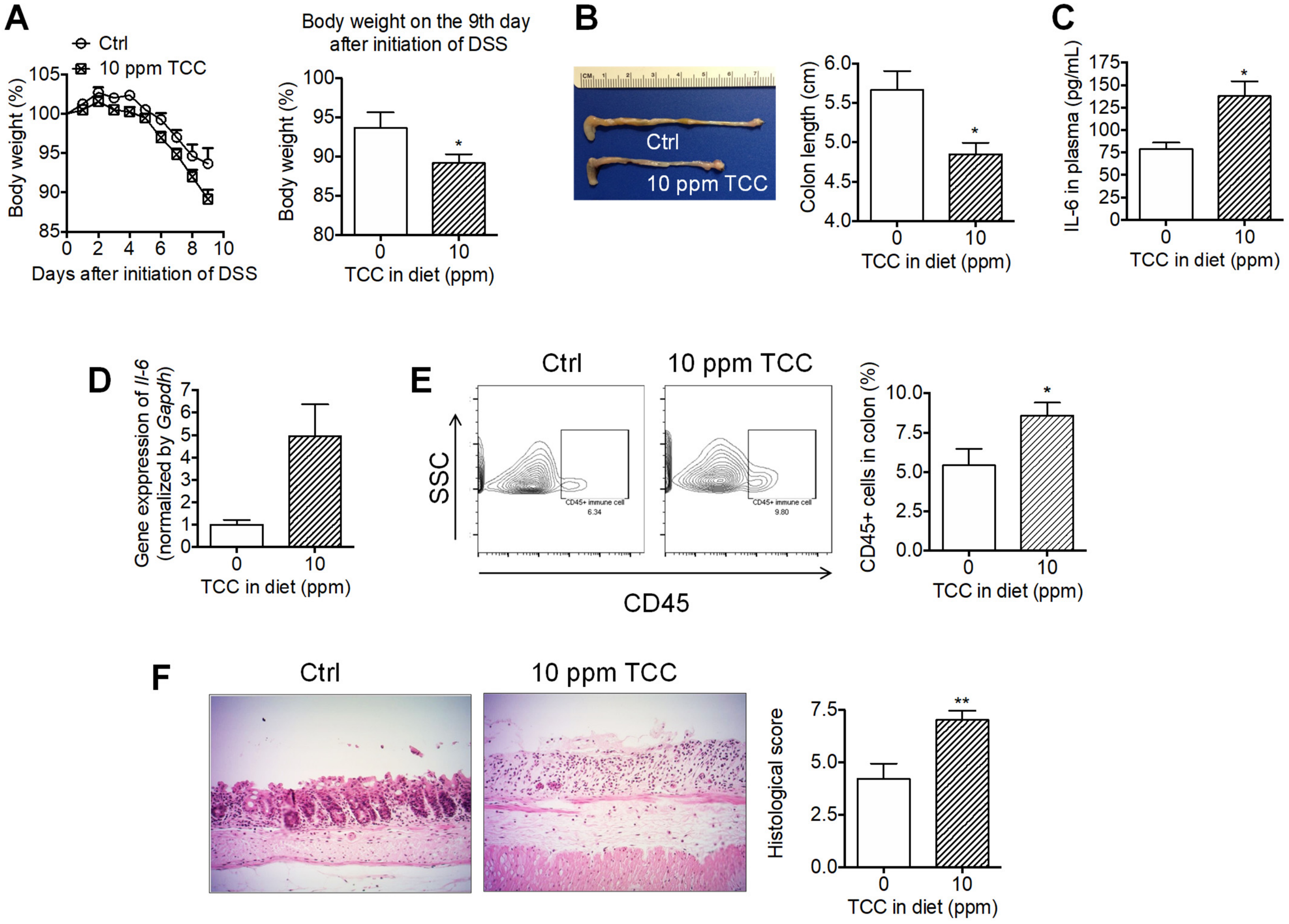

Fig. S1. Effect of a lower-dose TCC (10 ppm in diet) on DSS-induced colitis in mice. (A) Body weight. *Left:* time-course of body weight; *Right:* quantification of mouse body weight on the final day. (B) Colon length. (C) Concentration of IL-6 in plasma. (D) Gene expression of *Il-6* in colon. (E) FACS quantification of immune cell infiltration into colon. (F) H&E staining of the colon. The data are mean ± SEM, * $P < 0.05$, ** $P < 0.01$, n = 8 mice per group. Note: the control group (0 ppm TCC in diet) is the same as the control group in Fig. 1.

