**Supplementary\_Table\_1.xlsx** Clinical metadata for each sample, including host age, sex, geographic location, and labeled disease outcome (gastric vs non-gastric cancer).

**Supplementary\_Table\_2.xlsx** Binary matrix indicating presence (1) or absence (0) of known *H. pylori* virulence genes per genome, based on BLASTN results.

**Supplementary\_Table\_3.xlsx** Length-weighted numerical genome descriptors computed using iFeatureOmega and MathFeature for each *H. pylori* genome.

**Supplementary\_Table\_4.xlsx** Aggregated variant-level features including mutation types and functional annotations extracted from VCF files for each genome.

**Supplementary\_Table\_5.xlsx**Final merged dataset containing all the extracted features before model training.