Supplemental Figure 1: Discovery and validation sample analyses for colonic inflammation

a. *Citrobacter rodentium* levels were not significantly affected by stress in the discovery samples. b and c. iNOS and TNFα main effect of stress exposure (p<.05). d. IL-1β. e. IFNγ main effect of stress and infection exposure (p<.05). f. IL-22 main effect of infection exposure (p<.05 stress). g. REG3γ *p<.05 infection x sac day interaction. h. Histopathology. i. *Citrobacter rodentium* increased with stress in the validation samples *p<.05. j and k. iNOS and TNFα main effect of stress and infection exposure (p<.05). l. IL-1β *p<.05 stress x infection interaction. m. IFNγ *p<.05 stress x infection interaction. n. IL-22 *p<.05 stress x infection interaction. o. REG3γ *p<.05 stress x infection interaction. p. Histopathology *p<.05 stress x infection interaction.

Supplemental Figure 2: Discovery and validation sample analyses for SCFA levels and SCFA receptor expression

a-c. Acetic acid, Butyric acid, and Propionic acid were not significantly affected by stress or infection in the discovery samples. d. GPR43 receptor expression qPCR analysis main effect of infection exposure (p<.05). e. GPR41 receptor expression qPCR analysis *p<.05 stress x infection interaction. f. GPR109A receptor expression qPCR. g. Acetic acid analysis main effect of stress (p<.05). h. Butyric acid analysis *p<.05 infection day 12 compared to infection day 6. i. Propionic acid analysis *p<.05 stress and infection on day 6 and 12 compared to stress and no infection day 6 and 12. j. GPR43 receptor expression qPCR analysis main effect of infection exposure ($p<.05$). k. GPR41 receptor expression qPCR analysis *$p<.05$ stress x infection interaction. l. GPR109A receptor expression qPCR analysis *$p<.05$ stress x infection interaction.

Supplemental Figure 3: Genera combined sample analysis

a-f**.** The relative abundances of *Akkermansia, Anaerostipes, Butyricicoccus, Coprococcus, Parabacteroides,* and *SMB53* decreased with stress exposure ($p<.05$). g and h. The relative abundances of *Bacteroides* and *Butyricimonas* decreased with stress exposure ($p<.05$) and decreased when challenged with the infection ($p<.05$). i and j. The relative abundances of *Odoribacter* and *Sutterella* increased with stress exposure ($p<.05$).

Supplemental Figure 4: Genera combined sample analysis

a-c. The relative abundances of *AF12, Helicobacter, and Prevotella* decreased when challenged with the infection ($p<.05$) and increased with stress exposure ($p<.05$). d-k. The relative abundances of *Anaerococcus*, *Anaeroplasma*, *Bradyrhizobium*, *Enhydrobacter*, *Mucispirillum, Oscillospira*, *Peptoniphilus,* and *Roseburia* decreased when challenged with the infection ($p<.05$). l-o. The relative abundances of *Enterobacter*, *Flavobacterium, Flexispira,* and *Trabulsiella* increased when challenged with the infection ($p<.05$).

Supplemental Figure 5: Genera discovery sample analysis

a-f. The relative abundances of *Akkermansia, Anaerostipes, Butyricicoccus, Coprococcus, Parabacteroides*, and *SMB53* were not significantly affected with stress or infection exposure. g. The relative abundance of *Bacteroides* decreased with stress exposure (p<.05). h. The relative abundance of *Butyricimonas* was not significantly affected with stress or infection exposure. i. The relative abundance of *Odoribacter* was not significantly affected with stress or infection exposure. j. The relative abundance of S*utterella* increased with stress exposure (p<.05).

Supplemental Figure 6: Genera discovery sample analysis

a-c. The relative abundances of *AF12, Helicobacter,* and *Prevotella* decreased when challenged with the infection (p<.05) and increased with stress exposure (p<.05). d-g. The relative abundances of *Anaerococcus, Anaeroplasma, Bradyrhizobium*, and *Enhydrobacter* were not significantly affected with stress or infection exposure. h. The relative abundance of *Mucispirillum* decreased when challenged with the infection (p<.05). i-k. The relative abundances of *Oscillospira, Peptoniphilus*,and *Roseburia* were not significantly affected with stress or infection exposure. l. The relative abundance of *Enterobacter* increased when challenged with the infection (p<.05). m. The relative abundance of *Flavobacterium* was not significantly affected with stress or infection exposure. n and o. The relative abundances of *Flexispira*, and *Trabulsiella* increased when challenged with the infection (p<.05).

Supplemental Figure 7: Genera validation sample analysis

a. The relative abundance of *Akkermansia* decreased with stress exposure (p<.05). b. The relative abundance of *Anaerostipes* decreased with stress exposure (p<.05) and increased with infection exposure (p<.05). c. The relative abundance of *Butyricicoccus* decreased with stress exposure (p<.05). d. The relative abundance of *Coprococcus* was not significantly affected with stress or infection exposure. e and f. The relative abundances of *Parabacteroides and SMB53* decreased with stress exposure (p<.05). g and h. The relative abundances of *Bacteroides* and *Butyricimonas* decreased with stress exposure (p<.05) and decreased with infection exposure (p<.05). i and j. The relative abundances of *Odoribacter* and S*utterella* increased with stress exposure (p<.05).

Supplemental Figure 8: Genera validation sample analysis

a-c. The relative abundances of *AF12, Helicobacter,* and *Prevotella* decreased when challenged with the infection (p<.05) and increased with stress exposure (p<.05). d-f. The relative abundances of *Anaerococcus, Anaeroplasma,* and *Bradyrhizobium* decreased when challenged with the infection (p<.05). g. The relative abundance *Enhydrobacter* was not significantly affected with stress or infection exposure. h. The relative abundance of *Mucispirillum* decreased when challenged with the infection (p<.05). i. The relative abundance of *Oscillospira* was not significantly affected with stress or infection exposure. j and k. The relative abundances of *Peptoniphilus* and *Roseburia* decreased when challenged with the infection (p<.05). l and m. The relative abundances of *Enterobacter* and *Flavobacterium* increased when challenged with the infection (p<.05). n. The relative abundance of *Flexispira* increased with stress exposure (p<.05). o. The relative abundance of *Trabulsiella* increased when challenged with the infection (p<.05).

Supplemental Table 1. Sequences of primers and probes used for real-time PCR

Primers and probes were purchased from (Thermo Fisher, Waltham, MA).