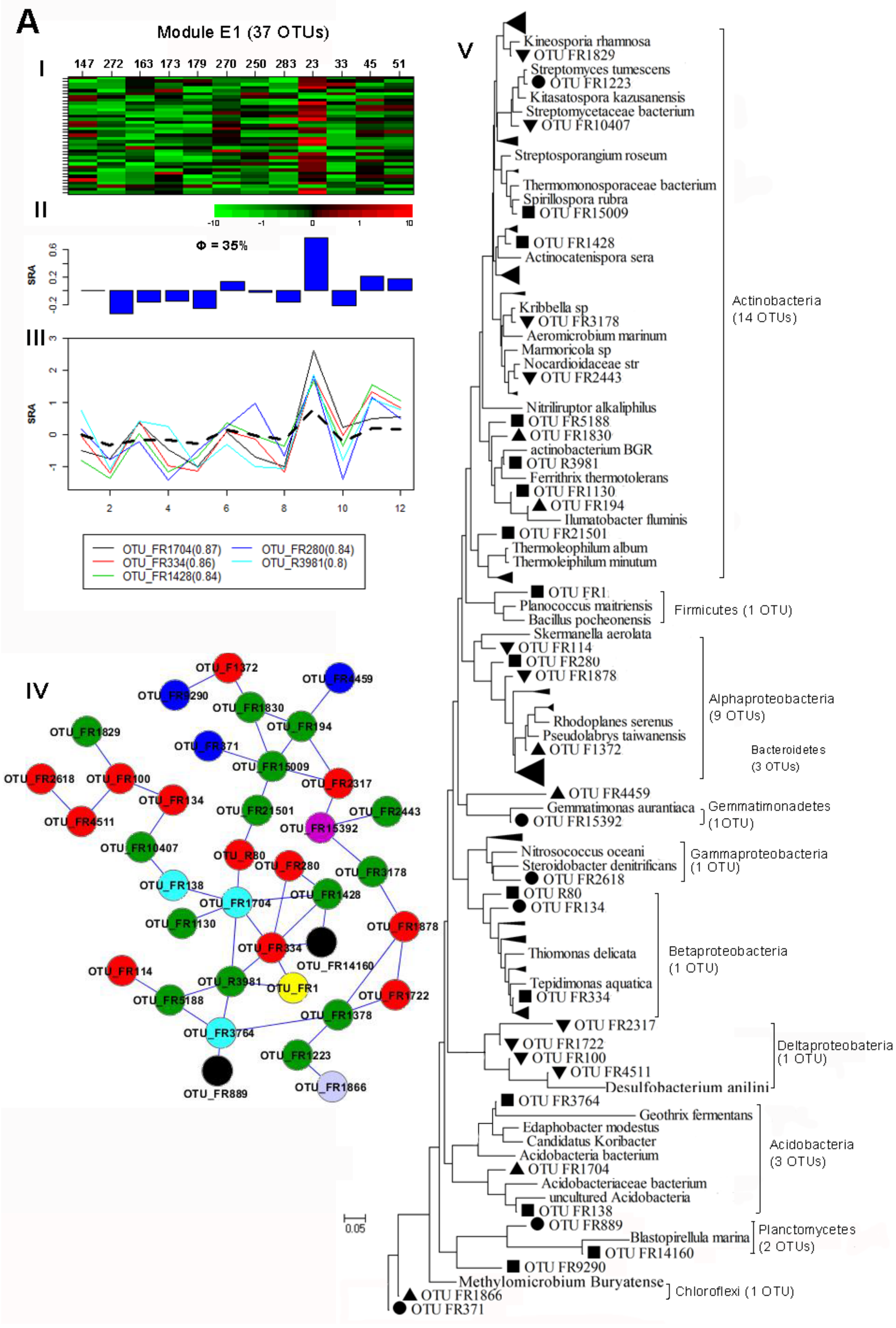
Supplemental text for “Phylogenetic Molecular Ecological Network of Soil Microbial Communities in Response to Elevated CO_2”

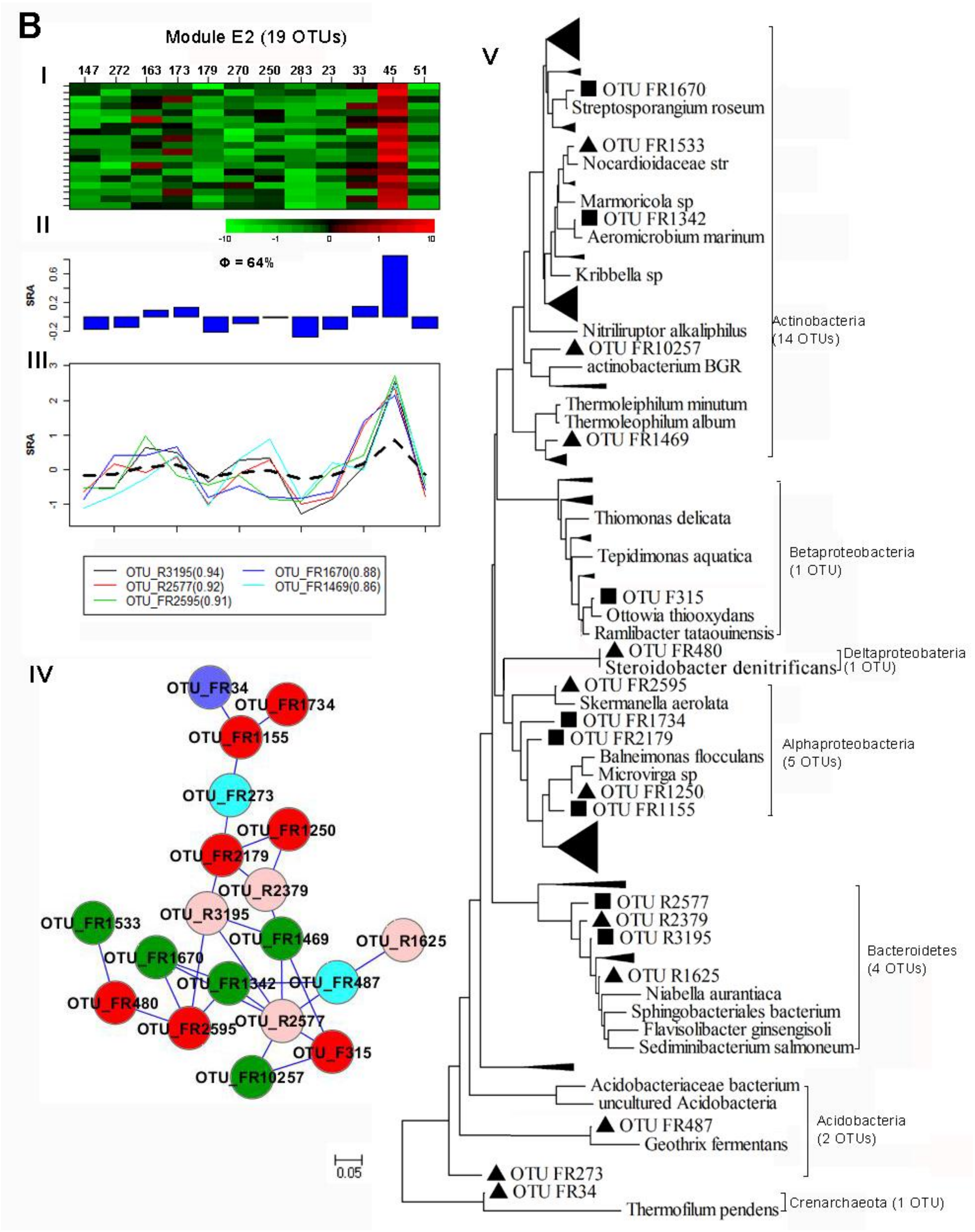
Module eigengene analyses on eCO2 and aCO2 phylogenetic molecular ecological network analysis

1) Supplemental Figures of module eigengene analyses

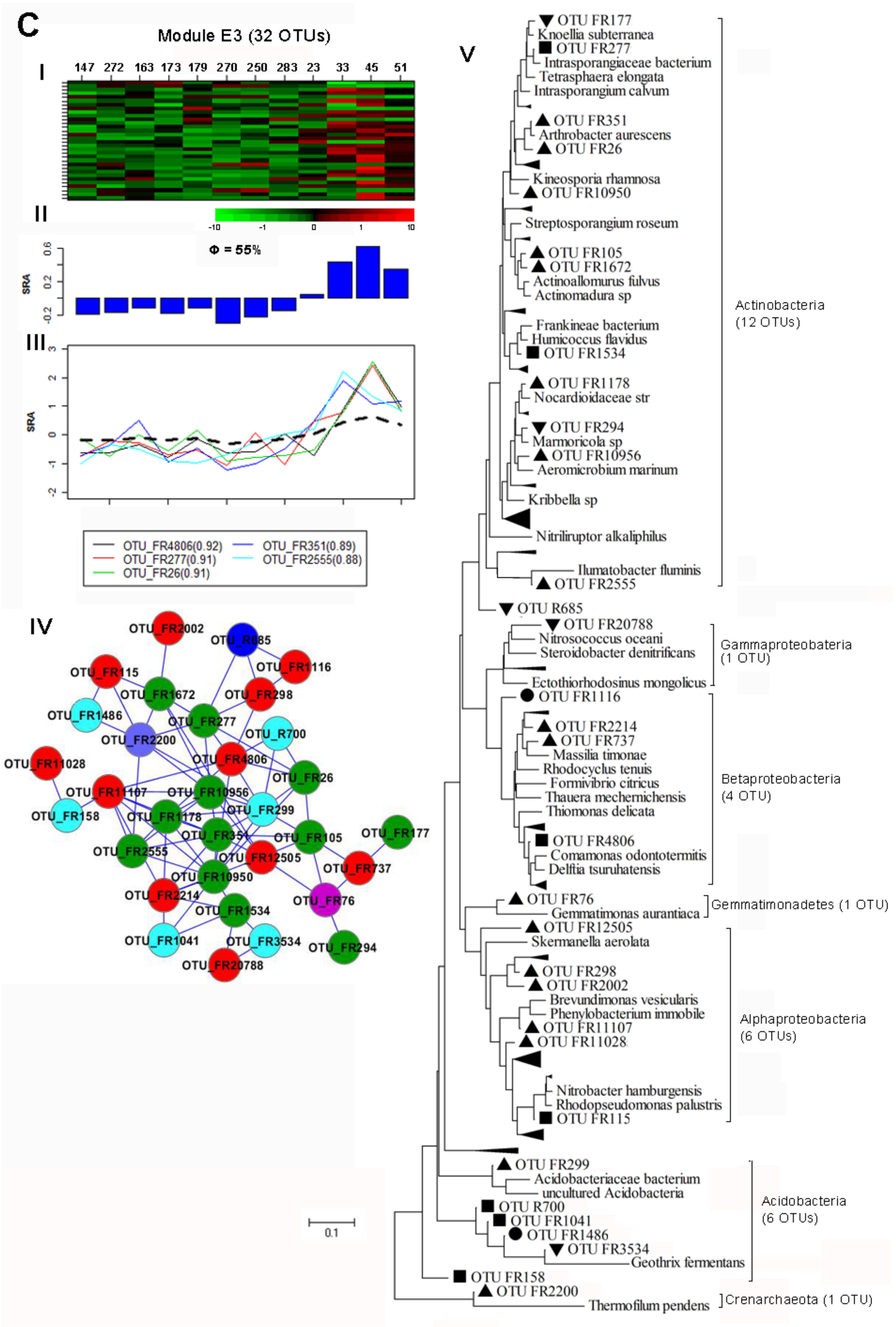
1. **Online Fig. 1**. Eigengene network analysis of individual modules (A-J) under eCO_2. Only the modules with ≥ 5 nodes were displayed here. (I) Heatmap of the standardized relative abundance (SRA) of OTUs across different samples. Rows correspond to individual OTUs in the module whereas columns are the samples. The number above each column is the experimental plot number in the BioCon experiment. Red color corresponds to the OTUs whose SRAs are > 0 and green color signifies those are < 0. (II). Eigengene. SRA of the corresponding eigengene (y-axis) across the samples (x-axis). The paramter (Φ) indicates the perecentage of the total variance expalined by the eigengene. (III) Module memberships identifies groups of OTUs that consistently co-exist in these microbial communities. Only 5 OTUs with signficant module memberships were shown in this figure where y-axis is SRA and x-axis is individual samples. The numbers in parenthesis indicate the values of module memberships. (IV) Module visualization to show the interactions among different OTUs within the module. Blue line, positive interactive (positive correlation), red line, negative interaction (negative correlation). The different colors of the shading of nodes represent different phylogenetic groups (see Fig. S5 for their meanings). (V) Phylogenetic tree to show the relationships of the OTUs observed in the corresponding module. The tree was constructed with Neighbor-Joining approach with 1,000 bootstrap. Due to space limitation, bootstrap percentages were not shown on the tree. The symbols before individual OTUs signified different features of nodes in the module. ▲ indicates that the OTU exists in both aCO_2 and eCO_2 networks with significant module memberships; ■ indicates that the OTU has significant module membership but not shared in the corresponding network under aCO_2; ● indicates that the OTU shared but without significant module membership; while ▼ indicates that the OTU neither shared nor had significant module membership.


A
Module E1 (37 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
II
-10 -1 0 1 10
Φ = 35%
SRA
0.6 0.2 -0.2
III
SRA
3 2 1 0 -1
2 4 6 8 10 12
OTU_FR1704(0.87)
OTU_FR334(0.86)
OTU_FR1428(0.84)
OTU_FR280(0.84)
OTU_R3981(0.8)
IV
OTU_F1372
OTU_FR9290
OTU_FR4459
OTU_FR1830
OTU_FR1829
OTU_FR194
OTU_FR371
OTU_FR15009
OTU_FR2618
OTU_FR100
OTU_FR2317
OTU_FR134
OTU_FR21501
OTU_FR2443
OTU_FR4511
OTU_FR15392
OTU_FR10407
OTU_R80
OTU_FR280
OTU_FR3178
OTU_FR138
OTU_FR1704
OTU_FR1428
OTU_FR1130
OTU_FR1878
OTU_FR334
OTU_FR14160
OTU_FR114
OTU_R3981
OTU_FR1
OTU_FR1722
OTU_FR5188
OTU_FR1378
OTU_FR3764
OTU_FR1223
OTU_FR889
OTU_FR1866
0.05
V
Kineosporia rhamnosa
OTU FR1829
Streptomyces tumescens
OTU FR1223
Kitasatospora kazusanensis
Streptomycetaceae bacterium
OTU FR10407
Streptosporangium roseum
Thermomonosporaceae bacterium
Spirillospora rubra
OTU FR15009
OTU FR1428
Actinocatenispora sera
Kribbella sp
OTU FR3178
Aeromicrobium marinum
Marmoricola sp
Nocardioidaceae str
OTU FR2443
Nitriliruptor alkaliphilus
OTU FR5188
OTU FR1830
actinobacterium BGR
OTU R3981
Ferrithrix thermotolerans
OTU FR1130
OTU FR194
Ilumatobacter fluminis
OTU FR21501
Thermoleophilum album
Thermoleiphilum minutum
Actinobacteria
(14 OTUs)
OTU FR1
Planococcus maitriensis
Bacillus pocheonensis
Firmicutes (1 OTU)
Skermanella aerolata
OTU FR114
OTU FR280
OTU FR1878
Rhodoplanes serenus
Pseudolabrys taiwanensis
OTU F1372
Alphaproteobacteria
(9 OTUs)
Bacteroidetes
(3 OTUs)
OTU FR4459
Gemmatimonas aurantiaca
OTU FR15392
Gemmatimonadetes
(1OTU)
Nitrosococcus oceani
Steroidobacter denitrificans
OTU FR2618
Gammaproteobacteria
(1 OTU)
OTU R80
OTU FR134
Thiomonas delicata
Tepidimonas aquatica
OTU FR334
Betaproteobacteria
(1 OTU)
OTU FR2317
OTU FR1722
OTU FR100
OTU FR4511
Desulfobacterium anilini
Deltaproteobateria
(1 OTU)
OTU FR3764
Geothrix fermentans
Edaphobacter modestus
Candidatus Koribacter
Acidobacteria bacterium
OTU FR1704
Acidobacteriaceae bacterium
uncultured Acidobacteria
OTU FR138
Acidobacteria
(3 OTUs)
OTU FR889
Blastopirellula marina
OTU FR14160
Planctomycetes
(2 OTUs)
OTU FR9290
Methylomicrobium Buryatense
Chloroflexi (1 OTU)
OTU FR1866
OTU FR371

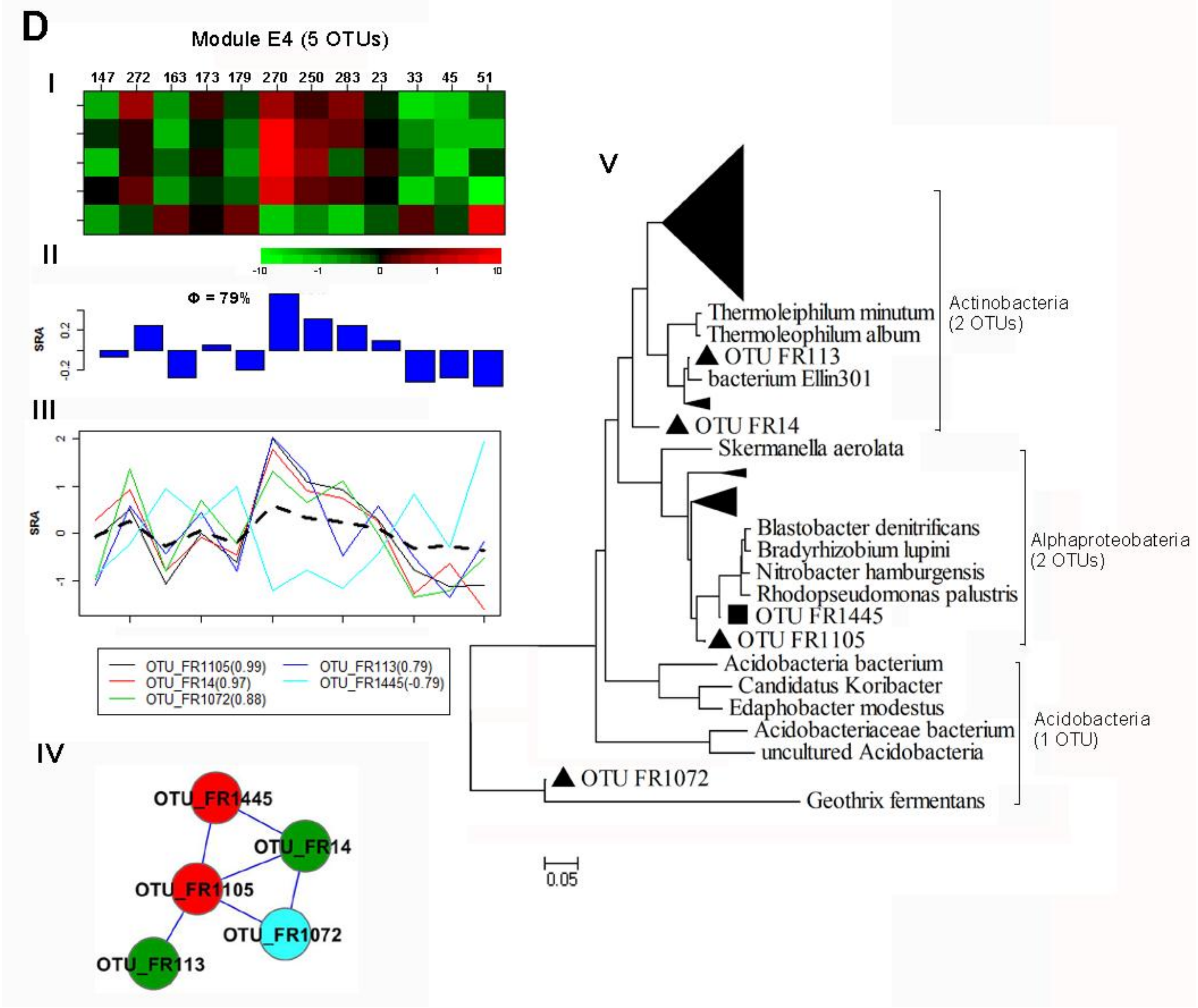
Online Fig. 1.


