

Microbial community composition in the rhizosphere of *Larix decidua* under different light regimes with additional focus on methane cycling microorganisms

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Supplementary Information

Supplementary Information Fig. S1-S7

Supplementary Information Table S1+S2

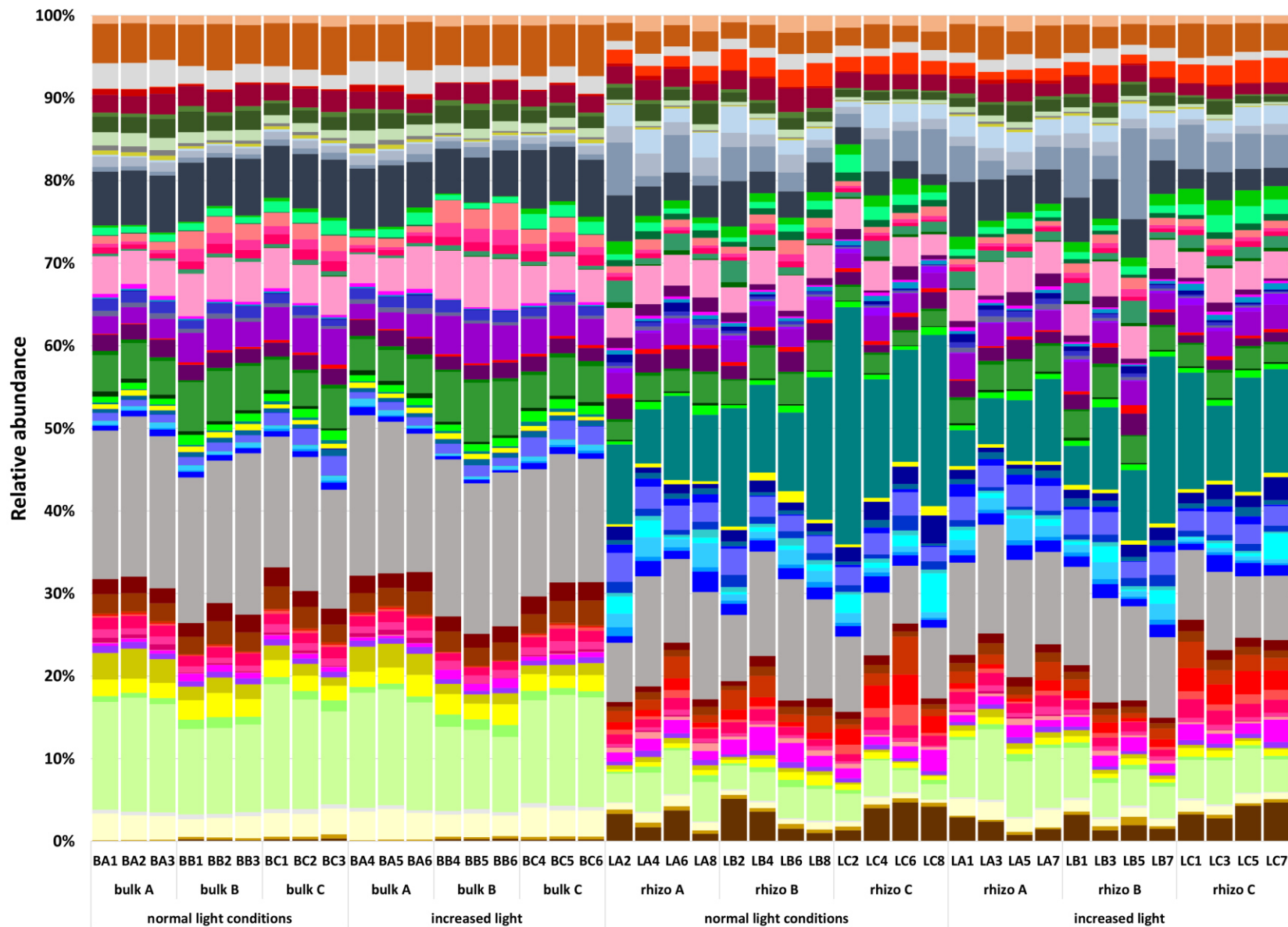


Figure S1: Community composition of prokaryotes on genus level representing most abundant genera (98% of relative abundance) in bulk and rhizosphere (rhizo) soils at normal and increased light conditions. A,B,C represent the replicate forest sites. BA, BB, BC stand for bulk soils on site replicate A, B and C. LA, LB, LC stand for rhizosphere soil of *L. decidua* (L) on site replicate A, B and C.

