**Figure 1.** Graphical depiction of the rhizobiome complexity from axenic culture to terrestrial, wild conditions.

**Figure 2.** (Left) Schematic of the aquaponics design used in the study. (Right) Diagram of the hydroponic boxes used in the experiment.

**Figure 3.** Relative crop head weights (wet) and root weights (dry) over experiment 1. Trial 1 is shown in panels A-B, Trial 2 is shown in panels C-D.

**Figure 4.** Genus rank cluster plot showing consolidation of hydroponic (HP) treatments into a single cluster. Controls include: RAS (recirculating aquaculture system water column), BF (biofilter effluent), WS (facility water source), Soil (rhizosphere from a terrestrial lettuce crop), HNS (hydroponic nutrient solution stock). HNS.basin refers to roots taken directly from the hydroponic basin. HNS.BF.basin refers to roots taken from the nutrient supplemented biofilter effluent basins. All other treatments refer to roots taken from box-grown plants. HNSm.1-3 were grown in mature hydroponic basin water. HNS.s.1-3 were grown on filter-sterilized HNS. BF.1-3 were grown on nutrient supplemented biofilter effluent taken directly from the stock solution. BF.s.1-3 refer to the same solution as for the BF treatments, but additionally filter sterilized. Soil.1-3 refer to soil inoculated boxes. Probio.s.1-3 refer to the addition of the probiotic *Bacillus amyloliquefaciens* to filter sterilized HNS; Probio.BF.1-3 refer to the same strain added to nutrient supplemented biofilter effluent.

**Figure 5.** Genus rank dendrogram showing consolidation of hydroponic (HP) treatments into a single cluster, labelled as in figure 4.

**Figure 6.** Genus rank unrooted, radial phylogenetic tree showing consolidation of hydroponic (HP) treatments into a single cluster, labelled as in figure 4.

**Figure 7.** Class rank heatmap of OTUs (y-axis) plotted across treatments (x-axis) and total frequency (z-axis). Both OTUs and treatments are organized by hierarchal clustering.

**Figure 8.** Family rank heatmap of OTUs (y-axis) plotted across treatments (x-axis) and total frequency (z-axis). Both OTUs and treatments are organized by hierarchal clustering.

**Figure 9.** Heatmap of OTUs (y-axis) plotted across treatments (x-axis) and KEGG gene prevalence for nitrogen metabolism (z-axis). Treatments in which the corresponding OTU is present are colored; gene prevalence here is the sum of mentions within the annotated genome to keywords surrounding a specific metabolism.