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

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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

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Identification of putative adaptive mutations

Fitness assays

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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.)

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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)