

Supplementary Data

Soil bacterial diversity responds to long-term establishment of perennial legumes in warm-season grassland at two soil depths

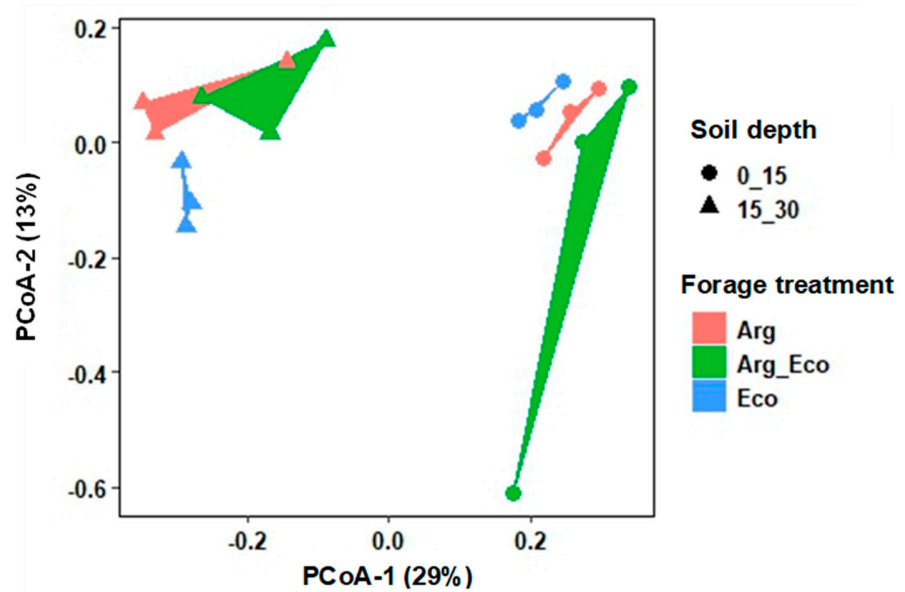


Figure S1. Soil bacterial beta diversity under different forage treatments at two soil depths (0-15 and 15-30 cm). Principle coordinates analysis (PCoA) of Bray-Curtis dissimilarities calculated using amplicon sequence variant counts.

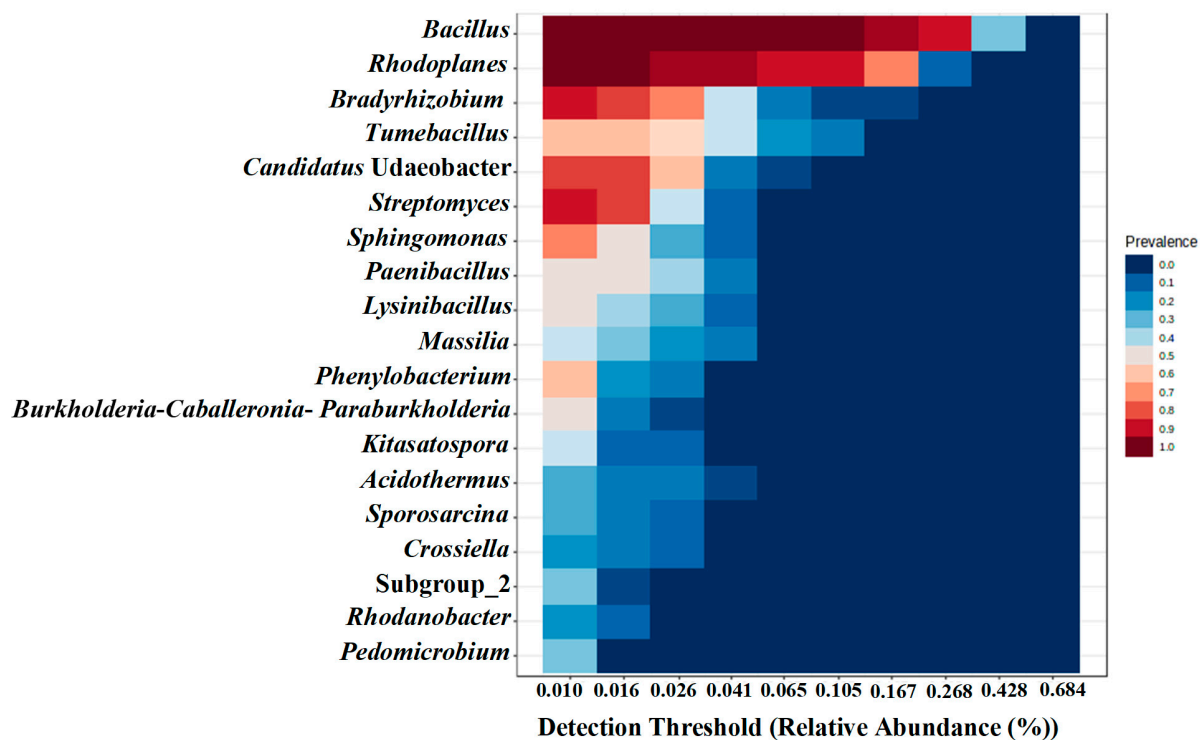


Figure S2. A heatmap showing core microbiome (identified at genus level) across all samples. Blue color indicates that the genus is either absent or present in low abundance, whereas the red color signifies that it is highly abundant.

