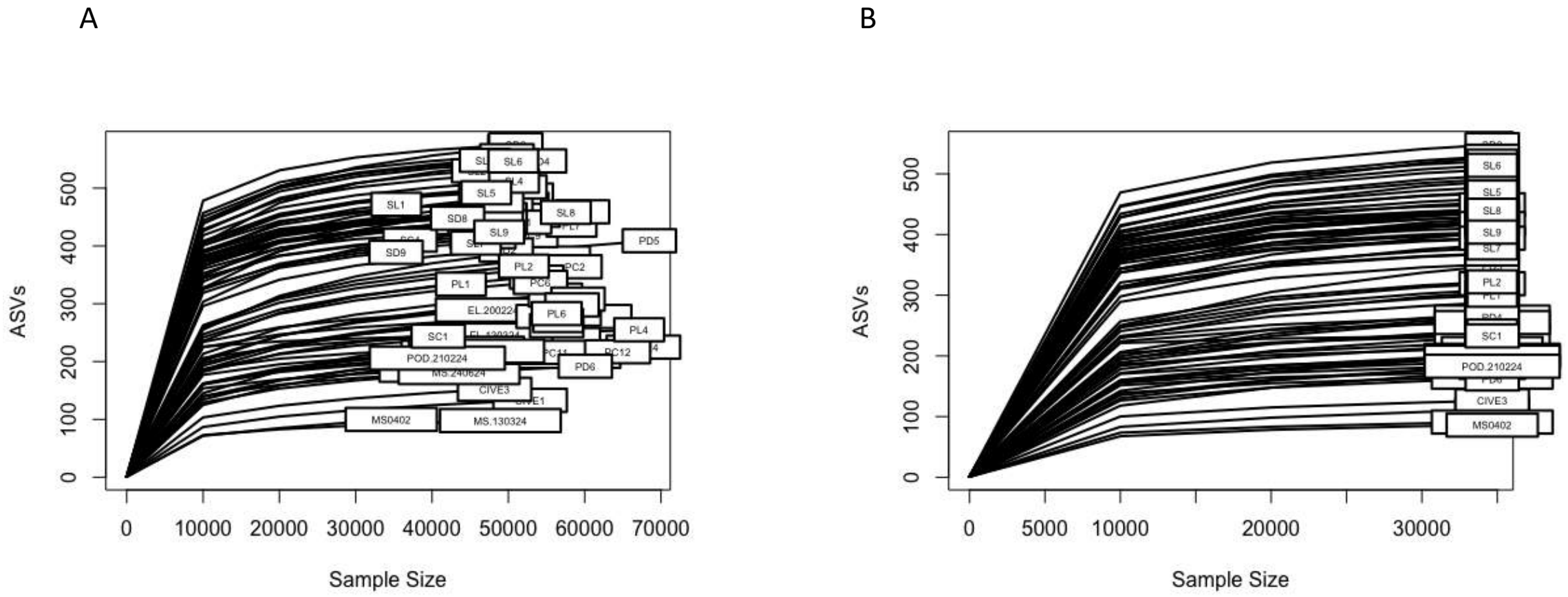
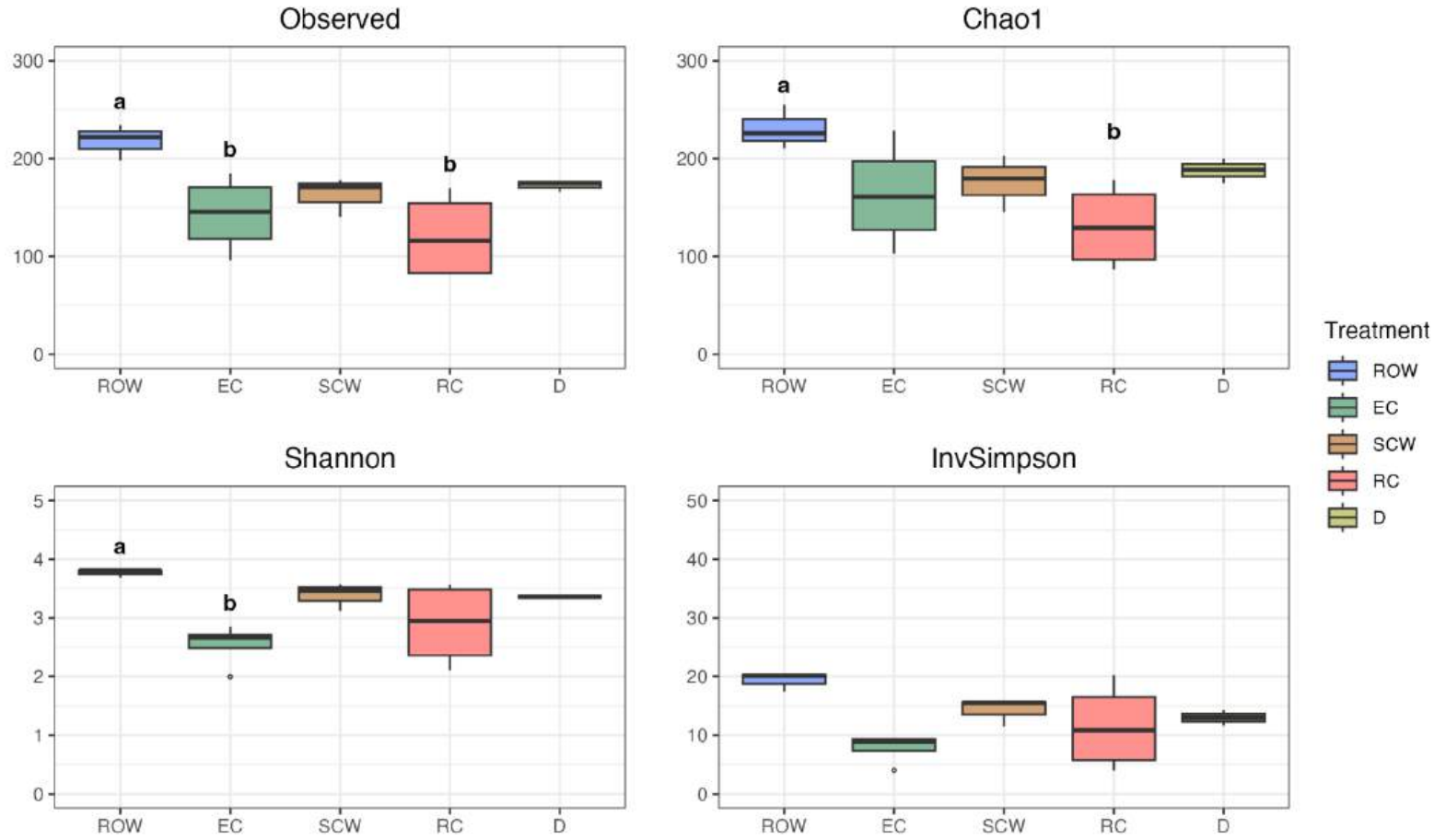
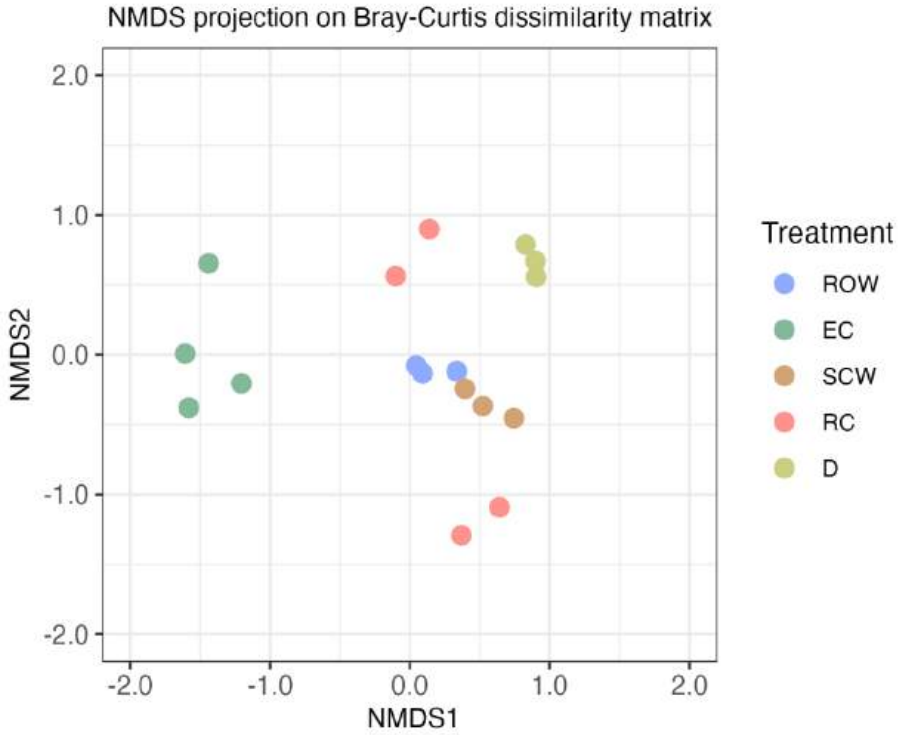


Supplementary Figure 1. Rarefaction curves based on (A) non-rarefied data and (B) data rarefied to the sequencing depth of the sample with the lowest read count (MS0402, 35,447 reads).



