

## Supplementary materials

**Table S1.** The genotypes and phenotypes of the *K. pneumoniae* isolates used in this study.

Strain	Source	<i>entb</i>	<i>fimh</i>	<i>mrkd</i>	<i>ybtA</i>	Resistance to Antibiotic	Tolerance to Heavy Metal	16S rRNA Gene (GenBank Accession No.)
7-5-4	<i>Misgurnus anguillicaudatus</i>	+	+	+	–	CHL/CIP/KAN/NOR/SXT/TET	Cr/Pb/Cu/Zn/Hg	OM816745
7-10-14	<i>Maoetra veneriformis</i>	+	–	–	–	AMP/CHL/GEN/KAN/SXT/TET	Cr/Pb/Cu/Zn/Hg	OM816746
7-13-2	<i>Eriocheir sinensis</i>	+	+	+	–	AMP	Cr/Pb/Cu/Mn/Zn	OM816747
7-17-8	<i>Cipangopaludina cahayensis</i>	+	+	+	+	AMP	Cr/Cu/Zn	OM816748
8-1-12-1	<i>Procambarus clarkii</i>	+	+	+	+	AMP	Cd/Cr/Pb/Cu/Mn/Zn/Hg	OM816750
8-2-5-4	<i>Tegillarca granosa</i>	+	+	+	–	AMP/CHL/TET	Cr/Pb/Cu/Zn/Hg	OM816752
8-2-10-5	<i>Epinephelus fuscoguttatus</i>	+	+	+	–	CHL/CIP/KAN/SXT/TET	Cd/Cr/Pb/Cu/Zn/Hg	OM816753

Note: AMP, ampicillin; CHL, Chloroamphenicol; KAN, Kanamycin; GEN, Gentamicin; SXT, Sulphamethoxazole-trimethoprim; TET, Tetracycline; NOR, Norfloxacin; CIP, Ciprofloxacin

**Table S2.** The oligonucleotide primers used in this study.

Target Gene	Primer	Sequence (5' to 3')	Predicted Size (bp)	Reference
16S rDNA	27-F	AGAGTTTGATCCTGGCTCAG	1540	[110]
	1492-R	TACGGCTACCTTGTACGAC		
<i>aerobactin</i>	<i>aerobactin</i> -F	GTGCTGTCGATGAGCGATGC	944	[111]
	<i>aerobactin</i> -R	GTGAGCCAGGTTTCAGCGTC		
<i>wcaG</i>	<i>wcaG</i> -F	GGTTGGTCAGCAATCGTA	169	[112]
	<i>wcaG</i> -R	ACTATTCGCCCAACTTTTGC		
<i>traT</i>	<i>traT</i> -F	GGTGTGGTGCGATGAGCACAG	290	[109]
	<i>traT</i> -R	CACGGTTCAGCCATCCCTGAG		
<i>iroN</i>	<i>iroN</i> -F	AAGTCAAAGCAGGGGTGCCCCG	665	[112]
	<i>iroN</i> -R	GACGCCGACATTAAGACGCAG		
<i>rmpA</i>	<i>rmpA</i> -F	ACTGGGCTACCTCTGCTTCA	535	[108]
	<i>rmpA</i> -R	CTTGCGATGAGCCATCTTTCA		
<i>magA</i>	<i>magA</i> -F	GGTGCTCTTTACATCATTGC	1283	[108]
	<i>magA</i> -R	GCAATGGCCATTTCGCTTAG		
<i>mrkD</i>	<i>mrkD</i> -F	CCACCAACTATTCCTCGAA	240	[110]
	<i>mrkD</i> -R	ATGGAACCCACATCGACATT		
<i>ybtA</i>	<i>ybtA</i> -F	ATGACGGAGTCACCGCAAAC	950	[110]
	<i>ybtA</i> -R	TTACATCAGCGTTTAAAGG		
<i>fimH</i>	<i>fimH</i> -F	TACTGCTGATGGGCTGGTC	640	[110]
	<i>fimH</i> -R	GCCGGAGAGGTAATACCCC		
<i>entB</i>	<i>entB</i> -F	ATTCCTCAACTTCTGGGGC	371	[110]
	<i>entB</i> -R	AGCATCGGTGGCGGTGGTCA		
K2	K2-F	GACCCGATATTCATACTTGACAGAG	641	[110]
	K2-R	CCTGAAGTAAAATCGTAAATAGATGGC		
K5	K5-F	TGGTAGTGATGCTCGCGA	280	[111]
	K5-R	CCTGAACCCACCCCAATC		
K20	K20-F	CGGTGCTACAGTGCATCATT	741	[113]
	K20-R	GTTATACGATGCTCAGTCGC		
K54	K54-F	CATTAGCTCAGTGGTTGGCT	881	[113]
	K54-R	GCTTGACAAACACCATAGCAG		
K57	K57-F	CTCAGGGCTAGAAGTGTCAT	1037	[113]
	K57-R	CACTAACCCAGAAAGTCGAG		

