



Supplement of

Only a minority of bacteria grow after wetting in both natural and post-mining biocrusts in a hyperarid phosphate mine

Talia Gabay et al.

Correspondence to: Roey Angel (roey.angel@bc.cas.cz) and Talia Gabay (taliajoann@gmail.com)

The copyright of individual parts of the supplement might differ from the article licence.

Supplementary figures

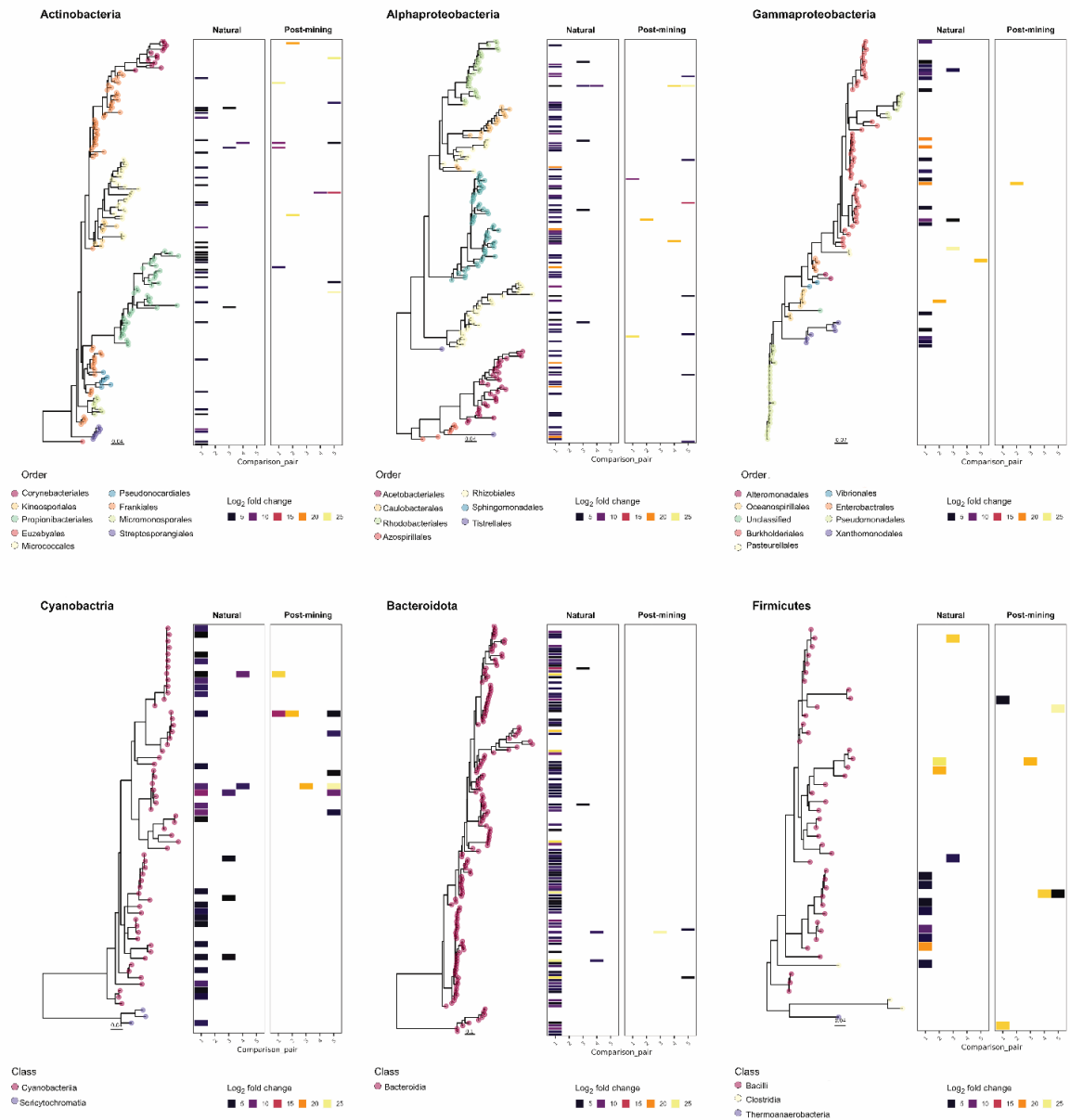


Figure S1. Heatmaps and phylogenetic trees of active bacterial ASVs. Each figure represents a different phylum or class, the different colors in the tips of the phylogenetic trees represent different orders/classes. The squares in the heatmaps represent active ASVs assigned to a specific taxa and the color of each square is the number of Log₂ fold change. Every column represents a natural or post-mining sample.

