

Modern microbial mats from the Chihuahuan Desert provide insights into ecological stability throughout Earth's history

Supplementary material

Supplementary figures

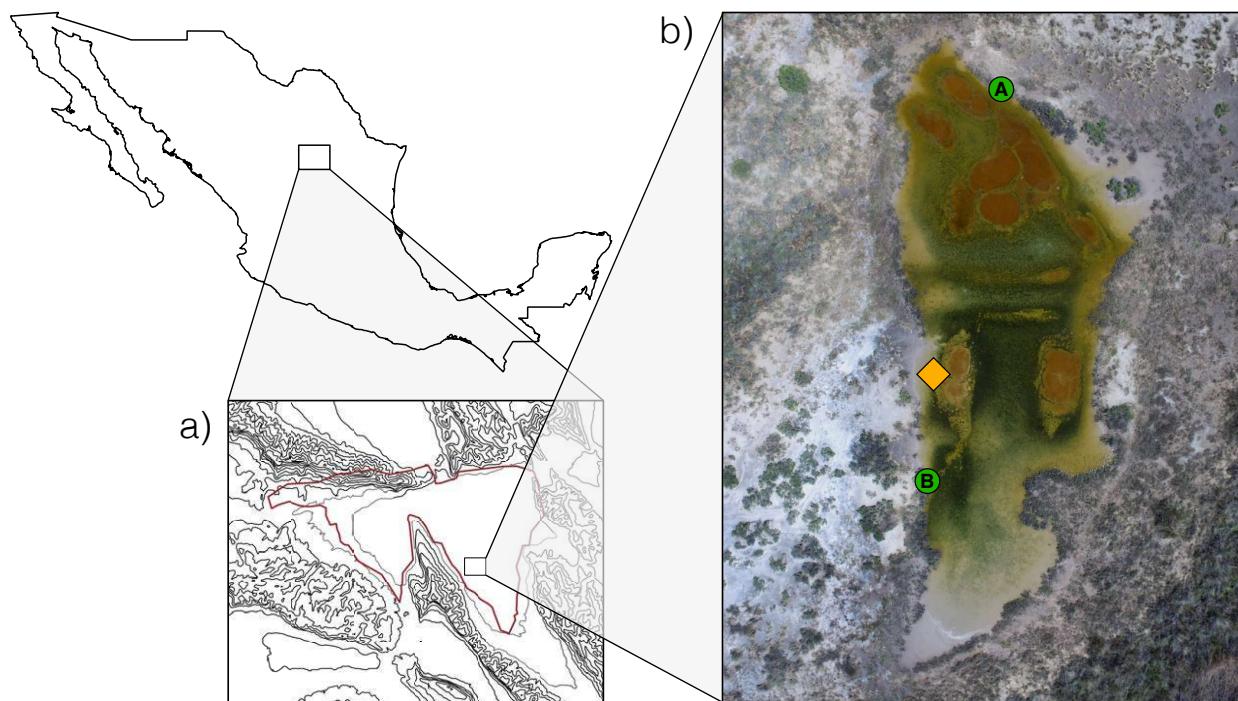


Fig. S1: Overview of the Archean Domes sample site. *a)* the Cuatro Ciénegas Basin, located in the Chihuahuan Desert. Depicted as a rectangle, the Pozas Azules ranch where the Archean Domes is located. *b)* Aerial view of the Archean Domes pond during the september 2019 sampling. The yellow diamond show the sampling point for the six metagenomes studied in this work. Green circles, A and B, indicate the picture location from Figure 1a and 1b, respectively.

