

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection Data collection did not require of any particular software.

Data analysis Resistance Gene Identifier v5.1.1; MMseqs2 v13.45111; parasail-python v1.2.4; HipMCL CPU version; InterProScan v5.59-91.0; HMMER v3.3.2; R v4.0.3; CSB Finder-S v0.6.3; Blast+ v2.9.0+; Cytoscape v3.10.1; PlasmidFinder v2.1.6; pMLST v2.0.3; MOB-suite v3.0.3; COPLA v1.0; MAFFT v7.475; IQ-Tree v2.1.2; iTOL v6.5.8; vegan v2.6-4

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Source data are provided with this paper. The genome data is publicly available (<https://ftp.ncbi.nlm.nih.gov/genomes/refseq/>). Antibiotic resistance genes in comprehensive antibiotic resistance database (CARD v3.1.0; <https://card.mcmaster.ca/>); intact transposable elements were collected from The Transposon Registry

(v10/2021; <https://transposon.lstmed.ac.uk/tn-registry>), TnCentral (v10/2021; <https://tncentral.ncc.unesp.br/>), and ISfinder database (v10/2020; <https://isfinder.biotoul.fr/>). Phylogenetic data of five transposase gene families, Rop, and RepB are supplied. The full CSB dataset and gene family information used in this study is available in Figshare (doi: 10.6084/m9.figshare.25605450).

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No experiment was included in this study. We studied the content evolution of antibiotic resistance genes in plasmids from 2,441 genomes of strains in the genera of Escherichia, Salmonella, and Klebsiella.
Data exclusions	This study aims to study the evolution of ARG content in natural plasmids, a total of 23 strains sequenced within the framework of laboratory experiments were excluded.
Replication	No experiment was included in this study, all genomes were analyzed.
Randomization	In the gene island analysis, we randomly sampled gene families as a control, where a similar number of gene families was sampled. Each sampled gene family has a similar family size to the corresponding gene family.
Blinding	Blinding was not relevant to this study, the data was not split into groups and we didn't estimate any effects between groups.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Plants

Seed stocks

N/A

Novel plant genotypes

N/A

Authentication

N/A