

SUPPLEMENTARY INFORMATION

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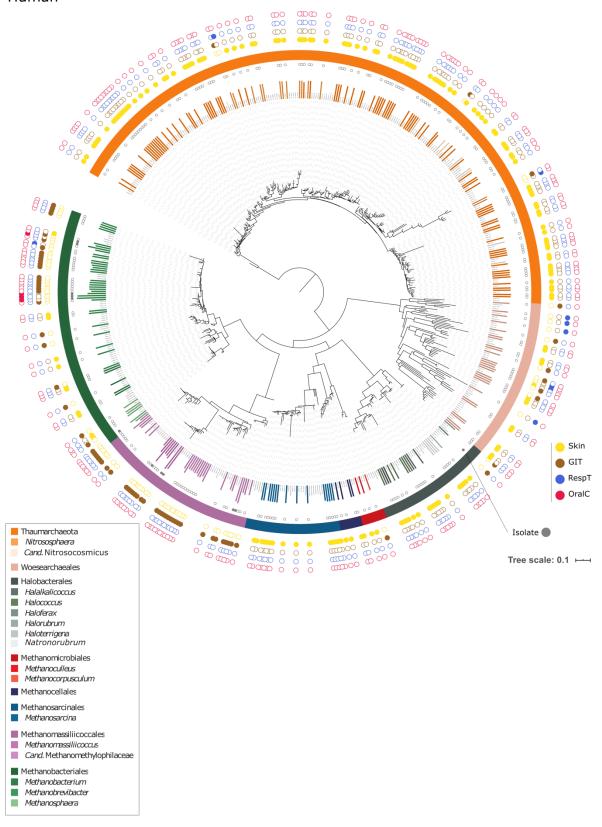
The host-associated archaeome

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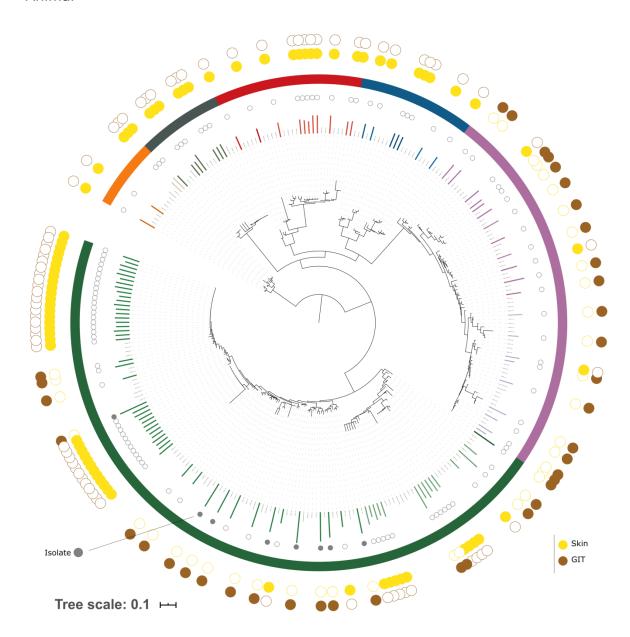
Supplementary figure: Archaeal taxa detected in human, animal and plant samples. 16S rRNA gene sequences from isolated strains, publicly available clone sequences (for example, Ref. 1), reconstructed metagenome assembled genomes (MAGs) from human microbiomes ^{2,3} and sequences from amplicon-based studies of animals ^{4,5}, humans ^{6,7} and plants 8-11 were quality filtered (no singletons, length > 100bp, alignment score > 30, alignment identity > 40%; 12), grouped at 97% similarity, and processed through SILVA SINA classification. Trees were calculated via RAxML, on the backbone of three neighbour sequences per query which were used to stabilize the tree ('add to neighbours tree' option; neighbor representatives are shown in the tree with an unlabeled node) (for a detailed overview please see supplementary figures). For the human archaeome tree (top panel), lineages found in only one publication are not shown; this filtering was not applied for the animal archaeome tree (bottom left panel) and plant archaeome tree (bottom right panel) due to the small number of available studies. Output was completed with metainformation (sample origin, isolate) using Itol¹³. Thaumarchaeota (correspond to Nitrososphaeria, in shades of orange), Woesearchaeota (in very soft red), and Halobacteriales (in grey/green), Methanomicrobiales (in shades of red), Methanocellales (in shades of dark blue), Methanosarcinales (in shades of blue), Methanomassiliicoccales (in shades of purple), and Methanobacteriales (in shades of green), were found in all groups in different sample types (that is, skin, gastrointestinal tract (GIT) (including faeces, gut biopsies and rumen samples), respiratory tract and oral cavity samples), as well as green plant and/or seed samples, as indicated by the circles outside, which is linked to an individual archaeal representative.

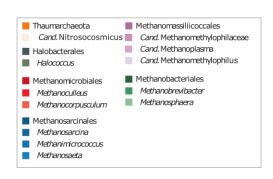
- 1. Probst, A. J., Auerbach, A. K. & Moissl-Eichinger, C. Archaea on Human Skin. *PLoS One* **8,** (2013).
- 2. Borrel, G. *et al.* Genomics and metagenomics of trimethylamine-utilizing Archaea in the human gut microbiome. *ISME J.* (2017).
- 3. Almeida, A. *et al.* A new genomic blueprint of the human gut microbiota. *Nature* **568**, 499 (2019).
- 4. Ross, A. A., Müller, K. M., Weese, J. S. & Neufeld, J. D. Comprehensive skin microbiome analysis reveals the uniqueness of human skin and evidence for phylosymbiosis within the class Mammalia. *Proc. Natl. Acad. Sci.* **115**, E5786–E5795 (2018).
- 5. Raymann, K., Moeller, A. H., Goodman, A. L. & Ochman, H. Unexplored archaeal diversity in the great ape gut microbiome. *mSphere* **2**, e00026-17 (2017).
- 6. Moissl-Eichinger, C. *et al.* Human age and skin physiology shape diversity and abundance of Archaea on skin. *Sci. Rep.* **7 (1)**, 4039 (2017).
- 7. Koskinen, K. *et al.* First insights into the diverse human archaeome: specific detection of archaea in the gastrointestinal tract, lung, and nose and on skin. *MBio* e00824-17 (2017).
- 8. Taffner, J. *et al.* What Is the Role of Archaea in Plants? New Insights from the Vegetation of Alpine Bogs. *mSphere* **3**, e00122-18 (2018).
- 9. Taffner, J., Cernava, T., Erlacher, A. & Berg, G. Novel insights into plant-associated archaea and their functioning in arugula (Eruca sativa Mill.). *J. Adv. Res.* (2019).
- 10. Taffner, J., Bergna, A., Cernava, T. & Berg, G. Tomato-associated archaea show a cultivar-specific rhizosphere effect but an unspecific transmission by seeds. *Phytobiomes J.* (2020).
- 11. Müller, H. *et al.* Plant genotype-specific archaeal and bacterial endophytes but similar Bacillus antagonists colonize Mediterranean olive trees. *Front. Microbiol.* **6**, (2015).
- 12. Quast, C. *et al.* The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Res.* **41**, D590–D596 (2013).
- 13. Letunic, I. & Bork, P. Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. *Bioinformatics* **23**, 127–128 (2007).

Human



Animal





Plant

