Supplemental Figures

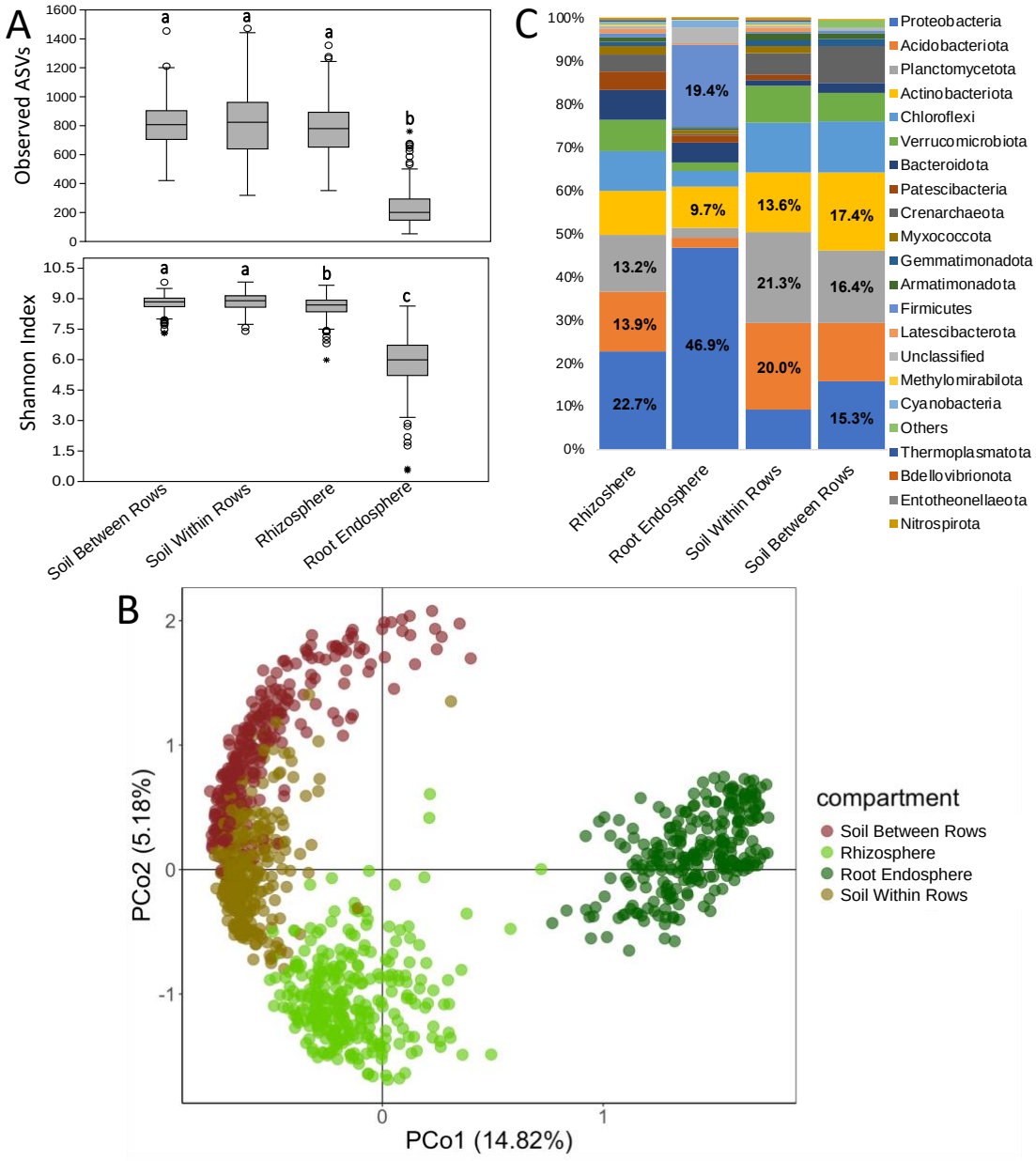

Figure S1. Bacterial community composition, α– and β–diversity in the soil and plant compartments analyzed. A) Species richness (Observeds ASVs) and diversity (Shannon Index) between root endosphere, rhizosphere, soil within rows and soil between rows bacterial communities. Different letters indicate significant shifts in the indices assessed between the compartments according to Kruskal-Wallis test ($p < 0.05$). B) Principal coordinate analysis (PCoA) showing bacterial community structure of samples from the four compartments based on the Bray-Curtis distance matrix. C) Bar chart showing the bacterial community composition at the phylum level for each compartment. Others are the sum of bacterial phyla with < 0.1% relative abundance. The proportion of the top three phyla is shown for each compartment.

