

Table S1. Primers used in the amplification of the amplicons.

Primer name	Predicted target group	Target region	Primer sequences (5'→3')
515F	Bacterial 16S rRNA	16S (V4+V5)	GTGCCAGCMGCCGCGGTAA
907R			CCGTCAATTCCTTTGAGTTT
Arch519F	Archaeal 16S rRNA	16S (V4+V5)	CAGCCGCCGCGGTAA
Arch915R			GTGCTCCCCCGCCAATTCCT

Table S2. Ionic chromatography analysis of brine samples from the Mahai potash area.

Sample ID	Anion concentrations (mg/L)				Cation concentrations (mg/L)				
	F ⁻	Cl ⁻	NO ₃ ⁻	SO ₄ ²⁻	Li ⁺	Na ⁺	K ⁺	Mg ²⁺	Ca ²⁺
ML	15003.43	4276.634	14849.78	15388.2	0	1752.437	1156.231	2951.274	3733.006
MSa	15008.67	157422.2	14876.42	21660.88	1048.775	68474.23	6127.609	17129.66	3958.655
MSb	15007.13	143291.8	14863.43	19374.23	1048.055	57633.01	5589.147	14234.05	4108.269
MWa1	14962.57	183747.7	15534.06	16970.09	1076.868	58005.92	8780.301	19554.33	4054.31
MWa2	14955.03	172267.5	15829.08	16849.51	1049.496	55424.79	1176.33	18605.3	4034.688
MWa3	14962.95	168074.3	15391.88	16547.81	1049.496	58640.92	8049.893	18693.78	4024.877
MWa4	14959.25	192179.7	15489.77	17130.95	1048.055	82309.46	2485.351	7152.701	3936.58
MWb1	14959.25	180899.7	15684.24	16003.92	1055.979	47078.67	9141.08	29525.59	4145.06
MWb2	14957.33	175603.9	15531.06	15986.73	1047.335	92249.42	1932.177	4700.917	4120.533
MWb3	14960.27	179258.3	15376.22	16023.42	1046.615	88844.11	1864.635	4548.216	4248.073
MWb4	14961.03	138688.1	15445.49	16619.9	1046.615	90848.92	1898.611	4750.866	4113.174
MWc1	14959.89	205499.2	15479.12	17161.22	1049.496	48882.24	2747.478	13967.18	4005.256
MWc2	14961.93	203283.7	15533.39	16996.01	1057.419	39564.63	23382.91	32715.19	5032.936
MWc3	14963.08	215179.1	15704.88	16861.83	1059.58	27149.8	18638.06	39640.98	4652.768
MWc4	14967.29	222592	15613.64	16735.35	1062.461	21301.77	20484.29	46138.63	4319.201
MWc5	14961.67	227679.6	15637.95	16687.12	1079.029	17609.27	19754.47	48784.51	3845.83
MWd1	14958.61	172371.6	14819.47	16569.36	1046.615	83249.3	2458.557	7272.579	3880.168
MWd2	14989.38	176794.6	14877.41	16812.57	1046.615	92986.42	2671.437	7866.259	3858.094
MWd3	14989.89	175264.2	14877.08	16769.21	1046.615	91957.87	2638.044	7830.581	3855.641
MWd4	-	-	-	-	-	-	-	-	-
MWe1	14958.61	175545.6	15335.27	17437.27	1047.335	83295.61	3731.664	8972.273	3811.493
MWe2	14961.29	187086.4	15415.52	17260.77	1056.699	36162.6	4862.85	35325.38	4412.404
MWe3	14960.27	189577.6	15457.14	16784.35	1064.622	9152.159	2913.536	50606.93	4221.093
MWe4	14960.14	213275.8	15428.17	17000.88	1067.504	13039.69	3201.55	55633.23	4417.309

“-”: data not aquired

Table S3. Sequence data of the 24 water samples.

