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Supplemental Material for: Applied and Environmental Microbiology

Soybean Root Nodule and Rhizosphere Microbiome: Distribution of Rhizobial and Non-rhizobial Endophytes

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Fig. S1. Roots from one of the soybean plants (L1P1N1-23). The 23 intact root nodules that were selected for the microbiome analysis are indicated (arrows).

Fig. S2: A comparison of bacterial genera identified by 16S rRNA gene sequences from the root nodules and rhizosphere soil of plant 1 (L1P1N1-23). The total number of DNA sequences obtained from root nodules (826,945) and rhizosphere soil (19,345) of plant 1 were used for this comparison.

Fig. S3: Species accumulation curve for the root nodules and a rhizosphere sample of plant 1 (L1P1N1-23).

Fig. S4 A&B: Nonmetric multidimensional scaling representation of 16S rRNA gene sequences from root nodules of plant 1 (L1P1N1-23). A). Describing the influence of root nodule location on a root system and B) size of the root nodules on bacterial endophytes. The two-dimensional stress was 0.11 and 0.10 for panels A and B, respectively.

Fig. S5: Maximum likelihood phylogenetic tree based on partial sequences of the 16S rRNA gene of the *Nitrobacter* related sequences detected within root nodules and rhizosphere soil of soybean plants. The distribution of related *Nitrobacter* sequences from GenBank is shown next to the cluster. The numbers at the nodes reflect bootstrap support values that were above 50%.

Fig. S6: Maximum likelihood phylogenetic tree based on partial sequences of the 16S rRNA gene of the *Tardiphaga* related sequences detected within root nodules and rhizosphere soil of soybean plants. The numbers at the nodes reflect bootstrap support values that were above 50%.

Fig. S7: Soil and plant samples were collected from three locations within the Kindrick farm.

Fig. S8: Soybean root nodules intact with the root system. **A**). before cleaning and **B**). after cleaning the nodule surfaces.

Fig. S9: Description of two step PCR approach for 16S rRNA gene amplification and library preparation for Illumina MiSeq paired-end DNA sequencing.

Supplemental Tables:

Table S1: Culture and culture-independent based studies focused on the non-rhizobial endophytes within soybean root nodules.

Table S2: Distribution of various non-rhizobial endophytes within root nodules of a plant (L1P1N1-23).

Table S3: Bacterial diversity within root nodules of a plant and rhizosphere soil. In sample ID, L1-3 represents three locations (1-3), P1-9 represents nine plant (1-9), N represents the nodules per plant (N1-23), and R is for rhizosphere samples.

Table S4: Soil physiochemical characteristics of soil attached with soybean plants from three locations within Kindrick farm.

Table S5: List of unique indices used for each of the root nodules and soil samples.

