Figure S2

Library preparation

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DNA library with approximately 500 bp fragments of *Helicobacter pylori* genome

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Illumina MiSeq control software

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Sequencing data with 151 bp paired-end reads

↓

Trimming automatically low quality reads (<Q30), index, and adaptor sequences

↓

CLC Genomics Workbench 6.0.1

↓

Mapping with CLC Assembly Cell 4.0

↓

Detection of SNVs/indels positions against reference genome NC_000915

↓

Discard indels position

↓

Selection of SNVs presented in >99% of mapped reads with minimum coverage of 100

↓

Identification of SNVs