

# Detection of hidden antibiotic resistance through real-time genomics

## Supplementary Information

Ela Sauerborn<sup>1,2,3,4</sup>, Nancy Carolina Corredor<sup>4</sup>, Tim Reska<sup>1,2,3</sup>, Albert Perlas<sup>1,2</sup>, Samir Vargas da Fonseca, Atum<sup>1,25,6</sup>, Nick Goldman<sup>7</sup>, Nina Wantia<sup>4</sup>, Clarissa Prazeres da Costa<sup>4,8,9</sup>, Ebenezer Foster-Nyarko<sup>10</sup>, Lara Urban<sup>1,2,3\*</sup>

<sup>1</sup>Helmholtz AI, Helmholtz Zentrum Muenchen, Neuherberg, Germany

<sup>2</sup>Helmholtz Pioneer Campus, Helmholtz Zentrum Muenchen, Neuherberg, Germany

<sup>3</sup>Technical University of Munich, School of Life Sciences, Freising, Germany

<sup>4</sup>Institute of Medical Microbiology, Immunology and Hygiene, TUM School of Medicine and Health, Technical University of Munich, Germany

<sup>5</sup>Departamento de Química Fundamental, Instituto de Química, Universidade de São Paulo, São Paulo, Brazil

<sup>6</sup>Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, São Paulo, Brazil

<sup>7</sup>European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Genome Campus, Cambridge, UK

<sup>8</sup>Center for Global Health, TUM School of Medicine and Health, Technical University of Munich, Munich, Germany

<sup>9</sup>German Center for Infection Research (DZIF), partner site Munich, Germany

<sup>10</sup>Department of Infection Biology, London School of Hygiene & Tropical Medicine, Keppel Street, London, UK

\*Corresponding author: [lara.h.urban@gmail.com](mailto:lara.h.urban@gmail.com)

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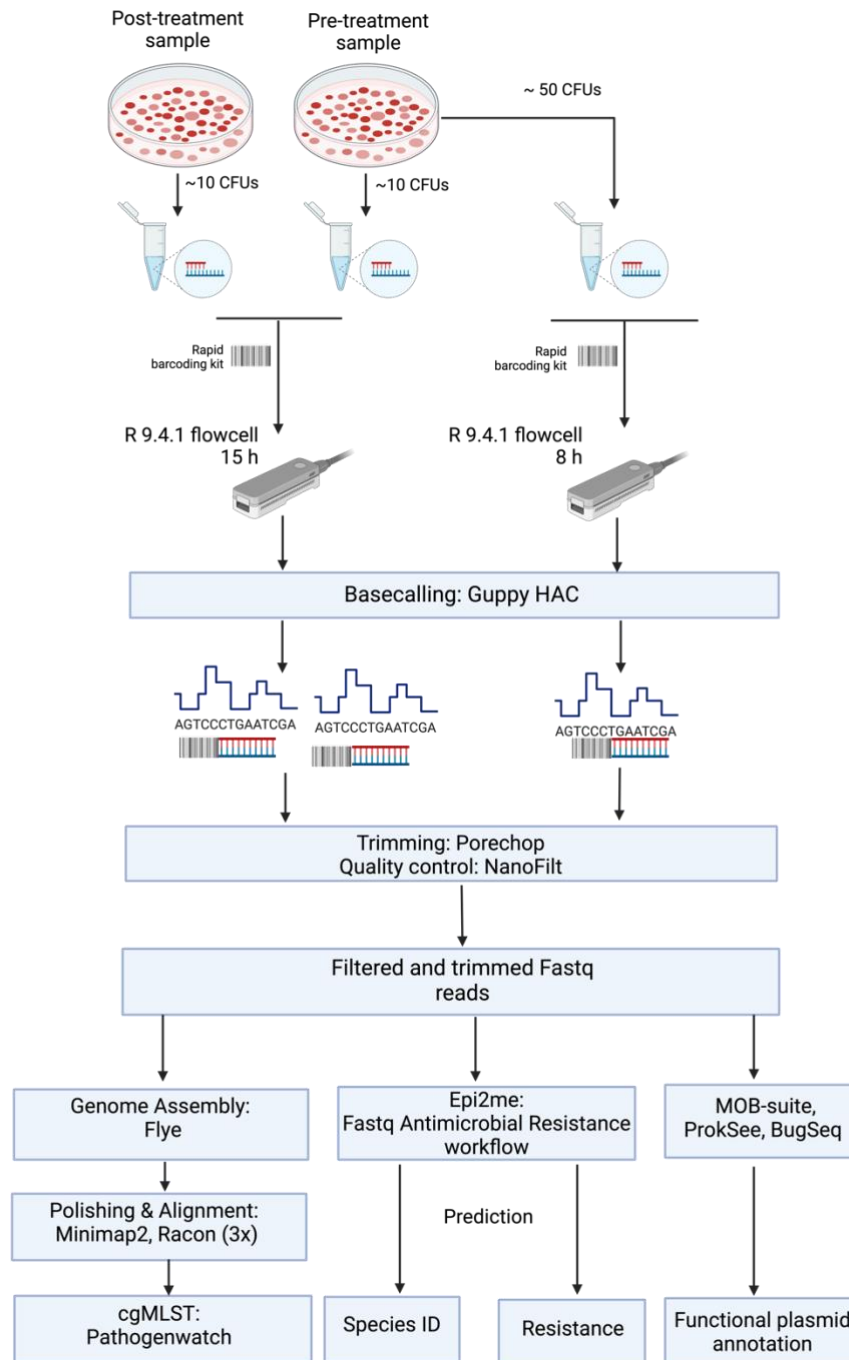
- Supplementary Table 1
- Supplementary Table 2
- Supplementary Figure 1

