***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/%22%20%5Ct%20%22_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info%3Adoi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

- Methods Section: Statistical analysis and quantification of the role each evolutionary force.

- Results section: Contributions of evolutionary forces under antibiotic treatment. Evolutionary tradeoffs arise from past antibiotic selection, Replaying the antibiotic treatment using a different antibiotic. Phenotypic divergence despite genetic parallelism

- Figures 2, 3, 4, Figure1-Figure supplement 1, Figure 2-Figure supplement 1, Figure 2-source data 1.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Full description of the experimental setup. Sections: Results and Experimental evolution (Methods)

MIC estimations (3 technical replicates per population). Section: Contributions of evolutionary forces under antibiotic treatment. Evolutionary tradeoffs arise from past antibiotic selection, Replaying the antibiotic treatment using a different antibiotic.
Populations sequenced: 44. Sections: Phenotypic divergence despite genetic parallelism, Collateral sensitivity resulting from genetic reversions, Genome sequencing and Data processing. Genomes can be found in <https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA485123> with the accession numbers shown in Supplementary File 1.

Code can be found in <https://github.com/sirmicrobe/chance_history_selection>.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

No group allocation in the manuscript

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Figure 1-source data 1. Concentrations of CAZ and IMI used at different intervals during the evolution experiments.

Figure 1-source data 2. MIC values of all ancestors and evolved clones by treatment.

Figure 2-source data 1. Raw data for the statistical analysis of the evolutionary forces

Figure 4-source data 1. Putative driver mutations and resistance levels.

Figure 4-source data 2. Complete list of mutated genes.

Supplementary File 1. Accession numbers to NCBI of the 44 populations sequenced.

All MICs data, and code processing can be found in: <https://github.com/sirmicrobe/chance_history_selection>.

Sequenced Genomes can be found in:
<https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA485123>