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Systematic analysis of plasmids of the *Serratia marcescens* complex using 142 closed genomes

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Abstract

Plasmids play important roles in bacterial genome diversification. In the *Serratia marcescens* complex (SMC), a notable contribution of plasmids to genome diversification was also suggested by our recent analysis of >600 draft genomes. As accurate analyses of plasmids in draft genomes are difficult, in this study we analysed 142 closed genomes covering the entire complex, 67 of which were obtained in this study, and identified 132 plasmids (1.9–244.4 kb in length) in 77 strains. While the average numbers of plasmids in clinical and non-clinical strains showed no significant difference, strains belonging to clade 2 (one of the two hospital-adapted lineages) contained more plasmids than the others. Pangenome analysis revealed that of the 28954 genes identified, 12.8% were plasmid-specific, and 1.4% were present in plasmids or chromosomes depending on the strain. In the latter group, while transposon-related genes were most prevalent (31.4% of the function-predicted genes), genes related to antimicrobial resistance and heavy metal resistance accounted for a notable proportion (22.7%). Mash distance-based clustering separated the 132 plasmids into 23 clusters and 50 singletons. Most clusters/singletons showed notably different GC contents compared to those of host chromosomes, suggesting their recent or relatively recent appearance in the SMC. Among the 23 clusters, 17 were found in only clinical or only non-clinical strains, suggesting the possible preference of their distribution on the environmental niches of host strains. Regarding the host strain phylogeny, 16 clusters were distributed in two or more clades, suggesting their interclade transmission. Moreover, for many plasmids, highly homologous plasmids were found in other species, indicating the broadness of their potential host ranges, beyond the genus, family, order, class or even phylum level. Importantly, highly homologous plasmids were most frequently found in *Klebsiella pneumoniae* and other species in the family *Enterobacteriaceae*, suggesting that this family, particularly *K. pneumoniae*, is the main source for plasmid exchanges with the SMC. These results highlight the power of closed genome-based analysis in the investigation of plasmids and provide important insights into the nature of plasmids distributed in the SMC.

DATA SUMMARY

The raw read sequences and closed genome sequences obtained in this study have been deposited in GenBank/EMBL/DBJ under the BioProject accession number PRJDB10568 (see also Table S1, available in the online version of this article, for the accession numbers of each strain), and the Sequence Read Archive (SRA) accession numbers DRR493224 to DRR493297. All supporting data have been provided within the article or through supplementary data files.

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Abbreviations: AMR, antimicrobial resistance; ANI, average nucleotide identity; ANOVA, analysis of variance; Chr/Pla, genes present in chromosome or plasmid depending on strain; DFAST, DNA Data Bank of Japan Fast Annotation and Submission Tool; HGT, horizontal gene transfer; HMR, heavy metal resistance; HMW, high-molecular-weight; ICE, integrative conjugative element; MGE, mobile genetic element; ML, maximum-likelihood; NJ, neighbour-joining; Sma, *Serratia marcescens*; Sma s.s., *Serratia marcescens* sensu stricto; SMC, *Serratia marcescens* complex; Sne, *Serratia nematodiphila*; Ssu, *Serratia surfactantfaciens*; Sur, *Serratia ureilytica*; Tn, transposon; T4SS, type 4 secretion system; T6SS, type 6 secretion system; WGS, whole genome sequencing.

The raw read sequences and closed genome sequences obtained in this study have been deposited in GenBank/EMBL/DBJ under the BioProject accession number PRJDB10568. The accession numbers for the raw read data in the Sequence Read Archive (SRA) are DRR493224 to DRR493297 and for the closed genomes in the GenBank/EMBL/DBJ are AP028462 to AP028600.

Data statement: All supporting data, code and protocols have been provided within the article or through supplementary data files. Six supplementary figures and six supplementary tables are available with the online version of this article.

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Impact Statement

Plasmids are important players in bacterial genome diversification. While growing numbers of bacterial draft genomes are rapidly accumulating, accurate analyses of plasmids in draft genomes are not easy. Here, we describe the results of a systematic plasmid analysis of the *Serratia marcescens* complex (SMC) using 142 closed genomes. We identified 132 plasmids in 77 strains, which were separated into 23 clusters and 50 singletons based on their pairwise Mash distances. A systematic analysis of these plasmids provided multiple lines of findings important for better understanding the nature of plasmids in the SMC. They included the notable difference in GC content between most plasmids and their host chromosomes, which suggests their recent appearance in the SMC, the intra-complex transmission of the SMC plasmids, and their broad potential host ranges beyond the genus, family, order, class or even phylum level. Moreover, members of the family *Enterobacteriaceae*, particularly *Klebsiella pneumoniae*, were suggested as the main sources for plasmid exchanges with the SMC. These results show the power and importance of closed genome-based analysis in better understanding the nature of plasmids in bacterial populations.

INTRODUCTION

Serratia marcescens (Sma) is a Gram-negative, rod-shaped bacterium ubiquitous in the environment but has attracted attention as an opportunistic pathogen in the last few decades. It causes a wide range of nosocomial infections, such as pneumonia, bacteraemia, meningitis and endocarditis, including outbreaks, in compromised patients, particularly in neonatal and other intensive care units [1–7]. Sma strains have also been isolated from hospital equipment (e.g. ventilators) and the environment (e.g. sinks) and spread by healthcare professionals, as recently described in hospitalized COVID-19 patients in a Portuguese hospital [8]. Moreover, in addition to the natural resistance of Sma to multiple antimicrobial classes, such as penicillins and first- and second-generation cephalosporins, their acquisition of mobile genetic elements (MGEs), primarily plasmids, carrying multiple antimicrobial resistance (AMR) genes has raised further public health concerns as their acquisition limits treatment options, making Sma strains potentially more harmful to compromised patients [6, 7].

Sma was formerly included in the family *Enterobacteriaceae* but is now classified as a member of the family *Yersiniaceae* [9]. Recently, we performed a whole genome sequence (WGS)-based analysis of a global set of Sma, including *S. marcescens* subsp. *sakuensis*, and its close relatives, *Serratia nematodiphila* (Sne), *Serratia ureilytica* (Sur), and *Serratia surfactantifaciens* (Ssu), collectively named the Sma complex (SMC). This analysis identified 14 clades with an average nucleotide identity (ANI) threshold of 97%, four of which corresponded to Sma *sensu stricto* (clade 11), Sne (clade 10), Sur (clade 12) and Ssu (clade 13) [6]. Importantly, many strains isolated from patients and hospital environments and identified as Sma in laboratories formed two clades (clades 1 and 2) distinct from the other clades, and the strains belonging to these two clades contained more AMR genes. Moreover, clade 2 strains have larger genomes with lower GC contents than the strains in the other clades, and it was suggested that this feature was due to the acquisition of more plasmids and integrative elements because more plasmid replicons and integrase genes were detected in clade 2 strains [6]. In several other clades, there were also negative correlations between genome size and GC content and positive correlations between genome size and the number of plasmid replicons and/or integrase genes. Similar findings were obtained by WGS analysis of the entire genus *Serratia* [10]. However, the draft genome sequences of MGEs, particularly those of large plasmids, are often fragmented [11, 12]. Thus, although several plasmid analysis tools based on replication systems and/or mobilization systems are now available, it is not easy to identify their sequences [13, 14]. This was also the case for the SMC strains, for which intensive plasmid analyses similar to those for the pathogens belonging to *Enterobacteriaceae*, such as *Escherichia coli* and *Klebsiella pneumoniae* [15, 16], have not yet been conducted. Therefore, accurate repertoires and natures of the plasmids in the SMC remain elusive.

In this study, to overcome the limitations of draft genome sequences in plasmid analysis, we obtained 67 SMC closed genome sequences and collected 75 SMC closed genomes from the National Center for Biotechnology Information (NCBI) database. In these closed genomes, we identified 132 plasmids in 77 genomes, which were separated into 23 clusters and 50 singletons based on their pairwise Mash distances. We performed systematic analyses of these plasmids, including of their sizes and GC contents, analysed relationships with the phylogeny of host strains, and conducted a database search for highly homologous plasmids outside the SMC. These analyses provided multiple lines of important findings on the nature of SMC plasmids, such as their potentially broad host ranges beyond family, order, class or even phylum level.

METHODS

Strain set, long-read sequencing and hybrid assembly to closure

Of the 142 closed genomes analysed in this study, 75 were obtained from the NCBI database (accessed 10 December 2021). The remaining 67 genomes were closed in this study. To obtain these 67 closed genomes, we initially selected 77 strains from a collection of 227 SMC strains that were previously draft-sequenced [6] based on the clades of strains, the results of plasmid detection by

local PlasmidFinder v2.0.1 [17] and MOBScan server (<https://castillo.dicom.unican.es/mobscan/>) [18], and an AMR gene search by SRST2 v0.2.0 [11] with the ARG-ANNOT_v3 database (<https://www.mediterranee-infection.com/wp-content/uploads/2019/03/arg-annot-nt-v3-march2017.txt>) to capture the diversity of plasmids and host strains as much as possible. Genomic DNA of the 77 strains was purified with the QIAGEN Genomic Tip 100 G⁻¹ kit (Qiagen) according to the manufacturer's instructions, except for the incubation temperature (55°C). When we failed to obtain high-molecular-weight (HMW) DNA, an additional step of 20 min of incubation at 65°C was included prior to the lysis step to prevent autodegradation [19]. As HMW DNA was not obtained from 10 strains even with this additional incubation, these strains were excluded from the subsequent analysis. The successfully purified genomic DNA of 67 strains was subjected to long-read sequencing by the Oxford Nanopore Technologies (ONT) sequencing technology. Libraries were prepared using the Rapid Barcoding Kit (ONT) and sequenced using MinION R9.4.1 flow cells (ONT). Sequence reads were base-called using the Albacore v2.3.1 and quality-filtered and adapter-trimmed (score: >10, read length: ≥2000 bp, initial 100 bp of reads trimmed) using the Nanofilt v2.7.1 [20]. When the long-read coverage was >100×, reads were half sampled using the SeqKit toolkit v2.3.0 [21]. Then, by using Unicycler v0.4.8 [22], closed genomes were obtained by hybrid assembly using the long-read sequences obtained in this study and the Illumina short reads previously obtained [6], except for seven strains. As the amounts and qualities of the Illumina short reads from these seven strains appeared insufficient to obtain closed genomes, these strains were sequenced again on the Illumina MiSeq platform using the libraries prepared with the NEBNext Ultra II FS DNA Library Prep Kit (New England Biolabs), and the obtained Illumina short reads were used for hybrid assembly to obtain their closed genomes. The position of nucleotide 1 of the chromosome sequences was adjusted to that of strain Db11 [1], and gene annotation was conducted using the DNA Data Bank of Japan (DDBJ) Fast Annotation and Submission Tool (DFAST) v1.2.0 [23].

Replicon and MOB typing of plasmids

We identified all extrachromosomal sequences in the 142 closed genomes, and then their replicon and MOB typing was performed via Mob-Typer v3.0.3 from the Mob-suite package [24] for both typings, local PlasmidFinder v2.0.1 [17] for replicon typing and MOBScan server (<https://castillo.dicom.unican.es/mobscan/>) [18] for MOB typing. MOB subfamilies were determined based on the previously described conserved residues and motifs of relaxases [14, 25], the results of BLASTp sequence similarity analysis with prototype relaxases, and neighbour-joining (NJ) phylogenetic trees reconstructed for each subfamily using the alignments generated by ClustalW [26] in MEGAX [27]. Truncated relaxases were excluded from the analysis. A diagram showing the correlation of replicon and MOB types was generated using the package networkD3 in R v4.2.3 [28].

Phylogenetic analyses

The clades of 52 closed genomes obtained from the NCBI database were unknown because they were not included in our previous analysis [6]. Therefore, their clades were determined by a core gene-based phylogenetic analysis of these 52 closed genomes, three draft genomes of type strains, the 775 previously analysed genomes [6] and *Serratia ficaria* NCTC 12148 (used as an outgroup). We first determined the core genes ($n=2429$) of these 831 genomes using Roary v3.12 [29] with an 80% BLASTp identity cutoff and generated a core-gene sequence alignment using mafft, as previously described [6]. Based on the 193503 SNPs identified in this alignment, we reconstructed a maximum-likelihood (ML) tree using RAxML v8.2.10 [30] with the GTRGAMMA model of nucleotide substitution and 100 bootstrap replicates (Fig. S1). Based on this result, we determined the clades of the 52 closed genomes newly obtained from NCBI and the three type strains. Afterwards, we repeated the phylogenetic analysis using only 146 closed genomes, which consisted of 67 genomes closed in this study and 79 closed genomes from the NCBI database. As four pairs of genomes in the NCBI genome set were identical in core genome sequence and did not carry plasmids, only one of each pair was included in further analyses. Thus, our final dataset included 142 closed genomes, from which we obtained 535875 SNPs, in the sequence alignment of 3189 core genes, and the ML tree of these 142 genomes was reconstructed as described above.

An additional ML tree including only 77 strains that carried plasmids was reconstructed based on the 565456 SNPs in 3311 core genes which were identified using the same tools and parameters as described above. This tree was used to visualize the correlation of the results of plasmid clustering with the phylogeny of host strains using the cophylo command of the phytools package in R v4.2.3 [28].

Pangenome analysis

The pangenome of the 142 closed genomes was determined by Roary v3.12 [29] with a 95% BLASTp identity for gene clustering to construct a presence/absence matrix. Based on the presence/absence matrix of the genes in the pangenome, genes were classified into three groups: (i) those specifically encoded by chromosomes, (ii) those specifically encoded by plasmids, and (iii) those encoded by chromosomes or plasmids depending on the strain. Annotations of the genes in the second and third groups were manually curated based on the results of the BLASTp homology search of the NCBI database.

Search for AMR and heavy metal resistance genes

AMR and heavy metal resistance (HMR) genes were identified with AMRFinderPlus v3.10.30, database v2022-05-26, with the --plus option [31]. The AMR genes and HMR genes identified were further manually checked for variant and operon composition, respectively.

Analysis of linear plasmids

In two genomes that we tried to close in this study, a contig sequence that appeared to represent a linear plasmid was generated in addition to a circular closed chromosome. To exclude the possibility that they were derived from gap-containing circular plasmid sequences, PCR analyses were performed using two sets of primers designed to fill the potential gaps between ends in each contig (Fig. S3). Non-digested genomic DNA of the two strains was also analysed by PFGE to detect linear extra-chromosomal DNA molecules using a 1% agarose gel prepared with Certified Megabase agarose (Bio-Rad) and the CHEF Mapper XA system (Bio-Rad) at 14 °C and 6 V cm⁻¹ for 20 h. Pulse times were ramped with 0.5 s at the beginning and 30 s at the end [19, 32, 33]. The gel was stained with SYBR Safe DNA Gel Stain (Thermo Fisher Scientific), and images were obtained using the Gel Doc XR Imaging Systems (Bio-Rad). The genome maps of the two linear plasmids were generated with GenomeMatcher v3.04 [34] and their nucleotide sequence identity was determined by BLASTn.

Mash distance-based clustering of plasmids

All-against-all Mash distances of the 132 plasmids were calculated using Mash v2.0 with default k-mer and sketch sizes [35]. Based on the distance matrix constructed, the plasmids were clustered by the complete linkage method with the hclust command and a cut-off of 0.06 [24]. The ggtree package in R v4.2.3 [28] was used for dendrogram construction and dataset visualization. Network diagrams of the 23 plasmid clusters were prepared and visualized with Cytoscape v3.10.0 [36] using Prefuse Force Directed layout weighted by pairwise Mash distances with default parameters.

Database search for plasmids highly homologous to the SMC plasmids

We initially searched the NCBI database for sequences highly homologous to the plasmids identified in this study using BLASTn with an identity threshold of ≥90%. After excluding the sequences labelled '*Serratia marcescens* (taxid:615)', '*Serratia ureilytica* (taxid:300181)', '*Serratia nematodiphila* (taxid:458197)' and '*Serratia surfactantifaciens* (taxid:2741499)', and those not indicated as plasmids, Mash distances of the remaining sequences from corresponding SMC plasmid sequences were calculated as described above, and those showing Mash distances <0.06 were selected as highly homologous plasmids.

Statistical analyses

Statistical analyses were performed in R v4.2.3 [28]. For the comparison of the average numbers of plasmids carried by strains belonging to different clades, one-way ANOVA followed by a Tukey–Kramer multiple comparison test was used. For the comparison of the average numbers of plasmids carried by strains from clinical/hospital environments and non-clinical sources, the Mann–Whitney U test was used. Simple linear regression analysis was used to analyse the relationship between plasmid GC content and plasmid size.

RESULTS AND DISCUSSION

Closed genome set

The closed genome set analysed in this study included 75 genomes obtained from the NCBI database and 67 genomes closed in this study. The clades of the 52 genomes from the NCBI database, which were not included in our previous study [6], were determined by core gene-based phylogenetic analyses with the SMC genomes used in our previous study. The 67 genomes closed in this study were selected to cover the entire complex and the variation in AMR gene repertoires in the complex as much as possible. The clade distribution of the 142 genomes and their isolation sources are summarized in Table 1 (see also Table S1 and Fig. S2 for details of each genome). Although some of the clades were poorly represented in this genome set, the number of strains belonging to these clades was small in the whole set (see Fig. S1 for the phylogenetic positions and clades of the 142 strains in the whole set of SMC strains). They were isolated from five geographical regions: Japan (*n*=58), North America (*n*=37), Europe (*n*=23), Asia excluding Japan or Oceania (*n*=23), and South America (*n*=1). The average size and GC content of the chromosomes were 5.23 Mb (4.93–5.64 Mb) and 59.58% (58.92–60.16%), respectively (Fig. S2). As expected, the total sizes of the 67 genomes closed in this study were larger than those of their draft sequences with an average difference of 38.9 kb (0.7–108.0 kb) (Table S2).

