Supplementary Material

Figure S1: Sunburst chart showing the total relative abundance of bacterial phyla detected in investigated samples. Percentage in each sector along with bacterial phyla represents the average relative abundance.

Figure S2: Rarefaction analyses of samples at genus level. Rarefaction curves of OTUs clustered at 97% sequence identity across different samples from agricultural and non-agricultural soils.
Figure S3: Unique and shared Kegg Orthologs (KOs) between the agricultural and non-agricultural soils.

Figure S4: Extended error bar plot for the six active features (high-level subsystems) that had significant differences between agricultural and non-agricultural samples. Each bar shows the mean proportion (%) of functional categories predicted in soil bacterial communities. Points indicate the differences between agricultural and non-agricultural soil (blue and green bars, respectively), and the values at the right show the corrected $p$-values that were derived from a White’s non-parametric t-test [71].
**Figure S5.** Extended error bar plot showing the abundances of functions associated with plant interaction that had significant differences between agricultural and non-agricultural samples. Each bar shows the mean proportion (%) of functional categories predicted in soil bacterial communities. Points indicate the differences between agricultural and non-agricultural soil (blue and green bars, respectively), and the values at the right show the corrected p-values that were derived from a White’s non-parametric t-test.
Figure S6: Heat map showing differences in relative abundance of the 50 most abundant bacterial genera as revealed by ClustVis statistical analysis. Relative abundance of each taxon in agricultural and non-agricultural soils is measured on a scale from dark blue = low abundance to bright red = high abundance.
Figure S7. Relative abundance of different genera involved in plant growth promotion and plant fitness between agricultural and non-agricultural soils.