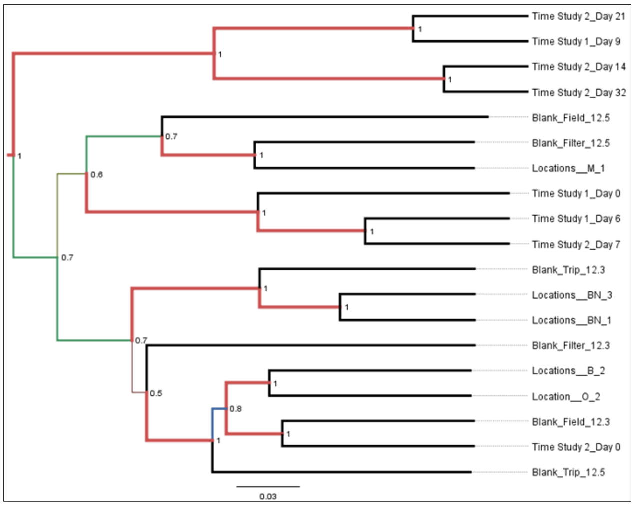

Figure S1. Phylogenetic Tree constructed from weighted Unifrac BootStrapped Jackknife analysis, performed in Qiime for pure water samples. Select samples from two independent time studies under both light (Time Study 1) and dark (Time Study 2) conditions are represented, as well as samples from several pure water systems (Locations) and blanks collected during that survey campaign. Differences in communities are calculated based both on presence and relative abundance of OTUs. Branching indicates a difference in the composition of the assemblage, length of each branch indicates extent of variation (see scale). Bootstrap values at nodes indicate confidence of clustering for each node, where 1 indicates 100% confidence.

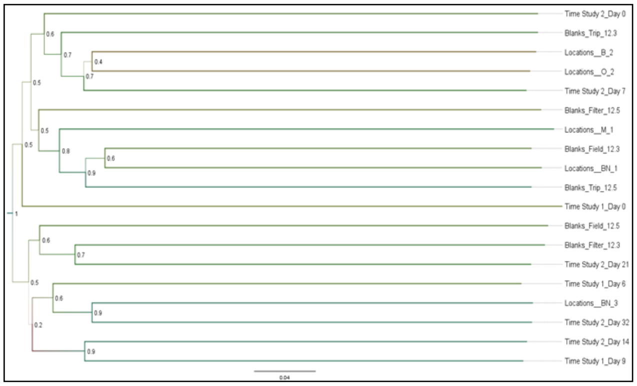

Figure S2. Phylogenetic Tree created by unweighted Unifrac BootStrapped Jackknife analysis, performed in Qiime for pure water samples. Select samples from two distinct time studies under both light (Time Study 1) and dark (Time Study 2) conditions are represented, as well as samples from several pure water systems (Locations) and blanks collected during that survey campaign. Differences in microbial assemblage composition are calculated given both the presence and relative abundance OTUs present and their relative abundance. Branching indicates a difference in microbial assemblage composition, length of each branch indicates extent of variation (see scale). Bootstrap values at nodes indicate confidence of clustering for each node, where 1 indicates 100% confidence.