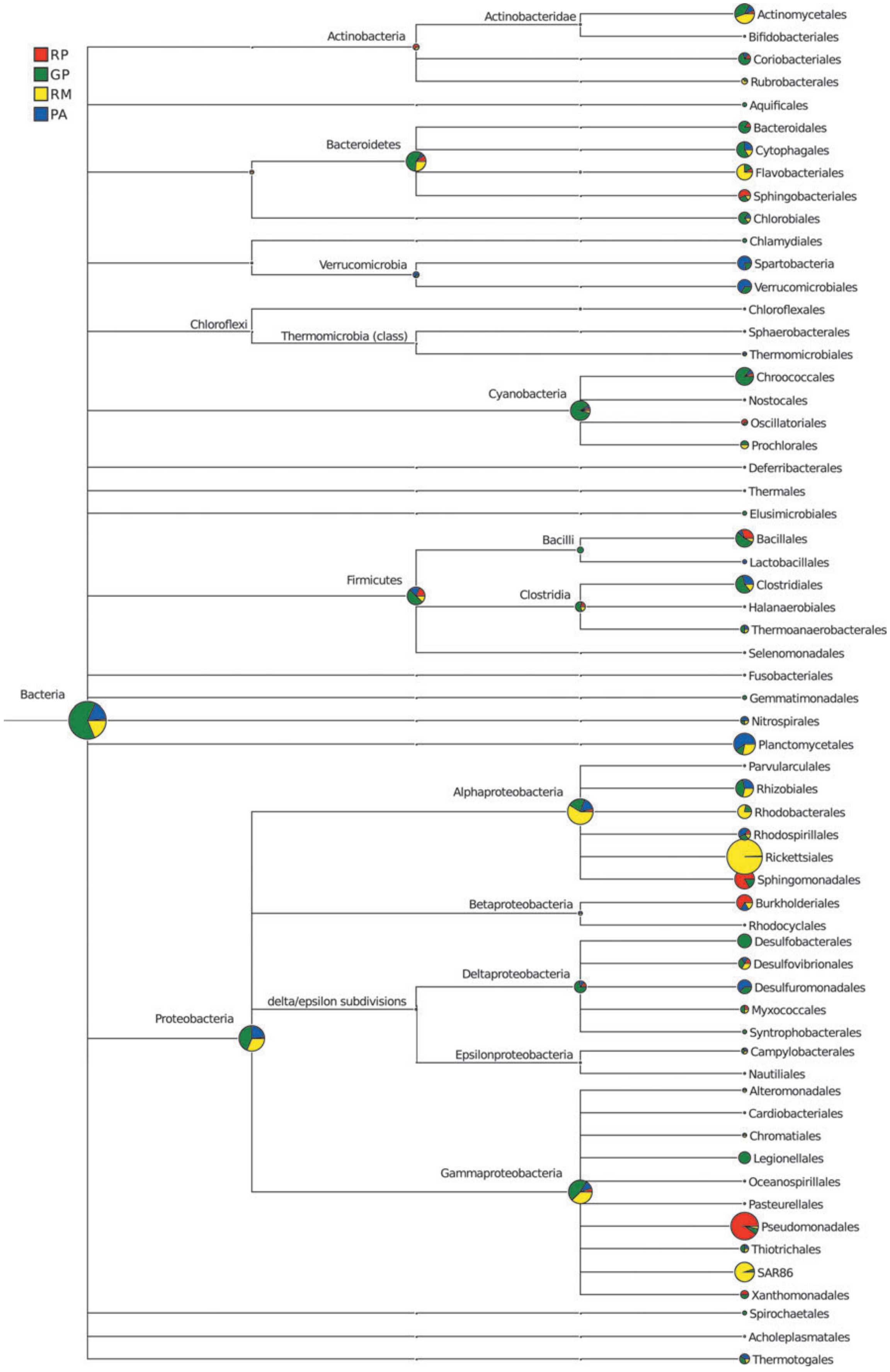
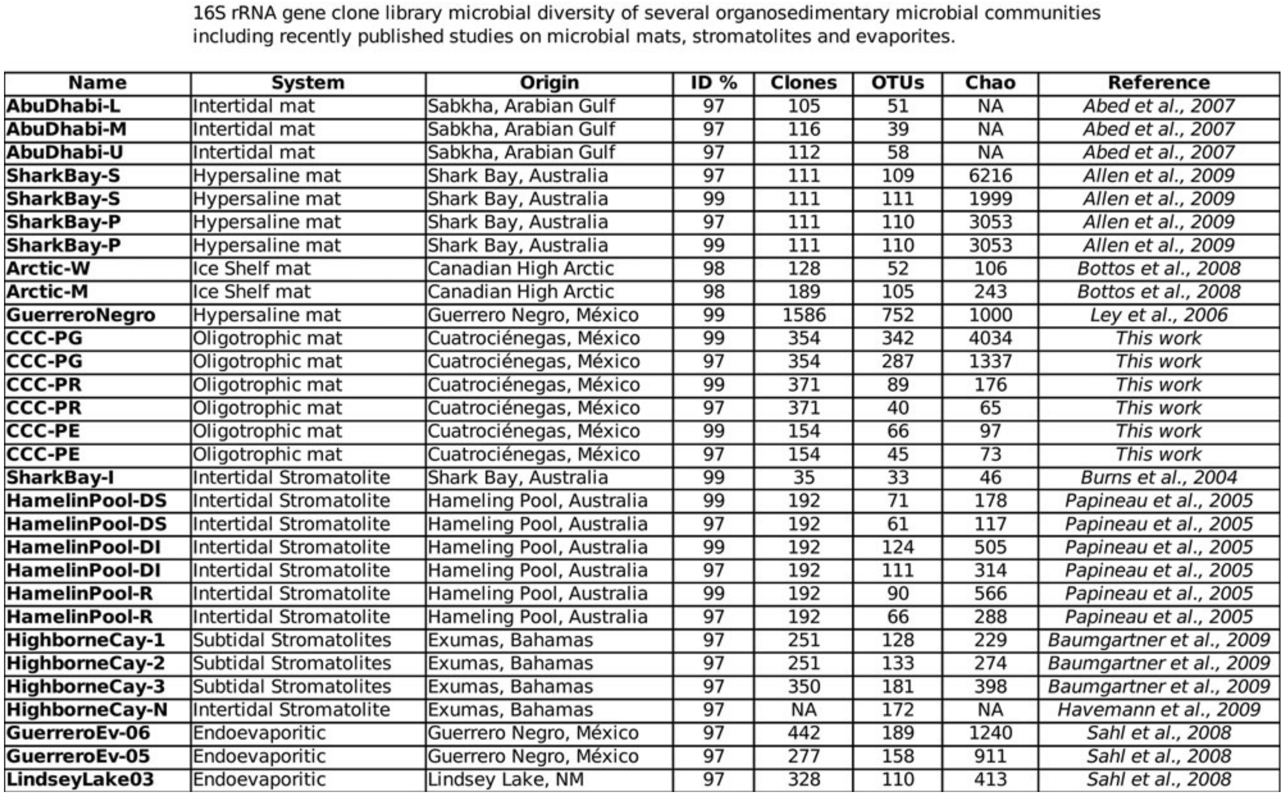


FIG. S1. Phylogram depicting the relative abundances at order level of the four CCB metagenomes according to the protein-coding gene abundance matrices.



