

Supplement of Biogeosciences, 17, 1181–1198, 2020
<https://doi.org/10.5194/bg-17-1181-2020-supplement>
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Supplement of

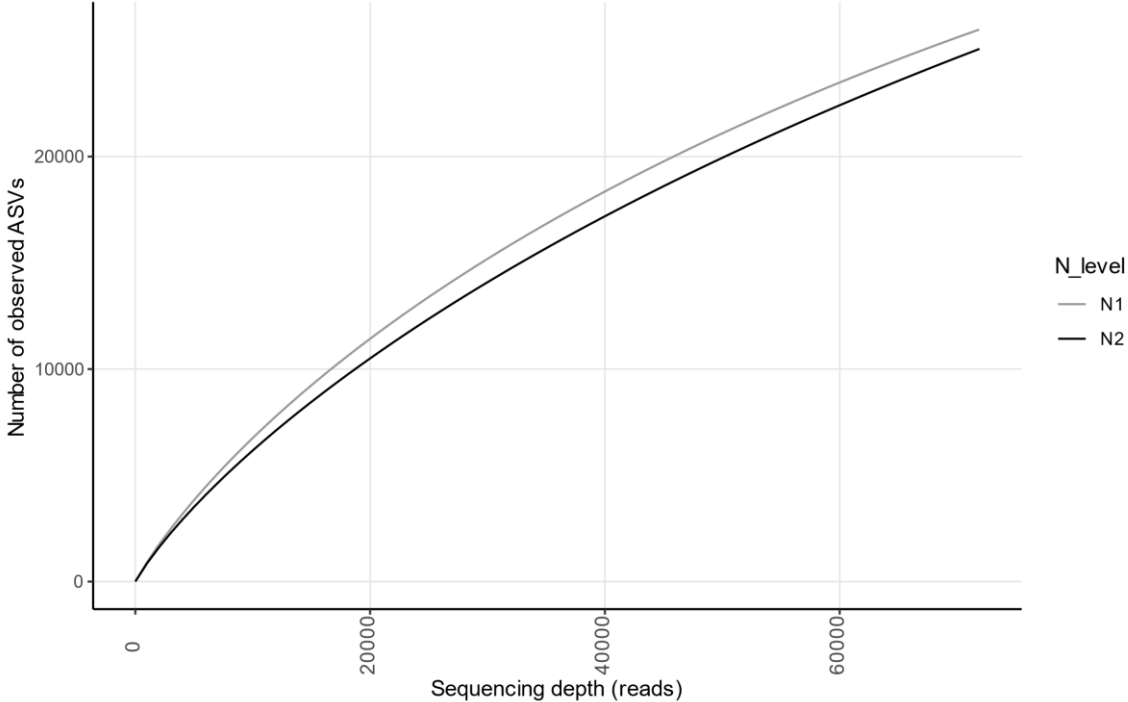
Maize root and shoot litter quality controls short-term CO₂ and N₂O emissions and bacterial community structure of arable soil

Pauline Sophie Rummel et al.