Fig. S1

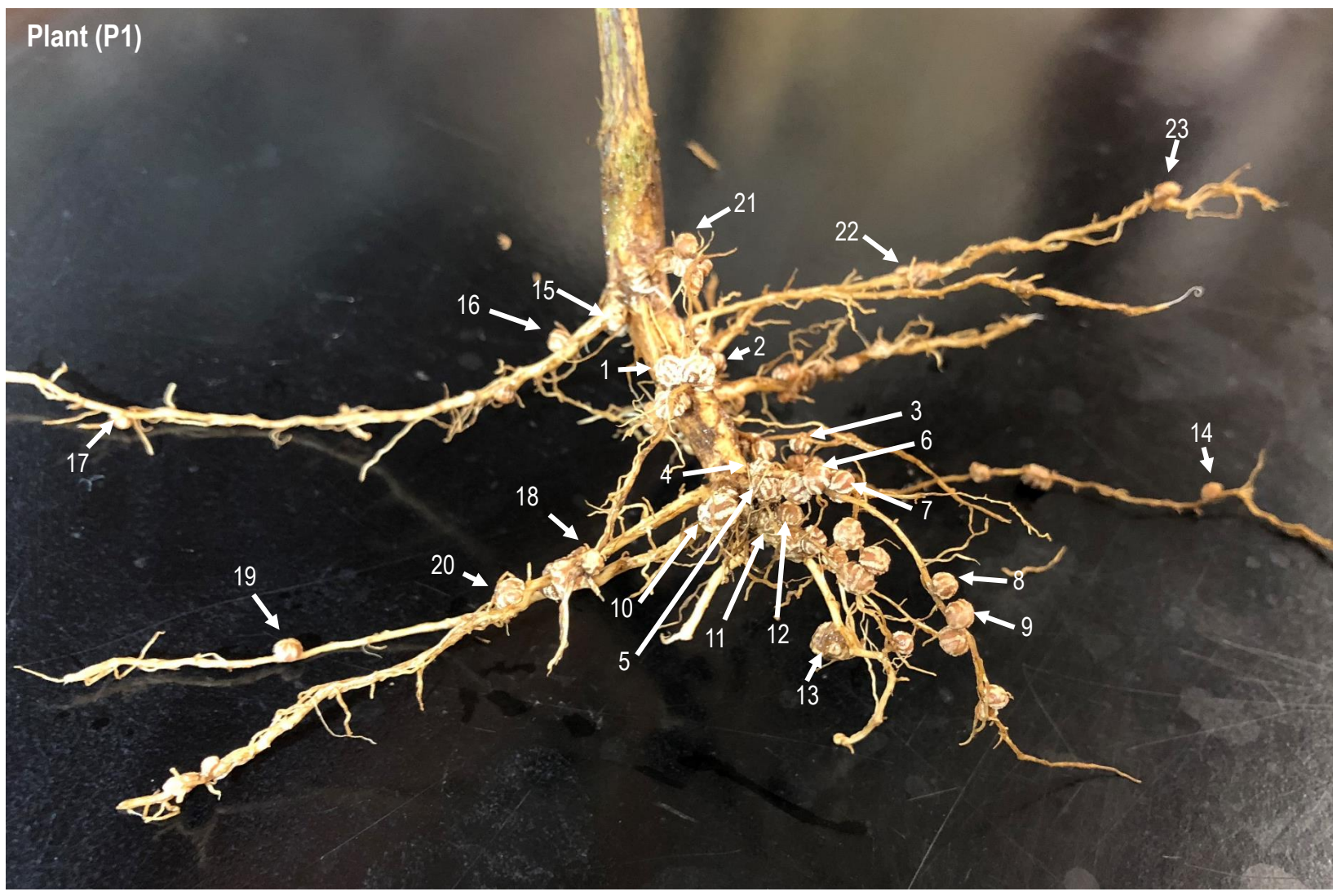


Fig. S2

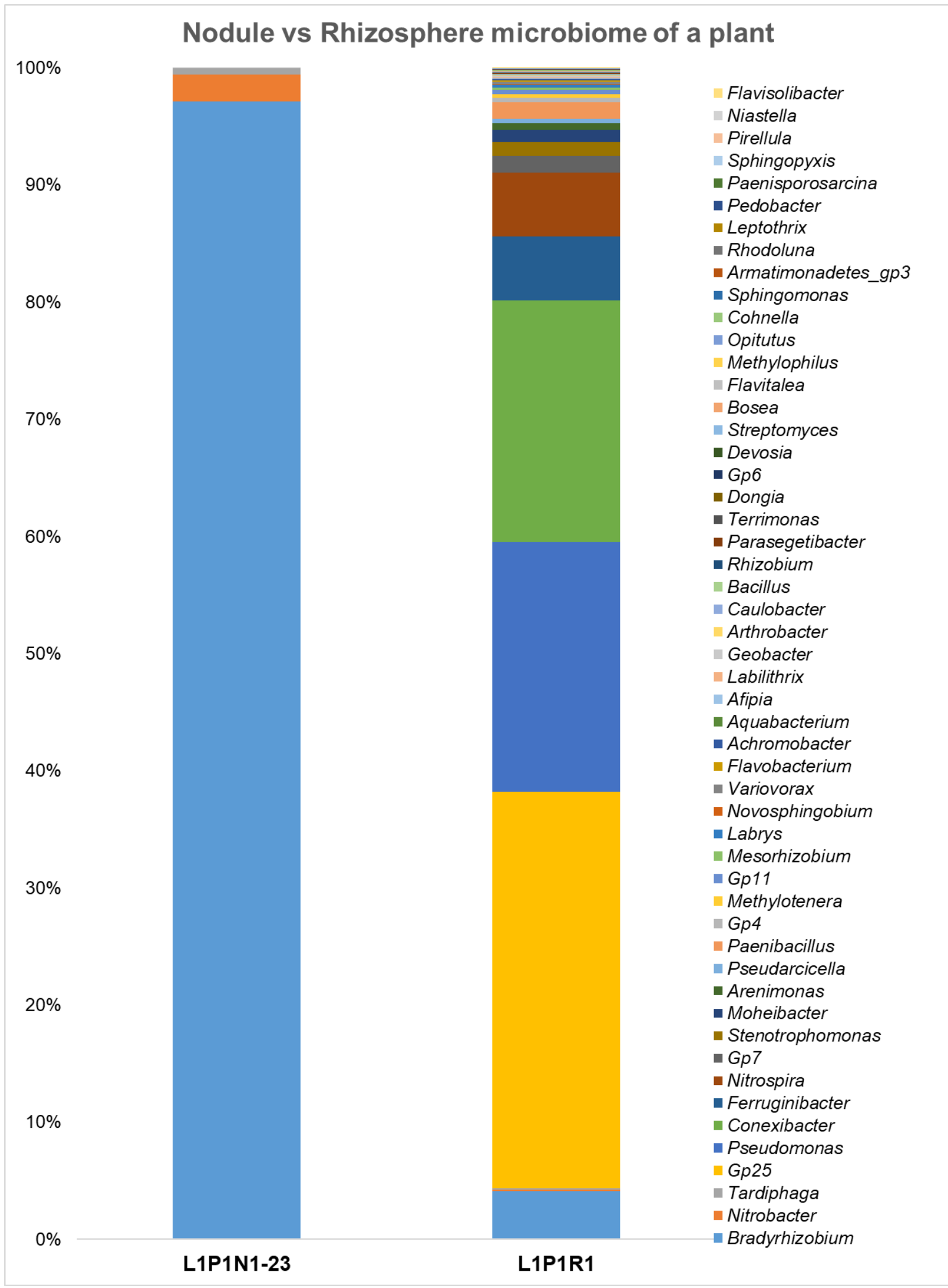

Nodule vs Rhizosphere microbiome of a plant
16S rRNA gene sequences (%)
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
L1P1N1-23
L1P1R1
Flavisolibacter
Niastella
Pirellula
Sphingopyxis
Paenisporosarcina
Pedobacter
Leptothrix
Rhodoluna
Armatimonadetes_gp3
Sphingomonas
Cohnella
Opitutus
Methylophilus
Flavitalea
Bosea
Streptomyces
Devosia
Gp6
Dongia
Terrimonas
Parasegetibacter
Rhizobium
Bacillus
Caulobacter
Arthrobacter
Geobacter
Labilithrix
Afipia
Aquabacterium
Achromobacter
Flavobacterium
Variovorax
Novosphingobium
Labrys
Mesorhizobium
Gp11
Methylotenera
Gp4
Paenibacillus
Pseudarcicella
Arenimonas
Moheibacter
Stenotrophomonas
Gp7
Nitrospira
Ferruginibacter
Conexibacter
Pseudomonas
Gp25
Tardiphaga
Nitrobacter
Bradyrhizobium

