

Table S1: Statistical evaluation of agronomic parameters and qPCR measurements tested using pairwise t-Test.

Test set	Category		CB	CF	P69B
complete	Emergence rate	CF	0.493	-	-
		P69B	0.15	0.435	-
		P69F	0.355	0.116	0.024
	Fresh weight	CF	0.168	-	-
		P69B	0.811	0.269	-
		P69F	0.021	0.339	0.043
	Yield	CF	0.74	-	-
		P69B	0.87	0.87	-
		P69F	0.94	0.69	0.82
Melk	Emergence rate	CF	0.434	-	-
		P69B	0.084	0.282	-
		P69F	0.915	0.496	0.099
	Fresh weight	CF	0.98	-	-
		P69B	0.85	0.88	-
		P69F	0.24	0.28	0.22
	Yield	CF	0.55	-	-
		P69B	0.53	0.98	-
		P69F	0.34	0.7	0.72
Mitterdorf	Emergence rate	CF	0.889	-	-
		P69B	0.414	0.493	-
		P69F	0.017	0.021	0.063
	Fresh weight	CF	0.031	-	-
		P69B	0.353	0.141	-
		P69F	0.017	0.713	0.078
	Yield	CF	0.58	-	-
		P69B	0.70	0.87	-
		P69F	0.78	0.78	0.91
qPCR		Bulk_soil	CB	CF	P69B
	CB	1	-	-	-
	CF	1	1	-	-
	P69B	0.00013	5.90E-05	2.00E-05	-
	P69F	6.30E-05	2.90E-05	1.00E-05	1

Table S2: Sequencing overview of 16S amplicons for each sample and observed alpha diversity.

Sample ID	Sample type	Field location	Treatment	Filtered quality sequences	Shannon diversity index
soil_Mitterdorf1_bacteria	soil	Mitterdorf	none	36260	6.3
soil_Mitterdorf2_bacteria	soil	Mitterdorf	none	33070	6.3
soil_Mitterdorf3_bacteria	soil	Mitterdorf	none	16690	5.9
soil_Mitterdorf4_bacteria	soil	Mitterdorf	none	9193	5.6
soil_Melk1_bacteria	soil	Melk	none	21547	6.2

soil_Melk2_bacteria	soil	Melk	none	12472	6.0
soil_Melk3_bacteria	soil	Melk	none	68602	6.8
soil_Melk4_bacteria	soil	Melk	none	37257	6.5
rhizosphere_Mitterdorf_CB1_bacteria	rhizosphere	Mitterdorf	CB	30527	6.2
rhizosphere_Mitterdorf_CB2_bacteria	rhizosphere	Mitterdorf	CB	53169	6.3
rhizosphere_Mitterdorf_CB3_bacteria	rhizosphere	Mitterdorf	CB	14234	5.9
rhizosphere_Melk_CB1_bacteria	rhizosphere	Melk	CB	30068	6.2
rhizosphere_Melk_CB2_bacteria	rhizosphere	Melk	CB	14246	5.1
rhizosphere_Melk_CB3_bacteria	rhizosphere	Melk	CB	40783	6.0
rhizosphere_Mitterdorf_CF1_bacteria	rhizosphere	Mitterdorf	CF	7766	5.5
rhizosphere_Mitterdorf_CF2_bacteria	rhizosphere	Mitterdorf	CF	2790	4.9
rhizosphere_Mitterdorf_CF3_bacteria	rhizosphere	Mitterdorf	CF	5393	5.2
rhizosphere_Melk_CF1_bacteria	rhizosphere	Melk	CF	40360	5.8
rhizosphere_Melk_CF2_bacteria	rhizosphere	Melk	CF	27217	5.2
rhizosphere_Melk_CF3_bacteria	rhizosphere	Melk	CF	11194	5.1
rhizosphere_Mitterdorf_P69B1_bacteria	rhizosphere	Mitterdorf	P69B	11280	5.6
rhizosphere_Mitterdorf_P69B2_bacteria	rhizosphere	Mitterdorf	P69B	32102	6.0
rhizosphere_Mitterdorf_P69B3_bacteria	rhizosphere	Mitterdorf	P69B	19881	5.7
rhizosphere_Melk_P69B1_bacteria	rhizosphere	Melk	P69B	106544	3.8
rhizosphere_Melk_P69B2_bacteria	rhizosphere	Melk	P69B	13501	5.7
rhizosphere_Melk_P69B3_bacteria	rhizosphere	Melk	P69B	48768	6.0
rhizosphere_Mitterdorf_P69F1_bacteria	rhizosphere	Mitterdorf	P69F	6503	5.5
rhizosphere_Mitterdorf_P69F2_bacteria	rhizosphere	Mitterdorf	P69F	31655	6.3
rhizosphere_Mitterdorf_P69F3_bacteria	rhizosphere	Mitterdorf	P69F	51874	6.6
rhizosphere_Melk_P69F1_bacteria	rhizosphere	Melk	P69F	48190	5.5
rhizosphere_Melk_P69F2_bacteria	rhizosphere	Melk	P69F	20570	5.5
rhizosphere_Melk_P69F3_bacteria	rhizosphere	Melk	P69F	23315	6.0

Table S3: Sequencing overview of ITS amplicons for each sample and observed alpha diversity.