**Supplementary Table 1.** Real-time genomic sequencing and assembly metrics before and after treatment with CAZ-AVI. Genomic material of each bacterial isolate was sequenced for 15 hours; the pre-treatment isolate was additionally sequenced for a further 8 hours to simulate adaptive sequencing in the clinical setting.

Genomic sequencing and assembly metrics	Pre-treatment sample		Post-treatment sample
	15h	+8h	15h
Median read quality (Phred)	12.3	13.0	12.3
Median read length [kb]	4.1	5.3	4.5
Total number of bases [Mb]	442	1,551	194
Assembly coverage (median)	68	271	30
Number of contigs (>50 kb)	5	5	5
Contig N50 [Mb]	5.2	5.2	5.3

**Supplementary Table 2.** MIC measurements with VITEK2 and Liofilchem®MIC test strip for CAZ-AVI. The colouring scheme indicates the interpretation of MICs according to EUCAST guidelines (green: susceptible/intermediate; red: resistant).

Antibiotic	Pre-treatment isolate MIC (mg/L)	Post-treatment isolate MIC (mg/L)
Ampicillin	>32	>32
Ampicillin-Sulbactam	>32	>32
Piperacillin	>128	>128
Piperacillin-Tazobactam	>128	>128
Cefuroxime	>64	>64
Cefotaxime	>64	>64
Ceftriaxone	>64	>64
Ceftazidime	>64	>64
Imipenem	>16	1
Meropenem	>16	2
Ertapenem	>8	>8
Gentamicin	>16	>16
Ciprofloxacin	>4	>4
Ceftazidime-Avibactam	2	>256



**Supplementary Figure 1.** Bioinformatic workflow for species identification and antibiotic resistance prediction from nanopore sequencing data of pre- and post-treatment isolates (HAC: High-accuracy basecalling; ID: Identification; cgMLST: core genome Multi-Locus Sequence Typing). All computational analyses were conducted on a portable laptop with an 8 GB NVIDIA GeForce RTX 4070 GPU, 16 GB 5200 MHz RAM, and an Intel i7-13800H CPU with 14 cores and 20 threads.