

Caribbean multi-centre study of *Klebsiella pneumoniae*: whole genome sequencing, antimicrobial resistance and virulence factors.

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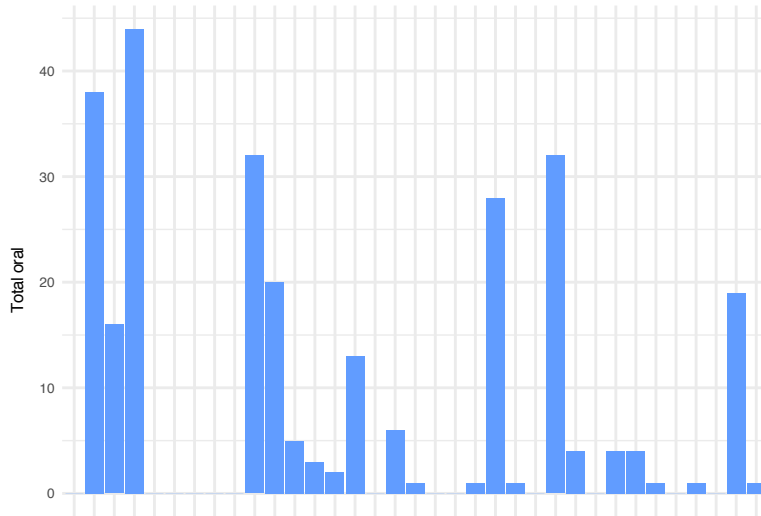
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Supplementary data

Figure S1: Numbers of all orally (A) and peritoneal (B) prescribed antibiotics reported in the PPS.

Figure S1

(A)



(B)

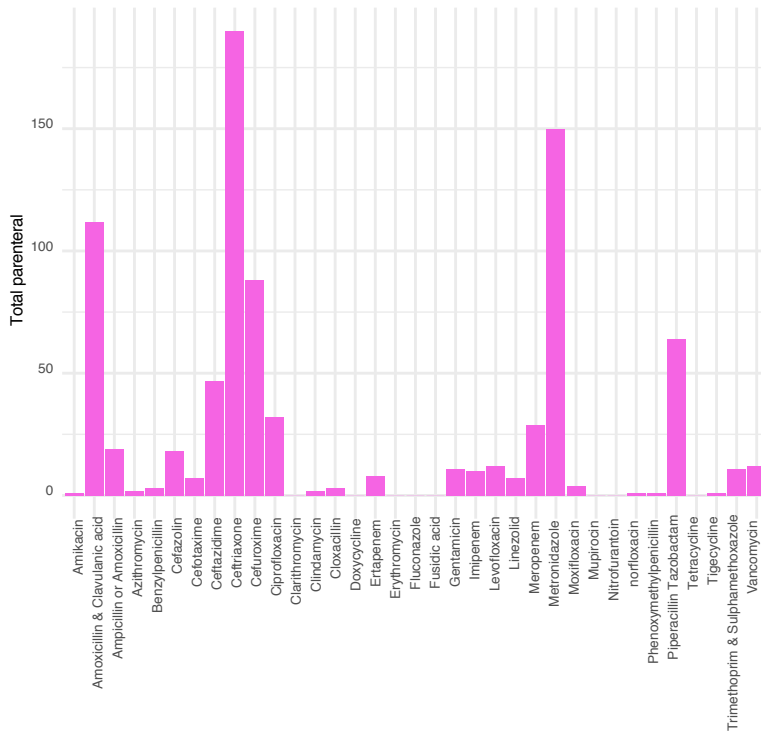
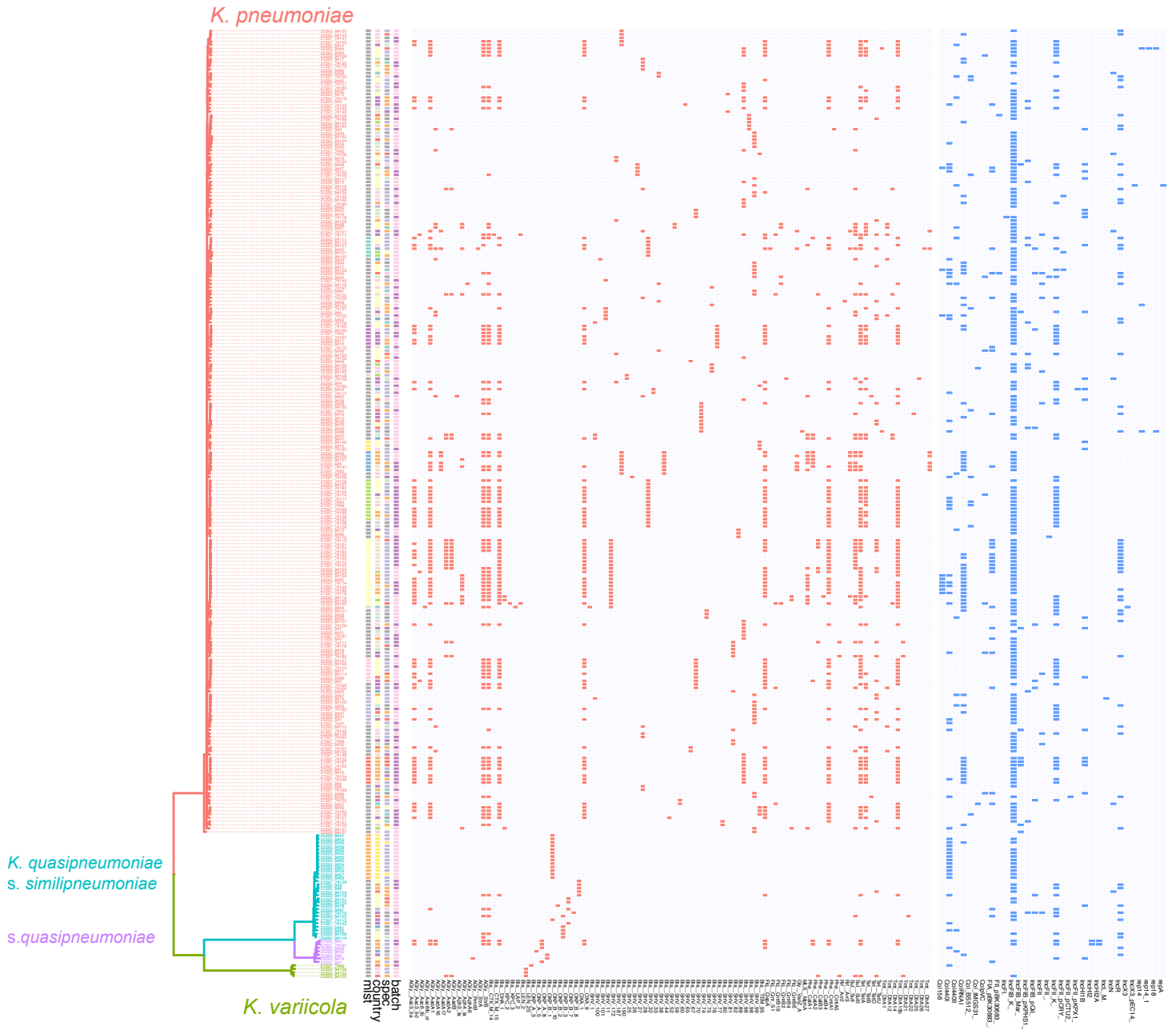