B
Module E2 (19 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
II
-10 -1 0 1 10
Φ = 64%
SRA
0.6 0.2 -0.2
III
SRA
3 2 1 0 -1
OTU_R3195(0.94)
OTU_R2577(0.92)
OTU_FR2595(0.91)
OTU_FR1670(0.88)
OTU_FR1469(0.86)
IV
OTU_FR34
OTU_FR1734
OTU_FR1155
OTU_FR273
OTU_FR1250
OTU_FR2179
OTU_R2379
OTU_R3195
OTU_FR1533
OTU_FR1469
OTU_R1625
OTU_FR1670
OTU_FR1342
OTU_FR487
OTU_FR480
OTU_FR2595
OTU_R2577
OTU_F315
OTU_FR10257
0.05
V
OTU FR1670
Streptosporangium roseum
OTU FR1533
Nocardioidaceae str
Marmoricola sp
OTU FR1342
Aeromicrobium marinum
Kribbella sp
Nitriliruptor alkaliphilus
OTU FR10257
actinobacterium BGR
Thermoleiphilum minutum
Thermoleophilum album
OTU FR1469
Actinobacteria (14 OTUs)
Thiomonas delicata
Tepidimonas aquatica
OTU F315
Ottowia thiooxydans
Ramlibacter tataouinensis
Betaproteobacteria (1 OTU)
OTU FR480
Steroidobacter denitrificans
Deltaproteobateria (1 OTU)
OTU FR2595
Skermanella aerolata
OTU FR1734
OTU FR2179
Balneimonas flocculans
Microvirga sp
OTU FR1250
OTU FR1155
Alphaproteobacteria (5 OTUs)
OTU R2577
OTU R2379
OTU R3195
OTU R1625
Niabella aurantiaca
Sphingobacteriales bacterium
Flavisolibacter ginsengisoli
Sediminibacterium salmoneum
Bacteroidetes (4 OTUs)
Acidobacteriaceae bacterium
uncultured Acidobacteria
OTU FR487
Geothrix fermentans
Acidobacteria (2 OTUs)
OTU FR273
OTU FR34
Thermofilum pendens
Crenarchaeota (1 OTU)

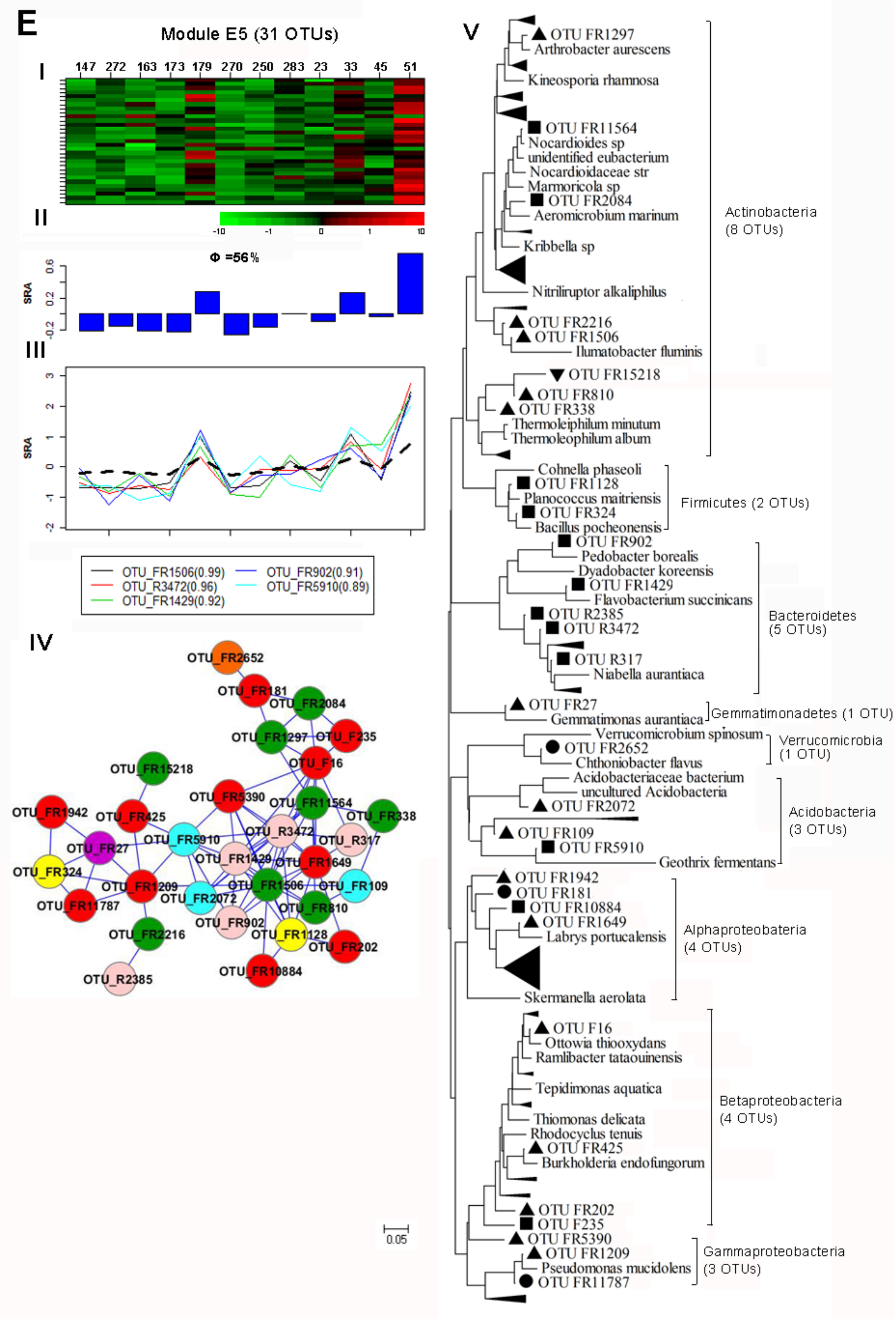
Online Fig. 1.

C
Module E3 (32 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
II
-10 -1 0 1 10
Φ = 55%
SRA
0.6 0.2 -0.2
III
SRA
3 2 1 0 -1 -2
OTU_FR4806(0.92)
OTU_FR277(0.91)
OTU_FR26(0.91)
OTU_FR351(0.89)
OTU_FR2555(0.88)
IV
OTU_FR2002
OTU_R685
OTU_FR115
OTU_FR1116
OTU_FR1672
OTU_FR298
OTU_FR1486
OTU_FR277
OTU_R700
OTU_FR2200
OTU_FR4806
OTU_FR11028
OTU_FR26
OTU_FR11107
OTU_FR10956
OTU_FR158
OTU_FR1178
OTU_FR299
OTU_FR351
OTU_FR105
OTU_FR177
OTU_FR2555
OTU_FR12505
OTU_FR737
OTU_FR10950
OTU_FR2214
OTU_FR76
OTU_FR1534
OTU_FR1041
OTU_FR3534
OTU_FR294
OTU_FR20788
V
OTU FR177
Knoellia subterranea
OTU FR277
Intrasporangiaceae bacterium
Tetrasphaera elongata
Intrasporangium calvum
OTU FR351
Arthrobacter aurescens
OTU FR26
Kineosporia rhamnosa
OTU FR10950
Streptosporangium roseum
OTU FR105
OTU FR1672
Actinoallomurus fulvus
Actinomadura sp
Frankineae bacterium
Humicoccus flavidus
OTU FR1534
OTU FR1178
Nocardioidaceae str
OTU FR294
Marmoricola sp
OTU FR10956
Aeromicrobium marinum
Kribbella sp
Nitriliruptor alkaliphilus
Ilumatobacter fluminis
OTU FR2555
Actinobacteria (12 OTUs)
OTU R685
OTU FR20788
Nitrosococcus oceani
Steroidobacter denitrificans
Ectothiorhodosinus mongolicus
Gammaproteobateria (1 OTU)
OTU FR1116
OTU FR2214
OTU FR737
Massilia timonae
Rhodocyclus tenuis
Formivibrio citricus
Thauera mechernichensis
Thiomonas delicata
OTU FR4806
Comamonas odontotermitis
Delftia tsuruhatensis
Betaproteobacteria (4 OTU)
OTU FR76
Gemmatimonas aurantiaca
Gemmatimonadetes (1 OTU)
OTU FR12505
Skermanella aerolata
OTU FR298
OTU FR2002
Brevundimonas vesicularis
Phenylobacterium immobile
OTU FR11107
OTU FR11028
Nitrobacter hamburgensis
Rhodopseudomonas palustris
OTU FR115
Alphaproteobacteria (6 OTUs)
OTU FR299
Acidobacteriaceae bacterium
uncultured Acidobacteria
OTU R700
OTU FR1041
OTU FR1486
OTU FR3534
Geothrix fermentans
Acidobacteria (6 OTUs)
OTU FR158
OTU FR2200
Thermofilum pendens
Crenarchaeota (1 OTU)
0.1

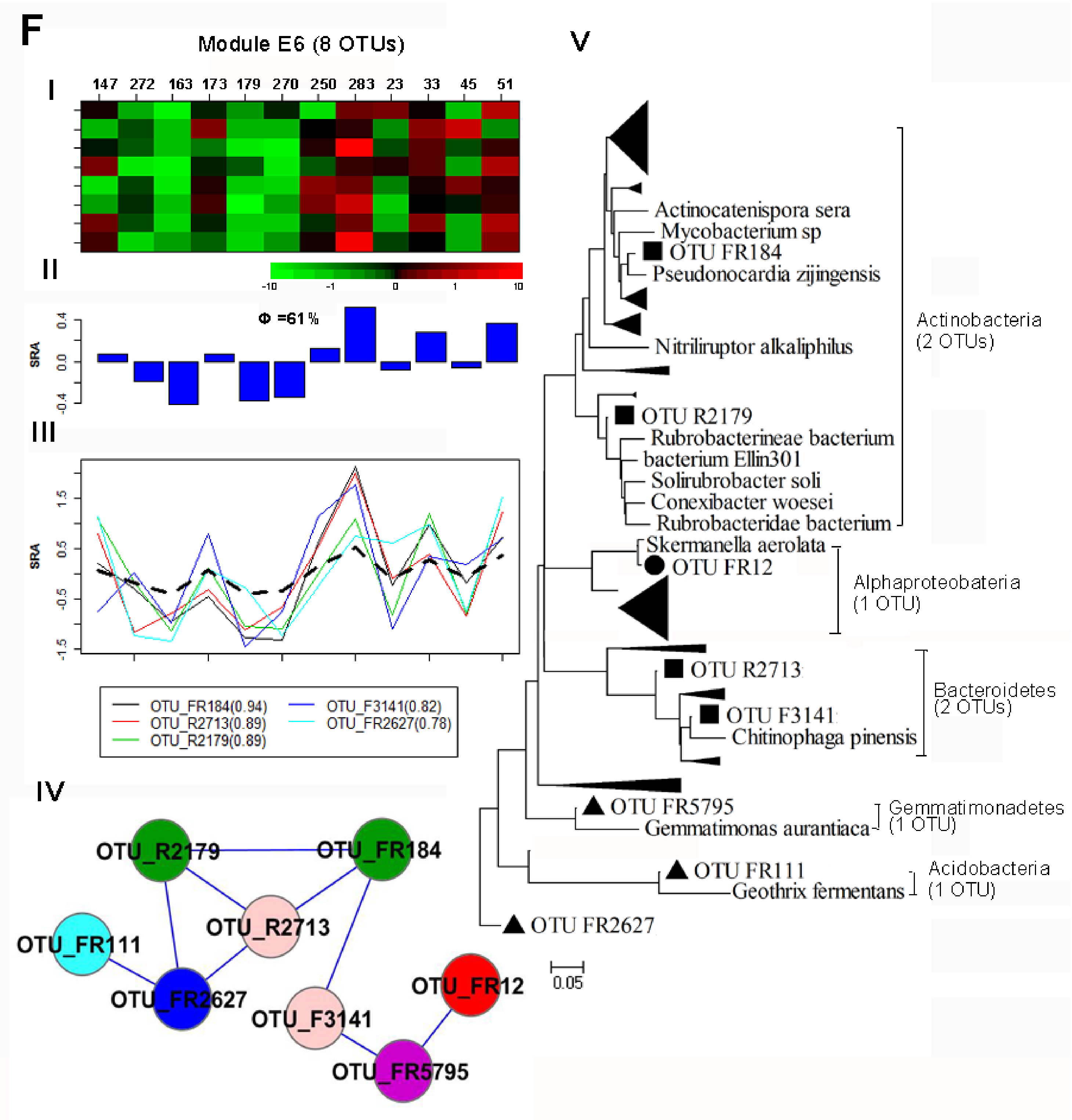
Online Fig. 1.


D
Module E4 (5 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
-10 -1 0 1 10
II
Φ = 79%
SRA
0.2
-0.2
III
SRA
2
1
0
-1
OTU_FR1105(0.99)
OTU_FR14(0.97)
OTU_FR1072(0.88)
OTU_FR113(0.79)
OTU_FR1445(-0.79)
IV
OTU_FR1445
OTU_FR14
OTU_FR1105
OTU_FR1072
OTU_FR113
V
Thermoleiphilum minutum
Thermoleophilum album
OTU FR113
bacterium Ellin301
OTU FR14
Actinobacteria
(2 OTUs)
Skermanella aerolata
Blastobacter denitrificans
Bradyrhizobium lupini
Nitrobacter hamburgensis
Rhodopseudomonas palustris
OTU FR1445
OTU FR1105
Alphaproteobateria
(2 OTUs)
Acidobacteria bacterium
Candidatus Koribacter
Edaphobacter modestus
Acidobacteriaceae bacterium
uncultured Acidobacteria
OTU FR1072
Geothrix fermentans
Acidobacteria
(1 OTU)
0.05

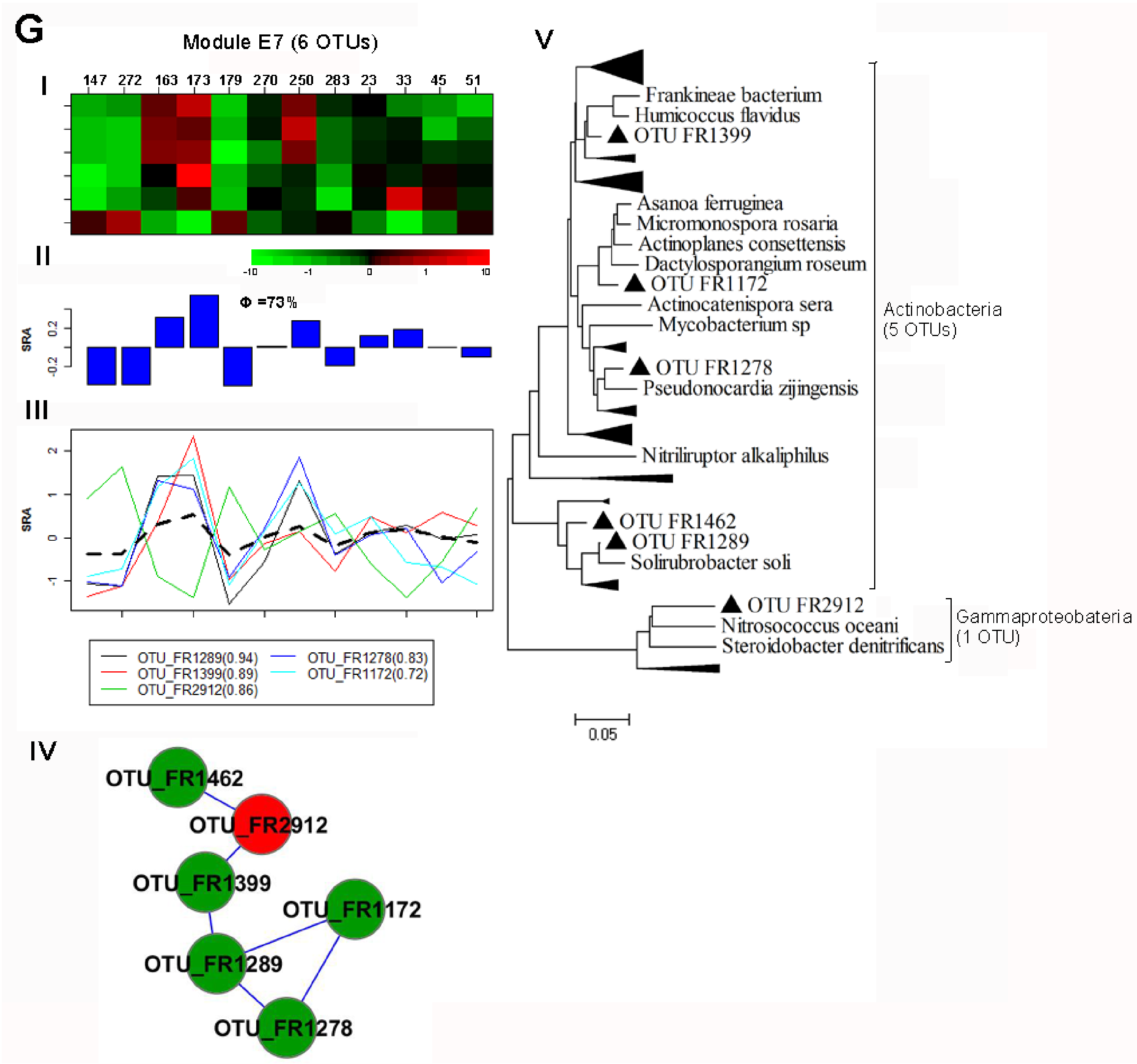
Online Fig. 1.


E
Module E5 (31 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
II
-10 -1 0 1 10
Φ =56%
SRA
0.6 0.2 -0.2
III
SRA
3 2 1 0 -1 -2
OTU_FR1506(0.99)
OTU_R3472(0.96)
OTU_FR1429(0.92)
OTU_FR902(0.91)
OTU_FR5910(0.89)
IV
OTU_FR2652
OTU_FR181
OTU_FR2084
OTU_FR1297
OTU_F235
OTU_FR15218
OTU_F16
OTU_FR5390
OTU_FR11564
OTU_FR338
OTU_FR1942
OTU_FR425
OTU_FR5910
OTU_R3472
OTU_R317
OTU_FR27
OTU_FR1429
OTU_FR1649
OTU_FR324
OTU_FR1209
OTU_FR1506
OTU_FR109
OTU_FR11787
OTU_FR2072
OTU_FR810
OTU_FR902
OTU_FR2216
OTU_FR1128
OTU_FR202
OTU_R2385
OTU_FR10884
0.05
V
▲ OTU FR1297
Arthrobacter aurescens
Kineosporia rhamnosa
■ OTU FR11564
Nocardioides sp
unidentified eubacterium
Nocardioidaceae str
Marmoricola sp
■ OTU FR2084
Aeromicrobium marinum
Kribbella sp
Nitriliruptor alkaliphilus
▲ OTU FR2216
▲ OTU FR1506
Ilumatobacter fluminis
▼ OTU FR15218
▲ OTU FR810
▲ OTU FR338
Thermoleiphilum minutum
Thermoleophilum album
Actinobacteria (8 OTUs)
Cohnella phaseoli
■ OTU FR1128
Planococcus maitriensis
■ OTU FR324
Bacillus pocheonensis
Firmicutes (2 OTUs)
■ OTU FR902
Pedobacter borealis
Dyadobacter koreensis
■ OTU FR1429
Flavobacterium succinicans
■ OTU R2385
■ OTU R3472
■ OTU R317
Niabella aurantiaca
Bacteroidetes (5 OTUs)
▲ OTU FR27
Gemmatimonas aurantiaca
Gemmatimonadetes (1 OTU)
Verrucomicrobium spinosum
● OTU FR2652
Chthoniobacter flavus
Verrucomicrobia (1 OTU)
Acidobacteriaceae bacterium
uncultured Acidobacteria
▲ OTU FR2072
▲ OTU FR109
■ OTU FR5910
Geothrix fermentans
Acidobacteria (3 OTUs)
▲ OTU FR1942
● OTU FR181
■ OTU FR10884
▲ OTU FR1649
Labrys portucalensis
Skermanella aerolata
Alphaproteobateria (4 OTUs)
▲ OTU F16
Ottowia thiooxydans
Ramlibacter tataouinensis
Tepidimonas aquatica
Thiomonas delicata
Rhodocyclus tenuis
▲ OTU FR425
Burkholderia endofungorum
Betaproteobacteria (4 OTUs)
▲ OTU FR202
■ OTU F235
▲ OTU FR5390
▲ OTU FR1209
Pseudomonas mucidolens
● OTU FR11787
Gammaproteobacteria (3 OTUs)

