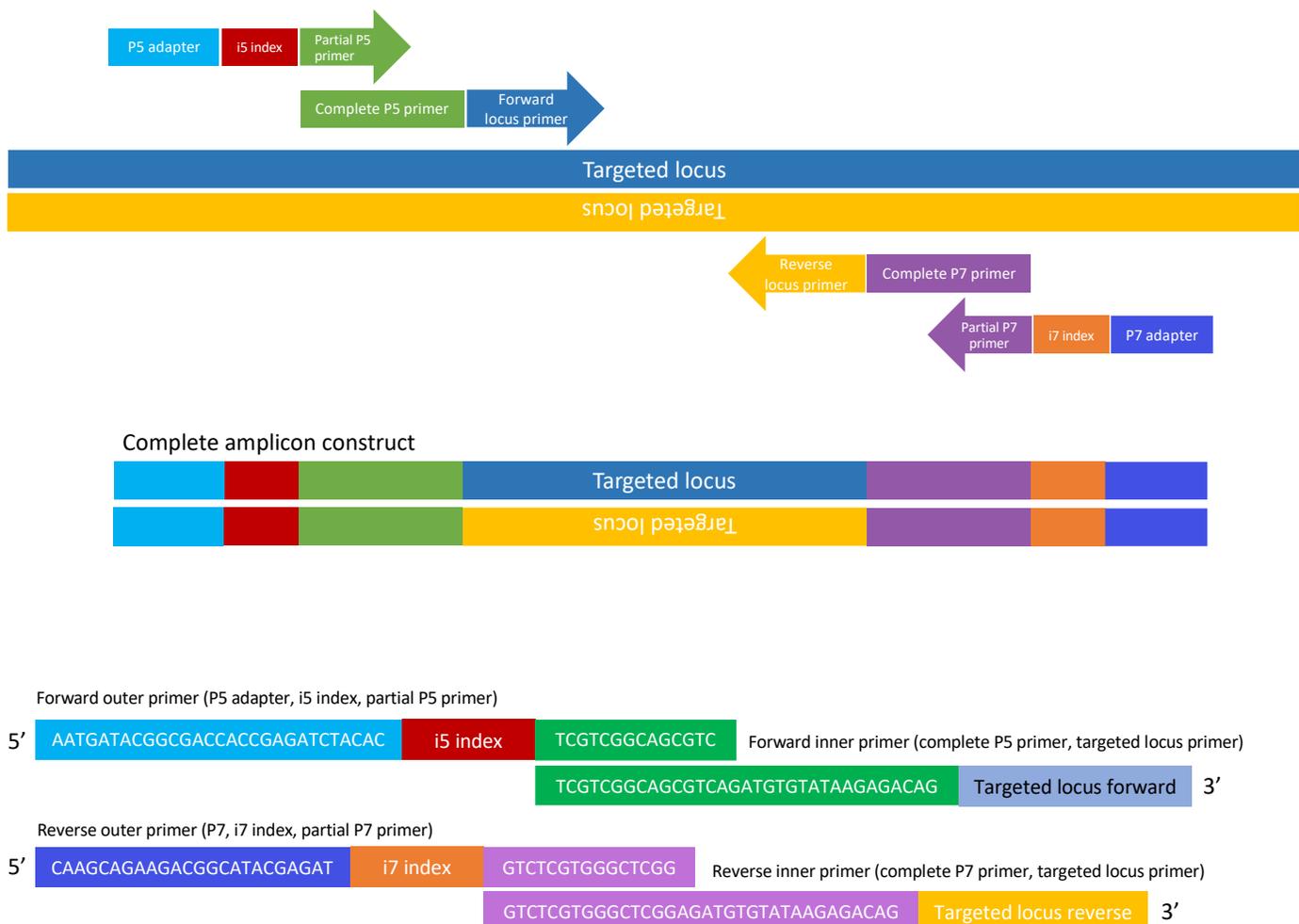
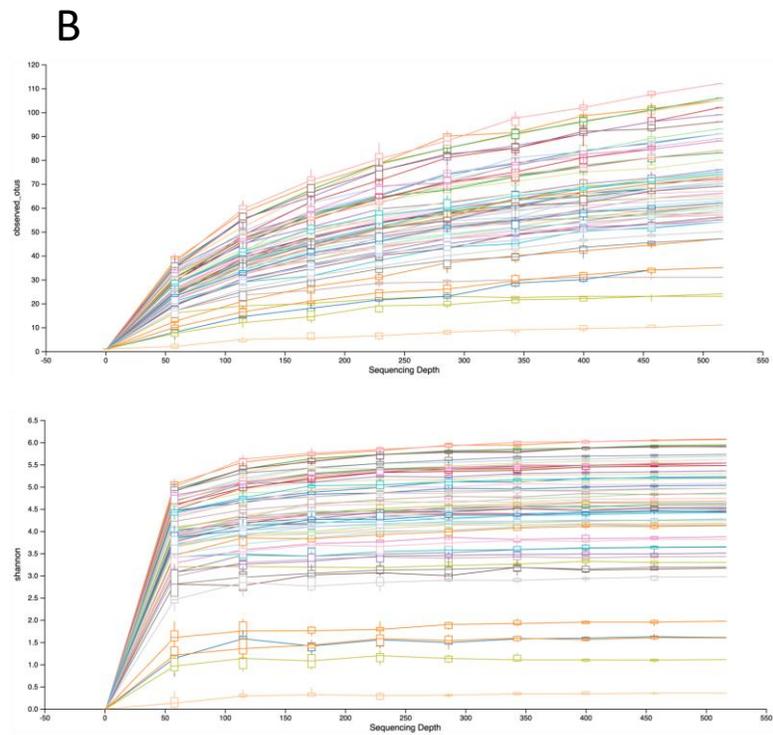
