SUPPORTING INFORMATION (SI) APPENDIX

Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms and limited clonal outbreaks

SI TEXT

Comparison of mechanisms identified in the prospective collection and those observed in a retrospective collection of 48 CRE collected from 2007-2012.

We sequenced a collection of 48 CRE isolated from patients at the same three Boston area hospitals in the six years prior (2007-2012) to the prospective sampling period (Table S1). Though this was not a comprehensive sample of CRE diversity at these hospitals over this time period, these isolates allowed us to compare historical strains and resistance determinants with those isolated more recently.

The historical collection comprised the three most common species that were recorded in the prospective collection (*E. coli*, *K. pneumoniae* and *E. cloacae*). Three out of the four most frequent non-susceptible STs from the Boston Prospective Collection were among the four most frequent non-susceptible STs in the Boston Historical Collection, including *K. pneumoniae* ST258, which was the most frequently isolated ST in both sets (35% and 33% of historical and prospective collection, respectively) (Table S3).

The diversity and frequency of resistance determinants among the historical collection was similar to that of the prospective collection (Tables S1 and S4); *bla*$_{\text{KPC}}$ was the most prevalent genetic determinant of meropenem resistance with *bla*$_{\text{KPC-3}}$ alleles being the most frequently observed followed by *bla*$_{\text{KPC-2}}$ and *bla*$_{\text{KPC-4}}$. We observed only one strain carrying *bla*$_{\text{NDM-1}}$, which was isolated from a patient in 2009. Though the species carrying the *bla*$_{\text{NDM-1}}$ gene differed between its appearance in 2009 (*E. cloacae*) and 2013 (*K. pneumoniae*), both strains were isolated from the same hospital. The only unique genetic determinant among the historical collection was *bla*$_{\text{OXA-48}}$, a less commonly reported beta-lactamase, which is found predominantly in North Africa and Europe[14]. This gene was observed in only one *K. pneumoniae* ST101 strain isolated in November 2011 - five months prior to the first report of *bla*$_{\text{OXA-48}}$ in the United States[49]. No strains from the historical collection were found to encode truncated forms of porins with or without other beta-lactamases, this fact could be either the result or the reason why historical collection being biased toward highly resistant isolates (the median meropenem MIC for the historical and prospective collections were ≥ 16 μg/mL and ≥ 8 μg/mL, respectively). Strains harboring porin mutations had lower meropenem resistance ranging in their MICs from ≥ 2 to ≥ 8 μg/mL.

SI MATERIALS AND METHODS

Specimen collection and phenotypic assessment. Meropenem resistant Enterobacteriaceae isolated from patients from four hospitals over a 16-month period (August 2012 through November 2013) were collected for genome sequencing. Species- and date-matched carbapenem susceptible controls, when available, were also collected. Three participating hospitals were located in Boston, Massachusetts, between 0.5-3 miles (0.8-4.8 kilometers) apart from one another (Boston Prospective Collection). The other participating hospital was located in Irvine, California, which is located ~3,000 miles (~4,828 kilometers) from Boston (Irvine Prospective Collection). Isolates were cultured in each hospital's respective microbiology lab from patient specimens sent for routine clinical management. Blood culture isolates were obtained using the BD BACTEC 9240 or BACTEC FX systems. Other isolates were cultured directly from clinical specimens by plating onto standard bacterial culture medium. In the case of multiple isolates from the same patient during a single admission, only the earliest collection was submitted for sequencing except in two cases when two isolates from the same patient were sequenced (BIDMC_43A, BIDMC_43B and BIDMC_42A, BIDMC_42B). Organism identification and susceptibility testing were performed using the bioMérieux Vitek 2. Carbapenem susceptibility was defined based on an *in vitro* MIC to meropenem: ≥ 2 ug/mL was considered non-susceptible with isolates having MIC below this threshold considered susceptible.

For historical context and comparison, carbapenem resistant bacteria that had been sporadically archived from three Boston-area hospitals between 2006 and 2012 were also selected for sequencing (Historical Collection). Strains from the Historical Collection were tested for carbapenem susceptibility by disk diffusion. Strains were then tested for presumptive carbapenemase activity by modified Hodge test per CLSI guidelines, and, if confirmed, the MIC was determined by manual micro broth dilution. A full list of isolates and characteristics is provided in Table S1 and summarized in Table S2.

DNA extraction. Bacterial DNA was extracted using either the BioRobot EZ1 or the QiaSymphony AS (Qiagen). For the BioRobot EZ1 extractions, the bacterial protocol using the EZ1 DNA Tissue Kit was followed and the DNA was extracted according to the specifications provided by the EZ1 DNA Bacterial Card. For the QiaSymphony DNA extractions, one bacterial colony was suspended in 400 mL of lysis buffer containing 180 mL of Qiagen P1 buffer, 20 mL of Qiagen PK and 200 mL of Qiagen AL buffer. The tube was vortexed for 1 minute and incubated at 56ºC for 30 minutes and then at 95ºC for 10 minutes. The tube was loaded onto the QiaSymphony. Bacterial DNA was extracted using the DSP Midi Virus/Pathogen Kit and the DSP Complex 400 Default IC protocol.

Library preparation and genome sequencing. Two Illumina sequencing libraries were prepared as previously described (1). Libraries were 101 bp, paired-end sequenced using the HiSeq2000 platform to achieve 100-200-fold coverage. Seven isolates were also selected for sequencing via the Pacific Bioscience RS platform: BIDMC_12C, BIDMC_16, BIDMC_19C, BIDMC_18C, MGH_8, MGH_14 and BWH_24. Libraries were prepared as previously described (2) and sequenced and analyzed on the PacBio-RS instrument (version 2 chemistry and 2.0.1 analysis software) following manufacturer's recommendations. The sequencing yielded ~10 KB reads, on average, at approximately 100x (range of 90x-146x) genome coverage.

Assembly. Data were assembled using ALLPATHS-LG (3) with the reference assisting option. Base call correction was performed by Pilon (4) according to BWA (5) read alignment. Potential mis-assemblies were manually corrected. Final assemblies were produced by post-assembly scaffolding using SSPACE (6) followed by a second round of assembly improvement using Pilon. The scaffolding consists of estimating the distance between contiguous sequences (contigs) and defines their relative order and orientation based on paired-end reads that are assigned to different contigs but derived from the same jumping library clone. Paired-end reads are reads derived from the insert ends of the same library clone. Jumping library clones contain the DNA from two fragments 3-5 Kb apart in the genome, which significantly improves the assembly of genomes and are critical in the resolution of repetitive regions. Strains sequenced with PacBio were assembled using HGAP (7). The accuracy of assemblies obtained by a second round of scaffolding using SSPACE was evaluated by comparing SSPACE assemblies to PacBio assemblies from the same strain. An average accuracy was estimated by dividing the number of correct joins by the total number of joins performed on all seven isolates (Table S10). SSPACE, like the scaffolding module embedded in ALLPATHS-LG, attempts to resolve contradictory assembly hypotheses by analysing the number and nature of paired-ends reads supporting each alternative. The SSPACE approach is less conservative, generating scaffolds in cases where ALLPATHS-LG will report separate and disconnected contigs.

Annotation. Protein-coding gene predictions were made by Prodigal (8). rRNA loci were predicted by RNAmmer (9), and tRNA by tRNAscan-SE (10). Protein-coding genes with 70% overlap with non-coding genes were filtered out. Gene product names were assigned based on BLAST best hit (E-value < 1e-10) against the following reference databases in the following order of precedence: curated set of *E. coli* virulence proteins (only *E. coli* assemblies; >= 60% identity and query coverage), Swiss-Prot (11) (>=70% identity and query coverage for *E. coli*; >= 60% for others), TIGRFam (12), *E. coli* K-12 MG1655 proteins (in-house sequence and annotation) and *E. coli* UTI89 (GenBank accession: NC_007946.1, NC_007941.1) proteins (only *E. coli* assemblies; >= 60% identity and query coverage), *K. pneumoniae* MGH 78578 (GenBank accession: NC_009648.1, NC_009649.1, NC_009650.1, NC_009651.1, NC_009652.1, NC_009653.1) proteins (only *K. pneumoniae* assemblies; >= 60% identity and query coverage) and *E. cloacae* ATCC 13047 (GenBank accession: NC_014121.1, NC_014107.1, NC_014108.1) proteins (only *E. cloacae* assemblies; >= 60% identity and query coverage). Genes without a match to any database had their product name defined as "hypothetical protein." These annotations were submitted to NCBI. Genes were also functionally re-annotated for secondary analysis of resistance genes based on BLAST searches against four databases: i) an internal custom-made database of genes encoding porins and beta-lactamases, including carbapenamases; ii) Resfinder (13); iii) genes with available sequences in the Lahey Clinic catalog of beta-lactamases (http://www.lahey.org/Studies) and (iv) ARDB (14). Gene names from best matches with e-value < 1e-10 with > 80% coverage of the database sequence were transferred. Matches against multiple genes in different databases were resolved by defining an order of precedence among databases, the same order in which those databases are listed above.

Clustering orthologs and phylogenetic reconstruction. Predicted genes were grouped into putative ortholog clusters using OrthoMCL 1.0 (15) using an inflation value of 1.5 and a E-value cutoff of $1e10^{-5}$. Genes conserved among isolates of each species and having one single copy per genome (single copy core) were concatenated and aligned using MUSCLE (16). For each species, phylogenetic reconstructions were generated using FastTree (17). Tree rendered by FigTree (18).

Reconstruction of recombination-free phylogenetic ST258 strain tree. Genomic sequences from all ST258 isolates and UCI_17, a closely related ST437 isolate, were aligned using progressive Mauve (19), multiple whole-genome alignment algorithm. Conserved regions in the Mauve XMFA output alignment were converted to FASTA format, and Gubbins (20) was used to predict regions of recombination (parameters: '--filter_percentage 60 --tree-builder raxml'). Gubbins intermediate trees were generated by RaxML (21). Putative sites of recombination were removed from the alignment and a new phylogenetic tree was constructed for ST258 strains using FastTree (22). Tanglegram, a visual comparison of taxa position in two alternative trees, was rendered by Dendroscope (23).

***cps* gene analysis and clade classification**. ST258 isolates may be further divided on the basis of distinct and divergent capsular loci, which form *cps* clades I and II (Fig. S1 and Table S1). *wzy* reference sequences were downloaded from GenBank as proxies for capsular polysaccharide clades I and II (24, 25) (AHJ80448.1 and AHJ80492.1, respectively). The *wzy* sequences were BLAST (26) similarity searched against each assembly. Matches (e-value < 1e-10, > 80% coverage of *wzy* sequence length) from all strains were aligned with the reference sequences using MAFFT (27) and a phylogenetic tree was constructed using FastTree (22) and rendered by FigTree (18). *cps* clade designations were based on the relatedness to each reference *wzy* sequence.

Plasmid identification. To identify plasmids, each scaffold was BLAST similarity searched against the GenBank NT database from May 2014. The best BLAST hit to each scaffold was manually inspected and binned into one of five reference datasets: all plasmid sequences, all mobile element sequences and chromosomal reference sequences for each of *E. cloacae, E. coli,* and *K. pneumoniae*. Plasmid scaffolds were defined when >70% of scaffold length matched the plasmid reference dataset and < 30% matched to either mobile element or chromosomal sequences, according to MUMMER alignment (28), a whole-genome pairwise alignment algorithm. Reference plasmids having ≥ 70% overall coverage by scaffolds of one isolate were considered as present in that isolate. The estimated length of each plasmid was calculated as the sum of the length of all scaffolds associated with a specific reference plasmid. Incompatibility groups were defined based on greater than 94% identity to replicons in PlasmidFinder database (29). Similarity among plasmids was evaluated by MUMMER (28); alignments overall pairwise coverage, and identity were calculated by internal scripts and rendered as a heat map by the heatmap.2 function of gplots package, R (30). We compared results using our approach for BIMDC_38, BWH_24 and BIDMC_20B to those reported by (31), which featured PLACNET, an alternative plasmid identification method. Eight of ten total predicted plasmids were found with both methods (Table S11).

Transposon Tn*4401* annotation. Tn*4401* sequences were identified by BLAT (32), a global-local (glocal) pairwise alignment algorithm; by aligning genomic sequences (local alignment) against the Tn*4401* transposon sequence (global alignment) from plasmid pKPC_FCF/3SP (GenBank accession NC_021660.2 coordinates 27,541 to 37,544). Identified transposon sequences from each isolate were aligned using MAFFT (27) (parameters "--globalpair --maxiterate 16") and the Tn*4401* phylogeny was reconstructed using FastTree (22) (default parameters). Tree rendered by FigTree (18). Transposons with gaps in the end of the multiple sequence alignment were considered 'truncated'. Only isoforms of the transposon present in more than one genome were annotated according to the appropriate nomenclature (33, 34). Isoforms not meeting this criterion were annotated as 'unique'. Copies of Tn*4401*b either carrying different variants of bla_{KPC} or containing a single nucleotide substitution were considered as distinct Tn*4401*b subtypes. Fig. 3 was rendered using Circos (35). Site of integration of chromosome-encoded Tn*4401* was examined by concatenating 5 KB regions flanking the transposon on both sides (10 Kb total). Flanking sequences were aligned in pairwise fashion by MUMMER (28). Sequences with more than 90% coverage with 90% identity were considered as representing the same integration site. Two instances of chromosomal Tn*4401* were located near scaffold breaks. In those cases only the available flanking region was evaluated. Manual inspection and Pilon (4) assisted evaluation of the alignment of UCI_1 and UCI_67 reads against their respective genomes revealed correct assembly of the 210 bp deletion in Tn*4401* that we propose as Tn*4401*i. Specifically, we observed no significant deviation in the average read depth across the element or enrichment of paired-end reads with longer or shorter than expected mapping distances between reads. UCI_1 and UCI_67 reads were also aligned against the assembly of isolate BIDMC_43B, which encodes isoform Tn*4401*b without the 210 bp deletion (Fig. S10). In this case and as expected, there were no reads spanning the region of 210 bp deletion, and paired-end reads flanking the deletion were mapped farther apart than expected based on the distribution of the insert size of the sequenced library. Alignments were performed using BWA-MEM (36) and visual inspection and figures were made using the Integrative Genomics Viewer (IGV) (37).

Search for genetic determinants of meropenem resistance in strains having unexplained resistance. Ortholog clusters containing genes from MGH_31 or MGH_59 predicted to be on plasmid scaffolds were identified. For each such cluster, the number of meropenem susceptible isolates contributing to that cluster was tallied, and clusters encoding "hypothetical proteins" were BLAST similarity searched against the NCBI non-redundant database (Table S7). Orthologs cluster containing genes from MGH_31 or MGH_59 that were either annotated as resistance genes (see SI Annotation section) or contained beta-lactamase domains according to similarity search against PFAM/TIGRFAM (38), in spite of their genomic location (chromosomal or plasmid), were also inspected (Table S9). BIDMC_35 genes predicted as part of plasmid scaffolds were identified and BLAST similarity searched against the PFAM domain database (Table S8). Alternatively, sequencing reads from all isolates with unexplained resistance were aligned against a nucleotide database of antibiotic resistance genes (AR genes). AR genes were considered present in an isolate if the mean read depth of aligned reads was higher than a specific threshold (median – 2 * standard deviation of the read depth of single copy genes in *K. pneumoniae*) and 60% of the AR gene was covered with aligned reads with a read depth above the same threshold. Results are shown in Table S12. For highly related families of AR genes (e.g., *bla*$_{\text{SHV}}$ family) the mapping results indicated the presence of multiple members even when a strain encoded only a single gene from that family.

PCR validation for presence of specific loci. The presence of *bla*$_{\text{KPC}}$ was verified in select strains by colony PCR using primers (5- GTCACTGTATCGCCGTCTAGTTC and 5-CTCGAGCGCGAGTCTAGC). Sanger sequencing was used to confirm all amplification products. The *wzi* gene from BIDMC_35 was amplified with primers 5-ATGATAAAAATTGCGCGCATTG and 5-CTAAATGGTATTTCAACCCCTGCG by colony PCR. Amplification resulted in a band with the expected length and Sanger sequencing confirmed that the *wzi* sequence was specific to BIDMC_35. The *bla*$_{\text{OXA-10}}$ from BIDMC_35 was amplified with primers 5- GCAACGATGTTACGCAGCAG and 5-GTTGAGTCGATACTTCGGCG by colony PCR. Amplification resulted in a band with the expected length and Sanger sequencing confirmed that the *bla*$_{\text{OXA-10}}$ sequence was specific to BIDMC_35.

Identifying plasmid-encoded resistance factors. A meropenem susceptible *K. pneumoniae* strain was transformed with the plasmid content from MGH_31 or MGH_59 and a meropenem susceptible *E. coli* NEB10beta strain was transformed with plasmid content from BIDMC_35 by electroporation. Meropenem susceptibility was determined by two-fold serial dilutions of meropenem in Mueller Hinton medium.

SI FIGURES

Figure S1. **Phylogenetic tree based on multiple sequence alignment of *wzy* orthologs across all *Klebsiella* ST258 isolates**. The *wzy* gene encodes the capsular polysaccharide (*cps*) polymerase and is a proxy for *cps* clades I and II. The OTU AHJ80492.1 (red) is associated with *cps* clade I. The OTU AHJ80448.1 (blue) is associated with *cps* clade II (see Materials and Methods). No *wzy* orthologs were found in UCI_22 and UCI_61 and BIDMC_18A. Branch length scale indicates the number of substitutions per site.

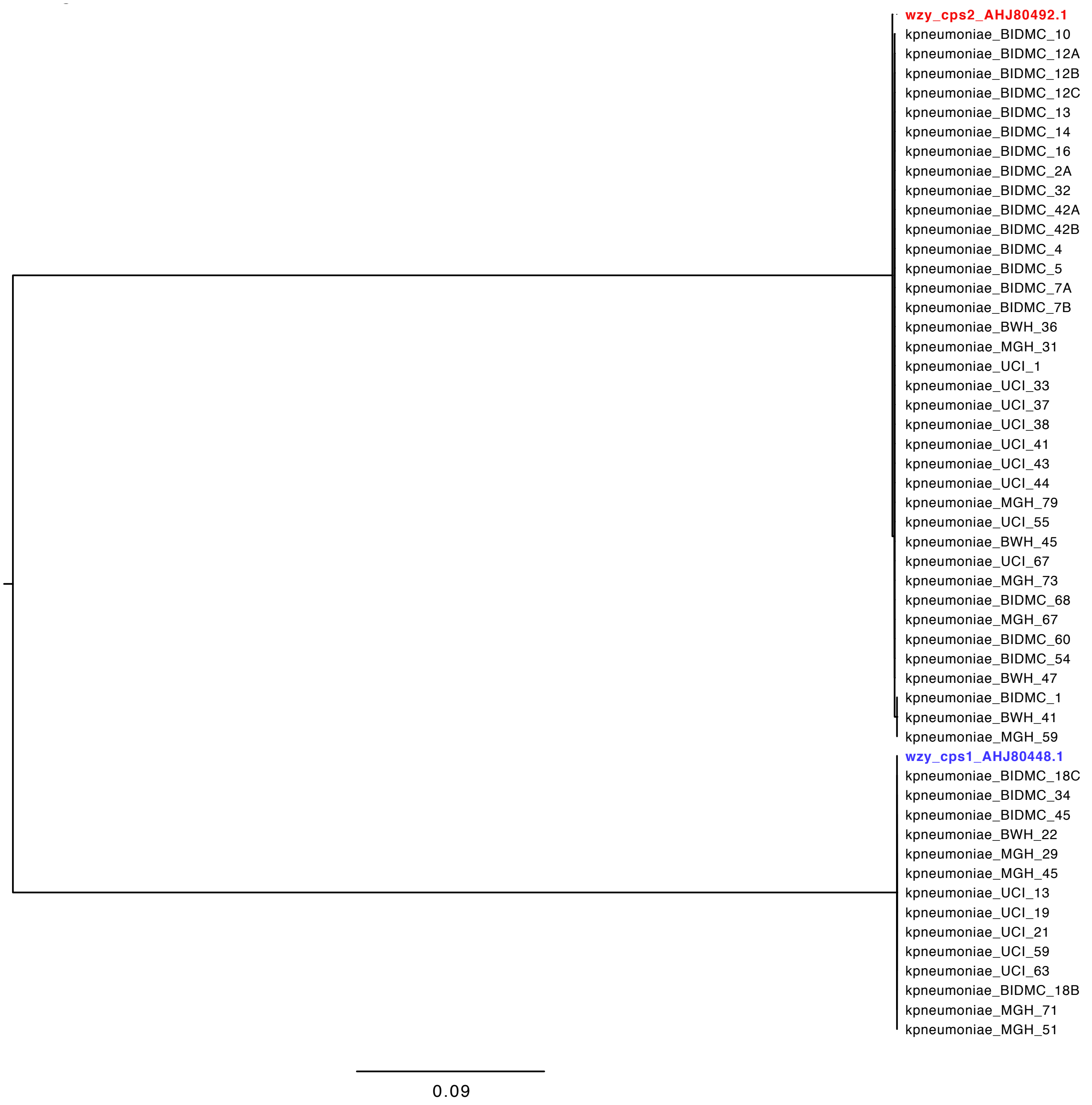


Figure S2. **Timeline of susceptible isolates.** Isolates are stratified based on species and MLST (vertical axis) and with respect to time of collection (horizontal axis). Shape of glyphs indicates the hospital from which each isolate was collected, according to the legend on the right.

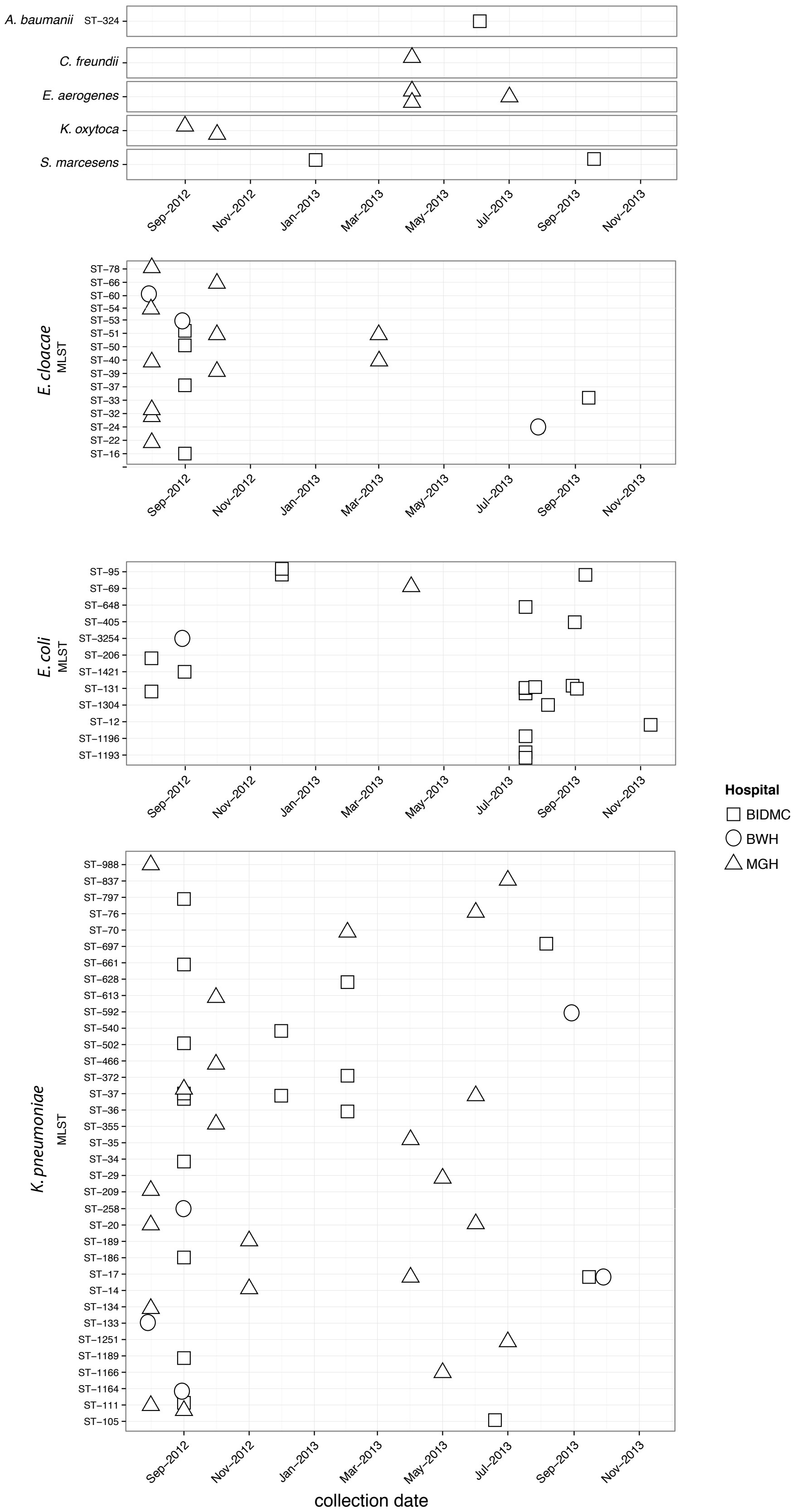


Figure S3. **Bar chart showing the MIC to meropenem (ug/mL) per predicted genetic determinant for resistance of isolates within Prospective Collection.** The multiplying factor on top of each bar indicates the number of isolates represented by each bar when the number was more than one.

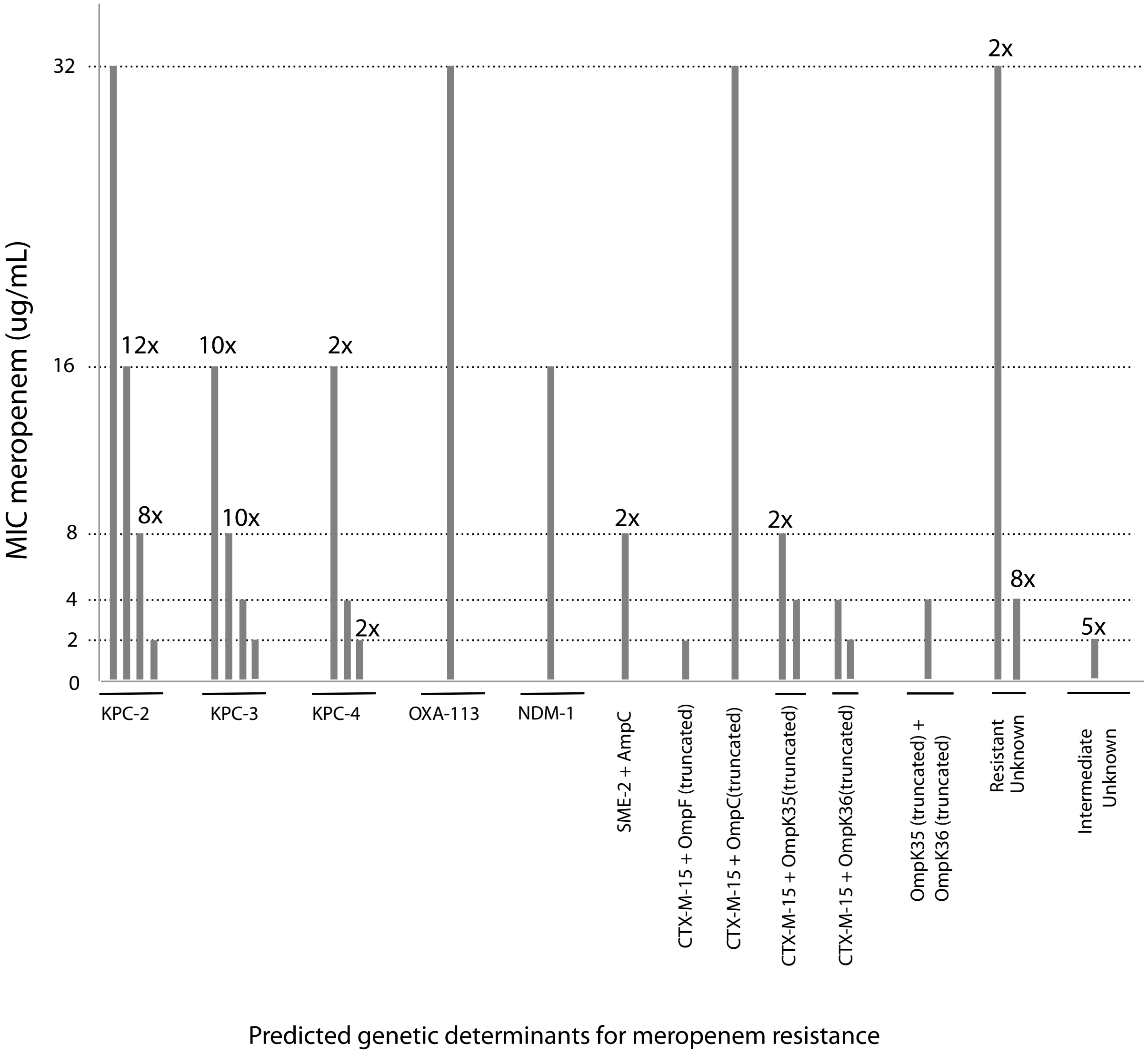


Figure S4. **Phylogeny of *K. pneumoniae* isolates** - Column containing green, gray, yellow and red rectangles indicate MIC of meropenem in ug/mL for each isolate according to the legend. Grid with blue rectangles indicates the plausible genotype conferring resistance for each specimen from the list of alternative genotypes located on the top. Labels near blue rectangles indicate if gene is located in the chromosome, or, in the case of plasmid encoded genes, the replicon and name or Genbank accession of similar plasmid (in brackets). Black rectangles indicate the city in which the isolate was collected. Vertical thick bars delimit clades associated with a MLST and containing resistant strains. Branch length scale indicates the number of substitutions per site.

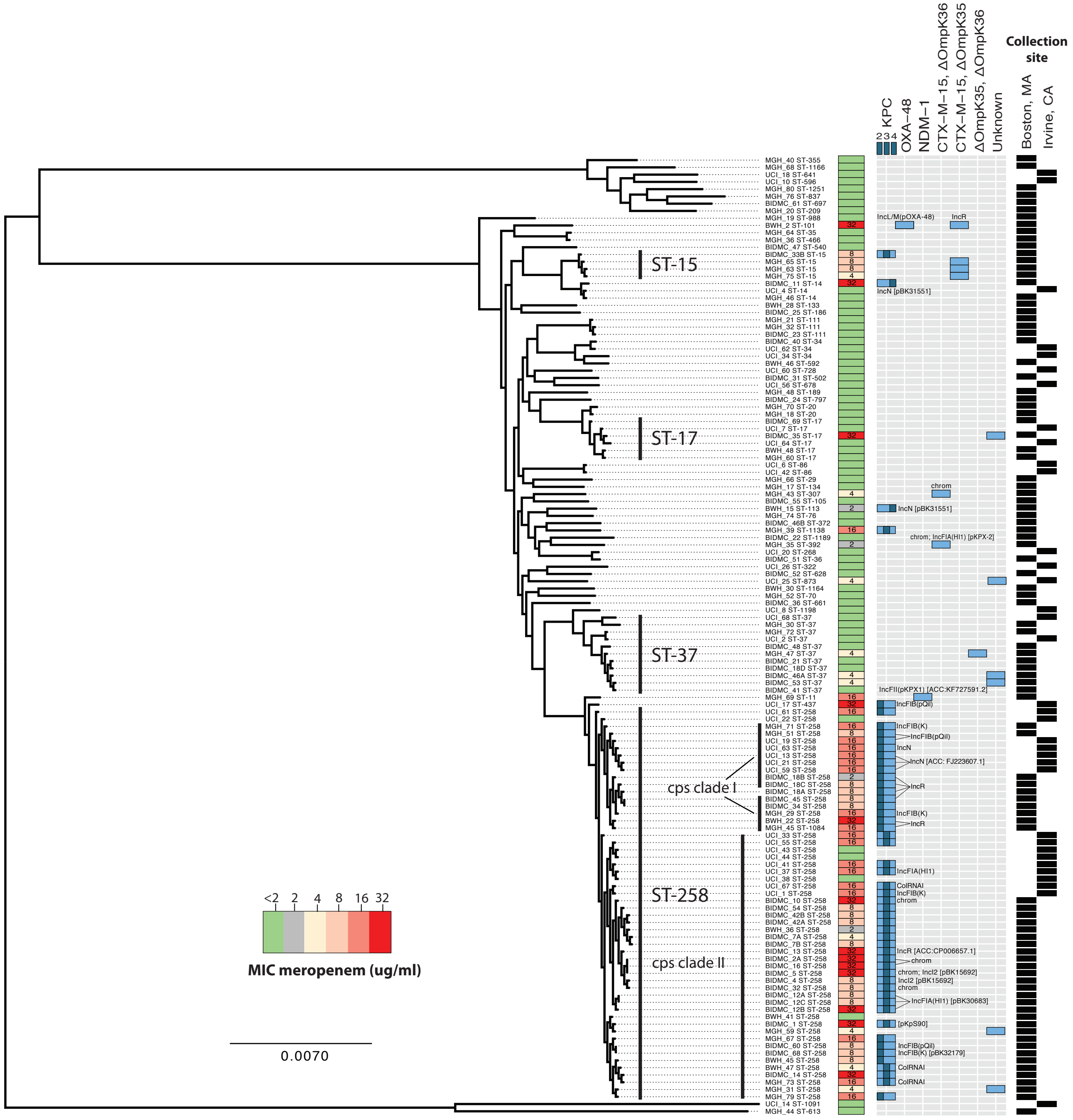


Figure S5. **Phylogeny of *E. coli* isolates** - Column containing green, gray, yellow and red rectangles indicate MIC of meropenem in ug/mL for each isolate according to the legend. Grid with blue rectangles indicates the plausible genotype conferring resistance for each specimen from the list of alternative genotypes located on the top. Labels near blue rectangles indicate if gene is located in the chromosome, or, in the case of plasmid encoded genes, the replicon and name or Genbank accession of similar plasmid (in brackets). Black rectangles indicate the city in which the isolate was collected. Vertical thick bars delimit clades associated with a MLST and containing resistant strains. Branch length scale indicates the number of substitutions per site.