16S rRNA gene clone library microbial diversity of several organosedimentary microbial communities including recently published studies on microbial mats, stromatolites and evaporites.

Name	System	Origin	ID %	Clones	OTUs	Chao	Reference
AbuDhabi-L	Intertidal mat	Sabkha, Arabian Gulf	97	105	51	NA	*Abed et al., 2007*
AbuDhabi-M	Intertidal mat	Sabkha, Arabian Gulf	97	116	39	NA	*Abed et al., 2007*
AbuDhabi-U	Intertidal mat	Sabkha, Arabian Gulf	97	112	58	NA	*Abed et al., 2007*
SharkBay-S	Hypersaline mat	Shark Bay, Australia	97	111	109	6216	*Allen et al., 2009*
SharkBay-S	Hypersaline mat	Shark Bay, Australia	99	111	111	1999	*Allen et al., 2009*
SharkBay-P	Hypersaline mat	Shark Bay, Australia	97	111	110	3053	*Allen et al., 2009*
SharkBay-P	Hypersaline mat	Shark Bay, Australia	99	111	110	3053	*Allen et al., 2009*
Arctic-W	Ice Shelf mat	Canadian High Arctic	98	128	52	106	*Bottos et al., 2008*
Arctic-M	Ice Shelf mat	Canadian High Arctic	98	189	105	243	*Bottos et al., 2008*
GuerreroNegro	Hypersaline mat	Guerrero Negro, México	99	1586	752	1000	*Ley et al., 2006*
CCC-PG	Oligotrophic mat	Cuatrociénegas, México	99	354	342	4034	*This work*
CCC-PG	Oligotrophic mat	Cuatrociénegas, México	97	354	287	1337	*This work*
CCC-PR	Oligotrophic mat	Cuatrociénegas, México	99	371	89	176	*This work*
CCC-PR	Oligotrophic mat	Cuatrociénegas, México	97	371	40	65	*This work*
CCC-PE	Oligotrophic mat	Cuatrociénegas, México	99	154	66	97	*This work*
CCC-PE	Oligotrophic mat	Cuatrociénegas, México	97	154	45	73	*This work*
SharkBay-I	Intertidal Stromatolite	Shark Bay, Australia	99	35	33	46	*Burns et al., 2004*
HamelinPool-DS	Intertidal Stromatolite	Hameling Pool, Australia	99	192	71	178	*Papineau et al., 2005*
HamelinPool-DS	Intertidal Stromatolite	Hameling Pool, Australia	97	192	61	117	*Papineau et al., 2005*
HamelinPool-DI	Intertidal Stromatolite	Hameling Pool, Australia	99	192	124	505	*Papineau et al., 2005*
HamelinPool-DI	Intertidal Stromatolite	Hameling Pool, Australia	97	192	111	314	*Papineau et al., 2005*
HamelinPool-R	Intertidal Stromatolite	Hameling Pool, Australia	99	192	90	566	*Papineau et al., 2005*
HamelinPool-R	Intertidal Stromatolite	Hameling Pool, Australia	97	192	66	288	*Papineau et al., 2005*
HighborneCay-1	Subtidal Stromatolites	Exumas, Bahamas	97	251	128	229	*Baumgartner et al., 2009*
HighborneCay-2	Subtidal Stromatolites	Exumas, Bahamas	97	251	133	274	*Baumgartner et al., 2009*
HighborneCay-3	Subtidal Stromatolites	Exumas, Bahamas	97	350	181	398	*Baumgartner et al., 2009*
HighborneCay-N	Intertidal Stromatolite	Exumas, Bahamas	97	NA	172	NA	*Havemann et al., 2009*
GuerreroEv-06	Endoevaporitic	Guerrero Negro, México	97	442	189	1240	*Sahl et al., 2008*
GuerreroEv-05	Endoevaporitic	Guerrero Negro, México	97	277	158	911	*Sahl et al., 2008*
LindseyLake03	Endoevaporitic	Lindsey Lake, NM	97	328	110	413	*Sahl et al., 2008*

FIG. S2. Supplementary tables of (**a**) species richness according to 16S rRNA clone libraries in previously published microbial mat studies; (**b**) relative frequency distributions of reads assigned to most-abundant orders according to the all-read metagenomic content.

Relative frequency distributions of reads assigned to most abundant orders by means of the all-reads metagenomic complement approach for the Green Mat (G), Red Mat (R), Guerrero Negro mat (GN) and Pozas Azules Stromatolite (PA). Different shades of gray are used to remark high frequency (>0.1, dark gray), medium frequency (>0.03, medium gray), and very low frequency (<0.003, light gray) of particular taxonomic groups.

	G	GN	PA	R
Chroococcales	0.084	0.048	0.088	0.043
Clostridiales	0.056	0.049	0.022	0.016
Bacillales	0.037	0.029	0.020	0.051
Burkholderiales	0.037	0.030	0.067	0.126
Nostocales	0.036	0.030	0.045	0.030
Rhizobiales	0.035	0.054	0.068	0.037
Actinomycetales	0.035	0.045	0.029	0.020
Pseudomonadales	0.034	0.016	0.015	0.326
Bacteroidales	0.032	0.034	0.013	0.013
Flavobacteriales	0.029	0.025	0.019	0.022
Oscillatoriales	0.028	0.033	0.032	0.038
Alteromonadales	0.026	0.017	0.012	0.014
Enterobacteriales	0.026	0.014	0.013	0.027
Legionellales	0.023	0.002	0.006	0.001
Cytophagales	0.022	0.016	0.017	0.011
Desulfuromonadales	0.021	0.027	0.018	0.005
Chlorobiales	0.019	0.014	0.012	0.004
Desulfovibrionales	0.017	0.024	0.007	0.005
Sphingobacteriales	0.016	0.014	0.016	0.011
Chloroflexales	0.016	0.023	0.015	0.005
Rhodobacterales	0.015	0.081	0.026	0.015
Planctomycetales	0.015	0.031	0.112	0.003
Thermoanaerobacterales	0.014	0.015	0.007	0.004
Chromatiales	0.014	0.014	0.009	0.004
Myxococcales	0.013	0.021	0.020	0.004
Vibrionales	0.012	0.007	0.006	0.006
Desulfobacterales	0.012	0.021	0.004	0.004
Lactobacillales	0.012	0.006	0.004	0.003
Rhodospirillales	0.011	0.015	0.015	0.008
Oceanospirillales	0.010	0.007	0.006	0.007
Spirochaetales	0.009	0.013	0.004	0.002
Campylobacterales	0.008	0.003	0.003	0.002
Syntrophobacterales	0.008	0.011	0.007	0.002
Xanthomonadales	0.007	0.006	0.008	0.010
Pasteurellales	0.007	0.003	0.003	0.002
Rickettsiales	0.007	0.002	0.004	0.001
Thiotrichales	0.006	0.003	0.002	0.001
Neisseriales	0.006	0.003	0.004	0.004
Chlamydiales	0.006	0.002	0.003	0.000
Sphingomonadales	0.005	0.007	0.011	0.047
Prochlorales	0.005	0.001	0.004	0.001
Gloeobacterales	0.005	0.003	0.006	0.001
Verrucomicrobiales	0.005	0.006	0.028	0.001
Nitrospirales	0.003	0.002	0.020	0.000
Thermotogales	0.001	0.007	0.002	0.001

FIG. S2. (Continued).