Phylum	Class	Order	Family	Genus		
Verrucomicrobia	Subdivision3	Subdivision3 unclassified	Subdivision3 unclassified	Subdivision3 unclassified		
	Spartobacteria	Spartobacteria unclassified	Spartobacteria unclassified	Spartobacteria unclassified		
	Proteobacteria unclassified	Proteobacteria unclassified	Proteobacteria unclassified	Proteobacteria unclassified		
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	<i>Steroidobacter</i> spp.		
		Gammaproteobacteria unclassified	Gammaproteobacteria unclassified	Sinobacteraceae unclassified		
	Deltaproteobacteria	Myxococcales	Polyangiaceae	Gammaproteobacteria unclassified	Gammaproteobacteria unclassified	
			Myxococcales unclassified	Polyangiaceae unclassified	Polyangiaceae unclassified	
	Betaproteobacteria	Deltaproteobacteria unclassified	Rhodocyclales	Rhodocyclaceae	Myxococcales unclassified	
			Nitrosomonadales	Nitrosomonadaceae	Deltaproteobacteria unclassified	
		Burkholderiales	Comamonadaceae	Rhodocyclaceae unclassified	Rhodocyclaceae unclassified	
			Burkholderiaceae	Burkholderiaceae unclassified	<i>Nitrospira</i> spp.	
	Alphaproteobacteria	Betaproteobacteria unclassified	Sphingomonadales	Sphingomonadaceae	Comamonadaceae unclassified	
				Burkholderia spp.	Burkholderiaceae unclassified	
		Rhodospirillales	Rhodospirillales unclassified	Rhodospirillaceae	Betaproteobacteria unclassified	Betaproteobacteria unclassified
				Reyranella	Sphingomonadaceae unclassified	<i>Sphingomonas</i> spp.
				Acetobacteraceae	Rhodospirillaceae unclassified	Sphingomonadaceae unclassified
				Xanthobacteraceae	Reyranella unclassified	<i>Rhizorhabdus</i> spp.
		Rhizobiales	Rhizobiales unclassified	Rhizobiaceae	Acetobacteraceae unclassified	Rhodospirillales unclassified
				Phyllobacteriaceae	<i>Labrys</i> spp.	Rhodospirillaceae unclassified
				Hypomicrobiaceae	Rhizobiales unclassified	Reyranella unclassified
Bradyrhizobiaceae				<i>Rhizobium</i> spp.	Acetobacteraceae unclassified	
Caulobacteraceae	Phyllobacteriaceae unclassified			<i>Labrys</i> spp.		
Alphaproteobacteria unclassified	Alphaproteobacteria unclassified			Rhizobiales unclassified		
Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	<i>Rhizobium</i> spp.		
			Planctomycetaceae unclassified	Planctomycetaceae unclassified	<i>Mesorhizobium</i> spp.	
Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	<i>Rhodomicrobium</i> spp.		
Candidatus Saccharibacteria	Candidatus Saccharibacteria	Candidatus Saccharibacteria unclassified	Candidatus Saccharibacteria unclassified	<i>Pedomicrobium</i> spp.		
Candidate division WPS-1	Candidate division WPS-1	Candidate division WPS-1 unclassified	Candidate division WPS-1 unclassified	<i>Hyphomicrobium</i> spp.		
Bacteroidetes	Sphingobacteria	Sphingobacteriales	Sphingobacteriaceae	<i>Devosia</i> spp.		
			Chitinophagaceae	<i>Bradyrhizobium</i> spp.		
	Flavobacteriia	Flavobacteriales	Cytophagales	Cryomorpaceae	<i>Phenylobacterium</i> spp.	
				Ohtaekwangia	Alphaproteobacteria unclassified	
				Cytophagaceae	<i>Singulisphaera</i> spp.	
				Chryseolinea	Planctomycetaceae unclassified	
	Cytophagia	Bacteroidetes unclassified	Bacteroidetes unclassified	Bacteroidetes unclassified	<i>Pirellula</i> spp.	
				Bacteroidetes unclassified	<i>Gemmatimonas</i> spp.	
	Bacteria unclassified	Bacteria unclassified	Bacteria unclassified	Bacteria unclassified	Candidatus Saccharibacteria unclassified	
	Actinobacteria	Actinobacteria	Actinobacteria unclassified	Actinobacteria unclassified	Candidate division WPS-1 unclassified	
Gaiellales				Gaiellales	<i>Mucilaginibacter</i> spp.	
Actinomycetales				Streptomycetaceae	<i>Terrimonas</i> spp.	
Actinobacteria unclassified		Actinobacteria unclassified	Actinobacteria unclassified	Nocardoidaceae	<i>Ferruginibacter</i> spp.	
				Mycobacteriaceae	Chitinophagaceae unclassified	
				Micromonosporaceae	<i>Chitinophaga</i> spp.	
				Microbacteriaceae	<i>Fluviicola</i> spp.	
				Actinospicaceae	Ohtaekwangia unclassified	
Actinobacteria unclassified		Actinobacteria unclassified	Actinobacteria unclassified	Actinomycetales unclassified	Cytophagaceae unclassified	
				Actinomycetales unclassified	Chryseolinea unclassified	
				Actinomycetales unclassified	Bacteroidetes unclassified	
Acidobacteria	Acidobacteria Gp17	Acidobacteria Gp16	Acidobacteria Gp17 unclassified	Bacteria unclassified		
				Acidobacteria Gp16 unclassified	Actinobacteria unclassified	
				Acidobacteria Gp7 unclassified	Gaiella spp.	
				Acidobacteria Gp6 unclassified	Streptomycetaceae unclassified	
				Acidobacteria Gp5 unclassified	<i>Streptomyces</i> spp.	
				Acidobacteria Gp4 unclassified	<i>Kribbella</i> spp.	
				Granulicella unclassified	<i>Mycobacterium</i> spp.	
				Acidobacteria Gp1 unclassified	Micromonosporaceae unclassified	
				Acidobacteria Gp1 unclassified	<i>Agromyces</i> spp.	
				Acidobacteria Gp1 unclassified	<i>Actinospica</i> spp.	
Acidobacteria Gp1 unclassified	Actinomycetales unclassified					
Acidobacteria Gp1 unclassified	Actinomycetales unclassified					
Acidobacteria Gp17 unclassified	Acidimicrobiales unclassified					
Acidobacteria Gp16 unclassified	Acidimicrobiales unclassified					
Acidobacteria Gp7 unclassified	Acidimicrobiales unclassified					
Acidobacteria Gp6 unclassified	Acidimicrobiales unclassified					
Acidobacteria Gp5 unclassified	Acidimicrobiales unclassified					
Acidobacteria Gp4 unclassified	Acidimicrobiales unclassified					
Acidobacteria Gp1 unclassified	Acidimicrobiales unclassified					

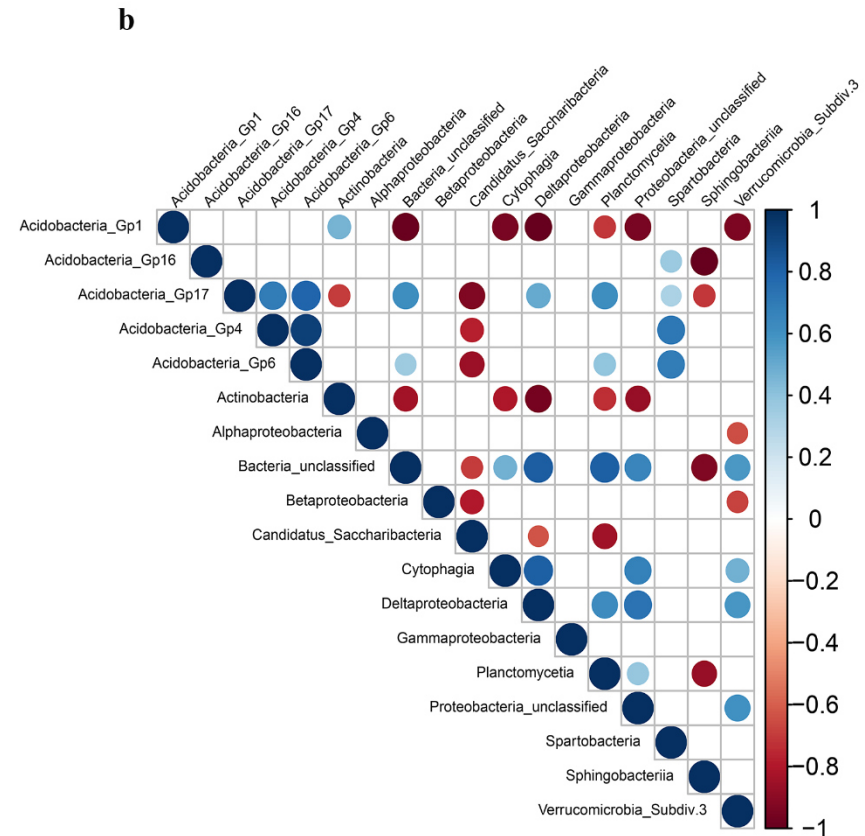
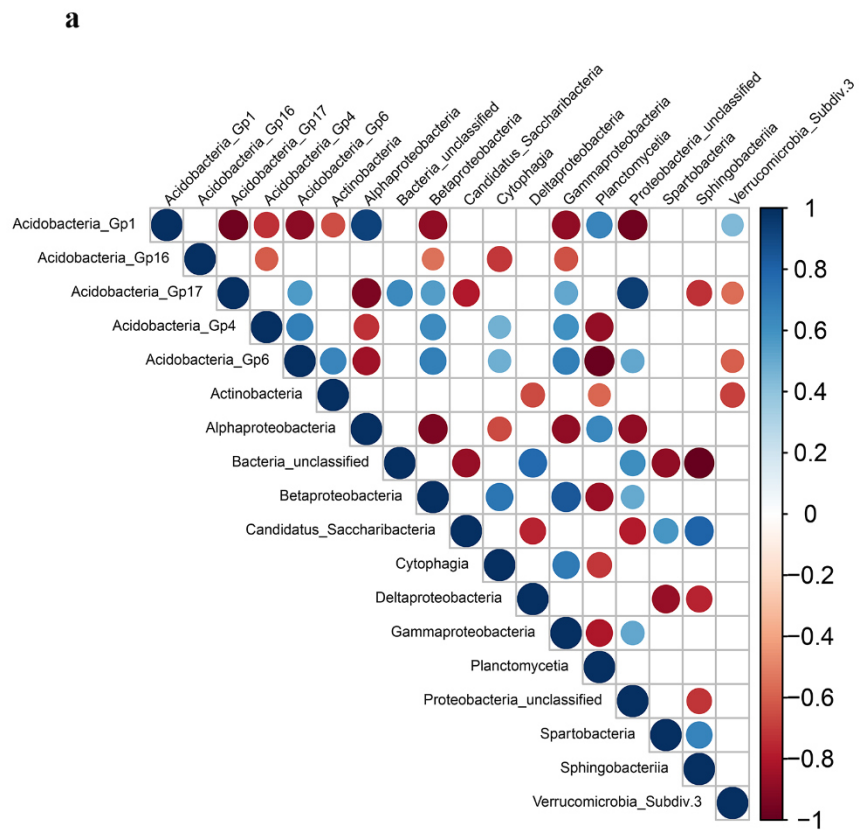