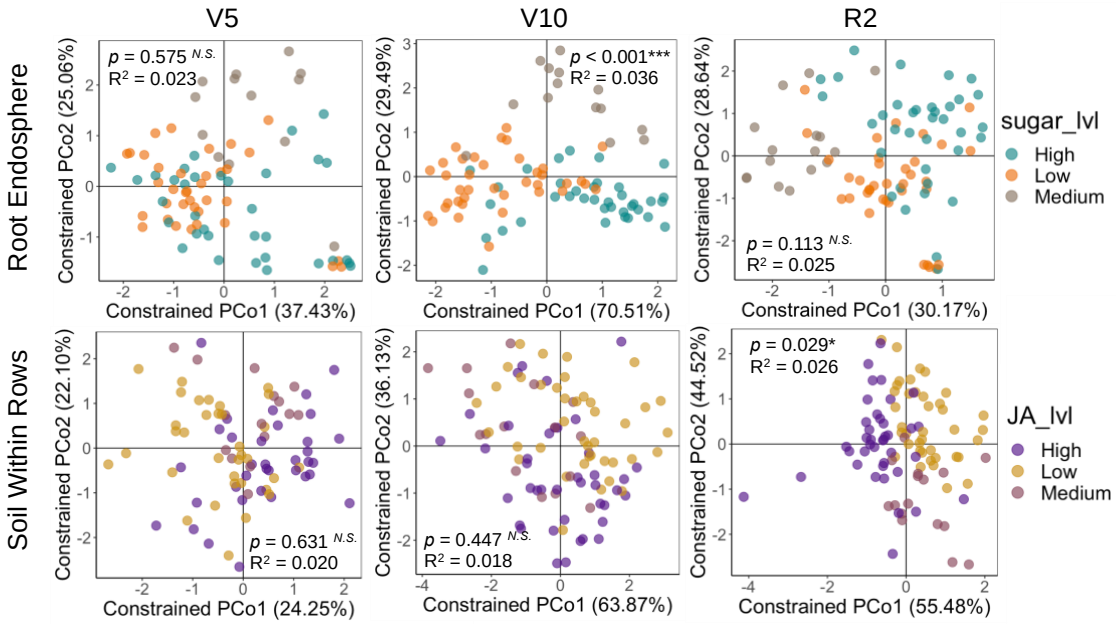

Figure S2. Specific growth stages where the bacterial communities of the root endosphere and soil within rows were affected by differences in total sugars or jasmonic acid concentration in root exudates. Constrained principal coordinates analysis (CAP) based on the Bray-Curtis distance matrix showing the separation of samples according to the different levels of total sugars and jasmonic acid concentrations in root exudates. PERMANOVA *p*-value and R^2 are shown in each graph to indicate the significance and effect size of sugars or jasmonic acid concentration in root exudates on the bacterial community structure of the root endosphere and soil within rows at each growth stage, respectively.

