

Supplementary Information for

**Bacteriome diversity in leaf and root of the resurrection species *Selaginella convoluta* and *S. sellowii* in the
Brazilian Cerrado**

Mayara Santana Zanella¹, Jeferson Vidart Ramos¹, Gecele Matos Paggi¹, Daniel Guerra Franco^{1,2},
Nalvo Franco de Almeida³, Denise Brentan da Silva^{2,4}, Aline Pedroso Lorenz^{1,2}

¹Laboratory of Ecology and Evolutionary Biology, Institute of Biosciences, Federal University of
Mato Grosso do Sul, Av. Costa e Silva, s/nº, Campo Grande, 79070-900, MS, Brazil

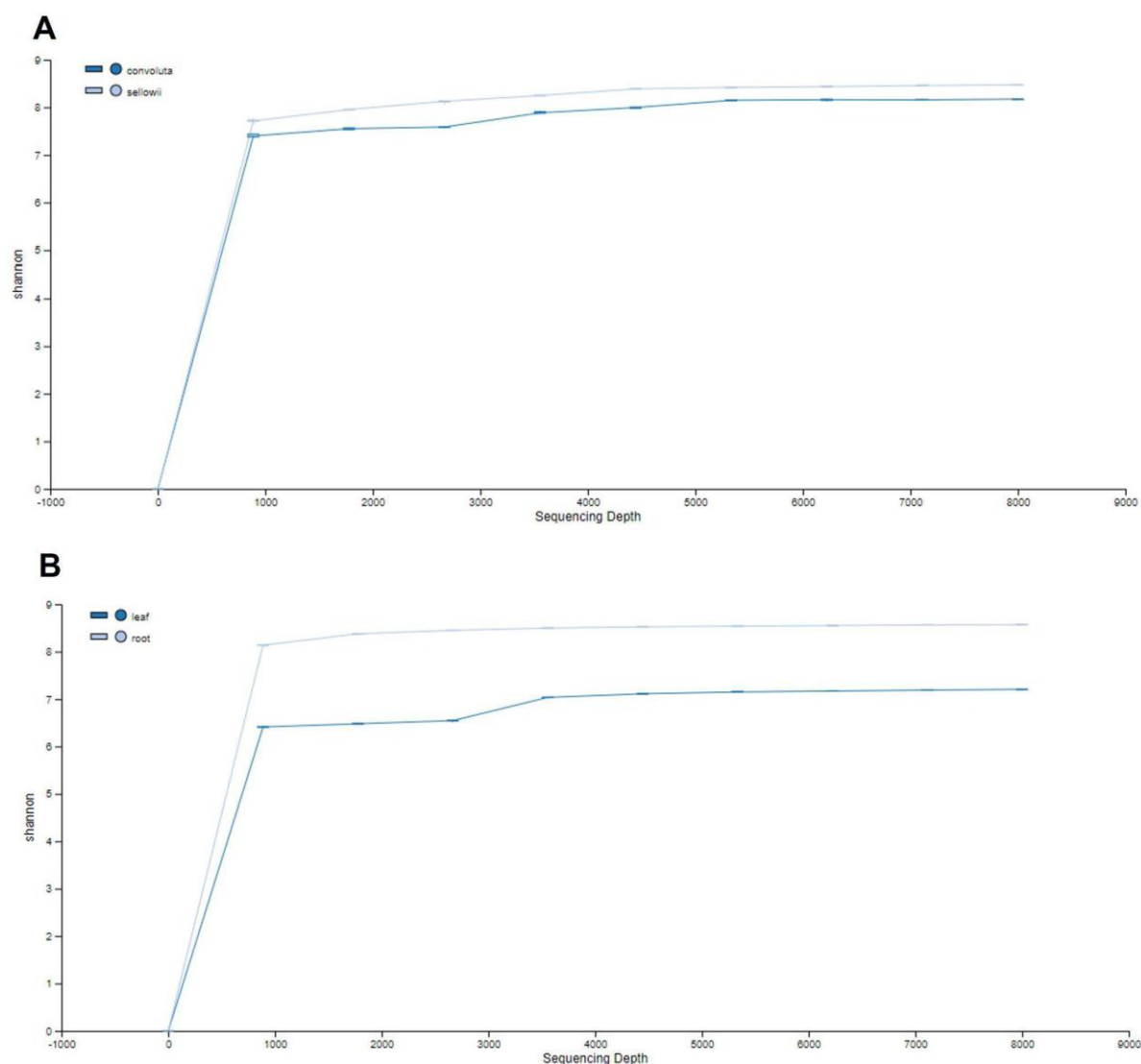
²Postgraduate Program in Ecology and Conservation, Institute of Biosciences, Federal University of
Mato Grosso do Sul, Campo Grande, 79070-900, MS, Brazil

