SUPPLEMENTARY LEGENDS

Figure S1: (a) Photograph of the Drexel biowall, and (b) a schematic of its operating principles.

Figure S2. Schematic of the aeroponic system used to conduct so-called Laboratory Experiments for Objective 2. (GC/FID = gas chromatograph/ flame ionization detector.)

Figure S3: Rarefaction curves illustrating alpha diversity for individual bacterial root communities from (A) the Laboratory Experiment, (B) the Drexel Experiment, and (C) the Dodge Experiment.

Figure S4. Taxonomic make-up of root bacterial communities from plants in the Laboratory (VOC exposure) experiments. Information on plant species and treatments can be found in Table S1. Classifications of sequence reads to the listed taxa had at least 50% bootstrap support, and were made to the order level or the next highest level with such support.

Figure S5: Principal coordinates analysis reveals differences between soil-grown versus biowall-grown plant root communities. This statistical map shows similarity of bacterial communities (individual symbols) based on their proximity in two-dimensional space. Filled symbols correspond to bacterial communities of plants collected from soil

or immediately before/after installation into a biowall. Open circles reveal bacterial communities from biowall-grown plants. Different colors reveal communities from different plant species, while shapes distinguish samples from the Drexel biowall experiment (shifts in communities within the same plants over time) and those from the Dodge foundation experiment (wall growth vs. greenhouse/soil growth, with comparisons between different plant individuals). Note that the communities from all wall-grown plants tend to cluster together regardless of plant species or wall identity, suggesting that transfer to this habitat has a predictable effect on bacterial communities. While these results were based on community similarity measures obtained with the Bray-Curtis metric at the 97% OTU level, weighted UniFrac yielded generally similar findings (data not shown).

Figure S6: Principal coordinates analysis reveals differences in root bacterial communities of VOC-exposed vs. clean-air-exposed plants belonging to two species. A) Bacterial communities from VOC exposed pothos plants (filled symbols) are positioned at the right-most portion of the 1st axis, while showing clustering in the mid-region of the 2nd axis. B) Bacterial communities from VOC exposed rubber tree plants (filled symbols) show clustering in the lower left quadrant of this plot. Combined, results suggest that VOC exposure alters root communities in predictable ways, though arguably to a greater extent in pothos. In both plots, different shapes reveal different sampling time points, whereas different colors help to distinguish individual plants used in this study (e.g. “Pothos A1” = red; “Pothos A3” = blue). While these results were based on

community similarity measures obtained with the Bray-Curtis metric, weighted UniFrac yielded generally similar findings (data not shown).

Table S1: Table S1: Metadata for samples used for amplicon sequence libraries

Table S2: 97% OTUs and their distributions across sequence libraries, along with information on alpha diversity after normalization.

Table S3: ADONIS statistics based on Bray-Curtis distances focused on family level root community composition.

Table S4: Bacterial families varying significantly in relative abundance across experimental treatments. Shown are all families with a significant shift in at least one controlled experiment (with the Laboratory Experiment broken up by plant host species). No data were shown for families exhibiting non-significant shifts in a given experiment before P-value FDR corrections for multiple comparisons. For those with significant changes, we use a blue-yellow-red heat map to illustrate relative abundance and how it changed across conditions.

Table S5: 97% OTUs varying significantly in relative abundance across experimental treatments. Shown are all OTUs with a significant shift in at least one controlled experiment (with the Laboratory Experiment broken up by plant host species). No data were shown for OTUs exhibiting non-significant shifts in a given experiment

before P-value FDR corrections for multiple comparisons. For those with significant changes, we use a blue-yellow-red heat map to illustrate relative abundance and how it changed across conditions.

Table S6: Genotypes at sites with ≥1% minor allele frequency across all raw *Hyphomicrobium* reads passing quality control assessment. Shown are nucleotides only at variable sites for each unique genotype/strain.

