Supplementary Information for:

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

Gherman Uritskiy, Samantha Getsin, Adam Munn, Benito Gomez-Silva, Alfonso Davila, Brian Glass, James Taylor\* and Jocelyne DiRuggiero\*

**Supplementary figure legends:**

**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.

**Fig. S2.** Regionalclimate 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.

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

**Data S1.** Summary table of 16S rRNA gene OTUs clustered at 97% for Site 1 and Site 2, including OTU abundances across replicates, taxonomy, and representative sequences.

**Data S2.** Summary of the taxonomic composition for Site 1 samples inferred from 16S rRNA gene sequences clustered into OTUs at 97% identity. Files “area\_charts.html” and “bar\_charts.html” contain interactive stacked taxonomy plots visualizing community composition across the time-points and replicates, out\_table.txt contains the raw OTU table, and rep\_sets.fna contains the representative OTU sequences. Other files are necessary for displaying the interactive html plots.

**Data S3.** Summary of the taxonomic composition for Site 2 samples inferred from 16S rRNA gene sequences clustered into OTUs at 97% identity. Files “area\_charts.html” and “bar\_charts.html” contain interactive stacked taxonomy plots visualizing community composition across the time-points and replicates, out\_table.txt contains the raw OTU table, and rep\_sets.fna contains the representative OTU sequences. Other files are necessary for displaying the interactive html plots.

**Data S4.** 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.