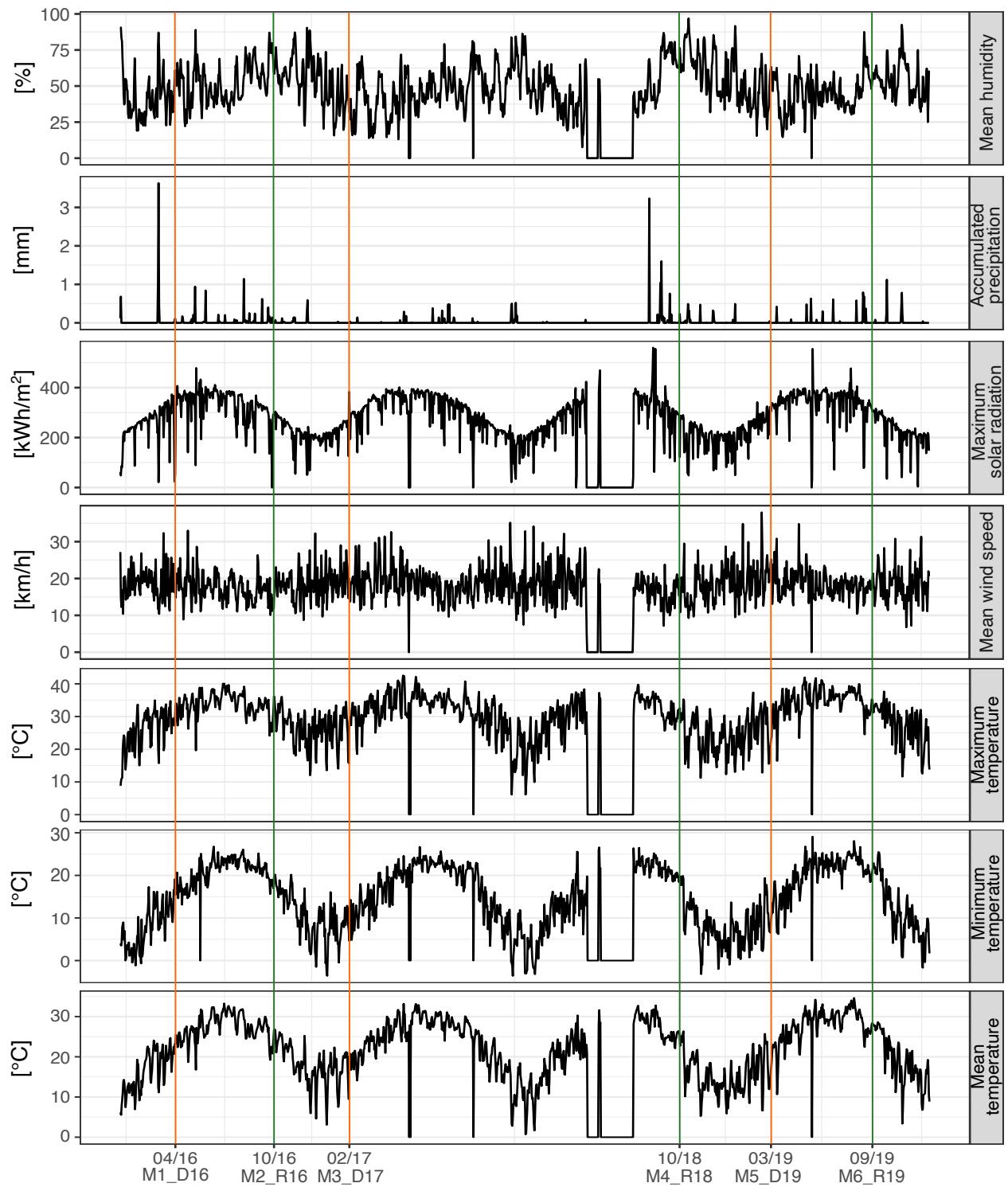


Fig. S2: Weather data retrieved from the EMA weather station No. 15DBB372, Cuatro Ciénelas, from 2016 to 2019. Data gaps during some months of 2018 represent that service was unavailable at that time. Lines show the sample day variables for each sample. Colors indicate rainy (green) and dry (orange) seasons.

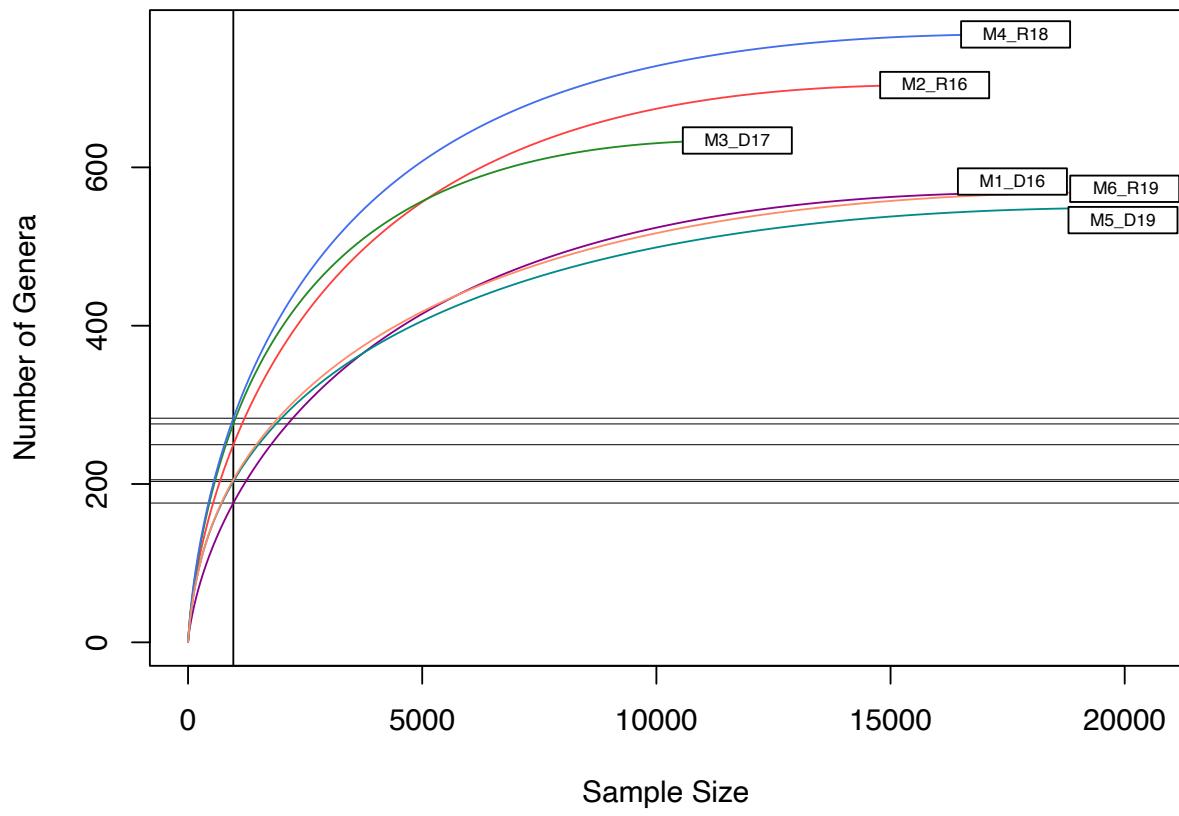


Fig. S3: Rarefaction curves for each sample studied. Sample size and number of genera are depicted in the horizontal and vertical axes, respectively. Each sample reaches saturation of genera richness and is suitable for sample comparison.