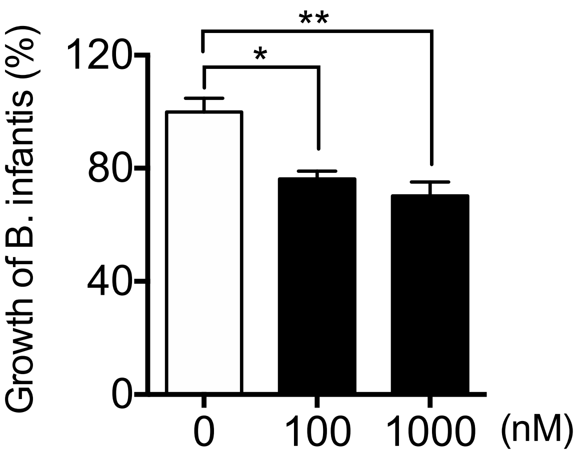

Fig. S2. Effect of TCC on *B. infantis 272* growth. *B. Infantis 272* was treated with TCC or vehicle (DMSO) under anaerobic conditions for 48 h, then bacterial growth was analyzed by measuring the turbidity at 600 nm. The results are expressed as mean ± SEM, from three independent experiments conducted in triplicates, * $P < 0.05$, ** $P < 0.01$.

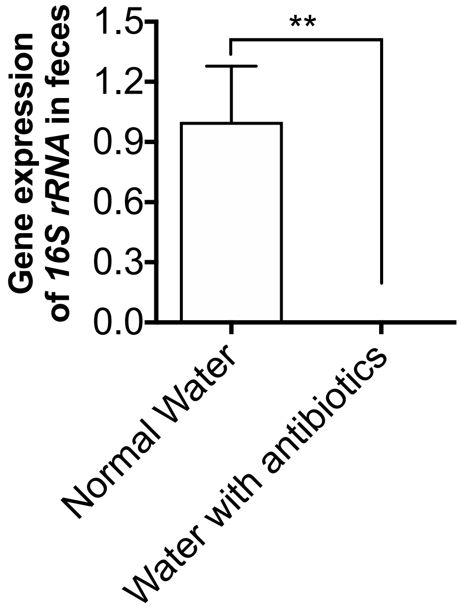

Fig. S3. Effect of the antibiotic cocktail on fecal bacteria load. The mice were given drinking water with or without the antibiotic cocktail (1.0 g/L ampicillin and 0.5 g/L neomycin) for 5 days. Feces were collected and *16S rRNA* gene expression in feces were analyzed by qRT-PCR (n = 7 per group). The results are expressed as mean ± SEM, ** $P < 0.01$.

