Supplementary Information for:

Halophilic microbial community composition shift after a rare rainfall in the Atacama Desert

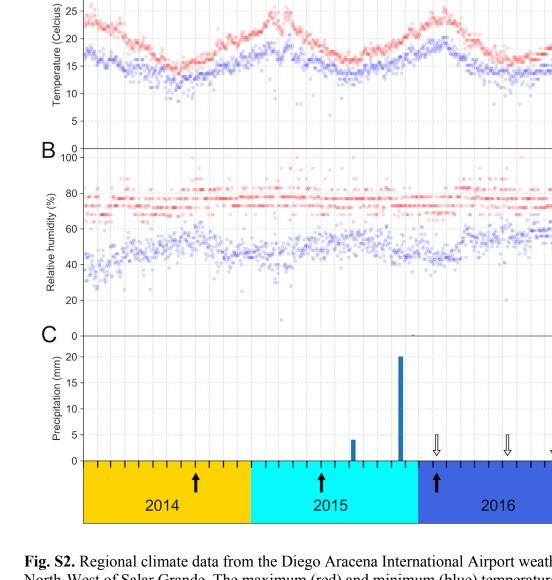
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Supplementary figures:





Fig. S1. Salar Grande landscape and halite nodules. (A) Aerial view of the evaporitic basin of Salar Grande, 5 km wide and 45 km long (N-S direction). (B) Halite nodules (salt rocks) 20 to 50 cm in size.



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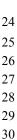
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Fig. S2. Regional climate data from the Diego Aracena International Airport weather station, 40km North-West of Salar Grande. The maximum (red) and minimum (blue) temperature (A) and relative humidity (B) values, and total daily precipitation (C), are plotted for each date along the x-axis. Colors denote the year (2014-2017), x-ticks denote months, black arrows show the main sampling dates at Site 1, and white arrows show the sampling dates at Site 2.



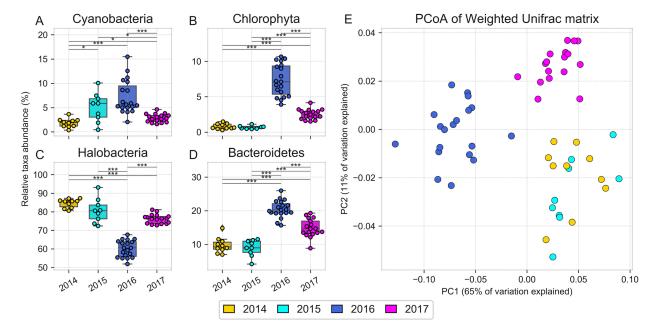


Fig. S3. Taxonomic composition of halite nodules from Site 1 over time inferred from 16S rRNA gene sequences clustered into OTUs at 97% identity and visualized through (A-D) relative abundance of the dominant phyla (Chloroplast was used as a proxy for Chlorophyta and Halobacteria was the only class of Euyarchaeota) whose abundance significantly shifted after the rain and a (E) PCoA plot of a Weighted Unifrac dissimilarity matrix comparing taxonomic composition. Error bars represent standard deviation; significance bars represent group significance based on a two tail t-test, and stars denote the p-value thresholds (*=0.01, **=0.001, ***=0.0001).





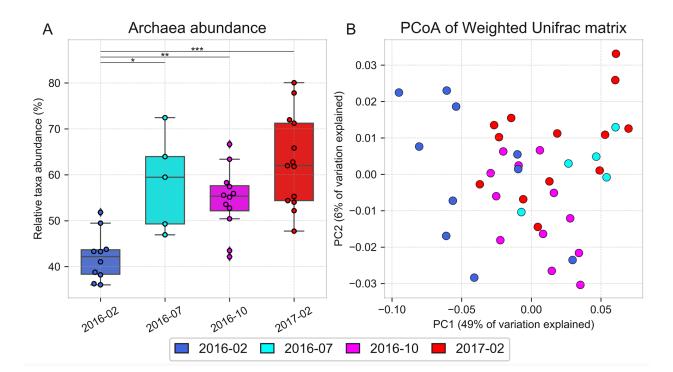


Fig. S4. Taxonomic composition of halite nodules harvested post-rain from Site 2 over time, inferred from 16S rRNA gene sequences clustered into OTUs at 97% identity and visualized through (A) relative abundance of Archaea, and (B) PCoA projection of the Weighted Unifrac dissimilarity matrix. Error bars represent standard deviation; significance bars represent group significance based on a two tail t-test, and stars denote the p-value thresholds (*=0.01, **=0.001, ***=0.0001).

