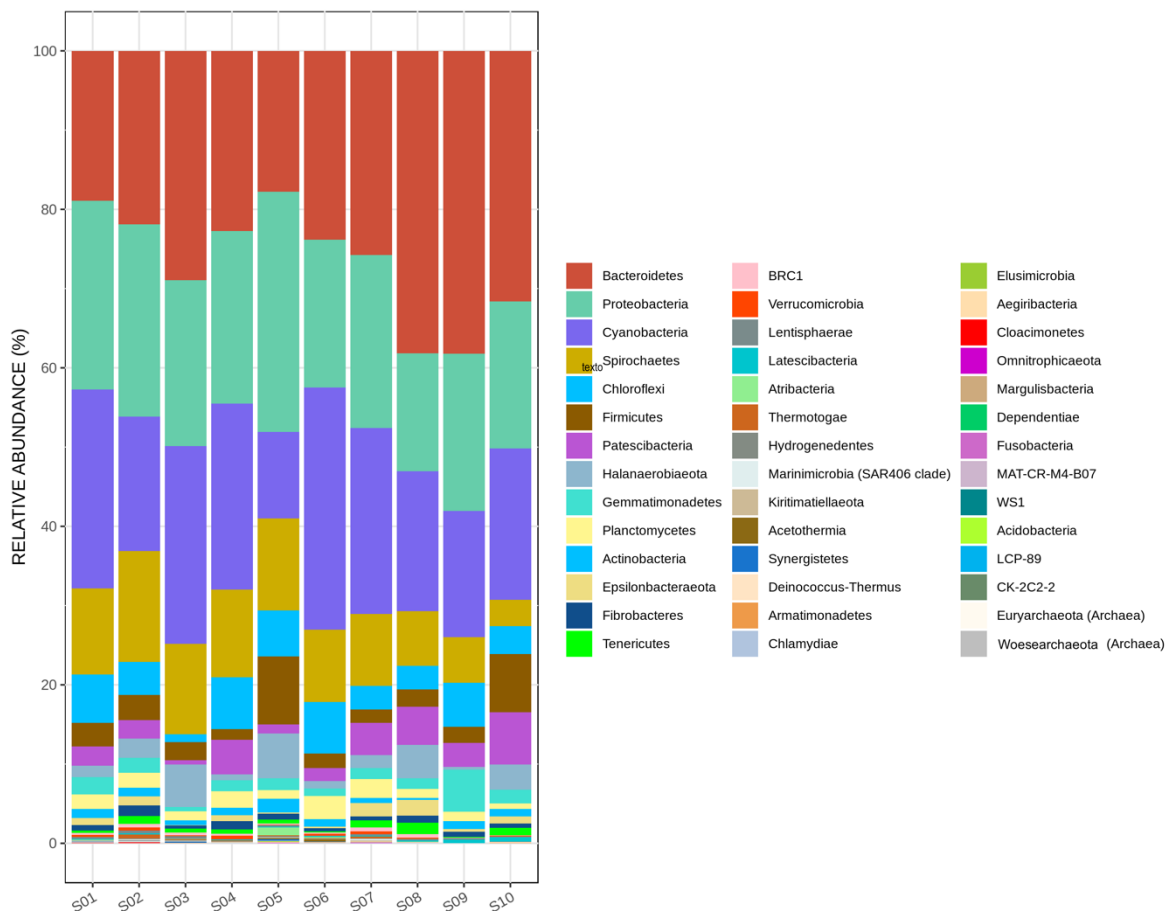


Supplementary materials

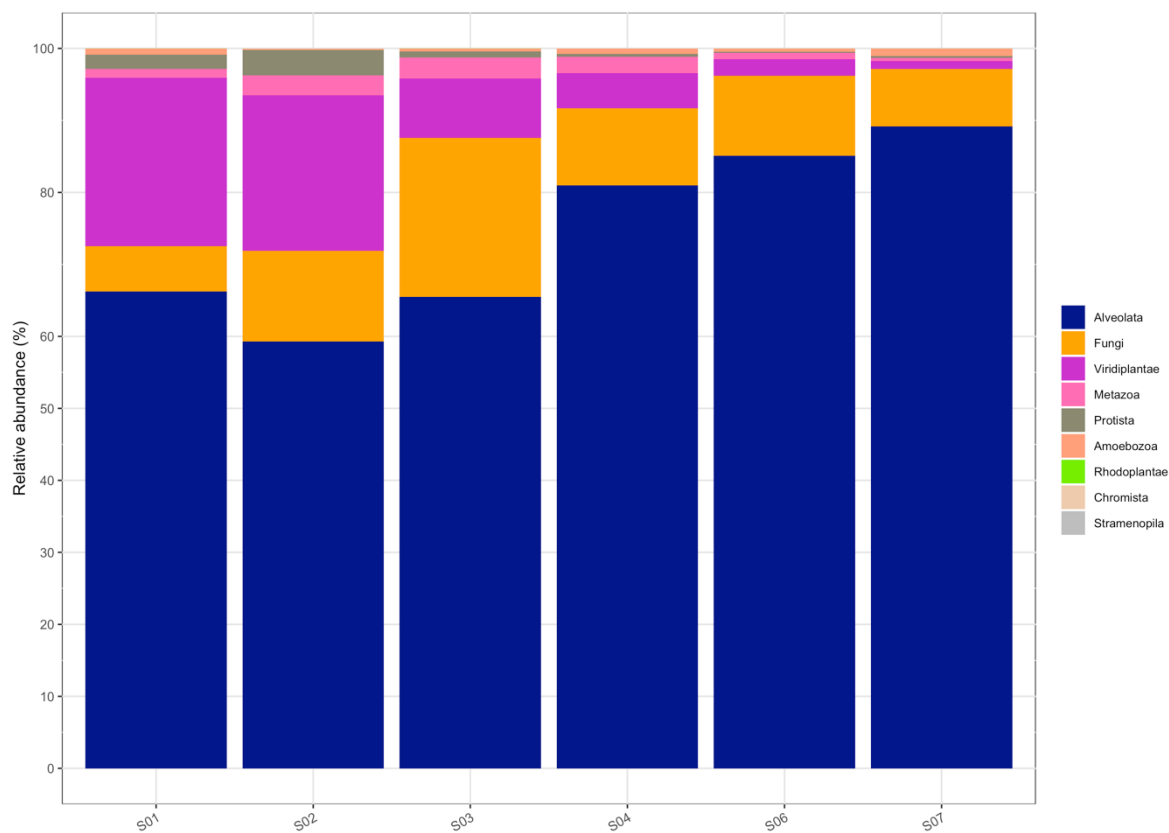
A



Suppl. Fig. 1

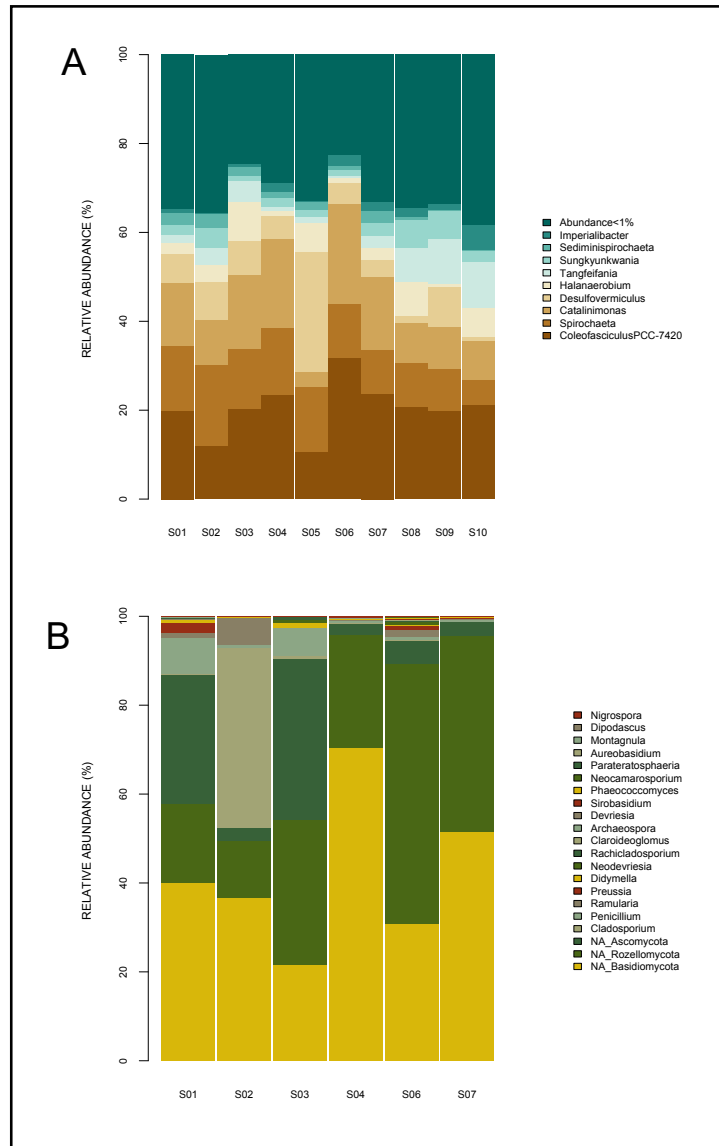