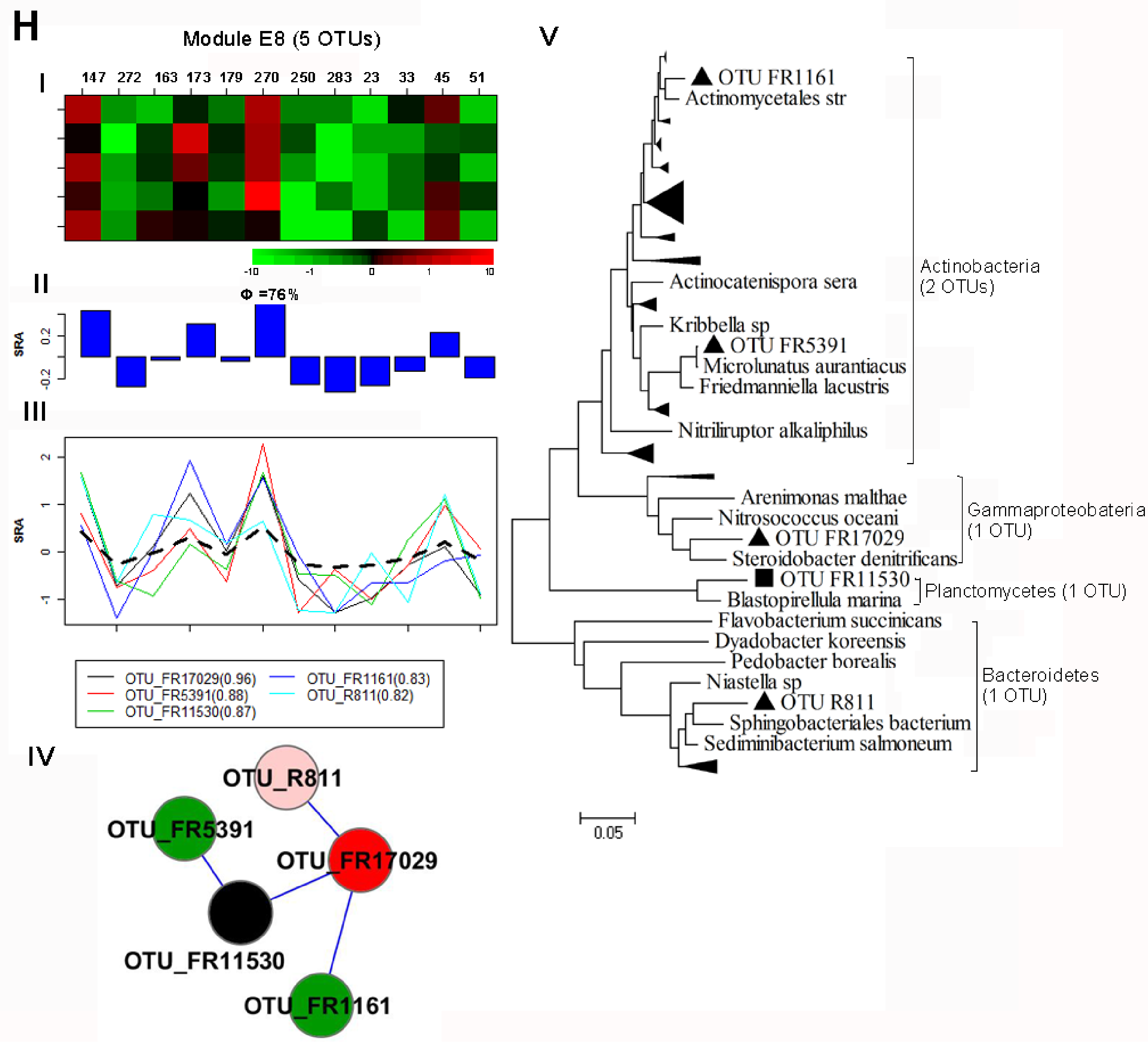
Online Fig. 1.


F
Module E6 (8 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
II
-10 -1 0 1 10
Φ =61 %
SRA
0.4 0.0 -0.4
III
SRA
1.5 0.5 -0.5 -1.5
OTU_FR184(0.94)
OTU_R2713(0.89)
OTU_R2179(0.89)
OTU_F3141(0.82)
OTU_FR2627(0.78)
IV
OTU_R2179
OTU_FR184
OTU_FR111
OTU_R2713
OTU_FR2627
OTU_F3141
OTU_FR12
OTU_FR5795
V
Actinocatenispora sera
Mycobacterium sp
OTU FR184
Pseudonocardia zijingensis
Nitriliruptor alkaliphilus
OTU R2179
Rubrobacterineae bacterium
bacterium Ellin301
Solirubrobacter soli
Conexibacter woesei
Rubrobacteridae bacterium
Actinobacteria (2 OTUs)
Skermanella aerolata
OTU FR12
Alphaproteobateria (1 OTU)
OTU R2713
OTU F3141
Chitinophaga pinensis
Bacteroidetes (2 OTUs)
OTU FR5795
Gemmatimonas aurantiaca
Gemmatimonadetes (1 OTU)
OTU FR111
Geothrix fermentans
Acidobacteria (1 OTU)
OTU FR2627
0.05

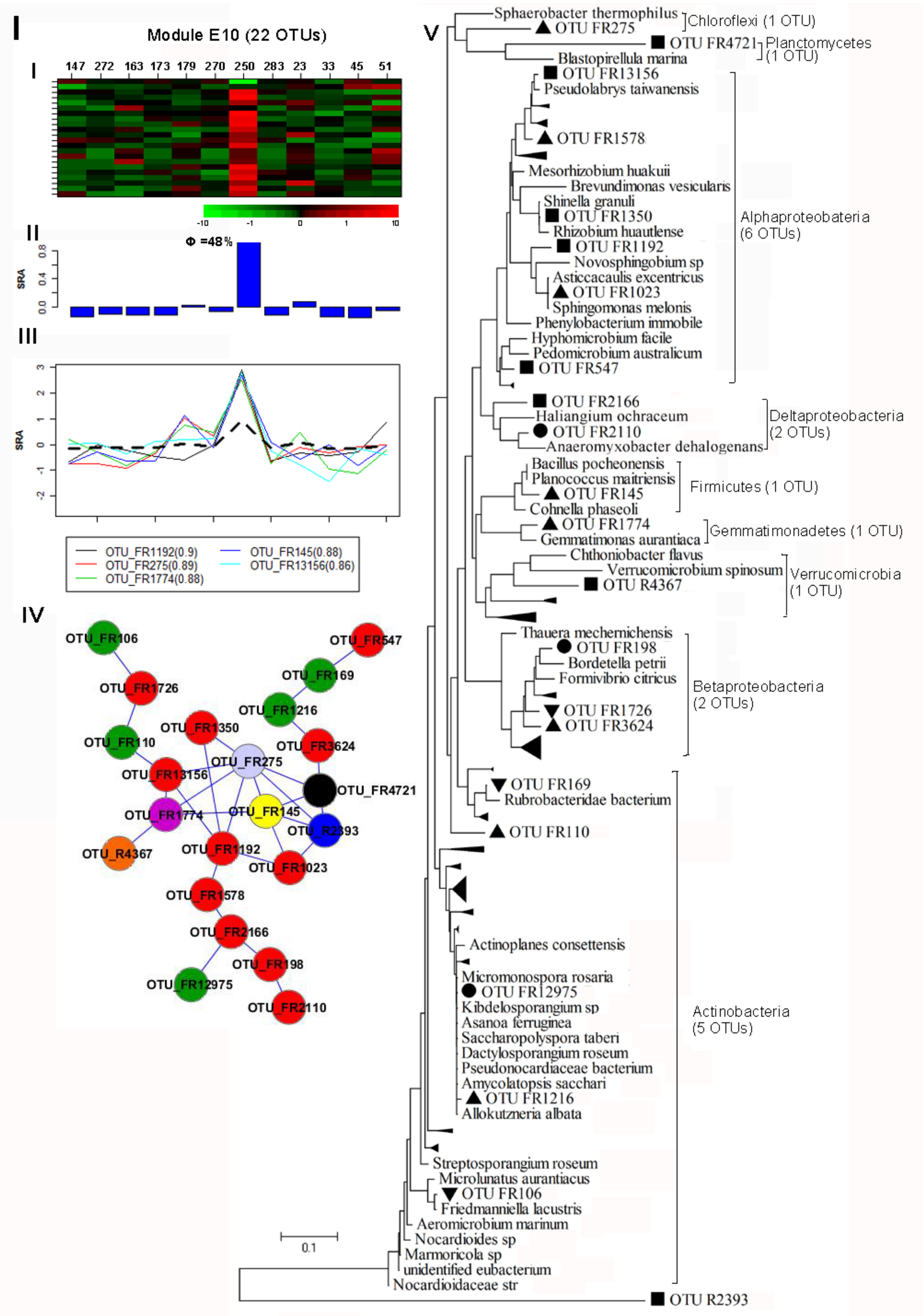
Online Fig. 1.


G
Module E7 (6 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
II
-10 -1 0 1 10
Φ =73%
SRA
0.2
-0.2
III
SRA
2
1
0
-1
OTU_FR1289(0.94)
OTU_FR1399(0.89)
OTU_FR2912(0.86)
OTU_FR1278(0.83)
OTU_FR1172(0.72)
IV
OTU_FR1462
OTU_FR2912
OTU_FR1399
OTU_FR1172
OTU_FR1289
OTU_FR1278
V
Frankineae bacterium
Humicoccus flavidus
▲ OTU FR1399
Asanoa ferruginea
Micromonospora rosaria
Actinoplanes consettensis
Dactylosporangium roseum
▲ OTU FR1172
Actinocatenispora sera
Mycobacterium sp
▲ OTU FR1278
Pseudonocardia zijingensis
Nitriliruptor alkaliphilus
▲ OTU FR1462
▲ OTU FR1289
Solirubrobacter soli
Actinobacteria
(5 OTUs)
▲ OTU FR2912
Nitrosococcus oceani
Steroidobacter denitrificans
Gammaproteobateria
(1 OTU)
0.05

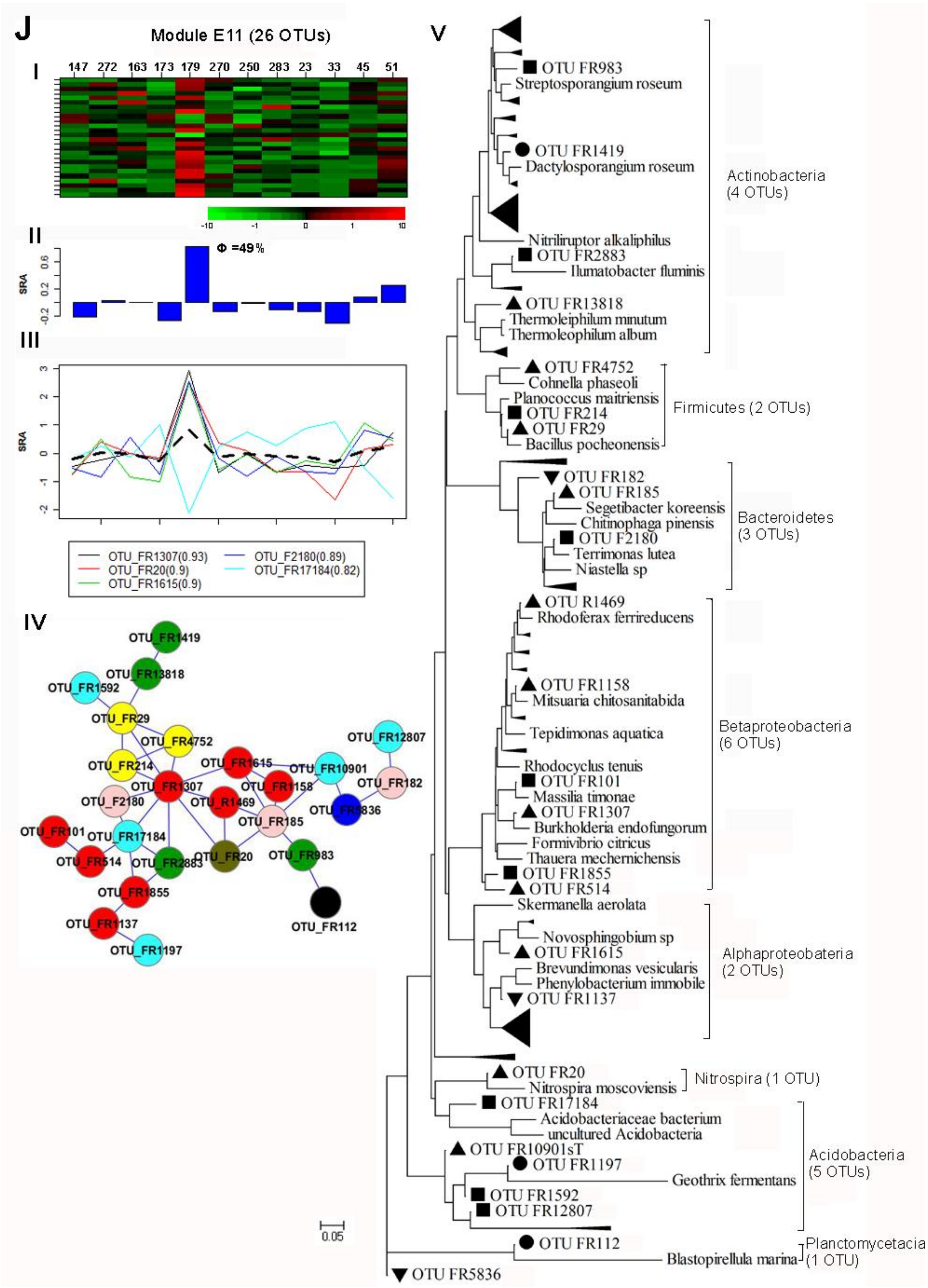
Online Fig. 1.


H
Module E8 (5 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
-10 -1 0 1 10
II
Φ =76%
SRA
0.2
-0.2
III
SRA
2
1
0
-1
OTU_FR17029(0.96)
OTU_FR5391(0.88)
OTU_FR11530(0.87)
OTU_FR1161(0.83)
OTU_R811(0.82)
IV
OTU_R811
OTU_FR5391
OTU_FR17029
OTU_FR11530
OTU_FR1161
V
OTU FR1161
Actinomycetales str
Actinocatenispora sera
Kribbella sp
OTU FR5391
Microlunatus aurantiacus
Friedmanniella lacustris
Nitriliruptor alkaliphilus
Actinobacteria (2 OTUs)
Arenimonas malthae
Nitrosococcus oceani
OTU FR17029
Steroidobacter denitrificans
Gammaproteobateria (1 OTU)
OTU FR11530
Blastopirellula marina
Planctomycetes (1 OTU)
Flavobacterium succinicans
Dyadobacter koreensis
Pedobacter borealis
Niastella sp
OTU R811
Sphingobacteriales bacterium
Sediminibacterium salmoneum
Bacteroidetes (1 OTU)
0.05

Online Fig. 1.

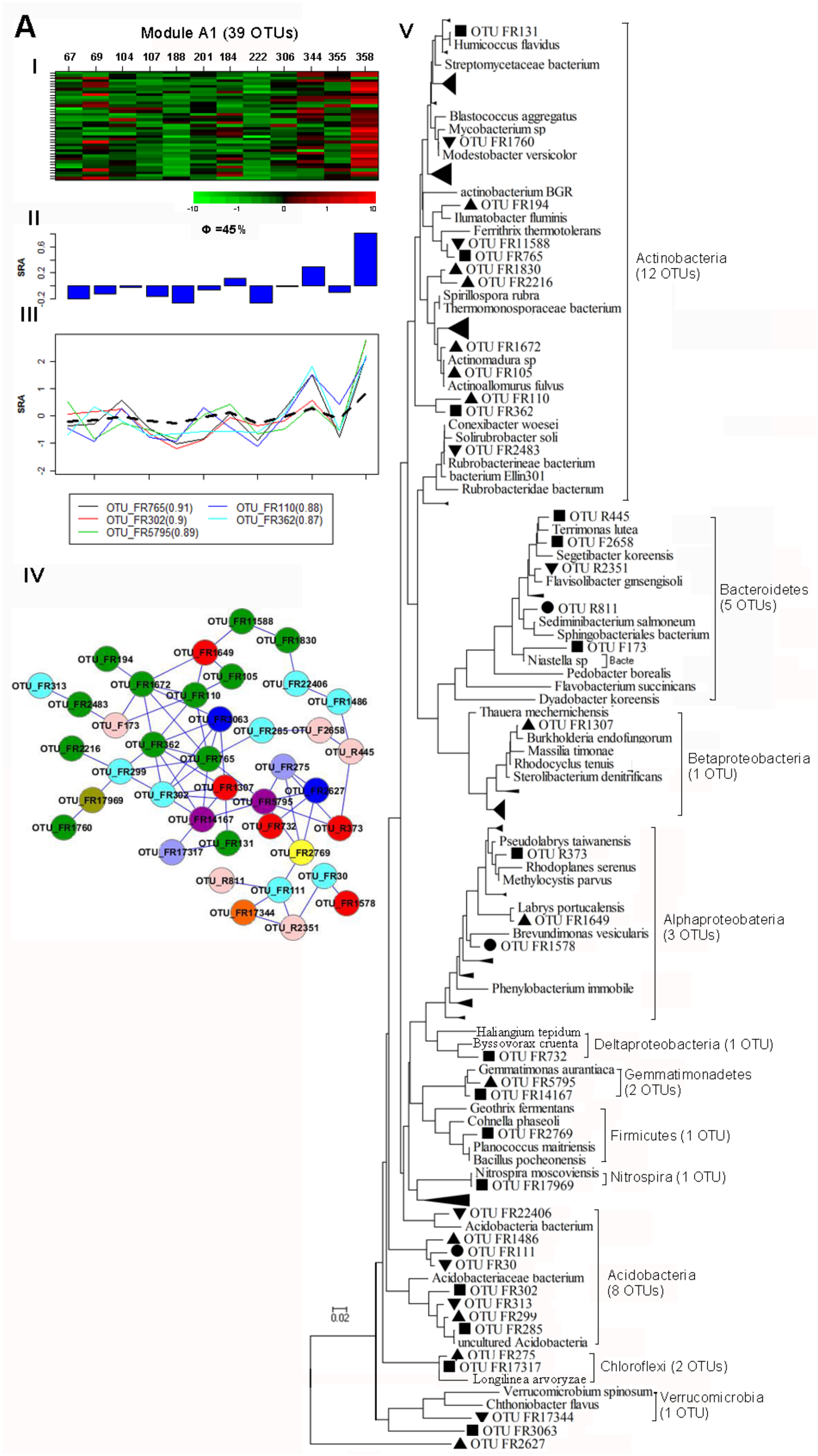

I
Module E10 (22 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
-10 -1 0 1 10
II
SRA
0.0 0.4 0.8
Φ =48%
III
SRA
-2 -1 0 1 2 3
OTU_FR1192(0.9)
OTU_FR275(0.89)
OTU_FR1774(0.88)
OTU_FR145(0.88)
OTU_FR13156(0.86)
IV
OTU_FR106
OTU_FR547
OTU_FR169
OTU_FR1726
OTU_FR1216
OTU_FR1350
OTU_FR110
OTU_FR3624
OTU_FR275
OTU_FR13156
OTU_FR4721
OTU_FR1774
OTU_FR145
OTU_R2393
OTU_R4367
OTU_FR1192
OTU_FR1023
OTU_FR1578
OTU_FR2166
OTU_FR198
OTU_FR12975
OTU_FR2110
V
Sphaerobacter thermophilus
OTU FR275
Chloroflexi (1 OTU)
OTU FR4721
Planctomycetes (1 OTU)
Blastopirellula marina
OTU FR13156
Pseudolabrys taiwanensis
OTU FR1578
Mesorhizobium huakuii
Brevundimonas vesicularis
Shinella granuli
OTU FR1350
Rhizobium huautlense
OTU FR1192
Novosphingobium sp
Asticcacaulis excentricus
OTU FR1023
Sphingomonas melonis
Phenylobacterium immobile
Hyphomicrobium facile
Pedomicrobium australicum
OTU FR547
Alphaproteobateria (6 OTUs)
OTU FR2166
Haliangium ochraceum
OTU FR2110
Anaeromyxobacter dehalogenans
Deltaproteobacteria (2 OTUs)
Bacillus pocheonensis
Planococcus maitriensis
OTU FR145
Cohnella phaseoli
Firmicutes (1 OTU)
OTU FR1774
Gemmatimonas aurantiaca
Gemmatimonadetes (1 OTU)
Chthoniobacter flavus
Verrucomicrobium spinosum
OTU R4367
Verrucomicrobia (1 OTU)
Thauera mechernichensis
OTU FR198
Bordetella petrii
Formivibrio citricus
OTU FR1726
OTU FR3624
Betaproteobacteria (2 OTUs)
OTU FR169
Rubrobacteridae bacterium
OTU FR110
Actinoplanes consettensis
Micromonospora rosaria
OTU FR12975
Kibdelosporangium sp
Asanoa ferruginea
Saccharopolyspora taberi
Dactylosporangium roseum
Pseudonocardiaceae bacterium
Amycolatopsis sacchari
OTU FR1216
Allokutzneria albata
Actinobacteria (5 OTUs)
Streptosporangium roseum
Microlunatus aurantiacus
OTU FR106
Friedmanniella lacustris
Aeromicrobium marinum
Nocardioides sp
Marmoricola sp
unidentified eubacterium
Nocardioidaceae str
0.1
OTU R2393

Online Fig. 1.

