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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 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	Data were not collected by software. We produced primary data through environmental sampling, DNA purification and 16S/18S rRNA gene amplicon sequencing.
Data analysis	Software used for sequence analysis: To clean chimeric sequences, VSEARCH (v2.3.4, Rognes et al., 2016) OTU clustering, CDHIT-EST (v4.6, Li et al., 2006) To align gene marckers, Codon Code Aligner (v8.0.1, CodonCode Corporation, www.codoncode.com) Database SILVA v.128 (Glöckner et al., 2017) To align sequencs retrieved from SILVA, MAFFT (v7.388, Katoh and Standley, 2013, accurate linsi option) TRIMAL (v.1.4rev15; Capella-Gutierrez et al., 2009, automated 1 option) IQ-TREE using using the GTR model of sequence evolution with a gamma law and taking into account invariable sites (GTR+G+I)

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

Sanger sequences have been deposited in GenBank (NCBI) with accession numbers MK894601-MK894820 and Illumina sequences in GenBank Short Read Archive

with BioProject number PRJNA541281.

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	This is an interdisciplinary study of the occurrence and diversity of microorganisms in samples collected along polyextreme gradients (low pH, high salt, high temperature) involving culture attempts, amplification and sequencing of 16S/18S rRNA genes followed by molecular phylogenetic analyses, chemical analyses, fluorescence-activated cell sorting and electron microscopy observations combined with energy dispersive X-ray spectrome
Research sample	A total of 69 different samples were analyzed for different purposes. The detailed list of samples, their description and the type of analyses carried out are specifically provided in Supplementary Table 1.
Sampling strategy	Samples were chosen by their distribution along defined gradients of extreme physico-chemical parameters.
Data collection	Solid and water samples for microbial diversity analyses and culturing assays were collected under the most possible aseptic conditions to prevent contamination (gloves, sterile forceps and containers). Samples for culture assays were kept at room temperature. Salts and mineral fragments for DNA-based analyses were conditioned in Falcon tubes and fixed with absolute ethanol. Water samples (volumes for each sample are indicated in Supplementary Table 1) were filtered through 30 µm pore-diameter filters to remove large particles and sequentially filtered either through 0.22 µm pore-diameter filters (Whatman®) or using 0.2 µm pore-size Cell-Trap units (MEM-TEQ Ventures Ltd, Wigan, UK). Filters or Cell-Trap concentrates retaining 0.2-30 µm particles were fixed in 2-ml cryotubes with absolute ethanol (>80% final concentration). Back in the laboratory, ethanol-fixed samples were stored at -20°C until use.
Timing and spatial scale	Samples were collected during two field trips carried out in January 2016 and January 2017 (when air temperature rarely exceeded 40-45°C); a few additional samples were collected in January 2018 (Fig. 1; Supplementary Fig. 1 and Supplementary Table 1). The exact collection date for each sample is provided in Supplementary Table 1.
Data exclusions	Data were not excluded from our study.
Reproducibility	This is a descriptive study involving only oridination methods and principal component analyses. Different samples collected from each specific area and bearing similar physico-chemical characteristics acts as replicate.
Randomization	Not applicable
Blinding	Not applicable

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Physicochemical parameters (Supplementary Table 1) were measured in situ with a YSI Professional Series Plus multiparameter probe (pH, temperature, dissolved oxygen, redox potential) up to 70°C and a Hanna HI93530 temperature probe (working range -200/1,000°C) and a Hanna HI991001 pH probe (working pH range -2.00/16.00) at higher temperatures. Salinity was measured on site with a refractometer on 1:10 dilutions in MilliQ water. Water samples for chemical analyses were collected in 50 ml glass bottles after prefiltration through 0.22 µm pore-diameter filters; bottles were filled to the top and sealed with rubber stoppers to prevent the (further) oxidation of reduced fluids.
Location	All sampling points and mapping data were georeferenced using a Trimble® handheld GPS (Juno SB series) equipped with ESRI software ArcPad® 10. Cartography of hydrogeothermal activity areas was generated using ESRI GIS ArcMap™ mapping software ArcGis® 10.1 over georeferenced Phantom-4 drone images taken by O. Grunewald during field campaigns, compared with and updating previous local geological cartography 4. Samples were collected in three major areas at the Dallol dome and its vicinity (Fig.1b): i) the top of the Dallol dome, comprising various hydrothermal pools with diverse degrees of oxidation (Fig.1c); ii) the Black Mountain area (Fig.1d), including the Black Lake and surrounding bischofite flows and the South-Western salt canyons harboring water reservoirs often influenced by the geothermal activity and iii) the Yellow Lake (Gaet'Ale) area (Fig.1e). We also collected water samples from the hypersaline Lake Assale (Karum), located a few kilometers to the South in the Danakil Depression (Fig1b).
Access and import/export	Our field expeditions were locally organized by Luigi Cantamessnna (Géodécouvertes) in collaboration with the University of Mekelle and the Afar and Ethiopian authorities. All our samples transited by the Ministry of Mines, Ethiopia, where they were inspected and sealed prior to their shipment to the airport for a Custom's declaration of export.

Disturbance	Not applicable

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

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Water samples were concentrated using CellTraps and directly used for fluorescent activated cell-sorting
Instrument	FACSAriaTMIII (Becton Dickinson)
Software	Sorting was conducted using the FACSDivaTM software (Becton Dickinson); figures were done with the FCSExpress 6 software (De Novo Software).
Cell population abundance	Cell population abundance varied and in some cases it was 0 - in these points only abiotic biomorphs could be detected
Gating strategy	The FACSAriaTMIII was set at purity sort mode triggering on the forward scatter (FSC). Fluorescent target cells/particles were gated based on the FSC and red or green fluorescence (SupplementaryFig. 6b) and flow-sorted at a rate of 1-1,000 particles per second

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.