Supplementary Material

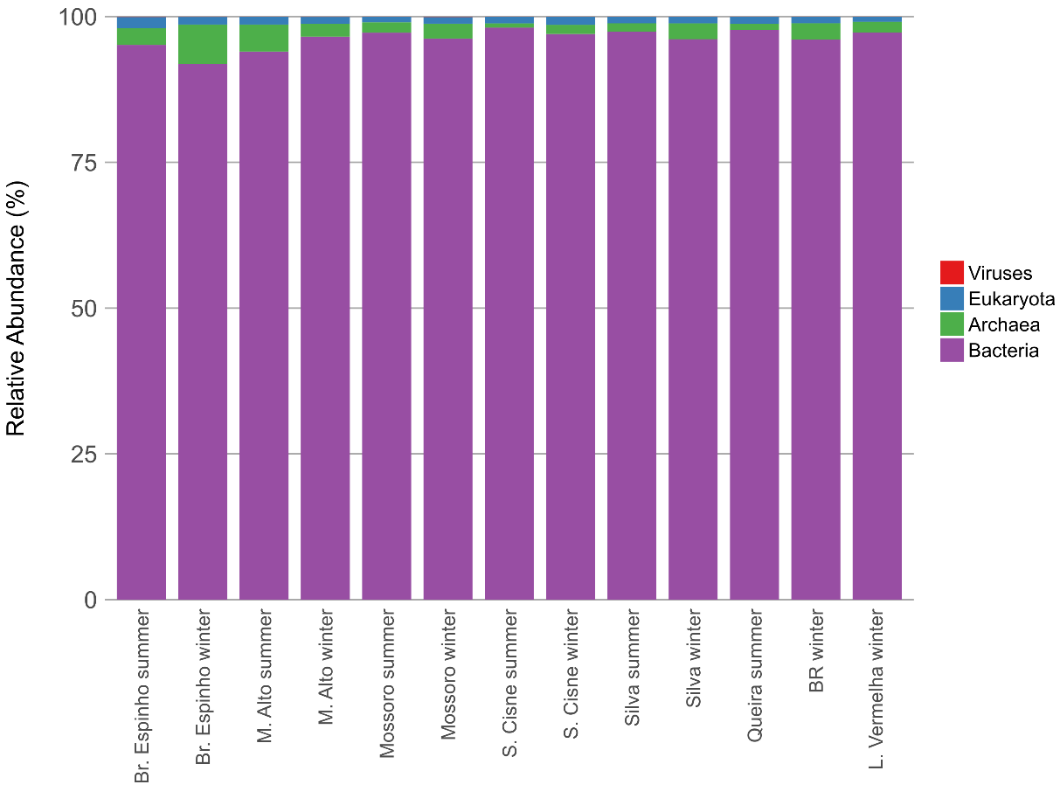
1 Supplementary Data

Supplementary scripts for our analyses can be found on GitHub (*https://github.com/juwal22/Araruama-metagenomes*).