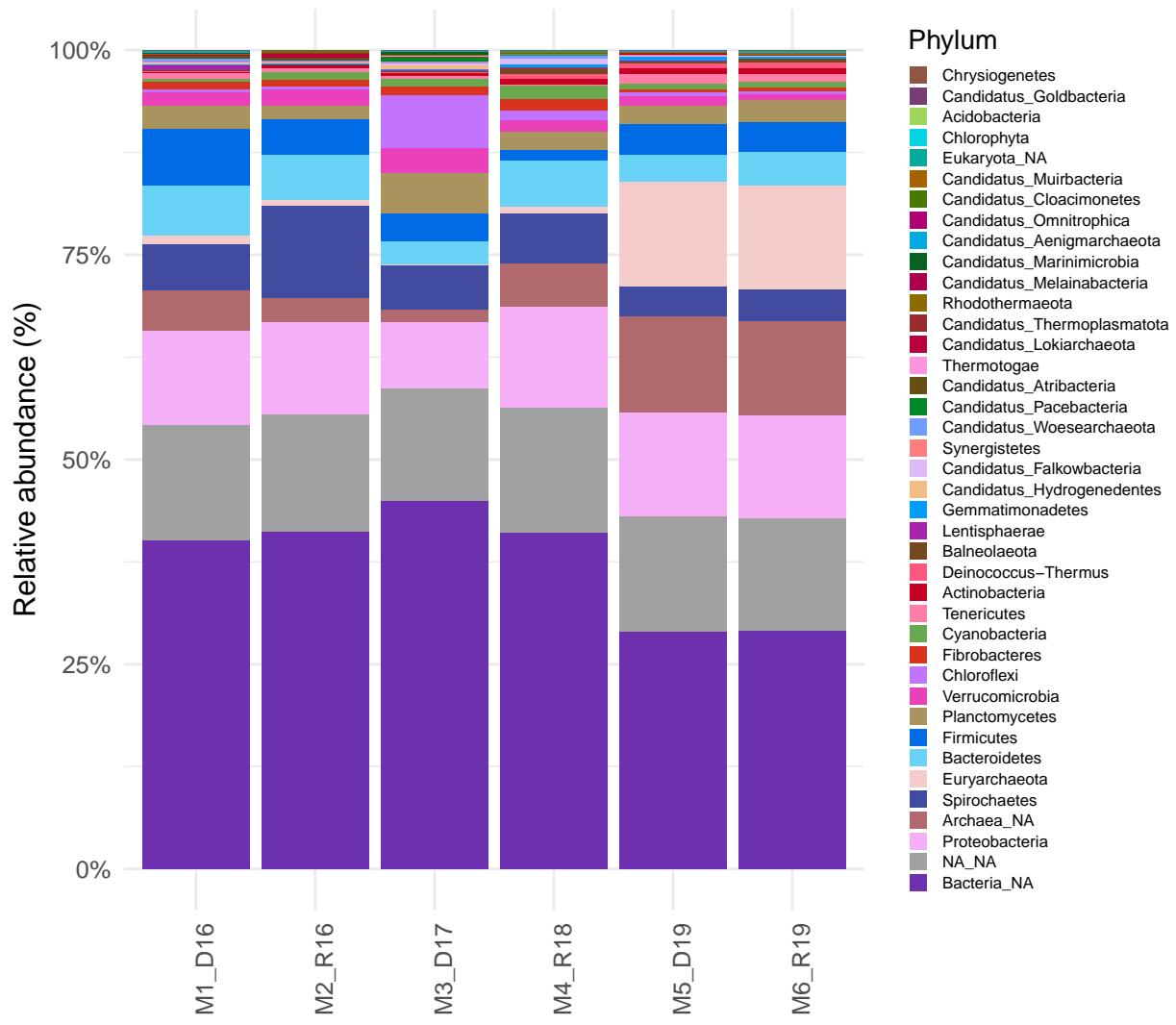


Fig. S4: Ribosomal-protein taxonomic profile of the Archean Domes system. Not annotated sequences were grouped in the NA categories.

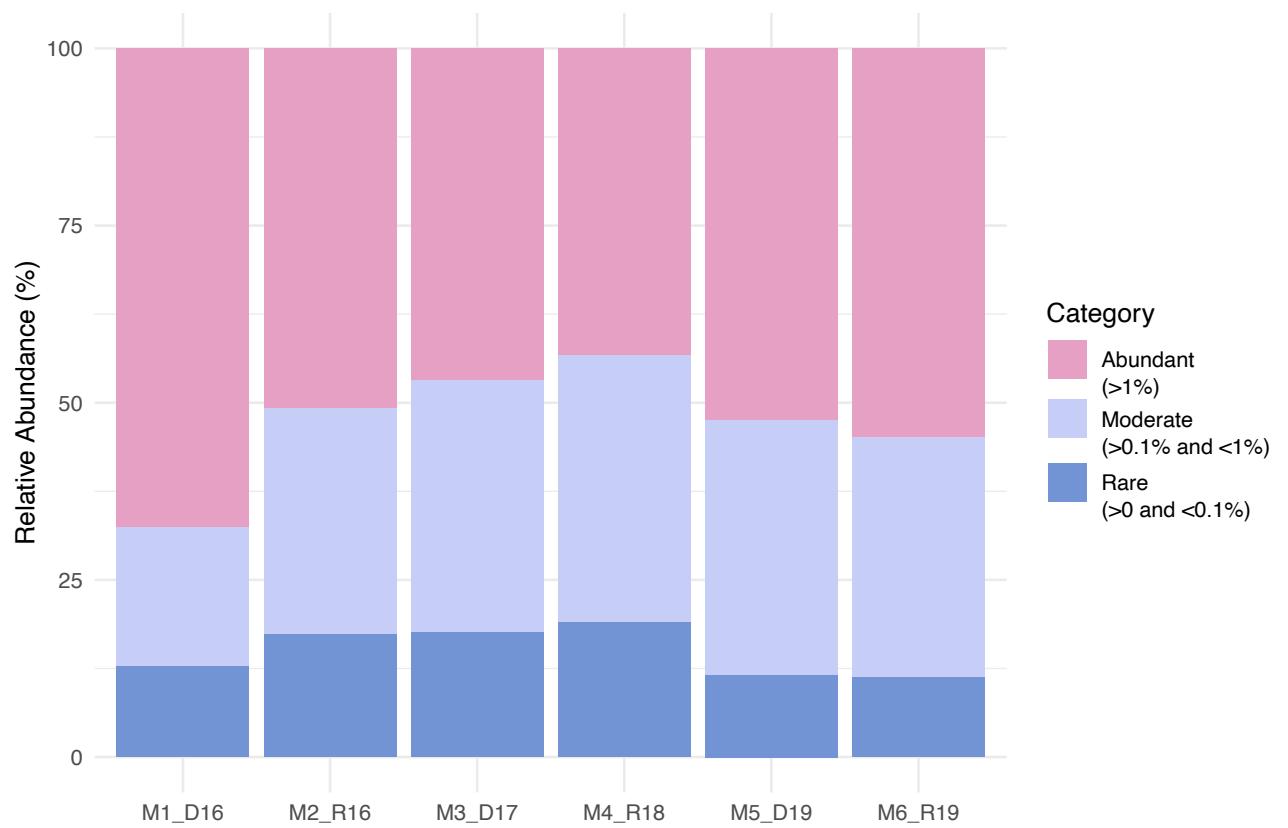


Fig. S5: The Archean Domes community based on their relative abundance at genus level. Abundant taxa comprise most of the whole community, in contrast to moderate and rare taxa abundance.

