TABLE S1

Table of *Klebsiella pneumoniae* isolates sequenced in this study and selected characteristics.

PUBLICATION_NAME	ENTRY	YEAR OF COLLECTION	MLST	HOSPITAL	PHENOTYPE
100SGR	ERS480596	2012	16	SAN GIOVANNI ROTONDO	ESBL
101BO	ERS480597	2012	512	BOLOGNA	KPC
102BO	ERS480598	2012	512	BOLOGNA	KPC
103BO	ERS480599	2012	512	BOLOGNA	KPC
104BO	ERS480600	2012	512	BOLOGNA	KPC
10PV	ERS480601	2012	307	PAVIA	ESBL
11PV	ERS480602	2013	258	PAVIA	KPC
12PV	ERS480603	2013	258	PAVIA	KPC
13PV	ERS480604	2013	258	PAVIA	KPC
14PV	ERS480605	2012	1624	PAVIA	Susceptible
15PV	ERS480606	2012	976	PAVIA	Susceptible
16BO	ERS480607	2011	37	BOLOGNA	ESBL
17PV	ERS480608	2012	307	PAVIA	ESBL
18PV	ERS480609	2013	15	PAVIA	ESBL
19PV	ERS480610	2013	15	PAVIA	ESBL
20PV	ERS480611	2012	1631	PAVIA	Susceptible
21PV	ERS480612	2012	240	PAVIA	Susceptible
22PV	ERS480613	2012	1625	PAVIA	Susceptible
23PV	ERS480614	2013	258	PAVIA	KPC
24PV	ERS480615	2013	258	PAVIA	KPC
25BO	ERS480616	2013	35	BOLOGNA	Susceptible
26BO	ERS480617	2013	35	BOLOGNA	Susceptible
27BO	ERS480618	2011	45	BOLOGNA	ESBL
28BO	ERS480619	2011	37	BOLOGNA	ESBL
29BO	ERS480620	2012	512	BOLOGNA	KPC
30BO	ERS480621	2012	512	BOLOGNA	KPC
31AVR	ERS480622	2013	512	CESENA	KPC
32AVR	ERS480623	2013	466	CESENA	Susceptible
34AVR	ERS480624	2013	405	CESENA	Susceptible
36AVR	ERS480625	2013	37	CESENA	Susceptible
37AVR	ERS480626	2013	323	CESENA	ESBL
39AVR	ERS480627	2013	395	CESENA	Susceptible
40AVR	ERS480628	2013	307	CESENA	ESBL
41AVR	ERS480629	2013	16	CESENA	ESBL
42AVR	ERS480630	2013	512	CESENA	KPC
43AVR	ERS480631	2013	512	CESENA	KPC
44AVR	ERS480632	2013	512	CESENA	KPC
45AVR	ERS480633	2013	160	CESENA	Susceptible
46AVR	ERS480634	2013	395	CESENA	ESBL
47AVR	ERS480635	2013	323	CESENA	ESBL
48AVR	ERS480636	2013	512	CESENA	KPC
49BG	ERS480637	2012	147	BERGAMO	Susceptible
50BG	ERS480638	2011	258	BERGAMO	KPC
51BG	ERS480639	2007	1626	BERGAMO	Susceptible
52BG	ERS480640	2006	268	BERGAMO	Susceptible
53BG	ERS480641	2009	321	BERGAMO	Susceptible
54BG	ERS480642	2011	258	BERGAMO	KPC
55BG	ERS480643	2012	466	BERGAMO	Susceptible
56BG	ERS480644	2011	258	BERGAMO	KPC