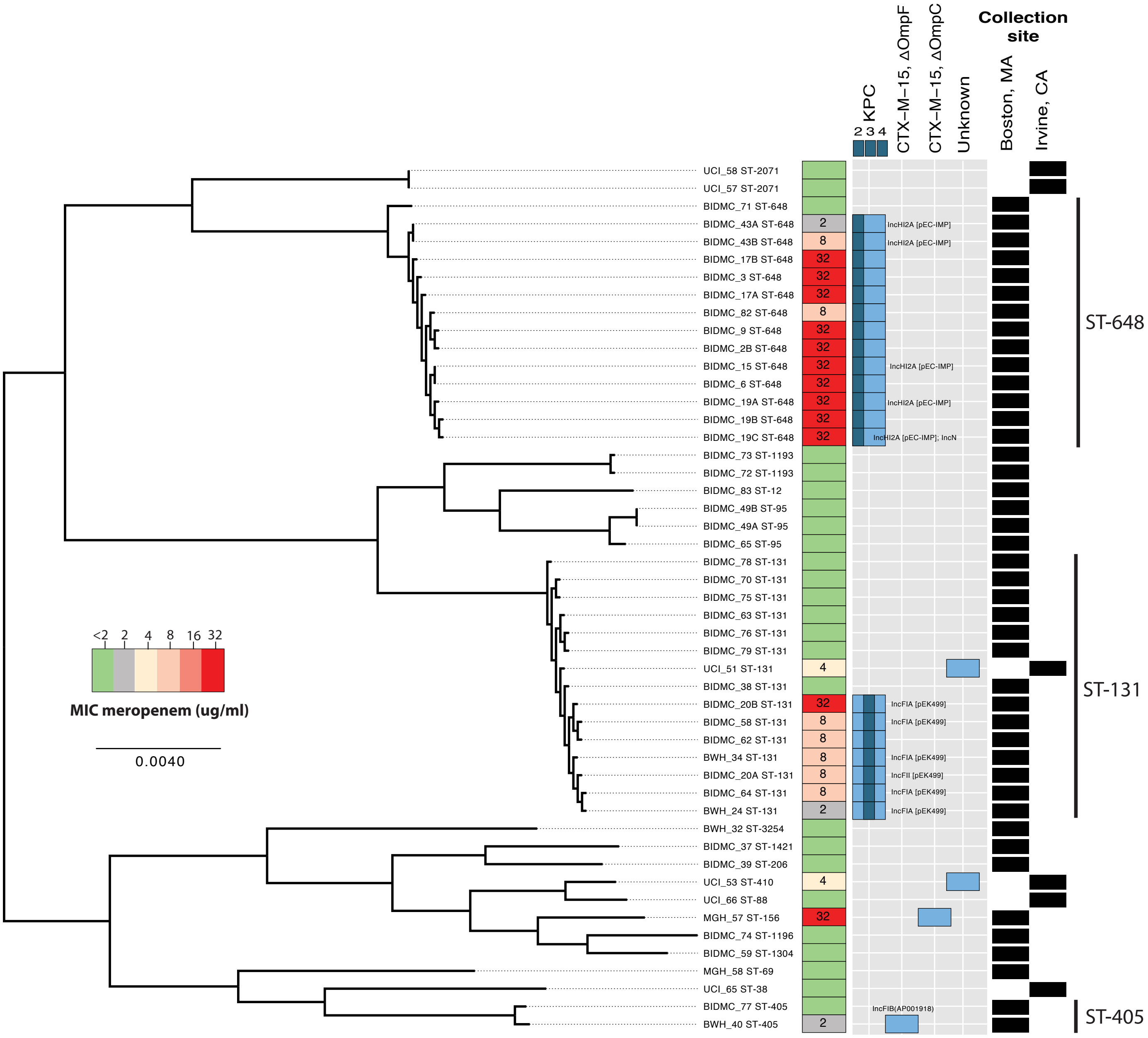


Figure S6. **Phylogeny of *E. cloacae* isolates** - Column containing green, gray, yellow and red rectangles indicate MIC of meropenem in ug/mL for each isolate according to the legend. Grid with blue rectangles indicates the plausible genotype conferring resistance for each specimen from the list of alternative genotypes located on the top. Labels near blue rectangles indicate if gene is located in the chromosome, or, in the case of plasmid encoded genes, the replicon and name or Genbank accession of similar plasmid (in brackets). Black rectangles indicate the city in which the isolate was collected. Vertical thick bars delimit clades associated with a MLST and containing resistant strains. Branch length scale indicates the number of substitutions per site.

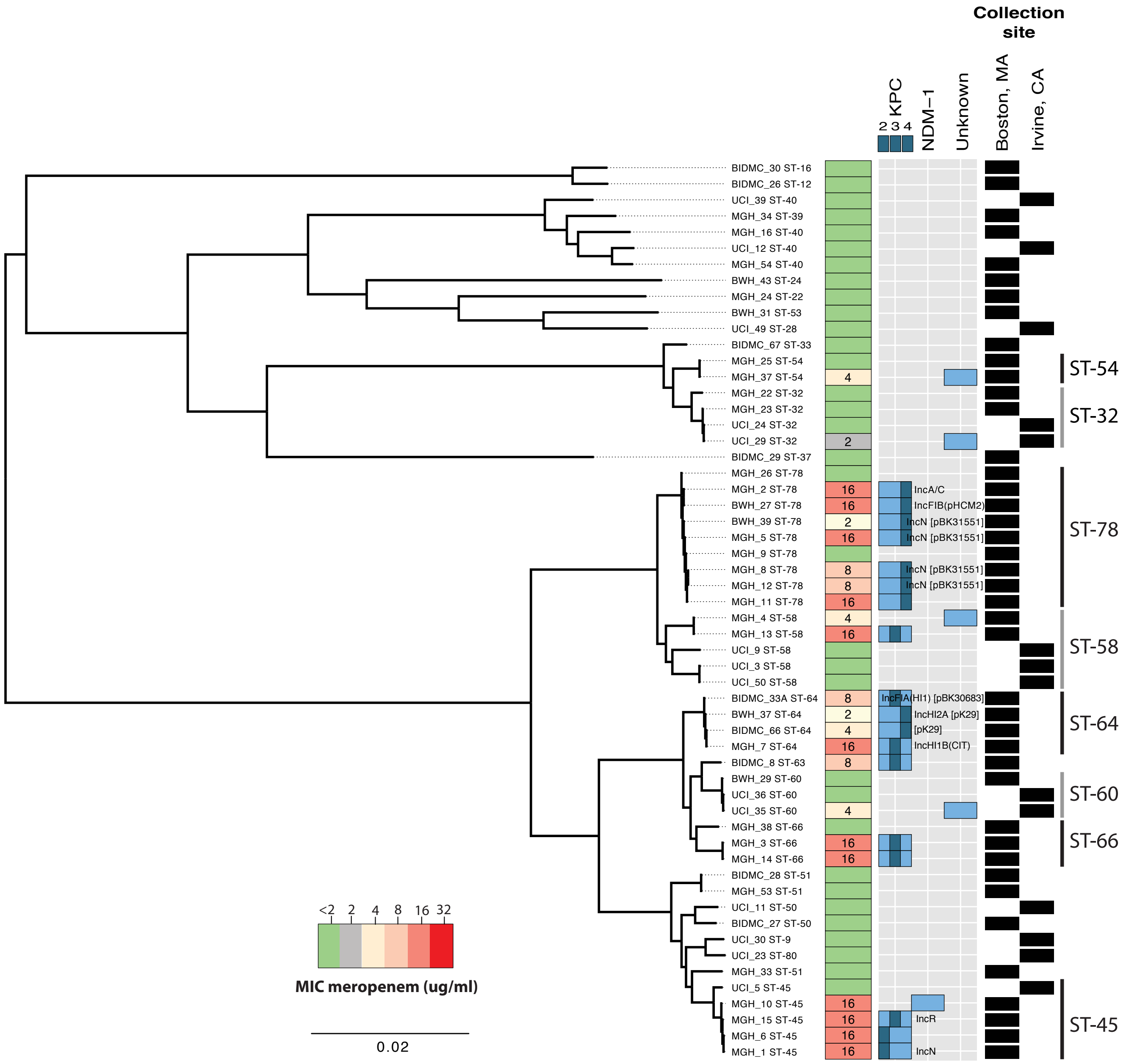
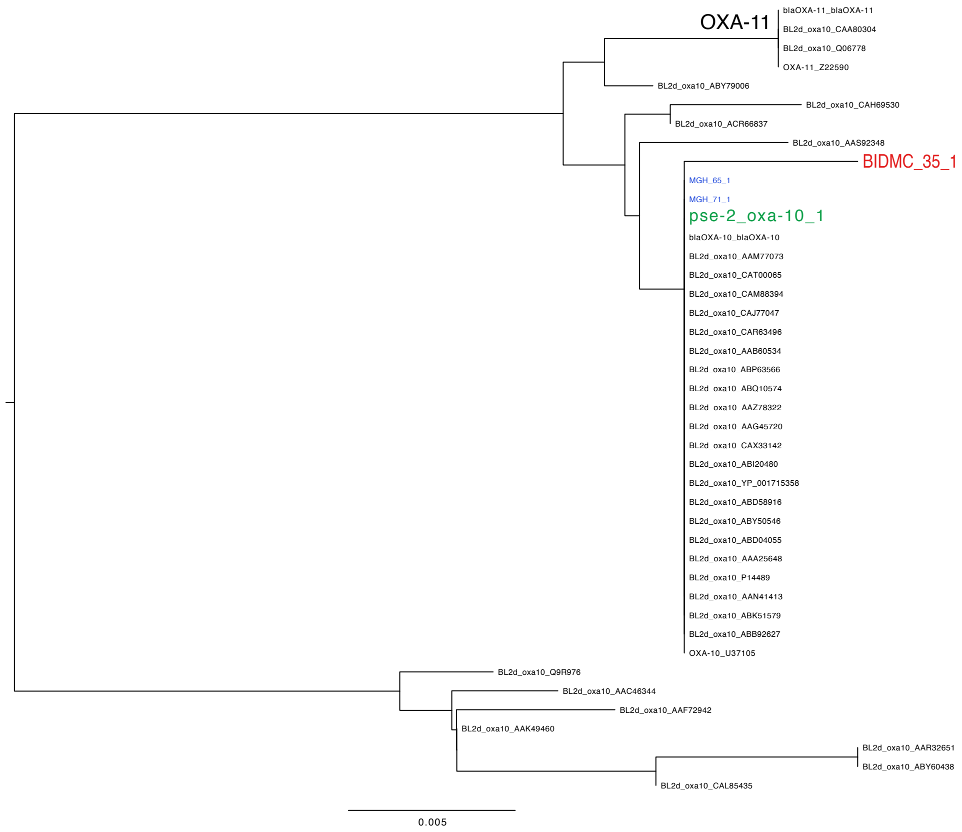


Figure S7. **Phylogenetic tree of amino acid alignment of $\textit{bla}_{\text{OXA-10}}$ and $\textit{bla}_{\text{OXA-11}}$ genes.** A) OTUs in black represent protein sequences of $\textit{bla}_{\text{OXA-10}}$ and $\textit{bla}_{\text{OXA-11}}$ genes from the antibiotic resistance databases used in the re-annotation of genes (see SI Materials and Methods). OTUs in blue correspond to $\textit{bla}_{\text{OXA-10}}$ representatives in two of our isolates. The OTU in green represents the first characterized $\textit{bla}_{\text{OXA-10}}$ gene (39) (originally named as PSE-2 *bla*). The OTU in red represents BIDMC_35's $\textit{bla}_{\text{OXA-10}}$. MAFFT (27) (--globalpair --maxiterate 16) was used in the alignment of sequences, FastTree (17) in the tree reconstruction and FigTree (18) in the rendering of the tree. Branch length scale indicates the number of substitutions per site. B) Partial visualization of multiple sequence alignment of few sequences depicted in the phylogenetic tree. Rendered by Seaview (40).

A



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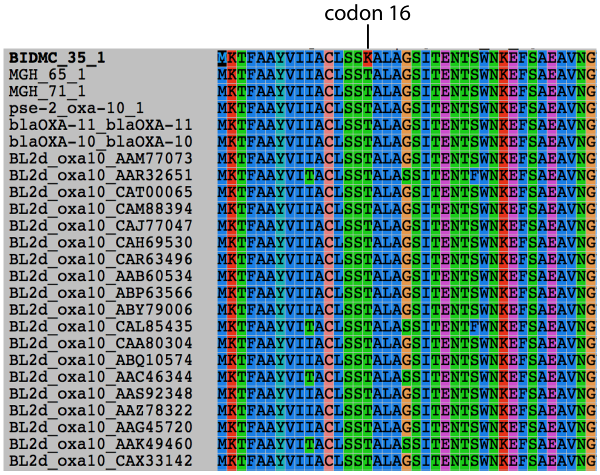

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BIDMC_35_1              MKTFAAYVIIACLSSKALAGSITENTSWNKEFSAEAVNG
MGH_65_1                MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
MGH_71_1                MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
pse-2_oxa-10_1          MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
blaOXA-11_blaOXA-11     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
blaOXA-10_blaOXA-10     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAM77073     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAR32651     MKTFAAYVITACLSSTALASSITENTFWNKEFSAEAVNG
BL2d_oxa10_CAT00065     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_CAM88394     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_CAJ77047     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_CAH69530     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_CAR63496     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAB60534     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_ABP63566     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_ABY79006     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_CAL85435     MKTFAAYVITACLSSTALASSITENTFWNKEFSAEAVNG
BL2d_oxa10_CAA80304     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_ABQ10574     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAC46344     MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAS92348     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAZ78322     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAG45720     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
BL2d_oxa10_AAK49460     MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNG
BL2d_oxa10_CAX33142     MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNG
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Figure S8. **Phylogenetic tree of nucleotide alignment of Tn*4401* isoforms** - Tn*4401* transposon isoforms are indicated according to the color legend. Only transposons encoded in the genomes of *K. pneumoniae*, *E. coli* and *E. cloacae* isolates were included in this analysis. Very large branches were contracted to facilitate visualization and indicated by scale breaks (two parallel lines). Branch length scales indicate the number of substitutions per site.

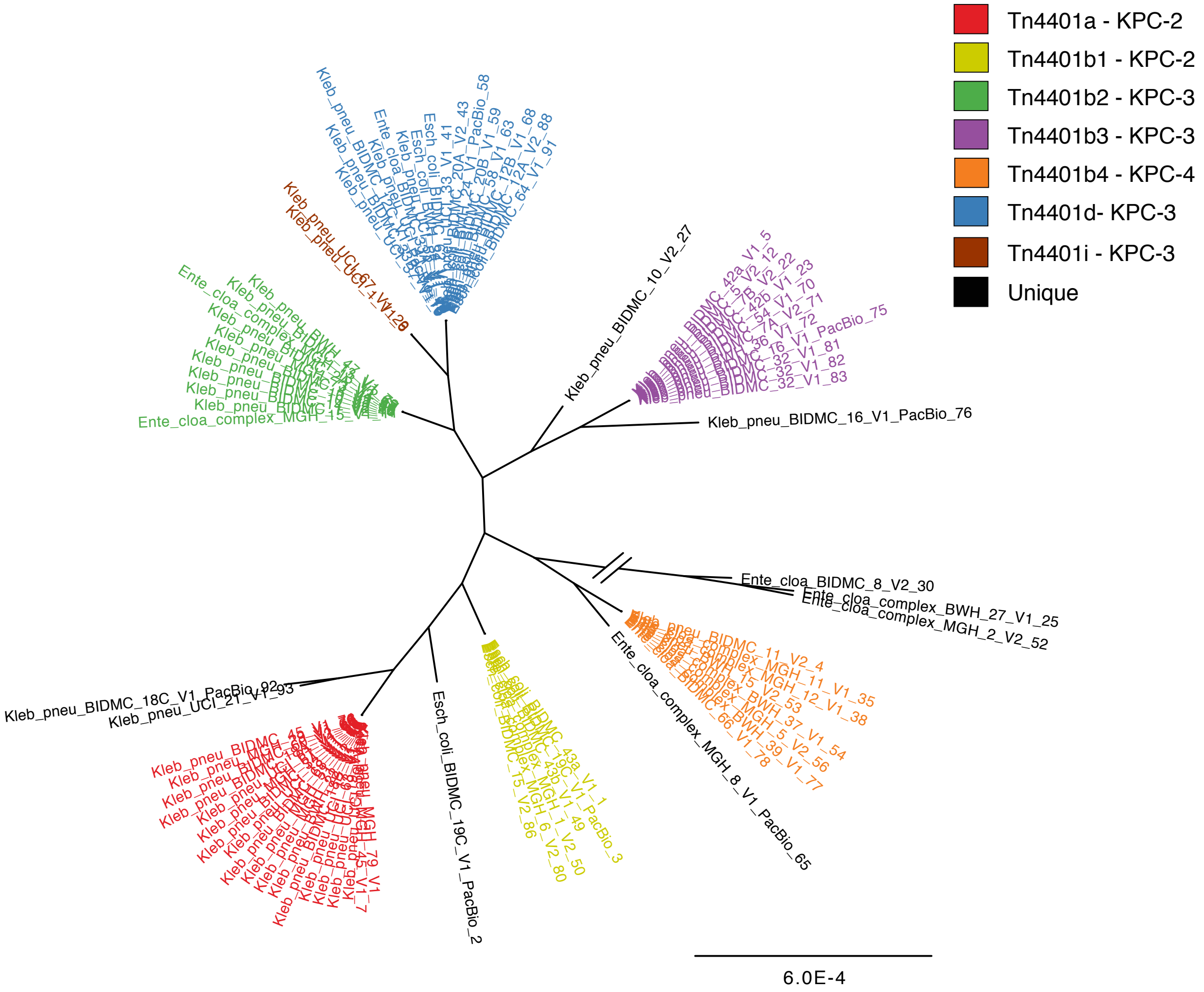


Figure S9. **Comparison of ST258 core genome phylogenies with and without predicted regions of recombination.** (A) ST258 phylogeny based on the single copy core of *K. pneumoniae* (see SI Materials and Methods), including sites predicted to be recently recombined. (B) ST258 phylogeny based on core genome of *K. pneumoniae* excluding sites predicted by Gubbins (20) to be recently recombined (see SI Materials and Methods). Blue and black strain identifiers correspond to isolates from U.S. West Coast and U.S. East Coast, respectively, UCI_17, in red, served as an outgroup for this analysis. Purple lines connect isolates with major differences in their relative location when comparing trees. Numbers near branches indicate local support values; values below 0.8 are not shown.

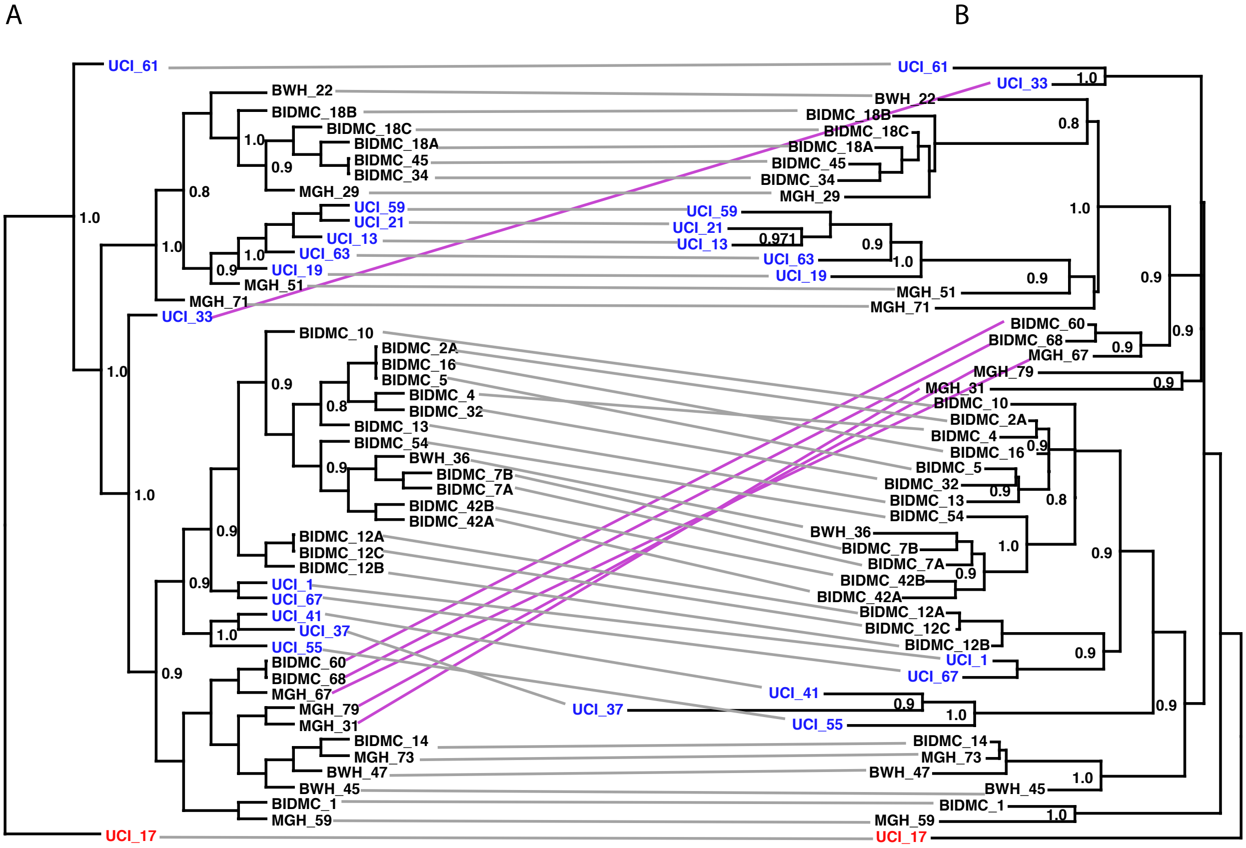
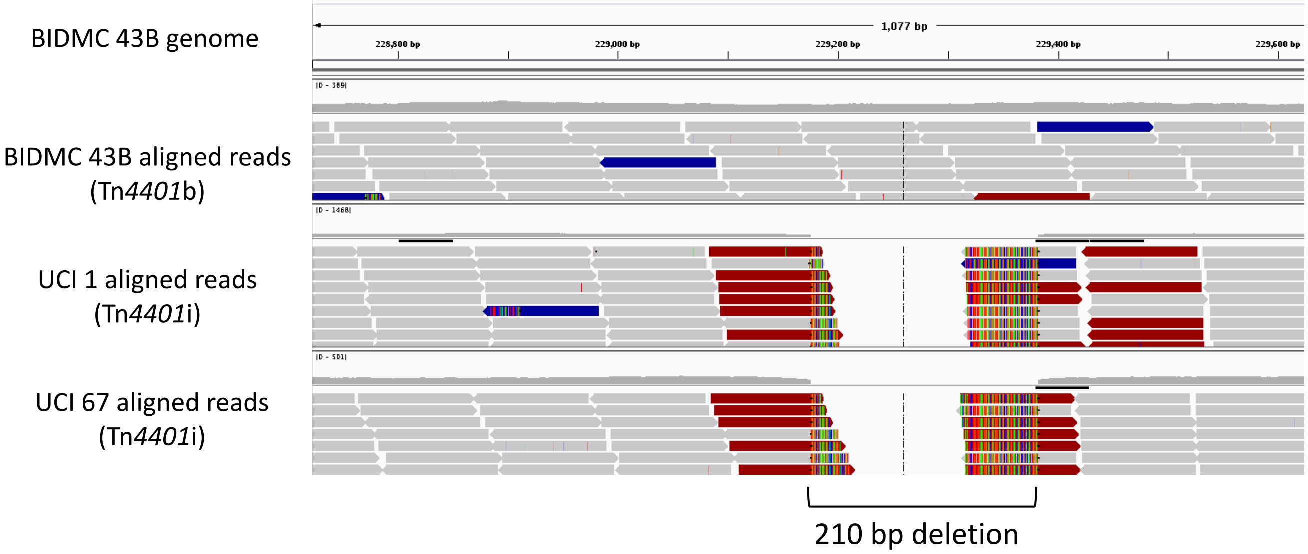


Figure S10. **Alignment of UCI_1 and UCI_67 reads against BIDMC_43B assembly confirms a 210 nt deletion in Tn*4401*.** Top track shows the Tn*4401b*-containing region of scaffold NZ_KI929662.1 from BIMDC_43B. Grey, blue and red arrows in the second, third and fourth track represent alignments of sequencing reads from isolates BIDMC_43B, UCI_1 and UCI_67 to BIDMC_43B assembly, respectively. The color of the arrows indicates paired-end reads (jumps) mapped farther apart then expected (red; farther than 99.5% of jumps), optimally mapped (grey) and closer than expected (blue; closer than 99.5% of jumps) based on the distribution of all jumps aligned to the reference. Colored vertical lines in the arrows correspond to nucleotide differences between reads and the reference genome, BIDMC_43B.



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SI TABLES

Table S1. List of strains, hospitals, collection date, ST, MIC to meropenem, predicted carbapenem resistance determinant, *cps* prediction and Tn*4401* isoform.

collection phase	collection date	clinical sample type	species	Isolate	MIC mero (ug/ml)	MLST	cps prediction	resistance phenotype	genotype conferring resistance	Tn4401 variant
Boston historical	September-07	Urine	*Enterobacter cloacae*	MGH_13	>=16	ST58		NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston historical	October-07	Urine	*Enterobacter cloacae*	MGH_5	>=16	ST78		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston historical	January-08	Wound	*Enterobacter cloacae*	MGH_7	>=16	ST64		NON-SUSCEPTIBLE	blaKPC-3	truncated
Boston historical	April-08	Urine	*Enterobacter cloacae*	MGH_9	0.5	ST78		SUSCEPTIBLE		
Boston historical	July-08	Blood Culture	*Klebsiella pneumoniae*	BIDMC_5	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	2 copies: Tn4401b3, truncated
Boston historical	December-08	Swab, Peritoneal Abscess	*Klebsiella pneumoniae*	BIDMC_11	>32	ST14		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston historical	April-09	Respiratory	*Enterobacter cloacae*	MGH_14	>=16	ST66		NON-SUSCEPTIBLE	blaKPC-3	truncated
Boston historical	May-09	Urine	*Enterobacter cloacae*	MGH_10	>=16	ST45		NON-SUSCEPTIBLE	NDM-1	
Boston historical	June-09	Urine	*Enterobacter cloacae*	MGH_12	8	ST78		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston historical	June-09	Urine	*Enterobacter cloacae*	MGH_11	>=16	ST78		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston historical	July-09	Urine	*Enterobacter cloacae*	MGH_8	8	ST78		NON-SUSCEPTIBLE	blaKPC-4	unique
Boston historical	July-09	Respiratory	*Enterobacter cloacae*	MGH_1	>=16	ST45		NON-SUSCEPTIBLE	blaKPC-2	Tn4401b1
Boston historical	August-09	Swab, abdominal incision	*Escherichia coli*	BIDMC_3	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	August-09	Foot Culture	*Klebsiella pneumoniae*	BIDMC_10	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	3 copies: 2xTn4401b2, unique
Boston historical	September-09	Wound	*Enterobacter cloacae*	MGH_2	>=16	ST78		NON-SUSCEPTIBLE	blaKPC-4	unique
Boston historical	September-09	Urine	*Escherichia coli*	BIDMC_9	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	September-09	Tissue, Abdomen	*Klebsiella pneumoniae*	BIDMC_4	>8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston historical	November-09	Urine	*Enterobacter cloacae*	MGH_6	>=16	ST45		NON-SUSCEPTIBLE	blaKPC-2	Tn4401b1
Boston historical	November-09	Urine	*Klebsiella pneumoniae*	BIDMC_14	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston historical	November-09	Blood Culture	*Klebsiella pneumoniae*	BIDMC_16	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	2 copies: Tn4401b3, unique
Boston historical	November-09	Blood Culture	*Klebsiella pneumoniae*	BIDMC_13	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston historical	December-09	Urine	*Enterobacter cloacae*	MGH_4	4	ST58		NON-SUSCEPTIBLE	UNKNOWN	
Boston historical	December-09	Respiratory	*Enterobacter cloacae*	MGH_3	>=16	ST66		NON-SUSCEPTIBLE	blaKPC-3	truncated
Boston historical	December-09	Peritoneal Fluid	*Escherichia coli*	BIDMC_17B	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	December-09	Blood Culture	*Escherichia coli*	BIDMC_17A	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	March-10	Swab, Abdomen	*Escherichia coli*	BIDMC_15	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	2 copies: Tn4401b1, truncated
Boston historical	March-10	Bile	*Escherichia coli*	BIDMC_6	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	April-10	Blood Culture	*Klebsiella pneumoniae*	BIDMC_12B	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston historical	May-10	Blood Culture	*Escherichia coli*	BIDMC_2B	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	May-10	Blood Culture	*Klebsiella pneumoniae*	BIDMC_2A	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston historical	August-10	Urine	*Klebsiella pneumoniae*	BIDMC_18D	<=0.25	ST37		SUSCEPTIBLE		
Boston historical	August-10	Bone Tissue, Toe	*Klebsiella pneumoniae*	BIDMC_1	>32	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston historical	September-10	Urine	*Escherichia coli*	BIDMC_19C	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	2 copies: Tn4401b1, unique
Boston historical	October-10	Bronchoalveolar Lavage	*Escherichia coli*	BIDMC_19A	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	October-10	Urine	*Escherichia coli*	BIDMC_19B	>32	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston historical	November-10	Urine	*Klebsiella pneumoniae*	BIDMC_18C	>8	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	unique
Boston historical	December-10	Urine	*Klebsiella pneumoniae*	BIDMC_18B	2	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston historical	July-11	Urine	*Enterobacter cloacae*	BIDMC_8	8	ST63		NON-SUSCEPTIBLE	blaKPC-3	unique
Boston historical	November-11	Tissue	*Klebsiella pneumoniae*	BWH_2	>32	ST101		NON-SUSCEPTIBLE	OXA-48	
Boston historical	March-12	Peritoneal	*Klebsiella pneumoniae*	BWH_15	2	ST113		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston historical	April-12	Urine	*Escherichia coli*	BIDMC_20A	8	ST131		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston historical	April-12	Urine	*Klebsiella pneumoniae*	BIDMC_7A	4	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b3
Boston historical	April-12	Sputum	*Klebsiella pneumoniae*	BIDMC_12A	>8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston historical	April-12	Urine	*Klebsiella pneumoniae*	BIDMC_7B	8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b3
Boston historical	May-12	Urine	*Escherichia coli*	BIDMC_20B	>32	ST131		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston historical	May-12	Urine	*Klebsiella pneumoniae*	BIDMC_18A	>8	ST258	UNKNOWN	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston historical	May-12	Endotrachael	*Klebsiella pneumoniae*	BIDMC_12C	>8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston historical	June-12	Urine	*Klebsiella pneumoniae*	BWH_22	>32	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston historical	July-12	Drainage	*Escherichia coli*	BWH_24	2	ST131		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston prospective	August-12	Tissue	*Enterobacter cloacae*	MGH_24	<=0.25	ST22		SUSCEPTIBLE		
Boston prospective	August-12	Urine	*Enterobacter cloacae*	MGH_22	<=0.25	ST32		SUSCEPTIBLE		
Boston prospective	August-12	Urine	*Enterobacter cloacae*	MGH_23	<=0.25	ST32		SUSCEPTIBLE		
Boston prospective	August-12	Respiratory	*Enterobacter cloacae*	MGH_16	<=0.25	ST40		SUSCEPTIBLE		
Boston prospective	August-12	Wound	*Enterobacter cloacae*	BWH_29	<=0.25	ST60		SUSCEPTIBLE		
Boston prospective	August-12	Urine	*Enterobacter cloacae*	MGH_26	<=0.25	ST78		SUSCEPTIBLE		
Boston prospective	August-12	Urine	*Enterobacter cloacae*	MGH_25	0.5	ST54		SUSCEPTIBLE		
Boston prospective	August-12	Respiratory	*Enterobacter cloacae*	BIDMC_33A	>8	ST64		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston prospective	August-12	Respiratory	*Enterobacter cloacae*	MGH_15	>=16	ST45		NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston prospective	August-12	Sputum	*Enterobacter cloacae*	BWH_27	16	ST78		NON-SUSCEPTIBLE	blaKPC-4	unique
Boston prospective	August-12	Blood	*Escherichia coli*	BIDMC_38	<=0.25	ST131		SUSCEPTIBLE		
Boston prospective	August-12	Blood	*Escherichia coli*	BIDMC_39	<=0.25	ST206		SUSCEPTIBLE		
Boston prospective	August-12	Urine	*Klebsiella pneumoniae*	MGH_21	<=0.25	ST111		SUSCEPTIBLE		
Boston prospective	August-12	Sputum	*Klebsiella pneumoniae*	BWH_28	<=0.25	ST133		SUSCEPTIBLE		
Boston prospective	August-12	Urine	*Klebsiella pneumoniae*	MGH_17	<=0.25	ST134		SUSCEPTIBLE		
Boston prospective	August-12	Respiratory	*Klebsiella pneumoniae*	MGH_18	<=0.25	ST20		SUSCEPTIBLE		
Boston prospective	August-12	Respiratory	*Klebsiella pneumoniae*	MGH_20	<=0.25	ST209		SUSCEPTIBLE		
Boston prospective	August-12	Urine	*Klebsiella pneumoniae*	MGH_19	<=0.25	ST988		SUSCEPTIBLE		
Boston prospective	August-12	Respiratory	*Klebsiella pneumoniae*	BIDMC_33B	>8	ST15		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d