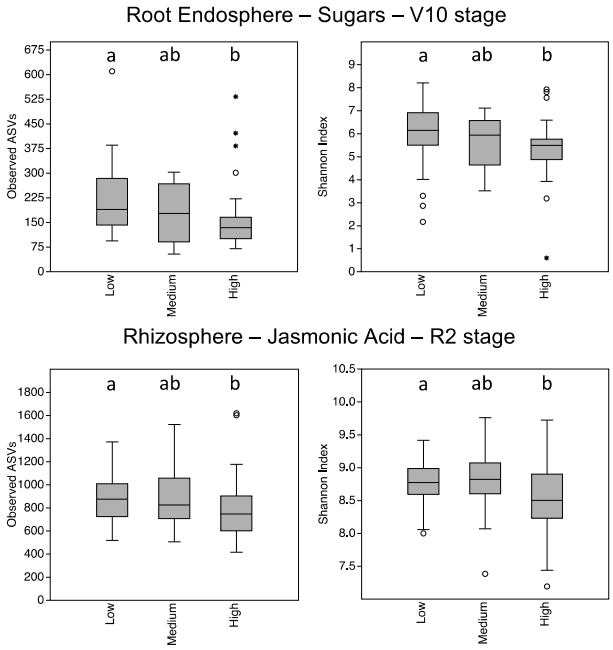

Figure S3. Specific growth stages where changes in bacterial α–diversity occur between genotypes exuding different sugars or jasmonic acid levels in the root exudates. Box plots showing the compartments and growth stages whose species richness (Observed ASVs) and diversity (Shannon index) were significantly different between genotypes exuding low, medium and high levels of sugars or jasmonic acid. Top: changes in species richness and diversity between genotypes exuding different sugar levels in the root endosphere compartment at the V10 stage. Bottom: changes in species richness and diversity between genotypes exuding different jasmonic acid levels in the rhizosphere compartment at the R2 stage. All other compartments and growth stages showed no differences in α–diversity according to sugars and jasmonic acid levels. Different letters indicate significant differences according to the Kruskal-Wallis test ($p < 0.05$).

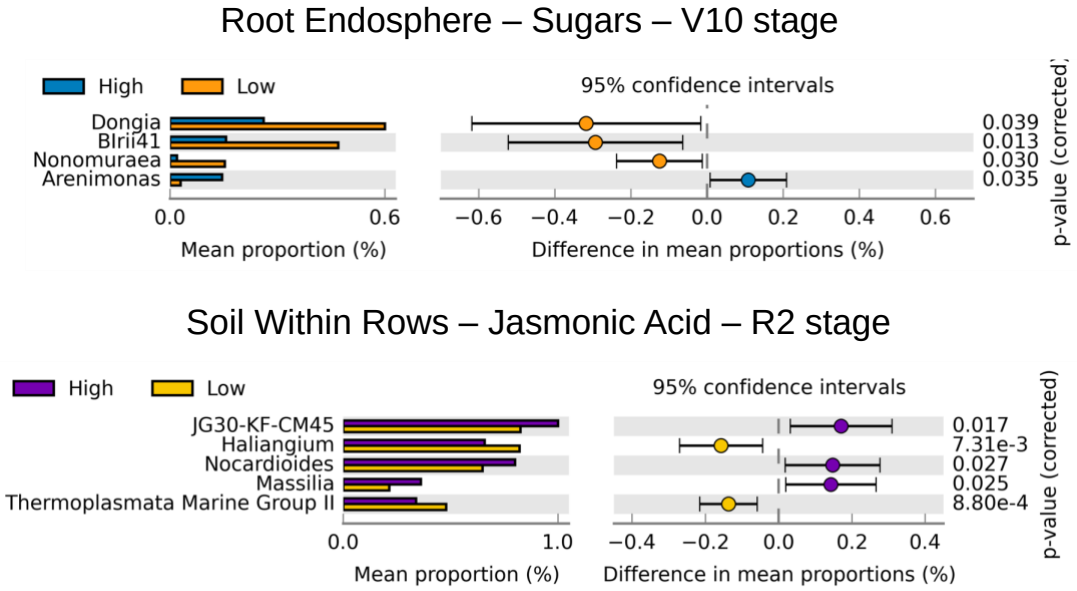

Figure S4. Specific growth stages where bacterial genera changed in relative abundance between genotypes exuding contrasting levels of sugars or jasmonic acid in the root endosphere and soil within rows compartments. Bacterial genera showing significant changes in relative abundance between genotypes with high or low concentrations of sugars or jasmonic acid in root exudates. Top: bacterial genera that changed in relative abundance between genotypes exuding different sugar levels at the V10 stage in the root endosphere. Bottom: bacterial genera that changed in relative abundance between genotypes exuding different jasmonic acid levels at the R2 stage in the soil within rows. The genera displayed in the graphs showed $p < 0.05$ in the Welch's t-test after the Benjamini-Hochberg FDR correction and differences between proportions of sequences were > 0.1%. Unclassified genera were filtered out.

