Factors associated with elevated levels of antibiotic resistance genes in sewer sediments and wastewater

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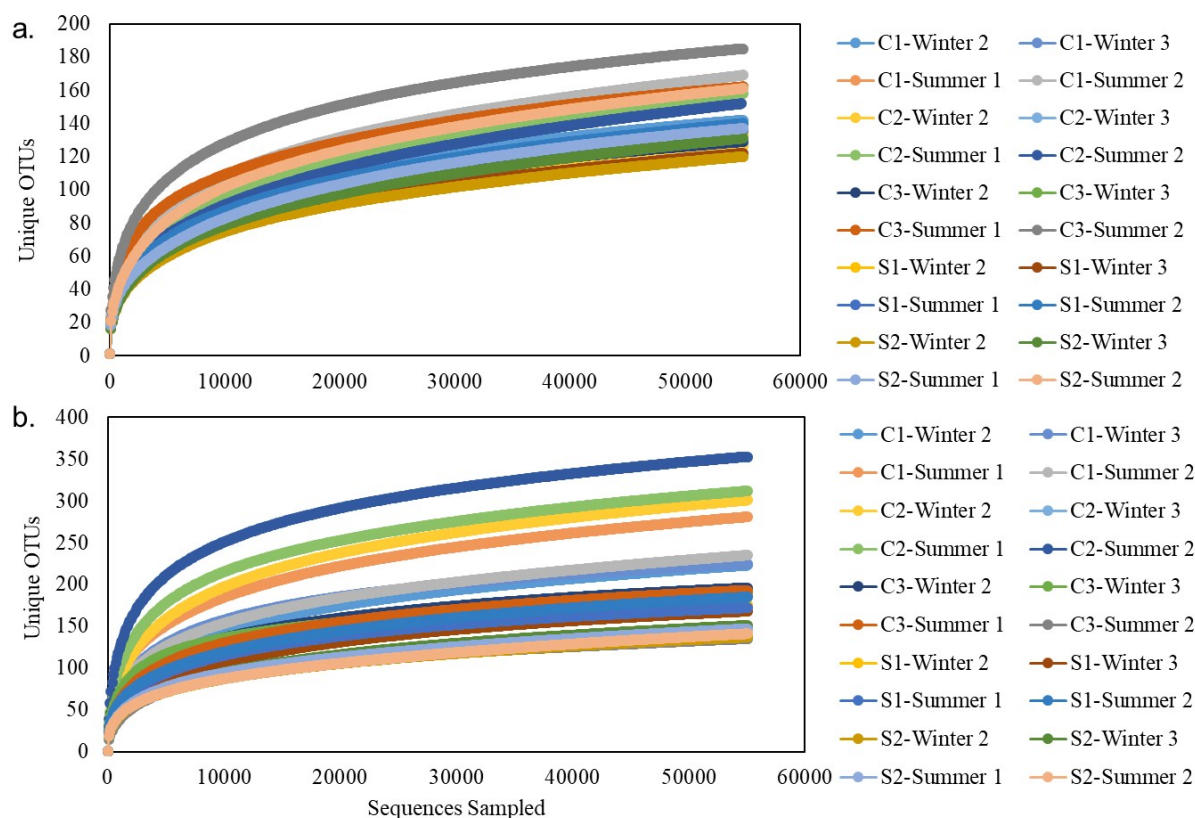*nfahrenf@rutgers.edu, 1-848-445-8416

Supplemental Material

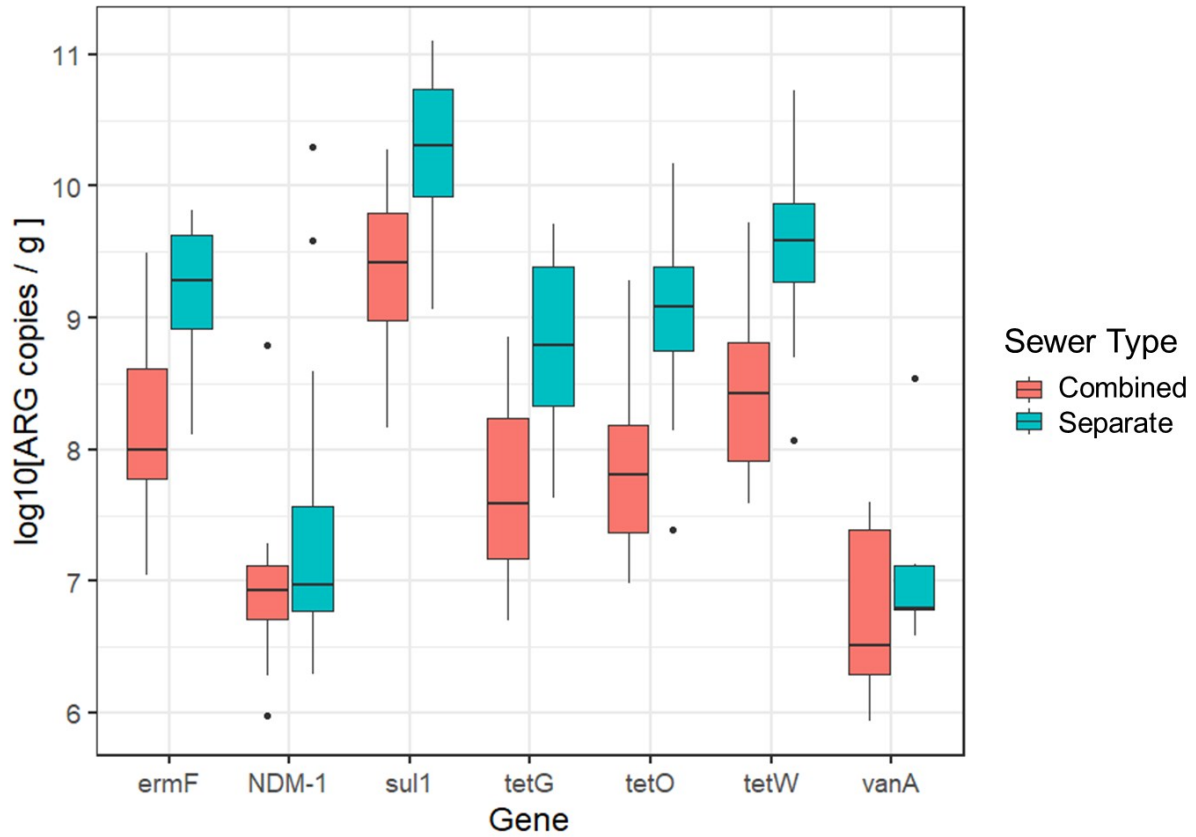**Fig. S1** Rarefaction curves for (a) wastewater influent and (b) sediment DNA samples.