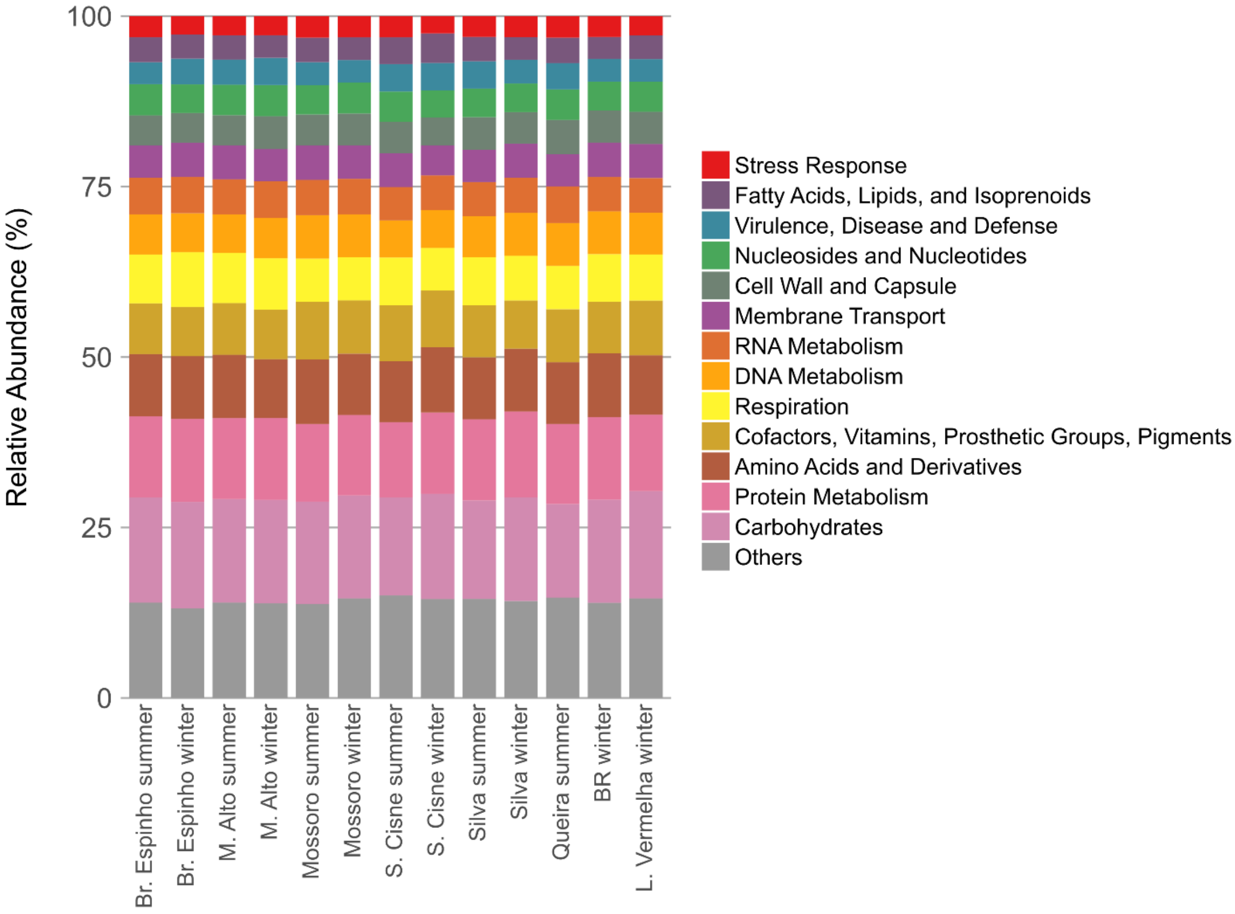
All metagenomic data are available at *http://metagenomics.anl.gov* (Metagenomics RAST Server) - MG-RAST IDs: from 4576344.3 to 4576356.3 (see Supplementary Table 1 below for details).