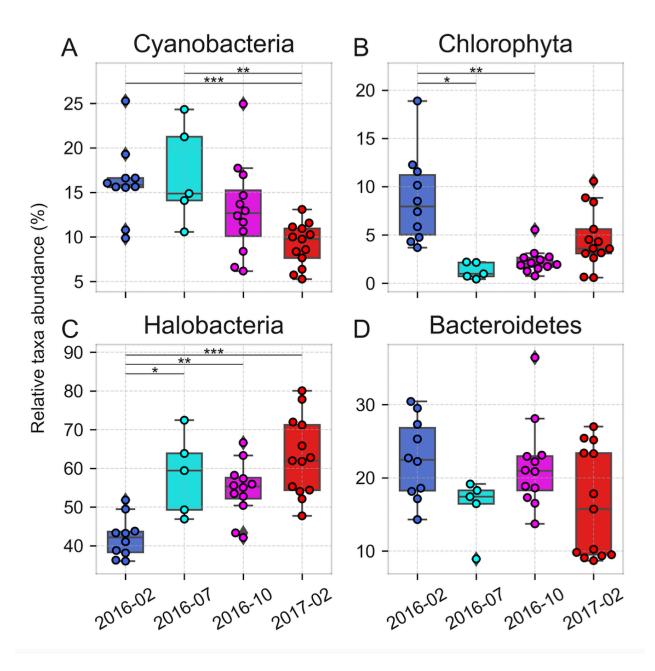


Fig. S5. Taxonomic composition of halite nodules harvested post-rain from Site 2 over time, inferred from 16S rRNA gene sequences clustered into OTUs at 97% identity and visualized through the relative abundance of dominant phyla (Chloroplast was used as a proxy for Chlorophyta and Halobacteria was the only class of Euyarchaeota) (A-D) Error bars represent standard deviation; significance bars represent group significance based on a two tail t-test, and stars denote the p-value thresholds (*=0.01, **=0.001, ***=0.0001).

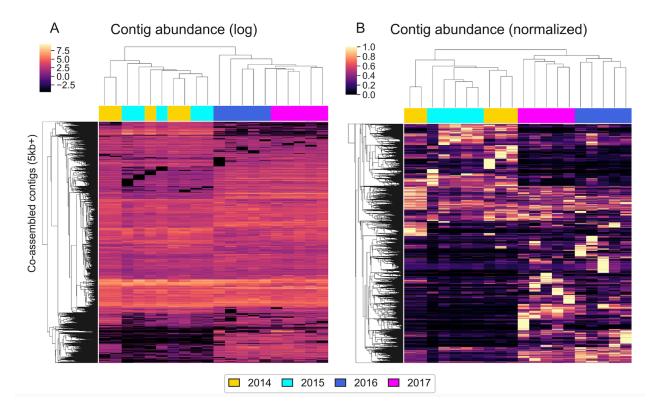


Fig. S6. Hierarchical clustering (Euclidean metric) of relative abundances (fragments per million) of contigs > 5kbp in the WMG co-assembly, quantified with reads from samples harvested at different dates and displayed on (A) a log scale and (B) standardized to the maximum abundance of each contig.

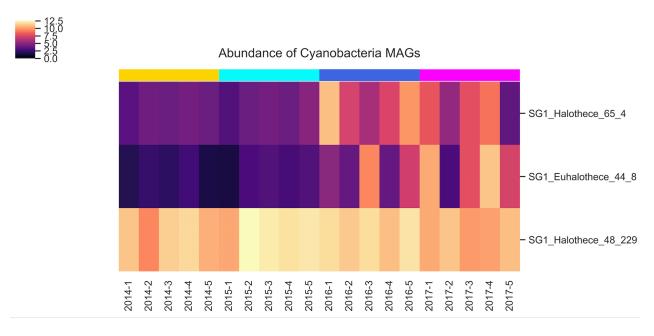


Fig. S7. Hierarchical clustering (Euclidean metric) of photosynthetic MAG relative abundances (fragments per million), quantified with metaWRAP's quant_bins module, showing the emergence of two new *Cyanobacteria* MAGs after the rain.

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Tables (Supplementary):

replicates.

Site	Latitude	Longitude	Elevation (asl)	Collection dates	Amplicon sequencing replicates	Shotgun sequencing replicates	Purpose
S1	20°57' 12.006"S	70°1' 10.5996"W	680m	Sep-14	10	5	Before-after rain comparison
				Jun-15	9	5	
				8-Feb-16	19	5	
				20-Feb-17	17	5	
S2	20°57' 8.5212"S	70°1' 1.2612''W	664m	8-Feb-16	12	NA	After rain recovery process
				11-Jul-16	5	NA	
				20-Oct-16	12	NA	
				20-Feb-17	13	NA	
S3	20°55' 48.18"S	70°0′ 49.32"W	676m	Misc.	NA	15	Assembly and binning improveme nt

Data S1. Summary table of 16S rRNA gene OTUs clustered at 97% for Site 1 and Site 2,

Data S2. Summary table of reconstructed metagenome-assembled genomes (MAGs) with

information about sequence statistics, binning accuracy estimated with CheckM, assembly

coverage, taxonomy, and abundance across replicates in the time series.

including OTU abundances across replicates, taxonomy, representative sequences, and

stacked taxonomy plots visualizing community composition across the time-points and

Table S1. Description of sampling locations, dates, and replicate counts of biological samples collected for this study.

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