Supplementary material for:
"Microbial response to deliquescence of nitrate-rich soil surfaces in the hyperarid Atacama Desert"
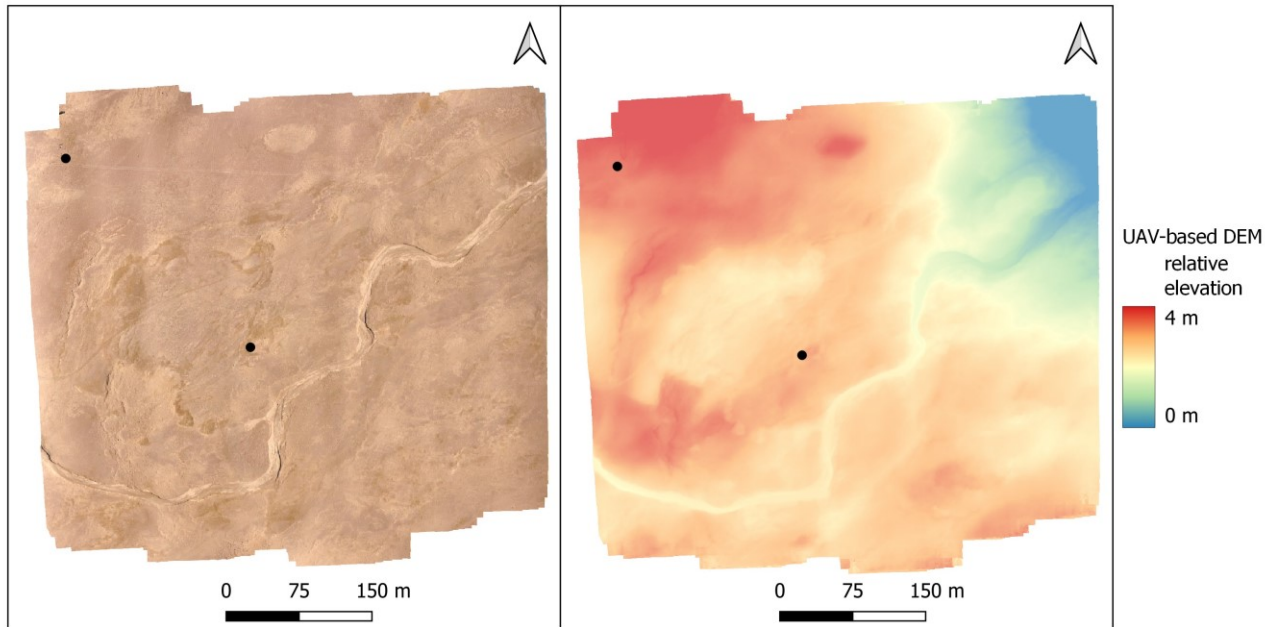
Figure S1: Orthographic image and DEM of the study area of EP1 and EP2
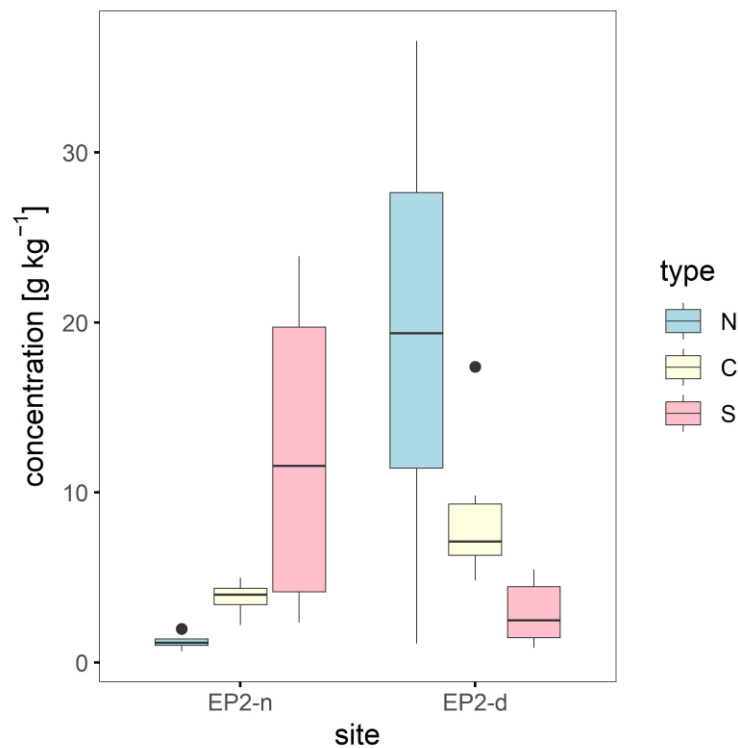
Figure S2: Elemental data (C,N,S) of the EP2 site
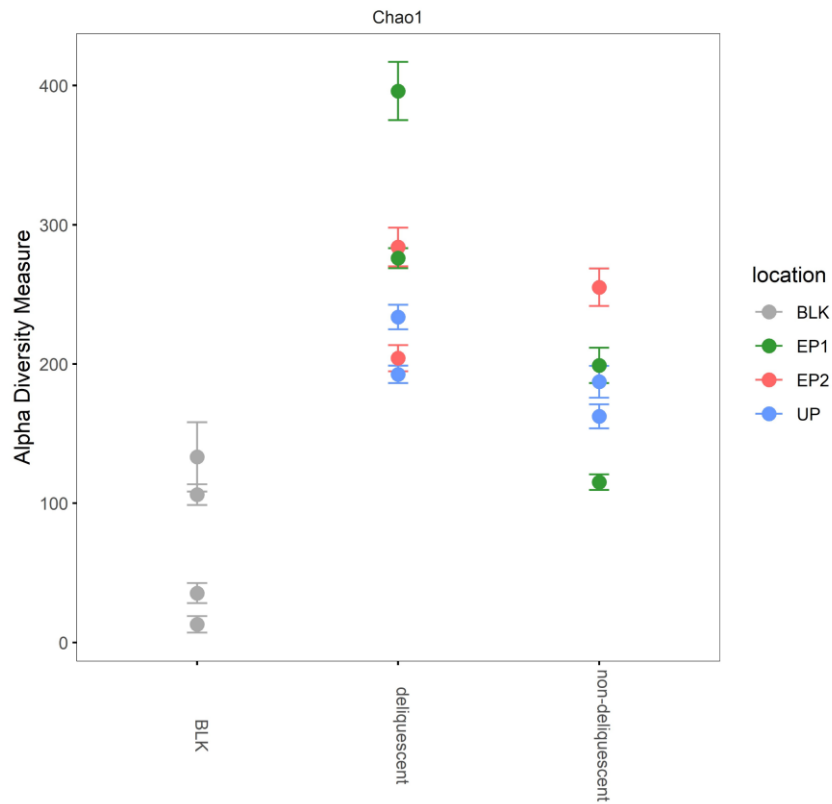
