

Supplementary Information

Table S1: Reference sequence accessions for each ST

Sequence type	Reference accession
ST15	NZ_CP062475.1
ST101	NZ_CP102940.1
ST147	NZ_CP029582.1
ST307	NZ_CP158302.1
ST983	NZ_CP021165.1
ST985	NZ_CP086724.1
ST2004	NZ_CP103579.1

Table S2: Isolates and sequence data included in the study

https://github.com/klebgenomics/SPINZ/blob/main/tables/Supplementary_table_S2.tsv

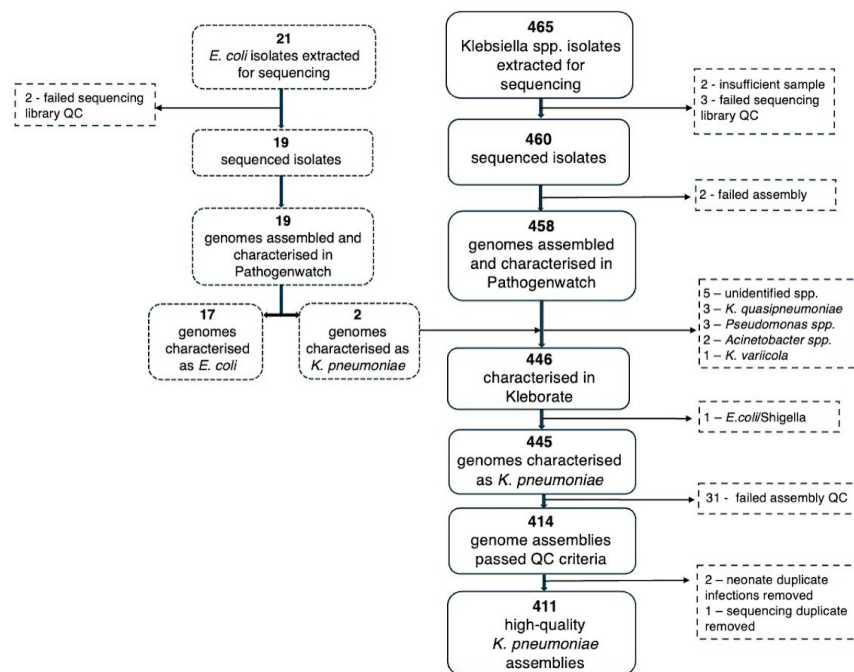


Figure S1. Pipeline of isolate from isolate extraction through to high-quality assembled genomes. Loss of isolates from the pipeline are indicated at each stage.

ST307		Temporal threshold (weeks)			
		1	2	3	4
SNP distance threshold 5-20	No of clusters	8	7	5	5
	No of clustered sequences	225/232	227/232	230/232	231/232
	Median cluster size	7	7	7	7
	Proportion of cases in a transmission cluster	97%	98%	99%	100%
	Proportion of cases due to transmission	94%	95%	97%	97%

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ST101		Temporal threshold (weeks)			
		1	2	3	4
SNP distance threshold 5	No of clusters	1	2	2	2
	No of clustered sequences	2/9	4/9	4/9	5/9
	Median cluster size	2	2	2	2
	Proportion of cases in a transmission cluster	22%	44%	44%	56%
	Proportion of cases due to transmission	11%	22%	22%	33%
SNP distance threshold 10 - 25	No of clusters	1	2	2	2
	No of clustered sequences	2/9	5/9	6/9	6/9
	Median cluster size	2	2	3	3
	Proportion of cases in a transmission cluster	22%	56%	67%	67%
	Proportion of cases due to transmission	11%	33%	44%	44%

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ST2004		Temporal threshold (weeks)			
		1	2	3	4
SNP distance threshold 5-25	No of clusters	6	2	2	2
	No of clustered sequences	44/47	47/47	47/47	47/47
	Median cluster size	4	24	24	24
	Proportion of cases in a transmission cluster	94%	100%	100%	100%
	Proportion of cases due to transmission	81%	96%	96%	96%

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ST983		Temporal threshold (weeks)			
		1	2	3	4
SNP distance threshold 5-25	No of clusters	2	1	1	1
	No of clustered sequences	9/9	9/9	9/9	9/9
	Median cluster size	4	9	9	9
	Proportion of cases in a transmission cluster	100%	100%	100%	100%
	Proportion of cases due to transmission	78%	89%	89%	89%

