

# Exploring the microbial communities in coastal cenote and their hidden biotechnological potential

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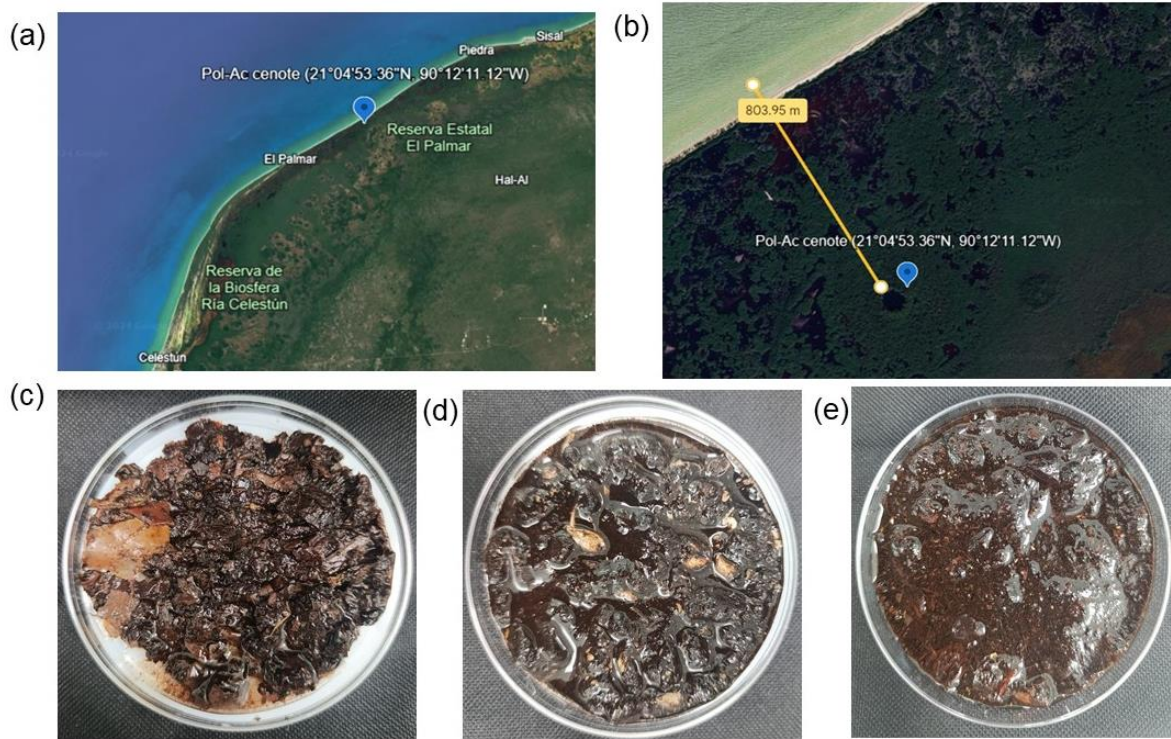
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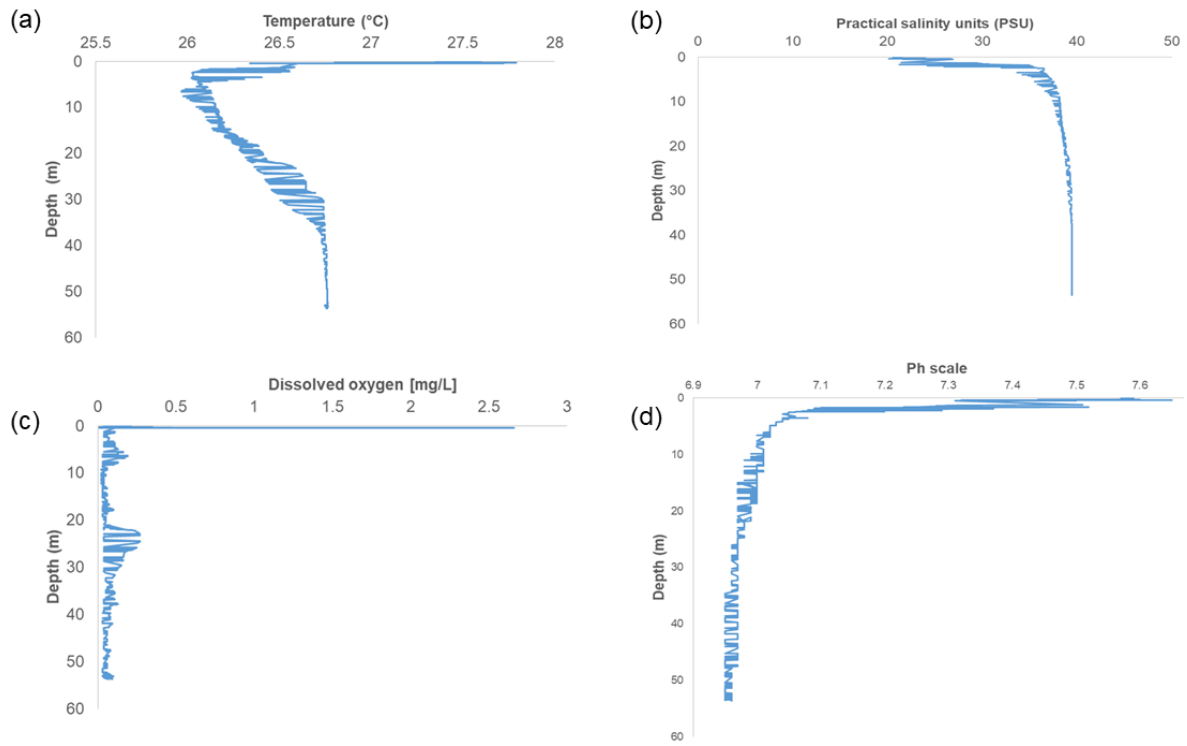