Plasmids in the 142 closed genomes

We identified 132 plasmids in the genomes of 77 strains, ranging from 1.4 to 244.4 kb in size with 71.9 kb on average (Table S1 and S3, and Fig. S2). Consistent with our previous result [[6]], the average number of plasmids found in the strains in clade 2, a hospital-adapted clade, was significantly higher than that in other clades (Fig. 1a). Most clade 2 strains contained three or more

Table 1. Clades and isolation sources of the strains analysed

Clade*	No. of strains	Clinical/non-clinical
1	33	33/0
2	11	10†/1
3	10	7/3
4	6	6/0
5	1	0/1
6	5	0/5
7	3	0/3
8	2	0/2
9	11	6/5
10 (Sne)	13	4/9
11 (Sma s.s.)	14	5/9
12 (Sur)	29	12/17
13 (Ssu)	4	0/4

*Sne; *S. nematodiphila*, Sma s.s.; *S. marcescens sensu stricto*, Sur; *S. ureilytica*, Ssu; *S. surfactantfaciens*.

†Including two hospital environmental strains.

plasmids, with one containing as many as nine plasmids, whereas two clade 2 strains contained only one plasmid (Fig. S2), of which one was from the natural environment (water) and contained only a small plasmid 5.3 kb in size (Table S3). In contrast, the strains in clade 1, another hospital-adapted clade, did not contain more plasmids than the other clades, which was also consistent with our previous results [6]. Consequently, the average numbers of plasmids between clinical ($n=83$; including two strains isolated from the hospital environment) and non-clinical strains ($n=59$) were not significantly different ($P=0.316$; Fig. 1b). However, when the total numbers of AMR genes and HMR operons encoded in each clade were analysed, notable differences

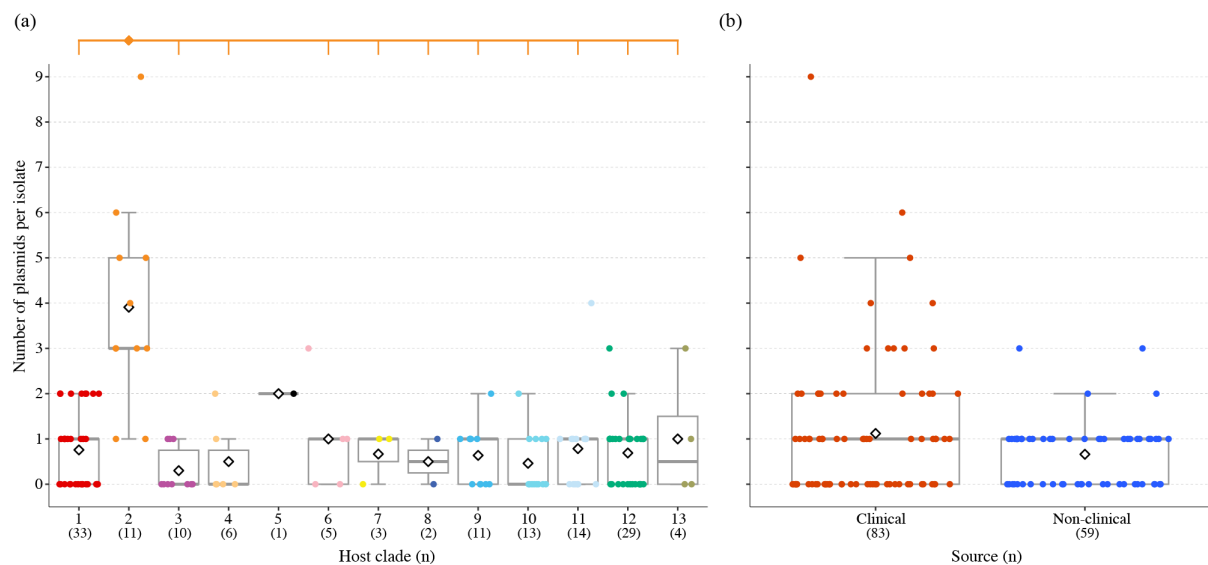


Fig. 1. The numbers of plasmids identified in the 142 closed genomes. (a) Comparison of the numbers of plasmids carried by SMC strains belonging to 13 clades. Open diamonds in the boxplot indicate mean values. A closed diamond indicates the clade which showed a significant difference ($P < 0.01$) from the clades indicated by short vertical lines. There was no significant difference between the 12 clades other than clade 2. (b) Comparison of the numbers of plasmids carried by the clinical/hospital environment and non-clinical strains. Open diamonds in the boxplot indicate mean values. A statistically significant difference was not detected between the two groups.

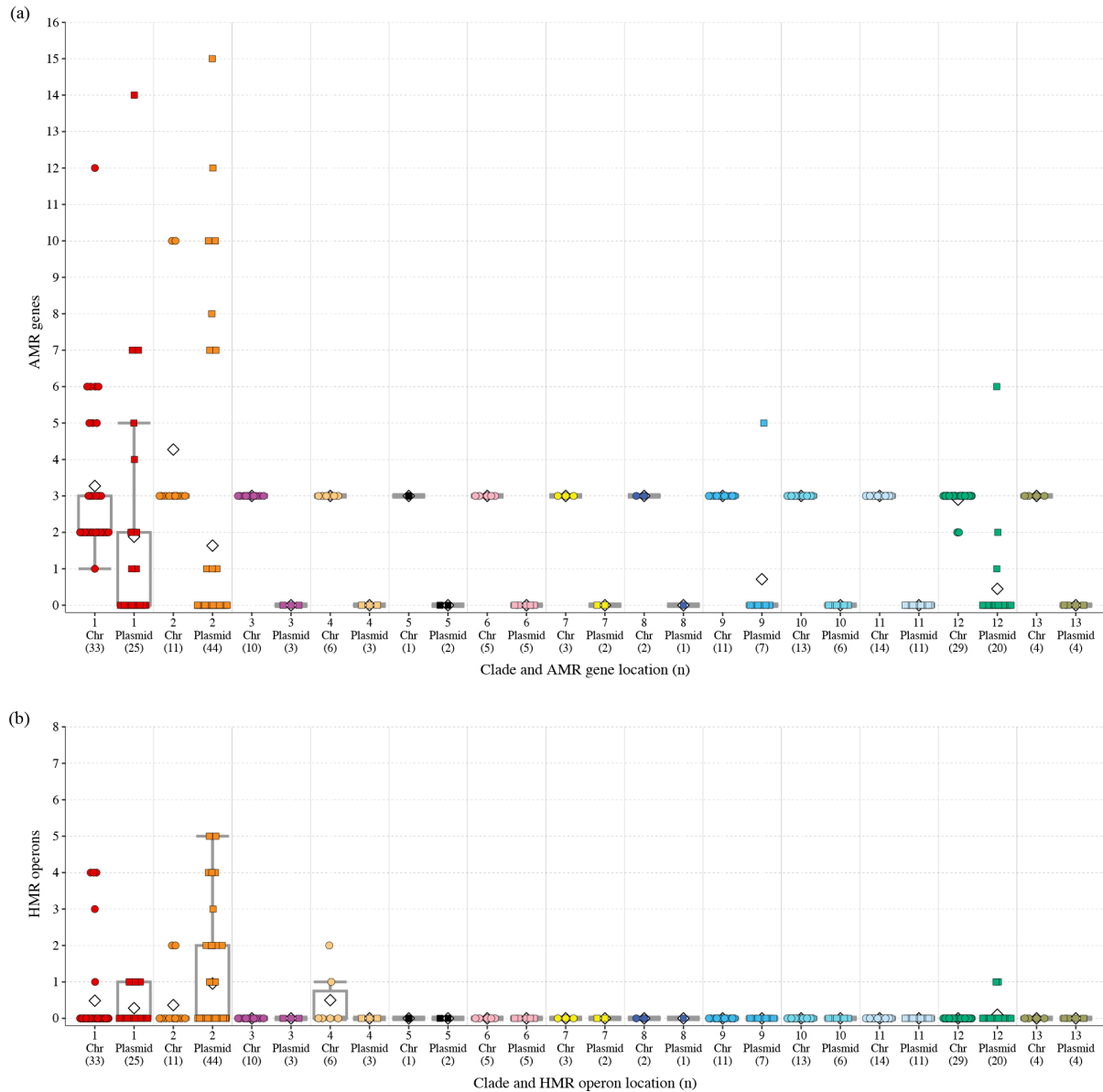


Fig. 2. AMR genes and HMR operons identified in the 142 closed genomes. The cumulative numbers of AMR genes (a) and HMR operons (b) in the chromosomes (circles) and plasmids (squares) of each strain are shown.

were observed between the two hospital-adapted clades and the other clades (Fig. 2). Although we identified 49 AMR genes and six HMR operons in the whole dataset (Table S1), the same pair of AMR genes [*aac(6')*-Ic and *bla*_{SRT}] was encoded in the chromosomes, and no genes/operons were encoded by the plasmids in most strains belonging to clades other than clades 1 and 2. In contrast, the numbers of these AMR genes and HMR operons in clades 1 and 2 were highly variable in both chromosomes and plasmids, indicating the acquisition of these genes/operons by these clades via horizontal gene transfer (HGT) mediated by both plasmids and some integrative elements.

Linear plasmids

The 132 plasmids included two similar linear plasmids 43.1 and 36.5 kb in size, showing >95% ANI values (Fig. S3). The linearity of their genomes was verified by PCR analysis with primers targeting each end of the genomes (see Fig. S3a for their positions), which yielded no amplicons (Fig. S3b). In addition, by PFGE analysis of undigested whole-genomic DNA of the two strains containing these linear plasmids, an extrachromosomal DNA band with the expected size was detected in both strains (Fig. S3c). Although we were unable to determine the exact terminal sequences of their genomes, a terminal inverted sequence of at least

Table 2. Replicon and MOB typing of 132 SMC plasmids by three typing tools

Typing tool	Replicon		MOB	
	Detected	Not detected	Detected	Not detected
MOB-Typer	108	24	112†	20
PlasmidFinder	69*	63	–	–
MOBScan	–	–	107‡	25

*All replicons detected by PlasmidFinder were also detected by MOB-Typer.

†Of these 112 plasmids, 105 contained apparently intact relaxases, the MOB subfamilies of which were determined as described in the Methods and used for further analyses.

‡Of these 107 plasmids, 103 contained apparently intact relaxases. Their MOB subfamilies were also determined as described in the Methods and used for further analyses. Note that the 103 plasmids were included in the 105 plasmids typed by MOB-Typer.

490 bp was identified. Moreover, the two plasmids showed >90% nucleotide sequence identity with the linear plasmids previously identified in *Klebsiella* and other *Enterobacteriaceae* [37].

Replicon and MOB types of plasmids

To determine the replicon and MOB types of the 132 plasmids, while we initially used three typing tools, PlasmidFinder, MOBScan and MOB-Typer, the largest number of plasmids were typed by MOB-Typer (Table 2; see Table S3 for the initial outputs of three tools). Therefore, we used the results predicted by this tool in this study. The replicon types of 108 plasmids (including uncharacterized types labelled ‘rep_cluster’) were determined by MOB-Typer (see Table S3 for details). Of the typed plasmids, 33 contained multiple replicons. Among the 24 untypeable plasmids, 13 were small plasmids (1.9–5.1 kb), but the remaining 11 ranged from 13.9 to 139.9 kb in size. They included the two linear plasmids, which probably use a 5′ terminus-binding protein as a primer for replication [37, 38]. The MOB types of 112 plasmids were determined by MOB-Typer. All known MOB families (MOB_C, MOB_P, MOB_H, MOB_P, MOB_Q and MOB_V) were detected in the 112 plasmids, and the MOB subfamilies were further determined for the 105 plasmids that encoded intact relaxases based on the sequence homologies of their protein sequences (Table S3). Of the 27 untypeable plasmids, 13 were small plasmids (1.9–6.3 kb). The remaining 14 plasmids, which included the two linear plasmids, ranged from 11.1 to 101.5 kb in size. The combinations of MOB types and replicon types were generally consistent with known combinations (MOB_F-IncF/IncN; MOB_H-IncH/IncC; MOB_P-IncP/Col/IncX/IncU) [14, 39], but most plasmids encoding the IncI1 replicon also contained the MOB_{F12} subfamily relaxase genes and only one IncI1 plasmid contained the MOB_{P12} subfamily relaxase gene (Fig. 3).

Genes specific to plasmids and those encoded by chromosomes or plasmids

To identify the genes specifically encoded by plasmids and those encoded by chromosomes or plasmids depending on the strain, we performed a pangenome analysis of the 142 genomes by Roary v3.12 [29] with a 95% sequence identity threshold. Among the 28954 genes identified, 24858 (85.8%) were specifically present in chromosomes, 3693 (12.8%) were specific to plasmids, and the remaining 403 (1.4%) were present in either chromosomes or plasmids (referred to as ‘Chr/Pla genes’; listed in Table S4). While a large proportion ($n=2285$, 61.9%) of the plasmid-specific genes encoded hypothetical proteins of unknown function, genes for conjugation ($n=259$) were most predominant among the 1408 function-predicted genes, followed by genes related to transposon (Tn) ($n=200$), AMR/HMR ($n=117$) and fimbria formation ($n=111$) (Fig. 4). Among the 299 function-predicted Chr/Pla genes, while Tn-related genes were most predominant ($n=94$), AMR/HMR genes ($n=68$) were also enriched (Fig. 4), indicating that a considerable number of AMR/HMR genes move between chromosomes and plasmids. Of note, genomic locations (chromosome or plasmid) of many genes were variable even between closely related strains (see Fig. S4 for the phylogeny of host strains and the genomic locations of the 299 genes in each strain). Consistent with this, the Chr/Pla genes also included notable numbers of conjugation-related genes ($n=18$), type 4 secretion system (T4SS)-related genes ($n=5$), which can also be involved in conjugation [40], and genes for plasmid maintenance ($n=8$), recombinases ($n=6$) and integrases ($n=4$) (see Table S4 and Fig S4 for details), suggesting that these AMR/HMR genes may be encoded by integrative conjugative elements (ICEs) and other integrative elements such as integrative plasmids. This result may partly explain why more AMR genes and HMR operons accumulated in clade 1 strains, because some of the clade 1 strains contained many AMR genes and multiple HMR operons in the chromosome (Fig. 2).

The presence of T6SS- and bacteriocin-related genes, both of which are involved in bacterial competition, in the Chr/Pla genes and fimbrial genes in both Chr/Pla and plasmid-specific genes may also be interesting, because inter-bacterial competition and fimbria-mediated adhesion can affect phenotypes that are important in niche colonization and specificity [41–43]. Some of the genes involved in bacterial competition may also be encoded by ICEs or other integrative elements, but a systematic and detailed analysis of these elements is required to clarify this issue.

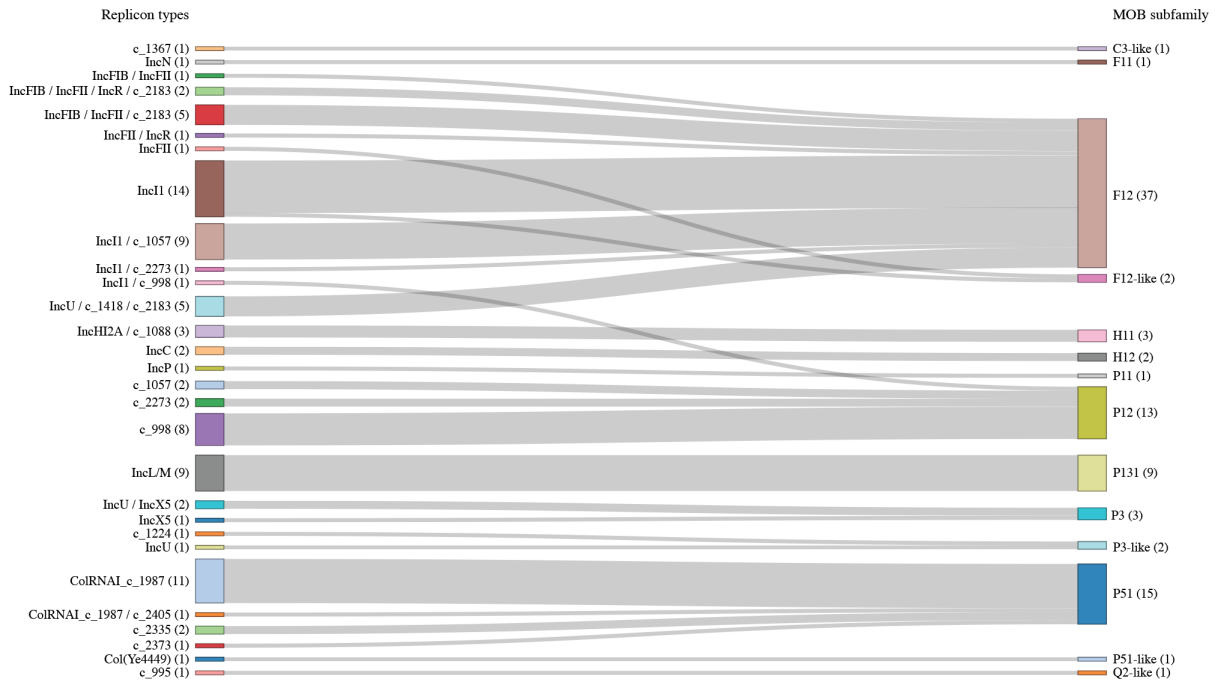


Fig. 3. Combinations of plasmid replicon types and MOB subfamilies. A Sankey diagram presenting the combinations of replicon types (left) and MOB subfamilies (right) identified in the 90 SMC plasmids, in which both replicon type and MOB subfamily were defined, is shown. The numbers of each replicon type and MOB subfamilies are indicated in parentheses. Replicon types indicated by c_XXXX are those defined as rep_cluster_XXXX by MOB-Typer.