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ST147		Temporal threshold (weeks)			
		1	2	3	4
SNP distance threshold 5-25	No of clusters	1	1	1	1
	No of clustered sequences	3/4	3/4	4/4	4/4
	Median cluster size	3	3	4	4
	Proportion of cases in a transmission cluster	75%	75%	100%	100%
	Proportion of cases due to transmission	50%	50%	75%	75%

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SNP distance threshold 5-25	ST15	Temporal threshold (weeks)	ST985	Temporal threshold (weeks)
		1-4		1-4
	No of clusters	1	No of clusters	1
	No of clustered sequences	4/4	No of clustered sequences	5/5
	Median cluster size	4	Median cluster size	5
	Proportion of cases in a transmission cluster	100%	Proportion of cases in a transmission cluster	100%
	Proportion of cases due to transmission	75%	Proportion of cases due to transmission	80%

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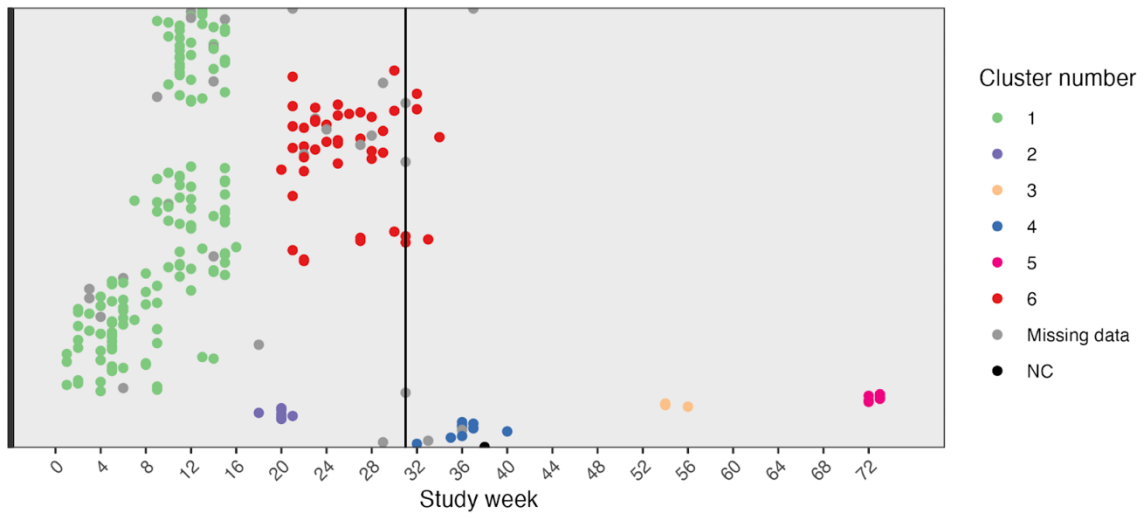
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ST985		Temporal threshold (weeks)
		1-4
SNP distance threshold 5-25	No of clusters	1
	No of clustered sequences	5/5
	Median cluster size	5
	Proportion of cases in a transmission cluster	100
	Proportion of cases due to transmission	80

Figure S2. Clustering sensitivity analyses. The sensitivity of clustering to choice of SNV threshold (between 5–25) and temporal threshold (between 7–28 days) was assessed for all STs.

