

***Cyanobacteria* and Alphaproteobacteria may facilitate cooperative interactions in niche communities**

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Figure S1. Venn diagram indicating the distribution of taxa between total and potentially-active hypolithic communities.

Figure S2. Significant differences (two-sided Welch's t-test; $P < 0.05$) in the relative abundances of microbial taxa between total (DNA, blue) and potentially-active (RNA, red) communities at the (A) domain and (B) phylum levels.

Figure S3. Significant differences (two-sided Welch's t-test; $P < 0.05$) in the relative abundances of microbial taxa between total (DNA, blue) and potentially-active (RNA, red) communities at the family level.

Figure S4. Highly-connected clusters (A-E) identified using the MCODE application within Cytoscape. Nodes represent *Cyanobacteria* (green), *Proteobacteria* (dark blue), heterotrophic bacteria (orange). Lines connecting nodes (edges) are significant ($P < 0.05$) positive (light blue) or negative (red) relationships. Node size is proportional to the number of reads assigned to the taxon. Module hubs are squares, connectors are shown as diamonds, and peripherals are indicated by circles.

Table S1. Network statistics of the potentially-active hypolith sub-cluster networks.

Figure S1.

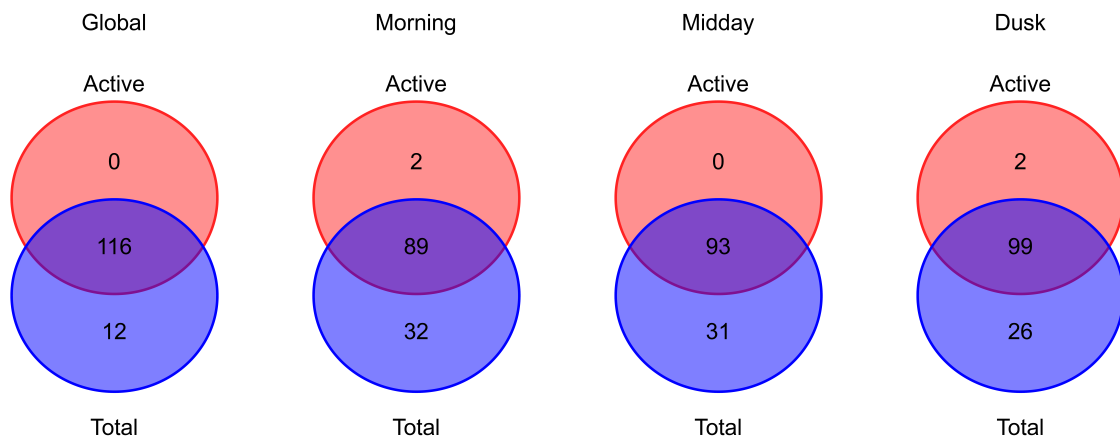


Figure S2.

