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**Sample-size estimation**

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* 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:

Sample size and statistical methods used can be found within the ‘Material and methods’ section, in the paragraph related to relevant techniques:

Convergent evolution on genes

Fitness assays

Cell cycle profiles

Premature sister chromatid separation assay

DNA replication profiles

Analysis of allele frequency by sanger sequencing

Segmental amplification detection by digital PCR

**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
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Cell cycle profiles

Premature sister chromatid separation assay

DNA replication profiles

Analysis of the allele frequency by sanger sequencing

Segmental amplification detection by digital PCR

**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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Information about statistical analysis performed can found within the ‘Material and methods’ section, in the paragraph related to relevant techniques:

Identification of putative adaptive mutations

Fitness assays

Premature sister chromatid separation assay

(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

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N/A because group allocation is not part of the experimental protocol used

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* 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
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Source data files are provided for all plots and graphs as excel files

Description of each source data file is provided in the manuscript

Additional data files related to the following figures are provided:

Figure 1D: Supplementary file 1, Supplementary file 2

Figure 1-figure supplement 3: Supplementary file 3

Figure 4-figure supplement 3: Supplementary file 4

Description of each Supplementary file is provided in the manuscript

Code used for the analysis for the following figures is provided with a link in the appropriate section of the material and methods:

Figure 1D: Whole genome sequencing, Identification of putative adaptive mutations

Figure 3A, Figure 3-figure supplement 1: Copy number variation (CNVs) detection by sequencing

Figure 4D-E, Figure 4-figure supplement 1: DNA replication profiles

A major dataset, containing the sequencing data used in the manuscript has been made publicly available at the EBI European Nucleotide Archive (Accession no: PRJEB34641)