

Diversity, taxonomic novelty, and encoded functions of Salar de Ascotán microbiota as revealed by metagenome-assembled genomes

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SUPPLEMENTARY MATERIAL

Contents of the Supplementary Material (this file and two spreadsheets):

Figure S1. Geographic location of Salar de Ascotán and the sampling sites.

Figure S2. Taxonomic assignment of the Illumina and Nanopore metagenomic reads.

Figure S3. Complete DRAM functional profile for archaeal and bacterial MAGs.

Figure S4. Functional profile of the Salar de Ascotán bacterial MAGs, according to the SUPER-FOCUS classification.

Figure S5. Functional profile of the Salar de Ascotán archaeal MAGs, according to the SUPER-FOCUS classification.

Table S1. Bacterial genera and their relative abundance in Salar de Ascotán water, sediment, and soil (provided as a separate spreadsheet).

Table S2. Sequencing and assembly stats of the Salar de Ascotán metagenomes.

Table S3. Main stats of the bacterial and archaeal MAGs recovered from Salar de Ascotán soil, sediment, and water (provided as a separate spreadsheet).

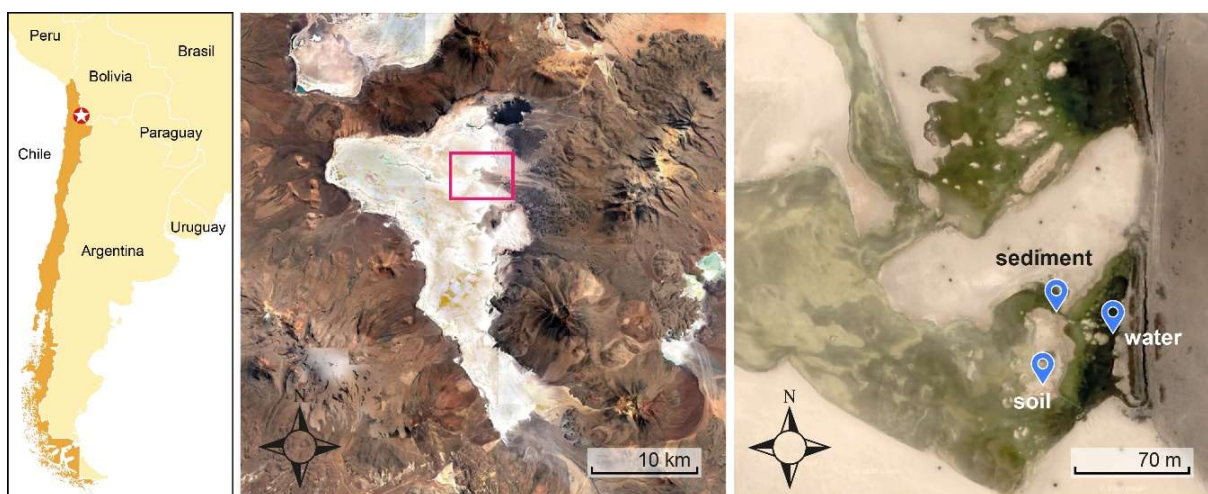


Figure S1. Geographic location of Salar de Ascotán and the sampling sites. The zoom of the view increases from the left to the right.

