Supplementary figures and tables

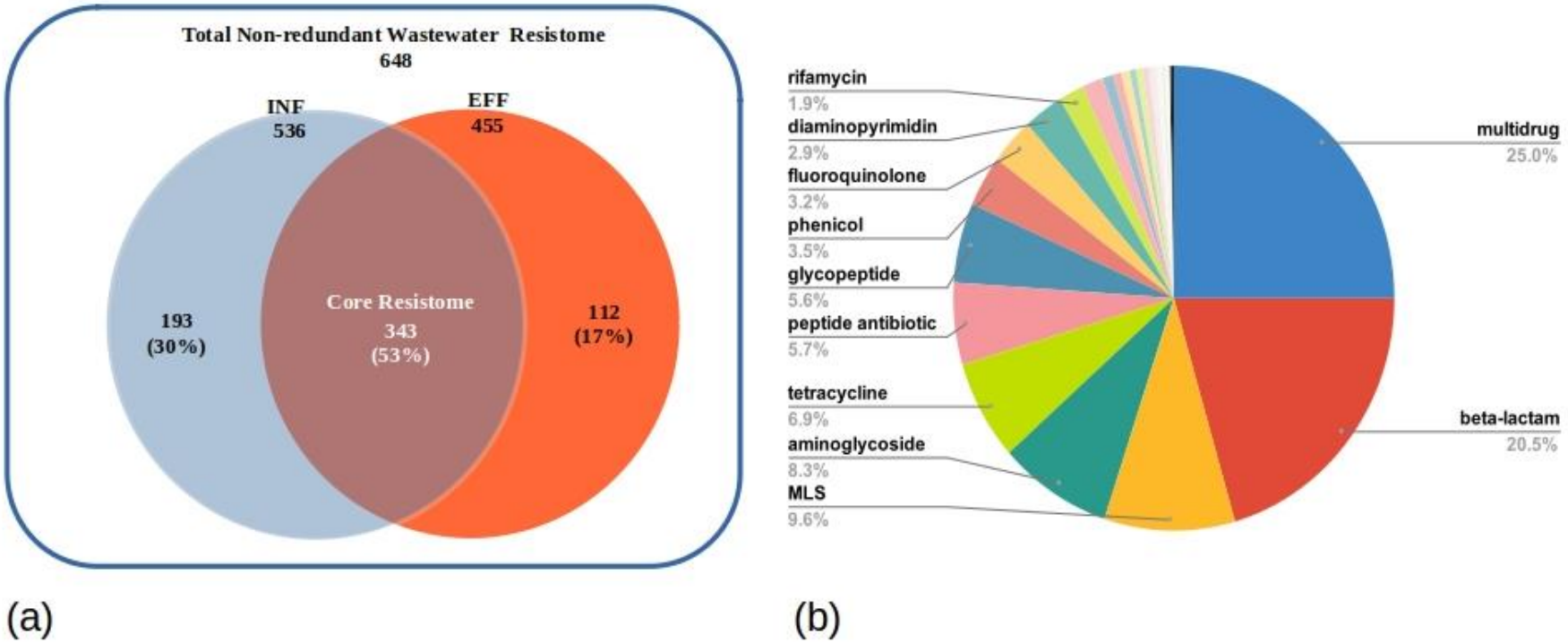


Figure S1. Resistome composition of the assembled metagenomes.

(a) Unique ARGs annotated in both INF and EFF (b) Distribution of ARGs per drug classes

(link to full resolution figure)