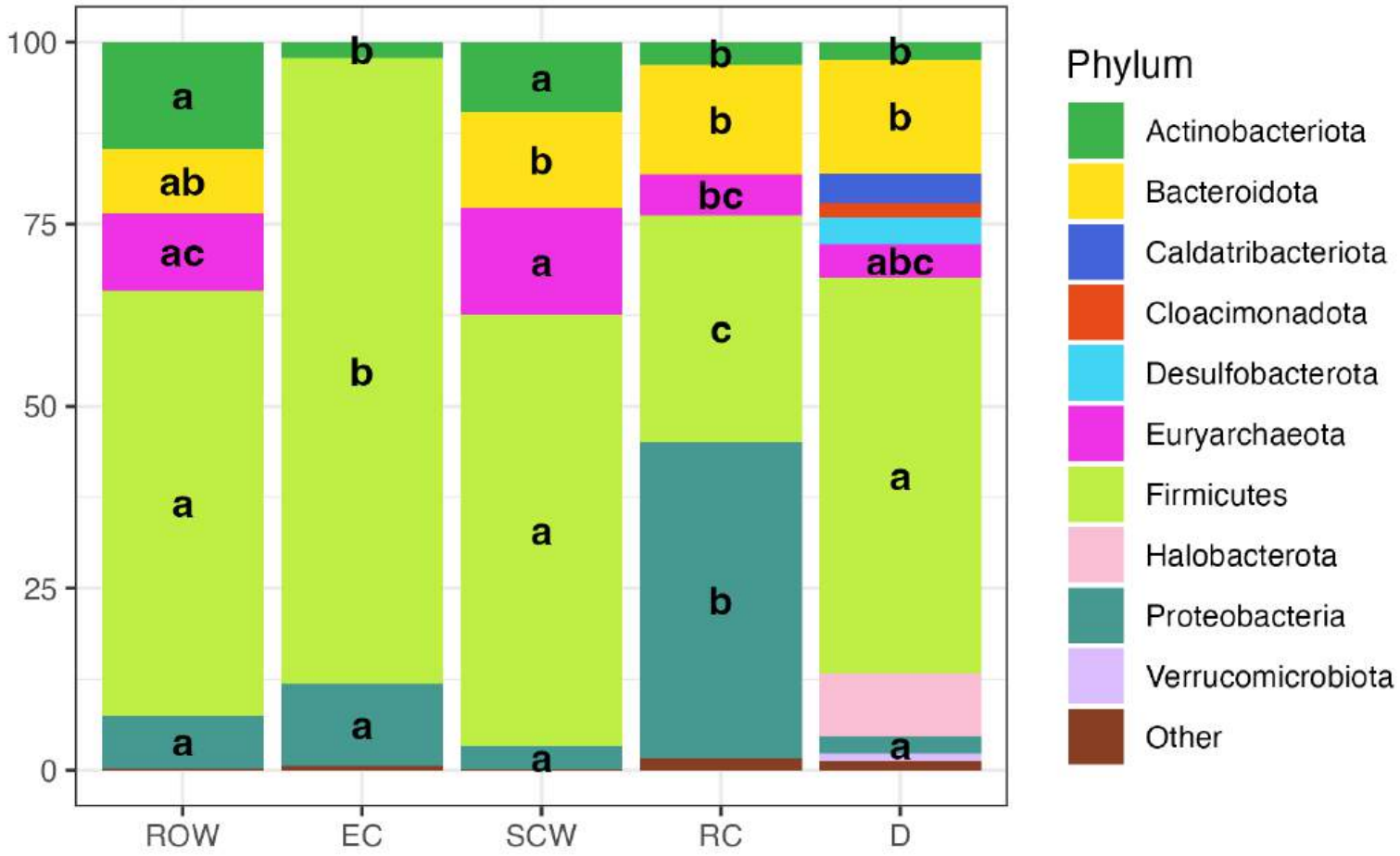
Supplementary Figure 2. Alpha diversity analysis of organic waste samples. Statistically significant differences in alpha diversities were calculated using ANOVA (Analysis of Variance) with the formula "Alpha diversity ~ Type of organic waste" using the aov function from the *stats* package in R. Pairwise comparisons were performed using estimated marginal means with the emmeans function from the *emmeans* package in R, with Tukey-adjusted *p*-values. Significant differences are indicated on the figure using lowercase letters. ROW: Raw Total Organic wastes; EC: Energy Crops; SCW: Cattle slurry enriched with 8–10% cheese whey; RC: Rumen Content, D: Digestate.



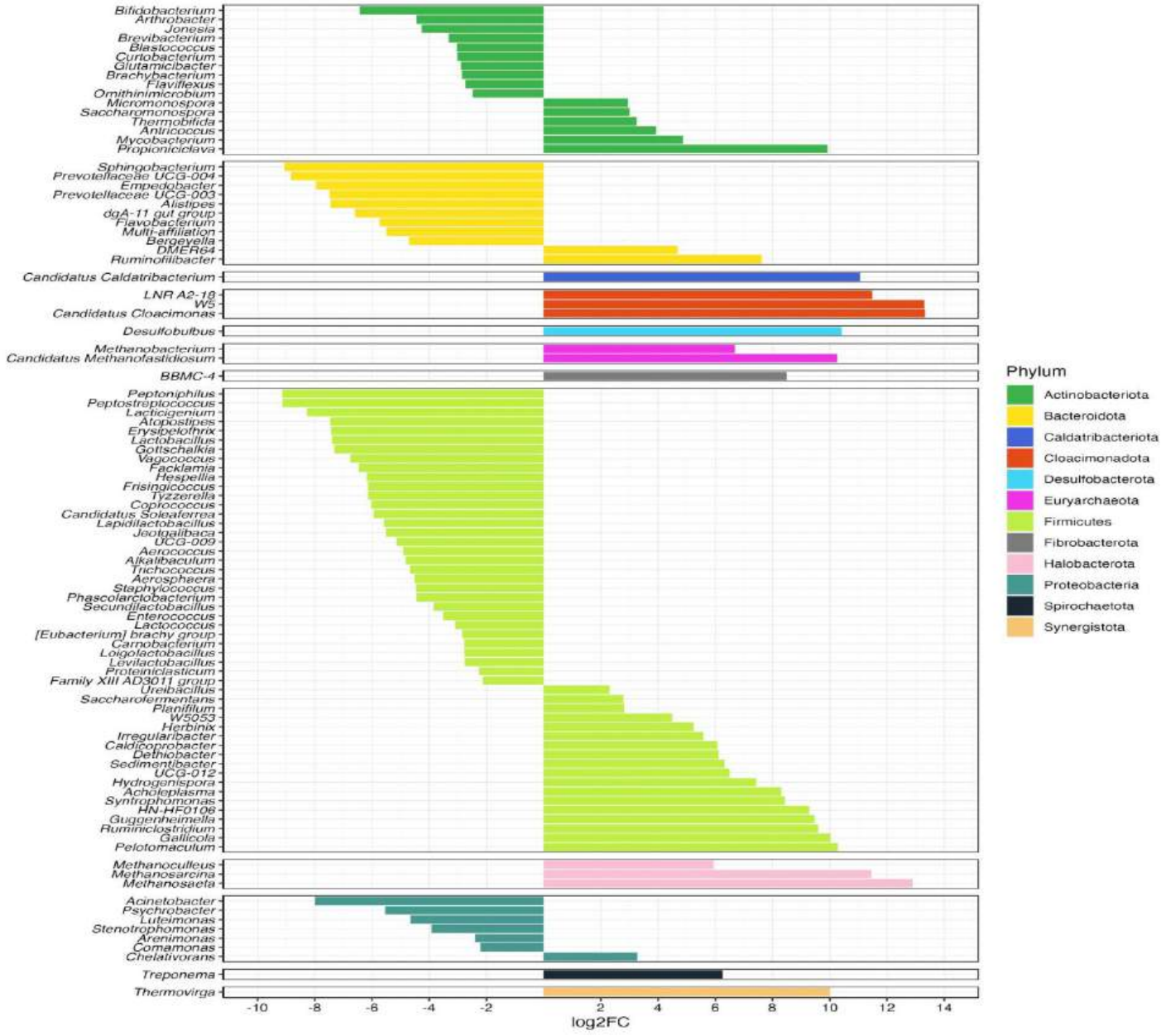
Supplementary Figure 3. Non-metric multidimensional scaling on Bray-Curtis dissimilarity matrix of organic waste samples. Statistically significant differences in Bray-Curtis dissimilarity were calculated using Permutational Multivariate Analysis of Variance (PERMANOVA) with the formula "Beta distance ~ Type of organic waste" using the adonis2 function from *vegan* package in R. Pairwise comparisons were performed with pairwise multilevel comparison using pairwise.adonis2 function from *pairwiseAdonis* R package (*n* = 999 permutations). Statistically significant differences are reported in Supplementary Table 6.
ROW: Raw total Organic Wastes; EC: Energy Crops, SCW: Cattle slurry enriched with 8–10% cheese whey; RC: Rumen Content; D: Digestate.

