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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 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	QGis (v3.4) and Microsoft Excel (2016) were used to obtain and organize the data. Custom code to download data from an online data set to Excel in a user-friendly and filtered format is not deemed central to the conclusions and is available upon request.
Data analysis	This study was conducted using Microsoft Excel (2016) and R (v. 3.6.1). For Excel we used the basic package including the "rand" function, whereas in R we used the "Pirateplot()" function from the "yarrr package" and "hclust(d, method="ward")" function for the hierarchical cluster.

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 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

All raw data will be available at the website (to be completed at acceptance). Figure 1 and Figure 5 are associated with the raw data. Custom codes are available upon request.

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

Ecological, evolutionary & environmental sciences study design

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

Study description	In this study we carried out an in-depth harmonization of sampling methods and analyzed the distribution of more than 12 million of litter items across aquatic habitats worldwide. A total of 36 data sets providing counts of litter by item typology were harmonized and combined for the present study. The items were classified by material, plastic type and probable origin of the litter found in seven major aquatic environments at global scale.
Research sample	The full database covered seven major aquatic environments globally, specifically river waters and riverbed, shoreline, nearshore waters and nearshore seafloor, open waters, and deep seafloor. Our analysis focused on the counts of items per environment (litter inventories), irrespective of whether there are estimates for the area or volume sampled. This approach allowed for expanding the size and coverage of the data set to provide a global multi-ecosystem perspective never used before in the analysis of the marine litter, specially due to the mainstreaming of the huge amount of information collected by citizen science in rivers, beaches and shallow seafloors. Data sources are provided in Table S1.
Sampling strategy	Litter sampling was performed in different ways as per table S1 Methods Floating barriers, retention booms, stationary-point visual census on surface waters, and census of stranded litter in river banks Visual census by diving, and nets anchored to river bed Beach cleanups Surface trawling mega-nets and strip-transect visual census from vessels. Surface trawling mega-nets, and strip-transect visual census from vessels. Scuba divers Video camera and bottom trawling nets
Data collection	Data collection varies for each of the 36 data sets used in the study. The data compilation was managed by the co-authors of the manuscript according to the different methodologies. C. Morales-Caselles and A. Cózar harmonized the collected data considering the different methodologies.
Timing and spatial scale	This study contains data ranging from 2008 to 2019 at a global scale.
Data exclusions	Some data was excluded from the analysis and the criteria has been explained in the text. The data set was populated with large identifiable items, while small pieces and fragments were removed from the counts. This was the case of fragments and broken pieces that cannot be associated straightaway to a particular identifiable primary object. Those items that had gone through an important degradation process making unfeasible to determine what the original feature was, were similarly excluded. Regarding ropes, strings, cords and threads, we only considered those tangles and pieces larger than ten centimeters. The smallest object size considered in the analyses was the equivalent to a small bottle cap about 3 cm in diameter. Cigarette filters and cigar tips were excluded, because these small items were not systematically sampled in all data sets.
Reproducibility	The reproducibility of the analysis needs to take into account the harmonizing factors used for each single item depending on the sampling strategy shown in Table S2 (Weighing factors (fw) and confidence intervals (CIs) applied for item category and sampling method. CIs are shown through lower and upper limits determining the interval of confidence)
Randomization	The category lists used to classify litter items in the different data sets were accommodated into a joint master litter category list (JML List, Table S2), made up of a total of 112 types of products. The criteria for harmonizing litter classifications are shown in table S2 (downloadable as independent htm file), where we show the correspondence between litter categories used by the different studies (e.g., OSPAR codes, UNEP codes) and the JML List. Moreover, an Excel tool for automatically convert any major category list into the JML List is provided at website (to be released at acceptance). The analysis did not consider non-identifiable items
Blinding	We feel that blinding is not relevant to the study of global flows of litter

Did the study involve field work?   ☐ Yes   ☒ No

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
☒	Antibodies
☒	Eukaryotic cell lines
☒	Palaeontology and archaeology
☒	Animals and other organisms
☒	Human research participants
☒	Clinical data
☒	Dual use research of concern

Methods

n/a	Involved in the study
☒	ChIP-seq
☒	Flow cytometry
☒	MRI-based neuroimaging