Fig. S3

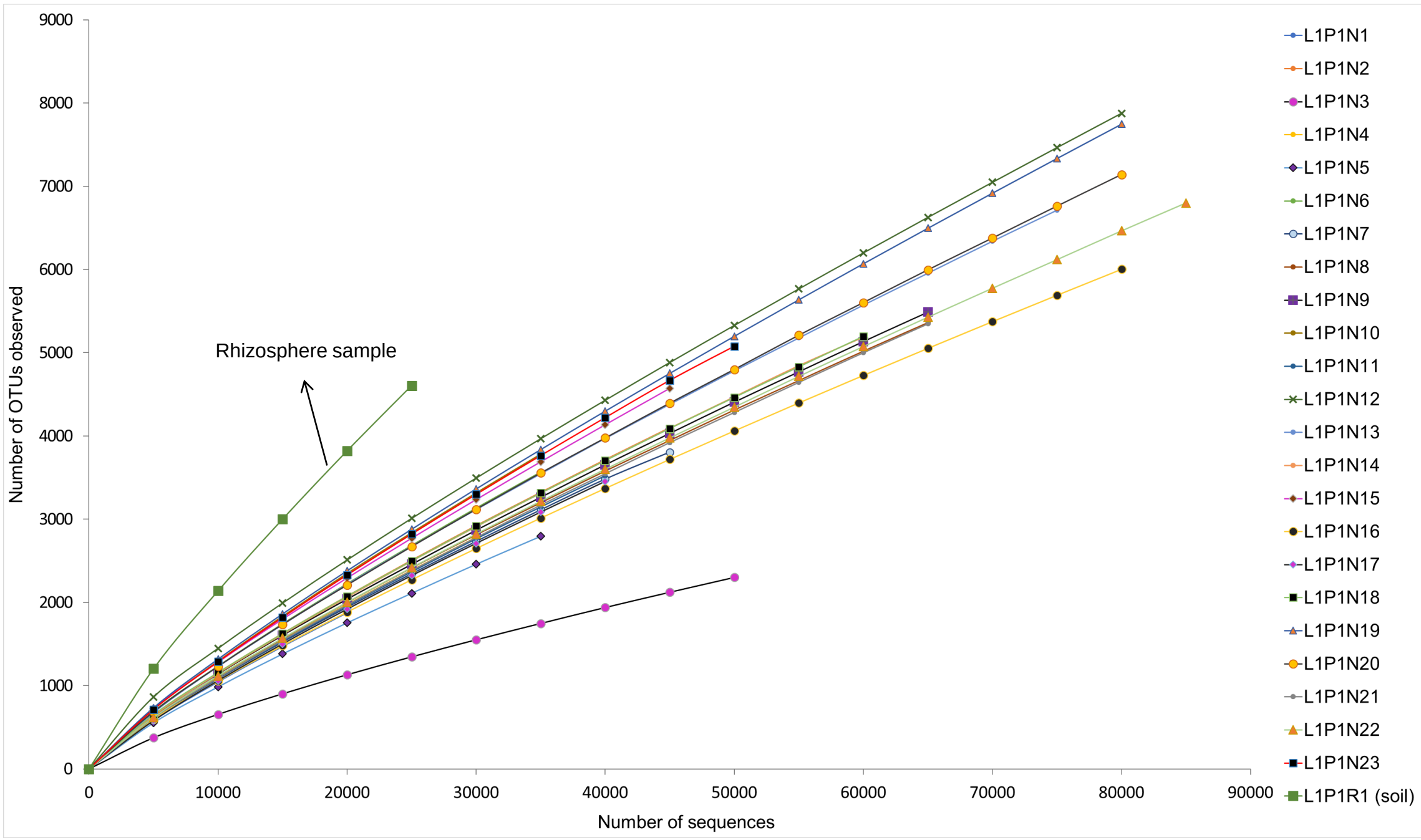

Number of OTUs observed
Number of sequences
Rhizosphere sample
0
1000
2000
3000
4000
5000
6000
7000
8000
9000
10000
20000
30000
40000
50000
60000
70000
80000
90000
L1P1N1
L1P1N2
L1P1N3
L1P1N4
L1P1N5
L1P1N6
L1P1N7
L1P1N8
L1P1N9
L1P1N10
L1P1N11
L1P1N12
L1P1N13
L1P1N14
L1P1N15
L1P1N16
L1P1N17
L1P1N18
L1P1N19
L1P1N20
L1P1N21
L1P1N22
L1P1N23
L1P1R1 (soil)

Fig. S4 A&B

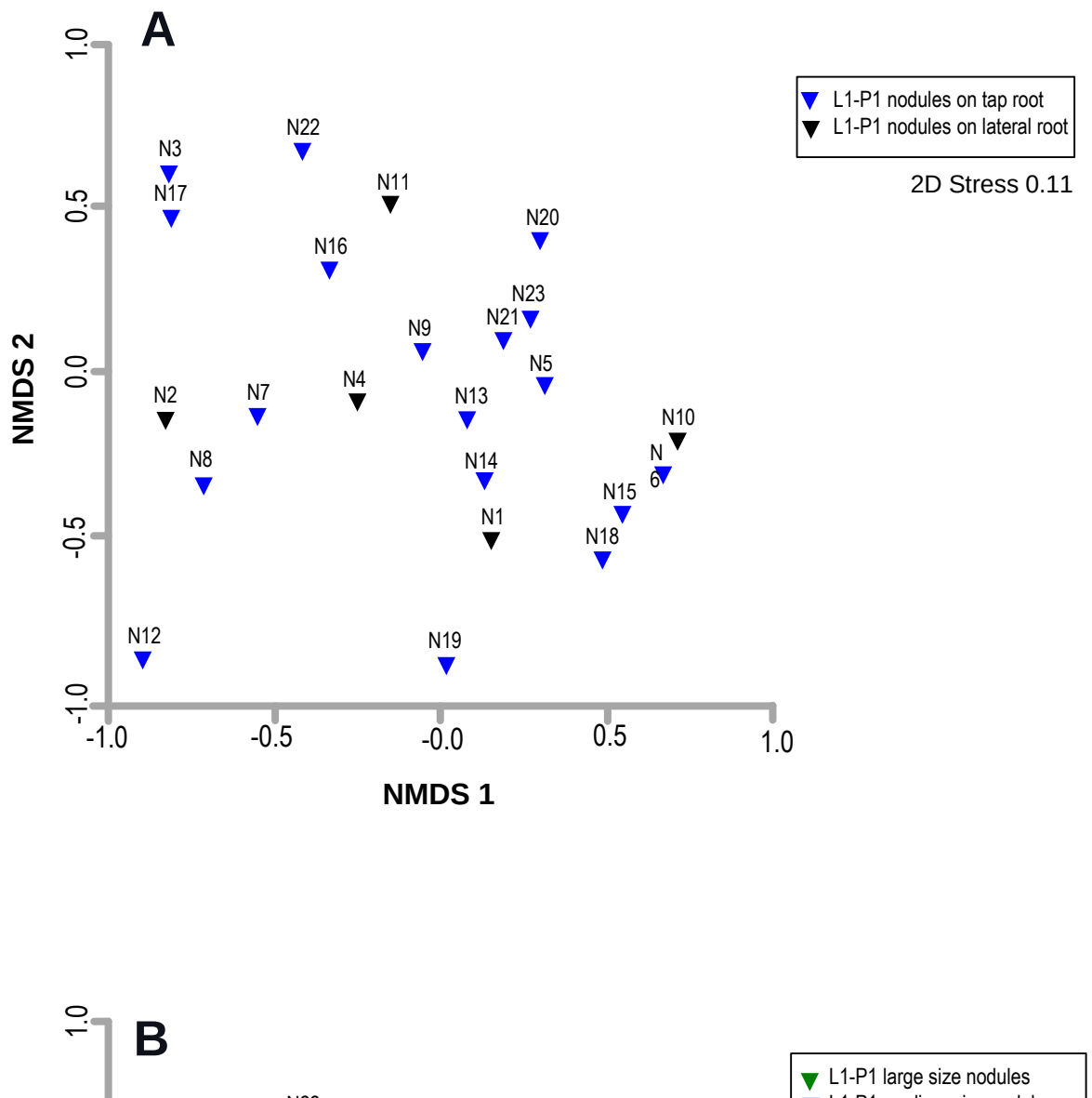
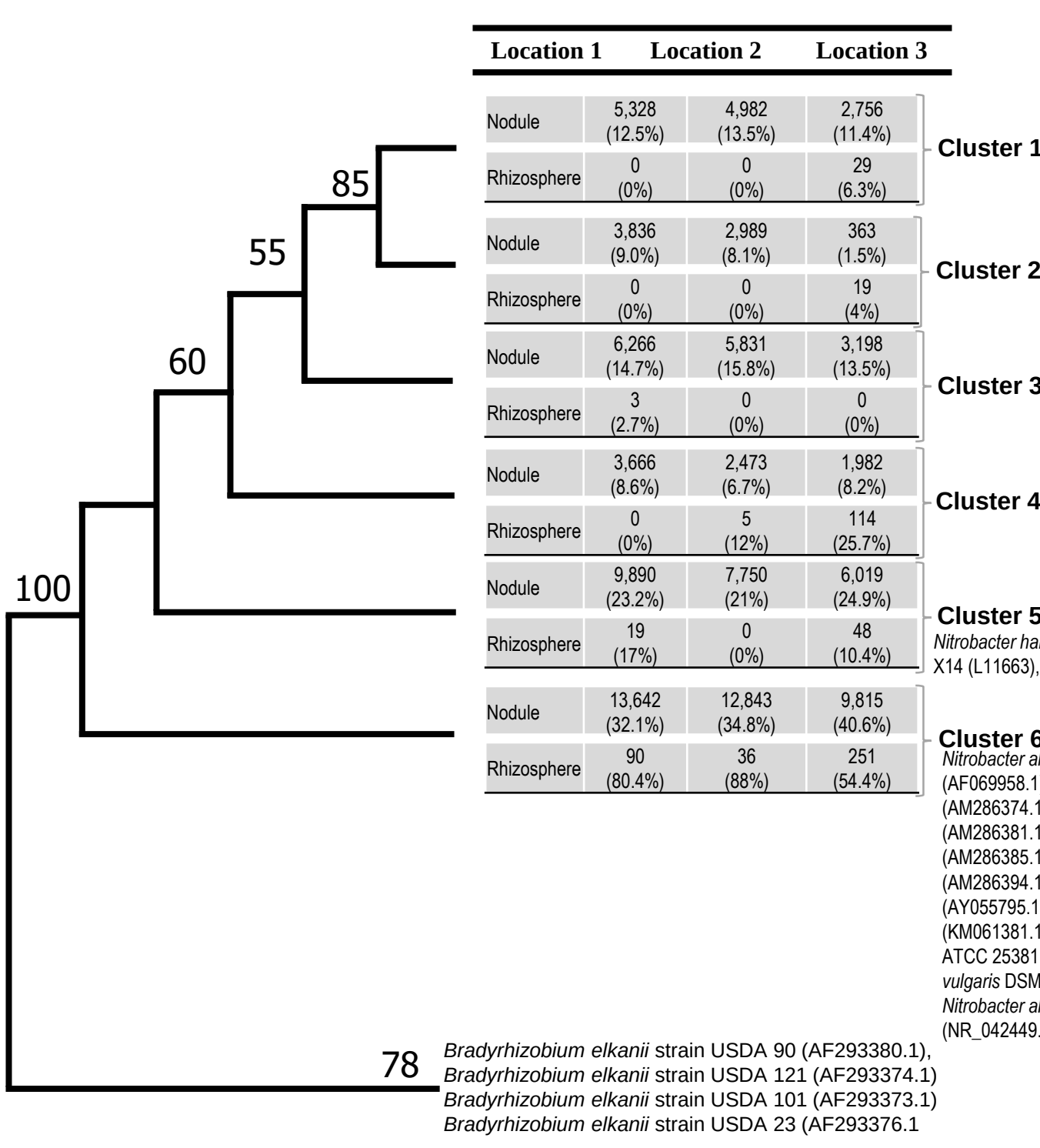

