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 |
|  |  |  |  |  |
|  | **CF** | 0.58 | - | - |
| Yield | **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 | |
| Fvalue | P value |  | Fvalue | 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 | padj | Class | Genus |
| CB:CF | 5.3 | 0.033 | *Holophagae* | *uncultured Subgroup 7* |
| 6.2 | 0.045 | *Gammaproteobacteria* | *Stenotrophomonas* |
| 6.2 | 0.006 | *Subgroup\_6* | *uncultured Subgroup 6* |
| 6.2 | 0.001 | *Bacteroidia* | *uncultured env.OPS17* |
| 6.2 | 0.048 | *Subgroup\_6* | *uncultured Subgroup 6* |
| 6.2 | 0.048 | *Gammaproteobacteria* | *Massilia* |
| 6.2 | 0.007 | *Gammaproteobacteria* | *Ellin6067* |
| 6.3 | 0.008 | *Subgroup\_6* | *uncultured Subgroup 6* |
| 6.4 | 0.045 | *Gammaproteobacteria* | *Ellin6067* |
| 6.4 | 0.002 | *Verrucomicrobiae* | *Candidatus Xiphinematobacter* |
| 6.6 | 0.001 | *KD4-96* | *uncultured KD4-96* |
| 6.6 | 0.030 | *Bacilli* | *Bacillus* |
| 6.8 | 0.031 | *Alphaproteobacteria* | *Nordella* |
| 7.4 | <0.001 | *Verrucomicrobiae* | *Candidatus Xiphinematobacter* |
| 7.4 | 0.010 | *Subgroup\_6* | *uncultured Subgroup 6* |
| 7.4 | 0.048 | *Bacteroidia* | *Flavobacterium* |
| 7.9 | 0.030 | *Gammaproteobacteria* | *Rhizobacter* |
|  |  |  |  |  |
| CB:P69B | -9.7 | 0.045 | *Verrucomicrobiae* | *Opitutaceae* |
| 7.7 | 0.030 | *Anaerolineae* | *uncultured Anaerolineaceae* |
| 7.7 | <0.001 | *KD4-96* | *uncultured KD4-96* |
|  |  |  |  |  |
| CB:P69F | 7.7 | <0.001 | *Verrucomicrobiae* | *Candidatus Xiphinematobacter* |

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

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

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Comparison | log2FoldChange | padj | Class | Genus |
|  |  |  |  |  |
| CB:CF | 22.0 | <0.001 | *Sordariomycetes* | *Unidentified Nectriaceae* |
| -20.2 | <0.001 | *Mortierellomycotina cls Incertae sedis* | *Mortierella* |
|  |  |  |  |  |
| CB:P69F | -21.2 | <0.001 | *Mortierellomycotina cls Incertae sedis* | *Mortierella* |

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 | *Mortierellomycotina cls Incertae sedis* | *Mortierella* |
| -21.3 | <0.001 | *Sordariomycetes* | *unidentified Nectriaceae* |
|  |  |  |  |  |
| CB:P69B | -22.6 | <0.001 | *Mortierellomycotina cls Incertae sedis* | *Mortierella* |
| 21.9 | <0.001 | *Spizellomycetes* | *Spizellomyces* |
| -22.0 | <0.001 | *Sordariomycetes* | *unidentified Nectriaceae* |
|  |  |  |  |  |
| CB:P69F | -24.2 | <0.001 | *Sordariomycetes* | *unidentified Nectriaceae* |
| -20.7 | <0.001 | *Mortierellomycotina cls Incertae sedis* | *Mortierella* |