Sample ID	No. of effective sequence		No. of assigned ASVs	
	Bacteria	Archaea	Bacteria	Archaea
ML	76051	104	727	34
MSa	74985	14020	640	60
MSb	74803	17732	1211	60
MWa1	75970	n.d.	1515	n.d.
MWa2	75853	20893	766	114
MWa3	75403	33230	1379	143
MWa4	74458	1487	1294	79
MWb1	76061	2044	924	10
MWb2	75936	737	1215	42
MWb3	75957	2365	759	47
MWb4	76001	10	886	6
MWc1	75673	1827	1220	73
MWc2	76032	37199	476	128
MWc3	75735	n.d.	2132	n.d.
MWc4	75984	12345	1688	77
MWc5	75917	5308	689	73
MWd1	74902	46018	875	104
MWd2	74578	40810	677	99
MWd3	75250	4464	694	64
MWd4	75498	162	734	43
MWe1	51246	14839	138	38
MWe2	75686	3978	2308	12
MWe3	75965	48	2014	12
MWe4	75906	92	96	5
Total	1789850	259712	3980	238

“n.d.”: not determined.

Table S4. Alpha diversity indices calculated for each sample.

Sample ID	Bacteria				Archaea			
	Richness	Chao1	Shannon	Invsimpson	Richness	Chao1	Shannon	Invsimpson
ML	727	1092.956	2.932158	5.582196	34	45.375	3.128652	16.09524
MSa	640	953.5119	2.803248	3.675312	60	61.5	3.053482	17.4974
MSb	1211	1639.879	3.395878	4.133344	60	77.5	3.112409	16.87359
MWa1	1515	1990.02	1.896605	2.047005	n.d.	n.d.	n.d.	n.d.
MWa2	766	1197.462	1.680828	2.319119	114	124.0435	1.654676	3.993343
MWa3	1379	1826.857	2.164484	2.310101	143	151.6364	2.058047	3.600064
MWa4	1294	1753.722	2.213416	2.393925	79	92.125	2.563019	5.445116
MWb1	924	1438.857	1.715922	2.446089	10	10.5	0.736642	2.011404
MWb2	1215	1682.708	2.813704	4.689674	42	49.33333	1.6573	2.860305
MWb3	759	1155.409	1.655671	1.963726	47	57.90909	1.873157	4.541625
MWb4	886	1281.189	1.93874	2.901035	6	7	1.695743	5
MWc1	1220	1623.077	3.101065	3.885334	73	108.4286	2.48619	7.669186
MWc2	476	799.0182	0.756326	1.232442	128	139.4	1.895657	3.497383
MWc3	2132	2502.722	3.968302	5.415725	n.d.	n.d.	n.d.	n.d.
MWc4	1688	2038.833	3.324904	5.010013	77	98.66667	2.108946	4.907463
MWc5	689	1084.116	1.871529	2.279554	73	90.76923	1.832427	4.431009
MWd1	875	1218.994	2.616186	4.732894	104	107.9286	3.391756	24.19337
MWd2	677	975.8095	2.010944	2.499024	99	108.5455	3.508113	27.84231
MWd3	694	1001.616	2.278593	2.298387	64	89	1.304112	2.641113
MWd4	734	1118.57	2.511628	2.516322	43	54.375	3.419129	23.18375
MWe1	138	159	3.915377	16.13991	38	38	2.81223	11.06877
MWe2	2308	2591.53	4.24077	7.103093	12	13.5	1.672916	4.828518
MWe3	2014	2379.889	4.099533	8.00471	12	33	1.995844	5.788945
MWe4	96	129	1.746239	2.073854	5	6	0.470767	1.252071

“n.d.”: not determined.



Figure S1. Sampling context. (A) The panorama of the Mahai potash area. (B) Mahai lake. (C) Monitoring station. (D) Sampling site of a Mining well. (E) Brine sampling from a mining well.