A
L1-P1 nodules on tap root
L1-P1 nodules on lateral root
2D Stress 0.11
NMDS 2
NMDS 1
1.0
0.5
0.0
-0.5
-1.0
N22
N3
N17
N11
N20
N16
N23
N21
N9
N5
N2
N7
N4
N13
N10
N8
N14
N6
N15
N1
N18
N12
N19
B
L1-P1 large size nodules
L1-P1 medium size nodules
L1-P1 Small size nodules
2D Stress 0.10

Fig. S5



	Location 1	Location 2	Location 3	
Nodule	5,328 (12.5%)	4,982 (13.5%)	2,756 (11.4%)	**Cluster 1**
Rhizosphere	0 (0%)	0 (0%)	29 (6.3%)	
Nodule	3,836 (9.0%)	2,989 (8.1%)	363 (1.5%)	**Cluster 2**
Rhizosphere	0 (0%)	0 (0%)	19 (4%)	
Nodule	6,266 (14.7%)	5,831 (15.8%)	3,198 (13.5%)	**Cluster 3**
Rhizosphere	3 (2.7%)	0 (0%)	0 (0%)	
Nodule	3,666 (8.6%)	2,473 (6.7%)	1,982 (8.2%)	**Cluster 4**
Rhizosphere	0 (0%)	5 (12%)	114 (25.7%)	
Nodule	9,890 (23.2%)	7,750 (21%)	6,019 (24.9%)	**Cluster 5**
Rhizosphere	19 (17%)	0 (0%)	48 (10.4%)	
Nodule	13,642 (32.1%)	12,843 (34.8%)	9,815 (40.6%)	**Cluster 6**
Rhizosphere	90 (80.4%)	36 (88%)	251 (54.4%)	

Nitrobacter hamburgensis strain Nb14 (L35502.1), *Nitrobacter hamburgensis* X14 (L11663), *Nitrobacter hamburgensis X14 (NR_074313.1)*

Nitrobacter alkalicus strain AN2 (AF069957.1), *Nitrobacter alkalicus* strain AN4 (AF069958.1), *Nitrobacter* sp. TH21 (AF080257.1), *Nitrobacter winogradskyi* (AM286374.1), *Nitrobacter vulgaris* (AM286378.1), *Nitrobacter vulgaris* (AM286381.1), *Nitrobacter* sp. 263 (AM286383.1), *Nitrobacter* sp. LIP (AM286385.1), *Nitrobacter* sp. BS5/19 (AM286387.1), *Nitrobacter* sp. D6/13 (AM286394.1), *Nitrobacter* sp. 311 (AM286397.1), *Nitrobacter* sp. PJN1 (AY055795.1), *Nitrobacter winogradskyi* (AY055796.1), *Nitrobacter* sp. NKU (KM061381.1), *Nitrobacter winogradskyi* (L11661.1), *Nitrobacter winogradskyi* ATCC 25381 (L35506.1), *Nitrobacter alkalicus* AN1 (AF069956), *Nitrobacter vulgaris* DSM 10236 (AM114522), *Nitrobacter winogradskyi* Nb-255 (CP000115), *Nitrobacter alkalicus* strain AN1 (NR_024920.1), *Nitrobacter vulgaris* strain Z (NR_042449.1), *Nitrobacter winogradskyi* strain Nb-255 (NR_074324.1)

Bradyrhizobium elkanii strain USDA 90 (AF293380.1),
Bradyrhizobium elkanii strain USDA 121 (AF293374.1)
Bradyrhizobium elkanii strain USDA 101 (AF293373.1)
Bradyrhizobium elkanii strain USDA 23 (AF293376.1