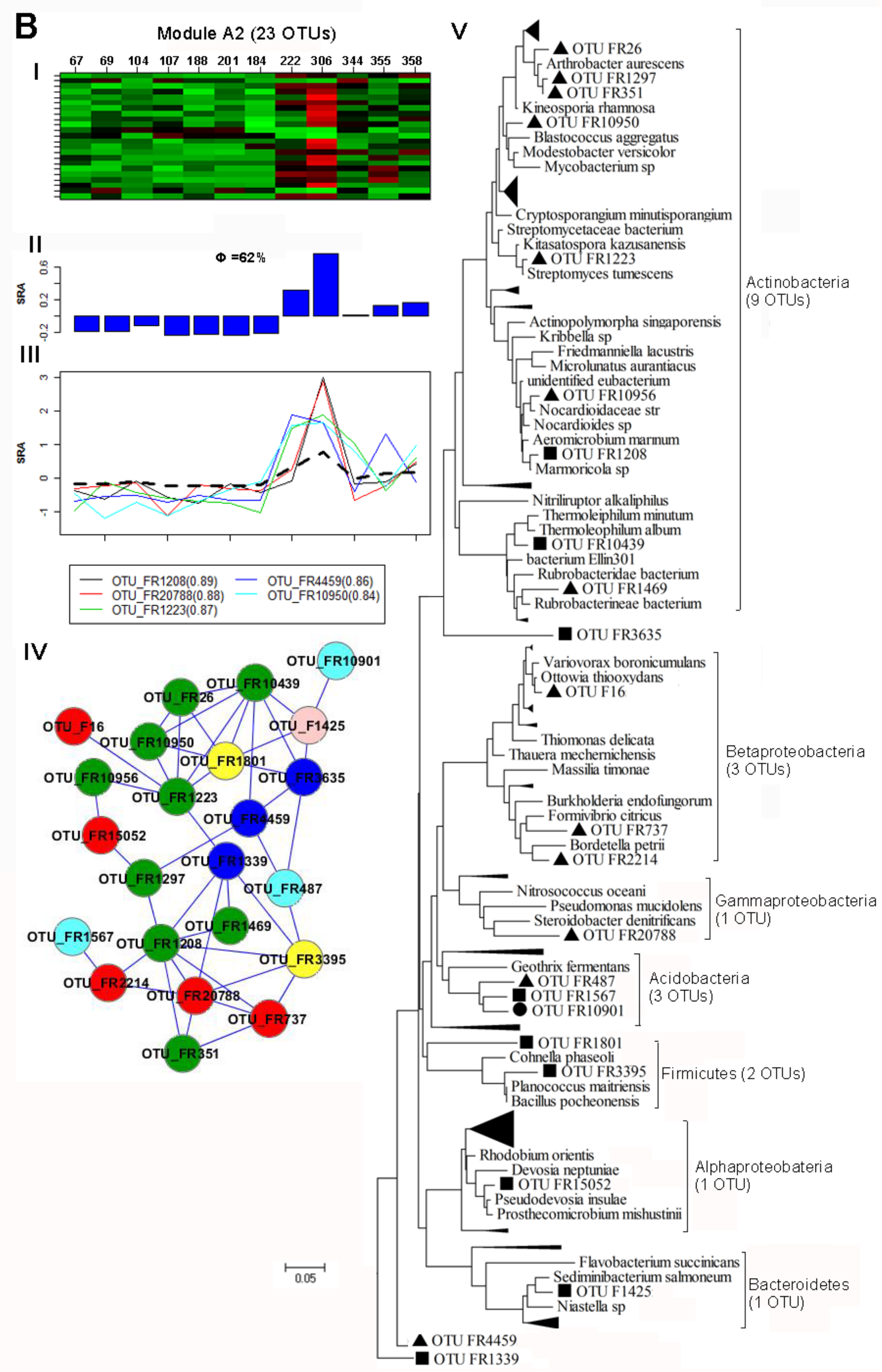

J
Module E11 (26 OTUs)
I
147 272 163 173 179 270 250 283 23 33 45 51
-10 -1 0 1 10
II
SRA
Φ =49%
0.6 0.2 -0.2
III
SRA
3 2 1 0 -1 -2
OTU_FR1307(0.93)
OTU_FR20(0.9)
OTU_FR1615(0.9)
OTU_F2180(0.89)
OTU_FR17184(0.82)
IV
OTU_FR1419
OTU_FR13818
OTU_FR1592
OTU_FR29
OTU_FR4752
OTU_FR12807
OTU_FR214
OTU_FR1615
OTU_FR10901
OTU_FR1307
OTU_FR1158
OTU_FR182
OTU_F2180
OTU_R1469
OTU_FR5836
OTU_FR185
OTU_FR101
OTU_FR17184
OTU_FR514
OTU_FR2883
OTU_FR20
OTU_FR983
OTU_FR1855
OTU_FR112
OTU_FR1137
OTU_FR1197
V
OTU FR983
Streptosporangium roseum
OTU FR1419
Dactylosporangium roseum
Nitriliruptor alkaliphilus
OTU FR2883
Ilumatobacter fluminis
OTU FR13818
Thermoleiphilum minutum
Thermoleophilum album
Actinobacteria (4 OTUs)
OTU FR4752
Cohnella phaseoli
Planococcus maitriensis
OTU FR214
OTU FR29
Bacillus pocheonensis
Firmicutes (2 OTUs)
OTU FR182
OTU FR185
Segetibacter koreensis
Chitinophaga pinensis
OTU F2180
Terrimonas lutea
Niastella sp
Bacteroidetes (3 OTUs)
OTU R1469
Rhodoferax ferrireducens
OTU FR1158
Mitsuaria chitosanitabida
Tepidimonas aquatica
Rhodocyclus tenuis
OTU FR101
Massilia timonae
OTU FR1307
Burkholderia endofungorum
Formivibrio citricus
Thauera mechernichensis
OTU FR1855
OTU FR514
Betaproteobacteria (6 OTUs)
Skermanella aerolata
Novosphingobium sp
OTU FR1615
Brevundimonas vesicularis
Phenylobacterium immobile
OTU FR1137
Alphaproteobateria (2 OTUs)
OTU FR20
Nitrospira moscoviensis
Nitrospira (1 OTU)
OTU FR17184
Acidobacteriaceae bacterium
uncultured Acidobacteria
OTU FR10901sT
OTU FR1197
Geothrix fermentans
OTU FR1592
OTU FR12807
Acidobacteria (5 OTUs)
OTU FR112
Blastopirellula marina
Planctomycetacia (1 OTU)
OTU FR5836
0.05

Online Fig. 1.

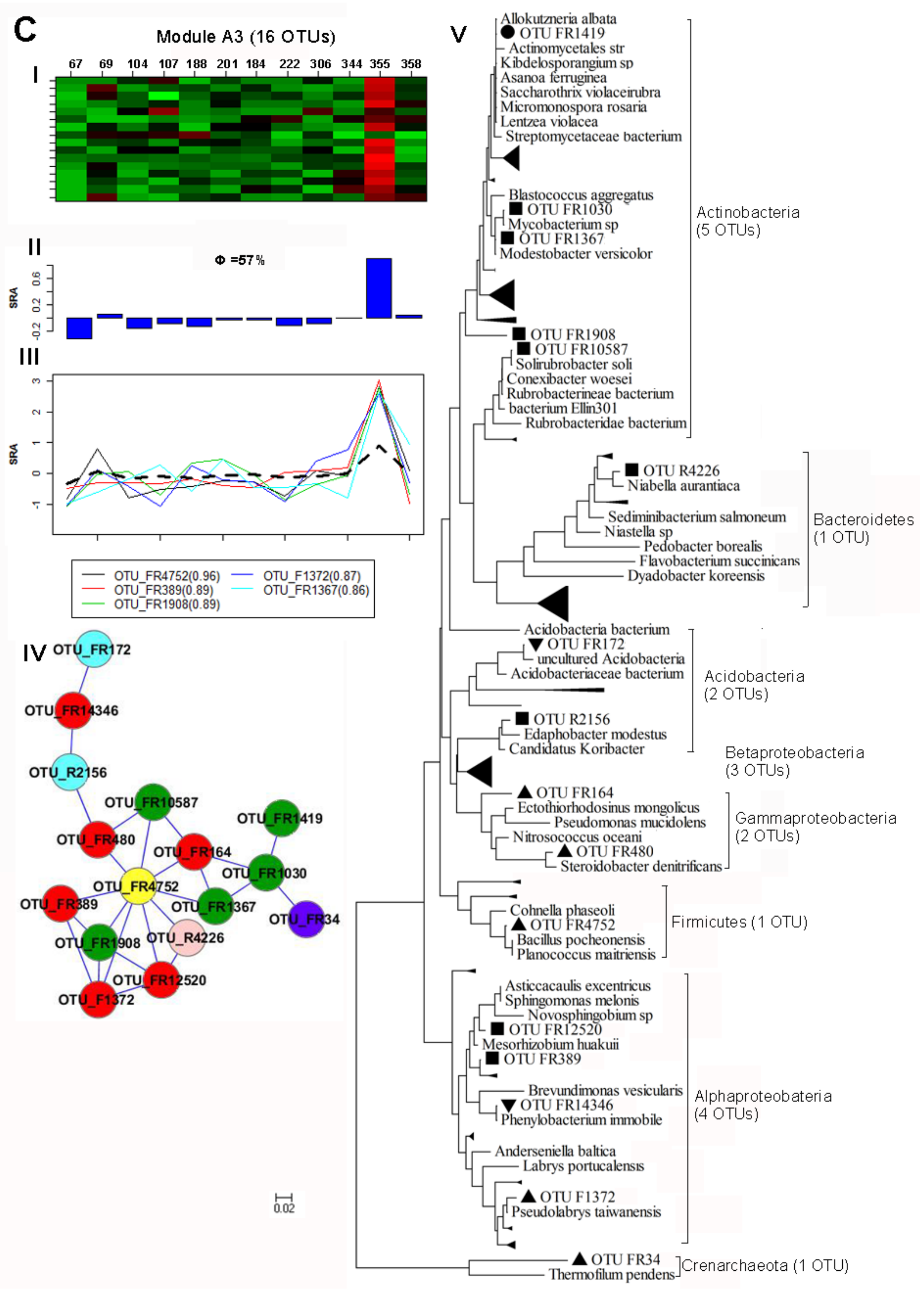
2. **Online Fig. 2.** Eigengene network analysis of individual modules (A-N) under aCO2. Only the modules with ≥ 5 nodes were displayed here. See above legend for details.


A
Module A1 (39 OTUs)
I
67 69 104 107 188 201 184 222 306 344 355 358
-10 -1 0 1 10
II
Φ =45%
SRA
0.6 0.2 -0.2
III
SRA
2 1 0 -1 -2
OTU_FR765(0.91)
OTU_FR302(0.9)
OTU_FR5795(0.89)
OTU_FR110(0.88)
OTU_FR362(0.87)
IV
OTU_FR11588
OTU_FR1830
OTU_FR1649
OTU_FR194
OTU_FR105
OTU_FR313
OTU_FR1672
OTU_FR22406
OTU_FR110
OTU_FR1486
OTU_FR2483
OTU_F173
OTU_FR3063
OTU_FR285
OTU_F2658
OTU_FR2216
OTU_FR362
OTU_R445
OTU_FR765
OTU_FR275
OTU_FR299
OTU_FR1307
OTU_FR2627
OTU_FR17969
OTU_FR302
OTU_FR5795
OTU_FR14167
OTU_FR732
OTU_R373
OTU_FR1760
OTU_FR131
OTU_FR17317
OTU_FR2769
OTU_FR30
OTU_R811
OTU_FR111
OTU_FR1578
OTU_FR17344
OTU_R2351
V
OTU FR131
Humicoccus flavidus
Streptomycetaceae bacterium
Blastococcus aggregatus
Mycobacterium sp
OTU FR1760
Modestobacter versicolor
actinobacterium BGR
OTU FR194
Ilumatobacter fluminis
Ferrithrix thermotolerans
OTU FR11588
OTU FR765
OTU FR1830
OTU FR2216
Spirillospora rubra
Thermomonosporaceae bacterium
OTU FR1672
Actinomadura sp
OTU FR105
Actinoallomurus fulvus
OTU FR110
OTU FR362
Conexibacter woesei
Solirubrobacter soli
OTU FR2483
Rubrobacterineae bacterium
bacterium Ellin301
Rubrobacteridae bacterium
Actinobacteria
(12 OTUs)
OTU R445
Terrimonas lutea
OTU F2658
Segetibacter koreensis
OTU R2351
Flavisolibacter ginsengisoli
OTU R811
Sediminibacterium salmoneum
Sphingobacteriales bacterium
OTU F173
Niastella sp
Bacte
Pedobacter borealis
Flavobacterium succinicans
Dyadobacter koreensis
Bacteroidetes
(5 OTUs)
Thauera mechernichensis
OTU FR1307
Burkholderia endofungorum
Massilia timonae
Rhodocyclus tenuis
Sterolibacterium denitrificans
Betaproteobacteria
(1 OTU)
Pseudolabrys taiwanensis
OTU R373
Rhodoplanes serenus
Methylocystis parvus
Labrys portucalensis
OTU FR1649
Brevundimonas vesicularis
OTU FR1578
Phenylobacterium immobile
Alphaproteobateria
(3 OTUs)
Haliangium tepidum
Byssovorax cruenta
OTU FR732
Deltaproteobacteria (1 OTU)
Gemmatimonas aurantiaca
OTU FR5795
OTU FR14167
Gemmatimonadetes
(2 OTUs)
Geothrix fermentans
Cohnella phaseoli
OTU FR2769
Planococcus maitriensis
Bacillus pocheonensis
Firmicutes (1 OTU)
Nitrospira moscoviensis
OTU FR17969
Nitrospira (1 OTU)
OTU FR22406
Acidobacteria bacterium
OTU FR1486
OTU FR111
OTU FR30
Acidobacteriaceae bacterium
OTU FR302
OTU FR313
OTU FR299
OTU FR285
uncultured Acidobacteria
Acidobacteria
(8 OTUs)
OTU FR275
OTU FR17317
Longilinea arvoryzae
Chloroflexi (2 OTUs)
Verrucomicrobium spinosum
Chthoniobacter flavus
OTU FR17344
Verrucomicrobia
(1 OTU)
OTU FR3063
OTU FR2627
0.02

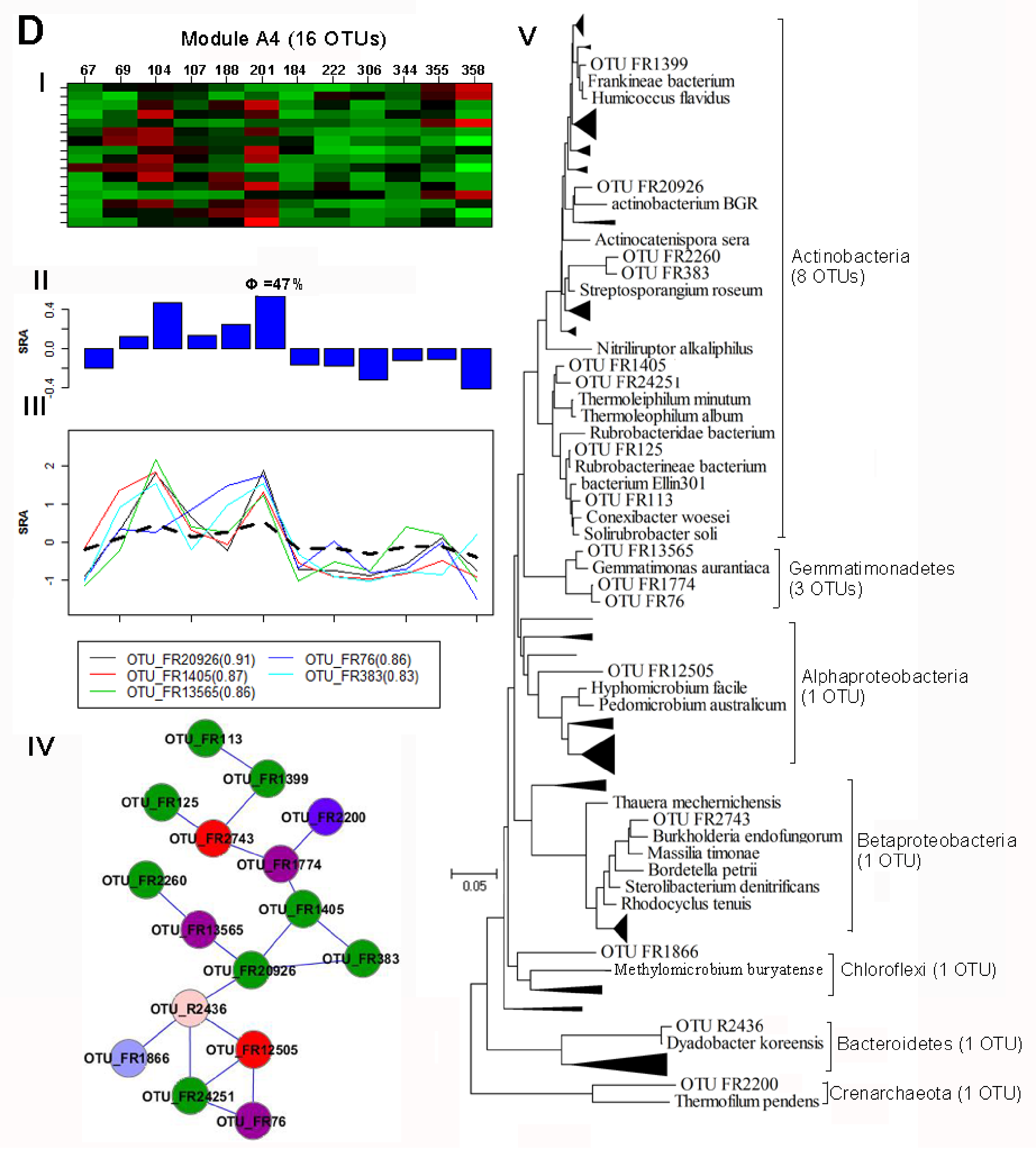
Online Fig. 2.