Pairwise Mash distance-based clustering of plasmids

To analyse the similarity of the 132 plasmids, we performed a clustering analysis of these plasmids based on their pairwise Mash distances. With a threshold of 0.06 [3], the 132 plasmids were divided into 23 clusters that contained 2–10 members, and 50 singletons (Fig. 5). The lengths and GC contents of plasmids belonging to the same cluster were principally similar although some variations were observed in a few cases (Clusters 4, 20 and 21) (Figs 5 and 6). While the MOB types in the same cluster were concordant, the replicon types showed variations in eight clusters, but most variations observed were due to the presence or absence of a single replicon (Fig. 5 and Table S3). Of the 23 clusters, 11 consisted of plasmids from strains isolated in the same country: six in Japan, three in USA and two in China (Fig. S5a and Table S3). Of the remaining 12 clusters, 11 consisted of plasmids from strains isolated in two or three different continents and Cluster 4 comprised one plasmid from Japan and one

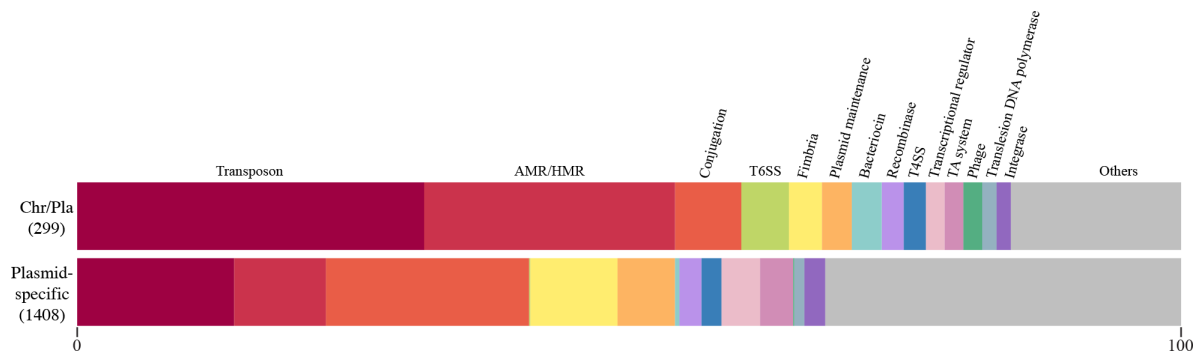


Fig. 4. Functions of the genes encoded by chromosomes or plasmids (Chr/Pla genes). The proportions of 14 functional gene groups containing four or more members in the 299 function-predicted Chr/Pla genes are shown. For comparison, the proportions of these 14 gene groups in the 1408 function-predicted plasmid-specific genes are also shown. Note that while 'Others' in the Chr/Pla genes included gene groups containing fewer than four members, 'Others' in the plasmid-specific genes included not only those containing fewer than four members but also those including four or more members (10 or fewer members in all but one group). Hypothetical genes were not included in this analysis.

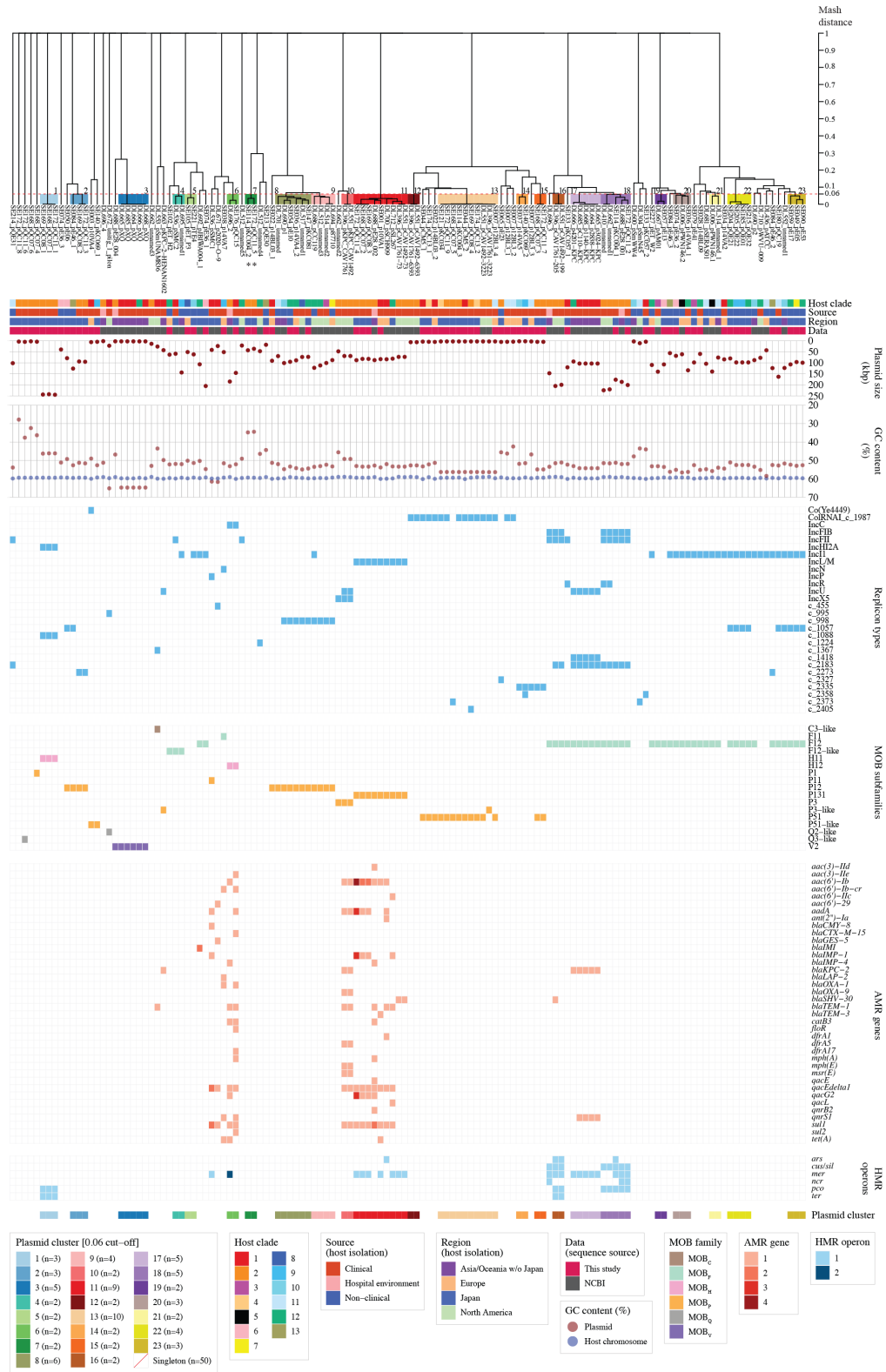


Fig. 5. Pairwise Mash distance-based clustering of SMC plasmids. The 132 plasmids analysed in this study were separated into 23 clusters and 50 singletons with a cut-off distance of 0.06. Two linear plasmids are indicated by asterisks. Clades, isolation sources, regions of host strain isolation and sequence sources are shown along with the sizes and GC contents of plasmids, host chromosome GC content, replicon types and MOB subfamilies of plasmids, and carriage of AMR genes and HMR operons by each plasmid.

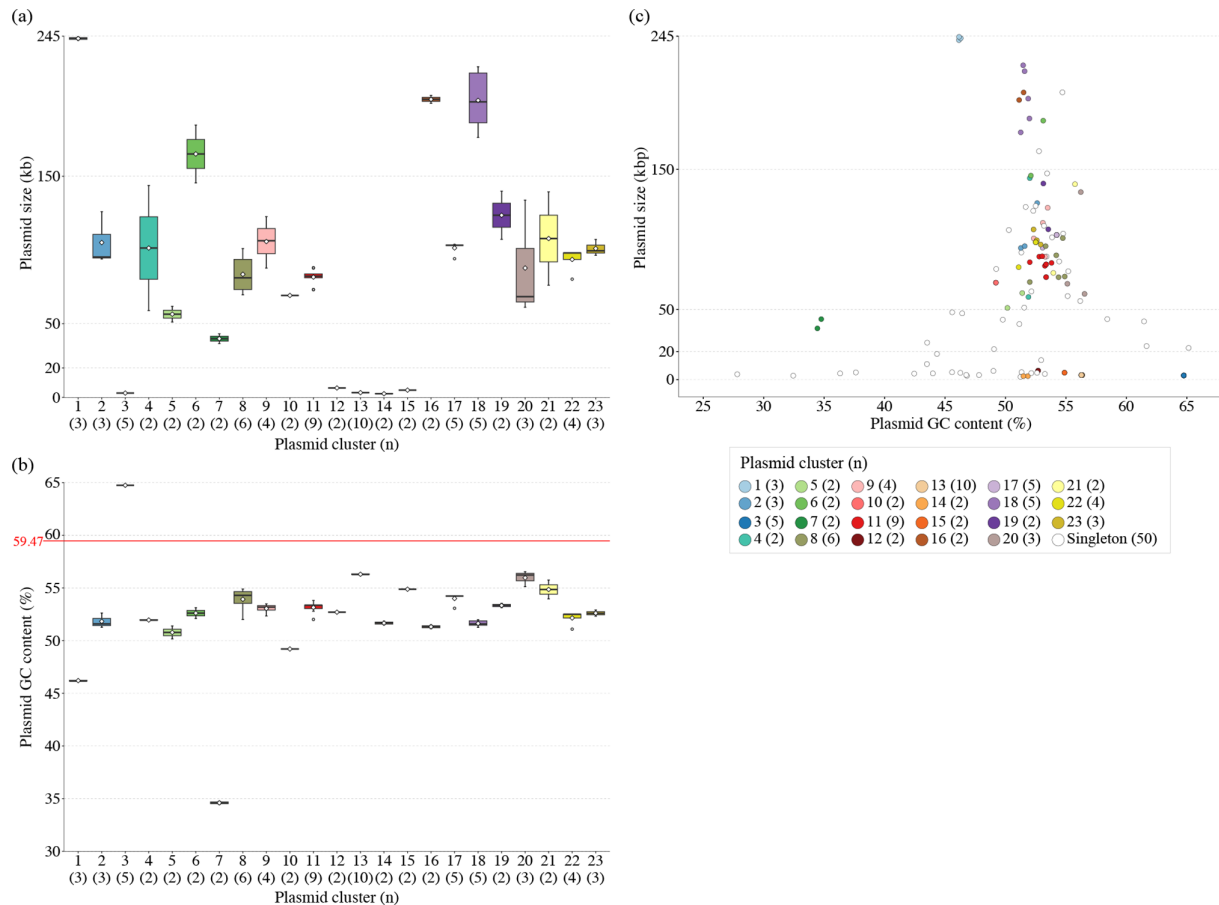


Fig. 6. Sizes and GC contents of the 23 plasmid clusters and 50 singletons. The ranges of plasmid size (a) and GC content (b) in each plasmid cluster are shown. Open diamonds in the boxplot indicate mean values. In (b), average GC content of SMC chromosomes is also indicated by a red line. In (c), the relationship between the GC content and size of plasmids is shown. No significant correlation was observed in this comparison.

from China (Fig. S5a and Table S3), indicating that the 11 plasmid clusters are globally distributed and not limited to a specific geographical region. Regarding the sources of host strains, clustered plasmids often shared the same source, clinical (including hospital environments) or non-clinical; 13 were exclusively found in clinical strains, and four were found only in non-clinical strains (Fig. 5; see Table S3 for details), suggesting the possible preference of plasmid distribution based on the environmental niches preferred by host strains, as previously observed with *Escherichia coli* plasmids [40]. Consistent with this, the carriage of AMR genes and HMR operons was also highly biased (Fig. 2), and these genes and operons were present in seven clusters and seven singletons, all of which were found in clinical/hospital environment strains except for one singleton (Fig. 5 and Table S3). Among these seven clusters, the plasmids in Clusters 6, 10 and 11 contained six or more different AMR genes and HMR operons (up to 14 AMR genes in one Cluster 6 plasmid) (Figs 5 and S6, and Table S3). Of note, the plasmids in Clusters 1, 16 and 18 carried two or more different HMR operons (up to four operons) but they carried no AMR genes except for one Cluster 16 plasmid that carried a single AMR gene (Figs 5 and S6, and Table S3). Thus, these plasmids can be regarded as specialized for HMR rather than AMR.

Sizes and GC contents of plasmids

While 22 plasmids belonging to five clusters (Clusters 3, 12, 13, 14 and 15) and 17 singletons were smaller than 6.3 kb in size, most of the other plasmids (79/94) were larger than 50 kb (Figs 5 and 6a, and Table S3). In particular, Clusters 1, 6, 16 and 18 comprised very large plasmids (>176 kb, except for a 145.5 kb plasmid in Cluster 6). One singleton plasmid was also 204.9 kb. Thus, the carriage of these plasmids has a considerable impact on the total genome size of each strain, as suggested by our previous study [6]. As expected, the sizes of potentially self-transmissible plasmids were much larger (109 287 bp on average) than non-self-transmissible plasmids (16 076 bp on average). More importantly, most plasmid genomes showed notably lower GC contents than their host chromosomes (58.9–60.1%; see Fig. S2), mostly ranging between 50 and 56%, with extreme cases of the plasmids in Clusters 1 and 7, which showed approximately 46.2–46.3 and 34.4–34.8% GC contents, respectively (Figs 5 and

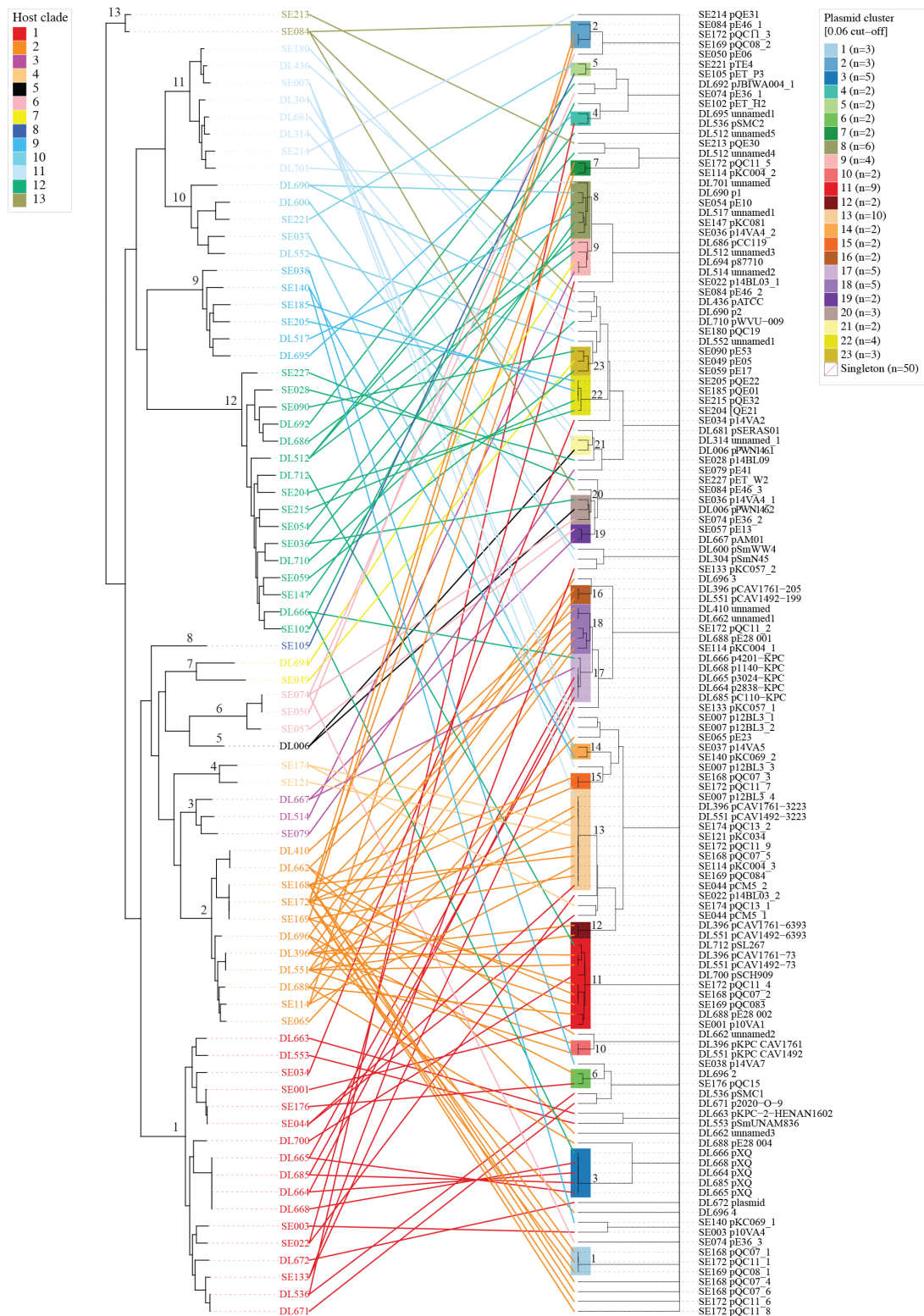


Fig. 7. The correlation of plasmid clustering with host strain phylogeny. A core gene-based ML phylogenetic tree of the 77 plasmid-containing strains is presented along with the dendrogram showing the Mash distance-based clustering of the 132 plasmids found in the 77 strains. Plasmids and their hosts are linked by lines coloured according to host strain clades. The plasmid dendrogram was rotated to best mirror the host phylogenetic tree using the cophylo command from the phytools package in R v4.2.3. Host clades and plasmid clusters are indicated in the ML tree and the dendrogram, respectively.

