

Appendix A Sequences of the designed LNA oligonucleotides and bacterial primers specific for the SSU rRNA genes from plant mitochondria and plastids

Name of the LNA oligonucleotide and bacterial primers		Sequence (5'----3')	Length (bases)
LNA oligonucleotide	LNA-Mit63	¹⁾ <u>GTCGAACGTTGTTTT</u> CGGp	18
	LNA-Mit1492	<u>CTTCACCCCAGTCGAAG</u> Ap	18
	LNA-Pla63b (soybean)	<u>TCGGACGGGAAGTGGT</u> p	16
	LNA-Pla1492b (soybean)	<u>CTTCACTCCAGTCACTAGC</u> p	19
	LNA-Pla63a (corn)	<u>GTCGAACGGGAAGTGGT</u> p	17
	LNA-Pla1492a (corn)	<u>CTTCACTCCAGTCGCAAGC</u> p	19
Bacterial primer	63f-mi	YRKGCYTWAYACATGCAAGTC	21
	1492r-y	GGYTACCTTGTTACGACTT	19
	A-Ns-341F	²⁾ A-Ns-CCTACGGGAGGCAGCAG	58
	B-907R	B-CCGTCAATTCCTTTGAGTTT	50

¹⁾LNA bases are indicated with bold letters. Underlined DNA bases are overlapped sequences with the bacterial primer. The 3' end of all LNA were phosphorylated to avoid extension during PCR. This was indicated with a small letter “p”.

²⁾The sequences of the A and B adapters are CCATCTCATCCCTGCGTGTCTCCGACGACT and CCTATCCCCTGTGTGCCTTGGCAGTCGACT, respectively. Ns represent an 11-base sample-specific barcode sequence.

Appendix B Distribution of root-associated bacteria in soybean and corn after excluded the sequences of plastids and mitochondria¹⁾

Phylum	Class	Genus	Soybean LNA (+)	Soybean LNA (-)	Corn LNA (+)	Corn LNA (-)		
Acidobacteria	Acidobacteria	11-24_norank	-	-	1	-		
		<i>Acidobacterium</i>	-	-	5	-		
		<i>Bryobacter</i>	-	6	17	-		
		<i>Candidatus_Koribacter</i>	-	-	2	-		
		<i>Candidatus_Solibacter</i>	-	-	12	-		
		<i>Blastocatella</i>	-	-	8	1		
		<i>Granulicella</i>	-	-	5	-		
		Subgroup_5_norank	-	-	2	-		
		Subgroup_6_norank	8	21	47	-		
		<i>Telmatobacter</i>	-	-	13	-		
		43F-1404R_norank	-	-	4	-		
		Subgroup_7_norank	-	-	2	-		
		Actinobacteria	Actinobacteria	<i>Actinoallomurus</i>	-	-	2	-
				<i>Actinocorallia</i>	-	2	1	-
				<i>Actinoplanes</i>	-	2	11	-
				<i>Actinospica</i>	-	-	1	-
				<i>Aeromicrobium</i>	3	7	9	1
<i>Amycolatopsis</i>	-			-	21	1		
<i>Angustibacter</i>	-			-	2	-		
<i>Agromyces</i>	4			1	-	-		
<i>Arthrobacter</i>	234			3	162	1		
<i>Bifidobacterium</i>	1			-	-	-		
<i>Blastococcus</i>	1			4	13	1		
<i>Corynebacterium</i>	2			-	-	-		
<i>Crossiella</i>	-			-	5	-		
CL500-29_marine_group	1			-	2	-		
<i>Catellatospora</i>	-			11	14	-		
<i>Catenulispora</i>	-			-	27	1		
<i>Cellulomonas</i>	3			-	-	-		
<i>Curtobacterium</i>	-			2	-	-		
<i>Dactylosporangium</i>	-			-	10	-		
<i>Frankia</i>	-			-	24	1		
<i>Frankiales_norank</i>	-	-	5	-				
<i>Friedmanniella</i>	-	-	2	-				
<i>Frigoribacterium</i>	3	-	7	-				
<i>Hamadaea</i>	-	-	3	-				
<i>Kibdelosporangium</i>	-	-	2	-				
<i>Kineosporia</i>	-	-	1	-				
<i>Kitasatospora</i>	-	-	9	-				
<i>Kribbella</i>	5	1	4	-				