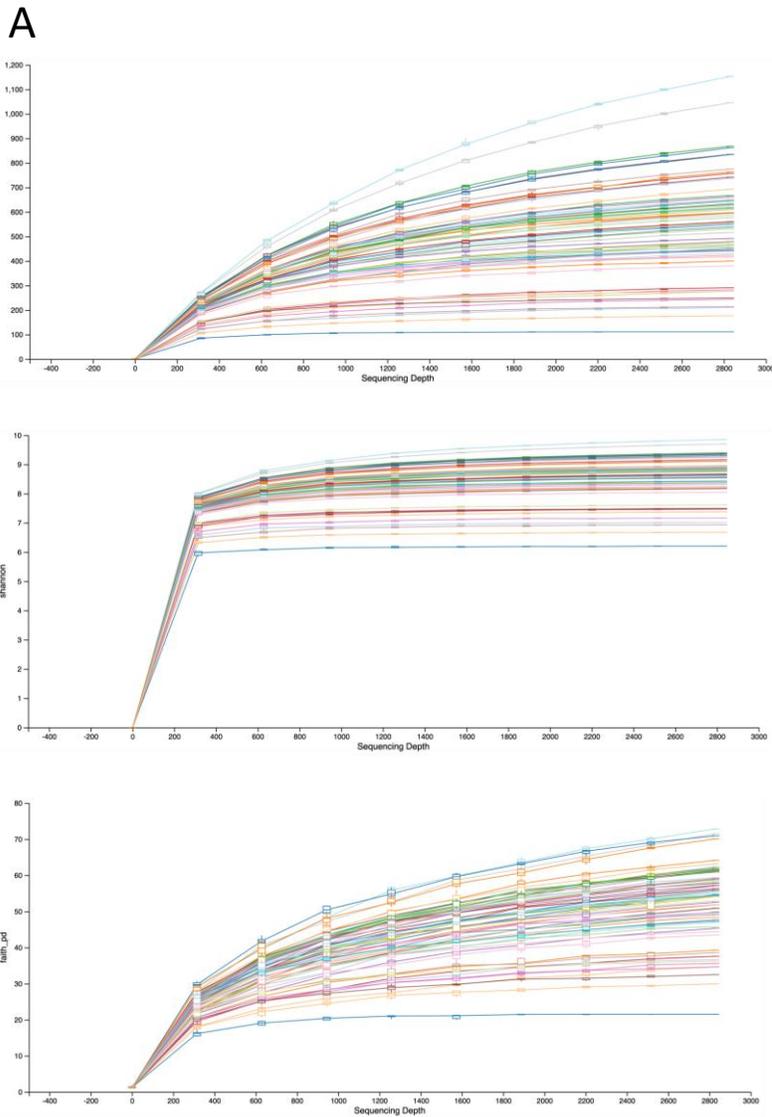


