SUPPLEMENTAL RESULTS AND DISCUSSION

Supp. Table 1. Predicted diversity coverage and inverse Simpson indices of 16S rRNA gene sequences recovered from microbialites-associated mat communities in seven locations from the SA of GSL.

Location	Average Coverage	Average Inverse Simpson
BB	0.90	32.4
BP	0.90	46.4
R	0.90	34.2
SI	0.89	29.6
SP	0.89	30.8
WE	0.91	35.4
WW	0.87	39.9

Abbreviations: BB, Bridger Bay; BP, Bison Point; R, Ridges; SI, Stansbury Island; SP, Stansbury Polygons; WE, Windward East; WW, Windward West.

Supp. Table 2. Bray-Curtis dissimilarity indices of community compositions recovered from seven sites in the SA of GSL. Bray-Curtis distances were calculated using the relative abundances of SSU rRNA gene OTUs as defined at 97% sequence similarity.

	BB	**BP**	**R**	**SI**	**SP**	**WE**	**WW**
BB	1.00	0.77	0.85	0.84	0.85	0.89	0.87
BP		1.00	0.71	0.70	0.70	0.79	0.77
R			1.00	0.82	0.91	0.80	0.80
SI				1.00	0.83	0.79	0.86
SP					1.00	0.78	0.81
WE						1.00	0.84
WW							1.00

Abbreviations: BB, Bridger Bay; BP, Bison Point; R, Ridges; SI, Stansbury Island; SP, Stansbury Polygons; WE, Windward East; WW, Windward West.

Supp. Table 3. Bray Curtis dissimilarity of the taxonomic composition of seven Great Salt Lake (GSL) microbialite communities and the average (Avg) GSL microbialite community calculated after organizing 16S rRNA gene sequences at the order level of taxonomic classification.

	Avg	**BB**	**BP**	**R**	**SI**	**SP**	**WE**	**WW**
Avg	1.00	0.92	0.87	0.90	0.92	0.92	0.91	0.91
BB		1.00	0.84	0.88	0.87	0.87	0.93	0.88
BP			1.00	0.80	0.82	0.82	0.84	0.82
R				1.00	0.87	0.92	0.86	0.84
SI					1.00	0.89	0.85	0.90
SP						1.00	0.84	0.86
WE							1.00	0.87
WW								1.00

Abbreviations: BB, Bridger Bay; BP, Bison Point; R, Ridges; SI, Stansbury Island; SP, Stansbury Polygons; WE, Windward East; WW, Windward West.

Supp. Table 4. Sequencing statistics associated with the Bridger Bay, Great Salt Lake, Utah, microbialite mat metagenome and its assembly.

Read Lengths	2x125
# Reads (Post Quality Filter)	79,692,256
Total Sequencing (bp)	10,026,675,156
# Contigs	212,139
Contig no. > 1 kbp	71,830
Longest Contig	233,003
Total Assembly Size	354,039,636
Assembly size > 1 kbp	284,850,691
N50	5,244

SUPPLEMENTAL RESULTS AND DISCUSSION

Bin 1: *Euhalothece* (Cyanobacteria; Chroococcales)

Estimated genome size = 4.82 Mb; completeness = 98.3%; contamination = 0.0%; abundance within community = 12.2%.

The beta subunit of the DNA directed RNA polymerase (RpoB) in the most abundant MAG from the microbialite metagenome (**Fig. 3A**) shared 97% sequence identity to that of *Euhalothece* sp. PCC 7418. The genus *Euhalothece* comprises thermo- and halotolerant members within the order Chroococcales (1). Consistent with the dominance of this MAG in the hypersaline GSL metagenome, *Euhalothece* spp. were also shown to be dominant members of microbial communities in several hypersaline environments including estuaries in South Africa (1) and salt lakes in India (2), among others. The *Euhalothece* GSL MAG encodes a complete Calvin cycle, both photosystems I and II, and pathways for fermentation of pyruvate into formate, lactate, and acetate. Further, *Euhalothece* encodes a molybdenum (Mo)-dependent nitrogenase (NifHDKENB) (**Supp. Dataset 2**). The presence of a molybdate importer and machinery for synthesizing the active site iron-molybdenum cofactor of Mo-nitrogenase is consistent with this population being capable of nitrogen fixation. This indicates that *Euhalothece* likely supplies both fixed carbon and nitrogen for secondary consumers in GSL, a finding that supports previous suggestions that this taxon is a keystone species in the GSL ecosystem (3). The GSL *Euhalothece* MAG also encodes a bidirectional type 3d [NiFe]-hydrogenase (HoxUFE), indicating a general ability to metabolize H_2 (4). The ability of this population to catalyze reversible H_2 oxidation via [NiFe]-hydrogenase is supported by the