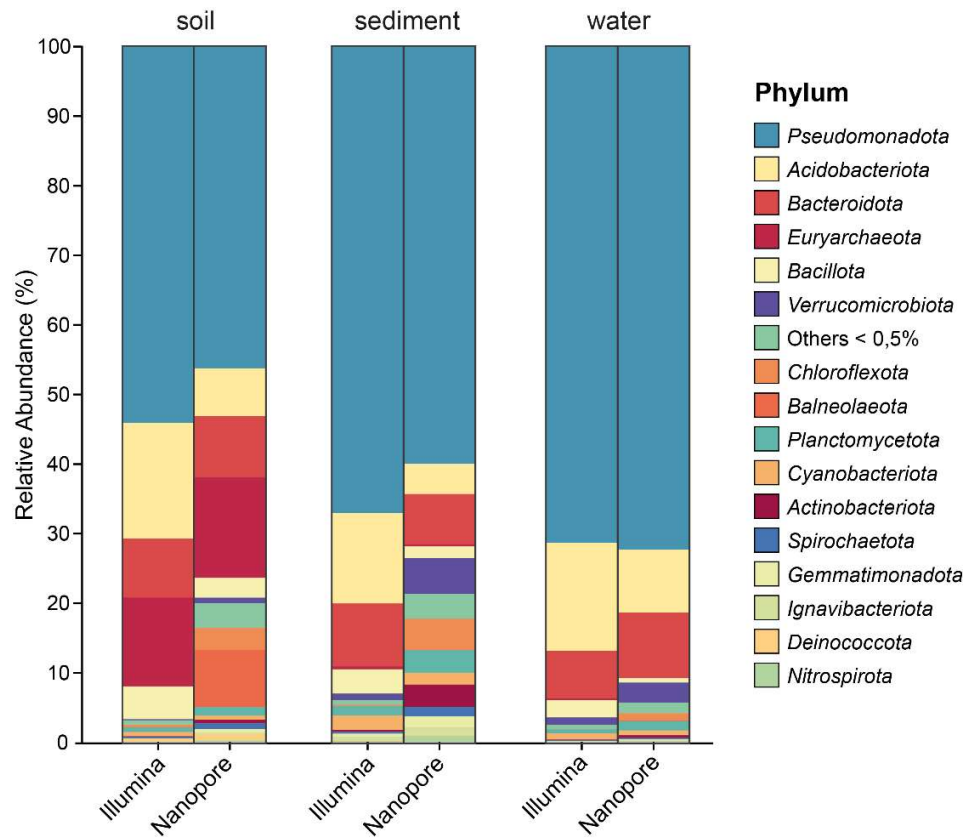


Figure S2. Taxonomic assignment of the Illumina and Nanopore metagenomic reads. The shotgun metagenomic reads obtained for each sample were classified using Kraken (Nanopore) and Kaiju (Illumina). The bars show the relative abundance of the reads classified at the phylum level. Phyla with abundances below 0.5% were grouped into the “others” category.

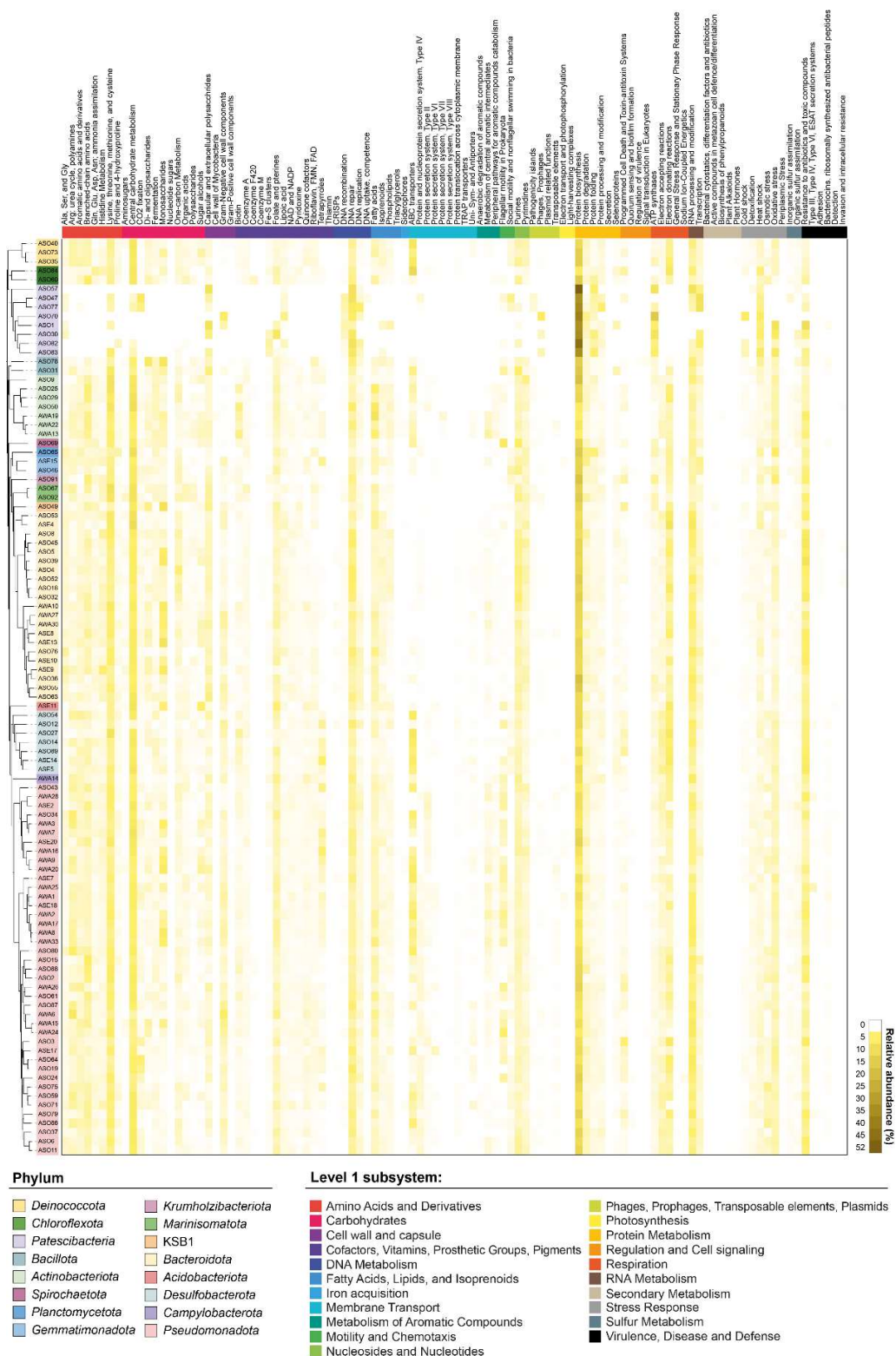


Figure S4. Functional profile of Salar de Ascotán bacterial MAGs, according to the SUPER-FOCUS classification in the hierarchical subsystem levels 1 and 2. The heatmap indicates each category's relative abundance among the total number of categories for each MAG.