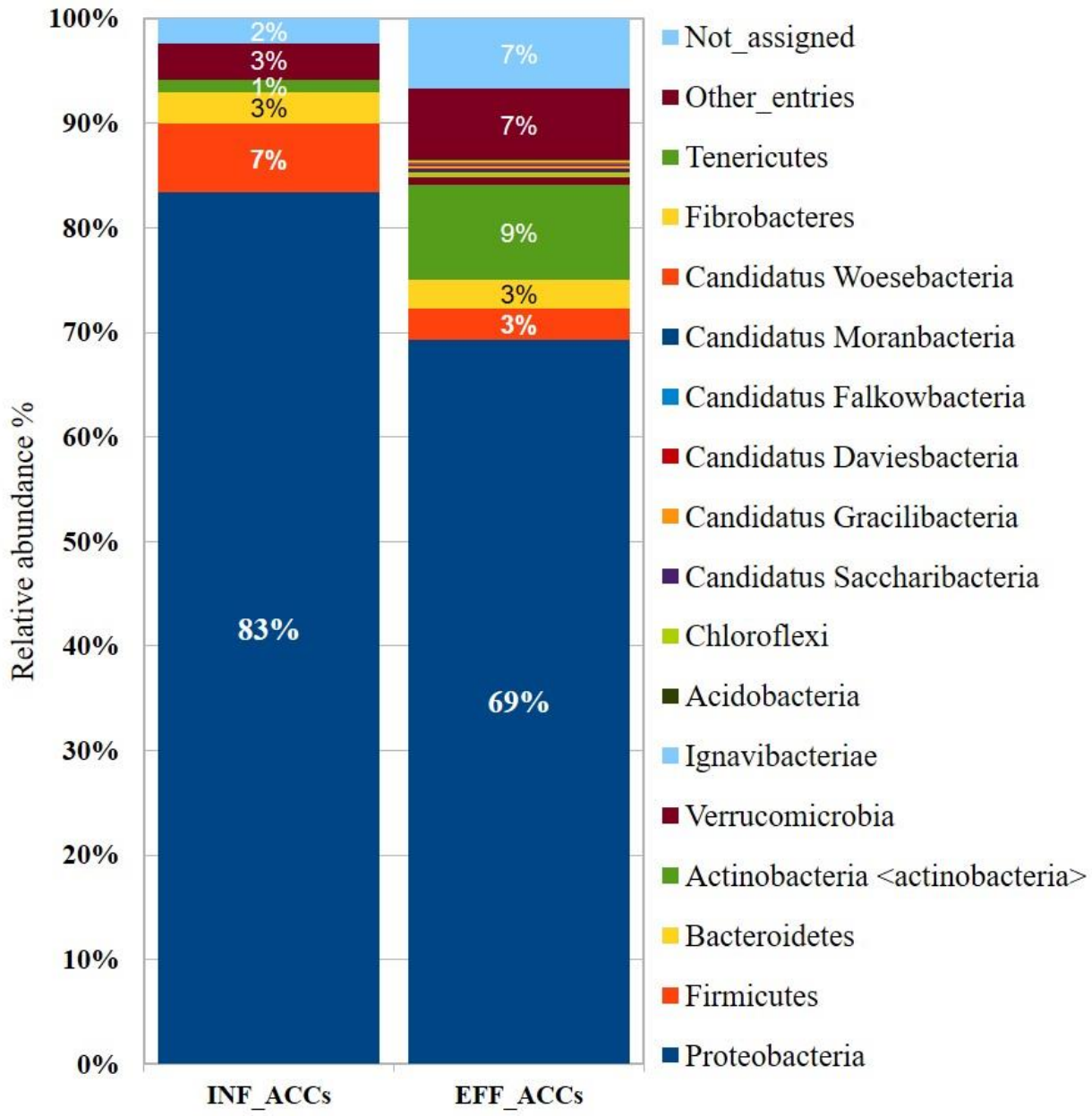


Figure S2. Taxonomic classification of ARG-carrying contigs (ACCs) at phylum level for INF and EFF assembled metagenomes using MEGAN analysis.

