

Supplementary Table S1. Plasmid born antibiotic resistance genes (ARG).

<i>K. pneumoniae</i> isolates														Gene	Anntotation	
CK1	CK2	CK3	CK4	CK5	CK6	CK7	CK8	CK9	CK10	K11	K12	K13	K14			K15
+	-	-	-	-	+	+	-	+	-	-	-	-	+	-	<i>AAC(3)-IIC</i>	Aminoglycoside acetyltransferase
+	-	-	+	+	+	+	+	+	+	+	+	+	+	+	<i>AAC(6)-Ib</i>	Aminoglycoside acetyltransferase
-	-	+	-	+	-	-	-	-	-	-	-	-	-	-	<i>AAC(6)-Ib-cr</i>	Aminoglycoside acetyltransferase
-	-	+	-	-	-	-	+	-	-	-	-	-	-	-	<i>aadA12</i>	Aminoglycoside nucleotidyltransferase
+	-	-	-	+	+	+	-	+	+	+	+	+	-	+	<i>APH(3)-IIa</i>	Aminoglycoside phosphotransferase
+	-	-	-	+	+	+	-	+	+	+	+	+	-	+	<i>APH(6)-Ic</i>	Aminoglycoside phosphotransferase
-	-	-	+	-	-	-	+	-	+	+	+	+	+	+	<i>arr-8</i>	Ribosyltransferase
+	-	-	-	+	+	+	+	+	-	-	-	-	-	-	<i>baeR</i>	Response regulator that promotes the expression of MdtABC and AcrD efflux complexes
+	-	-	+	+	+	+	+	+	+	+	+	+	+	+	<i>catB11</i>	Chloramphenicol acetyltransferase
-	-	+	-	+	-	-	+	-	-	-	-	-	-	-	<i>catI</i>	Chloramphenicol acetyltransferases
-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	<i>cmlB</i>	Chloramphenicol exporter
+	-	-	-	+	+	+	+	+	-	-	-	-	-	-	<i>cpxA</i>	Membrane-localized sensor kinase that is activated by envelope stress and promotes efflux complex expression
+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<i>CTX-M-130</i>	Beta-lactamase
-	-	+	-	-	-	-	+	-	-	-	-	-	-	-	<i>dfrA13</i>	Dihydrofolate reductase
-	-	+	-	-	-	-	+	-	-	-	+	+	+	+	<i>emrE</i>	Ethidium bromide and erythromycin efflux transporter
-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	<i>emrR</i>	Negative regulator of multidrug efflux pumps
-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	<i>ereA</i>	Erythromycin esterase
+	-	-	-	-	+	+	-	+	-	-	-	-	-	-	<i>evgS</i>	Sensor regulatory protein involved in drug resistance
-	-	+	-	-	-	-	+	-	-	-	-	-	-	-	<i>floR</i>	Chloramphenicol exporter
-	-	-	-	-	+	+	+	+	+	+	+	+	-	+	<i>H-NS</i>	Histone-like protein involved in global gene regulation including RND-type multidrug exporters.
+	-	-	-	+	+	+	-	+	-	-	-	-	-	-	<i>kdpE</i>	Transcriptional activator involved in the virulence and intracellular survival of pathogenic bacteria
-	-	+	-	-	-	-	+	-	-	-	-	-	-	-	<i>marA</i>	Global activator protein inducing MDR efflux pump AcrAB and porin OmpF
+	+	-	-	+	+	+	+	+	-	-	-	-	-	-	<i>mdtA</i>	Membrane fusion protein of the multidrug efflux complex
+	+	-	-	+	+	+	+	+	-	-	-	-	-	-	<i>mdtF</i>	Multidrug inner membrane transporter for the MdtEF-TolC efflux complex
-	-	-	+	-	-	-	-	-	-	-	-	+	-	-	<i>mdtG</i>	Major facilitator superfamily of transporters increasing fosfomycin and deoxycholate resistance
-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	<i>mdtM</i>	Multidrug resistance protein
+	-	-	-	+	+	+	-	+	-	-	-	-	-	-	<i>mdtP</i>	Multidrug resistance efflux pump
-	-	+	+	+	-	-	+	-	+	+	+	+	+	+	<i>mphA</i>	Resistance enzymewhich preferentially inactivate 14-membered macrolides
+	+	+	-	-	+	+	+	+	-	-	-	-	-	-	<i>msbA</i>	Multidrug resistance transporter
-	-	-	-	+	+	+	-	+	-	-	-	-	-	-	<i>NDM-6</i>	Beta-lactamase
+	-	-	+	+	+	+	+	+	-	-	+	+	+	+	<i>OXA-232</i>	Beta-lactamase
-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	<i>OXA-9</i>	Beta-lactamase
+	-	-	+	+	+	+	+	+	-	-	-	-	-	-	<i>qnrS8</i>	Quinolone resistance protein
-	-	-	+	-	-	-	+	-	+	+	+	+	-	+	<i>rmtH</i>	16s Ribosomal RNA methyltransferase that confers high resistance to all aminoglycosides
+	-	+	-	+	+	+	-	+	+	+	+	+	+	+	<i>SHV-52</i>	Beta-lactamase
+	-	+	-	+	+	+	+	+	+	+	+	+	+	+	<i>sul3</i>	Sulfonamide resistant dihydropteroate synthase
-	-	-	-	-	+	+	-	+	-	-	-	-	-	-	<i>TEM-126</i>	Beta-lactamase
+	-	-	-	+	+	+	-	+	-	-	-	-	-	-	<i>tet(E)</i>	Tetracycline efflux pump
19	4	11	8	19	21	21	20	21	10	10	12	13	13	12	Total DRG	