PUBLICATION_NAME	ENTRY	YEAR OF COLLECTION	MLST	HOSPITAL	PHENOTYPE
57BG	ERS480645	2011	258	BERGAMO	KPC
58BG	ERS480646	2011	512	BERGAMO	KPC
60BG	ERS480647	2012	45	BERGAMO	ESBL
62BG	ERS480648	2011	147	BERGAMO	ESBL
63BG	ERS480649	2011	1627	BERGAMO	ESBL
65BO	ERS480650	2013	1243	BOLOGNA	Susceptible
66BO	ERS480651	2013	416	BOLOGNA	Susceptible
67BO	ERS480652	2013	1628	BOLOGNA	Susceptible
68BO	ERS480653	2011	37	BOLOGNA	ESBL
69BO	ERS480654	2011	277	BOLOGNA	ESBL
70BO	ERS480655	2011	37	BOLOGNA	ESBL
71RE	ERS480656	2011	258	REGGIO EMILIA	KPC
72RE	ERS480657	2011	258	REGGIO EMILIA	KPC
73RE	ERS480658	2011	258	REGGIO EMILIA	KPC
74RE	ERS480659	2011	512	REGGIO EMILIA	KPC
75RE	ERS480660	2011	258	REGGIO EMILIA	KPC
76RE	ERS480661	2012	1243	REGGIO EMILIA	Susceptible
77RE	ERS480662	2012	1629	REGGIO EMILIA	Susceptible
78RE	ERS480663	2012	1164	REGGIO EMILIA	Susceptible
79RE	ERS480664	2012	35	REGGIO EMILIA	Susceptible
81RE	ERS480665	2011	147	REGGIO EMILIA	ESBL
82RE	ERS480666	2012	405	REGGIO EMILIA	ESBL
83RE	ERS480667	2012	147	REGGIO EMILIA	ESBL
84RE	ERS480668	2012	322	REGGIO EMILIA	ESBL
85RE	ERS480669	2012	37	REGGIO EMILIA	ESBL
86SGR	ERS480670	2011	512	SAN GIOVANNI ROTONDO	KPC
87SGR	ERS480671	2011	512	SAN GIOVANNI ROTONDO	KPC
88SGR	ERS480672	2011	512	SAN GIOVANNI ROTONDO	KPC
89SGR	ERS480673	2011	512	SAN GIOVANNI ROTONDO	KPC
90SGR	ERS480674	2011	512	SAN GIOVANNI ROTONDO	KPC
91SGR	ERS480675	2012	29	SAN GIOVANNI ROTONDO	Susceptible
92SGR	ERS480676	2012	70	SAN GIOVANNI ROTONDO	Susceptible
93SGR	ERS480677	2012	35	SAN GIOVANNI ROTONDO	Susceptible
94SGR	ERS480678	2012	45	SAN GIOVANNI ROTONDO	Susceptible
95SGR	ERS480679	2012	1307	SAN GIOVANNI ROTONDO	Susceptible
96SGR	ERS480680	2012	1630	SAN GIOVANNI ROTONDO	ESBL
97SGR	ERS480681	2012	512	CESENA	ESBL
98SGR	ERS480682	2012	20	SAN GIOVANNI ROTONDO	ESBL
99SGR	ERS480683	2012	15	SAN GIOVANNI ROTONDO	ESBL
9PV	ERS480684	2012	307	PAVIA	ESBL

TABLE S2

Genes with potential effect on virulence or antibiotic resistance phenotype comprised in recombined region of ~1.3 Mb described in this work. Coordinates and strand are referred to the genome of the reference strain NJST258_1, annotation was obtained by BLAST search against a specifically designed database, as reported in the materials and methods section.