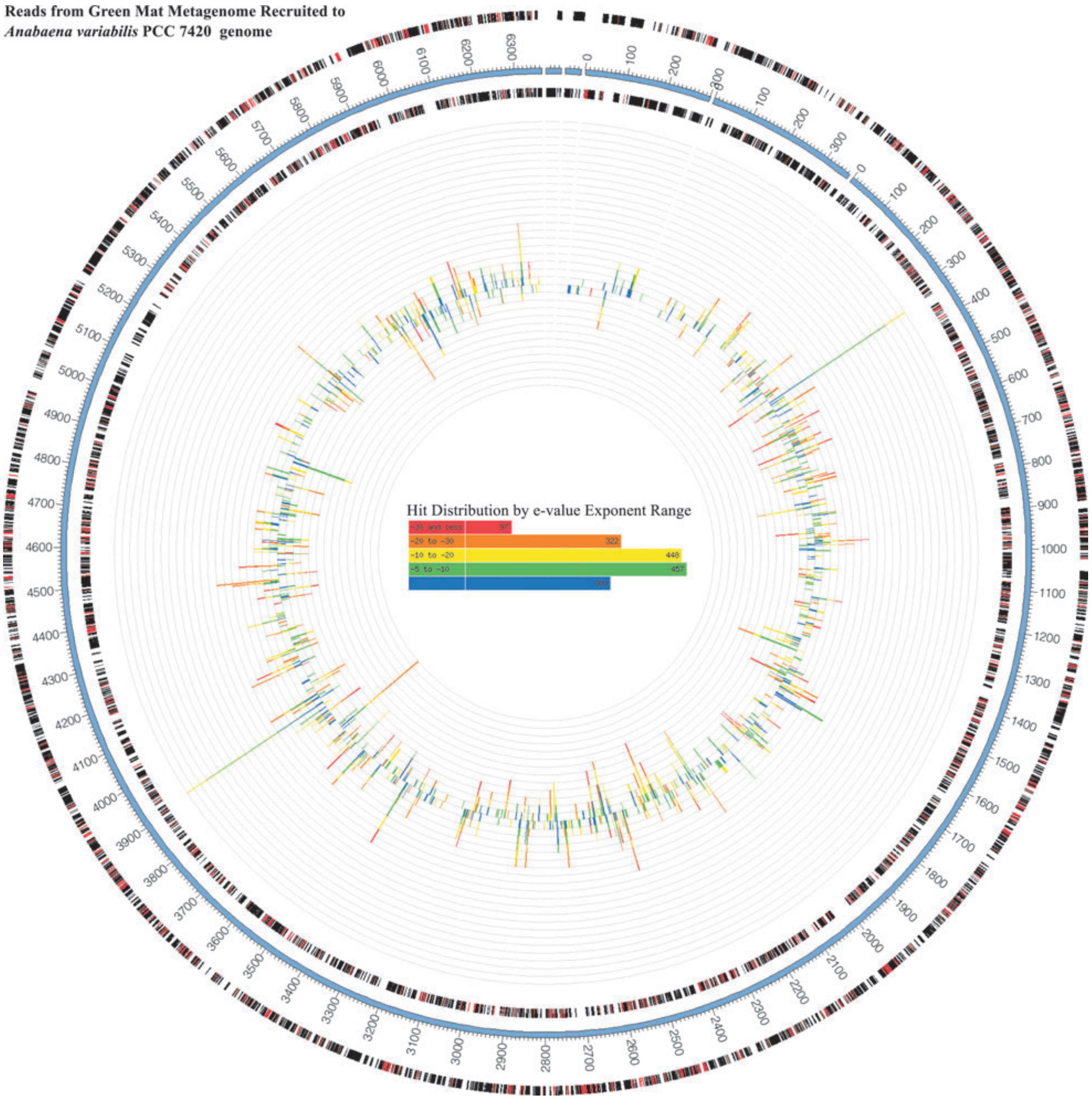


FIG. S3. Fragment recruitment diagrams of the reference genomes recruiting the highest amount of reads from the green and red mats' metagenomes.

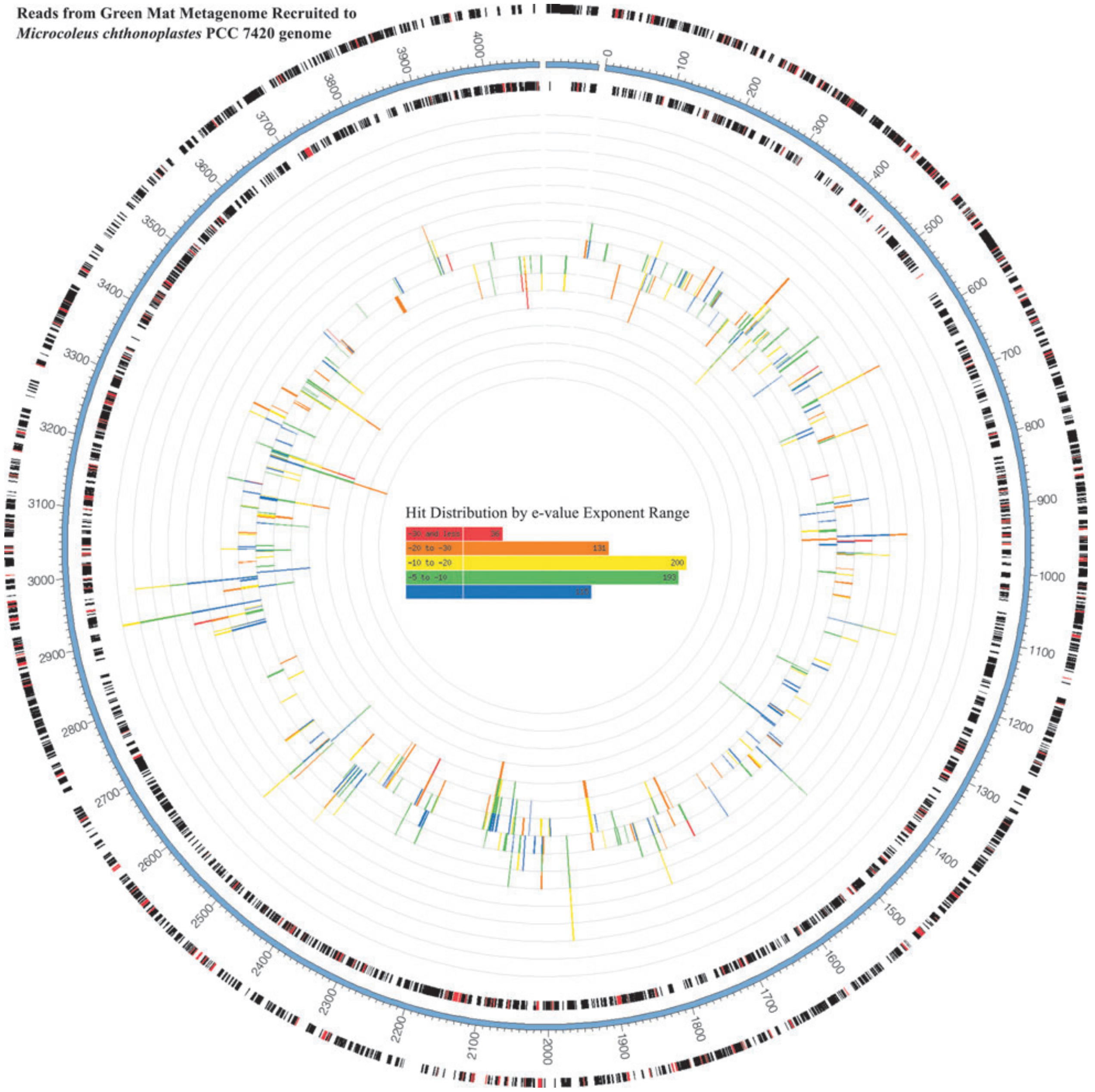


FIG. S3. (Continued).