detection of homologs of proteins involved in the synthesis of the [NiFe] active site as well as nickel import proteins. Hydrogenase may allow *Euhalothece* to re-capture H_2 generated as a byproduct of nitrogen fixation activity, or may function to regenerate oxidized pyridine nucleotides that accumulate when these cells ferment organic carbon reserves at night (5). The NifD protein from the GSL *Euhalothece* MAG clusters phylogenetically with NifD genes from canonical nitrogen fixing cyanobacteria including *Trichodesmium erythraeum* (data not shown), which temporally segregates the O_2 sensitive process of N_2 fixation from oxygenic photosynthesis by only fixing N_2 at night (6). This suggests that the GSL *Euhalothece* population may also temporally segregate N_2 fixation. Further, the GSL *Euhalothece* MAG encodes CikA, Pex, KaiA, KaiB, KaiC, and SASa, genes required for circadian timing (7). In addition, this MAG encodes xanthorhodopsin, a retinal-based green-light absorbing proton pump (8), and for apocarotenoid-15,15' oxygenase, a protein that synthesizes retinal (9). This suggests this to be an additional mechanism allowing it to generate an electrochemical gradient across the membranes of these cells (8). Other pathways encoded by this MAG include two-component signaling, quorum sensing, and carbohydrate secretory systems, the latter of which may function to facilitate cross-feeding of secondary consumers in the community and thus contribute to microbialite community structure and function.

Bin 2: *Fabibacter* (Bacteroidetes; Bacteroidetes Order II. Incertae sedis)

Estimated genome size = 3.34 Mb; completeness = 94.8%; contamination = 1.7%; abundance within community = 9.3%.

The second most abundant MAG (**Fig. 3A**; 9.3% of total reads) in the GSL microbialite metagenome is distantly related (60% RpoB identity) to the genus *Fabibacter* within the Bacteroidetes Order II. Incertae sedis. The *Fabibacter*-affiliated MAG encodes complete glycolytic, pentose phosphate, and TCA cycle pathways (**Supp. Dataset 2**). The closest cultured representative, *F. pacificus,* was shown to be obligately aerobic (10). Consistent with this, the GSL MAG encodes homologs for cytochrome *c* oxidase (complex IV), indicating it too may respire O_2. This MAG can likely use starch as a carbon source and electron donor based on the presence of homologs of isoamylase that hydrolyze starch into maltodextrin. Maltodextrin can then be hydrolyzed to maltose and glucose by alpha amylase. Maltodextrin can also be hydrolyzed to yield glucose polymers by maltodextrin glucosidase. This organism may also utilize glycerolipids and fatty acids as sources of carbon and electrons as evidenced by the MAG encoding multiple lipases, including triacylglycerol lipase, and fatty acid degradation pathways. The GSL MAG does not encode glycerate 2-kinase for entry of glycerate from glycerol metabolism into glycolysis but it does encode other enzymes that allow for processing glycerol into glycerate. Thus, it is unclear if this MAG can utilize glycerol as a carbon and/or energy source, like has been demonstrated for *F. pacificus* (10). The GSL MAG encodes pathways for the degradation of leucine and isoleucine as other potential reduced carbon sources accessible to this population. In addition, homologs for sodium ion-transporting rhodopsin (11) and halorhodopsin, a retinal-based green/yellow light-absorbing unidirectional chloride pump (12), were identified. This suggesting the organism can use light to maintain its cytoplasmic osmotic balance. Collectively, these observations point to the *Fabibacter*-affiliated GSL population as being an aerobic photoheterotroph that is cross-fed reduced carbon compounds that serve as sources of carbon and reductant.

Bin 3: *Longibacter* (Bacteroidetes; Bacteroidetes Order II, *Incertae sedis*)

Estimated genome size = 4.05 Mb; completeness = 88.8%; contamination = 1.4%; abundance within community = 5.8%.

A MAG was recovered from the GSL microbial mat that was most closely affiliated (97% RpoB identity) with *L. salinarum* and this MAG comprised 5.8% of the total reads (**Fig. 3A**). The detection of sequences affiliated with *L. salinarum* in hypersaline GSL is consistent with the environment where the type strain was isolated: a marine solar saltern in China (13). Moreover, the type strain was shown to grow over a salinity range of 5-20% (14), which is similar to the salinity of GSL waters (14.5 to 17.0%) when mat samples for the metagenome were collected. The MAG encoded nearly complete glycolysis, pentose phosphate, and starch/sucrose degradation pathways but did not encode any known autotrophic pathways (**Supp. Dataset 2**). The MAG also encodes for xanthorhodopsin, a retinal-based green-light absorbing proton pump (8), and for β-carotene 15,15′-dioxygenase, a protein involved in the synthesis of the carotenoid salinixanthin (15). This suggests a possible role in supplementing the generation of electrochemical gradients across the membrane of the cell. The organism also encoded cytochrome *c* oxidase (complex IV) but did not encode other protein complexes (e.g., nitrate reductase) allowing for anaerobic respiration. Together, these data suggest that the organism is an aerobic photoheterotroph. To this end, the predicted metabolism of the GSL *Longibacter*-affiliated population is consistent with previous studies of the type strain that showed that aerobic growth of the organism was supported by oxidation of glycerol, sucrose, starch, and mannitol (13), however, it differs in the suggested ability to use light.

