

## Appendix

**Supplementary materials - Tables S1\_S8. See online Excel file.**

**Table S1. Two-way ANOVA F-values for production data. G: Factor genotype, R: Factor water regime.**

**Table S2. Soil physical-chemical features.**

**Table S3. Amount of starting material for DNA extraction for each sample (mg).**

**Table S4. List of primer pairs used for RT-qPCR.**

**Table S5. P-values from multiple comparison one-way ANOVA with an LSD post-hoc test for data presented in Figure 3.**

**Table S5. OTU from soil samples.**

**Table S6. OTU from roots.**

**Table S7. Analysis of variance on single variables (Water regime, Genotype, interaction between Water regime and Genotype) of gene expression data.**

Supplementary materials - *Figures*

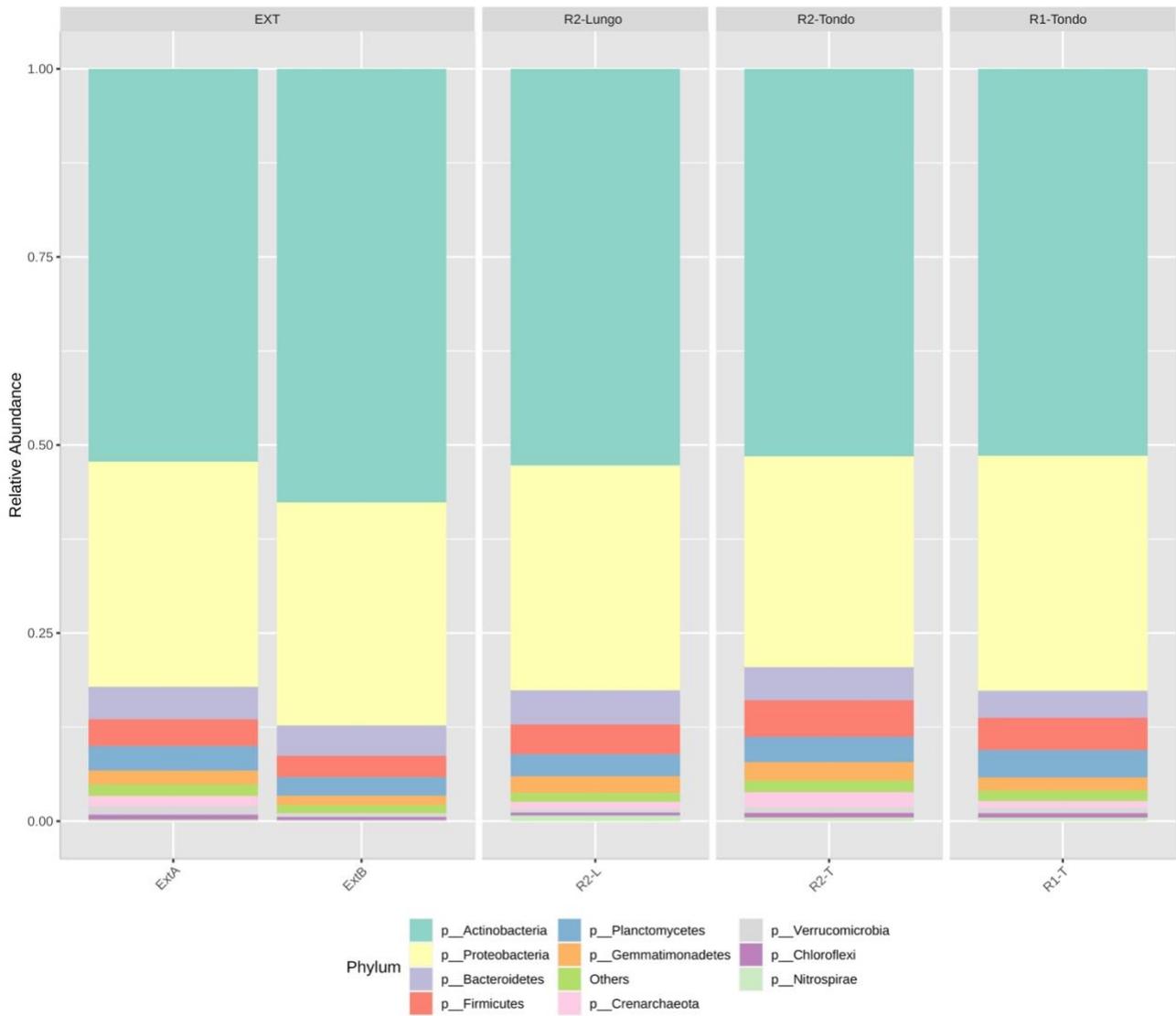
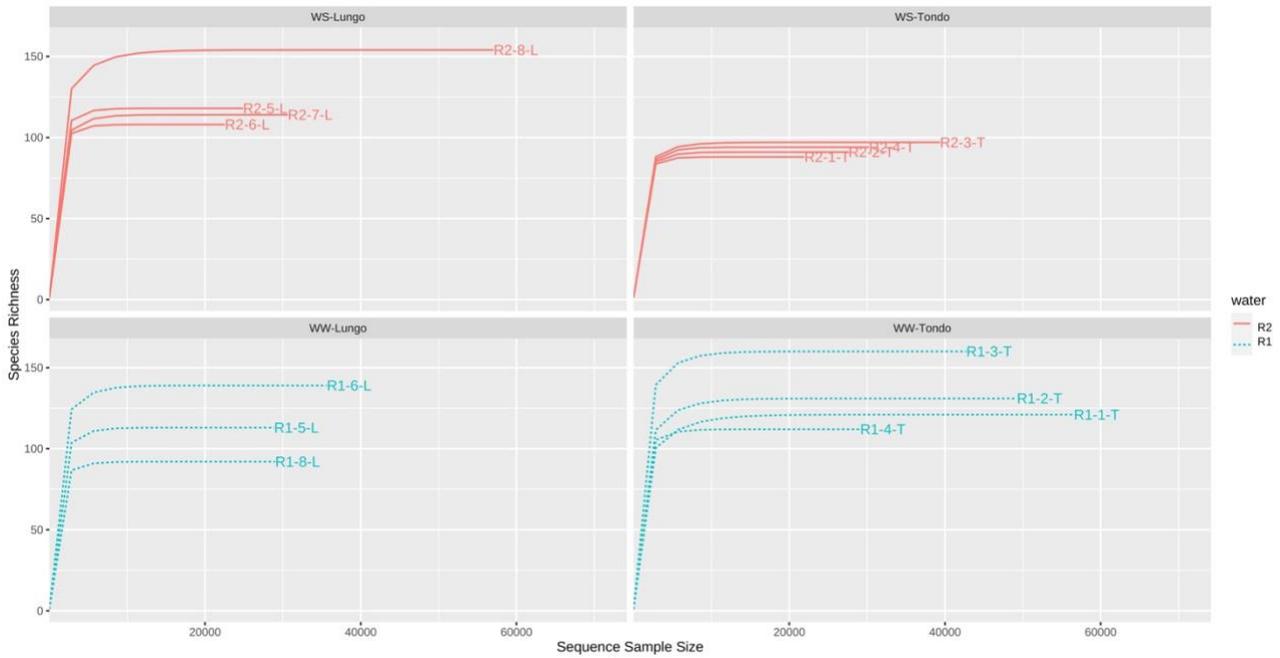
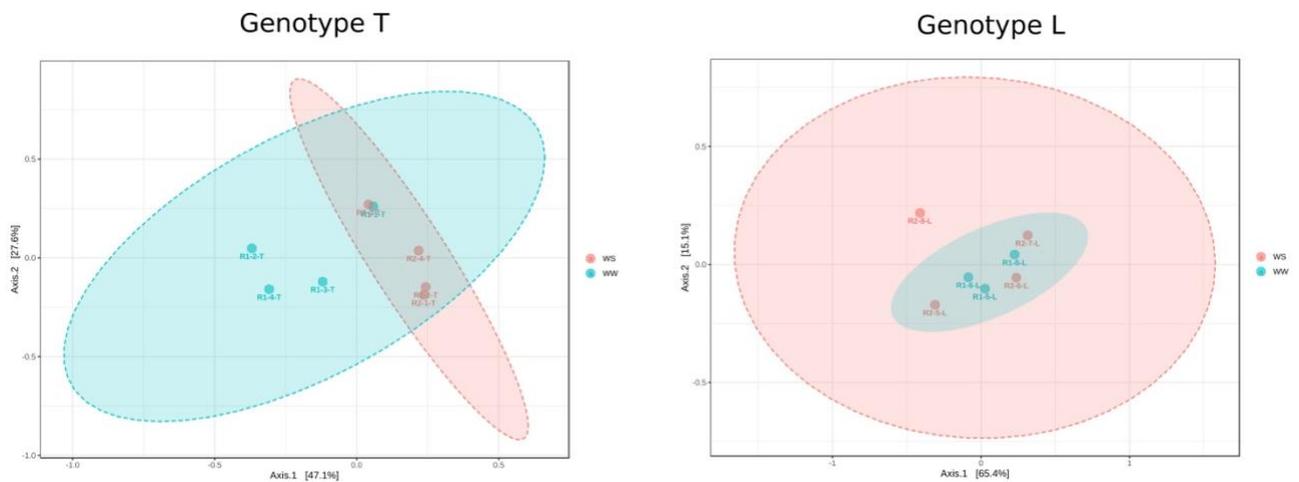


Figure S1. Stacked taxa barplots of bacterial relative abundance at phylum level in soil samples.



**Figure S2. Rarefaction curves of detected microbial OTUs in rhizosphere samples. Rarefaction curves showed the number of OTUs defined at a 97% sequence similarity relative to total sequence number.**



**Figure S3. Beta diversity calculated with Bray Curtis index and reported as PCoA, for both Tondo and Lungo genotypes. Different colours represent different conditions (R1 and R2).**