

Description of Additional Supplementary Files:

Supplementary Data 1: Sequence statistics of 226 activated sludge metagenomes.

Supplementary Data 2: The relative abundance of core ARGs across activated sludge samples. Core genes are defined as those detected in all 266 sample. The ORF annotated to Resfam were represented as gene families.

Supplementary Data 3: The abundance of MGE sequences across 226 activated sludge samples.