TABLE S1. Primers used in this study

Primers	Sequence (5'-3')	Purpose	Reference
iutA-F	CCAACTCCGTCCGTACCCTGTCA	*iucABCDiutA* detection	1
iutA-R	CGAGGGATCGACGATGGTGTTCT		
iroB-F	AGAGGCTGGATTGGTGGCGTTTG	*iroBCDN* detection	1
iroB-R	CGATCTGTGGAATACCGGCGTGTAG		
rmpA-F	ACTGGGCTACCTCTGCTTCA	*rmpA* detection	1
rmpA-R	CTTGCATGAGCCATCTTTCA		
rmpA2-F	AGAGTATTGGTTGATAGCCGGA	*rmpA2* detection	1
rmpA2-R	GAAATGTCAAGCCACATCCATTG		
orf7-F	AGCTTAAACTCGCCGTTATC	Left junction of virulence cluster	This study
iroN-R	CCAGAATAAGATCTTGGCCG		
rmpA-J-F	CTGCAGTCAACCAATACTCT	Right junction of virulence cluster	This study
Orf16-R	TTGTTCCTGGTAGACAATGG		
ompC-F	TTCAGACCAAAGCGAACATA	Left junction of ICE*Kp1*	This study
int-R	CATGCTTCCAGATAATCCGA		
orf40-F	TACGAGATCATAGCGAGACT	Right junction of ICE*Kp1*	This study
yeaP-R	TGAAATTAGCCGGACTTCAT		
KPC-F	CGTCTAGTTCTGCTGTCTTG	*bla*$_{KPC}$ detection	2
KPC-R	CTTGTCATCCTTGTTAGGCG		
NDM-F	GGTTTGGCGATCTGGTTTTC	*bla*$_{NDM}$ detection	2
NDM-R	CGGAATGGCTCATCACGATC		
IMP-F	GGAATAGAGTGGCTTAAYTCTC	*bla*$_{IMP}$ detection	2
IMP-R	GGTTTAAYAAAACAACCACC		
VIM-F	GATGGTGTTTGGTCGCATA	*bla*$_{VIM}$ detection	2
VIM-R	CGAATGCGCAGCACCAG		
OXA-48-F	GCGTGGTTAAGGATGAACAC	*bla*$_{OXA-48}$ detection	2
OXA-48-R	CATCAAGTTCAACCCAACCG		

TABLE S2. Antimicrobial susceptibility testing of *K. pneumoniae* RJY9645 and the control strains

Strain	ST	MIC (μg/ml)									
		CAZ	FEP	ATM	TZP	IMP	MEM	AMK	LEV	TGC	Polymycin B
RJY9645	35	≥64	≥64	≤1	≥128	16	64	0.5	≤0.25	≤0.25	0.5
HAP-Kp11	11	≥64	≥64	≥64	≥128	>128	>128	≥64	≥8	≤0.25	0.5
LA-Kp23	23	≤1	≤1	≤1	≤4	≤0.5	≤0.5	0.5	≤0.25	≤0.25	≤0.25

[a] CAZ, ceftazidime; FEP, cefepime; ATM, aztreonam; TZP, piperacillin/tazobactam; IMP, imipenem; MEM, meropenem; AMK, amikacin; LVX, levofloxacin; TGC, tigecycline.

TABLE S3. Reference strains used for the whole genome based phylogenetic analysis