Fig. S2 Antibiotic resistance gene copies per mass of sewer sediment for combined and separate sewer systems. (N=12 for combined sewers, N=6 for separate sewers).
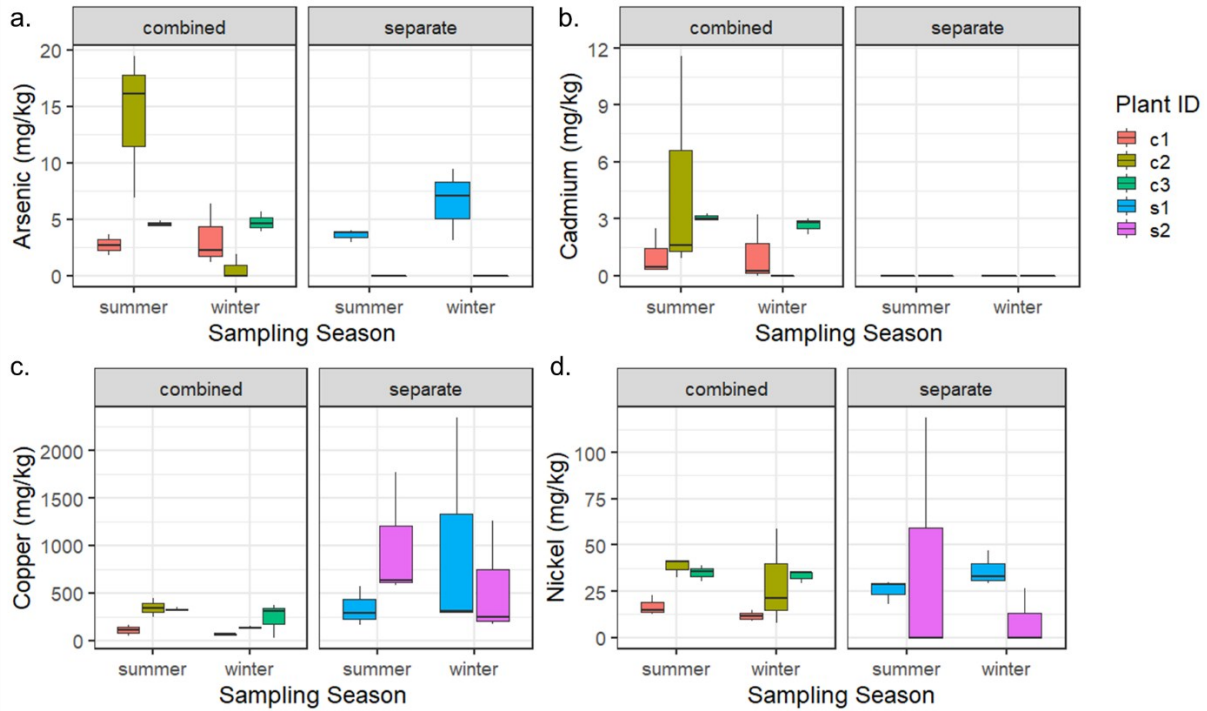
Fig. S3 Concentration of heavy metals (mg/kg dry sewer sediment) for (a) arsenic, (b) cadmium, (c) copper, and (d) nickel.