Figure S3: Alpha diversity of the 16S rRNA gene sequencing data
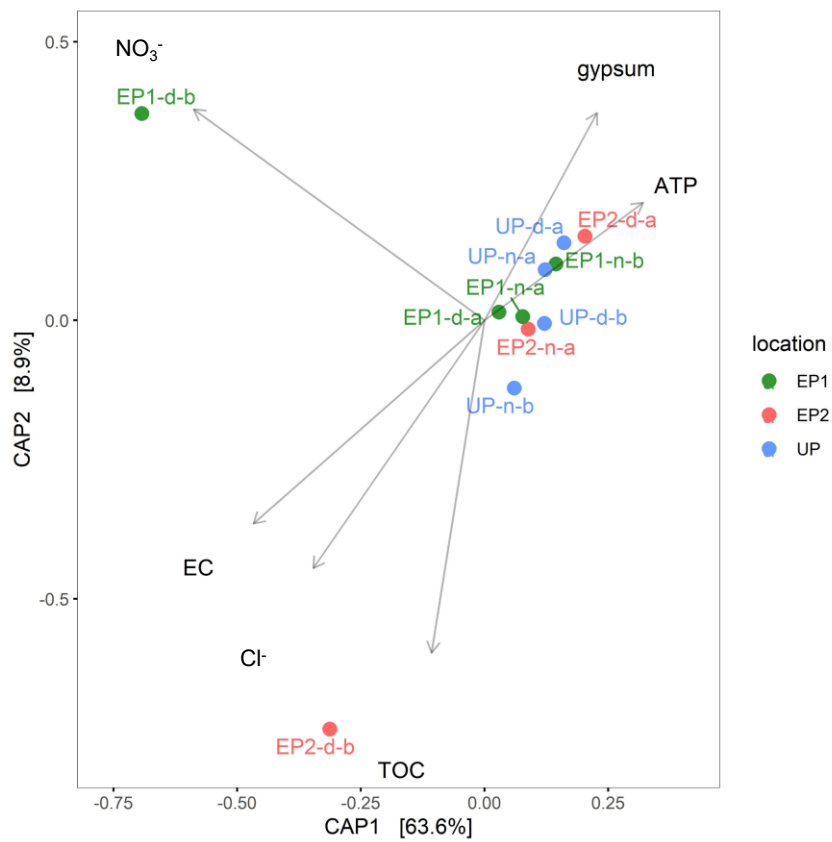
Figure S4: Canonical analysis of Principal Coordinates (CAP) compare the bacterial communities based on 16S rRNA gene sequencing data to different environmental variables (including EC and concentration of gypsum, Cl^-, NO_3^-, ATP, and TOC).