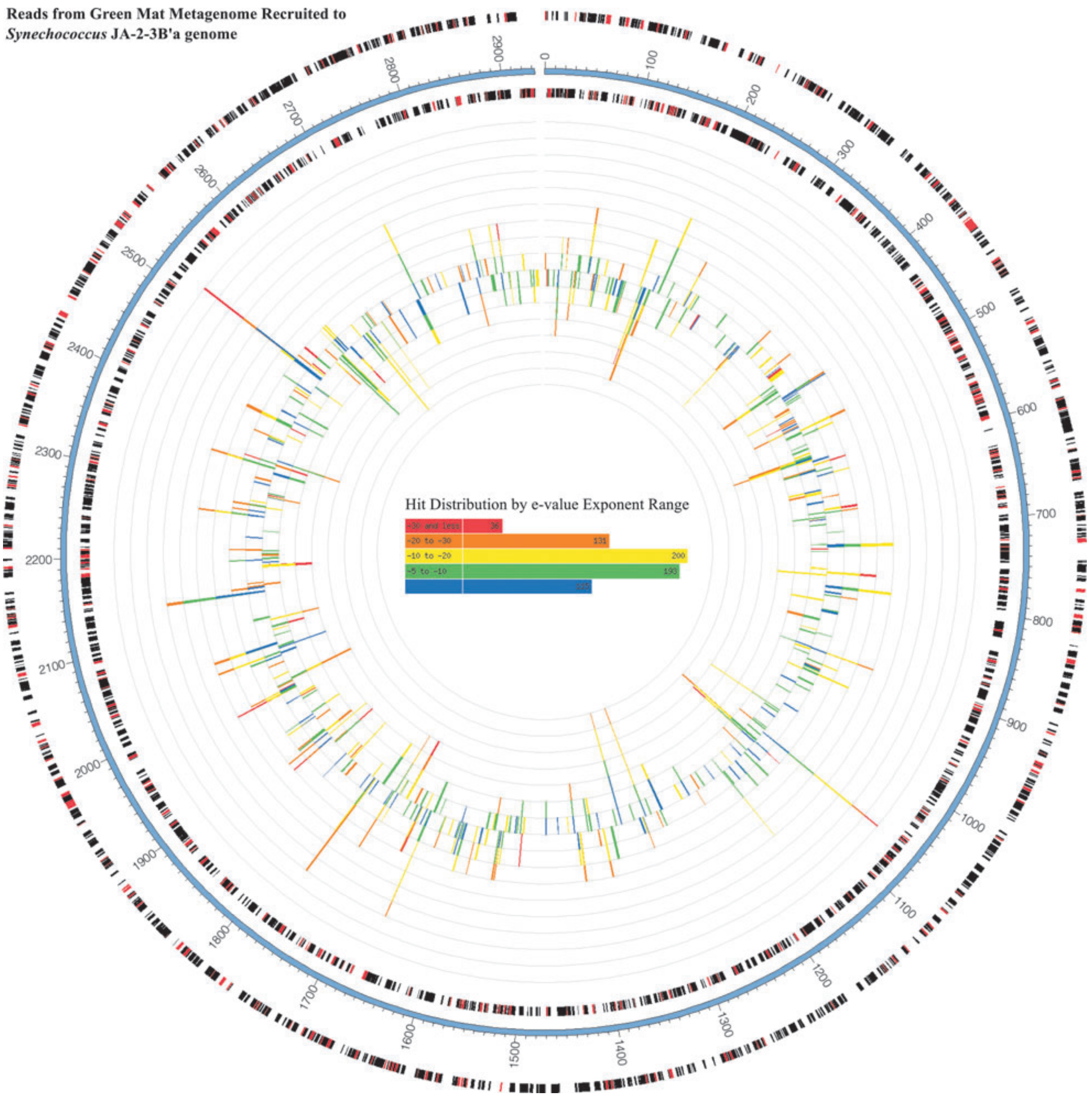


FIG. S3. (Continued).