Bin 4: *Pelagibaca* (Proteobacteria; Rhodobacterales)

Estimated genome size = 3.00 Mb; completeness = 86.2%; contamination = 0.0%; abundance within community = 3.7%.

A MAG closely affiliated with *P. abyssi* (94% 50S ribosomal protein L2 identity) and that represented 5.8% of the total reads was identified in the GSL microbial mat metagenome (**Fig. 3A**). Consistent with its detection within GSL mats, the type strain of *P. abyssi* was isolated from a marine habitat and exhibited growth across a range of salinities (5 to 13%) (16). The type strain was reported as an aerobic heterotroph. Consistent with this report, the GSL *P. abyssi* MAG encodes cytochrome *c* oxidase (complex IV) and lacked homologs of other identifiable protein complexes that would allow for respiration of additional oxidants such as nitrate or sulfate (**Supp. Dataset 2**). Homologs for nearly complete TCA, glycolytic, and pentose phosphate pathways were also identified in the GSL MAG. Like the genome of *P. abyssi*, the GSL MAG encodes a wide range of carbohydrate, oligopeptide, and amino acid transporters, suggesting it can import and degrade organic carbon substrates (17). Specific carbohydrate transporters identified in the MAG include those for maltose/maltodextrin, raffinose/stachyose/melibiose, and glucose/mannose. Maltose is possibly hydrolyzed to glucose by alpha-glucosidase and raffinose/stachyose/melibiose could be hydrolyzed to glucose by alpha-galactosidase; glucose released from these hydrolysis reactions could then enter glycolysis. Alternatively, homologs of an ABC transporter for glucose/mannose could allow glucose to enter glycolysis in the absence of a phosphotransferase system for this sugar. Additional ABC transporters were identified for alpha-glucoside, ribose/xylose, sn-glycerol-3-phosphate and

phospholipids. In addition, two of the three genes for transport of urea were identified. The type strain was shown to encode the Calvin cycle allowing for CO_2 fixation, with electrons likely coming from thiosulfate oxidation via the Sox system (17). However, while the GSL MAG encodes for the Sox system, it does not encode for the Calvin Cycle or any other autotrophic pathways. This suggests an ability to oxidize thiosulfate to potentially supplement heterotrophic growth in what has been described as chemolithoheterotrophy (18). Intriguingly, the GSL MAG encodes an antenna complex, bacteriochlorophyll biosynthesis genes, and photosynthetic reaction center L, M and H, which could also supplement heterotrophic growth through what has been described as aerobic anoxygenic photoheterotrophy.

Bin 5: *Wenzhouxiangella* (Proteobacteria; Chromatiales)

Estimated genome size = 2.94 Mb; completeness = 82.8%; contamination = 1.7%; abundance within community = 3.1%.

A MAG closely affiliated to *Wenzhouxiangella sediminis* (96% RpoB identity) that accounts for 3.1% of the total reads was identified in the GSL microbialite mat metagenome (**Fig. 3A**). The MAG encodes cytochrome *c* oxidase (complex IV), which when combined with the absence of other canonical protein complexes that allow for anaerobic respiration (e.g., nitrate reductases; **Supp. Dataset 2**), suggests the population to be aerobic. This agrees with previous characterizations of closely related strains that were also shown to be aerobes . The MAG encodes an incomplete glycolytic pathway and lacks homologs of glucose-6-phosphate isomerase, phosphofructokinase, diphosphate--fructose-6-phosphate 1-phosphotransferase, and aldose reductase, suggesting a limited ability to metabolize sugars. However, the MAG encodes

a complete TCA cycle suggesting that the organism may be acquiring acetyl-CoA via pathways other than glycolysis. Perhaps consistent with this hypothesis, the GSL MAG encodes fructose 1,6-bisphosphatase, an enzyme that functions in gluconeogenesis. The MAG has all the genes required for the transport of oligopeptides and encodes valine, leucine, and isoleucine degradation pathways. When taken together, these data suggest that the bacterium may acquire acetyl-CoA for biosynthesis via amino acid degradation. The presence of phospholipid transport genes also points toward the possibility of lipid degradation as a source of carbon and reductant. Consistent with this hypothesis, fatty acid degradation pathways are encoded by the MAG. Considering that an endpoint of fatty acid degradation is acetyl-CoA, the genome data provide a possible path for how this organism may be acquiring acetyl-CoA.