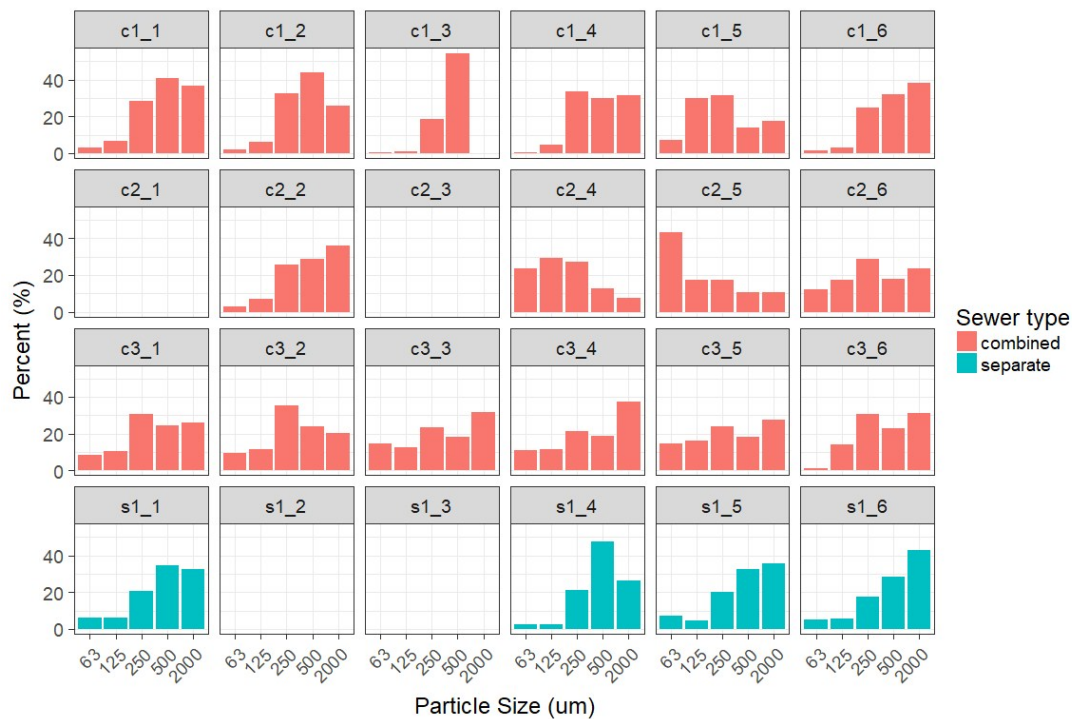

Fig. S4 Percent (mass) versus particle size for sewer sediment samples collected from combined or separate sanitary sewers. Sample names formatting: "c" for combined "s" for separate

sanitary sewers and number referring to the system number. The number following the underscore represents the sampling event. Events 1-3 were in the fall/winter and 4-6 were in the summer.