Fig. S6

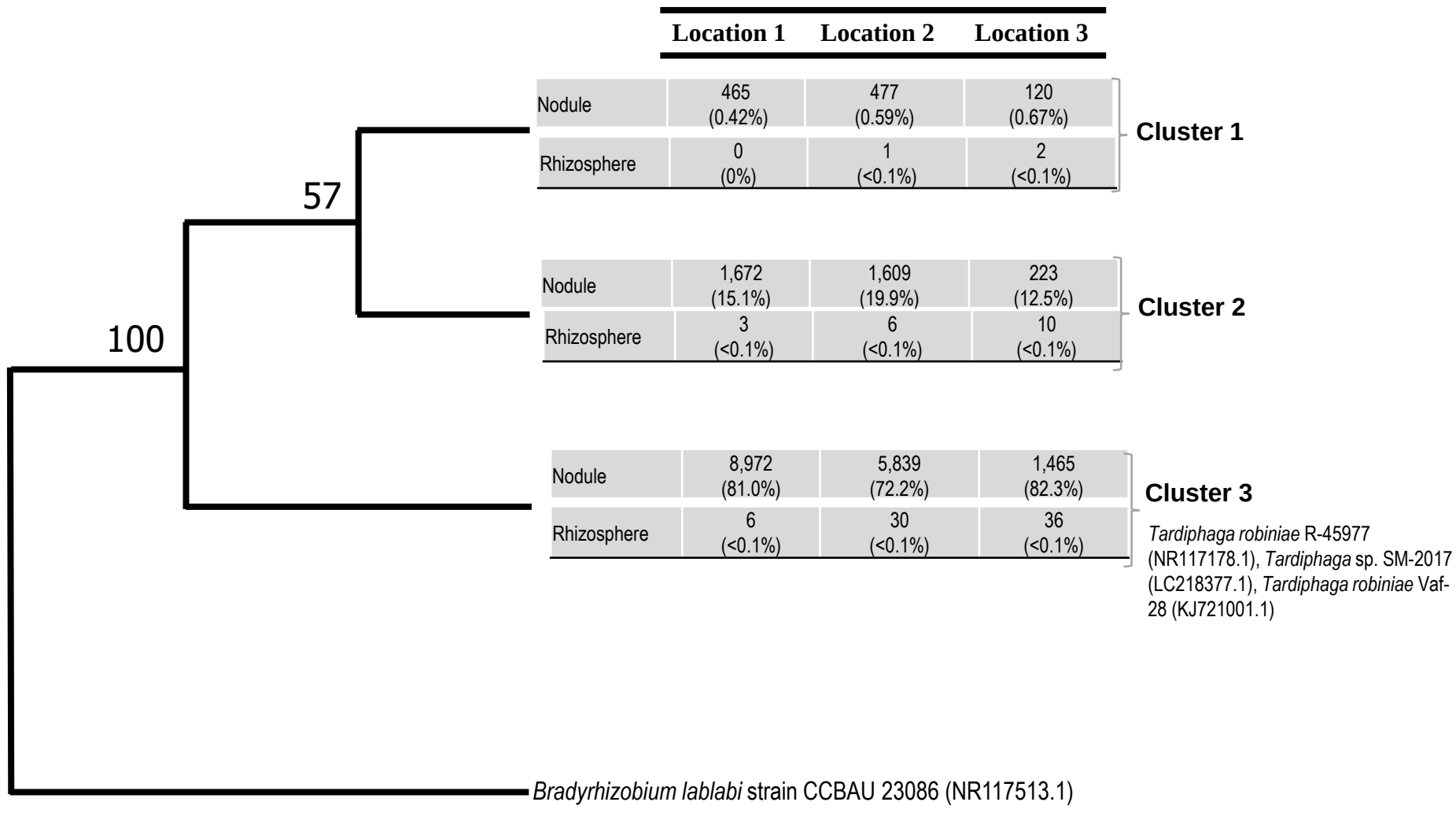

Location 1
Location 2
Location 3
Nodule
465 (0.42%)
477 (0.59%)
120 (0.67%)
Rhizosphere
0 (0%)
1 (<0.1%)
2 (<0.1%)
Cluster 1
Nodule
1,672 (15.1%)
1,609 (19.9%)
223 (12.5%)
Rhizosphere
3 (<0.1%)
6 (<0.1%)
10 (<0.1%)
Cluster 2
Nodule
8,972 (81.0%)
5,839 (72.2%)
1,465 (82.3%)
Rhizosphere
6 (<0.1%)
30 (<0.1%)
36 (<0.1%)
Cluster 3
57
100
Tardiphaga robiniae R-45977 (NR117178.1), *Tardiphaga* sp. SM-2017 (LC218377.1), *Tardiphaga robiniae* Vaf-28 (KJ721001.1)
Bradyrhizobium lablabi strain CCBAU 23086 (NR117513.1)

