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.** 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 major differentially abundant phyla 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. S2. Taxonomic composition differences between halite samples harvested from Site 2 at different dates post-rain, infeed from 16S rRNA gene sequences clustered into OTUs at 97% identity and visualized through (A-D) relative abundance of major differentially abundant phyla and (E) archaea abundance. 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. 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. S4. 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.