Supplementary Table S2. Output of analysis of *K. pneumoniae* genomes by Kleborate software

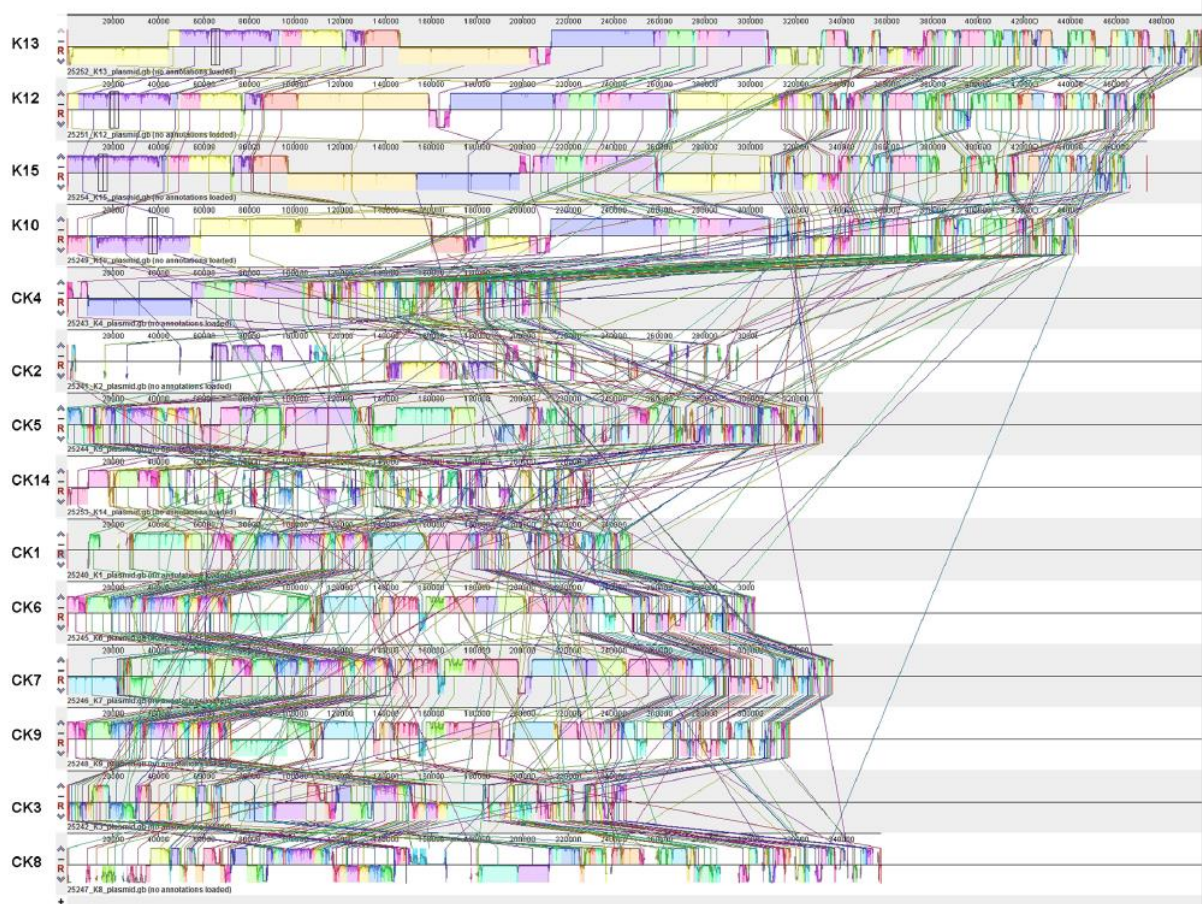
Metrics*	<i>Klebsiella pneumoniae</i> strains															
	CK1	CK2	CK3	CK4	CK5	CK6	CK7	CK8	CK9	K10	K11	K12	K13	K14	K15	
species_match	strong	strong	strong	strong	strong	strong	strong	strong	strong	strong	strong	strong	strong	strong	strong	
contig_count	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
N50	5463570	5409351	5483106	5502003	5495443	5568378	5580866	5332283	5570665	5753154	5664041	5719068	5717081	5519244	5718783	
largest_contig	5463570	5409351	5483106	5502003	5495443	5568378	5580866	5332283	5570665	5753154	5664041	5719068	5717081	5519244	5718783	
total_size	5463570	5409351	5483106	5502003	5495443	5568378	5580866	5332283	5570665	5753154	5664041	5719068	5717081	5519244	5718783	
ambiguous_bases	yes (1800)	yes (5000)	yes (3400)	yes (5800)	yes (3700)	yes (3400)	yes (3500)	yes (9200)	yes (3500)	yes (3600)	yes (4800)	yes (4900)	yes (4100)	yes (4200)	yes (5300)	
QC_warnings	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	ambiguous_bases	
ST	ST1801	ST1634	ST231-1LV	ST147	ST11	ST147	ST147	ST231	ST147	ST147	ST147-1LV	ST147	ST147-1LV	ST14	ST147-1LV	
virulence_score	0	1	4	1	1	0	0	4	0	1	1	1	1	1	1	
resistance_score	0	0	1	1	2	1	1	1	1	2	2	2	1	1	2	
num_resistance_classes	2	0	2	2	5	2	2	2	2	6	6	5	5	5	5	
num_resistance_genes	2	0	1	1	5	1	1	1	1	8	8	7	7	4	7	
Yersiniabactin	-	ybt 4; plasmid	ybt 14; ICEKp5	ybt 10; ICEKp4	ybt 15; ICEKp11	-	-	ybt 14; ICEKp5	-	ybt 10; ICEKp4	ybt 10; ICEKp4	ybt 10; ICEKp4 (truncated)	ybt 14; ICEKp4 (truncated)	ybt 14; ICEKp5	ybt 10; ICEKp4 (truncated)	