**Table S3.** The sixty-five *K. pneumoniae* strains with complete genomes used in the phylogenetic tree.

<i>K. pneumoniae</i> Strain	Source	Collected Date	Serotype	Location	GenBank Accession No.
MN-03	bovine	2014	K22	USA	NZ_CP081897.1
AR142_2b	cat	2018	KN2	Switzerland	NZ_CP039954.1
18KM1950	dog	2018	KL105	Switzerland	NZ_CP039936.1
F1	human	2014	K47	China	NZ_CP026130.1
AJ218	human	2002	KUT	Australia	NZ_LR130541.1
B31	human	missing	K19	missing	NZ_CP035929.1
KP1677	human	2015	K20	China	NZ_CP041022.1
LH102-A	human	2012	K22	Laos	NZ_CP035194.1
158590	human	2018-2	K47	China	NZ_CP047649.1
QD23	human	2015	K45	China	NZ_CP042858.1
BA25665	human	2019	K2	India	NZ_CP059468.1
N16-03892	human	2016	KUT	Canada	NZ_CP047271.1
ATCC 43816	human	missing	KUT	missing	NZ_CP064352.1
RIVM_C014073	human	2017	K24	Netherlands	NZ_CP068797.1
IRQBAS102c	human	missing	K11	Irap	NZ_CP071150.1
SB1139	human	2002	KUT	Netherlands	NZ_CP084859.1
TH12852	human	missing	KUT	China	NZ_CP087122.1
KP29105	human	2020	K1	China	NZ_CP091061.1
TAKPN-1	human	2020	K54	China	NZ_CP091650.1
Bio4	human	2018	KN2	Turkey	CP093850.1
2N3	human	2009	KUT	China	NZ_CP025541.3
GSU10-3	human	2017	K47	Japan	NZ_AP018671.1
KSB1_7F-sc-2280268	human	2015	KUT	missing	NZ_CP031814.1
NFY0065	human	2014	K28	China	NZ_CP035531.1
NCTC11698	human	2015	K3	missing	NZ_LR588408.1
LEMB18	human	2017	KUT	UK	NZ_CP045782.1
Bckp067	human	2019	KUT	China	NZ_CP050829.1
SB612	water	2000	O1:K1	Netherlands	NZ_CP084830.1
74-17	human	2017	KUT	Italy	NZ_CP042317.1
RHB38-C06	human	2017	K6	UK	NZ_CP057099.1
KP63	human	2020	K64	China	NZ_CP077763.1
R32	human	2021	K19	China	NZ_CP083443.1
M164-1	human	2018	KUT	China	NZ_CP063992.1
R50	rabbit	2017	K5	China	NZ_CP040363.1
SB617	water	2000	KL124	Netherlands	NZ_CP084825.1
SB615	water	1999	KL124	Netherlands	NZ_CP084829.1
AR_0141	human	missing	K57	missing	NZ_CP028953.1
INF078	human	2015	KN2	missing	NZ_CP032831.1
NCTC11359	human	2015	KUT	United kingdom	NZ_LR133964.1
EC-12536	human	2019	K51	missing	NZ_LR025099.1
K2606	human	2012	K20	China	NZ_CP047633.1