Interestingly, the MAG encodes several proteins that form photosystem II, reaction center proteins PufM, PufL, PufC, PucC, PuhE, PuhA and alpha/beta subunits of an antenna complex. It also encodes most of the proteins required for the biosynthesis of the carotenoid, spheroidene, which forms a complex with the reaction center in *Rhodobacter sphaeroides* (19). It is unlikely that the organism can synthesize bacteriochlorophyll, however, since the MAG lacks most of the proteins required including dark-operative protochlorophyllide oxidoreductase (DPOR; BchLNB) and chlorophyllide *a* oxidoreductase (COR; BchXYZ) (20). Intriguing, the MAG encodes the large subunit of RuBisCO but not the small subunit. When taken together, the genome data suggests this organism is a facultative anaerobe and heterotroph that relies on amino acid and fatty acid degradation to generate ATP and acquire carbon. The incomplete glycolytic pathway might indicate that this aerobic organism specializes in utilizing select amino and fatty acids to minimize niche overlap with co-inhabiting heterotrophs that utilize sugars to

support their energy metabolism**s.** The presence of reaction center proteins and an antenna complex but no Calvin Cycle suggest that the organism may also be capable of anoxygenic photoheterotrophic carbon assimilation.

Bin 6: *Arboriscoccos* (Proteobacteria; Geminicoccales)

Estimated genome size = 3.36 Mb; completeness = 99.7%; contamination = 3.6%; abundance within community = 2.9%.

A MAG distantly affiliated (80% RpoB identity) with *Arboriscoccos pini* (21) was identified in the GSL metagenome and it comprised 2.9% of the total reads (**Fig. 3A**). The MAG encodes nearly complete glycolytic and pentose phosphate pathways, as well as the TCA cycle (**Supp. Dataset 2**). The MAG also encodes transporters for glycerol, lipoproteins, and lipopolysaccharides and encodes pathways allowing for starch metabolism, a hallmark of other closely related alphaproteobacterial (e.g., *A. pini* and free-living *Geminicoccus roseus* and *Alysiosphaera europaea*) (21-23). The MAG also encodes for a bidirectional [NiFe]-hydrogenase, suggesting an ability to reversibly oxidize H_2 (4). The MAG also encodes for cytochrome *c* oxidase (complex IV) and the supporting proteins necessary for oxidative phosphorylation. The MAG encodes a homolog of xanthorhodopsin, a retinal-based green-light absorbing proton pump (8). To this end, the MAG appears to be an aerobic photoheterotroph with the capacity to use oxygen as its terminal electron acceptor to metabolize sugars and starch.

Bin 7: *Roseibaca* (Proteobacteria; Rhodobacteriales)

Estimated genome size = 2.58 Mb; completeness = 82.8%; contamination = 2.6%; abundance within community = 2.2%.

A MAG closely affiliated with *Roseibaca calidilacus* (93% 50S rRNA sequence identities) within the proteobacterial order Rhodobacteriales was identified in the metagenome, representing 2.2% of the total reads (**Fig. 3A**). These findings are consistent with previous studies that identified *Roseibaca* to be abundant components of waters and phototroph mats from hypersaline, alkaline habitats [e.g., (24)]. The GSL *Roseibaca* MAG encodes full glycolytic, TCA, and pentose phosphate (PP) pathways, as well as transporter for xylose that can be input into the PP pathway (**Supp. Dataset 2**). Other homologs of transport systems identified in the MAG include those for urea, glucose, glycerol, lipoproteins, and lipopolysaccharides. Based on these identified protein homologs and the absence of homologs of autotrophic pathways, the bacterium is hypothesized to be a heterotroph. Likewise, the presence of several homologs of cytochrome *c* oxidase (complex IV) and the absence of identifiable pathways for anaerobic respiration, suggests that the GSL *Roseibaca*-affiliated bacterium is aerobic. Intriguingly, this MAG encodes homologs for genes involved in bacteriochlorophyll synthesis but only encodes one reaction center (PufH) homolog. This might be due to the MAG incompleteness (82.8%) and suggests this organism is a photoheterotroph.

Bin 8: *Longibacter* (Bacteroidetes; Bacteroidetes Order II. Incertae sedis)

Estimated genome size = 4.27 Mb; completeness = 87.9%; contamination = 5.9%; abundance within community = 1.9%.