Figure S1

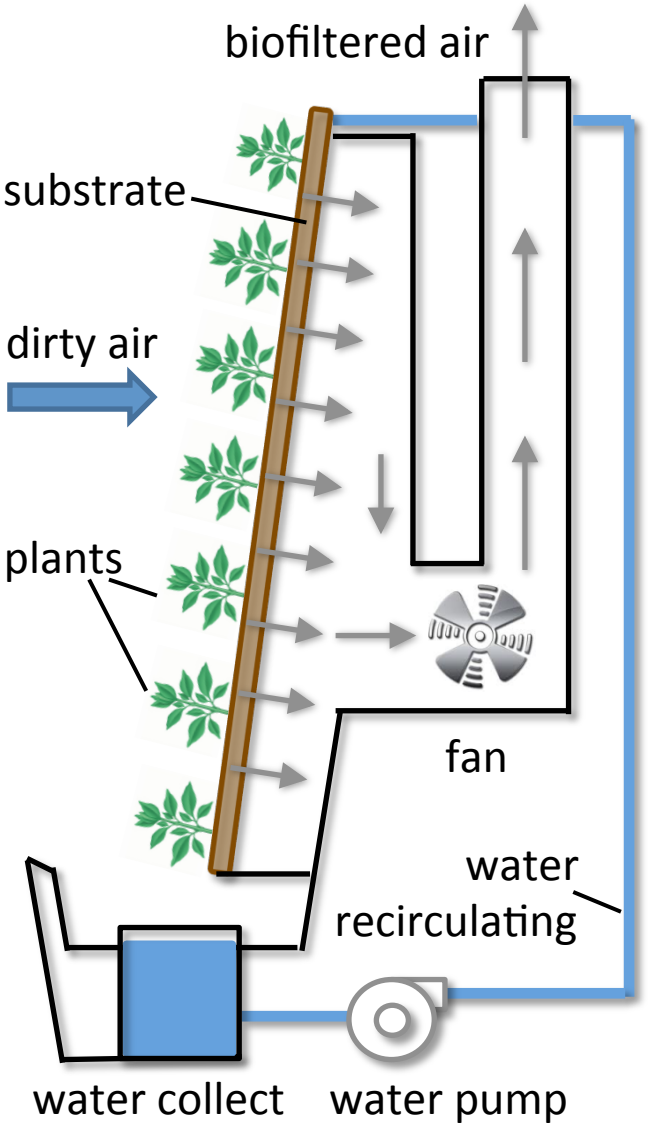

biofiltered air
substrate
dirty air
plants
fan
water
recirculating
water collect
water pump