START	END	STRAND	PRODUCT NAME
18482	20224	+	Integral membrane protein with trka domains
29471	30706	-	Multidrug resistance protein emrD
69212	72319	-	multidrug transporter
72319	73443	-	acriflavine resistance protein E
138949	140223	-	3-deoxy-D-manno-octulosonic acid transferase WaaA
142431	143558	-	glycosyl transferase family 1 WabG
143555	144631	-	glycosyl transferase family 9 WaaQ
148902	149873	-	ADP-heptose--LPS heptosyltransferase WaaC
149877	150935	-	ADP-heptose--LPS heptosyltransferase WaaF
150945	151877	-	ADP-L-glycero-D-manno-heptose-6-epimerase RfaD
188732	190165	+	Xylose isomerase
291995	293161	+	UDP-4-amino-L-arabinose synthase PmrH
293109	294146	+	Undecaprenyl-phosphate alpha-4-amino-L-arabinosyltransferase ArnC
294143	296128	+	UDP-4-amino-4-deoxy-L-arabinose formyltransferase ArnA
296125	297027	+	4-deoxy-4-formamido-L-arabinose-phospho-UDP deformylase PmrJ
297024	298682	+	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase ArnT
298679	299017	+	4-amino-4-deoxy-L-arabinose-phospho-UDP flippase PmrL
299017	299397	+	4-amino-4-deoxy-L-arabinose-phospho-UDP flippase PmrM
373562	374329	+	Transcriptional regulatory protein ompR
374326	375681	+	osmolarity sensor protein envZ
408428	409060	-	Crp/Fnr family transcriptional regulator
424107	425291	+	Elongation factor Tu
457426	460536	-	multidrug transporter AcrB
460549	461688	-	acrE
462055	462717	+	AcrAB operon repressor
532636	532923	-	yhbH
536245	536811	-	yrbI
540606	541172	+	yrbD/mlad
541191	541826	+	mlac
553941	554792	+	dihydropteroate synthase
4632900	4634141	+	multidrug transporter
4638808	4639326	-	Transcriptional regulator, MarR family protein
4646942	4648030	-	ABC-type_sugar_transport_system,_periplasmic_component
4682645	4683964	-	xylose isomerase
4684337	4685830	+	Xyloside transporter
4685889	4687568	+	beta-xylosidase
4845809	4846771	+	Phosphatidylserine_decarboxylase psd
4853100	4854890	+	fumarate reductase frdA
4854835	4855617	+	frdB
4855628	4856023	+	fumarate reductase frdC
4856004	4856393	+	frdD
4856507	4857040	+	Bacterial_lipocalin
4857037	4857354	-	Membrane_transporter_of_cations_and_cationic_drugs sugE
4874086	4875387	+	C4-dicarboxylate ABC transporter DcuA
4901698	4904016	-	Ferrienterobactin receptor precursor fepA
4996917	5000978	-	rpoB
5005173	5006357	-	elongation factor Tu
5149976	5150674	+	cpxR
5150671	5152044	+	Sensor protein cpxA
5160685	5161671	+	ABC-type_sugar_transport_system,_periplasmic_component rhaS
5256865	5258115	-	Chloramphenicol resistance protein