		<i>Kutzneria</i>	-	-	3	-
		<i>Lechevalieria</i>	-	-	3	-
		<i>Leifsonia</i>	1	6	14	1
		<i>Luedemannella</i>	-	-	2	-
		<i>Marmoricola</i>	2	-	16	1
		<i>Microbacterium</i>	22	12	9	-
		<i>Micrococcus</i>	1	-	-	-
		<i>Microlumatus</i>	-	-	6	-
		<i>Mycetocola</i>	3	1	2	-
		<i>Mycobacterium</i>	2	2	7	-
		<i>Nocardioiodes</i>	10	-	29	-
		<i>Nonomuraea</i>	-	-	1	-
		<i>Phycococcus</i>	1	4	2	-
		<i>Plantibacter</i>	-	-	3	-
		<i>Promicromonospora</i>	1	-	-	-
		<i>Propionibacterium</i>	-	5	5	-
		<i>Pseudonocardia</i>	-	-	7	-
		<i>Streptomyces</i>	114	119	1288	15
		<i>Streptosporangium</i>	-	-	1	-
		<i>Terrabacter</i>	5	21	6	-
		<i>Williamsia</i>	-	-	1	1
	Acidimicrobiia	<i>Iamia</i>	1	-	-	1
		OCS155_marine_group_norank	-	-	1	-
	Thermoleophilia	480-2_norank	-	-	1	-
		<i>Gaiella</i>	-	-	19	1
Armatimonadetes	MB-A2-108	MB-A2-108_norank	-	20	6	-
Bacteroidetes	norank	Armatimonadetes_norank	-	-	1	-
	Bacteroidia	<i>Bacteroides</i>	1	-	1	-
		<i>Dysgonomonas</i>	-	-	1	-
		<i>Prevotella</i>	1	-	-	-
		RC9_gut_group	1	-	-	-
	Cytophagia	<i>Candidatus_Paenicardinium</i>	1	-	-	-
		<i>Cytophaga</i>	1	-	1	-
		<i>Dyadobacter</i>	6	-	-	-
		<i>Flexibacter</i>	1	-	56	-
		<i>Ohtaekwangia</i>	7	-	-	-
		<i>Siphonobacter</i>	-	-	4	-
	Flavobacteria	<i>Chryseobacterium</i>	10	-	2	-
		<i>Flavobacterium</i>	744	28	1	-
		<i>Fluviicola</i>	3	-	-	-
		<i>Weeksella</i>	-	-	2	-
	Sphingobacteria	AKYH767_norank	-	-	3	-
		<i>Chitinophaga</i>	7	11	79	-
		<i>Ferruginibacter</i>	-	-	1	-
		<i>Flaviumibacter</i>	-	-	1	-
		<i>Flavisolibacter</i>	-	-	14	-
		<i>Flavitalea</i>	-	-	4	-
		<i>Mucilagimibacter</i>	2	6	87	1
		<i>Niastella</i>	7	-	1030	7
		<i>Pedobacter</i>	46	-	1	-
		<i>Sediminibacterium</i>	1	-	-	-
		<i>Segetibacter</i>	-	-	4	-