Supplementary Material

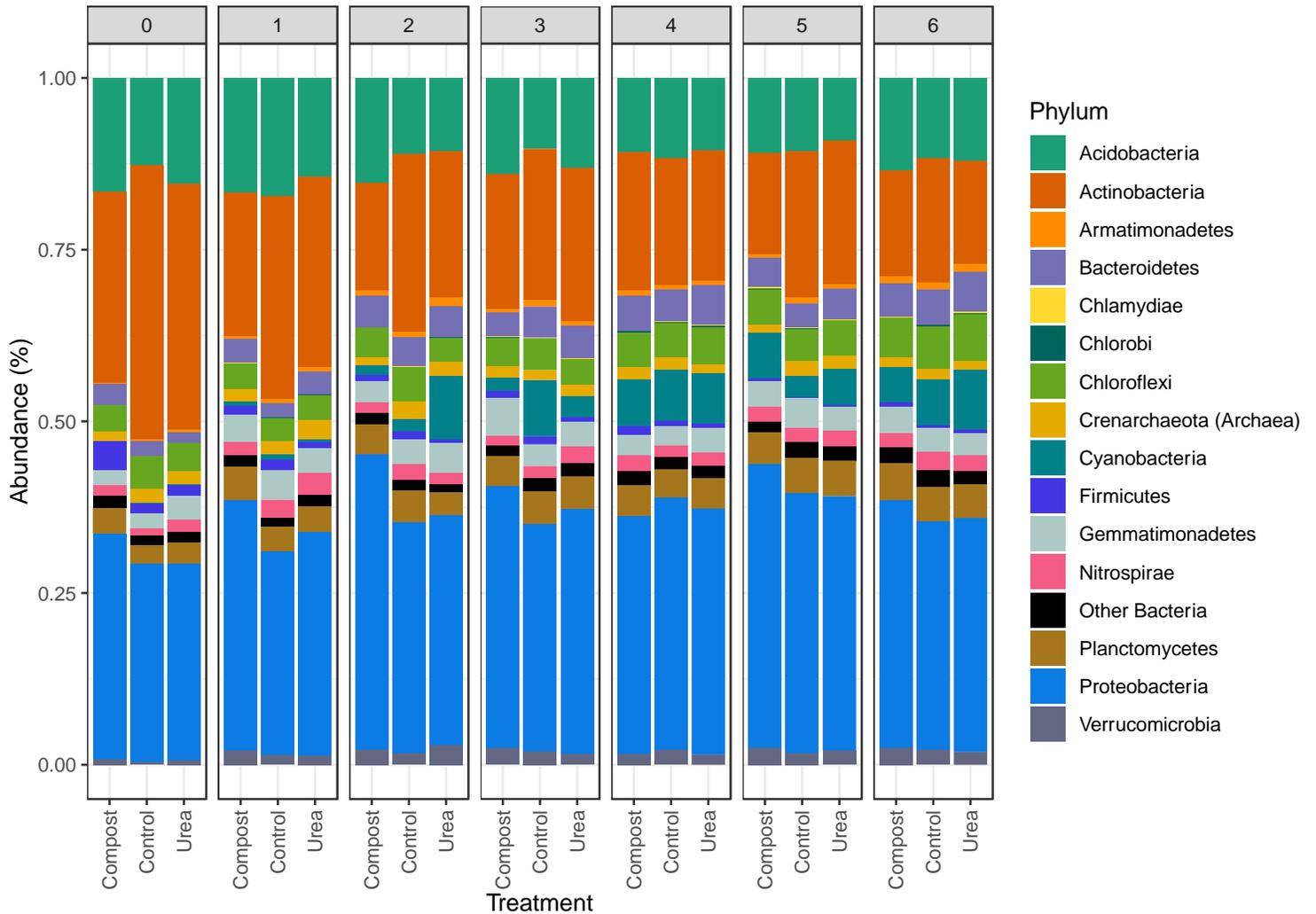
Supplementary Figures



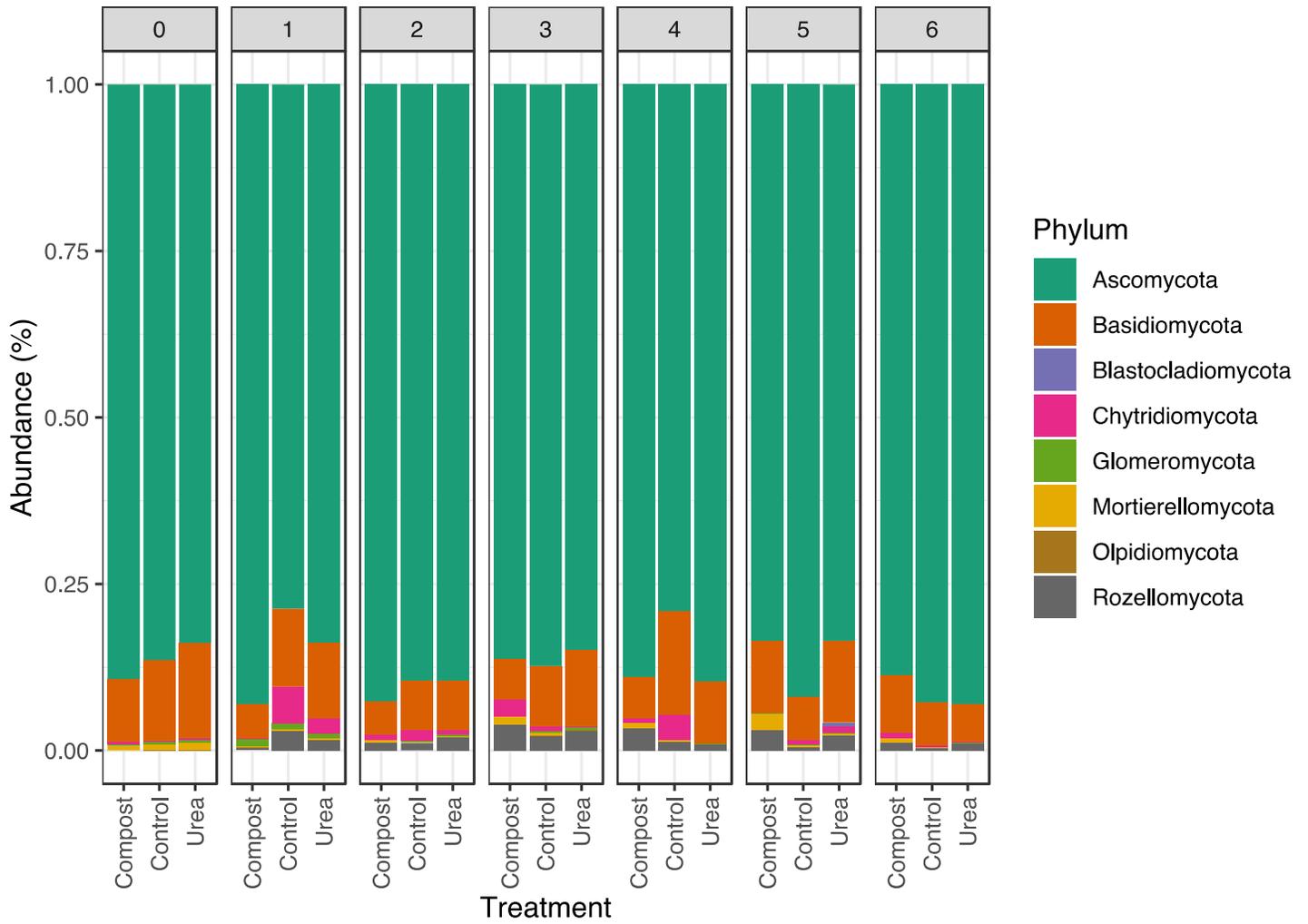
Supplementary Figure 1. Dual-barcode Illumina MiSeq primer design for a 2-step PCR process used in this work. The first primer pair amplifies the target and includes an overhang of the P5 and P7 primers. The second primer pair includes the full P5 and P7 primer, an 8 bp index (barcode) on each primer, and the P5 and P7 Illumina adapter.



Supplementary Figure 2. Rarefaction curves for all samples used in this study, showing various levels of sequencing depths across the samples. **(A)** 16S data showing observed OTU count, Shannon's Index, and Faith's PD. **(B)** ITS data showing observed OTU count and Shannon's Index. The sequence run contained 9 million reads passing initial filter with an overall Q30 > 84%. The 16S dataset contained 6,648,965 sequences with an average of 63,932 per sample. The ITS dataset contained 2,624,849 sequences with an average of 25,238 per samples. Post quality control, the 16S dataset contains 2,322,126 sequences with a median frequency of 21,800, and the ITS dataset contained 872,027 fungal OTUs with a median frequency of 7,042 per sample. There was no evidence of tag bleeding from positive nor negative controls.