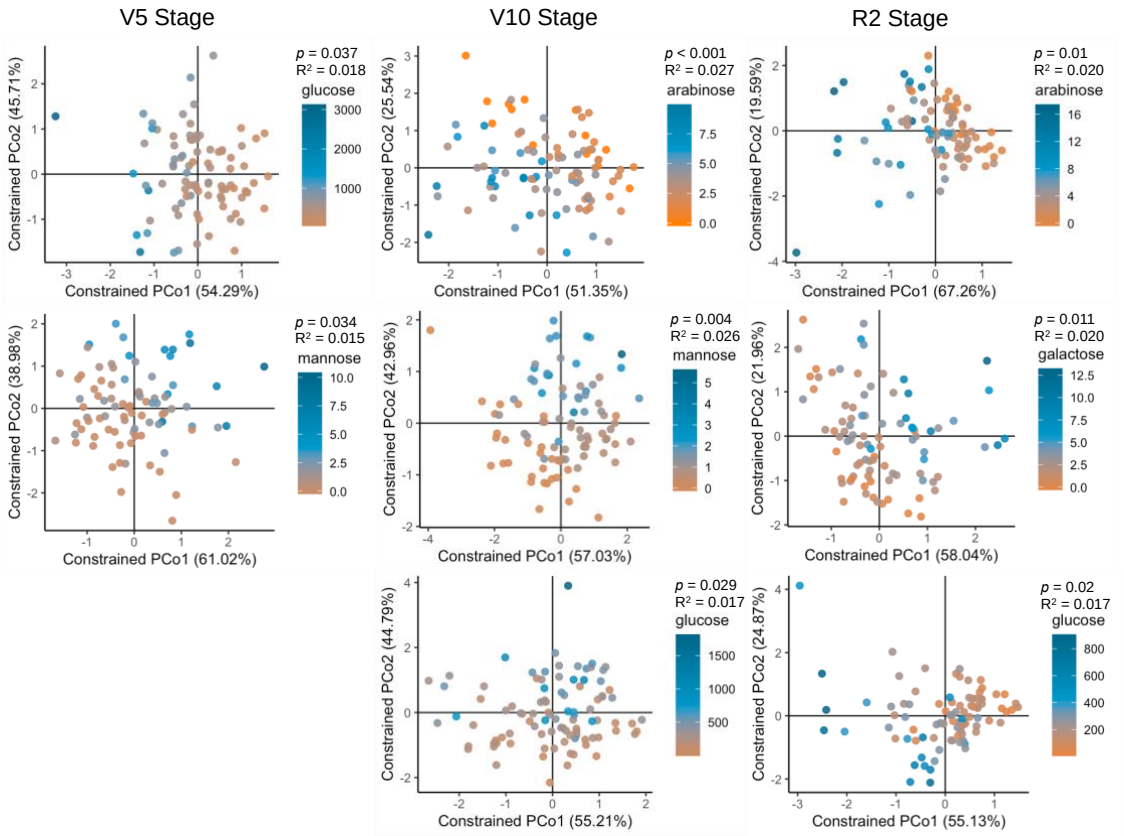

Figure S5. The individual sugars that had a significant impact on the rhizobacterial communities at each maize growth stage. Constrained principal coordinates analyses (CAPs) based on the Bray-Curtis distance matrices showing the specific sugars that significantly affected the rhizobacterial communities at each growth stage according to Table S3. The sugars with the largest effects at each growth stage (sucrose at V5 and trehalose at V10 and R2) are not shown here because they are shown in Figure 6A. PERMANOVA *p*-value and R^2 are shown in each graph to indicate the significance and effect size of each sugar at each growth stage. The concentrations of the specific sugars were used as numeric factors in the multivariate analyses. Each sample had a corresponding value of each sugar as quantified in the rhizosphere field samples whose variation (ng soil g^{-1}) is shown in the legends of each graph. The CAP ordinations were constrained according to the concentration of the sugar in each respective graph.