B
Module A2 (23 OTUs)
I
67
69
104
107
188
201
184
222
306
344
355
358
II
Φ =62%
SRA
0.6
0.2
-0.2
III
SRA
3
2
1
0
-1
OTU_FR1208(0.89)
OTU_FR20788(0.88)
OTU_FR1223(0.87)
OTU_FR4459(0.86)
OTU_FR10950(0.84)
IV
OTU_FR10901
OTU_FR10439
OTU_FR26
OTU_F1425
OTU_F16
OTU_FR10950
OTU_FR1801
OTU_FR10956
OTU_FR3635
OTU_FR1223
OTU_FR4459
OTU_FR15052
OTU_FR1339
OTU_FR1297
OTU_FR487
OTU_FR1469
OTU_FR1567
OTU_FR1208
OTU_FR3395
OTU_FR2214
OTU_FR20788
OTU_FR737
OTU_FR351
0.05
V
▲ OTU FR26
Arthrobacter aurescens
▲ OTU FR1297
▲ OTU FR351
Kineosporia rhamnosa
▲ OTU FR10950
Blastococcus aggregatus
Modestobacter versicolor
Mycobacterium sp
Cryptosporangium minutisporangium
Streptomycetaceae bacterium
Kitasatospora kazusanensis
▲ OTU FR1223
Streptomyces tumescens
Actinopolymorpha singaporensis
Kribbella sp
Friedmanniella lacustris
Microlunatus aurantiacus
unidentified eubacterium
▲ OTU FR10956
Nocardioidaceae str
Nocardioides sp
Aeromicrobium marinum
■ OTU FR1208
Marmoricola sp
Nitriliruptor alkaliphilus
Thermoleiphilum minutum
Thermoleophilum album
■ OTU FR10439
bacterium Ellin301
Rubrobacteridae bacterium
▲ OTU FR1469
Rubrobacterineae bacterium
Actinobacteria (9 OTUs)
■ OTU FR3635
Variovorax boronicumulans
Ottowia thiooxydans
▲ OTU F16
Thiomonas delicata
Thauera mechernichensis
Massilia timonae
Burkholderia endofungorum
Formivibrio citricus
▲ OTU FR737
Bordetella petrii
▲ OTU FR2214
Betaproteobacteria (3 OTUs)
Nitrosococcus oceani
Pseudomonas mucidolens
Steroidobacter denitrificans
▲ OTU FR20788
Gammaproteobacteria (1 OTU)
Geothrix fermentans
▲ OTU FR487
■ OTU FR1567
● OTU FR10901
Acidobacteria (3 OTUs)
■ OTU FR1801
Cohnella phaseoli
■ OTU FR3395
Planococcus maitriensis
Bacillus pocheonensis
Firmicutes (2 OTUs)
Rhodobium orientis
Devosia neptuniae
■ OTU FR15052
Pseudodevosia insulae
Prosthecomicrobium mishustinii
Alphaproteobateria (1 OTU)
Flavobacterium succinicans
Sediminibacterium salmoneum
■ OTU F1425
Niastella sp
Bacteroidetes (1 OTU)
▲ OTU FR4459
■ OTU FR1339

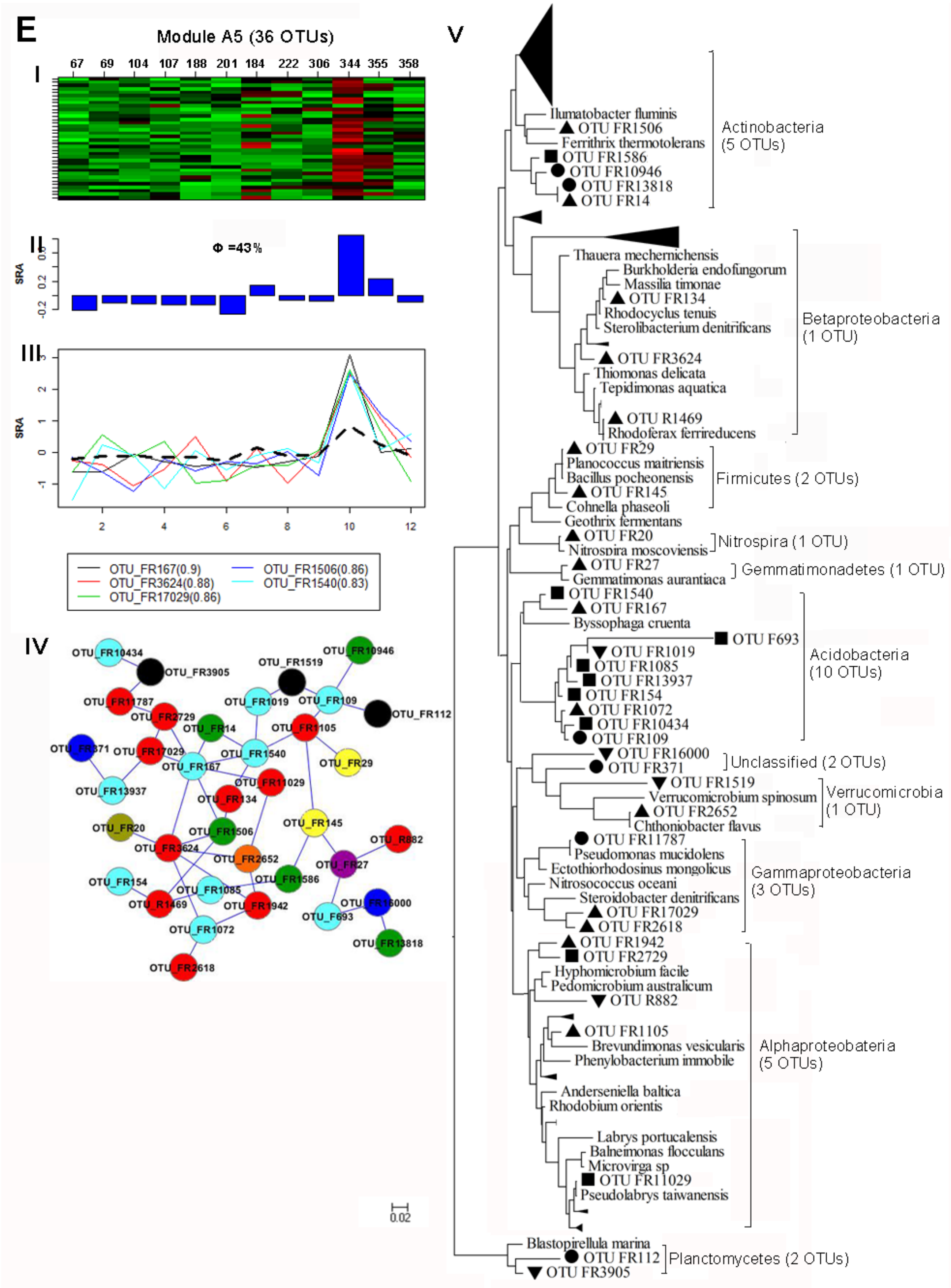
Online Fig. 2.


C
Module A3 (16 OTUs)
I
67
69
104
107
188
201
184
222
306
344
355
358
II
Φ =57 %
SRA
0.6
0.2
-0.2
III
SRA
3
2
1
0
-1
OTU_FR4752(0.96)
OTU_FR389(0.89)
OTU_FR1908(0.89)
OTU_F1372(0.87)
OTU_FR1367(0.86)
IV
OTU_FR172
OTU_FR14346
OTU_R2156
OTU_FR10587
OTU_FR1419
OTU_FR480
OTU_FR164
OTU_FR1030
OTU_FR4752
OTU_FR389
OTU_FR1367
OTU_FR34
OTU_FR1908
OTU_R4226
OTU_FR12520
OTU_F1372
0.02
V
Allokutzneria albata
OTU FR1419
Actinomycetales str
Kibdelosporangium sp
Asanoa ferruginea
Saccharothrix violaceirubra
Micromonospora rosaria
Lentzea violacea
Streptomycetaceae bacterium
Blastococcus aggregatus
OTU FR1030
Mycobacterium sp
OTU FR1367
Modestobacter versicolor
OTU FR1908
OTU FR10587
Solirubrobacter soli
Conexibacter woesei
Rubrobacterineae bacterium
bacterium Ellin301
Rubrobacteridae bacterium
Actinobacteria
(5 OTUs)
OTU R4226
Niabella aurantiaca
Sediminibacterium salmoneum
Niastella sp
Pedobacter borealis
Flavobacterium succinicans
Dyadobacter koreensis
Bacteroidetes
(1 OTU)
Acidobacteria bacterium
OTU FR172
uncultured Acidobacteria
Acidobacteriaceae bacterium
OTU R2156
Edaphobacter modestus
Candidatus Koribacter
Acidobacteria
(2 OTUs)
Betaproteobacteria
(3 OTUs)
OTU FR164
Ectothiorhodosinus mongolicus
Pseudomonas mucidolens
Nitrosococcus oceani
OTU FR480
Steroidobacter denitrificans
Gammaproteobacteria
(2 OTUs)
Cohnella phaseoli
OTU FR4752
Bacillus pocheonensis
Planococcus maitriensis
Firmicutes (1 OTU)
Asticcacaulis excentricus
Sphingomonas melonis
Novosphingobium sp
OTU FR12520
Mesorhizobium huakuii
OTU FR389
Brevundimonas vesicularis
OTU FR14346
Phenylobacterium immobile
Anderseniella baltica
Labrys portucalensis
OTU F1372
Pseudolabrys taiwanensis
Alphaproteobateria
(4 OTUs)
OTU FR34
Thermofilum pendens
Crenarchaeota (1 OTU)

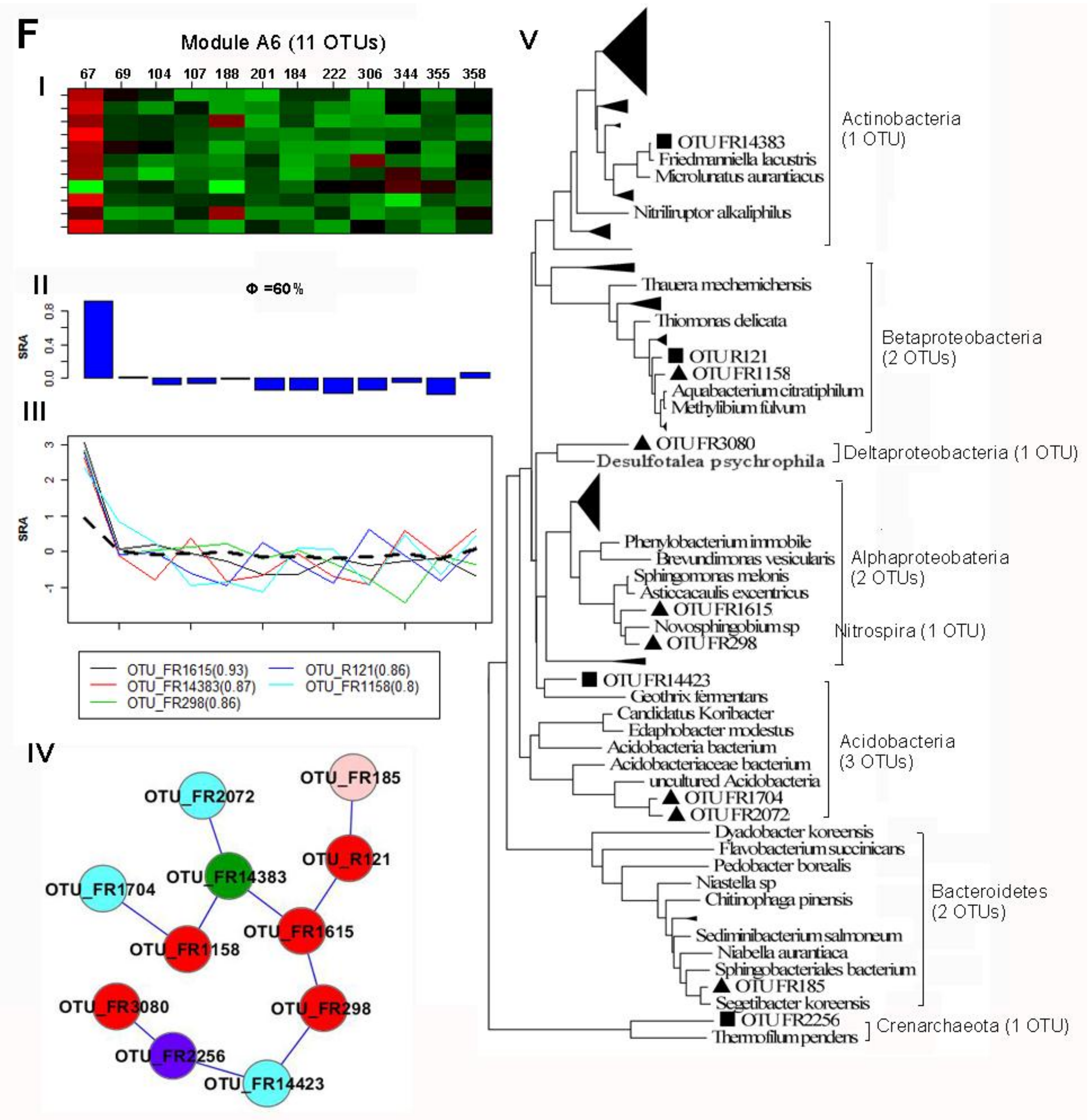
Online Fig. 2.


D
Module A4 (16 OTUs)
I
67
69
104
107
188
201
184
222
306
344
355
358
II
Φ =47%
SRA
0.4
0.0
-0.4
III
SRA
2
1
0
-1
OTU_FR20926(0.91)
OTU_FR1405(0.87)
OTU_FR13565(0.86)
OTU_FR76(0.86)
OTU_FR383(0.83)
IV
OTU_FR113
OTU_FR1399
OTU_FR125
OTU_FR2200
OTU_FR2743
OTU_FR1774
OTU_FR2260
OTU_FR1405
OTU_FR13565
OTU_FR383
OTU_FR20926
OTU_R2436
OTU_FR1866
OTU_FR12505
OTU_FR24251
OTU_FR76
V
OTU FR1399
Frankineae bacterium
Humicoccus flavidus
OTU FR20926
actinobacterium BGR
Actinocatenispora sera
OTU FR2260
OTU FR383
Streptosporangium roseum
Nitriliruptor alkaliphilus
OTU FR1405
OTU FR24251
Thermoleiphilum minutum
Thermoleophilum album
Rubrobacteridae bacterium
OTU FR125
Rubrobacterineae bacterium
bacterium Ellin301
OTU FR113
Conexibacter woesei
Solirubrobacter soli
Actinobacteria
(8 OTUs)
OTU FR13565
Gemmatimonas aurantiaca
OTU FR1774
OTU FR76
Gemmatimonadetes
(3 OTUs)
OTU FR12505
Hyphomicrobium facile
Pedomicrobium australicum
Alphaproteobacteria
(1 OTU)
Thauera mechernichensis
OTU FR2743
Burkholderia endofungorum
Massilia timonae
Bordetella petrii
Sterolibacterium denitrificans
Rhodocyclus tenuis
Betaproteobacteria
(1 OTU)
0.05
OTU FR1866
Methylomicrobium buryatense
Chloroflexi (1 OTU)
OTU R2436
Dyadobacter koreensis
Bacteroidetes (1 OTU)
OTU FR2200
Thermofilum pendens
Crenarchaeota (1 OTU)

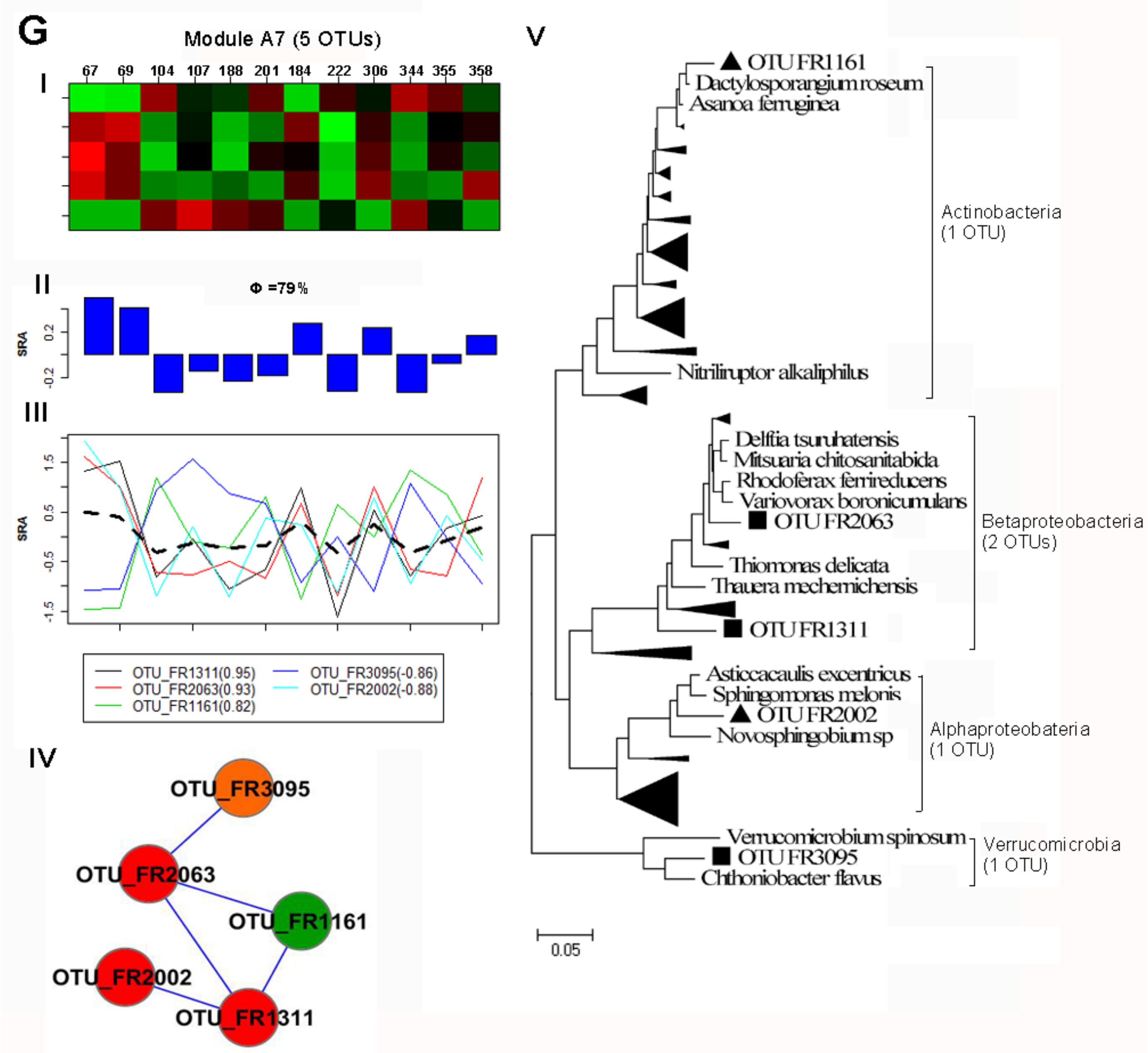
Online Fig. 2.


E
Module A5 (36 OTUs)
I
67 69 104 107 188 201 184 222 306 344 355 358
II
SRA
Φ =43%
0.5
0.2
-0.2
III
SRA
3
2
1
0
-1
2 4 6 8 10 12
OTU_FR167(0.9)
OTU_FR3624(0.88)
OTU_FR17029(0.86)
OTU_FR1506(0.86)
OTU_FR1540(0.83)
IV
OTU_FR10434
OTU_FR3905
OTU_FR1519
OTU_FR10946
OTU_FR11787
OTU_FR2729
OTU_FR1019
OTU_FR109
OTU_FR112
OTU_FR14
OTU_FR1105
OTU_FR371
OTU_FR17029
OTU_FR1540
OTU_FR167
OTU_FR29
OTU_FR11029
OTU_FR13937
OTU_FR134
OTU_FR145
OTU_FR20
OTU_FR1506
OTU_R882
OTU_FR3624
OTU_FR2652
OTU_FR27
OTU_FR154
OTU_FR1586
OTU_FR1085
OTU_FR16000
OTU_R1469
OTU_FR1942
OTU_F693
OTU_FR1072
OTU_FR13818
OTU_FR2618
0.02
V
Ilumatobacter fluminis
OTU FR1506
Ferrithrix thermotolerans
OTU FR1586
OTU FR10946
OTU FR13818
OTU FR14
Actinobacteria (5 OTUs)
Thauera mechernichensis
Burkholderia endofungorum
Massilia timonae
OTU FR134
Rhodocyclus tenuis
Sterolibacterium denitrificans
OTU FR3624
Thiomonas delicata
Tepidimonas aquatica
OTU R1469
Rhodoferax ferrireducens
Betaproteobacteria (1 OTU)
OTU FR29
Planococcus maitriensis
Bacillus pocheonensis
OTU FR145
Cohnella phaseoli
Geothrix fermentans
Firmicutes (2 OTUs)
OTU FR20
Nitrospira moscoviensis
Nitrospira (1 OTU)
OTU FR27
Gemmatimonas aurantiaca
Gemmatimonadetes (1 OTU)
OTU FR1540
OTU FR167
Byssophaga cruenta
OTU F693
OTU FR1019
OTU FR1085
OTU FR13937
OTU FR154
OTU FR1072
OTU FR10434
OTU FR109
Acidobacteria (10 OTUs)
OTU FR16000
OTU FR371
Unclassified (2 OTUs)
OTU FR1519
Verrucomicrobium spinosum
OTU FR2652
Chthoniobacter flavus
Verrucomicrobia (1 OTU)
OTU FR11787
Pseudomonas mucidolens
Ectothiorhodosinus mongolicus
Nitrosococcus oceani
Steroidobacter denitrificans
OTU FR17029
OTU FR2618
Gammaproteobacteria (3 OTUs)
OTU FR1942
OTU FR2729
Hyphomicrobium facile
Pedomicrobium australicum
OTU R882
OTU FR1105
Brevundimonas vesicularis
Phenylobacterium immobile
Anderseniella baltica
Rhodobium orientis
Labrys portucalensis
Balneimonas flocculans
Microvirga sp
OTU FR11029
Pseudolabrys taiwanensis
Alphaproteobateria (5 OTUs)
Blastopirellula marina
OTU FR112
OTU FR3905
Planctomycetes (2 OTUs)

