

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 No software was used to collect data

Data analysis

Hi-C data processing:

```
- https://github.com/dekkerlab/cMapping
- python=2.7.9
- bowtie2=2.3.0
- numpy=1.13.3
- h5py=2.6.0
- cMapping/scripts/utilities/processFlowCell.pl
- cMapping/scripts/utilities/combineHiC.pl

- https://github.com/mirnylab/distiller-nf v0.3.3
- python=3.7
```

- samtools =1.4

- bwa

- pairtools

- cooler=0.8.5

Genome assembly:

- <https://github.com/dekkerlab/DNATriangulation>

- numpy=1.10.4

- scipy=0.18.1

- matplotlib=1.5

- scikit-learn=0.18

- hmmlearn=0.2.0

- h5py

- matplotlib=1.5.1

- DNATriangulation/scripts/chromosome_scaffold.py

- DNATriangulation/scripts/karyotype.py

- DNATriangulation/scripts/triangulation.py

Data Analysis:

- <https://github.com/dekkerlab/cworld-dekker>

- cworld-dekker/scripts/perl/scaleMatrix.pl

- cworld-dekker/scripts/perl/binMatrix.pl

- cworld-dekker/scripts/perl/heatmap.pl

- cworld-dekker/scripts/perl/matrix2insulation.pl

- <https://github.com/open2c/cooltools> v0.3.2

- cooltools/cooltools/cli/dump_cworld.py

- cooltools/cooltools/cli/compute_expected.py

- cooltools/cooltools/cli/expected.py

- cooltools/docs/notebooks/01_scaling-curves.ipynb

- cooltools/docs/notebooks/07_pileups2.ipynb

- <https://github.com/open2c/pairtools> v0.3.0

- pairtools/pairtools/pairtools_merge.py

- pairtools/pairtools/pairtools_sort.py

- pairtools/pairtools/pairtools_stats.py

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 Hi-C and PacBio sequencing data and Smic1.0 and Smic1.1 genome sequences are available in GEO (accession number: GSE152150). RNAseq data used here are from Liew et al. 11 and available in NCBI Short Read Archive (SRA), BioProject PRJNA315758.

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

Life sciences study design

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

Sample size	<input type="text" value="N/A"/>
Data exclusions	<input type="text" value="N/A"/>
Replication	<input type="text" value="All Hi-C and PacBio experiments are performed in at least duplicate"/>
Randomization	<input type="text" value="N/A"/>
Blinding	<input type="text" value="N/A"/>

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

Methods

- | | |
|-------------------------------------|---|
| n/a | Involvement in the study |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input type="checkbox"/> | <input checked="" 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"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern |

- | | |
|-------------------------------------|---|
| 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 |

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	<input type="text" value="S. microadriaticum clade A cultures were obtained from the Gulf of Aqaba near Asia, vendor NCMA (National Center for Marine Algae and Microbiota) – Bigelow Laboratory for Ocean Sciences (CCMP2467-SC)"/>
Authentication	<input type="text" value="Genome sequencing, morphology, single cell cloning"/>
Mycoplasma contamination	<input type="text" value="N/A"/>

Commonly misidentified lines
(See [ICLAC](#) register)

N/A