Supplementary Information

Table S1. Pyrosequencing primers using in diversity analyses.

Name [1]	Primer Sequence [2]
454B-27F	5'-GCCTTGCCAGCCCGCTCAG*TC***AGAGTTTGATCCTGGCTCAG**-3'
454A-338R-C1-T0	5'-GCCTCCCTCGCGCCATCAGAACCAACC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C1-T2	5'-GCCTCCCTCGCGCCATCAGAACGAAGC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C1-T4	5'-GCCTCCCTCGCGCCATCAGCCCCAACC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C1-T6	5'-GCCTCCCTCGCGCCATCAGCCGGCCTT*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C2-T0	5'-GCCTCCCTCGCGCCATCAGGGAATTGG*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C2-T2	5'-GCCTCCCTCGCGCCATCAGAAGGCCTT*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C2-T4	5'-GCCTCCCTCGCGCCATCAGCCTACCGC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C2-T6	5'-GCCTCCCTCGCGCCATCAGCCCGCCAT*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C3-T0	5'-GCCTCCCTCGCGCCATCAGCCAACCTT*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C3-T2	5'-GCCTCCCTCGCGCCATCAGTTCGAAGC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C3-T4	5'-GCCTCCCTCGCGCCATCAGAATACCGC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C3-T6	5'-GCCTCCCTCGCGCCATCAGAACGCCAT*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C4-T0	5'-GCCTCCCTCGCGCCATCAGTTAAGGCC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C4-T2	5'-GCCTCCCTCGCGCCATCAGAAGGAACC*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C4-T4	5'-GCCTCCCTCGCGCCATCAGAAGCAACG*CA***TGCTGCCTCCCGTAGGAGT**-3'
454A-338R-C4-T6	5'-GCCTCCCTCGCGCCATCAGCCTACGCC*CA***TGCTGCCTCCCGTAGGAGT**-3'

Notes: [1] Name reflects the 454 Life Sciences Primer; the location within the 16S rRNA gene; the experimental chamber (C1, C2, C3, C4); and the time period the sample was collected (T0, T2, T4, T6 months). Note the forward primer 454B-27F was used for all samples; [2] Sequence reflects 454 Life Sciences Primer A/B (underlined); eight-base unique barcode; two-base linker (red italics); and the bacterial 16S rRNA gene primer (bold).

Figure S1. Diagrammatic representation of the environmental manipulation chambers. (**A**) Atmospheric gas flow control into the four environmental chambers. CO_2 flow is denoted in green; (**B**) Opto 22 hardware monitoring that controls CO_2 gas flow and records data to database server.