A



B

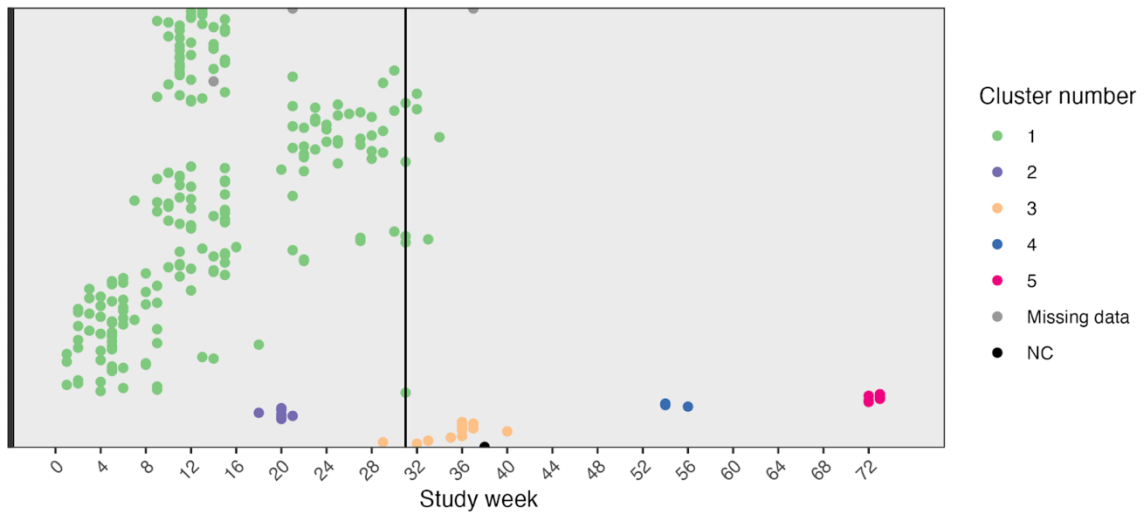


Figure S3. Sensitivity analysis of ST307 clusters. (A) Using culture date to define clusters if available, and admission date if not (n=233), compared to **(B)** using only culture date (n=206).