Figure S2: Spearman's rank correlation matrix of bacterial classes in bulk (a) and rhizosphere (b) soils. Strong correlations are indicated by large circles and weak correlations are indicated by small circles. The colours of the scale bar denote the nature of the correlation with 1 indicating perfect positive correlation (dark blue) and -1 indicating perfect negative correlation (dark red) between two bacterial classes. Only significant correlations are shown ($p < 0.05$).

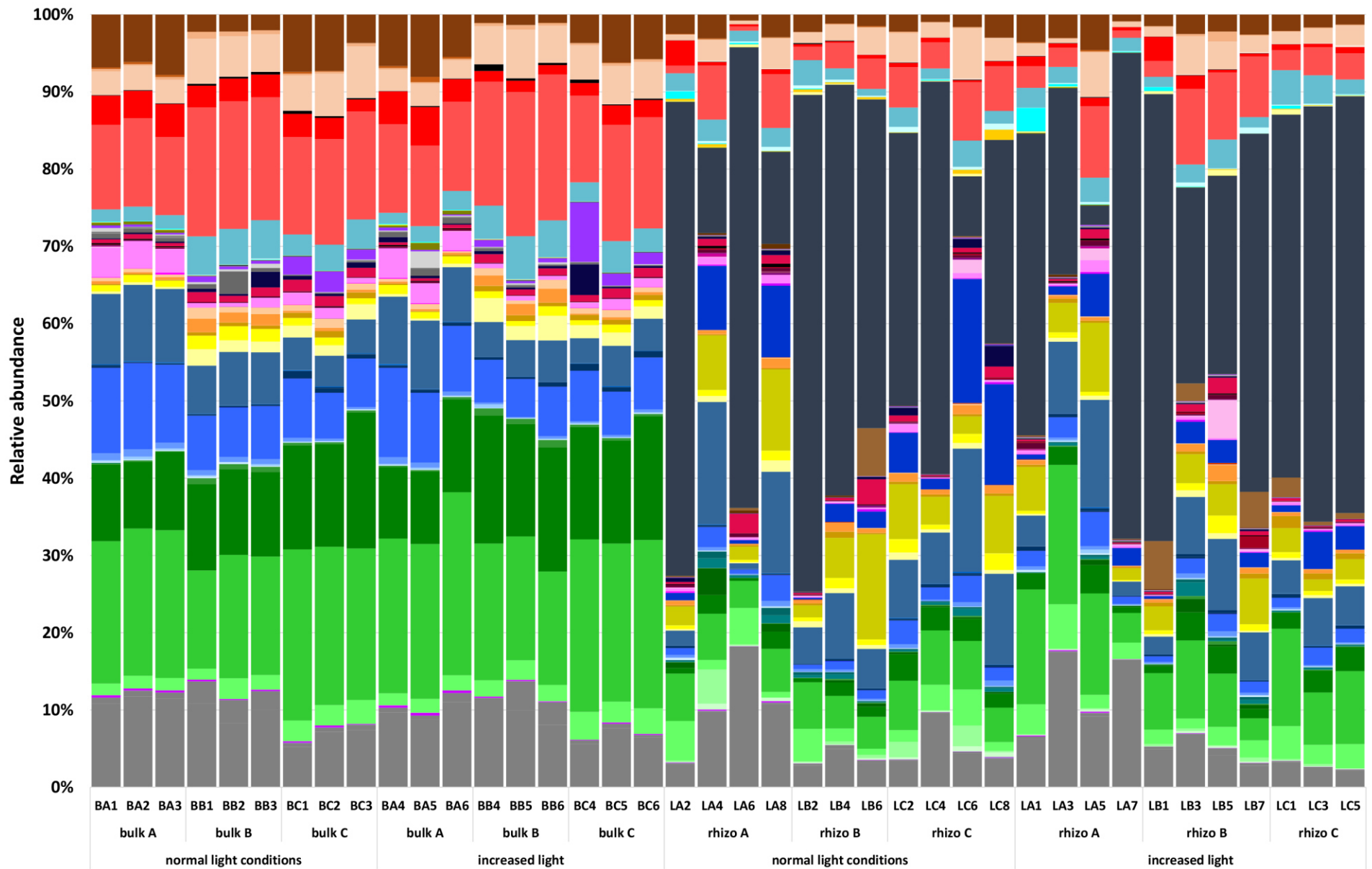


Figure S3: Community composition of fungi on genus level representing most abundant genera (99% of relative abundance) in bulk and rhizosphere (rhizo) soils at normal and increased light conditions. A,B,C represent the replicate forest sites. BA, BB, BC stand for bulk soils on site replicate A, B and C. LA, LB, LC stand for rhizosphere soil of *L. decidua* (L) on site replicate A, B and C. LB8 and LC7 were excluded for the description of the fungal community composition as the samples did not meet the quality requirements.