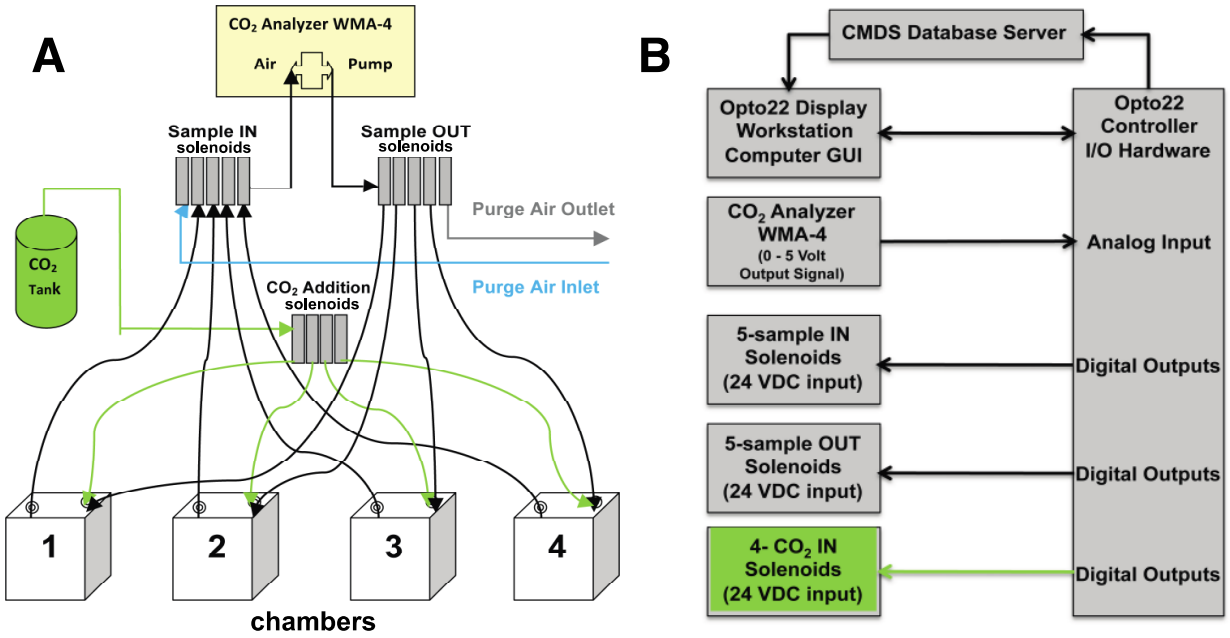

Figure S2. Representative month of CO_2 readins taken throughout the six-month microbialite in cubation. Readings taken every 8 min with CO_2 analyzer depict the tight regulation of the atmospheric headspace within each environmental chamber. Colors depict the four treatments: blue (Chamber 1, 400 ppmv CO_2, 35‰ salinity); green (Chamber 2, 1200 ppmv CO_2, 35‰ salinity); red (Chamber 3, 400 ppmv CO_2, 85‰ salinity); and grey (Chamber 4, 1200 ppmv CO_2, 85‰ salinity). Asterisk denotes a sampling event.

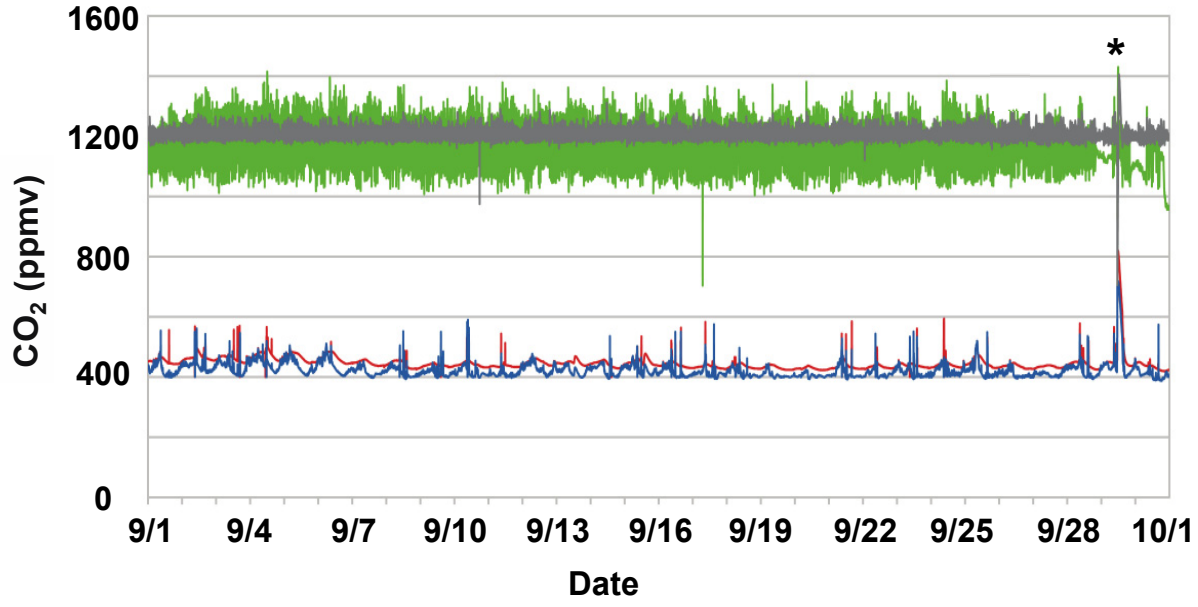

Figure S3. Rarefaction curves plotted 16S rRNA gene amplicon library from microbialites exposed to variable CO_2 and salinity levels. The blue curve represents the average OUTs observed at a 97% similarity threshold, while the grey and orange curves represent the upper and lower bounds, respectively, of the 95% confidence interval for that average. The *X*- and *Y*-axes represent the number of the sequences and OUTs, respectively.