

Supplementary Materials:

Impact of Various Grass Species on Soil Bacteriobiome

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Table S1 One-way significance tests carried out using the analysis of variance (ANOVA)

| Parameters | | Depending on species grass | | Depending on type grass (fodder or lawn) | |
|---------------------------------------|------------------------|----------------------------|-------|--|-------|
| | | F | P | F | P |
| Numbers of microorganisms | Organotrophic bacteria | 60.801 | 0.000 | 8.598 | 0.002 |
| | Actinobacteria | 84.311 | 0.000 | 4.405 | 0.028 |
| Ecophysiological diversity index (EP) | Organotrophic bacteria | 20.858 | 0.000 | 3.553 | 0.050 |
| | Actinobacteria | 3.797 | 0.019 | 0.012 | 0.988 |
| Colony development index (CD) | Organotrophic bacteria | 51.343 | 0.000 | 69.160 | 0.000 |
| | Actinobacteria | 5.174 | 0.005 | 4.143 | 0.033 |
| Shannon-Weiner's diversity index | Phylum | 19.591 | 0.000 | 3.908 | 0.082 |
| | Class | 10.225 | 0.000 | 2.136 | 0.199 |
| | Order | 4.888 | 0.007 | 1.981 | 0.218 |
| | Family | 48.856 | 0.000 | 56.327 | 0.000 |
| | Genus | 67.997 | 0.000 | 58.136 | 0.000 |
| Simpson's diversity index | Phylum | 8.335 | 0.000 | 4.792 | 0.057 |
| | Class | 1.730 | 0.186 | 0.359 | 0.713 |
| | Order | 3.143 | 0.036 | 0.032 | 0.969 |
| | Family | 47.289 | 0.000 | 32.574 | 0.001 |
| | Genus | 96.735 | 0.000 | 54.938 | 0.000 |
| Enzymes | Dehydrogenases | 575.037 | 0.000 | 287.428 | 0.000 |
| | Catalase | 93.143 | 0.000 | 238.634 | 0.000 |
| | Urease | 4.058 | 0.014 | 15.028 | 0.005 |
| | Acid phosphatase | 28.522 | 0.000 | 20.103 | 0.002 |