Phylum	Class	Order	Family	Genus			
Zygomycota	Zygomycota class Incertae sedis	Mucorales	Umbelopsidaceae	<i>Umbelopsis</i> spp.			
			Mucoraceae	<i>Mucor</i> spp. Mucoraceae unclassified			
		Mortierellales	Mortierellaceae	<i>Mortierella</i> spp.			
		Kickxellales	Kickxellaceae	<i>Ramicandelaber</i> spp.			
Basidiomycota	Basidiomycota unclassified	Basidiomycota unclassified	Basidiomycota unclassified	Basidiomycota unclassified			
			Wallemiomycetes	Geminibasidiales	Geminibasidiaceae	<i>Geminibasidium</i> spp.	
	Tremellomycetes	Filobasidiales	Filobasidiaceae	<i>Cryptococcus</i> spp.			
	Microbotryomycetes	Sporidiobolales	unclassified Sporidiobolales	unclassified Sporidiobolales			
			Sporidiobolales family Incertae sedis	<i>Rhodotorula</i> spp.			
	Agaricostilbomycetes	Agaricostilbales	Chionosphaeraceae	<i>Kurtzmanomyces</i> spp.			
			Trechisporales	unclassified Trechisporales	unclassified Trechisporales		
			Thelephorales	Hydnodontaceae	<i>Trechispora</i> spp.		
				Thelephoraceae	<i>Tomentella</i> spp.		
				Sebacinales	Sebacinaceae unclassified		
			Boletales	Suillaceae	<i>Suillus</i> spp.		
				Gomphidiaceae	unclassified Gomphidiaceae		
			Auriculariales	unclassified Auriculariales	unclassified Auriculariales		
				Agaricales	Agaricales unclassified	Agaricales unclassified	
						Tricholomataceae	unclassified Tricholomataceae
						Mycenaceae	Mycenaceae unclassified
						Inocybaceae	<i>Inocybe</i> spp.
						Hygrophoraceae	<i>Hygrocybe</i> spp.
				Agaricaceae	<i>Echinoderma</i> spp.		
				Agaricomycetes unclassified	Agaricomycetes unclassified		
	Ascomycota	Ascomycota unclassified	Ascomycota unclassified	Ascomycota unclassified	Ascomycota unclassified		
				Xylariales	Hyponectriaceae	unclassified Hyponectriaceae	
				Amphisphaeriaceae	unclassified Amphisphaeriaceae		
Sordariales unclassified				Sordariales unclassified			
Hypocreales unclassified				Hypocreales unclassified	Hypocreales unclassified	Hypocreales unclassified	
					<i>Stachybotrys</i> spp.		
Hypocreales family Incertae sedis				Hypocreales family Incertae sedis	<i>Ilyonectria</i> spp.		
					<i>Acremonium</i> spp.		
						<i>Hypocrea</i> spp.	
						Hypocreaceae unclassified	
						Cordycipitaceae unclassified	
						Cordycipitaceae	<i>Metarhizium</i> spp.
Pezizomycetes				Pezizales	Pyronemataceae	<i>Wilcoxina</i> spp.	
	Leotiomycetes order Incertae sedis	<i>Meliniomyces</i> spp.					
			<i>Leohumicola</i> spp.				
			Helotiales unclassified	Helotiales unclassified			
			Leotiomycetes unclassified	<i>Leptodontidium</i> spp.			
			Eurotiales	Eurotiales	Dermateaceae unclassified	<i>Cadophora</i> spp.	
					Leotiomycetes unclassified	Dermateaceae unclassified	
						Trichocomaceae unclassified	
						<i>Penicillium</i> spp.	
						<i>Paecilomyces</i> spp.	
						Chaetothyriales unclassified	Chaetothyriales unclassified
						<i>Exophiala</i> spp.	
						Herpotrichiellaceae unclassified	<i>Cladophialophora</i> spp.
			Herpotrichiellaceae unclassified				
			Eurotiomycetes unclassified	Eurotiomycetes unclassified			
			<i>Phoma</i> spp.				
			Pleosporales family Incertae sedis unclassified				
			Pleomassariaceae unclassified				
			<i>Cenococcum</i> spp.				
			unclassified Pseudeurotiaceae				
			<i>Oidiodendron</i> spp.				
			Myxotrichaceae unclassified				
			<i>Aureobasidium</i> spp.				
			Davidiellaceae unclassified				
			<i>Tetrachaetum</i> spp.				
			<i>Chalara</i> spp.				
			Ascomycota class Incertae sedis	Ascomycota family Incertae sedis			
Fungi unclassified	Fungi unclassified	Fungi unclassified	Fungi unclassified	Fungi unclassified			