collection phase	collection date	clinical sample type	species	Isolate	MIC mero (ug/ml)	MLST	cps prediction	resistance phenotype	genotype conferring resistance	Tn4401 variant
Boston prospective	August-12	Abscess	*Klebsiella pneumoniae*	BIDMC_32	>8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	3 copies: 3xTn4401b3
Boston prospective	September-12	Blood	*Enterobacter cloacae*	BIDMC_26	<=0.25	ST12		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Enterobacter cloacae*	BIDMC_30	<=0.25	ST16		SUSCEPTIBLE		
Boston prospective	September-12	Wound	*Enterobacter cloacae*	BIDMC_29	<=0.25	ST37		SUSCEPTIBLE		
Boston prospective	September-12	Wound	*Enterobacter cloacae*	BIDMC_27	<=0.25	ST50		SUSCEPTIBLE		
Boston prospective	September-12	Blood	*Enterobacter cloacae*	BIDMC_28	<=0.25	ST51		SUSCEPTIBLE		
Boston prospective	September-12	Bile	*Enterobacter cloacae*	BWH_31	<=0.25	ST53		SUSCEPTIBLE		
Boston prospective	September-12	Rectal Swab	*Enterobacter cloacae*	BWH_37	2	ST64		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston prospective	September-12	Urine	*Enterobacter cloacae*	BWH_39	2	ST78		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston prospective	September-12	Blood	*Escherichia coli*	BIDMC_37	<=0.25	ST1421		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Escherichia coli*	BWH_32	<=0.25	ST3254		SUSCEPTIBLE		
Boston prospective	September-12	Wound	*Escherichia coli*	BWH_34	>8	ST131		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston prospective	September-12	Tissue	*Klebsiella oxytoca*	MGH_28	<=0.25			SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella oxytoca*	MGH_27	>=16			NON-SUSCEPTIBLE	blaKPC-3	unique
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_31	<=0.25	ST502		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_23	<=0.25	ST111		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	MGH_32	<=0.25	ST111		SUSCEPTIBLE		
Boston prospective	September-12	Blood	*Klebsiella pneumoniae*	BWH_30	<=0.25	ST1164		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_22	<=0.25	ST1189		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_25	<=0.25	ST186		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_40	<=0.25	ST34		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_21	<=0.25	ST37		SUSCEPTIBLE		
Boston prospective	September-12	Blood	*Klebsiella pneumoniae*	BIDMC_41	<=0.25	ST37		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	MGH_30	<=0.25	ST37		SUSCEPTIBLE		
Boston prospective	September-12	Blood	*Klebsiella pneumoniae*	BIDMC_36	<=0.25	ST661		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_24	<=0.25	ST797		SUSCEPTIBLE		
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BWH_41	0.5	ST258	II	SUSCEPTIBLE		
Boston prospective	September-12	Bronchoalveolar Lavage	*Klebsiella pneumoniae*	BWH_36	2	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b3
Boston prospective	September-12	Tissue	*Klebsiella pneumoniae*	MGH_31	4	ST258	II	NON-SUSCEPTIBLE	UNKNOWN	
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_34	>8	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	September-12	Respiratory	*Klebsiella pneumoniae*	MGH_29	>=16	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	September-12	Urine	*Klebsiella pneumoniae*	BIDMC_35	>32	ST17		NON-SUSCEPTIBLE	UNKNOWN	
Boston prospective	October-12	Abdominal Surgical Drain Flui	*Enterobacter cloacae*	MGH_33	<=0.25	ST51		SUSCEPTIBLE		
Boston prospective	October-12	Urine	*Enterobacter cloacae*	MGH_34	<=0.25	ST39		SUSCEPTIBLE		
Boston prospective	October-12	Urine	*Enterobacter cloacae*	MGH_38	<=0.25	ST66		SUSCEPTIBLE		
Boston prospective	October-12	Urine	*Enterobacter cloacae*	MGH_37	4	ST54		NON-SUSCEPTIBLE	UNKNOWN	
Boston prospective	October-12	Urine	*Escherichia coli*	BWH_40	2	ST405		NON-SUSCEPTIBLE	blaCTX-M-15 + OmpF(truncated)	
Boston prospective	October-12	Respiratory	*Klebsiella oxytoca*	MGH_42	<=0.25			SUSCEPTIBLE		
Boston prospective	October-12	Urine	*Klebsiella oxytoca*	MGH_41	>=16			NON-SUSCEPTIBLE	blaKPC-2	unique
Boston prospective	October-12	Urine	*Klebsiella pneumoniae*	MGH_40	<=0.25	ST355		SUSCEPTIBLE		
Boston prospective	October-12	Urine	*Klebsiella pneumoniae*	MGH_36	<=0.25	ST466		SUSCEPTIBLE		
Boston prospective	October-12	Respiratory	*Klebsiella pneumoniae*	MGH_44	<=0.25	ST613		SUSCEPTIBLE		
Boston prospective	October-12	Bile (fluid)	*Klebsiella pneumoniae*	MGH_35	2	ST392		NON-SUSCEPTIBLE	blaCTX-M-15 + OmpK36(truncated)	
Boston prospective	October-12	Urine	*Klebsiella pneumoniae*	MGH_43	4	ST307		NON-SUSCEPTIBLE	blaCTX-M-15 + OmpK36(truncated)	
Boston prospective	October-12	Urine	*Klebsiella pneumoniae*	MGH_39	>=16	ST1138		NON-SUSCEPTIBLE	blaKPC-3	truncated
Boston prospective	November-12	Urine	*Klebsiella pneumoniae*	MGH_46	<=0.25	ST14		SUSCEPTIBLE		
Boston prospective	November-12	Urine	*Klebsiella pneumoniae*	MGH_48	<=0.25	ST189		SUSCEPTIBLE		
Boston prospective	November-12	Wound fluid	*Klebsiella pneumoniae*	MGH_47	4	ST37		NON-SUSCEPTIBLE	OmpK35(truncated) + OmpK36(truncated)	
Boston prospective	November-12	Urine	*Klebsiella pneumoniae*	MGH_45	>=16	ST1084	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	December-12	Blood Culture	*Escherichia coli*	BIDMC_49B	0.5	ST95		SUSCEPTIBLE		
Boston prospective	December-12	Blood Culture	*Escherichia coli*	BIDMC_49A	<=0.25	ST95		SUSCEPTIBLE		
Boston prospective	December-12	Blood Culture	*Escherichia coli*	BIDMC_43A	2	ST648		NON-SUSCEPTIBLE	blaKPC-2	Tn4401b1
Boston prospective	December-12	Blood Culture	*Escherichia coli*	BIDMC_43B	8	ST648		NON-SUSCEPTIBLE	blaKPC-2	Tn4401b1
Boston prospective	December-12	Urine	*Klebsiella pneumoniae*	BIDMC_47	<=0.25	ST540		SUSCEPTIBLE		
Boston prospective	December-12	Sputum	*Klebsiella pneumoniae*	BIDMC_48	<=0.25	ST37		SUSCEPTIBLE		
Boston prospective	December-12	Blood Culture	*Klebsiella pneumoniae*	BIDMC_42A	>8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b3
Boston prospective	December-12	Blood Culture	*Klebsiella pneumoniae*	BIDMC_42B	>8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b3
Boston prospective	January-13	Bronchoalveolar Lavage	*Serratia marcesens*	BIDMC_50	<=0.25			SUSCEPTIBLE		
Boston prospective	January-13	Urine	*Serratia marcesens*	BIDMC_44	>8			NON-SUSCEPTIBLE	blaSME-2 + AmpC	
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	BIDMC_46B	<=0.25	ST372		SUSCEPTIBLE		
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	BIDMC_51	<=0.25	ST36		SUSCEPTIBLE		
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	BIDMC_52	<=0.25	ST628		SUSCEPTIBLE		
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	MGH_52	<=0.25	ST70		SUSCEPTIBLE		
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	BIDMC_46A	2	ST37		NON-SUSCEPTIBLE	UNKNOWN	
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	BIDMC_53	2	ST37		NON-SUSCEPTIBLE	UNKNOWN	
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	BIDMC_45	>8	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	February-13	Urine	*Klebsiella pneumoniae*	MGH_51	8	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	March-13	Urine	*Enterobacter cloacae*	MGH_53	1	ST51		SUSCEPTIBLE		
Boston prospective	March-13	Urine	*Enterobacter cloacae*	MGH_54	1	ST40		SUSCEPTIBLE		
Boston prospective	April-13	Renal Stone	*Citrobacter freundii*	MGH_56	<=0.25			SUSCEPTIBLE		
Boston prospective	April-13	Urine	*Citrobacter species*	MGH_55	16			NON-SUSCEPTIBLE	blaKPC-4	truncated

collection phase	collection date	clinical sample type	species	Isolate	MIC mero (ug/ml)	MLST	cps prediction	resistance phenotype	genotype conferring resistance	Tn4401 variant
Boston prospective	April-13	Wound	*Enterobacter aerogenes*	MGH_62	<=0.25			SUSCEPTIBLE		
Boston prospective	April-13	Blood	*Enterobacter aerogenes*	MGH_61	1			SUSCEPTIBLE		
Boston prospective	April-13	Urine	*Escherichia coli*	MGH_58	<=0.25	ST69		SUSCEPTIBLE		
Boston prospective	April-13	Wound abscess	*Escherichia coli*	MGH_57	>32	ST156		NON-SUSCEPTIBLE	blaCTX-M-15 + OmpC(truncated)	
Boston prospective	April-13	Sputum	*Klebsiella pneumoniae*	MGH_60	<=0.25	ST17		SUSCEPTIBLE		
Boston prospective	April-13	Urine	*Klebsiella pneumoniae*	MGH_64	<=0.25	ST35		SUSCEPTIBLE		
Boston prospective	April-13	Urine	*Klebsiella pneumoniae*	MGH_59	>4	ST258	II	NON-SUSCEPTIBLE	UNKNOWN	
Boston prospective	April-13	Bile (fluid)	*Klebsiella pneumoniae*	MGH_63	8	ST15		NON-SUSCEPTIBLE	blaCTX-M-15 + OmpK35(truncated)	
Boston prospective	May-13	Urine	*Klebsiella pneumoniae*	MGH_66	<=0.25	ST29		SUSCEPTIBLE		
Boston prospective	May-13	Urine	*Klebsiella pneumoniae*	MGH_68	<=0.25	ST1166		SUSCEPTIBLE		
Boston prospective	May-13	Bile (fluid)	*Klebsiella pneumoniae*	MGH_65	8	ST15		NON-SUSCEPTIBLE	blaCTX-M-15 + OmpK35(truncated)	
Boston prospective	May-13	Pleural Tissue	*Klebsiella pneumoniae*	MGH_67	16	ST258	II	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	June-13	Urine	*Klebsiella pneumoniae*	MGH_70	<=0.25	ST20		SUSCEPTIBLE		
Boston prospective	June-13	Urine	*Klebsiella pneumoniae*	MGH_72	<=0.25	ST37		SUSCEPTIBLE		
Boston prospective	June-13	Urine	*Klebsiella pneumoniae*	MGH_74	<=0.25	ST76		SUSCEPTIBLE		
Boston prospective	June-13	Sputum	*Klebsiella pneumoniae*	MGH_69	16	ST11		NON-SUSCEPTIBLE	NDM-1	
Boston prospective	June-13	Urine	*Klebsiella pneumoniae*	MGH_71	16	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	June-13	Wound - Deep Sinus	*Klebsiella pneumoniae*	MGH_73	16	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston prospective	June-13	Urine	*Acinetobacter baumanii*	BIDMC_56	>32	ST208		NON-SUSCEPTIBLE	OXA-113	
Boston prospective	June-13	Urine	*Klebsiella pneumoniae*	BIDMC_54	8	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b3
Boston prospective	June-13	Urine	*Klebsiella pneumoniae*	BIDMC_55	<=0.25	ST105		SUSCEPTIBLE		
Boston prospective	June-13	Bronchoalveolar Lavage	*Acinetobacter baumanii*	BIDMC_57	1	ST324		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Enterobacter aerogenes*	MGH_78	<=0.25			SUSCEPTIBLE		
Boston prospective	July-13	Wound - Abdominal	*Enterobacter aerogenes*	MGH_77	>4			NON-SUSCEPTIBLE	UNKNOWN	
Boston prospective	July-13	Bile (fluid)	*Klebsiella pneumoniae*	MGH_76	<=0.25	ST837		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Klebsiella pneumoniae*	MGH_80	<=0.25	ST1251		SUSCEPTIBLE		
Boston prospective	July-13	Wound - Abdominal	*Klebsiella pneumoniae*	MGH_75	4	ST15		NON-SUSCEPTIBLE	blaCTX-M-15 + OmpK35(truncated)	
Boston prospective	July-13	Urine	*Klebsiella pneumoniae*	MGH_79	16	ST258	II	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_70	<=0.25	ST131		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_71	<=0.25	ST648		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_72	<=0.25	ST1193		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_73	<=0.25	ST1193		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_74	<=0.25	ST1196		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_75	<=0.25	ST131		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_76	<=0.25	ST131		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_79	<=0.25	ST131		SUSCEPTIBLE		
Boston prospective	July-13	Urine	*Escherichia coli*	BIDMC_58	8	ST131		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston prospective	August-13	Urine	*Enterobacter cloacae*	BWH_43	<=0.25	ST24		SUSCEPTIBLE		
Boston prospective	August-13	Peritoneal Fluid	*Klebsiella pneumoniae*	BIDMC_60	8	ST258	II	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	August-13	Urine	*Klebsiella pneumoniae*	BIDMC_61	<=0.25	ST697		SUSCEPTIBLE		
Boston prospective	August-13	Urine	*Escherichia coli*	BIDMC_59	<=0.25	ST1304		SUSCEPTIBLE		
Boston prospective	August-13	Blood Culture	*Escherichia coli*	BIDMC_78	<=0.25	ST131		SUSCEPTIBLE		
Boston prospective	August-13	Bronchoalveolar Lavage	*Escherichia coli*	BIDMC_62	8	ST131		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston prospective	September-13	Blood Culture	*Escherichia coli*	BIDMC_77	<=0.25	ST405		SUSCEPTIBLE		
Boston prospective	September-13	Sputum	*Klebsiella pneumoniae*	BWH_46	<=0.25	ST592		SUSCEPTIBLE		
Boston prospective	September-13	Tissue	*Klebsiella pneumoniae*	BWH_47	4	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401b2
Boston prospective	September-13	Tissue	*Klebsiella pneumoniae*	BWH_45	8	ST258	II	NON-SUSCEPTIBLE	blaKPC-2	truncated
Boston prospective	September-13	Swab	*Escherichia coli*	BIDMC_63	<=0.25	ST131		SUSCEPTIBLE		
Boston prospective	September-13	Urine	*Escherichia coli*	BIDMC_64	8	ST131		NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Boston prospective	September-13	Tissue	*Enterobacter cloacae*	BIDMC_66	4	ST64		NON-SUSCEPTIBLE	blaKPC-4	Tn4401b4
Boston prospective	September-13	Abscess	*Escherichia coli*	BIDMC_65	<=0.25	ST95		SUSCEPTIBLE		
Boston prospective	September-13	Abscess, Pelvic Drain	*Enterobacter cloacae*	BIDMC_67	<=0.25	ST33		SUSCEPTIBLE		
Boston prospective	September-13	Blood Culture	*Klebsiella pneumoniae*	BIDMC_68	8	ST258	II	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Boston prospective	September-13	Sputum	*Klebsiella pneumoniae*	BIDMC_69	<=0.25	ST17		SUSCEPTIBLE		
Boston prospective	September-13	Tissue	*Serratia marcesens*	BIDMC_81	<=0.25			SUSCEPTIBLE		
Boston prospective	September-13	Blood Culture	*Serratia marcesens*	BIDMC_80	8			NON-SUSCEPTIBLE	blaSME-2 + AmpC	
Boston prospective	October-13	Urine	*Klebsiella pneumoniae*	BWH_48	<=0.25	ST17		SUSCEPTIBLE		
Boston prospective	November-13	Urine	*Escherichia coli*	BIDMC_83	<=0.25	ST12		SUSCEPTIBLE		
Boston prospective	November-13	Urine	*Escherichia coli*	BIDMC_82	8	ST648		NON-SUSCEPTIBLE	blaKPC-2	truncated
Irvine prospective	2012	Urine	*Enterobacter cloacae*	UCI_11	<=0.25	ST50		SUSCEPTIBLE		
Irvine prospective	2012	Bronchoalveolar Lavage	*Enterobacter cloacae*	UCI_12	<=0.25	ST40		SUSCEPTIBLE		
Irvine prospective	2012	Sputum	*Enterobacter cloacae*	UCI_3	<=0.25	ST58		SUSCEPTIBLE		
Irvine prospective	2012	Perirectal abscess	*Enterobacter cloacae*	UCI_5	<=0.25	ST45		SUSCEPTIBLE		
Irvine prospective	2012	Sputum	*Enterobacter cloacae*	UCI_9	<=0.25	ST58		SUSCEPTIBLE		
Irvine prospective	2012	Blood	*Klebsiella pneumoniae*	UCI_10	<=0.25	ST596		SUSCEPTIBLE		
Irvine prospective	2012	Sputum	*Klebsiella pneumoniae*	UCI_14	<=0.25	ST1091		SUSCEPTIBLE		
Irvine prospective	2012	Sputum	*Klebsiella pneumoniae*	UCI_2	<=0.25	ST37		SUSCEPTIBLE		
Irvine prospective	2012	Blood	*Klebsiella pneumoniae*	UCI_4	<=0.25	ST14		SUSCEPTIBLE		
Irvine prospective	2012	Sputum	*Klebsiella pneumoniae*	UCI_6	<=0.25	ST86		SUSCEPTIBLE		
Irvine prospective	2012	Urine	*Klebsiella pneumoniae*	UCI_7	<=0.25	ST17		SUSCEPTIBLE		
Irvine prospective	2012	Urine	*Klebsiella pneumoniae*	UCI_8	<=0.25	ST1198		SUSCEPTIBLE		

collection phase	collection date	clinical sample type	species	Isolate	MIC mero (ug/ml)	MLST	cps prediction	resistance phenotype	genotype conferring resistance	Tn4401 variant
Irvine prospective	2012	Sputum	*Klebsiella pneumoniae*	UCI_1	>=16	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401i
Irvine prospective	2012	Urine	*Klebsiella pneumoniae*	UCI_13	>=16	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Irvine prospective	2013	Urine	*Citrobacter freundii*	UCI_31	<=0.25			SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Citrobacter freundii*	UCI_32	<=0.25			SUSCEPTIBLE		
Irvine prospective	2013	Sputum	*Enterobacter aerogenes*	UCI_45	<=0.25			SUSCEPTIBLE		
Irvine prospective	2013	Blood	*Enterobacter aerogenes*	UCI_16	<=0.25			SUSCEPTIBLE		
Irvine prospective	2013	Drainage	*Enterobacter aerogenes*	UCI_28	<=0.25			SUSCEPTIBLE		
Irvine prospective	2013	CSF	*Enterobacter aerogenes*	UCI_46	<=0.25			SUSCEPTIBLE		
Irvine prospective	2013	Sputum	*Enterobacter aerogenes*	UCI_48	<=0.25			SUSCEPTIBLE		
Irvine prospective	2013	Sputum	*Enterobacter aerogenes*	UCI_47	1			SUSCEPTIBLE		
Irvine prospective	2013	Blood	*Enterobacter aerogenes*	UCI_27	2			NON-SUSCEPTIBLE	UNKNOWN	
Irvine prospective	2013	Aspirate	*Enterobacter aerogenes*	UCI_15	>32			NON-SUSCEPTIBLE	UNKNOWN	
Irvine prospective	2013	Aspirate	*Enterobacter cloacae*	UCI_23	<=0.25	ST80		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Enterobacter cloacae*	UCI_24	<=0.25	ST32		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Enterobacter cloacae*	UCI_30	<=0.25	ST9		SUSCEPTIBLE		
Irvine prospective	2013	Tissue	*Enterobacter cloacae*	UCI_36	<=0.25	ST60		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Enterobacter cloacae*	UCI_39	<=0.25	ST40		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Enterobacter cloacae*	UCI_49	<=0.25	ST28		SUSCEPTIBLE		
Irvine prospective	2013	Aspirate, JP drain	*Enterobacter cloacae*	UCI_50	<=0.25	ST58		SUSCEPTIBLE		
Irvine prospective	2013	Blood	*Enterobacter cloacae*	UCI_29	2	ST32		NON-SUSCEPTIBLE	UNKNOWN	
Irvine prospective	2013	Surgical Procedure Specimen	*Enterobacter cloacae*	UCI_35	4	ST60		NON-SUSCEPTIBLE	UNKNOWN	
Irvine prospective	2013	Urine	*Escherichia coli*	UCI_57	<=0.25	ST2071		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Escherichia coli*	UCI_58	<=0.25	ST2071		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Escherichia coli*	UCI_65	<=0.25	ST38		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Escherichia coli*	UCI_66	<=0.25	ST88		SUSCEPTIBLE		
Irvine prospective	2013	Aspirate, biliary drain	*Escherichia coli*	UCI_53	2	ST410		NON-SUSCEPTIBLE	UNKNOWN	
Irvine prospective	2013	Urine	*Escherichia coli*	UCI_51	>=4	ST131		NON-SUSCEPTIBLE	UNKNOWN	
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_18	<=0.25	ST641		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_20	<=0.25	ST268		SUSCEPTIBLE		
Irvine prospective	2013	Sputum	*Klebsiella pneumoniae*	UCI_22	<=0.25	ST258	UNKNOWN	SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_26	<=0.25	ST322		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_34	<=0.25	ST34		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_38	<=0.25	ST258	II	SUSCEPTIBLE		
Irvine prospective	2013	Sputum	*Klebsiella pneumoniae*	UCI_42	<=0.25	ST86		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_43	<=0.25	ST258	II	SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_44	<=0.25	ST258	II	SUSCEPTIBLE		
Irvine prospective	2013	Sputum	*Klebsiella pneumoniae*	UCI_56	<=0.25	ST678		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_60	<=0.25	ST728		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_62	<=0.25	ST34		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_64	<=0.25	ST17		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_68	<=0.25	ST37		SUSCEPTIBLE		
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_25	>=4	ST873		NON-SUSCEPTIBLE	UNKNOWN	
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_19	>=16	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Irvine prospective	2013	rectal	*Klebsiella pneumoniae*	UCI_21	>=16	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	unique
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_33	>=16	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_37	>=16	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_41	>=16	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Irvine prospective	2013	Wound	*Klebsiella pneumoniae*	UCI_55	16	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401d
Irvine prospective	2013	Wound	*Klebsiella pneumoniae*	UCI_59	16	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_61	16	ST258	UNKNOWN	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Irvine prospective	2013	Wound	*Klebsiella pneumoniae*	UCI_63	16	ST258	I	NON-SUSCEPTIBLE	blaKPC-2	Tn4401a
Irvine prospective	2013	Sputum	*Klebsiella pneumoniae*	UCI_67	16	ST258	II	NON-SUSCEPTIBLE	blaKPC-3	Tn4401i
Irvine prospective	2013	Urine	*Klebsiella pneumoniae*	UCI_17	>32	ST437		NON-SUSCEPTIBLE	blaKPC-2	Tn4401a

Table S2. Breakdown of number of meropenem non-susceptible and susceptible strains and STs in Boston Prospective Collection by species

	Number of NON-SUSCEPTIBLE strains	Number of SUSCEPTIBLE strains	Number of NON-SUSCEPTIBLE **STs**	Number of SUSCEPTIBLE **STs**
Klebsiella pneumoniae	32	44	9	35
Enterobacter cloacae	7	20	4	16
Escherichia coli	9	21	4	12
Klebsiella oxytoca	2	2	-	-
Serratia marcesens	2	2	-	-
Enterobacter aerogenes	1	3	-	-
Acinetobacter baumanii	1	1	1	1
Citrobacter species	1	1	-	-
TOTALS	55	94	18	64

Table S3. Breakdown of number of strains in Boston Prospective Collection, Boston Historical Collection and Irvine Prospective Collection by phenotype and STs

	Boston Prospective		Boston Historical		Irvine Prospective	
	Non-susceptible	Susceptibles	Non-susceptible	Susceptible	Non-susceptible	Susceptible
Total	55	94	47	2	20	45
Overall total	149		49		65	
Klebsiella_pneumoniae_ST258	19	1	17	0	12	4
Escherichia_coli_ST131	4	7	3	0	1	0
Klebsiella_pneumoniae_ST15	4	0	0	0	0	0
Escherichia_coli_ST648	3	1	10	0	0	0
Enterobacter_cloacae_ST64	3	0	1	0	0	0
Klebsiella_pneumoniae_ST37	3	5	0	1	0	2
Enterobacter_aerogenes_	1	3	0	0	2	6
Enterobacter_cloacae_ST54	1	1	0	0	0	0
Enterobacter_cloacae_ST78	2	1	5	1	0	0
Klebsiella_oxytoca_	2	2	0	0	0	0
Serratia_marcesens_	2	2	0	0	0	0
Acinetobacter_baumanii_ST208	1	0	0	0	0	0
Acinetobacter_baumanii_ST324	0	1	0	0	0	0
Citrobacter_species_	1	0	0	0	0	0
Enterobacter_cloacae_ST40	0	2	0	0	0	2
Enterobacter_cloacae_ST45	1	0	3	0	0	1
Enterobacter_cloacae_ST51	0	3	0	0	0	0
Escherichia_coli_ST156	1	0	0	0	0	0
Escherichia_coli_ST405	1	1	0	0	0	0
Klebsiella_pneumoniae_ST1084	1	0	0	0	0	0
Klebsiella_pneumoniae_ST11	1	0	0	0	0	0
Klebsiella_pneumoniae_ST1138	1	0	0	0	0	0
Klebsiella_pneumoniae_ST17	1	3	0	0	0	2
Klebsiella_pneumoniae_ST307	1	0	0	0	0	0
Klebsiella_pneumoniae_ST392	1	0	0	0	0	0
Citrobacter_freundii_	0	1	0	0	0	2
Enterobacter_cloacae_ST12	0	1	0	0	0	0
Enterobacter_cloacae_ST16	0	1	0	0	0	0
Enterobacter_cloacae_ST22	0	1	0	0	0	0

	Boston Prospective		Boston Historical		Irvine Prospective	
	Non-susceptible	Susceptibles	Non-susceptible	Susceptible	Non-susceptible	Susceptible
Enterobacter_cloacae_ST24	0	1	0	0	0	0
Enterobacter_cloacae_ST28	0	0	0	0	0	1
Enterobacter_cloacae_ST32	0	2	0	0	1	1
Enterobacter_cloacae_ST33	0	1	0	0	0	0
Enterobacter_cloacae_ST37	0	1	0	0	0	0
Enterobacter_cloacae_ST39	0	1	0	0	0	0
Enterobacter_cloacae_ST50	0	1	0	0	0	1
Enterobacter_cloacae_ST53	0	1	0	0	0	0
Enterobacter_cloacae_ST58	0	0	2	0	0	3
Enterobacter_cloacae_ST60	0	1	0	0	1	1
Enterobacter_cloacae_ST63	0	0	1	0	0	0
Enterobacter_cloacae_ST66	0	1	2	0	0	0
Enterobacter_cloacae_ST80	0	0	0	0	0	1
Enterobacter_cloacae_ST9	0	0	0	0	0	1
Escherichia_coli_ST1193	0	2	0	0	0	0
Escherichia_coli_ST1196	0	1	0	0	0	0
Escherichia_coli_ST12	0	1	0	0	0	0
Escherichia_coli_ST1304	0	1	0	0	0	0
Escherichia_coli_ST1421	0	1	0	0	0	0
Escherichia_coli_ST206	0	1	0	0	0	0
Escherichia_coli_ST2071	0	0	0	0	0	2
Escherichia_coli_ST3254	0	1	0	0	0	0
Escherichia_coli_ST38	0	0	0	0	0	1
Escherichia_coli_ST410	0	0	0	0	1	0
Escherichia_coli_ST69	0	1	0	0	0	0
Escherichia_coli_ST88	0	0	0	0	0	1
Escherichia_coli_ST95	0	3	0	0	0	0
Klebsiella_pneumoniae_ST101	0	0	1	0	0	0
Klebsiella_pneumoniae_ST105	0	1	0	0	0	0
Klebsiella_pneumoniae_ST1091	0	0	0	0	0	1
Klebsiella_pneumoniae_ST111	0	3	0	0	0	0
Klebsiella_pneumoniae_ST113	0	0	1	0	0	0
Klebsiella_pneumoniae_ST1164	0	1	0	0	0	0
Klebsiella_pneumoniae_ST1166	0	1	0	0	0	0

	Boston Prospective		Boston Historical		Irvine Prospective	
	Non-susceptible	Susceptibles	Non-susceptible	Susceptible	Non-susceptible	Susceptible
Klebsiella_pneumoniae_ST1189	0	1	0	0	0	0
Klebsiella_pneumoniae_ST1198	0	0	0	0	0	1
Klebsiella_pneumoniae_ST1251	0	1	0	0	0	0
Klebsiella_pneumoniae_ST133	0	1	0	0	0	0
Klebsiella_pneumoniae_ST134	0	1	0	0	0	0
Klebsiella_pneumoniae_ST14	0	1	1	0	0	1
Klebsiella_pneumoniae_ST186	0	1	0	0	0	0
Klebsiella_pneumoniae_ST189	0	1	0	0	0	0
Klebsiella_pneumoniae_ST20	0	2	0	0	0	0
Klebsiella_pneumoniae_ST209	0	1	0	0	0	0
Klebsiella_pneumoniae_ST268	0	0	0	0	0	1
Klebsiella_pneumoniae_ST29	0	1	0	0	0	0
Klebsiella_pneumoniae_ST322	0	0	0	0	0	1
Klebsiella_pneumoniae_ST34	0	1	0	0	0	2
Klebsiella_pneumoniae_ST35	0	1	0	0	0	0
Klebsiella_pneumoniae_ST355	0	1	0	0	0	0
Klebsiella_pneumoniae_ST36	0	1	0	0	0	0
Klebsiella_pneumoniae_ST372	0	1	0	0	0	0
Klebsiella_pneumoniae_ST437	0	0	0	0	1	0
Klebsiella_pneumoniae_ST466	0	1	0	0	0	0
Klebsiella_pneumoniae_ST502	0	1	0	0	0	0
Klebsiella_pneumoniae_ST540	0	1	0	0	0	0
Klebsiella_pneumoniae_ST592	0	1	0	0	0	0
Klebsiella_pneumoniae_ST596	0	0	0	0	0	1
Klebsiella_pneumoniae_ST613	0	1	0	0	0	0
Klebsiella_pneumoniae_ST628	0	1	0	0	0	0
Klebsiella_pneumoniae_ST641	0	0	0	0	0	1
Klebsiella_pneumoniae_ST661	0	1	0	0	0	0
Klebsiella_pneumoniae_ST678	0	0	0	0	0	1
Klebsiella_pneumoniae_ST697	0	1	0	0	0	0
Klebsiella_pneumoniae_ST70	0	1	0	0	0	0
Klebsiella_pneumoniae_ST728	0	0	0	0	0	1
Klebsiella_pneumoniae_ST76	0	1	0	0	0	0
Klebsiella_pneumoniae_ST797	0	1	0	0	0	0

	Boston Prospective		Boston Historical		Irvine Prospective	
	Non-susceptible	Susceptibles	Non-susceptible	Susceptible	Non-susceptible	Susceptible
Klebsiella_pneumoniae_ST837	0	1	0	0	0	0
Klebsiella_pneumoniae_ST86	0	0	0	0	0	2
Klebsiella_pneumoniae_ST873	0	0	0	0	1	0
Klebsiella_pneumoniae_ST988	0	1	0	0	0	0

Table S4. Breakdown of number of meropenem non-susceptible strains in Boston Prospective Collection, Boston Historical Collection and Irvine Prospective Collection by predicted resistance determinant.

	BOSTON PROSPECTIVE COLLECTION	BOSTON HISTORICAL COLLECTION	IRVINE PROSPECTIVE COLLECTION	TOTAL
KPC	36	44	13	93
KPC-3	16	21	6	43
KPC-2	15	16	7	38
KPC-4	5	7	0	12
NDM-1	1	1	0	2
OXA-48	0	1	0	1
SME-2 + AmpC	2	0	0	2
OXA-113	1	0	0	1
CTX-M-15 + OmpK35(truncated)	3	0	0	3
CTX-M-15 + OmpK36(truncated)	2	0	0	2
CTX-M-15 + OmpF(truncated)	1	0	0	1
CTX-M-15 + OmpC(truncated)	1	0	0	1
OmpK35(truncated) + OmpK36(truncated)	1	0	0	1
Non-susceptible unknown	7	1	7	15
SUM	55	47	20	122