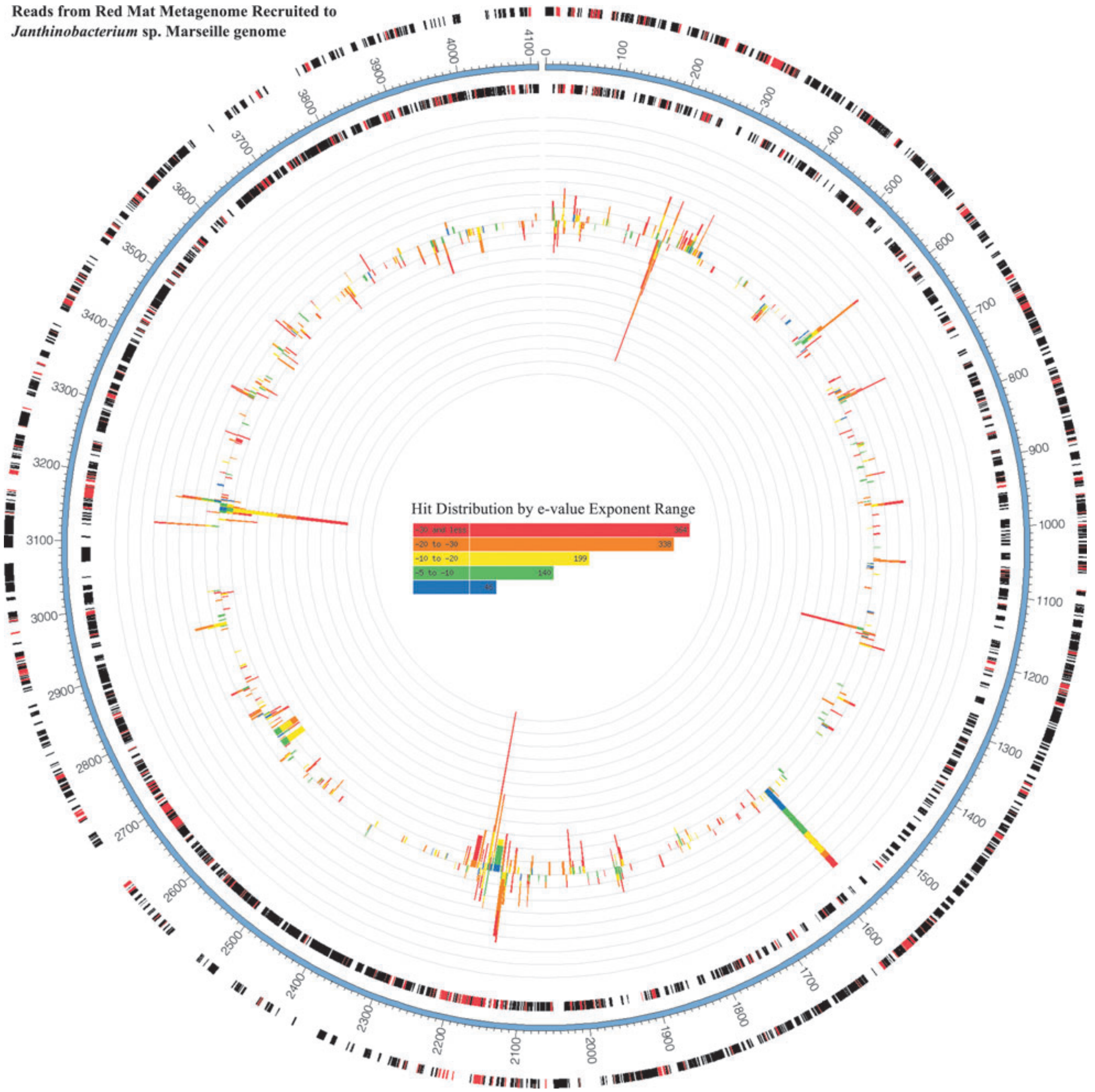
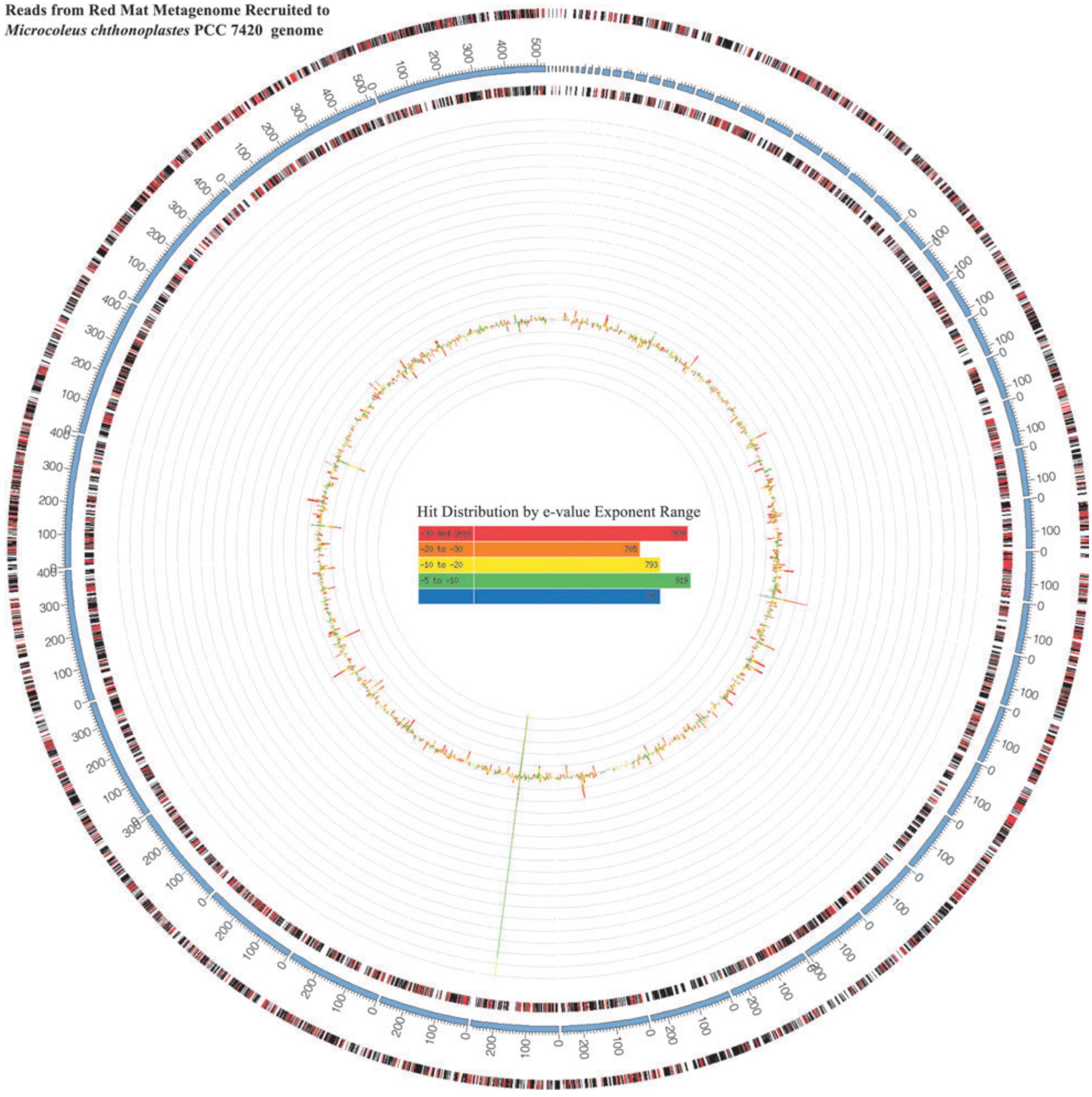


FIG. S3. (Continued).



Reads from Red Mat Metagenome Recruited to
***Microcoleus chthonoplastes* PCC 7420 genome**

FIG. S3. (Continued).