Comparison of permutational multivariate analysis of variance (PERMANOVA) was done using adonis function from vegan package on different beta-diversity metrics computed from organic matters samples (ROW,EC, SCW, RC, D). Pr(>F) indicates the permutation-based p-value.									
Beta-diversity metric	Bray-Curtis	Jaccard							
Pr(>F)	0.001 ***	0.002 **							

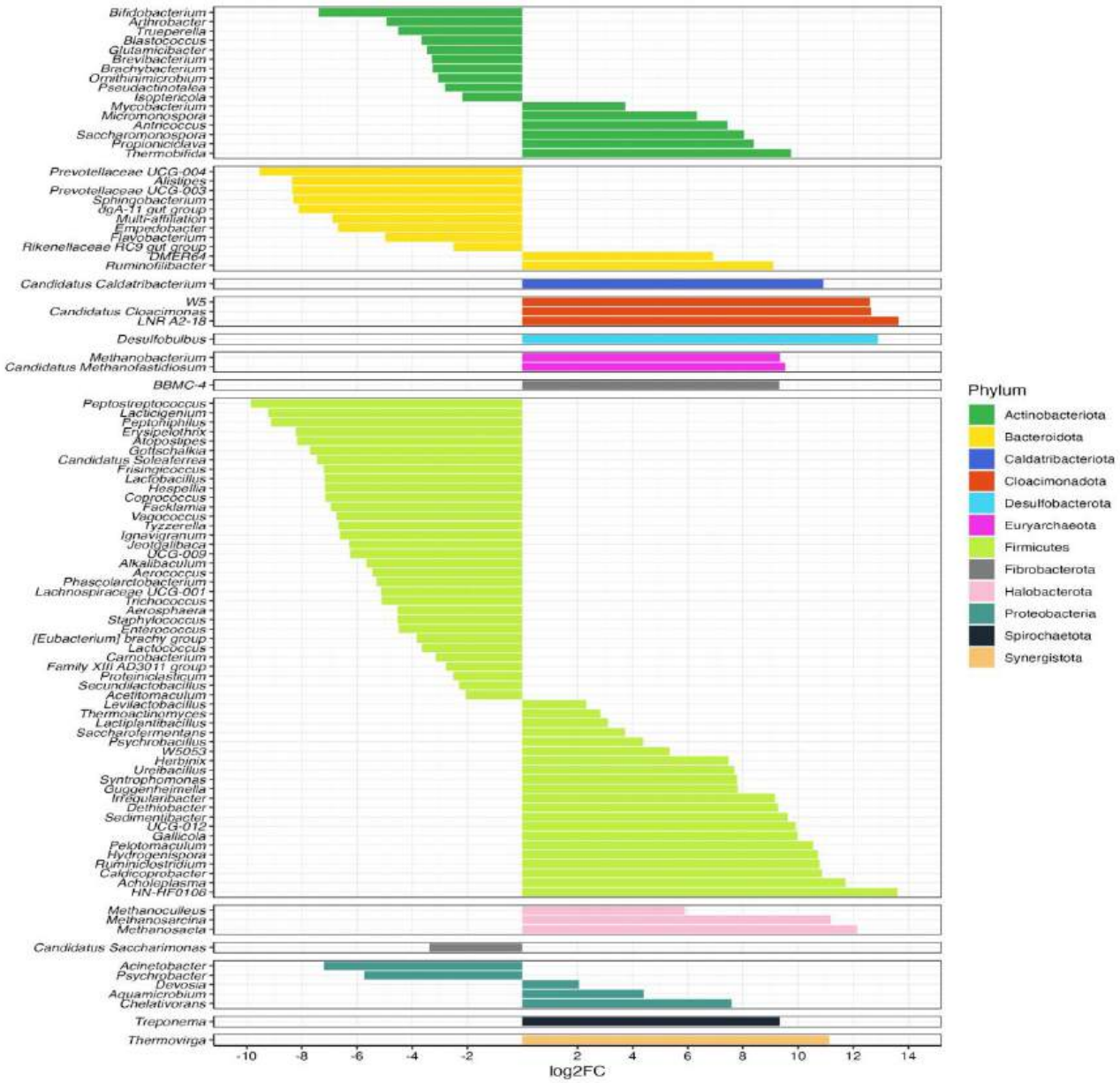
Pas de différences significatives en comparaisons multiples



Supplementary Figure 4. Relative average abundance (%) of V4 16S rRNA gene reads assigned to bacterial phyla in organic waste samples. Only phyla with a mean relative abundance above 1% are shown; phyla below this threshold are grouped under "Other." Statistically significant differences in phylum abundances are indicated by lowercase letters. Differences were tested using Analysis of Variance (ANOVA) with the model *Relative abundance ~ Organic waste*, implemented via the aov function from the stats package in R. Pairwise comparisons were conducted using estimated marginal means (emmeans function, emmeans package) with Tukey-adjusted p-values. Abbreviations: ROW, Raw Organic Wastes; SCW, Cattle slurry enriched with 8–10% cheese whey; RC, Rumen Content; EC, Energy Crops.