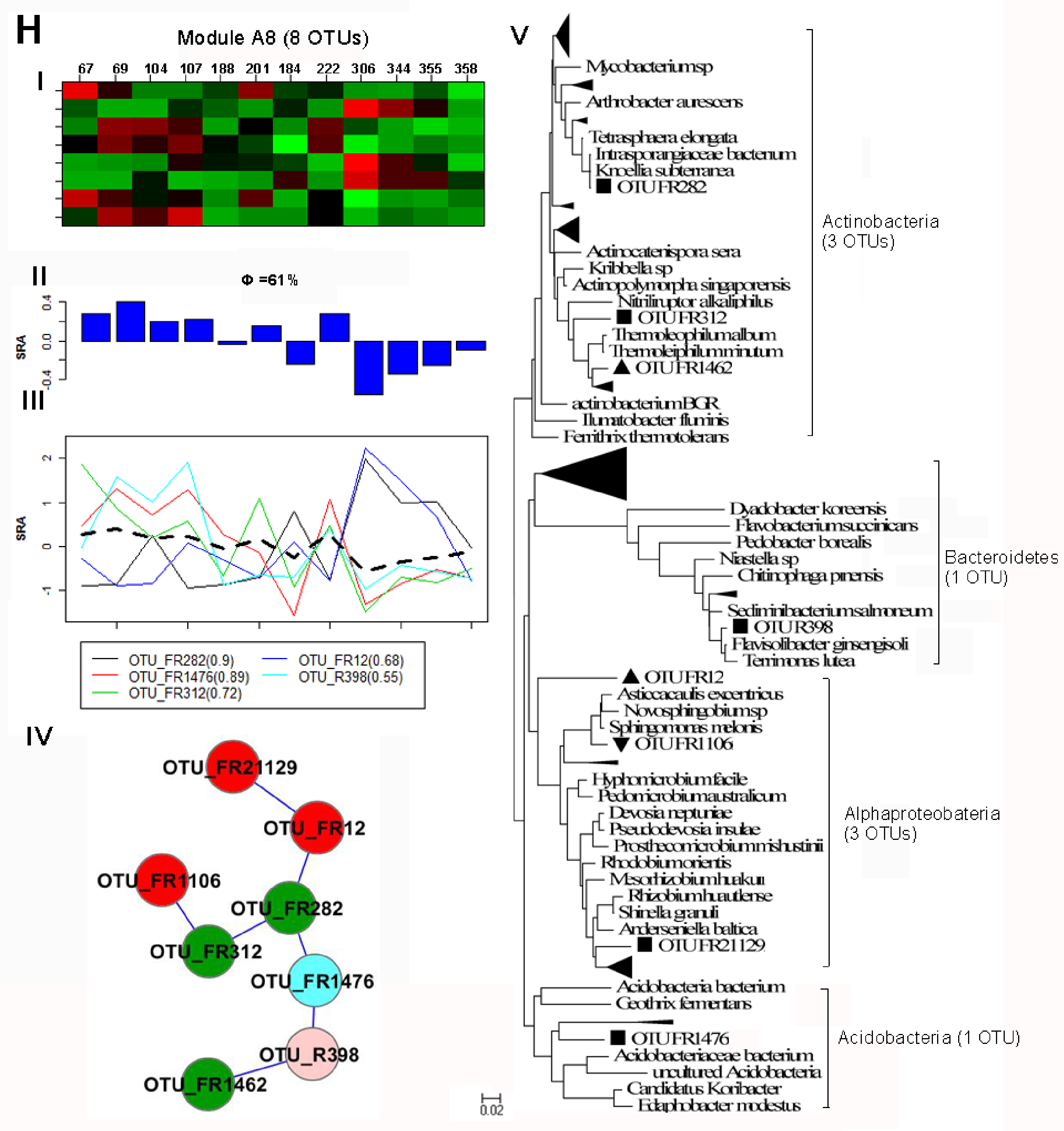
Online Fig. 2.


F
Module A6 (11 OTUs)
I
67 69 104 107 188 201 184 222 306 344 355 358
II
Φ =60%
SRA
0.0 0.4 0.8
III
SRA
3 2 1 0 -1
OTU_FR1615(0.93)
OTU_FR14383(0.87)
OTU_FR298(0.86)
OTU_R121(0.86)
OTU_FR1158(0.8)
IV
OTU_FR185
OTU_FR2072
OTU_R121
OTU_FR14383
OTU_FR1704
OTU_FR1615
OTU_FR1158
OTU_FR3080
OTU_FR298
OTU_FR2256
OTU_FR14423
V
OTU FR14383
Friedmanniella lacustris
Microlunatus aurantiacus
Nitriliruptor alkaliphilus
Actinobacteria (1 OTU)
Thauera mechernichensis
Thiomonas delicata
OTU R121
OTU FR1158
Aquabacterium citratiphilum
Methylibium fulvum
Betaproteobacteria (2 OTUs)
OTU FR3080
Desulfotalea psychrophila
Deltaproteobacteria (1 OTU)
Phenylobacterium immobile
Brevundimonas vesicularis
Sphingomonas melonis
Asticcacaulis excentricus
OTU FR1615
Novosphingobium sp
OTU FR298
Alphaproteobateria (2 OTUs)
Nitrospira (1 OTU)
OTU FR14423
Geothrix fermentans
Candidatus Koribacter
Edaphobacter modestus
Acidobacteria bacterium
Acidobacteriaceae bacterium
uncultured Acidobacteria
OTU FR1704
OTU FR2072
Acidobacteria (3 OTUs)
Dyadobacter koreensis
Flavobacterium succinicans
Pedobacter borealis
Niastella sp
Chitinophaga pinensis
Sediminibacterium salmoneum
Niabella aurantiaca
Sphingobacteriales bacterium
OTU FR185
Segetibacter koreensis
Bacteroidetes (2 OTUs)
OTU FR2256
Thermofilum pendens
Crenarchaeota (1 OTU)

Online Fig. 2.

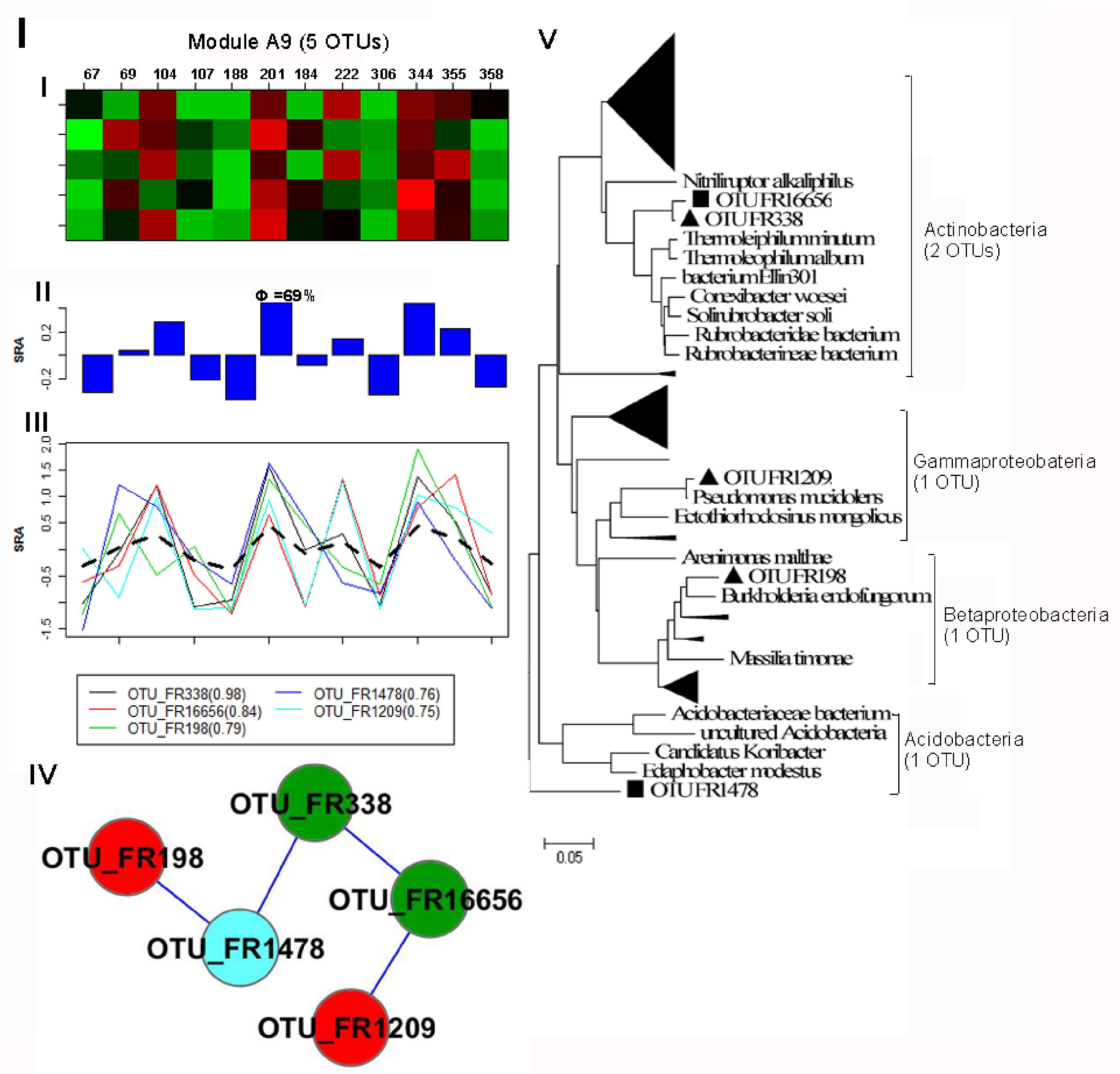

G
Module A7 (5 OTUs)
I
67
69
104
107
188
201
184
222
306
344
355
358
II
Φ =79%
SRA
0.2
-0.2
III
SRA
1.5
0.5
-0.5
-1.5
OTU_FR1311(0.95)
OTU_FR2063(0.93)
OTU_FR1161(0.82)
OTU_FR3095(-0.86)
OTU_FR2002(-0.88)
IV
OTU_FR3095
OTU_FR2063
OTU_FR1161
OTU_FR2002
OTU_FR1311
V
OTU FR1161
Dactylosporangium roseum
Asanoa ferruginea
Nitriliruptor alkaliphilus
Actinobacteria (1 OTU)
Delftia tsuruhatensis
Mitsuaria chitosanitabida
Rhodoferax ferrireducens
Variovorax boronicumulans
OTU FR2063
Thiomonas delicata
Thauera mechernichensis
OTU FR1311
Betaproteobacteria (2 OTUs)
Asticcacaulis excentricus
Sphingomonas melonis
OTU FR2002
Novosphingobium sp
Alphaproteobateria (1 OTU)
Verrucomicrobium spinosum
OTU FR3095
Chthoniobacter flavus
Verrucomicrobia (1 OTU)
0.05

Online Fig. 2.

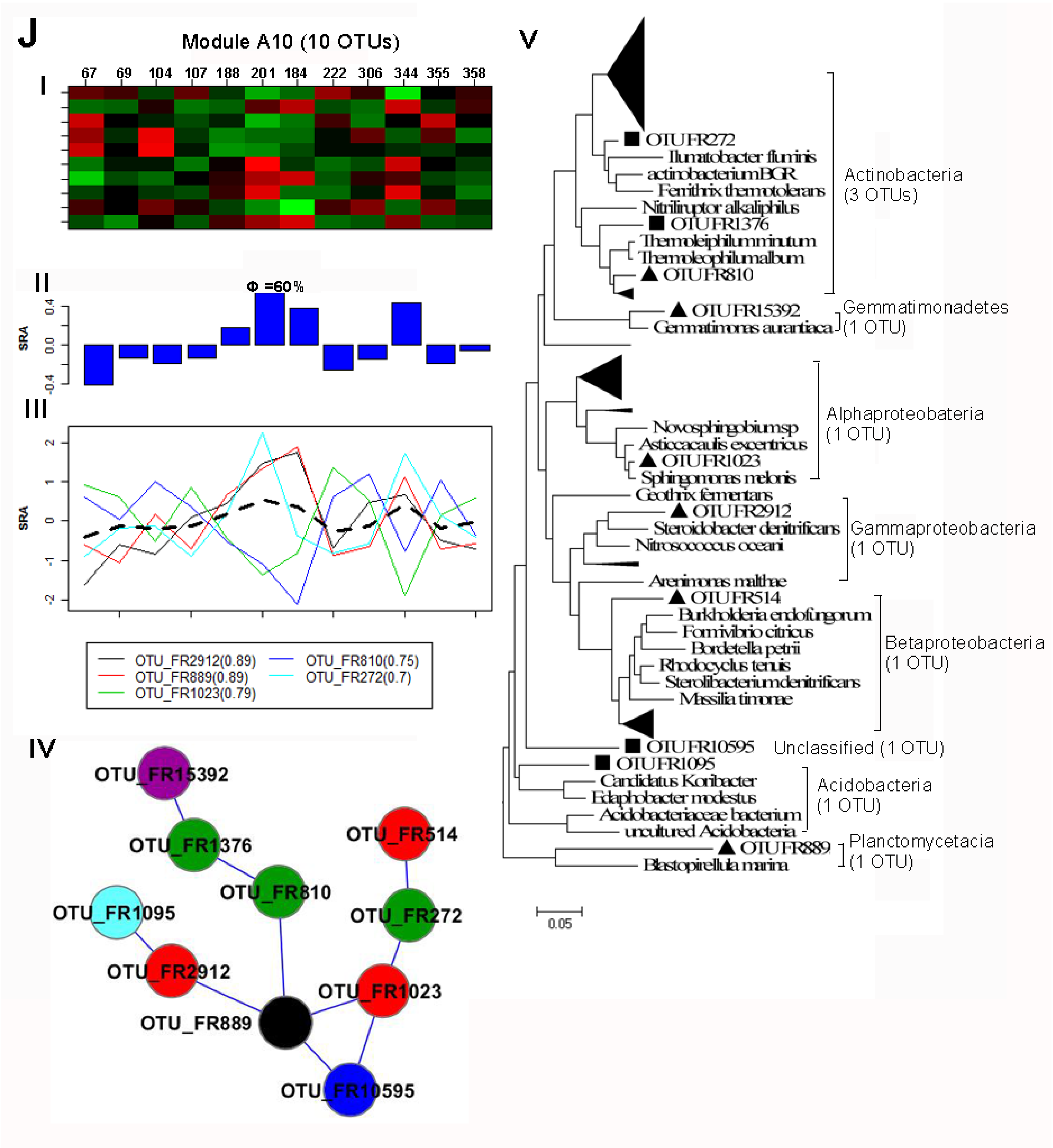


H
Module A8 (8 OTUs)
I
67 69 104 107 188 201 184 222 306 344 355 358
II
Φ =61 %
SRA
0.4
0.0
-0.4
III
SRA
2
1
0
-1
OTU_FR282(0.9)
OTU_FR1476(0.89)
OTU_FR312(0.72)
OTU_FR12(0.68)
OTU_R398(0.55)
IV
OTU_FR21129
OTU_FR12
OTU_FR1106
OTU_FR282
OTU_FR312
OTU_FR1476
OTU_R398
OTU_FR1462
V
Mycobacterium sp
Arthrobacter aurescens
Tetrasphaera elongata
Intrasporangiaceae bacterium
Knoellia subterranea
OTU FR282
Actinocatenispora sera
Kribbella sp
Actinopolymorpha singaporensis
Nitriliruptor alkaliphilus
OTU FR312
Thermoleophilum album
Thermoleiphilum minutum
OTU FR1462
actinobacterium BGR
Ilumatobacter fluminis
Ferrithrix thermotolerans
Actinobacteria (3 OTUs)
Dyadobacter koreensis
Flavobacterium succinicans
Pedobacter borealis
Niastella sp
Chitinophaga pinensis
Sediminibacterium salmoneum
OTU R398
Flavisolibacter ginsengisoli
Terrimonas lutea
Bacteroidetes (1 OTU)
OTU FR12
Asticcacaulis excentricus
Novosphingobium sp
Sphingomonas melonis
OTU FR1106
Hyphomicrobium facile
Pedomicrobium australicum
Devosia neptuniae
Pseudodevosia insulae
Prosthecomicrobium mishustinii
Rhodobium orientis
Mesorhizobium huakuii
Rhizobium huautlense
Shinella granuli
Aminobacter-like Andersenella baltica
OTU FR21129
Alphaproteobateria (3 OTUs)
Acidobacteria bacterium
Geothrix fermentans
OTU FR1476
Acidobacteriaceae bacterium
uncultured Acidobacteria
Candidatus Koribacter
Edaphobacter modestus
Acidobacteria (1 OTU)
0.02

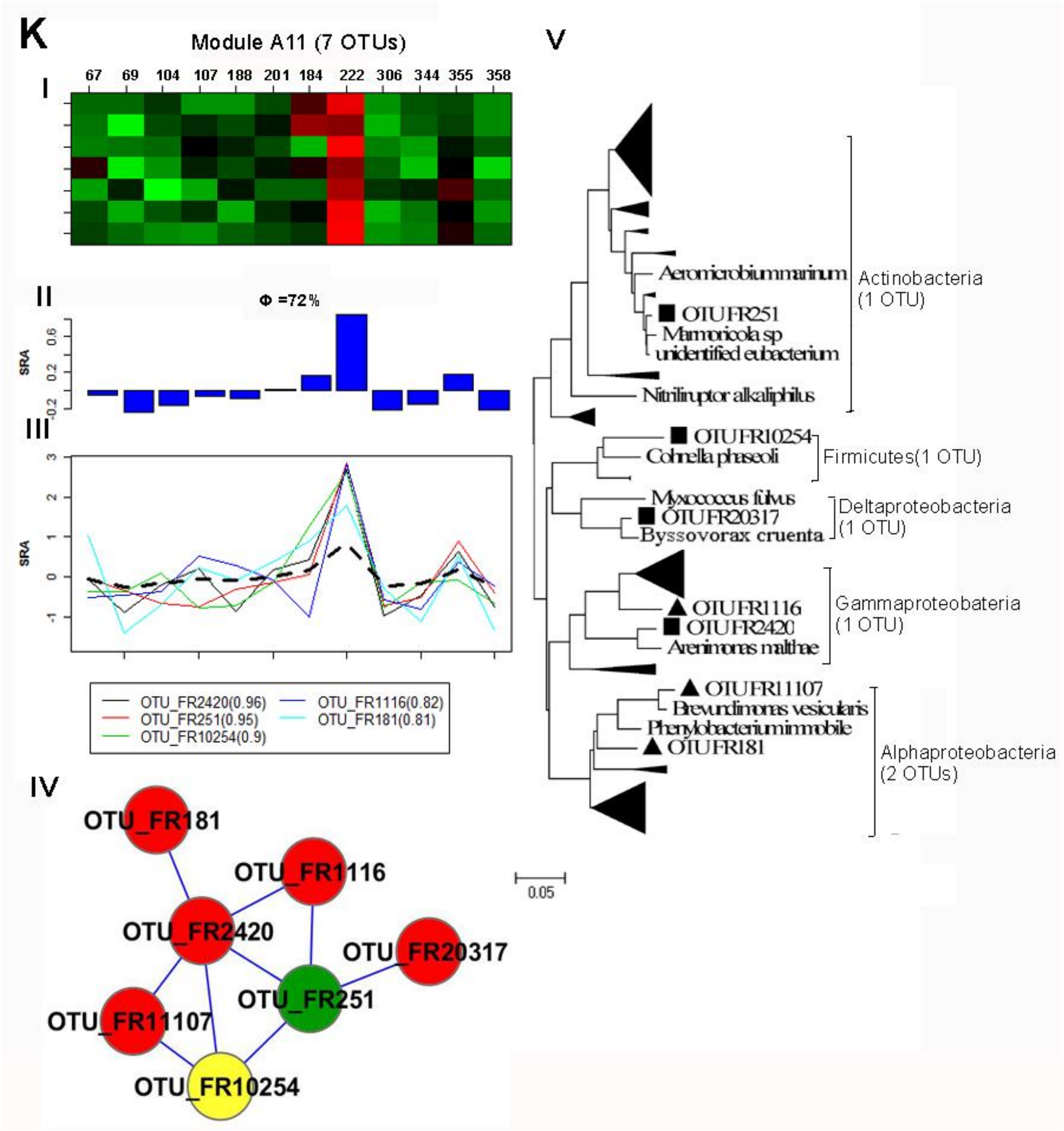
Online Fig. 2.