KPN41053	human	2016	K16	China	NZ_CP052036.1
KP20191015	human	2019	K15	missing	NZ_CP051160.1
16BU137	human	2016	KUT	missing	NZ_CP051161.1
89-17	human	2017	KUT	Italy	NZ_CP042315.1
RHBSTW-00128	human	2017	KUT	UK	NZ_CP056830.1
S130-1	human	2019	KUT	China	NZ_CP063865.1
JX-CR-hvKP-7	human	2019	K64	China	NZ_CP064223.1
JX-CR-hvKP-9	human	2019	K64	China	NZ_CP064211.1
ZG2017CW 1-1-1	human	2017	KUT	China	NZ_CP065341.1
JX-CR-hvKP-10	human	2018	K64	China	NZ_CP064258.1
JX-CR-hvKP-8	human	2019	K64	China	NZ_CP064217.1
JX-CR-hvKP-11	human	2019	KUT	China	NZ_CP064208.1
ABFQB	human	2015	K22	USA	NZ_CP036438.1
TA6363	human	2016	K20	missing	NZ_AP019665.1
49210	human	missing	K1	missing	NZ_CP089024.1
KpWEA1	human	2016	KUT	China	NZ_AP024568.1
SWHIN_114	human	2018	KUT	Hong Kong	NZ_CP055087.1
STIN_79	human	2017	K54	Hong Kong	NZ_CP055003.1
Kp6	human	2015	KUT	missing	NZ_CP082290.1
SB611	water	2000	KL111	Netherlands	NZ_CP084843.1
555	chicken	2018	KL125	China	NZ_CP043932.1
ZYST1	pig	2017	KL110	China	NZ_CP031613.1
SWHE3	human	2018	K62	Hong Kong	NZ_CP055061.1
K41	pig	2020	KUT	China	NZ_CP094237.1

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**Table S4.** The identified GIs in the *K. pneumoniae* genomes.

<i>K. pneumoniae</i> Isolate	GI ID	Location	Scaffold Size (bp)	Start (bp)	End (bp)	CDS Gene	COG Gene
7-5-4	GI 1	Scaffold2	432753	339787	349536	9	9
	GI 2	Scaffold2	432753	59860	81676	21	19
	GI 3	Scaffold3	324215	246768	254874	7	6
	GI 4	Scaffold5	301401	123785	141119	14	14
	GI 5	Scaffold6	296280	155929	166357	15	11
	GI 6	Scaffold7	282157	210027	221984	17	7
	GI 7	Scaffold8	250732	188109	195940	9	9
	GI 8	Scaffold8	250732	207234	223806	12	7
	GI 9	Scaffold8	250732	236150	241954	10	8
	GI 10	Scaffold8	250732	244943	248389	7	4
	GI 11	Scaffold9	244480	194447	224127	34	27
	GI 12	Scaffold9	244480	232891	238915	7	7
	GI 13	Scaffold10	241143	2585	47180	47	32
	GI 14	Scaffold15	178058	139007	147213	11	4
	GI 15	Scaffold16	175428	37424	45691	7	5
	GI 16	Scaffold17	168697	135196	143810	9	8
	GI 17	Scaffold20	111494	58142	67650	9	7
7-10-14	GI 1	Scaffold1	460602	152376	167750	13	10
	GI 2	Scaffold1	460602	192747	225949	27	23
	GI 3	Scaffold1	460602	244863	254883	16	9
	GI 4	Scaffold2	382437	330434	343331	14	12
	GI 5	Scaffold4	360045	106846	117570	9	9
	GI 6	Scaffold4	360045	15346	45673	26	24
	GI 7	Scaffold5	351815	233798	243191	10	10
	GI 8	Scaffold27	42946	32741	40516	7	4
7-13-2	GI 1	Scaffold1	736977	104781	113741	8	8
	GI 2	Scaffold1	736977	358360	379490	21	19
	GI 3	Scaffold2	645154	394682	412023	14	14
	GI 4	Scaffold3	477586	151492	184440	35	26
	GI 5	Scaffold7	301221	21487	48214	25	24
	GI 6	Scaffold9	217230	193520	212882	21	17
	GI 7	Scaffold12	132361	60442	74780	15	11
	GI 8	Scaffold28	25989	9693	16319	8	5
7-17-8	GI 1	Scaffold2	473222	231286	247698	16	16
	GI 2	Scaffold2	473222	25130	46124	25	17
	GI 3	Scaffold2	473222	266070	279222	9	8
	GI 4	Scaffold3	460977	47399	59446	12	3
	GI 5	Scaffold4	421210	341088	363942	23	21
	GI 6	Scaffold4	421210	87549	97802	9	9
	GI 7	Scaffold5	410758	241686	249882	11	10
	GI 8	Scaffold6	365567	18564	43243	26	23
	GI 9	Scaffold6	365567	3647	11072	7	7
	GI 10	Scaffold7	337469	85252	90471	8	8
	GI 11	Scaffold8	332908	240567	283312	47	33
	GI 12	Scaffold9	299567	166248	178841	15	9
	GI 13	Scaffold9	299567	45703	62418	15	12
	GI 14	Scaffold12	206470	198350	204258	5	5
	GI 15	Scaffold14	109983	81272	86612	8	3
8-1-12-1	GI 1	Scaffold2	609221	249438	258820	9	9
	GI 2	Scaffold2	609221	60590	74393	16	7
	GI 3	Scaffold3	427492	19136	36739	19	19
	GI 4	Scaffold3	427492	347004	368133	21	19
	GI 5	Scaffold3	427492	93338	104200	9	9
	GI 6	Scaffold4	269760	38398	46229	9	9
	GI 7	Scaffold7	207876	1522	13898	17	10
	GI 8	Scaffold9	182244	159775	162808	8	2