YbST	0	65-1LV	376	384	230-2LV	0	0	376	0	384	384-1LV	384-2LV	384-2LV	140	384-2LV	
Colibactin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
CbST	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Aerobactin	-	-	iuc 5	-	-	-	-	iuc 5	-	-	-	-	-	-	-	
AbST	0	0	61-3LV	0	0	0	0	0	61-3LV	0	0	0	0	0	0	
Salmocheilin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
SmST	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
RmpADC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
RmST	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
rmpA2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
wzi	wzi433	wzi2	wzi104	wzi64	wzi24	wzi420	wzi420	wzi104	wzi420	wzi64	wzi64	wzi64	wzi64	wzi2	wzi64	
K_locus	KL35	(KL107)	KL51	KL64	KL24	KL10	KL10	(KL107)	KL10	KL64	(KL64)	KL64	(KL64)	KL2	KL64	
K_type	K35	(KL107)	K51	K64	K24	K10	K10	(KL107)	K10	K64	(K64)	K64	(K64)	K2	K64	
K_locus_problems	none	?-+*	-	?-	?-	none	none	?+	none	none	-	?-	?-	none	?-	
K_locus_confidence	Very high	None	High	Good	Good	Very high	Very high	None	Very high	Perfect	None	Good	None	Very high	Good	
K_locus_identity	99.33%	83.35%	99.40%	100.00%	99.99%	96.76%	96.74%	81.68%	96.75%	100.00%	100.00%	100.00%	100.00%	99.73%	99.98%	
K_locus_missing_genes		KL107_05_w zb, KL107_06 _wzc, KL107 _07_wbaP, K L107_08, KL1 07_09, KL10 7_10, KL107 _11_gnd, KL 107_12, KL1 07_13, KL10 7_14, KL107 _15, KL107_	KL51_14_wc oZ	KL64_10_wz y	KL24_13_wc uG						KL64_08_wc oV, KL64_09, KL64_10_wz		KL64_10_wz y, KL64_11_ oU, KL64_12 wcoU, KL64_		KL64_11_wc oU, KL64_12 _wcoT	