I
Module A9 (5 OTUs)
I
67
69
104
107
188
201
184
222
306
344
355
358
II
Φ =69%
SRA
0.2
-0.2
III
SRA
2.0
1.5
1.0
0.5
-0.5
-1.5
OTU_FR338(0.98)
OTU_FR16656(0.84)
OTU_FR198(0.79)
OTU_FR1478(0.76)
OTU_FR1209(0.75)
IV
OTU_FR338
OTU_FR198
OTU_FR16656
OTU_FR1478
OTU_FR1209
V
Nitriliruptor alkaliphilus
OTUFR16656
OTUFR338
Thermoleiphilum minutum
Thermoleophilum album
bacterium Ellin301
Conexibacter woesei
Solirubrobacter soli
Rubrobacteridae bacterium
Rubrobacterineae bacterium
Actinobacteria
(2 OTUs)
OTUFR1209
Pseudomonas mucidolens
Ectothiorhodosinus mongolicus
Gammaproteobateria
(1 OTU)
Arenimonas malthae
OTUFR198
Burkholderia endofungorum
Massilia timonae
Betaproteobacteria
(1 OTU)
Acidobacteriaceae bacterium
uncultured Acidobacteria
Candidatus Koribacter
Edaphobacter modestus
OTUFR1478
Acidobacteria
(1 OTU)
0.05

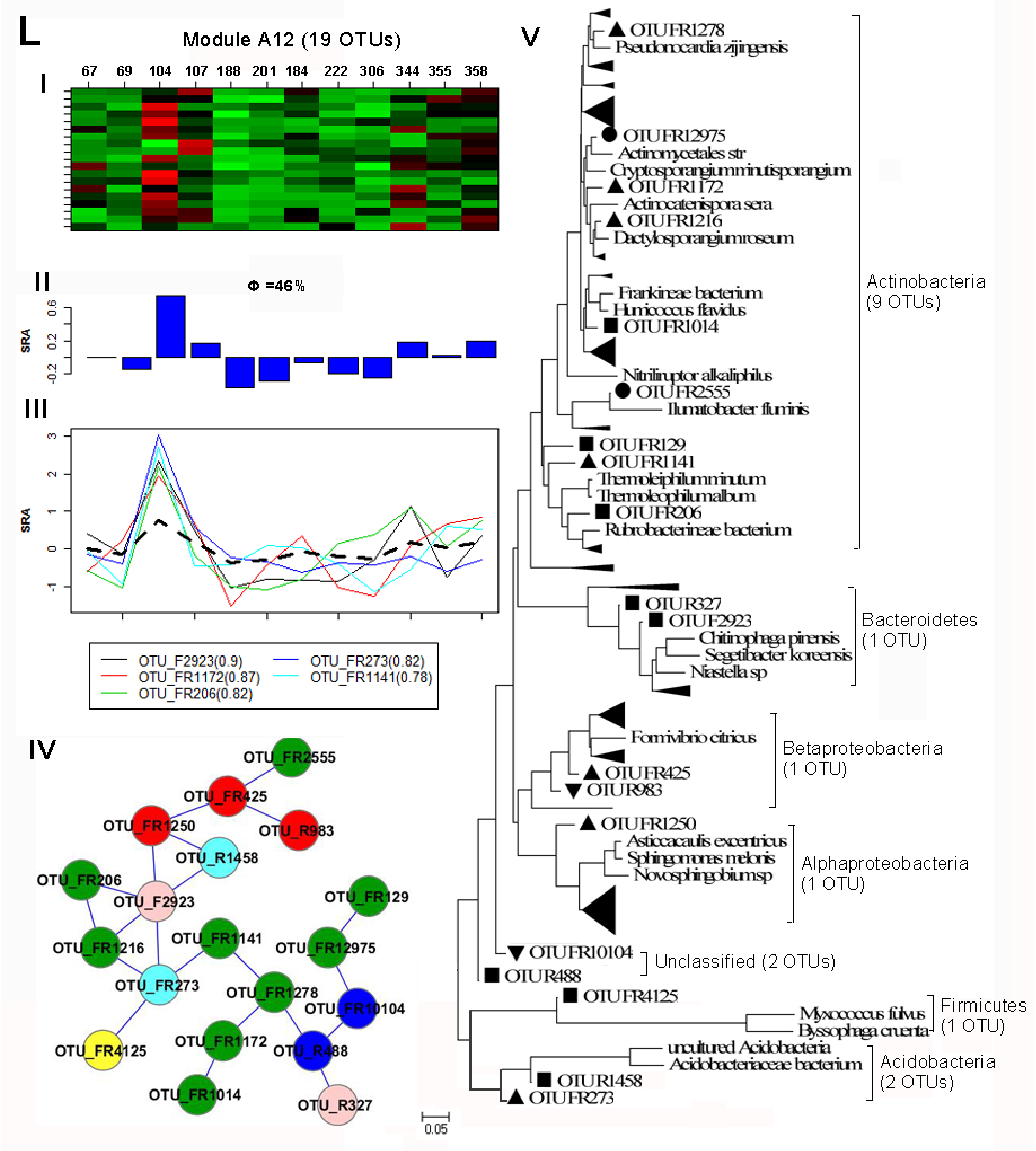
Online Fig. 2.


J
Module A10 (10 OTUs)
I
67
69
104
107
188
201
184
222
306
344
355
358
II
Φ =60%
SRA
0.4
0.0
-0.4
III
SRA
2
1
0
-1
-2
OTU_FR2912(0.89)
OTU_FR889(0.89)
OTU_FR1023(0.79)
OTU_FR810(0.75)
OTU_FR272(0.7)
IV
OTU_FR15392
OTU_FR1376
OTU_FR514
OTU_FR810
OTU_FR1095
OTU_FR272
OTU_FR2912
OTU_FR1023
OTU_FR889
OTU_FR10595
V
OTUFR272
Ilumatobacter fluminis
actinobacteriumBGR
Ferrithrix thermotolerans
Nitriliruptor alkaliphilus
OTUFR1376
Thermoleiphilumminutum
Thermoleophilumalbum
OTUFR810
Actinobacteria
(3 OTUs)
OTUFR15392
Gemmatimonas aurantiaca
Gemmatimonadetes
(1 OTU)
Novosphingobiumsp
Asticcacaulis excentricus
OTUFR1023
Sphingomonas melonis
Alphaproteobateria
(1 OTU)
Geothrix fermentans
OTUFR2912
Steroidobacter denitrificans
Nitrosococcus oceani
Arenimonas malthae
Gammaproteobacteria
(1 OTU)
OTUFR514
Burkholderia endofungorum
Formivibrio citricus
Bordetella petrii
Rhodocyclus tenuis
Sterolibacteriumdenitrificans
Massilia timonae
Betaproteobacteria
(1 OTU)
OTUFR10595
Unclassified (1 OTU)
OTUFR1095
Candidatus Koribacter
Edaphobacter modestus
Acidobacteriaceae bacterium
uncultured Acidobacteria
Acidobacteria
(1 OTU)
OTUFR889
Blastopirellula marina
Planctomycetacia
(1 OTU)
0.05

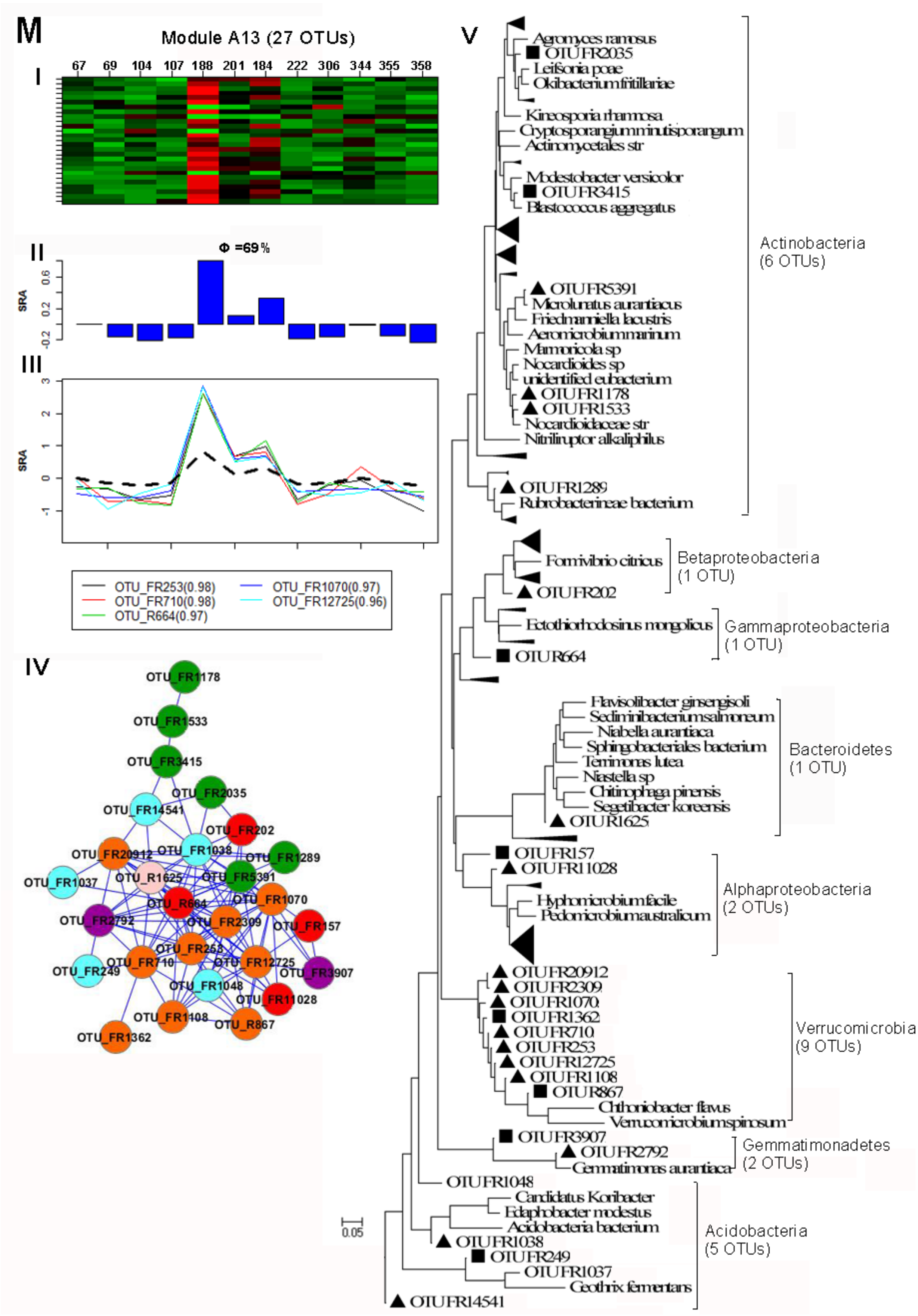
Online Fig. 2.


K
Module A11 (7 OTUs)
67
69
104
107
188
201
184
222
306
344
355
358
I
II
Φ =72%
SRA
0.6
0.2
-0.2
III
SRA
3
2
1
0
-1
OTU_FR2420(0.96)
OTU_FR251(0.95)
OTU_FR10254(0.9)
OTU_FR1116(0.82)
OTU_FR181(0.81)
IV
OTU_FR181
OTU_FR1116
OTU_FR2420
OTU_FR20317
OTU_FR251
OTU_FR11107
OTU_FR10254
V
Aeromicrobium marinum
OTUFR251
Marmoricola sp
unidentified eubacterium
Nitriliruptor alkaliphilus
Actinobacteria (1 OTU)
OTUFR10254
Cohnella phaseoli
Firmicutes(1 OTU)
Myxococcus fulvus
OTUFR20317
Byssovorax cruenta
Deltaproteobacteria (1 OTU)
OTUFR1116
OTUFR2420
Arenimonas malthae
Gammaproteobateria (1 OTU)
OTUFR11107
Brevundimonas vesicularis
Phenylobacterium immobile
OTUFR181
Alphaproteobacteria (2 OTUs)
0.05

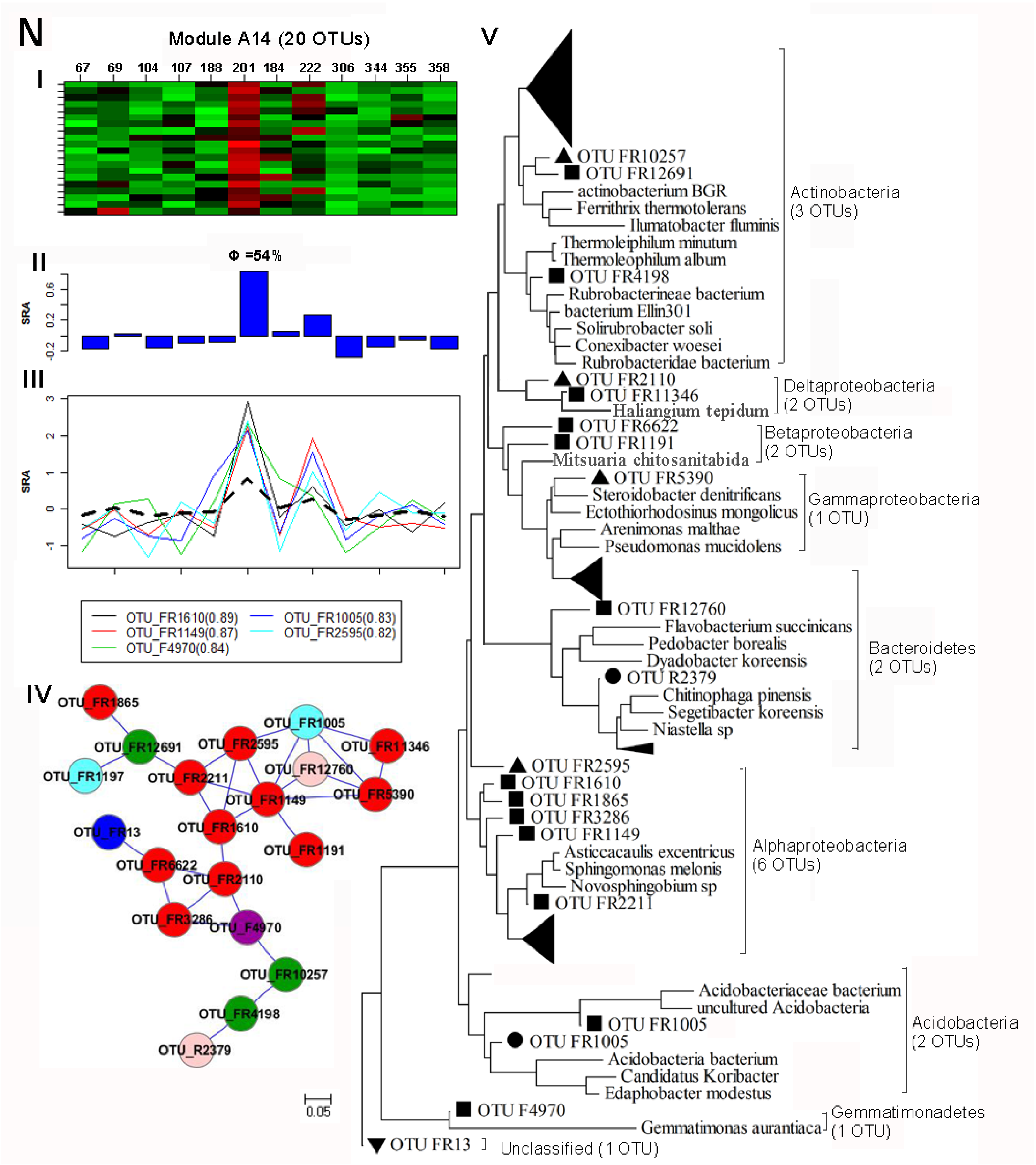
Online Fig. 2.


L
Module A12 (19 OTUs)
I
67 69 104 107 188 201 184 222 306 344 355 358
II
Φ =46%
SRA
0.6
0.2
-0.2
III
SRA
3
2
1
0
-1
OTU_F2923(0.9)
OTU_FR1172(0.87)
OTU_FR206(0.82)
OTU_FR273(0.82)
OTU_FR1141(0.78)
IV
OTU_FR2555
OTU_FR425
OTU_FR1250
OTU_R983
OTU_R1458
OTU_FR206
OTU_F2923
OTU_FR129
OTU_FR1216
OTU_FR1141
OTU_FR12975
OTU_FR273
OTU_FR1278
OTU_FR10104
OTU_FR4125
OTU_FR1172
OTU_R488
OTU_FR1014
OTU_R327
V
OTUFR1278
Pseudonocardia zijingensis
OTUFR12975
Actinomycetales str
Cryptosporangium minutisporangium
OTUFR1172
Actinocatenispora sera
OTUFR1216
Dactylosporangium roseum
Frankineae bacterium
Humicoccus flavidus
OTUFR1014
Nitriliruptor alkaliphilus
OTUFR2555
Ilumatobacter fluminis
OTUFR129
OTUFR1141
Thermoleiphilum minutum
Thermoleophilum album
OTUFR206
Rubrobacterineae bacterium
Actinobacteria
(9 OTUs)
OTUR327
OTUF2923
Chitinophaga pinensis
Segetibacter koreensis
Niastella sp
Bacteroidetes
(1 OTU)
Formivibrio citricus
OTUFR425
OTUR983
Betaproteobacteria
(1 OTU)
OTUFR1250
Asticcacaulis excentricus
Sphingomonas melonis
Novosphingobium sp
Alphaproteobacteria
(1 OTU)
OTUFR10104
Unclassified (2 OTUs)
OTUR488
OTUFR4125
Myxococcus fulvus
Byssophaga cruenta
Firmicutes
(1 OTU)
uncultured Acidobacteria
Acidobacteriaceae bacterium
OTUR1458
OTUFR273
Acidobacteria
(2 OTUs)
0.05

Online Fig. 2.


M
Module A13 (27 OTUs)
I
67
69
104
107
188
201
184
222
306
344
355
358
II
Φ =69%
SRA
0.6
0.2
-0.2
III
SRA
3
2
1
0
-1
OTU_FR253(0.98)
OTU_FR710(0.98)
OTU_R664(0.97)
OTU_FR1070(0.97)
OTU_FR12725(0.96)
IV
OTU_FR1178
OTU_FR1533
OTU_FR3415
OTU_FR2035
OTU_FR14541
OTU_FR202
OTU_FR20912
OTU_FR1038
OTU_FR1289
OTU_FR1037
OTU_R1625
OTU_FR5391
OTU_R664
OTU_FR1070
OTU_FR2792
OTU_FR2309
OTU_FR157
OTU_FR253
OTU_FR249
OTU_FR710
OTU_FR12725
OTU_FR3907
OTU_FR1048
OTU_FR11028
OTU_FR1108
OTU_R867
OTU_FR1362
V
Agromyces ramosus
OTUFR2035
Leifsonia poae
Okibacterium fritillariae
Kineosporia rhamnosa
Cryptosporangium minutisporangium
Actinomycetales str
Modestobacter versicolor
OTUFR3415
Blastococcus aggregatus
OTUFR5391
Microlunatus aurantiacus
Friedmanniella lacustris
Aeromicrobium marinum
Marmoricola sp
Nocardioides sp
unidentified eubacterium
OTUFR1178
OTUFR1533
Nocardioidaceae str
Nitriliruptor alkaliphilus
OTUFR1289
Rubrobacterineae bacterium
Actinobacteria
(6 OTUs)
Formivibrio citricus
OTUFR202
Betaproteobacteria
(1 OTU)
Ectothiorhodosinus mongolicus
OTUR664
Gammaproteobacteria
(1 OTU)
Flavisolibacter ginsengisoli
Sediminibacterium salmoneum
Niabella aurantiaca
Sphingobacteriales bacterium
Terrimonas lutea
Niastella sp
Chitinophaga pinensis
Segetibacter koreensis
OTUR1625
Bacteroidetes
(1 OTU)
OTUFR157
OTUFR11028
Hyphomicrobium facile
Pedomicrobium australicum
Alphaproteobacteria
(2 OTUs)
OTUFR20912
OTUFR2309
OTUFR1070
OTUFR1362
OTUFR710
OTUFR253
OTUFR12725
OTUFR1108
OTUR867
Chthoniobacter flavus
Verrucomicrobium spinosum
Verrucomicrobia
(9 OTUs)
OTUFR3907
OTUFR2792
Gemmatimonas aurantiaca
Gemmatimonadetes
(2 OTUs)
OTUFR1048
Candidatus Koribacter
Edaphobacter modestus
Acidobacteria bacterium
OTUFR1038
OTUFR249
OTUFR1037
Geothrix fermentans
OTUFR14541
Acidobacteria
(5 OTUs)
0.05

Online Fig. 2.


