**Supplemental methods**

*Colonic myeloperoxidase (MPO) assay*

Neutrophil influx in tissue was analyzed by assaying the enzymatic activity of MPO, a marker for neutrophils. Briefly, tissue (50 mg/mL) were thoroughly washed in PBS and homogenized in 0.5% hexadecyltrimethylammonium bromide (Sigma, St. Louis, MO) in 50 mM PBS, (pH 6.0), freeze-thawed 3 times, sonicated and centrifuged. MPO was assayed in the clear supernatant by adding 1 mg/mL of dianisidine dihydrochloride (Sigma, St. Louis, MO) and 5x10-4% H2O2 and the change in optical density measured at 450 nm. Human neutrophil MPO (Sigma, St. Louis, MO) was used as standard. One unit of MPO activity was defined as the amount that degraded 1.0 mol of peroxide/min at 25**°**C ([1](#_ENREF_1)).

*Quantification of fecal Lcn-2 by ELISA*

For quantification of fecal Lcn-2 by ELISA, frozen fecal samples were reconstituted in PBS containing 0.1% Tween 20 to a final concentration of 100 mg/mL and vortexed for 20 min to get a homogenous fecal suspension ([2](#_ENREF_2)). These samples were then centrifuged and supernatants were collected and used for estimating Lcn-2 levels using Duoset murine Lcn-2 ELISA kit (R&D Systems, Minneapolis, Minnesota, USA).

*Quantification of serum CXCL-1 and IL-6 by ELISA*

Serum CXCL1 (KC) and IL-6 concentration were determined using Duoset cytokine ELISA kits (R&D Systems, Minneapolis, MN) according to manufacturer’s instructions.

*Fecal flagellin and lipopolysaccharide load quantification*

We quantified flagellin and lipopolysaccharide (LPS) as previously described ([3](#_ENREF_3)) using human embryonic kidney (HEK)-Blue-mTLR5 and HEK-BluemTLR4 cells, respectively (Invivogen, San Diego, California, USA). We resuspended fecal material in PBS to a final concentration of 100 mg/mL and homogenized using a Mini-Beadbeater-24 without the addition of beads to avoid bacteria disruption. Supernatants were serially diluted and applied to mammalian cells. Purified *E. coli* flagellin and LPS (Sigma, St Louis, Missouri, USA) were used for standard curve determination. After 24 h of stimulation, we applied cell culture supernatant to QUANTI-Blue medium (Invivogen, San Diego, California, USA) and measured alkaline phosphatase activity at 620 nm after 30 min.

*RNA Extraction and Real-Time RT-PCR*

Total RNAs were isolated from a piece of distal colon devoid of tumor, using TRIzol (Invitrogen, Carlsbad, CA) according to the manufacturer’s instructions. Quantitative RT-PCR was performed using the iScriptTM One-Step RT-PCR Kit with SYBR Green (Bio-Rad, Hercules, CA) in a CFX96 apparatus (Bio-Rad, Hercules, CA) with specific mouse oligonucleotides. The sense and antisense oligonucleotides used are listed in **table S1**.

*Bacterial quantification by qPCR*

For quantification of total fecal bacterial load, total bacterial DNA was isolated from weighted feces using QIAamp DNA Stool Mini Kit (Qiagen). DNA was then subjected to quantitative PCR using QuantiFast SYBR Green PCR kit (Biorad) with universal 16S rRNA primers (**Table S1**) to measure total bacteria ([4](#_ENREF_4)). Results are expressed as bacteria number per mg of stool, using a standard curve. The sense and antisense oligonucleotides used are listed in **table S1** ([5-8](#_ENREF_5))

*Food intake measurement*

Groups of mice were placed in a clean cage with a known amount of food. Twenty-four hours later, amount of remaining food was measured with the difference viewed as food intake per 24h. Error bars reflect S.E.M. of 3 measurements made one week apart.

*Overnight fasting blood glucose measurement*

Mice were placed in a clean cage and fasted for 15h. Blood glucose concentration was then determined using a Nova Max Plus Glucose Meter and expressed in mg/dL.

*H&E staining and histopathologic analysis*

Following euthanasia, mouse colons and small intestines were fixed in 10% buffered formalin for 24 hours at room temperature and then embedded in paraffin. Tissues (containing tumors in AOM/DSS-treated animals) were sectioned at 5-m thickness and stained with hematoxylin & eosin (H&E) using standard protocols.

*Fecal microbiota analysis by 16S rRNA gene sequencing using Illumina technology and metagenome prediction*

16S rRNA gene sequencing was performed as previously described ([9](#_ENREF_9)), with data deposited in the European Nucleotide Archive under accession number PRJEB8035. Sequences were demultiplexed, quality filtered using the Quantitative Insights Into Microbial Ecology (QIIME, version 1.8.0) software package ([10](#_ENREF_10)), and forward and reverse Illumina reads were joined using the fastq-joinmethod ([11](#_ENREF_11)). We used QIIME default parameters for quality filtering (reads truncated at first low-quality base and excluded if: (1) there were more than three consecutive low quality base calls; (2) less than 75% of read length was consecutive high quality base calls; (3) at least one uncalled base was present; (4) more than 1.5 errors were present in the barcode; (5) any Phred qualities were below 20; or (6) the length was less than 75 bases). Sequences were assigned to OTUs using the UCLUST algorithm ([12](#_ENREF_12)) with a 97% threshold of pairwise identity (without the creation of new clusters with sequences that do not match the reference sequences), and classified taxonomically using the Greengenes reference database ([13](#_ENREF_13)). Alpha diversity curves were determined using the determination of the number of observed OTUs. OTUs were summarized at the phylum, class and order levels. LEfSE (LDA Effect Size) was used to investigate bacterial members that drive differences between groups ([14](#_ENREF_14)).

PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) was used to predict the metagenome based on microbiota composition analysis ([15](#_ENREF_15)). A closed-OTU picking strategy was using against the Greengenes reference database 13-5 ([13](#_ENREF_13)), and predicted metagenomes were analyzed by principal coordinates analysis of the beta diversity using binary jaccard method with QIIME. Predicted metagenomes were categorized at level 3 of the Kyoto Encyclopedia of genes and genomes (KEGG) pathways. Gene-E ([16](#_ENREF_16)) was used for heatmap representation of pathways with an altered abundance following emulsifier consumption compared with water-treated control group. KEGG pathways were visualized on volcano plot using R software.

**Supplemental references**

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