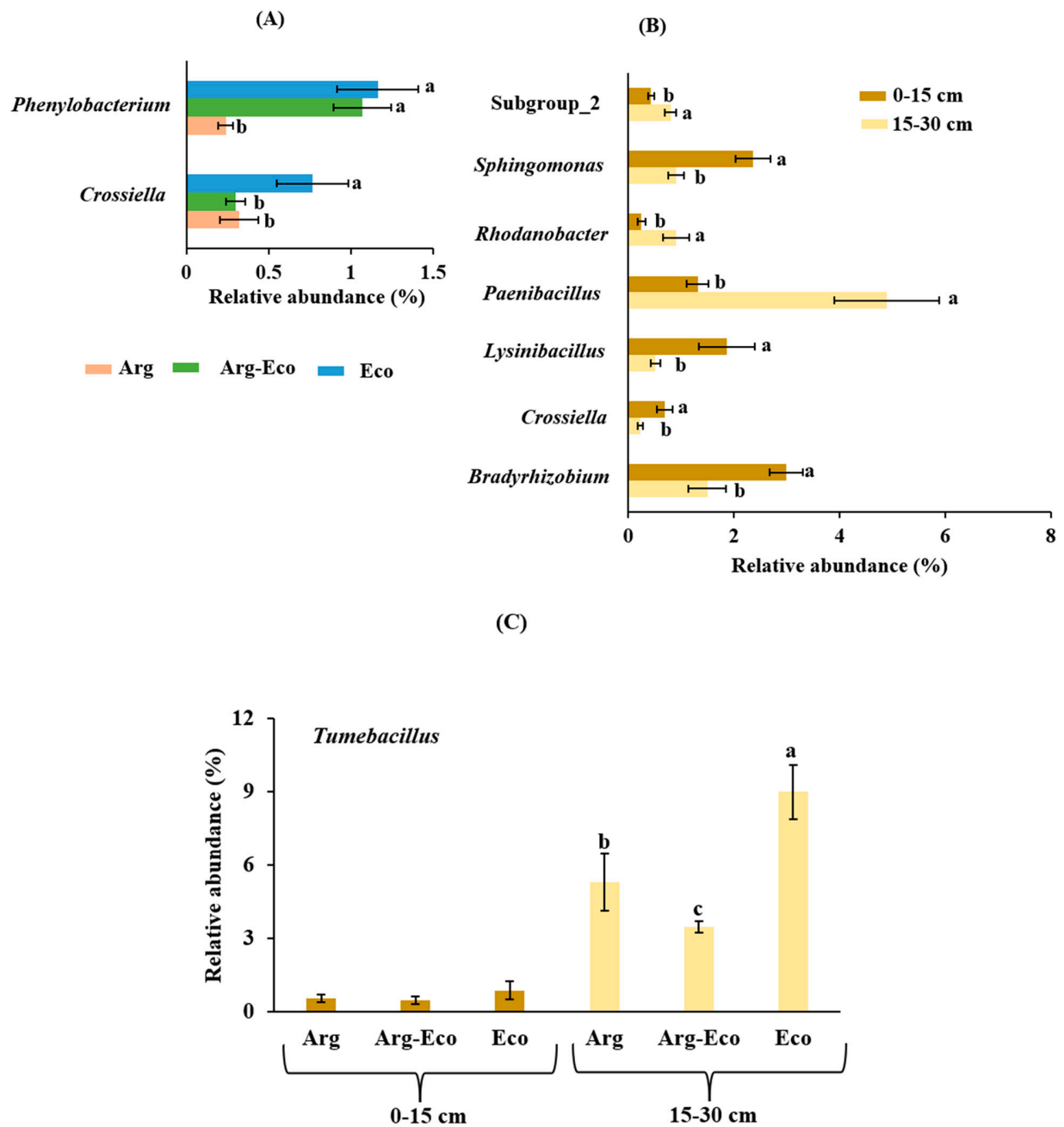


Figure S3. The effect of A) forage treatment, B) soil depth, and C) forage treatment x soil depth on the relative abundance of significant core microbiome based on the P values from ANOVA on table 3. Lowercase letters show significant differences among forage treatments and between soil depths for figure A and B. For figure C, lowercase and uppercase letters show significant differences among forage treatments at 0- 15 and 15- 30 cm, respectively.

Table S1. *P* values from ANOVA table showing the effect of forage treatment (FT), soil depth (D), and their interactions (FT x D) on the relative abundance of core soil microbiome at the genus level.

Bacterial genera	FT	D	FT x D
<i>Acidothermus</i>	0.512	0.232	0.615
<i>Bacillus</i>	0.176	0.182	0.770
<i>Bradyrhizobium</i>	0.114	0.035*	0.531
<i>Burkholderia-Caballeronia-Paraburkholderia</i>	0.535	0.136	0.214
<i>Candidatus Udaeobacter</i>	0.825	0.683	0.283
<i>Crossiella</i>	0.011*	0.003**	0.140
<i>Kitasatospora</i>	0.963	0.747	0.209
<i>Lysinibacillus</i>	0.830	0.048*	0.608
<i>Massilia</i>	0.762	0.176	0.281
<i>Paenibacillus</i>	0.080	0.008**	0.340
<i>Pedomicrobium</i>	0.583	0.783	0.123
<i>Phenyllobacterium</i>	0.009**	0.648	0.804
<i>Rhodanobacter</i>	0.650	0.029*	0.384
<i>Rhodoplanes</i>	0.389	0.053	0.387
<i>Sphingomonas</i>	0.131	0.003**	0.473
<i>Sporosarcina</i>	0.431	0.094	0.150
<i>Streptomyces</i>	0.576	0.177	0.051
Subgroup_2	0.395	0.025*	0.851
<i>Tumebacillus</i>	0.003**	0.0001***	0.008**

*, **, and *** indicate significance at $P < 0.05$, 0.01 and < 0.0001 , respectively.