N
Module A14 (20 OTUs)
67 69 104 107 188 201 184 222 306 344 355 358
I
II
Φ =54%
SRA
0.6 0.2 -0.2
III
SRA
3 2 1 0 -1
OTU_FR1610(0.89)
OTU_FR1149(0.87)
OTU_F4970(0.84)
OTU_FR1005(0.83)
OTU_FR2595(0.82)
IV
OTU_FR1865
OTU_FR12691
OTU_FR1197
OTU_FR2595
OTU_FR1005
OTU_FR11346
OTU_FR2211
OTU_FR12760
OTU_FR1149
OTU_FR5390
OTU_FR13
OTU_FR1610
OTU_FR1191
OTU_FR6622
OTU_FR2110
OTU_FR3286
OTU_F4970
OTU_FR10257
OTU_FR4198
OTU_R2379
V
OTU FR10257
OTU FR12691
actinobacterium BGR
Ferrithrix thermotolerans
Ilumatobacter fluminis
Thermoleiphilum minutum
Thermoleophilum album
OTU FR4198
Rubrobacterineae bacterium
bacterium Ellin301
Solirubrobacter soli
Conexibacter woesei
Rubrobacteridae bacterium
Actinobacteria (3 OTUs)
OTU FR2110
OTU FR11346
Haliangium tepidum
Deltaproteobacteria (2 OTUs)
OTU FR6622
OTU FR1191
Mitsuaria chitosanitabida
Betaproteobacteria (2 OTUs)
OTU FR5390
Steroidobacter denitrificans
Ectothiorhodosinus mongolicus
Arenimonas malthae
Pseudomonas mucidolens
Gammaproteobacteria (1 OTU)
OTU FR12760
Flavobacterium succinicans
Pedobacter borealis
Dyadobacter koreensis
OTU R2379
Chitinophaga pinensis
Segetibacter koreensis
Niastella sp
Bacteroidetes (2 OTUs)
OTU FR2595
OTU FR1610
OTU FR1865
OTU FR3286
OTU FR1149
Asticcacaulis excentricus
Sphingomonas melonis
Novosphingobium sp
OTU FR2211
Alphaproteobacteria (6 OTUs)
Acidobacteriaceae bacterium
uncultured Acidobacteria
OTU FR1005
OTU FR1005
Acidobacteria bacterium
Candidatus Koribacter
Edaphobacter modestus
Acidobacteria (2 OTUs)
OTU F4970
Gemmatimonas aurantiaca
Gemmatimonadetes (1 OTU)
OTU FR13
Unclassified (1 OTU)
0.05

Online Fig. 2.

2) Supplemental Text for module eigengene analyses

Detailed description of individual modules

Since the pair-wise correlations of OTU abundance across different samples are used to define the adjacency matrix, the pMENs constructed here in fact describe the co-occurrence of OTUs in microbial communities. Thus a module in a pMEN could indicate that the microbial populations within a module may have similar ecological niches. Detailed examination of the module memberships of individual OTUs are rich sources of new hypotheses for understanding the potential interactions and ecological roles of various microbial species/populations in microbial communities, detailed analyses of individual modules are described as below.

a. Modules under elevated CO_2

Module E1. This module contained 37 members, making it the largest module in eCO_2 network. The change pattern of the eigengene across all 12 samples was more or less consistent with those of individual OTUs (Fig. S6A-I, II). The eigengene explained 35% of the total OTU abundance variance for this module (Fig. S6A-II). About 54% of the OTUs had significant module memberships with their eigengene of this module (Fig. S6A-III). This module was enriched with *Actinobacteria* (38%) and *Proteobacteria* (32%). As a group, *Actinobacteria* include some of the most common soil, freshwater and marine bacteria. They play an important role in the decomposition of organic materials, such as cellulose and chitin, playing a vital part in organic matter turnover and carbon cycling, replenishing the supply of nutrients in the soil and is an important part of humus formation. OTU FR21501 in *Actinobacteria* is closely related to *Thermoleophilum album* and *Thermoleophilum minutum* (Fig. S6A-V), obligately aerobic thermophilic bacteria restricted to growth on a narrow range of *n*-alkane substrates from C13 to C20, who have been isolated from mud samples obtained from both thermal and nonthermal environments (1).

Module E2. This module contained 19 members. The change pattern of the eigengene across all 12 samples was more or less consistent with those of individual OTUs (Fig. S6B-I, II). The eigengene explained 64% of total OTU abundance variance for this module (Fig. S6B-II). All OTUs had significant module memberships with their eigengene of this module and more than half of them (10) were shared with aCO_2 network (Fig. S6B-V). Although this module was composed of diverse groups, 4 of the 15 *Bacteroidetes* from the network were enriched in this module and one (OTU R2577) was a module hub (Fig. 3). Members of the *Bacteroidetes* phylum are found in a wide variety of environments, including soil (2), aquatic habitats (3), insect symbionts (4), and are also dominant in the human gut as beneficial bacteria (5).

Module E3. This module had 32 members. The change pattern of the eigengene across all 12 samples was more or less consistent with those of individual OTUs (Fig. S6C-I, II). The eigengene explained 55% of total OTU abundance variance in this module (Fig. S6C-II). About 78% of the OTUs had significant module memberships with their eigengene of this module. This module was primarily enriched with *Actinobacteria* (38%), *α-Proteobacteria* (19%) and *Acidobacteria* (19%) (Fig. S6C-V). OTU FR351 had the highest connectivity within the module and is closely related to *Arthrobacter aurescens* (Fig. S6C-V), which was originally isolated from soil at an atrazine spill site (6). *Arthrobacter* species are among the most frequently isolated, indigenous, aerobic bacteria found in soils, are metabolically and ecologically diverse, and have the ability to survive harsh environmental conditions (e.g., starvation, radiation, oxygen radicals, and toxic chemicals) for extended periods of time (6).

Module E4. This small module contained only 5 members. The change pattern of the eigengene across all 12 samples was very consistent with those of individual OTUs (Fig. S6D-I, II). The eigengene explained 79% of total OTU abundance variance of in this module (Fig. S6D-II). All of the OTUs had significant module memberships with their eigengene of this module. This module was composed of two *Actinobacteria*, two *α-Proteobacteria* and one *Acidobacteria*, but most of them were a little bit far away from the known isolates except OTU FR113 close to bacterium Ellin301 (Fig. S6D-V) (7, 8).

Module E5. This module contained 31 members. The change pattern of the eigengene across all 12 samples was more or less consistent with those of individual OTUs (Fig. S6D-I, II). The eigengene explained 56% of total the OTU abundance variance for this module (Fig. S6D-II). About 87% of the OTUs had significant module memberships with their eigengene of this module. Similar to module E2, 5 of 15 Bacteroidetes were enriched in this module (Fig. S6E-V). OTU FR1506, most significantly correlated with the eigengene, was detected as the module hub as well. Its closest known relative is *Ilumatobacter fluminis*, a Gram-positive, , aerobic *Actinobacterium* estuary sediment isolate (9).

Module E6. This is a small module with 8 members. The change patterns of the eigengene across all 12 samples were consistent with those of individual OTUs (Fig. S6F-I, II). The eigengene explained 61% of total variance of the OTU abundance in this module (Fig. S6F-II). All except one OTU had significant module memberships with their eigengene of this module. This module was composed by diverse groups (Fig. S6F-V), and OTU FR184, most significantly correlated with the eigengene, is closely related to *Pseudonocardia zijingensis* that was isolated on an enrichment culture (10).

Module E7. This module had 6 members. The change pattern of the eigengene across all 12 samples was very consistent with those of individual OTUs (Fig. S6G-I, II). The eigengene explained 73% of total OTU abundance variance in this module (Fig. S6G-II). All OTUs had significant module memberships with their eigengene of this module and shared with aCO_2 network. Most of the OTUs belonged to *Actinobacteria* (83%) (Fig. S6G-V). OTU FR1399 is closely related to *Humicoccus flavidus* a strictly aerobic soil isolate that grows under conditions of 4~32^{o}C, pH 5.0-8.5 with less than 5% of NaCl. It can use cellobiose, trehalose or arabinose as a sole carbon and energy source, but not benzoate, citrate, or formate (11).

Module E8. This is a small module with 5 members. The change pattern of the eigengene across all 12 samples was highly consistent with those of individual OTUs (Fig. S6H-I, II). The eigengene explained 76% of total OTU abundance variance in this module (Fig. S6H-II). All OTUs had significant module memberships with their eigengene of this module. This module was composed of two *Actinobacteria*, a *Planctomycetes*, a *Bacteroidetes* and a *γ-Proteobacteria* (Fig. S6H-V). OTU FR17029, most significantly correlated with the eigengene, was close to *Steroidobacter denitrificans* that is a steroidal hormone-degrading *γ*-proteobacterium (12).

Module E9. This is an intermediate module with 20 members. The change pattern of the eigengene across all 12 samples was very consistent with those of individual OTUs (Fig. 2-I, II). The eigengene explained 63% of total variance of the OTU abundance in this module (Fig. 2-II). All OTUs except one had significant module memberships with their eigengene of this module. This module was dominated by *Verrucomicrobia* (35%) that were closely related to *Chthoniobacter flavus* and *Verrucomicrobium spinosum*, which were enteric bacterium found in aquatic and soil habitats and in the gastrointestinal tract of humans. These organisms can ferment sugars without generating gas as end product (7). *Verrucomicrobium* species can make up to 3% of soil microbiota (7, 8). All OTUs were significantly correlated with the module eigengene and all were shared in both eCO_2 and aCO_2 networks.

Module E10. This module had 22 members. The change pattern of the eigengene across all 12 samples was more or less consistent with those of individual OTUs (Fig. S6I-I, II). The eigengene explained 48% of total variance of the OTU abundance in this module (Fig. S6I-II). Most OTUs (68%) had significant module memberships with their eigengene of this module. Although this module was dominated by *Actinobacteria* (23%) and *α–Proteobacteria* (28%), OTU FR275 from the *Chloroflexi* was found to serve as the module hub (Fig. 3; Fig. S6I-V). As yet this OTU does not have any closely related isolates. OTU FR106 was identified as a module connector, which was the only one in eCO_2 network. It was closely related to *Friedmanniella lacustris*, a bacterium isolated from a water sample of the hyper-saline Ekho Lake, Antarctica water sample (13).

Module E11. This module contained 26 members. The change pattern of the eigengene across all 12 samples was consistent with those of individual OTUs (Fig. S6J-I, II). The eigengene explained 49% of total variance of the OTU abundance in this module (Fig. S6J-II). About 69% of the OTUs had significant module memberships with their eigengene of this module. This module was enriched with *β-Proteobacteria* (23%) and *Acidobacteria* (19%) (Fig. S6J-V). OTU FR1307 which had highest connectivity within the module and mostly correlated with the module eigengene, was closely related with *Burkholderia endofungorum*. The members of genus *Burkholderia* are very abundant and widely spread, including soil and hospital environments (14). Many strains have been found as plant-associated bacteria (14), including both obligate endosybionts and phytopathogens (14).

b. Modules under ambient CO_2

Module A1: With 39 members, A1 was the largest module in the aCO_2 network. The change pattern of the eigengene across all 12 samples was consistent with those of individual OTUs (Fig. S7A-I, II). The eigengene explained 45% of total variance of the OTU abundance in this module (Fig. S7A-II). This module was enriched with *Actinobacteria* (31%), *Acidobacteria* (21%). About 69% of the OTUs had significant module memberships with their eigengene of this module (Fig. S7A-III). OTU FR765 acted as a module hub and OTU FR11588 acted as a connector in this module (Fig. 3). Both are closely related to *Ferrithrix thermotolerans*, an extremely acidophilic, iron-oxidizing *Actinobacteria* isolated from a geothermal site in Yellowstone National Park, Wyoming, USA (15). Under anaerobic conditions it catalyzes the dissimilatory reduction of ferric iron in oxygen-free medium with glycerol as the electron donor (15).

Module A2. This module had 23 members. The change pattern of the eigengene across all 12 samples was quite consistent with those of individual OTUs (Fig. S7B-I, II). The eigengene explained 62% of total variance of the OTU abundance in this module (Fig. S7B-II). All OTUs except one had significant module memberships with their eigengene of this module (Fig. S7B-III). This module was still primarily enriched with Actinobacteria (39%). OTU FR1208 had highest connectivity within modules and most correlated with the module eigengene and it was close to *Marmoricola sp.*. The members of *Marmoricola* genus were widely isolated from quite different habitats, such as marine sediment (16), soil (17), volcanic ash (18) and even marble statue (19). They were aerobic and Gram-positive coccoid *Actinobacterium*.

Module A3. This module had 16 members. The change pattern of the eigengene across all 12 samples was well consistent with those of individual OTUs (Fig. S7C-I, II). The eigengene explained 57% of total variance of the OTU abundance in this module (Fig. S7C-II). About 81% of the OTUs had significant module memberships with their eigengene of this module (Fig. S7C-III). This module was composed of diverse groups, with the module hub OTU FR4752 that was closely related to *Bacillus pocheonensis*. *B. pocheonensis* is an aerobic, halotolerant bacterium originally isolated from a ginseng field soil (20). OTU FR4752 was identified as a connector in this module and it was closely related to *Edaphobacter modestus* in *Firmicutes* phylum. *E. modestus* was isolated from alpine and forest soils and adapted to low carbon concentrations and to neutral to slightly acidic conditions (21).

Module A4. This module contained 16 members. The change pattern of the eigengene across all 12 samples was more or less consistent with those of individual OTUs (Fig. S7D-I, II). The eigengene explained 47% of total variance of the OTU abundance in this module (Fig. S7D-II). Majority of the OTUs (69%) in this module had significant module memberships with their eigengene (Fig. S7D-III). This module still was enriched by *Actinobacteria* (50%) (Fig. S7D-V). OTU FR383 and OTU FR125 were both identified as connectors in this module, which were close to *Streptosporangium roseum* and *Rubrobacterineae bacterium* in *Actinobacteria*, respectively. OTU FR113 is closely related to *Conexibacter woesei*, another member of the common soil *Actinobacteria*, that is able to use a variety of substrates and reduce nitrate to nitrite (22).

Module A5. This module had 36 members, which was the second largest module in this network. The change pattern of the eigengene across all 12 samples was not so consistent with those of individual OTUs (Fig. S7E-I, II). The eigengene explained 43% of total OTU abundance variance in this module (Fig. S7E-II) and 69% of the OTUs had significant module memberships with their eigengene of this module. This module was composed of a diverse group of bacteria with *Acidobacteria* (28%) as most abundant (Fig. S9E-V). Among them, OTU FR167, as a module hub, was closely related to *Byssophaga cruenta* that degraded crystalline cellulose completely and could be cultivated on filter paper as the only carbon source with inorganic nitrogen source (23) (Fig S7E-V). Besides, The OTU R882 in *α-Proteobacteria* was closely related to *Rhodopseudomonas palustris* and *Hyphomicrobium facile* (Fig. S7E-V). *Rhodopseudomonas* bacteria are purple nonsulfur phototrophic organisms that can be found in many types of marine environments and soils (24).

Module A6. This module had 11 members. The change pattern of the eigengene across all 12 samples was highly consistent with those of individual OTUs (Fig. S7F-I, II). The eigengene explained 60% of total OTU abundance variance in this module (Fig. S7F-II). All of the OTUs had significant module memberships with their eigengene of this module. This module was dominated by *Proteobacteria* (64%) and one, OTU FR1615, has highest correlation with the module eigengene. This OTU is close to *Novosphingobium* species, which are capable of degradation of a variety of organic contaminants, such as naphthalene (25) and carbofuran, a broad-spectrum pesticide (26).

Module A7. This small module had 5 members only. The change pattern of the eigengene across all 12 samples was very consistent with those of individual OTUs (Fig. S7G-I, II). The eigengene explained 79% of total OTU abundance variance in this module (Fig. S7G-II). All the OTUs had significant module memberships with their eigengene but only two of them were shared with eCO_2 network (Fig. S7G-III). This module was dominated by *Proteobacteria* (60%), one *α-Proteobacteria* and two *β-Proteobacteria*. OTU FR1311 had the most connectivity and highest correlation with the module eigengene, but it was not close to any isolates within the *β-Proteobacteria*.

Module A8. This module had 8 members. The change patterns of the eigengene across all 12 samples were quite consistent with those of individual OTUs (Fig. S7H-I, II). The eigengene explained 61% of total variance of the OTU abundance in this module (Fig. S7H-II). The majority (88%) of the OTUs had significant module memberships with their eigengene of this module (Fig. S7H-III). This module was primarily enriched with *Actinobacteria* (38%), and *α-Protoebacteria* (38%) (Fig. S7H-V). The central node OTU FR282 was significantly negative correlated the module eigengene. This OTU was closely related with *Intrasporangiaceae bacterium* and *Knoellia subterranea* of the *Actinobacteria*. *K. subterranea* was isolated from a soil sample in the Reed Flute Cave near Guilin, China (27) and is an aerobic to microaerophilic bacterium, capable of growth on acetate, formate, malate or succinate as a carbon source, but not aconitate, benzoate, citrate or tartrate (27).

Module A9. This is a small module with 5 members. The change patterns of the eigengene across all 12 samples were quite consistent with those of individual OTUs (Fig. S7I-I, II). The eigengene explained 69% of total variance of the OTU abundance in this module (Fig. S7I-II) and all of the OTUs had significant module memberships with their eigengene of this module. This module was composed by *Actinobacteria*, *γ-Proteobacteria, β-Proteobacteria* and *Acidobacteria* (Fig S9I-V). The top two significant OTUs correlated to their eigengene were both from *Actinobacteria* and clustered together but do not have any closely related isolates.

Module A10. This module had 10 members. The change pattern of the eigengene across all 12 samples was well consistent with those of individual OTUs (Fig. S7J-I, II). The eigengene explained 60% of total OTU abundance variance in this module (Fig. S7J-II) and all had significant (positively or negatively) module memberships with their eigengene of this module (Fig. S7J-III). Although this module was relatively small it was composed of several bacterial groups (Fig. S7J-IV, V). OTU FR889 had the highest connectivity and most significant correlation with the module eigengene, but its taxonomy is unclear. The nearest relative was *Blastopirellula marina*, a strictly aerobic *Planctomycetacia* (28).

Module A11. This module had 7 members. The change pattern of the eigengene across all 12 samples was quite consistent with those of individual OTUs (Fig. S7K-I, II). The eigengene explained 72% of total OTU abundance variance in this module (Fig. S7K-II) and all of the OTUs had significant module memberships with their eigengene of this module (Fig. S7K-III). This module was dominated by *Proteobacteria* (71%), including two *α*-, one *δ*- and two *γ-Proteobacteria* (Fig. S7K-IV, V). One of the *γ-Proteobacteria*, OTU FR2420, had most connectivity and highest correlation with the module eigengene. It is closely related to *Arenimonas malthae*, an isolate from oil-contaminated soil from Taiwan, China (29).

Module A12. This module had 19 members. The change pattern of the eigengene across all 12 samples was more or less consistent with those of individual OTUs (Fig. S7L-I, II). The eigengene explained 46% of total OTU abundance variance in this module (Fig. S7L-II) and 76% of the OTUs had significant module memberships with their eigengene of this module. This module was dominated by *Actinobacteria* (47%) however the identified module hub belonged to a *Bacteroidetes*, OTU F2923 (Fig. 3), which had no known close relatives(Fig. S7L-V).

Module A13. This module had 27 members. The change pattern of the eigengene across all 12 samples was well consistent with those of individual OTUs (Fig. S7M-I, II). The eigengene explained 69% of total variance of the OTU abundance in this module (Fig. S7M-II) and all of the OTUs had significant module memberships with their eigengene of this module. Most of this network's *Verrucomicrobia* OTUs (9 of 12) were concentrated in this module (accounting for 33% of the members). All these nine OTUs had significant module memberships with their eigengene (Fig. S7M-V). Although most of them (78%) were shared in both eCO_2 and aCO_2 networks, they had many more connections among themselves and neighbors under the aCO_2 network than eCO_2 network (Fig. S4). Similar to the OTUs in the module E9 (Fig. 2), these OTUs were closely related to *Chthoniobacter flavus* and *Verrucomicrobium spinosum,* which were enteric bacterium found in aquatic and soil habitats and in the gastrointestinal tract of humans. They can ferment sugars without making gas as a product (7).

Module A14. This module had 20 members. The change pattern of the eigengene across all 12 samples was consistent with those of individual OTUs (Fig. S7N-I, II). The eigengene explained 54% of total variance of the OTU abundance in this module (Fig. S7N-II) and 85% of the OTUs had significant module memberships with their eigengene of this module. This module was composed of diverse bacterial groups but the major one was Proteobacteria, including six *α*-, two *β*-, two *δ*- and one *γ-Proteobacteria*. OTU FR1149 was identified as module hub (Fig. 3) but OTU FR1610 was most correlated with the module eigengene. Both of them belonged to *α-Proteobacteria* (Fig. S7N-V).

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