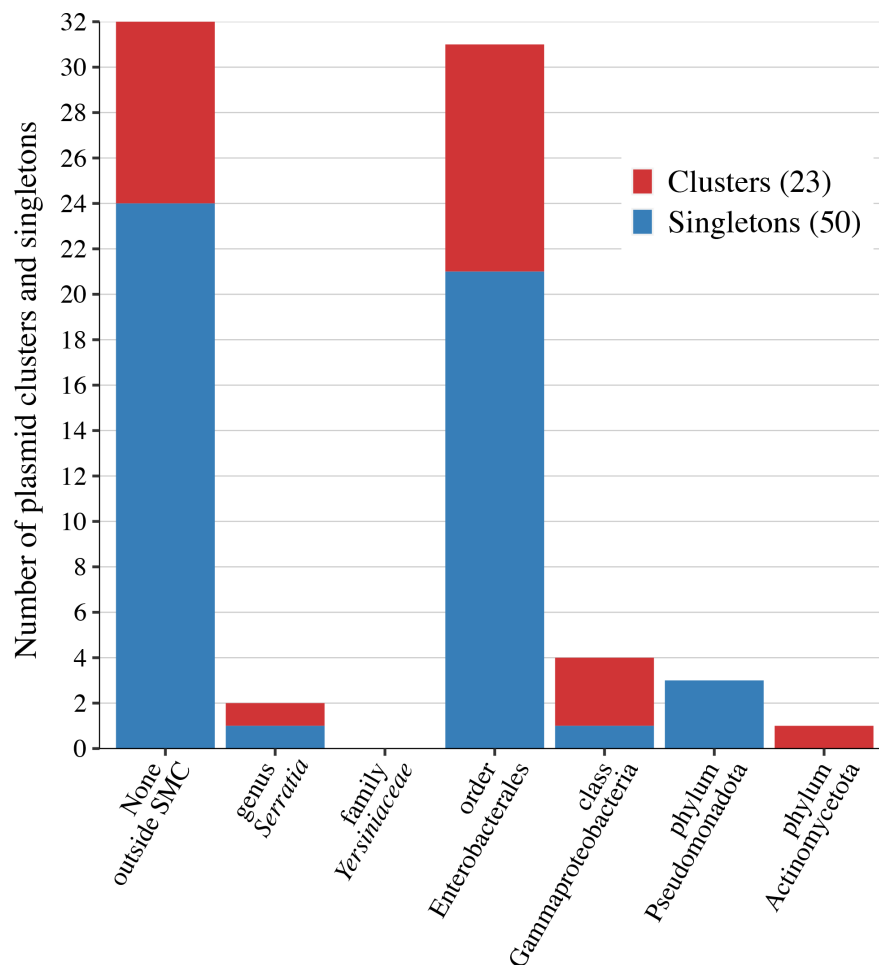


Fig. 8. Potential host ranges of the 23 plasmid clusters and 50 singleton plasmids. Potential host ranges were predicted based on the detection of plasmids that were highly homologous (<0.06 Mash distance) to each plasmid cluster and singleton in the NCBI database (see Tables 3 and S5 for more details).

6b, and Table S3). The GC contents of 11 singleton plasmids were also lower than 46%, with one showing a 27.8% GC content (Fig. 5). In addition, Cluster 3 plasmids showed much higher GC contents (64.8%) than their host chromosomes (Figs 5 and 6b). The size and GC content of the 132 plasmids were not correlated (Fig. 6c), although smaller plasmids showed a wider range of GC contents than larger plasmids, as shown in an analysis of plasmids from a wide range of bacterial species [44]. These results suggest that the acquisitions of most plasmids (and/or their gene contents) by the strains analysed in this study were recent or relatively recent genetic events.

Within-SMC transmission and potential host ranges of plasmids

Of the 23 plasmid clusters, 16 comprised plasmids distributed in two or more different host clades (Fig. 7, see also network diagrams of each plasmid cluster shown in Fig. S5b). Among these multiclade clusters, Clusters 8 and 13 consisted of plasmids from four clades (Fig. 7). This finding suggests the interclade transmission of the 16 plasmid clusters.

To analyse the potential host ranges of the SMC plasmids in a wider taxonomic scope, we first searched the NCBI database by BLASTn for plasmids similar to each of the 132 plasmids. Then, among the plasmid hits in this initial screening, we selected highly homologous plasmids with the same Mash distance threshold (0.06) as used for the clustering of SMC plasmids. This analysis identified 1955 plasmids outside the SMC (listed in Table S5), which should share very recent common ancestors with SMC plasmids, indicative of their potential transmission abilities. As summarized in Fig. 8 and Table 3, eight clusters and 24 singletons had no highly homologous plasmids in the database, and one cluster and one singleton had such plasmids only within the genus *Serratia*. However, for the plasmids in the other clusters and singletons, highly homologous plasmids were found in different species belonging to the order *Enterobacterales*, class *Gammaproteobacteria* or phylum *Pseudomonadota*. Moreover, a plasmid highly homologous to Cluster 15 was found in *Corynebacterium jeikeium*, a Gram-positive, rod-shaped bacterium

Moreover, members of the family *Enterobacteriaceae*, particularly *K. pneumoniae*, were suggested as the main sources for plasmid exchanges with the SMC. These results highlight the power of closed genome-based analysis in studies of plasmids and provide important insights into the nature of plasmids distributed in the SMC. The 67 closed genomes obtained in this study will also be important genomic resources for future studies of the SMC and other species in the genus *Serratia*, particularly for accurate analyses of their MGEs.

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Author contributions

Conceptualization: T.H. Data curation: D.S.N., T.H. Formal analysis: D.S.N., T.H. Funding acquisition: T.H. Investigation: D.S.N., I.T., T.H. Methodology: D.S.N., I.T., K.N., Y.G. Project administration: T.H. Resources: T.O. Validation: D.S.N., T.H. Visualization: D.S.N., I.T., T.H. Writing – original draft: D.S.N., T.H. Writing – review and editing: D.S.N., I.T., T.O., K.N., Y.G., T.H.

Conflicts of interest

The authors declare that there are no conflicts of interest.

Ethical statement

There are no ethical considerations applicable to the work presented.

Consent to publish

The authors agree with the publication of this article in Microbial Genomics.

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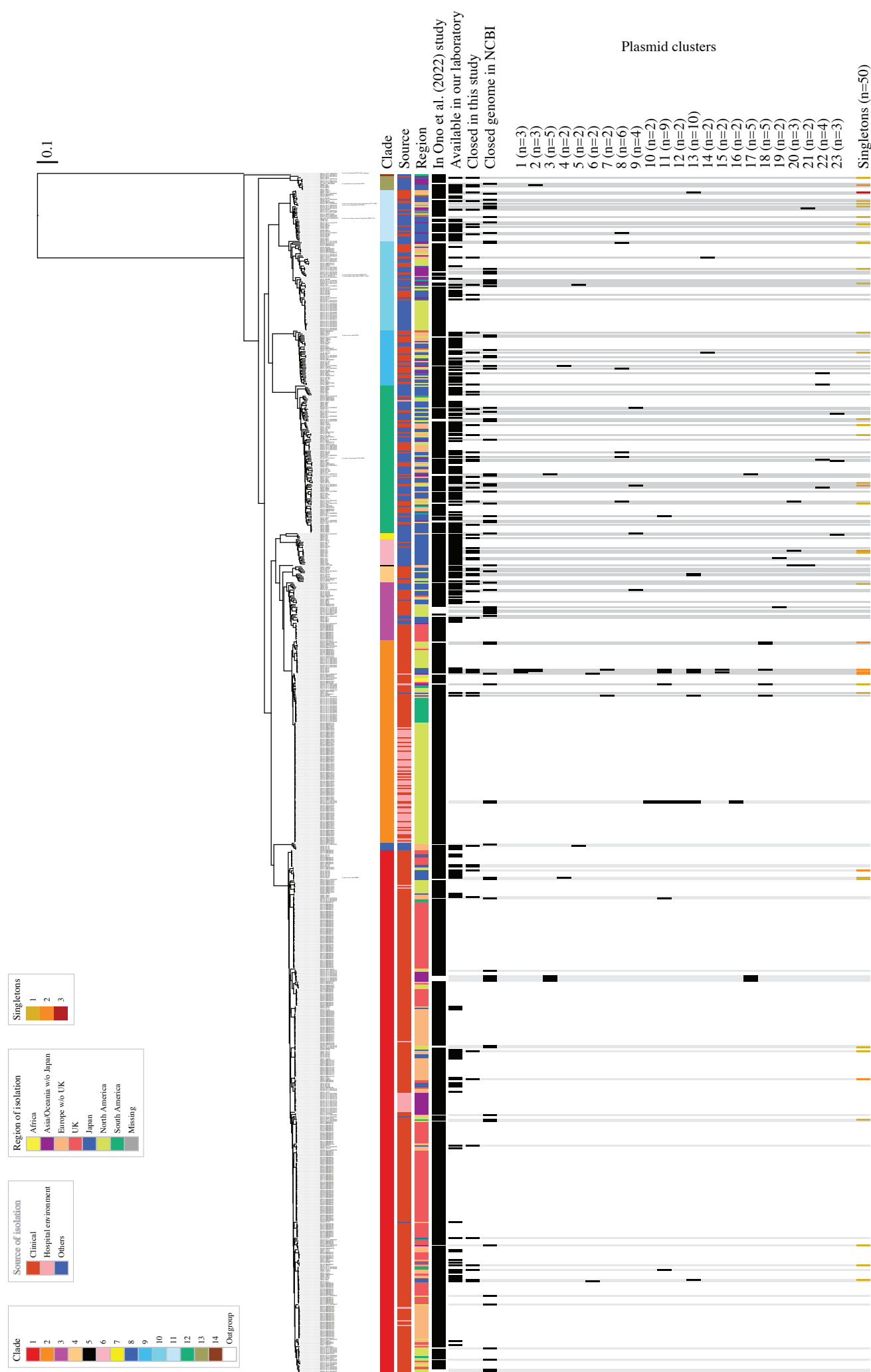


Fig. S1. Phylogenetic positions of the 142 genomes in the SMC. The core gene-based ML tree of the 775 SMC genomes that we previously analysed (Ono et al., 2022; Ref. 6 in the main text), 52 closed genomes and three draft genomes of type strains of three SMC species newly obtained from the NCBI database were constructed with a *S. ficaria* strain as an outgroup. The type strains and two SMC strains (Db11 and SM39) are indicated by their names. The clade, isolation source, isolation region are indicated for each strain. Strains analysed in the Ono et al. (2022) study, strains available in our laboratory, genomes closed in this study, and closed genomes obtained from NCBI are also indicated. The 142 closed genomes analysed in this study were highlighted by gray backgrounds and the distribution of plasmid clusters and singletons in these genomes were also indicated.

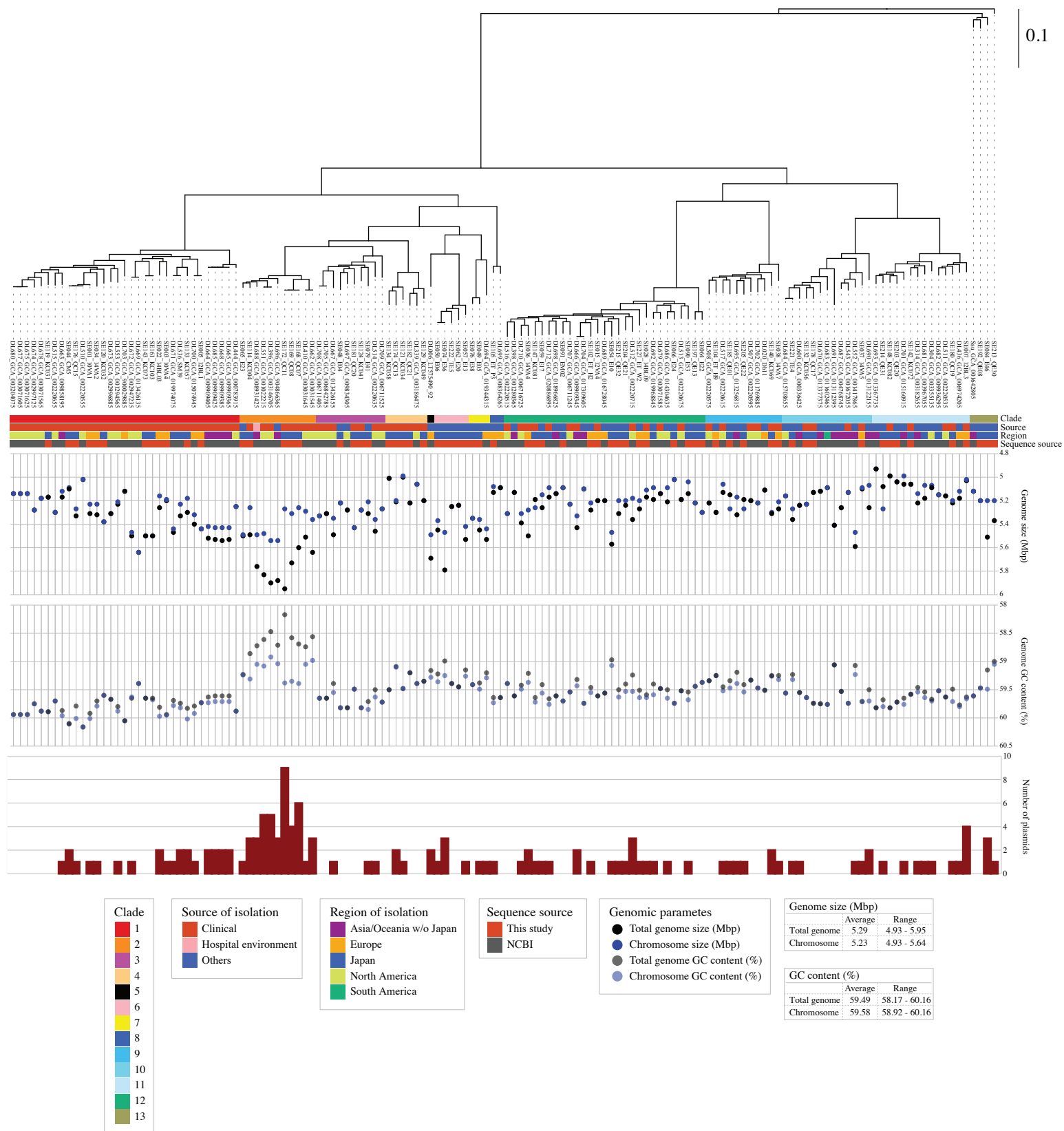
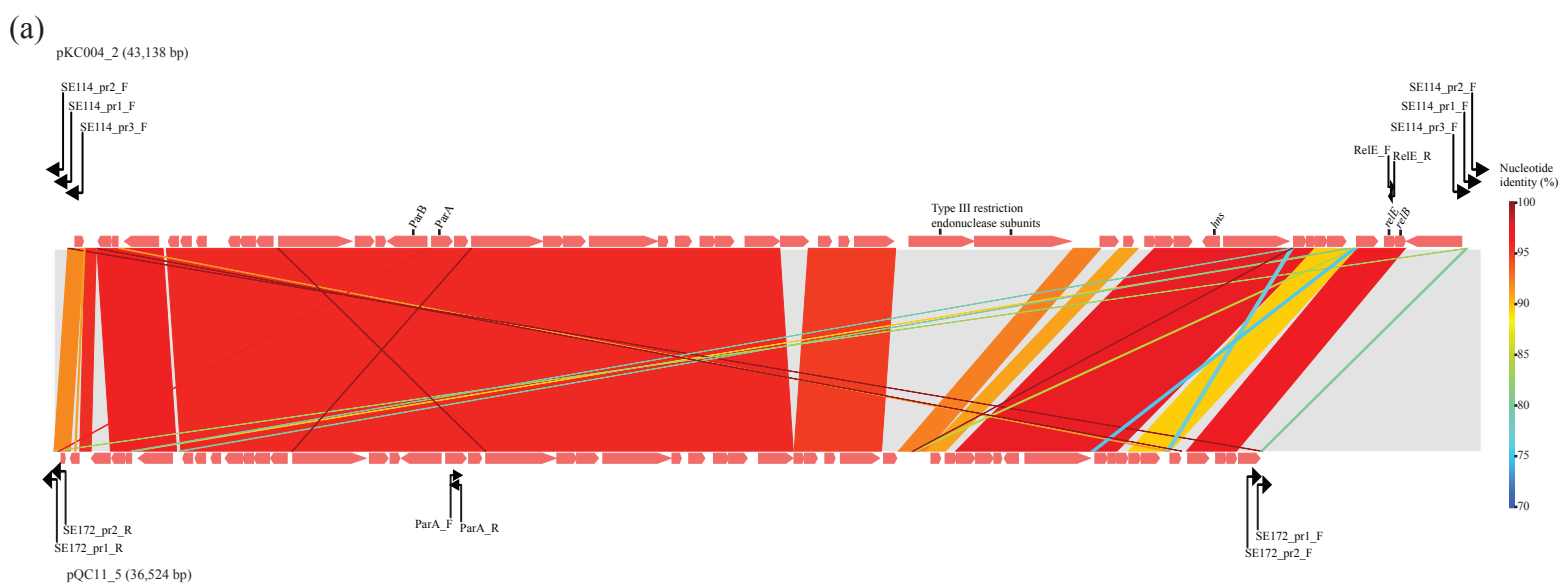
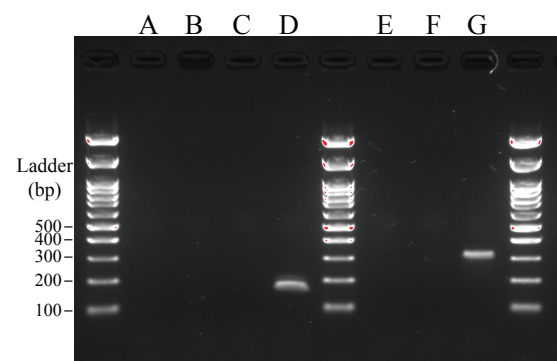


Fig. S2. Phylogenetic relationships of the 142 closed genomes analysed in this study. An ML tree was constructed based on the 535,875 SNPs identified in 3,189 core genes. The clade, isolation source, isolation region, genome sequence source (closed in this study and obtained from NCBI) are indicated for each genome. The sizes and GC content of the total genome and chromosome of each genome and the numbers of plasmids found in each genome are also shown.