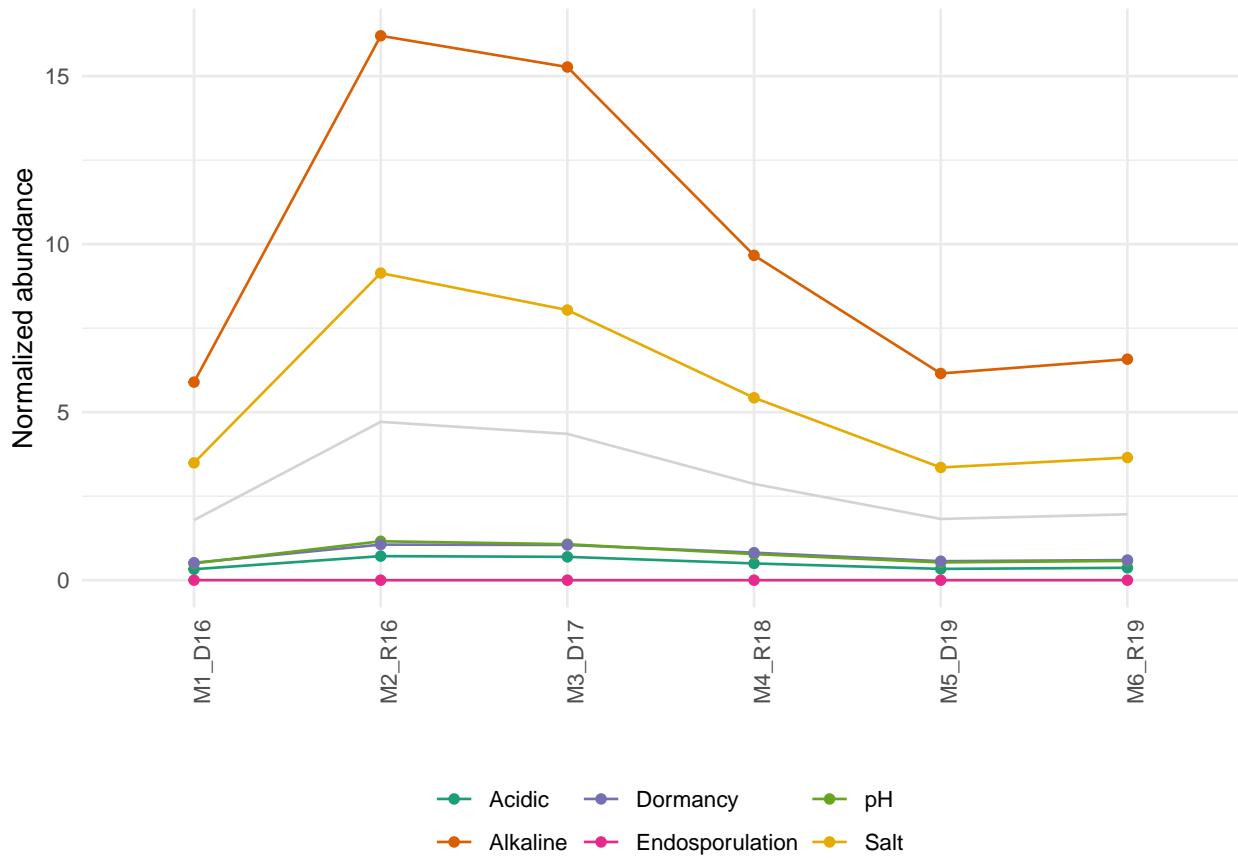


Fig. S6: Resistance genes found at the Archean Domes. Through all samples, most resistance genes associate to alkaline and salt response genes.