8-2-5-4	GI 9	Scaffold9	182244	171864	179868	12	10
	GI 10	Scaffold9	182244	3225	17849	12	11
	GI 11	Scaffold11	169042	149704	165535	20	19
	GI 12	Scaffold13	157700	2136	8395	7	6
	GI 13	Scaffold19	120128	96233	115744	19	19
	GI 14	Scaffold24	85775	67696	72101	7	5
	GI 15	Scaffold28	55673	1737	10262	8	8
	GI 16	Scaffold29	54121	5582	11865	7	6
	GI 1	Scaffold1	636683	206607	219426	11	9
	GI 2	Scaffold1	636683	551676	585628	45	31
	GI 3	Scaffold1	636683	595042	634014	32	25
	GI 4	Scaffold3	390132	309488	332409	23	21
	GI 5	Scaffold3	390132	58735	68796	9	9
	GI 6	Scaffold6	318675	43690	61028	12	12
	GI 7	Scaffold7	314071	57029	74367	14	14
8-2-10-5	GI 8	Scaffold9	220110	142820	155334	16	2
	GI 9	Scaffold9	220110	187363	203780	15	15
	GI 10	Scaffold13	125592	84580	109357	15	14
	GI 11	Scaffold16	106294	70327	86892	10	7
	GI 1	Scaffold1	1044252	774060	791396	14	14
	GI 2	Scaffold1	1044252	955105	990617	25	19
	GI 3	Scaffold2	745848	565466	579015	13	13
	GI 4	Scaffold2	745848	734622	743007	12	11
	GI 5	Scaffold3	636023	109198	118393	8	8
	GI 6	Scaffold3	636023	19101	43733	21	19
	GI 7	Scaffold3	636023	357129	384338	28	25
	GI 8	Scaffold3	636023	408988	413997	7	7
	GI 9	Scaffold4	546665	235463	248298	10	8
	GI 10	Scaffold4	546665	661	34755	33	26
	GI 11	Scaffold9	216588	2681	36647	37	28
	GI 12	Scaffold20	20995	14194	18002	5	5

**Table S5.** Various functions of the identified GIs in the in the *K. pneumoniae* genomes.

<i>K. pneumoniae</i> Isolate	Related Gene				
	Prophage regulatory	Antibiotic and Heavy Metal Resistance	Virulence	Conjugative Transfer	Metabolism
7-5-4	GI 5, GI 11	GI 4	GI 2, GI 4		GI 17
7-10-14	GI 2, GI 4, GI 8	GI 7	GI 1		GI 6, GI 7
7-13-2	GI 5, GI 7	GI 3, GI 8	GI 2, GI 3		GI 3
7-17-8	GI 1, GI 8		GI 5, GI 3	GI 11	GI 5
8-1-12-1	GI 6, GI 11		GI 4		GI 1
8-2-5-4	GI 2,	GI 7	GI 3		GI 7
8-2-10-5	GI 3, GI 11	GI 1, GI 12	GI 7		GI 1, GI 10

