Supplementary Information
Direct utilization of long-chain fatty acid for methane production by thermophilic *Archaeoglobi*

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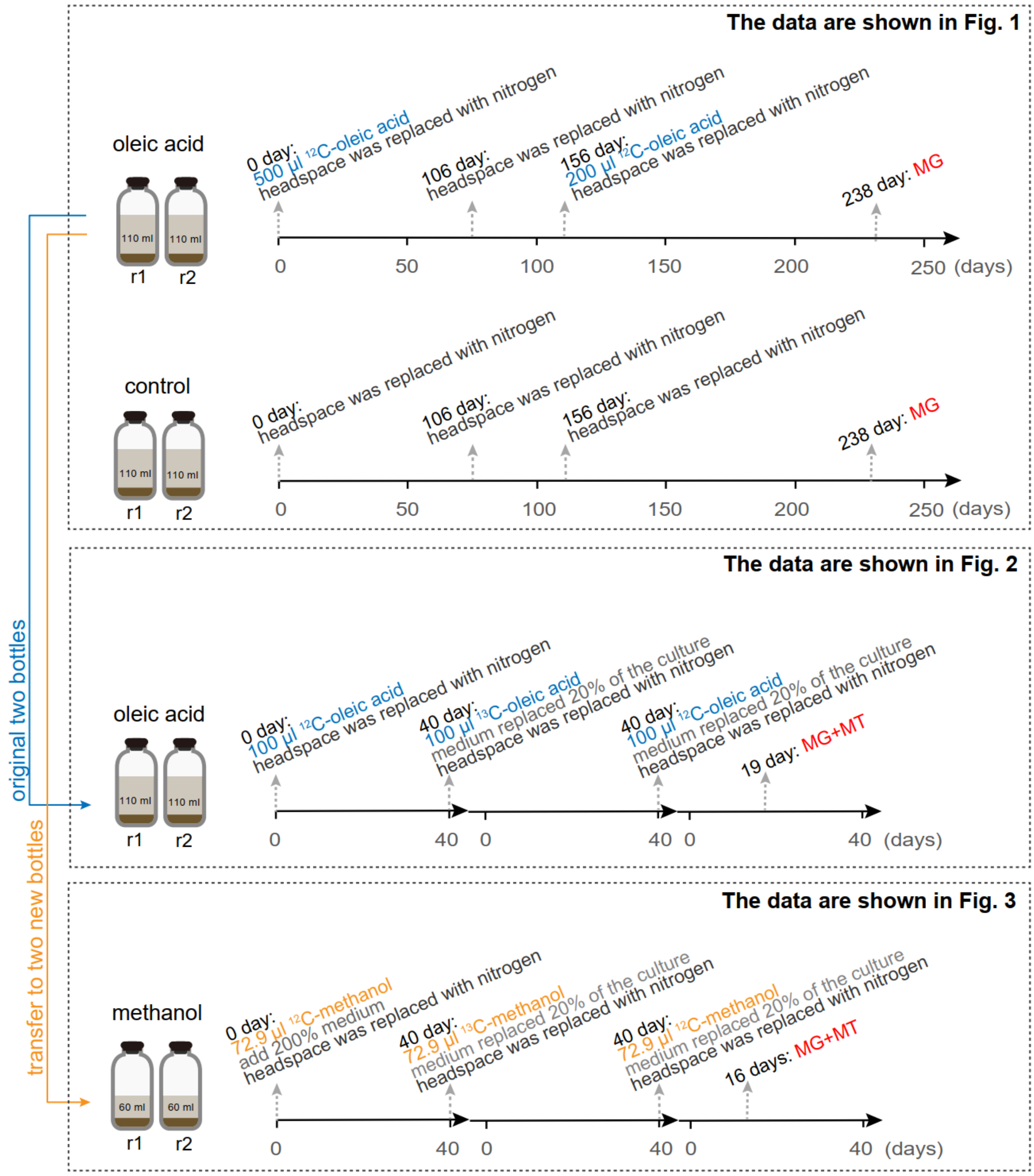
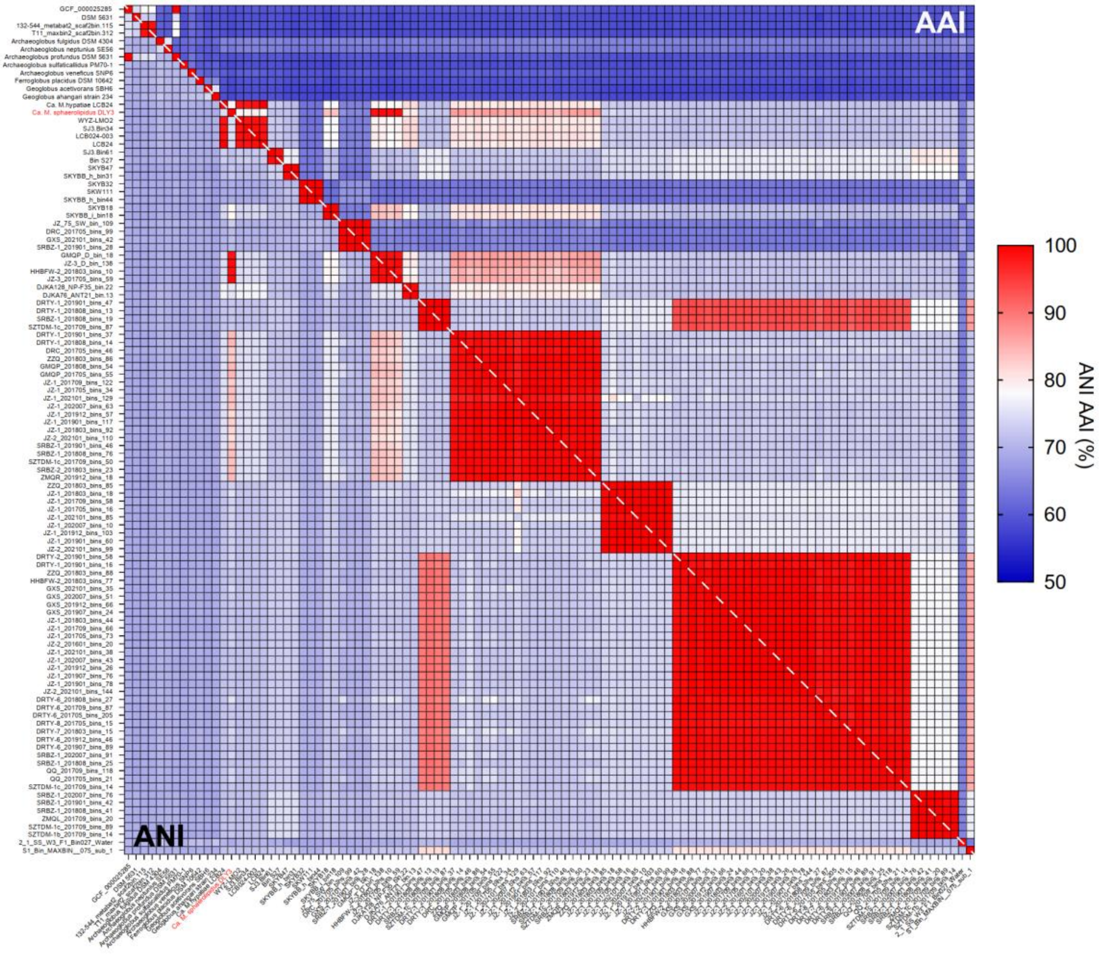
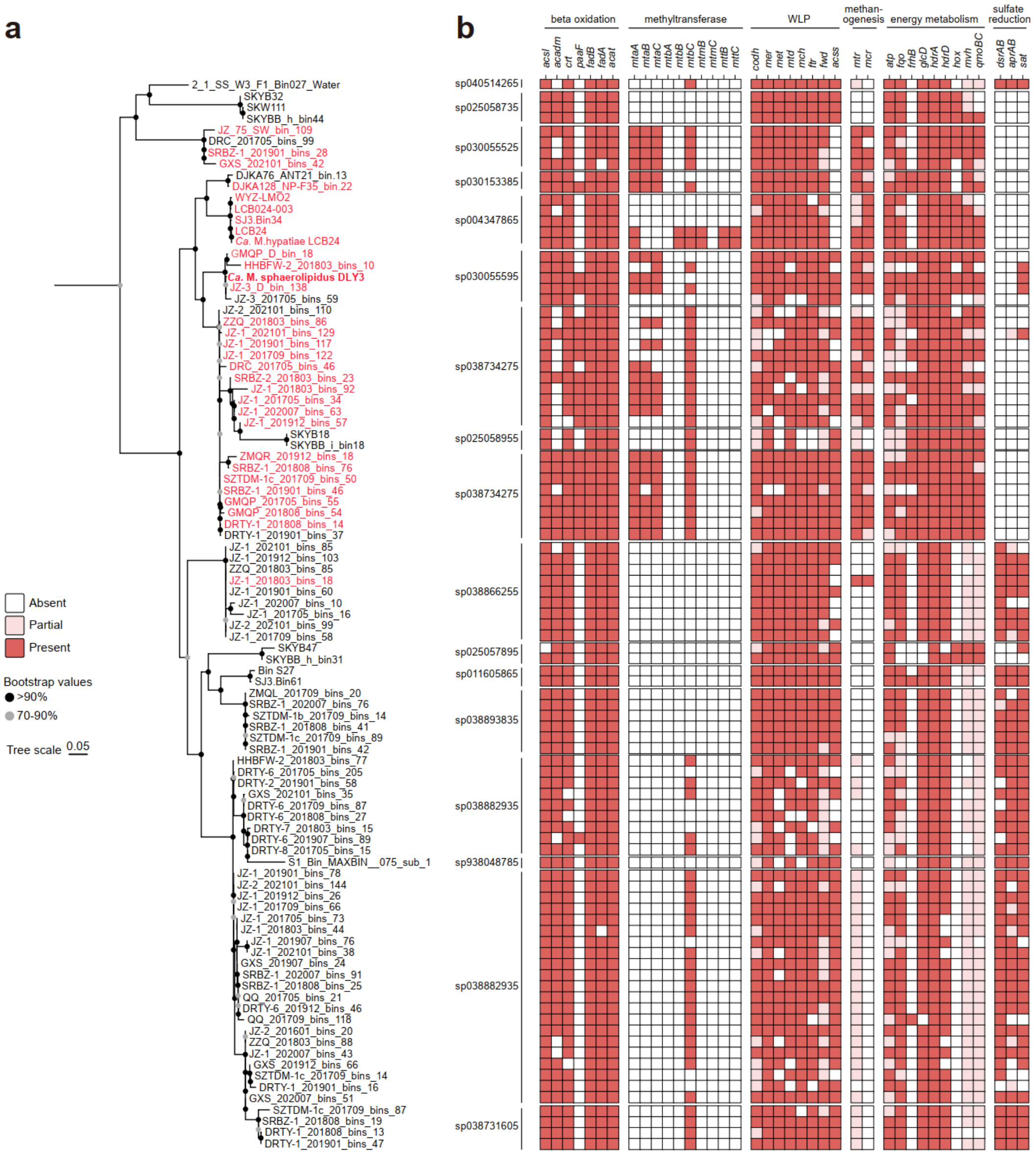