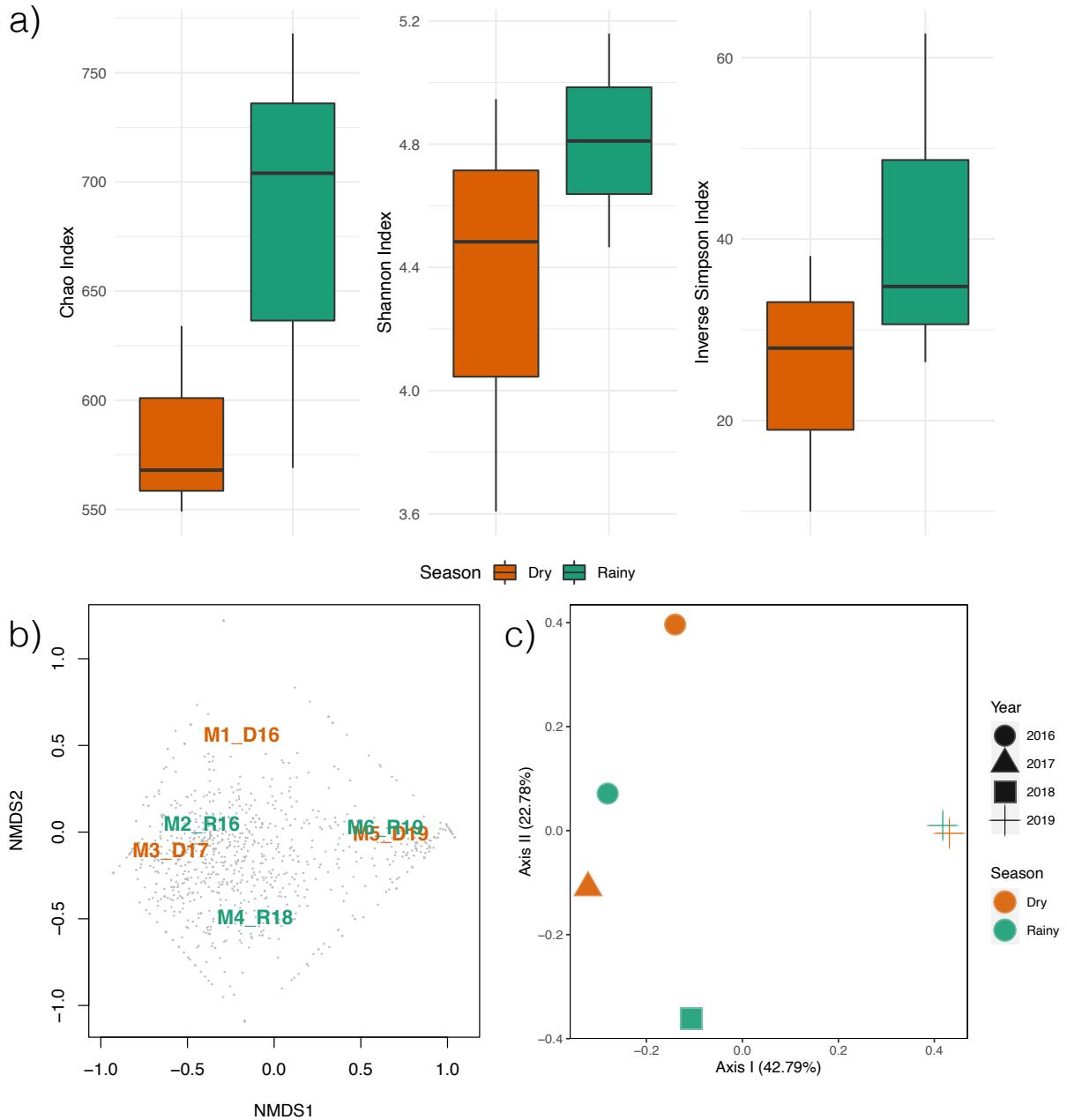


Fig. S7: Seasonal comparison of communities in the Archean Domes. *a)* Boxplots for diversity comparison for each seasonal state. performing Wilcoxon Rank Sum test showed no statistical differences between seasonal diversity. *b)* NMDS and *c)* PCoA analyses at genus level with Bray-Curtis measure. Both analyses showed no seasonal aggregation. NMDS and PCoA analyses at order level showed similar results to the ones at genus level.

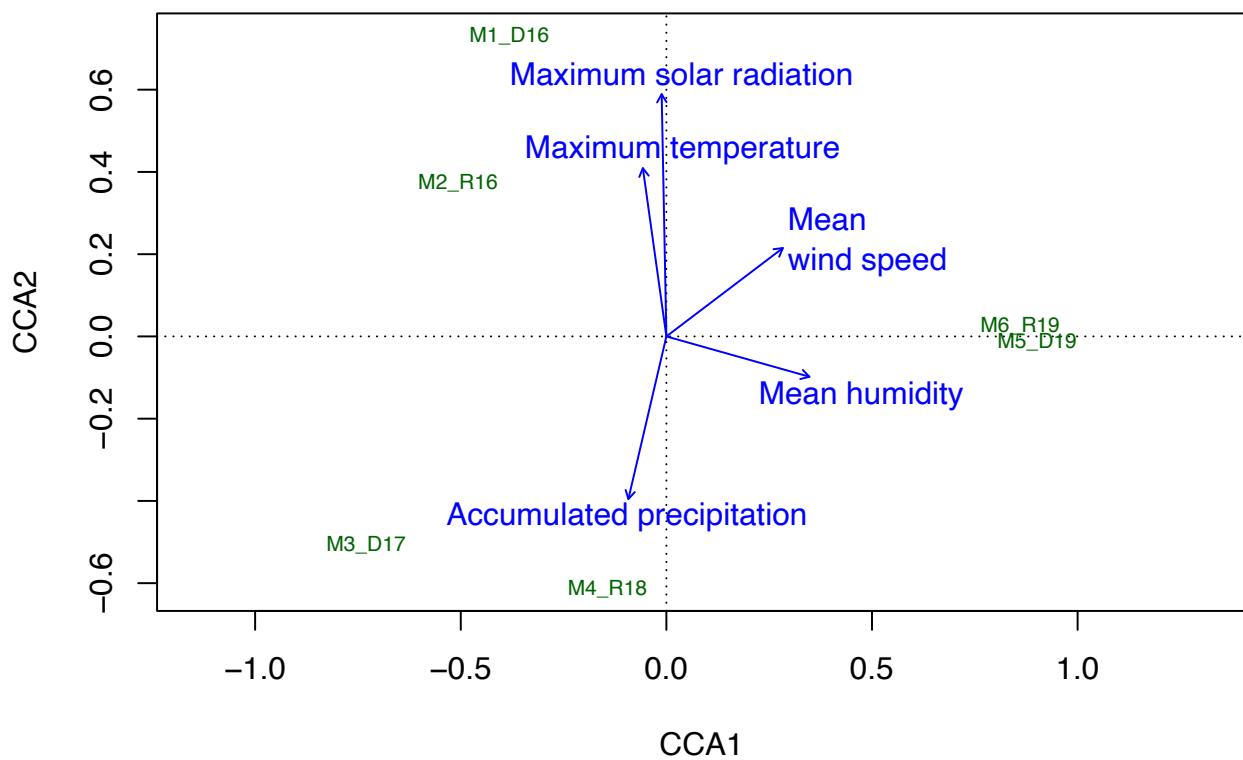


Fig. S8: CCA analysis with the environmental data provided by the EMA meteorological station. Meteorological data mean values for each sample month was input.