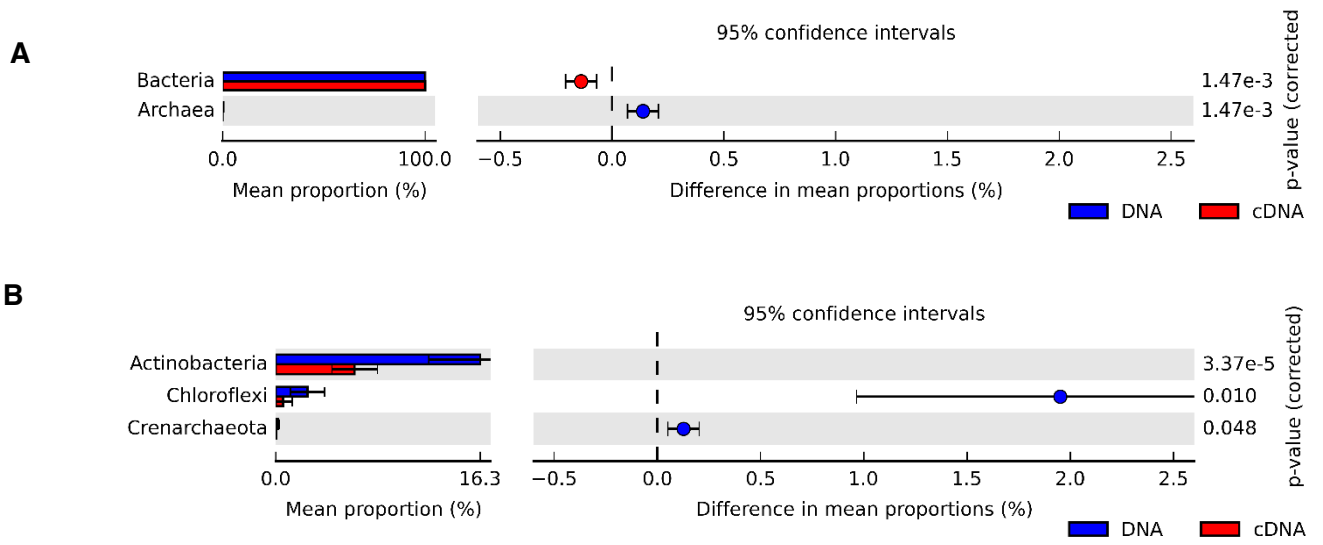


Figure S3.

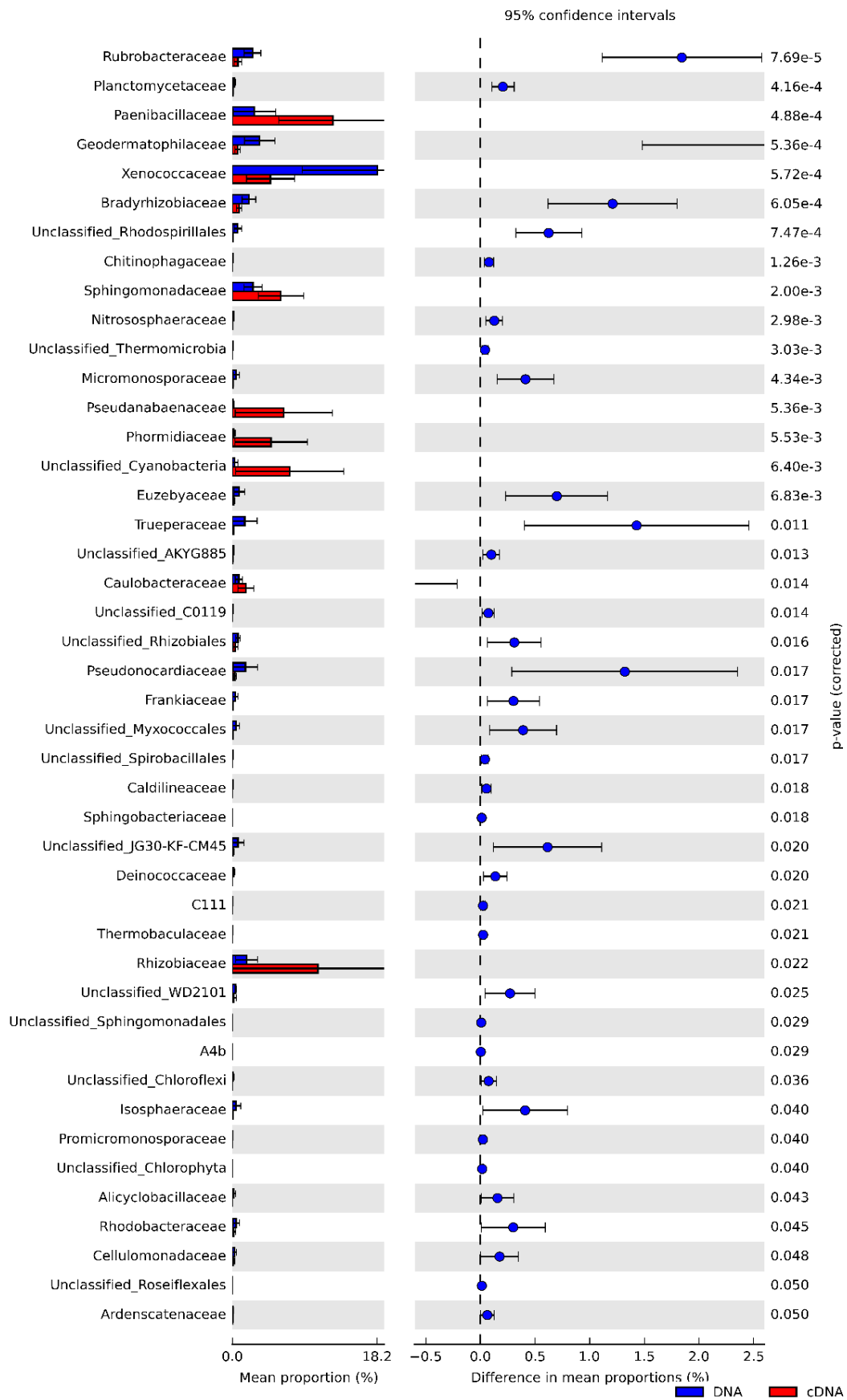


Figure S4.