Compositional profiles of organic molecules
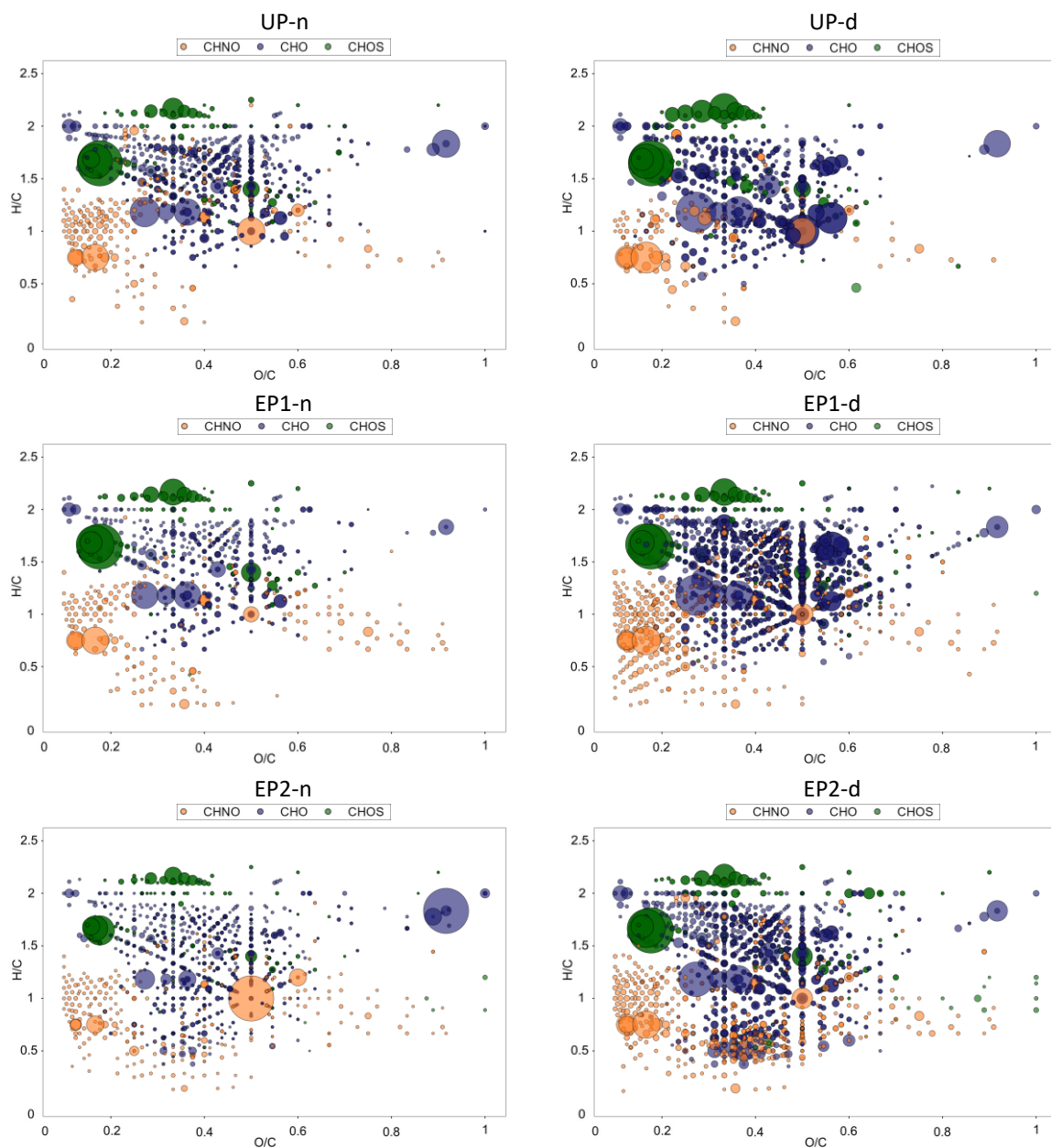
Figure S5: Organic molecule compositional profiles plotted in Van Krevelen diagrams. The hydrogen:carbon atomic ratio (H/C) as a function of the oxygen:carbon (O/C) atomic ratio of organic compounds. The elemental compositions are plotted as CHO (blue), CHOS (green), and CHNO (orange), and bubble sizes depict mass signal intensities.