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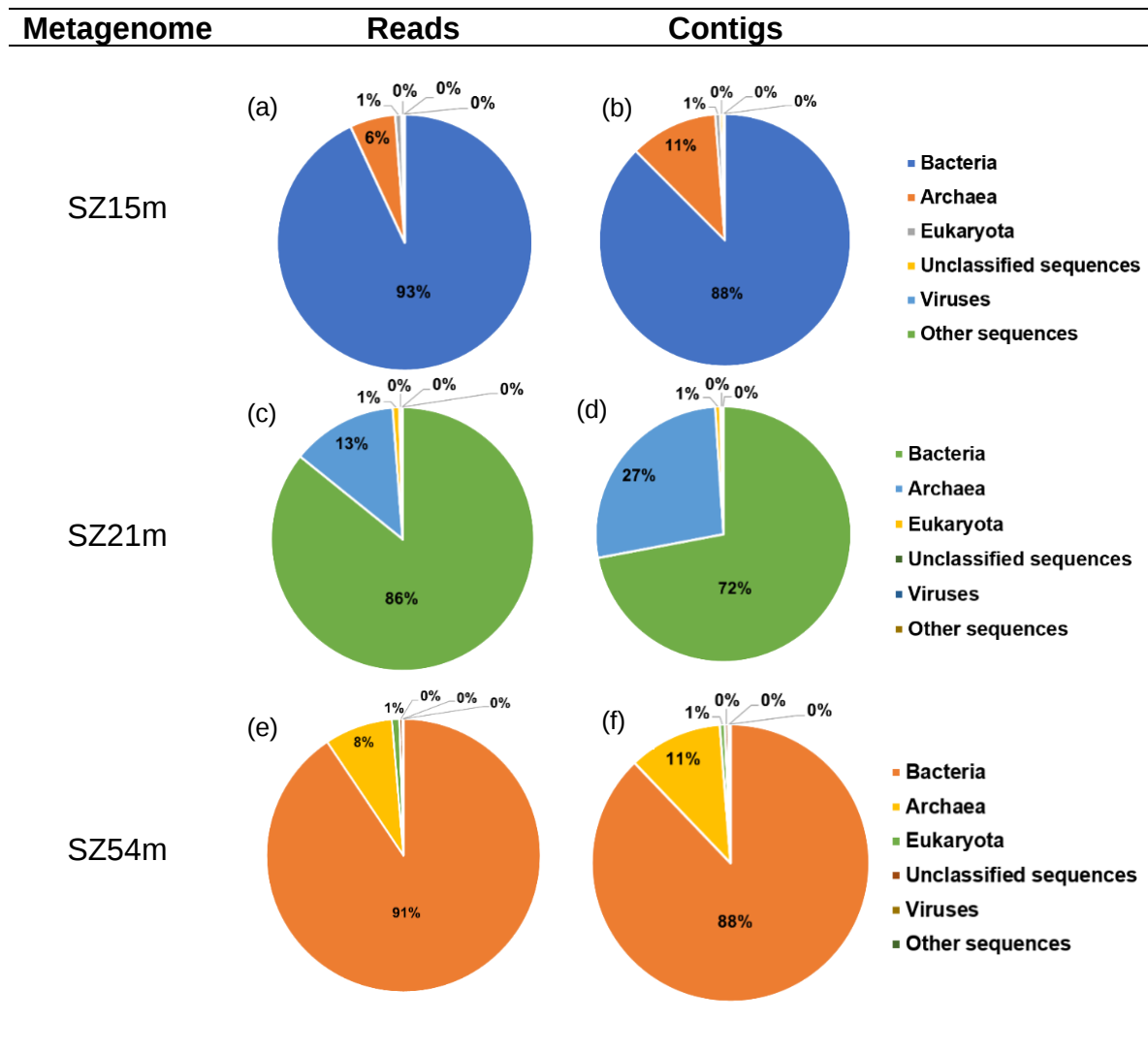
## Supplementary figures material