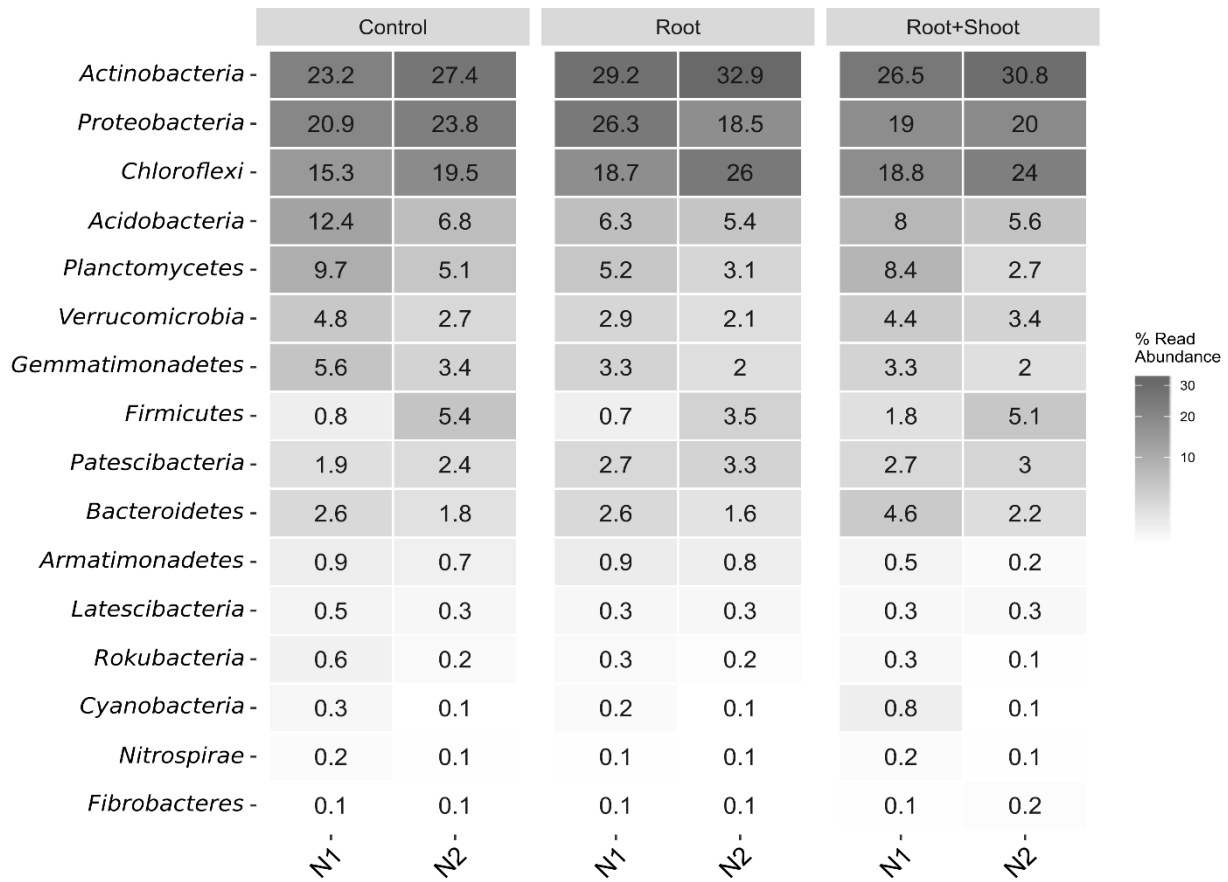
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Supplement



5 **Figure S1: Rarefaction curve of the observed amplicon sequence variants (ASVs) of the soil inhabiting bacterial communities within the two different N-fertilizer treatments (N1 and N2). Samples of the same N treatment were aggregated and rarefied to the same number of raw reads (61206).**



10 **Figure S2: Heatmap of the 16 most abundant phyla (>0.1 %) in the analyzed soil samples grouped by N levels and litter input (n=4, except for N2 Root: n=3).**