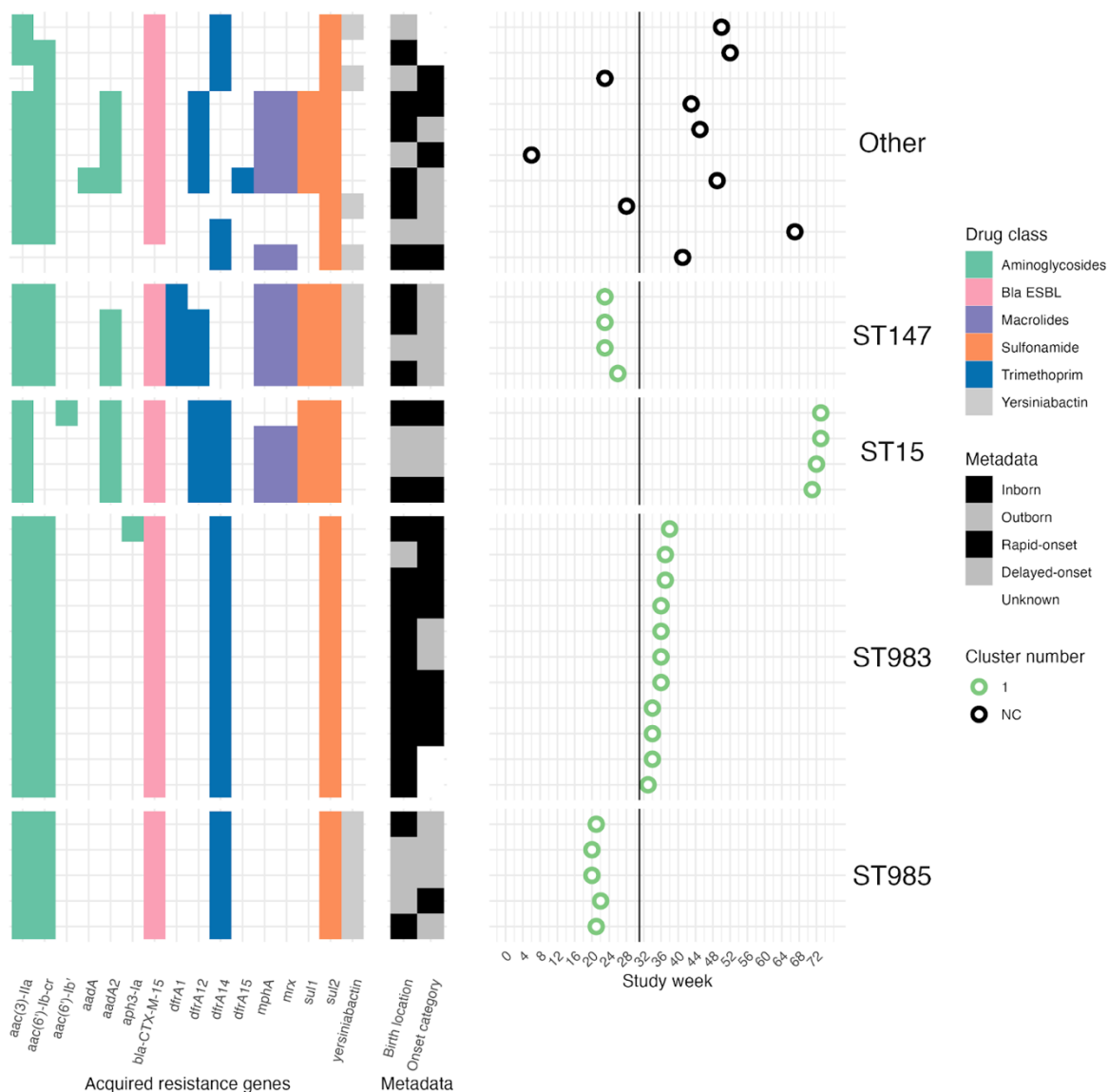


Figure S4. Acquired resistance genes, hypervirulence genes and birth location and onset metadata aligned to study week of infection for all other STs (of ≥ 4 genomes). In all other STs for which a phylogenetic tree could not be constructed. The presence of an isolate in a cluster is indicated by the colour of the circle plotted by study week of infection. The solid vertical line represents the start of the implementation of the IPC bundle.

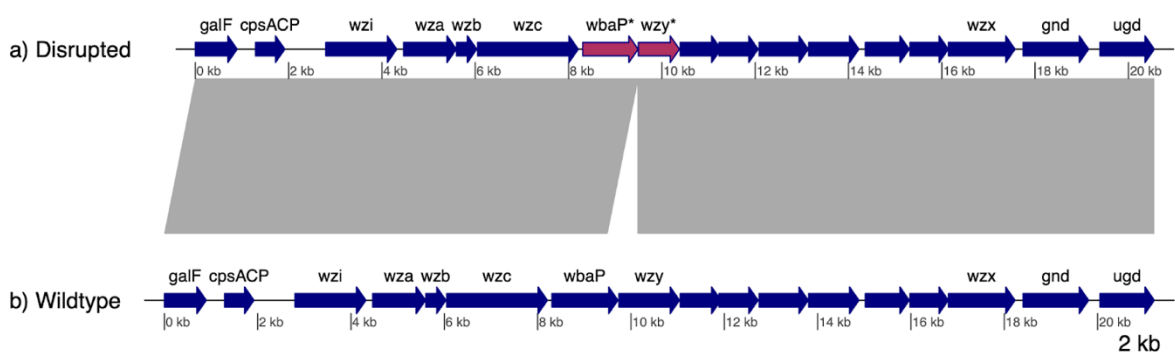


Figure S5. Comparison of KL102 loci in ST307. (a) Disrupted form conserved in ST307 cluster 1 isolates from this study. (b) Wildtype reference form (GenBank accession, AB371290). Arrows show annotated protein-coding genes, navy blue arrows indicate intact open reading frames, maroon arrows indicate truncated open reading frames. Grey shows homology blocks between the two KL102 locus sequences, revealing a 661 bp deletion stretching from the end of *wbaP* into the beginning of *wzy* thus truncating both genes and presumably rendering both non-functional.