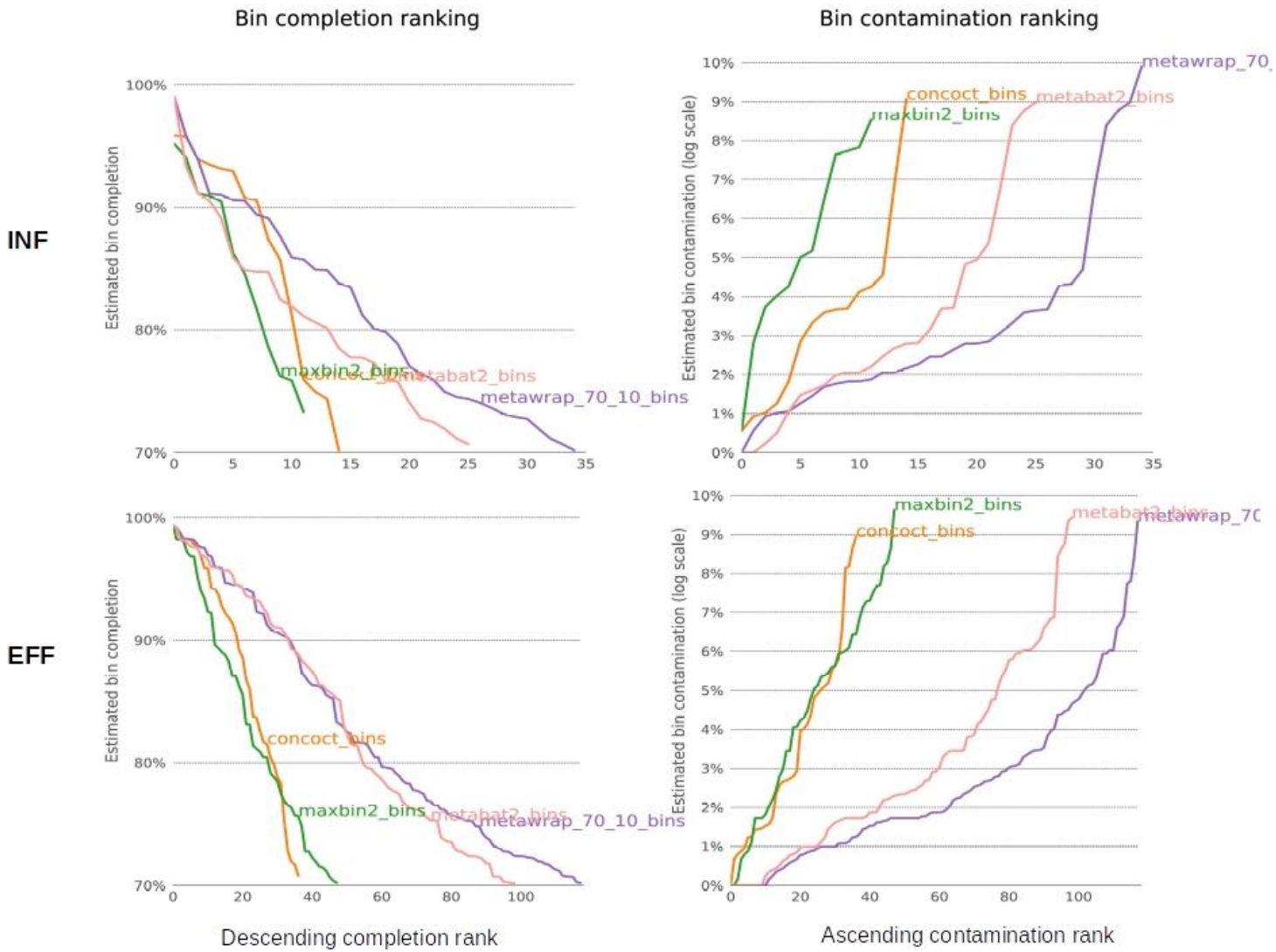


Figure S4. Comparison of genome binning results of wastewater influent and effluent assembled metagenomes showing the improvement in the bin completion and contamination percentages at the selection cutoff thresholds as a result of using hybrid binning approach by MetaWrap software. (Diagram is adapted from MetaWrap pipeline results) **INF:** Influent assembled contigs, **EFF**: Effluent assembled contigs