³Faculty of Computing, Federal University of Mato Grosso do Sul, Av. Costa e Silva, s/nº, Campo
Grande, 79070-900, MS, Brazil

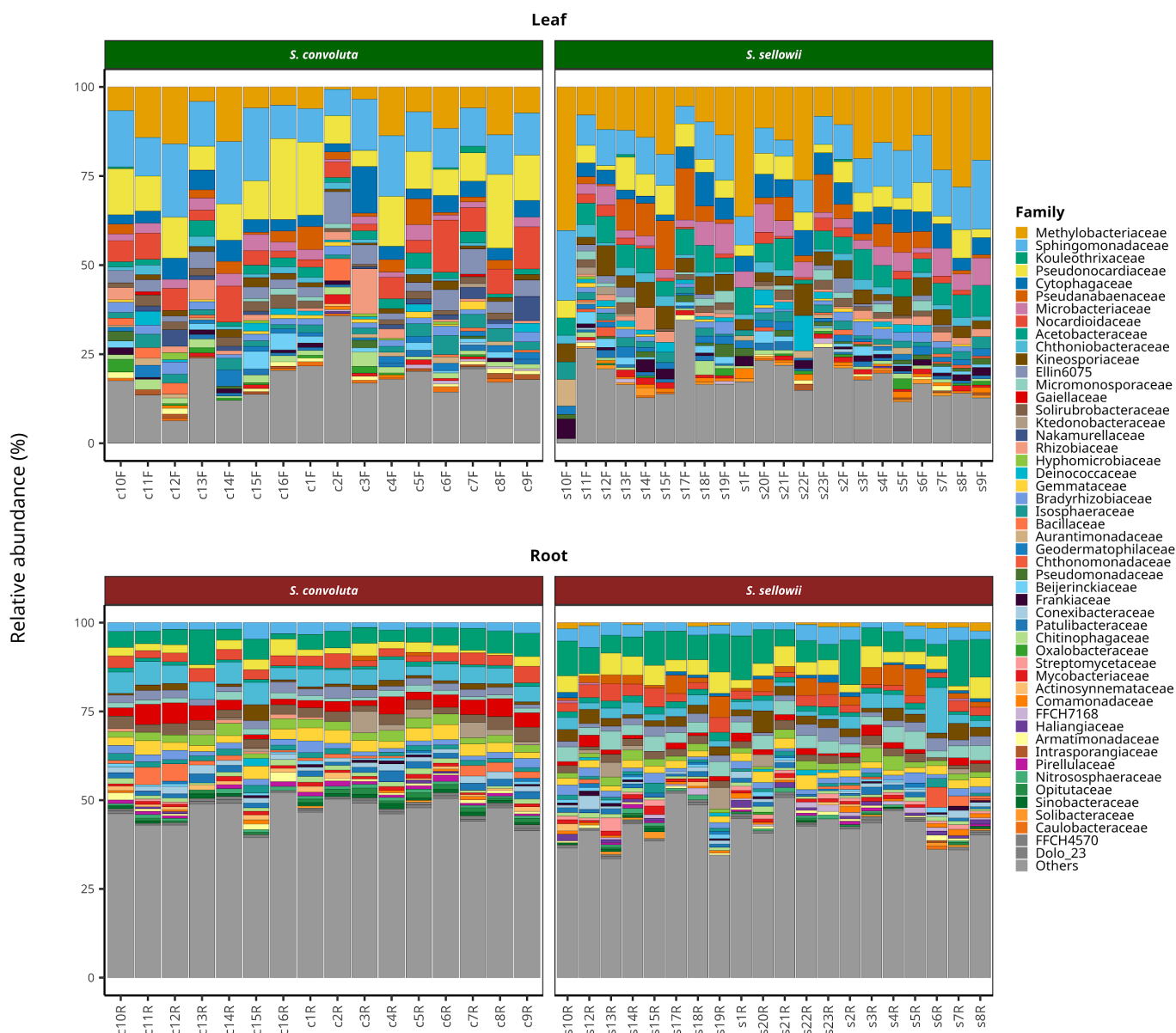
⁴Laboratory of Natural Products and Mass Spectrometry, Faculty of Pharmaceutical Sciences, Food
and Nutrition, Federal University of Mato Grosso do Sul, Av. Costa e Silva, s/nº, Campo Grande,
79070-900, MS, Brazil

Correspondence to: Jeferson Vidart Ramos, jeff.bioinfo@gmail.com

This supplementary file contains the following: Supplementary Figures 1 to 2 and Supplementary
Tables 1 to 4.