A MAG closely related to *Longibacter salinarum* (84% RpoB identity) was detected in the GSL mat metagenome at an abundance of 1.9% of total reads (**Fig. 3A**). The type strain of *L. salinarum* was isolated in a marine system in China (13) and has been shown to grow over a salinity range of 5-20% (14), which is comparable to conditions within GSL (14-17%, **Table 1**). The MAG encoded a nearly complete glycolytic pathway (exceptions being genes coding for phosphofructokinase and hexokinase), a complete TCA cycle, and a complete pentose phosphate pathway (**Supp. Dataset 2**). Homologs of enzymes involved in autotrophic pathways were not detected. The MAG encodes cytochrome *c* oxidase (complex IV) suggesting an ability to respire O_2 but it does not encode homologs of proteins that would allow it to respire other oxidants. These findings suggest that this MAG is from an aerobic heterotroph. This is consistent with a physiological characterization of the type strain that showed the organism could grow aerobically using glycerol and starch, among other carbon sources (13). In addition, this MAG encodes the enzyme lactate dehydrogenase, which can convert lactate to pyruvate and pyruvate to lactate. This MAG also contains the sequences for lactate utilization suggesting that the bacterium could potentially use lactate as a carbon source (25). Some of the transporters encoded in the MAG include a sodium/glucose co-transporter in addition to amino acid and metal transporters. This MAG does not encode for reaction centers, bacteriochlorophyll biosynthesis genes, or rhodopsins.

Bin 9: *Coraliomargarita* (Verrucomicrobia; Puniceicoccaceae)

Estimated genome size = 4.30 Mb; completeness = 92.2%; contamination = 7.1%; abundance within community = 1.8%.

A MAG distantly related to *Coraliomargarita akajimensis* (78% RpoB identity), a member of the bacterial phylum Verrucomicrobia, order Puniceicoccales, was detected in the GSL at a relative abundance of ~1.8% total reads (**Fig. 3A**). This strain is an obligate aerobe isolated from seawater (26). The GSL MAG encodes complete glycolytic, TCA, and PP pathways. In addition, this MAG encodes cytochrome *c* oxidase (complex IV), suggesting an ability to respire O_2 (**Supp. Dataset 2**). This MAG does not encode homologs for proteins involved in autotrophy. Homologs for transporters for the following reduced organic carbon compounds are encoded in this MAG: polysaccharides, lipopolysaccharides, lipoproteins, glycine betaine/proline, oligopeptides, and a sodium/glucose cotransporter. This MAG may utilize fructose by first converting it to glucose using the encoded xylose isomerase. Glycogen can be phosphorylated to 1P-glucose by the encoded glycogen phosphorylase or converted to maltose and dextrin by the encoded alpha-amylases, and sucrose can be converted to fructose by alpha-glucosidase. The potential for fermentation is suggested by the presence of alcohol dehydrogenase and the ability to convert acetate to acetyl-CoA. Moreover, a suite of enzymes allowing for the conversion of propanoate to propanoyl-CoA, which can be converted to succinyl CoA or succinate to feed other metabolic pathways, are also encoded by the GSL MAG. It may also be possible for this population to reduce nitrous oxide, as a homolog for nitrous oxide reductase was encoded in this MAG; however, no other denitrification genes were identified. In addition, this MAG encodes for β-carotene 15,15'-dioxygenase, a protein involved in the synthesis of the carotenoid salinixanthin (15), and for two proteorhodopsinss: one is a homolog of xanthorhodopsin, a retinal-based green-light absorbing proton pump (8), and the other is a homolog of the partially characterized blue-light absorbing rhodopsin (27). Either of these likely allow the organism to support the generation of an electrochemical gradient across its membrane

using light (8). Altogether, these observations suggest that this population is a facultative anaerobic photoheterotroph.

Bin 10: *Psychroflexus* (Bacteroidota; Flavobacteriales)

Estimated genome size = 2.58 Mb; completeness = 98.3%; contamination = 1.7%; abundance within community = 1.8%.

A MAG closely affiliated (100% RpoB identity) with *Psychroflexus* sp. WDS2C27, a member of the bacterial order Flavobacteriales, was detected in the GSL metagenome where it comprised 2.29% of the total reads (**Fig. 3A**). The detection of sequences affiliated with *Psychroflexus* in hypersaline GSL is consistent with the detection of related strains in hypersaline lakes (28), salt pans (29), among other brine habitats [e.g., (30)]. The GSL *Psychroflexus* MAG encodes near complete glycolysis and TCA pathways and lacks evidence for autotrophic metabolism (**Supp. Dataset 2**). The MAG also encodes cytochrome *c* oxidase (complex IV) but did not encode other canonical protein complexes that would allow it to respire other oxidants such as nitrate or sulfate. Additionally, the organism encodes a homolog of a rhodopsin, allowing the bacterium to use light to generate/supplement an electrochemical gradient that could be used to drive ATP synthesis or to perform work. The MAG encodes a group 2a [NiFe] Hydrogenase, suggesting a generalized ability to metabolize H_2 as a source of reductant (4). Together, these data suggest that the organism is an aerobic photoheterotroph

Bin 11: *Henriciella* (Proteobacteria; Caulobacterales)

Estimated genome size = 2.49 Mb; completeness = 87.9%; contamination = 0.0%; abundance within community = 1.6%.

