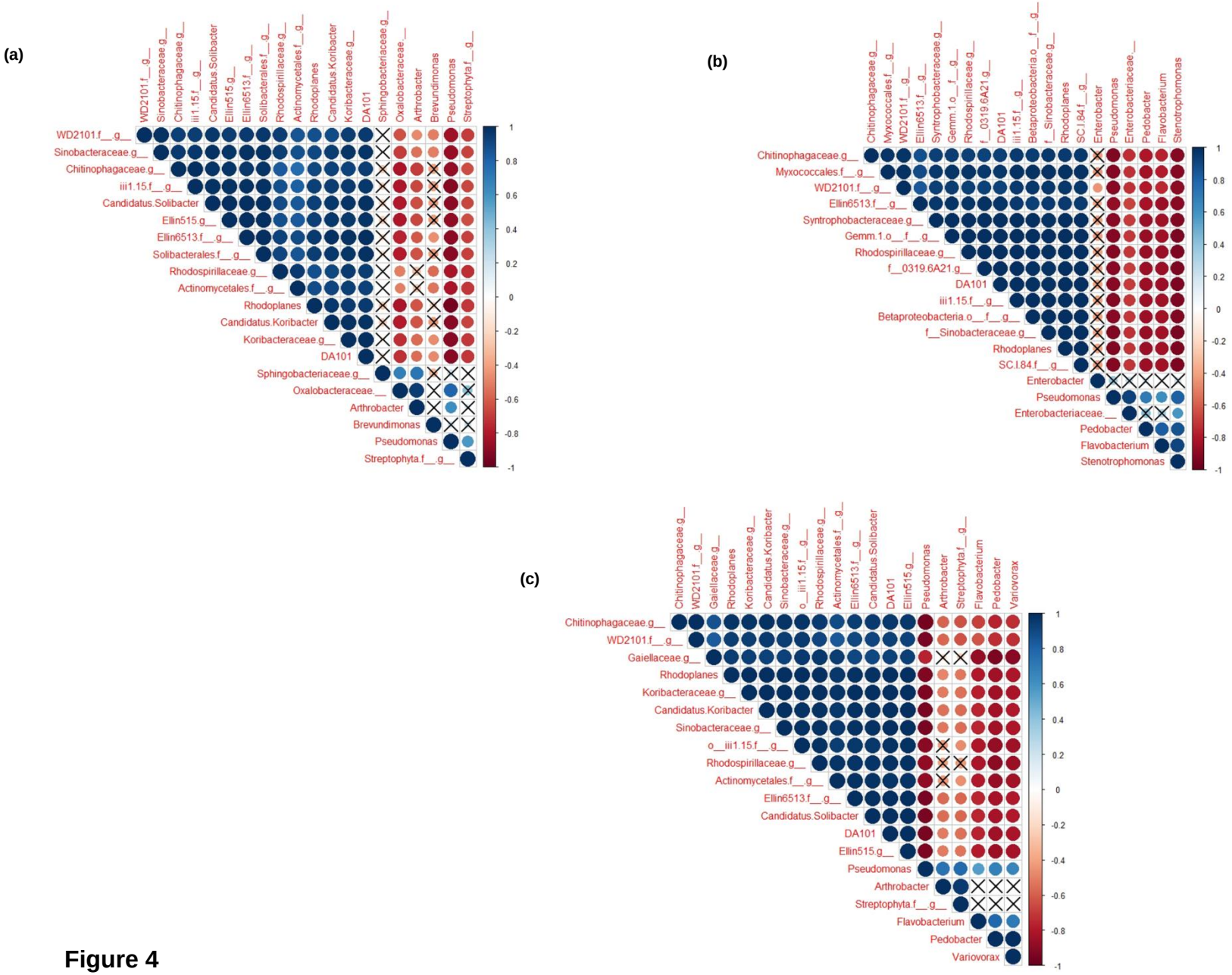
(a)
WD2101.f__g__
Sinobacteraceae.g__
Chitinophagaceae.g__
iii1.15.f__g__
Candidatus.Solibacter
Ellin515.g__
Ellin6513.f__g__
Solibacterales.f__g__
Rhodospirillaceae.g__
Actinomycetales.f__g__
Rhodoplanes
Candidatus.Koribacter
Koribacteraceae.g__
DA101
Sphingobacteriaceae.g__
Oxalobacteraceae.__
Arthrobacter
Brevundimonas
Pseudomonas
Streptophyta.f__g__
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1
(b)
Chitinophagaceae.g__
Myxococcales.f__g__
WD2101.f__g__
Ellin6513.f__g__
Syntrophobacteraceae.g__
Gemm.1.o__f__g__
Rhodospirillaceae.g__
f__0319.6A21.g__
DA101
iii1.15.f__g__
Betaproteobacteria.o__f__g__
f__Sinobacteraceae.g__
Rhodoplanes
SC.I.84.f__g__
Enterobacter
Pseudomonas
Enterobacteriaceae.__
Pedobacter
Flavobacterium
Stenotrophomonas
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1
(c)
Chitinophagaceae.g__
WD2101.f__g__
Gaiellaceae.g__
Rhodoplanes
Koribacteraceae.g__
Candidatus.Koribacter
Sinobacteraceae.g__
o__iii1.15.f__g__
Rhodospirillaceae.g__
Actinomycetales.f__g__
Ellin6513.f__g__
Candidatus.Solibacter
DA101
Ellin515.g__
Pseudomonas
Arthrobacter
Streptophyta.f__g__
Flavobacterium
Pedobacter
Variovorax
1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
-0.8
-1

Figure 4