**Figure 1.** The distribution of OTUs across treatments indicates a sharp drop in the amount of OTUs present per treatment at the 1000 OUT threshold.

**Figure 2.** The phylum rank phylogenetic diagram (a), cluster plot (b), and dendrogram (c) show the same hydroponic (HP) consolidation pattern as for lower ranks (compare to genus rank in the main text). 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 3.** Heatmaps of OTUs (y-axis) plotted across treatments (x-axis) and total frequency (z-axis). Both OTUs and treatments are organized by hierarchal clustering. Heatmaps resolution is lower at higher ranks but more legible in comparison to lower ranks. Heatmaps presented here correspond to phylum, order, class, and family. Despite slight reorganization in the clustering pattern across ranks, the general trend is clearly visible as a consolidation away from the diverse profiles of the controls (RAS, BF, WS, Soil) with the notable exception of the HNS stock control. Treatment acronyms are identical to those used in figure 2.

**Figure 4.** Phylogenetic diagram consisting of only HNS treatment cluster (controls RAS, WS, Soil were removed). Of note are the groupings visible: sterilized treatments groups on one branch, HNSm.1-3 grouped on a second branch, probiotic treatments grouped on a third branch (one exception). A fourth branch consisted of the least similar (most divergent clusters): HNS stock, BF stock, two of the three soil samples, and both basin root samples fall into this category.

**Figure 5.** Clustering analysis done after removing the common HNS stock microbiome, equivalent to considering the HNS stock as a background signal. Across the cluster plot (a), dendrogram (b), and phylogenetic diagram (c) the same trend is visible as with the normal dataset.

**Figure 6.** Heatmaps of OTUs (y-axis) plotted across treatments (x-axis) and KEGG gene prevalence (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. Each plot (a-h) represents a different search in the database.