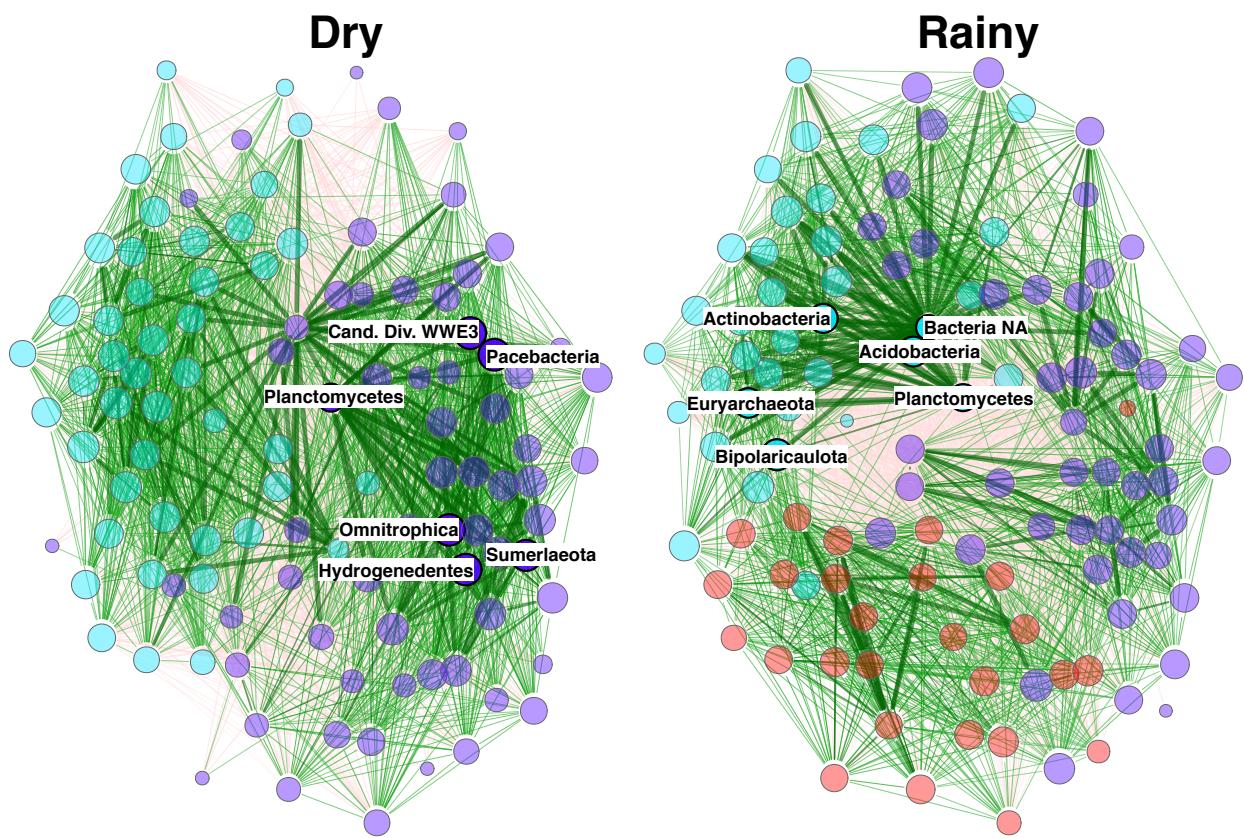


Fig. S9: Global network of shared phyla between seasons. Networks were built with the top 120 phyla across samples. Colors show clusters, and the same colors in both networks correspond to the same structural cluster. It can be appreciated the addition of a new cluster (red) during the rainy season. Green edges represent positive relationships, while red edges represent negative ones.