Strain	Sequence type (ST)	GenBank accession no.	Virulence genes [a]			
			rmpA	*rmpA2*	*iroBCDN*	*iucABCDiutA*
NY9	ST340	NZ_CP012300	-	-	-	-
Kp-Goe-33208	ST101	CP018447	-	-	-	-
AR-0049	ST11	CP018816	-	-	-	-
HS11286	ST11	NC_016845	-	-	-	-
SWU01	ST11	CP018454	-	-	-	-
J1	ST111	NZ_CP013711	-	-	-	-
NUHL24835	ST14	NZ_CP014004	-	-	-	-
342	ST146	NC_011283	-	-	-	-
AATZP	ST147	CP014755	-	-	-	-
KP5	ST147	CP012426	-	-	-	-
KP36	ST15	CP017385	-	-	-	-
Kp-Goe-39795	ST15	CP018458	-	-	-	-
KPNIH29	ST1518	NZ_CP009863	-	-	-	-
W14	ST1536	CP015753	-	-	-	-
UCLAOXA232KP	ST16	CP012561	-	-	-	-
XH209	ST17	NZ_CP009461	-	-	-	-
1084	ST23	NC_018522	-	-	-	-
NTUH-K2044	ST23	NC_012731	+	-	+	+
RJF999	ST23	NZ_CP014010	+	+	+	+
CAV1042	ST244	CP018671	-	-	-	-
1756	ST2549	CP019219	-	-	-	-
CAV1453	ST258	CP018356	-	-	-	-
KPNIH36	ST258	CP014647	-	-	-	-
MNCRE69	ST258	CP018427	-	-	-	-
Kpn223	ST273	CP015025	-	-	-	-
KpN01	ST278	NZ_CP012987	-	-	-	-

KpN06	ST279	NZ_CP012992	-	-	-	-
KP-1	ST29	NZ_CP012883	-	-	-	-
DHQP1002001	ST34	CP016811	-	-	-	-
CAV1417	ST340	CP018352	-	-	-	-
KPNIH39	ST37	CP014762	-	-	-	-
RJF293	ST374	NZ_CP014008	+	+	+	+
KCTC-2242	ST375	NC_017540	+	+	+	+
MGH-78578	ST38	NC_009648	-	-	-	-
TGH10	ST383	NZ_CP012744	-	-	-	-
CN1	ST392	CP015382	-	-	-	-
Kp-Goe-62629	ST395	CP018364	-	-	-	-
Kp13	ST442	NZ_CP003999	-	-	-	-
CAV1016	ST45	CP017934	-	-	-	-
KPPR1	ST493	NZ_CP009208	-	-	-	-
GCA-001705385	ST512	CP015822	-	-	-	-
234-12	ST514	NZ_CP011313	-	-	-	-
1158	ST65	NZ_CP006722	-	-	-	-
Kp52.145	ST66	NZ_FO834906	-	-	+	+
CG43	ST86	NC_022566	+	+	+	+

[a] -, negative; +, positive.

TABLE S4. Integrative and conjugative elements (ICEs) identified on *K. pneumoniae* RJY9645 chromosome

ICE	Region	Length (kb)	G+C%	Features
ICE1	1,324,606-1,346,038	21.4	58.9	Prophage
ICE2	1,728,519-1,803,969	75.4	51.4	ICE*Kp1*(Yersiniabactin, salmochelin and type IV secretion system)
ICE3	1,982,844-2,005,955	23.1	56.8	Type VI secretion system (T6SS-1)
ICE4	2,905,079-2,932,166	27.1	60.4	Type VI secretion system (T6SS-2)
ICE5	2,987,984-3,055,008	67.0	52.5	Prophage

FIGURE S1. PFGE and S1-PFGE analysis of *K. pneumoniae* RJY9645. (A) PFGE analysis of *K. pneumoniae* RJY9645 and RJY9699. The two strains shared identical PFGE patterns. (B) S1-PFGE analysis of *K. pneumoniae* RJY9645. The black arrows indicted the three plasmids in this strain.
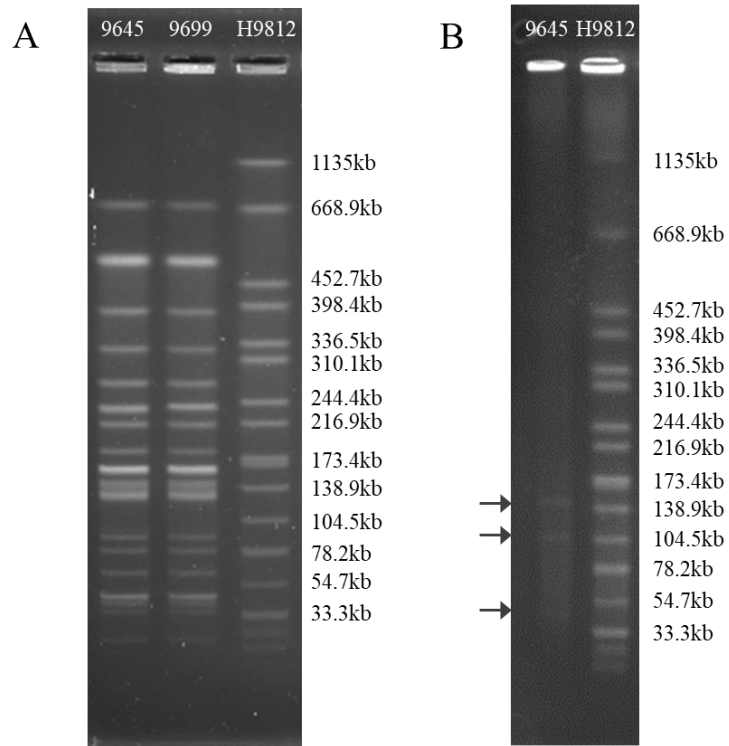
Figure S2. Phylogenetic analysis of *K. pneumoniae* RJY9645. The whole genomes of