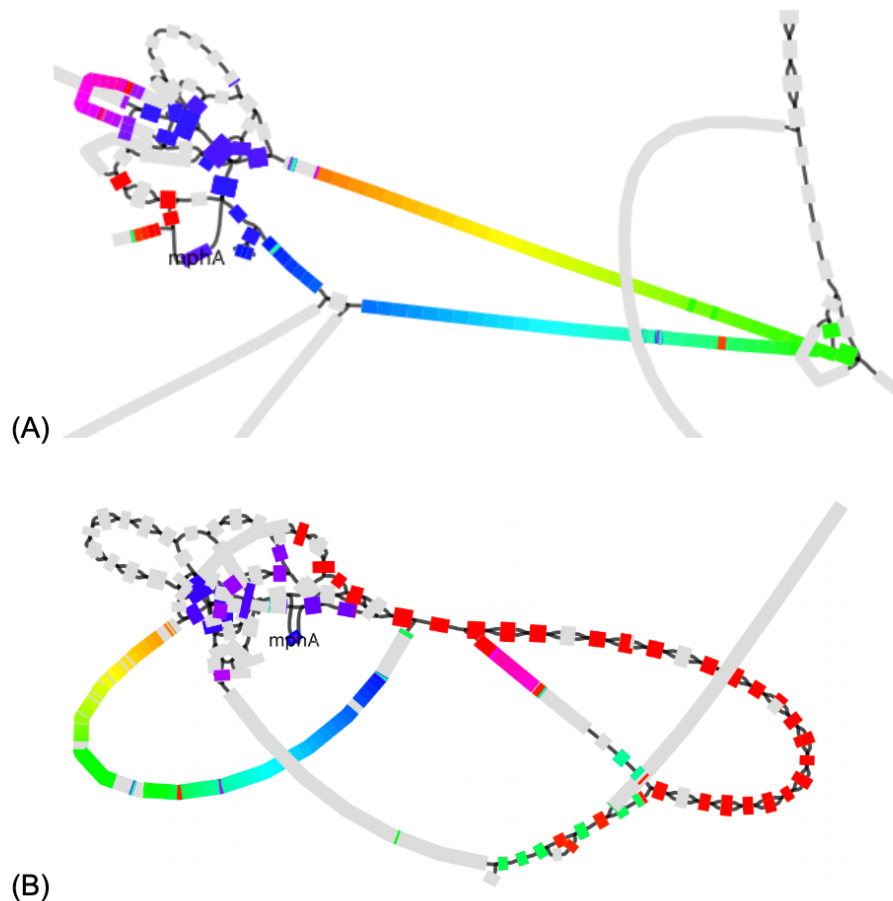


Figure S6. BLAST hits to *mphA* reference plasmid (GenBank accession: CP021752.1) in representative assembly graphs for ST307 cluster 3 and 4 genomes. BLAST search and visualisation of the graph was done using Bandage. In each graph, rectangles indicate contigs, sized to indicate their relative length in base pairs. Contigs are coloured to indicate hits to the reference plasmid (GenBank accession CP021752.1), using a rainbow scale such that red indicates hits to the start of the reference plasmid sequence, colours yellow through green indicate hits in the middle of the reference sequence, through to blue for hits at the end of the reference sequence. The contig containing the *mphA* gene is labelled. (A) Cluster 4 genome, read accession ERR15165518. Zoomed in on the part of the graph with hits to the reference plasmid (96.9% coverage at mean 98.6% identity), note this part is connected to the rest of the graph including the chromosome. (B) Cluster 3 genome, ZN2356 (accession ERR15165559). Note the part of the graph shown is disconnected from the rest of the graph including the chromosome. Coverage of the reference plasmid is 74%.

ST101

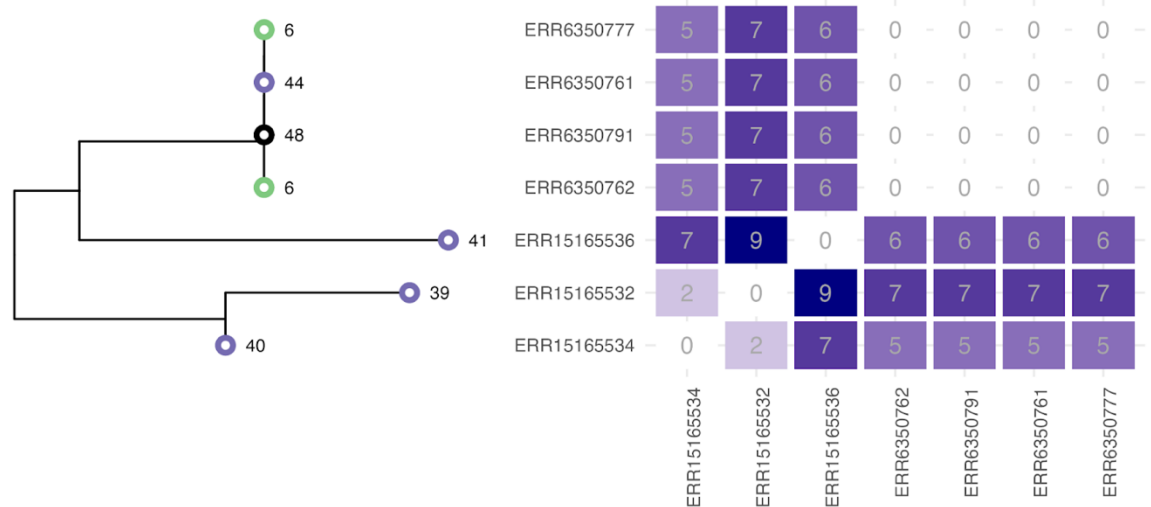


Figure S7. Maximum likelihood phylogenetic tree and pairwise SNV distance matrix of a subset of ST101 infections. Tree tips labelled with cluster number (colour) and week of infection. Two infections observed in week 6 during the baseline period (cluster 1, green tree tips), and four infections during weeks 39-44 in the post-implementation period (cluster 2, purple tree tips) as well as a single non-clustered infection (black tree tip) at week 48.