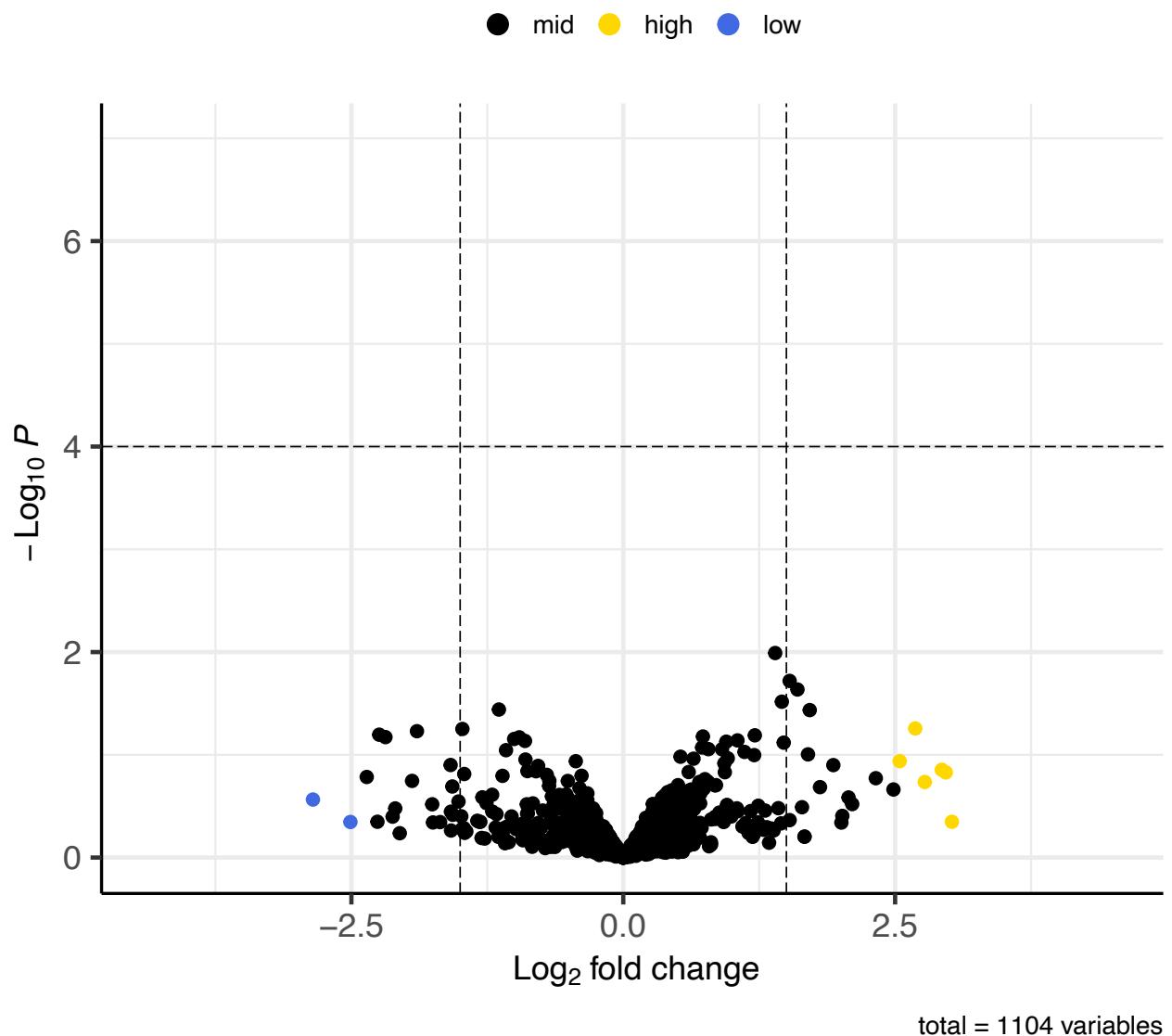


Fig. S10: Differential expression analysis of fuctions adapted to a metagenomic study (gene functions). No statistical significance was found for each function, although there are slight increases in both rainy (high) and dry (low) seasons.

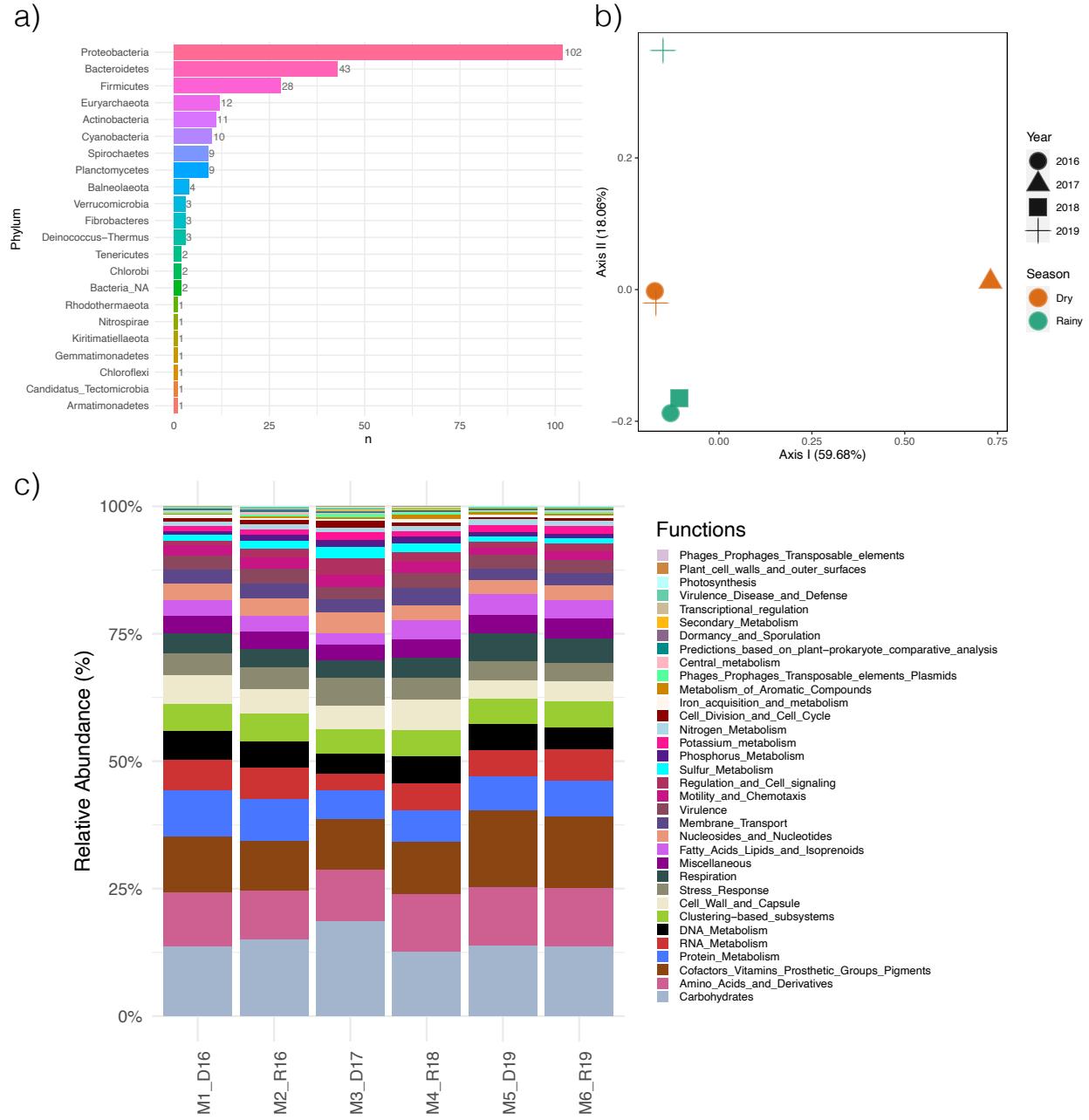


Fig. S11: Core taxonomic and functional details. *a)* Core composition at phylum level. *b*) Core functions under a PCoA ordination method. Roughly, there appears to be a seasonal pattern with a close association between two dry and rainy season samples, although the rainy sample from 2019 and the dry sample from 2017 does not group with any other sample. *c)* Function composition for core genera. Overall, similar compositions between samples can be appreciated.



Fig. S12: Core composition at the genus level. Each of the 250 genera that constitute the core is shown in order to emphasize in the taxonomic replacement.

Supplementary tables

Table S1: Sample-day weather parameters from EMA weather station No. 15DBB372, Cuatro Ciénelas.