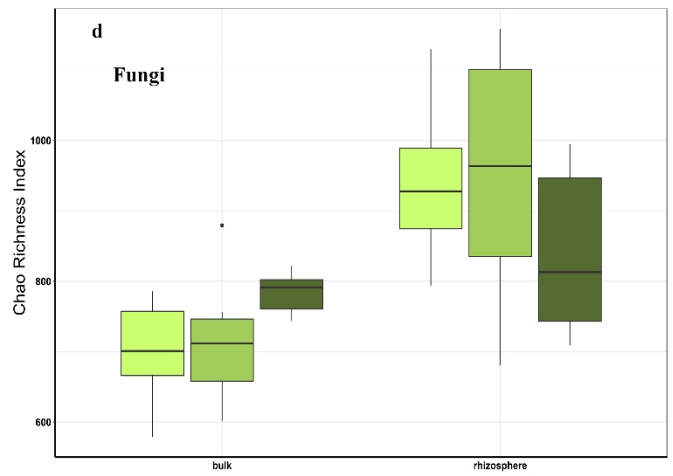
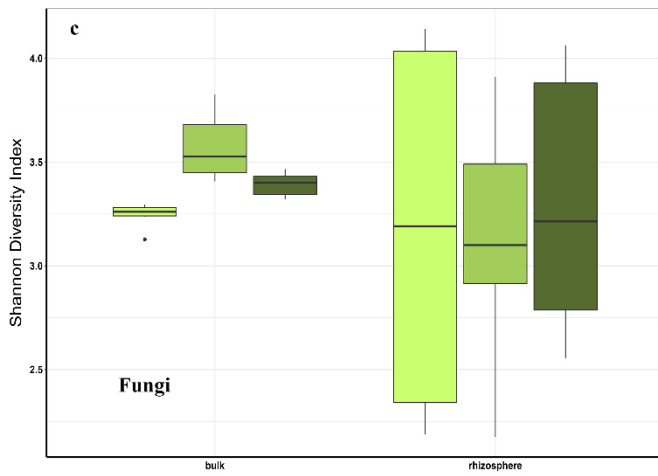
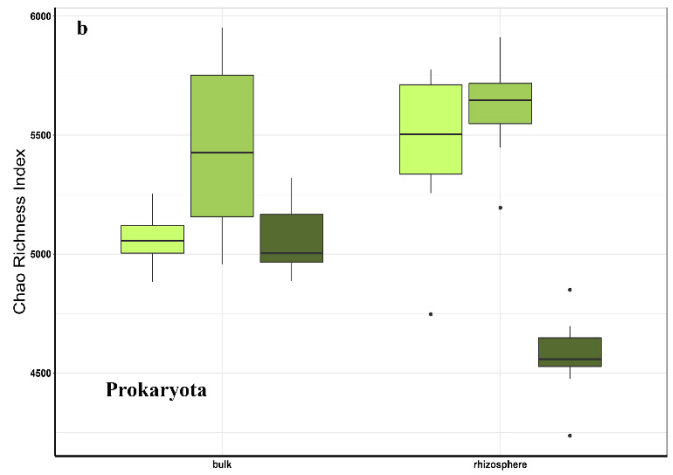
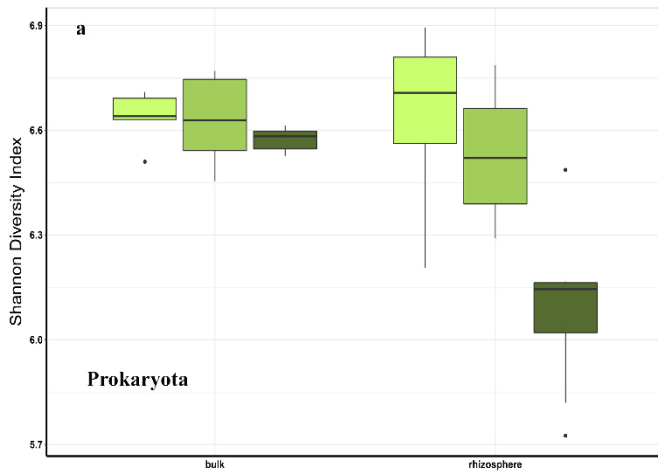


Figure S4: Shannon–Wiener Diversity Index (H') (a) and Chao Richness Index (b) of prokaryotic communities and Shannon–Wiener Diversity Index (H') (c) and Chao Richness Index (d) of fungal communities in all bulk and rhizosphere soils of *Larix decidua* (L). The different green colors refer to the replicate sites (A, B, C) in the forest. Boxes represent 25–75% of values, black lines medians ($n = 3$), and whiskers 1.5 interquartile ranges.

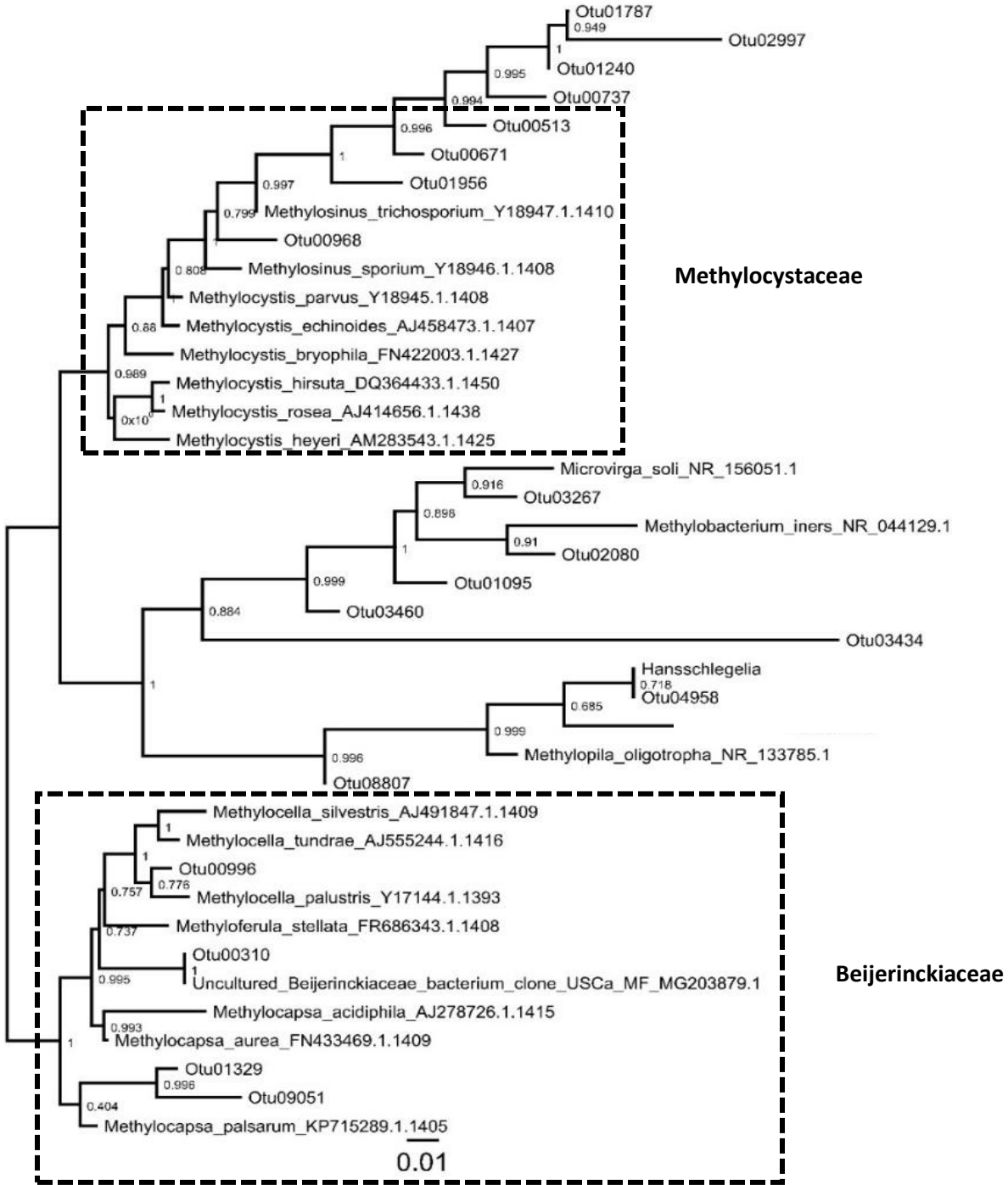


Figure S5: Unrooted Maximum likelihood tree (PhyML) showing the relationship between selected OTUs that were classified as ‘Rhizobiales unclassified’ as the highest taxonomic resolution and selected reference methanotrophs (and methylotrophic species) within Alphaproteobacteria known from the literature and a reconstructed draft genome of the uncultivated upland soil cluster α (USC α) methanotroph (Pratscher et al., 2018). The scale bar represents 1% nucleotide substitution per site and numbers at nodes of the tree indicate Chi2 values.

