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## Data Article

# Data on gut metagenomes of the patients with *Helicobacter pylori* infection before and after the antibiotic therapy



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## ABSTRACT

Antibiotic therapy can lead to the disruption of gut microbiota community with possible negative outcomes for human health. One of the diseases for which the treatment scheme commonly included antibiotic intake is *Helicobacter pylori* infection. The changes in taxonomic and functional composition of microbiota in patients can be assessed using “shotgun” metagenomic sequencing. Ten stool samples were collected from 4 patients with *Helicobacter pylori* infection before and directly after the *H. pylori* eradication course. Additionally, for two of the subjects, the samples were collected 1 month after the end of the treatment. The samples were subject to “shotgun” (whole-genome) metagenomic sequencing using Illumina HiSeq platform. The reads are deposited in the ENA (project ID: PRJEB18265).

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