

Description of Additional Supplementary Files

Supplementary Data 1: Concentration distribution of various antibiotic residues in wastewater samples. The various sheets in the Excel file provide data on the concentrations of different antibiotics detected in sewage water viz. a. Ampicillin; b. Azithromycin; c. Nalidixic acid; d. Amoxicillin; e. Kanamycin; f. Erythromycin; g. Rifampicin; h. Tetracycline; i. Spectinomycin; j. Polymyxin-B; k. Colistin.

Supplementary Data 2: Detection of antibiotic resistant genes (ARGs) using dipstick based assay. Four sets of multiplex PCR assay were performed to target 16 ARGs, Group 1 (*bla_{NDM}*, *bla_{CTX-M}*, *bla_{KPC}*, *bla_{TEM}*); Group 2 (*cat*, *aac*, *sul2*, *oqxA*); Group 3 (*bla_{OXA}*, *tet*, *aadA*, *sul1*); Group 4 (*ermB*, *dfrA*, *qnrS*, *mphA*) and detected using dipstick based detection assay. A value of '1' indicates the presence of a resistance gene in the sample, while '0' denotes its absence.

Supplementary Data 3: a) Comparative analysis of antibiotic residues detected in QTRAP MS analysis with the ARGs detected in dipstick based assay b) Comparison of ARGs detected in dipstick assay with the ARGs detected in Shotgun analysis

Supplementary Data 4: a) Read information from 16S sequencing samples processed by DADA2 pipeline b) Concentration of metagenomic DNA extracted from sewage water samples

Supplementary Data 5: Distribution of total sewage resistome data in 167 samples (includes both community and hospital sites of India) as identified from Illumina shotgun metagenomic sequencing.

Supplementary Data 6: Distribution of total sewage resistome data a) ARGs b) Efflux pump, in 167 samples as identified from Illumina shotgun sequencing which are associated with taxonomically resolved metagenome assembled genome (MAGs)

Supplementary Data 7: Bacterial isolates and their susceptibility profile a) Bacterial Isolates along with their total counts identified in the study using Sanger sequencing b) Isolates were checked towards different classes of antibiotics using Kirby-Bauer disc diffusion method

and were categorized as resistant, susceptible, and intermediate. The diameter of each of the antibiotics are also mentioned along with the antibiotics which are intrinsically resistant (IR) to the isolate. c) Screening of vancomycin-resistant *Enterococcus faecium* isolates (VRE) among the sewage isolates.

Supplementary Data 8: Percentage of resistance among isolates a) Overall count of resistance towards antibiotics b) Percentage of isolates resistant to different classes of antibiotics

Supplementary Data 9: Sample information of the sewage whole genome sequences and the NCBI-downloaded clinical sequences. a) Information of whole genome sequences from sewage isolates. The sheets b-k are the metadata of the clinical isolates downloaded from the NCBI b) *E. coli* c) *K. pneumoniae* d) *A. baumannii* e) *P. aeruginosa* f) *E. faecium* g) *P. mirabilis* h) *M. morganii* i) *P. rettgeri* k) *C. werkmanii*

Supplementary Data 10: Genomic analysis information on the ARGs, MGEs, plasmids and integrons.

The sheets a-i represent the presence of ARGs in different clinical isolates a) *A. baumannii* b) *E. coli* c) *K. pneumoniae* d) *P. aeruginosa* e) *M. morganii* f) *P. mirabilis* g) *P. rettgeri* h) *C. werkmanii* i) *E. faecium* j) MGEs associated with ARGs in sewage isolates k) ARGs associated with plasmid genes in sewage isolates l) Integrons linked with ARGs in sewage isolates.

Supplementary Data 11: Details of the study sampling sites along with the geographical locations a) Different sampling sites of Faridabad, Haryana along with the geographical locations b) Geographical locations of the samples collected from other parts of the India.