Supplementary Figure 1. Rarefaction curves of alpha diversity (Shannon index) as a function of sequencing depth. A) Comparison between the species *S. convoluta* (dark blue) and *S. sellowii* (light blue). B) Comparison between plant compartments: root (dark blue) and leaf (light blue).



Supplementary Figure 2. Relative abundance of the top 50 bacterial families associated with *S. convoluta* and *S. sellowii* in leaf and root compartments. Samples are grouped by plant species and compartment, with leaf samples shown in the upper panels and root samples in the lower panels. Each bar represents an individual sample, and colors indicate different bacterial families. Families with low abundance were grouped as “Others”.

Supplementary Table 1. Beta diversity analysis considering the overview and pairwise PERMANOVA results from Jaccard distance analysis for each species and plant compartments of *Selaginella*. conv: *Selaginella convoluta*; sell: *Selaginella sellowii*.

Overview						
Method name		PERMANOVA				
Test statistic name		pseudo-F				
Sample size		51				
Number of groups		4				
Test statistic		1.83832				
p-value		0.001				
Number of permutations		999				
Pairwise PERMANOVA results						
Group 1	Group 2	Sample size	Permutations	pseudo-F	p- value	q-value
conv-leaf	conv-root	25	999	2.279003	0.001	0.001
	sell-leaf	15	999	1.428483	0.001	0.001
conv-root	sell-root	29	999	2.086366	0.001	0.001
	sell-leaf	22	999	1.994651	0.001	0.001
	sell-root	36	999	1.544665	0.001	0.001
sell-leaf	sell-root	26	999	1.654736	0.001	0.001

Supplementary Table 2. Exclusive bacteria taxa for *Selaginella convoluta*, in the leaf (convoluta-leaf) and root (convoluta-root), and for *S. sellowii*, in the leaf (sellowii-leaf), and root (sellowii-root).

p = phylum; c = class; o = order; f = family.

Sample	Exclusive taxa
convoluta-leaf	p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bartonellaceae p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Flammeovirgaceae p_Planctomycetes;c_Planctomycetia;; p_GN02;c_3BR-5F;o_;f p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae p_Bacteroidetes;c_At12OctB3;o_;f p_Chlamydiae;c_Chlamydiia;o_Chlamydiales;f p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;
convoluta-root	p_Tenericutes;c_Mollicutes;; p_Acidobacteria;c_S035;o_;f p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Bogoriellaceae p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae p_Verrucomicrobia;c_;o_;f p_OP3;c_PBS-25;o_;f p_Planctomycetes;c_C6;o_MVS-107;f p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_auto67_4W p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae p_Verrucomicrobia;;; p_WS2;c_SHA-109;o_;f k_Archaea;p_Euryarchaeota;c_Thermoplasmata;o_E2;f_[Methanomassiliicoccaceae] p_OP11;c_;o_;f p_Verrucomicrobia;c_Opitutae;o_;f p_Acidobacteria;c_[Chloracidobacteria];o_;f p_Tenericutes;c_Mollicutes;o_;f p_Bacteroidetes;c_[Rhodothermi];o_[Rhodothermales];f_Rhodothermaceae p_Chlorobi;c_SJA-28;o_;f p_Planctomycetes;c_028H05-P-BN-P5;o_;f p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae p_OD1;c_ABY1;o_;f p_Verrucomicrobia;c_[Methylacidiphilae];o_S-BQ2-57;f
sellowii-leaf	p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Williamsiaceae p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae

sellowii-root	p_Cyanobacteria;c_Synechococcophycidae;o_Pseudanabaenales;f
	p_Cyanobacteria;c_Oscillatoriophycidae;o_Chroococcales;
	p_Proteobacteria;c_Deltaproteobacteria;;
	p_Fibrobacteres;c_Fibrobacteria;o_258ds10;f
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae
	p_AD3;c_JG37-AG-4;o_;f
	p_Acidobacteria;c_[Chloracidobacteria];o_RB41;
	p_Cyanobacteria;c_Nostocophycidae;o_Nostocales;f
	p_Planctomycetes;c_vadinHA49;o_DH61;f
	p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_Microthrixaceae
	p_Bacteroidetes;c_Cytophagia;o_Cytophagales;
	p_Proteobacteria;c_TA18;o_CV90;f
	p_Cyanobacteria;c_Synechococcophycidae;o_Pseudanabaenales;
	p_WS3;c_PRR-12;o_Sediment-1;f
	p_OD1;c_SM2F11;o_;f
	p_Chloroflexi;c_Thermomicrobia;;
	p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];
	p_Cyanobacteria;c_4C0d-2;o_MLE1-12;f
	p_FBP;c_;o_;f
	p_Chloroflexi;c_Chloroflexi;;
	p_Actinobacteria;c_MB-A2-108;o_;f
	p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoracaceae
	p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;
	p_Cyanobacteria;c_Oscillatoriophycidae;o_Chroococcales;f_Chroococcaceae
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f
	p_Verrucomicrobia;c_[Methylocidiphilae];o_Methylocidiphilales;f
	p_Actinobacteria;c_Thermoleophilia;;