(A) Phylum composition within 16S rRNA gene database (B) Kingdom composition (based on UNITE database eukaryotic taxonomy) within Forward-Only ITS region database.

B



Suppl. Fig. 1

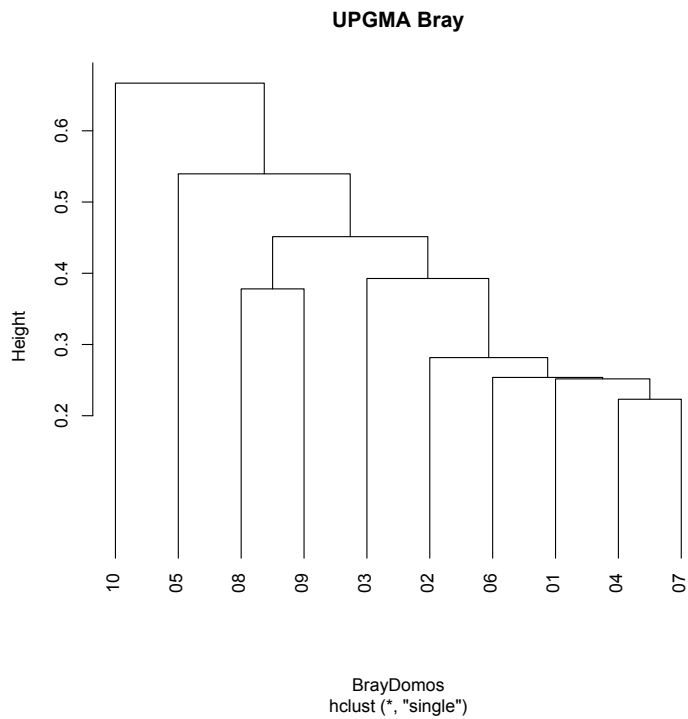
(A) Phylum composition within 16S rRNA gene database (B) Kingdom composition (based on UNITE database eukaryotic taxonomy) within Forward-Only ITS region database.