Table S5. Genes associated with antibiotic resistance in each sequenced isolate

Resistance to meropenem phenotype

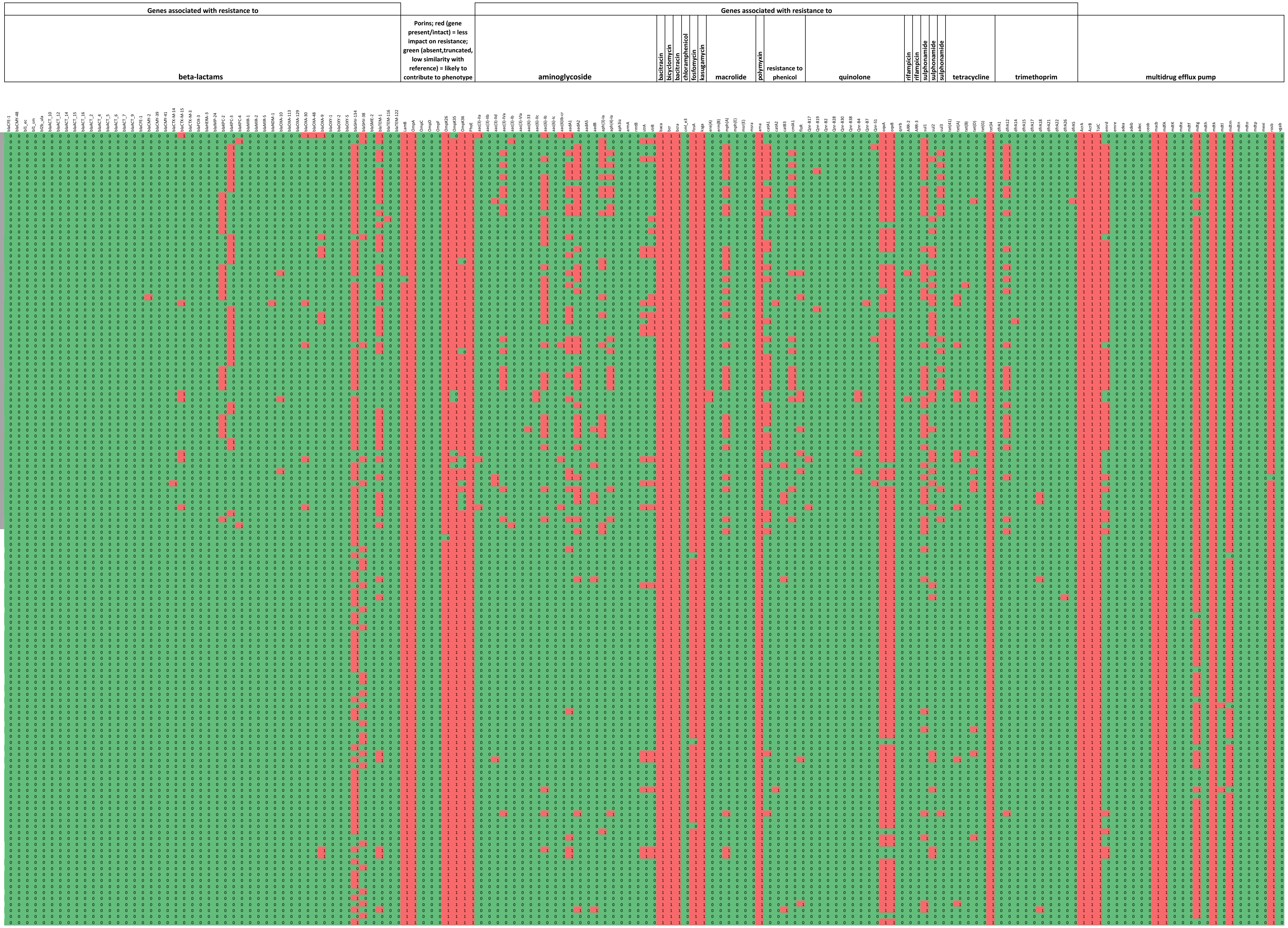
N = NON-SUSCEPTIBLE strains

S= SUSCEPTIBLE strains

🟥 Gene present/intact

🟩 Gene absent/truncated/less than 80% similarity with reference gene

species	Isolate name	City/Collection	ST	Resistance to meropenem phenotype	meropenem mic (ug/mg)	Genetic determinant of resistance
kpneumoniae	BWH_2	Boston historical	ST101	N	>32	OXA-48
kpneumoniae	BIDMC_11	Boston historical	ST14	N	>32	KPC-4
kpneumoniae	BIDMC_1	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BIDMC_10	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BIDMC_12B	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BIDMC_13	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BIDMC_14	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BIDMC_16	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BIDMC_2A	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BIDMC_5	Boston historical	ST258	N	>32	KPC-3
kpneumoniae	BWH_22	Boston historical	ST258	N	>32	KPC-2
kpneumoniae	UCI_17	Irvine prospective	ST437	N	>32	KPC-2
kpneumoniae	MGH_29	Boston prospective	ST258	N	>=16	KPC-2
kpneumoniae	MGH_45	Boston prospective	ST1084	N	>=16	KPC-2
kpneumoniae	UCI_13	Irvine prospective	ST258	N	>=16	KPC-2
kpneumoniae	UCI_19	Irvine prospective	ST258	N	>=16	KPC-2
kpneumoniae	UCI_21	Irvine prospective	ST258	N	>=16	KPC-2
kpneumoniae	MGH_39	Boston prospective	ST1138	N	>=16	KPC-3
kpneumoniae	UCI_1	Irvine prospective	ST258	N	>=16	KPC-3
kpneumoniae	UCI_33	Irvine prospective	ST258	N	>=16	KPC-3
kpneumoniae	UCI_37	Irvine prospective	ST258	N	>=16	KPC-3
kpneumoniae	UCI_41	Irvine prospective	ST258	N	>=16	KPC-3
kpneumoniae	MGH_67	Boston prospective	ST258	N	16	KPC-2
kpneumoniae	MGH_71	Boston prospective	ST258	N	16	KPC-2
kpneumoniae	MGH_79	Boston prospective	ST258	N	16	KPC-2
kpneumoniae	UCI_59	Irvine prospective	ST258	N	16	KPC-2
kpneumoniae	UCI_61	Irvine prospective	ST258	N	16	KPC-2
kpneumoniae	UCI_63	Irvine prospective	ST258	N	16	KPC-2
kpneumoniae	MGH_69	Boston prospective	ST11	N	16	NDM-1
kpneumoniae	MGH_73	Boston prospective	ST258	N	16	KPC-3
kpneumoniae	UCI_55	Irvine prospective	ST258	N	16	KPC-3
kpneumoniae	UCI_67	Irvine prospective	ST258	N	16	KPC-3
kpneumoniae	BIDMC_12A	Boston historical	ST258	N	>8	KPC-3
kpneumoniae	BIDMC_12C	Boston historical	ST258	N	>8	KPC-3
kpneumoniae	BIDMC_32	Boston prospective	ST258	N	>8	KPC-3
kpneumoniae	BIDMC_33B	Boston prospective	ST15	N	>8	KPC-3
kpneumoniae	BIDMC_4	Boston historical	ST258	N	>8	KPC-3
kpneumoniae	BIDMC_42A	Boston prospective	ST258	N	>8	KPC-3
kpneumoniae	BIDMC_42B	Boston prospective	ST258	N	>8	KPC-3
kpneumoniae	BIDMC_18A	Boston historical	ST258	N	>8	KPC-2
kpneumoniae	BIDMC_18C	Boston historical	ST258	N	>8	KPC-2
kpneumoniae	BIDMC_34	Boston prospective	ST258	N	>8	KPC-2
kpneumoniae	BIDMC_45	Boston prospective	ST258	N	>8	KPC-2
kpneumoniae	MGH_63	Boston prospective	ST15	N	8	CTX-M-15 + OmpK35(truncated)
kpneumoniae	MGH_65	Boston prospective	ST15	N	8	CTX-M-15 + OmpK35(truncated)
kpneumoniae	BIDMC_54	Boston prospective	ST258	N	8	KPC-3
kpneumoniae	BIDMC_7B	Boston historical	ST258	N	8	KPC-3
kpneumoniae	BIDMC_60	Boston prospective	ST258	N	8	KPC-2
kpneumoniae	BIDMC_68	Boston prospective	ST258	N	8	KPC-2
kpneumoniae	BWH_45	Boston prospective	ST258	N	8	KPC-2
kpneumoniae	MGH_51	Boston prospective	ST258	N	8	KPC-2
kpneumoniae	BIDMC_7A	Boston historical	ST258	N	4	KPC-3
kpneumoniae	BWH_47	Boston prospective	ST258	N	4	KPC-3
kpneumoniae	MGH_75	Boston prospective	ST15	N	4	CTX-M-15 + OmpK35(truncated)
kpneumoniae	MGH_43	Boston prospective	ST307	N	4	CTX-M-15 + OmpK36(truncated)
kpneumoniae	MGH_47	Boston prospective	ST37	N	4	OmpK35(truncated) + OmpK36(truncated)
kpneumoniae	BIDMC_35	Boston prospective	ST17	N	>32	UNKNOWN
kpneumoniae	MGH_59	Boston prospective	ST258	N	>4	UNKNOWN
kpneumoniae	UCI_25	Irvine prospective	ST873	N	>=4	UNKNOWN
kpneumoniae	MGH_31	Boston prospective	ST258	N	4	UNKNOWN
kpneumoniae	BIDMC_46A	Boston prospective	ST37	N	2	UNKNOWN
kpneumoniae	BIDMC_53	Boston prospective	ST37	N	2	UNKNOWN
kpneumoniae	MGH_35	Boston prospective	ST392	N	2	CTX-M-15 + OmpK36(truncated)
kpneumoniae	BWH_36	Boston prospective	ST258	N	2	KPC-3
kpneumoniae	BIDMC_18B	Boston historical	ST258	N	2	KPC-2
kpneumoniae	BWH_15	Boston historical	ST113	N	2	KPC-4
kpneumoniae	BWH_41	Boston prospective	ST258	S	0.5	
kpneumoniae	BIDMC_21	Boston prospective	ST37	S	<=0.25	
kpneumoniae	BIDMC_22	Boston prospective	ST1189	S	<=0.25	
kpneumoniae	BIDMC_23	Boston prospective	ST111	S	<=0.25	
kpneumoniae	BIDMC_24	Boston prospective	ST797	S	<=0.25	
kpneumoniae	BIDMC_25	Boston prospective	ST186	S	<=0.25	
kpneumoniae	BIDMC_36	Boston prospective	ST661	S	<=0.25	
kpneumoniae	BIDMC_40	Boston prospective	ST34	S	<=0.25	
kpneumoniae	BIDMC_41	Boston prospective	ST37	S	<=0.25	
kpneumoniae	BIDMC_47	Boston prospective	ST540	S	<=0.25	
kpneumoniae	BIDMC_48	Boston prospective	ST37	S	<=0.25	
kpneumoniae	BIDMC_51	Boston prospective	ST36	S	<=0.25	
kpneumoniae	BIDMC_52	Boston prospective	ST628	S	<=0.25	
kpneumoniae	BIDMC_55	Boston prospective	ST105	S	<=0.25	
kpneumoniae	BIDMC_61	Boston prospective	ST697	S	<=0.25	
kpneumoniae	BIDMC_69	Boston prospective	ST17	S	<=0.25	
kpneumoniae	BWH_28	Boston prospective	ST133	S	<=0.25	
kpneumoniae	BWH_30	Boston prospective	ST1164	S	<=0.25	
kpneumoniae	BWH_46	Boston prospective	ST592	S	<=0.25	
kpneumoniae	BWH_48	Boston prospective	ST17	S	<=0.25	
kpneumoniae	MGH_17	Boston prospective	ST134	S	<=0.25	
kpneumoniae	MGH_18	Boston prospective	ST20	S	<=0.25	
kpneumoniae	MGH_19	Boston prospective	ST988	S	<=0.25	
kpneumoniae	MGH_20	Boston prospective	ST209	S	<=0.25	
kpneumoniae	MGH_21	Boston prospective	ST111	S	<=0.25	
kpneumoniae	MGH_30	Boston prospective	ST37	S	<=0.25	
kpneumoniae	MGH_32	Boston prospective	ST111	S	<=0.25	
kpneumoniae	MGH_36	Boston prospective	ST466	S	<=0.25	
kpneumoniae	MGH_40	Boston prospective	ST355	S	<=0.25	
kpneumoniae	MGH_44	Boston prospective	ST613	S	<=0.25	
kpneumoniae	MGH_46	Boston prospective	ST14	S	<=0.25	
kpneumoniae	MGH_48	Boston prospective	ST189	S	<=0.25	
kpneumoniae	MGH_52	Boston prospective	ST70	S	<=0.25	
kpneumoniae	MGH_60	Boston prospective	ST17	S	<=0.25	
kpneumoniae	MGH_64	Boston prospective	ST35	S	<=0.25	
kpneumoniae	MGH_66	Boston prospective	ST29	S	<=0.25	
kpneumoniae	MGH_68	Boston prospective	ST1166	S	<=0.25	
kpneumoniae	MGH_70	Boston prospective	ST20	S	<=0.25	
kpneumoniae	MGH_72	Boston prospective	ST37	S	<=0.25	
kpneumoniae	MGH_74	Boston prospective	ST76	S	<=0.25	
kpneumoniae	MGH_76	Boston prospective	ST837	S	<=0.25	
kpneumoniae	MGH_80	Boston prospective	ST1251	S	<=0.25	
kpneumoniae	UCI_10	Irvine prospective	ST596	S	<=0.25	
kpneumoniae	UCI_14	Irvine prospective	ST1091	S	<=0.25	
kpneumoniae	UCI_18	Irvine prospective	ST641	S	<=0.25	
kpneumoniae	UCI_2	Irvine prospective	ST37	S	<=0.25	
kpneumoniae	UCI_20	Irvine prospective	ST268	S	<=0.25	
kpneumoniae	UCI_22	Irvine prospective	ST258	S	<=0.25	
kpneumoniae	UCI_26	Irvine prospective	ST322	S	<=0.25	
kpneumoniae	UCI_34	Irvine prospective	ST34	S	<=0.25	
kpneumoniae	UCI_38	Irvine prospective	ST258	S	<=0.25	
kpneumoniae	UCI_4	Irvine prospective	ST14	S	<=0.25	
kpneumoniae	UCI_42	Irvine prospective	ST86	S	<=0.25	
kpneumoniae	UCI_43	Irvine prospective	ST258	S	<=0.25	
kpneumoniae	UCI_44	Irvine prospective	ST258	S	<=0.25	
kpneumoniae	UCI_56	Irvine prospective	ST678	S	<=0.25	
kpneumoniae	UCI_6	Irvine prospective	ST86	S	<=0.25	
kpneumoniae	UCI_60	Irvine prospective	ST728	S	<=0.25	
kpneumoniae	UCI_62	Irvine prospective	ST34	S	<=0.25	
kpneumoniae	UCI_64	Irvine prospective	ST17	S	<=0.25	
kpneumoniae	UCI_68	Irvine prospective	ST37	S	<=0.25	
kpneumoniae	UCI_7	Irvine prospective	ST17	S	<=0.25	
kpneumoniae	UCI_8	Irvine prospective	ST1198	S	<=0.25	
kpneumoniae	BIDMC_18D	Boston historical	ST37	S	<=0.25	
kpneumoniae	BIDMC_31	Boston prospective	ST502	S	<=0.25	
kpneumoniae	BIDMC_46B	Boston prospective	ST372	S	<=0.25	



species	Isolate name	City/Collection	ST	Resistance to meropenem phenotype	meropenem mic (ug/mg)	Genetic determinant of resistance
ecloacae	MGH_1	Boston historical	ST45	N	>=16	KPC-2
ecloacae	MGH_6	Boston historical	ST45	N	>=16	KPC-2
ecloacae	MGH_13	Boston historical	ST58	N	>=16	KPC-3
ecloacae	MGH_14	Boston historical	ST66	N	>=16	KPC-3
ecloacae	MGH_15	Boston prospective	ST45	N	>=16	KPC-3
ecloacae	MGH_3	Boston historical	ST66	N	>=16	KPC-3
ecloacae	MGH_7	Boston historical	ST64	N	>=16	KPC-3
ecloacae	MGH_2	Boston historical	ST78	N	>=16	KPC-4
ecloacae	MGH_5	Boston historical	ST78	N	>=16	KPC-4
ecloacae	MGH_11	Boston historical	ST78	N	>=16	KPC-4
ecloacae	MGH_10	Boston historical	ST45	N	>=16	NDM-1
ecloacae	BWH_27	Boston prospective	ST78	N	16	KPC-4
ecloacae	BIDMC_33A	Boston prospective	ST64	N	>8	KPC-3
ecloacae	BIDMC_8	Boston historical	ST63	N	8	KPC-3
ecloacae	MGH_12	Boston historical	ST78	N	8	KPC-4
ecloacae	MGH_8	Boston historical	ST78	N	8	KPC-4
ecloacae	BIDMC_66	Boston prospective	ST64	N	4	KPC-4
ecloacae	MGH_37	Boston prospective	ST54	N	4	UNKNOWN
ecloacae	MGH_4	Boston historical	ST58	N	4	UNKNOWN
ecloacae	UCI_35	Irvine prospective	ST60	N	4	UNKNOWN
ecloacae	UCI_29	Irvine prospective	ST32	N	2	UNKNOWN
ecloacae	BWH_37	Boston prospective	ST64	N	2	KPC-4
ecloacae	BWH_39	Boston prospective	ST78	N	2	KPC-4
ecloacae	MGH_54	Boston prospective	ST40	S	1	
ecloacae	MGH_53	Boston prospective	ST51	S	1	
ecloacae	MGH_25	Boston prospective	ST54	S	0.5	
ecloacae	MGH_9	Boston historical	ST78	S	0.5	
ecloacae	BIDMC_26	Boston prospective	ST12	S	<=0.25	
ecloacae	BIDMC_27	Boston prospective	ST50	S	<=0.25	
ecloacae	BIDMC_28	Boston prospective	ST51	S	<=0.25	
ecloacae	BIDMC_29	Boston prospective	ST37	S	<=0.25	
ecloacae	BIDMC_30	Boston prospective	ST16	S	<=0.25	
ecloacae	BIDMC_67	Boston prospective	ST33	S	<=0.25	
ecloacae	BWH_29	Boston prospective	ST60	S	<=0.25	
ecloacae	BWH_31	Boston prospective	ST53	S	<=0.25	
ecloacae	BWH_43	Boston prospective	ST24	S	<=0.25	
ecloacae	MGH_16	Boston prospective	ST40	S	<=0.25	
ecloacae	MGH_22	Boston prospective	ST32	S	<=0.25	
ecloacae	MGH_23	Boston prospective	ST32	S	<=0.25	
ecloacae	MGH_24	Boston prospective	ST22	S	<=0.25	
ecloacae	MGH_26	Boston prospective	ST78	S	<=0.25	
ecloacae	MGH_34	Boston prospective	ST39	S	<=0.25	
ecloacae	MGH_38	Boston prospective	ST66	S	<=0.25	
ecloacae	UCI_11	Irvine prospective	ST50	S	<=0.25	
ecloacae	UCI_12	Irvine prospective	ST40	S	<=0.25	
ecloacae	UCI_23	Irvine prospective	ST80	S	<=0.25	
ecloacae	UCI_24	Irvine prospective	ST32	S	<=0.25	
ecloacae	UCI_3	Irvine prospective	ST58	S	<=0.25	
ecloacae	UCI_30	Irvine prospective	ST9	S	<=0.25	
ecloacae	UCI_36	Irvine prospective	ST60	S	<=0.25	
ecloacae	UCI_39	Irvine prospective	ST40	S	<=0.25	
ecloacae	UCI_49	Irvine prospective	ST28	S	<=0.25	
ecloacae	UCI_5	Irvine prospective	ST45	S	<=0.25	
ecloacae	UCI_50	Irvine prospective	ST58	S	<=0.25	
ecloacae	UCI_9	Irvine prospective	ST58	S	<=0.25	
ecloacae	MGH_33	Boston prospective	ST51	S	<=0.25	
ecoli	BIDMC_15	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_17A	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_17B	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_19A	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_19B	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_19C	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_2B	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_3	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_6	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_9	Boston historical	ST648	N	>32	KPC-2
ecoli	BIDMC_20B	Boston historical	ST131	N	>32	KPC-3
ecoli	BWH_34	Boston prospective	ST131	N	>8	KPC-3
ecoli	BIDMC_43B	Boston prospective	ST648	N	8	KPC-2
ecoli	BIDMC_82	Boston prospective	ST648	N	8	KPC-2
ecoli	BIDMC_20A	Boston historical	ST131	N	8	KPC-3
ecoli	BIDMC_58	Boston prospective	ST131	N	8	KPC-3
ecoli	BIDMC_62	Boston prospective	ST131	N	8	KPC-3
ecoli	BIDMC_64	Boston prospective	ST131	N	8	KPC-3
ecoli	MGH_57	Boston prospective	ST156	N	>32	UNKNOWN
ecoli	UCI_51	Irvine prospective	ST131	N	>=4	UNKNOWN
ecoli	UCI_53	Irvine prospective	ST410	N	2	UNKNOWN
ecoli	BIDMC_43A	Boston prospective	ST648	N	2	KPC-2
ecoli	BWH_24	Boston historical	ST131	N	2	KPC-3
ecoli	BWH_40	Boston prospective	ST405	N	2	CTX-M-15 + OmpF(truncated)
ecoli	BIDMC_37	Boston prospective	ST1421	S	<=0.25	
ecoli	BIDMC_38	Boston prospective	ST131	S	<=0.25	
ecoli	BIDMC_39	Boston prospective	ST206	S	<=0.25	
ecoli	BIDMC_49A	Boston prospective	ST95	S	<=0.25	
ecoli	BIDMC_59	Boston prospective	ST1304	S	<=0.25	
ecoli	BIDMC_63	Boston prospective	ST131	S	<=0.25	
ecoli	BIDMC_65	Boston prospective	ST95	S	<=0.25	
ecoli	BIDMC_70	Boston prospective	ST131	S	<=0.25	
ecoli	BIDMC_71	Boston prospective	ST648	S	<=0.25	
ecoli	BIDMC_72	Boston prospective	ST1193	S	<=0.25	
ecoli	BIDMC_73	Boston prospective	ST1193	S	<=0.25	
ecoli	BIDMC_74	Boston prospective	ST1196	S	<=0.25	
ecoli	BIDMC_75	Boston prospective	ST131	S	<=0.25	
ecoli	BIDMC_76	Boston prospective	ST131	S	<=0.25	
ecoli	BIDMC_77	Boston prospective	ST405	S	<=0.25	
ecoli	BIDMC_78	Boston prospective	ST131	S	<=0.25	
ecoli	BIDMC_79	Boston prospective	ST131	S	<=0.25	
ecoli	BIDMC_83	Boston prospective	ST12	S	<=0.25	
ecoli	BWH_32	Boston prospective	ST3254	S	<=0.25	
ecoli	MGH_58	Boston prospective	ST69	S	<=0.25	
ecoli	UCI_57	Irvine prospective	ST2071	S	<=0.25	
ecoli	UCI_58	Irvine prospective	ST2071	S	<=0.25	
ecoli	UCI_65	Irvine prospective	ST38	S	<=0.25	
ecoli	UCI_66	Irvine prospective	ST88	S	<=0.25	
ecoli	BIDMC_49B	Boston prospective	ST95	S	0.5	
eaerogenes	UCI_15	Irvine prospective		N	>32	UNKNOWN
eaerogenes	MGH_77	Boston prospective		N	>4	UNKNOWN
eaerogenes	UCI_27	Irvine prospective		N	2	UNKNOWN
eaerogenes	MGH_61	Boston prospective		S	1	
eaerogenes	UCI_47	Irvine prospective		S	1	
eaerogenes	MGH_62	Boston prospective		S	<=0.25	
eaerogenes	MGH_78	Boston prospective		S	<=0.25	
eaerogenes	UCI_16	Irvine prospective		S	<=0.25	
eaerogenes	UCI_28	Irvine prospective		S	<=0.25	
eaerogenes	UCI_46	Irvine prospective		S	<=0.25	
eaerogenes	UCI_48	Irvine prospective		S	<=0.25	
eaerogenes	UCI_45	Irvine prospective		S	<=0.25	
koxytoca	MGH_27	Boston prospective		N	>=16	KPC-3
koxytoca	MGH_41	Boston prospective		N	>=16	KPC-2
koxytoca	MGH_28	Boston prospective		S	<=0.25	
koxytoca	MGH_42			S	<=0.25	
smarcesens	BIDMC_44	Boston prospective		N	>8	SME-2 + AmpC
smarcesens	BIDMC_80	Boston prospective		N	8	SME-2 + AmpC
smarcesens	BIDMC_50	Boston prospective		S	<=0.25	
smarcesens	BIDMC_81	Boston prospective		S	<=0.25	
cfreundii	MGH_56	Boston prospective		S	<=0.25	
cfreundii	UCI_31	Irvine prospective		S	<=0.25	
cfreundii	UCI_32	Irvine prospective		S	<=0.25	
cspecies	MGH_55	Boston prospective		N	16	KPC-4
abaumanii	BIDMC_56	Boston prospective	ST208	N	>32	blaOXA-113
abaumanii	BIDMC_57	Boston prospective	ST324	S	1	

Table S6. Incompatibility groups replicons found in the scaffolds of MGH_31 and MGH_59

MGH_31	MGH_59
IncFIB(K);	ColpVC
IncFIB(pQil)	IncFIB(AP001918)
IncFII(K)	IncFII(pRSB107)
IncR	IncN
	IncI1

Table S7. List of genes located in non-chromosomal scaffolds and having orthologs in MGH_31 and MGH_59

					BLAST NR of unannotated clusters	
#cluster id	isolate	Genbank locus name	functional annotation	location of gene	(hit description, #accession, e-value)	Number of orthologous genes among susceptible K. pneumoniae isolates
737	MGH_31	L377_05470	hypothetical protein	plasm	phage protein, CAJ49067.1, 4e-07	23
737	MGH_59	AF45_05325	hypothetical protein	plasm		
936	MGH_31	L377_05449	transposase insH for insertion sequence element IS5T	plasm		112
936	MGH_31	L377_05283	transposase insH for insertion sequence element IS5I	plasm		
936	MGH_59	AF45_05125	transposase insH for insertion sequence element IS5Y	plasm		
936	MGH_59	AF45_05321	transposase insH for insertion sequence element IS5Y	undetermined		
936	MGH_59	AF45_05255	transposase insH for insertion sequence element IS5H	undetermined		
1173	MGH_31	L377_05485	hypothetical protein	plasm	StbA, WP_012561140.1, 2e-49	14
1173	MGH_59	AF45_05333	hypothetical protein	plasm		
1243	MGH_31	L377_05482	insertion element IS1 protein insB	plasm		218
1243	MGH_31	L377_05202	insertion element IS1 protein insB	plasm		
1243	MGH_31	L377_05205	insertion element IS1 protein insB	plasm		
1243	MGH_31	L377_05282	insertion element IS1 protein insB	plasm		
1243	MGH_59	AF45_05127	insertion element IS1 protein insB	plasm		
1243	MGH_59	AF45_05399	insertion element IS1 protein insB	plasm		
1243	MGH_59	AF45_05240	insertion element IS1 5 protein insB	undetermined		
1243	MGH_59	AF45_05260	insertion element IS1 3 protein insB	undetermined		
2267	MGH_31	L377_05191	protein sopB	plasm		43
2267	MGH_59	AF45_05232	protein sopB	undetermined		
2911	MGH_31	L377_05513	resolvase	plasm		44
2911	MGH_31	L377_05372	resolvase	plasm		
2911	MGH_59	AF45_05235	resolvase	undetermined		
2974	MGH_31	L377_05194	integrase	plasm		54
2974	MGH_59	AF45_05263	hypothetical protein	undetermined		
3206	MGH_31	L377_05478	protein samB	plasm		84
3206	MGH_31	L377_05380	protein samB	plasm		
3206	MGH_31	L377_05390	protein samB	plasm		
3206	MGH_31	L377_05187	protein samB	plasm		
3206	MGH_59	AF45_05420	protein impB	undetermined		
3309	MGH_31	L377_05192	protein sopA	plasm		43
3309	MGH_59	AF45_05233	protein sopA	undetermined		
3447	MGH_31	L377_05473	hypothetical protein	plasm	transposase, WP_033179069.1, 4e-36	20
3447	MGH_59	AF45_05328	hypothetical protein	plasm		
3458	MGH_31	L377_05361	hypothetical protein	plasm	plasmid stability protein StbA family protein, CNI36763.1, 1e-14	50
3458	MGH_31	L377_05294	hypothetical protein	plasm		
3458	MGH_31	L377_05305	hypothetical protein	plasm		
3458	MGH_59	AF45_05304	hypothetical protein	undetermined		
4082	MGH_31	L377_05472	hypothetical protein	plasm	putative toxin-antitoxin system, antitoxin component, ADP40712.1, 9e-39	20
4082	MGH_59	AF45_05327	hypothetical protein	plasm		
4402	MGH_31	L377_05481	insertion element IS1 protein insA	plasm		89
4402	MGH_59	AF45_05126	insertion element IS1 1 protein insA	plasm		
4415	MGH_31	L377_05333	conjugal transfer transcriptional regulator TraJ	plasm		203
4415	MGH_59	AF45_05331	hypothetical protein	plasm		
4415	MGH_59	AF45_05332	hypothetical protein	plasm		
4764	MGH_31	L377_05501	transposase	plasm		112
4764	MGH_31	L377_05235	transposase	plasm		
4764	MGH_31	L377_05273	transposase	plasm		
4764	MGH_59	AF45_05162	hypothetical protein	plasm		
4764	MGH_59	AF45_05310	hypothetical protein	undetermined		
4764	MGH_59	AF45_05312	hypothetical protein	undetermined		
4764	MGH_59	AF45_05405	hypothetical protein	plasm		
4839	MGH_31	L377_05471	hypothetical protein	plasm	Thermophilic glucose-6-phosphate isomerase, WP_031942309.1, 1e-60	17
4839	MGH_59	AF45_05326	hypothetical protein	plasm		
4845	MGH_31	L377_05445	transposon Tn3 resolvase	plasm		21
4845	MGH_31	L377_05232	transposon Tn3 resolvase	plasm		
4845	MGH_31	L377_05276	transposon Tn3 resolvase	plasm		
4845	MGH_59	AF45_05417	transposon Tn3 resolvase	undetermined		
4845	MGH_59	AF45_05152	transposon Tn3 resolvase	plasm		
4867	MGH_31	L377_05484	hypothetical protein	plasm	StdB, WP_012561139.1, 3e-169	12
4867	MGH_59	AF45_05334	hypothetical protein	plasm		
4936	MGH_31	L377_05446	beta-lactamase TEM-12	plasm		7
4936	MGH_31	L377_05447	beta-lactamase TEM	plasm		
4936	MGH_59	AF45_05418	blaTEM-1B1, resistance to beta-lactam	undetermined		
4936	MGH_59	AF45_05151	blaTEM-1A4, resistance to beta-lactam	plasm		
4936	MGH_59	AF45_05409	blaTEM-1A4, resistance to beta-lactam	plasm		
4938	MGH_31	L377_05301	transposase	plasm		7
4938	MGH_59	AF45_05166	hypothetical protein	plasm		
4996	MGH_31	L377_05307	type-F conjugative transfer system pilin assembly thiol-disulfide isomera	plasm		31
4996	MGH_59	AF45_05129	type-F conjugative transfer system pilin assembly thiol-disulfide isomera	plasm		
5057	MGH_31	L377_05407	inner membrane protein	plasm		71
5057	MGH_31	L377_05418	inner membrane protein	plasm		
5057	MGH_31	L377_05432	protein traI	plasm		
5057	MGH_31	L377_05436	conjugative transfer relaxase TraI	plasm		
5057	MGH_59	AF45_05138	protein traI	plasm		
5061	MGH_31	L377_05313	type-F conjugative transfer system mating-pair stabilization protein TraN	plasm		30
5061	MGH_59	AF45_05122	type-F conjugative transfer system mating-pair stabilization protein TraN	plasm		
5068	MGH_31	L377_05360	transposase	plasm		67
5068	MGH_31	L377_05293	transposase	plasm		
5068	MGH_31	L377_05304	transposase	plasm		
5068	MGH_59	AF45_05169	hypothetical protein	plasm		
5092	MGH_31	L377_05427	conjugal transfer mating pair stabilization protein TraG	plasm		75
5092	MGH_31	L377_05431	type IV conjugative transfer system coupling protein TraD	plasm		
5092	MGH_31	L377_05435	type IV conjugative transfer system coupling protein TraD	plasm		

					BLAST NR of unnannotated clusters	
#cluster id	isolate	Genbank locus name	functional annotation	location of gene	(hit description, #accession, e-value)	Number of orthologous genes among susceptible K. pneumoniae isolates
5092	MGH_59	AF45_05137	protein traD	plasm		
5160	MGH_31	L377_05179	hypothetical protein	plasm	only hits against genes encoding hypothetical proteins	41
5160	MGH_59	AF45_05416	hypothetical protein	plasm		
5170	MGH_31	L377_05319	protein traC	plasm		35
5170	MGH_59	AF45_05117	protein traC	plasm		
5195	MGH_31	L377_05521	protein traB	plasm		32
5195	MGH_31	L377_05328	protein traB	plasm		
5195	MGH_59	AF45_05114	protein traB	plasm		
5207	MGH_31	L377_05178	hypothetical protein	plasm	hydrolase, WP_009310030.1, 0.0	26
5207	MGH_59	AF45_05415	hypothetical protein	plasm		
5235	MGH_31	L377_05309	type-F conjugative transfer system pilin assembly protein TraF	plasm		30
5235	MGH_59	AF45_05124	type-F conjugative transfer system pilin assembly protein TraF	plasm		
5254	MGH_31	L377_05451	hypothetical protein	plasm		11
5254	MGH_59	AF45_05173	replication initiation protein	plasm		
5295	MGH_31	L377_05314	type-F conjugative transfer system pilin assembly protein TrbC	plasm		29
5295	MGH_59	AF45_05121	type-F conjugative transfer system pilin assembly protein TrbC	plasm		
5421	MGH_31	L377_05315	conjugal transfer pilus assembly protein TraU	plasm		31
5421	MGH_59	AF45_05120	hypothetical protein	plasm		
5437	MGH_31	L377_05429	TraT complement resistance protein	plasm		31
5437	MGH_31	L377_05433	TraT complement resistance protein	plasm		
5437	MGH_59	AF45_05135	TraT complement resistance protein	plasm		
5444	MGH_31	L377_05426	conjugative transfer pilus assembly protein TraH	plasm		32
5444	MGH_59	AF45_05132	hypothetical protein	plasm		
5465	MGH_31	L377_05298	mph(A)1, resistance to macrolide	plasm		3
5465	MGH_59	AF45_05163	mph(A)1, resistance to macrolide	plasm		
5467	MGH_31	L377_05303	hypothetical protein	plasm	chromate transporter, CHR family, partial, ESD86461.1, 0.0	3
5467	MGH_59	AF45_05168	hypothetical protein	plasm		
5471	MGH_31	L377_05302	hypothetical protein	plasm	PadR family transcriptional regulator, WP_038612200.1, 5e-40	3
5471	MGH_59	AF45_05167	hypothetical protein	plasm		
5476	MGH_31	L377_05299	hypothetical protein	plasm	Mrx, AHA87067.1, e-145	3
5476	MGH_59	AF45_05164	hypothetical protein	plasm		

Table S8. List of genes located in non-chromosomal scaffolds of BIDMC_35 isolate

Genbank locus name	functional annotation	PFAM/TIGRFAM domains
L472_05108	hypothetical protein	
L472_05109	hypothetical protein	
L472_05110	hypothetical protein	
L472_05111	hypothetical protein	
L472_05112	hypothetical protein	
L472_05114	hypothetical protein	
L472_05113	hypothetical protein	
L472_05115	hypothetical protein	
L472_05116	hypothetical protein	
L472_05117	hypothetical protein	
L472_05118	hypothetical protein	
L472_05119	hypothetical protein	
L472_05120	hypothetical protein	
L472_05121	hypothetical protein	Methyltransferase domain
L472_05122	hypothetical protein	HD domain
L472_05124	hypothetical protein	
L472_05123	hypothetical protein	
L472_05125	hypothetical protein	
L472_05126	hypothetical protein	
L472_05127	hypothetical protein	
L472_05128	hypothetical protein	Gram-negative bacterial TonB protein C-terminal
L472_05129	hypothetical protein	
L472_05130	hypothetical protein	Phage regulatory protein Rha (Phage_pRha)
L472_05132	hypothetical protein	Protein of unknown function (DUF3927)
L472_05131	hypothetical protein	Protein of unknown function (DUF3927)
L472_05133	hypothetical protein	
L472_05134	hypothetical protein	RNase H
L472_05135	hypothetical protein	
L472_05136	phage N-6-adenine-methyltransferase	DNA N-6-adenine-methyltransferase (Dam)
L472_05138	hypothetical protein	
L472_05137	hypothetical protein	
L472_05139	hypothetical protein	Exonuclease, RNase_H superfamily, DNA polymerase family B, exonuclease domain
L472_05140	hypothetical protein	DNA polymerase family B, exonuclease domain
L472_05141	hypothetical protein	AAA domain
L472_05142	hypothetical protein	AAA domain, Dihydrofolate reductase
L472_05143	hypothetical protein	Dihydrofolate reductase
L472_05144	hypothetical protein	Thymidylate synthase
L472_05145	hypothetical protein	
L472_05146	hypothetical protein	
L472_05147	RNA one modulator-like protein	Rop protein
L472_05019	hypothetical protein	Phosphoribosyl-ATP pyrophosphohydrolase
L472_05020	ribonucleoside-diphosphate reductase 1 subunit beta	Ribonucleotide reductase, small chain
L472_05021	ribonucleoside-diphosphate reductase, alpha subunit	Ribonucleotide reductase, barrel domain, Ribonucleotide reductase, all-alpha domain, ATP cone domain
L472_05022	hypothetical protein	
L472_05025	hypothetical protein	Calcineurin-like phosphoesterase superfamily domain, Calcineurin-like phosphoesterase
L472_05023	hypothetical protein	
L472_05024	hypothetical protein	RecF/RecN/SMC N terminal domain, AAA domain
L472_05026	hypothetical protein	
L472_05028	hypothetical protein	Initiator Replication protein
L472_05029	hypothetical protein	
L472_05030	hypothetical protein	
L472_05031	hypothetical protein	
L472_05032	hypothetical protein	
L472_05027	hypothetical protein	
L472_05034	hypothetical protein	
L472_05033	hypothetical protein	
L472_05036	hypothetical protein	
L472_05035	hypothetical protein	SPFH domain / Band 7 family
L472_05037	hypothetical protein	
L472_05038	protein RecA	recA bacterial DNA recombination protein
L472_05040	hypothetical protein	5'-3' exonuclease, N-terminal resolvase-like domain, 5'-3' exonuclease, C-terminal SAM fold
L472_05039	hypothetical protein	
L472_05041	hypothetical protein	
L472_05042	hypothetical protein	
L472_05043	hypothetical protein	
L472_05044	hypothetical protein	
L472_05045	hypothetical protein	Helix-hairpin-helix motif, Uracil DNA glycosylase superfamily
L472_05046	hypothetical protein	PHP domain, Bacterial DNA polymerase III alpha subunit
L472_05047	hypothetical protein	AAA domain (dynein-related subfamily)
L472_05048	hypothetical protein	Cobalamin biosynthesis protein CobT, Cobalamin biosynthesis protein CobT VWA domain, von Willebrand factor type A domain
L472_05049	hypothetical protein	
L472_05051	hypothetical protein	
L472_05052	hypothetical protein	
L472_05050	hypothetical protein	Phage integrase family
L472_05053	GrxA family glutaredoxin	Glutaredoxin-like domain (DUF836), Glutaredoxin
L472_05054	hypothetical protein	
L472_05055	hypothetical protein	
L472_05056	hypothetical protein	Protein of unknown function (DUF2829)
L472_05057	protein phoH	PhoH-like protein, Zonular occludens toxin (Zot)
L472_05058	hypothetical protein	
L472_05060	hypothetical protein	
L472_05061	hypothetical protein	
L472_05062	hypothetical protein	
L472_05065	hypothetical protein	
L472_05064	hypothetical protein	
L472_05063	hypothetical protein	ATP dependent DNA ligase domain, DNA ligase OB-like domain
L472_05066	hypothetical protein	
L472_05067	hypothetical protein	
L472_05068	hypothetical protein	DnaB-like helicase C terminal domain, AAA domain
L472_05069	hypothetical protein	
L472_05070	hypothetical protein	
L472_05071	hypothetical protein	
L472_05072	hypothetical protein	ATPase MipZ, VirC1 protein, CobQ/CobB/MinD/ParA nucleotide binding domain
L472_05075	hypothetical protein	
L472_05074	hypothetical protein	
L472_05073	hypothetical protein	
L472_05076	hypothetical protein	
L472_05077	hypothetical protein	Chaperone of endosialidase
L472_05078	hypothetical protein	Domain of unknown function (DUF1983), Fibronectin type III domain, Putative phage tail protein
L472_05080	hypothetical protein	Prokaryotic homologs of the JAB domain, Phage minor tail protein L, NlpC/P60 family