tATP quantification via standard addition method
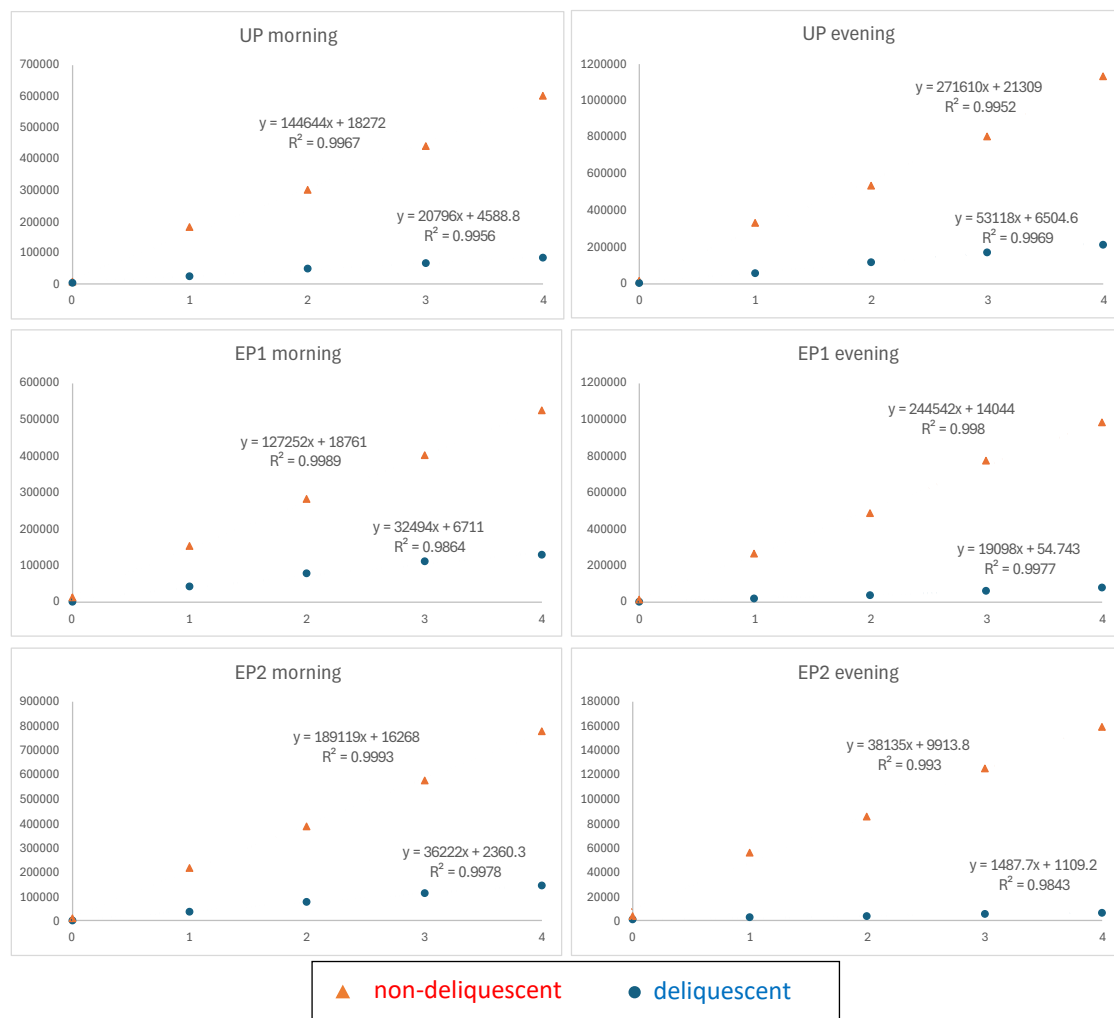
Figure S6: ATP standard addition. Linear fits are plotted for each sample site during morning and evening. y-axis shows the relative light unit (RLU) and the x-axis the standard addition steps in µL. The linear regression function and the coefficient of determination (R^2) are plotted above.

Calculation:
$c_x = (b \cdot c_{Sdt})/(m \cdot v_x)$ in mol/L
where c_x is the ATP concentration, v_x the sample volume, c_{Sdt} the concentration of the added standard of the sample. b is the y-intersection and m the slope of the linear regression from the measured standard addition 0 - 4 µL 1µM ATP.
Linear regression: $y = m \cdot x + b$

Table S1 16S rRNA gene sequencing results of the CFUs given in genus level

Phylum	Genus	EP2-d	EP2-n	SUM
Proteobacteria	Pseudomonas	6	0	6
Proteobacteria	Variovorax	0	3	3
Proteobacteria	Agrobacterium	4	5	9
Proteobacteria	Advenella	5	0	5
Proteobacteria	Hydrogenophaga	0	1	1
Bacillota	Bacillus	0	1	1
Actinomycetota	Microbacterium	6	0	6
Proteobacteria	Rhizobium	4	0	4
n sequences		*25*	*10*	*35*