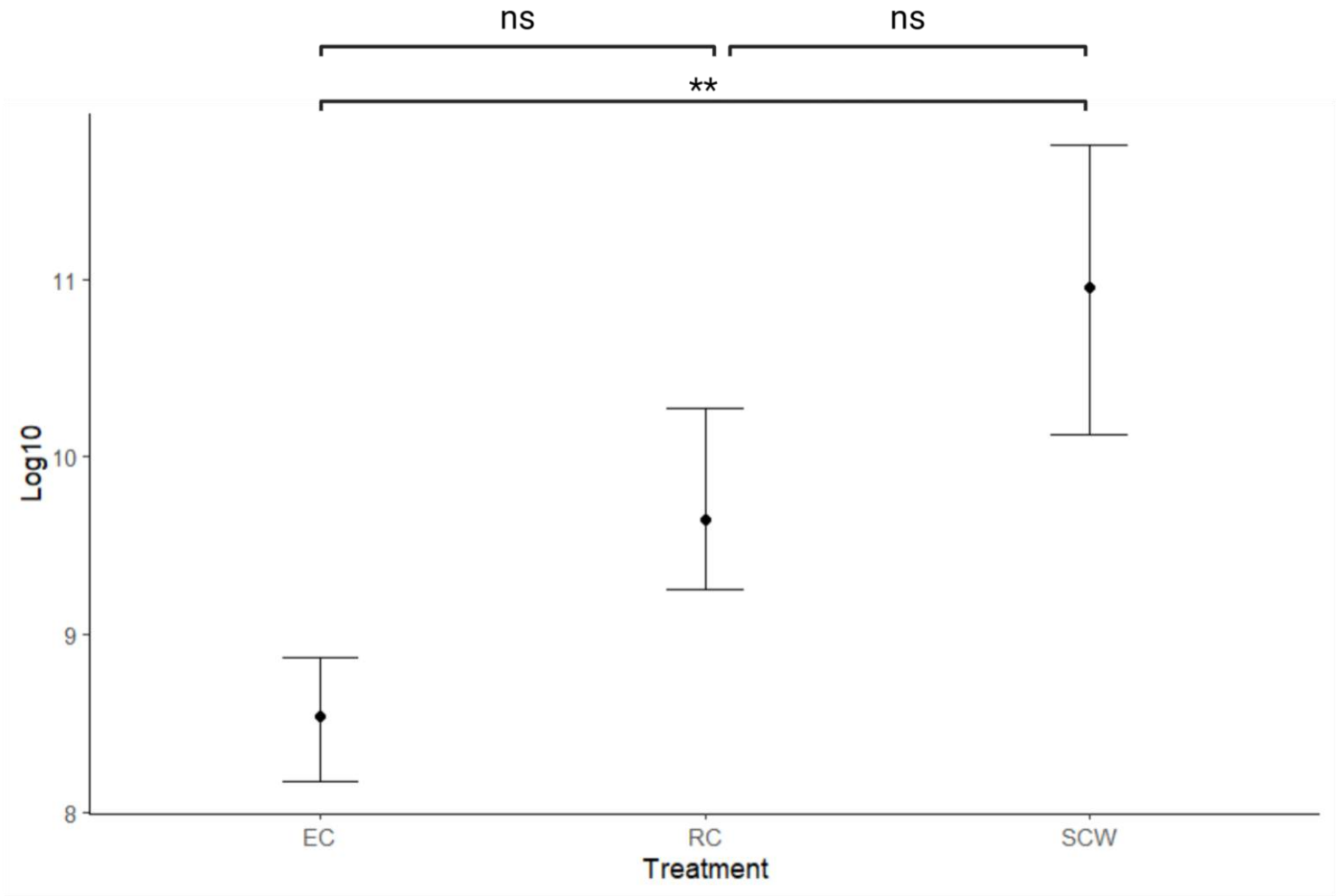


Supplementary Figure 4a. Significant changes in the relative abundance of bacterial genera, as inferred from V4 16S rDNA ASV contingency tables comparing total raw organic wastes and their corresponding digestates. Differential abundance was assessed using DESeq2. Only genera meeting the following criteria are shown: log2 fold change ≤ –2 or ≥ +2, *padj* < 0.05, and a minimum normalized read count of 10. Genera of unknown identity were excluded from the figure for clarity but are listed in Supplementary Table 15. A positive log2FC indicates a higher relative abundance in digestates compared to raw wastes. Genera are color-coded according to their phylum.

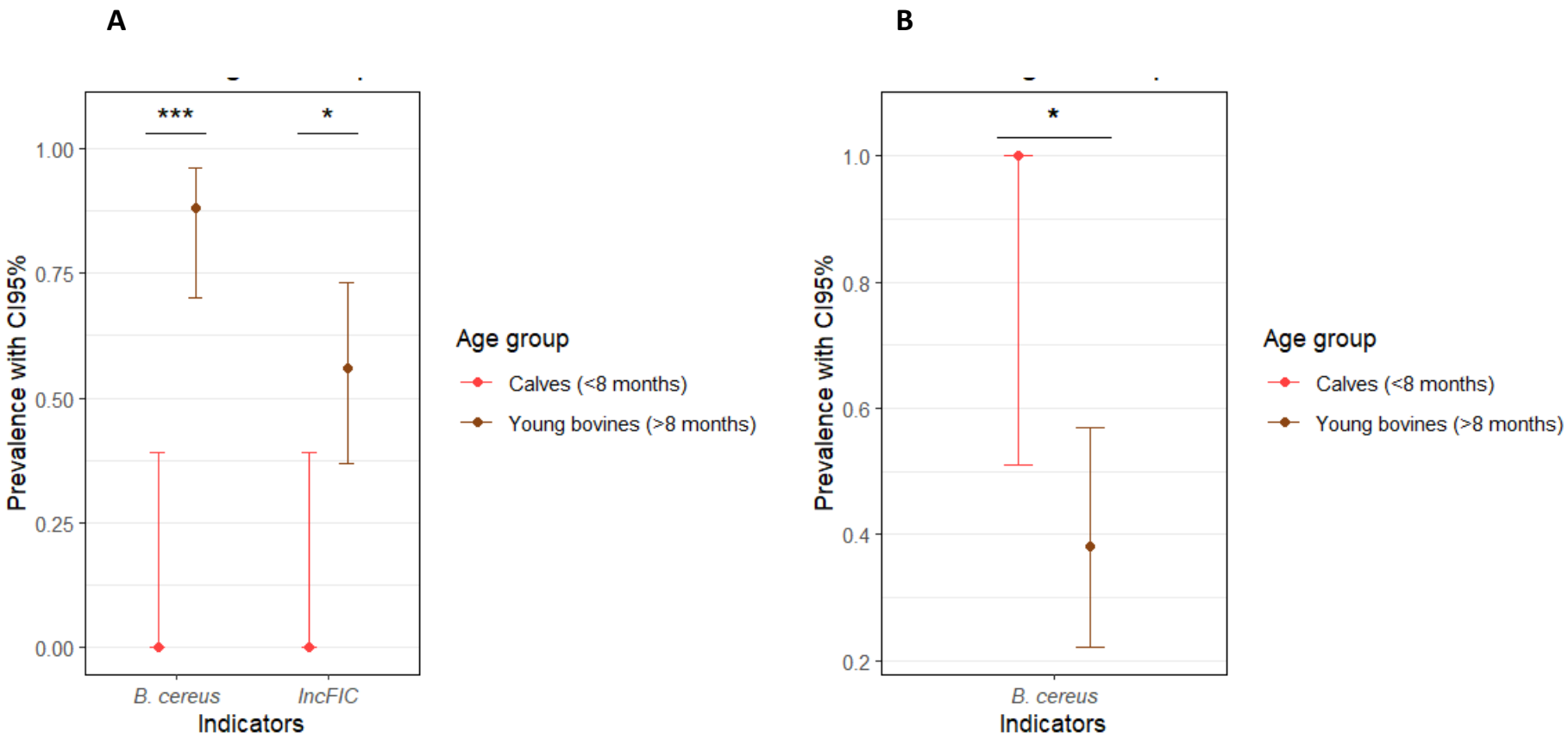


Supplementary Figure 4b. Significant shifts in bacterial genera between cattle slurry enriched with 8–10% cheese whey (SCW) and its corresponding digestate, both used as biofertilizers. SCW was also used as an input material for anaerobic digestion to produce the digestate. Differential abundance was assessed using DESeq2. Only genera with $\log_2$ fold-change ≤ -2 or $\geq +2$, *padj* < 0.05, and a minimum normalized read count of 10 are shown. Genera of unknown identity were excluded for clarity (their distribution is provided in Supplementary Table 15). Positive $\log_2$ FC values indicate greater relative abundance in the digestate than in SCW. Genera are colour-coded by phylum.