Genbank locus name	functional annotation	PFAM/TIGRFAM domains
L472_05081	phage minor tail protein L	Phage minor tail protein L
L472_05082	hypothetical protein	Phage minor tail protein
L472_05083	hypothetical protein	Lambda phage tail tape-measure protein (Tape_meas_lam_C)
L472_05079	hypothetical protein	
L472_05084	hypothetical protein	
L472_05085	hypothetical protein	
L472_05086	hypothetical protein	
L472_05088	hypothetical protein	
L472_05087	hypothetical protein	
L472_05089	hypothetical protein	
L472_05091	hypothetical protein	
L472_05090	hypothetical protein	
L472_05092	hypothetical protein	Bacterial Ig-like domain (group 2)
L472_05093	hypothetical protein	
L472_05094	hypothetical protein	
L472_05095	hypothetical protein	
L472_05096	hypothetical protein	Phage terminase large subunit, Terminase-like family
L472_05097	hypothetical protein	
L472_05098	hypothetical protein	
L472_05101	hypothetical protein	ABC transporter
L472_05099	hypothetical protein	
L472_05100	hypothetical protein	
L472_05103	hypothetical protein	ParB-like nuclease domain
L472_05102	hypothetical protein	ParB-like nuclease domain
L472_05104	hypothetical protein	Type III restriction enzyme, res subunit, Helicase conserved C-terminal domain, DEAD/DEAH box helicase
L472_05105	hypothetical protein	
L472_05106	hypothetical protein	Repressor of phase-1 flagellin
L472_05107	hypothetical protein	
L472_04901	hypothetical protein	Bacterial regulatory helix-turn-helix protein, lysR family
L472_04902	floR2, resistance to phenicol	Major Facilitator Superfamily, Sugar (and other) transporter
L472_04903	hypothetical protein	Protein of unknown function (DUF3363)
L472_04904	transposase	Integrase core domain, DDE domain, Transposase IS66 family
L472_04905	S-formylglutathione hydrolase	Putative esterase
L472_04906	S-(hydroxymethyl)glutathione dehydrogenase	Alcohol dehydrogenase GroES-like domain, Zinc-binding dehydrogenase
L472_04907	tet(D)1, resistance to tetracycline	Major Facilitator Superfamily, Sugar (and other) transporter
L472_04908	tetracycline repressor protein class D	Tetracyclin repressor, C-terminal all-alpha domain, Bacterial regulatory proteins, tetR family
L472_04909	transposase	Transposase IS66 family, DDE domain, Integrase core domain
L472_04910	Na(+)/H(+) antiporter nhaA 2	Na+/H+ antiporter 1
L472_04911	hypothetical protein	
L472_04912	hypothetical protein	Cupin domain, Mannose-6-phosphate isomerase
L472_04913	hypothetical protein	Protein of unknown function DUF86, Nucleotidyltransferase domain
L472_04914	hypothetical protein	Nucleotidyltransferase domain
L472_04915	transposase for transposon Tn21	Tn3 transposase DDE domain, Domain of unknown function (DUF4158)
L472_04916	transposase	Transposase, Transposase IS116/IS110/IS902 family
L472_04917	hypothetical protein	Predicted membrane protein (DUF2254)
L472_04918	hypothetical protein	
L472_04919	high-affinity choline transporter	BCCT family transporter
L472_04921	hypothetical protein	
L472_04920	insertion element IS1 protein insB	IS1 transposase
L472_04922	hypothetical protein	
L472_04923	hypothetical protein	
L472_04924	transposase	Transposase DDE domain
L472_04925	hypothetical protein	UvrD-like helicase C-terminal domain, Part of AAA domain, PIF1-like helicase
L472_04926	hypothetical protein	
L472_04927	transposase	Transposase DDE domain
L472_04928	DNA polymerase V	Peptidase S24-like
L472_04929	protein samB	Domain of unknown function (DUF4113), IMS family HHH motif, impB/mucB/samB family, impB/mucB/samB family C-terminal domain
L472_04931	plasmid partition protein ParA	CobQ/CobB/MinD/ParA nucleotide binding domain
L472_04930	ParB family chromosome partitioning protein	ParB-like nuclease domain, ParB family
L472_04932	hypothetical protein	
L472_04933	hypothetical protein	
L472_04934	DNA replication protein RepB	Initiator Replication protein
L472_04935	hypothetical protein	
L472_04936	hypothetical protein	
L472_04937	resolvase	Phage integrase family
L472_04938	hypothetical protein	
L472_04939	hypothetical protein	
L472_04940	virulence-associated protein vagC	Antidote-toxin recognition MazE
L472_04941	plasmid maintenance protein VagD	PIN domain
L472_04942	hypothetical protein	AAA ATPase domain, P-loop containing region of AAA domain
L472_04943	transposase	Transposase IS66 family, Integrase core domain, DDE domain
L472_04944	hypothetical protein	Electron transfer DM13
L472_04945	hypothetical protein	Protein of unknown function (DUF1471)
L472_04946	hypothetical protein	Bacterial regulatory proteins, tetR family
L472_04947	hypothetical protein	EamA-like transporter family
L472_04948	hypothetical protein	Alpha/beta hydrolase family, Prolyl oligopeptidase family
L472_04949	transposase	Transposase IS116/IS110/IS902 family, Transposase
L472_04950	hypothetical protein	
L472_04951	hypothetical protein	
L472_04952	hypothetical protein	RHS Repeat, RHS protein
L472_04953	hypothetical protein	
L472_04954	hypothetical protein	
L472_04955	hypothetical protein	
L472_04956	hypothetical protein	
L472_04957	hypothetical protein	
L472_04958	hypothetical protein	Phage integrase family, Phage integrase, N-terminal SAM-like domain
L472_04959	hypothetical protein	Exonuclease
L472_04960	hypothetical protein	
L472_04961	DNA replicatio site-binding protein	DNA replication terminus site-binding protein (Ter protein)
L472_04962	hypothetical protein	Plasmid replication region DNA-binding N-term, Leucine-rich repeats of kinetochore protein Cenp-F/LEK1
L472_04963	hypothetical protein	
L472_04964	hypothetical protein	UvrD-like helicase C-terminal domain, Part of AAA domain, UvrD/REP helicase N-terminal domain
L472_04965	hypothetical protein	
L472_04966	hypothetical protein	Conjugative relaxosome accessory transposon protein
L472_04967	hypothetical protein	TraG-like protein, N-terminal region
L472_04968	hypothetical protein	Transglycosylase SLT domain
L472_04969	hypothetical protein	
L472_04970	hypothetical protein	Flagellar transcriptional activator (FlhC)
L472_04971	hypothetical protein	H-NS histone family
L472_04972	PRTRC system protein D	
L472_04973	hypothetical protein	
L472_04974	hypothetical protein	

Genbank locus name	**functional annotation**	**PFAM/TIGRFAM domains**
L472_04975	hypothetical protein	Initiator Replication protein
L472_04976	hypothetical protein	
L472_04977	hypothetical protein	Phosphoadenosine phosphosulfate reductase family
L472_04978	hypothetical protein	
L472_04979	hypothetical protein	
L472_04980	hypothetical protein	
L472_04982	hypothetical protein	
L472_04981	hypothetical protein	
L472_04984	signal peptide peptidase SppA, 36K type	Serine dehydrogenase proteinase, Clp protease, Peptidase family S49
L472_04983	hypothetical protein	
L472_04985	hypothetical protein	DSBA-like thioredoxin domain, Thioredoxin-like domain, Thioredoxin
L472_04986	hypothetical protein	
L472_04989	hypothetical protein	
L472_04988	hypothetical protein	
L472_04987	hypothetical protein	
L472_04990	hypothetical protein	
L472_04991	hypothetical protein	
L472_04992	hypothetical protein	
L472_04993	hypothetical protein	Staphylococcal nuclease homologue
L472_04994	DNA-binding protein HU-beta	Bacterial DNA-binding protein
L472_04995	hypothetical protein	Helix-turn-helix, Helix-turn-helix domain
L472_04996	hypothetical protein	Phage derived protein Gp49-like (DUF891)
L472_04997	hypothetical protein	
L472_04998	hypothetical protein	
L472_04999	hypothetical protein	
L472_05000	hypothetical protein	
L472_05001	hypothetical protein	
L472_05002	hypothetical protein	Protein of unknown function (DUF1643)
L472_05003	hypothetical protein	
L472_05004	hypothetical protein	
L472_05005	hypothetical protein	ATPase family associated with various cellular activities (AAA)
L472_05006	hypothetical protein	
L472_05007	hypothetical protein	
L472_05009	hypothetical protein	
L472_05008	hypothetical protein	
L472_05012	hypothetical protein	
L472_05011	hypothetical protein	
L472_05010	hypothetical protein	
L472_05014	hypothetical protein	VirB8 protein
L472_05013	hypothetical protein	VirB8 protein
L472_05016	hypothetical protein	Bacterial conjugation TrbI-like protein
L472_05015	P-type conjugative transfer protein VirB9	Conjugal transfer protein
L472_05017	P-type DNA transfer ATPase VirB11	Type II/IV secretion system protein
L472_05018	transposase	Transposase IS66 family, Integrase core domain, DDE domain
L472_04842	QnrB41, resistance to quinolone	Pentapeptide repeats (9 copies), Pentapeptide repeats (8 copies)
L472_04843	psp operon transcriptional activator	Bacterial regulatory protein, Fis family, AAA domain (dynein-related subfamily), Sigma-54 interaction domain
L472_04844	phage shock protein A	PspA/IM30 family
L472_04845	phage shock protein B	Phage shock protein B
L472_04846	phage shock protein C	PspC domain
L472_04847	phage shock protein D	Phage shock protein PspD (Phageshock_PspD)
L472_04848	hypothetical protein	
L472_04849	transposase	Transposase IS66 family, Integrase core domain, DDE domain
L472_04851	hypothetical protein	PhoH-like protein, IstB-like ATP binding protein, ATPase family associated with various cellular activities (AAA), Bacterial dnaA protein
L472_04850	hypothetical protein	Homeodomain-like domain, Integrase core domain
L472_04853	blaOXA-10, resistance to beta-lactam	Penicillin binding protein transpeptidase domain
L472_04852	aadA12, resistance to aminoglycoside	Domain of unknown function (DUF4111), Nucleotidyltransferase domain
L472_04854	integrase/recombinase	Phage integrase, N-terminal SAM-like domain, Phage integrase family
L472_04855	transposase	Integrase core domain, DDE domain, Transposase IS66 family
L472_04856	hypothetical protein	Tn3 transposase DDE domain, Domain of unknown function (DUF4158)
L472_04857	transposase	Transposase IS116/IS110/IS902 family, Transposase
L472_04858	transposase for transposon	Tn3 transposase DDE domain
L472_04859	transposase	Transposase, Transposase IS116/IS110/IS902 family
L472_04860	hypothetical protein	
L472_04861	peptide-methionine (S)-S-oxide reductase	Peptide methionine sulfoxide reductase
L472_04862	methionine-R-sulfoxide reductase	SelR domain, Peptide methionine sulfoxide reductase
L472_04863	hypothetical protein	
L472_04864	hypothetical protein	Protein of unknown function, DUF417
L472_04865	hypothetical protein	Protein of unknown function (DUF1471)
L472_04866	hypothetical protein	Bacterial regulatory proteins, tetR family
L472_04867	hypothetical protein	Protein of unknown function (DUF1471)
L472_04868	transposase	Transposase IS116/IS110/IS902 family, Transposase
L472_04869	transposase for transposon	Tn3 transposase DDE domain
L472_04870	transposase	Integrase core domain, DDE domain, Transposase IS66 family
L472_04871	hypothetical protein	Transposase
L472_04872	hypothetical protein	IS66 Orf2 like protein
L472_04875	hypothetical protein	
L472_04873	hypothetical protein	Transposase C of IS166 homeodomain, Transposase IS66 family, zinc-finger binding domain of transposase IS66, IS66 C-terminal element
L472_04874	hypothetical protein	
L472_04876	hypothetical protein	
L472_04877	hypothetical protein	Domain of unknown function (DUF4400)
L472_04878	hypothetical protein	Domain of unknown function (DUF4400)
L472_04879	hypothetical protein	Type IV secretion-system coupling protein DNA-binding domain, Domain of unknown function DUF87, TraM recognition site of TraD and TraG, AAA-like domain, Bacterial protein of unknown function (DUF853)
L472_04880	hypothetical protein	Putative helicase
L472_04881	hypothetical protein	
L472_04882	hypothetical protein	DNA topoisomerase, Toprim domain, Topoisomerase DNA binding C4 zinc finger
L472_04883	hypothetical protein	
L472_04884	hypothetical protein	
L472_04886	hypothetical protein	C-5 cytosine-specific DNA methylase
L472_04885	hypothetical protein	
L472_04887	hypothetical protein	
L472_04888	hypothetical protein	
L472_04890	hypothetical protein	
L472_04891	hypothetical protein	
L472_04889	hypothetical protein	
L472_04892	hypothetical protein	
L472_04893	hypothetical protein	N-6 DNA Methylase
L472_04894	hypothetical protein	Winged helix-turn helix, M protein trans-acting positive regulator (MGA) HTH domain
L472_04895	hypothetical protein	KorB domain, ParB-like nuclease domain
L472_04896	hypothetical protein	AAA domain, CobQ/CobB/MinD/ParA nucleotide binding domain, ATPase MipZ
L472_04897	hypothetical protein	
L472_04898	sul22, resistance to sulphonamide	Pterin binding enzyme

Genbank locus name	functional annotation	PFAM/TIGRFAM domains
L472_04899	phosphoglucosamine mutase	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I
L472_04900	transposase	Putative transposase, Transposase zinc-binding domain

Table S9. List of MGH_31 and MGH_59 genes associated antibiotic resistance and belonging to COGs shared by the two isolates.

#cluster id	isolate	Genbank locus name	functional annotation	location of gene	Has beta-lactamase PFAM domain	PFAM domain e-value
55	MGH_31	L377_05492	aadA21, resistance to aminoglycoside	plasm		
55	MGH_31	L377_05494	aadA13, resistance to aminoglycoside	plasm		
55	MGH_31	L377_01167	aadA21, resistance to aminoglycoside	chrom		
55	MGH_59	AF45_05307	aadA21, resistance to aminoglycoside	undetermined		
55	MGH_59	AF45_05411	aadA15, resistance to aminoglycoside	plasm		
246	MGH_31	L377_02898	ribonuclease Z	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	4.1e-28, 1.8e-11
246	MGH_59	AF45_02421	ribonuclease Z	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	4.1e-28, 1.8e-11
388	MGH_31	L377_02805	D-alanyl-D-alanine endopeptidase	chrom	Beta-lactamase enzyme family	3.20E-12
388	MGH_59	AF45_02327	D-alanyl-D-alanine endopeptidase	chrom	Beta-lactamase enzyme family	3.20E-12
432	MGH_31	L377_02314	penicillin-binding protein AmpH	chrom	Beta-lactamase	0
432	MGH_59	AF45_04918	penicillin-binding protein AmpH	chrom	Beta-lactamase	0
544	MGH_31	L377_01986	beta-lactamase	chrom	Beta-lactamase superfamily domain	1.5e-35, 2.1e-22
544	MGH_59	AF45_00161	hypothetical protein	chrom	Beta-lactamase superfamily domain	2.1e-22, 1.5e-35
604	MGH_31	L377_02852	beta-lactamase	chrom	Beta-lactamase	7.10E-38
604	MGH_59	AF45_02374	hypothetical protein	chrom	Beta-lactamase	7.10E-38
642	MGH_31	L377_04342	beta-lactamase	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	4.2e-12, 8.8e-18, 2.8e-05
642	MGH_59	AF45_03763	hypothetical protein	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	4.2e-12, 8.8e-18, 2.8e-05
711	MGH_31	L377_04742	LamB, LamB	chrom		
711	MGH_59	AF45_04157	LamB, LamB	chrom		
810	MGH_31	L377_04903	L-ascorbate 6-phosphate lactonase	chrom	Beta-lactamase superfamily domain	1.3e-24, 1.7e-16
810	MGH_59	AF45_04323	hypothetical protein	chrom	Beta-lactamase superfamily domain	1.3e-24, 1.7e-16
1054	MGH_31	L377_05076	mdtm, Major facilitator superfamily transporter. Multidrug resista	chrom		
1054	MGH_59	AF45_04497	mdtm, Major facilitator superfamily transporter. Multidrug resista	chrom		
1155	MGH_31	L377_02699	D-alanyl-D-alanine carboxypeptidase dacD	chrom	Beta-lactamase enzyme family	4.50E-12
1155	MGH_59	AF45_02222	D-alanyl-D-alanine carboxypeptidase dacD	chrom	Beta-lactamase enzyme family	4.50E-12
1179	MGH_31	L377_02594	ksga, Specifically dimethylates two adjacent adenosines in the l	chrom		
1179	MGH_59	AF45_04638	ksga, Specifically dimethylates two adjacent adenosines in the l	chrom		
1217	MGH_31	L377_01674	multidrug transporter MdfA	chrom		
1217	MGH_59	AF45_00477	multidrug transporter MdfA	chrom		
1345	MGH_31	L377_00441	mdtk, Major facilitator superfamily transporter. Multidrug resista	chrom		
1345	MGH_59	AF45_01719	mdtk, Major facilitator superfamily transporter. Multidrug resista	chrom		
1437	MGH_31	L377_01570	competence protein ComEC	chrom	Metallo-beta-lactamase superfamily	4.20E-14
1437	MGH_59	AF45_00590	hypothetical protein	chrom	Metallo-beta-lactamase superfamily	4.20E-14
1439	MGH_31	L377_02350	PhoE, PhoE	chrom		
1439	MGH_59	AF45_04882	PhoE, PhoE	chrom		
1468	MGH_31	L377_00433	beta-lactamase	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	2e-10, 2.8e-05, 5.6e-23
1468	MGH_59	AF45_01727	hypothetical protein	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	2e-10, 2.8e-05, 5.6e-23
1641	MGH_31	L377_01729	bcra, ABC transporter system, bacitracin efflux pump.	chrom		
1641	MGH_59	AF45_00422	bcra, ABC transporter system, bacitracin efflux pump.	chrom		
1730	MGH_31	L377_05066	fosA3_NZ, resistance to fosfomycin	chrom		
1730	MGH_59	AF45_04487	fosA3_NZ, resistance to fosfomycin	chrom		
2049	MGH_31	L377_03744	tolc, Resistance-nodulation-cell division transporter system. Mul	chrom		
2049	MGH_59	AF45_03164	tolc, Resistance-nodulation-cell division transporter system. Mul	chrom		
2103	MGH_31	L377_01677	D-alanyl-D-alanine carboxypeptidase dacC	chrom	Beta-lactamase enzyme family	9.00E-14
2103	MGH_59	AF45_00474	D-alanyl-D-alanine carboxypeptidase dacC	chrom	Beta-lactamase enzyme family	9.00E-14
2292	MGH_31	L377_02187	AcrB, acriflavine resistance protein B, multidrug resistance efflux	chrom		
2292	MGH_59	AF45_05047	AcrB, acriflavine resistance protein B, multidrug resistance efflux	chrom		
2307	MGH_31	L377_01454	mdtg, Major facilitator superfamily transporter. Multidrug resista	chrom		
2307	MGH_59	AF45_00706	mdtg, Major facilitator superfamily transporter. Multidrug resista	chrom		
2345	MGH_31	L377_03986	acrb, Resistance-nodulation-cell division transporter system. Mu	chrom		
2345	MGH_59	AF45_03407	acrb, Resistance-nodulation-cell division transporter system. Mu	chrom		
2362	MGH_31	L377_01599	macb, Resistance-nodulation-cell division transporter system. M	chrom		
2362	MGH_59	AF45_00562	macb, Resistance-nodulation-cell division transporter system. M	chrom		
2598	MGH_31	L377_04159	arna, Bifunctional enzyme that catalyzes the oxidative decarbox	chrom		
2598	MGH_59	AF45_03580	arna, Bifunctional enzyme that catalyzes the oxidative decarbox	chrom		
2640	MGH_31	L377_01555	metallo-beta-lactamase	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	7.6e-07, 7.6e-32
2640	MGH_59	AF45_00605	hypothetical protein	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	7.6e-07, 7.6e-32
2669	MGH_31	L377_03891	D-alanyl-D-alanine carboxypeptidase dacB	chrom	Beta-lactamase enzyme family	2.10E-08
2669	MGH_59	AF45_03312	D-alanyl-D-alanine carboxypeptidase dacB	chrom	Beta-lactamase enzyme family	2.10E-08

#cluster id	isolate	Genbank locus name	functional annotation	location of gene	Has beta-lactamase PFAM domain	PFAM domain e-value
2724	MGH_31	L377_00598	metallo-beta-lactamase	chrom	Metallo-beta-lactamase superfamily	2.60E-13
2724	MGH_59	AF45_01562	hypothetical protein	chrom	Metallo-beta-lactamase superfamily	2.60E-13
2858	MGH_31	L377_01034	metallo-beta-lactamase	chrom	Metallo-beta-lactamase superfamily	2.60E-20
2858	MGH_59	AF45_01125	hypothetical protein	chrom	Metallo-beta-lactamase superfamily	2.60E-20
2894	MGH_31	L377_01877	D-alanyl-D-alanine carboxypeptidase dacA	chrom	Beta-lactamase enzyme family	1.50E-08
2894	MGH_59	AF45_00270	D-alanyl-D-alanine carboxypeptidase dacA	chrom	Beta-lactamase enzyme family	1.50E-08
2899	MGH_31	L377_02847	bcr, bicyclomycin resistance protein	chrom		
2899	MGH_59	AF45_02369	bcr, bicyclomycin resistance protein	chrom		
2943	MGH_31	L377_02389	tet34, Xanthine-guanine phosphoribosyltransferase. Mechanism	chrom		
2943	MGH_59	AF45_04843	tet34, Xanthine-guanine phosphoribosyltransferase. Mechanism	chrom		
3014	MGH_31	L377_00634	coenzyme PQQ synthesis protein B	chrom	Beta-lactamase superfamily domain	1.00E-21
3014	MGH_59	AF45_01527	coenzyme PQQ synthesis protein B	chrom	Beta-lactamase superfamily domain	1.00E-21
3070	MGH_31	L377_02186	acra, Resistance-nodulation-cell division transporter system. Mu	chrom		
3070	MGH_59	AF45_05048	acra, Resistance-nodulation-cell division transporter system. Mu	chrom		
3281	MGH_31	L377_03757	baca, Undecaprenyl pyrophosphate phosphatase, which consist	chrom		
3281	MGH_59	AF45_03177	baca, Undecaprenyl pyrophosphate phosphatase, which consist	chrom		
3373	MGH_31	L377_03301	anaerobic nitric oxide reductase flavorubredoxin	chrom	Metallo-beta-lactamase superfamily	3.10E-27
3373	MGH_59	AF45_02778	anaerobic nitric oxide reductase flavorubredoxin	chrom	Metallo-beta-lactamase superfamily	3.10E-27
3525	MGH_31	L377_00858	blaSHV-134, SHV	chrom	Beta-lactamase, Beta-lactamase enzyme family	1.9e-32, 5.5e-37
3525	MGH_59	AF45_05311	blaSHV-134, SHV	undetermined	Beta-lactamase, Beta-lactamase enzyme family	1.2e-32, 5.6e-37
3525	MGH_59	AF45_01303	blaSHV-134, SHV	chrom	Beta-lactamase, Beta-lactamase enzyme family	1.9e-32, 3.8e-37
3990	MGH_31	L377_04808	protein phnP	chrom	Beta-lactamase superfamily domain	3.40E-12
3990	MGH_59	AF45_04223	protein phnP	chrom	Beta-lactamase superfamily domain	3.40E-12
4100	MGH_31	L377_00628	pbp2, The enzyme has a penicillin-insensitive transglycosylase	chrom		
4100	MGH_59	AF45_01533	pbp2, The enzyme has a penicillin-insensitive transglycosylase	chrom		
4135	MGH_31	L377_04396	emrd, Multidrug resistance efflux pump.	chrom		
4135	MGH_59	AF45_03817	emrd, Multidrug resistance efflux pump.	chrom		
4179	MGH_31	L377_02412	hydroxyacylglutathione hydrolase	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	8.9e-07, 8.2e-31
4179	MGH_59	AF45_04820	hydroxyacylglutathione hydrolase	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	8.9e-07, 8.2e-31
4184	MGH_31	L377_04772	metallo-beta-lactamase	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	2.4e-18, 1.3e-10
4184	MGH_59	AF45_04187	hypothetical protein	chrom	Beta-lactamase superfamily domain, Metallo-beta-lactamase superfamily	2.4e-18, 1.3e-10
4774	MGH_31	L377_03223	oqxB1, resistance to quinolone	chrom		
4774	MGH_59	AF45_02700	oqxB1, resistance to quinolone	chrom		
4832	MGH_31	L377_01165	sul11, resistance to sulphonamide	chrom		
4832	MGH_59	AF45_05305	sul11, resistance to sulphonamide	undetermined		
4881	MGH_31	L377_03222	oqxA1, resistance to quinolone	chrom		
4881	MGH_59	AF45_02699	oqxA1, resistance to quinolone	chrom		
4903	MGH_31	L377_00714	N-acylhomoserine lactone degredation protein AhlK	chrom	Metallo-beta-lactamase superfamily	4.90E-19
4903	MGH_59	AF45_01447	hypothetical protein	chrom	Metallo-beta-lactamase superfamily	5.40E-19
4936	MGH_31	L377_05446	beta-lactamase TEM-12	plasm	Beta-lactamase, Beta-lactamase enzyme family	1.4e-06, 1.1e-07
4936	MGH_31	L377_05447	beta-lactamase TEM	plasm	Beta-lactamase, Beta-lactamase enzyme family	6.5e-20, 1.1e-26
4936	MGH_59	AF45_05418	blaTEM-1B1, resistance to beta-lactam	undetermined	Beta-lactamase, Beta-lactamase enzyme family	1.7e-30, 3e-39
4936	MGH_59	AF45_05151	blaTEM-1A4, resistance to beta-lactam	plasm	Beta-lactamase, Beta-lactamase enzyme family	1.7e-30, 3e-39
4936	MGH_59	AF45_05409	blaTEM-1A4, resistance to beta-lactam	plasm	Beta-lactamase, Beta-lactamase enzyme family	1.7e-30, 3e-39
5465	MGH_31	L377_05298	mph(A)1, resistance to macrolide	plasm		
5465	MGH_59	AF45_05163	mph(A)1, resistance to macrolide	plasm		

Table S10. Evaluating accuracy of second round of scaffolding (SSPACE), using SMRT sequencing assemblies as gold standard.

Accuracy of assemblies of a second round of scaffolding using SSPACE was evaluated by comparing SSPACE assemblies to PacBio assemblies from the same strain.
An average accuracy was estimated by dividing the number of correct joins by the total number of joins performed on all seven isolates.

Isolate	#scaffolds (Illumina based assembly)	#scaffolds after SSPACE (Illumina based assembly)	#number of joins performed by SSPACE	#correct joins	correct joins (%)
G25860	52	14	38	35	92
G25823	74	30	44	37	84
G25824	26	14	12	11	92
G25833	28	14	14	11	79
G25837	28	11	17	16	94
G25847	27	10	17	15	88
G25858	9	7	2	2	100
G25863	12	11	1	0	0

Average accuracy (%): 88

Table S11. Comparison of plasmid detection methods presented by this work and PLACNET.

	This work		PLACNET		Comparison this work vs PLACNET
Isolate	Genbank accession of plasmidial scaffolds	Length (kb)	Plasmid name	Length (Kb)	Coverage/Identity
BIDMC_20B	NZ_KI929680.1	142.2	pBIDMC20B_1	128	> 90 % coverage; > 90% identity
BIDMC_20B	NZ_KI929681.1	109	pBIDMC20B_2	109	> 90 % coverage; > 90% identity
BWH_24	NZ_AXLH01000002.1	164.7	pBWH24_1	123	> 90 % coverage; > 90% identity
BWH_24	NZ_AXLH01000001.1	109.1	pBWH24_2	109	> 90 % coverage; > 90% identity
BWH_24	NZ_AXLH01000004.1	60.8	pBWH24_3	60.3	> 90 % coverage; > 90% identity
BIDMC_38			pBIDMC38_1	11.8	Not rerported as a plasmidial sequence by this work
BIDMC_38	NZ_KI535397.1	5.2	pBIDMC38_2	5.3	> 90 % coverage; > 90% identity
BIDMC_38	NZ_KI535402.1	1.6	pBIDMC38_3	1.6	> 90 % coverage; > 90% identity
BIDMC_38	NZ_KI535395.1	3.8	pBIDMC38_4	4.2	< 30 % coverage (different sequences)
BIDMC_38	NZ_KI535393.1	127	pBIDMC38_5	123	> 90 % coverage; > 90% identity

Table S12. Read based analysis of presence(1)/absence(0) of genes associated with antibiotic resistance among isolates with unknown cause of resistance.