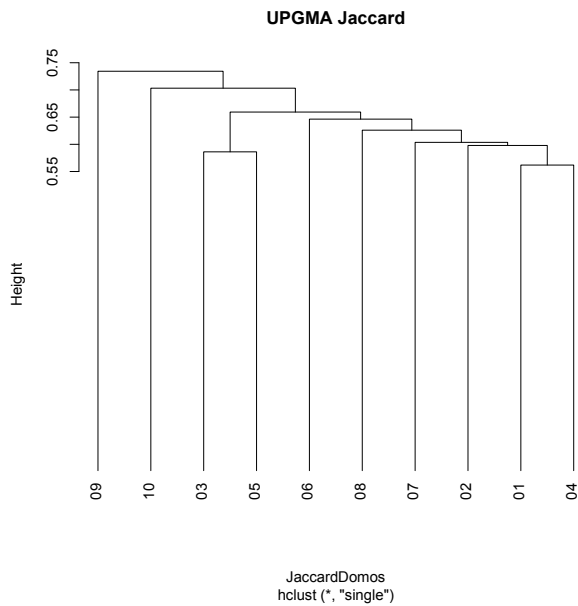
Suppl. Fig. 2

Rarefaction curves for 16S rRNA gene database (A) and ITS region Forward-Only ITS database (B).

A 16S Bray-Curtis



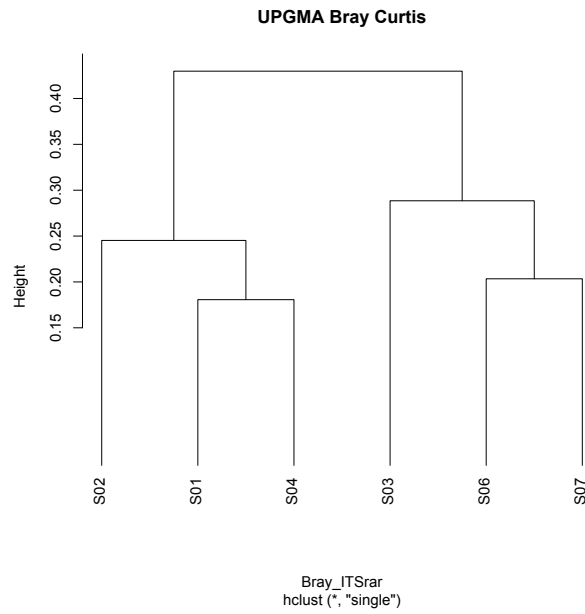
A 16S Jaccard



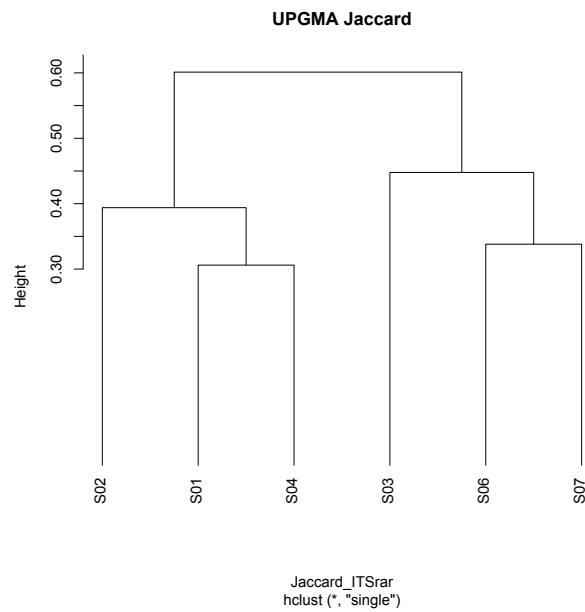
Suppl. Fig. 3

UPGMA dendrogram showing composition similarities among sampling sites (Forward-Only ITS database for Eucarya UPGMA). Branch length represent Bray-Curtis and Jaccard-1 dissimilarity coefficient, based on (A) abundance of 16S rDNA sequences ASVs, and (B) abundance of ITS region database ASVs. The numbers (height) are Bray-Curtis and Jaccard values.