Figure S2

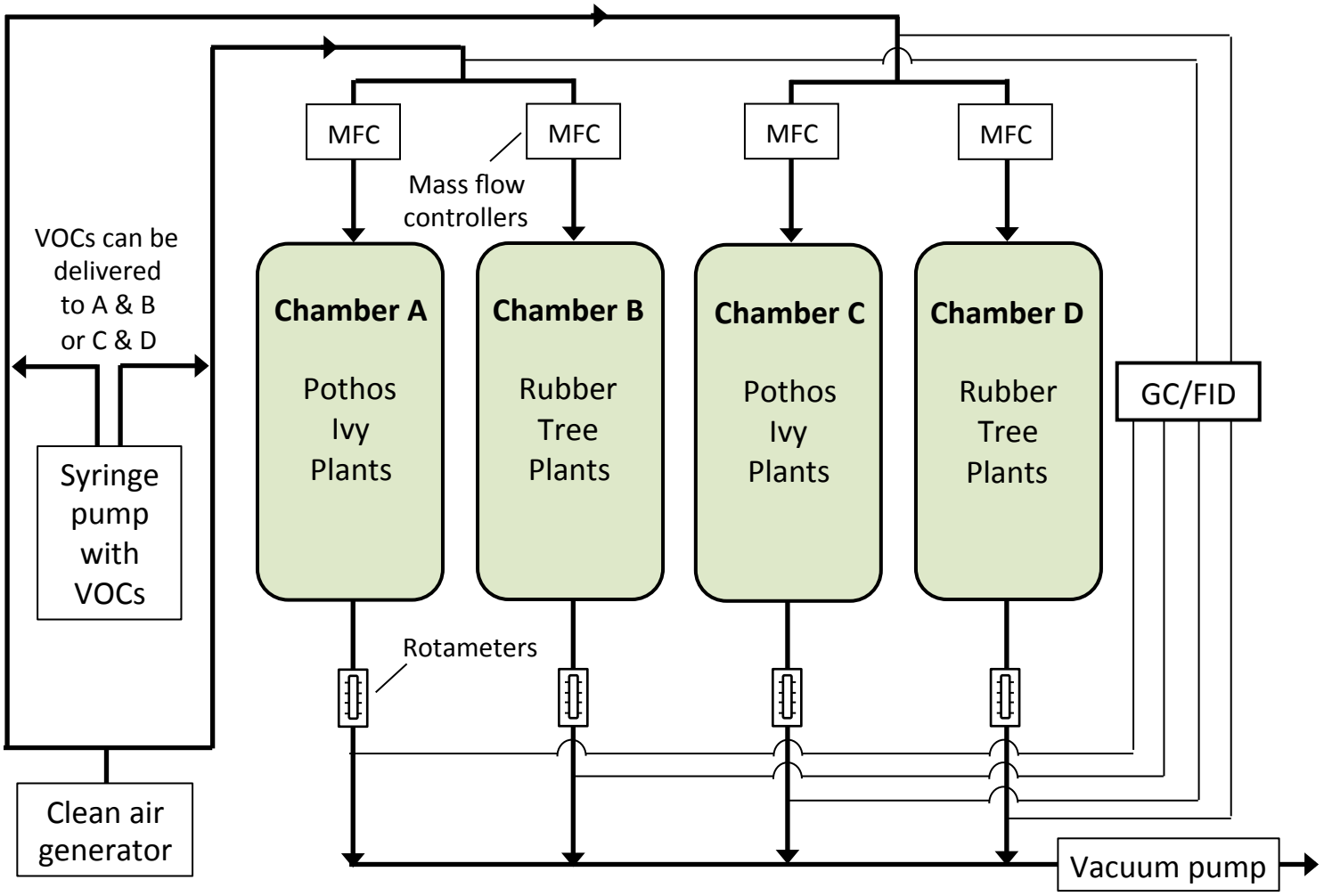

MFC
MFC
MFC
MFC
Mass flow controllers
VOCs can be delivered to A & B or C & D
Chamber A
Pothos Ivy Plants
Chamber B
Rubber Tree Plants
Chamber C
Pothos Ivy Plants
Chamber D
Rubber Tree Plants
GC/FID
Syringe pump with VOCs
Rotameters
Clean air generator
Vacuum pump