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
aac	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac2-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac2-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac2-Ic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac2-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac2-Ie	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Ib-aac6-Ib	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
aac3-Ic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-If	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Ig	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Ih	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Ii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-IIa	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1	0
aac3-IIb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-IIc	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1	0
aac3-IId	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1	0
aac3-IIe	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1	0
aac3-IIIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-IIIb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-IIIc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Ik	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-IVa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-IXa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-VIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-VIIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-VIIIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac3-Xa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
aac6-31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-aph2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-I30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iaa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iad	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iaf	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iai	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ib	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0
aac6Ib-cr	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0
aac6-Ic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-If	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ig	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ih	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ii	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-IIb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-IIc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ij	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ik	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Il	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Im	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iq	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Ir	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Is	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-It	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iu	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iv	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iw	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aac6-Iy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
aac6-Iz	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aacA29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aacA43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA12	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA15	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA17	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA2	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
aadA21	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA22	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA23	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA3	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
aadA4	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
aadA5	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
aadA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadA8	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
aadA8b	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
aadA9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadB	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
aadC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aadD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AcrA	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
AcrB	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
ampH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ampS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ant2-Ia	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
ant4-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
ant4-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ant4-IIb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ant6-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ant6-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ant9-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph2-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph2-Ic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph2-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph2-Ie	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-Ic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-Id	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-IIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-IIb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-IIc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-III	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-IV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-Va	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-Vb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-Vc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-VIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-VIb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-VIIa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-VIII	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph3-XV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph4-Ia	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph4-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph6-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph6-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph6-Ic	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph9-Ia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
aph9-Ib	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
apmA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
armA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARR-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARR-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARR-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARR-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARR-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ARR-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BL2apc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BL2bectxm	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BL2beoxy1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BL2beshv2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BL2dmoxa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BL2efpm	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BL2fnmca	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACC-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACC-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACC-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACC-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACI-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACT-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACT-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACT-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACT-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACT-5	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
blaACT-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaACT-7	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
blaAER-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaAST-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaB-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaB-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaBEL-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaBEL-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaBEL-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaBES-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaBIC-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaBIL-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCARB-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCEPA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCEPA-29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCEPA-44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCEPA-49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCEPA-85	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCEPH-A3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCFE-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCGB-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCGB-1b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCKO-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaCME-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaCMY-49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCMY-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-1	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-10	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-101	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-102	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-105	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-106	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-107	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-108	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-109	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-11	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-110	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-111	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-112	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-113	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-114	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-116	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-12	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaCTX-M-13	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-15	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-16	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-17	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-19	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-21	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-22	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-23	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-24	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-27	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-28	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-29	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-3	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-30	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-32	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-34	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-36	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-37	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-38	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-42	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-45	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaCTX-M-46	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-47	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-48	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-49	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-50	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-51	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-52	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-53	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-54	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-55	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-58	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-60	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-61	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-62	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-65	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-66	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-67	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-68	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-69	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-71	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-79	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-80	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-81	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaCTX-M-82	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-83	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-84	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-85	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-86	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-87	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-88	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-9	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-93	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-94	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-95	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-96	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0
blaCTX-M-97	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaCTX-M-98	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaCTX-M-99	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
blaDES-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaDHA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaDHA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaDHA-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaDHA-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaDHA-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaDHA-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaDIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaEBR-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaERP-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFAR-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFONA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFONA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFONA-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFONA-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFONA-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaFONA-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaFOX-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGES-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaGOB-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-13B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaGOB-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaHERA-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMI-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMI-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMI-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaIMP-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIMP-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-2a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-2b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-2c	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaIND-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaIND-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaJOHN-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKHM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaKPC-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaL1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLAT-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLCR-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaLEN23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLEN9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaLUT-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMAL-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMIR-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMIR-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMIR-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMIR-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMIR-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOR-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOX-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOX-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOX-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOX-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOX-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOX-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMOX-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaMUS-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaNDM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaNDM-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaNDM-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaNDM-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaNDM-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaNDM-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaNMC-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaNPS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOCH-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOCH-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOCH-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOCH-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOCH-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOCH-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOCH-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-A-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaOKP-B-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOKP-B-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-104	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-106	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-108	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-109	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-110	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-112	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-113	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-114	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-116	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-117	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-118	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-130	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaOXA-131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-132	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-137	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-138	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-142	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-162	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-163	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-166	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-169	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-17	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-171	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaOXA-173	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-174	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-176	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-177	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-178	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-179	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-180	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-181	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-182	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-183	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-192	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-194	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-195	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-196	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-197	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-198	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-199	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-200	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-201	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-202	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-203	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-205	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-208	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-209	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-210	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-216	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-219	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaOXA-223	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-225	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-31	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
blaOXA-32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-4	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
blaOXA-40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-47	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
blaOXA-48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaOXA-58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-74	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-79	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-83	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-86	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-9	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-90	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaOXA-92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-94	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-95	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-96	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-97	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXA-99	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXY-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXY-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXY-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXY-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXY-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaOXY-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPAO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPER-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPER-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPER-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPER-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPER-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPER-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPER-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaPME-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaRAHN-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaRAHN-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaROB-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSED1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSFB-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSFC-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSFO-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSHV-1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-100	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-101	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-102	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaSHV-103	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-104	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-105	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-106	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-107	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-108	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-109	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-11	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-110	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-12	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-122	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-128	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-129	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-13	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-132	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-133	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-134	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-135	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-136	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-137	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-14	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-140	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-15	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-16	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-18	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-2	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-24	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-25	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-26	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-27	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-28	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-29	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-2a	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-30	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaSHV-31	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-33	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-34	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-35	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-36	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-37	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-38	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-39	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-40	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-41	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-42	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-43	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-44	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-45	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-46	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-48	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-49	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-5	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-50	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-51	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-52	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-53	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-55	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-56	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-57	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-59	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-6	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-60	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-61	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-62	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-63	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-64	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-65	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-66	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaSHV-67	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-69	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-7	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-70	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-71	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-72	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-77	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-8	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-84	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-85	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-86	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-89	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-92	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-93	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-94	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-95	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-96	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-97	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-98	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSHV-99	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
blaSIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSLB-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSME-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSME-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSME-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSMP-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaSPM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaTEM-1	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-10	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-101	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-102	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-104	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-105	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-106	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaTEM-107	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-108	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-109	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-11	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-110	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-111	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-112	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-113	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-114	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-115	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-116	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-117	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-118	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-12	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-120	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-121	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-122	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-123	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-124	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-125	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-126	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-127	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-128	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-129	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-130	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-131	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-132	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-133	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-134	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-135	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-136	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-137	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-138	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-139	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaTEM-141	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-142	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-143	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-144	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-145	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-146	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-147	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-148	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-149	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-15	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-150	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-151	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-152	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-154	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-155	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-156	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-157	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-158	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-159	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-160	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-162	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-163	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-166	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-167	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-168	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-169	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-17	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-171	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-176	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-177	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-178	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-183	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-187	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-188	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaTEM-189	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-190	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-2	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-20	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-21	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-22	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-24	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-28	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-29	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-3	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-30	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-33	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-42	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-43	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-47	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-48	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-49	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-52	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-53	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-54	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-55	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-57	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-59	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-6	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-60	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-63	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-67	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-68	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-7	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-70	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-71	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-72	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-75	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-76	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaTEM-77	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-78	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-79	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-80	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-81	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-82	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-83	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-84	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-85	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-86	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-87	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-88	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-89	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-90	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-91	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-93	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-94	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-95	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-96	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-97	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-98	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTEM-99	0	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0
blaTLA-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaTRU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaTUS-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVEB-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVEB-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVEB-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVEB-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVEB-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVEB-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVEB-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
blaVIM-11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaVIM-9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
blaZEG-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
carA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cat	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cat86	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
catB10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB3	0	0	0	1	1	0	0	1	1	0	0	0	0	0	0	0
catB7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catB9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catpC194	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catpC221	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catpC233	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catQ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
catS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfiA9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfxA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfxA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfxA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfxA4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cfxA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
cfxA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cml	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlA1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmlV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cmx	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CMY-2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CMY-23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cphA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cphA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cphA4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cphA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cphA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cphA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cphA8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA12	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
dfrA15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA15b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA17	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
dfrA18	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
dfrA20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA22	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
dfrA23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
dfrA29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA33	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
dfrA3b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrA9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrB8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
dfrK	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ereA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ereB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
erm39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
erm42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ErmE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermQ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermW	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ermZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
fexA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
floR	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
fosA	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0
fosB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
fosC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
fusA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
fusB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
hugA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
imiH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
imiS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
lmrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lmrB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lnuF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lsaA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lsaB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
lsaC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mdfA	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
mdtK	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
mecA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MecR1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mefA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mefB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphA	0	1	1	0	0	0	0	1	0	0	0	0	0	0	1	0
mphB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mphE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
msrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
msrC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
msrD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
msrE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NMC-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
norA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
npmA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oleB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oleC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
oqxA	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
oqxB	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
ortB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otrA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
otrC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
penA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
pexA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
qepA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
qepA2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-A2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-A3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-A4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-A5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-A6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-A7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-AS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B10	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B11	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B13	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B15	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B17	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B18	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B19	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B20	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B23	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B24	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B26	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B29	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
Qnr-B3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B32	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B36	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B40	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B41	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B5	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B6	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Qnr-B8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-B9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-S1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Qnr-S2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Qnr-S3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Qnr-S4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Qnr-S5	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
rmtA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtD2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rmtE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
spc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sph	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
srmB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
str	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
strA	0	0	0	0	0	1	0	1	0	0	1	0	0	0	1	0
strB	0	0	0	0	0	1	0	1	0	0	1	0	0	0	1	0
sul1	0	1	1	1	1	0	0	1	0	0	1	0	0	0	1	0
sul2	1	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0
sul3	0	1	1	1	1	0	0	1	0	0	1	0	0	0	1	0
tcr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tet44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetA	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0
tetAP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetBP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetD	1	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0
tetE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetH	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetJ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetK	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
tetM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetQ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetW	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetX	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tetZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tlrC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TolC	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
VanA-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-Ao2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanAE-Pp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-L	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-Pt2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanA-Sc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-ABc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-Ac1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-Ac2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-Ao1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-Ao2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
VanH-E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanHE-Pp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-Pt2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanH-Sc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-F	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-L	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanR-Pt2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-F	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-L	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanS-Pt2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanT-C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanT-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanTm-L	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanTr-L	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanU-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanW-B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanW-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanW-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						***E. coli***			***E. cloacae***				***E. aerogenes***		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
VanX-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-Ac1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-Ac2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-Ao1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-Ao2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanXE-Pp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-Pt2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanX-Sc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanXY-C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanXY-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanXY-L	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-B	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-F	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanYF-Pp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanY-Pt2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanZ-A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanZ-F	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanZF-Pp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VanZ-Pt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vatA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vatB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vatC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vatD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vatE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	Presence(1)/absence(0) on isolates															
	K. pneumoniae						*E. coli*			*E. cloacae*				*E. aerogenes*		
Genes associated with antibiotic resistance	**BIDMC_35**	**MGH_31**	**MGH_59**	**BIDMC_46A**	**BIDMC_53**	**UCI_25**	**MGH_57**	**UCI_51**	**UCI_53**	**UCI_29**	**UCI_35**	**MGH_37**	**MGH_4**	**MGH_77**	**UCI_15**	**UCI_27**
vatF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vgaA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vgaALC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vgaB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vgaC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vgaE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vgbA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vgbB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S13. Beta-lactamases and porin truncations detected in isolates with unknown genetic determinants for carbapenem resistance.

Beta-lactamases and porin truncations found in isolates from Boston Prospective Collection with unknown genetic determinant for carbapenem resistance

Species	Collection	Isolate	Genes in the assembly that might be associated with meropenem resistance	Additional genes detected by read-based analysis
K. pneumoniae	Boston prospective	BIDMC_46A	*bla* TEM-1, truncated OmpK36	
K. pneumoniae	Boston prospective	BIDMC_53	*bla* TEM-1, truncated OmpK36	
E. cloacae	Boston prospective	MGH_37	*bla* ACT-9-like	
K. pneumoniae	Boston prospective	MGH_31		*bla* TEM-like; gene spans a contig break
K. pneumoniae	Boston prospective	MGH_59	*bla* TEM	*bla* CTX-like, *bla* OXA; both are truncated genes in the assembly
K. pneumoniae	Boston prospective	BIDMC_35	*bla* OXA-10	
E. aerogenes	Boston prospective	MGH_77		

Beta-lactamases and porin truncations found in isolates from Irvine with unknown genetic determinant for carbapenem resistance

E. cloacae	Irvine prospective	UCI_35	*bla* ACT-16-like, truncated OmpC, absent OmpD	
E. coli	Irvine prospective	UCI_51	*bla* CTX-M-15, *bla* OXA-30, *bla* TEM-1	
E. coli	Irvine prospective	UCI_53	*bla* CTX-M-15, *bla* OXA-30	
K. pneumoniae	Irvine prospective	UCI_25	*bla* CTX-M-14, truncated OmpK36	
E. cloacae	Irvine prospective	UCI_29	*bla* ACT-9-like	
E. aerogenes	Irvine prospective	UCI_27		

Beta-lactamases and porin truncations found in isolates from Boston Historical Collection with unknown genetic determinant for carbapenem resistance

E. cloacae	Boston historical	MGH_4	*bla* ACT-14-like, truncated OmpF	

Table S14. Detailed analysis of porin encoding genes from non-susceptible isolates.

Grey cells indicate porins from the same isolate

species	isolate name	collection	MIC meropenem (ug/ml)	beta-lactamases possibly associated with meropenem resistance	putatively inactivated porin	Events detected in porins	Length of CDS when compared to reference gene (only for truncated porins)
E. coli	BWH_40	Boston prospective	2	blaCTX-M-15	OmpF	indel frameshift/premature STOP codon	71%
K. pneumoniae	MGH_63	Boston prospective	8	*bla* CTX-M-15	OmpK35	indel frameshift/premature STOP codon	70%
K. pneumoniae	MGH_65	Boston prospective	8	*bla* CTX-M-15	OmpK35	indel frameshift/premature STOP codon	70%
K. pneumoniae	MGH_75	Boston prospective	4	*bla* CTX-M-15	OmpK35	indel frameshift/premature STOP codon	70%
K. pneumoniae	MGH_43	Boston prospective	4	*bla* CTX-M-15, *bla* OXA-30, *bla* TEM-1	OmpK36	non-sense mutation + non-synonymous substitutions	86%
K. pneumoniae	MGH_35	Boston prospective	2	*bla* CTX-M-15	OmpK36	indel frameshift/premature STOP codon	32%
K. pneumoniae	MGH_47	Boston prospective	4		OmpK35	disruption by IS element	78%
K. pneumoniae	MGH_47	Boston prospective	4		OmpK36	non-sense mutation	34%
K. pneumoniae	BIDMC_46A	Boston prospective	2	*bla* TEM-1	OmpK36 copy 1	non-sense mutation	26%
K. pneumoniae	BIDMC_46A	Boston prospective	2	*bla* TEM-1	OmpK36 copy 2	indel frameshift/premature STOP codon	56%
K. pneumoniae	BIDMC_53	Boston prospective	2	*bla* TEM-1	OmpK36	non-sense mutation	26%
K. pneumoniae	BIDMC_53	Boston prospective	2	*bla* TEM-1	OmpK36	indel frameshift/premature STOP codon	56%
E. coli	MGH_57	Boston prospective	>32	*bla* CTX-M-15	OmpC	non-sense mutation	32%
K. pneumoniae	BIDMC_35	Boston prospective	>32	*bla* OXA-10	OmpK36	first 25 aa and 3 aa along the sequence are different than orhtologs in susceptible and non-susceptible isolates.	
K. pneumoniae	MGH_31	Boston prospective	4		OmpK36	two aa different then orthologs in susceptible and non-susceptible isolates	
E. cloacae	MGH_37	Boston prospective	4	blaACT-9-like	OmpC	no truncation, less than 80% similarity with reference OmpC.	
E. cloacae	MGH_37	Boston prospective	4	blaACT-9-like	OmpF	no truncation, less than 80% similarity with reference OmpF	
E. cloacae	MGH_4	Boston historical	4	*bla* ACT-14-like	OmpF	indel frameshift/premature STOP codon	67%
K. pneumoniae	UCI_25	Irvine prospective	>=4	*bla* CTX-M-14	OmpK36	non-sense mutation	50%
E. cloacae	UCI_35	Irvine prospective	4	*bla* ACT-16-like	OmpC	indel frameshift/premature STOP codon	67%
E. cloacae	UCI_35	Irvine prospective	4	*bla* ACT-16-like	OmpD	absent in assembly and reads	
E. coli	UCI_51	Irvine prospective	>=4	*bla* CTX-M-15, *bla* OXA-30, *bla* TEM-1	OmpC	one aa different than orthologs in susceptible and non-susceptible isolates	
E. cloacae	UCI_29	Irvine prospective	2	blaACT-9-like	OmpC	no truncation, less than 80% similarity with reference OmpC.	
E. cloacae	UCI_29	Irvine prospective	2	blaACT-9-like	OmpF	no truncation, less than 80% similarity with reference OmpF	

Table S15. Location of plasmidial genes associated with antibiotic resistance							
species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	BIDMC_35	N	1			IncA/C2	Qnr-B4
kpneumoniae	BIDMC_35	N	1			IncA/C2	aadA1
kpneumoniae	BIDMC_35	N	1			IncA/C2	blaOXA-10
kpneumoniae	BIDMC_35	N	1			IncA/C2	floR
kpneumoniae	BIDMC_35	N	1			IncA/C2	sul2
kpneumoniae	BIDMC_35	N	1			IncA/C2	tet(D)
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	aadA5
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	blaKPC-3
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	dfrA17
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	strA
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	strB
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	sul1
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	sul2
ecoli	BIDMC_20B	N	1	pEK499	EU935739.1	IncFIA	tet(A)
kpneumoniae	UCI_59	N	1	plasmid_9_strain_9	FJ223607.1	IncN	blaKPC-2
kpneumoniae	UCI_59	N	1	plasmid_9_strain_9	FJ223607.1	IncN	blaTEM-1
kpneumoniae	UCI_59	N	2			ColRNAI	aac(6)-Ib
kpneumoniae	UCI_59	N	2			ColRNAI	blaTEM-1
kpneumoniae	UCI_59	N	3				aadA1
kpneumoniae	UCI_59	N	3				sul2
kpneumoniae	UCI_59	N	3				tet(B)
kpneumoniae	UCI_59	N	4				aac(6)-Ib
kpneumoniae	UCI_38	S	1			IncX3	aph(3)-Ia
kpneumoniae	BWH_22	N	1			IncR	aac(3)-IVa
kpneumoniae	BWH_22	N	1			IncR	aac(6)-Ib
kpneumoniae	BWH_22	N	1			IncR	aadA1
kpneumoniae	BWH_22	N	1			IncR	aadA2
kpneumoniae	BWH_22	N	1			IncR	aph(4)-Ia
kpneumoniae	BWH_22	N	1			IncR	blaKPC-2
kpneumoniae	BWH_22	N	1			IncR	blaTEM-1
kpneumoniae	BWH_22	N	1			IncR	cmlA1
kpneumoniae	BWH_22	N	1			IncR	sul3
ecloacae	MGH_3	N	1				aac3iia
ecloacae	MGH_3	N	1				aph(3)-Ia
ecloacae	MGH_3	N	1				blaTEM-1
ecloacae	MGH_3	N	2				aac(6)-Ib
ecloacae	MGH_3	N	2				aadA1
ecloacae	MGH_3	N	2				blaKPC-3
ecloacae	MGH_3	N	2				blaOXA-9
ecloacae	MGH_3	N	2				blaSHV-38

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	MGH_3	N	3				sul2
ecloacae	MGH_3	N	3				tet(D)
ecloacae	MGH_3	N	4				aac(6)-IIc
ecloacae	MGH_3	N	4				ere(A)
kpneumoniae	MGH_46	S	1			IncFIB(K)	aadA1
kpneumoniae	MGH_46	S	1			IncFIB(K)	sul1
ecoli	MGH_57	N	1				blaTEM-1
kpneumoniae	BIDMC_18C	N	1			IncR	aac(3)-IVa
kpneumoniae	BIDMC_18C	N	1			IncR	aadA1
kpneumoniae	BIDMC_18C	N	1			IncR	aadA2
kpneumoniae	BIDMC_18C	N	1			IncR	aph(4)-Ia
kpneumoniae	BIDMC_18C	N	1			IncR	blaKPC-2
kpneumoniae	BIDMC_18C	N	1			IncR	cmlA1
kpneumoniae	BIDMC_18C	N	2	pKpS90	JX461340.1	IncX3	blaSHV-134
kpneumoniae	BIDMC_18C	N	3			ColRNAI	aac(6)-Ib
kpneumoniae	BIDMC_18C	N	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_18C	N	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_18C	N	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_18C	N	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_18C	N	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	MGH_79	N	1			IncFIB(K)	aadA2
kpneumoniae	MGH_79	N	1			IncFIB(K)	catA1
kpneumoniae	MGH_79	N	1			IncFIB(K)	dfrA12
kpneumoniae	MGH_79	N	1			IncFIB(K)	mph(A)
kpneumoniae	MGH_79	N	1			IncFIB(K)	sul1
kpneumoniae	MGH_79	N	2				blaKPC-2
kpneumoniae	UCI_33	N	1				catA1
kpneumoniae	UCI_33	N	2				blaOXA-9
kpneumoniae	UCI_33	N	3	pKpS90	JX461340.1	IncX3	aadA2
kpneumoniae	UCI_33	N	3	pKpS90	JX461340.1	IncX3	blaSHV-134
kpneumoniae	UCI_33	N	3	pKpS90	JX461340.1	IncX3	dfrA12
kpneumoniae	UCI_33	N	3	pKpS90	JX461340.1	IncX3	mph(A)
kpneumoniae	UCI_33	N	3	pKpS90	JX461340.1	IncX3	sul1
kpneumoniae	UCI_33	N	4	pNJST258C1	CP006922.1		blaTEM-1
kpneumoniae	UCI_33	N	4	pNJST258C1	CP006922.1		strA
kpneumoniae	UCI_33	N	4	pNJST258C1	CP006922.1		strB
kpneumoniae	UCI_33	N	4	pNJST258C1	CP006922.1		sul2
kpneumoniae	UCI_33	N	5				blaKPC-3
kpneumoniae	UCI_13	N	1	plasmid_9_strain_9	FJ223607.1	IncN	blaKPC-2
kpneumoniae	UCI_13	N	1	plasmid_9_strain_9	FJ223607.1	IncN	blaTEM-116
kpneumoniae	UCI_13	N	2	pQ1-1	HM371192.1	ColRNAI	strB
kpneumoniae	UCI_13	N	2	pQ1-1	HM371192.1	ColRNAI	sul2

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
eaerogenes	MGH_77	N	1				bcra
eaerogenes	MGH_77	N	1				fosA
eaerogenes	MGH_77	N	1				ksga
eaerogenes	MGH_77	N	2				baca
eaerogenes	MGH_77	N	3				CMY-48
eaerogenes	MGH_77	N	3				bcr
eaerogenes	MGH_77	N	3				bcra
eaerogenes	MGH_77	N	3				mdfa
eaerogenes	MGH_77	N	3				oqxB
eaerogenes	MGH_77	N	3				tet34
kpneumoniae	BIDMC_42B	N	1				catA1
kpneumoniae	BIDMC_45	N	1			ColRNAI	aac(6)-Ib
kpneumoniae	BIDMC_45	N	2			IncR	aac(3)-IVa
kpneumoniae	BIDMC_45	N	2			IncR	aadA2
kpneumoniae	BIDMC_45	N	2			IncR	aph(4)-Ia
kpneumoniae	BIDMC_45	N	2			IncR	blaKPC-2
kpneumoniae	BIDMC_45	N	2			IncR	cmlA1
kpneumoniae	BIDMC_45	N	2			IncR	sul3
kpneumoniae	BIDMC_45	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_45	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_45	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_45	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_45	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
cfreundii	UCI_31	S	1				Qnr-B38
cfreundii	UCI_31	S	1				arna
cfreundii	UCI_31	S	1				baca
cfreundii	UCI_31	S	1				bcr
cfreundii	UCI_31	S	1				bcra
cfreundii	UCI_31	S	1				blaCMY-41
cfreundii	UCI_31	S	1				ksga
cfreundii	UCI_31	S	1				mdfa
cfreundii	UCI_31	S	1				tet34
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	aac(6)Ib-cr
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	aph(3)-Ia
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	blaOXA-30
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	blaTEM-1
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_33B	N	1	pUUH239.2	CP002474.1	IncFIB(K)	tet(A)
kpneumoniae	BIDMC_33B	N	2				aac(6)-Ib
kpneumoniae	BIDMC_33B	N	2				aadA1
kpneumoniae	BIDMC_33B	N	2				blaKPC-3

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	MGH_31	N	1			IncFIB(K)	aac(6)-Ib
kpneumoniae	MGH_31	N	1			IncFIB(K)	mph(A)
kpneumoniae	MGH_31	N	2			IncR	aac(3)-IVa
kpneumoniae	MGH_31	N	2			IncR	aadA1
kpneumoniae	MGH_31	N	2			IncR	aadA2
kpneumoniae	MGH_31	N	2			IncR	aph(4)-Ia
kpneumoniae	MGH_31	N	2			IncR	cmlA1
kpneumoniae	MGH_31	N	2			IncR	sul3
kpneumoniae	MGH_31	N	3				tet(D)
ecoli	BIDMC_20A	N	1				strA
ecoli	BIDMC_20A	N	1				strB
ecoli	BIDMC_20A	N	1				sul2
ecoli	BIDMC_20A	N	2	pEK499	EU935739.1	IncFIA	aadA5
ecoli	BIDMC_20A	N	2	pEK499	EU935739.1	IncFIA	dfrA17
ecoli	BIDMC_20A	N	2	pEK499	EU935739.1	IncFIA	sul1
ecoli	BIDMC_20A	N	3	pEK499	EU935739.1	IncFII	tet(A)
ecoli	BIDMC_20A	N	3	pEK499	EU935739.1	IncFII	blaKPC-3
ecoli	BIDMC_76	S	1			IncFIB(AP001918)	blaTEM-1
kpneumoniae	MGH_72	S	1				aac(3)-IId
kpneumoniae	MGH_72	S	1				blaTEM-1
kpneumoniae	MGH_72	S	1				floR
kpneumoniae	MGH_72	S	1				strA
kpneumoniae	MGH_72	S	1				strB
kpneumoniae	MGH_72	S	1				sul2
kpneumoniae	MGH_72	S	1				tet(A)
kpneumoniae	MGH_72	S	2				tet(A)
smarcesens	BIDMC_81	S	1				tet34
smarcesens	BIDMC_81	S	2				aac(6)-Ic
smarcesens	BIDMC_81	S	2				baca
smarcesens	BIDMC_81	S	3				arna
smarcesens	BIDMC_81	S	4				bl1_sm
smarcesens	BIDMC_81	S	4				tet(41)
smarcesens	BIDMC_81	S	5				bcra
smarcesens	BIDMC_81	S	6				ksga
smarcesens	BIDMC_81	S	7				qnrb
smarcesens	BIDMC_81	S	8				oqxB
ecoli	BIDMC_62	N	1				blaKPC-3
ecoli	BIDMC_62	N	1				strA
ecoli	BIDMC_62	N	1				strB
ecoli	BIDMC_62	N	1				sul2
ecoli	BIDMC_62	N	2			IncN	aadA5
ecoli	BIDMC_62	N	2			IncN	dfrA17
ecoli	BIDMC_62	N	2			IncN	sul1
ecoli	BIDMC_62	N	2			IncN	tet(A)

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	MGH_5	N	1				Qnr-S1
ecloacae	MGH_5	N	2	pHCM2	AL513384.1	IncFIB(pHCM2)	dfrA15
ecloacae	MGH_5	N	3	pBK31551	JX193301.1	IncN	aac(3)-Ib
ecloacae	MGH_5	N	3	pBK31551	JX193301.1	IncN	aph(3)-Ia
ecloacae	MGH_5	N	3	pBK31551	JX193301.1	IncN	blaKPC-4
ecloacae	MGH_5	N	3	pBK31551	JX193301.1	IncN	blaTEM-1
ecloacae	MGH_5	N	3	pBK31551	JX193301.1	IncN	dfrA14
ecloacae	MGH_5	N	3	pBK31551	JX193301.1	IncN	sul1
kpneumoniae	MGH_45	N	1			IncR	aac(3)-IVa
kpneumoniae	MGH_45	N	1			IncR	aadA1
kpneumoniae	MGH_45	N	1			IncR	aadA2
kpneumoniae	MGH_45	N	1			IncR	aph(4)-Ia
kpneumoniae	MGH_45	N	1			IncR	blaKPC-2
kpneumoniae	MGH_45	N	1			IncR	blaTEM-1
kpneumoniae	MGH_45	N	1			IncR	cmlA1
kpneumoniae	MGH_45	N	1			IncR	sul3
kpneumoniae	UCI_22	S	1			IncFIB(K)	aac(6)-Ib
kpneumoniae	UCI_22	S	1			IncFIB(K)	aadA2
kpneumoniae	UCI_22	S	1			IncFIB(K)	catA1
kpneumoniae	UCI_22	S	1			IncFIB(K)	dfrA12
kpneumoniae	UCI_22	S	1			IncFIB(K)	mph(A)
kpneumoniae	UCI_22	S	1			IncFIB(K)	sul1
kpneumoniae	UCI_22	S	2				aac(3)-IVa
kpneumoniae	UCI_22	S	2				aadA2
kpneumoniae	UCI_22	S	2				aph(4)-Ia
kpneumoniae	UCI_22	S	2				sul3
kpneumoniae	BIDMC_12B	N	1	pNJST258N3	CP006925.1	ColRNAI	aac(6)-Ib
kpneumoniae	BIDMC_12B	N	1	pNJST258N3	CP006925.1	ColRNAI	blaTEM-1
kpneumoniae	BIDMC_12B	N	2	pBK30683	KF954760.1	IncFIA(HI1)	blaKPC-3
kpneumoniae	BIDMC_12B	N	2	pBK30683	KF954760.1	IncFIA(HI1)	blaTEM-1
kpneumoniae	BIDMC_12B	N	2	pBK30683	KF954760.1	IncFIA(HI1)	strA
kpneumoniae	BIDMC_12B	N	2	pBK30683	KF954760.1	IncFIA(HI1)	strB
kpneumoniae	BIDMC_12B	N	2	pBK30683	KF954760.1	IncFIA(HI1)	sul2
kpneumoniae	BIDMC_12B	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_12B	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aph(3)-Ia
kpneumoniae	BIDMC_12B	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_12B	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_12B	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_12B	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	UCI_8	S	1			IncR	floR
kpneumoniae	UCI_8	S	1			IncR	sul1
kpneumoniae	UCI_8	S	1			IncR	tet(A)
ecloacae	MGH_7	N	1			IncHI1B(CIT)	aac(6)-Ib

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	MGH_7	N	1			IncHI1B(CIT)	aadA1
ecloacae	MGH_7	N	1			IncHI1B(CIT)	blaKPC-3
ecloacae	MGH_7	N	1			IncHI1B(CIT)	blaOXA-9
ecloacae	MGH_7	N	1			IncHI1B(CIT)	blaSHV-38
ecloacae	MGH_7	N	1			IncHI1B(CIT)	blaTEM-1
ecoli	BIDMC_19B	N	1			IncN	dfrA14
ecoli	BIDMC_19B	N	2	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_19B	N	2	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_19B	N	2	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_19B	N	2	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_19B	N	2	pEC-IMP	EU855787.1	IncHI2A	sul2
ecoli	BIDMC_19B	N	3				blaKPC-2
kpneumoniae	BIDMC_4	N	1			IncR	aac(3)-IVa
kpneumoniae	BIDMC_4	N	1			IncR	aadA1
kpneumoniae	BIDMC_4	N	1			IncR	aadA2
kpneumoniae	BIDMC_4	N	1			IncR	aph(4)-Ia
kpneumoniae	BIDMC_4	N	1			IncR	cmlA1
kpneumoniae	BIDMC_4	N	1			IncR	sul3
kpneumoniae	BIDMC_4	N	2	pBK15692	KC845573.1	IncI2	blaKPC-3
kpneumoniae	BIDMC_4	N	2	pBK15692	KC845573.1	IncI2	blaTEM-1
kpneumoniae	BWH_36	I	1			IncFIB(K)	catA1
kpneumoniae	BWH_36	I	2	pBK15692	KC845573.1	IncI2	blaTEM-1
kpneumoniae	BIDMC_54	N	1				aadA2
kpneumoniae	BIDMC_54	N	1				dfrA12
kpneumoniae	BIDMC_54	N	1				sul1
kpneumoniae	BIDMC_54	N	2	pNJST258C1	CP006922.1		catA1
kpneumoniae	UCI_67	N	1				dfrA14
kpneumoniae	UCI_67	N	1				strB
kpneumoniae	UCI_67	N	1				sul2
kpneumoniae	UCI_67	N	2				aadA1
kpneumoniae	UCI_67	N	2				blaOXA-9
kpneumoniae	UCI_67	N	3			ColRNAI	aac(6)-Ib
kpneumoniae	UCI_67	N	3			ColRNAI	blaKPC-3
kpneumoniae	UCI_67	N	3			ColRNAI	blaTEM-1
kpneumoniae	UCI_67	N	4			IncI2	catA1
kpneumoniae	MGH_59	N	1				aadA2
kpneumoniae	MGH_59	N	1				blaSHV-134
kpneumoniae	MGH_59	N	1				dfrA12
kpneumoniae	MGH_59	N	1				sul1
kpneumoniae	MGH_59	N	2				blaTEM-1
kpneumoniae	MGH_59	N	3				aadA1
kpneumoniae	MGH_59	N	3				blaTEM-1
kpneumoniae	MGH_59	N	4			IncFII(pRSB107)	aac(3)-IId

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	MGH_59	N	4			IncFII(pRSB107)	blaTEM-1
kpneumoniae	MGH_59	N	4			IncFII(pRSB107)	mph(A)
kpneumoniae	MGH_69	N	1	CCBH_10892_plasmid	KF727591.2	IncFII(pKPX1)	blaNDM-1
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	Qnr-B7
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	aac(6)-Ib
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	blaCTX-M-15
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	blaOXA-30
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	catA2
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	strA
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	strB
kpneumoniae	MGH_69	N	2	pHg	CP006662.1	IncR	sul2
kpneumoniae	MGH_69	N	3			IncFIB(K)	mph(A)
kpneumoniae	MGH_69	N	3			IncFIB(K)	tet(A)
ecoli	UCI_66	S	1	pS1400_89	JN796410.1	IncI1	blaCMY-2
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	Qnr-B2
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	aac(6)Ib-cr
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	aadA2
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	aph(3)-Ia
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	blaSHV-134
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	blaTEM-1
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	catA2
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	dfrA18
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	strB
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	sul1
ecloacae	MGH_15	N	1	pEC-IMPQ	EU855788.1	IncHI2A	sul2
ecloacae	MGH_15	N	2			IncR	aadA1
ecloacae	MGH_15	N	2			IncR	blaKPC-3
ecloacae	MGH_15	N	2			IncR	blaOXA-9
ecloacae	MGH_15	N	2			IncR	blaTEM-1
ecloacae	MGH_15	N	2			IncR	floR
ecloacae	MGH_15	N	2			IncR	sul1
ecloacae	MGH_15	N	2			IncR	tet(G)
ecoli	UCI_58	S	1			IncP	aac(3)-VIa
ecoli	UCI_58	S	1			IncP	aadA1
ecoli	UCI_58	S	1			IncP	blaCMY-2
ecoli	UCI_58	S	1			IncP	sul1
ecoli	UCI_58	S	1			IncP	tet(A)
kpneumoniae	MGH_63	N	1				aac(6)-IIc
kpneumoniae	MGH_63	N	1				ere(A)
kpneumoniae	MGH_63	N	2				tet34
kpneumoniae	MGH_63	N	3				tet(D)
kpneumoniae	MGH_63	N	4				blaCTX-M-15
kpneumoniae	MGH_63	N	5				floR
kpneumoniae	MGH_63	N	5				sul2

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	MGH_63	N	6				Qnr-B4
kpneumoniae	MGH_63	N	7				tet(A)
kpneumoniae	MGH_29	N	1			ColRNAI	aac(6)-Ib
kpneumoniae	MGH_29	N	2			IncFIB(K)	aac(3)-IVa
kpneumoniae	MGH_29	N	2			IncFIB(K)	aadA1
kpneumoniae	MGH_29	N	2			IncFIB(K)	aadA2
kpneumoniae	MGH_29	N	2			IncFIB(K)	aph(4)-Ia
kpneumoniae	MGH_29	N	2			IncFIB(K)	blaKPC-2
kpneumoniae	MGH_29	N	2			IncFIB(K)	cmlA1
kpneumoniae	MGH_29	N	2			IncFIB(K)	mph(A)
kpneumoniae	MGH_29	N	2			IncFIB(K)	sul3
kpneumoniae	BWH_15	I	1	pBK31551	JX193301.1	IncN	aac(3)-Ib
kpneumoniae	BWH_15	I	1	pBK31551	JX193301.1	IncN	aph(3)-Ia
kpneumoniae	BWH_15	I	1	pBK31551	JX193301.1	IncN	blaKPC-4
kpneumoniae	BWH_15	I	1	pBK31551	JX193301.1	IncN	blaTEM-1
kpneumoniae	BWH_15	I	1	pBK31551	JX193301.1	IncN	sul1
ecoli	BIDMC_79	S	1			Col156	aadA5
ecoli	BIDMC_79	S	1			Col156	dfrA17
ecoli	BIDMC_79	S	1			Col156	mph(A)
ecoli	BIDMC_79	S	1			Col156	strA
ecoli	BIDMC_79	S	1			Col156	strB
ecoli	BIDMC_79	S	1			Col156	sul1
ecoli	BIDMC_79	S	1			Col156	sul2
ecoli	BIDMC_79	S	1			Col156	tet(A)
ecoli	BIDMC_79	S	2			IncFII	blaTEM-1
kpneumoniae	UCI_37	N	1			IncFIA(HI1)	blaKPC-3
kpneumoniae	UCI_37	N	2				aadA1
kpneumoniae	UCI_37	N	2				blaOXA-9
kpneumoniae	UCI_37	N	2				mph(A)
kpneumoniae	UCI_37	N	2				strA
kpneumoniae	UCI_37	N	2				strB
kpneumoniae	UCI_37	N	2				sul2
ecloacae	BIDMC_8	N	1				Qnr-S1
ecloacae	BIDMC_8	N	1				blaKPC-3
ecloacae	BIDMC_8	N	2			IncFII(pECLA)	blaTEM-1
ecloacae	BIDMC_8	N	2			IncFII(pECLA)	catA2
ecloacae	BIDMC_8	N	2			IncFII(pECLA)	dfrA14
ecloacae	BIDMC_8	N	2			IncFII(pECLA)	strA
ecloacae	BIDMC_8	N	2			IncFII(pECLA)	strB
ecloacae	BIDMC_8	N	2			IncFII(pECLA)	sul2
ecloacae	BIDMC_8	N	2			IncFII(pECLA)	tet(D)
ecloacae	MGH_1	N	1			IncN	aac(6)-Ib
ecloacae	MGH_1	N	1			IncN	aadA1