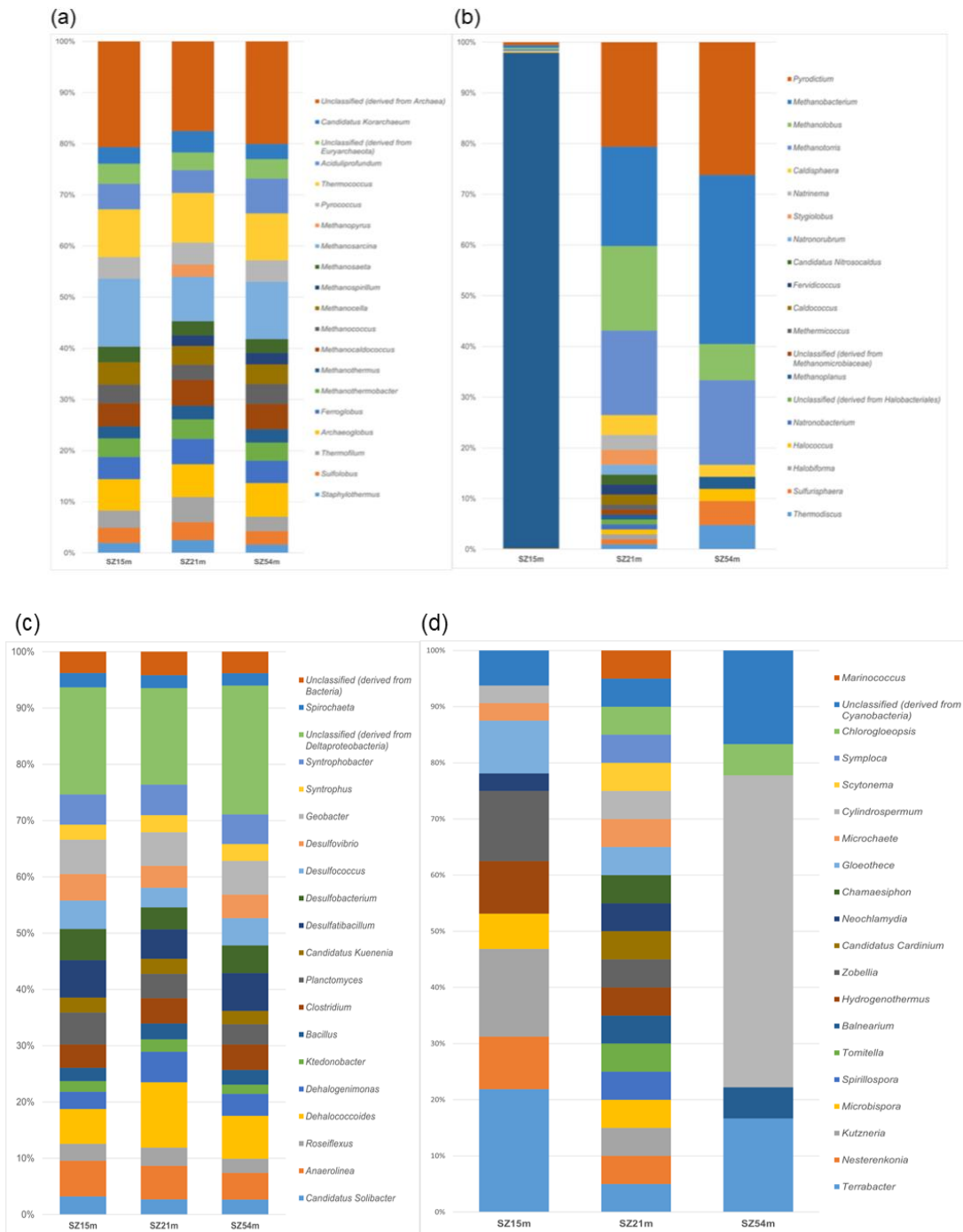
**Fig. S1. Sample site and physical characteristics of sediment samples.** The upper section shows “Pol-Ac” location maps and the lower section shows sediment images. (a) A map showing geographical location of the Pol-Ac cenote within the ecological reserve “El Palmar.” (b) A map depicting the distance between the Pol-Ac cenote to the coastline. (c–e) Images of sediment samples collected at different depths: (c) sediments from 15 m (SZ15m), (d) sediment from 21 m (SZ21m), and (e) sediment from 54 m (SZ54m). The sediment samples are shown in petri dishes to highlight their physical appearance.