**Table S6.** The identified prophages in the *K. pneumoniae* genomes.

<i>K. pneumoniae</i> Isolate	Prophage ID	Location	Scaffold Size (bp)	Start (bp)	End (bp)	Possible Phage	NCBI Accession No.
7-5-4	Ph01	Scaffold6	296280	149191	187586	<i>Enterobacteria</i> _phage_186	NC_001317
	Ph02	Scaffold8	250732	203517	250731	<i>Pseudomonas</i> _phage_D3	NC_002484
7-10-14	Ph01	Scaffold1	460602	208039	271213	<i>Pseudomonas</i> _phage_D3	NC_002484
	Ph02	Scaffold1	460602	380887	416860	<i>Enterobacteria</i> _phage_P2	NC_001895
7-13-2	Ph01	Scaffold12	132361	58921	91462	Phage_phiO18P	NC_009542
	Ph02	Scaffold3	477586	167679	204848	<i>Enterobacteria</i> _phage_ES18	NC_006949
7-17-8	Ph01	Scaffold2	473222	27482	73299	<i>Klebsiella</i> _phage_phiKO2	NC_005857
	Ph02	Scaffold14	109983	1015	109982	<i>Enterobacteria</i> _phage_P1	NC_005856
8-1-12-1	Ph01	Scaffold11	169042	147704	169042	<i>Enterobacteria</i> _phage_186	NC_001317
	Ph02	Scaffold9	182244	154869	182244	<i>Ralstonia</i> _phage_RSA1	NC_009382
	Ph03	Scaffold4	269760	198579	249652	<i>Klebsiella</i> _phage_phiKO2	NC_005857
8-2-5-4	Ph01	Scaffold1	636683	556279	599619	<i>Enterobacteria</i> _phage_HK022	NC_002166
8-2-10-5	Ph01	Scaffold9	216588	6585	40967	<i>Enterobacteria</i> _phage_N15	NC_001901
	Ph02	Scaffold1	53616	3208	53418	<i>Klebsiella</i> _phage_phiKO2	NC_005857

**Table S7.** The identified INs in the *K. pneumoniae* genomes.

<i>K. pneumoniae</i> Isolate	IN ID	Location	Scaffold Size (bp)	Start (bp)	End (bp)	CDS Gene
7-5-4	IN 1	Scaffold43	5287	1829	5286	1
7-10-14	IN 1	Scaffold66	1899	34	1864	2
	IN 2	Scaffold76	1265	3	1232	0
8-2-10-5	IN 1	Scaffold1	1044252	318724	323056	2