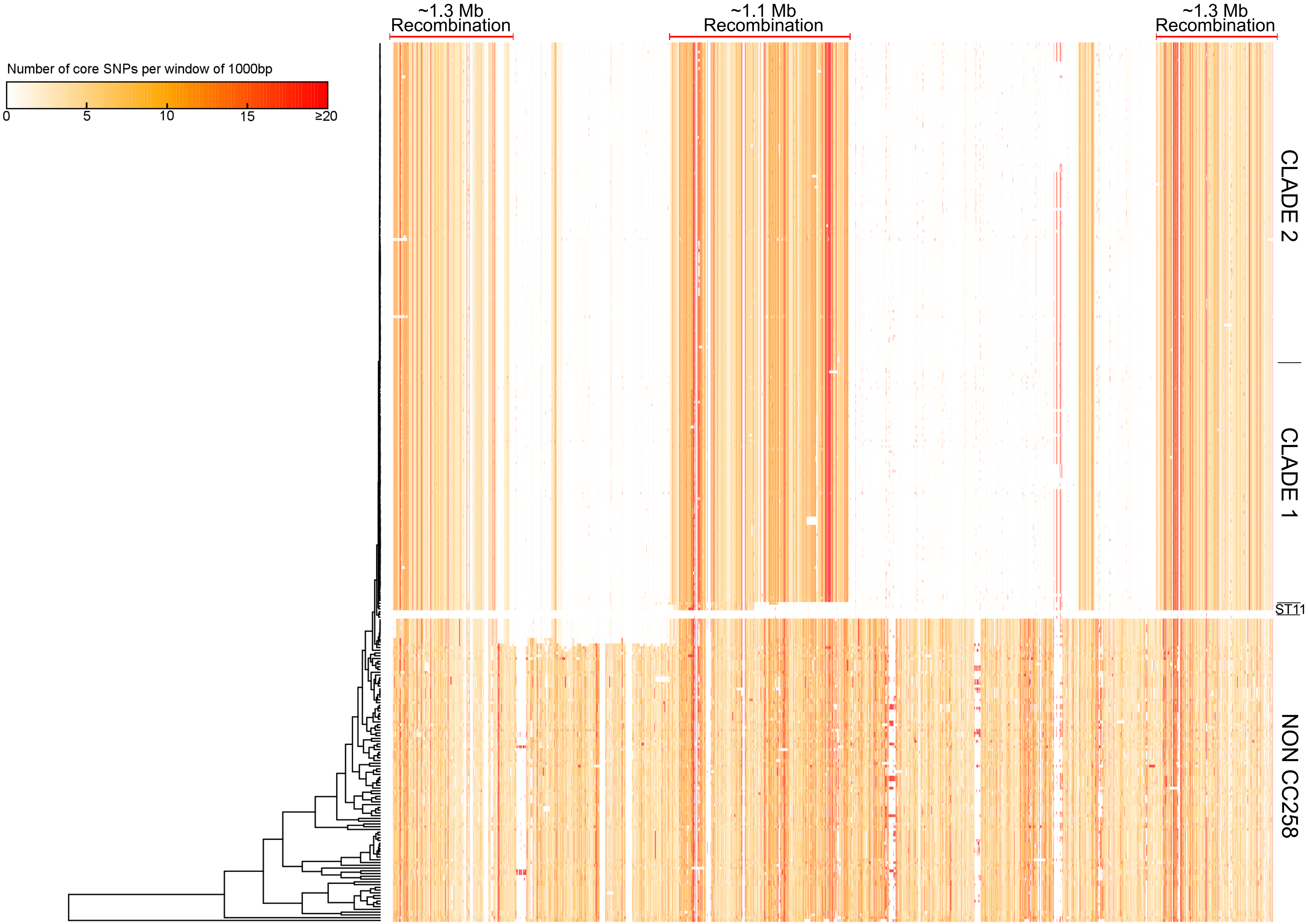

FIGURE S1

Clustering of core SNPs in the 319 Klebsiella pneumoniae genomes. The phylogenetic reconstruction is shown on the left, while the core SNP frequency is shown on the right, in shades of red representing number of core SNPs per 1000bp windows for each genome. Detected recombinations are indicated on the top of the figure, main clades detected in the phylogenetic analysis are indicated on the right side of the figure.