A MAG that is related (88% RpoB identity) to *Henriciella pelagia* accounted for 1.6% of the total reads (**Fig. 3A**). Like *H. pelagia* which was classified as oxidase positive (31), the GSL MAG encodes cytochrome *c* oxidase (complex IV) (**Supp. Dataset 2**). Homologs of protein complexes allowing for anaerobic respiration (e.g., nitrate reductase, bisulfite reductase) were not identified. The MAG encodes a full glycolytic and TCA cycle but does not encode autotrophic pathways. Together, these observations suggest that the bacterium is an aerobic heterotroph. The MAG encodes alpha-amylase that converts starch into glucose and maltose as well as maltase that converts maltose into glucose. These data suggest that the organism utilizes starch. Interestingly, the MAG encodes for xanthorhodopsin, a retinal-based green-light absorbing unidirectional proton pump (8). Xanthorhodopsin is a retinal protein/carotenoid complex (8) and the MAG encodes β-carotene 15,15'-dioxygenase that is involved in the synthesis of the carotenoid salinixanthin (15), suggesting that one of the ways that the organism is generating an electrochemical gradient is via light energy. Overall, the bacterium represented by this MAG is likely an aerobic photoheterotroph.

Bin 12: *Rhodohalobacter* (Bacteroidota; Balneolales)

Estimated genome size = 3.81 Mb; completeness = 66.8%; contamination = 6.0%; abundance within community = 1.5%.

A MAG closely affiliated (91% RpoB) with *Rhodohalobacter halophilus* that represented 1.5% of the total reads was identified in the GSL microbial mat (**Fig. 3A**). *Rhodohalobacter halophilus*, the first species identified for this genus, was isolated from seawater and is reported as a halophilic heterotroph and facultative anaerobe capable of fermenting carbohydrates (32). The GSL *Rhodohalobacter halophilus* MAG encodes cytochrome *c* oxidase (complex IV), suggesting the ability to respire O_2 (**Supp. Dataset 2**). A homolog for nitrous-oxide reductase, which converts N_2O to N_2, was also identified suggesting the possibility for anaerobic respiration (33). Partially complete TCA, glycolytic, and pentose phosphate pathways were also identified, which may be due to the incompleteness of the MAG (66.8% complete). Homologs for phospholipid and ribose transporters were also identified. The former could be degraded by the nearly complete fatty acid degradation pathway while the latter could be metabolized through the pentose phosphate pathway. The ability to ferment pyruvate to acetate is suggested by the detection of homologs of phosphotransacetylase and acetate kinase. Homologs for autotrophic carbon fixation pathways were not detected. A fragment of a halorhodopsin homolog was identified in this MAG. Halorhodopsins are retinal-based green/yellow light-absorbing unidirectional chloride pumps that might enable this organism to maintain cytoplasmic osmotic balance (12). Thus, these observations suggest that *Rhodohalobacter halophilus* MAG is a photoheterotroph and possibly a facultative anaerobe, pending the strains ability to respire N_2O or ferment organic compounds.

Bin 13: *Rhodohalobacter* (Bacteroidetes; Balneolales)

Estimated genome size = 3.79 Mb; completeness = 93.1%; contamination = 0.0%; abundance within community = 1.3%.

A MAG closely affiliated (96% RpoB identity) to *Rhodohalobacter halophilus* (bacterial order Balneolales) represented 1.3% of the total reads (**Fig. 3A**). The MAG encodes nearly complete glycolysis, gluconeogenesis, pentose phosphate, and TCA cycle pathways (**Supp. Dataset 2**). It also encodes cytochrome *c* oxidase (complex IV), a key enzyme complex involved in respiration of O_2. The MAG lacks evidence for autotrophic pathways or protein complexes that allow for anaerobic respiration. However, the MAG encodes alcohol dehydrogenase and five other key enzymes required for fermentation, suggesting the possibility that it can ferment organic carbon substrates. These findings are consistent with the previous characterizations of members of this genus as facultative anaerobes (32) and supports the notion that this GSL population can survive under oxic and anoxic conditions. The ability to ferment and thus metabolize organic carbon substrates under anoxic conditions potentially differentiates this bacterium from the other putatively aerobic heterotrophs in the mat community. This MAG also encodes halorhodopsin, a retinal-based green/yellow-light absorbing chloride pump that could support cytoplasmic osmotic balance through the use of light (12). These observations suggest this organism is a facultative anaerobic photoheterotroph.

Bin 14: *Thiohalocapsa* (Proteobacteria; Chromatiales)

Estimated genome size = 4.28 Mb; completeness = 98.3%; contamination = 0.0%; abundance within community = 1.3%.