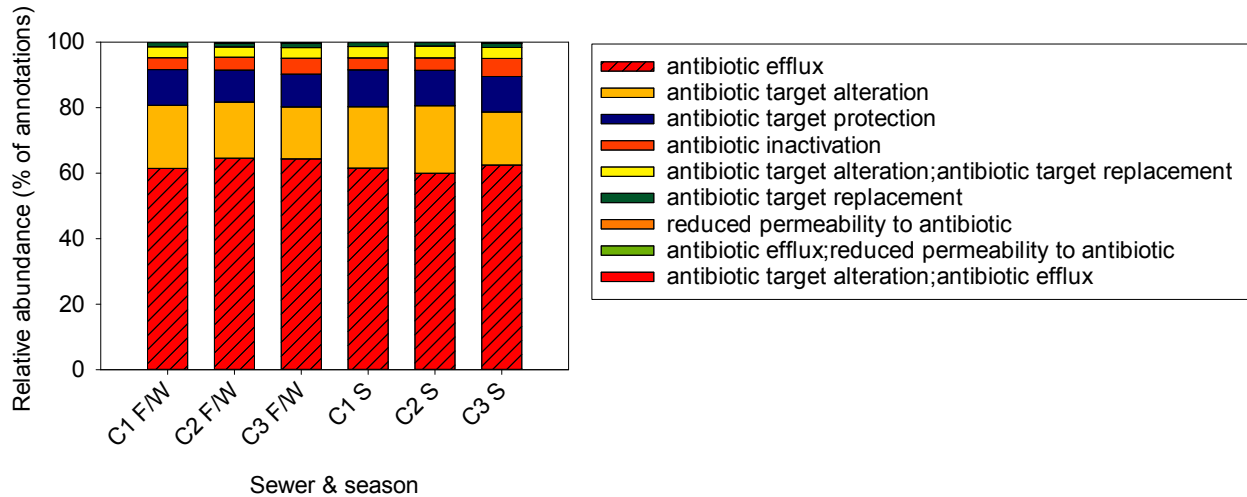

Fig. S5 Antibiotic resistance mechanisms observed in combined sewer sediment metagenomes annotated with CARD. Three combined sewers were sampled (C1, C2, and C3) during fall/winter (F/W) or summer (S). Two replicate samples from a given season and sewer system were pooled to generate each metagenome.
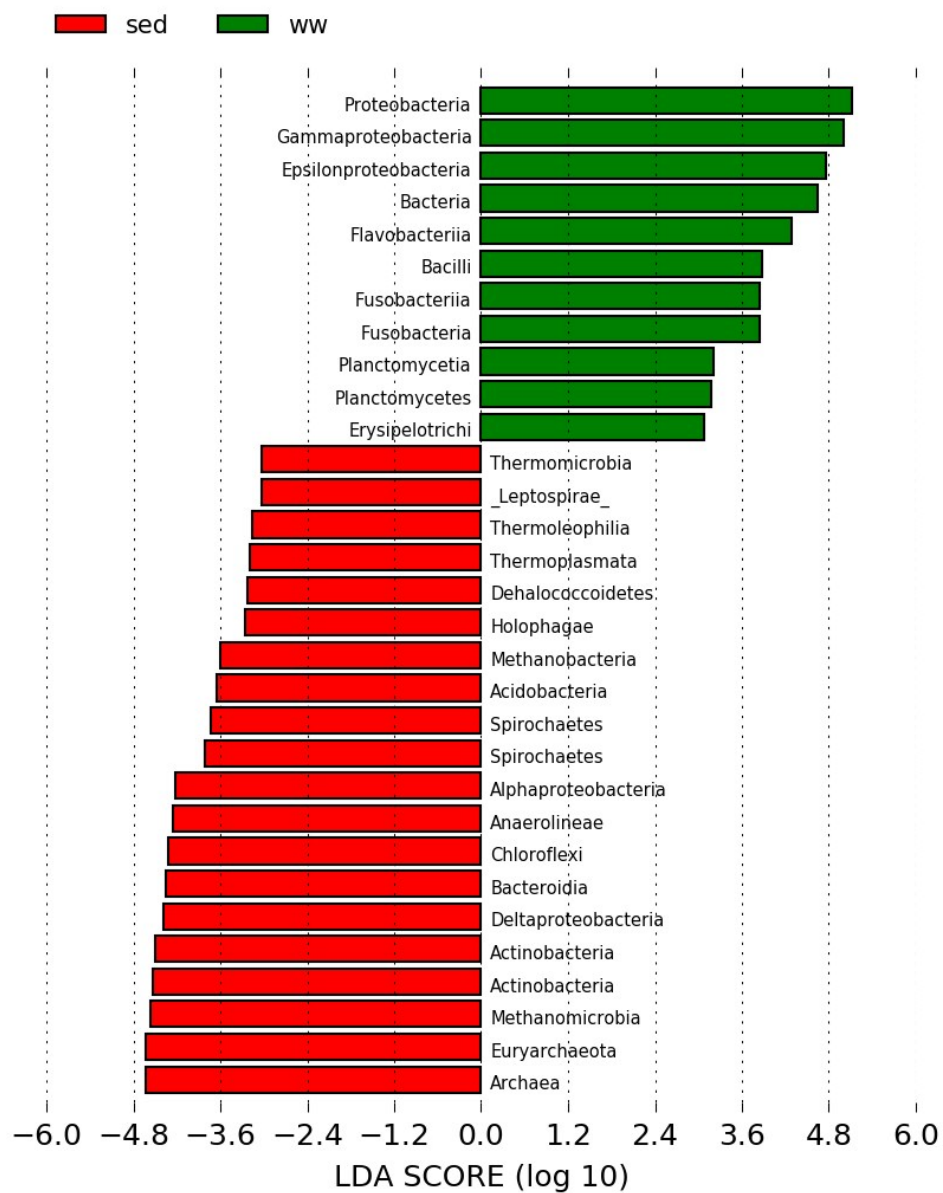
