Supplementary data

 Fig S1: Rarefaction curves of bacterial 16S rRNA gene sequences recovered from the ectomycorrhizospheres of

 oak. The expected number of phylotypes (OTUs) was calculated from the number of sequences, with inclusion in

 the same species based on 97% sequence similarity. The five samples considered are presented as follow:

 Xerocomus pruinatus samples (C1B, grey line; C3A, black line) and *Scleroderma citrinum* samples (C3B, green

 line; C4A, blue line and C4B, red line).







of 100 reads are presented.

Xerocomus pruinatus Scleroderma citrinum	
	unassigned Candidatus Koribacter
	Rubrivivax Bacillus Bacilythizobium
	Burkholderia Microscilla
	Ricinus Chitinophaga
	Daucus Francisella Caulobactor
	unclassified (derived from Bacteria) Rhodopseudomonas
	Acidobacterium Curtobacterium
	Phenylobacterium Desulfobacterium Acetobacter
	Candidatus Solibacter Methylocystis
	Desulfothermus Desulfotibrio
	Wohifahrliimonas Nocardiopsis uuclassilied (derived from Gammaproteobacteria)
	Xylella unclassified (derived from Verrucomicrobia subdivision 3)
	Chiamydophila Methylosinus Pinus
	Dyella Geminicoccus Desulfotomaculum
	Mycobacterium Cytophaga
	Rhodoplanes Piscirickettsia
	Thioalkalivibrio Brevundimonas Gluconacetobacter
	Herbaspirilium Pedobacter
	Cupriavidus Phaeospirillum
	Veillonella Anaeromyxobacter Lysinbacillus
	Zymononas Isosphaera
	Opitutis unclassified (derived from Desulfuromonadales)
	unclassified (derived from Opitutaceae) Hyphomicrobium Rubritepida
	Prosthecobacter Oxalicibacterium usclassified (derived from Thermomonosporaceae)
	Biatabacterium Stenotrophomonas
	Methylocaldum Nitrosococcus Streptomyces
	Trabulsiella unclassified (derived from Beijerincklaceae) Nocardia
	Exiguobacterium Geobacillus Desulfoastronum
	Thioalkalibacter Azoarcus
	Janthiobacterium Acidithiobacillus
	Erwinia Nocardioldes Kiebsiela
	Dialister Denalobacter Menadblachter
	Bosea Ectothiorhodospira
	Thermobaculum Coraliomargarita Geoalkalibacter
	unclassified (derived from Thiotrichales) Bdellovibrio Actinocorallia
	Afipia Stenoxybacter
	Ideonella Conexibacter
	Neisseria Variovorax Candidatus Liberibacter
	Rhizobium Legionella Regulamonae
	Asia Alifella
	Rhodoblastus Aeromonas Verrucomicrobium
	Acinetobacter Shigelia Shipeomonas
	Raistonia Acidocella
	unclassified (derived from Actinobacteria (class)) Streptomonospora
	Acidovorax Moorella Xanthomonas
	Salinibacter Flexibacter Halomonas
	Ktedonobacter Lactobacillus
	Aciaiphilium Streptococcus Kineococcus
	Flavobacterium Denitromonas Selenomonas
	unclassified (derived from Sphingobacteriaceae) Rhodothermus
	Solimonas Solimonas Frankia
	Pseudonocardia Geobacter Acidimicrobium
	Rhodothalassium Pandoraea

Fig S3: Bacterial community membership similarities between ectomycorrhizosphere, the global rhizosphere and the surrounding bulk soil samples. The cluster analysis was performed using Mothur. (A) Bacterial community membership similarities between ectomycorrhizosphere samples. C1B and C3A correspond to *X. pruinatus* ectomycorrhizospheres; and C3B, C4A and C4B correspond to *S. citrinum* ectomycorrhizospheres. (B) Comparison of all the samples (rhizosphere samples: C1R-C3R and bulk soil samples: C1BS-C3BS). Values are based on 0.03 distances.



- 1 Fig S4: Venn diagram comparing the OTUs (97%) from the ectomycorrhizosphere, the total rhizosphere and the
- surrounding bulk soil. This figure presents the number of OTUs shared or only present in one the three
 environments considered, as well as the relative percentage they represent in brackets.
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Table S1: Number of OTUs and Richness estimators based on Mothur analyses detected in the different ectomycorrhizosphere samples

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	Label	Number of reads	OTU	OTU 97%	shannon	Chao1	ACE
			(97%)	normalized*		(lower and upper	(lower and upper
				with C1B		95% confidence intervals)	95% confidence intervals)
X. pruinatus	C1B	28,516	11,277	11,277	8.30	31,019 (29,742/32,383)	57,599 (56,748/ 58,466)
	СЗА	34,913	13,060	11,333	8.31	35,474 (34,121/36,914)	66,362 (65,477/ 67,262)
S. citrinum	СЗВ	31,428	12,145	11,361	8.32	32,671 (31,391/34,035)	59,776
							(58,940/ 60,627)
	C4A	37,358	14,516	12,523	8.63	39,268 (37,856/40,766)	73,792 (72,856/ 74,743)
	C4B	28,686	12,058	12,032	8.49	33,062 (31,746/34,465)	62,043 (61,183/ 62,917)

5 * the number of OTUs 97% was calculated using the same number of reads for each sample, which corresponds to the minimal number of reads of the sample C1B of the X.

pruinatus ectomycorrhizosphere.

2 Table S2: Bacterial genera associated with known functions (number of reads detected)

	X. prui	S. citrinum			
Sample name	C1B	C3A	C3B	C4A	C4B
Nitrifying bacteria					
Nitrospira	4	6	1	20	7
Nitrosospira	0	0	0	0	0
Nitrosomonas	1	6	14	7	0
Nitrobacter	1	1	0	0	0
Nitrogen-fixing bacteria					
Bradyrhizobium	1111	1735	1494	1131	1253
Rhizobium	61	63	46	8	6
Sinorhizobium	0	1	1	0	0
Mesorhizobium	4	7	3	2	10
Methane-oxidizing bacteria					
Methylocystis	14	1	3	10	10

Planctomycete anammox (anaerobic ammonium	71	179	163	135	90
oxidation)					
Other genera with functions of interest (mineral					
weathering, antibiotic production, chitin hydrolysis)					
Burkholderia	2279	2907	2654	1161	1215
Rhodoplane	974	1796	1514	2011	1268
Alterococcus	769	331	270	470	211
Streptomyces	26	13	25	51	60
Pseudomonas	6	3	4	8	0
Collimonas	8	0	1	5	0
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