

Supplementary Material

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TABLE S1 Summary of *Klebsiella pneumoniae* strains used for the phylogenetic tree and SNPs analysis

Strains	Year	NCBI accession number or SRA data base	Breadth of coverage (%)	Depth of coverage (fold)	No. of SNPs including recombination site	No. of SNPs excluding recombination site
reference	before 1937	FO834906	-	-	-	-
KUN4843*	2009	DRX052508	87.2	46.0	25,742	24,132
KUN5033*	2009	DRX052507	83.3	42.4	25,741	24,131
ERR1014123*	2011	ERR1014123	84.9	92.0	27,063	25,068
ERR204293	unknown	ERR204293	86.5	60.1	26,883	24,976
ERR303231	unknown	ERR303231	90.2	63.0	25,769	23,610
ERR303236	unknown	ERR303236	80.1	69.1	27,170	25,530
ERR317530*	2012	ERR317530	81.9	62.3	26,976	25,008
ERR317531*	2012	ERR317531	81.0	60.9	26,976	25,008
ERR317532*	2012	ERR317532	81.9	56.5	26,976	25,008
ERR317533*	2012	ERR317533	80.6	58.3	26,976	25,008
ERR317535*	2012	ERR317535	86.6	62.4	26,379	24,646
ERR317536*	2012	ERR317536	85.9	61.0	26,379	24,646
ERR323219	unknown	ERR323219	84.9	72.4	26,049	24,334
ERR323220	unknown	ERR323220	87.0	72.2	26,050	24,335
ERR323222	unknown	ERR323222	82.3	66.2	26,050	24,335
ERR455536	unknown	ERR455536	82.4	56.9	26,691	24,791
ERR455538	unknown	ERR455538	81.1	55.8	26,695	24,795
ERR459452	unknown	ERR459452	83.6	70.4	27,690	24,315
ERR459453	unknown	ERR459453	87.1	77.0	27,689	24,315
ERR459456	unknown	ERR459456	81.0	68.7	27,208	25,138
ERR459458	unknown	ERR459458	85.5	66.4	25,392	23,245
ERR559460	unknown	ERR559460	83.7	62.0	25,592	23,916
ERR706870	unknown	ERR706870	87.0	102.8	26,796	25,002
ERR712623	unknown	ERR712623	90.3	95.8	26,777	24,980
ERR712626	unknown	ERR712626	88.8	94.7	26,798	25,005
ERR712793	unknown	ERR712793	85.6	107.2	26,786	24,995
ERR712901	unknown	ERR712901	86.6	85.3	26,753	24,963
ERR713522	unknown	ERR713522	86.3	89.7	26,765	24,975
ERR926757*	2014	ERR926757	89.9	99.8	26,295	24,316
SRR1510963*	2012	SRR1510963	86.3	96.5	27,168	25,527
SRR2033748*	2012	SRR2033748	84.1	70.3	27,132	25,490
SRR2244243	unknown	SRR2244243	80.6	98.7	26,414	24,566
SRR2724078*	2007	SRR2724078	82.3	90.0	27,124	25,484
SRR2724097*	2012	SRR2724097	87.7	92.8	26,467	24,578
SRR2724109*	2012	SRR2724109	86.8	99.7	25,659	23,979
SRR2724116*	2013	SRR2724116	87.3	88.6	27,242	25,602
SRR2724117*	2013	SRR2724117	84.7	111.2	27,243	25,603
Average			85.0 ± 2.9	76.4 ± 18.4	26,636 ± 589	24,739 ± 564

* indicates the strains used for molecular clock analysis.