Figure S3

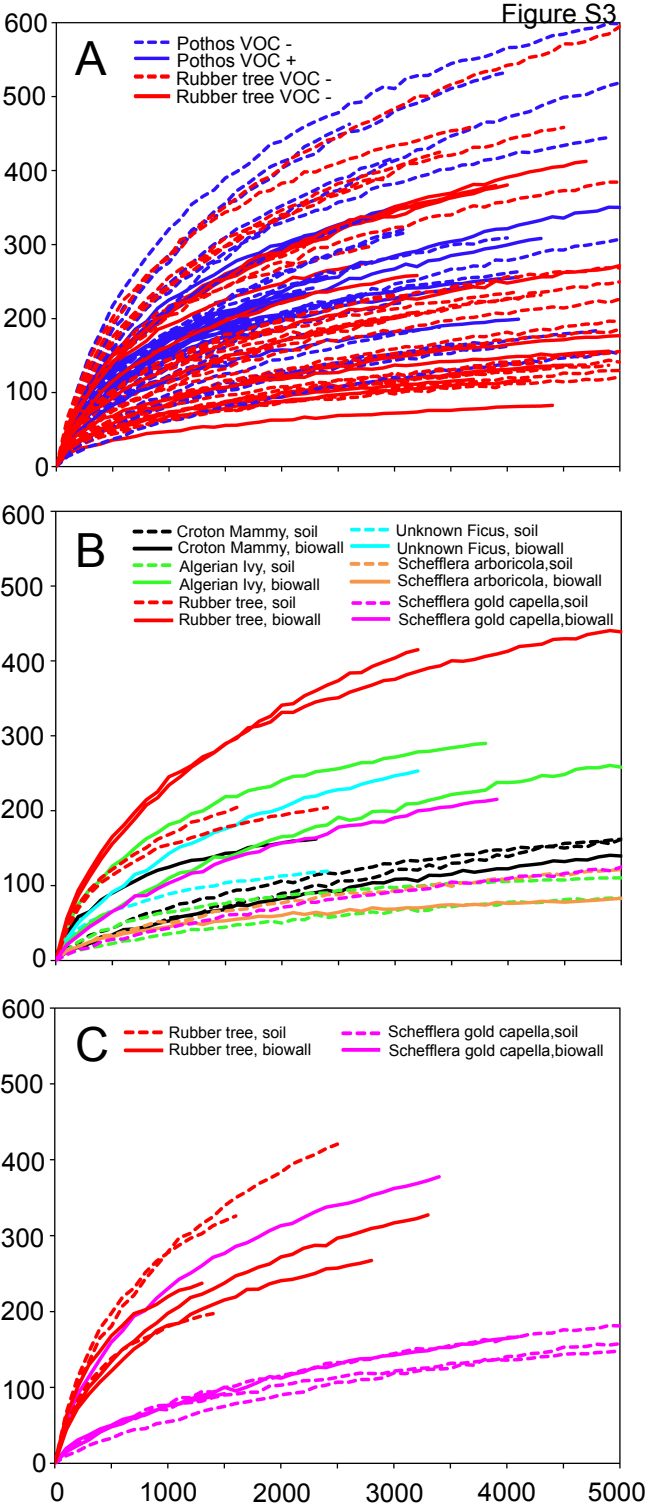

A
Pothos VOC -
Pothos VOC +
Rubber tree VOC -
Rubber tree VOC -
B
Croton Mammy, soil
Croton Mammy, biowall
Algerian Ivy, soil
Algerian Ivy, biowall
Rubber tree, soil
Rubber tree, biowall
Unknown Ficus, soil
Unknown Ficus, biowall
Schefflera arboricola,soil
Schefflera arboricola, biowall
Schefflera gold capella,soil
Schefflera gold capella,biowall
C
Rubber tree, soil
Rubber tree, biowall
Schefflera gold capella,soil
Schefflera gold capella,biowall
0
100
200
300
400
500
600
0
1000
2000
3000
4000
5000

Figure S4


D7.8
D7.6
D7.3
D7.2
D6.8
D6.6
D6.3
D6.2
D5.8
D5.6
D5.3
D5.2
D3.8
D3.6
D3.3
D3.2
D1.8
D1.6
D1.3
D1.2
C7.8
C7.6
C7.3
C7.2
C6.8
C6.6
C6.3
C6.2
C5.8
C5.6
C5.3
C5.2
C3.8
C3.6
C3.3
C3.2
C1.8
C1.6
C1.3
C1.2
B7.8
B7.6
B7.3
B7.2
B6.8
B6.6
B6.3
B6.2
B5.8
B5.6
B5.3
B5.2
B3.8
B3.6
B3.3
B3.2
B1.8
B1.6
B1.3
B1.2
A7.8
A7.6
A7.3
A7.2
A6.8
A6.6
A6.3
A6.2
A5.8
A5.6
A5.3
A5.2
A3.8
A3.6
A3.3
A3.2
A1.8
A1.6
A1.3
A1.2
0%
10%
20%
30%
40%
50%
60%
70%
80%
90%
100%
Burkholderiales
Rhizobiales
Sphingomonadales
Sphingobacteriales
unclassified Proteobacteria
Flavobacteriales
Pseudomonadales
Xanthomonadales
unclassified Alphaproteobacteria
Actinomycetales
Rhodobacterales
Ohtaekwangia
unclassified bacteria
unclassified Gammaproteobacteria
Rhodocyclales
Caulobacterales
Enterobacteriales
Enterobacteriales
Myxococcales
Planctomycetales
Rhodospirillales
Gp4
Opitutales
Methylophilales
Others