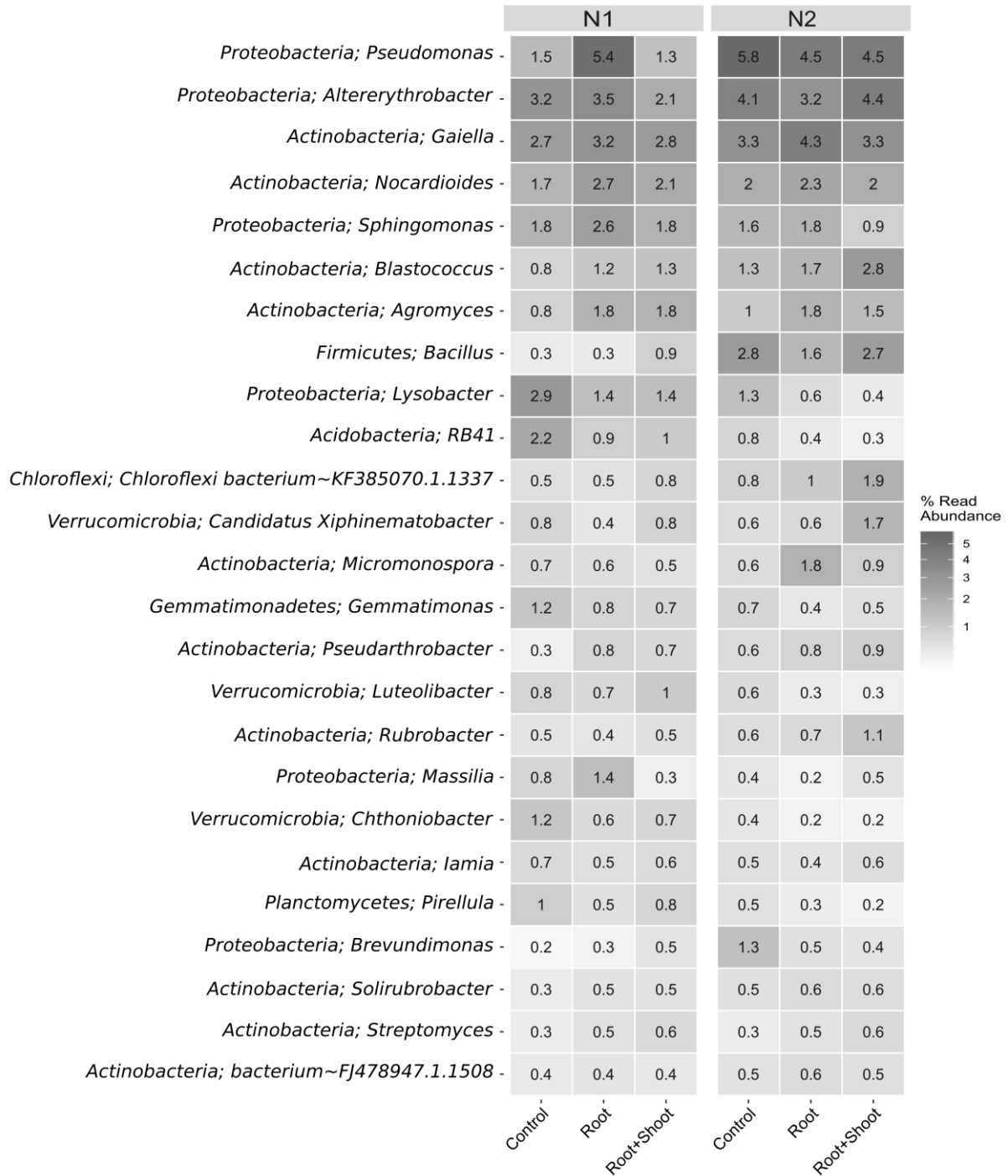


Figure S3: Heatmap of the 25 most abundant bacterial genera in the analyzed soil samples grouped by N levels and litter input (n=4, except for N2 Root: n=3).

Table S4: Sequence summary, alpha diversity indices and PD (phylogenetic diversity) for each treatment. Shown are read sums and mean values of diversity indices (ASV = amplicon sequence variant).

Sample ID	Number of Replicates	Raw Reads	Reads after Pipeline	Reads after Taxonomy filter	Subsample size	Observed ASVs	Shannon	Simpson	PD
N1_C	4	537242	443228	442610	61206	21113	9.22	0.9997	423.2
N1_R	4	590494	492088	491280	61206	21447	9.10	0.9995	431.0
N1_RS	4	557072	439132	438456	61206	21789	9.29	0.9997	436.6
N2_C	4	531926	441286	440968	61206	19142	8.79	0.9992	420.4
N2_R	3	848974	735676	735366	61206	18891	8.78	0.9991	409.2
N2_RS	4	536532	463944	463504	61206	20301	8.89	0.9990	403.3