(b)

Agarose gel lane	Primers ID	Primers sequences (5' -> 3')	Expected size (bp)
A	SE114_pr1_F	CATGCACTTACATTCTCTGAAC	
	SE114_pr1_R	TCGCCAGTTCAGTATTTCC	
B	SE114_p2r_F	ATCCGGGTTTTACTCATACCA	
	SE114_pr2_R	TTCCTGATACCACATCGAATG	
C	SE114_pr3_F	ACACTTAATGAGCTGTCATCTGC	
	SE114_pr3_R	GCCAGCTTCTTGATCTGTTC	
D	RelE_F (positive control)	ATAGTAGGAAGTGGCGGTG	175
	RelE_R (positive control)	GAGCTGGTTTTTCTCTGCTG	
E	SE172_pr1_F	CTCAGGCTTCTCAGGTTTCATTG	
	SE172_pr1_R	TCCCCCTGATAACATCGTACTATC	
F	SE172_pr2_F	GGGATGATTGGGAAAGGCATATAC	
	SE172_pr2_R	CAGGATACTACTGGTTCAGAGTC	
G	ParA_F (positive control)	TGCGGAGAAAAACGGTAAAC	318
	ParA_R (positive control)	TTACGGATGTAGGGCTGTTC	



(c)

PFGE gel lane	Description	Circular plasmids (kb)	Linear plasmids (kb)
L8	PFGE standards 8 kb ladder		
L5	PFGE standards 5 kb ladder		
λ	Lambda PFG ladder		
Db	Strain Db11	-	-
E6	Strain E6	78.9	-
E36	Strain E36	204.9, 68.3 and 39.6	-
KC	Strain KC004	176.4 and 3.2	43.1
QC	Strain QC11	244.4, 200.4, 95.2, 87.9, 5.1, 4.9, 3.8 and 3.2	36.5

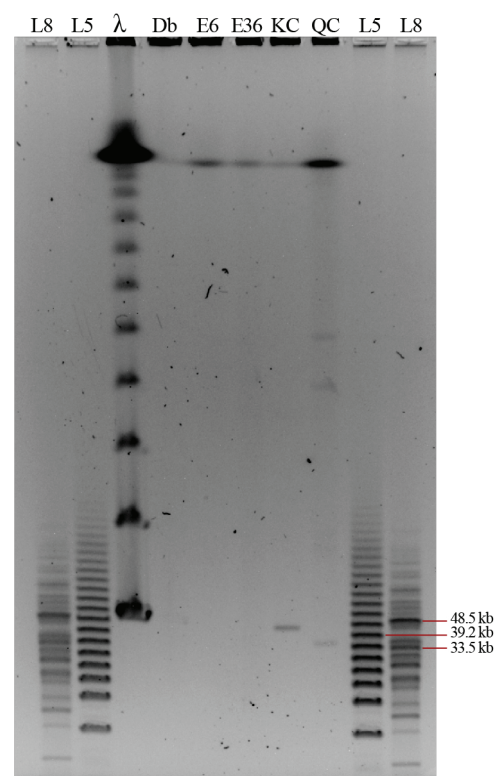
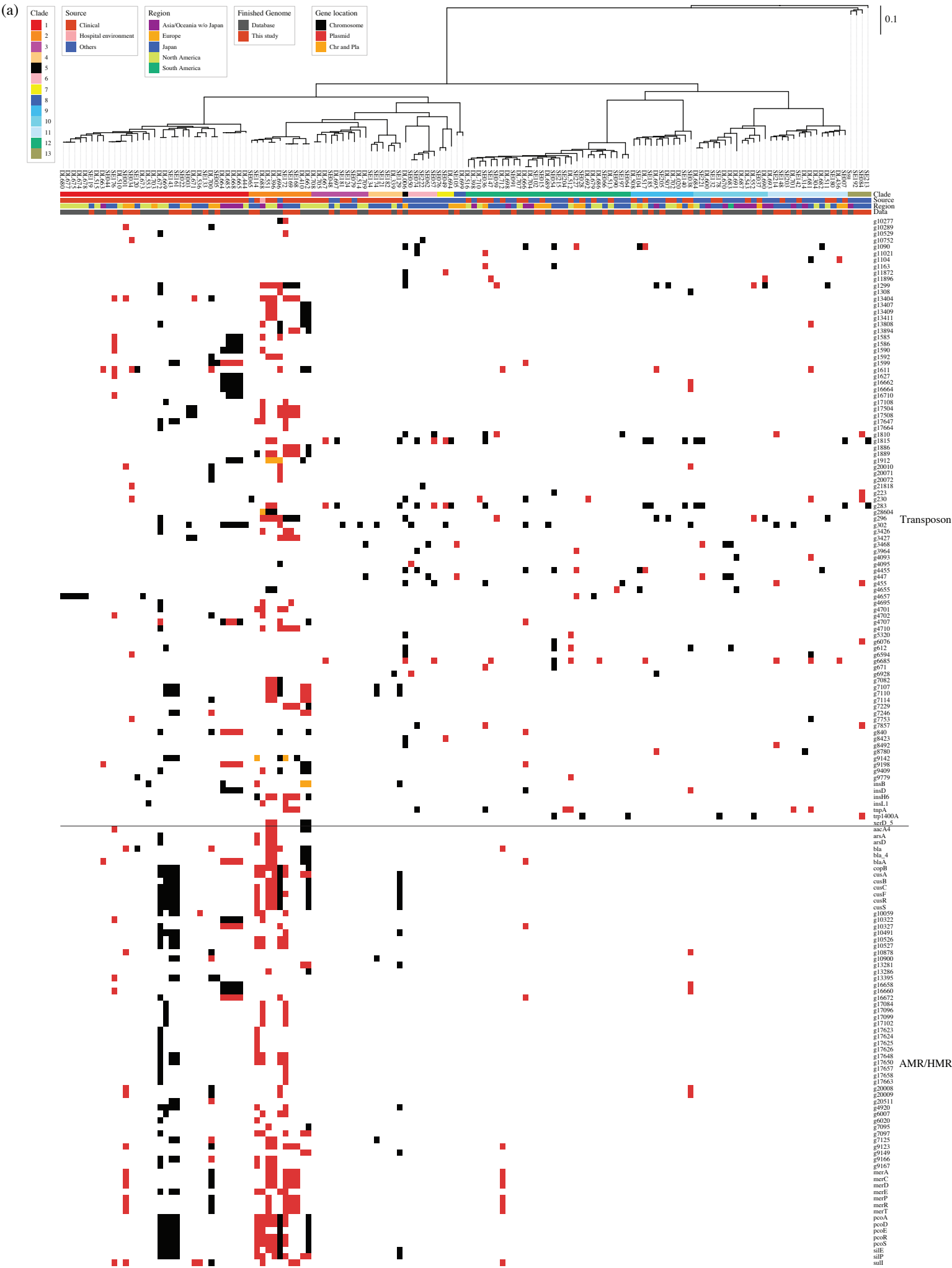


Fig. S3. Linear plasmids found in two SMC strains. (a) Genetic maps of the two linear plasmids and their nucleotide sequence identity are shown. These plasmids constituted Cluster 7. Genes indicated were previously described in similar linear plasmids from *Enterobacteriaceae* [37]. Positions and directions of the primers designed for PCR analysis shown in Panel (b) are also indicated. (b) Sequences of the PCR primers and the results of PCR analysis using these primers are shown. While the primer pair designed at the middle of the plasmid sequence yielded a band of the expected size in each strain (positive controls), the primer pairs targeting the ends of each plasmid sequence yielded no amplicons. (c) The result of PFGE analysis of undigested genomic DNA of the two strains carrying these linear plasmids is shown. A band with an expected size was detected in each strain, confirming the linearity of the two plasmids.



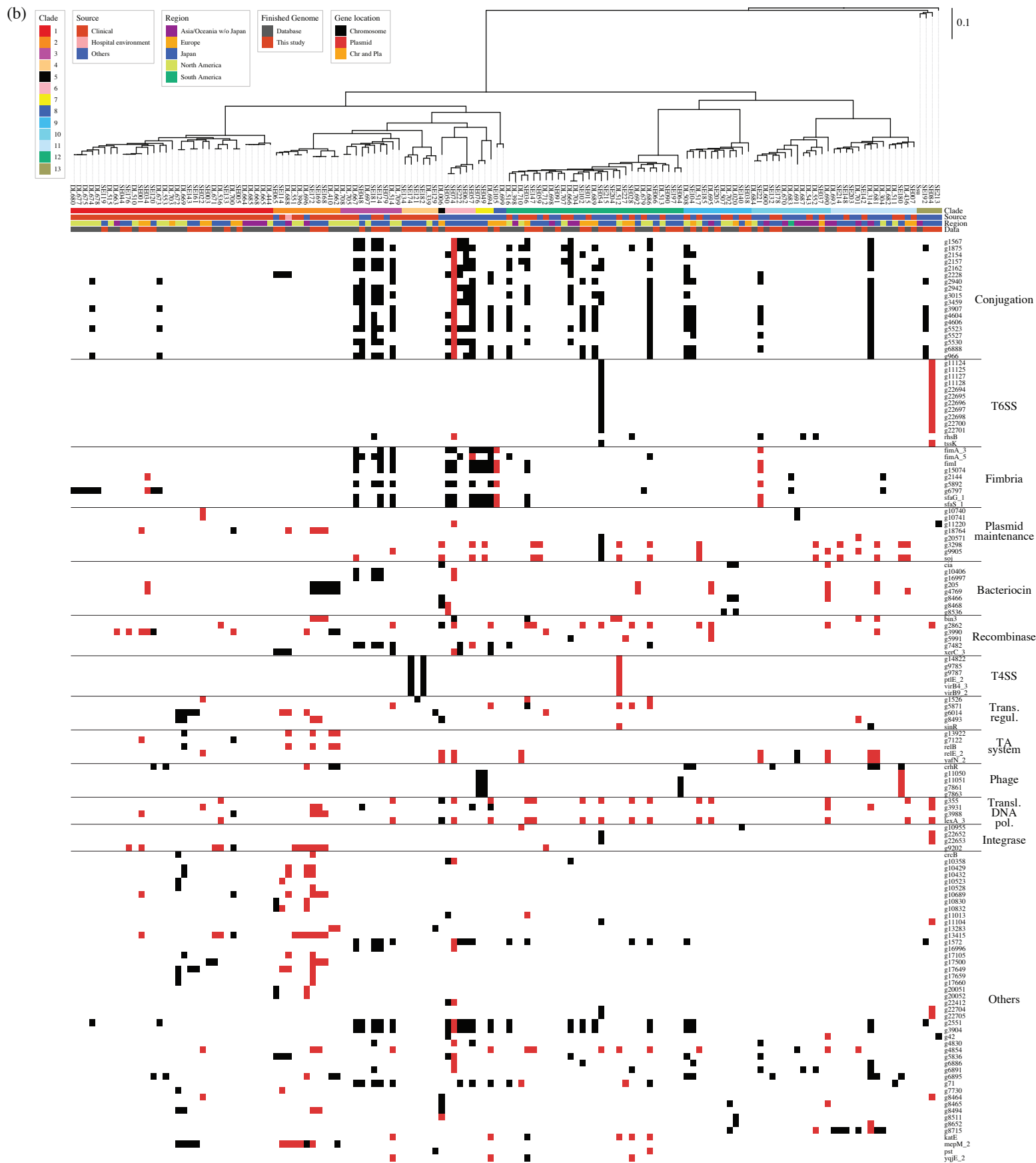
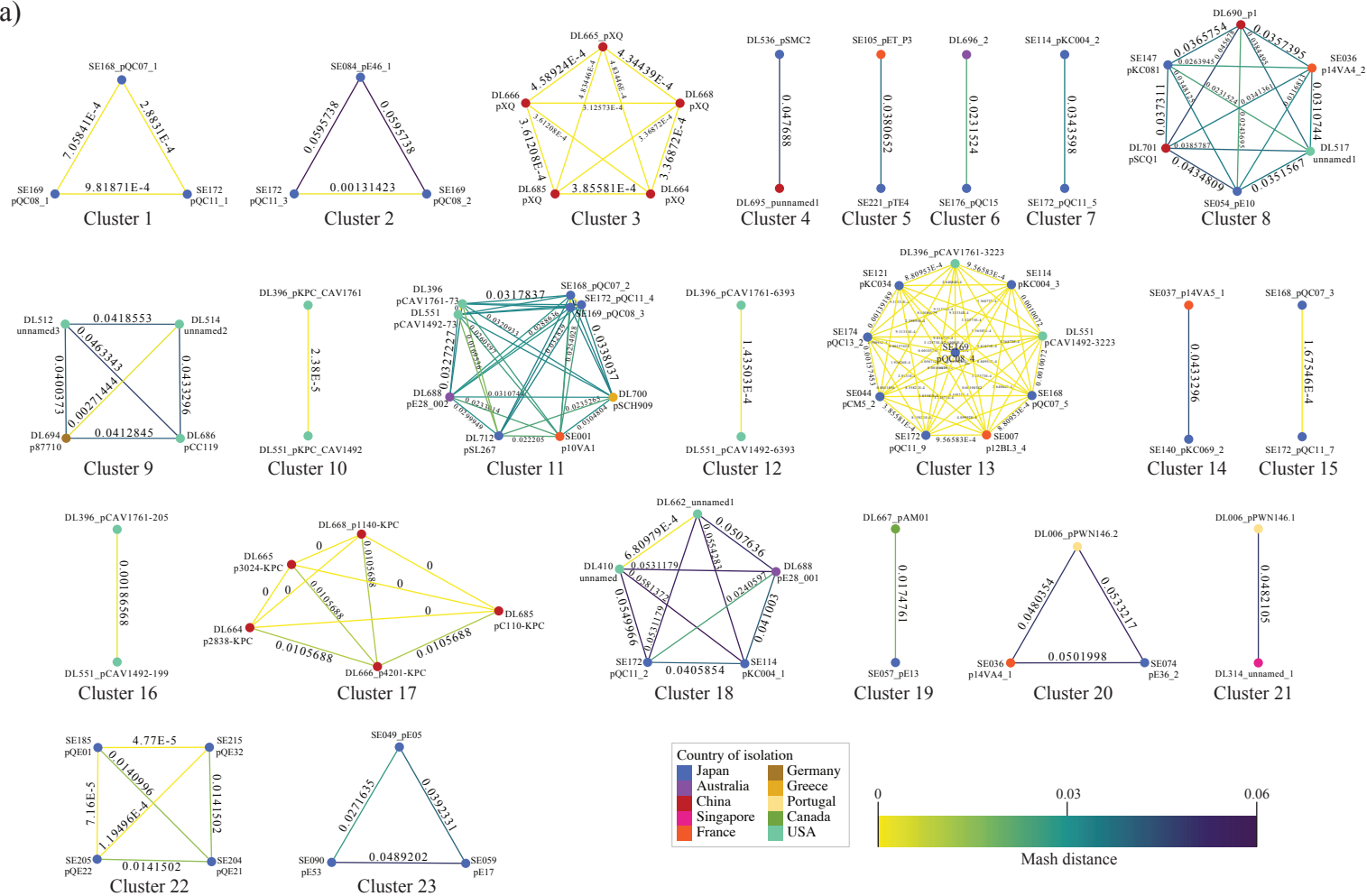


Fig. S4. Distribution of the 299 function-predicted Chr/Pla genes among the 142 closed SMC genomes. Genomic locations of each gene (chromosome or plasmid) are also indicated. Genes related to Transposon and AMR/HMR are shown in panel (a) and others are in panel (b). Trans. Regul.; Transcriptional Regulator, Transl. DNA pol.; Translesion DNA polymerase. See Table S4 for predicted functions of 299 genes.