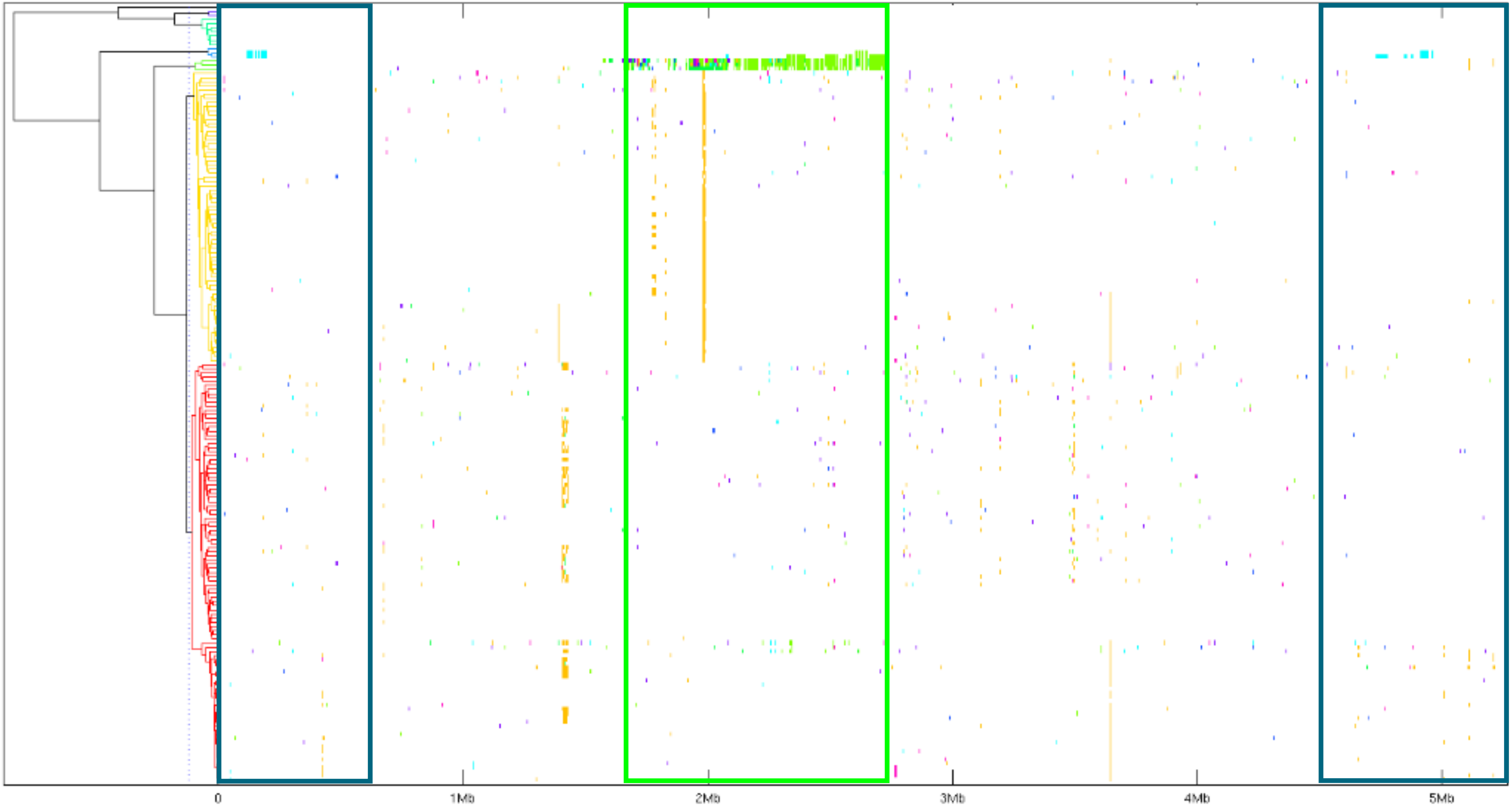

FIGURE S2

Recombination analysis obtained with BRATnextgen. A subdataset of 187 genomes was used as input for a 100 iteration analysis with 100 replicates with the BRATnextgen software. The recombination proposed by Chen and coworkers is detected in green while the recombination proposed in this work is detected in blue. Recombined regions as detected with the SNP-based method are indicated with boxes, using the same colors as those chosen by the BRATnextgen software.