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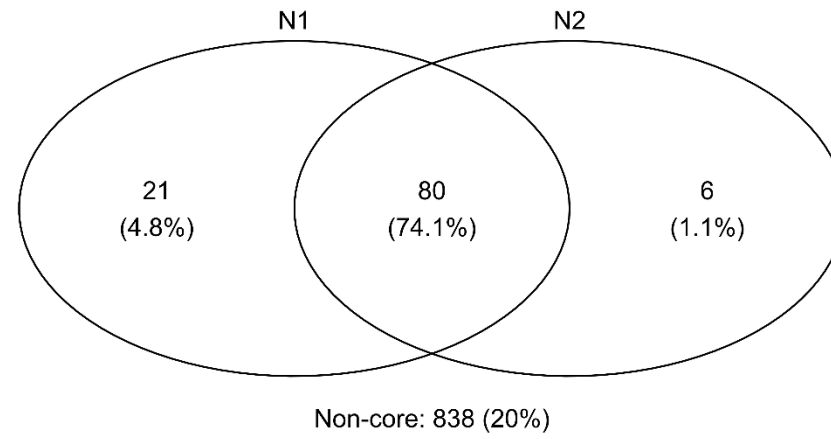
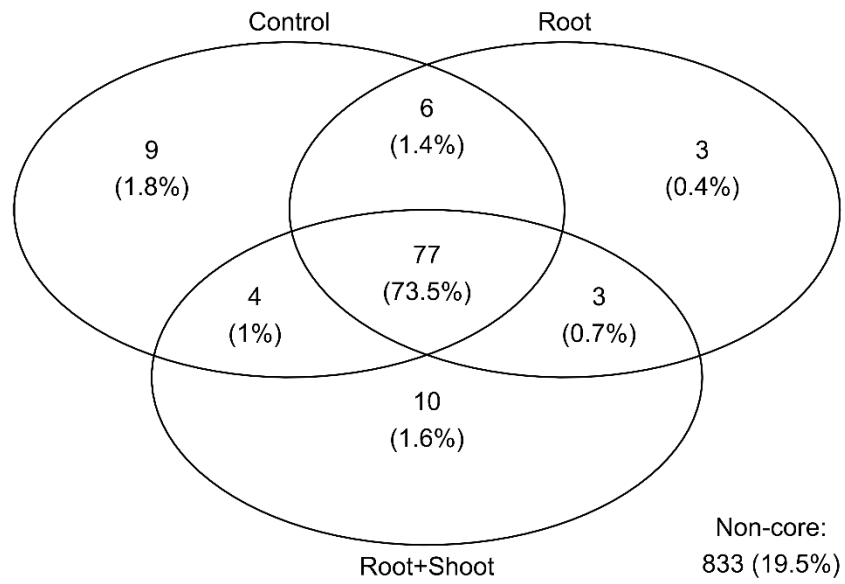


Fig. S5 a + b: Venn diagrams displaying core and non-core microbiomes of the soil inhabiting bacterial community analyzed at the end of the incubation experiment grouped by either litter input or N level (for Control and Root+Shoot n=8, for Root: n=7, for N1 n=12, for N2 n=11).

Table S6: The core microbiome of the soil inhabiting bacterial community analyzed at the end of the incubation experiment grouped by litter input (for Control and Root+Shoot n=8, for Root: n=7).

Phylum	Class	Order	Family	Genus	Relative abundance in %
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	<i>Pyrinomonadales</i>	<i>Pyrinomonadaceae</i>	RB41	1.01
	<i>Holophagae</i>	Subgroup 7	uncultured bacterium		0.29
	<i>Subgroup 6</i>	metagenome			0.27
		uncultured <i>Acidobacteria</i> bacterium			2.42
		uncultured <i>Acidobacteriales</i> bacterium			0.22
uncultured bacterium			1.77		
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Actinomarinales</i>	uncultured bacterium		0.54
		IMCC26256	uncultured bacterium		0.24
		<i>Microtrichales</i>	<i>Iamiaceae</i>	<i>Iamia</i>	0.55
			<i>Ilumatobacteraceae</i>	<i>Ilumatobacter</i>	0.23
				uncultured bacterium	0.69
	uncultured bacterium			0.23	
	<i>Actinobacteria</i>	<i>Corynebacteriales</i>	<i>Mycobacteriaceae</i>	<i>Mycobacterium</i>	0.16
		<i>Frankiales</i>	<i>Geodermatophilaceae</i>	<i>Blastococcus</i>	1.54
			<i>Sporichthyaceae</i>	uncultured bacterium	0.31
		<i>Micrococcales</i>	<i>Intrasporangiaceae</i>	<i>Intrasporangium</i>	0.36
				<i>Tetrasphaera</i>	0.20
				uncultured bacterium	0.67
			<i>Microbacteriaceae</i>	<i>Agromyces</i>	1.48
<i>Micrococcaceae</i>	<i>Pseudarthrobacter</i>	0.65			
uncultured bacterium			0.25		