Supplementary Figure 3. Stacked bar plots comparing the relative abundance of bacteria and archaea among the compost, urea, and unamended control across the six time points.



Supplementary Figure 4. Stacked bar plots comparing the relative abundance of fungi among the compost, urea, and unamended control across the six time points.

Supplementary Table

Fungi			
Crop Cycle	Taxa	w-score	Treatment(s) where most abundant
1	<i>Thermomyces lanuginosus</i>	142	Compost
2	<i>Myceliophthora sp. 1</i>	283	Compost
3	<i>Myceliophthora sp. 1</i>	245	Compost
4	<i>Myceliophthora sp. 1</i>	227	Compost
	<i>Pezizaceae sp. 1</i>	206	Control and Urea
5	<i>Myceliophthora sp. 1</i>	205	Compost
6	<i>Thermomyces lanuginosus</i>	146	Compost
Bacteria			
Crop Cycle	Taxa	w-score	Treatment(s) where most abundant
1	<i>Acidimicrobiales sp. 1</i>	3952	Control

Supplementary Table 1. Fungal and bacterial taxa that were differentially abundant across fertilizer types (compost, urea, and control) and time. Results are from ANCOM analysis with corresponding significance as determined by w-scores, which can be interpreted as the count of the number of sub-hypotheses that have not been rejected for a given species.