FIGURE S3

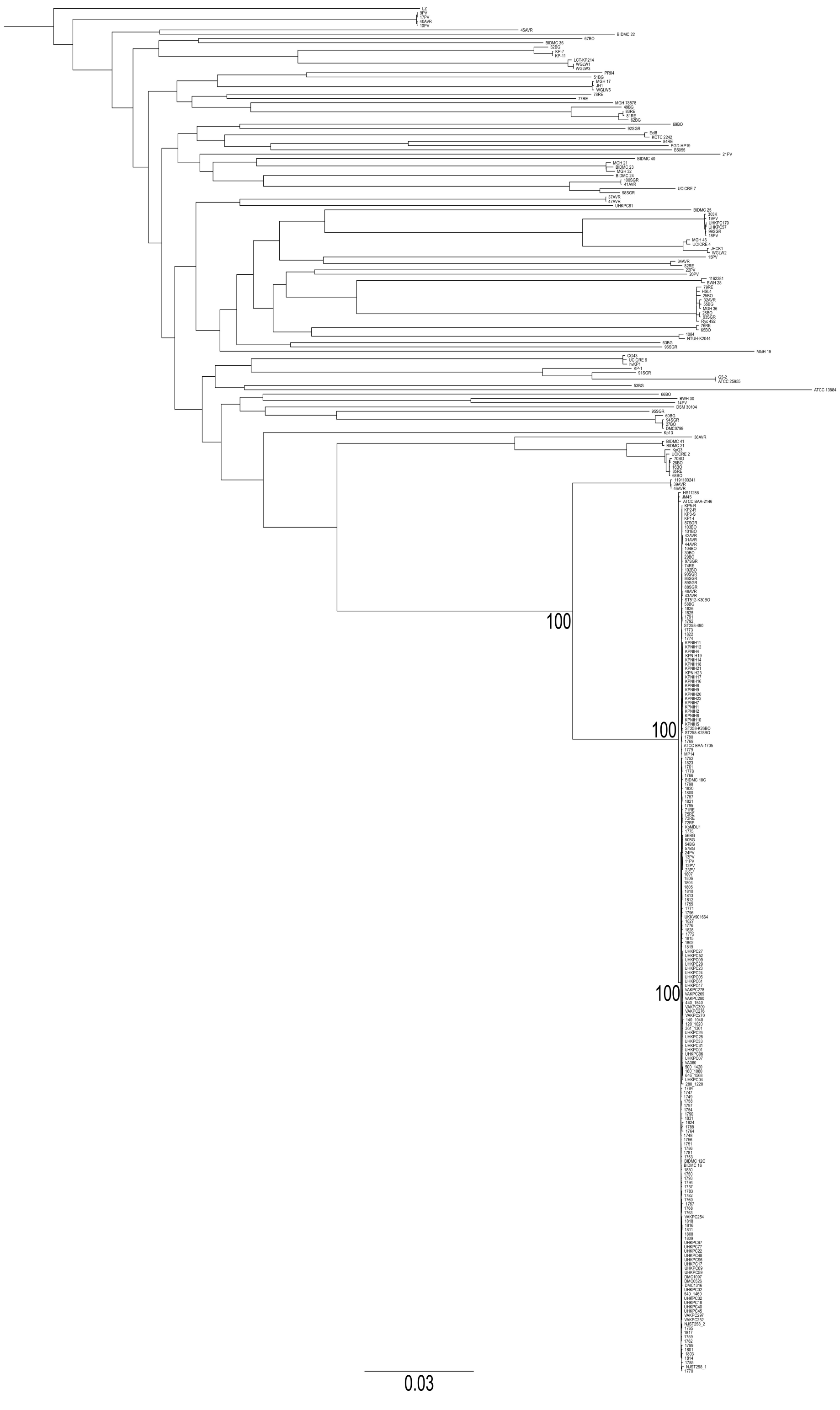

FIGURE S3. Phylogeny of the 319 *Klebsiella pneumoniae* genomes based on core SNPs in non-recombined regions. Phylogeny was reconstructed starting from an alignment of 55,368 core SNPs, located outside of the two main recombined regions of the genome, using the software RAxML, with the Generalised time-reversible (GTR) model and 100 bootstrap replicates. Bootstrap is shown only for the three main nodes of Clonal Complex 258.