Fig. S7

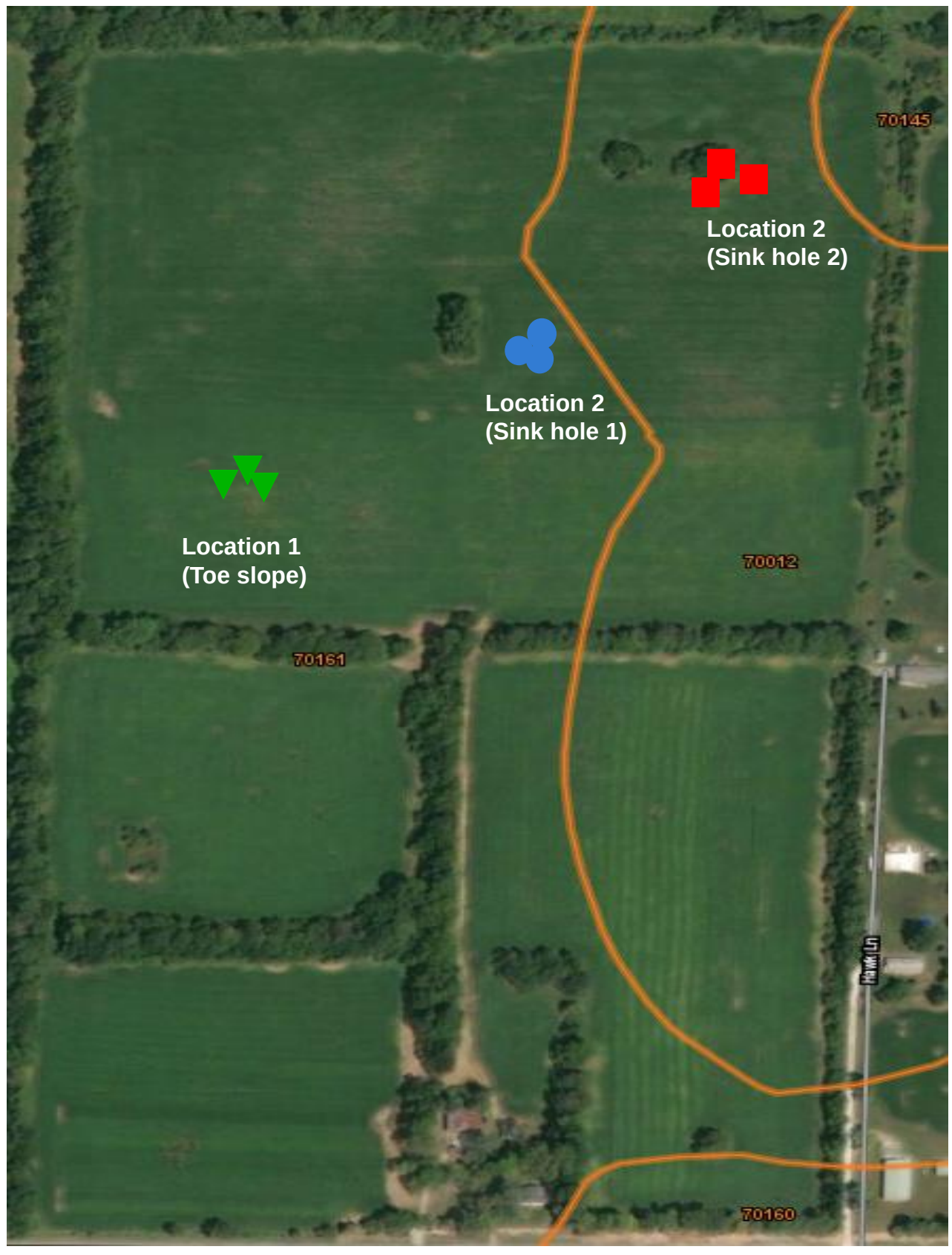

70145
Location 2
(Sink hole 2)
Location 2
(Sink hole 1)
Location 1
(Toe slope)
70012
70161
Hawk Ln
70160

Fig. S8

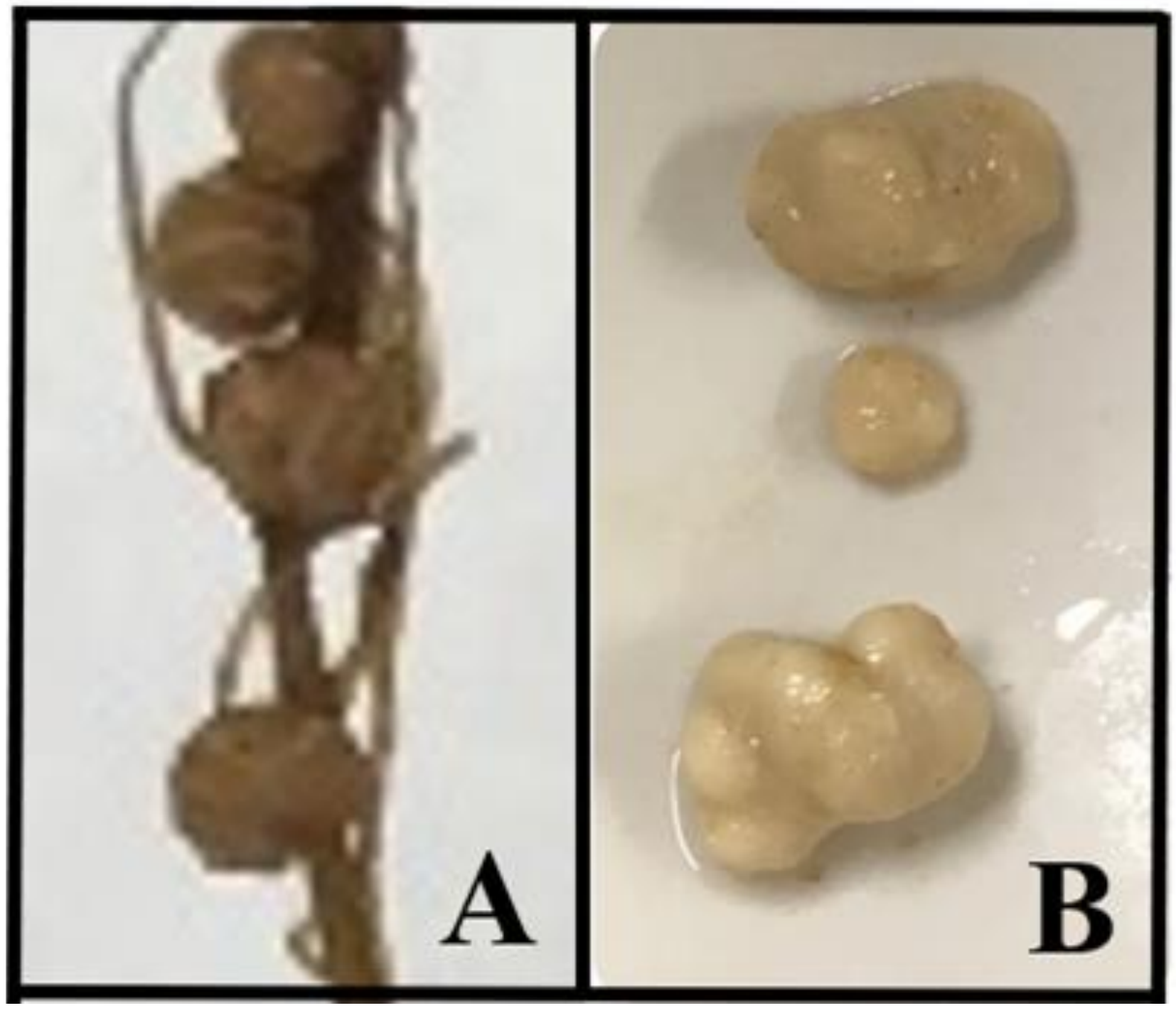
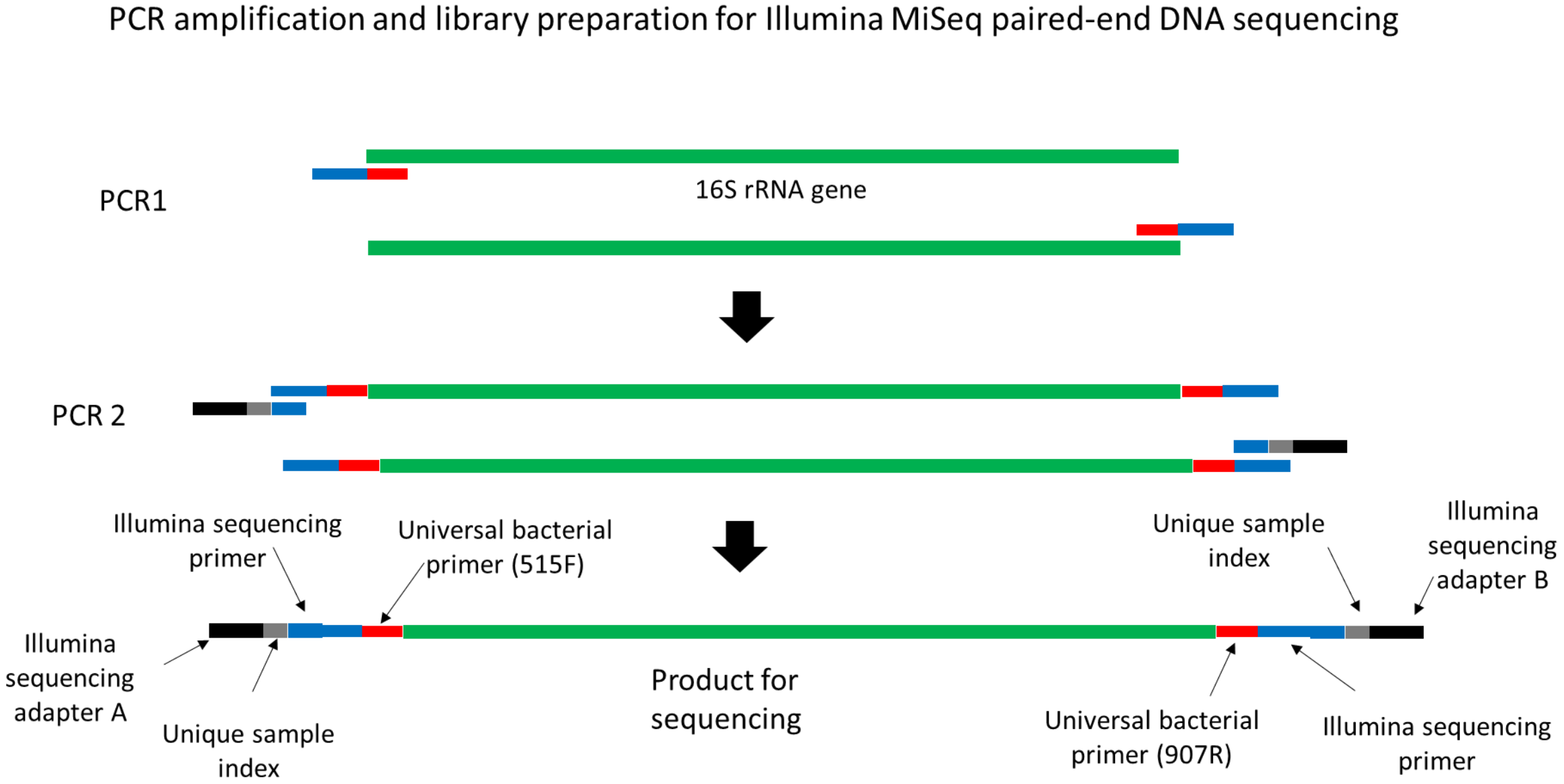


