Supplementary Information for:

Halophilic microbial community composition turnover following a rare rainfall in the Atacama Desert

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**Supplementary figure legends:**

**Fig. S1.** Regionalclimate data collected at the Diego Aracena International Airport, 40km West of Salar Grande. The maximum (red) and minimum (blue) temperature (A) and relative humidity (B) values, as well as 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 while arrows show the sampling dates at Site 2.

**Fig. S2.** Taxonomic composition differences between halite samples harvested from Site 1 at different dates, infeed from 16S rRNA gene sequences clustered into OTUs at 97% identity and visualized through (A-D) relative abundance of phyla whose abundnace signifficantly shifter 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. S3. Taxonomic composition differences between halite samples harvested post-rain from Site 2 at different dates post-rain, infered from 16S rRNA gene sequences clustered into OTUs at 97% identity and visualized through (A) relative abundance 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. S4. Taxonomic composition differences between halite samples harvested post-rain from Site 2 at different dates post-rain, infered from 16S rRNA gene sequences clustered into OTUs at 97% identity and visualized through the relative abundance of four of the dominant phyla (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. S5. 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. S6. 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. Information on the 16S rRNA gene OTUs clustered at 97% from Site 1 and Site 2, including OTU abundances across replicates, their estimated taxonomy, and representative sequences.

Data S2. Summary of the taxonomic composition of 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 of 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), including information about their sequence statistics, binning accuracy estimated with CheckM, assembly coverage, taxonomy, and abundance across the replicates in the time series.