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 meta-information (sample origin, isolate) using Itol13. Thaumarchaeota (correspond to Nitrososphaeria, in shades of orange), Woesearchaeota (in very soft red), and Halobacteriales (in shades of dark blue), Methanomicrobiales (in shades of blue), Methanocellales (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.

Human

![Image of a phylogenetic tree showing various bacterial and archaeal groups associated with different body sites such as Skin, GIT, RespT, and GenIC. The tree includes branches for Thaumarchaeota, Nitrosophama, Candida Nitrosococcosicus, Woesearchaeales, Haloarchaeales, Halalkalicoccus, Halococcus, Haloferax, Halobacterium, Haloferax, Halococcus, Halobacterium, Methanomicrobiales, Methanococcales, Methanocorpusculum, Methanocellales, Methanosaetales, Methanomassiliicoccales, Methanoplasticum, Candida Methanomethylophilaceae, Methanosarcinales, Methanobacterium, Methanobrevibacter, and Methanosphaera.]