| | Alkaline phosphatase | 105.743 | 0.000 | 644.848 | 0.000 |
| | Arylsulfatase | 21.551 | 0.000 | 35.873 | 0.000 |
| | β -glucosidase | 58.140 | 0.000 | 64.605 | 0.000 |
| The yield of grasses | Cut I | 111.010 | 0.000 | 11.076 | 0.004 |
| | Cut II | 232.688 | 0.000 | 5.118 | 0.038 |
| | Cut III | 21.821 | 0.000 | 0.529 | 0.477 |

F – F-test; P – level of probability.

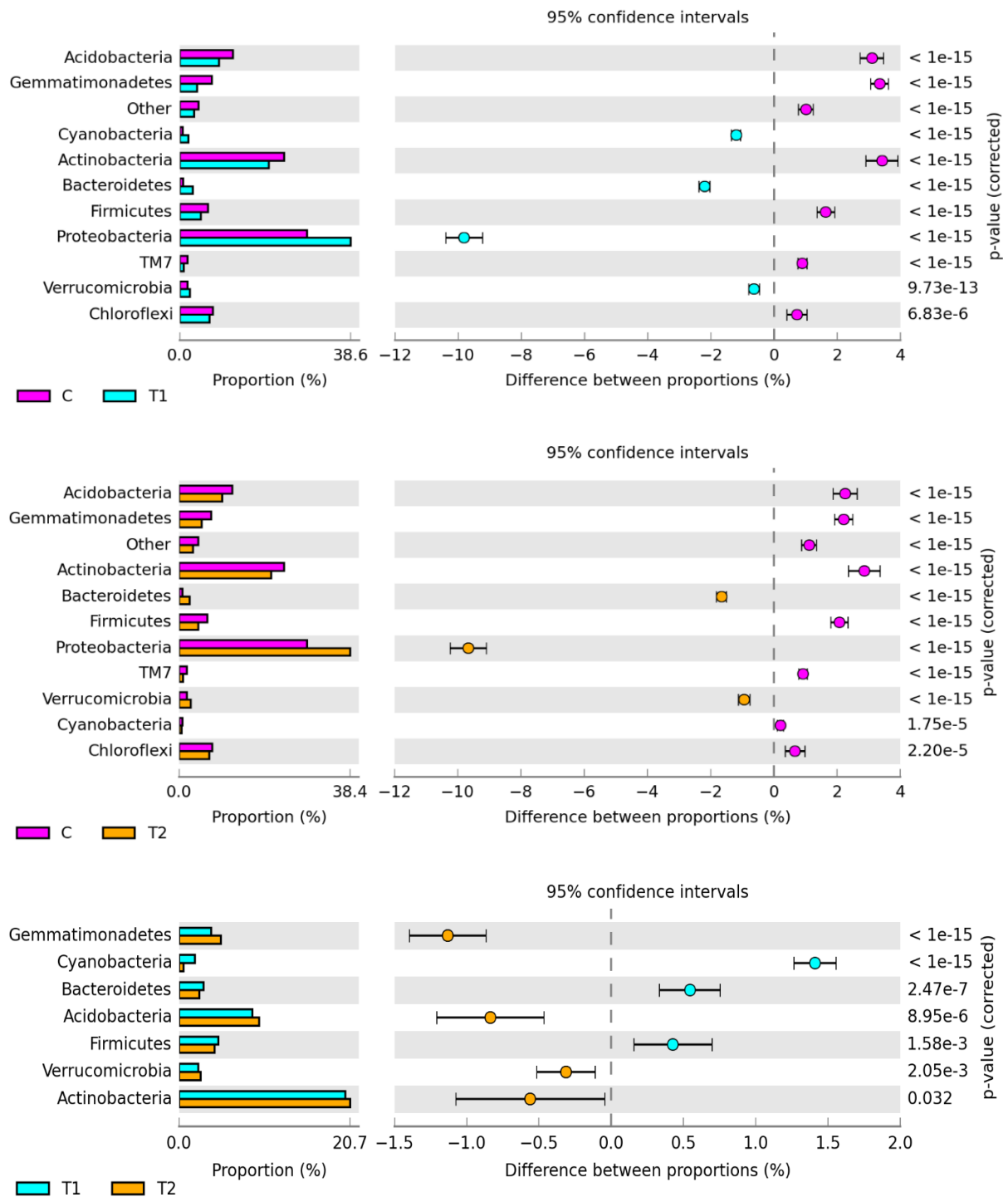
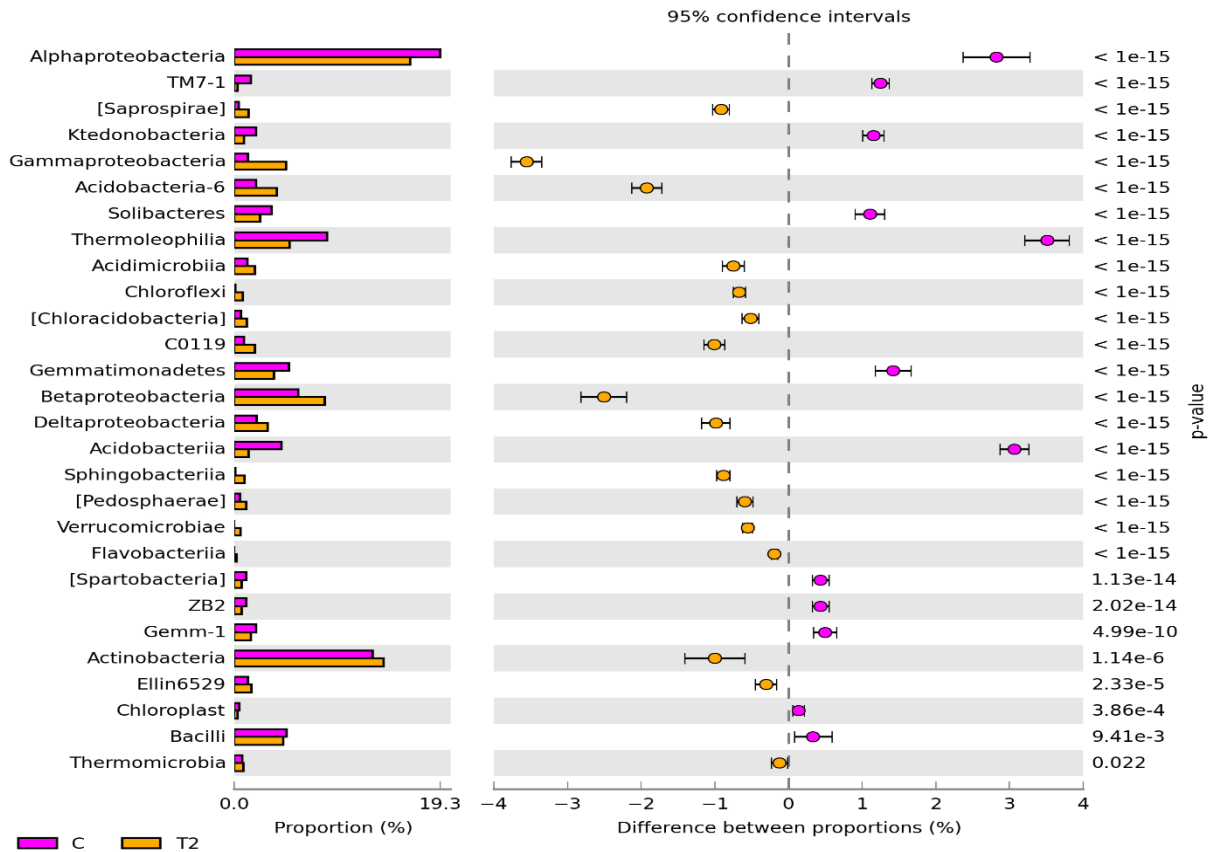
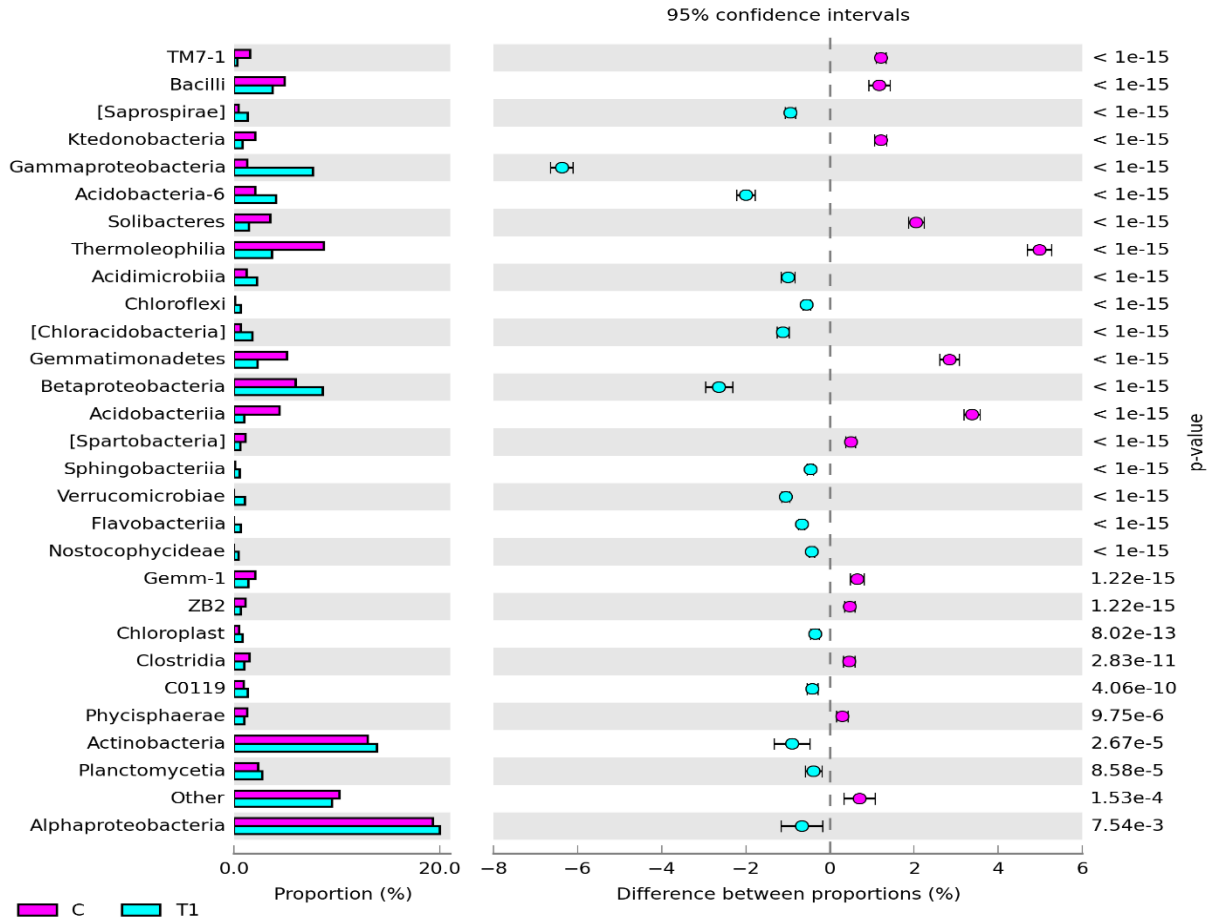


Figure S1. The relative abundance of dominant phylum bacteria in soil. Data on the number of readings greater than 1% of all OTUs. C – unsown soil; T1 - average bacteria abundance in soils sown with fodder grasses; T2 - average bacteria abundance in soils sown with lawn grasses.