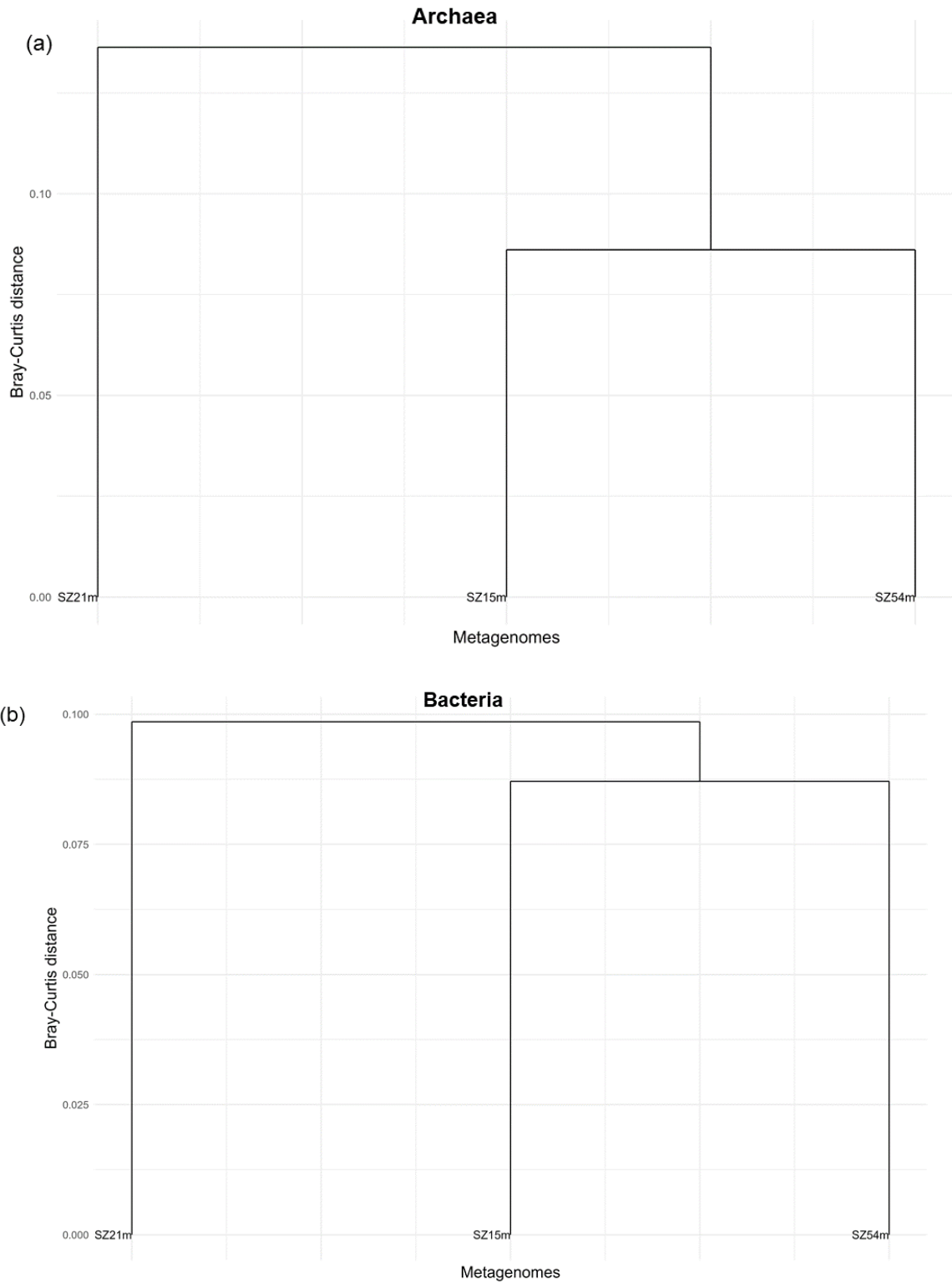
**Fig. S2.** *In situ* parameters measured per meter of depth, including (a) temperature, (b) salinity, (c) dissolved oxygen, and (d) pH, quantified within the water column (0-54 m) of the Pol-Ac cenote.