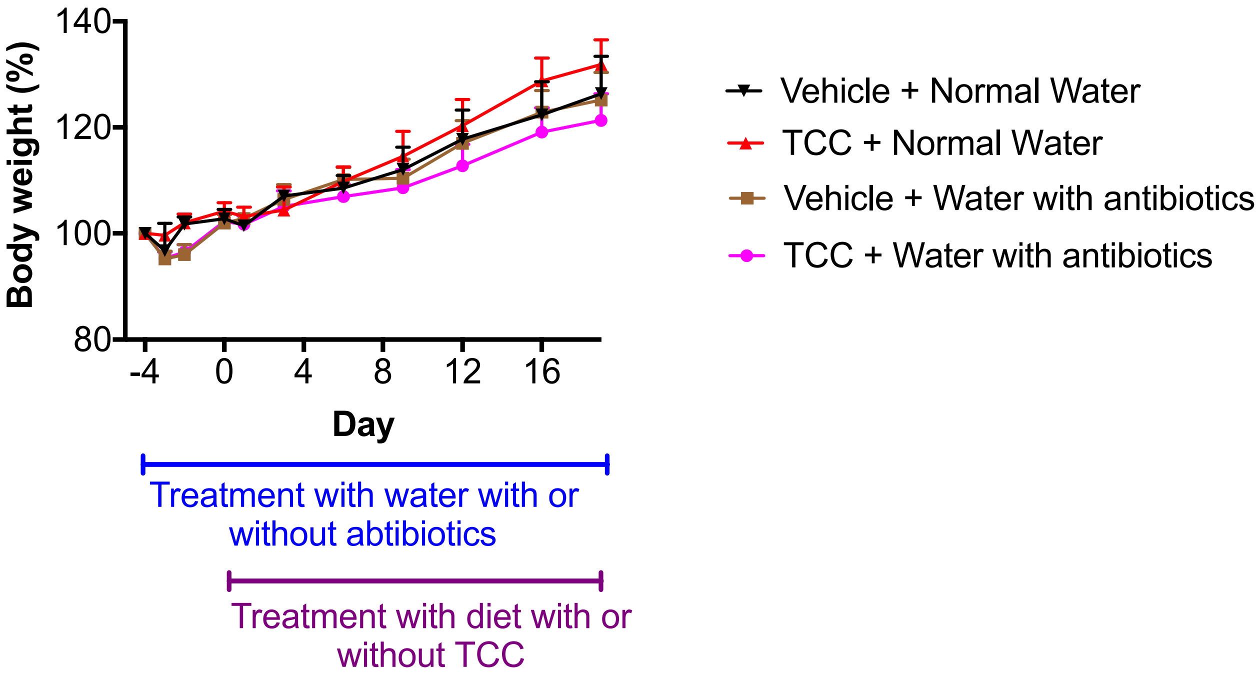

Fig. S4. Effect of TCC and/or antibiotic cocktail on mouse body weight (before the DSS stimulation). The results are expressed as mean ± SEM.

Table S1. Composition of the modified AIN-93G diet used in the animal experiment

Ingredients	g/kg
Casein	200
L-cystine	3
Sucrose	100
Dyetrose	132
Cornstarch	397.486
Cellulose	50
Mineral mix #210025	35
Vitamin mix #310025	10
Choline Bitartrate	2.5
Corn oil (purified) *	70
Vitamin A Palmitate	0.016

* All ingredients, except corn oil, were purchased from Dyets Inc (Bethlehem, PA). Corn oil has a high abundance of polyunsaturated fatty acids which are prone to lipid oxidation during production and storage; therefore, we purchased commercial samples of fresh corn oil and purified the oils using a chromatography column to minimize the potential variation of oxidized components in corn oil. Briefly, commercial corn oil (Mazola®, ACH Food company, Inc., Cordova, TN) was purchased from a local market in Amherst, MA, and purified by a silicic acid-activated charcoal chromatography to remove any pre-existing oxidized compounds, then the purified oil was fortified with 400 ppm tocopherols, flushed with N_2, and stored at -80°C until use.

Table S2. Sequences of primers in qRT-PCR and 16S rRNA sequencing

Gene	Forward	Reverse
Primers for qRT-PCR		
Gapdh	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA
Tnf-α	CCCTCACACTCAGATCATCTTCT	GCTACGACGTGGGCTACAG
Il-6	TAGTCCTTCCTACCCCAATTTCC	TTGGTCCTTAGCCACTCCTTC
Ifnγ	ATGAACGCTACACACTGCATC	CCATCCTTTTGCCAGTTCCTC
Tlr4	ATGGCATGGCTTACACCACC	GAGGCCAATTTTGTCTCCACA
Il-10	GCTCTTACTGACTGGCATGAG	CGCAGCTCTAGGAGCATGTG
Il-1β	GCAACTGTTCCTGAACTCAACT	ATCTTTTGGGGTCCGTCAACT
C-myc	TGAAGTTCACGTTGAGGGG	AGAGCTCCTCGAGCTGTTTG
Axin 2	TGCATCTCTCTCTGGAGCTG	ACTGACCGACGATTCCATGT
Primers for sequencing		
16S rRNA	TCGTCGGCAGCGTCAGATGTGTAT	GTCTCGTGGGCTCGGAGATGTGTATA
	AAGAGACAGCCTACGGGNGGCWGCAG	AGAGACAGGACTACHVGGGTATCTAATCC

Table S3. Effects of TCC on composition of the microbiota at phylum levels (* *P* < 0.05, ** *P* < 0.01, * *P* < 0.001). The results are expressed as relative abundance (%).**

	Ctrl		**TCC**		
Phylum Name	**Average**	**SEM**	**Average**		**SEM**
Unassigned	1.290	0.111	0.547	***	0.092
Actinobacteria	3.505	0.930	1.091		0.509
Bacteroidetes	52.984	1.841	32.209	**	5.054
Cyanobacteria	0.734	0.163	0.137	***	0.079
Deferribacteres	1.686	0.478	0.004	***	0.002
Firmicutes	38.873	1.670	62.104	***	4.437
Proteobacteria	0.385	0.096	2.048	***	0.567
Tenericutes	0.031	0.004	0.054		0.027
Verrucomicrobia	0.511	0.193	1.806		1.231

Table S4. Effects of TCC on composition of the microbiota at genus levels. The results are expressed as relative abundance (%).