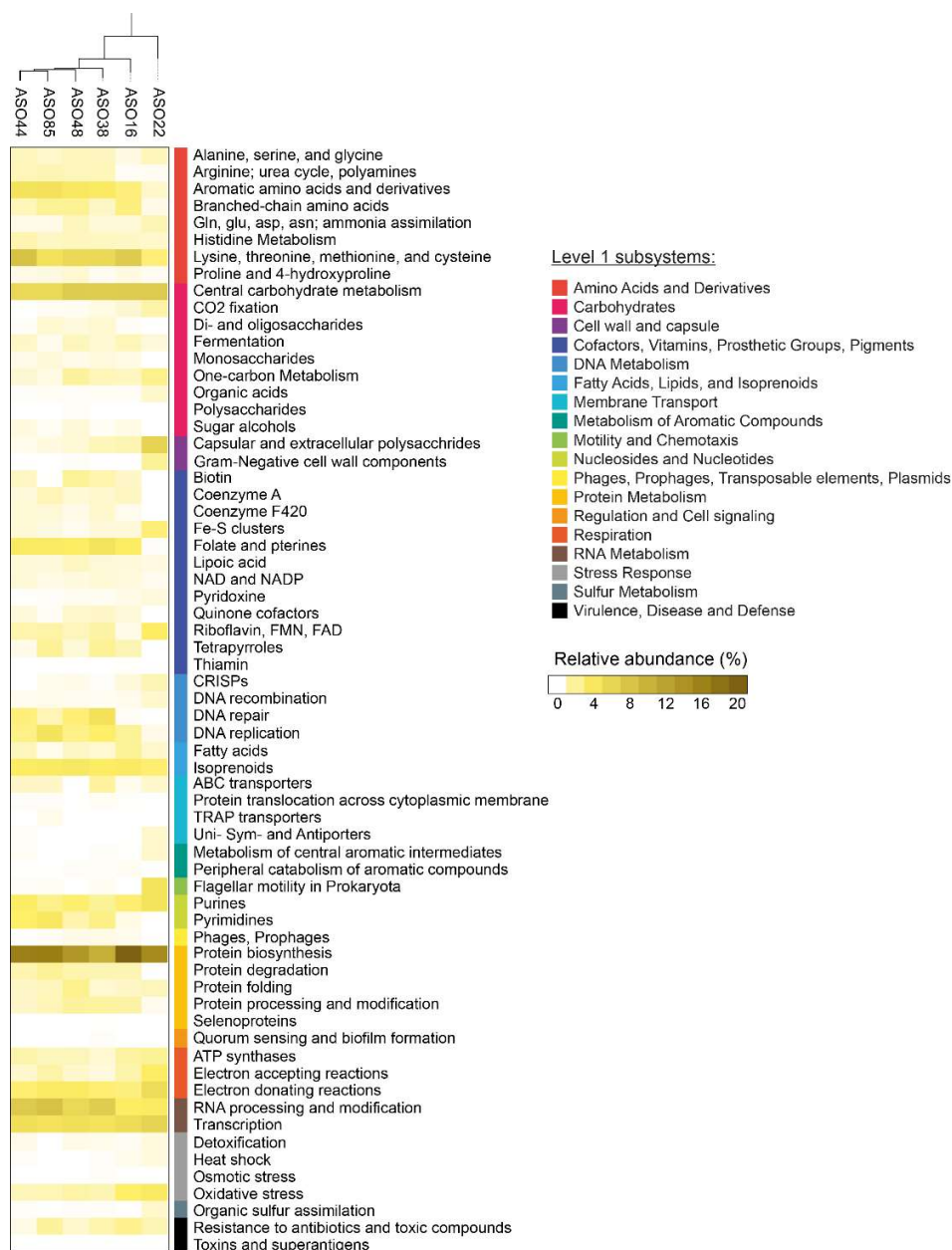


Figure S5. Functional profile of Salar de Ascotán archaeal MAGs, according to the SUPER-FOCUS classification in the hierarchical subsystem levels 1 and 2. The heatmap indicates each category's relative abundance among the total number of categories for each MAG.

Table S2. Sequencing and assembly stats of the Salar de Ascotán metagenomes.

Parameter	Sample		
	Soil	Sediment	Water
Nanopore total bases	9.77 Gbp	6.71 Gbp	9.49 Gbp
Nanopore average read length	6,518 bp	6,219 bp	3,742 bp
Nanopore average read quality (Q)	11.8	11.3	12.2
Illumina total bases	11.60 Gbp	12.62 Gbp	12.37 Gbp
Illumina average read length	151 bp	151 bp	151 bp
Illumina average read quality (Q)	33.2	31.5	30.7
Total assembly length	697 Mbp	292 Mbp	330 Mbp
# assembled contigs	12,152	7,514	16,370
Largest contig	5.2 Mbp	1.2 Mbp	2.4 Mbp
GC content	56.1 %	57.6%	57.0%
N50	135.4 Kbp	63.6 Kpb	39.6 Kbp
L50	1069	1182	1679