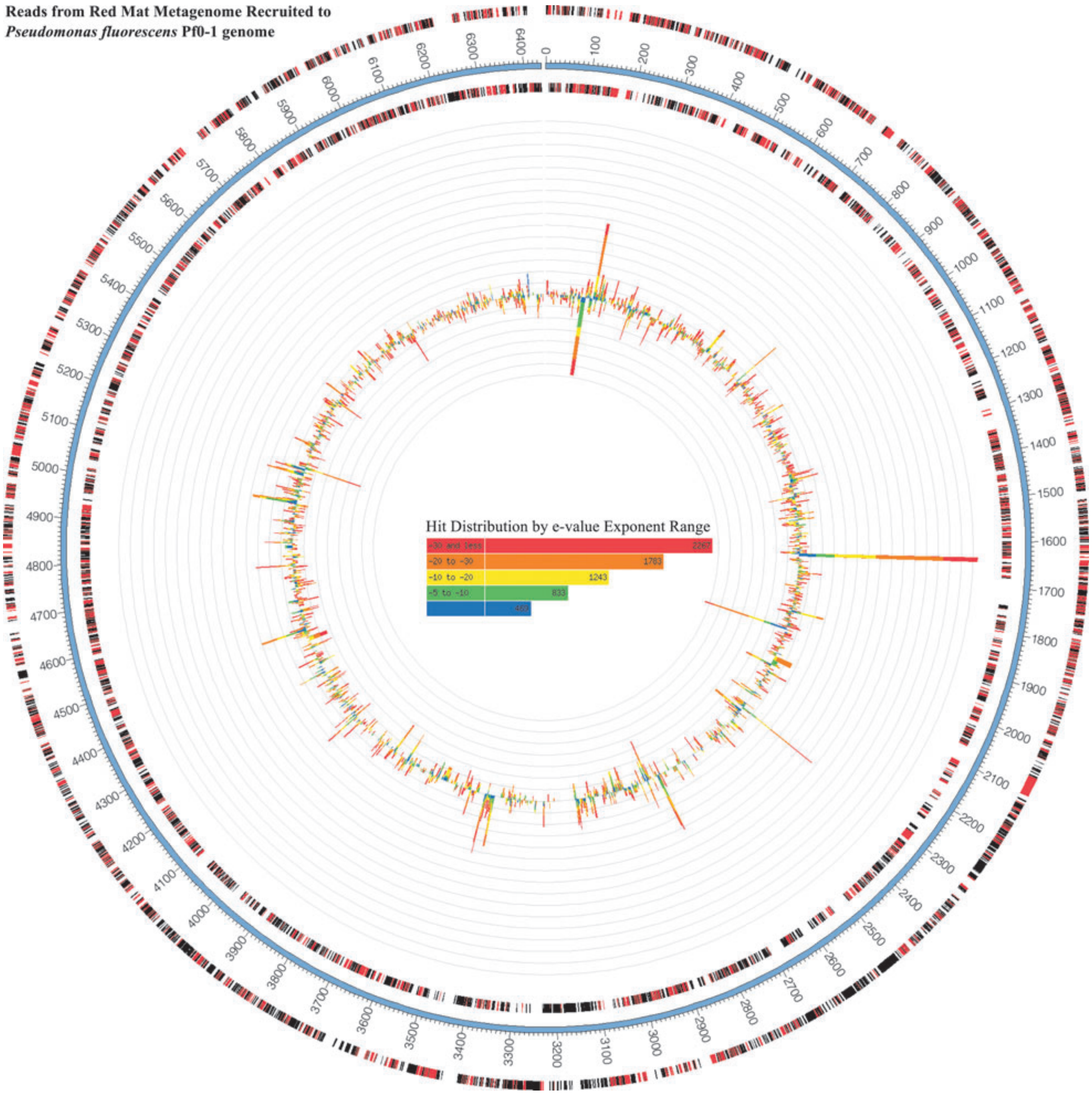


FIG. S3. (Continued).

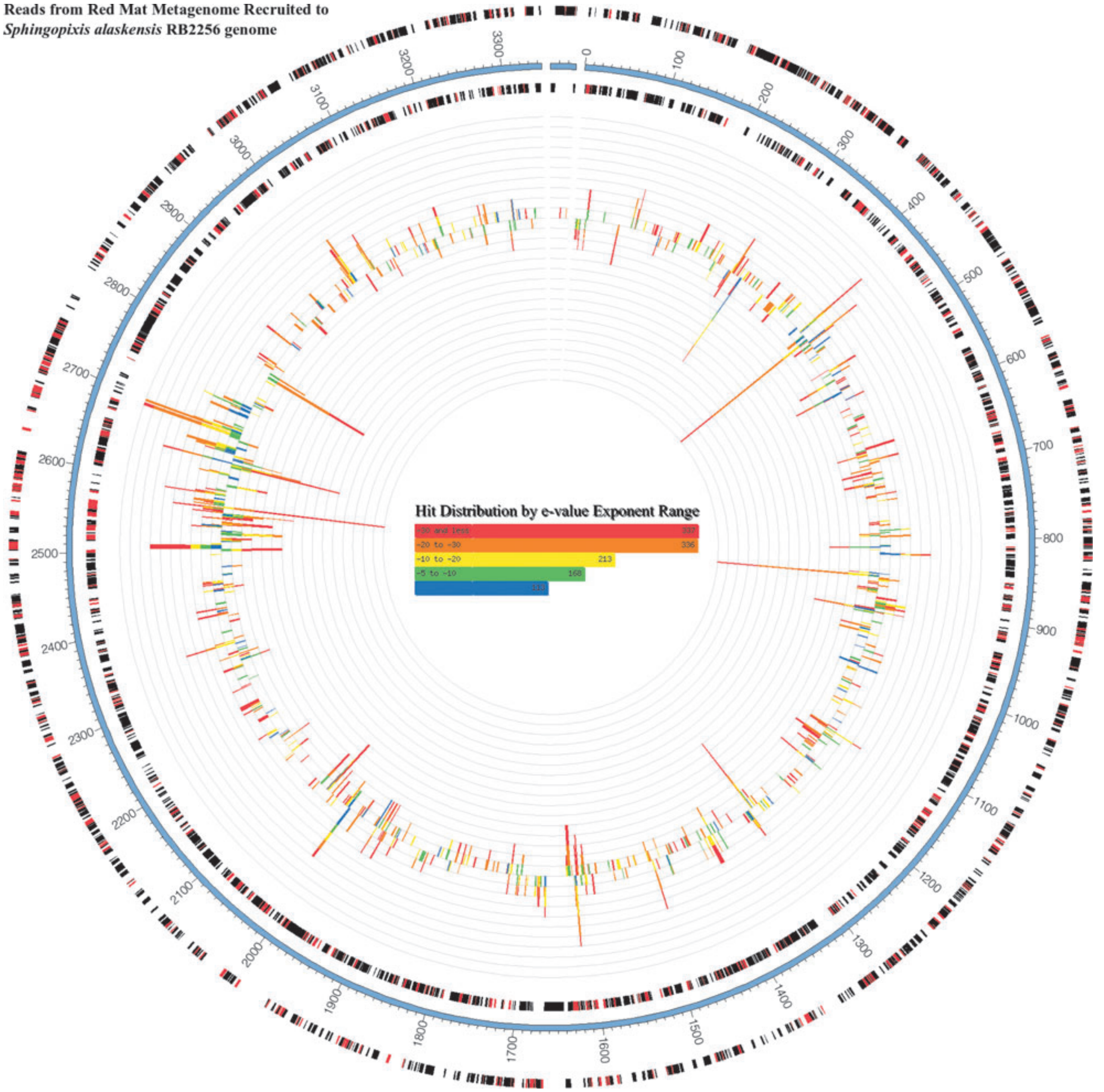
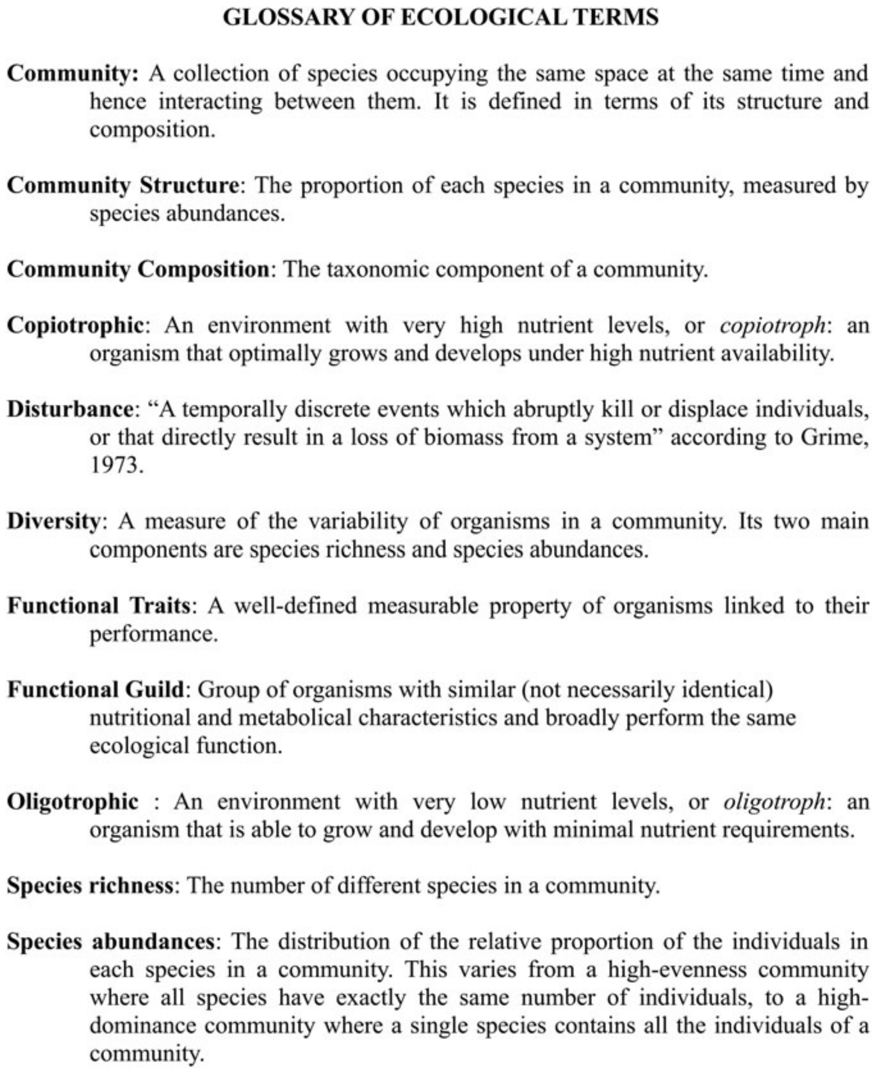