reference strains were downloaded from GenBank and were listed with strain name

and sequence type (ST). The genomes were aligned using Muscle (http://www.drive5.

com/muscle) and homologous blocks from each genome were concatenated. A

maximum-likelihood phylogeny was generated with 1000 bootstrap replicates using

RAxML version 8.0.
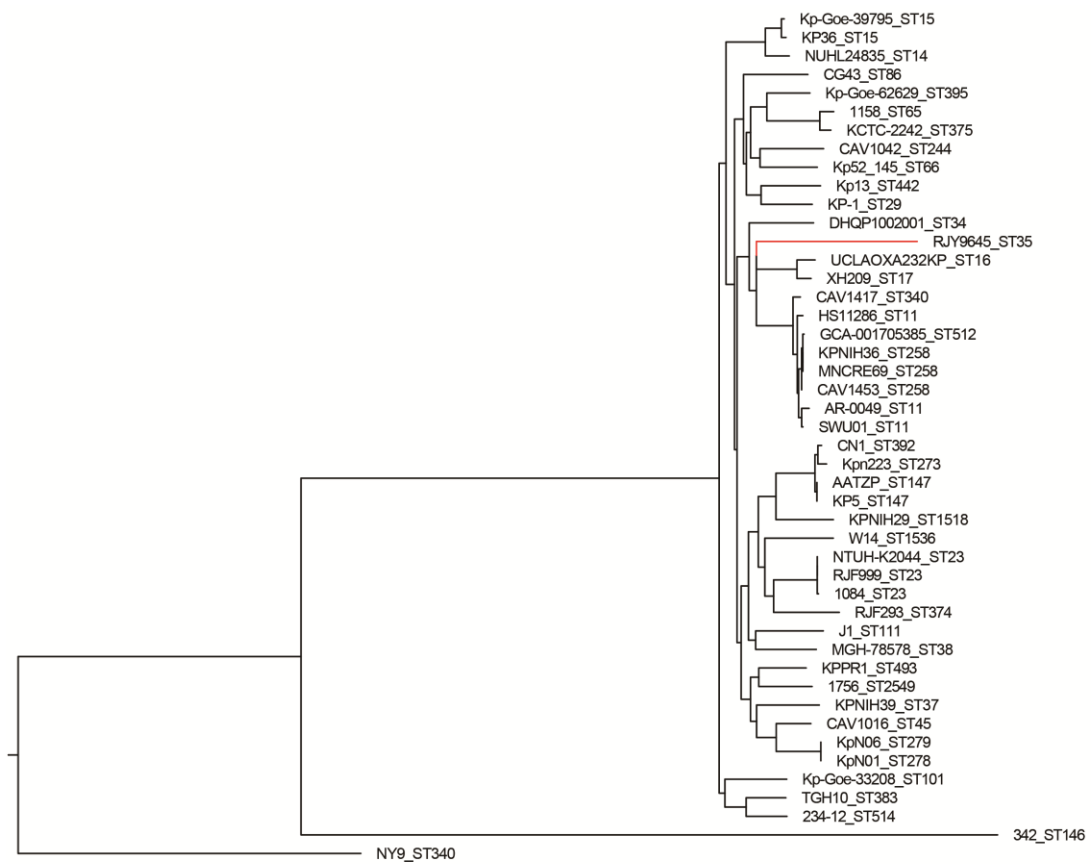
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