Sample ID	Sample type	Field location	Treatment	Filtered quality sequences	Shannon diversity index
soil_Mitterdorf1_fungi	soil	Mitterdorf	none	5541	1.9
soil_Mitterdorf2_fungi	soil	Mitterdorf	none	1293	1.8
soil_Mitterdorf3_fungi	soil	Mitterdorf	none	4181	2.2
soil_Mitterdorf4_fungi	soil	Mitterdorf	none	1944	1.6
soil_Melk1_fungi	soil	Melk	none	1540	2.4
soil_Melk2_fungi	soil	Melk	none	2825	2.8
soil_Melk3_fungi	soil	Melk	none	15208	2.9
soil_Melk4_fungi	soil	Melk	none	5733	2.9
rhizosphere_Mitterdorf_CB1_fungi	rhizosphere	Mitterdorf	CB	3109	2.7
rhizosphere_Mitterdorf_CB2_fungi	rhizosphere	Mitterdorf	CB	1072	3.0

rhizosphere_Mitterdorf_CB3_fungi	rhizosphere	Mitterdorf	CB	9758	2.4
rhizosphere_Melk_CB1_fungi	rhizosphere	Melk	CB	4016	3.1
rhizosphere_Melk_CB2_fungi	rhizosphere	Melk	CB	1936	3.0
rhizosphere_Melk_CB3_fungi	rhizosphere	Melk	CB	7557	2.7
rhizosphere_Mitterdorf_CF1_fungi	rhizosphere	Mitterdorf	CF	6712	3.2
rhizosphere_Mitterdorf_CF2_fungi	rhizosphere	Mitterdorf	CF	3837	2.3
rhizosphere_Mitterdorf_CF3_fungi	rhizosphere	Mitterdorf	CF	5318	2.4
rhizosphere_Melk_CF1_fungi	rhizosphere	Melk	CF	5581	2.9
rhizosphere_Melk_CF2_fungi	rhizosphere	Melk	CF	2948	1.7
rhizosphere_Melk_CF3_fungi	rhizosphere	Melk	CF	4714	2.5
rhizosphere_Mitterdorf_P69B1_fungi	rhizosphere	Mitterdorf	P69B	13190	2.2
rhizosphere_Mitterdorf_P69B2_fungi	rhizosphere	Mitterdorf	P69B	5307	3.0
rhizosphere_Mitterdorf_P69B3_fungi	rhizosphere	Mitterdorf	P69B	5263	1.4
rhizosphere_Melk_P69B1_fungi	rhizosphere	Melk	P69B	4183	2.4
rhizosphere_Melk_P69B2_fungi	rhizosphere	Melk	P69B	6224	2.5
rhizosphere_Melk_P69B3_fungi	rhizosphere	Melk	P69B	10616	2.4
rhizosphere_Mitterdorf_P69F1_fungi	rhizosphere	Mitterdorf	P69F	7158	2.9
rhizosphere_Mitterdorf_P69F2_fungi	rhizosphere	Mitterdorf	P69F	5744	2.7
rhizosphere_Mitterdorf_P69F3_fungi	rhizosphere	Mitterdorf	P69F	7342	1.7
rhizosphere_Melk_P69F1_fungi	rhizosphere	Melk	P69F	1626	2.9
rhizosphere_Melk_P69F2_fungi	rhizosphere	Melk	P69F	4077	2.5
rhizosphere_Melk_P69F3_fungi	rhizosphere	Melk	P69F	780	3.0

Table S4: Statistical evaluation of explained impact of different factors on bacterial and fungal diversity.

Factor	Bacterial richness analysis		Fungal richness analysis	
	F value	P value	F value	P value
Soil only dataset				
Location	2.019	0.205	23.63	0.003
Rhizosphere Mitterdorf dataset				
Treatment	3.97	0.052	0.483	0.703
Rhizosphere Melk dataset				
Treatment	0.384	0.767	1.812	0.223

Table S5: DESeq2 analysis of bacterial ASVs on the site Mitterdorf. Significantly different ASVs with log-change above 2 are shown.