2 Supplementary Figures and Tables

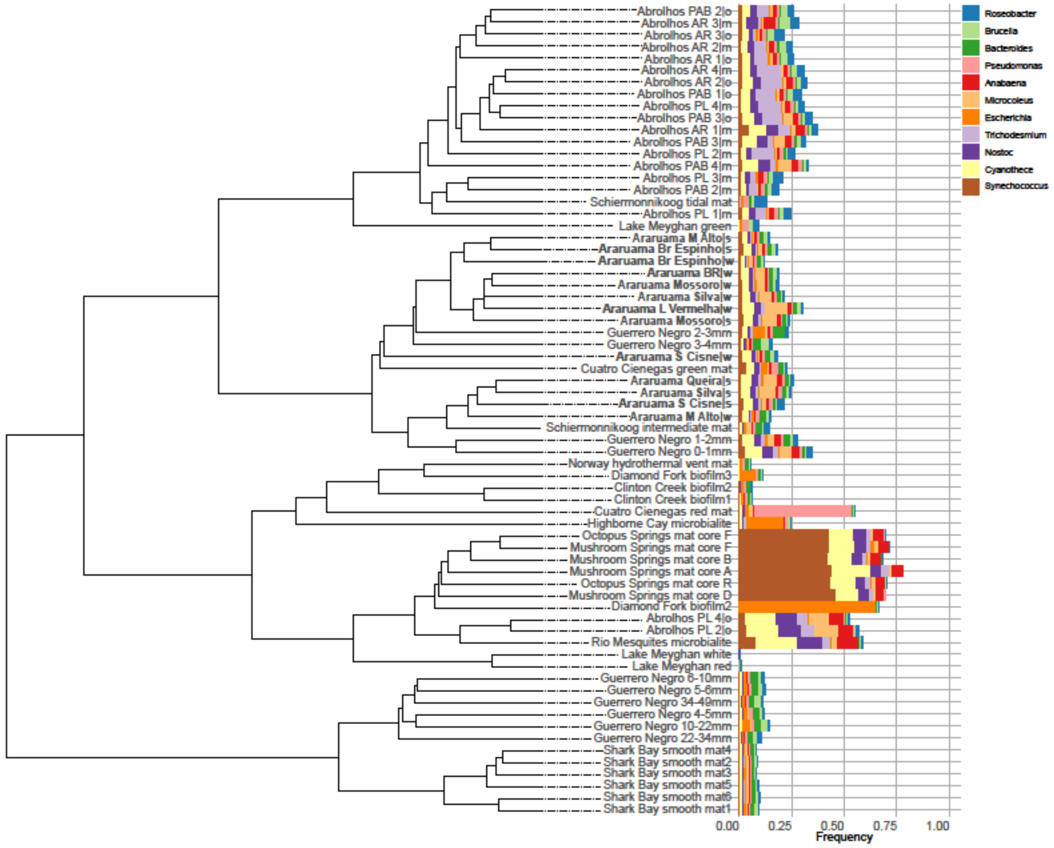
2.1 Supplementary Figures



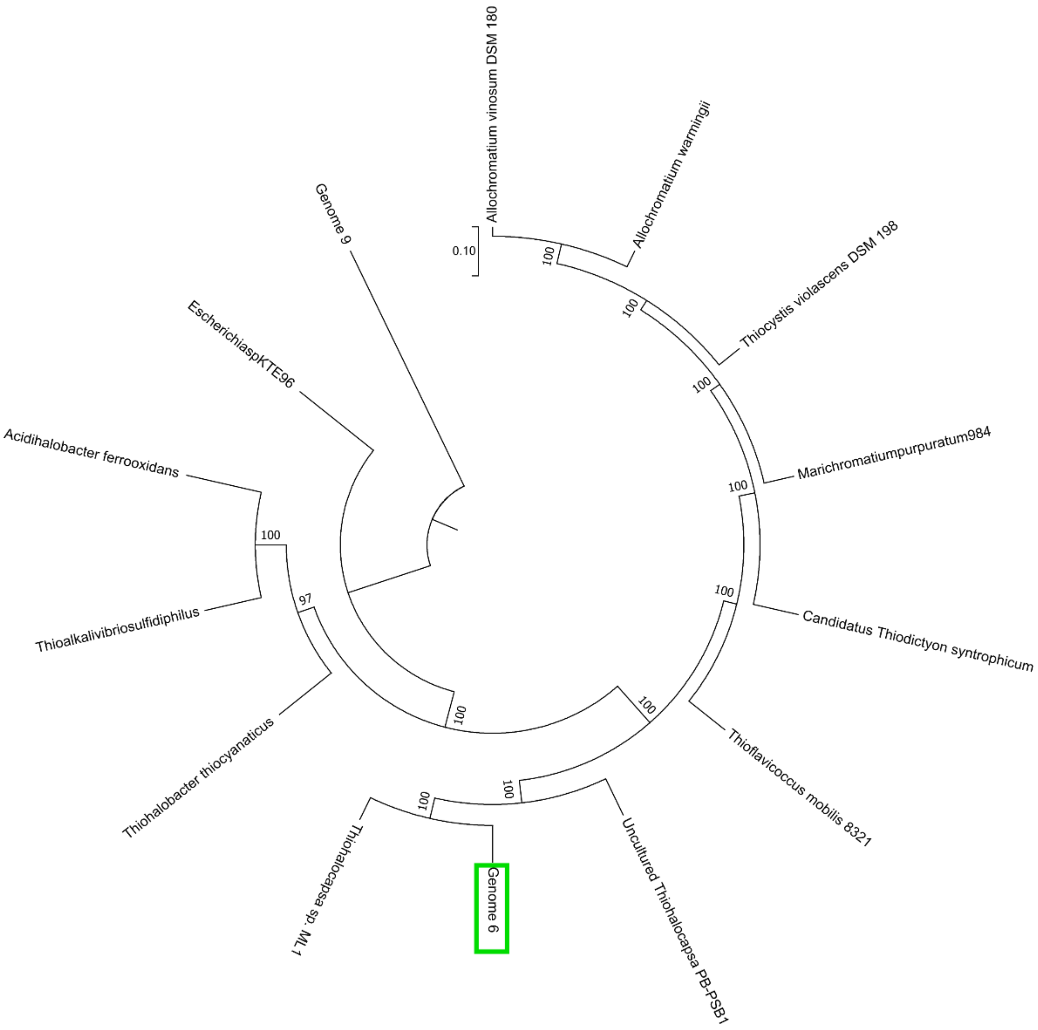
Supplementary Figure 1. Taxonomic composition at the domain level of microbial mats from the hypersaline lagoon system of Araruama. Among eukaryotes, the most abundant phyla included Bacillariophyta, which was represented mainly by the order Naviculales (0.01% in Mossoró summer to 0.2% in Queira summer), and Ascomycota (0.1% in S. Cisne summer to 0.2% in Br. Espinho summer). Among viruses, the only identified order was Caudovirales (0.02% in Mossoró summer to 0.1% in Mossoró winter).