Fig. S9



First PCR primer set

515F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTGCCAGCMGCCGCGG
907R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCGTCAATTCMTTTRAGTTT

An example of a 2nd PCR primer set

U701	**CAAGCAGAAGACGGCATACGAGAT**TCGCCTTAGTGACTGGAGTTCAGACGTGTG
U501	**AATGATACGGCGACCACCGAGATCTACAC**TAGATCGCACACTCTTTCCCTACACGACG

Table S1: Important bacterial genera identified as non-rhizobial endophytes within soybean root nodules

Isolates (genera)	Proposed Beneficial Feature	Reference
Culturing-based studies		
Pseudomonas, Burkholderia, Enterobacter, Agrobacterium, Ochrobactrum, Acinetobacter, Proteus	Biocontrol agents	(1)
Pseudomonas, Bacillus, Enterobacter, Klebsiella, Acetobacter Burkholderia, Rhizobium, Xanthomonas	Phytohromone and Siderophore production, Biocontrol agents	(2)
Enterobacter, Microbacterium, Agrobacterium, Serratia marcescens, Chryseobacterium, Xanthomonas.	Increase plant growth	(3)
Pseudomonas, Acinetobacter, Enterobacter, Bacillus, Ochrobacterum	BNF, IAA synthesis, nutrient availability	(4)
Agrobacterium, Bacillus, Pantoea, Serratia, Burkholderia, Acinetobacter	BNF, IAA synthesis, nutrient availability	(5)
Bacillus, Paenibacillus	IAA synthesis and biocontrol agent	(6)
Tardiphaga, Afipia	-	(7)
Bacillus spp. (*subtilis* and *thuringiensis*)	PGPR activity	(8,9)
Bacillus endoradicis	-	(10)
Achromobacter, Agrobacterium, Burkholderia, Cronobacter, Enterobacter, Novosphingobium, Pantoea, Pseudomonas, Rahnella, Serratia, and Variovorax.	PGPR properties in vitro	(11)
Achromobacter xylosoxidans	BNF	(12)
Paenibacillus polymyxa		(13)
35 Non-rhizobial endophytes	IAA synthesis, cellulose, pectinase	(14)
Enterobacter ludwigii, *Variovorax paradoxus* (isolates from roots)	IAA synthesis, P-solublization, PGPR	(15)
Pseudomonas, Ralstonia, Enterobacter, Pantoea, Acinetobacter.	IAA synthesis, P-solublization, BNF	(16)
Culture-independent studies		
Pseudomonas, Enterobacter, Bacillus, Paenibacillus and some others (pooled root nodules from multiple plants) 1-40%		(17)
Members of Proteobacteria, Actinobacteria, Firmicutes and Bacteroidetes. (pooled root nodules from multiple plants) 435 bacterial genera of 21 phyla		(18)
Pseudomonas, Agrobacterium, Bacillus, Burkholderia, Microbacterium, Streptomyces and others (pooled root nodules from multiple plants) 2434 OTUs of NREs		(19)

BNF = Biological N fixation; IAA = Indole acetic Acid; PGPR = Plant growth promoting rhizobacteria

Table S2: Distribution of various non-rhizobial endophytes within root nodules of a plant (L1P1N1-23).

Organism	N1	N2	N3	N4	N5	N6	N7	N8	N9	N10	N11	N12	N13	N14	N15	N16	N17	N18	N19	N20	N21	N22	N23
Nitrobacter	820	253	118	160	179	1416	254	328	340	1296	184	247	2685	2105	19	334	218	2104	3096	363	307	399	1684
Tardiphaga	43	110	32	144	183	187	143	247	301	171	152	200	246	185	3	351	89	237	416	416	271	325	282
Novosphingobium	0	2	1	1	1	0	0	1	0	0	1	2	7	1	0	0	0	0	0	0	0	0	0
Variovorax	0	2	0	2	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudomonas	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Paenibacillus	0	0	0	0	1	0	0	0	0	2	0	2	3	0	0	0	0	0	0	1	0	0	1
Flavobacterium	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	1	2
Achromobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sphingobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planococcaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arthrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nitrospira	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stenotrophomonas	0	0	0	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0

Table S3: Bacterial diversity within root nodules of a plant and rhizosphere soil. In sample ID, L1-3 represents locations 1-3, P1-9 represents plant 1-9, N represents the nodules per plant, and R is for rhizosphere samples.

Sample ID	Nodules per plant or soil samples	Average number sequences per plant	Chao 1 estimator	Shannon Diversity
L1P1N1-23	23	56781 ± 4064	29263 ± 2547	2.60 ± 0.09
L1P2N1-23	23	44829 ± 7763	27932 ± 2986	2.83 ± 0.15
L1P3N1-20	20	25356 ± 2873	13846 ± 1161	2.55 ± 0.10
L2P4N1-22	22	42484 ± 6579	20072 ± 2681	2.50 ± 0.08
L2P5N1-24	24	35969 ± 3513	22991 ± 2238	2.49 ± 0.09
L2P6N1-24	24	40697 ± 4773	19554 ± 2210	2.32 ± 0.11
L3P4N1-21	21	20031 ± 1995	9051 ± 853	2.03 ± 0.12
L3P5N1-17	17	14221 ± 1698	8327 ± 451	2.04 ± 0.19
L3P6N1-19	19	43637 ± 7497	17939 ± 2412	2.27 ± 0.07
L1RP1-3	3	55296 ± 17176	45861 ± 11477	5.78 ± 0.28
*L2RP6	1	104715	55208	5.72
L3RP7-9	3	61554 ± 24622	46193 ± 16634	6.40 ± 0.29

* Location 2, the two of three rhizosphere samples resulted in less than 5,000 sequences. These two samples were not included the diversity analysis.

Table S4: Soil physiochemical characteristics of soil attached with soybean plants from three locations within Kindrick farm.

Sample ID	pH	OM	NO_3-N	NH_4-N	P	K	Ca	Mg	CEC
Location 1 (Toe slope)	6.6±.2	3.5±0.1	9.7±.8	22.4±4.5	33±1.5	104±3	1223±216	31±8	9.3±1.8
Location 2 (Sink hole 1)	6.5±0.1	3.1±0.2	8.7±1	11.4±3.5	16±2	103±2	1113±114	24±5	8.7±1
Location 3 (Sink hole 2)	6.8±0.1	3.5±.02	26.7±1.8	8.2±2.5	34±2.7	134±7	1358±12	28±4	10±0.2

Measured soil variables: pH, organic matter (OM %), Nitrate N (ppm), Ammonium N (ppm), P (phosphorus); K (potassium); Ca (calcium); Mg (magnesium); P, K, Ca, Mg, are expressed as mg/L, CEC, potential cation exchange capacity (meq/100g).
Sampling locations: Location 1 & 2 were related to (Keeno-Bona complex, Karst, 2 to 5 % slopes), whereas, Location 3 was related to (Hoberg, silt loam, 2 to 5 percent slopes).

Table S5: List of unique indices used for each of the root nodules and soil samples.