Supplementary Table 3. Exclusive taxa for the species, *Selaginella convoluta* and *S. sellowii*, considering leaf and root together. k = kingdom; p = phylum; c = class; o = order; f = family.

Species	Exclusive taxa
<i>S. convoluta</i>	k_Archaea;p_Euryarchaeota;c_Thermoplasmata;o_E2;f_[Methanomassiliicoccace ae]
	k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_;f_____
	k_Bacteria;p_Acidobacteria;c_S035;o_;f_____
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f__Bogoriellaceae
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f__Nocardiaceae
	k_Bacteria;p_Bacteroidetes;c_[Rhodothermi];o_[Rhodothermales];f_Rhodothermaceae
	k_Bacteria;p_Bacteroidetes;c_At12OctB3;o_;f_____
	k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Flammeovirgaceae
	k_Bacteria;p_Chlamydiae;c_Chlamydiia;o_Chlamydiales;f_____
	k_Bacteria;p_Chlorobi;c_SJA-28;o_;f_____
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae
	k_Bacteria;p_GN02;c_3BR-5F;o_;f_____
	k_Bacteria;p_OD1;c__ABY1;o_;f_____
	k_Bacteria;p_OP11;c__o_;f_____
	k_Bacteria;p_OP3;c_PBS-25;o_;f_____
	k_Bacteria;p_Planctomycetes;c_028H05-P-BN-P5;o_;f_____
	k_Bacteria;p_Planctomycetes;c_C6;o_MVS-107;f_____
	k_Bacteria;p_Planctomycetes;c_Planctomycetia;_;f_____
	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bartonellaceae
	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae
	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae
	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_____
	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_____
	k_Bacteria;p_Tenericutes;c_Mollicutes;_;f_____
	k_Bacteria;p_Tenericutes;c_Mollicutes;o_;f_____
	k_Bacteria;p_Verrucomicrobia;_;f_____
	k_Bacteria;p_Verrucomicrobia;c_;o_;f_____
	k_Bacteria;p_Verrucomicrobia;c_[Methylacidiphilae];o_S-BQ2-57;f_____
	k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_auto67_4W
	k_Bacteria;p_Verrucomicrobia;c_Opitutae;o_;f_____
	k_Bacteria;p_WS2;c_SHA-109;o_;f_____
<i>S. sellowii</i>	k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_RB41;f_____
	k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_____
	k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_Microthrixaceae
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f__Williamsiaceae
	k_Bacteria;p_Actinobacteria;c_MB-A2-108;o_;f_____
	k_Bacteria;p_Actinobacteria;c_Thermoleophilia;_;f_____
	k_Bacteria;p_AD3;c__JG37-AG-4;o_;f_____

k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_____

k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;_____

k_Bacteria;p_Chloroflexi;c_Chloroflexi;_____

k_Bacteria;p_Chloroflexi;c_Thermomicrobia;_____

k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_MLE1-12;f_____

k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Nostocales;f_____

k_Bacteria;p_Cyanobacteria;c_Oscillatoriohaptophyceae;o_Chroococcales;_____

k_Bacteria;p_Cyanobacteria;c_Oscillatoriohaptophyceae;o_Chroococcales;f_Chroococcaceae

k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;_____

k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;f_____

k_Bacteria;p_FBP;c_o;f_____

k_Bacteria;p_Fibrobacteres;c_Fibrobacteria;o__258ds10;f_____

k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae

k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_____

Gemmatimonadaceae

k_Bacteria;p_OD1;c__SM2F11;o;f_____

k_Bacteria;p_Planctomycetes;c_vadinHA49;o_DH61;f_____

k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;_____

k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoracaceae

k_Bacteria;p_Proteobacteria;c_TA18;o_CV90;f_____

k_Bacteria;p_Verrucomicrobia;c_[Methylophilales];o_Methylophilales;f_____

k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];_____

k_Bacteria;p_WS3;c_PRR-12;o_Sediment-1;f_____

Supplementary Table 4. Exclusive taxa for the plant compartments, leaf and root, considering both species, *Selaginella convoluta* and *S. sellowii*. k = kingdom; p = phylum; c = class; o = order; f = family.