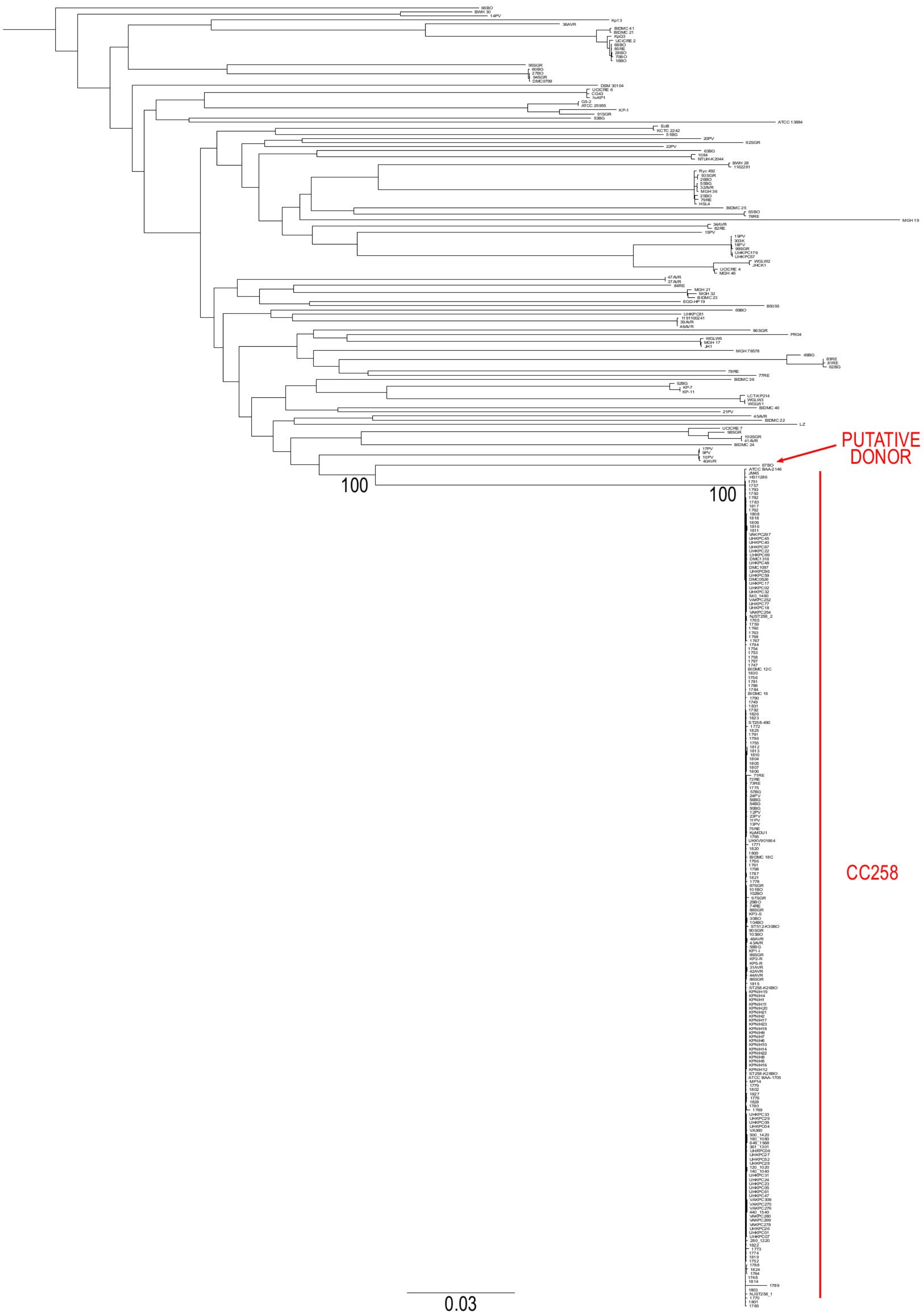

FIGURE S4

phylogeny of the 319 *Klebsiella pneumoniae* genomes based on core SNPs in the ~1.3Mb recombined region. Phylogeny was reconstructed starting from an alignment of 24,537 core SNPs present only in the recombined region located from 4,554,906 to 629,621, spanning the origin of replication, using coordinates of genome NJST258_1. The tree was obtained using the software RAxML, with the Generalised time-reversible (GTR) model and 100 bootstrap replicates, bootstraps are shown only for nodes of interest. The putative donor of the ~1.3Mb recombined region, 67BO, results as sister clade of the recipient CC258.

FIGURE S5. phylogeny of the 319 *Klebsiella pneumoniae* genomes based on core SNPs in the ~1.1Mb recombined region. Phylogeny was reconstructed starting from an alignment of 14,905 core SNPs present only in the recombined region located from 1,675,550 to 2,740,033, using coordinates of genome NJST258_1. The tree was obtained using the software RAxML, with the Generalised time-reversible (GTR) model and 100 bootstrap replicates, bootstraps are shown only for nodes of interest. The putative donor of the ~1.1Mb recombined region, Kp13, results as sister clade of the recipient CC258 clade, with the exclusion of the ST11 clade.