(a)



(b)

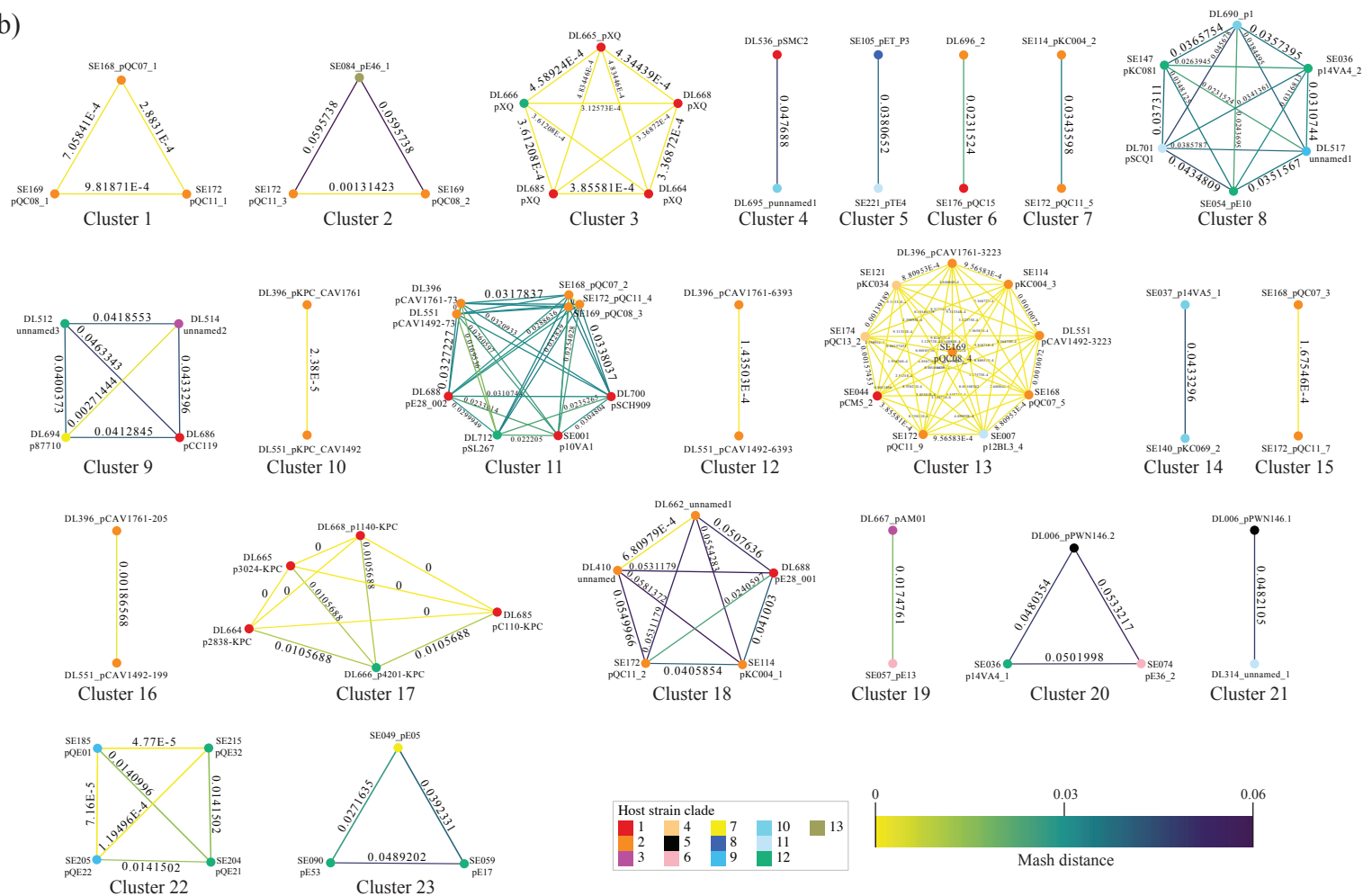


Fig. S5. Network diagrams of the 23 plasmid clusters prepared and visualized with Cytoscape v.3.10.0 [36] using Prefuse Force Directed layout weighted by pairwise Mash distances with default parameters. Geographic (country) information and clades of host strains are shown in (a) and (b), respectively.

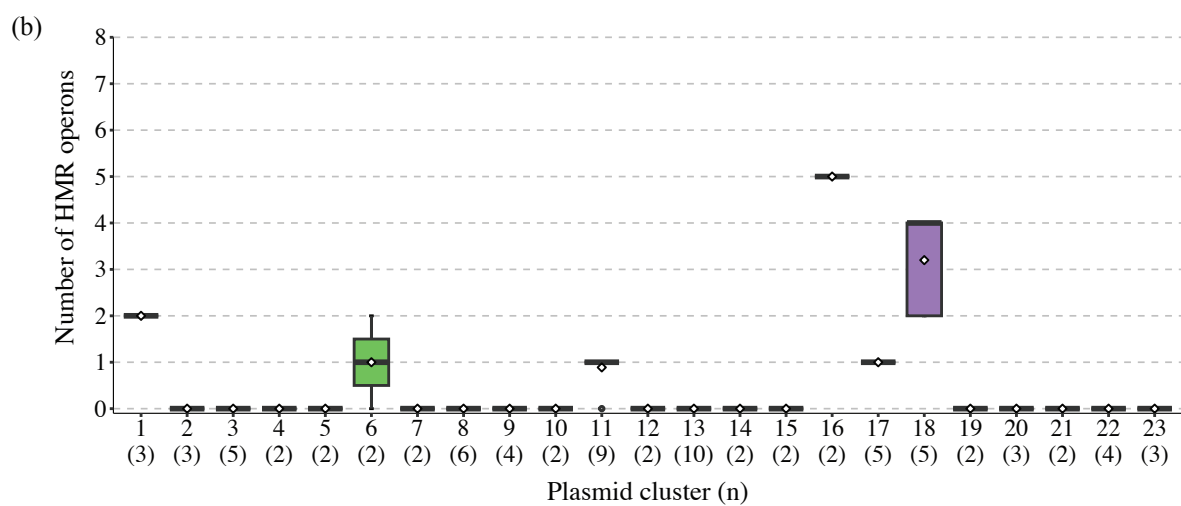
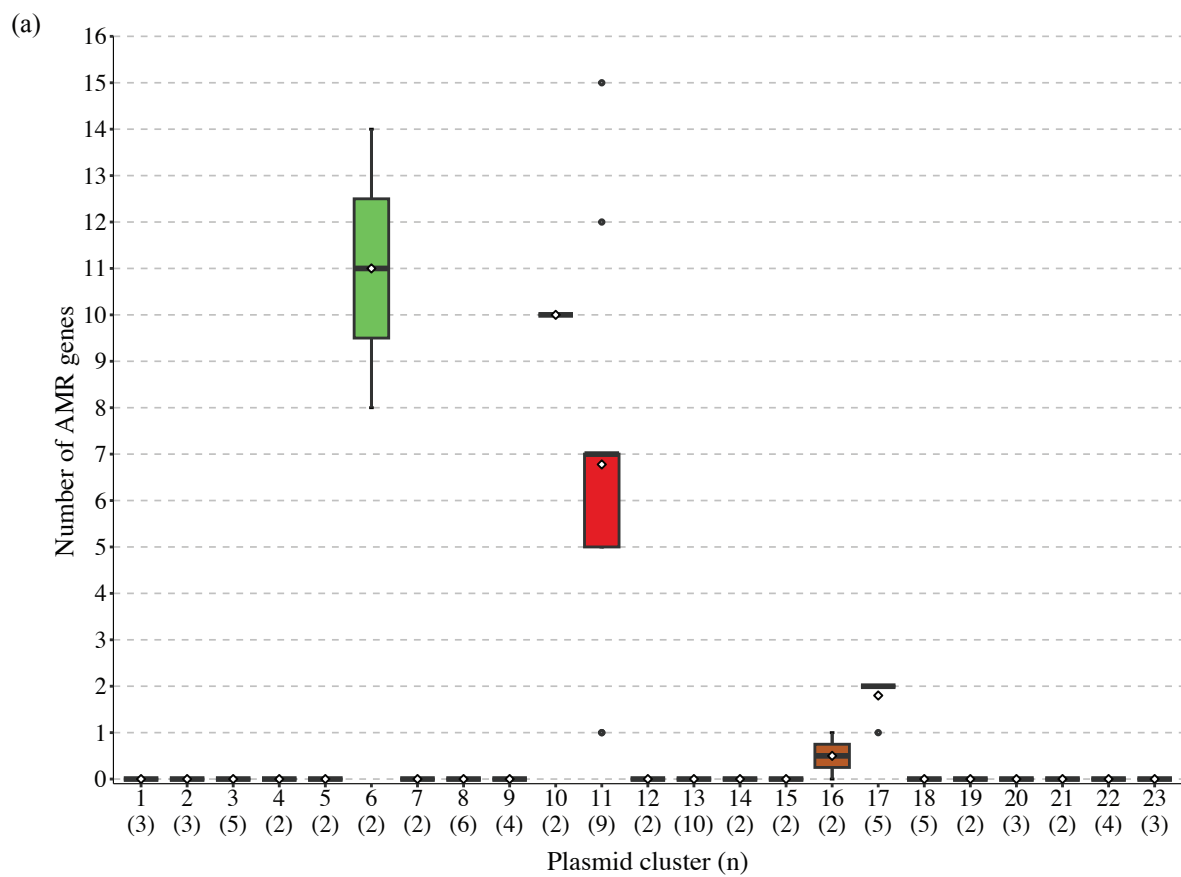


Fig. S6. The numbers of AMR genes (a) and HMR operons (b) encoded by each plasmid cluster.

Table S1: List of closed genomes analyzed in this study.

[illegible]

Table S2: Differences in genome size between closed and draft sequences.

Strains	Closed genome (bp)	Draft assembly (bp)	Closed - Draft (bp)	Number of plasmids
SE001_10VA1	5,308,278	5,281,151	27,127	1
SE003_10VA4	5,199,493	5,173,090	26,403	1
SE005_12BL1	5,437,989	5,401,809	36,180	
SE007_12BL3	5,033,039	5,004,976	28,063	4
SE015_12VA4	5,197,128	5,167,718	29,410	
SE022_14BL03	5,260,390	5,232,934	27,456	2
SE028_14BL09	5,169,281	5,139,913	29,368	1
SE034_14VA2	5,317,462	5,290,464	26,998	1
SE036_14VA4	5,498,766	5,429,188	69,578	2
SE037_14VA5	5,095,222	5,066,421	28,801	1
SE038_14VA7	5,265,848	5,222,721	43,127	1
SE044_CM5	5,100,511	5,072,689	27,822	2
SE048_E04	5,224,855	5,177,593	47,262	
SE049_E05	5,453,398	5,417,810	35,588	1
SE050_E06	5,451,727	5,399,667	52,060	1
SE054_E10	5,567,346	5,515,303	52,043	1
SE057_E13	5,526,983	5,483,633	43,350	1
SE059_E17	5,260,136	5,223,053	37,083	1
SE062_E20	5,241,956	5,211,643	30,313	
SE064_E22	5,296,927	5,252,992	43,935	
SE065_E23	5,497,510	5,456,044	41,466	1
SE066_E24	5,015,878	4,989,616	26,262	
SE074_E36	5,785,264	5,677,281	107,983	3
SE076_E38	5,353,302	5,315,227	38,075	
SE079_E41	5,306,402	5,273,603	32,799	1
SE084_E46	5,506,736	5,450,613	56,123	3
SE090_E53	5,136,471	5,101,902	34,569	1
SE091_EM02	5,085,848	5,055,685	30,163	
SE102_ET_H2	5,279,826	5,247,410	32,416	1
SE104_ET_H9	5,302,314	5,269,487	32,827	
SE105_ET_P3	5,129,805	5,096,828	32,977	1
SE114_KC004	5,485,222	5,437,048	48,174	3
SE119_KC031	5,172,316	5,138,363	33,953	
SE120_KC032	5,381,407	5,352,714	28,693	
SE121_KC034	4,998,008	4,981,697	16,311	1
SE124_KC041	5,277,442	5,227,849	49,593	
SE129_KC049	5,197,553	5,166,241	31,312	
SE132_KC056	5,232,355	5,200,258	32,097	
SE133_KC057	5,301,187	5,296,927	4,260	2
SE134_KC058	5,010,344	4,972,181	38,163	
SE140_KC069	5,310,191	5,285,042	25,149	2
SE142_KC072	5,063,566	5,032,441	31,125	
SE143_KC073	5,504,482	5,503,780	702	
SE147_KC081	5,187,304	5,161,049	26,255	1
SE148_KC082	4,992,650	4,959,857	32,793	
SE161_KC103	5,504,908	5,474,475	30,433	
SE168_QC07	5,603,850	5,551,889	51,961	6
SE169_QC08	5,728,036	5,626,840	101,196	4
SE172_QC11	5,951,644	5,876,380	75,264	9
SE174_QC13	5,207,203	5,176,819	30,384	2
SE176_QC15	5,332,150	5,299,096	33,054	1
SE178_QC17	5,125,610	5,095,276	30,334	
SE180_QC19	5,216,117	5,179,684	36,433	1
SE181_QC20	5,431,434	5,386,113	45,321	
SE182_QC21	5,220,978	5,182,041	38,937	
SE185_QE01	5,150,568	5,121,027	29,541	1
SE192_QE08	5,199,566	5,165,632	33,934	
SE197_QE13	5,219,101	5,169,890	49,211	
SE203_QE20	5,036,689	4,998,645	38,044	
SE204_QE21	5,240,357	5,202,480	37,877	1
SE205_QE22	5,194,597	5,151,712	42,885	1
SE213_QE30	5,369,835	5,275,779	94,056	1
SE214_QE31	5,082,691	5,019,115	63,576	1
SE215_QE32	5,309,714	5,271,964	37,750	1
SE221_TE4	5,360,887	5,329,852	31,035	1
SE222_TE5	5,251,009	5,211,538	39,471	
SE227_ET_W2	5,267,928	5,239,257	28,671	1
Average			38,889	

^{**} MOR type detected after changing start position of sequence in which relaxase was separated at ends of sequence.

Table 5d: Cases encoded by chromosomes or phenids depending on circles.

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Table S5: Plasmids highly homologous to the SMC plasmids.