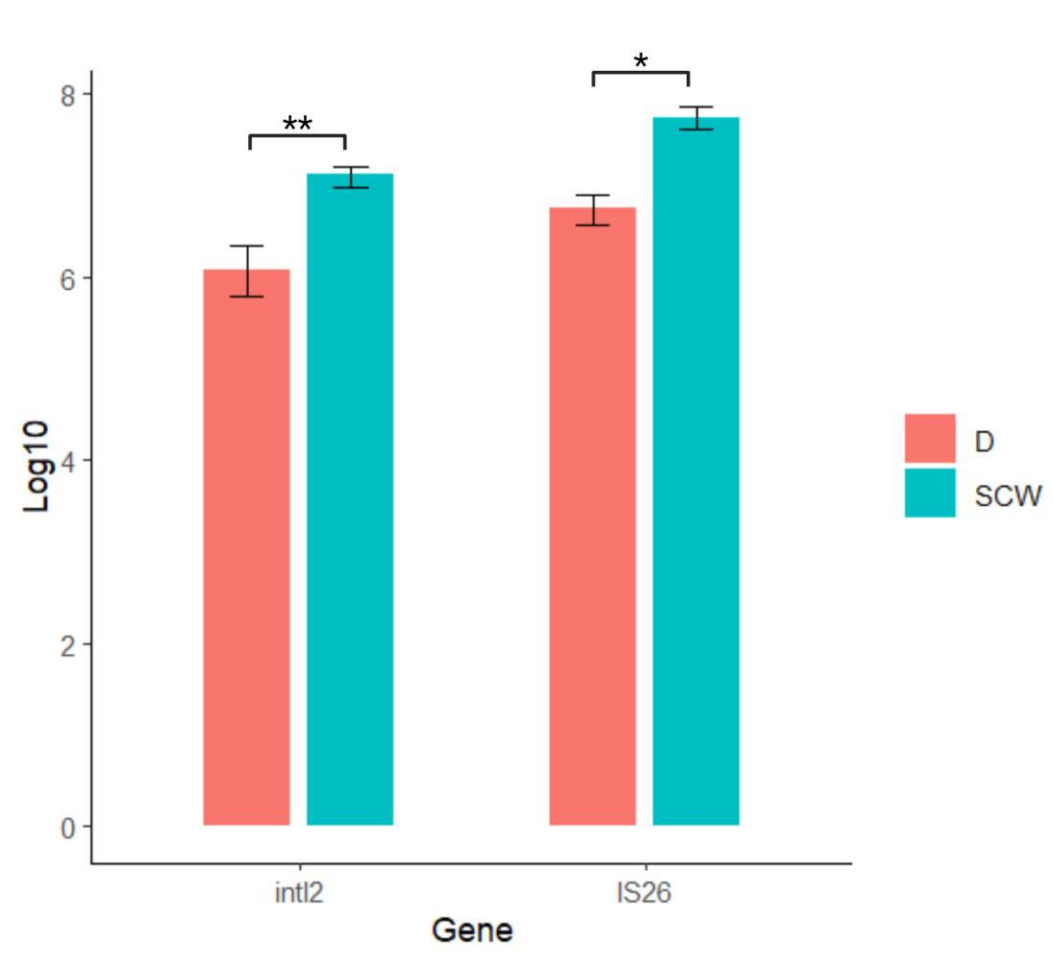
Supplementary Figure 4c. Significant changes in the relative abundance of bacterial genera between rumen content (RC) and its corresponding digestate, as inferred from V4 16S rDNA ASV contingency tables. Differential abundance was assessed using DESeq2. Only genera with significant changes ($\log_2$ fold-change ≤ -2 or $\geq +2$, *padj* < 0.05, and a minimum normalized read count of 10) are shown. Genera of unknown identity are excluded for clarity, but their distribution is detailed in Supplementary Table 15. Positive $\log_2$ FC values indicate higher relative abundance in the digestate than in RC. Genera are colour-coded by their respective phylum.



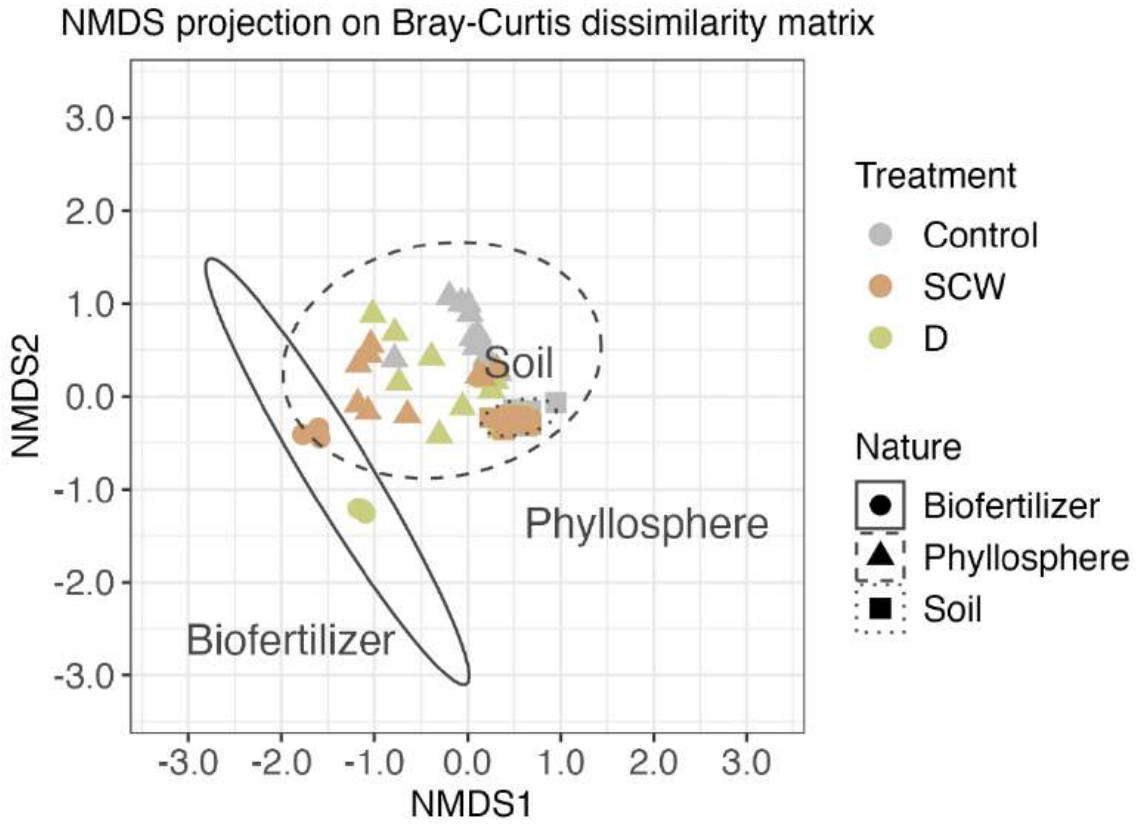
Supplementary Figure 5. Absolute abundance of total bacteria, estimated via 16S rDNA quantification, in three emerging organic substrates: energy crops (EC), rumen content (RC), and slurry enriched with cheese whey (SCW). Points represent gene abundance (log_{10} copies g^{-1} dry matter); whiskers indicate 95% confidence intervals. Generalized linear models (GLMs) with a gamma distribution were fitted, and significance was assessed using Anova() from the car package (R). Estimated marginal means and 95% confidence intervals were computed with emmeans_test(). *P*-values were adjusted using the Bonferroni–Holm method (ns = not significant; $p < 0.05$*; $p < 0.01$**; $p < 0.001$***). Gene abundances are not normalized to 16S rDNA copy numbers. Figure created with BioRender.com.



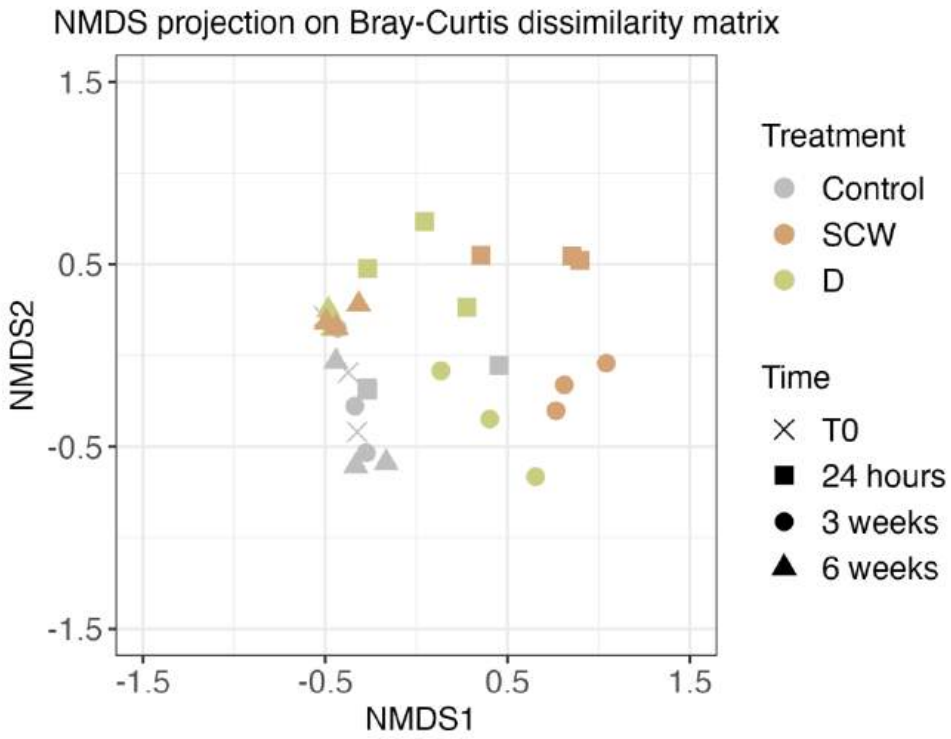
Supplementary Figure 6. Prevalence of RT-PCR-detected indicators in the recto-anal junction (A) and rumen (B) of calves (n = 6; < 8 months) and young cattle (n = 26; > 8 months). Dots represent prevalence estimates; error bars indicate 95% confidence intervals calculated using the Wilson method (*BinomCI* function, *DescTools* package, R), as recommended by Agresti & Coull (1998) and Brown et al. (2001). Differences between age groups were assessed using Fisher's exact test (*fisher.test*, *stats* package). Only statistically significant differences are shown, indicated by horizontal bars and asterisks ($p < 0.05$*; $p < 0.01$**; $p < 0.001$***).