B ITS Bray-Curtis



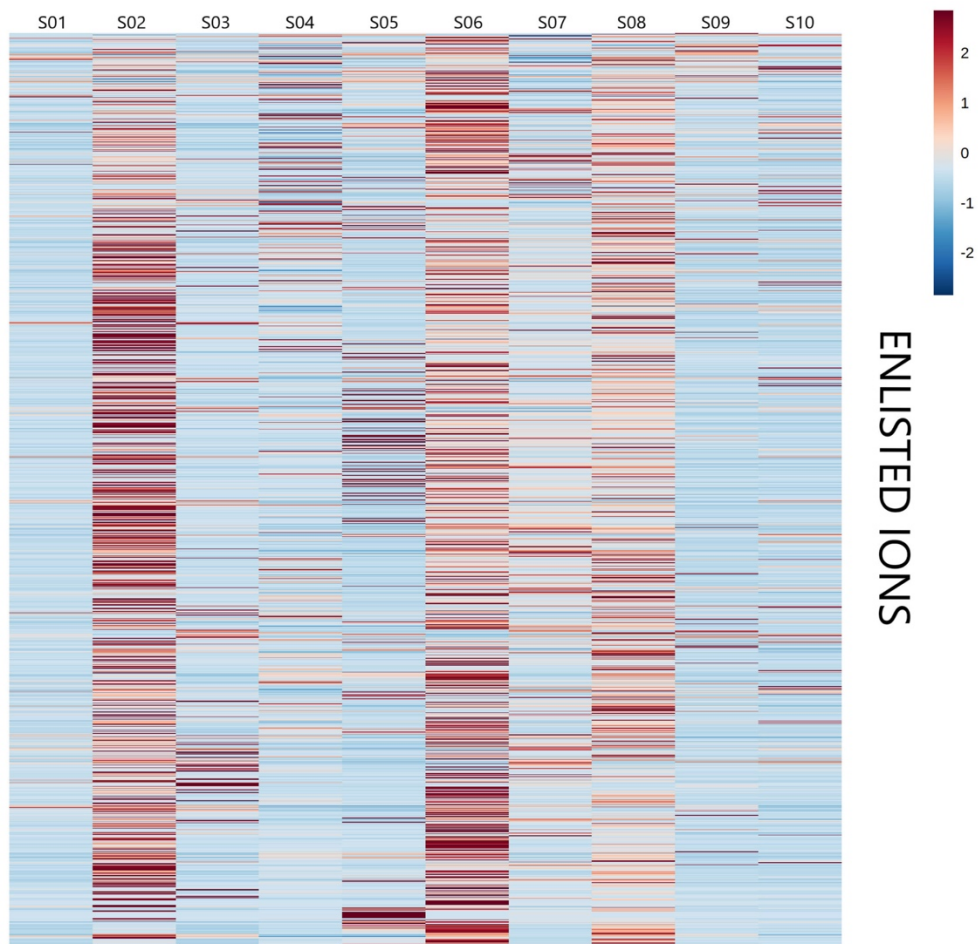
B ITS Jaccard



Suppl. Fig. 3

UPGMA dendrogram showing composition similarities among sampling sites (Forward-Only ITS database for Eucarya UPGMA). Branch length represent Bray-Curtis and Jaccard-1 dissimilarity coefficient, based on (A) abundance of 16S rDNA sequences ASVs, and (B) abundance of ITS region database ASVs. The numbers (height) are Bray-Curtis and Jaccard values.