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	MGH_1	N	1			IncN	blaKPC-2
ecloacae	MGH_1	N	1			IncN	blaOXA-9
ecloacae	MGH_1	N	1			IncN	blaTEM-1
ecloacae	MGH_1	N	1			IncN	blaTEM-122
ecloacae	MGH_1	N	1			IncN	dfrA14
kpneumoniae	BIDMC_13	N	1				aph(3)-Ia
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncR	aac(3)-IVa
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncR	aadA1
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncR	aadA2
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncR	aph(4)-Ia
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncR	blaKPC-3
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncR	cmlA1
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_13	N	2	strain_JM45_plasmid_p1	CP006657.1	IncR	sul3
kpneumoniae	BWH_47	N	1				aadA2
kpneumoniae	BWH_47	N	1				catA1
kpneumoniae	BWH_47	N	1				dfrA12
kpneumoniae	BWH_47	N	1				mph(A)
kpneumoniae	BWH_47	N	1				sul1
kpneumoniae	BWH_47	N	2			ColRNAI	aac(6)-Ib
kpneumoniae	BWH_47	N	2			ColRNAI	blaKPC-3
kpneumoniae	BWH_47	N	2			ColRNAI	blaTEM-1
kpneumoniae	BWH_47	N	3	pKpS90	JX461340.1	IncX3	blaSHV-134
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	aadA1
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	aadA2
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	blaTEM-1
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	cmlA1
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	dfrA12
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	strA
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	strB
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	sul2
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	sul3
ecoli	BIDMC_74	S	1			IncFIB(AP001918)	tet(A)
kpneumoniae	BIDMC_7B	N	1			IncFIB(K)	catA1
kpneumoniae	BIDMC_7B	N	2	pBK15692	KC845573.1	IncI2	blaTEM-1
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	aadA5
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	blaTEM-1
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	dfrA17
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	mph(A)
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	strA

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	strB
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	sul1
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	sul2
ecoli	BIDMC_72	S	1			IncFIB(AP001918)	tet(A)
ecloacae	BWH_29	S	1			IncR	Qnr-S1
ecloacae	BWH_29	S	1			IncR	aadA2
ecloacae	BWH_29	S	1			IncR	dfrA12
ecloacae	BWH_29	S	1			IncR	floR
ecloacae	BWH_29	S	1			IncR	strA
ecloacae	BWH_29	S	1			IncR	strB
ecloacae	BWH_29	S	1			IncR	sul1
ecloacae	BWH_29	S	1			IncR	sul2
ecloacae	BWH_29	S	1			IncR	tet(A)
ecloacae	BIDMC_66	N	1	pK29	EF382672.1		blaKPC-4
ecloacae	BIDMC_66	N	1	pK29	EF382672.1		tet(B)
ecloacae	BIDMC_66	N	2				aadA2
ecloacae	BIDMC_66	N	2				aadB
ecloacae	BIDMC_66	N	2				blaACT-7
ecloacae	BIDMC_66	N	2				blaIMP-24
ecloacae	BIDMC_66	N	2				cmlA1
ecloacae	BIDMC_66	N	2				mph(A)
ecloacae	BIDMC_66	N	2				strB
ecloacae	BIDMC_66	N	2				sul1
smarcesens	BIDMC_80	N	1				tet34
smarcesens	BIDMC_80	N	2				arna
smarcesens	BIDMC_80	N	2				bcra
smarcesens	BIDMC_80	N	2				qnrb
smarcesens	BIDMC_80	N	3				ksga
smarcesens	BIDMC_80	N	4				bl1_sm
smarcesens	BIDMC_80	N	5				blaSME-2
smarcesens	BIDMC_80	N	6				aac(6)-Ic
smarcesens	BIDMC_80	N	6				baca
smarcesens	BIDMC_80	N	7				Qnr-S1
smarcesens	BIDMC_80	N	7				blaCTX-M-15
kpneumoniae	MGH_70	S	1				blaTEM-1
kpneumoniae	MGH_70	S	1				catA1
kpneumoniae	MGH_70	S	1				strA
kpneumoniae	MGH_70	S	1				strB
kpneumoniae	MGH_70	S	1				sul2
kpneumoniae	MGH_70	S	1				tet(D)
ecloacae	UCI_35	N	1			IncFIA(HI1)	dfrA22
ecloacae	UCI_35	N	1			IncFIA(HI1)	strA
ecloacae	UCI_35	N	1			IncFIA(HI1)	sul1
ecloacae	UCI_35	N	1			IncFIA(HI1)	tet(D)

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	ARR-3
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	aac(6)Ib-cr
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	aph(3)-Ia
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	blaKPC-4
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	blaOXA-30
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	blaTEM-1
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	catB3
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	dfrA15
ecloacae	BWH_27	N	1			IncFIB(pHCM2)	sul1
ecloacae	BWH_27	N	2				Qnr-S1
kpneumoniae	UCI_21	N	1	plasmid_9_strain_9	FJ223607.1	IncN	blaKPC-2
kpneumoniae	UCI_21	N	2	pQ1-1	HM371192.1		strB
kpneumoniae	UCI_21	N	2	pQ1-1	HM371192.1		sul2
kpneumoniae	UCI_21	N	3			ColRNAI	aac(6)-Ib
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	aac(6)Ib-cr
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	aadA5
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	blaOXA-30
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	blaTEM-1
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	catA1
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	catB3
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	dfrA17
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	erm(B)
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	mph(A)
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	strA
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	strB
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	sul1
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	sul2
ecoli	BIDMC_71	S	1	pRSB225	JX127248.1	IncFIB(AP001918)	tet(B)
eaerogenes	MGH_62	S	1				baca
eaerogenes	MGH_62	S	2				CMY-48
eaerogenes	MGH_62	S	2				arna
eaerogenes	MGH_62	S	2				bcr
eaerogenes	MGH_62	S	2				bcra
eaerogenes	MGH_62	S	2				mdfa
eaerogenes	MGH_62	S	2				oqxB
eaerogenes	MGH_62	S	2				tet34
eaerogenes	MGH_62	S	3				fosA
eaerogenes	MGH_62	S	3				ksga
kpneumoniae	BIDMC_2A	N	1				blaKPC-3
kpneumoniae	BIDMC_2A	N	2	pNJST258C1	CP006922.1	IncI2	blaTEM-1
ecoli	BIDMC_38	S	1			IncFIA	aadA5
ecoli	BIDMC_38	S	1			IncFIA	blaTEM-1
ecoli	BIDMC_38	S	1			IncFIA	dfrA17

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ecoli	BIDMC_38	S	1			IncFIA	mph(A)
ecoli	BIDMC_38	S	1			IncFIA	sul1
ecoli	BIDMC_38	S	1			IncFIA	tet(A)
kpneumoniae	UCI_44	S	1			IncX3	mph(A)
kpneumoniae	UCI_44	S	2				blaTEM-1
kpneumoniae	UCI_44	S	2				strA
kpneumoniae	UCI_44	S	2				strB
kpneumoniae	UCI_44	S	2				sul2
kpneumoniae	UCI_44	S	3				aadA1
kpneumoniae	UCI_44	S	3				blaOXA-9
eaerogenes	MGH_61	S	1				CMY-48
eaerogenes	MGH_61	S	1				bcra
eaerogenes	MGH_61	S	1				tet34
eaerogenes	MGH_61	S	2				bcra
eaerogenes	MGH_61	S	2				fosA
eaerogenes	MGH_61	S	2				ksga
eaerogenes	MGH_61	S	3				baca
eaerogenes	MGH_61	S	3				bcr
eaerogenes	MGH_61	S	3				mdfa
eaerogenes	MGH_61	S	3				oqxB
eaerogenes	MGH_61	S	4				arna
abaumanii	BIDMC_56	N	1				aph3ia
abaumanii	BIDMC_56	N	1				strA
abaumanii	BIDMC_56	N	1				strB
abaumanii	BIDMC_56	N	1				tet(B)
abaumanii	BIDMC_56	N	2				aac(6)Ib-cr
abaumanii	BIDMC_56	N	2				aadA1
abaumanii	BIDMC_56	N	2				armA
abaumanii	BIDMC_56	N	2				bcra
abaumanii	BIDMC_56	N	2				blaOXA-113
abaumanii	BIDMC_56	N	2				blaTEM-1
abaumanii	BIDMC_56	N	2				catB3
abaumanii	BIDMC_56	N	2				mph(E)
abaumanii	BIDMC_56	N	2				msr(E)
abaumanii	BIDMC_56	N	2				sul1
ecloacae	MGH_10	N	1				blaNDM-1
ecloacae	MGH_10	N	1				sul1
ecloacae	MGH_10	N	2			IncR	aac(3)-IId
ecloacae	MGH_10	N	2			IncR	aac(6)-Ib
ecloacae	MGH_10	N	2			IncR	aac(6)Ib-cr
ecloacae	MGH_10	N	2			IncR	aadA1
ecloacae	MGH_10	N	2			IncR	aadA2
ecloacae	MGH_10	N	2			IncR	armA
ecloacae	MGH_10	N	2			IncR	blaCTX-M-15
ecloacae	MGH_10	N	2			IncR	blaOXA-30

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	MGH_10	N	2			IncR	blaOXA-9
ecloacae	MGH_10	N	2			IncR	blaTEM-1
ecloacae	MGH_10	N	2			IncR	dfrA12
ecloacae	MGH_10	N	2			IncR	mph(E)
ecloacae	MGH_10	N	2			IncR	msr(E)
ecloacae	MGH_10	N	2			IncR	sul1
ecloacae	MGH_10	N	3				Qnr-S1
ecoli	BIDMC_15	N	1			IncN	blaTEM-1
ecoli	BIDMC_15	N	1			IncN	dfrA14
ecoli	BIDMC_15	N	2				mph(A)
ecoli	BIDMC_15	N	3	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_15	N	3	pEC-IMP	EU855787.1	IncHI2A	blaKPC-2
ecoli	BIDMC_15	N	3	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_15	N	3	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_15	N	3	pEC-IMP	EU855787.1	IncHI2A	sul2
koxytoca	MGH_27	N	1			IncN	aac(6)-Ib
koxytoca	MGH_27	N	1			IncN	aadA1
koxytoca	MGH_27	N	1			IncN	blaKPC-3
koxytoca	MGH_27	N	1			IncN	blaOXA-9
koxytoca	MGH_27	N	1			IncN	blaTEM-1
koxytoca	MGH_27	N	1			IncN	dfrA14
koxytoca	MGH_27	N	1			IncN	strA
koxytoca	MGH_27	N	1			IncN	strB
koxytoca	MGH_27	N	1			IncN	sul2
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	Qnr-B17
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	aac(3)-IIa
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	aac(6)Ib-cr
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	blaCTX-M-15
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	blaOXA-30
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	blaTEM-1
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	strA
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	strB
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	sul2
kpneumoniae	MGH_35	I	1	pKPX-2	AP012056.1	IncFIA(HI1)	tet(A)
kpneumoniae	BIDMC_51	S	1			IncR	blaTEM-1
kpneumoniae	BIDMC_51	S	1			IncR	dfrA26
kpneumoniae	BIDMC_51	S	1			IncR	sul2
kpneumoniae	BWH_41	S	1			IncFIB(K)	aadA2
kpneumoniae	BWH_41	S	1			IncFIB(K)	aph(3)-Ia
kpneumoniae	BWH_41	S	1			IncFIB(K)	catA1
kpneumoniae	BWH_41	S	1			IncFIB(K)	dfrA12
kpneumoniae	BWH_41	S	1			IncFIB(K)	mph(A)
kpneumoniae	BWH_41	S	1			IncFIB(K)	sul1

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	BIDMC_60	N	1				aadA2
kpneumoniae	BIDMC_60	N	1				aph(3)-Ia
kpneumoniae	BIDMC_60	N	1				catA1
kpneumoniae	BIDMC_60	N	1				dfrA12
kpneumoniae	BIDMC_60	N	1				mph(A)
kpneumoniae	BIDMC_60	N	1				sul1
kpneumoniae	BIDMC_60	N	2	pAAC154	JF828150.1	ColRNAI	aac(6)-Ib
kpneumoniae	BIDMC_60	N	3			IncFIB(pQil)	blaKPC-2
kpneumoniae	BIDMC_60	N	3			IncFIB(pQil)	blaTEM-1
kpneumoniae	MGH_65	N	1			IncHI1B	ARR-2
kpneumoniae	MGH_65	N	1			IncHI1B	aac(6)-IIc
kpneumoniae	MGH_65	N	1			IncHI1B	aadA1
kpneumoniae	MGH_65	N	1			IncHI1B	blaOXA-10
kpneumoniae	MGH_65	N	1			IncHI1B	cmlA1
kpneumoniae	MGH_65	N	1			IncHI1B	ere(A)
kpneumoniae	MGH_65	N	1			IncHI1B	floR
kpneumoniae	MGH_65	N	1			IncHI1B	sul1
kpneumoniae	MGH_65	N	1			IncHI1B	sul2
kpneumoniae	MGH_65	N	1			IncHI1B	tet(A)
kpneumoniae	MGH_65	N	2				blaSHV-134
kpneumoniae	MGH_65	N	2				tet(D)
kpneumoniae	MGH_65	N	3				Qnr-B4
kpneumoniae	MGH_39	N	1				aac(6)-Ib
kpneumoniae	MGH_39	N	1				aadA1
kpneumoniae	MGH_39	N	1				blaKPC-3
kpneumoniae	MGH_39	N	1				blaOXA-9
kpneumoniae	MGH_39	N	1				blaTEM-1
ecloacae	MGH_53	S	1				aac(6)-Ib
ecloacae	MGH_2	N	1			IncA/C	ARR-3
ecloacae	MGH_2	N	1			IncA/C	aac(3)-VIa
ecloacae	MGH_2	N	1			IncA/C	aac(6)Ib-cr
ecloacae	MGH_2	N	1			IncA/C	aadA1
ecloacae	MGH_2	N	1			IncA/C	aph(3)-Ia
ecloacae	MGH_2	N	1			IncA/C	blaKPC-4
ecloacae	MGH_2	N	1			IncA/C	blaOXA-30
ecloacae	MGH_2	N	1			IncA/C	blaTEM-1
ecloacae	MGH_2	N	1			IncA/C	catB3
ecloacae	MGH_2	N	1			IncA/C	mph(A)
ecloacae	MGH_2	N	1			IncA/C	sul1
ecloacae	MGH_2	N	2	pHCM2	AL513384.1	IncFIB(pHCM2)	sul1
ecloacae	MGH_2	N	3				Qnr-S1
kpneumoniae	UCI_25	N	1			IncFIB(K)	strA
kpneumoniae	UCI_25	N	1			IncFIB(K)	strB
kpneumoniae	UCI_25	N	1			IncFIB(K)	sul2

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	UCI_25	N	1			IncFIB(K)	tet(D)
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	aadA5
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	blaKPC-3
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	dfrA17
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	strA
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	strB
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	sul1
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	sul2
ecoli	BWH_34	N	1	pEK499	EU935739.1	IncFIA	tet(A)
ecloacae	MGH_13	N	1				aac(6)-Ib
ecloacae	MGH_13	N	1				aadA1
ecloacae	MGH_13	N	1				blaKPC-3
ecloacae	MGH_13	N	1				blaOXA-9
ecloacae	MGH_13	N	1				blaTEM-1
kpneumoniae	BIDMC_12A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	blaKPC-3
kpneumoniae	BIDMC_12A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	blaTEM-1
kpneumoniae	BIDMC_12A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	strA
kpneumoniae	BIDMC_12A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	strB
kpneumoniae	BIDMC_12A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	sul2
kpneumoniae	UCI_14	S	1			IncFIA(HI1)	catA2
kpneumoniae	UCI_14	S	1			IncFIA(HI1)	strA
kpneumoniae	UCI_14	S	1			IncFIA(HI1)	strB
kpneumoniae	UCI_14	S	1			IncFIA(HI1)	sul2
kpneumoniae	UCI_14	S	2				aac(6)-Ib
ecoli	BIDMC_43B	N	1	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_43B	N	1	pEC-IMP	EU855787.1	IncHI2A	blaKPC-2
ecoli	BIDMC_43B	N	1	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_43B	N	1	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_43B	N	1	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_43B	N	1	pEC-IMP	EU855787.1	IncHI2A	sul2
kpneumoniae	UCI_61	N	1				blaKPC-2
kpneumoniae	UCI_61	N	2				aadA2
kpneumoniae	UCI_61	N	2				dfrA12
kpneumoniae	UCI_61	N	2				mph(A)
kpneumoniae	UCI_61	N	2				sul1
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	aadA5
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	blaKPC-3
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	dfrA17
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	strA
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	strB
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	sul1
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	sul2

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecoli	BIDMC_64	N	1	pEK499	EU935739.1	IncFIA	tet(A)
kpneumoniae	BIDMC_32	N	1			IncFIB(K)	catA1
kpneumoniae	BIDMC_32	N	2				aac(3)-IVa
kpneumoniae	BIDMC_32	N	2				aadA1
kpneumoniae	BIDMC_32	N	2				aadA2
kpneumoniae	BIDMC_32	N	2				aph(4)-Ia
kpneumoniae	BIDMC_32	N	2				cmlA1
kpneumoniae	BIDMC_32	N	2				sul3
kpneumoniae	BIDMC_32	N	3				blaKPC-3
kpneumoniae	BIDMC_32	N	4				Qnr-S1
kpneumoniae	BIDMC_7A	N	1				catA1
kpneumoniae	BIDMC_7A	N	2			IncI2	blaTEM-1
kpneumoniae	BIDMC_46A	I	1			IncFIB(K)	aadA2
kpneumoniae	BIDMC_46A	I	1			IncFIB(K)	aadB
kpneumoniae	BIDMC_46A	I	1			IncFIB(K)	catB3
kpneumoniae	BIDMC_46A	I	1			IncFIB(K)	dfrA18
kpneumoniae	BIDMC_46A	I	1			IncFIB(K)	sul1
kpneumoniae	BIDMC_46A	I	2			IncFIB(pQil)	blaSHV-134
kpneumoniae	BIDMC_46A	I	2			IncFIB(pQil)	blaTEM-1
ecoli	BIDMC_19A	N	1				blaKPC-2
ecoli	BIDMC_19A	N	2	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_19A	N	2	pEC-IMP	EU855787.1	IncHI2A	blaKPC-2
ecoli	BIDMC_19A	N	2	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_19A	N	2	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_19A	N	2	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_19A	N	2	pEC-IMP	EU855787.1	IncHI2A	sul2
ecoli	BIDMC_19A	N	3				blaKPC-2
ecoli	BIDMC_19A	N	3				blaTEM-1
ecoli	BIDMC_19A	N	3				dfrA14
ecoli	BIDMC_19A	N	3				mph(A)
kpneumoniae	MGH_60	S	1			IncFIB(K)	tet(D)
kpneumoniae	MGH_60	S	2				sul1
kpneumoniae	BIDMC_18B	I	1				aac(6)-Ib
kpneumoniae	BIDMC_18B	I	2			IncR	aac(3)-IVa
kpneumoniae	BIDMC_18B	I	2			IncR	aadA1
kpneumoniae	BIDMC_18B	I	2			IncR	aadA2
kpneumoniae	BIDMC_18B	I	2			IncR	aph(4)-Ia
kpneumoniae	BIDMC_18B	I	2			IncR	blaKPC-2
kpneumoniae	BIDMC_18B	I	2			IncR	cmlA1
kpneumoniae	BIDMC_18B	I	2			IncR	sul3
kpneumoniae	BIDMC_18B	I	3	pKpS90	JX461340.1	IncX3	aac(6)-Ib
kpneumoniae	BIDMC_18B	I	3	pKpS90	JX461340.1	IncX3	blaSHV-134
kpneumoniae	BIDMC_18B	I	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	BIDMC_18B	I	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_18B	I	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_18B	I	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_18B	I	4	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_18B	I	5				aac(6)-Ib
cfreundii	MGH_56	S	1			ColRNAI	aac(6)-Ib
cfreundii	MGH_56	S	2				Qnr-B28
cfreundii	MGH_56	S	2				arna
cfreundii	MGH_56	S	2				baca
cfreundii	MGH_56	S	2				bcr
cfreundii	MGH_56	S	2				bcra
cfreundii	MGH_56	S	2				mdfa
cfreundii	MGH_56	S	2				tet34
cfreundii	MGH_56	S	3			IncA/C2	aadB
cfreundii	MGH_56	S	3			IncA/C2	dfrA14
cfreundii	MGH_56	S	3			IncA/C2	sul1
cfreundii	MGH_56	S	4				bcra
cfreundii	MGH_56	S	5				blaCFE-1
cfreundii	MGH_56	S	5				ksga
eaerogenes	MGH_78	S	1				bcra
eaerogenes	MGH_78	S	1				fosA
eaerogenes	MGH_78	S	1				ksga
eaerogenes	MGH_78	S	2				CMY-48
eaerogenes	MGH_78	S	2				arna
eaerogenes	MGH_78	S	2				baca
eaerogenes	MGH_78	S	2				bcr
eaerogenes	MGH_78	S	2				bcra
eaerogenes	MGH_78	S	2				mdfa
eaerogenes	MGH_78	S	2				oqxB
eaerogenes	MGH_78	S	2				tet34
ecloacae	MGH_9	S	1	pHCM2	AL513384.1	IncFIB(pHCM2)	dfrA15
ecloacae	MGH_9	S	1	pHCM2	AL513384.1	IncFIB(pHCM2)	sul1
ecloacae	MGH_9	S	2				Qnr-S1
ecloacae	MGH_6	N	1			IncN	aac(6)-Ib
ecloacae	MGH_6	N	1			IncN	aadA1
ecloacae	MGH_6	N	1			IncN	blaKPC-2
ecloacae	MGH_6	N	1			IncN	blaOXA-9
ecloacae	MGH_6	N	1			IncN	blaTEM-1
ecloacae	MGH_6	N	1			IncN	dfrA14
kpneumoniae	MGH_47	N	1			IncFIB(K)	aadB
kpneumoniae	MGH_47	N	1			IncFIB(K)	catA1
kpneumoniae	MGH_47	N	1			IncFIB(K)	catB3
kpneumoniae	MGH_47	N	1			IncFIB(K)	sul1

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	BIDMC_12C	N	1	pBK30683	KF954760.1	IncFII(p14)	blaKPC-3
kpneumoniae	BIDMC_12C	N	1	pBK30683	KF954760.1	IncFII(p14)	blaTEM-1
kpneumoniae	BIDMC_12C	N	1	pBK30683	KF954760.1	IncFII(p14)	strA
kpneumoniae	BIDMC_12C	N	1	pBK30683	KF954760.1	IncFII(p14)	strB
kpneumoniae	BIDMC_12C	N	1	pBK30683	KF954760.1	IncFII(p14)	sul2
kpneumoniae	UCI_55	N	1				aph(3)-Ia
kpneumoniae	UCI_55	N	2	pKpS90	JX461340.1	IncX3	blaSHV-134
kpneumoniae	UCI_55	N	3				aac(6)-Ib
kpneumoniae	UCI_55	N	3				aadA1
kpneumoniae	UCI_55	N	3				blaOXA-9
kpneumoniae	UCI_55	N	4				blaTEM-1
kpneumoniae	UCI_55	N	4				strA
kpneumoniae	UCI_55	N	4				strB
kpneumoniae	UCI_55	N	4				sul2
kpneumoniae	UCI_55	N	5				blaKPC-3
kpneumoniae	UCI_55	N	6	pNJST258C1	CP006922.1	IncFII(p14)	mph(A)
kpneumoniae	BIDMC_1	N	1	pNE1280	JQ837276.1	IncL/M(pMU407)	Qnr-S1
kpneumoniae	BIDMC_1	N	2	pKpS90	JX461340.1		blaKPC-3
kpneumoniae	BIDMC_1	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_1	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aph(3)-Ia
kpneumoniae	BIDMC_1	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_1	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_1	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_1	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
ecoli	BIDMC_9	N	1				blaKPC-2
ecoli	BIDMC_9	N	2			IncN	blaTEM-1
ecoli	BIDMC_9	N	2			IncN	dfrA14
ecoli	BIDMC_9	N	2			IncN	mph(A)
ecoli	BIDMC_9	N	3	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_9	N	3	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_9	N	3	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_9	N	3	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_9	N	3	pEC-IMP	EU855787.1	IncHI2A	sul2
kpneumoniae	UCI_43	S	1				blaSHV-134
kpneumoniae	UCI_43	S	1				mph(A)
kpneumoniae	UCI_43	S	2	pNJST258C1	CP006922.1		aac(6)-Ib
kpneumoniae	UCI_43	S	2	pNJST258C1	CP006922.1		aadA1
kpneumoniae	UCI_43	S	2	pNJST258C1	CP006922.1		blaOXA-9
kpneumoniae	UCI_1	N	1	pNJST258N3	CP006925.1		aac(6)-Ib
kpneumoniae	UCI_1	N	2			IncFIB(K)	blaKPC-3
kpneumoniae	UCI_1	N	2			IncFIB(K)	catA1
kpneumoniae	UCI_1	N	3			IncI2	blaTEM-1
ecloacae	BIDMC_33A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	aac(6)-Ib

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	BIDMC_33A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	aadA1
ecloacae	BIDMC_33A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	blaKPC-3
ecloacae	BIDMC_33A	N	1	pBK30683	KF954760.1	IncFIA(HI1)	dfrA14
ecoli	UCI_51	N	1				blaTEM-1
ecoli	UCI_51	N	1				strA
ecoli	UCI_51	N	1				strB
ecoli	UCI_51	N	1				sul2
ecoli	UCI_51	N	2			IncFIA	tet(A)
ecoli	UCI_51	N	3				aadA5
ecoli	UCI_51	N	3				dfrA17
ecoli	UCI_51	N	3				mph(A)
ecoli	UCI_51	N	3				sul1
kpneumoniae	BIDMC_34	N	1	pKpS90	JX461340.1	IncX3	blaSHV-134
kpneumoniae	BIDMC_34	N	2				aac(3)-IVa
kpneumoniae	BIDMC_34	N	2				aadA2
kpneumoniae	BIDMC_34	N	2				aph(4)-Ia
kpneumoniae	BIDMC_34	N	2				blaKPC-2
kpneumoniae	BIDMC_34	N	2				cmlA1
kpneumoniae	BIDMC_34	N	2				sul3
kpneumoniae	BIDMC_34	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_34	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_34	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_34	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_34	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_34	N	4			ColRNAI	aac(6)-Ib
ecoli	BIDMC_82	N	1				aac(6)-IIc
ecoli	BIDMC_82	N	1				ere(A)
ecoli	BIDMC_82	N	1				sul1
ecoli	BIDMC_82	N	2				dfrA14
ecoli	BIDMC_82	N	3				mph(A)
ecoli	BIDMC_82	N	4				sul2
ecoli	BIDMC_82	N	5				blaKPC-2
ecoli	BIDMC_82	N	6			IncB/O/K/Z	blaCTX-M-14
ecoli	BIDMC_82	N	7				blaTEM-1
ecoli	BIDMC_82	N	8				blaSHV-134
kpneumoniae	UCI_19	N	1	pKpQIL	GU595196.1	IncFIB(pQil)	aac(6)-Ib
kpneumoniae	UCI_19	N	1	pKpQIL	GU595196.1	IncFIB(pQil)	blaKPC-2
kpneumoniae	UCI_19	N	1	pKpQIL	GU595196.1	IncFIB(pQil)	blaTEM-1
ecoli	BIDMC_19C	N	1			IncN	blaKPC-2
ecoli	BIDMC_19C	N	1			IncN	blaTEM-1
ecoli	BIDMC_19C	N	1			IncN	dfrA14
ecoli	BIDMC_19C	N	1			IncN	mph(A)
ecoli	BIDMC_19C	N	2	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_19C	N	2	pEC-IMP	EU855787.1	IncHI2A	blaKPC-2

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ecoli	BIDMC_19C	N	2	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_19C	N	2	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_19C	N	2	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_19C	N	2	pEC-IMP	EU855787.1	IncHI2A	sul2
kpneumoniae	UCI_4	S	1			IncFIB(K)	aadA1
kpneumoniae	UCI_4	S	1			IncFIB(K)	sul1
kpneumoniae	UCI_4	S	1			IncFIB(K)	tet(D)
kpneumoniae	UCI_63	N	1				blaCMY-2
kpneumoniae	UCI_63	N	1				sul1
kpneumoniae	UCI_63	N	2				floR
kpneumoniae	UCI_63	N	2				tet(A)
kpneumoniae	UCI_63	N	3				aac(6)-Ib
kpneumoniae	UCI_63	N	4				strB
kpneumoniae	UCI_63	N	4				sul2
kpneumoniae	UCI_63	N	5			IncN	aph(3)-Ia
kpneumoniae	UCI_63	N	5			IncN	blaKPC-2
kpneumoniae	UCI_63	N	5			IncN	blaTEM-1
kpneumoniae	UCI_63	N	6				aac(6)-Ib
ecoli	BIDMC_3	N	1				blaKPC-2
ecoli	BIDMC_3	N	2			IncN	blaTEM-1
ecoli	BIDMC_3	N	2			IncN	dfrA14
ecoli	BIDMC_3	N	2			IncN	mph(A)
ecoli	BIDMC_3	N	3	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_3	N	3	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_3	N	3	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_3	N	3	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_3	N	3	pEC-IMP	EU855787.1	IncHI2A	sul2
kpneumoniae	MGH_67	N	1				blaKPC-2
kpneumoniae	MGH_67	N	2	pAAC154	JF828150.1	ColRNAI	aac(6)-Ib
kpneumoniae	MGH_67	N	3				blaTEM-1
kpneumoniae	MGH_67	N	4				aadA2
kpneumoniae	MGH_67	N	4				aph(3)-Ia
kpneumoniae	MGH_67	N	4				catA1
kpneumoniae	MGH_67	N	4				dfrA12
kpneumoniae	MGH_67	N	4				mph(A)
kpneumoniae	MGH_67	N	4				sul1
ecoli	BIDMC_49B	S	1			IncFIB(AP001918)	dfrA5
ecoli	BIDMC_49B	S	1			IncFIB(AP001918)	tet(A)
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aac(3)-IVa
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA1
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aph(3)-Ia
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aph(4)-Ia

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kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	cmlA1
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_5	N	1	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul3
kpneumoniae	BIDMC_5	N	2	pBK15692	KC845573.1	IncI2	blaKPC-3
kpneumoniae	BIDMC_5	N	2	pBK15692	KC845573.1	IncI2	blaTEM-1
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	aadA5
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	blaKPC-3
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	dfrA17
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	strA
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	strB
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	sul1
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	sul2
ecoli	BWH_24	I	1	pEK499	EU935739.1	IncFIA	tet(A)
ecloacae	MGH_26	S	1	pHCM2	AL513384.1	IncFIB(pHCM2)	dfrA15
ecloacae	MGH_26	S	1	pHCM2	AL513384.1	IncFIB(pHCM2)	sul1
kpneumoniae	BIDMC_53	I	1			IncFIB(pQil)	blaSHV-134
kpneumoniae	BIDMC_53	I	1			IncFIB(pQil)	blaTEM-1
kpneumoniae	BIDMC_53	I	2			IncFIB(K)	aadA2
kpneumoniae	BIDMC_53	I	2			IncFIB(K)	aadB
kpneumoniae	BIDMC_53	I	2			IncFIB(K)	catB3
kpneumoniae	BIDMC_53	I	2			IncFIB(K)	dfrA18
kpneumoniae	BIDMC_53	I	2			IncFIB(K)	sul1
cfreundii	UCI_32	S	1				baca
cfreundii	UCI_32	S	1				bcra
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	aadA5
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	blaKPC-3
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	dfrA17
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	strA
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	strB
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	sul1
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	sul2
ecoli	BIDMC_58	N	1	pEK499	EU935739.1	IncFIA	tet(A)
ecoli	BIDMC_63	S	1			IncFIB(AP001918)	blaTEM-1
kpneumoniae	BWH_2	N	1			IncR	aac(6)-Ib
kpneumoniae	BWH_2	N	1			IncR	aadA1
kpneumoniae	BWH_2	N	1			IncR	blaCTX-M-15
kpneumoniae	BWH_2	N	1			IncR	blaOXA-9
kpneumoniae	BWH_2	N	1			IncR	blaTEM-1
kpneumoniae	BWH_2	N	2			IncL/M(pOXA-48)	blaOXA-48

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kpneumoniae	BWH_2	N	3			IncFIA(HI1)	aac(3)-IIa
kpneumoniae	BWH_2	N	3			IncFIA(HI1)	aac(6)Ib-cr
kpneumoniae	BWH_2	N	3			IncFIA(HI1)	blaOXA-30
ecoli	BWH_40	I	1			IncFIB(AP001918)	aadA5
ecoli	BWH_40	I	1			IncFIB(AP001918)	blaCTX-M-15
ecoli	BWH_40	I	1			IncFIB(AP001918)	dfrA17
ecoli	BWH_40	I	1			IncFIB(AP001918)	mph(A)
ecoli	BWH_40	I	1			IncFIB(AP001918)	sul1
ecoli	BWH_40	I	1			IncFIB(AP001918)	tet(B)
kpneumoniae	MGH_51	N	1				aac(6)-Ib
kpneumoniae	MGH_51	N	2				aac(6)-Ib
kpneumoniae	MGH_51	N	3			IncFIB(K)	aadA2
kpneumoniae	MGH_51	N	3			IncFIB(K)	aph(3)-Ia
kpneumoniae	MGH_51	N	3			IncFIB(K)	catA1
kpneumoniae	MGH_51	N	3			IncFIB(K)	dfrA12
kpneumoniae	MGH_51	N	3			IncFIB(K)	mph(A)
kpneumoniae	MGH_51	N	3			IncFIB(K)	sul1
kpneumoniae	MGH_51	N	4	pKpS90	JX461340.1	IncX3	blaSHV-134
kpneumoniae	MGH_51	N	5				aac(6)-Ib
kpneumoniae	MGH_51	N	6			IncFIB(pQil)	blaKPC-2
kpneumoniae	MGH_51	N	6			IncFIB(pQil)	blaTEM-1
ecoli	MGH_58	S	1			IncFIB(AP001918)	blaTEM-1
ecoli	MGH_58	S	1			IncFIB(AP001918)	dfrA14
ecoli	MGH_58	S	1			IncFIB(AP001918)	mph(A)
ecoli	MGH_58	S	1			IncFIB(AP001918)	strA
ecoli	MGH_58	S	1			IncFIB(AP001918)	strB
ecoli	MGH_58	S	1			IncFIB(AP001918)	tet(B)
ecoli	MGH_58	S	2			IncB/O/K/Z	sul2
ecoli	BIDMC_43A	I	1	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_43A	I	1	pEC-IMP	EU855787.1	IncHI2A	blaKPC-2
ecoli	BIDMC_43A	I	1	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_43A	I	1	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_43A	I	1	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_43A	I	1	pEC-IMP	EU855787.1	IncHI2A	sul2
cspecies	MGH_55	N	1				arna
cspecies	MGH_55	N	1				baca
cspecies	MGH_55	N	1				bcr
cspecies	MGH_55	N	1				bcra
cspecies	MGH_55	N	1				bl2b_ula
cspecies	MGH_55	N	1				ksga
cspecies	MGH_55	N	1				mdfa
cspecies	MGH_55	N	1				oqxB
cspecies	MGH_55	N	1				tet34
cspecies	MGH_55	N	2				ARR-3