Strain ID	Plasmid name	Plasmid class	Phylum	Class	Order	Family	Genus	Species	Description	Accession	Highest Mash distance
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar 4:5,12:-1-4:551 plasmid pSAL4551-1 DNA, complete sequence	AP028305.1	0.026819
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar 4:5,12:-1-4:481 plasmid pSAL4681-1 DNA, complete sequence	AP028308.1	0.026478
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli str. Stx1 plasmid pStx_255, complete sequence	CP011602.1	0.0146626
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Shigella	Shigella flexneri	Shigella flexneri 4c strain 1205 plasmid pShf1205, complete sequence	CP012561.1	0.013294
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain N13-01290 plasmid pN13-01290_23, complete sequence	CP012911.1	0.015616
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain C829 plasmid pC829, complete sequence	CP015725.1	0.0294234
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli O157 strain 180-PT24 plasmid, complete sequence	CP015833.1	0.0139988
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain 13C10657 plasmid p13C10657-1, complete sequence	CP016203.1	0.012872
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica strain 98-04615 plasmid pSf98-04615-1, complete sequence	CP016291.1	0.013294
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain FDAARGOS_319 plasmid unannoted, complete sequence	CP027411.1	0.015998
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain AMSH001 plasmid pAMSH1, complete sequence	CP030401.1	0.0133547
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia fergusonii	Escherichia fergusonii strain 404 plasmid p280_404, complete sequence	CP031284.1	0.0186195
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain CT39 plasmid pCT39-PT1, complete sequence	CP032839.1	0.0242917
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica strain CFSA244 plasmid pCFSA244_1, complete sequence	CP033432.2	0.0250005
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica strain CFSA1096 plasmid pCFSA1096, complete sequence	CP033472.2	0.0170006
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain WCHEC025970 plasmid pCTX0199_025970, complete sequence	CP036178.1	0.0141502
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Newport strain VNSEC023 plasmid pCFSA080857, complete sequence	CP039438.1	0.0150813
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain TYP0001 plasmid pTYP0001, complete sequence	CP040472.1	0.0146626
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Enteritidis strain STU121519-2 plasmid p12519A, complete sequence	CP041174.1	0.0141502
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Bredeney strain SA20114778W7 plasmid pET1.1-hcII, complete sequence	CP042231.1	0.0134255
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain ST95-32 plasmid pST95-32-1, complete sequence	CP043951.1	0.0126347
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Schwarzengrund strain 9355 plasmid p230_9355, complete sequence	CP045446.1	0.0165552
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Schwarzengrund strain 1288 plasmid p230_1288, complete sequence	CP054491.1	0.0165552
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Kluyvera	Kluyvera intermedia	Kluyvera intermedia strain 182 plasmid p182-1, complete sequence	CP045444.1	0.0138985
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Kluyvera	Kluyvera intermedia	Kluyvera intermedia strain N2-1 plasmid pN2-1, complete sequence	CP045446.1	0.0138985
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF11216 plasmid unannotedA, complete sequence	CP047523.1	0.0234513
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF11077 plasmid unannoted, complete sequence	CP047526.1	0.0142009
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10469 plasmid unannoted, complete sequence	CP047528.1	0.0142009
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10484 plasmid unannotedA, complete sequence	CP047532.1	0.0135259
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10452 plasmid unannoted, complete sequence	CP047536.1	0.0137488
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10485 plasmid unannotedA, complete sequence	CP047538.1	0.0127093
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10517 plasmid unannoted, complete sequence	CP047540.1	0.0136967
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10330 plasmid unannoted, complete sequence	CP047543.1	0.0132087
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10250 plasmid unannoted, complete sequence	CP047545.1	0.0138985
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain STJUF10169 plasmid unannoted, complete sequence	CP047549.1	0.0142009
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella aerogenes	Klebsiella aerogenes strain IN0871 plasmid pKIN0871_NDM-5, complete sequence	CP047608.1	0.0125875
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Schwarzengrund strain VAPHI_SAL-400527 plasmid p1566-2, complete sequence	CP047609.1	0.0136967
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Schwarzengrund strain VAPHI_SAL-400757 plasmid p2045-2, complete sequence	CP048303.1	0.0143337
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain pV01-18-E02-025-051 plasmid pKCE1005, complete sequence	CP049001.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain GS20117-Sal-008 plasmid unannoted, complete sequence	CP050131.1	0.0175349
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain ST106 plasmid pST106-1, complete sequence	CP050729.1	0.010124
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain ST546 plasmid pST546-1, complete sequence	CP050731.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain ST545 plasmid pST45-1, complete sequence	CP050754.1	0.0137395
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Indiana strain SI115 plasmid pSI115-1, complete sequence	CP050763.1	0.020747
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Indiana strain SI102 plasmid pSI102-1, complete sequence	CP050772.1	0.0236339
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Indiana strain SI057 plasmid pSI057-1, complete sequence	CP050775.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain CVM 31561 plasmid p31561-1, complete sequence	CP051113.1	0.0167259
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain CVM 28322 plasmid p28322-1, complete sequence	CP051599.1	0.0160531
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain CVM 24359 plasmid p24359-1, complete sequence	CP051592.1	0.013998
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain CVM 20760 plasmid p20760-2, complete sequence	CP051423.1	0.013998
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Escherichia coli strain SC148 plasmid pSC148, complete sequence	CP051424.1	0.0136967
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Bredeney strain CVM 24358 plasmid p24358-1, complete sequence	CP051442.1	0.0231031
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Indiana strain K16S897 plasmid pK16S897, complete sequence	CP052538.1	0.0160531
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain RH841-C01 plasmid pRH841-C01_2, complete sequence	CP057008.1	0.0121679
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain AMPCN024 plasmid pAMPD03, complete sequence	CP058311.1	0.0122604
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Escherichia coli strain M17-1 plasmid pM17-1_2, complete sequence	CP059161.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 453 plasmid p453-MDR, complete sequence	CP060856.1	0.0127293
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain S585 plasmid pS585_1, complete sequence	CP061161.1	0.0161084
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain LD67-1 plasmid pLD67-1-157ab, complete sequence	CP061187.1	0.0272429
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain S150D9511 plasmid unannot1	CP061807.1	0.0117112
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Salmonella enterica strain S150D9511 plasmid unannot3	CP061809.1	0.0114419
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain R274 plasmid unannot0	CP061906.1	0.0134036
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain R274 plasmid unannot1	CP061907.1	0.0172424
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella sp.	Salmonella sp. STJUF10479 plasmid p4076A, complete sequence	CP064675.1	0.0137986
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 172 plasmid p172, complete sequence	CP064680.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain GS2016-Sal-016 plasmid pS016A, complete sequence	CP065922.1	0.0146996
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli O176:H45 strain MN09 plasmid pMUB-MN9-1, complete sequence	CP066083.1	0.0174175
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain CFSA083829 plasmid pCFSA083829_1, complete sequence	CP070934.1	0.0142518
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain CFSA083827 plasmid pCFSA083827_1, complete sequence	CP070866.1	0.0154006
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain EC20871-C9 plasmid pE20871-C9, complete sequence	CP071121.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain E105 plasmid pE105-4, complete sequence	CP072315.1	0.0137986
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain PK5074 plasmid pPK5074-MCR1, complete sequence	CP072803.1	0.0145452
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain X152 plasmid unannot1, complete sequence	CP074555.1	0.0119385
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Choleraesuis strain CFSA02626 plasmid pCFSA02626, complete sequence	CP075027.1	0.0191008
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain C97 plasmid unannot1, complete sequence	CP075491.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain PK5217 plasmid pPK5217-MCR1, complete sequence	CP080123.1	0.0145452
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Derby strain F8S1609398 plasmid pF18S029-1	CP082427.1	0.0162749
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Bredeney strain CVM N18S0406 plasmid pN18S0406-1, complete sequence	CP082485.1	0.0124178
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Bredeney strain CVM N18S0406 plasmid pN18S0406-1, complete sequence	CP082486.1	0.0124178
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain EC29 plasmid pEC29, complete sequence	CP083043.1	0.0139943
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain EC29 plasmid pEC22-CTX-M-15, complete sequence	CP084001.1	0.0139595
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Saintpaul strain S23 plasmid pS23-hcII, complete sequence	CP085977.1	0.0129677
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain EF940 plasmid pMADE-1, complete sequence	CP086679.1	0.0127767
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 2080987-Sf plasmid p2080987-241, complete sequence	CP090530.1	0.0134496
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 2017005-Sf plasmid p2017005-292, complete sequence	CP090531.1	0.0134496
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 2016089-Sf plasmid p2016089-170, complete sequence	CP090536.1	0.0204919
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 2016062-Sf plasmid p2016062-242, complete sequence	CP090540.1	0.0145076
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 2010112-Sf plasmid p2010112-144, complete sequence	CP090542.1	0.0245258
			Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain 2017028-Sf plasmid p2017028-205, complete sequence	CP090546.1	0.0150813

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Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella	Klebsiella michiganensis	Klebsiella michiganensis strain B0-50 Kpn plasmid pB0-50_KM_VIM-1, complete sequence	CP049191.1	0.020546
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain 13002 plasmid p1_130002, complete sequence	CP064854.1	0.026365
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica subsp. enterica serovar Newport strain CFSAN024415 plasmid pCFSAN024415, complete sequence	CPO74361.1	0.029797
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae subsp. pneumoniae strain WRIC17 plasmid pKMC30P77, full complete sequence	CPO76626.1	0.023299
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Salmonella enterica	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain 364.05 plasmid pH3-364.05, complete sequence	CPO80424.1	0.023785
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Salmonella enterica	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain 364.65 plasmid pH3-364.65, complete sequence	CPO80424.1	0.033787
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Salmonella enterica	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain 363.78 plasmid pH3-363.78, complete sequence	CPO80425.1	0.038329
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Salmonella enterica	Salmonella enterica	Salmonella enterica subsp. enterica serovar Heidelberg strain 35.62 plasmid pH3-35.62, complete sequence	CPO80428.1	0.033787
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Ranella planticola	Ranella planticola	Ranella planticola strain SCL2562 plasmid p_SCL2562, complete sequence	CP082173.1	0.024419
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Salmonella enterica	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain T33106097 plasmid pT33106097	CPO84415.1	0.051179
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Salmonella enterica	Salmonella enterica	Salmonella enterica subsp. enterica serovar Typhimurium strain CVN M18161 plasmid pH18S163-2, complete sequence	CPO82551.1	0.027689
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain 7008.29 plasmid p1-7008.29, complete sequence	CPO82891.1	0.00957263
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain AE-2247421-720-SHSL, plasmid p2247421-720-SHSL, 1, complete sequence	CPO86417.1	0.166031
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain AE-2247421-720-MAC, plasmid p2247421-720-MAC, 1, complete sequence	CPO86417.1	0.166031
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain AE-2247421-TS-MAC plasmid p2247421-TS-MAC, 1, complete sequence	CPO86440.1	0.166031
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain AE-2247421-TS-MAC plasmid p2247421-TS-MAC, 1, complete sequence	CPO86440.1	0.166031
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain h7-01 plasmid pKH06, complete sequence	CPO85751.1	0.029231
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Proteus mirabilis	Proteus mirabilis	Proteus mirabilis strain E27105 plasmid pND2A_E27105, complete sequence	CPO88441.1	0.024115
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain 5531 plasmid pMDP906_2, complete sequence	CPO13554.1	0.00999714
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain BSHPKN-11 plasmid unannoted, complete sequence	CPI06091.1	0.031002
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain BSHPKN-9 plasmid unannoted, complete sequence	CPI06091.1	0.031748
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain 202CK-0498 plasmid unannoted, complete sequence	CPI14504.1	0.0171265
Pseudomonas	Gammaproteobacteria	Aeromonadaceae	Aeromonadaceae	Aeromonas hydrophila	Aeromonas hydrophila	Aeromonas hydrophila plasmid pH1, complete sequence	XJ314173.1	0.023014
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strain CRE114 plasmid pMP-PH114, complete sequence	KF250428.1	0.016899
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae plasmid pKAZA, complete sequence	KFY94622.2	0.021602
NA	NA	NA	NA	NA	NA	Uncultured bacterium plasmid pKAZA, complete sequence	KCR77393.1	0.024168
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain A-261 plasmid pJC0610, complete sequence	SX04263.1	0.027855
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain K-12 plasmid R166, complete sequence	KU156773.1	0.024208
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain E-coli plasmid pEci, complete sequence	EY878790.1	0.0206126
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain E-coli plasmid pEci, complete sequence	EY878791.1	0.016532
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Citrobacter freundii	Citrobacter freundii	Citrobacter freundii strain CTS2 plasmid pCTS2, complete sequence	EY878791.1	0.015425
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Citrobacter	Citrobacter freundii	Citrobacter freundii strain CTS2 plasmid pCTS2, complete sequence	EY878791.1	0.015425
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain E-coli plasmid pEci, complete sequence	EY878791.1	0.016532
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae plasmid pKH1091 DNA, complete sequence, strain: Y881	LC058550.1	0.012141
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli plasmid p2064-DNA, contig: V206-4, scaffold: 2, strain: V206	LC064733.1	0.047316
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Klebsiella pneumoniae MycK0475 plasmid pMyCNC0475 plasmid, complete sequence, strain: Y881	LC08822.1	0.014525
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae plasmid pMYCNC0475 plasmid, complete sequence, strain: Y881	LC08822.1	0.014525
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain MyL780 plasmid pMyL780 DNA, complete sequence	LC144483.1	0.021499
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain MYNCM012_1 plasmid pMyNCM012_1 DNA, complete sequence	LC144483.1	0.026735
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain MYNCM015 plasmid pMyNCM015 DNA, complete sequence	LC144483.1	0.026855
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain MYNCM001 plasmid pMyNCM001 DNA, complete sequence	LC144502.1	0.026043
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain MYNCM014 plasmid pMyNCM014 DNA, complete sequence	LC144514.1	0.026945
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae isolate K32626-A364-116-8998-4859976838 genome assembly, plasmid: p1ARS, OMCM099-1	LR607990.1	0.020822
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae isolate K31764-A364-116-8998-4859976838 genome assembly, plasmid: p1ARS, VISM899-1	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Citrobacter freundii	Citrobacter freundii	Citrobacter freundii strain BHI-472 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Citrobacter	Citrobacter werkmanii	Citrobacter werkmanii isolate BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae isolate BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
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Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
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Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enterobacteriaceae	Escherichia coli	Escherichia coli	Escherichia coli strain BHI-495 genome assembly, plasmid: pCWX-CTX-M-15B	LR607923.1	0.020806
Pseudomonas	Gammaproteobacteria	Enterobacteriaceae	Enter					

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CPO5234.1	0.0046329
CPO5234.1	0.0043296
CPO5251.2	0.0030933
CPO5240.0	0.0037767
CPO7036.1	0.0031881
CPO5890.1	0.0076371
CPO6808.1	0.0026795
CPO3015.1	0.0031502
CPO4769.1	0.0053589
CPO4671.1	2.38E-05
CPO7607.1	0.0045634
CPO2607.1	0.0052139
CPO1311.1	0.0029154
CPO5550.1	0.0053149
CPO5958.1	0.0049544
CPO5600.1	0.0038838
CPO5626.1	0.0049002
CPO5647.1	0.0029231
CPO5654.1	0.0039101
CPO5623.1	0.0048202
CPI0095.1	0.0056462
CPI0099.1	0.0054702
CPI0013.1	0.0051782
CPI0010.1	0.0046974
CPI0057.1	0.0052318
CPI0011.1	0.0052118
F3628.672	0.022205
K7C1214.1-3	0.0037767
KV174332.1	0.0284967
MS48923.3	0.0058883
CPO57750.2	0.0016691
MAZ57570.1	0.0016691
LN05820.5.1	0.0002852
OW06710.1	0.009819
OW06766.1	0.0047612
CPO2267.1	0.0057466
CPO1769.1	0.0039303
CPO6268.1	0.0072108
LW02178.1	0.0076371
OW49210.1	0.0049802
OW06765.1	0.0058883
CPO2389.1	0.007671
CPO5327.1	0.0049997
CPO2486.1	0.0058883
CPI1460.1	0.0054461
MI09344.1	0.0054461
ANC2079.1	0.007671
CPO2454.1	0.0050746
CPO2521.1	0.0050851
CPO5225.1	0.0049802
CPO5311.1	0.0053589
CPO5423.1	0.0056966
CPO5386.1	0.007214
CPO7480.1	0.0052714
CPO4980.1	0.0039303
CPO3769.1	0.0054283
CPO3776.1	0.0039303
CPO4807.1	0.0051248
PI10485.1	0.0051504
PI14465.1	0.0074601
PI14313.1	0.0074601
PI14317.1	0.0074601
PI14321.1	0.0074601
PI14325.1	0.0074601
PI14329.1	0.0074601
PI14333.1	0.0072108
PI14355.1	0.0074601
PI14362.1	0.0072108
LRK09210.1	0.0050746
LRK0934.1	0.0059738
LRK4903.1	0.0059738
OW06939.1	0.009819
PI18670.1	0.0056966
CPO7634.1	0.0053589
CPO79762.1	0.0058376
LRK0950.8	0.0058883
MAZ5769.1	0.0058885
MAZ5769.1	0.0059403
CPO7636.1	0.0056966
CPI4877.1	0.0056966
CPI4877.1	0.0056966
MAZ1166.1	0.0053217
CPO4397.1	0.022205
CPO2599.1	0.0056966
CPO5674.1	0.0038209
CPO5652.1	0.0053002
CPO5660.1	0.0052445
CPO7823.1	0.0054702
CPO7581.1	0.0054702
CPO9940.1	0.0023623
CPO99410.1	0.0023623
CPI0355.1	0.0054702
CPI03640.1	0.0054702
PI10579.1	0.0028145
PI15645.1	0.0057827
LRK09477.1	0.0024234
LRK09477.1	0.0024788
CPO7774.1	0.0054283
CPI1623.1	0.0031746
CPI3232.1	0.0024062
CPO4605.1	0.0057671
CPO5426.1	0.0026997
CPO6991.1	0.0056966
CPI88124.1	0.0048408
CPO88129.1	0.0045159
CPO4809.1	0.0023762
CPI02693.1	0.0048626
CPI03580.1	0.0054702
CPI03583.1	0.0054702
PI10615.1	0.0054702
PI03728.1	0.0039403
PI06655.1	0.0043296
MAZ15679.1	0.0053002
CPI07780.1	0.0039303
CPI78807.1	0.0054702
CPI78828.1	0.0072108
OW06782.1	0.0040354
OW06960.1	0.0059738
CPO2801.1	0.0059738
CPO2917.1	0.0026735
CPO2843.1	0.0023137
CPO2917.1	0.0021368
CPI02186.1	0.0021478
CPI03402.1	0.0026131
CPI06188.1	0.0027107
CPO3632.1	0.0029113
CPI06317.1	0.0016307
CPO39796.1	0.0016307
CPO19801.1	0.0029951
CPI09809.1	0.0029123
CPO14640.1	0.0028781
CPI49283.1	0.0019862
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CPO0379.1	0.0023613
CPI2164.8	0.00277
CPO2245.1	0.0025655
CPO2485.1	0.0024435
CPO2408.1	0.0016084
CPO2415.1	0.0026378
CPO2435.1	0.0023014
CPO2477.1	0.0022623
CPO2620.1	0.0025655
CPO2836.1	0.0025655
CPO2680.1	0.0024097
CPO2699.1	0.0024097
CPO2738.1	0.0026378
CPO5211.1	0.0022766
CPO5902.1	0.0024917
CPO5679.1	0.0029767
CPO6884.1	0.0029767
CPO5894.1	0.0067675
CPO9891.1	0.0021524
CPO6806.1	0.0027938
CPO6806.1	0.0019213
CPO7990.1	0.0017432
CPO7580.1	0.0029501
CPO789.1	0.0022142
CPO7751.1	0.003826
CPO7883.1	0.0024927
CPO7900.1	0.0024142
CPO7097.1	0.0034151
CPI7043.6	0.0025655
CPI07123.1	0.0028815
CPO0304.1	0.0016613
CPO2011.1	0.0021234
CPO3053.1	0.0017549
CPI1311.1	0.0025265
CPO4369.1	0.0019625
CPO5913.1	0.0027795
CPI7028.1	0.0017673
CPI0085.1	0.0021693
CPI0089.1	0.0027292
CPI0095.1	0.0024813
CPI0099.1	0.0025005
CPI0013.1	0.0025766
CPI0017.1	0.0025005
CPI0011.1	0.0025005
CPI0189.1	0.0025005
CPI0302.1	0.0021293
CPI03619.1	0.0029501
CPI04798.1	0.0019862
CPI0749.1	0.0019862
CPI0743.1	0.0019862
CPI07199.1	0.0020167
CPI07427.1	0.0019862
CPI07477.1	0.0019862
CPI07442.1	0.0019213
CPI07448.1	0.0019756
CPI07439.1	0.0019514
CPI0749.1	0.0019213
CPI0753.1	0.0019514