TABLE S2 List of primers used in this study

Primer	Nucleotide sequence	Amplicon size (bp)	Location
Used for gap closing			
pKUN4507_2 L	5'-CCCCACCACTCGACGATATG-3'		pKUN4507_2
pKUN4507_2 R	5'-CTCATCGCCAGAAGTGACGA-3'		
Used for conjugation analysis			
FwA16S	5'-GCTTCACACGTCATACAATG-3'	200	<i>Achromobacter xylosoxidans</i> 16S rRNA
RvA16S	5'-TTCTGGTAAAACCCACTCC-3'		
FwK16S	5'-GCATTGAAAACCTGGCAGGCTA-3'	383	<i>Klebsiella pneumoniae</i> 16S rRNA
RvK16S	5'-CTCTGGAAAAGTTCTGTGGAT-3'		
IMP19F	5'-TTTCTAAACACGGTTTGGTG-3'	493	<i>bla</i> _{IMP-19}
IMP19R	5'-GAAACAACCAAGTTTTGCTTT-3'		

TABLE S3 Summary of the strains used in the conjugation analysis

Isolates	Year	Conjugation analysis
<i>Achromobacter xylosoxidans</i>		
KUN4507	2009	Donor
<i>Klebsiella pneumoniae</i>		
KUN4843	2009	Recipient
<i>Escherichia coli</i>		
ME8067	-	Recipient
ME8568	-	Recipient

TABLE S4 Summary of strains isolated from this patient

Isolates	Year	Total reads	Reads passing filter	% \geq Q30 ^a	No. of contigs (\geq 0 bp)	No. of contigs (\geq 1000 bp)	N50 (bp)	NCBI accession number
<i>Achromobacter xylosoxidans</i>								
KUN4507	2009	1,225,422	1,200,026	80%	148	124	82,254	DRX052506
<i>Klebsiella pneumoniae</i>								
KUN4843	2009	1,215,126	1,199,009	81%	98	54	361,546	DRX052508
KUN5033	2009	1,149,922	1,134,327	82%	135	84	330,754	DRX052507

^a % \geq Q30 of filtered reads.

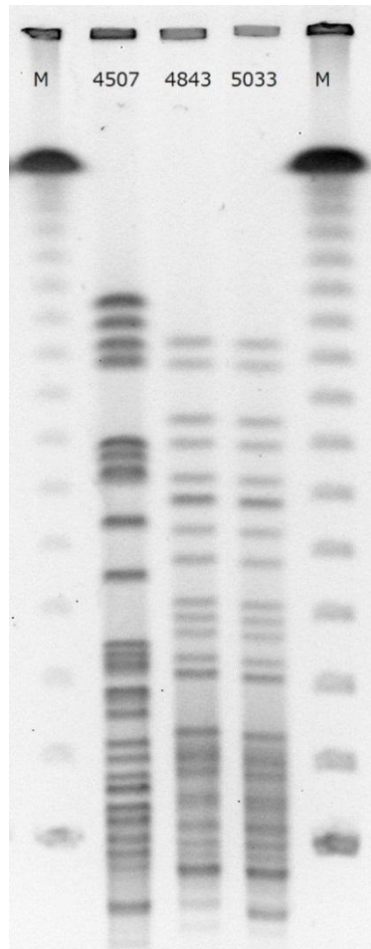


FIG S1 Pulsed-Field Gel Electrophoresis of XbaI-digested genome. M: lambda marker; 4507: *Achromobacter xylosoxidans* KUN4507 isolate; 4843: *Klebsiella pneumoniae* KUN4843 isolate; 5033: *K. pneumoniae* KUN503 isolate. *K. pneumoniae* KUN4843 and KUN5033 revealed the same PFGE pattern.