Figure S2: Core genome analysis of *K. quasipneumoniae* subsp. *similipneumoniae* isolates. Phylogenetic tree of the isolates (left) and corresponding pairwise SNP distances in a heatmap (right).

Figure S3: Antimicrobial resistance gene alleles for all analysed genomes in this study.

Figure S3



Main STs	Country	Specimen	Batch	
15	1	Blood	1	AMR genes present
11	2	Urine	2	Plasmid replicon present
258	3	Wound		
45	4	Abscess		
39	5	Liver abscess		
152	6	Sputum		
23	7	CSF		
307	8	Ear		
392	9	Vaginal		
405	10	Pus		
86	11	Other		
1605	12			
	13			

Figure S4: Core genome analysis for main antimicrobial resistant, globally spread STs. Mapping tree (left) in the context of public data and the corresponding pairwise SNP distances after removing recombination shown as heatmap (right) for **(A) ST11, (B) ST15, (C) ST307, (D) ST405**. The published strains included in the analyses are given in Dataset S2.

Figure S4

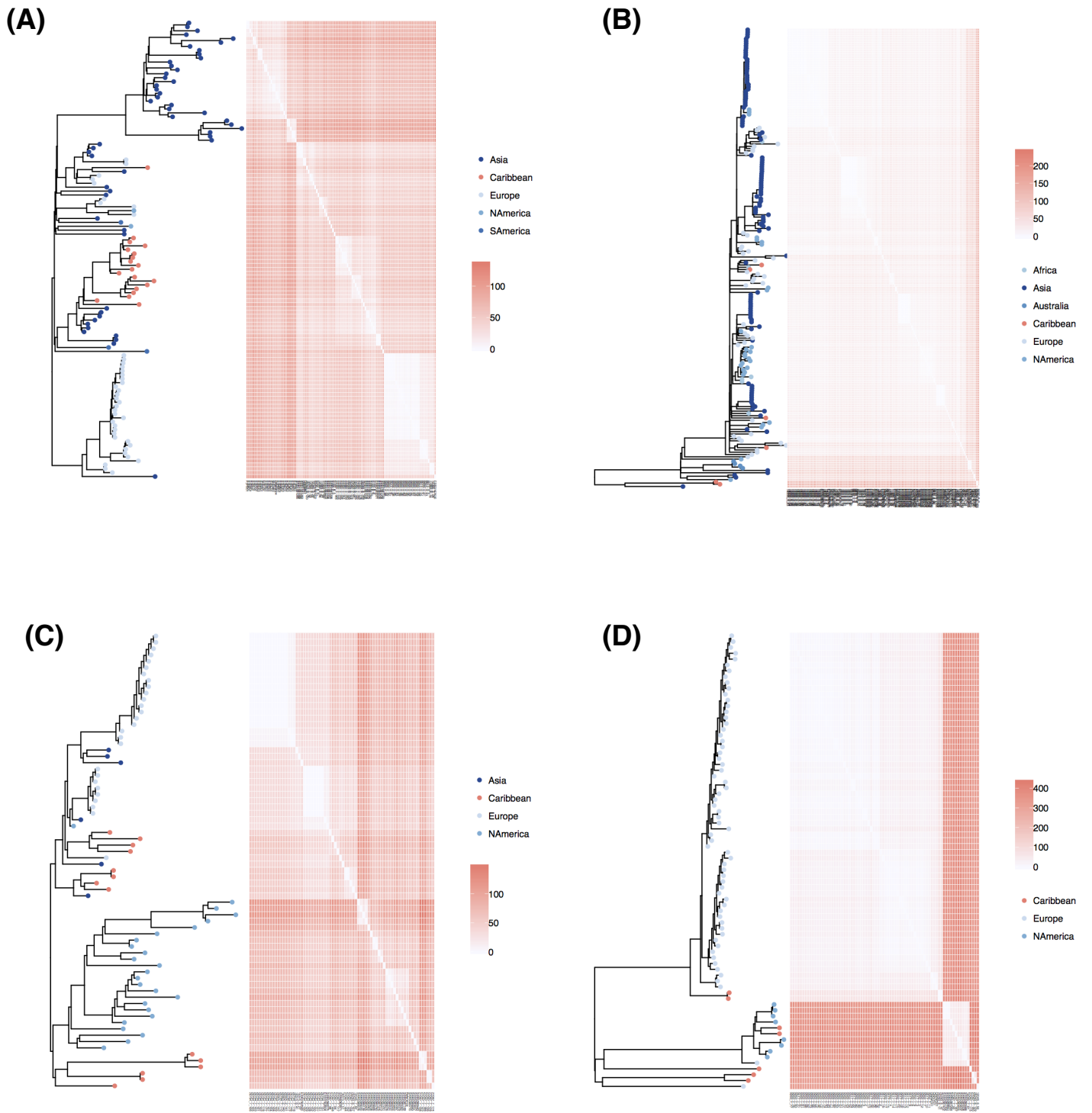


Figure S5: Comparison of two meningitis cases in the Caribbean. The mapping tree shows the two cases ([61], this study) in the context of other isolates. The core genome tree alignment was used to calculate pairwise SNP distances as in Figure S4 (middle panel), and the presence or absence of *K. pneumoniae*-specific virulence determinants associated with invasive disease [5] is shown on the right panel.

Figure S5

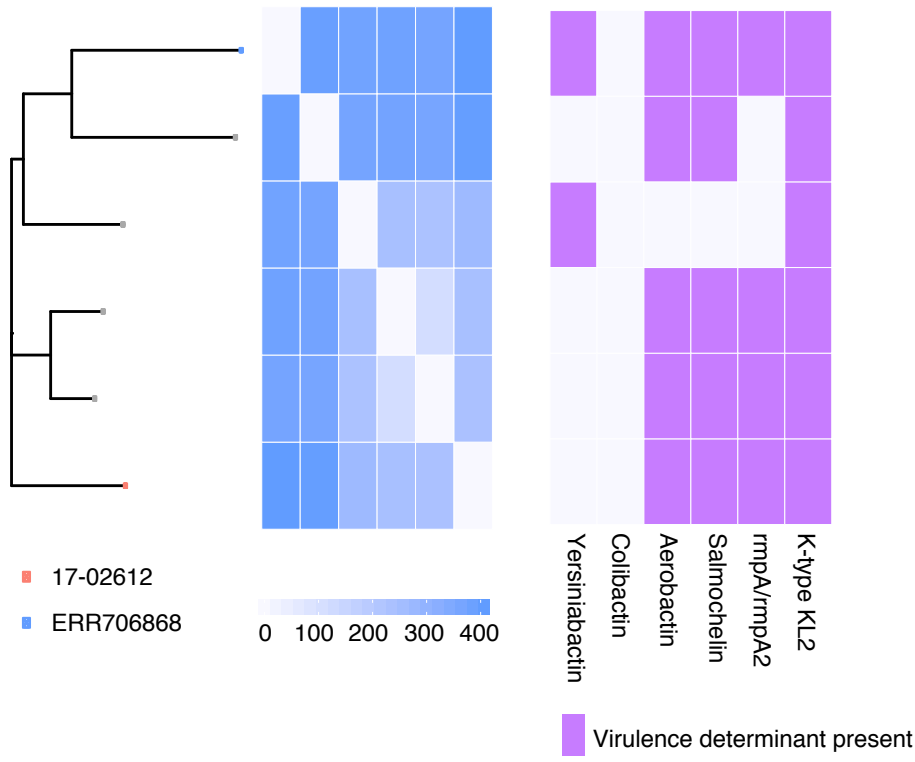


Figure S6: Capsule (K-) and LPS O-antigen (O-type) genotype distribution in all isolates.

Figure S6