Supplementary Figure 7. Statistically significant differences in absolute abundances of sanitary indicator genes between cattle slurry enriched with 8–10% cheese whey (SCW) and its corresponding digestate (D), both used as biofertilizers. SCW was also used as an input for anaerobic digestion to produce the digestate. Generalized linear models (GLMs) with a gamma distribution were fitted using the Anova() function from the **car** package in R. Only significant results (IS26 and IntI2) are shown. Points represent gene abundance (log_{10} copies/g dry matter); error bars indicate 95% confidence intervals. Estimated marginal means (EMMs) and confidence intervals were calculated using the emmeans_test() function in R. *P*-values were adjusted using the Bonferroni–Holm method (ns = not significant; $p < 0.05$*; $p < 0.01$**; $p < 0.001$***). Gene abundances are not normalized to 16S rDNA copy numbers. Figure created with BioRender.com.

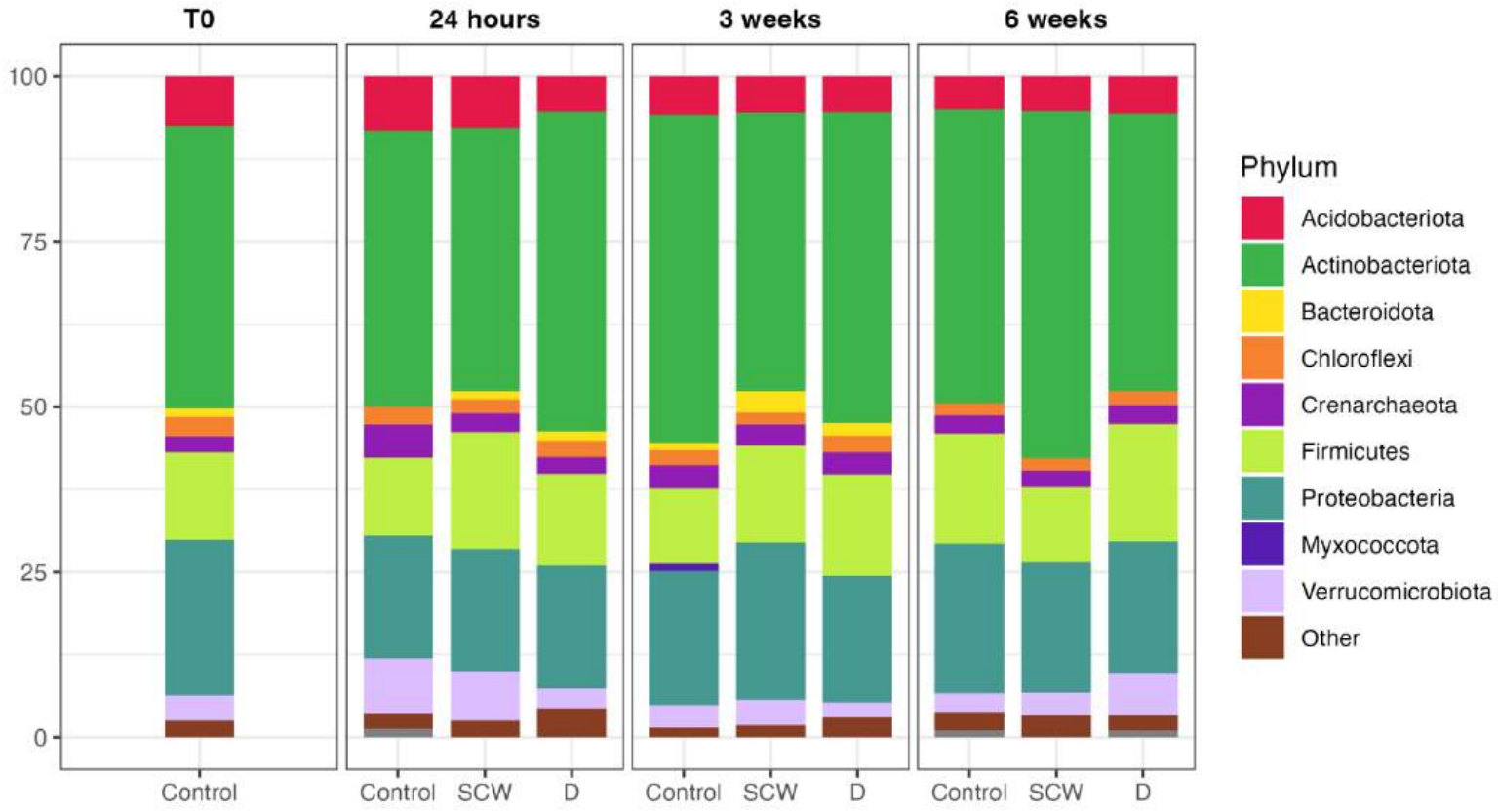


Supplementary Figure 8. Non-metric multidimensional scaling (NMDS) ordination based on Bray–Curtis dissimilarities of biofertilizers (SCW, D), fertilized phyllosphere, and soil samples. Differences in community composition (beta diversity) were assessed using permutational multivariate analysis of variance (PERMANOVA) with the model *Bray–Curtis distance ~ Sample type × Treatment*, implemented via the adonis2 function from the vegan package in R. Pairwise comparisons were performed using the pairwise.adonis2 function from the pairwiseAdonis package (999 permutations). Statistically significant comparisons are reported in Supplementary Table 11. SCW: cattle slurry enriched with 8–10% cheese whey; D: digestate.