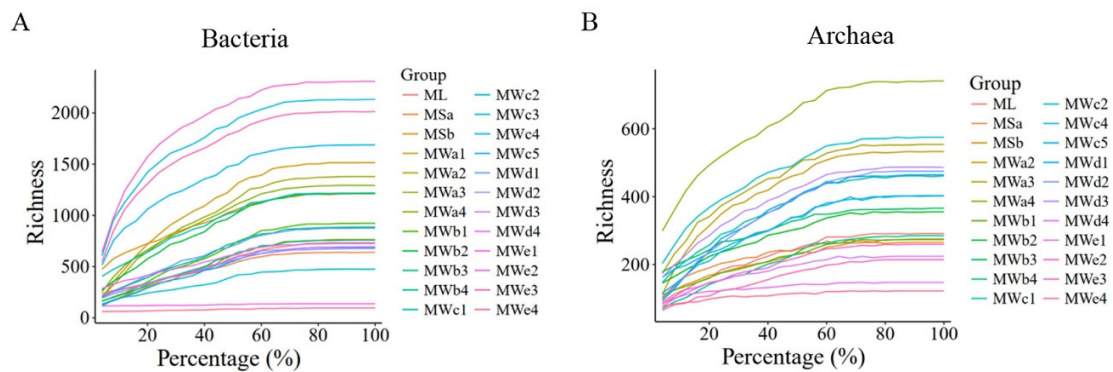
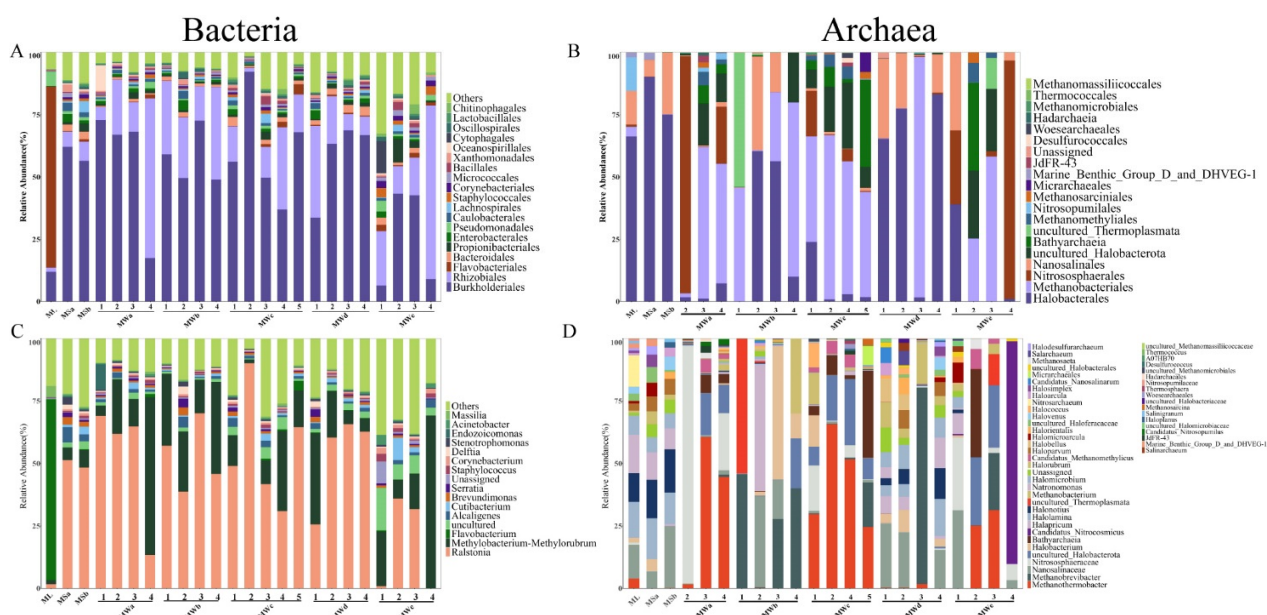


Figure S2. Rarefaction analysis of bacteria (A) and archaea (B) amplicon obtained from different brine samples of the Mahai potash region.