		<i>Micromonosporales</i>	<i>Micromonosporaceae</i>	<i>Micromonospora</i>	0.87	
		<i>Propionibacteriales</i>	<i>Nocardiodaceae</i>	<i>Aeromicrobium</i>	0.31	
				<i>Marmoricola</i>	0.35	
				<i>Nocardioides</i>	2.03	
			<i>Propionibacteriaceae</i>	uncultured bacterium	0.26	
		<i>Streptomyces</i>	<i>Streptomycetaceae</i>	<i>Streptomyces</i>	0.56	
	MB-A2-108	uncultured bacterium			1.87	
	<i>Rubrobacteria</i>	<i>Rubrobacterales</i>	<i>Rubrobacteriaceae</i>	<i>Rubrobacter</i>	0.60	
	<i>Thermoleophilia</i>	<i>Gaiellales</i>	<i>Gaiellaceae</i>	<i>Gaiella</i>	3.08	
			uncultured bacterium			3.67
		<i>Solirubrobacterales</i>	67-14	uncultured bacterium		1.53
			<i>Solirubrobacteraceae</i>	<i>Solirubrobacter</i>	0.48	
	uncultured bacterium			0.27		
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>Chthonomonadales</i>	uncultured bacterium		0.66	
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Cytophagales</i>	<i>Microscillaceae</i>	uncultured bacterium	0.45	
<i>Chloroflexi</i>	<i>Anaerolineae</i>	<i>Caldilineales</i>	<i>Caldilineaceae</i>	uncultured bacterium	0.54	
	<i>Chloroflexia</i>	<i>Chloroflexales</i>	<i>Herpetosiphonaceae</i>	<i>Herpetosiphon</i>	0.24	
			<i>Roseiflexaceae</i>	uncultured bacterium	0.61	
		<i>Thermomicrobiales</i>	JG30-KF-CM45	metagenome		0.30
				uncultured bacterium		2.72
	uncultured <i>Chloroflexi</i> bacterium		1.98			
	<i>Dehalococcoidia</i>	S085	uncultured bacterium			0.34
	Gitt-GS-136	uncultured bacterium			3.89	
uncultured <i>Chloroflexus</i> sp.			0.35			

	JG30-KF-CM66	uncultured bacterium			0.19
	KD4-96	metagenome			0.48
		uncultured <i>Anaerolineaceae</i> bacterium			0.55
		uncultured bacterium			3.08
		uncultured <i>Chloroflexi</i> bacterium			1.05
	<i>Ktedonobacteria</i>	C0119	uncultured bacterium		0.91
	TK10	uncultured bacterium			0.31
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Bacillaceae</i>	<i>Bacillus</i>	1.38
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonadales</i>	<i>Gemmatimonadaceae</i>	<i>Gemmatimonas</i>	0.71
				uncultured bacterium	1.65
	<i>Longimicrobia</i>	<i>Longimicrobiales</i>	<i>Longimicrobiaceae</i>	uncultured bacterium	0.21
<i>Latescibacteria</i>	uncultured bacterium				0.20
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>Saccharimonadales</i>	uncultured bacterium		1.31
			uncultured soil bacterium		0.30
<i>Planctomycetes</i>	OM190	uncultured bacterium			0.35
	<i>Phycisphaerae</i>	<i>Tepidisphaerales</i>	WD2101 soil group	uncultured bacterium	1.61
				uncultured <i>planctomycetes</i>	0.65
	<i>Planctomycetacia</i>	<i>Pirellulales</i>	<i>Pirellulaceae</i>	<i>Pirellula</i>	0.54
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacterales</i>	<i>Caulobacteraceae</i>	<i>Brevundimonas</i>	0.61
		<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Altererythrobacter</i>	3.75
				<i>Sphingomonas</i>	1.86
	<i>Deltaproteobacteria</i>	<i>Myxococcales</i>	<i>Haliangiaceae</i>	<i>Haliangium</i>	0.37
	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>	<i>Massilia</i>	0.79
			<i>Burkholderiaceae</i>	uncultured bacterium	0.30
<i>Nitrosomonadales</i>		<i>Nitrosomonadaceae</i>	MND1	0.51	

	<i>Gamma</i> proteobacteria	<i>Gamma</i> proteobacteria <i>Incertae Sedis</i>	Unknown Family	<i>Acidibacter</i>	0.18
		<i>Pseudomonadales</i>	<i>Pseudomonadaceae</i>	<i>Pseudomonas</i>	3.64
		<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Lysobacter</i>	1.31
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacterales</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus</i> <i>Xiphinematobacter</i>	0.89
		<i>Pedosphaerales</i>	<i>Pedosphaeraceae</i>	uncultured bacterium	0.43
		<i>Verrucomicrobiales</i>	<i>Rubritaleaceae</i>	<i>Luteolibacter</i>	0.71

25 Table S7: The responders of the soil inhabiting bacterial community analyzed at the end of the incubation experiment grouped by litter input (for Control and Root+Shoot n=8, for Root: n=7).