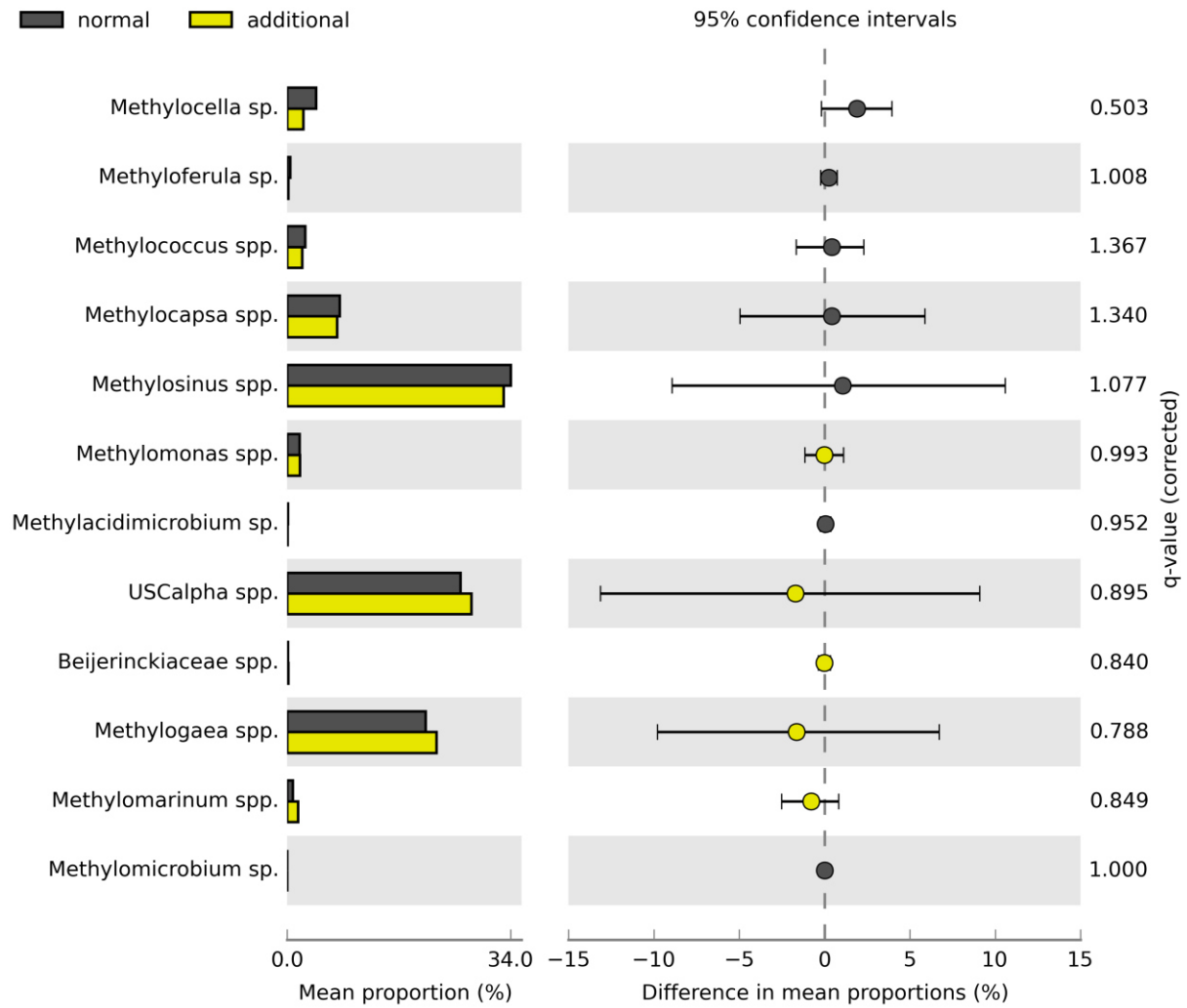
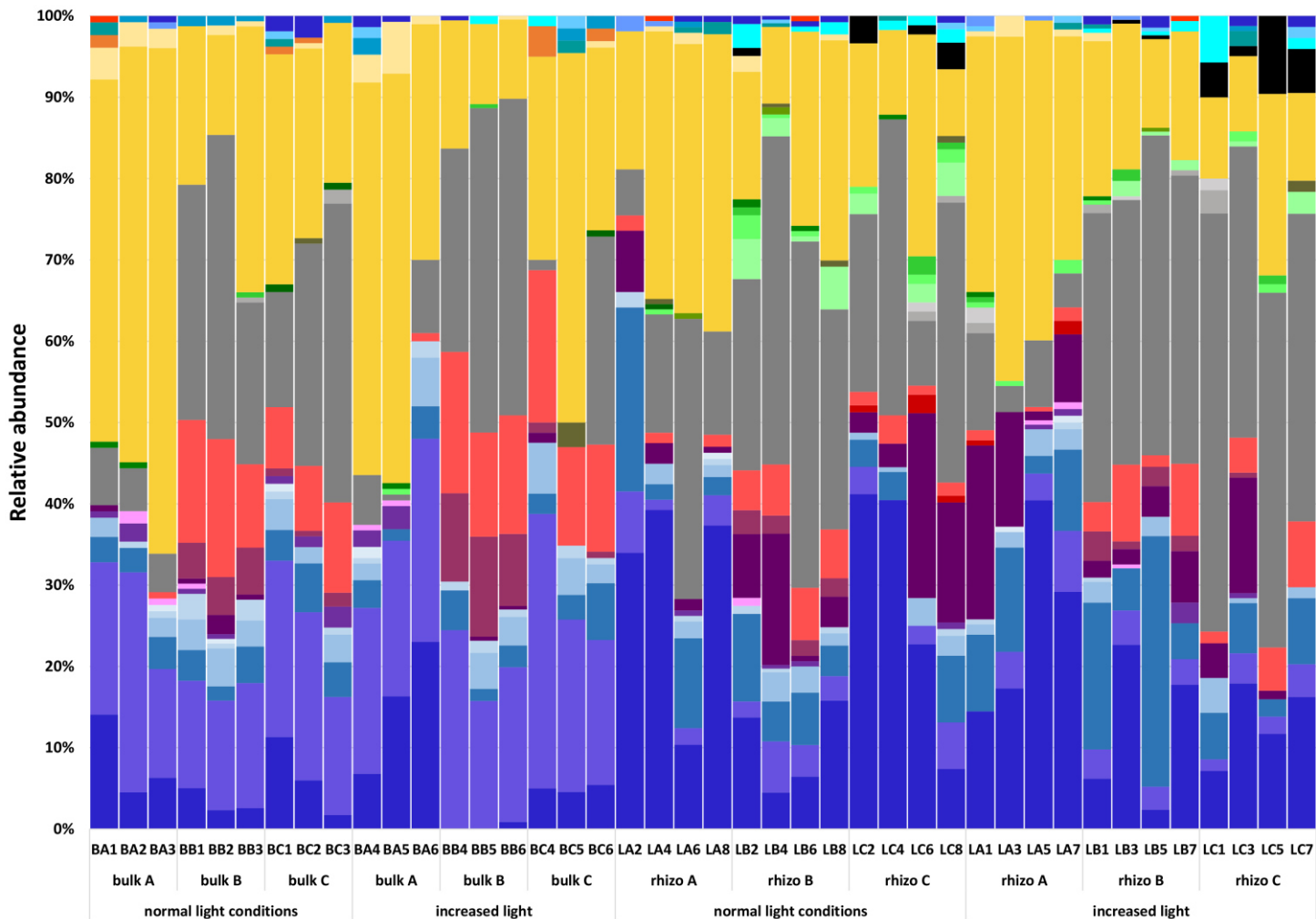