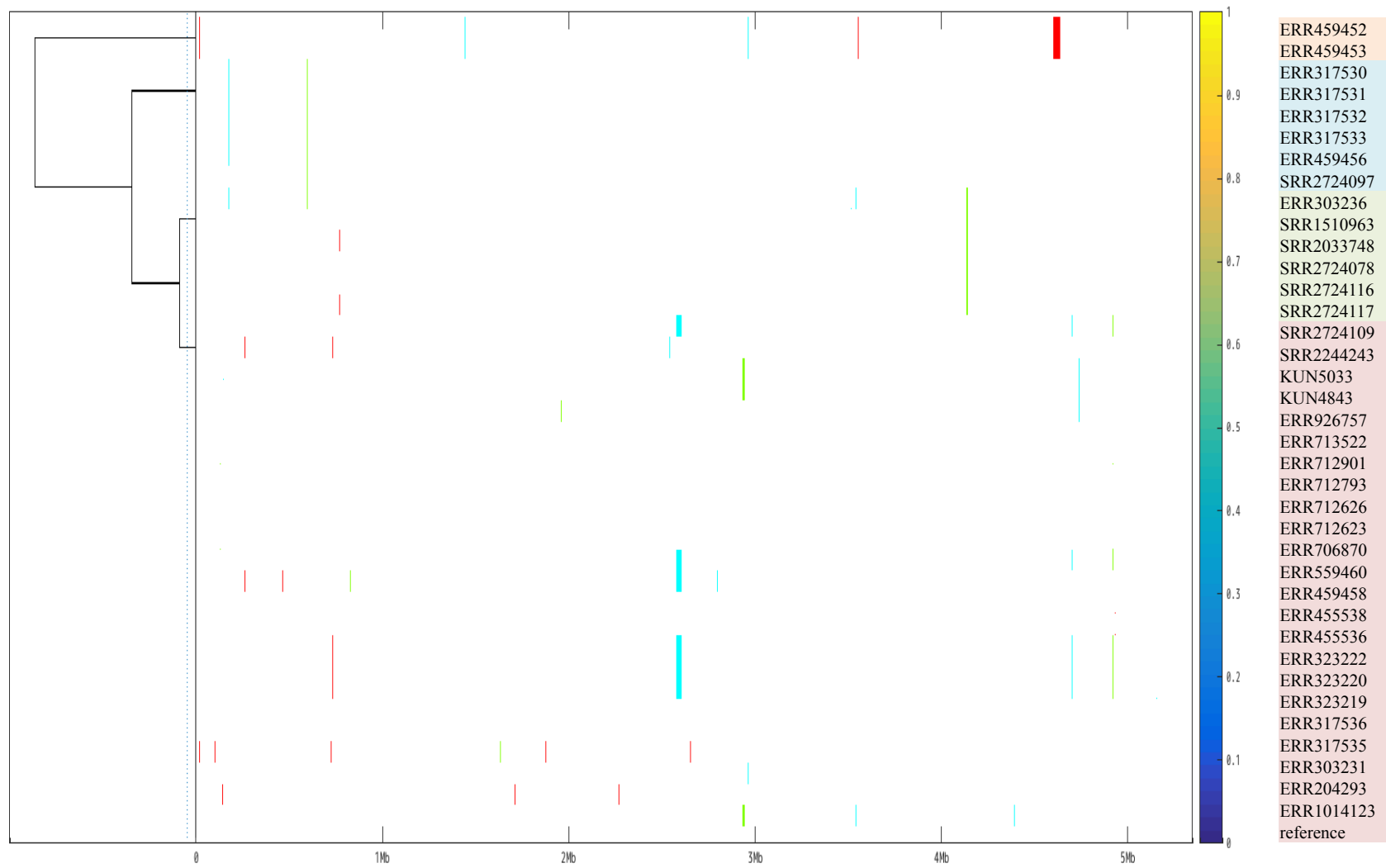


FIG S2 Recombination site analysis. A total of 346 recombination sites were detected using BRATNextGen. The total length of recombination site was 193,842 bp (average $560 \pm 2,643$ bp).