Figure S5

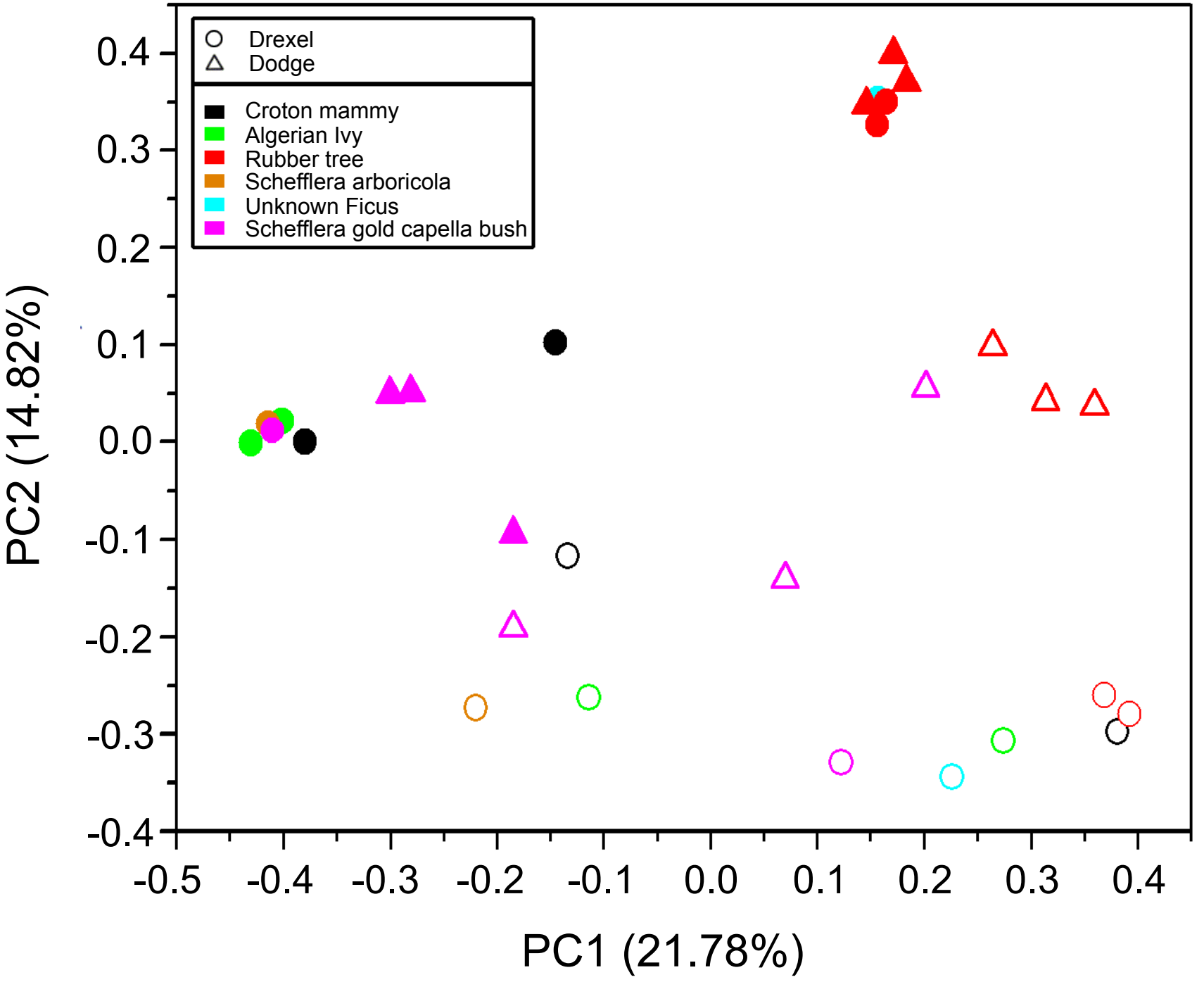
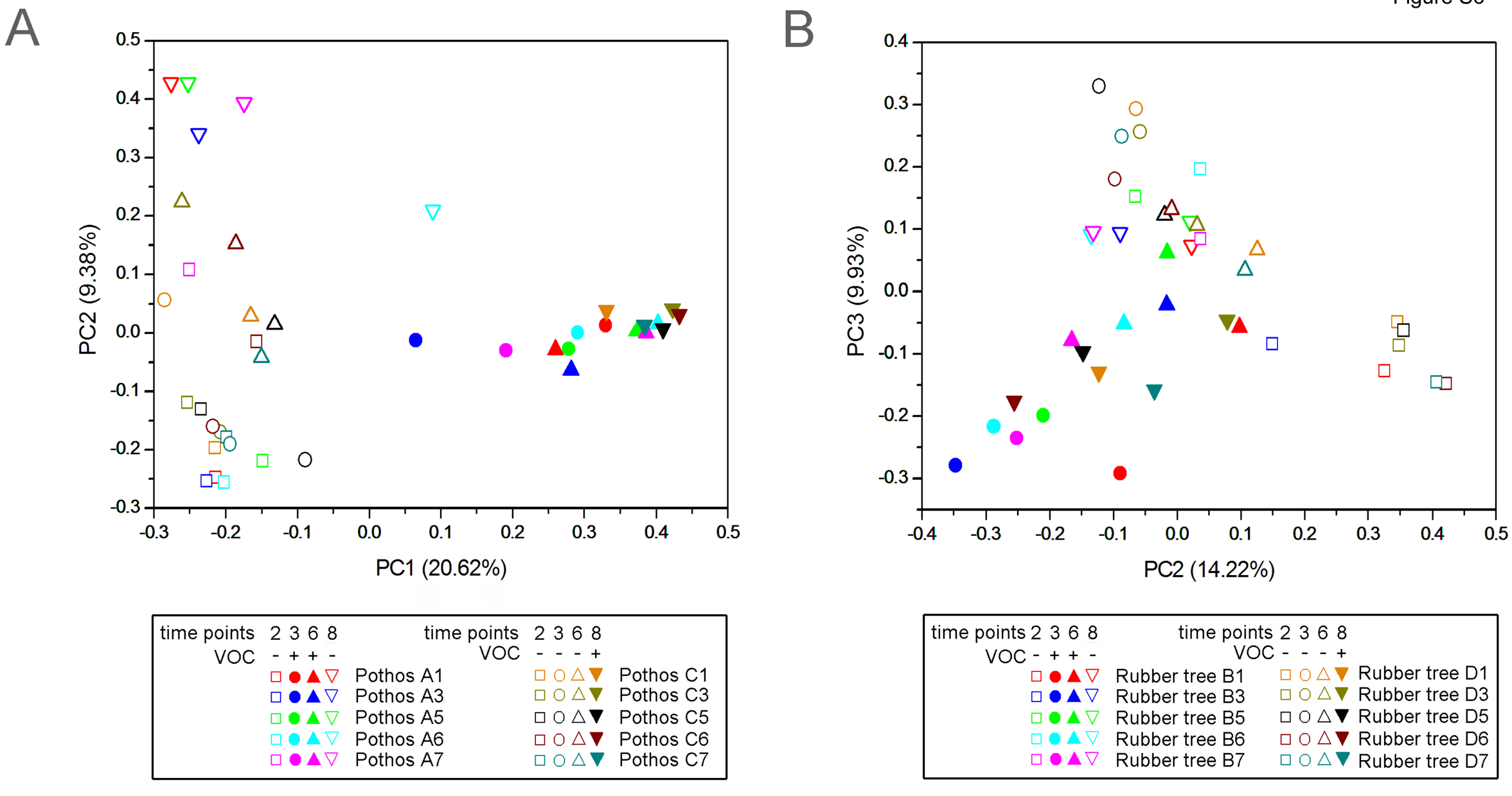

Drexel
Dodge
Croton mammy
Algerian Ivy
Rubber tree
Schefflera arboricola
Unknown Ficus
Schefflera gold capella bush
PC2 (14.82%)
PC1 (21.78%)
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.4
-0.3
-0.2
-0.1
0.0
0.1
0.2
0.3
0.4

Figure S6


A
PC2 (9.38%)
PC1 (20.62%)
time points 2 3 6 8
VOC - + + -
Pothos A1
Pothos A3
Pothos A5
Pothos A6
Pothos A7
time points 2 3 6 8
VOC - - - +
Pothos C1
Pothos C3
Pothos C5
Pothos C6
Pothos C7
B
PC3 (9.93%)
PC2 (14.22%)
time points 2 3 6 8
VOC - + + -
Rubber tree B1
Rubber tree B3
Rubber tree B5
Rubber tree B6
Rubber tree B7
time points 2 3 6 8
VOC - - - +
Rubber tree D1
Rubber tree D3
Rubber tree D5
Rubber tree D6
Rubber tree D7