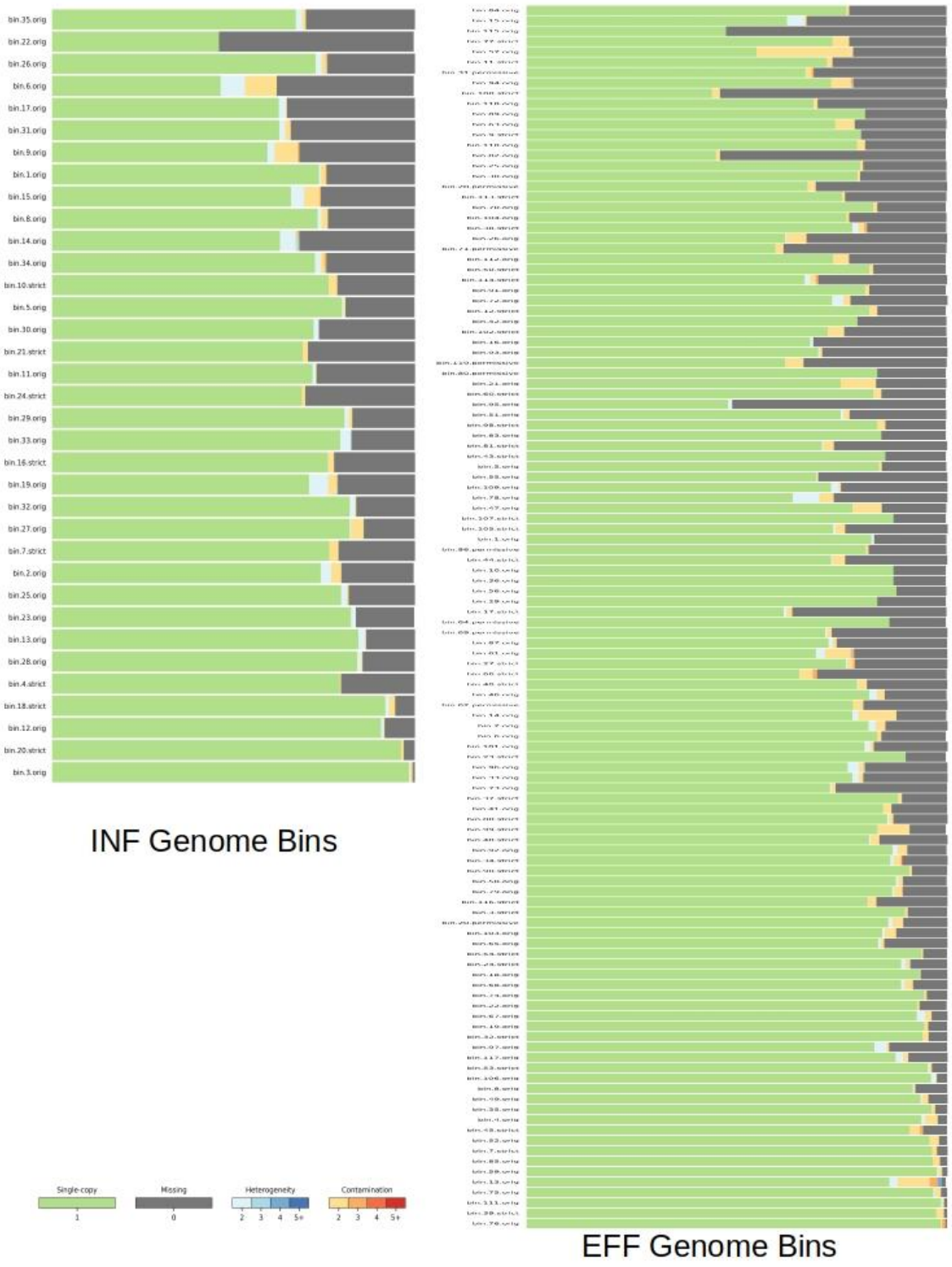


Figure S5. Heatmap diagram shows the level of completeness and contamination in the recovered genomic bins of INF and EFF MAGs.(link to full resolution images for the heatmap of INF genomes and EFF genomes)