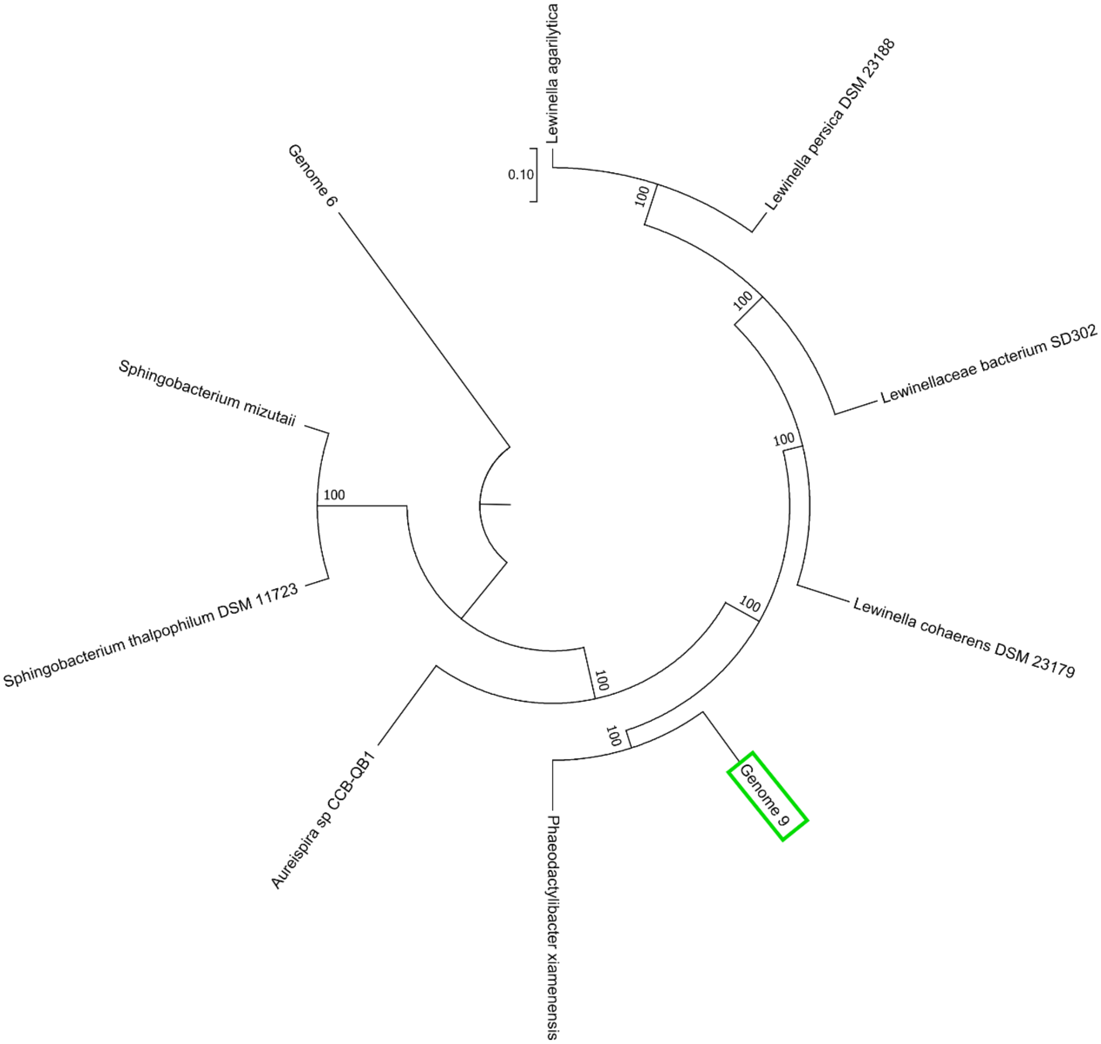
Supplementary Figure 2. Metabolic potential of microbial mats from the hypersaline lagoon system of Araruama.



