Supplementary Figure legends:

Figure S1 *Distribution of Molecular atrophy and its relation to ATP4 expression*

A) Mean ATP4 (*ATP4A* and *ATP4B*) expression shown in counts per million reads. Samples are marked according to Pathology stage: ""Min"; *H. pylori*-uninfected in green, "Gast"; Gastritis with no atrophy or metaplasia in blue, "Atr"; atrophic gastritis in orange, "EA"; Extensive atrophy in red, and "Met"; Intestinal metaplasia in black. B) Distribution of Molecular atrophy score in the pathology groups. C) Correlation between Molecular atrophy score and mean ATP4 expression. R and p-values are shown for the Spearman correlation between the two variables.

Figure S2. *Mapping statistics of bacterial 16S and reads mapping to H. pylori.*

A) Amount of reads identified as bacterial 16S per million total reads. B) Proportion of reads mapping to *H. pylori* transcripts using kallisto. Tpm; number of reads mapping to a transcript per million total reads.

Figure S3. *PCA plots based on log-transformed abundances, RNA-seq 16S data*

A) Phylum level. The phyla driving the differentiation are shown as red arrows. B) Genus level. "Min"; *H. pylori*-uninfected, "Gast"; Gastritis with no atrophy or metaplasia, "Atr"; Atrophic gastritis, "EA"; Extensive atrophy, and "Met"; Intestinal metaplasia. The asterisks denote the individuals that were H.p. negative according to clinical methods. Ellipses represent the normal distribution of the samples in each group.

Figure S4. *Genus-level abundance in the gastric corpus and antrum, based on 16S amplicon data.*

A) Genus level abundances in raw reads. B) Genus level relative abundances in percent. "Min"; *H. pylori*-uninfected, "Gast"; Gastritis with no atrophy or metaplasia, "Atr"; Atrophic gastritis, "EA"; Extensive atrophy, and "Met"; Intestinal metaplasia. Both antrum (-A) and corpus (-C) data shown. Reads from the 16S cDNA amplicon sequencing data were classified using Metaxa2. Asterisks represent individuals negative for *H. pylori* infection as determined by clinical tests.

Figure S5. *PCA plots based on log-transformed genus abundances, 16S amplicon data*

"Min"; *H. pylori*-uninfected, "Gast"; Gastritis with no atrophy or metaplasia, "Atr"; Atrophic gastritis, "EA"; Extensive atrophy, and "Met"; Intestinal metaplasia. Both antrum (-A) and corpus (-C) data shown. The asterisks denote the individuals that were Hp negative according to clinical methods. Ellipses represent the normal distribution of the samples in each group.