SE172

PCJ1_2

DL667

pAMH1

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		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Citrobacter yongae	Citrobacter yongae	Citrobacter yongae strain CT10 plasmid pCTY-6, complete sequence	CPY0259.1	0.01014
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Citrobacter yongae	Citrobacter yongae	Citrobacter yongae strain CT107 plasmid pCTY-81, complete sequence	CPY1086.1	0.034268
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Escherichia coli strain rzy3 plasmid pRZY3, complete sequence	MR02436.1	0.0120404
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Enterobacter cloacae strain T522 plasmid pT522-T52M, complete sequence	MJ061307	0.0161037
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strains 1390 plasmid pK1390-KPC, complete sequence	MR14455.1	0.0018006
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Enterobacter	Enterobacter	Enterobacter cloacae strain 18060 plasmid pB060-NK, complete sequence	MR14455.1	0.0018172
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Escherichia coli plasmid pE1-057, complete sequence	U0251218	0.0251218
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Serratia enterocolitica	Serratia enterocolitica	Serratia enterocolitica strain AG-44 plasmid unannounced, complete sequence	MR13455.1	0.0411716
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Serratia enterocolitica	Serratia enterocolitica	Serratia enterocolitica strain AG-44, plasmid unannounced, complete sequence	MR13455.1	0.0411716
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Rosellula solitaria	Rosellula solitaria	Enterobacter cloacae strain P3C1160.1, complete sequence	PF03549.1	0.0181568
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Rosellula solitaria	Rosellula solitaria	Rosellula solitaria strains 1706215 plasmid pRS128, complete sequence	MF73348.1	0.0155442
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Enterobacter cloacae isolate 16 genome assembly, plasmid PZ	U0247606	0.0247606
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Escherichia coli strain EC00N1 plasmid pEC0-615, complete sequence	CPD6402.1	0.00070741
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strains RHISTV-8095 plasmid pHISTV-8095, 5 complete sequences	CP02915.1	0.0593103
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Enterobacter regensburgensis	Enterobacter regensburgensis	Enterobacter regensburgensis strain RHISTV-8039 plasmid pHISTV-8039, 4 complete sequences	CP02915.1	0.00991131
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Citrobacter freundii	Citrobacter freundii	Citrobacter freundii strains 11-1 plasmid pKCIT-181, complete sequence	CP02276.1	0.0021918
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Proteus mirabilis	Proteus mirabilis	Proteus mirabilis strain XHP6 plasmid pXHP6, complete sequence	CP021847.1	0.0555655
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Enterobacter hormchei	Enterobacter hormchei	Enterobacter hormchei strain ccs4 plasmid unannounced	CP09849.1	0.0109154
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Rosellula planticola	Rosellula planticola	Rosellula planticola strain SC12562 plasmid pK_C12562, complete sequence	CP082176.1	0.000304208
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Enterobacter aerogenes	Enterobacter aerogenes	Citrobacter freundii strain SC1247 plasmid pK_C1247, SC1247, complete sequence	CP082176.1	0.000304208
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Morganella morganii	Proteus mirabilis	Proteus mirabilis strain FZ2726 plasmid pKPC_FZ2726, complete sequence	CP09849.1	0.0555655
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Morganella morganii	Proteus mirabilis	Proteus mirabilis strain FZ2715 plasmid pKPC_FZ2715, complete sequence	CP09849.1	0.0555655
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Enterobacter hormchei	Enterobacter hormchei	Enterobacter hormchei strain ECCT75 plasmid pECT75, 8 complete sequences	CP09849.1	0.0002851
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Citrobacter freundii	Citrobacter freundii	Citrobacter freundii strain FFP103 plasmid pCFP103, complete sequence	CP110886.1	0.0217903
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Citrobacter freundii	Citrobacter freundii	Citrobacter freundii strain CA7107 plasmid pCA7107-A, complete sequence	CP110886.1	0.0217903
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Klebsiella pneumoniae strain HS0261 plasmid pHS0261-1, complete sequence	CP110953.1	0.00113443
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Escherichia coli strain H1181 plasmid pJS11128, partial sequence	CP110953.1	0.000134965
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae strains K138 plasmid pK515, complete sequence	U0262455.1	0.0260265
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Enterobacter cloacae	Enterobacter cloacae	Enterobacter cloacae strain FCN49 plasmid pKPC_FCEN49, complete sequence	U0262455.1	0.0011089
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Citrobacter freundii	Citrobacter freundii	Citrobacter freundii strain P0159 plasmid pP0159-93, complete sequence	MF72693.1	0.0010803
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Citrobacter parvulus	Citrobacter parvulus	Escherichia coli strain 40 plasmid pC40, complete sequence	CP021847.1	0.000312571
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Escherichia coli strain 16 plasmid pC36, complete sequence	MB12807.1	0.0155442
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae plasmid pK31	MR107553.1	0.048143
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Klebsiella pneumoniae	Klebsiella pneumoniae	Klebsiella pneumoniae plasmid pK76.1	MR107553.1	0.048143
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Escherichia coli	Escherichia coli	Escherichia coli strain CAV17.4 plasmid pCAV17.4, complete sequence	CP11628.1	0.0262266
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Klebsiella pneumoniae	Klebsiella pneumoniae	Commensal bacterium, plasmid pK1	CP11628.1	0.0262266
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Aeromonas caviae	Aeromonas caviae	Aeromonas caviae KAM39 plasmid pKAM39, 3 DNA, complete sequence	AP02483.1	0.024831
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Burkholderia	Burkholderia	Burkholderia cenocepacia strain VC1209 plasmid unannounced, complete sequence	CP01761.1	0.0451199
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Burkholderia	Burkholderia	Burkholderia cenocepacia strain vggpl2 plasmid unannounced, complete sequence	U04634.1	0.046341
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Burkholderia	Burkholderia	Burkholderia cenocepacia strain vggpl3 plasmid unannounced, complete sequence	CP01761.1	0.0451199
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Burkholderia	Burkholderia	Burkholderia cenocepacia strain vggpl4 plasmid unannounced, complete sequence	CP01761.1	0.0451199
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales	Comamonas	Comamonas	Comamonas sp. C11 plasmid unannounced, complete sequence	U01917.1	0.016454
		Pseudomonas	Gammoproteobacteria	Enterobacterales	Enterobacterales</					

[illegible]

Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Salmonella	Salmonella enterica	Salmonella enterica strain SC2016091 plasmid pSC2016091-5k, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Raoultella	Raoultella erwinii	Raoultella erwinii strain JCM 360_108 plasmid pMR08_S108.1, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli ETEC H10407 p58 plasmid	
ND	ND	ND	ND	ND	ND	Uncultured prokaryote from Rat gut metagenome metatranscriptome, plasmid pRERHB09	
ND	ND	ND	ND	ND	ND	Uncultured prokaryote from Rat gut metagenome metatranscriptome, plasmid pRERHB15	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Citrobacter	Citrobacter portucalensis	Citrobacter portucalensis STW0522-30 plasmid pSTW0522-30.5 DNA, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter kobei	Enterobacter kobei STW0522-42 plasmid pSTW0522-42.4 DNA, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae strain WCRP11508 plasmid pJ_11508, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain RHBSTW-00093 plasmid pRHBSTW-00093_5, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae strain RHBSTW-00036 plasmid pRHBSTW-00036_7, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain 48947CZ_1, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae strain SCPM-O-B-8912 (11PKP196) plasmid p6, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae strain SCPM-B-8921 (12PKP196) plasmid p8-0921_6, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae strain SCPM-O-B-8919 (12PKP196) plasmid p8-8919_5, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Escherichia	Escherichia coli	Escherichia coli strain 2023CK-0867 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate N7375-sc-228039 genome assembly, plasmid: 3	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain K432 plasmid pK432-NR, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella sp. WPS-518-ESBL-05 plasmid pWPS-518-ESBL-05_9 DNA, complete genome, strain WPS-518-ESBL-05	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae subsp. pneumoniae strain KPCTRSRTB7 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter	Enterobacter sp. MGH 3 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter	Enterobacter sp. MGH 14 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain 59732CZ plasmid p59732CZ_1, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Enterobacter hormaechei strain 49589CZ plasmid p49589CZ_2, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae strain strain	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P8	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P7	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P8	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P7	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P8	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P7	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P6	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P5	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P7	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P7	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P8	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P7	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P7	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae isolate 147 genome assembly, plasmid: P6	
SE172	pQC11_6	Singleton	ND	ND	ND	-	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter kobei	Enterobacter kobei STW0522-42 plasmid pSTW0522-42.6 DNA, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Citrobacter	Citrobacter freundii	Citrobacter freundii KAM61 plasmid pKAM61_7 DNA, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain EB_P9_1_1_03.19 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae strain RHBSTW-00066 plasmid pRHBSTW-00066_5, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Citrobacter	Citrobacter freundii	Citrobacter freundii strain RHBSTW-00085 plasmid pRHBSTW-00085_8, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella quasipneumoniae	Klebsiella quasipneumoniae subsp. quasipneumoniae strain U41 plasmid pKqg_U41_10, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain 49W47CZ plasmid p49W47CZ_3, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Klebsiella	Klebsiella pneumoniae	Klebsiella pneumoniae plasmid p5710B DNA, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter cloacae	Enterobacter cloacae STN071-73 plasmid pSTN071-73.4 DNA, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter cloacae	Enterobacter cloacae CP20-4P1 plasmid pCP20-4P1-4 DNA, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain 48_138 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain RHBSTW-00211 plasmid unannoted	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain RHBSTW-00101 plasmid unannoted	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter roggenkampii	Enterobacter roggenkampii strain RHBSTW-00045 plasmid pRHBSTW-00045_5, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter cloacae	Enterobacter cloacae strain RHBSTW-00490 plasmid pRHBSTW-00490_6, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain RHBSTW-00642 plasmid pRHBSTW-00642_4, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain RHBSTW-00626 plasmid pRHBSTW-00626_4, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain RHBSTW-00313 plasmid pRHBSTW-00313_4, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain RHBSTW-00229 plasmid pRHBSTW-00229_4, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain RHBSTW-00216 plasmid pRHBSTW-00216_4, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter hormaechei	Enterobacter hormaechei strain MSB1_33 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter aerobius	Enterobacter aerobius strain 2023CK-00757 plasmid unannoted, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter cloacae	Enterobacter cloacae strain SZECL1 plasmid pSZECL1_4, complete sequence	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter cloacae	Enterobacter cloacae isolate 114 genome assembly, plasmid: P3	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter cloacae	Enterobacter cloacae isolate 114 genome assembly, plasmid: P2	
Pseudomonadota	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	Enterobacter cloacae	Enterobacter cloacae isolate 114 genome assembly, plasmid: P3	
ND	ND	ND	ND	ND	ND	-	
ND	ND	ND	ND	ND	ND	-	
ND	ND	ND	ND	ND	ND	-	
ND	ND	ND	ND	ND	ND	-	
ND	ND	ND	ND	ND	ND	-	

Table S6: Comparison of observed and predicted host ranges.

Clusters/Singletons	Observed by Mash distance approach		Prediction by MOB-Typer		Comparison	Host range
	Taxonomic rank	Taxon	Taxonomic rank	Taxon		
1 (n=3)	Order	Enterobacterales	Order	Enterobacterales	same	
2 (n=3)	Genus	Non-SMC Serratia	Genus	Serratia	same	
3 (n=5)	Class	Gammaproteobacteria	-	-	different	MOB-Typer unpredictable
4 (n=2)	Order	Enterobacterales	Order	Enterobacterales	same	
5 (n=2)	SMC	SMC	Order	Enterobacterales	different	observed < predicted
6 (n=2)	Class	Gammaproteobacteria	Phylum	Proteobacteria	different	observed < predicted
7 (n=2)	Order	Enterobacterales	Order	Enterobacterales	same	
8 (n=6)	SMC	SMC	Genus	Serratia	different	observed ≤ predicted
9 (n=4)	SMC	SMC	Order	Enterobacterales	different	observed < predicted
10 (n=2)	Order	Enterobacterales	Phylum	Proteobacteria	different	observed < predicted
11 (n=9)	Order	Enterobacterales	Phylum	Proteobacteria	different	observed < predicted
12 (n=2)	Order	Enterobacterales	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
13 (n=10)	Order	Enterobacterales	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
14 (n=2)	Class	Gammaproteobacteria	Multi-phylla	Firmicutes,Proteobacteria,Actinobacteria	different	observed < predicted
15 (n=2)	multi-phylla	Actinomycetota	Multi-phylla	Firmicutes,Proteobacteria,Actinobacteria	same	
16 (n=2)	Order	Enterobacterales	Order	Enterobacterales	same	
17 (n=5)	Order	Enterobacterales	Phylum	Proteobacteria	different	observed < predicted
18 (n=5)	Order	Enterobacterales	Order	Enterobacterales	same	
19 (n=2)	SMC	SMC	Genus	Serratia	different	observed ≤ predicted
20 (n=3)	SMC	SMC	Order	Enterobacterales	different	observed < predicted
21 (n=2)	SMC	SMC	Order	Enterobacterales	different	observed < predicted
22 (n=4)	SMC	SMC	Order	Enterobacterales	different	observed < predicted
23 (n=3)	SMC	SMC	Order	Enterobacterales	different	observed < predicted
DL304_GCA_003355135_pSmN45	SMC	SMC	Order	Enterobacterales	different	observed < predicted
DL436_GCA_006974205_pATCC	SMC	SMC	Order	Enterobacterales	different	observed < predicted
DL512_GCA_002220715_punnamed4	SMC	SMC	Genus	Serratia	different	observed ≤ predicted
DL512_GCA_002220715_punnamed5	Order	Enterobacterales	Order	Enterobacterales	same	
DL536_SM39_pSMC1	Phylum	Pseudomonadota	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
DL552_GCA_001417865_punnamed1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
DL553_GCA_001294565_pSmUNAM836	Order	Enterobacterales	Order	Enterobacterales	same	
DL600_GCA_000336425_pSmWW4	SMC	SMC	Genus	Serratia	different	observed ≤ predicted
DL662_GCA_003031545_punnamed2	Order	Enterobacterales	Order	Enterobacterales	same	
DL662_GCA_003031545_punnamed3	Order	Enterobacterales	Order	Enterobacterales	same	
DL663_GCA_009858195_pKPC-2-HENAN1602	Order	Enterobacterales	Phylum	Proteobacteria	different	observed < predicted
DL671_GCA_019974075_p2020-O-9	Phylum	Pseudomonadota	Phylum	Proteobacteria	same	
DL672_GCA_002947235_plasmid	Phylum	Pseudomonadota	Phylum	Proteobacteria	same	
DL681_GCA_003967055_pSERAS01	SMC	SMC	Order	Enterobacterales	different	observed < predicted
DL688_GCA_008931425_pE28_004	Class	Gammaproteobacteria	Order	Enterobacterales	different	observed > predicted
DL690_GCA_013122155_p2	SMC	SMC	Order	Enterobacterales	different	observed < predicted
DL692_GCA_019968845_pBIWA004_1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
DL696_GCA_904866365_plasmid3	Order	Enterobacterales	Order	Enterobacterales	same	
DL696_GCA_904866365_plasmid4	Order	Enterobacterales	Family	Enterobacteriaceae	different	observed > predicted
DL710_GCA_006716725_pWVU-009	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE003_10VA4_plasmid1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE007_12BL3_plasmid1	Order	Enterobacterales	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
SE007_12BL3_plasmid2	Order	Enterobacterales	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
SE007_12BL3_plasmid3	Order	Enterobacterales	Multi-phylla	Firmicutes,Proteobacteria,Actinobacteria	different	observed < predicted
SE022_14BL03_plasmid1	SMC	SMC	-	-	different	MOB-Typer unpredictable
SE022_14BL03_plasmid2	Order	Enterobacterales	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
SE028_14BL09_plasmid1	Genus	Non-SMC Serratia	Order	Enterobacterales	different	observed < predicted
SE034_14VA2_plasmid1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE038_14VA7_plasmid1	Order	Enterobacterales	Class	Gammaproteobacteria	different	observed < predicted
SE044_CM5_plasmid1	Order	Enterobacterales	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
SE050_E06_neb_plasmid1	SMC	SMC	Genus	Serratia	different	observed ≤ predicted
SE065_E23_plasmid1	Order	Enterobacterales	Family	Enterobacteriaceae	different	observed > predicted
SE074_E36_neb_plasmid1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE074_E36_neb_plasmid3	SMC	SMC	-	-	different	MOB-Typer unpredictable
SE079_E41_plasmid1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE084_E46_plasmid2	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE084_E46_plasmid3	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE102_ET_H2_plasmid1	SMC	SMC	Genus	Serratia	different	observed ≤ predicted
SE133_KC057_plasmid1	Order	Enterobacterales	Order	Enterobacterales	same	
SE133_KC057_plasmid2	Order	Enterobacterales	Phylum	Proteobacteria	different	observed < predicted
SE140_KC069_plasmid1	Order	Enterobacterales	Family	Enterobacteriaceae	different	observed > predicted
SE168_QC07_plasmid4	Order	Enterobacterales	-	-	different	MOB-Typer unpredictable
SE168_QC07_plasmid6	Order	Enterobacterales	Genus	Klebsiella	different	observed > predicted
SE172_QC11_plasmid6	SMC	SMC	Genus	Enterobacter	different	observed > predicted
SE172_QC11_plasmid8	Order	Enterobacterales	Genus	Enterobacter	different	observed > predicted
SE174_QC13_plasmid1	Order	Enterobacterales	Multi-phylla	Proteobacteria,Actinobacteria	different	observed < predicted
SE180_QC19_plasmid1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE213_QE30_neb_plasmid1	SMC	SMC	-	-	different	MOB-Typer unpredictable
SE214_QE31_neb_plasmid1	SMC	SMC	Order	Enterobacterales	different	observed < predicted
SE227_ET_W2_plasmid1	SMC	SMC	Order	Enterobacterales	different	observed < predicted