Supplementary Figure 3. Hierarchical clustering and bar plots of relative abundances of the major bacterial genera found within 68 metagenomes of microbial mats from different habitats. Clustering was based on Euclidian distances and Ward's clustering method.



Supplementary Figure 4. Maximum likelihood phylogenetic tree placing the metagenome-assembled Bin6, a purple sulfur Chromatiaceae bacteria, from the hypersaline lagoon system of Araruama. The tree was inferred from the concatenation of 43 conserved gene sequences from the reconstructed genome and publicly available microbial genomes.



Supplementary Figure 4. Maximum likelihood phylogenetic tree placing the metagenome-assembled Bin9, a bacteria belonging to the Saprospiraceae family, from the hypersaline lagoon system of Araruama. The tree was inferred from the concatenation of 43 conserved gene sequences from the reconstructed genome and publicly available microbial genomes.

2.2 Supplementary Tables

Supplementary Table 2. General characterization and MG-RAST IDs of the 68 metagenomes used in this study.

MG-RAST ID	Location	Samples	Reference
4576345.3	Araruama Lagoon	Araruama Brejo|s	This study
4576354.3	Araruama Lagoon	Araruama Silva|s	This study
4576344.3	Araruama Lagoon	Araruama Silva|w	This study
4576353.3	Araruama Lagoon	Araruama Sal Cisne|s	This study
4576351.3	Araruama Lagoon	Araruama Brejo|w	This study
4576355.3	Araruama Lagoon	Araruama Mossoro|s	This study
4576352.3	Araruama Lagoon	Araruama M Alto|w	This study
4576346.3	Araruama Lagoon	Araruama Mossoro|w	This study
4576347.3	Araruama Lagoon	Araruama M Alto|s	This study
4576349.3	Araruama Lagoon	Araruama BR|w	This study
4576350.3	Araruama Lagoon	Araruama L Vermelha|w	This study
4576356.3	Araruama Lagoon	Araruama Queira|s	This study
4576348.3	Araruama Lagoon	Araruama Sal Cisne|w	This study
4561212.3	Abrolhos Bank, Brazil	Abrolhos PL 1|m	Walter et al., 2016
4561207.3	Abrolhos Bank, Brazil	Abrolhos PL 2|m	Walter et al., 2016
4561206.3	Abrolhos Bank, Brazil	Abrolhos PL 3|m	Walter et al., 2016
4561211.3	Abrolhos Bank, Brazil	Abrolhos PL 4|m	Walter et al., 2016
4561210.3	Abrolhos Bank, Brazil	Abrolhos AR 1|m	Walter et al., 2016
4561205.3	Abrolhos Bank, Brazil	Abrolhos AR 2|m	Walter et al., 2016
4561203.3	Abrolhos Bank, Brazil	Abrolhos AR 3|m	Walter et al., 2016
4561213.3	Abrolhos Bank, Brazil	Abrolhos AR 4|m	Walter et al., 2016
4561208.3	Abrolhos Bank, Brazil	Abrolhos PAB 2|m	Walter et al., 2016
4561202.3	Abrolhos Bank, Brazil	Abrolhos PAB 3|m	Walter et al., 2016
4561209.3	Abrolhos Bank, Brazil	Abrolhos PAB 4|m	Walter et al., 2016
4564639.3	Abrolhos Bank, Brazil	Abrolhos PL 2|o	Walter et al., 2016
4564642.3	Abrolhos Bank, Brazil	Abrolhos PL 4|o	Walter et al., 2016
4564647.3	Abrolhos Bank, Brazil	Abrolhos AR 1|o	Walter et al., 2016
4564646.3	Abrolhos Bank, Brazil	Abrolhos AR 2|o	Walter et al., 2016