		<i>Sphingobacterium</i>	5	-	-	-
		env.OPS_17_norank	-	-	3	-
	VC2.1_Bac22	VC2.1_Bac22_norank	-	-	1	-
Candidate_division_TM7	norank	Candidate_division_TM7_norank	4	-	5	1
Chloroflexi	Chloroflexia	<i>Roseiflexus</i>	1	-	-	-
	Ktedonobacteria	CO119_norank	-	-	6	-
	Thermomicrobia	AKYG1722_norank	-	3	-	-
		JG30-KF-CM45_norank	-	1	1	-
Elusimicrobia	TK10	TK10_norank	-	1	2	-
	Elusimicrobia	<i>Lineage_Ila_norank</i>	-	-	1	-
		MVP-88_norank	-	-	2	-
Firmicutes	Bacilli	<i>Anoxybacillus</i>	-	8	-	-
		<i>Bacillus</i>	10	5	174	3
		<i>Cohnella</i>	-	-	2	-
		<i>Exiguobacterium</i>	9	-	-	-
		<i>Gemella</i>	1	-	-	-
		<i>Lactococcus</i>	2	-	-	-
		<i>Lysinibacillus</i>	-	-	1	-
		<i>Paenibacillus</i>	3	-	24	-
		<i>Paenisporosarcina</i>	2	-	4	-
		<i>Paucisalibacillus</i>	-	-	1	-
		<i>Solibacillus</i>	1	-	-	-
		<i>Sporosarcina</i>	1	-	3	-
		<i>Staphylococcus</i>	-	34	3	-
		<i>Streptococcus</i>	1	-	-	-
	Clostridia	<i>Anaerococcus</i>	1	-	-	-
		<i>Caldicoprobacter</i>	-	-	1	-
		<i>Clostridium</i>	1	-	3	-
		<i>Fastidiosipila</i>	1	-	-	-
		<i>Helcococcus</i>	2	-	-	-
		<i>Incertae_Sedis</i>	1	-	6	-
		<i>Tepidimicrobium</i>	-	-	1	-
		<i>Tissierella</i>	-	-	1	-
	Erysipelotrichia	<i>Asteroleplasma</i>	-	-	70	1
Gemmatimonadetes	Negativicutes	<i>Anaerovibrio</i>	1	-	-	-
	Gemmatimonadetes	AT425-EubC11_terrestrial_group_norank	-	-	4	-
		<i>Gemmatimonas</i>	-	2	9	-
Nitrospirae	Nitrospira	<i>Nitrospira</i>	-	-	6	-
Proteobacteria	Alphaproteobacteria	<i>Afpia</i>	9	1	-	-
		<i>Altererythrobacter</i>	1	-	-	-
		<i>Aquamicrobium</i>	1	-	-	-
		<i>Asticcacaulis</i>	11	-	-	-
		<i>Azospirillum</i>	-	-	-	2
		<i>Bosea</i>	11	8	-	-
		<i>Bradyrhizobium</i>	1133	23	-	3
		<i>Brevundimonas</i>	-	7	-	-
		<i>Caulobacter</i>	14	-	2	-

