Supplementary Figure Legends

Figure S1. A phylogenetic tree displaying the 109 families present in all five of the uninfected mice demonstrates the diversity of the microbiota in the mouse stomach. Clades are color-coded based on the phylum and collapsed branches had branch lengths < 0.05. The leaf labels indicate the phylum and the family of the identified bacteria. Blue, *Bacteroidetes*; Red, *Proteobacteria*; Pink, *Firmicutes*; Orange, *Acidobacteria*; Yellow, *Chloroflexi*; Light blue, *Verrucomicrobia*; Green, *Actinobacteria*.

Figure S2. *H. pylori* infection for four weeks does not alter the gastric microbiota. Non-metric multidimensional scaling (NMDS) based on Bray-Curtis distance between samples given the abundance of 12032 taxa present in at least one sample; each dot represents one mouse in the study. *H. p.*=4 week *H. pylori* infection; UI=uninfected.

Figure S3. Pie charts illustrate phylum level distribution between bacterial taxa that inversely correlated **(A;** 19 taxa) or co-correlated **(B;** 29 taxa) with *H. pylori* infection compared with uninfected controls. * Indicates class-level breakouts of the *Proteobacteria* phylum to highlight the class containing *H. pylori.*

Figure S4. Antibiotic treatment does not significantly change the numbers of total bacteria or *H. pylori* present in the stomach. **(A)** DNA was isolated from total mouse stomach tissue and used for qPCR of the bacterial 16s rRNA gene. N ≥ 4. No significant differences were found between groups by Mann Whitney U test. **(B)** Colonization level of *H. pylori* in the three infected groups was determined by plating and is presented as Log CFU/g stomach tissue. *H. pylori* was not detected in any uninfected groups. *P<0.05, Two way ANOVA and Tukey's Range Test. *H.p.*= *H. pylori* infected; Ab.= antibiotic treatment; RC.= reconstituted with gastric microbiota.

Figure S5. Antibiotic treatment alters the gastric microbiota. Non-metric multidimensional scaling (NMDS) based on Bray-Curtis distance between samples given the abundance of 12765 taxa present in at least one sample; each dot represents one mouse in the study. *H. p.*=4 week *H. pylori* infection; Ab.=antibiotic pretreatment.

Figure S6. *Clostridium* increased in the antibiotic treated mice all map to Cluster IV and XIVa. The phylogenetic tree displays all the unknown *Clostridium* increased in the antibiotic treated mice (green labels) with some known *Clostridium* species (black labels) to anchor the tree. Collapsed branches had branch lengths < 0.05 and bootstrap values are displayed at branch junctions.

Supplemental Tables

Table S1. 2056 OTUs present in all 5 uninfected mice

Table S2. 47 OTUs found to be different by abundance comparing 5 uninfected samples to 4 infected samples

Table S3. 2424 OTUs found to be decreased in antibiotic treated mice by abundance comparison with 10 non-antibiotic pretreated samples

Table S4. 1984 OTUs found to be increased in antibiotic treated mice by abundance comparison with 10 non-antibiotic pretreatment samples