Sample	F (indices)	R (indices)	Sample	F (indices)	R (indices)	Sample	F (indices)	R (indices)	Sample	F (indices)	R (indices)	Sample	F (indices)	R (indices)	Sample	F (indices)	R (indices)	Sample	F (indices)	R (indices)
L1P1N1	U701	U509	**L1P2N12**	U734	U509	**L2P4N3**	U739	511	**L2P5N12**	U724	512	**L2P6N21**	U709	513	**L3P8N11**	U718	515	**L3P9N19**	U742	515
L1P1N2	U702	U509	**L1P2N13**	U735	U509	**L2P4N4**	U740	511	**L2P5N13**	U725	512	**L2P6N22**	U710	513	**L3P8N14**	U719	515	**L3P9N20**	U743	515
L1P1N3	U703	U509	**L1P2N14**	U736	U509	**L2P4N5**	U741	511	**L2P5N14**	U726	512	**L2P6N23**	U711	513	**L3P8N15**	U720	515	**L3P9N21**	U744	515
L1P1N4	U704	U509	**L1P2N15**	U737	U509	**L2P4N6**	U742	511	**L2P5N15**	U727	512	**L2P6N24**	U712	513	**L3P8N18**	U721	515	**L3P9N24**	U745	515
L1P1N6	U705	U509	**L1P2N16**	U738	U509	**L2P4N7**	U743	511	**L2P5N16**	U728	512	**L3P7N1**	U737	514	**L3P8N19**	U722	515	**LP1R1**	U725	524
L1P1N7	U706	U509	**L1P2N17**	U739	U509	**L2P4N8**	U744	511	**L2P5N17**	U729	512	**L3P7N2**	U738	514	**L3P8N20**	U723	515	**LP2R2**	U726	524
L1P1N8	U707	U509	**L1P2N18**	U740	U509	**L2P4N9**	U745	511	**L2P5N18**	U730	512	**L3P7N3**	U739	514	**L3P8N21**	U724	515	**LP3R3**	U727	524
L1P1N9	U708	U509	**L1P2N19**	U741	U509	**L2P4N10**	U746	511	**L2P5N19**	U731	512	**L3P7N6**	U740	514	**L3P8N22**	U725	515	**LP4R4**	U728	524
L1P1N10	U709	U509	**L1P2N20**	U742	U509	**L2P4N11**	U747	511	**L2P5N20**	U732	512	**L3P7N7**	U741	514	**L3P8N23**	U726	515	**LP5R5**	U729	524
L1P1N11	U710	U509	**L1P2N21**	U743	U509	**L2P4N12**	U748	511	**L2P5N21**	U733	512	**L3P7N8**	U742	514	**L3P8N11**	U718	515	**LP6R6**	U730	524
L1P1N12	U711	U509	**L1P2N22**	U744	U509	**L2P4N13**	U701	512	**L2P5N22**	U734	512	**L3P7N9**	U743	514	**L3P8N14**	U719	515	**LP7R7**	U731	524
L1P1N13	U712	U509	**L1P2N23**	U745	U509	**L2P4N14**	U702	512	**L2P5N23**	U735	512	**L3P7N10**	U744	514	**L3P8N15**	U720	515	**LP8R8**	U732	524
L1P1N14	U713	U509	**L1P2N24**	U746	U509	**L2P4N15**	U703	512	**L2P5N24**	U736	512	**L3P7N11**	U745	514	**L3P8N18**	U721	515	**LP9R9**	U733	524
L1P1N15	U714	U509	**L1P3N1**	U747	U509	**L2P4N16**	U704	512	**L2P6N1**	U737	512	**L3P7N12**	U746	514	**L3P8N19**	U722	515			
L1P1N16	U715	U509	**L1P3N2**	U748	U509	**L2P4N17**	U705	512	**L2P6N2**	U738	512	**L3P7N13**	U747	514	**L3P8N20**	U723	515			
L1P1N17	U716	U509	**L1P3N3**	U701	U510	**L2P4N18**	U706	512	**L2P6N3**	U739	512	**L3P7N14**	U748	514	**L3P8N21**	U724	515			
L1P1N18	U717	U509	**L1P3N4**	U702	U510	**L2P4N19**	U707	512	**L2P6N4**	U740	512	**L3P7N15**	U701	515	**L3P8N22**	U725	515			
L1P1N19	U718	U509	**L1P3N5**	U703	U510	**L2P4N20**	U708	512	**L2P6N5**	U741	512	**L3P7N16**	U702	515	**L3P8N23**	U726	515			
L1P1N20	U719	U509	**L1P3N6**	U704	U510	**L2P4N21**	U709	512	**L2P6N6**	U742	512	**L3P7N18**	U703	515	**L3P9N2**	U727	515			
L1P1N21	U720	U509	**L1P3N7**	U705	U510	**L2P4N22**	U710	512	**L2P6N7**	U743	512	**L3P7N19**	U704	515	**L3P9N3**	U728	515			
L1P1N22	U721	U509	**L1P3N8**	U706	U510	**L2P4N23**	U711	512	**L2P6N8**	U744	512	**L3P7N20**	U705	515	**L3P9N4**	U729	515			
L1P1N23	U722	U509	**L1P3N9**	U707	U510	**L2P4N24**	U712	512	**L2P6N9**	U745	512	**L3P7N21**	U706	515	**L3P9N6**	U730	515			
L1P1N24	U723	U509	**L1P3N10**	U708	U510	**L2P5N1**	U713	512	**L2P6N10**	U746	512	**L3P7N22**	U707	515	**L3P9N7**	U731	515			
L1P2N1	U724	U509	**L1P3N13**	U709	U510	**L2P5N2**	U714	512	**L2P6N11**	U747	512	**L3P7N23**	U708	515	**L3P9N8**	U732	515			
L1P2N2	U725	U509	**L1P3N14**	U710	U510	**L2P5N3**	U715	512	**L2P6N12**	U748	512	**L3P7N24**	U709	515	**L3P9N9**	U733	515			
L1P2N3	U726	U509	**L1P3N15**	U711	U510	**L2P5N4**	U716	512	**L2P6N13**	U701	513	**L3P8N1**	U710	515	**L3P9N10**	U734	515			
L1P2N5	U727	U509	**L1P3N16**	U712	U510	**L2P5N5**	U717	512	**L2P6N14**	U702	513	**L3P8N2**	U711	515	**L3P9N11**	U735	515			
L1P2N6	U728	U509	**L1P3N17**	U713	U510	**L2P5N6**	U718	512	**L2P6N15**	U703	513	**L3P8N3**	U712	515	**L3P9N13**	U736	515			
L1P2N7	U729	U509	**L1P3N19**	U714	U510	**L2P5N7**	U719	512	**L2P6N16**	U704	513	**L3P8N6**	U713	515	**L3P9N14**	U737	515			
L1P2N8	U730	U509	**L1P3N20**	U715	U510	**L2P5N8**	U720	512	**L2P6N17**	U705	513	**L3P8N7**	U714	515	**L3P9N15**	U738	515			
L1P2N9	U731	U509	**L1P3N21**	U716	U510	**L2P5N9**	U721	512	**L2P6N18**	U706	513	**L3P8N8**	U715	515	**L3P9N16**	U739	515			
L1P2N10	U732	U509	**L1P3N22**	U717	U510	**L2P5N10**	U722	512	**L2P6N19**	U707	513	**L3P8N9**	U716	515	**L3P9N17**	U740	515			
L1P2N11	U733	U509	**L1P3N23**	U718	U510	**L2P5N11**	U723	512	**L2P6N20**	U708	513	**L3P8N10**	U717	515	**L3P9N18**	U741	515			

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