Phylum	Class	Order	Family	Genus	Relative abundance in %
Root					
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Micrococcales</i>	<i>Intrasporangiaceae</i>	<i>Lapillicoccus</i>	0.09
	<i>Thermoleophilia</i>	<i>Solirubrobacterales</i>	67-14	Uncultured bacterium <i>Rubrobacteria</i>	0.13
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Cytophagales</i>	<i>Hymenobacteraceae</i>	<i>Adhaeribacter</i>	0.17
Root+Shoot					
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptosporangiales</i>	<i>Streptosporangiaceae</i>	<i>Nonomuraea</i>	0.10
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Chitinophagales</i>	<i>Chitinophagaceae</i>	uncultured bacterium	0.27
		<i>Flavobacteriales</i>	<i>Crocinitomicaceae</i>	<i>Fluviicola</i>	0.18
<i>Chloroflexi</i>	<i>Anaerolineae</i>	SBR1031	uncultured bacterium		0.13
<i>Chloroflexi</i>	Gitt-GS-136	uncultured <i>Anaerolineae</i> bacterium			0.16
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospirales</i>	<i>Nitrospiraceae</i>	<i>Nitrospira</i>	0.13
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>Candidatus</i> Kaiserbacteria	uncultured bacterium		0.15
		uncultured bacterium			0.22
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Rhizobiaceae</i>	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium</i>	0.21
	<i>Gammaproteobacteria</i>	<i>Cellvibrionales</i>	<i>Cellvibrionaceae</i>	<i>Cellvibrio</i>	0.10
Root & Root+Shoot					
<i>Chloroflexi</i>	<i>Anaerolineae</i>	SBR1031	A4b	uncultured bacterium	0.23
	<i>Chloroflexia</i>	<i>Kallotenuales</i>	AKIW781	uncultured bacterium	0.19
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Sphingobium</i>	0.31
Control & Root					

<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	<i>Blastocatellales</i>	<i>Blastocatellaceae</i>	<i>uncultured bacterium</i>	0.34
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardiales</i>	<i>Pseudonocardiaceae</i>	<i>Pseudonocardia</i>	0.16
	<i>Thermoleophilia</i>	<i>Gaiellales</i>	<i>uncultured actinobacterium</i>		
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	Ellin6055	0.21
				<i>uncultured bacterium</i>	0.22
	<i>Tistrellales</i>	<i>Geminicoccaceae</i>	<i>Candidatus Alysiosphaera</i>	0.29	
Control & Root+Shoot					
<i>Gemmatimonadetes</i>	S0134 terrestrial group	<i>uncultured bacterium</i>			0.14
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	NB1-j	<i>uncultured bacterium</i>		0.17
	<i>Gammaproteobacteria</i>	PLTA13	<i>uncultured bacterium</i>		0.14
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacterales</i>	<i>Chthoniobacteraceae</i>	<i>Chthoniobacter</i>	0.56
Control					
<i>Acidobacteria</i>	<i>Thermoanaerobaculia</i>	<i>Thermoanaerobaculales</i>	<i>Thermoanaerobaculaceae</i>	Subgroup 10	0.15
<i>Chloroflexi</i>	<i>Anaerolineae</i>	<i>Caldilineales</i>	<i>Caldilineaceae</i>	<i>Litorilinea</i>	0.12
<i>Gemmatimonadetes</i>	AKAU4049	<i>uncultured bacterium</i>			0.23
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmatales</i>	<i>Gemmataceae</i>	<i>Gemmata</i>	0.20
				<i>uncultured bacterium</i>	0.47
		<i>Pirellulales</i>	<i>Pirellulaceae</i>	Pir4 lineage	0.18
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Novosphingobium</i>	0.13
		<i>Tistrellales</i>	<i>Geminicoccaceae</i>	<i>uncultured bacterium</i>	0.15
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Opitutales</i>	<i>Opitutaceae</i>	<i>Opitutus</i>	0.19

Table S8: The core microbiome and responders of the soil inhabiting bacterial community analyzed at the end of the incubation experiment grouped by soil N level (for N1 n=12, for N2 n=11).