4564644.3	Abrolhos Bank, Brazil	Abrolhos AR 3|o	Walter et al., 2016
4564648.3	Abrolhos Bank, Brazil	Abrolhos PAB 1|o	Walter et al., 2016
4564643.3	Abrolhos Bank, Brazil	Abrolhos PAB 2|o	Walter et al., 2016
4564645.3	Abrolhos Bank, Brazil	Abrolhos PAB 3|o	Walter et al., 2016
4440964.3	Baja California Sur, Mexico	Guerrero Negro 0-1mm	Harris et al., 2013
4440963.3	Baja California Sur, Mexico	Guerrero Negro 1-2mm	Harris et al., 2013
4440965.3	Baja California Sur, Mexico	Guerrero Negro 2-3mm	Harris et al., 2013
4440966.3	Baja California Sur, Mexico	Guerrero Negro 3-4mm	Harris et al., 2013
4440967.3	Baja California Sur, Mexico	Guerrero Negro 4-5mm	Harris et al., 2013
4440969.3	Baja California Sur, Mexico	Guerrero Negro 5-6mm	Harris et al., 2013
4440970.3	Baja California Sur, Mexico	Guerrero Negro 6-10mm	Harris et al., 2013
4440968.3	Baja California Sur, Mexico	Guerrero Negro 10-22mm	Harris et al., 2013
4440971.3	Baja California Sur, Mexico	Guerrero Negro 22-34mm	Harris et al., 2013
4440972.3	Baja California Sur, Mexico	Guerrero Negro 34-49mm	Harris et al., 2013
4674239.3	Clinton Creek, Canada	Clinton Creek biofilm	Unpublished (McCormick M)
4674238.3	Clinton Creek, Canada	Clinton Creek biofilm	Unpublished (McCormick M)
4441363.3	Cuatro Cienegas, Mexico	Cuatro Cienegas green mat	Breitbart et al., 2009
4442467.3	Cuatro Cienegas, Mexico	Cuatro Cienegas red mat	Breitbart et al., 2009
4440060.4	Cuatro Cienegas, Mexico	Rio Mesquites microbialite	Breitbart et al., 2009
4460448.3	Diamond Fork Utah, USA	Diamond Fork biofilm	Gomez-Alvarez et al., 2012
4460449.3	Diamond Fork Utah, USA	Diamond Fork biofilm	Gomez-Alvarez et al., 2012
4440061.3	Highborne Cay Island, Bahamas	Highborne Cay microbialite	Dinsdale et al., 2008
4683415.3	Lake Meyghan, Iran	Lake Meyghan green	Naghoni et al., 2017
4683416.3	Lake Meyghan, Iran	Lake Meyghan red	Naghoni et al., 2017
4683417.3	Lake Meyghan, Iran	Lake Meyghan white	Naghoni et al., 2017
4460441.3	Neutral Zone, Norway	Norway hydrothermal vent mat	Stokke et al, 2015
4548349.3	Schiermonnikoog, The Netherlands	Schiermonnikoog tidal mat	Bolhuis and Stal, 2011
4548350.3	Schiermonnikoog, The Netherlands	Schiermonnikoog intermediate mat	Bolhuis and Stal, 2011

4761319.3	Shark Bay, Australia	Shark Bay smooth mat	Wong et al., 2018; Ruvindy et al., 2016
4761321.3	Shark Bay, Australia	Shark Bay smooth mat	Wong et al., 2018; Ruvindy et al., 2016
4761322.3	Shark Bay, Australia	Shark Bay smooth mat	Wong et al., 2018; Ruvindy et al., 2016
4761314.3	Shark Bay, Australia	Shark Bay smooth mat	Wong et al., 2018; Ruvindy et al., 2016
4761316.3	Shark Bay, Australia	Shark Bay smooth mat	Wong et al., 2018; Ruvindy et al., 2016
4761325.3	Shark Bay, Australia	Shark Bay smooth mat	Wong et al., 2018; Ruvindy et al., 2016
4443745.3	Yellowstone, USA	Mushroom Springs mat core A	Bolhuis et al., 2014
4443746.3	Yellowstone, USA	Mushroom Springs mat core B	Bolhuis et al., 2014
4443747.3	Yellowstone, USA	Mushroom Springs mat core D	Bolhuis et al., 2014
4443762.3	Yellowstone, USA	Mushroom Springs mat core F	Bolhuis et al., 2014
4443749.3	Yellowstone, USA	Octopus Springs mat core F	Bolhuis et al., 2014
4443750.3	Yellowstone, USA	Octopus Springs mat core R	Bolhuis et al., 2014

Supplementary Table 2. Summary of individual metagenome-assembled genomes obtained from the microbial mats metagenomes of the hypersaline lagoon system of Araruama. Taxonomy of Chromatiaceae family: Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales. Taxonomy of Saprospiraceae family: Bacteria, Bacteroidetes, Sphingobacteria, Sphingobacteriales.

MAG	Family	Estimated Genome size (Mbp)	Number of Contigs	G+C Content (%)	Estimated Completeness (%)	Estimated Contamination (%)	CDS Number
Bin6	Chromatiaceae	3.7	661	66.7	91.59	4.49	3,302
Bin9	Saprospiraceae	3.7	678	58.6	87.98	4.73	3,305

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