	DBI-14_norank	-	-	2	-
	<i>Devosia</i>	40	26	-	3
	<i>Dongia</i>	1	26	-	-
	<i>Ensifer</i>	1	-	-	-
	GOBB3-C201_norank	-	33	-	-
	<i>Hyphomicrobium</i>	10	33	-	-
	JG34-KF-161_norank	1	-	-	-
	JG37-AG-20_norank	-	-	1	-
	<i>Labrys</i>	3	17	-	-
	<i>Mesorhizobium</i>	13	12	-	6
	<i>Methylobacterium</i>	2	3	-	-
	<i>Microvirga</i>	1	-	-	-
	<i>Nordella</i>	2	8	-	-
	<i>Novosphingobium</i>	28	261	-	2
	<i>Pedomicrobium</i>	1	-	-	1
	<i>Phenylobacterium</i>	9	-	-	1
	<i>Phyllobacterium</i>	10	-	-	-
	<i>Pseudolabrys</i>	3	12	-	-
	<i>Reyranella</i>	-	7	8	-
	<i>Rhizobium</i>	80	174	-	4
	<i>Rhizomicrobium</i>	-	-	8	-
	<i>Rhodopseudomonas</i>	5	-	-	-
	<i>Rubellimicrobium</i>	-	15	-	-
	SM2D12_norank	-	-	2	1
	<i>Shinella</i>	22	14	-	-
	<i>Skermanella</i>	-	-	1	-
	<i>Sphingobium</i>	8	-	3	1
	<i>Sphingomonas</i>	13	31	-	12
	<i>Sphingopyxis</i>	1	-	-	-
Betaproteobacteria	<i>Achromobacter</i>	4	-	-	-
	<i>Acidovorax</i>	6	-	-	-
	<i>Alcaligenes</i>	-	39	2	-
	<i>Burkholderia</i>	3	83	117	1
	<i>Caenimonas</i>	34	-	9	-
	<i>Candidatus_Glomeribacter</i>	-	-	6	-
	<i>Cupriavidus</i>	1	-	-	-
	<i>Delftia</i>	7	1	-	-
	<i>Herbaspirillum</i>	1	18	2	-
	<i>Hydrogenophaga</i>	4	-	-	-
	<i>Massilia</i>	22	62	135	5
	<i>Methylotenera</i>	111	5	2	-
	<i>Methyloversatilis</i>	-	12	-	-
	<i>Nitrosospira</i>	-	-	1	-
	<i>Pandoraea</i>	-	-	2	-
	<i>Paucimonas</i>	-	-	2	-
	<i>Polaromonas</i>	78	-	7	1
	<i>Pseudorhodoferrax</i>	14	-	-	-
	<i>Pusillimonas</i>	1	-	4	-
	<i>Ralstonia</i>	-	-	1	-
	<i>Ramlibacter</i>	5	-	2	-
	<i>Rhizobacter</i>	2	-	85	5
	<i>Roseateles</i>	1	-	-	-
	SC-1-84_norank	-	-	20	-
	<i>Schlegelella</i>	-	4	-	-
	<i>Undibacterium</i>	-	-	1	1
	<i>Variovorax</i>	101	-	29	-
	<i>Vogesella</i>	-	-	1	-
Deltaproteobacteria	0319-6G20_norank	1	-	6	1
	<i>Bacteriovorax</i>	-	-	6	1
	<i>Bdellovibrio</i>	1	13	9	-
	<i>Byssovorax</i>	-	-	15	-
	<i>Cystobacteraceae_norank</i>	-	-	1	-
	GR-WP33-30_norank	-	-	-	2
	<i>Haliangium</i>	1	31	49	-
	<i>Phaselicystis</i>	-	-	2	-
	<i>Sandaracinus</i>	-	-	3	-
	<i>Sorangium</i>	-	-	21	-
	mle1-27_norank	-	-	4	-
Gammaproteobacteria	<i>Acinetobacter</i>	7	-	-	1
	<i>Aeromonas</i>	2	-	-	-
	<i>Aquicella</i>	3	-	12	-
	<i>Arenimonas</i>	3	8	10	-
	CHAB-XI-27_norank	-	-	3	-
	<i>Cedecea</i>	13	30	-	-
	CrystalBog021C3_norank	-	-	1	-
	<i>Dokdonella</i>	1	15	18	-
	<i>Enhydrobacter</i>	1	-	-	-
	<i>Enterobacter</i>	26	-	-	-
	<i>Erwinia</i>	113	-	-	-
	<i>Ignatzschineria</i>	-	-	9	-
	<i>Klebsiella</i>	1	-	-	-
	<i>Legionella</i>	1	-	7	-
	<i>Luteibacter</i>	-	-	4	-
	<i>Luteimonas</i>	2	-	-	-
	<i>Lysobacter</i>	11	-	2	-
	NKB5_norank	-	-	60	1
	<i>Pantoea</i>	100	19	-	-
	<i>Pseudomonas</i>	1666	-	3	-
	<i>Pseudoxanthomonas</i>	1	-	-	-
	<i>Rhodanobacter</i>	5	1	87	2
	<i>Rudaea</i>	-	-	2	-
	<i>Serratia</i>	7	-	-	-
	<i>Stenotrophomonas</i>	69	62	-	-
	<i>Steroidobacter</i>	5	-	5	-
	<i>Thermomonas</i>	-	-	2	-
	<i>Xanthomonas</i>	-	-	4	1
Tenericutes	<i>Acholeplasma</i>	1	-	-	-
TM6	TM6_norank	-	-	1	-

WCHB1-60	norank	WCHB1-60_norank	-	-	1	-
Unclassified		Other	109	92	453	24
		uncultured	18	105	439	11
		uncultured_norank	6	54	99	5
		Total	5317	1714	5306	139

¹⁾ The number represents the root-associated bacteria sequences detected in the sample and “-” means no sequence was detected in the sample.