A MAG closely related (93% RpoB identity) to *Thiohalocapsa* sp. ML 1 represented 1.3% of total reads in the GSL mat metagenome (**Fig. 3A**). *Thiohalocapsa* is commonly

identified in anoxic, sulfidic environments (34). The GSL *Thiohalocapsa* shows many genomic similarities to *Thiohalocapsa* sp. ML1 (34, 35) including encoding complete glycolytic and TCA cycles (**Supp. Dataset 2**). Consistent with the genus *Thiohalocapsa* comprising anoxygenic phototrophs (36), the GSL MAG encodes photosynthetic reaction centers proteins L, M, and H, as well as genes required to synthesize bacteriochlorophyll (BchLNBXYZ). The MAG also encodes phosphoribulokinase which is involved in the Calvin Cycle. However, homologs of Type I or Type II ribulose-1,5- bisphosphate carboxylase oxygenase (CbbS and CbbM, respectively) were not detected in the MAG. A BLASTp search of unbinned contigs identified homologs of CbbSL and CbbM that exhibited close identities (95%, 86%, and 85%, respectively) to homologs from *Thiocapsa* sp. ML 1, suggesting that the GSL *Thiohalocapsa* strain is capable of CO_2 fixation via the Calvin Cycle. Based on genomic data, the most likely electron donor fueling anoxygenic photosynthesis is sulfide, which can be oxidized by sulfide:quinone oxidoreductase encoded in the GSL MAG. Sulfide is likely supplied to this bacterium by sulfate reducing bacteria that are widely distributed in sediments and anoxic zones in GSL (37, 38). The GSL MAG also encodes Mo-nitrogenase and all of the proteins needed for dissimilatory nitrate reduction/denitrification (i.e., NapAB). Cytochrome *cbb3* oxidase, which is typically only expressed in microorganisms living in microaerobic or anoxic conditions (39), was also identified in the MAG. Additionally, the MAG contains the enzymes for the fermentation of pyruvate to acetate. These enzymes include pyruvate dehydrogenase, phosphotransacetylase, and acetate kinase. Thus, the organism is hypothesized to be either an anaerobe or to be facultatively anaerobic and is capable of anoxygenic photosynthesis.

Bin 15: *Coraliomargarita* (Verrucomicrobia; Puniceicoccales)

Estimated genome size = 2.71 Mb; completeness = 93.1%; contamination = 8.6%; abundance within community = 1.2%.

A MAG closely related (80.6% RpoB identity) to *Coraliomargarita akajimensis* that represented 1.2% of the total reads was identified in the GSL microbial mat (**Fig. 3A**). Previous physiological characterizations indicate *C. akajimensis* is an obligately aerobic heterotroph (26). Unlike the genome of *C. akajimensis*, the GSL MAG does not encode a complete glycolytic pathway but might be able to assimilate glycerate-3P via a complete gluconeogenesis pathway (**Supp. Dataset 2)**. This population may obtain glycerate-3P from CO_2 fixed via the Calvin cycle. The GSL MAG encodes complete TCA and pentose phosphate pathways. Like *C. akajimensis*, the GSL MAG appears capable of utilizing fructose based on encoded homologs for fructokinase, phospofructokinase, and xylose isomerase. This MAG can also convert lactose to glucose and galactose via β-galactosidase. This MAG encodes a sodium/glucose cotransporter and a suite of subunits for the ABC oligopeptide transport system. This MAG encodes several, but not all, subunits for a cytochrome *c* oxidase making it unclear if it can respire O_2 like *C. akajimensis* (26). The GSL population appears capable of fermentation by the encoded alcohol dehydrogenase, lactate dehydrogenase, and malate dehydrogenase. This organism can also convert acetate to acetyl-CoA by acetyl-CoA synthetase. In addition, a group 3d (bidirectional) NiFe hydrogenase is encoded in the MAG suggesting the ability to reversibly transform H_2. The fitness of the organism is likely enhanced by xanthorhodopsin, a retinal-based green-light absorbing unidirectional proton pump that it may use to support the generation of an electrochemical gradient (8). In addition, this MAG encodes the full suite of genes for the glycine betaine/proline ABC transport system, as well as a chlorine/proton antiporter for

maintaining osmotic balance. Together, these observations suggest this GSL *Coraliomargarita*-affiliated population to be a facultative autotroph capable of fermentation and phototrophy.

Bin 16: *Wenzhouxiangella* (Proteobacteria; Chromatiales)

Estimated genome size = 1.88 Mb; completeness = 51.7%; contamination = 5.2%; abundance within community = 1.2%.