Comparison	log2FoldChange	p <sub>adj</sub>	Class	Genus
CB:CF	5.3	0.033	<i>Holophagae</i>	<i>uncultured Subgroup 7</i>
	6.2	0.045	<i>Gammaproteobacteria</i>	<i>Stenotrophomonas</i>
	6.2	0.006	<i>Subgroup_6</i>	<i>uncultured Subgroup 6</i>
	6.2	0.001	<i>Bacteroidia</i>	<i>uncultured env.OPS17</i>
	6.2	0.048	<i>Subgroup_6</i>	<i>uncultured Subgroup 6</i>
	6.2	0.048	<i>Gammaproteobacteria</i>	<i>Massilia</i>

	6.2	0.007	<i>Gammaproteobacteria</i>	<i>Ellin6067</i>
	6.3	0.008	<i>Subgroup_6</i>	<i>uncultured Subgroup 6</i>
	6.4	0.045	<i>Gammaproteobacteria</i>	<i>Ellin6067</i>
	6.4	0.002	<i>Verrucomicrobiae</i>	<i>Candidatus Xiphinematobacter</i>
	6.6	0.001	<i>KD4-96</i>	<i>uncultured KD4-96</i>
	6.6	0.030	<i>Bacilli</i>	<i>Bacillus</i>
	6.8	0.031	<i>Alphaproteobacteria</i>	<i>Nordella</i>
	7.4	<0.001	<i>Verrucomicrobiae</i>	<i>Candidatus Xiphinematobacter</i>
	7.4	0.010	<i>Subgroup_6</i>	<i>uncultured Subgroup 6</i>
	7.4	0.048	<i>Bacteroidia</i>	<i>Flavobacterium</i>
	7.9	0.030	<i>Gammaproteobacteria</i>	<i>Rhizobacter</i>
	<hr/>			
CB:P69B	-9.7	0.045	<i>Verrucomicrobiae</i>	<i>Opitutaceae</i>
	7.7	0.030	<i>Anaerolineae</i>	<i>uncultured Anaerolineaceae</i>
	7.7	<0.001	<i>KD4-96</i>	<i>uncultured KD4-96</i>
	<hr/>			
CB:P69F	7.7	<0.001	<i>Verrucomicrobiae</i>	<i>Candidatus Xiphinematobacter</i>

Table S6: DESeq2 analysis of bacterial ASVs on the site Melk. Significantly different ASVs with log-change above 2 are shown.

Comparison	log2FoldChange	p <sub>adj</sub>	Class	Genus
CB:CF	-23.0	<0.001	<i>Gammaproteobacteria</i>	<i>Janthinobacterium</i>
	-22.2	<0.001	<i>Bacteroidia</i>	<i>Pedobacter</i>
	-10.3	0.005	<i>Gammaproteobacteria</i>	<i>Luteibacter</i>
	7.0	0.001	<i>Holophagae</i>	<i>uncultured Subgroup 7</i>
	8.0	<0.001	<i>Subgroup 6</i>	<i>uncultured Subgroup 6</i>
	11.0	0.002	<i>Gammaproteobacteria</i>	<i>Achromobacter</i>
	<hr/>			
CB:P69B	-20.6	<0.001	<i>Bacteroidia</i>	<i>Pedobacter</i>
	-20.4	<0.001	<i>Gammaproteobacteria</i>	<i>Janthinobacterium</i>
	-11.6	0.002	<i>Gammaproteobacteria</i>	<i>Luteibacter</i>
	9.7	0.020	<i>Gammaproteobacteria</i>	<i>Massilia</i>
	<hr/>			
CB:P69F	-21.0	<0.001	<i>Gammaproteobacteria</i>	<i>Janthinobacterium</i>
	-19.3	<0.001	<i>Bacteroidia</i>	<i>Pedobacter</i>
	11.5	0.001	<i>Gammaproteobacteria</i>	<i>Achromobacter</i>

Table S7: DESeq2 analysis of fungal ASVs on the site Mitterdorf. Significantly different ASVs with log-change above 2 are shown.

Comparison	log2FoldChange	p <sub>adj</sub>	Class	Genus
CB:CF	22.0	<0.001	<i>Sordariomycetes</i>	<i>Unidentified Nectriaceae</i>
	-20.2	<0.001	<i>Mortierellomycotina cls Incertae sedis</i>	<i>Mortierella</i>

CB:P69F	-21.2	<0.001	<i>Mortierellomycotina cls Incertae sedis</i>	<i>Mortierella</i>
---------	-------	--------	---	--------------------

Table S8: DESeq2 analysis of fungal ASVs on the site Melk. Significantly different ASVs with log-change above 2 are shown.

Comparison	log2FoldChange	padj	Class	Genus
CB:CF	-20.5	<0.001	<i>Mortierellomycotina cls Incertae sedis</i>	<i>Mortierella</i>
	-21.3	<0.001	<i>Sordariomycetes</i>	<i>unidentified Nectriaceae</i>
CB:P69B	-22.6	<0.001	<i>Mortierellomycotina cls Incertae sedis</i>	<i>Mortierella</i>
	21.9	<0.001	<i>Spizellomycetes</i>	<i>Spizellomyces</i>
	-22.0	<0.001	<i>Sordariomycetes</i>	<i>unidentified Nectriaceae</i>
CB:P69F	-24.2	<0.001	<i>Sordariomycetes</i>	<i>unidentified Nectriaceae</i>
	-20.7	<0.001	<i>Mortierellomycotina cls Incertae sedis</i>	<i>Mortierella</i>