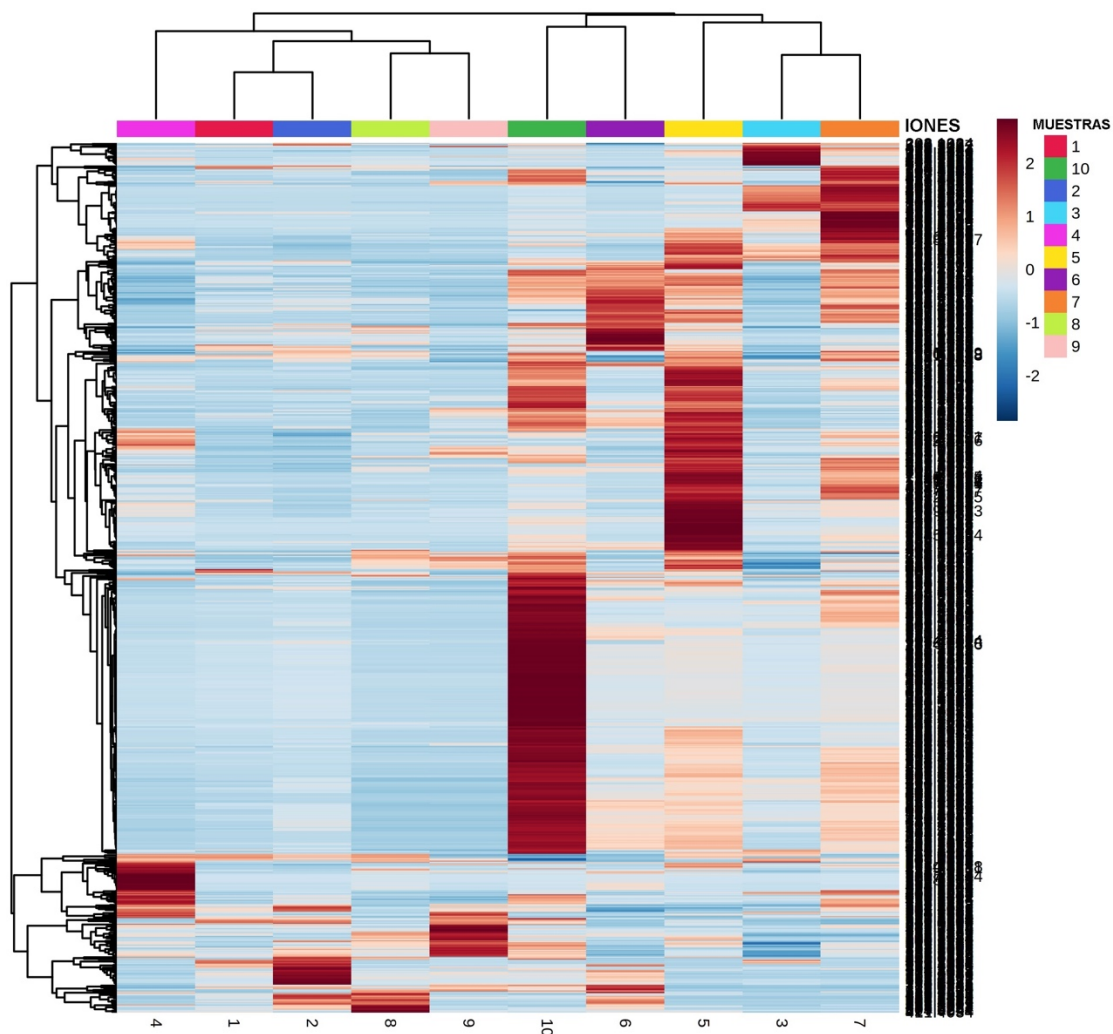
A



Suppl. Figure 4

Heatmap analysis showing relative abundance of metabolite features (MS ions in positive mode) in the Archaeal Domes mats samples. On the scale bar, brick red color indicates increased metabolite levels, and blue color represents decreased levels. A shows non clustered samples and sites, B clustered samples and sites.

B



Suppl. Figure 4

Heatmap analysis showing relative abundance of metabolite features (MS ions in positive mode) in the Archaeal Domes mats samples. On the scale bar, brick red color indicates increased metabolite levels, and blue color represents decreased levels. A shows non clustered samples and sites, B clustered samples and sites.

	% ITS library
<i>Fuscheria nodosa</i> (Alveolata)	0.0261
<i>Enchelys gasterosteus</i> (Alveolata)	0.0014
<i>Strombidium guangdongense</i> (Alveolata)	0.0214
<i>Fabrea salina</i> (Alveolata)	0.5524
<i>Nassula labiata</i> (Alveolata)	0.0007
<i>Paracladotricha salina</i> (Alveolata)	0.0207
<i>Thraustochytrium aureum</i> (Stramenopila)	0.0021
Uncultured Amoebozoa (Amoebozoa)	0.0043
<i>Vannella simplex</i> (Amoebozoa)	0.6675
<i>Chlamydomonadales</i> sp. (Viridiplantae)	0.0035
<i>Hamakko caudatus</i> (Viridiplantae)	0.0018
<i>Eleusine indica</i> (Viridiplantae)	0.0078
<i>Nephelochloa orientalis</i> (Viridiplantae)	0.0086

Suppl. Table 1.