A MAG closely related to *Wenzhouxiangella sediminis* (97% ribosomal protein S1 identity) was identified that accounted for 1.2% of the total GSL microbialite metagenome sequences (**Fig. 3A**). The MAG encodes two out of three subunits of the cytochrome bd complex, CydA and CydB (**Supp. Dataset 2**). The MAG is 51.7% complete which means it could encode the missing protein (CydX) as well as a complete cytochrome *c* oxidase but these were just not sequenced or they were excluded from the bin during assembly. Indeed, the bin 5 MAG, which is closely related to the bin 16 MAG, encodes a complete cytochrome *c* oxidase and is inferred to be an aerobe (described above). The less complete MAG (bin 16) does not encode pathways allowing for respiration of other electron acceptors such as nitrate. When combined with the finding that the more complete bin (bin 5) appears to be from an aerobe, it is plausible that the less complete MAG also corresponds to an aerobic organism. Like bin 5, the bin 16 MAG encodes an incomplete glycolytic pathway and lacks homologs of glucose-6-phosphate isomerase, phosphofructokinase, and diphosphate-fructose-6-phosphate 1-phosphotransferase. This suggests that the organism cannot metabolize sugars. Interestingly, the MAG encodes endoglucanase that is involved in the hydrolysis of cellulose for use in glycolysis. However, for reasons mentioned above, it is not clear if the organism is capable of glycolysis.

The MAG encodes isocitrate lyase and malate synthase involved in the glyoxylate cycle and this could provide substrates for gluconeogenesis. The MAG encodes a complete TCA cycle but has incomplete valine, leucine, and isoleucine degradation pathways. The MAG encodes most of the genes for phospholipid transport but lacks most of the genes for beta oxidation of fatty acids. Similar to the more complete bin 5, bin 16 encodes for photosystem II including the reaction center proteins PufM, PufL, PufC, PucC, PuhE, PuhA and alpha/beta subunits of an antenna complex. It also encodes most of the proteins required for the biosynthesis of the carotenoid, spheroidene, which forms a complex with the reaction center in *R. sphaeroides* (19). It is unlikely that the organism can synthesize bacteriochlorophyll, however, since the MAG lacks homologs of COR and DPOR (20). In addition, the MAG encodes a fragment of a xanthorhodopsin homolog and a homolog of β-carotene 15,15′-dioxygenase, a protein involved in the synthesis of the carotenoid salinixanthin (15). This suggests that xanthorhodopsin could function to support the generation of an electrochemical gradient across the membrane of the cell using light energy. Intriguing, the MAG encodes the large subunit of RuBisCO but not the small subunit. Thus, the organism could be a facultative aerobe that can perform anoxygenic photoheterotrophic carbon assimilation.

Bin 17: Rhodothermaceae (Bacteroidetes; Bacteroidetes Order II, *Incertae sedis*)

Estimated genome size = 4.07 Mb; completeness = 82.8%; contamination = 3.6%; abundance within community = 1.2%.

A MAG distantly affiliated (77% RpoB identity) with *Rhodothermaceae* bacterium RA was identified that represented 1.2% of the GSL mat community (**Fig. 3A**). *Rhodothermaceae*

bacterium RA is halo- and thermophilic aerobic heterotroph isolated from a saline hot spring (40). The GSL *Rhodothermaceae* MAG encodes near complete glycolysis, TCA cycle, and pyruvate metabolism pathways and lacks homologs of key proteins for anaerobic respiration or autotrophy (**Supp. Dataset 2**). This suggests aerobic heterotrophy and is consistent with a previous characterization of a member of this family (40). Further, this MAG encodes for a sodium ion-pump rhodopsin (11) and for halorhodopsin, a retinal-based green/yellow-light absorbing chloride pump (12). This suggests this organism could be a photoheterotroph that uses light to support the generation of an electrochemical gradient across its membrane and maintain its cytoplasmic osmotic balance.

Bin 18: *Inquilinus* (Proteobacteria; Inquilinaceae)

Estimated genome size = 4.23 Mb; completeness = 98.3%; contamination = 0.0%; abundance within community = 1.2%.

A MAG distantly related (86% RpoB identity) to the bacterium *Inquilinus limosus* (α-proteobacteria; Inquilinaceae) was detected in the GSL mat metagenome (**Fig. 3A**). *I. limosus* was originally isolated from the lung of a cystic fibrosis patient but related sequences have since been identified in hypersaline mats (41). The GSL MAG encodes for glycolysis, the TCA cycle, and pentose phosphate pathways but does not encode for known autotrophic pathways. This suggests the organism is a heterotroph. The MAG encodes for Mo-nitrogenase suggesting it can reduce atmospheric nitrogen for biosynthetic purposes. The MAG also encodes the dissimilatory nitrate reductase suggesting an ability to respire nitrate. A homolog for xanthorhodopsin, a retinal-based green-light absorbing proton pump (8), and a homolog for β-carotene 15,15′-

dioxygenase, a protein involved in the synthesis of the carotenoid salinixanthin (15), were identified. This suggests an ability to use light energy to support the generation of an electrochemical gradient across its cytoplasmic membrane. When combined with the presence of genes encoding cytochrome *c* oxidase (complex IV), the organism is predicted to be a facultative anaerobe photoheterotroph.

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