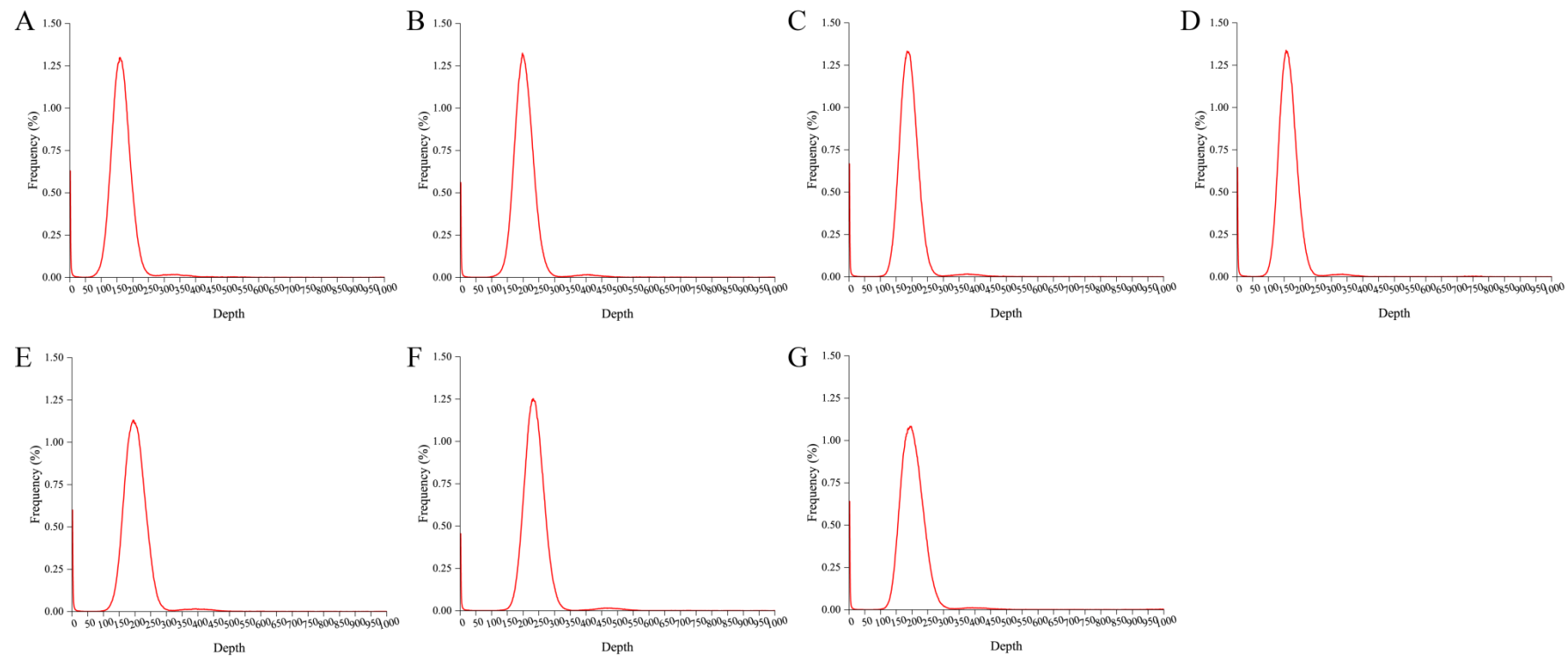
**Table S8.** The identified ISs in the *K. pneumoniae* genomes.

<i>K. pneumoniae</i> Isolate	IS ID	Location	Scaffold Size (bp)	Start (bp)	End (bp)	IS Family
7-5-4	IS001	Scaffold52	3429	2043	3359	IS110
	IS002	Scaffold9	244480	226072	227233	IS3
7-10-14	IS001	Scaffold42	8805	6302	7043	IS3
	IS002	Scaffold5	351815	276447	277895	IS91
7-13-2	IS001	Scaffold1	736977	371640	372447	IS91
	IS002	Scaffold17	90033	189	1454	IS110
	IS003	Scaffold21	50695	42679	43840	IS3
	IS004	Scaffold25	27431	26176	27349	IS5
	IS005	Scaffold57	1258	1	1258	IS3
	IS006	Scaffold66	820	1	820	IS6
7-17-8	IS001	Scaffold2	473222	279350	280531	IS3
	IS002	Scaffold4	421210	354404	355181	IS91
8-1-12-1	IS001	Scaffold2	609221	63591	65027	IS91
	IS002	Scaffold27	58708	55130	56718	IS3
	IS003	Scaffold3	427492	360319	361096	IS91
	IS004	Scaffold30	44634	37645	38824	IS5
8-2-5-4	IS003	Scaffold1	636683	224411	225631	IS3
	IS001	Scaffold13	125592	106372	107533	IS3
	IS002	Scaffold13	125592	113920	115084	IS3
	IS004	Scaffold3	390132	322874	323651	IS91
8-2-10-5	IS001	Scaffold3	636023	374276	375378	IS91
	IS002	Scaffold3	636023	375309	376585	IS91

