

Life Sciences Reporting Summary

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► Experimental design

1. Sample size

Describe how sample size was determined.

We used all the samples of structures with high-quality preservation, excavation and reporting, and where household use of space could be reconstructed with reasonable assurance, that were personally known to the author(s) responsible for each region.

2. Data exclusions

Describe any data exclusions.

Some regions are not represented because we did not have a regional specialist available. Some samples within regions for which we did have a specialist were excluded because of poor preservation, excavation, recording, or inability to assign households to spaces. In Fig. 3a, the !Kung San data point is eliminated, since it poorly represents diversity in house size in the Old World ca. 1970.

3. Replication

Describe whether the experimental findings were reliably reproduced.

Replication, strictly speaking, is impossible in archaeology. We do believe that our samples are large enough to see that the patterns we note are becoming redundant.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

No randomization in sample selection was possible, although we used a randomization approach to determine the Gini for Tenochtitlan, as described in the Methods section. Samples were allocated into regions by geography; into temporal periods based on criteria (e.g., tree-ring dates, 14C dates, textual sources) appropriate to each sample; and into groupings based on subsistence regime or political scale based on the expert judgment of the regional specialists

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

The regional specialists who provided the Gini coefficients also provided the geographic and temporal assignments, and the allocation into subsistence regimes and political scales, for the sample(s) for which they were responsible. However, they did this independently of each other, and prior to the pattern-seeking exercises described in this paper were undertaken. Our main result (the greater post-Neolithic wealth disparities in the Old World) was not recognized by any of the authors when these assignments were made and the Gini coefficients calculated.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- A statement indicating how many times each experiment was replicated
- The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted
- A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

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

7. Software

Describe the software used to analyze the data in this study.

We used R and R Studio for all graphics and analyses, invoking various libraries depending on the analysis. No custom computer code was employed, beyond the minimum necessary to generate the figures.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

n/a

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

n/a

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

n/a

b. Describe the method of cell line authentication used.

n/a

c. Report whether the cell lines were tested for mycoplasma contamination.

n/a

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

n/a

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

n/a

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

n/a