Fig. S6 Linear discriminant analysis score for biomarkers discriminating between sewer sediment microbiome ("sed") and wastewater microbiome ("ww").
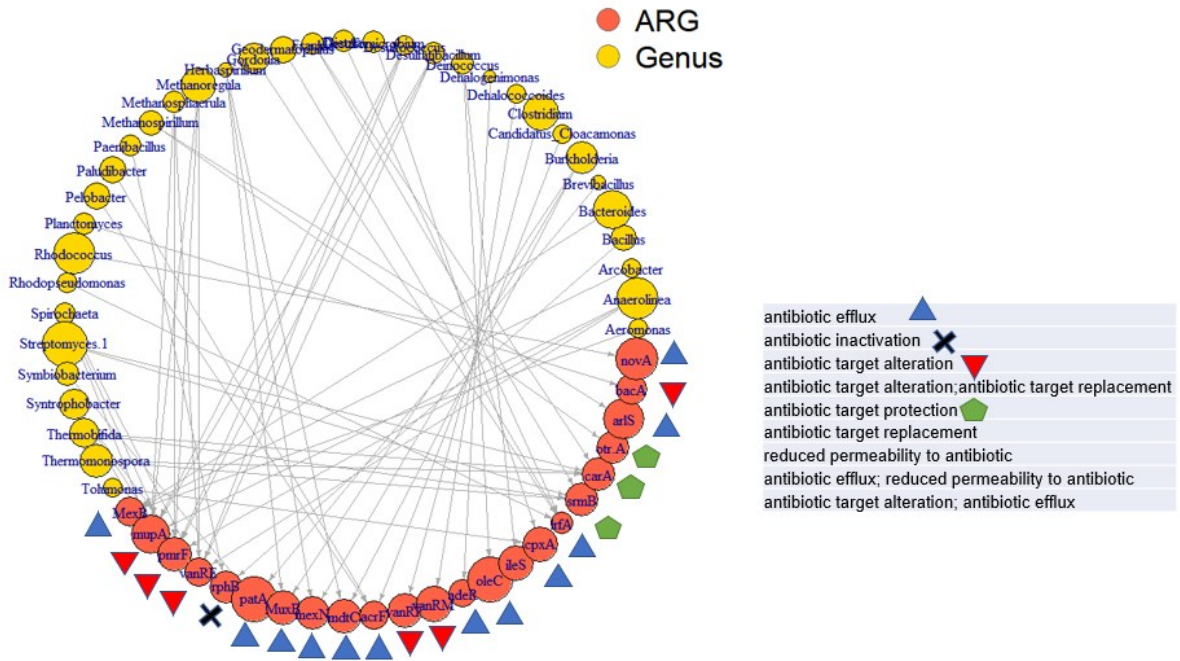
Fig. S7 Representation of network analysis results for ARGs annotated on the sewer sediment metagenome and taxonomy at the genus level. The functional classification of the ARGs are illustrated with symbols defined in the lower legend.