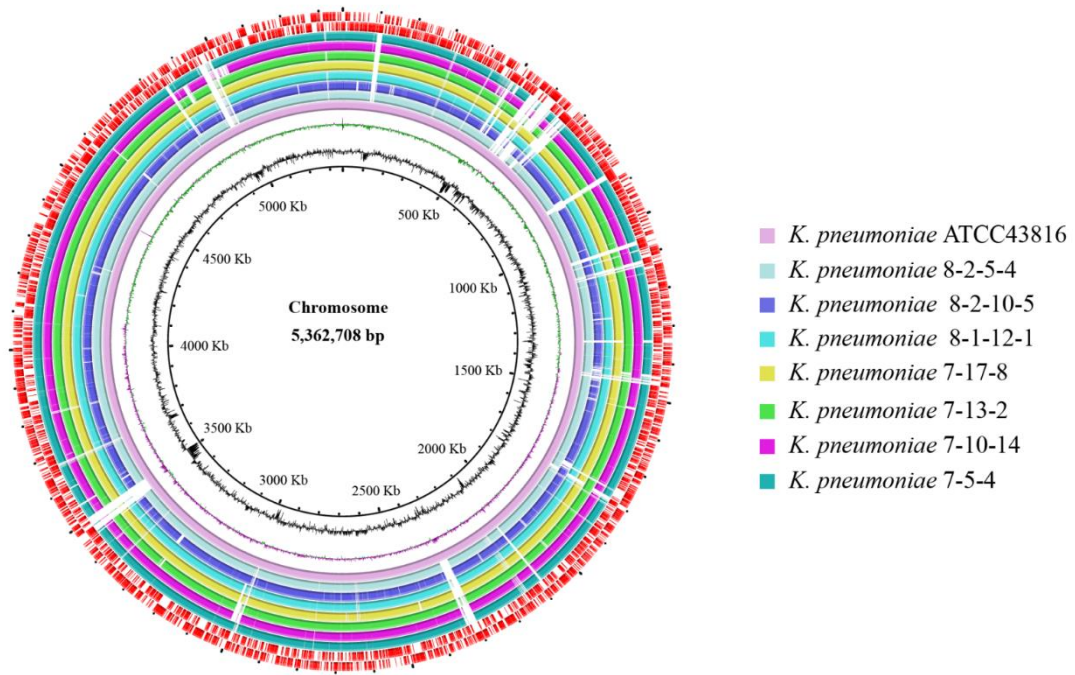


**Table S9.** The identified repeats in the *K. pneumoniae* genomes

<i>K. pneumoniae</i> Isolate	Repeat ID	Location	Scaffold Size (bp)	Repeat		
				Start	End	Length (bp)
7-5-4	Scaffold14_TR056	Scaffold14	196754	1	522	522
7-10-14	Scaffold3_TR004	Scaffold3	379227	1	223	223
	Scaffold6_TR014	Scaffold6	341057	1	270	270
	Scaffold7_TR022	Scaffold7	295176	1	447	447
	Scaffold15_TR051	Scaffold15	130236	129760	130236	477
	Scaffold32_TR069	Scaffold32	29415	1	267	267
7-13-2	Scaffold16_TR051	Scaffold16	95537	1	554	554
	Scaffold22_TR061	Scaffold22	48713	48189	48713	525
7-17-8	Scaffold24_TR60	Scaffold24	25052	1	341	341
8-2-5-4	Scaffold7_TR035	Scaffold7	314071	1	305	305
	Scaffold16_TR067	Scaffold16	106294	106184	106294	111
	Scaffold31_TR071	Scaffold31	25321	1	883	883
8-2-10-5	Scaffold36_TR074	Scaffold36	6671	1	98	98
	Scaffold6_TR38	Scaffold6	322274	322215	322274	60
	Scaffold8_TR50	Scaffold8	277101	276823	277101	279
	Scaffold19_TR63	Scaffold19	22479	1	85	85



**Figure S1.** The k-mer analysis for *K. pneumoniae* subread data based on the number of unique 17-mers.(A–G): *K. pneumoniae* 7-5-4, 7-10-14, 7-13-2, 7-17-8, 8-1-12-1, 8-2-5-4, and 8-2-10-5, respectively.



**Figure S2.** Genome circle maps of the seven *K. pneumoniae* isolates. Circles from the inwards to outside represented GC content (outward parts mean higher than average, while inward parts mean lower than average); GC-skew (purple values are higher than zero, while green values are lower than zero); the reference genome of *K. pneumoniae* ATCC43816 (GenBank accession no. NZ\_CP064352); *K. pneumoniae* 8-2-5-4, 8-2-10-5, 8-1-12-1, 7-17-8, 7-13-2, 7-10-14, and 7-5-4 genomes, respectively; and CDSs on the negative and positive chains (inward and outward parts), respectively.