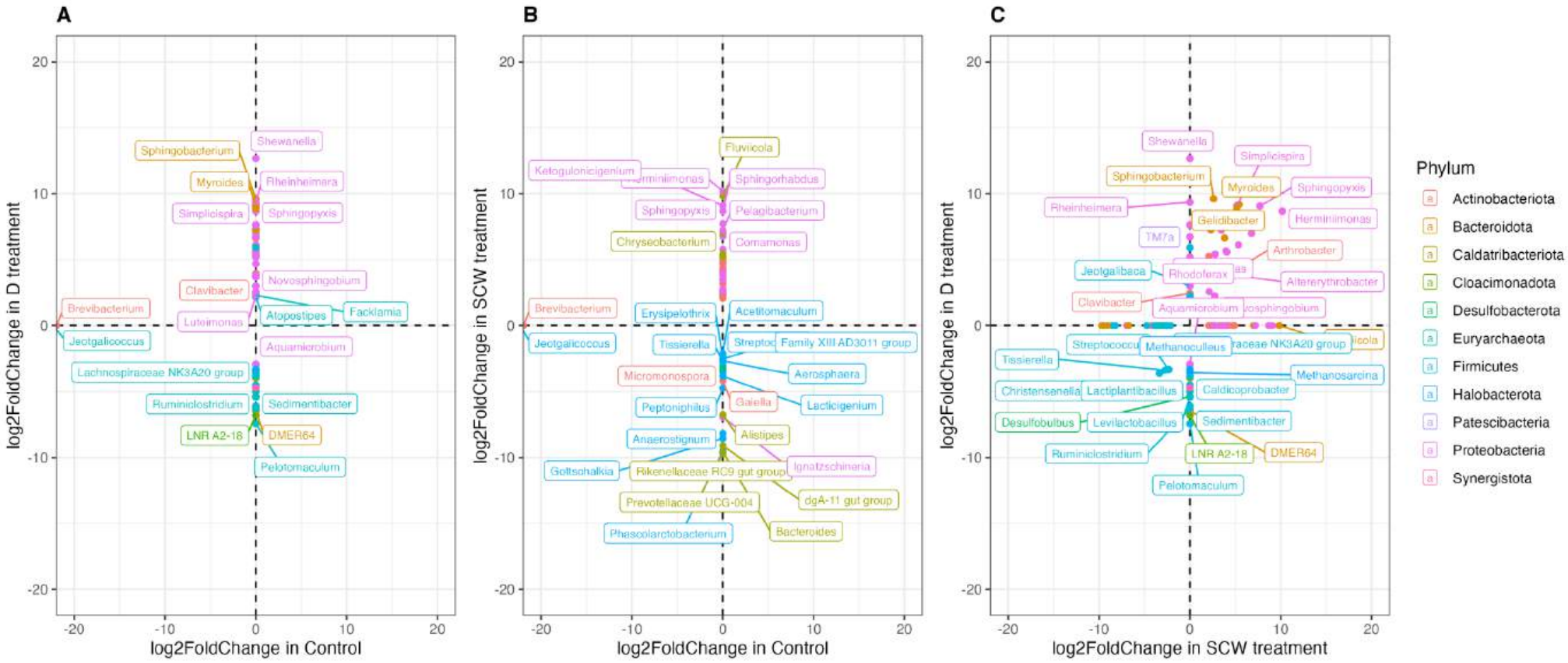


Supplementary Figure 9. Non-metric multidimensional scaling on Bray-Curtis dissimilarity matrix of phyllosphere samples. Statistically significant differences in Bray-Curtis dissimilarity were calculated using Permutational Multivariate Analysis of Variance (PERMANOVA) with the formula "Beta distance ~ Time (T0, 24 hours, 3 weeks or 6 weeks) * Treatment (Digestate, SCW or Control)" using the adonis2 function from *vegan* package in R. Pairwise comparisons were performed with pairwise multilevel comparison using pairwise.adonis2 function from *pairwiseAdonis* R package (n = 999 permutations). Statistically significant differences are reported in Supplementary Table 11. SCW: Cattle slurry enriched with 8–10% cheese whey, D: Digestate.

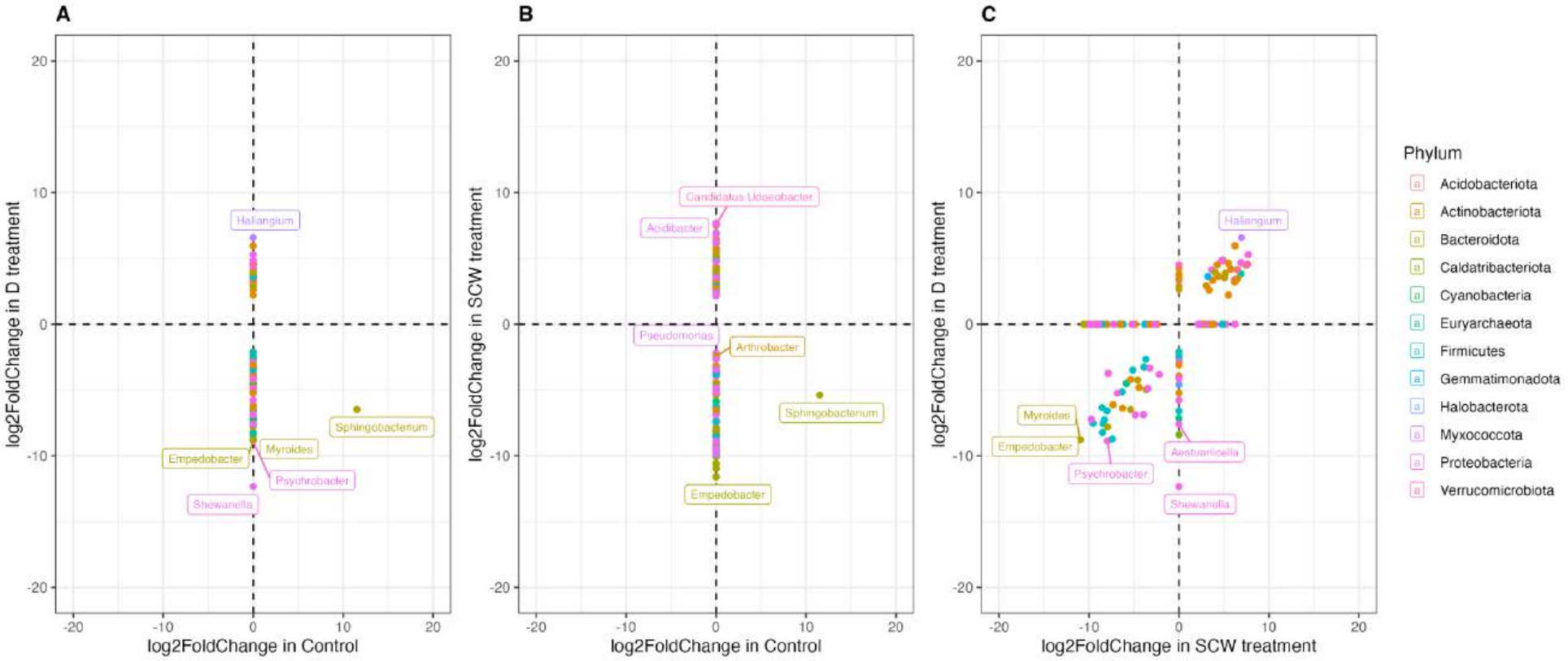
Abondance relative au niveau du phylum pour le sol



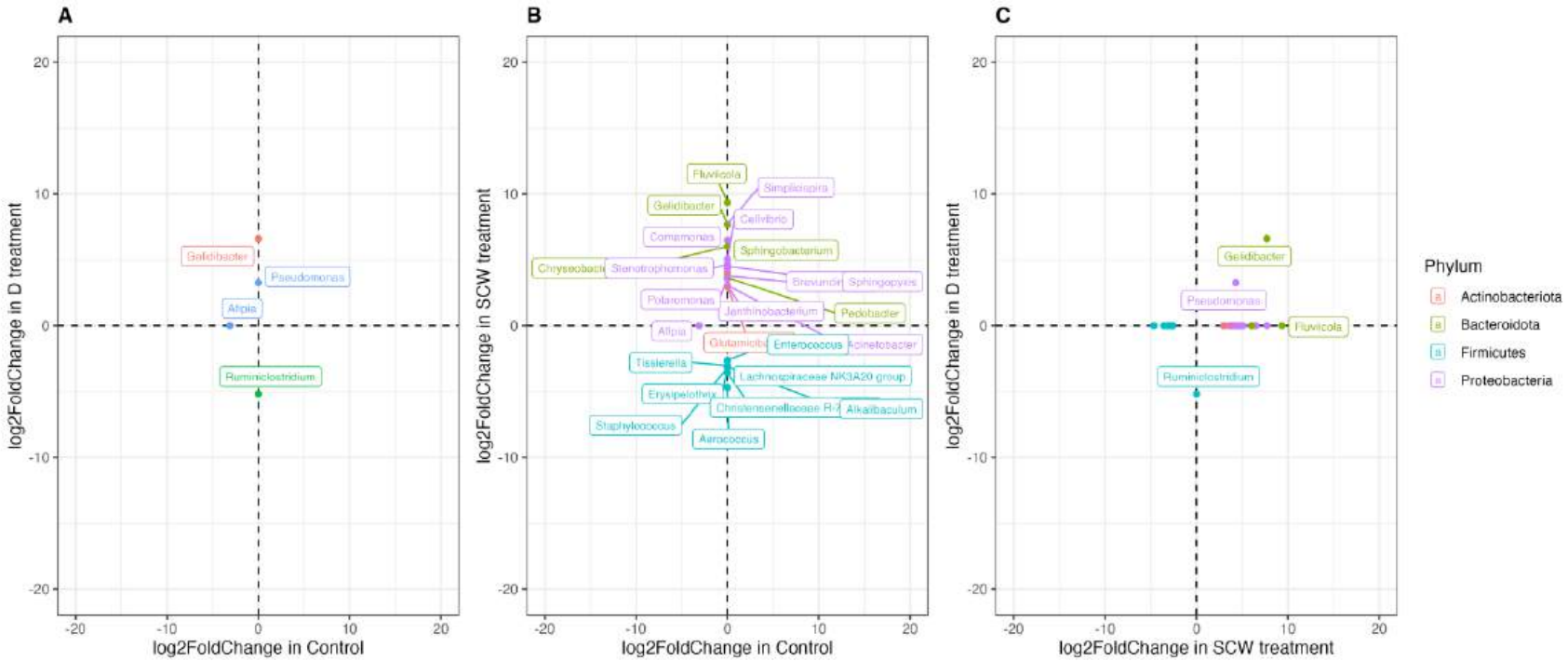
Supplementary Figure 10. Relative averaged abundance (%) of V4 16S rRNA gene reads allocated to phyla in soil samples. Only phyla with a relative abundance above 1% are displayed. Phyla with a relative abundance less than 1% are grouped in Other. Differences between abundances were computed using Analysis of Variance (ANOVA) with the formula "Relative abundance ~ Time * Treatment" using the aov function from the *stats* package in R. Pairwise comparisons were performed using estimated marginal means with the emmeans function from the *emmeans* package in R, with Tukey-adjusted *p*-values.
SCW: Cattle slurry enriched with 8–10% cheese whey, D: Digestate. For more details, see Supplementary Table 21.