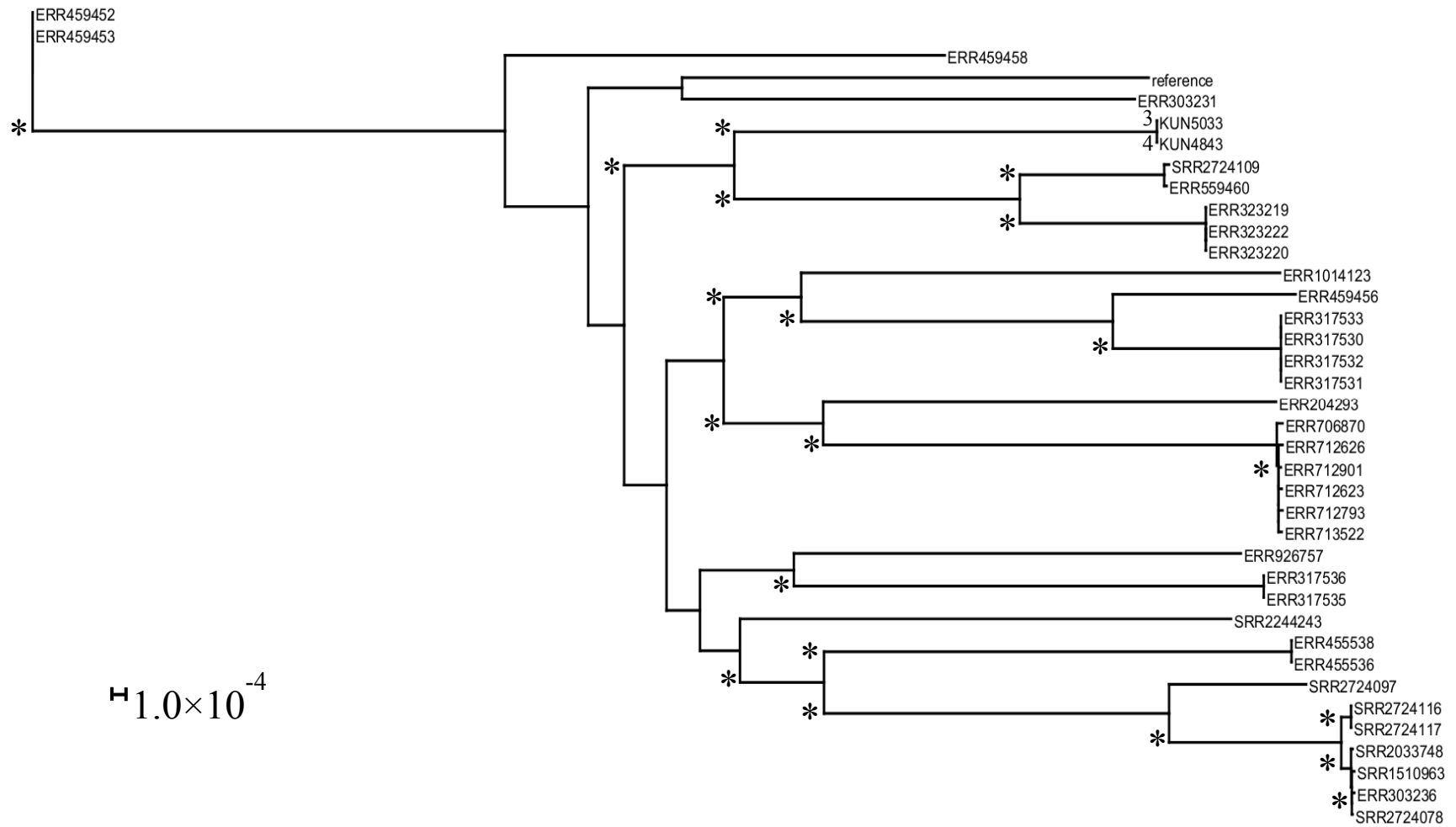


FIG S3 Phylogenetic tree of 37 *Klebsiella pneumoniae* isolates. The asterisk represents 100% bootstrap support. The scale bar indicates substitutions per SNP site. The numbers indicates number of distinguishing SNPs. *K. pneumoniae* KUN4843 encoded four SNPs from the most recent common ancestor and *K. pneumoniae* KUN5033 had three SNPs.