FIG. S3. (Continued).



GLOSSARY OF ECOLOGICAL TERMS

Community: A collection of species occupying the same space at the same time and hence interacting between them. It is defined in terms of its structure and composition.

Community Structure: The proportion of each species in a community, measured by species abundances.

Community Composition: The taxonomic component of a community.

Copiotrophic: An environment with very high nutrient levels, or *copiotroph*: an organism that optimally grows and develops under high nutrient availability.

Disturbance: "A temporally discrete events which abruptly kill or displace individuals, or that directly result in a loss of biomass from a system" according to Grime, 1973.

Diversity: A measure of the variability of organisms in a community. Its two main components are species richness and species abundances.

Functional Traits: A well-defined measurable property of organisms linked to their performance.

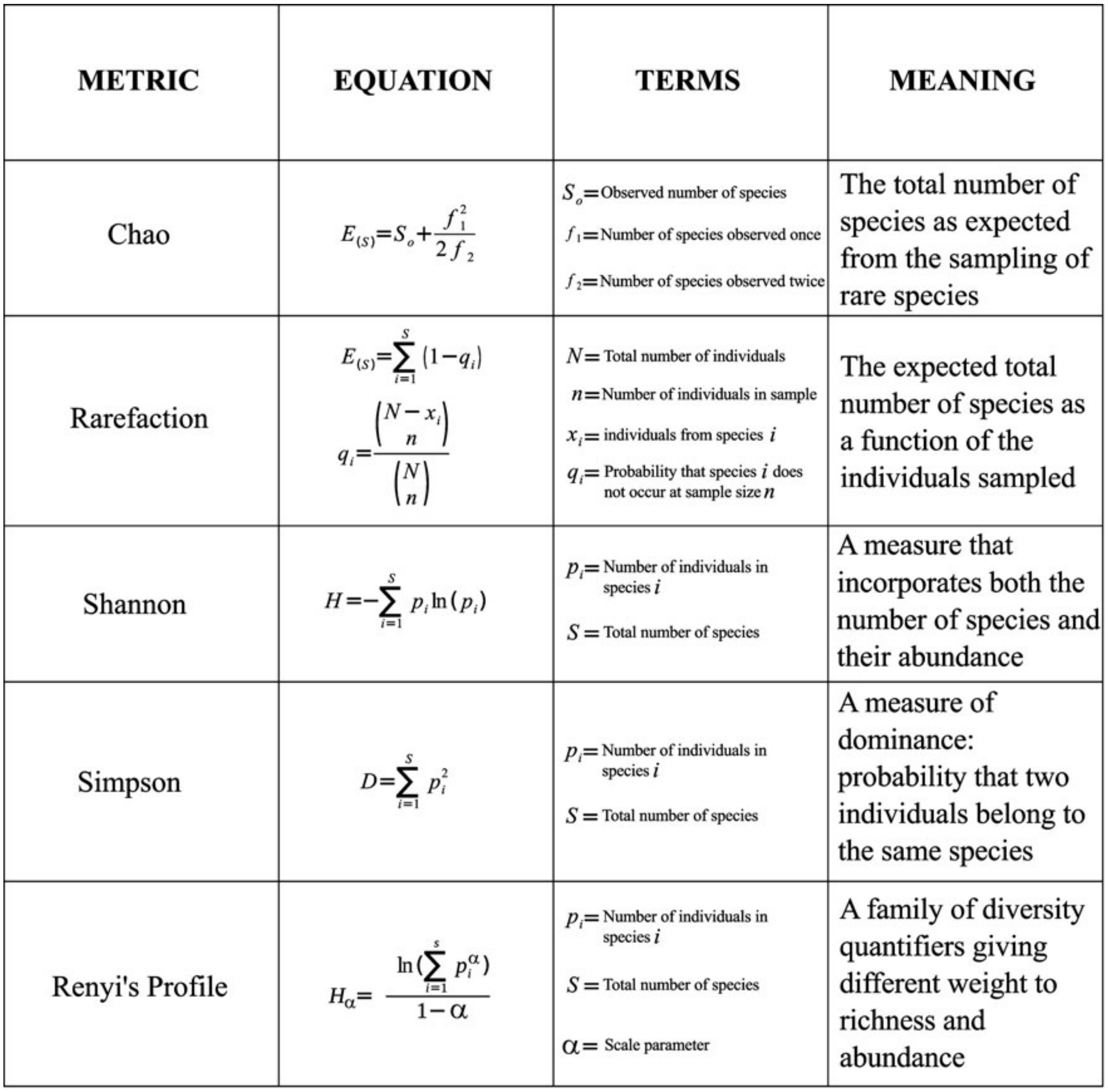
Functional Guild: Group of organisms with similar (not necessarily identical) nutritional and metabolical characteristics and broadly perform the same ecological function.

Oligotrophic : An environment with very low nutrient levels, or *oligotroph*: an organism that is able to grow and develop with minimal nutrient requirements.

Species richness: The number of different species in a community.

Species abundances: The distribution of the relative proportion of the individuals in each species in a community. This varies from a high-evenness community where all species have exactly the same number of individuals, to a high-dominance community where a single species contains all the individuals of a community.