Figure S6: Extended error bar plot showing mean proportions [%] of methanotrophic genera in rhizosphere soils of *L. decidua* and the respective differences in mean proportions [%] according to normal (grey) and additional (yellow) light conditions. q-values are adjusted p-values following Benjamini-Hochberg method for multiple test correction.



Order	Family	Genus	Order	Family	Genus
Verrucomicrobia	unclassified Verrucomicrobia	<i>Methylacidimicrobium</i> sp. (Otu08201)	Rhizobiales	Beijerinckiaceae	USCα Beijerinckiaceae cluster (Otu06160)
Methylococales	Methylococcaceae	<i>Methylomonas</i> sp. (Otu03260)			USCα Beijerinckiaceae cluster (Otu04834)
		<i>Methylomonas</i> sp. (Otu07875)			USCα Beijerinckiaceae cluster (Otu00310)
		<i>Methylomonas</i> sp. (Otu06015)			<i>Methylotella</i> sp. (Otu00996)
		<i>Methylomonas</i> sp. (Otu04993)			<i>Methylocapsa</i> sp. (Otu09051)
		<i>Methylomonas</i> sp. (Otu04444)			<i>Methylocapsa</i> sp. (Otu01445)
		<i>Methylomonas</i> sp. (Otu03413)			<i>Methylocapsa</i> sp. (Otu01329)
		<i>Methylomicrobium</i> sp. (Otu06027)			Beijerinckiaceae (Otu07689)
		<i>Methylomarinum</i> sp. (Otu03685)			<i>Methyloferula</i> sp. (Otu04528)
		<i>Methylogaea</i> sp. (Otu02547)		Methylocystaceae	<i>Methylosinus</i> sp. (Otu06414)
		<i>Methylogaea</i> sp. (Otu00163)			<i>Methylosinus</i> sp. (Otu02756)
		<i>Methylococcus</i> sp. (Otu12861)			<i>Methylosinus</i> sp. (Otu01956)
		<i>Methylococcus</i> sp. (Otu07827)			<i>Methylosinus</i> sp. (Otu00968)
		<i>Methylococcus</i> sp. (Otu07764)			<i>Methylosinus</i> sp. (Otu00671)
		<i>Methylococcus</i> sp. (Otu07643)			<i>Methylosinus</i> sp. (Otu00513)
		<i>Methylococcus</i> sp. (Otu07070)			
		<i>Methylococcus</i> sp. (Otu05641)			
		<i>Methylococcus</i> sp. (Otu03759)			
		<i>Methylococcus</i> sp. (Otu02779)			

Figure S7: Community composition of methanotrophs on OTU level in bulk and rhizosphere (rhizo) soils at normal and increased light conditions. A,B,C represent the replicate forest sites. BA, BB, BC stand for bulk soils on site replicate A, B and C. LA, LB, LC stand for rhizosphere soil of *L. decidua* (L) on site replicate A, B and C. OTU, operational taxonomic unit.

Table S1: Prokaryotic and fungal community description with dominant phyla, classes, orders and families including the respective relative abundances [%] both, in bulk and rhizosphere soils. Significant differences regarding dominant phyla, classes, families and species are indicated in blue (bulk) and red (rhizosphere). Black colors point to no significant differences between bulk and rhizosphere soils. 1) Abundances are given in the order: bulk, rhizosphere, 2) Significant differences regarding dominant phyla, classes, families and species are indicated in blue (bulk) and red (rhizosphere). Black colors point to no significant differences between bulk and rhizosphere soils.

Domain or kingdom	dominant phyla	relative abundance [%] ^{1, 2)}	dominant class	class abundance [%] ^{1, 2)}	dominant order	order abundance [%] ^{1, 2)}	dominant family ²⁾	dominant or exclusive species ²⁾		
Bacteria	Proteobacteria	34, 37.3	α -Proteobacteria	17, 18	Rhizobiales	9.9, 10.1	Bradyrhizobiaceae	<i>Bradyrhizobium</i> sp.		
							Hyphomicrobiaceae	<i>Pedomicrobium</i> sp.		
							Rhizobiaceae	<i>Rhizobium</i> sp.		
							Rhodospirillales	3.7, 3.8	Acetobacteriaceae	<i>Acidocella</i> sp.
							Rhodospirillaceae	<i>Inquillus</i> sp.		
							Sphingomonadales	1.3, 2.3	Erythrobacteraceae, Sphingomonadaceae	<i>Altererythrobacter</i> sp.
			β -Proteobacteria	8, 10	Burkholderiales	1.9, 6.5	Burkholderiaceae	<i>Burkholderia</i> sp.		
							Comamonadaceae			
							Oxalobacteraceae			
			γ -Proteobacteria	3.6, 5.4	Xanthomonadales	1.4, 3.4	Xanthomonadaceae	<i>Rhodanobacter</i> sp., <i>Pseudoxanthomonas</i> sp.		
							Sinobacteraceae	<i>Steroidobacter</i> sp.		
			Acidobacteria	22.2, 11.6	δ -Proteobacteria	3.5, 2.4	Myxococcales	2.3, 1.5	Acidobacteria_Gp6	10.6, 3.9
									Acidobacteria_Gp4	2.6, 0.9
									Acidobacteria_Gp1	0.1, 2.3
Acidobacteria_Gp16	1.8, 0.6									
Acidobacteria_Gp17	1.7, 0.4									
Bacteria unclassified	15.1, 8.8	Bacteria unclassified							15, 9	
Actinobacteria	9.8, 11.0	Actinobacteria	9, 10.6	Actinomycetales	4.2, 8.2	Streptomycetaceae	<i>Streptomyces</i> sp.			
						Mycobacteriaceae	<i>Mycobacterium</i> sp.			
						Micromonosporaceae	<i>Actinoplanes</i> sp.			
						Nocardiodaceae	<i>Nocardioides</i> sp., <i>Kribbella</i> sp.			
						Gaiellales	2.1, 0.8	Gaiellaceae	<i>Gaiella</i> sp.	
						Acidimicrobiales	1.1, 0.7	Acidimicrobiaceae	<i>Ilumatobacter</i> sp.	
						Bacteroidetes	3.6, 10.17	Sphingobacteriia	2, 6	Sphingobacteriales
Sphingobacteriaceae	<i>Mucilaginibacter</i> sp.									
Cytophagaceae	<i>Dyadobacter</i> sp.									
Verrucomicrobia	5.8, 4.6	Cd. Saccharibacteria	0.7, 2.6	Cytophagales	0.7, 2.6	Cd. Saccharibacteria	0.3, 10			
						Spartobacteria	4.5, 2.4	Spartobacteria unclassified	4.5, 2.4	
			0.1, 0.5	Opitutales	0.1, 0.5	Opitutaceae	<i>Opitutus</i> sp.			
			0.9, 1.1	Subdivision3	0.9, 1.1					

