

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](#).

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 Illumina software at sequencing facility.

Data analysis We used only the following tools, which are all publicly available: bbttools; SPAdes version: 3.11.1; minimus2; Virsorter; Virfinder; Prodigal v2.6.2; BLAST v2.2.3; bowtie2 v2.2.6; VirHostMatcher-Net; Samtools v1.2; Fast-Virome Explorer; Their specific use and parameters are noted in the methods section. Custom code available at <https://doi.org/10.6084/m9.figshare.8872796.v1>.

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. 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 manuscript includes the statement: "All sequencing data is available at the JGI Genome portal under the proposal ID 2799 (to NA and JF). All data needed to evaluate the conclusions in the paper are present in the paper or the supplementary materials."

The Supplemental GenBank-like file includes all contig sequences

The Supplemental Excel spreadsheet includes raw contig length, %GC, abundance, identity information, and abundance in all samples.

Final cross-assembled sequences are deposited at NCBI under the BioProject ID PRJNA550983.

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)

Ecological, evolutionary & environmental sciences study design

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

Study description	Community DNA from operationally identified virus-size fraction was collected monthly for 5 years without experimental manipulation.
Research sample	Seawater virus assemblages (as defined from being retained in between 0.02 - 0.2 um filters) were collected monthly. No experimental manipulation was done.
Sampling strategy	Seawater virus assemblages (as defined from being retained in between 0.02 - 0.2 um filters) were collected monthly. No experimental manipulation was done.
Data collection	Viromes were collected monthly; Seawater was filtered through a 0.2 um filter and then to 0.02 um filter, the latter was then used for DNA extraction. DNA amplification and sequencing was done at JGI as described in the methods section.
Timing and spatial scale	Viromes were collected monthly; Seawater was filtered through a 0.2 um filter and then to 0.02 um filter, the latter was then used for DNA extraction.
Data exclusions	Not all months are represented due to weather conditions, equipment failure, and failed DNA extractions; missing dates are noted in the figures as blank columns.
Reproducibility	Not relevant for an environmental time series.
Randomization	N/A. We described an ecological time series. Continuous sampling for ~20 years.
Blinding	NA
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Field conditions varied monthly, this project is the result of 53 cruises. For all environmental data associated please see: https://dornsife.usc.edu/spot/datasets-summary/ . We also cited publications by Cram et al., and Chow et al., that overlapped in time with this study, and reported and used these environmental conditions for interpretation.
Location	San Pedro Ocean Time series is located at 33°33'N and 118°24'W.
Access and import/export	NA
Disturbance	NA

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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