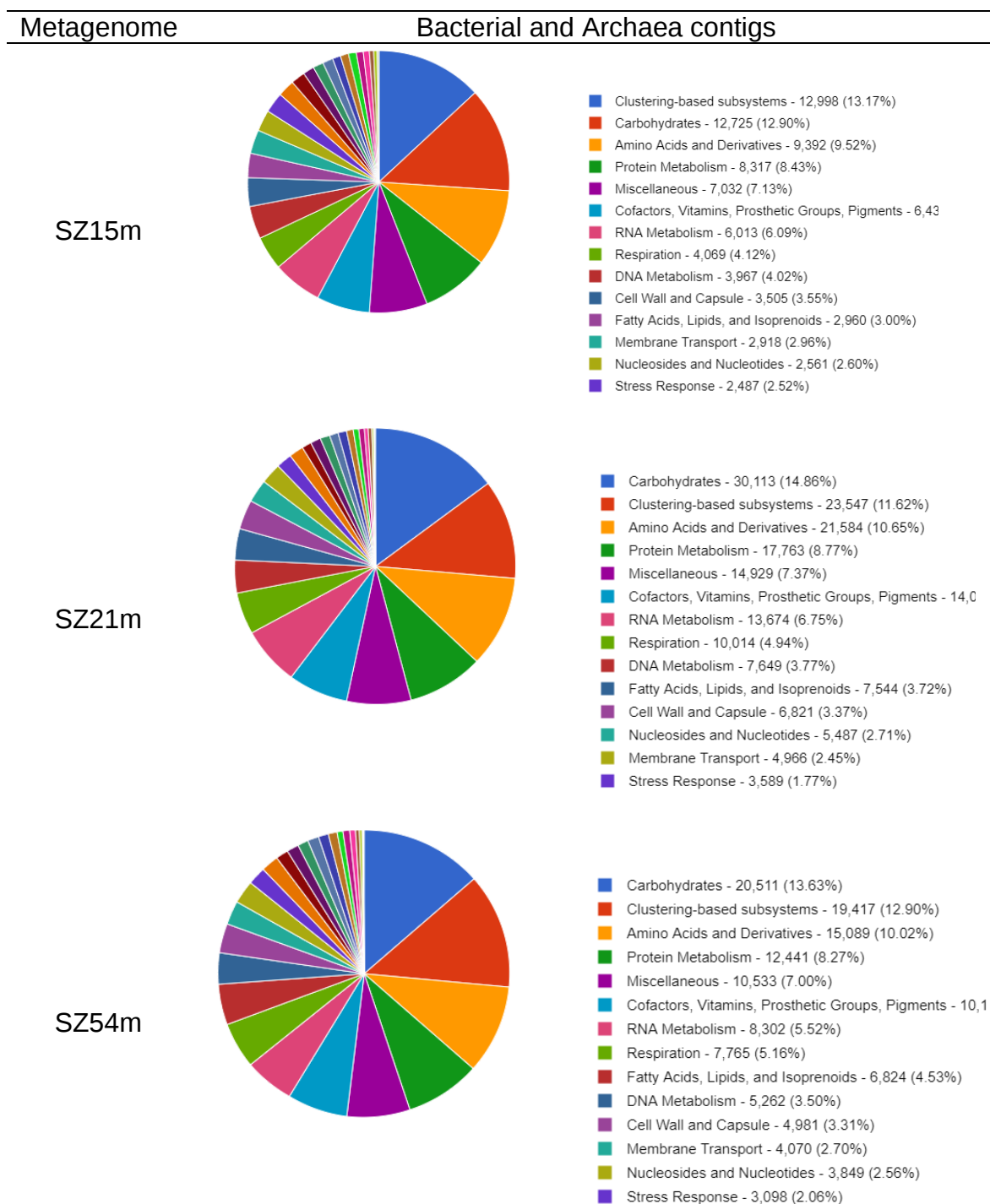
**Fig. S3.** MG-RAST report showing the relative abundances at the domain level for taxonomically annotated reads and contigs of microbial communities. (a-b) SZ15m metagenome, (c-d) SZ21m metagenome, and (e-f) SZ54m metagenome.