FIG. S4. Ecological appendix: (**a**) Glossary of ecological terms, (**b**) interpretation of the diversity metrics used in this study and (**c**) guide to the interpretation of Renyi profiles.

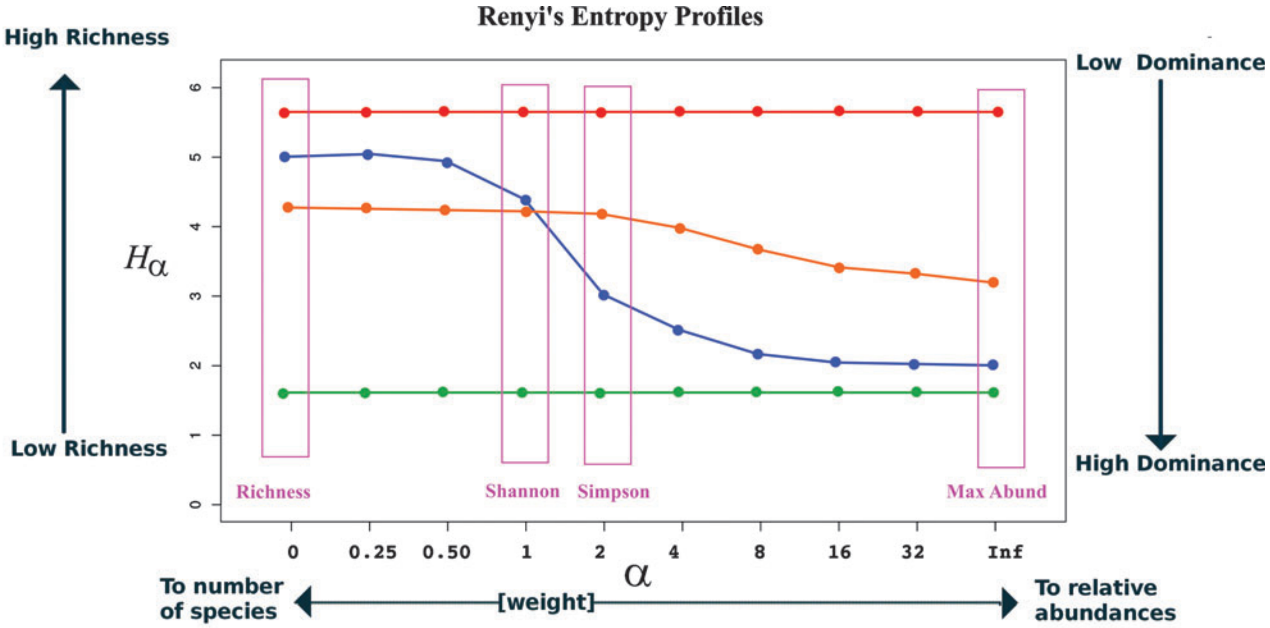


METRIC	EQUATION	TERMS	MEANING
Chao	$E_{(S)}=S_o+\frac{f_1^2}{2f_2}$	$S_o=$ Observed number of species $f_1=$ Number of species observed once $f_2=$ Number of species observed twice	The total number of species as expected from the sampling of rare species
Rarefaction	$E_{(S)}=\sum_{i=1}^{S}(1-q_i)$ $q_i=\frac{\binom{N-x_i}{n}}{\binom{N}{n}}$	$N=$ Total number of individuals $n=$ Number of individuals in sample $x_i=$ individuals from species i $q_i=$ Probability that species i does not occur at sample size n	The expected total number of species as a function of the individuals sampled
Shannon	$H=-\sum_{i=1}^{S}p_i\ln(p_i)$	$p_i=$ Number of individuals in species i $S=$ Total number of species	A measure that incorporates both the number of species and their abundance
Simpson	$D=\sum_{i=1}^{S}p_i^2$	$p_i=$ Number of individuals in species i $S=$ Total number of species	A measure of dominance: probability that two individuals belong to the same species
Renyi's Profile	$H_\alpha=\frac{\ln(\sum_{i=1}^{s}p_i^\alpha)}{1-\alpha}$	$p_i=$ Number of individuals in species i $S=$ Total number of species $\alpha=$ Scale parameter	A family of diversity quantifiers giving different weight to richness and abundance

FIG. S4. (Continued).

METRIC	EQUATION	TERMS	MEANING
Sorensen	$D_S=1-\frac{2\,S_{AB}}{S_A+S_B}$	$S_{AB}=$ Number of species shared between communities A and B $S_A=$ Number of species in A $S_B=$ Number of species in B	A measure of the similarity based on species composition
Morisita-Horn	$D_{MH}=1-2\frac{\sum(\frac{S_{A,i}}{n})(\frac{S_{B,i}}{m})}{\sum(\frac{S_{A,i}}{n})^2\sum(\frac{S_{B,i}}{m})^2}$	$S_{A,i}=$ Number of individuals from species *i* in community *A* $S_{B,i}=$ Number of individuals from species *i* in community *B* $n=$ Total individuals in *A* $m=$ Total individuals in *B*	A measure of similarity based on species composition and abundance
UniFrac	$U=\frac{\sum_{i=1}^{N} l_i\lvert A_i-B_i\rvert}{\sum_{i=1}^{N} l_i\,max(A_i, Bi)}$	$l_i=$ branch length between node *i* and its parental node $A_i=$ Binary indicator of the presence or absence of node *i* in sample *A* $B_i=$ Binary indicator of the presence or absence of node *i* in sample *A*	A measure of similarity based on the phylogenetic distance between members of two communities
Weighted UniFrac	$W=\frac{\sum_{i=1}^{N} l_i\left\lvert\frac{A_i}{A_T}-\frac{B_i}{B_T}\right\rvert}{\sum_{j=1}^{N} L_j(\frac{A_j}{A_T}+\frac{B_j}{B_T})}$	$l_i=$ branch length between tip node *i* and its parental node $L_j=$ Total branch length from the root to tip node *i* $A_i=$ Number of tip nodes in *A* that descend from node *j* $B_i=$ Number of tip nodes in *B* that descend from node *j* $A_T=$ Total number of tip nodes in *A* $B_T=$ Total number of tip nodes in *B*	A measure of similarity based on phylogenetic distance and relative abundance

FIG. S4. (Continued).



Renyi's Entropy profiles were developed as an extension of Shannon's entropy index to a scaling series that gives increasing weight to the relative abundance of species and decreasing weight to the number of species in a community. Common diversity indices are single moments of this function. In this sense, a measure of species richness is given when the scaling parameter equals to zero ($\alpha = 0$); Shannon's index is given when $\alpha = 1$; Simpson's index is given when $\alpha = 2$; and the relative abundance of the most abundant species (the proportion of the most dominant species) is given when α tends to infinity.

In a profile plot, a community is more diverse if it is higher in the plot, with more richness as it is higher on the left side and less dominant as it gets higher on the right side. In theory, a community can be called more diverse than another if each and every of the points along its profile line are above the points of the other communities (red profile in the figure above), and a community will be less diverse if all points are below the others (green profile). When profiles intersect, they can not be ranked in total diversity, since the one with higher points on the left side (blue profile) has more species, but it will be more dominated by few species than its intersect (orange profile). The latter will have less species since it has lower points on the left side, but its individuals will be more evenly distributed across all species.

FIG. S4. (Continued).