Plant compartment	Exclusive taxa
Leaf	k_Bacteria;p_Bacteroidetes;c_At12OctB3;o_f_____
	k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Flammeovirgaceae
	k_Bacteria;p_Chlamydiae;c_Chlamydia;o_Chlamydiales;f_____
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae
	k_Bacteria;p_GN02;c_3BR-5F;o_f_____
	k_Bacteria;p_Planctomycetes;c_Planctomycetia;_____
	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bartonellaceae
	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;_____
	k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_____
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Williamsiaceae
	k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae
	k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae
Root	k_Archaea;p_Euryarchaeota;c_Thermoplasmata;o_E2;f_[Methanomassiliicoccaceae]
	k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_f_____
	k_Bacteria;p_Acidobacteria;c_S035;o_f_____
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Bogoriellaceae
	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae
	k_Bacteria;p_Bacteroidetes;c_[Rhodothermi];o_[Rhodothermales];f_Rhodothermaceae
	k_Bacteria;p_Chlorobi;c_SJA-28;o_f_____
	k_Bacteria;p_OD1;c_ABY1;o_f_____
	k_Bacteria;p_OP11;c_;;o_f_____
	k_Bacteria;p_OP3;c_PBS-25;o_f_____
	k_Bacteria;p_Planctomycetes;c_028H05-P-BN-P5;o_f_____
	k_Bacteria;p_Planctomycetes;c_C6;o_MVS-107;f_____
	k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Hyphomonadaceae
	k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae
	k_Bacteria;p_Tenericutes;c_Mollicutes;_____
	k_Bacteria;p_Tenericutes;c_Mollicutes;o_f_____
	k_Bacteria;p_Verrucomicrobia;_____
	k_Bacteria;p_Verrucomicrobia;c_;;o_f_____
	k_Bacteria;p_Verrucomicrobia;c_[Methylacidiphilae];o_S-BQ2-57;f_____
	k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];f_auto67_4W
	k_Bacteria;p_Verrucomicrobia;c_Opitutae;o_;;f_____
	k_Bacteria;p_WS2;c_SHA-109;o_f_____
	k_Bacteria;p_Acidobacteria;c_[Chloracidobacteria];o_RB41;_____
	k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;_____
	k_Bacteria;p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_Microthrixaceae
	k_Bacteria;p_Actinobacteria;c_MB-A2-108;o_f_____
	k_Bacteria;p_Actinobacteria;c_Thermoleophilia;_____
	k_Bacteria;p_AD3;c_JG37-AG-4;o_f_____
	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_____

k_Bacteria;p_Bacteroidetes;c_Cytophagia;o_Cytophagales;_____

k_Bacteria;p_Chloroflexi;c_Chloroflexi;____;

k_Bacteria;p_Chloroflexi;c_Thermomicrobia;____;

k_Bacteria;p_Cyanobacteria;c_4C0d-2;o_MLE1-12;f_____

k_Bacteria;p_Cyanobacteria;c_Nostocophycideae;o_Nostocales;f_____

k_Bacteria;p_Cyanobacteria;c_Oscillatoriothycideae;o_Chroococcales;_____

k_Bacteria;p_Cyanobacteria;c_Oscillatoriothycideae;o_Chroococcales;f_Chroococcaceae

k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;_____

k_Bacteria;p_Cyanobacteria;c_Synechococcophycideae;o_Pseudanabaenales;f_____

k_Bacteria;p_FBP;c_o;f_____

k_Bacteria;p_Fibrobacteres;c_Fibrobacteria;o__258ds10;f_____

k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae

k_Bacteria;p_OD1;c__SM2F11;o;f_____

k_Bacteria;p_Planctomycetes;c_vadinHA49;o_DH61;f_____

k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;____;

k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoraceae

k_Bacteria;p_Proteobacteria;c_TA18;o_CV90;f_____

k_Bacteria;p_Verrucomicrobia;c_[Methylacidiphilae];o_Methylacidiphilales;f_____

k_Bacteria;p_Verrucomicrobia;c_[Pedosphaerae];o_[Pedosphaerales];_____

k_Bacteria;p_WS3;c_PRR-12;o_Sediment-1;f_____