Triclosan is a widely-used antimicrobial found in numerous household items from cosmetics and soap to plastics and fabrics. Triclosan is also commonly detected in untreated wastewater where it could act as a selective agent for antibiotic resistance in bioreactors used for treatment. The goal of our research is to understand the effect of triclosan on wastewater microbial communities. Replicate enrichment cultures were grown in the presence of different concentrations of triclosan (0 to 15 μg/L) for eight weeks. Bacterial community composition was determined by deep sequencing (Illumina MiSeq) of PCR-amplified 16S rRNA gene fragments. Antibiotic resistance profiles were investigated using shotgun metagenomic sequencing (Illumina HiSeq). Bacterial community composition exhibited statistically significant differences in response to higher triclosan concentrations. Antibiotic resistance profiles showed increases in select resistance genes but did not demonstrate broad responses to triclosan. From these results, we conclude that triclosan exposure impacts bacterial communities and antibiotic resistance in distinct ways. These results paint a more nuanced picture of the effect of the ubiquitous chemical and may help us understand its long-term impacts on wastewater microbial communities and their receiving environments.