Phylum	Class	Order	Family	Genus	Relative abundance in %
Core Microbiome					
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	<i>Pyrinomonadales</i>	<i>Pyrinomonadaceae</i>	RB41	1.01
	<i>Holophagae</i>	Subgroup 7	uncultured bacterium		0.29
	<i>Subgroup 6</i>	metagenome			0.27
		uncultured <i>Acidobacteria</i> bacterium			2.42
		uncultured <i>Acidobacteriales</i> bacterium			0.22
		uncultured bacterium			1.77
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Actinomarinales</i>	uncultured bacterium		0.54
		IMCC26256	uncultured bacterium		0.24
		<i>Microtrichales</i>	<i>Iamiaceae</i>	<i>Iamia</i>	0.55
			<i>Ilumatobacteraceae</i>	<i>Ilumatobacter</i>	0.23
			<i>Ilumatobacteraceae</i>	uncultured bacterium	0.69
			uncultured bacterium		0.23
	<i>Actinobacteria</i>	<i>Corynebacteriales</i>	<i>Mycobacteriaceae</i>	<i>Mycobacterium</i>	0.16
		<i>Frankiales</i>	<i>Geodermatophilaceae</i>	<i>Blastococcus</i>	1.54
			<i>Sporichthyaceae</i>	uncultured bacterium	0.31
		<i>Micrococcales</i>	<i>Intrasporangiaceae</i>	<i>Intrasporangium</i>	0.36
				<i>Tetrasphaera</i>	0.20
			uncultured bacterium		0.67
			<i>Microbacteriaceae</i>	<i>Agromyces</i>	1.48
			<i>Micrococcaceae</i>	<i>Pseudarthrobacter</i>	0.65
			uncultured bacterium		0.25
		<i>Micromonosporales</i>	<i>Micromonosporaceae</i>	<i>Micromonospora</i>	0.87
		<i>Propionibacteriales</i>	<i>Nocardioideaceae</i>	<i>Aeromicrobium</i>	0.31
				<i>Marmoricola</i>	0.35
			<i>Nocardioides</i>		2.03
			<i>Propionibacteriaceae</i>	uncultured bacterium	0.26
	<i>Pseudonocardiales</i>	<i>Pseudonocardaceae</i>	<i>Pseudonocardia</i>	0.16	
	<i>Streptomycetales</i>	<i>Streptomycetaceae</i>	<i>Streptomyces</i>	0.56	
	MB-A2-108	uncultured bacterium			1.87
<i>Rubrobacteria</i>	<i>Rubrobacterales</i>	<i>Rubrobacteriaceae</i>	<i>Rubrobacter</i>	0.60	
<i>Thermoleophilia</i>	<i>Gaiellales</i>	<i>Gaiellaceae</i>	<i>Gaiella</i>	3.08	
		uncultured <i>actinobacterium</i>		0.18	
		uncultured bacterium		3.67	

		<i>Solirubrobacterales</i>	67-14	uncultured bacterium	1.53
			<i>Solirubrobacteraceae</i>	<i>Solirubrobacter</i>	0.48
			uncultured bacterium		0.27
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>Chthonomonadales</i>	uncultured bacterium		0.66
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Cytophagales</i>	<i>Microscillaceae</i>	uncultured bacterium	0.45
	<i>Anaerolineae</i>	<i>Caldilineales</i>	<i>Caldilineaceae</i>	uncultured bacterium	0.54
		<i>Chloroflexales</i>	<i>Herpetosiphonaceae</i>	<i>Herpetosiphon</i>	0.24
			<i>Roseiflexaceae</i>	uncultured bacterium	0.61
	<i>Chloroflexia</i>	<i>Thermomicrobiales</i>	JG30-KF-CM45	metagenome	0.30
				uncultured bacterium	2.72
				uncultured <i>Chloroflexi</i> bacterium	1.98
	<i>Dehalococcoidia</i>	S085	uncultured bacterium		0.34
<i>Chloroflexi</i>	Gitt-GS-136	uncultured bacterium			3.89
		uncultured <i>Chloroflexus</i> sp.			0.35
	JG30-KF-CM66	uncultured bacterium			0.19
	KD4-96	metagenome			0.48
		uncultured <i>Anaerolineaceae</i> bacterium			0.55
		uncultured bacterium			3.08
		uncultured <i>Chloroflexi</i> bacterium			1.05
	<i>Ktedonobacteria</i>	C0119	uncultured bacterium		0.91
	TK10	uncultured bacterium			0.31
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillales</i>	<i>Bacillaceae</i>	<i>Bacillus</i>	1.38
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonadales</i>	<i>Gemmatimonadaceae</i>	<i>Gemmatimonas</i>	0.71
				uncultured bacterium	1.65
<i>Latescibacteria</i>	uncultured bacterium				0.20
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>Saccharimonadales</i>	uncultured bacterium		1.31
			uncultured soil bacterium		0.30
	OM190	uncultured bacterium			0.35
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>Tepidisphaerales</i>	WD2101 soil group	uncultured bacterium	1.61
				uncultured planctomycete	0.65
	<i>Planctomycetacia</i>	<i>Pirellulales</i>	<i>Pirellulaceae</i>	<i>Pirellula</i>	0.54
	<i>Alphaproteobacteria</i>	<i>Caulobacterales</i>	<i>Caulobacteraceae</i>	<i>Brevundimonas</i>	0.61
		<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Altererythrobacter</i>	3.75
				<i>Sphingomonas</i>	1.86
		<i>Tistrellales</i>	<i>Geminicoccaceae</i>	<i>Candidatus Alysiosphaera</i>	0.29
	<i>Deltaproteobacteria</i>	<i>Myxococcales</i>	<i>Haliangiaceae</i>	<i>Haliangium</i>	0.37
			NB1-j	uncultured bacterium	

