**Supplemental figure legends**

**Figure S1: Schematic representation of the AOM-DSS experimental design.**

**Figure S2: Dietary emulsifiers promote metabolic syndrome and low-grade intestinal inflammation in WT mice.** WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 13 weeks. (**A-C**) fecal Lcn2 concentration at day 0 (**A**), day 28 (**B**) and day 63 (**C**). (**D**) Body weight over time, (**E**) 15-hours fasting blood glucose concentration and (**F**) food intake. Data are the means +/- S.E.M. (*n*=5-8). Significance was determined using *t*-test (\* indicates *p*<0.05) or two-way group ANOVA corrected for multiple comparisons with a Bonferroni test (# indicates statistical significance).

**Figure S3: Colonic histology analysis of emulsifiers promotion of colitis-associated cancer.** WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 13 weeks. Mice were then injected intraperitoneally with AOM (10 mg/kg body weight), maintained for 7 days, and then subjected to a two-cycle DSS treatment (each cycle consisted of 7 days of 2.5% DSS and 14 days of H2O). Representative images of H&E staining of the colon. Arrow = inflammatory cell infiltration. Scale bar, 200m.

**Figure S4: Dietary emulsifiers induce alterations of the microbiota.** WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 13 weeks. Mice were then injected intraperitoneally with AOM (10 mg/kg body weight), maintained for 7 days, and then subjected to a two-cycle DSS treatment (each cycle consisted of 7 days of 2.5% DSS and 14 days of H2O). (**A-D)** Proteobacteria levels, (**E-H**) Enterobacteriaceae levels, (**I-L**) *Escherichia coli* levels and (**M-P**) ClbB encoding gene were estimated at day 0 (**A, E, I, M**), day 21 (**B, F, J, N**), day 63 (**C, G, K, O**) and day 141 (**D, H, L, P**). (*n*=5-8).

**Figure S5: Alpha diversity and summarized taxa of the fecal bacterial community following emulsifier treatment.** WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 13 weeks. (**A-B**) Alpha diversity analysis (observed OTUs) at day 0 (**A**) and day 63 (**B**). At day 63, OTUs were summarized at the phylum (**C**), class (**D**) and order (**E**) levels. Data are the means +/- S.E.M. (*n*=5-8). Significance was determined using two-way group ANOVA corrected for multiple comparisons with a Bonferroni test (# indicates statistical significance).

**Figure S6: Identification of bacterial members differentially expressed between experimental groups.** WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 13 weeks. LEfSE (LDA Effect Size) was used to investigate bacterial members that drive differences between groups at day 63. (**A**) Taxonomic cladogram obtained from LEfSe analysis of 16S sequences. Blue, water-enriched taxa; red, CMC-enriched taxa; green, P80-enriched taxa. The brightness of each dot is proportional to its effect size. (**B**) LDA scores for the differentially altered taxa. Blue, water-enriched taxa; red, CMC-enriched taxa; green, P80-enriched taxa. Only taxa meeting an LDA significant threshold >2.0 are represented.

**Figure S7: Dietary emulsifiers favor a pro-inflammatory microbiota.** WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 13 weeks. Mice were then injected intraperitoneally with AOM (10 mg/kg body weight), maintained for 7 days, and then subjected to a two-cycle DSS treatment (each cycle consisted of 7 days of 2.5% DSS and 14 days of H2O). Total fecal bacterial load was evaluated by q-PCR. Data are the means +/- S.E.M. (*n*=5-8).

**Figure S8: Metagenome prediction analysis following CMC consumption.** WT mice were exposed to drinking water containing CMC (1.0%) for 13 weeks. PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) was used to predict the metagenomes at day 63, and predicted metagenomes were categorized at level 3 of the Kyoto Encyclopedia of genes and genomes (KEGG) pathways. Heatmap representation of pathways with an altered abundance following CMC consumption compare to water-treated control group. Data are expressed as relative value, from blue for low expression to red for high expression. Hierarchical clustering of pathways (rows) and samples (columns) was performed using one minus pearson correlation.

**Figure S9: Metagenome prediction analysis following P80 consumption.** WT mice were exposed to drinking water containing P80 (1.0%) for 13 weeks. PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) was used to predict the metagenomes at day 63, and predicted metagenomes were categorized at level 3 of the Kyoto Encyclopedia of genes and genomes (KEGG) pathways. Heatmap representation of pathways with an altered abundance following P80 consumption compare to water-treated control group. Data are expressed as relative value, from blue for low expression to red for high expression. Hierarchical clustering of pathways (rows) and samples (columns) was performed using one minus pearson correlation.

**Figure S10: Dietary emulsifiers alter epithelial cell proliferation and apoptosis during colitis-associated cancer development.** WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 13 weeks. Mice were then injected intraperitoneally with AOM (10 mg/kg body weight), maintained for 7 days, and then subjected to a two-cycle DSS treatment (each cycle consisted of 7 days of 2.5% DSS and 14 days of H2O). Analysis of (**A**-**B**) CTNNBL and (**C**-**D**) LEF1mRNA expression by q-RT-PCR in the colon following emulsifier treatment (**A and** **C**) and following the induction of colonic neoplasia (**B** and **D**).

**Figure S11: Dietary emulsifier and AOM injection experiment.** (**A**) Schematic representation of the AOM alone experimental design. WT mice were exposed to drinking water containing CMC or P80 (1.0%) for 12 weeks. Mice were injected intraperitoneally with AOM (10 mg/kg body weight) weekly for a total of seven injections. (**B**) Body weight over time. Data are the means +/- S.E.M. (*n*=10). Significance was determined using two-way group ANOVA corrected for multiple comparisons with a Bonferroni test (# indicates statistical significance).