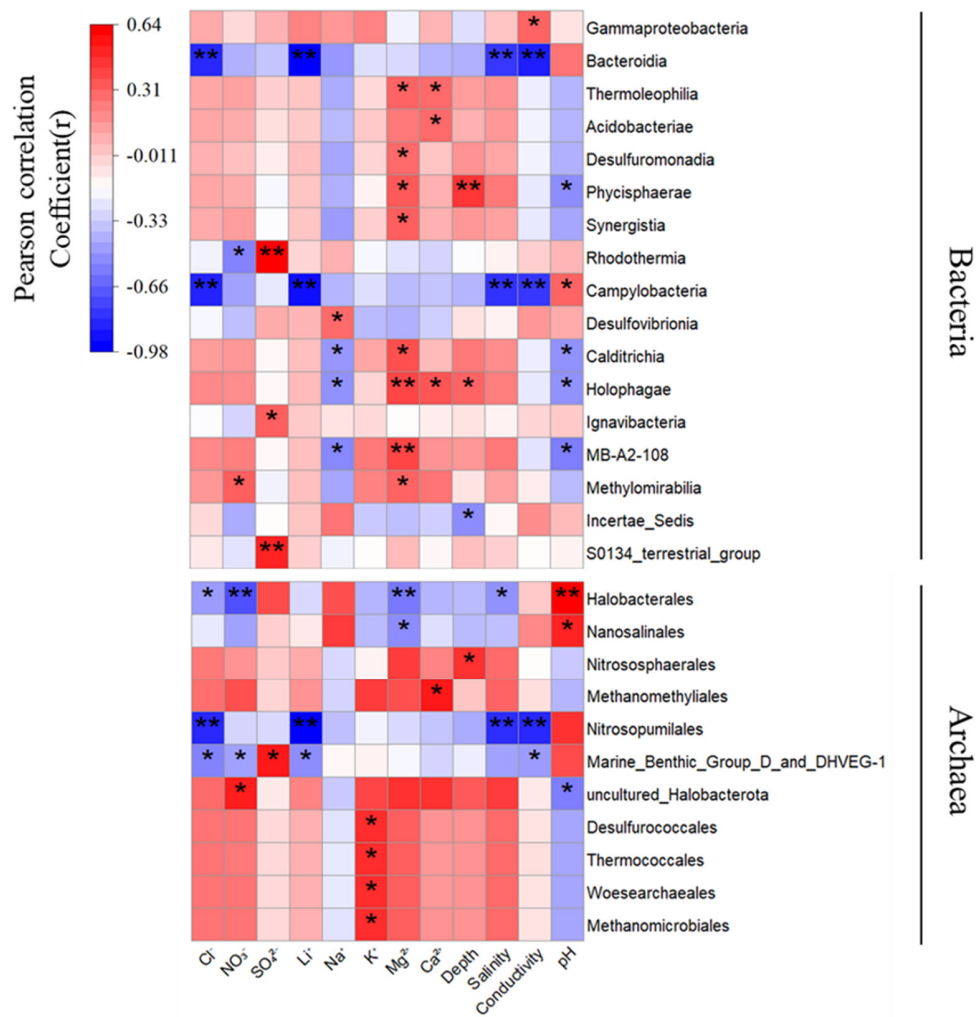


Figure S4. Heatmap of values of Pearson's correlation between species and environmental factors. The heatmap shows the species of bacteria at class level with relative abundance greater than 0.2 % and archaea at order level that are significantly associated with any environmental factor. Lines represent different microbial groups, columns represent different environmental factors. The color of the color block represents the correlation coefficient (r), and red indicates positive correlation, blue negative correlation. If the p value of the correlation between an environmental factor and the abundance of a species is less than 0.05, one star number "*" is marked in the corresponding color block, indicating significant indigenous correlation. If the $p \leq 0.01$, two-star numbers "**" are marked, indicating extremely significant indigenous correlation.