			GyrA-831;GyrA-87G;ParC-801		GyrA-83F;GyrA-87A;ParC-801		GyrA-83Y;GyrA-87A;ParC-801		GyrA-83Y;GyrA-87A;ParC-801		GyrA-831;ParC-801		GyrA-831;ParC-801		GyrA-831;ParC-801		GyrA-831;ParC-801	
Flq_mutations	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
truncated_resistance_hits	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
spurious_resistance_hits	fosA7*?-0%																	
Chr_ST	ST1801	ST1634	ST231-1LV	ST147	ST11	ST147	ST147	ST231	ST147	ST147	ST147-1LV	ST147	ST147-1LV	ST14	ST147-1LV			
gapA	2	1	2	3	3	3	3	3	2	3	3	3	3	3	1	3		
infB	1	6	6	4	3	4	4	6	4	4	4	4	4	4	6	4		
mdh	1	1	1	6	1	6	1	6	1	6	6	6	6	6	1	6		
pgi	26	26	3	1	1	1	1	3	1	1	1	1	1	1	1	1		
phoE	3	12	26	7	1	7	7	26	7	7	7	7	7	7	1	7		
rpoB	5	25	46	4	1	4	4	1	4	4	4	4	4	4	1	4		
tonB	54	9	77	38	4	38	38	77	38	38	38	38	38	38	1	38		
ybtS	-	23	4	16	65	-	-	4	-	16	16	16	16	16	4	16		
ybtX	-	27	4	12	15	-	-	4	-	12	12	12	12	12	4	12		
ybtQ	-	30	5	4	22	-	-	5	-	4	4	4	4	4	31	4		
ybtP	-	18	4	3	4	-	-	4	-	3	3	3	3	3	4	3		
ybtA	-	13	1	3	1	-	-	1	-	3	3	3	3	3	1	3		
irp2	-	65	8	61	37*	-	-	8	-	61	61	61	61	61	67	61		
irp1	-	61*	8	54	34	-	-	8	-	54	54	54	54	54	171	54		
ybtU	-	9	2	3	14	-	-	2	-	3	3	3	3	3	2	3		
ybtT	-	18	4	10	1	-	-	4	-	10	10	10	10	10	4	10		
ybtE	-	26	4	9	4	-	-	4	-	9	9	9	9	9	4	9		
fyuA	-	35	2	39	17	-	-	2	-	39	39	39	39	39	36	39		
clbA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbB	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbE	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbF	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbM	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbN	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbO	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbP	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
clbQ	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
iucA	-	-	29	-	-	-	-	29	-	-	-	-	-	-	-	-		
iucB	-	-	17	-	-	-	-	17	-	-	-	-	-	-	-	-		
iucC	-	-	28	-	-	-	-	28	-	-	-	-	-	-	-	-		
iucD	-	-	35	-	-	-	-	35	-	-	-	-	-	-	-	-		
iutA	-	-	61	-	-	-	-	61	-	-	-	-	-	-	-	-		
iroB	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
iroC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
iroD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
iroN	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
rmpA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
rmpD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
rmpC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
spurious_virulence_hits	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		

*Detailed description of the metrics can be found on Kleborate Web-page <https://github.com/klebgonomics/Kleborate>

reported_host_range_lit_name	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales	Enterobacterales
								10773089; 11254626;								
			10773089;		10773089;			25389419;								
			11254626;		16940067;			30761100;								
			25389419;		25389419;			19482926;								
			20547789;		20547789;			20547789;								
			19482926;		19482926;	11254626;	11254626;	21911569;	11254626;	18606786;						
			19897651;		19897651;	30761100;	30761100;	19897651;	30761100;	11254626;	17122402;	17122402;	17122402;	6263753;	19482926;	19897651;
		18606786;	26169555;	17122402;	23711894;	19482926;	19482926;	24247128;	19482926;	16940067;	19482926;	19482926;	20008783;	23711894;	23711894;	19482926;
	11254626;	11254626;	15781495;	16940067;	15781495;	15781495;	15781495;	15781495;	15781495;	19482926;	16257053;	16257053;	16257053;	15781495;	20008783;	20008783;
	19482926;	19482926;	24247128;	6263753;	24247128;	26842776;	26842776;	26842776;	26842776;	23711894;	23711894;	23711894;	23711894;	24247128;	23711894;	23711894;
	15781495;	15781495;	20851899;	20008783;	20851899;	20851899;	20851899;	20851899;	20851899;	15781495;	15781495;	15781495;	15781495;	15781495;	20851899;	15781495;
	20851899;	20851899;	22511964;	23711894;	22511964;	16257053;	16257053;	22511964;	16257053;	20851899;	20851899;	20851899;	20851899;	22511964;	22511964;	20851899;
associated_pmid(s)	16257053	16257053	16257053	26802429	16257053	22470007	22470007	16257053	22470007	16257053	26802429	26802429	26802429	26802429	16257053	16257053

*Detailed description of the metrics can be found on Mob-Suite Web-page <https://github.com/phac-nmi/mob-suite>



Supplementary Figure S1. Alignment of sequences of the plasmids from different strains of *K. pneumoniae* produced by Mauve 20150226.

Each sequence is represented by a row with a central line and sequence length values. Blocks filled with the same colour and connected by thin vertical lines represent homologous sequences found in different plasmids. Blocks above the central line are located on the forward strand and those below the line are located on the reverse complement strand of the plasmids.