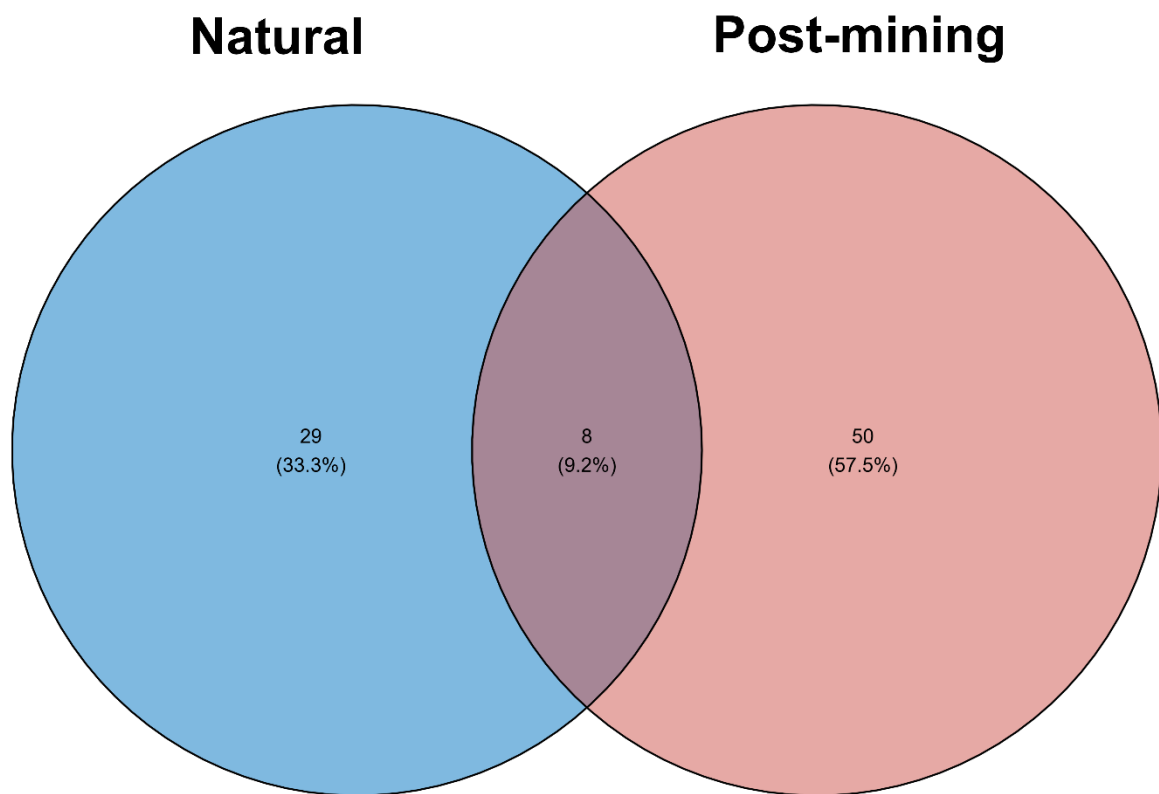


Figure S2. Venn diagram representing unique sequences in natural (blue) and post-mining (pink) samples. Overlap represents sequences that appear in both groups.

Supplementary tables

Table S1. Chlorophyll *a* concentration of all collected biocrust samples. Highlighted samples are the ones chosen for the SIP assay. The positive control consisted of 0.01 gr spirulina mixed with 30 gr of soil.

Plot type	Sample Number	Chla/gr soil
Positive control	Positive control	9.98
Natural	2	9.11
Natural	7	6.81
Natural	3	6.73
Natural	1	6.26
Natural	4	5.30
Natural	6	5.10
Natural	9	4.92
Natural	8	4.91
Natural	5	4.90
Natural	10	4.77
Post-mining	7	9.05
Post-mining	8	8.02
Post-mining	3	7.79
Post-mining	4	7.37
Post-mining	5	6.28
Post-mining	10	6.09
Post-mining	9	5.41
Post-mining	6	5.07
Post-mining	2	4.92
Post-mining	1	4.91
Negative control	Negative control	4.42

Table S2. Read information for samples.

Min.	602
Max.	29,1129
Median	23,739
Mean	47,311

Table S3. Numbers of ASVs throughout the pipeline.

Non-chimera ASVs	10,275
Number of ASVs after decontamination	10,100
Number of ASVs after prevalence filtering	1,404
Labelled ASVs (used for differential abundance modelling)	1,266

Table S4. Mean relative abundance of phyla and p-values of Mann-Whitney test comparing natural and post-mining abundances.

Phylum	Natural	Post-mining	p-value
Actinobacteriota	10.60	25.92	0.26
Bacteroidota	1.79	3.06	0.89
Cyanobacteria	7.16	16.76	0.26
Firmicutes	21.05	7.13	1
Gemmatimonadota	13.35	3.45	1
Myxococcota	0.01	2.03	0.56
Patescibacteria	0.65	16.18	0.22
Proteobacteria	40.81	24.99	0.9
Unclassified	4.58	0.48	0.86

Table S5. Means and Standard Deviation of functional gene abundances of the 11 function categories.

Function category	Natural abundance	Post-mining abundance
Autotrophy	1,233.16 ± 163.63	2,245 ± 1,890.48
DNA conservation	27,724.12 ± 14,087.9	75,650.46 ± 68,237.54
DNA repair and degradation	47,773.57 ± 27,991.98	92,325.27 ± 87,069.01
Inorganic and gaseous energy sources	4,919.22 ± 2,600.75	37,345.44 ± 33,585.23
Nitrogen	18,868.56 ± 12,281.28	53,779.92 ± 52,389.59
Organic energy source	26,0292.75 ± 87,385.81	57,4701.52 ± 58,3317.8
Phototrophy	12,436.05 ± 9,531.33	114,470.9 ± 96,555.88
ROS-damage prevention	47,572.92 ± 2,4443.2	116,383.04 ± 96,627.67
Sensing and motility	128,620.08 ± 86,886.19	189,995.54 ± 190,637.5
Sporulation capsule and C-storage	45,891.06 ± 34,684.91	101,349.6 ± 105,002.3