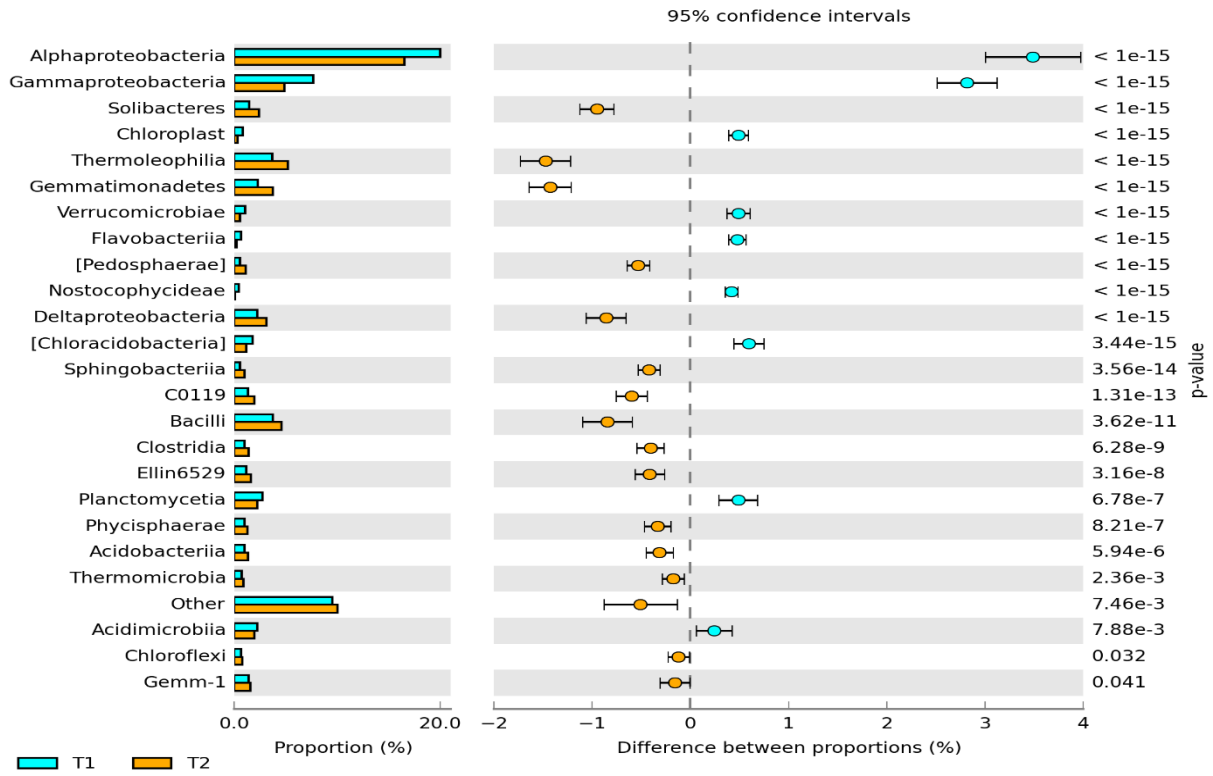
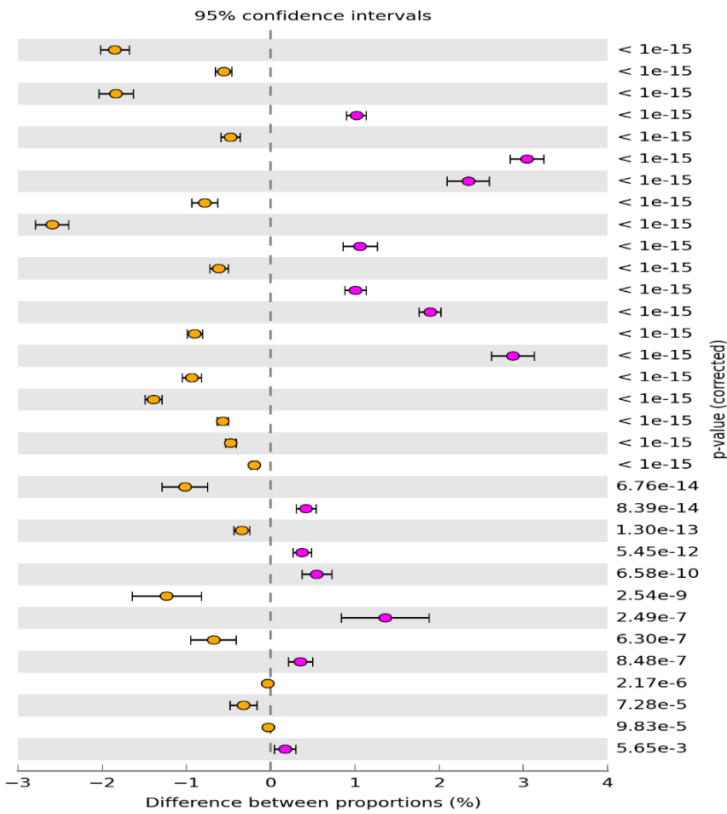
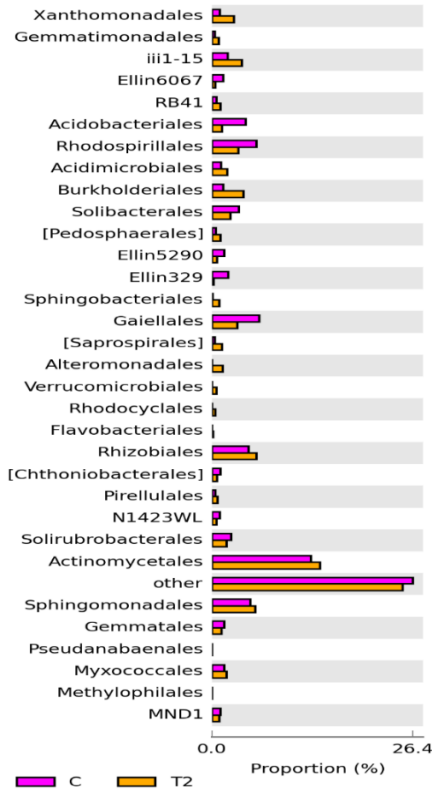
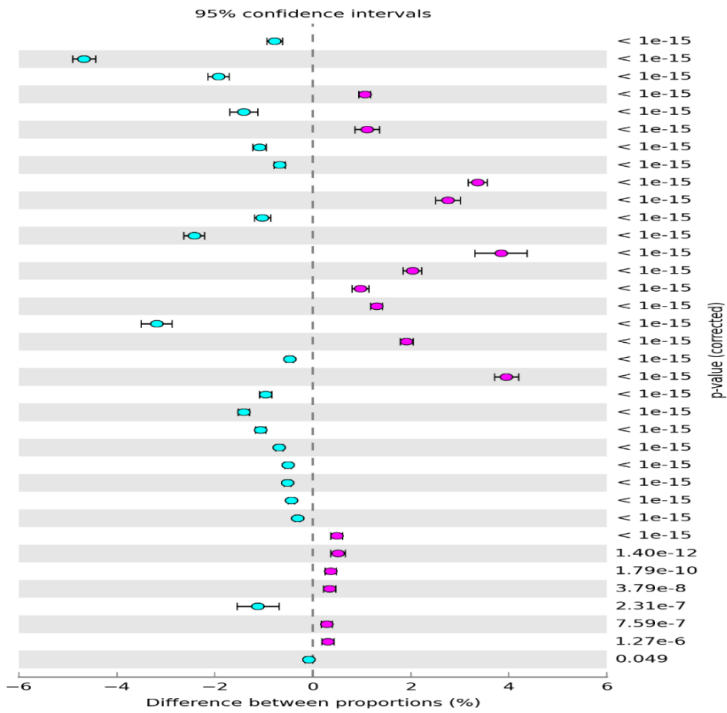
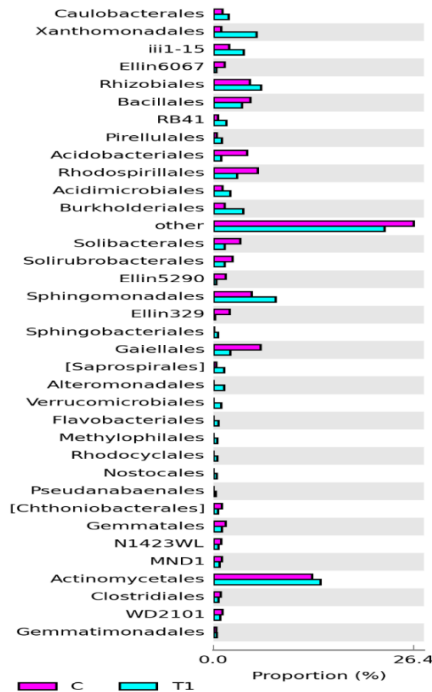


Figure S2. The relative abundance of dominant class bacteria in soil. Data on the number of readings greater than 1% of all OTUs. C – unsown soil; T1 - average bacteria abundance in soils sown with fodder grasses; T2 - average bacteria abundance in soils sown with lawn grasses.