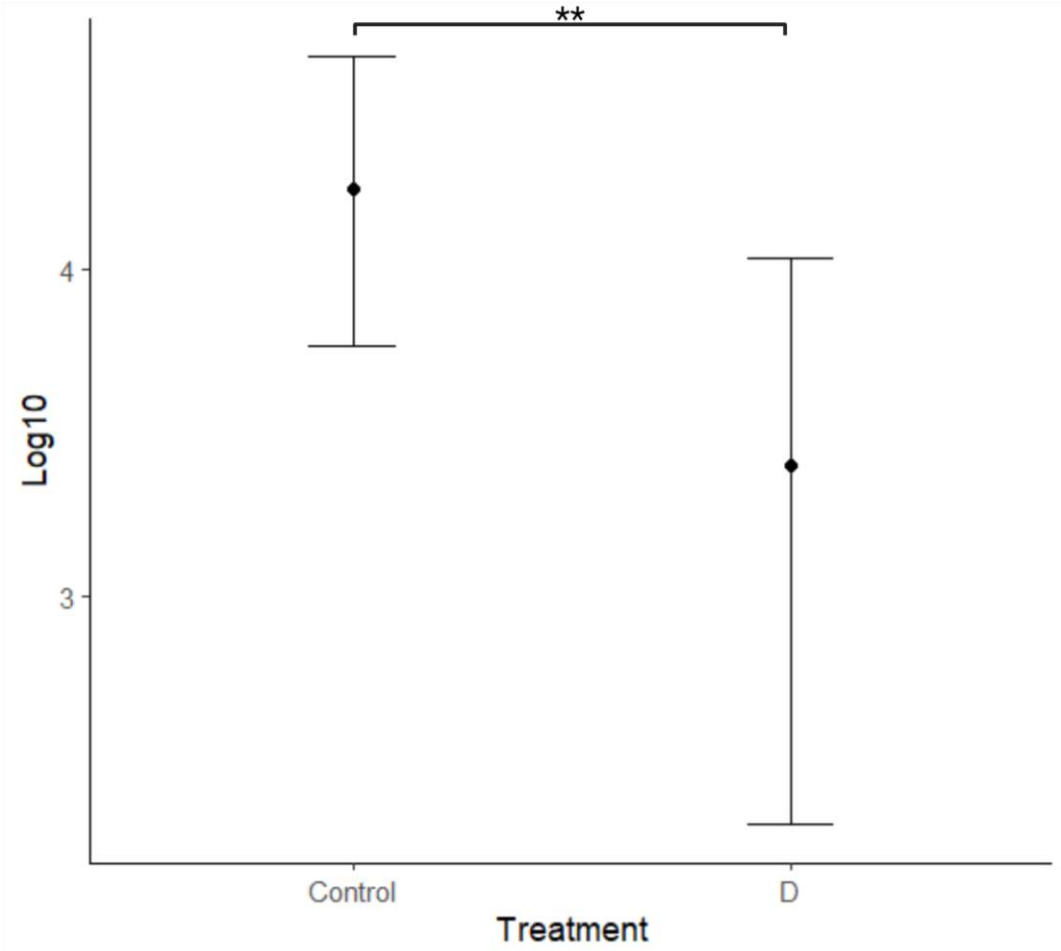
Supplementary Figure 11. Plots of genera with significant changes in relative abundance between 24 hours and 3 weeks. Evolutions are compared for **(A)** without treatment (control) *vs* digestate treated phyllosphere **(B)** without treatment (control) *vs* S+W treated phyllosphere **(C)** S+W *vs* digestate treated phyllosphere. Log2 fold-change was calculated using DESeq2 and based on the bacterial genera inferred from the 16S rRNA gene ASVs contingency tables (Supplementary Table 2). Samples were collected at 0-15 cm. Only genera with significant changes ($-2 \geq \text{Log2 FC} \geq +2$, padj < 0.05, minimum normalized read count = 10) were shown. Genera with unknown affiliation at genus level or multi-affiliated were excluded from the plots. For better lisibility not all genus annotation are shown (see Supplementary Tables 24 and 25 for the complete dataset). Genera are colored according to the phylum to which they belong.



Supplementary Figure 12. Plots of genera with significant changes in relative abundance between 3 weeks and 6 weeks. Evolutions are compared for **(A)** without treatment (control) *vs* digestate treated phyllosphere **(B)** without treatment (control) *vs* S+W treated phyllosphere **(C)** S+W *vs* digestate treated phyllosphere. Log2 fold-change was calculated using DESeq2 and based on the bacterial genera inferred from the 16S rRNA gene ASVs contingency tables (Supplementary Table 2). Only genera with significant changes ($-2 \geq \text{Log2 FC} \geq +2$, padj < 0.05, minimum normalized read count = 10) were shown. Genera with unknown affiliation at genus level or multi-affiliated were excluded from the plots. For better lisibility not all genus annotation are shown (see Supplementary Table 25 for the complete dataset). Genera are colored according to the phylum to which they belong.



Supplementary Figure 13. Plots of genera with significant changes in relative abundance between 24 hours *vs* 3 weeks. Evolutions are compared for **(A)** without treatment (control) *vs* digestate treated soil **(B)** without treatment (control) *vs* S+W treated soil **(C)** S+W *vs* digestate treated soil. Log2 fold-change was calculated using DESeq2 and based on the bacterial genera inferred from the 16S rRNA gene ASVs contingency tables (Supplementary Table 2). Samples were collected at 0-15 cm. Only genera with significant changes ($-2 \geq \text{Log2 FC} \geq +2$, padj < 0.05, minimum normalized read count = 10) were shown. Genera with unknown affiliation at genus level or multi-affiliated were excluded from the plots. For better lisibility not all genus annotation are shown (see Supplementary Tables 26 and 27 for the complete dataset). Genera are colored according to the phylum to which they belong.



Supplementary Figure 14. Absolute abundance of the sanitary-indicator gene *ermB* in phyllosphere samples from permanent grassland plots left unamended (control) or amended with digestate (D). Points represent gene abundance (log_{10} copies g^{-1} dry matter); whiskers show 95 % confidence intervals. Statistical analysis was restricted to samples quantifiable by ddPCR and only significant results (*ermB*) are shown. Generalized linear models with a gamma error structure were fitted, and significance was assessed with Anova() (package car, R). Estimated marginal means and their 95 % confidence intervals were computed with emmeans_test(). *P*-values were adjusted using the Bonferroni–Holm method (ns = not significant; $p < 0.05$*; $p < 0.01$**; $p < 0.001$***). Gene abundances are reported without normalization to 16S rRNA gene copy numbers. Figure created with BioRender.com.