

Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- An indication of 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 statistics 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
- Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

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

Data collection

Sample-based driver attribution data were collected using Google Earth (freely available at <https://www.google.com/earth/>)

Data analysis

The regression tree algorithm used to generate VCF layers was developed by Breiman et al. (1984). An R implementation is freely available at <https://cran.r-project.org/web/packages/rpart/>. Land-cover change characterization was implemented in Python using the Mann-Kendall-Trend package (freely available on GitHub at <https://github.com/mps9506/Mann-Kendall-Trend>), the SciPy library (freely available at <https://www.scipy.org/>) and the GDAL library (freely available at <http://www.gdal.org/>). Visualization maps were created using ArcMap 10.2.2 and PCI Geomatica 2014.

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

The generated AVHRR VCF products will be distributed through Land Processes Distributed Active Archive Center (LP DAAC, <https://lpdaac.usgs.gov/>). VCF change and uncertainty layers are also provided at <http://glad.geog.umd.edu/dataset/long-term-global-land-change> for download.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Ecological, evolutionary & environmental sciences study design

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

Study description	This study mapped annual global land cover between 1982 and 2016 using satellite data and quantified land-cover change over the study period.
Research sample	Two separate probability samples were selected, one used for land cover validation and one used for the driver attribution analysis. The validation sample used existing datasets described in Olofsson et al. (2012), Stehman et al. (2012) and Pengra et al. (2015) (available at https://landcover.usgs.gov/glc/SitesDescriptionAndDownloads.php). The population from which the validation sample was selected was the global land surface. The driver attribution sample used high-resolution satellite images from Google Earth. The population represented by the driver attribution sample was the global land-cover change area.
Sampling strategy	A complete description of the sampling design for the validation sample is available in Olofsson et al. (2012) and Stehman et al. (2012). For the driver attribution sample, an a priori sample size calculation was not employed. An initial sample size of 300 was selected and reported in the original submission. Upon reviewing the standard errors for the estimated proportion of change attributable to land use, we increased the sample size to 1500. The standard errors reported in the revised manuscript are accordingly much smaller, but this sample size was not chosen based on a formal sample size planning calculation.
Data collection	A complete description of data collection for the validation sample is available in Pengra et al. (2015). For the driver attribution sample, data were collected by the authors via visualizing high-resolution images in Google Earth.
Timing and spatial scale	The timing of the validation sample ranges from year 2002 to 2014. The spatial scale of the validation sample data is 5-km x 5-km. The timing of the driver attribution sample ranges from year 1982 to 2016. The spatial scale of the driver attribution sample is 0.05 degree x 0.05 degree.
Data exclusions	No data were excluded from analysis.
Reproducibility	Our study did not involve comparisons of treatment groups or populations so we did not employ traditional experimental design and analysis of variance techniques. Consequently replication of experimental units is not applicable to our study design. The reliability of our findings was evaluated based on the reported uncertainty analyses, the accuracy assessment results, and the standard errors accompanying sample-based estimates.
Randomization	Randomization was incorporated in the sample selection process following standard protocols of probability sampling design.
Blinding	The typical use of “blinding” observers to the identity of treatment and control groups was not applicable in our study. However, a similar concept of “blinding” was incorporated in our accuracy assessment work as the interpreters collecting the reference condition data for comparison to the map classification did not know the map label for the sample units being interpreted.
Did the study involve field work?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

Methods

n/a	Involvement 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