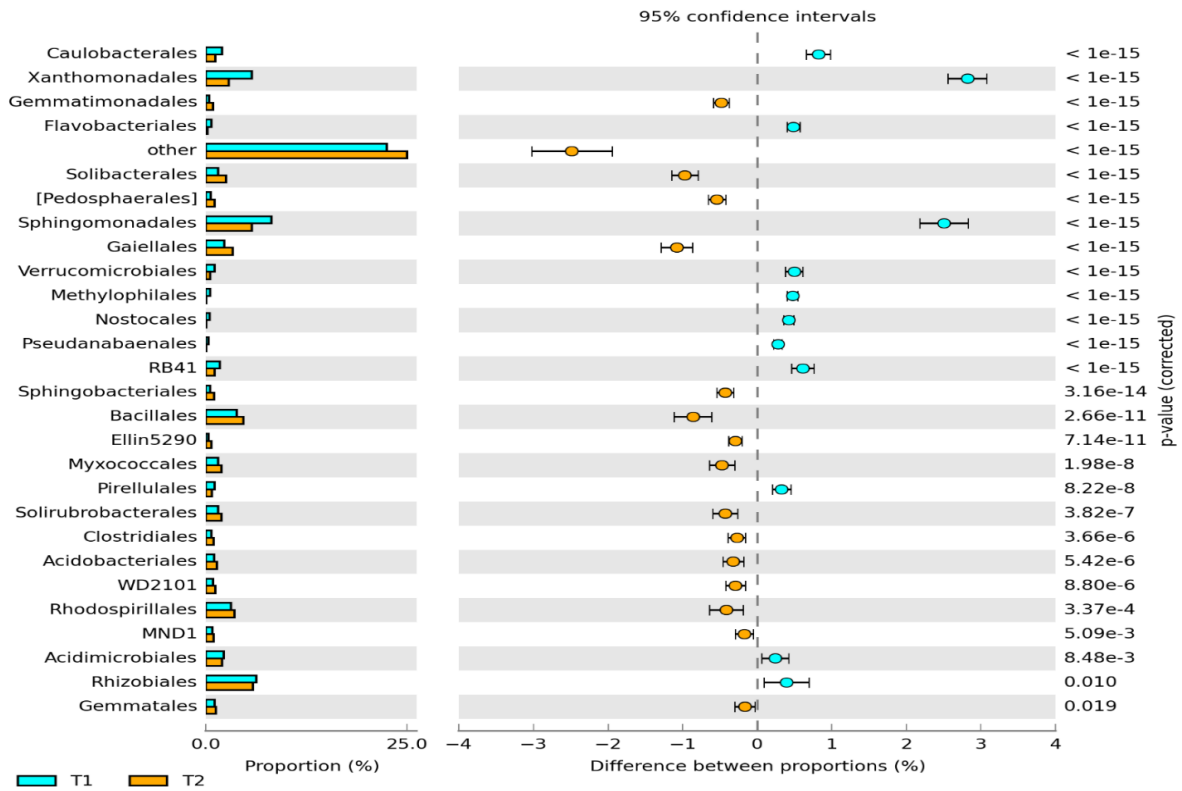
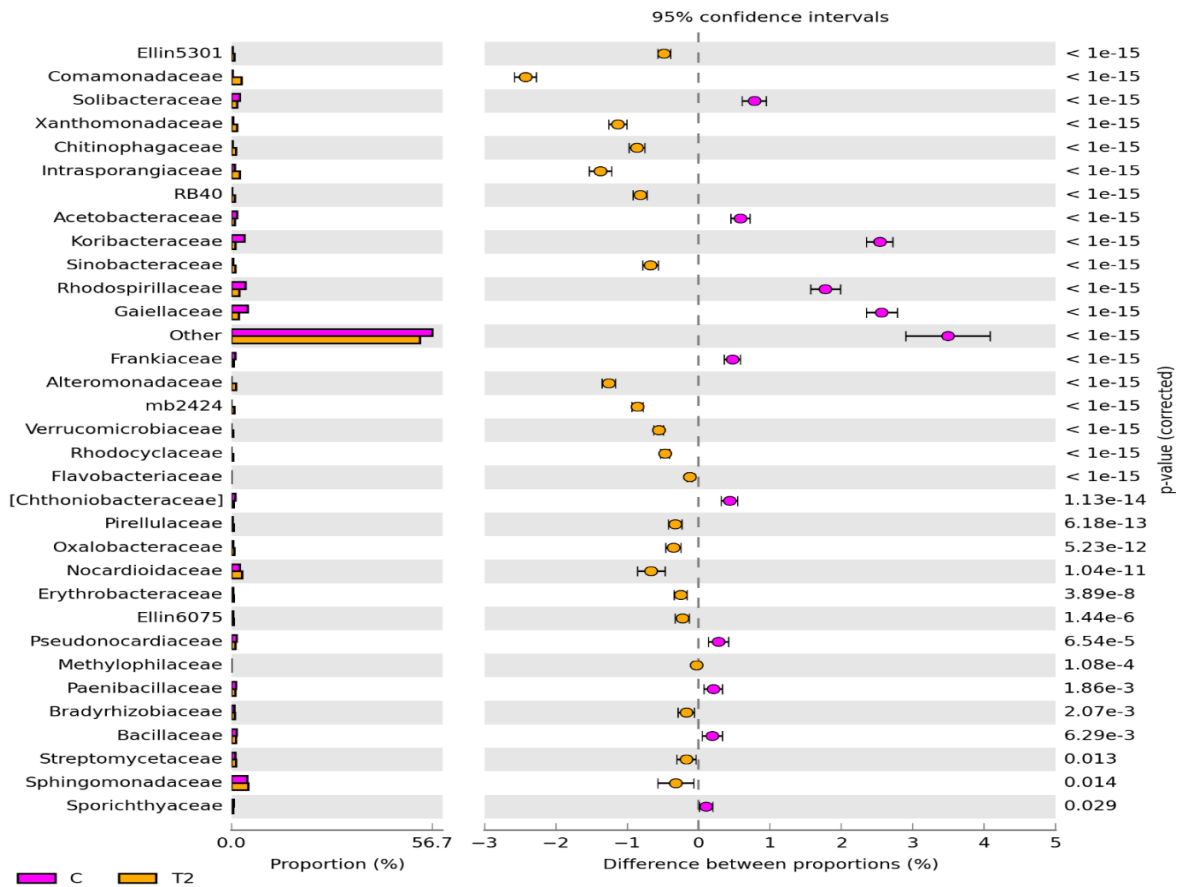
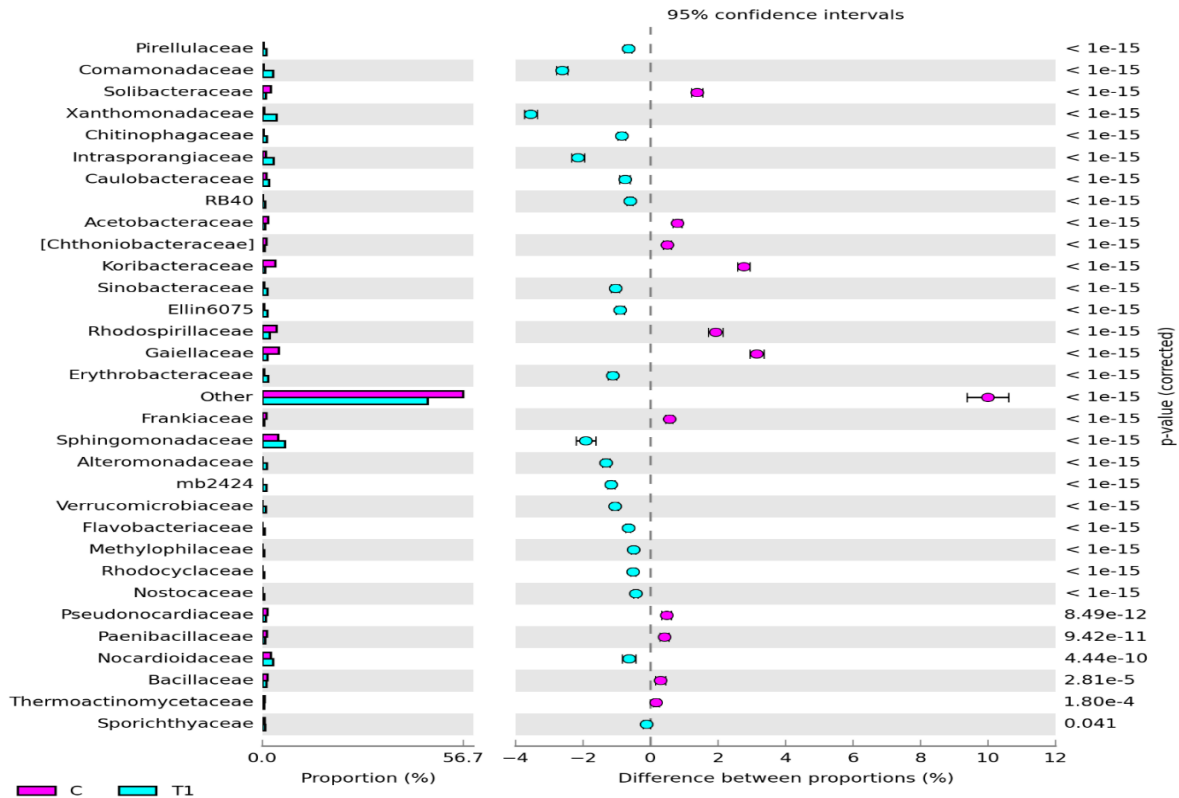


Figure S3. The relative abundance of dominant order bacteria in soil. Data on the number of readings greater than 1% of all OTUs. – unsown soil; T1 - average bacteria abundance in soils sown with fodder grasses; T2 - average bacteria abundance in soils sown with lawn grasses.