				unclassified			
	Planctomycetes	5.7, 3.2	Planctomycetia	5.7, 3.2	Planctomycetales	5.7, 3.2	Planctomycetaceae <i>Singulisphaera sp.</i> , <i>Pirellula sp.</i>
	Firmicutes	0.8, 0.7	Bacilli	0.8, 0.7	Bacillales	0.8, 0.7	
	Gemmatimonadetes	0.8, 0.6	Gemmatimonadetes	0.8, 0.6	Gemmatimonadales	0.8, 0.6	
	Chloroflexi	0.5, 0.8	Ktedonobacteria	0.1, 0.5	Ktedonobacterales	0.1, 0.5	
	candidate_division WPS-1	0.5, 0.5	candidate_division WPS-1 unclassified	0.5, 0.5			
	Armatimonadetes	0.2, 0.4	Armatimonadia	0.2, 0.4			
Archaea	Thaumarchaeota	0.03, 0.06	Nitrososphaerales	0.03, 0.06	Nitrososphaeria	0.01, 0.03	Nitrososphaeraceae
	Euryarchaeota	0.02, 0.02					
Fungi	Ascomycota	56.5, 38.9	Dothideomycetes	33.5, 15.0	Dothideomycetes order incertae sedis	33, 12	Myxotrichaceae <i>Oidiodendron sp.</i>
							Pseudeurotiaceae
					Pleosporales	0.5, 1.35	Pleosporales family incertae sedis <i>Phoma sp.</i> , <i>Setomelanomma sp.</i>
							Pleomassariaceae
					Dothideales	0, 0.7	Dothioraceae <i>Aureobasidium sp.</i>
					Capnodiales	0.05, 0.3	Davidiellaceae
					Hysteriales	0.01, 0.5	Gloniaceae <i>Cenococcum sp.</i>
			Eurotiomycetes	15, 10.6	Eurotiales	6.6, 7.5	Trichocomaceae <i>Penicillium sp.</i>
					Chaetothyriales	8.3, 2.5	Herpotrichiellaceae <i>Exophiala sp.</i>
			Leotiomycetes	4.6, 7.3	Helotiales	2.5, 6.7	Helotiales family incertae sedis <i>Cadophora sp.</i>
			Sordariomycetes	2.3, 2.0	Hypocreales	2.0, 1.7	Hypocreaceae
			Pezizomycetes	0.01, 3.7	Pezizales	0.01, 3.7	Pyronemataceae <i>Wilcoxina sp.</i>
	Basidiomycota	23.9, 49.4	Agaricomycetes	3.7, 40.6	Boletales	0.07, 38.6	Suillaceae <i>Suillus sp.</i>
					Agaricales	2.5, 0.4	Hygrophoraceae <i>Hygrocybe sp.</i>
					Trechisporales		
			Tremellomycetes	13.6, 4.7	Filobasidiales	8.8, 2.6	Filobasidiaceae
			Tremellomycetes		Tremellales	4.8, 2.1	Tremellales family incertae sedis <i>Cryptococcus sp.</i>
			Microbotryomycetes	3.5, 2.8	Sporidiobolales	3.3, 2.7	
			Wallemiomycetes	2.7, 0.8	Geminibasidiales	2.7, 0.8	Geminibasidiaceae <i>Geminibasidium sp.</i>
	Zygomycota	9.5, 5	Zygomycota class incertae sedis	9.5, 5.0	Mortierellales	4.4, 2.6	Mortierellaceae <i>Mortierella sp.</i>
					Mucorales	5.1, 2.3	Umbelopsidaceae <i>Umbelopsis sp.</i>

Table S2: Site description and physical and chemical soil characteristics of the replicate study sites (soil site) including dry matter content (DM), pH, electrical conductivity (EC), soil organic matter content (OM), dissolved organic carbon (DOC), maximum water holding capacity (MWHC), total carbon (C) and nitrogen (N) content, carbon/nitrogen ratio (C/N), and plant-available ammonium concentration (NH₄⁺-N). Data represent means ± standard deviations (*n* = 3) in italics.

<i>Soil site</i>	Replicate site	DM [g g ⁻¹]	pH	EC [μS m ⁻¹]	OM [g g ⁻¹ DM]	DOC [μg g ⁻¹ DM]	MWHC [g g ⁻¹ DM]	C [%]	N [%]	C/N	NH₄⁺-N [μg g ⁻¹ DM]
<i>Gschwandtkopf Seefeld/Austria</i>	A	0.67	6.86	82.67	0.11	135.40	0.98	5.45	0.28	19.57	5.29
		<i>0.00</i>	<i>0.05</i>	<i>3.51</i>	<i>0.00</i>	<i>19.60</i>	<i>0.04</i>	<i>0.36</i>	<i>0.01</i>	<i>1.52</i>	<i>0.70</i>
	B	0.65	6.34	103.67	0.11	165.94	1.14	5.53	0.26	21.79	11.82
		<i>0.00</i>	<i>0.05</i>	<i>0.58</i>	<i>0.00</i>	<i>2.13</i>	<i>0.01</i>	<i>0.42</i>	<i>0.01</i>	<i>2.21</i>	<i>1.20</i>
	C	0.71	6.16	89.33	0.09	147.36	0.81	3.95	0.18	21.99	12.51
		<i>0.00</i>	<i>0.19</i>	<i>4.62</i>	<i>0.00</i>	<i>9.11</i>	<i>0.01</i>	<i>0.32</i>	<i>0.01</i>	<i>2.14</i>	<i>1.11</i>

References

Pratscher, J., Dumont, M. G. & Conrad, R. Assimilation of acetate by the putative atmospheric methane oxidizers belonging to the USCα clade. *Environ. Microbiol.* **13**, 2692–2701; 10.1111/j.1462-2920.2011.02537.x (2011).