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☐ Initial submission   ☐ Revised version   ☑ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

▶ Experimental design

1. **Sample size**

   Describe how sample size was determined.

   > We obtained as many samples as possible form the chosen species to perform our metagenomics comparisons.

2. **Data exclusions**

   Describe any data exclusions.

   > We used all the generated data. Different sets for the different analyses, each one described in the extended methods. For example, the identification of the microbiome cores was done using all the datasets, and the microbiome profiles distances were obtained both using all the sets downsampled, and excluding the 3 most heavily sequenced samples to avoid bias

3. **Replication**

   Describe whether the experimental findings were reliably reproduced.

   > All attempts at replication were successful

4. **Randomization**

   Describe how samples/organisms/participants were allocated into experimental groups.

   > Allocation was done by species. This is not relevant to the comparatve genomics. And for the metagenomics, we controled the variability by normalizing the sequencing depths and performed the appropriate tests for finding enrichments. For identification of the microbial cores that is also not relevant.

5. **Blinding**

   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

   > Blinding is not relevant to our analyses, which compare the genomes and metagenomes of the species, our analyses do not make predictions of their microbes/genes, but characterize their identifications.

   Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. **Statistical parameters**

   For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒	A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	A statement indicating how many times each experiment was replicated
☐	☒	The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒	A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒	The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted
☐	☒	A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☒	☐	Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

▶ Software

7. Software

Describe the software used to analyze the data in this study.

> We used many different softwares. All of them are specified in the Methods sections in the main and supplementary text, including the versions. In house scripts upon request.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

▶ Materials and reagents

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

> Laboratory reagents are all comercially available. The unique materials are the bat fecal samples and *Desmodus rotundus* skin cells, which were all used for the generation of the sequencing data.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

> We did not use any antibodies

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

> We did not use any cell line. We generated the D. rotundus genome with cultured cells from the San Diego Zoo collection, that were originally derived from a skin sample, as mentioned in the methods section

b. Describe the method of cell line authentication used.

> No eukaryotic cell lines were used

c. Report whether the cell lines were tested for mycoplasma contamination.

> No eukaryotic cell lines were used

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

> N/A

▶ Animals and human research participants

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

> We used samples from *Desmodus rotundus*, *Rousettus aegyptiacus*, *Rhinolophus ferrumequinum*, *Macroderma gigas*, *Rhinolophus euryale*, *Miniopterus schreibersii*, *Nyctalus leisleri*, and *Nyctalus lasiopterus*. Physiological information of the vampire individuals sampled by net capturing is presented in the Supplementary Information.

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

> The study did not involve human research participants