Sample/parameter	M1_D16	M2_R16	M3_D17	M4_R18	M5_D19	M6_R19
Sample day/time	2016/04/09 9:48:38	2016/10/04 12:02:35	2017/02/17 11:38:28	2018/10/06 9:10:20	2019/03/20 11:32:19	2019/09/19 12:53:19
Mean wind direction (°)	153.5	149.5	245	170.5	123.5	111.5
Mean wind speed (km/h)	5.55	5.1	15.45	14.15	23.9	36.25
Max. wind speed (km/h)	14.3	12.1	43	22.5	39.1	63.2
Min. Temperature (°C)	23.1	28.1	21.1	24.6	16.8	29.5
Mean Temperature (°C)	23.9	29.2	22.53	25.13	17.3	29.73
Max. Temperature (°C)	24.8	29.8	23.1	25.9	17.9	29.9
Mean humidity (%)	63.83	50.5	28.5	70	45.67	54.15
Mean pressure (mbar)	923.52	925.07	927.82	928.43	935.37	929.6
Max. solar radiation (kWh/m ²)	721	859	864	607	971	942

Table S2: Raw reads and quality control (QC) metadata for each shotgun metagenome studied.

Sample/ parameter	Raw reads	Low QC reads	Total reads	Paired reads	Forward Unpaired	Reverse Unpaired
M1_D16	28,859,454	2,425,863	26,433,591	21,012,271	4,755,240	666,080
M2_R16	4,772,053	287,632	4,484,421	3,722,418	671,964	90,039
M3_D17	8,203,484	790,818	7,412,666	5,915,153	1,255,747	241,766
M4_R18	10,030,782	1,561,639	8,469,143	6,115,153	2,098,789	255,201
M5_D19	25,873,990	3,589,352	22,284,638	17,676,424	3,645,559	962,655
M6_R19	20,153,088	1,471,902	18,681,186	16,378,340	1,784,198	518,648

Table S3: Metagenome assembly metadata for each sample. Minimum, average, and maximum contig length is also shown

Sample/ parameter	Total base pairs	Assembled (bp)	Not assembled (bp)	Min. contig length (bp)	Avg. contig length (bp)	Max. contig length (bp)
M1_D16	9,838,571,624	857,058,612	8,981,513,012	500	1,274.80	159,881
M2_R16	1,491,700,706	190,580,164	1,301,120,542	500	1,243.70	86,189
M3_D17	2,627,434,540	304,829,428	2,322,605,112	500	1,291.70	121,677
M4_R18	2,985,543,837	329,842,768	2,655,701,069	500	1,089.90	75,330
M5_D19	7,799,883,462	588,197,199	7,211,686,263	500	1,142.20	142,626
M6_R19	7,744,171,739	621,571,725	7,122,600,014	500	1,108.90	124,235

Table S4: Metagenome assembly metadata for sequences not initially assembled.

Sample/ parameter	Assembled sequences	Not assembled sequences (Forward)	Not assembled sequences (Reverse)
M1_D16	672,295	1,263,688	197,513
M2_R16	153,232	244,559	26,150
M3_D17	235,985	323,183	66,130
M4_R18	302,633	735,840	91,703
M5_D19	515,141	888,820	242,019
M6_R19	560,549	427,091	121,222

Table S5: Taxonomic annotation metadata for each sample and relative abundances for each domain of life.

Sample/parameter	Reads processed				Relative abundance (%)			
	Total Found	Unclassified	Classified	Phylotypes	Archaea	Bacteria	Eukaryota	Viruses
M1_D16	1,562,120	1,083,248	478,872	8,699	3.06	96.65	0.20	0.08
M2_R16	1,288,875	578,442	710,433	10,969	4.27	95.45	0.17	0.11
M3_D17	285,524	190,940	94,584	3,872	1.44	98.38	0.13	0.05
M4_R18	1,791,166	867,900	923,266	12,370	7.27	92.01	0.51	0.21
M5_D19	1,833,943	1,020,352	813,591	10,079	33.61	65.83	0.19	0.36
M6_R19	2,142,378	884,359	1,258,019	11,840	33.60	65.83	0.19	0.39

Table S6: Alpha diversity indexes for each sample studied.

Sample/Index	Chao	Shannon	Simpson	Inverse Simpson
M1_D16	271.2500	2.792135	0.8184993	5.509622
M2_R16	143.4000	2.642506	0.8068319	5.176839
M3_D17	200.0833	2.592936	0.7840716	4.631164
M4_R18	205.1154	2.716131	0.8082304	5.214591
M5_D19	233.0000	3.128192	0.8797076	8.313074
M6_R19	231.3750	3.077123	0.8787593	8.248053

Table S7: Network metrics for global network (phylum level) and core network (genus level). Hub taxa found by NetCoMi is also shown.

	Phylum-level Global network		Genus-level Core network	
Category/ parameter	Dry season	Rainy season	Dry season	Rainy season
Number of components	1.0	1.0	1.0	1.0
Clustering coefficient	0.75980	0.73311	0.11670	0.12789
Modularity	0.01279	0.06986	0.16715	0.21577
Positive edge percentage	49.01681	48.77283	41.94115	41.41117
Edge density	0.57415	0.56764	0.07316	0.07650
Natural connectivity	0.21904	0.20453	0.01452	0.01545
Vertex connectivity	3.0	1.0	6.0	7.0
Edge connectivity	3.0	1.0	6.0	7.0
Average dissimilarity	0.78332	0.78216	0.97908	0.97812
Average path length	0.82592	0.84478	1.45398	1.44128
Hub taxa	cand.div. WWE3 Hydrogenedentes Omnitrophica Pacebacteria Planctomycetes Sumerlaeota	Acidobacteria Actinobacteria Bacteria NA Bipolaricaulota Euryarchaeota Planctomycetes	Chitinispirillum Coleofasciculus Desulfonatronovibrio Desulfovermiculus Halanaerobium Halomonas Halorhabdus Halorubrum Marinilabilia Mariniphaga Marinobacter Spiribacter Tangfeifania	Bradymonas cand. Izimaplasma Chitinispirillum Coleofasciculus Desulfohalobium Desulfonatronovibrio Desulfovermiculus Halanaerobium Halomonas Halorhabdus Halorubrum Mariniphaga Marinobacter Spiribacter Tangfeifania