	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>	<i>Massilia</i>	0.79	
			<i>Burkholderiaceae</i>	uncultured bacterium	0.30	
		<i>Nitrosomonadales</i>	<i>Nitrosomonadaceae</i>	MND1	0.51	
	<i>Gammaproteobacteria</i>	<i>Gammaproteobacteria Incertae Sedis</i>		Unknown Family	<i>Acidibacter</i>	0.18
			<i>Pseudomonadales</i>	<i>Pseudomonadaceae</i>	<i>Pseudomonas</i>	3.64
			<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Lysobacter</i>	1.31
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacterales</i>	<i>Xiphinematobacteraceae</i>	<i>Candidatus Xiphinematobacter</i>	0.89	
		<i>Pedosphaerales</i>	<i>Pedosphaeraceae</i>	uncultured bacterium	0.43	
		<i>Verrucomicrobiales</i>	<i>Rubritaleaceae</i>	<i>Luteolibacter</i>	0.71	
Responders						
N1						
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	<i>Blastocatellales</i>	<i>Blastocatellaceae</i>	uncultured bacterium	0.34	
	<i>Thermoanaerobaculia</i>	<i>Thermoanaerobaculales</i>	<i>Thermoanaerobaculaceae</i>	Subgroup 10	0.15	
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Chitinophagales</i>	<i>Chitinophagaceae</i>	uncultured bacterium	0.27	
		<i>Cytophagales</i>	<i>Hymenobacteraceae</i>	<i>Adhaeribacter</i>	0.17	
<i>Gemmatimonadetes</i>	AKAU4049			uncultured bacterium	0.23	
	<i>Longimicrobia</i>	<i>Longimicrobiales</i>	<i>Longimicrobiaceae</i>	uncultured bacterium	0.21	
	S0134 terrestrial group			uncultured bacterium	0.14	
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospirales</i>	<i>Nitrospiraceae</i>	<i>Nitrospira</i>	0.13	
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmatales</i>	<i>Gemmataceae</i>	<i>Gemmata</i>	0.20	
				uncultured bacterium	0.47	
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacterales</i>	<i>Caulobacteraceae</i>	<i>Phenylobacterium</i>	0.14	
		<i>Rhizobiales</i>	<i>Devosiaceae</i>	<i>Devosia</i>	0.15	
			<i>Xanthobacteraceae</i>	uncultured bacterium	0.13	
		<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	Ellin6055	0.21	
				<i>Novosphingobium</i>	0.13	
				<i>Sphingobium</i>	0.31	
	uncultured bacterium	0.22				
	<i>Gammaproteobacteria</i>	PLTA13		uncultured bacterium	0.14	
<i>Xanthomonadales</i>		<i>Xanthomonadaceae</i>	<i>Luteimonas</i>	0.22		
<i>Rokubacteria</i>	NC10	<i>Rokubacterales</i>	uncultured bacterium	0.27		
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacterales</i>	<i>Chthoniobacteraceae</i>	<i>Chthoniobacter</i>	0.56	
N2						
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacterales</i>	67-14	uncultured <i>Rubrobacteria</i> bacterium	0.13	
			<i>Solirubrobacteraceae</i>	<i>Conexibacter</i>	0.15	

<i>Chloroflexi</i>	<i>Anaerolineae</i>	SBR1031	A4b	uncultured bacterium	0.23
	<i>Chloroflexia</i>	<i>Kallotenuales</i>	AKIW781	uncultured bacterium	0.19
	Gitt-GS-136	uncultured <i>Anaerolineae</i> bacterium			0.16
<i>Patescibacteria</i>	<i>Parcubacteria</i>	uncultured bacterium			0.22