

Table S1 Patient Characteristics of the Study

Number	Gender	Age (years old)	Sampling Site	Disease Subtype	Healing Score (Table S2)
1	Male	72	Descending colon	Inflammatory polyp	None
2	Male	72	Sigmoid colon	Hyperplastic polyp	None
3	Male	51	Sigmoid colon	Hyperplastic polyp	None
4	Male	33	Transverse colon	Inactive UC	5
5	Male	33	Sigmoid colon	Inactive UC	4
6	Male	36	Descending colon	Inactive UC	4
7	Male	59	Sigmoid colon	Active UC	1
8	Male	25	Rectum	Active UC	1
9	Female	33	Descending colon	Active UC	1

Table S2 Guidelines for Histological Grading Assessment of Mucosal Healing after IBD Treatment

Healing Score	Histological Features
5 points	Completely normal
4 points	Quiescent colitis, no increase in basal plasma cells
3 points	Quiescent colitis, with significant increase in basal plasma cells
2 points	Chronic active colitis, without significant increase in basal plasma cells
1 point	Chronic active colitis, with significant increase in basal plasma cells
0 points	Severe crypt atrophy or complete disappearance

Table S3. Histopathological Scoring

Mucosal Epithelial Damage	Inflammatory Cell Infiltration	Score
No epithelial damage; intact crypt architecture	Rare inflammatory cell infiltration in the lamina propria	0
Focal epithelial damage with focal crypt injury (involving $\leq 1/3$ of crypt length)	Increased inflammatory cells and neutrophil infiltration in the lamina propria	1
Mucosal erosion, crypt fusion, and ulceration with moderate crypt loss (involving $\leq 2/3$ of crypt length)	Inflammatory cell infiltration also found in the submucosa	2
Extensive damage involving the entire mucosal epithelium with complete crypt loss and disappearance of glandular structure	Full-thickness inflammatory cell infiltration in the submucosa	3

Table S4 Primer sequences used for realtime-PCR

Primers		Sequence
GAPDH	Forward	5'-CATCACTGCCACCCAGAAGACTG-3'
GAPDH	Reverse	5'-ATGCCAGTGAGCTTCCCGTTCAG-3'
IL-6	Forward	5'-ATGCCAGTGAGCTTCCCGTTCAG-3'
IL-6	Reverse	5'-CTGCAAGTGCATCATCGTTGTTC-3'
TNF- α	Forward	5'-TTAGAAAGGGGATTATGGCTCA-3'
TNF- α	Reverse	5'-ACTCTCCCTTTGCAGAACTCAG-3'
iNOS2	Forward	5'-CCCTTCCGAAGTTTCTGGCAGCAGC-3'
iNOS2-R	Reverse	5'-GGCTGTCAGAGCCTCGTGGCTTTGG-3'
IL-10	Forward	5'-CGGGAAGACAATAACTGCACCC-3'
IL-10	Reverse	5'-CGGTTAGCAGTATGTTGTCCAGC-3'
ZO-1	Forward	5'-GTTGGTACGGTGCCCTGAAAGA-3'
ZO-1	Reverse	5'-GCTGACAGGTAGGACAGACGAT-3'
Occludin1	Forward	5'-TGGCAAGCGATCATACCCAGAG-3'
Occludin1	Reverse	5'-CTGCCTGAAGTCATCCACACTC-3'
MUC2	Forward	5'-CCCAGAAGGGACTGTGTATG-3'
MUC2	Reverse	5'-TGCAGACACACTGCTCACA-3'
Claudin1	Forward	5'-GGACTGTGGATGTCCTGCGTTT-3'
Claudin1	Reverse	5'-GCCAATTACCATCAAGGCTCGG-3'
IL-18	Forward	5'-GACAGCCTGTGTTCGAGGATATG-3'
IL-18	Reverse	5'-TGTTCTTACAGGAGAGGGTAGAC-3'
IL-1 β	Forward	5'-TGGACCTTCCAGGATGAGGACA-3'
IL-1 β	Reverse	5'-GTTTCATCTCGGAGCCTGTAGTG-3'
NLRP3	Forward	5'-TCACAACTCGCCCAAGGAGGAA-3'
NLRP3	Reverse	5'-AAGAGACCACGGCAGAAGCTAG-3'
GSDMD	Forward	5'-GGTGCTTGACTCTGGAGAACTG-3'
GSDMD	Reverse	5'-GCTGCTTTGACAGCACCGTTGT-3'

Table S5 Individual fecal short-chain fatty acid concentrations in each experimental group

Group	Acetic acid (ng/mg feces)	Propionic acid (ng/mg feces)	Butyric acid (ng/mg feces)	Isobutyric acid (ng/mg feces)	Isovaleric acid (ng/mg feces)
WT-Control-1	1558.5	493.2	947.2	501.2	10.5
WT-Control-2	1445.8	486.7	761.2	29.8	18.9
WT-Control-3	1207.8	483.9	597.6	30.6	24.0
WT-Control-4	2101.7	683.6	1315.4	27.4	16.6
WT-Control-5	2283.2	805.9	1102.1	50.4	21.0
WT-DSS-1	663.3	149.3	61.6	4.8	6.9
WT-DSS-2	783.0	199.8	118.4	11.2	17.3
WT-DSS-3	811.7	208.2	245.6	27.5	33.2
WT-DSS-4	579.7	130.7	215.2	16.7	23.9
WT-DSS-5	617.7	122.5	100.1	7.0	8.8
<i>Nlrp3</i> ^{-/-} -Control-1	2869.3	838.2	604.1	51.8	34.8
<i>Nlrp3</i> ^{-/-} -Control-2	1633.3	474.6	450.5	29.0	19.2
<i>Nlrp3</i> ^{-/-} -Control-3	1684.5	584.8	867.0	53.7	51.5
<i>Nlrp3</i> ^{-/-} -Control-4	2135.8	744.5	563.4	48.0	35.6
<i>Nlrp3</i> ^{-/-} -DSS-1	1721.7	640.4	442.5	44.2	54.1
<i>Nlrp3</i> ^{-/-} -DSS-2	1480.5	566.1	601.3	65.6	93.1
<i>Nlrp3</i> ^{-/-} -DSS-3	1447.5	562.4	400.9	94.0	163.9
<i>Nlrp3</i> ^{-/-} -DSS-4	2257.6	745.2	567.3	75.4	76.6

Values represent fecal short-chain fatty acid concentrations from individual mice.

Concentrations were converted from ng/g to ng/mg feces by dividing the original values by 1,000. Each row represents one biological replicate.