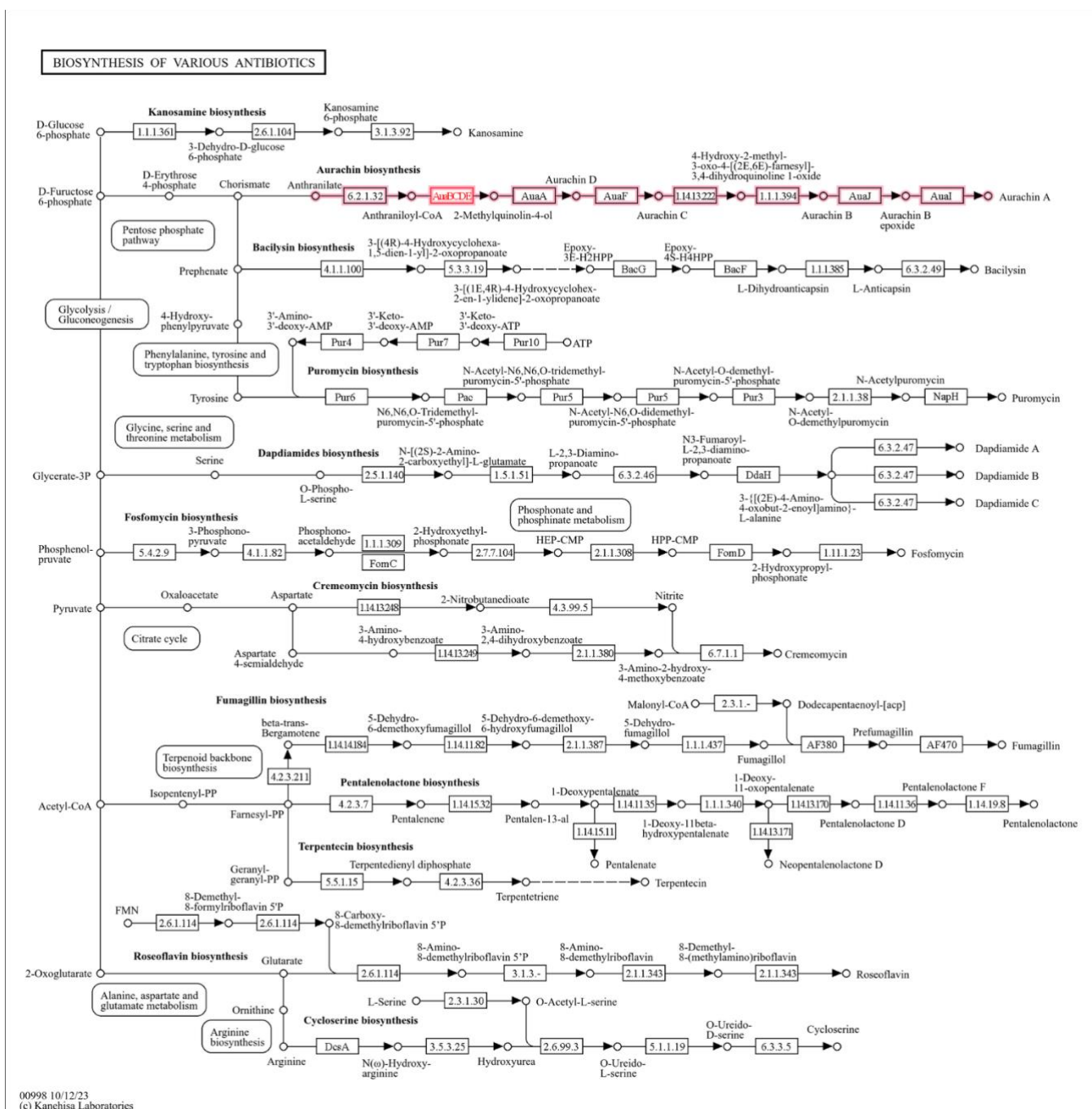
**Fig. S4.** Relative abundance of the 20 most abundant archaeal (a, b) and bacterial (c, d) genera at different depths. Less abundant genera are considered those with a relative abundance of 1%.



**Fig. S5.** Bray-Curtis dissimilarity index for bacterial (a) and archaeal (b) genera at different depths.



**Fig. S6.** Different functional hit category using KEGG Orthology (KO) database sub-system annotation.



**Fig. S7.** Map of the biosynthetic pathways for various antibiotics, highlighting the involvement of the *ctg4577\_2* gene within the BGC *Lbgc1\_15*, specifically in the biosynthesis of Aurachin A. The pathway associated with Aurachin A is highlighted in red.

## References

Oksanen, J. et al. Vegan: Community Ecology Package. R Package. 2022. Available from: <https://cran.r-project.org/web/packages/vegan/vegan.pdf>

Kanehisa M, Furumichi M, Sato Y, Kawashima M, Ishiguro-Watanabe M. KEGG for taxonomy-based analysis of pathways and genomes. *Nucleic Acids Res.* 2023 Jan 6;51(D1):D587–92.

Kanehisa M, Sato Y, Morishima K. BlastKOALA and GhostKOALA: KEGG Tools for Functional Characterization of Genome and Metagenome Sequences. *J Mol Biol.* 2016 Feb;428(4):726–31.