Supplementary Figure 1 Scheme of incubation experiments. r1 and r2 represent two replicates; MG and MT represent metagenomic and metatranscriptomic sequencing respectively; details see Materials and Methods.



Supplementary Figure 2 ANI and AAI analysis of reference *Archaeoglobales* genomes. AAI and ANI values are provided in Supplementary Table 3.



Supplementary Figure 3 Phylogenomic affiliation and proposed methane production pathway of genus *Ca.* Methanoglobus. a, phylogenomic affiliation of the *Ca.* Methanoglobus MAGs based on 37 conserved protein sequences and using 95 representative archaeal genomes. Maximum-likelihood tree, alignments were generated using MAFFT[1] and then filtered with trimAl[2], and the trees were built by the IQ-Tree[3] method with the model LG + C60 + F + G with 1,000 bootstrap replicates. Bootstrap values >90% shown in black dots, 70-90% shown in grey dots. MCR carrying MAGs shown in red. **b,** proposed methane production pathway of genus *Ca.* Methanoglobus, Presence and absence of key metabolic genes and methanogenesis marker proteins. See Supplementary Table 6 for details.

Supplementary References

1. Katoh, K. & Standley, D. M. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol. Biol. Evol.* **30**, 772-80 (2013).

2. Capella-Gutiérrez, S. et al. trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* **25**, 1972-1973 (2009).

3. Nguyen, L. T. et al. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol. Biol. Evol.* **32**, 268-274 (2015).