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
cspecies	MGH_55	N	2				aac(3)-Ib
cspecies	MGH_55	N	2				aac(6)Ib-cr
cspecies	MGH_55	N	2				blaKPC-4
cspecies	MGH_55	N	2				blaOXA-30
cspecies	MGH_55	N	2				blaTEM-1
cspecies	MGH_55	N	2				catB3
cspecies	MGH_55	N	2				sul1
ecoli	UCI_57	S	1				blaCMY-2
ecoli	UCI_57	S	2				aac(3)-VIa
ecoli	UCI_57	S	2				aadA1
ecoli	UCI_57	S	2				sul1
ecoli	UCI_57	S	2				tet(A)
eaerogenes	UCI_15	N	1				aadA5
eaerogenes	UCI_15	N	1				dfrA17
eaerogenes	UCI_15	N	1				mph(A)
eaerogenes	UCI_15	N	1				strB
eaerogenes	UCI_15	N	1				sul1
eaerogenes	UCI_15	N	1				sul2
eaerogenes	UCI_15	N	1				tet(A)
eaerogenes	UCI_15	N	2			IncFIB(AP001918)	aac(3)-IId
eaerogenes	UCI_15	N	2			IncFIB(AP001918)	blaTEM-1
ecoli	BIDMC_17A	N	1				blaSHV-134
ecoli	BIDMC_17A	N	2			IncN	blaTEM-1
ecoli	BIDMC_17A	N	2			IncN	dfrA14
ecoli	BIDMC_17A	N	2			IncN	mph(A)
ecoli	BIDMC_17A	N	3				blaKPC-2
ecoli	BIDMC_17A	N	4				blaSHV-134
ecoli	BIDMC_17A	N	5	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_17A	N	5	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_17A	N	5	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_17A	N	5	pEC-IMP	EU855787.1	IncHI2A	sul2
kpneumoniae	BIDMC_47	S	1			IncFIA(HI1)	strA
kpneumoniae	BIDMC_47	S	1			IncFIA(HI1)	strB
kpneumoniae	BIDMC_47	S	1			IncFIA(HI1)	sul2
kpneumoniae	MGH_71	N	1			IncFIB(K)	blaKPC-2
kpneumoniae	MGH_71	N	1			IncFIB(K)	blaTEM-1
kpneumoniae	MGH_71	N	2	pEA1509_A	FO203354.1	IncA/C2	floR
kpneumoniae	MGH_71	N	2	pEA1509_A	FO203354.1	IncA/C2	sul2
kpneumoniae	MGH_71	N	3				ARR-2
kpneumoniae	MGH_71	N	3				aadA1
kpneumoniae	MGH_71	N	3				blaOXA-10
kpneumoniae	MGH_71	N	3				cmlA1
kpneumoniae	MGH_71	N	3				sul1

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecoli	UCI_65	S	1			IncFII(pRSB107)	aac(3)-IId
ecoli	UCI_65	S	1			IncFII(pRSB107)	aadA5
ecoli	UCI_65	S	1			IncFII(pRSB107)	blaTEM-1
ecoli	UCI_65	S	1			IncFII(pRSB107)	dfrA17
ecoli	UCI_65	S	1			IncFII(pRSB107)	mph(A)
ecoli	UCI_65	S	1			IncFII(pRSB107)	strA
ecoli	UCI_65	S	1			IncFII(pRSB107)	strB
ecoli	UCI_65	S	1			IncFII(pRSB107)	sul1
ecoli	UCI_65	S	1			IncFII(pRSB107)	sul2
ecoli	UCI_65	S	1			IncFII(pRSB107)	tet(A)
kpneumoniae	BIDMC_18A	N	1			IncR	aac(3)-IVa
kpneumoniae	BIDMC_18A	N	1			IncR	aadA2
kpneumoniae	BIDMC_18A	N	1			IncR	aph(4)-Ia
kpneumoniae	BIDMC_18A	N	1			IncR	blaKPC-2
kpneumoniae	BIDMC_18A	N	1			IncR	cmlA1
kpneumoniae	BIDMC_18A	N	1			IncR	sul3
kpneumoniae	BIDMC_18A	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_18A	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_18A	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_18A	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_18A	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_23	S	1			IncR	aadA1
kpneumoniae	BIDMC_23	S	1			IncR	sul1
ecoli	BIDMC_78	S	1			IncFII	blaTEM-1
kpneumoniae	BIDMC_16	N	1			IncI2	blaTEM-1
kpneumoniae	BIDMC_16	N	2			ColRNAI	aac(6)-Ib
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncR	aac(3)-IVa
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncR	aac(6)-Ib
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncR	aadA1
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncR	aadA2
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aph(3)-Ia
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncR	aph(4)-Ia
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncR	cmlA1
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_16	N	3	strain_JM45_plasmid_p1	CP006657.1	IncR	sul3
kpneumoniae	BIDMC_16	N	4	pNJST258C1	CP006922.1		blaSHV-134
kpneumoniae	BIDMC_11	N	1			IncFIB(K)	strA
kpneumoniae	BIDMC_11	N	1			IncFIB(K)	strB
kpneumoniae	BIDMC_11	N	1			IncFIB(K)	sul1
kpneumoniae	BIDMC_11	N	2	pBK31551	JX193301.1	IncN	aac(3)-Ib

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
kpneumoniae	BIDMC_11	N	2	pBK31551	JX193301.1	IncN	aph(3)-Ia
kpneumoniae	BIDMC_11	N	2	pBK31551	JX193301.1	IncN	blaKPC-4
kpneumoniae	BIDMC_11	N	2	pBK31551	JX193301.1	IncN	blaTEM-1
kpneumoniae	BIDMC_18D	S	1			IncFIB(pQil)	aadA2
kpneumoniae	BIDMC_18D	S	1			IncFIB(pQil)	aadB
kpneumoniae	BIDMC_18D	S	1			IncFIB(pQil)	blaTEM-1
kpneumoniae	BIDMC_18D	S	1			IncFIB(pQil)	catB3
kpneumoniae	BIDMC_18D	S	1			IncFIB(pQil)	dfrA18
kpneumoniae	BIDMC_18D	S	1			IncFIB(pQil)	sul1
ecoli	BIDMC_70	S	1				sul2
ecoli	BIDMC_70	S	2	pUTI89	CP000244.1	IncFIB(AP001918)	blaTEM-1
ecoli	BIDMC_70	S	2	pUTI89	CP000244.1	IncFIB(AP001918)	tet(B)
ecoli	BIDMC_70	S	3				aadA1
ecoli	BIDMC_70	S	3				dfrA1
kpneumoniae	BIDMC_10	N	1				aph(3)-Ia
kpneumoniae	BIDMC_10	N	2				aac(3)-IVa
kpneumoniae	BIDMC_10	N	2				aadA1
kpneumoniae	BIDMC_10	N	2				aadA2
kpneumoniae	BIDMC_10	N	2				aph(4)-Ia
kpneumoniae	BIDMC_10	N	2				cmlA1
kpneumoniae	BIDMC_10	N	2				sul3
kpneumoniae	BIDMC_10	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_10	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_10	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_10	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_10	N	3	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_10	N	4	pBK15692	KC845573.1	IncI2	blaTEM-1
ecoli	UCI_53	I	1			IncFIB(AP001918)	aac(6)Ib-cr
ecoli	UCI_53	I	1			IncFIB(AP001918)	blaCTX-M-15
ecoli	UCI_53	I	1			IncFIB(AP001918)	blaOXA-30
ecoli	UCI_53	I	1			IncFIB(AP001918)	tet(A)
abaumanii	BIDMC_57	S	1				aph3ia
abaumanii	BIDMC_57	S	1				bcra
kpneumoniae	MGH_73	N	1	pKpS90	JX461340.1	IncX3	blaSHV-134
kpneumoniae	MGH_73	N	2			ColRNAI	aac(6)-Ib
kpneumoniae	MGH_73	N	2			ColRNAI	aadA1
kpneumoniae	MGH_73	N	2			ColRNAI	blaKPC-3
kpneumoniae	MGH_73	N	2			ColRNAI	blaTEM-1
ecloacae	UCI_36	S	1			IncFIA(HI1)	dfrA22
ecloacae	UCI_36	S	1			IncFIA(HI1)	strA
ecloacae	UCI_36	S	1			IncFIA(HI1)	sul1
ecloacae	UCI_36	S	1			IncFIA(HI1)	tet(D)

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecoli	BIDMC_77	S	1				aac(6)Ib-cr
ecoli	BIDMC_77	S	1				aadA5
ecoli	BIDMC_77	S	1				blaCTX-M-15
ecoli	BIDMC_77	S	1				blaOXA-30
ecoli	BIDMC_77	S	1				dfrA17
ecoli	BIDMC_77	S	1				sul1
ecoli	BIDMC_77	S	2				mph(A)
ecoli	BIDMC_77	S	2				tet(B)
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	aadA1
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	blaKPC-4
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	blaOXA-129
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	dfrA21
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	strA
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	strB
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	sul1
ecloacae	BWH_37	I	1	pK29	EF382672.1	IncHI2A	tet(B)
ecoli	BIDMC_6	N	1			IncN	blaTEM-1
ecoli	BIDMC_6	N	1			IncN	dfrA14
ecoli	BIDMC_6	N	1			IncN	mph(A)
ecoli	BIDMC_6	N	2				blaKPC-2
ecoli	BIDMC_6	N	3	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_6	N	3	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_6	N	3	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_6	N	3	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_6	N	3	pEC-IMP	EU855787.1	IncHI2A	sul2
ecloacae	MGH_14	N	1				aac(6)-IIc
ecloacae	MGH_14	N	1				aac3iia
ecloacae	MGH_14	N	1				aph(3)-Ia
ecloacae	MGH_14	N	1				blaTEM-1
ecloacae	MGH_14	N	1				ere(A)
ecloacae	MGH_14	N	1				sul1
ecloacae	MGH_14	N	1				sul2
ecloacae	MGH_14	N	1				tet(D)
ecloacae	MGH_14	N	2				aadA2
ecloacae	MGH_14	N	2				sul1
ecloacae	MGH_14	N	3				Qnr-B2
ecloacae	MGH_14	N	3				aac(6)-Ib
ecloacae	MGH_14	N	3				aadA1
ecloacae	MGH_14	N	3				aadA2
ecloacae	MGH_14	N	3				blaKPC-3
ecloacae	MGH_14	N	3				blaOXA-9
ecloacae	MGH_14	N	3				blaSHV-38
ecloacae	MGH_14	N	3				blaTEM-1
ecloacae	MGH_14	N	3				sul1
ecloacae	MGH_14	N	4				aph(3)-Ia

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	MGH_14	N	4				dfrA18
ecloacae	MGH_14	N	4				strB
ecloacae	MGH_14	N	4				sul1
koxytoca	MGH_41	N	1				aac(6)-Ib
koxytoca	MGH_41	N	1				aadA1
koxytoca	MGH_41	N	1				blaKPC-2
koxytoca	MGH_41	N	1				blaOXA-9
koxytoca	MGH_41	N	1				blaTEM-1
kpneumoniae	UCI_41	N	1				blaKPC-3
kpneumoniae	UCI_41	N	2	pKpS90	JX461340.1	IncX3	aph(3)-Ia
kpneumoniae	UCI_41	N	2	pKpS90	JX461340.1	IncX3	mph(A)
kpneumoniae	UCI_17	N	1			IncFIB(pQil)	aac(3)-IId
kpneumoniae	UCI_17	N	1			IncFIB(pQil)	blaKPC-2
kpneumoniae	UCI_17	N	1			IncFIB(pQil)	blaTEM-1
kpneumoniae	UCI_17	N	1			IncFIB(pQil)	dfrA5
kpneumoniae	UCI_17	N	1			IncFIB(pQil)	tet(D)
kpneumoniae	UCI_17	N	2				aac(6)-Ib
kpneumoniae	MGH_75	N	1				tet(D)
kpneumoniae	MGH_75	N	2				tet34
kpneumoniae	MGH_75	N	3				blaCTX-M-15
kpneumoniae	MGH_75	N	4				tet(A)
kpneumoniae	MGH_75	N	5				Qnr-B4
kpneumoniae	MGH_75	N	6				floR
kpneumoniae	MGH_75	N	6				sul2
ecloacae	UCI_49	S	1			IncFII(pECLA)	aac(3)-IIb
ecloacae	UCI_49	S	2				ARR-3
ecloacae	UCI_49	S	2				aac(6)Ib-cr
ecloacae	UCI_49	S	2				blaFOX-3
ecloacae	UCI_49	S	2				blaOXA-30
ecloacae	UCI_49	S	2				blaTEM-1
ecloacae	UCI_49	S	2				catB3
ecloacae	UCI_49	S	2				mph(A)
ecloacae	UCI_49	S	2				sul1
kpneumoniae	BIDMC_68	N	1			IncFIB(pQil)	blaTEM-1
kpneumoniae	BIDMC_68	N	2	pBK32179	JX430448.1	IncFIB(K)	blaKPC-2
kpneumoniae	BIDMC_68	N	3			ColRNAI	aac(6)-Ib
kpneumoniae	BIDMC_68	N	3			ColRNAI	blaTEM-1
kpneumoniae	BIDMC_68	N	4				aadA2
kpneumoniae	BIDMC_68	N	4				aph(3)-Ia
kpneumoniae	BIDMC_68	N	4				catA1
kpneumoniae	BIDMC_68	N	4				dfrA12
kpneumoniae	BIDMC_68	N	4				mph(A)
kpneumoniae	BIDMC_68	N	4				sul1

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	BIDMC_28	S	1			IncFII(pECLA)	dfrA14
ecloacae	BIDMC_28	S	1			IncFII(pECLA)	strA
ecloacae	BIDMC_28	S	1			IncFII(pECLA)	strB
ecloacae	BIDMC_28	S	1			IncFII(pECLA)	sul2
ecoli	BIDMC_2B	N	1			IncN	blaTEM-1
ecoli	BIDMC_2B	N	1			IncN	dfrA14
ecoli	BIDMC_2B	N	1			IncN	mph(A)
ecoli	BIDMC_2B	N	2				blaKPC-2
ecoli	BIDMC_2B	N	3	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_2B	N	3	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_2B	N	3	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_2B	N	3	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_2B	N	3	pEC-IMP	EU855787.1	IncHI2A	sul2
ecloacae	BWH_39	I	1				Qnr-S1
ecloacae	BWH_39	I	2	pBK31551	JX193301.1	IncN	aac(3)-Ib
ecloacae	BWH_39	I	2	pBK31551	JX193301.1	IncN	aph(3)-Ia
ecloacae	BWH_39	I	2	pBK31551	JX193301.1	IncN	blaKPC-4
ecloacae	BWH_39	I	2	pBK31551	JX193301.1	IncN	blaTEM-1
ecloacae	BWH_39	I	2	pBK31551	JX193301.1	IncN	dfrA14
ecloacae	BWH_39	I	2	pBK31551	JX193301.1	IncN	sul1
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	aadA5
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	dfrA17
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	mph(A)
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	strA
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	strB
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	sul1
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	sul2
ecoli	BIDMC_75	S	1			IncFIB(AP001918)	tet(A)
ecoli	BIDMC_75	S	2				aac(3)-IId
ecoli	BIDMC_75	S	3			IncFII(29)	blaTEM-1
ecoli	BIDMC_17B	N	1				blaKPC-2
ecoli	BIDMC_17B	N	2	pEC-IMP	EU855787.1	IncHI2A	aac(6)-IIc
ecoli	BIDMC_17B	N	2	pEC-IMP	EU855787.1	IncHI2A	blaSHV-134
ecoli	BIDMC_17B	N	2	pEC-IMP	EU855787.1	IncHI2A	ere(A)
ecoli	BIDMC_17B	N	2	pEC-IMP	EU855787.1	IncHI2A	sul1
ecoli	BIDMC_17B	N	2	pEC-IMP	EU855787.1	IncHI2A	sul2
ecoli	BIDMC_17B	N	3			IncN	blaTEM-1
ecoli	BIDMC_17B	N	3			IncN	dfrA14
ecoli	BIDMC_17B	N	3			IncN	mph(A)
ecloacae	MGH_8	N	1	pHCM2	AL513384.1	IncFIB(pHCM2)	dfrA15
ecloacae	MGH_8	N	1	pHCM2	AL513384.1	IncFIB(pHCM2)	sul1
ecloacae	MGH_8	N	2	pBK31551	JX193301.1	IncN	aac(3)-Ib
ecloacae	MGH_8	N	2	pBK31551	JX193301.1	IncN	aph(3)-Ia

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecloacae	MGH_8	N	2	pBK31551	JX193301.1	IncN	blaKPC-4
ecloacae	MGH_8	N	2	pBK31551	JX193301.1	IncN	blaTEM-1
ecloacae	MGH_8	N	2	pBK31551	JX193301.1	IncN	dfrA14
ecloacae	MGH_8	N	2	pBK31551	JX193301.1	IncN	sul1
ecloacae	MGH_8	N	3				Qnr-S1
ecloacae	MGH_11	N	1			IncFIB(pHCM2)	aac(3)-Ib
ecloacae	MGH_11	N	1			IncFIB(pHCM2)	aph(3)-Ia
ecloacae	MGH_11	N	1			IncFIB(pHCM2)	blaTEM-1
ecloacae	MGH_11	N	1			IncFIB(pHCM2)	dfrA14
ecloacae	MGH_11	N	1			IncFIB(pHCM2)	dfrA15
ecloacae	MGH_11	N	1			IncFIB(pHCM2)	sul1
ecloacae	MGH_11	N	2				Qnr-S1
ecloacae	MGH_11	N	3				blaKPC-4
ecoli	BIDMC_73	S	1			IncFIB(AP001918)	strA
ecoli	BIDMC_73	S	1			IncFIB(AP001918)	strB
ecoli	BIDMC_73	S	1			IncFIB(AP001918)	sul2
ecoli	BIDMC_73	S	2				dfrA17
ecoli	BIDMC_73	S	2				mph(A)
ecoli	BIDMC_73	S	2				tet(B)
kpneumoniae	BWH_45	N	1				sul2
kpneumoniae	BWH_45	N	2				aadA2
kpneumoniae	BWH_45	N	2				blaKPC-2
kpneumoniae	BWH_45	N	2				dfrA12
kpneumoniae	BWH_45	N	3				aadA2
kpneumoniae	BWH_45	N	3				dfrA12
kpneumoniae	BWH_45	N	3				sul1
kpneumoniae	BWH_45	N	4			ColRNAI	aac(6)-Ib
kpneumoniae	BWH_45	N	4			ColRNAI	blaTEM-1
kpneumoniae	BWH_45	N	5				aac(6)-33
kpneumoniae	BWH_45	N	5				aadB
kpneumoniae	BWH_45	N	5				sul1
kpneumoniae	BWH_45	N	6			IncA/C2	floR
kpneumoniae	BWH_45	N	7				aph(3)-Ia
kpneumoniae	BWH_45	N	7				mph(A)
kpneumoniae	BIDMC_14	N	1				Qnr-B19
kpneumoniae	BIDMC_14	N	1				aadA1
kpneumoniae	BIDMC_14	N	1				blaKPC-3
kpneumoniae	BIDMC_14	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	aadA2
kpneumoniae	BIDMC_14	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	catA1
kpneumoniae	BIDMC_14	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	dfrA12
kpneumoniae	BIDMC_14	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	mph(A)
kpneumoniae	BIDMC_14	N	2	strain_JM45_plasmid_p1	CP006657.1	IncFIB(K)	sul1
kpneumoniae	BIDMC_14	N	3				blaTEM-1
ecoli	BIDMC_49A	S	1	pECOS88	CU928146.1	IncFIB(AP001918)	dfrA5

species	isolate name	resistance phenotype (N=NON-SUSCEPTIBLE; S=SUSCEPTIBLE)	putative plasmid	Best hit Genbank	Genbank accession of best hit	plasmid replicon	gene name
ecoli	BIDMC_49A	S	1	pECOS88	CU928146.1	IncFIB(AP001918)	tet(A)
kpneumoniae	BIDMC_41	S	1			IncFIB(pQil)	blaSHV-134
kpneumoniae	BIDMC_41	S	1			IncFIB(pQil)	blaTEM-1
kpneumoniae	BIDMC_41	S	2				aadB
kpneumoniae	BIDMC_41	S	2				catB3
kpneumoniae	BIDMC_41	S	2				dfrA18
kpneumoniae	BIDMC_41	S	2				sul1
kpneumoniae	BIDMC_41	S	3			IncFIB(K)	aadA2
ecloacae	MGH_12	N	1				Qnr-S1
ecloacae	MGH_12	N	2	pHCM2	AL513384.1	IncFIB(pHCM2)	dfrA15
ecloacae	MGH_12	N	2	pHCM2	AL513384.1	IncFIB(pHCM2)	sul1
ecloacae	MGH_12	N	3	pBK31551	JX193301.1	IncN	aac(3)-Ib
ecloacae	MGH_12	N	3	pBK31551	JX193301.1	IncN	aph(3)-Ia
ecloacae	MGH_12	N	3	pBK31551	JX193301.1	IncN	blaKPC-4
ecloacae	MGH_12	N	3	pBK31551	JX193301.1	IncN	blaTEM-1
ecloacae	MGH_12	N	3	pBK31551	JX193301.1	IncN	dfrA14
ecoli	BIDMC_39	S	1			IncFIB(K)	aac(3)-VIa
ecoli	BIDMC_39	S	1			IncFIB(K)	aadA1
ecoli	BIDMC_39	S	1			IncFIB(K)	blaHERA-3
ecoli	BIDMC_39	S	1			IncFIB(K)	strA
ecoli	BIDMC_39	S	1			IncFIB(K)	strB
ecoli	BIDMC_39	S	1			IncFIB(K)	sul1

Table S16. Number of substitutions between ST258 isolates when accounting recombination free regions

	BIDMC_1	BIDMC_10	BIDMC_12A	BIDMC_12B	BIDMC_12C	BIDMC_13	BIDMC_14	BIDMC_16	BIDMC_18A	BIDMC_18B	BIDMC_18C	BIDMC_2A	BIDMC_32	BIDMC_34	BIDMC_4	BIDMC_42A	BIDMC_42B	BIDMC_45	BIDMC_5	BIDMC_54	BIDMC_60	BIDMC_68	BIDMC_7A	BIDMC_7B	BWH_22	BWH_36	BWH_45	BWH_47	MGH_29	MGH_31	MGH_51	MGH_59	MGH_67	MGH_71	MGH_73	MGH_79	UCI_1	UCI_13	UCI_17	UCI_19	UCI_21	UCI_33	UCI_37	UCI_41	UCI_55	UCI_59	UCI_61	UCI_63	UCI_67
BIDMC_1		129	155	133	152	142	131	127	178	171	167	120	151	188	127	153	159	178	136	142	120	124	141	137	158	163	123	155	184	146	148	70	107	145	134	135	142	233	136	201	225	132	244	182	189	232	156	206	155
BIDMC_10	129		96	75	96	55	110	36	145	144	137	35	50	146	39	58	56	147	41	55	96	99	50	60	131	74	99	131	144	106	126	144	88	120	108	109	81	188	115	166	184	104	200	143	140	191	126	165	95
BIDMC_12A	155	96		23	6	101	144	94	170	170	163	91	107	176	96	118	123	166	94	115	123	126	110	111	149	126	127	158	174	143	145	168	111	138	137	138	99	218	132	187	214	124	234	182	177	219	145	193	108
BIDMC_12B	133	75	23		20	80	124	75	151	151	141	72	81	160	74	98	96	153	70	93	103	106	84	95	129	92	110	141	154	119	127	151	93	126	119	121	81	199	121	171	195	110	221	168	161	199	131	174	90
BIDMC_12C	152	96	6	20		104	141	91	167	170	159	91	110	173	93	114	119	166	97	112	120	122	107	108	146	123	126	157	170	140	145	169	110	138	136	139	96	216	128	184	212	124	237	185	178	216	144	191	105
BIDMC_13	142	55	101	80	104		125	31	152	151	144	23	33	158	38	76	74	150	26	65	106	108	59	72	134	66	116	142	150	104	130	147	94	130	121	114	90	197	137	171	197	113	211	164	154	196	127	171	104
BIDMC_14	131	110	144	124	141	125		105	153	153	145	112	126	163	117	133	135	160	116	134	95	98	126	131	138	146	54	31	152	114	134	157	86	129	7	108	130	206	123	174	197	118	212	161	149	207	142	181	138
BIDMC_16	127	36	94	75	91	31	105		140	138	132	8	31	154	18	63	56	146	24	49	89	91	53	54	128	68	94	122	140	104	117	135	80	114	101	104	77	187	117	158	182	95	207	150	136	182	119	160	90
BIDMC_18A	178	145	170	151	167	152	153	140		29	16	135	165	29	142	163	167	23	149	153	116	118	168	156	121	172	143	168	42	164	124	197	99	118	150	145	160	192	161	165	194	146	261	205	203	192	173	167	169
BIDMC_18B	171	144	170	151	170	151	153	138	29		22	135	164	43	142	166	168	38	148	153	113	113	164	159	114	178	143	168	45	166	115	190	102	117	147	147	159	184	166	153	186	146	255	199	199	180	167	156	169
BIDMC_18C	167	137	163	141	159	144	145	132	16	22		125	157	28	132	155	158	21	141	146	107	108	154	149	108	168	135	160	34	159	107	183	97	110	142	142	149	178	153	150	180	139	255	197	196	177	162	150	159
BIDMC_2A	120	35	91	72	91	23	112	8	135	135	125		30	145	14	55	60	144	21	45	89	91	51	56	126	74	93	129	143	105	115	139	80	110	106	101	76	185	117	157	182	100	199	147	140	184	120	160	86
BIDMC_32	151	50	107	81	110	33	126	31	165	164	157	30		175	43	78	71	162	28	73	117	119	65	72	145	69	110	143	161	112	144	158	103	131	122	125	97	200	132	179	199	117	221	166	158	206	139	180	110
BIDMC_34	188	146	176	160	173	158	163	154	29	43	28	145	175		155	174	170	19	159	169	128	131	159	169	108	177	156	178	47	171	126	197	116	125	160	160	168	190	164	170	191	153	265	208	212	197	177	170	178
BIDMC_4	127	39	96	74	93	38	117	18	142	142	132	14	43	155		59	64	150	30	50	93	95	54	58	132	76	101	134	150	111	121	145	84	116	113	106	79	191	122	163	189	104	213	156	148	191	124	166	89
BIDMC_42A	153	58	118	98	114	76	133	63	163	166	155	55	78	174	59		29	165	71	37	122	120	25	32	146	46	132	156	159	137	147	171	106	137	134	133	105	211	135	186	209	124	230	170	170	212	143	190	116
BIDMC_42B	159	56	123	96	119	74	135	56	167	168	158	60	71	170	64	29		165	61	47	126	127	29	38	142	42	128	157	161	133	147	168	117	129	136	138	104	208	131	184	202	127	230	175	170	211	144	186	114
BIDMC_45	178	147	166	153	166	150	160	146	23	38	21	144	162	19	150	165	165		150	159	120	121	155	158	118	173	146	173	48	175	121	206	107	122	152	155	163	199	162	172	195	151	261	206	203	192	180	172	173
BIDMC_5	136	41	94	70	97	26	116	24	149	148	141	21	28	159	30	71	61	150		60	103	105	62	64	127	55	106	135	153	105	125	146	91	122	114	112	89	195	127	171	188	105	211	159	150	196	130	173	102
BIDMC_54	142	55	115	93	112	65	134	49	153	153	146	45	73	169	50	37	47	159	60		106	107	48	43	146	60	117	151	163	125	136	160	98	130	127	120	99	206	133	179	201	120	222	162	158	206	138	182	106
BIDMC_60	120	96	123	103	120	106	95	89	116	113	107	89	117	128	93	122	126	120	103	106		13	120	112	103	130	89	117	120	103	95	141	37	93	98	85	106	171	117	136	165	96	213	152	148	170	117	146	114
BIDMC_68	124	99	126	106	122	108	98	91	118	113	108	91	119	131	95	120	127	121	105	107	13		122	114	103	133	91	120	119	107	98	145	34	92	101	90	109	175	120	140	169	98	201	148	147	173	120	150	116
BIDMC_7A	141	50	110	84	107	59	126	53	168	164	154	51	65	159	54	25	29	155	62	48	120	122		24	138	36	121	153	157	119	152	160	111	127	131	133	93	209	129	183	207	126	221	170	166	214	140	181	114
BIDMC_7B	137	60	111	95	108	72	131	54	156	159	149	56	72	169	58	32	38	158	64	43	112	114	24		138	38	126	152	154	126	142	160	100	134	133	121	98	208	133	185	205	127	231	177	168	208	141	180	112
BWH_22	158	131	149	129	146	134	138	128	121	114	108	126	145	108	132	146	142	118	127	146	103	103	138	138		140	131	153	114	145	100	175	95	99	136	139	145	161	140	135	153	133	243	187	186	166	155	140	155
BWH_36	163	74	126	92	123	66	146	68	172	178	168	74	69	177	76	46	42	173	55	60	130	133	36	38	140		133	163	166	122	157	174	118	137	139	143	117	213	141	195	210	140	227	180	175	218	151	193	129
BWH_45	123	99	127	110	126	116	54	94	143	143	135	93	110	156	101	132	128	146	106	117	89	91	121	126	131	133		75	148	112	121	144	75	116	60	102	116	198	125	164	193	97	207	157	146	196	126	173	122
BWH_47	155	131	158	141	157	142	31	122	168	168	160	129	143	178	134	156	157	173	135	151	117	120	153	152	153	163	75		168	134	149	170	108	141	30	130	144	219	140	186	214	135	231	177	166	220	155	196	151
MGH_29	184	144	174	154	170	150	152	140	42	45	34	143	161	47	150	159	161	48	153	163	120	119	157	154	114	166	148	168		168	125	196	111	116	153	149	162	190	167	161	188	153	257	203	203	188	177	161	171
MGH_31	146	106	143	119	140	104	114	104	164	166	159	105	112	171	111	137	133	175	105	125	103	107	119	126	145	122	112	134	168		146	167	95	147	118	110	130	211	146	189	211	110	235	174	168	216	141	190	139
MGH_51	148	126	145	127	145	130	134	117	124	115	107	115	144	126	121	147	147	121	125	136	95	98	152	142	100	157	121	149	125	146		170	87	94	129	130	140	148	140	114	152	130	242	189	181	144	149	118	149
MGH_59	70	144	168	151	169	147	157	135	197	190	183	139	158	197	145	171	168	206	146	160	141	145	160	160	175	174	144	170	196	167	170		132	165	150	156	157	238	150	208	240	148	263	211	202	236	168	210	166
MGH_67	107	88	111	93	110	94	86	80	99	102	97	80	103	116	84	106	117	107	91	98	37	34	111	100	95	118	75	108	111	95	87	132		84	87	81	98	164	109	128	155	87	189	134	134	161	110	138	105
MGH_71	145	120	138	126	138	130	129	114	118	117	110	110	131	125	116	137	129	122	122	130	93	92	127	134	99	137	116	141	116	147	94	165	84		122	127	131	162	133	134	155	123	227	174	172	161	152	137	141
MGH_73	134	108	137	119	136	121	7	101	150	147	142	106	122	160	113	134	136	152	114	127	98	101	131	133	136	139	60	30	153	118	129	150	87	122		109	125	200	127	166	195	113	208	152	144	201	135	177	132
MGH_79	135	109	138	121	139	114	108	104	145	147	142	101	125	160	106	133	138	155	112	120	85	90	133	121	139	143	102	130	149	110	130	156	81	127	109		124	205	138	171	194	109	220	158	156	204	127	180	133
UCI_1	142	81	99	81	96	90	130	77	160	159	149	76	97	168	79	105	104	163	89	99	106	109	93	98	145	117	116	144	162	130	140	157	98	131	125	124		202	132	177	201	113	226	168	161	203	135	177	30
UCI_13	233	188	218	199	216	197	206	187	192	184	178	185	200	190	191	211	208	199	195	206	171	175	209	208	161	213	198	219	190	211	148	238	164	162	200	205	202		188	94	47	196	310	248	251	66	225	82	212
UCI_17	136	115	132	121	128	137	123	117	161	166	153	117	132	164	122	135	131	162	127	133	117	120	129	133	140	141	125	140	167	146	140	150	109	133	127	138	132	188		165	187	128	221	170	174	197	141	181	136
UCI_19	201	166	187	171	184	171	174	158	165	153	150	157	179	170	163	186	184	172	171	179	136	140	183	185	135	195	164	186	161	189	114	208	128	134	166	171	177	94	165		96	168	274	221	219	94	189	67	186
UCI_21	225	184	214	195	212	197	197	182	194	186	180	182	199	191	189	209	202	195	188	201	165	169	207	205	153	210	193	214	188	211	152	240	155	155	195	194	201	47	187	96		193	309	242	246	61	220	84	211
UCI_33	132	104	124	110	124	113	118	95	146	146	139	100	117	153	104	124	127	151	105	120	96	98	126	127	133	140	97	135	153	110	130	148	87	123	113	109	113	196	128	168	193		221	167	165	197	67	173	121
UCI_37	244	200	234	221	237	211	212	207	261	255	255	199	221	265	213	230	230	261	211	222	213	201	221	231	243	227	207	231	257	235	242	263	189	227	208	220	226	310	221	274	309	221		132	157	309	225	290	233
UCI_41	182	143	182	168	185	164	161	150	205	199	197	147	166	208	156	170	175	206	159	162	152	148	170	177	187	180	157	177	203	174	189	211	134	174	152	158	168	248	170	221	242	167	132		100	254	180	236	175
UCI_55	189	140	177	161	178	154	149	136	203	199	196	140	158	212	148	170	170	203	150	158	148	147	166	168	186	175	146	166	203	168	181	202	134	172	144	156	161	251	174	219	246	165	157	100		249	178	228	168
UCI_59	232	191	219	199	216	196	207	182	192	180	177	184	206	197	191	212	211	192	196	206	170	173	214	208	166	218	196	220	188	216	144	236	161	161	201	204	203	66	197	94	61	197	309	254	249		219	78	210
UCI_61	156	126	145	131	144	127	142	119	173	167	162	120	139	177	124	143	144	180	130	138	117	120	140	141	155	151	126	155	177	141	149	168	110	152	135	127	135	225	141	189	220	67	225	180	178	219		195	143
UCI_63	206	165	193	174	191	171	181	160	167	156	150	160	180	170	166	190	186	172	173	182	146	150	181	180	140	193	173	196	161	190	118	210	138	137	177	180	177	82	181	67	84	173	290	236	228	78	195		187
UCI_67	155	95	108	90	105	104	138	90	169	169	159	86	110	178	89	116	114	173	102	106	114	116	114	112	155	129	122	151	171	139	149	166	105	141	132	133	30	212	136	186	211	121	233	175	168	210	143	187	