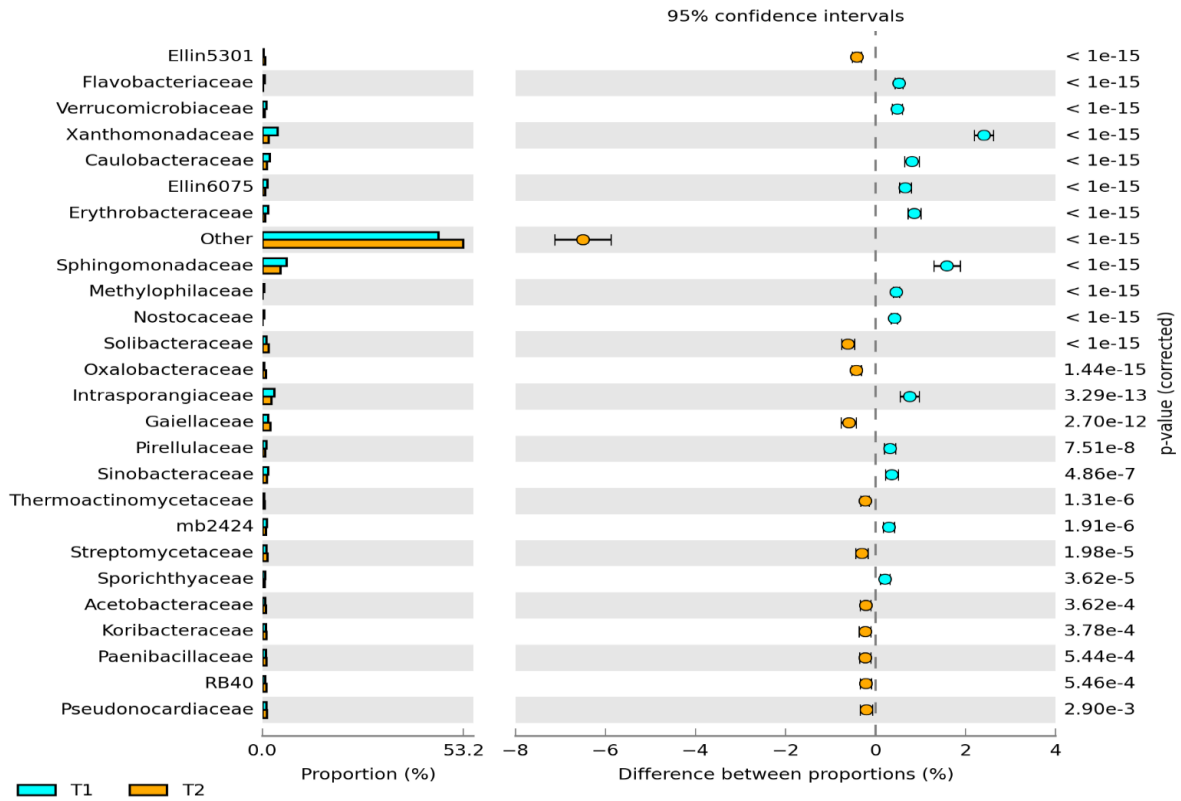


Figure S4. The relative abundance of dominant family bacteria in soil. Data on the number of readings greater than 1% of all OTUs. – unsown soil; T1 - average bacteria abundance in soils sown with fodder grasses; T2 - average bacteria abundance in soils sown with lawn grasses.