	Ctrl		**TCC**		
Genus Name	**Average**	**SEM**	**Average**		**SEM**
Unassigned	1.290	0.111	0.547	***	0.092
Prauseria	0.004	0.001	0.012	**	0.004
Bifidobacterium	3.352	0.922	0.889	*	0.490
Adlercreutzia	0.145	0.014	0.159		0.034
Eggerthella	0.000	0.000	0.019	*	0.012
o__Bacteroidales;Other;Other	0.022	0.007	0.002	***	0.001
Bacteroides	19.876	2.123	17.980		2.163
Parabacteroides	13.855	2.009	10.540		2.958
f__Rikenellaceae;g__	0.336	0.053	0.224		0.065
f__S24-7;g__	13.529	3.403	0.004	***	0.002
Butyricimonas	5.362	0.358	3.451		0.935
o__YS2;f__;g__	0.734	0.163	0.137	***	0.079
Mucispirillum	1.686	0.478	0.004	***	0.002
f__Bacillaceae;g__	0.015	0.002	0.058	*	0.021
Staphylococcus	0.004	0.002	0.117		0.108
Enterococcus	0.020	0.007	0.036		0.023
Lactobacillus	5.887	1.179	2.831	*	1.644
Streptococcus	0.008	0.001	0.097		0.086
Turicibacter	0.139	0.053	0.008	*	0.007
o__Clostridiales;Other;Other	0.037	0.008	0.070	*	0.012
o__Clostridiales;f__;g__	11.102	1.453	22.917	**	3.528
f__Christensenellaceae;g__	0.110	0.014	0.084		0.020
f__Clostridiaceae;Other	0.014	0.010	0.002	*	0.002
f__Clostridiaceae;g__	0.081	0.015	0.390	**	0.112
Clostridium	0.009	0.002	0.013		0.003
Dehalobacterium	0.232	0.027	0.061	***	0.017
f__Lachnospiraceae;Other	0.339	0.064	0.330		0.025
f__Lachnospiraceae;g__	3.937	0.554	7.393	**	1.097
Anaerostipes	0.002	0.000	0.011	*	0.003
Blautia	0.001	0.000	0.003		0.001
Coprococcus	0.251	0.024	0.771	***	0.128
Dorea	0.273	0.117	0.541	*	0.134
Pseudobutyrivibrio	0.037	0.009	0.007	**	0.004
Roseburia	0.013	0.007	0.016		0.006
[Ruminococcus]	0.528	0.047	1.369	***	0.211
f__Peptococcaceae;g__	0.058	0.012	0.046		0.017
rc4-4	1.163	0.269	1.762		0.962
f__Peptostreptococcaceae;g__	0.010	0.006	0.027		0.027
f__Ruminococcaceae;Other	0.806	0.091	0.875		0.169
f__Ruminococcaceae;g__	3.514	0.390	7.578	**	1.361
Anaerotruncus	0.013	0.004	0.019		0.007
Oscillospira	5.521	0.531	6.877		0.851
Ruminococcus	3.863	0.422	6.806		2.216
f__[Mogibacteriaceae];g__	0.031	0.005	0.017	*	0.004
o__SHA-98;f__;g__	0.002	0.001	0.000		0.000
f__Erysipelotrichaceae;Other	0.019	0.006	0.011		0.003
f__Erysipelotrichaceae;g__	0.795	0.140	0.873		0.179
Clostridium	0.026	0.006	0.027		0.006
Coprobacillus	0.007	0.003	0.044		0.025
o__RF32;f__;g__	0.125	0.040	0.199		0.092

Burkholderia	0.019	0.002	0.082	***	0.044
f__Oxalobacteraceae;Other	0.006	0.001	0.016	**	0.004
f__Enterobacteriaceae;Other	0.000	0.000	0.004		0.002
f__Enterobacteriaceae;g__	0.164	0.038	1.395	***	0.458
Enterobacter	0.048	0.031	0.123		0.050
Klebsiella	0.000	0.000	0.187	**	0.127
Stenotrophomonas	0.006	0.001	0.008		0.002
o__RF39;f__;g__	0.031	0.004	0.054		0.027
Akkermansia	0.511	0.193	1.806		1.231