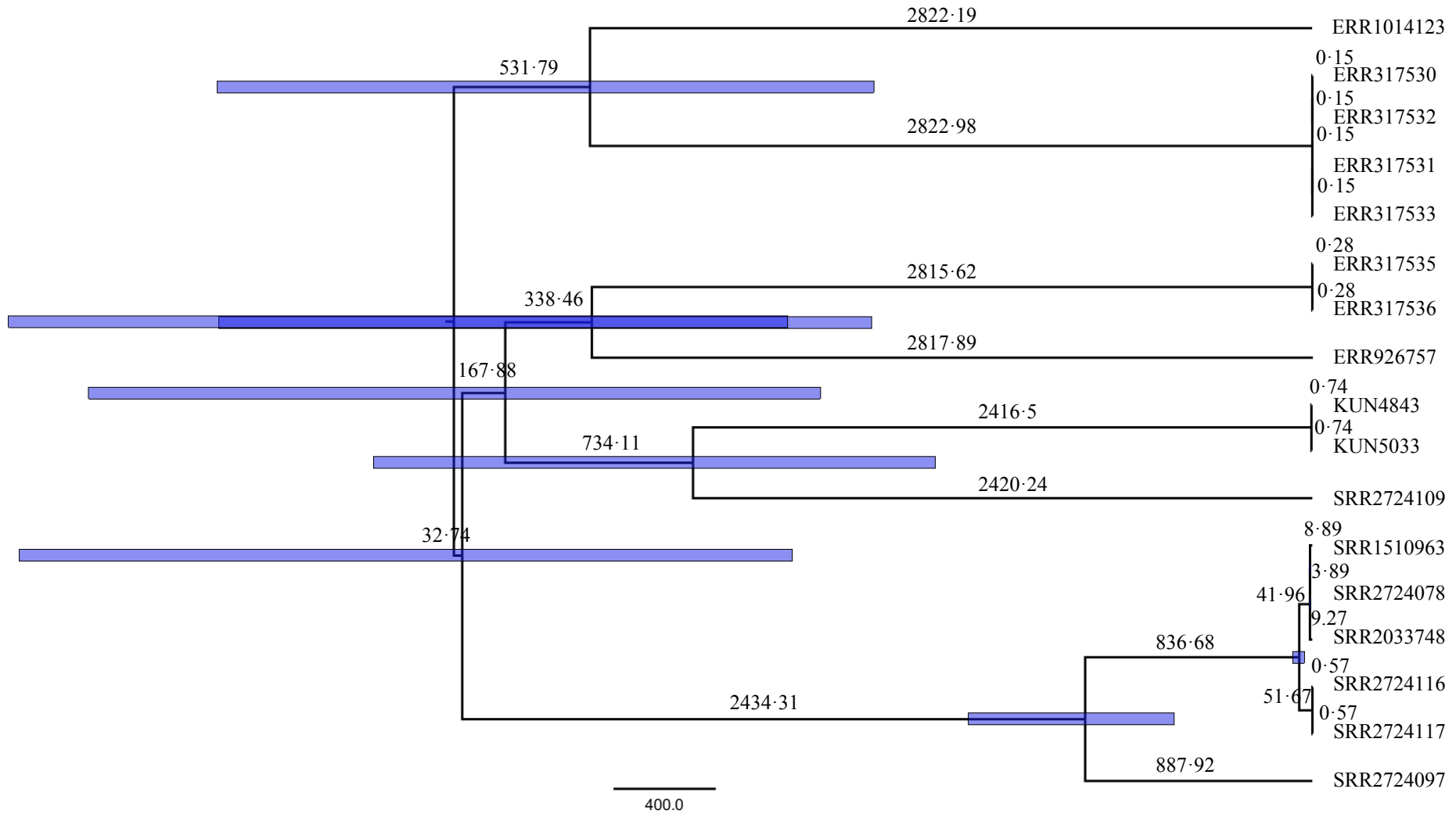


FIG S4 Molecular clock analysis of 17 *Klebsiella pneumoniae* isolates. The MRCA diverged into two groups of descendant 0.74 years before *K. pneumoniae* KUN4843 and KUN5033 appeared (95% highest posterior density [HPD]; 0.21-1.38).