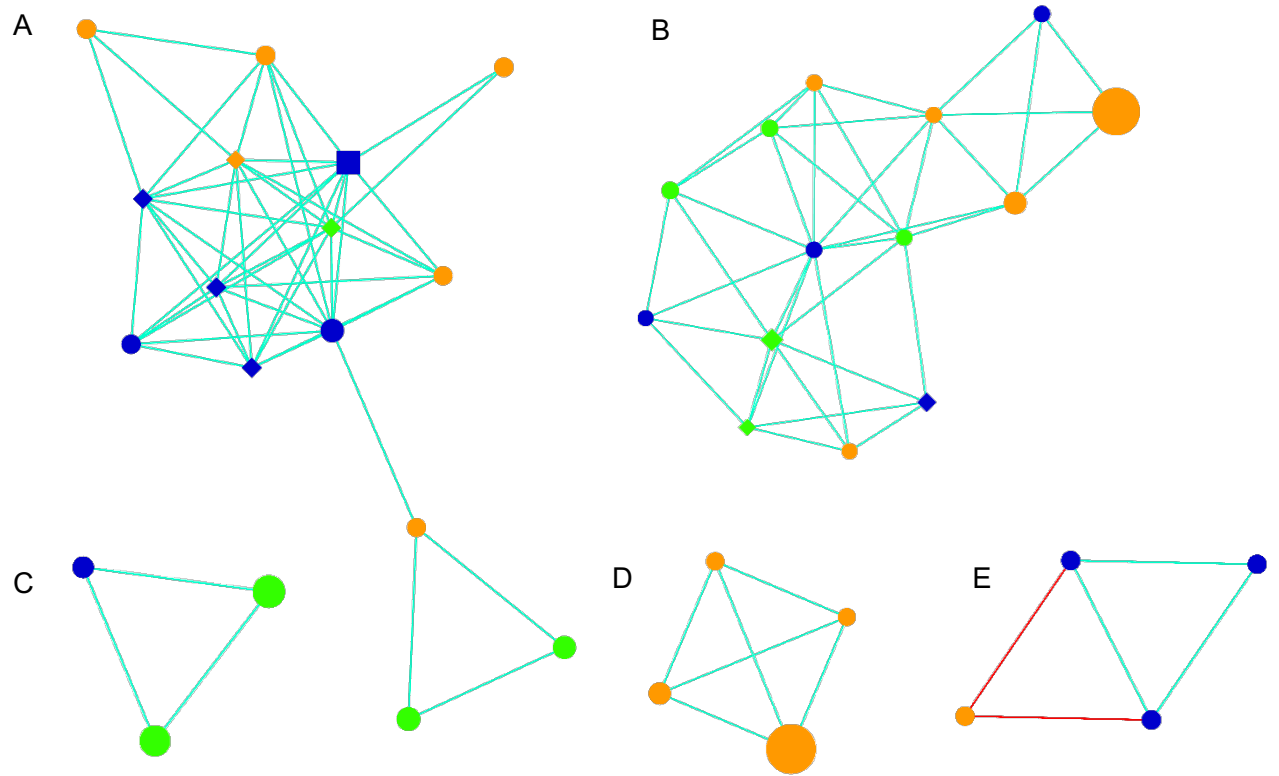


Table S1. Network statistics of the potentially-active hypolith sub-cluster networks.

Topological Features	Cluster A	Cluster B	Cluster C	Cluster D	Cluster E
Average node connectivity	7.33	5.75	2.67	-	-
Average path distance (GD)	1.83	1.73	1.17	1	1
Network diameter	4	3	2	1	1
Average clustering coefficient (avgCC)	0.786	0.697	0.833	1	1
Nodes	17	14	4	3	3
Edges (total)	60	37	5	3	3
Positive edges	60	37	3	3	3
Negative edges	0	0	2	0	0