List of ASVs Blast hits with <90%, of non-fungal Merge ITS database.

	Possitive	Negative
Arquea total	80	9
Arch-Bact	18	5
Arch-Arch	32	0
Arch-Fung	19	4
Arch-Euk	11	0
Bacteria total	63	22
Bac-Bact	18	9
Bact-Arch	18	5
Bact-Fung	9	5
Bact-Euk	18	3
Fungi total	49	14
Fung-Bact	9	5
Fung-Arch	19	4
Fung-Fung	10	3
Fung-Euk	11	2
Euk total	44	6
Euk-Bact	18	3
Euk-Arch	11	0
Euk-Fung	11	2
Euk-Euk	4	1

Suppl. Table 3.

Counts of significant negative and positive correlations from Pearson Correlation Analysis (Figure 5).

Tentatively identified microbial metabolites in samples S1-S10 by GNPS and detailed metabolomic analysis.

Observed <i>m/z</i> [M+H] ⁺	Molecular formula	Mass error (in ppm)	Tentative identification	Sample
290.0811	C ₁₈ H ₁₁ NO ₃	-0.2	nostodione A	S2,S6-S8
316.2032	C ₁₈ H ₂₅ N ₃ O ₂	+3.9	indolactam 1, martensine A	S1-S10
317.2229	C ₁₉ H ₂₈ N ₂ O ₂	+1.9	benzastatin A	S2,S4,S5,S7,S9,S10
318.2433	C ₂₀ H ₃₁ NO ₂	+1.7	periconiasin G	S1-3,S6,S7,S9,S10
319.1182	C ₁₇ H ₁₈ O ₆	+1.7	dechlorogriseofulvin	S7
319.1655	C ₁₇ H ₂₂ N ₂ O ₄	+0.8	phomamide, daryamide C, yomaymycin I	S1-S10
353.0792	C ₁₇ H ₁₇ ClO ₆	+1.6	griseofulvin	S7
387.1797	C ₂₂ H ₂₆ O ₆	-1.3	gibbestatin B, furaquinocin H, colletofragarone A1, pitholide B, dideacetylparasiticolide A.	S1-S10
496.3401	C ₃₁ H ₄₅ NO ₄	-4.1	8,9-dihydroindanomycin, neindanomycin	S1-S9
515.2636	C ₂₉ H ₃₈ O ₈	-0.7	citreo hybridone B, setosusin, roridin E, ganoboninone A	S1-S9
256.1026	ND	ND	^a	S1-S10
304.2995	ND	ND	^a	S1-S10
1068.4847	ND	ND	^a	S1-S10

ND, not determined; ^a, potentially new compound.

Suppl. Table 4.

Tentatively identified microbial metabolites in samples S1-S10 by GNPS and detailed metabolomic analysis.

	psc_16S	psc_rar_16S	psc_abun_16S	psc_ITS	psc_rar_ITS	psc_abun_ITS
S1	0.11060947	0.30236487	0.04866875	0.10968344	0.30487551	0.10002044
S2	0.10863735	0.29149669	0.0605547	0.09490329	0.2868876	0.10927695
S3	0.09063427	0.27552425	0.05493335	0.08496886	0.26553793	0.12463795
S4	0.11408563	0.32433312	0.05225602	0.11582347	0.30695845	0.09225003
S5	0.07809136	0.24593114	0.04262518			
S6	0.11513793	0.30216016	0.08670753	0.11553622	0.29763445	0.1295801
S7	0.11590233	0.30581557	0.07509745	0.12709692	0.37551424	0.11824146
S8	0.07955718	0.24829185	0.04620871			
S9	0.13062694	0.34927144	0.07490645			
S10		0.1354835	0.33490847	0.08888336		

Suppl. Table 5
nmdPSC values