

Figure S1. Short-read coverage against against NCTC9394 (RefSeq: NC_021046.1) for *E. cloacae* strains (A) or MGH78578 (GenBank: CP000647.1) for *K. pneumoniae* strains (B).

A

Strain ID	Organism	KPC	Tn4401	Plasmid Finder	% coverage of a reference plasmid (NZ_CP008826)	233 plasmid (10192bp) NG_041614.1	pKPC_CAV1392 (43621bp) NZ_CP011575.1	p34399 (43500bp) NZ_CP010387.1	pKPC-f91 (47290bp) NZ_CP008826.1	pRYCKPC3.1 (9803bp) NC_019151.1
Ec01	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec02	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec03	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec04	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec05	<i>E. cloacae</i>	KPC-3	b	repA	93					
Kp06	<i>K. pneumoniae</i>	KPC-3	d	IncFIA(HI1)	32					
Kp07	<i>K. pneumoniae</i>	KPC-3	b	repA	92					
Kp08	<i>K. pneumoniae</i>	KPC-3	b	IncI2	32					
Ec09	<i>E. cloacae</i>	KPC-3	b	repA	89					
Ec10	<i>E. cloacae</i>	KPC-3	b	repA	92					
Kp11	<i>K. pneumoniae</i>	KPC-3	b	repA	92					
Ec12	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec13	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec14	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec15	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec114	<i>E. cloacae</i>	KPC-3	b	repA	92					
Ec149	<i>E. cloacae</i>	KPC-3	b	repA	94					
Kp150	<i>K. pneumoniae</i>	KPC-2	a	IncFII(K)	39					
Kp152	<i>K. pneumoniae</i>	KPC-3	d	N/A	39					
Kp156	<i>K. pneumoniae</i>	KPC-3	d	N/A	39					

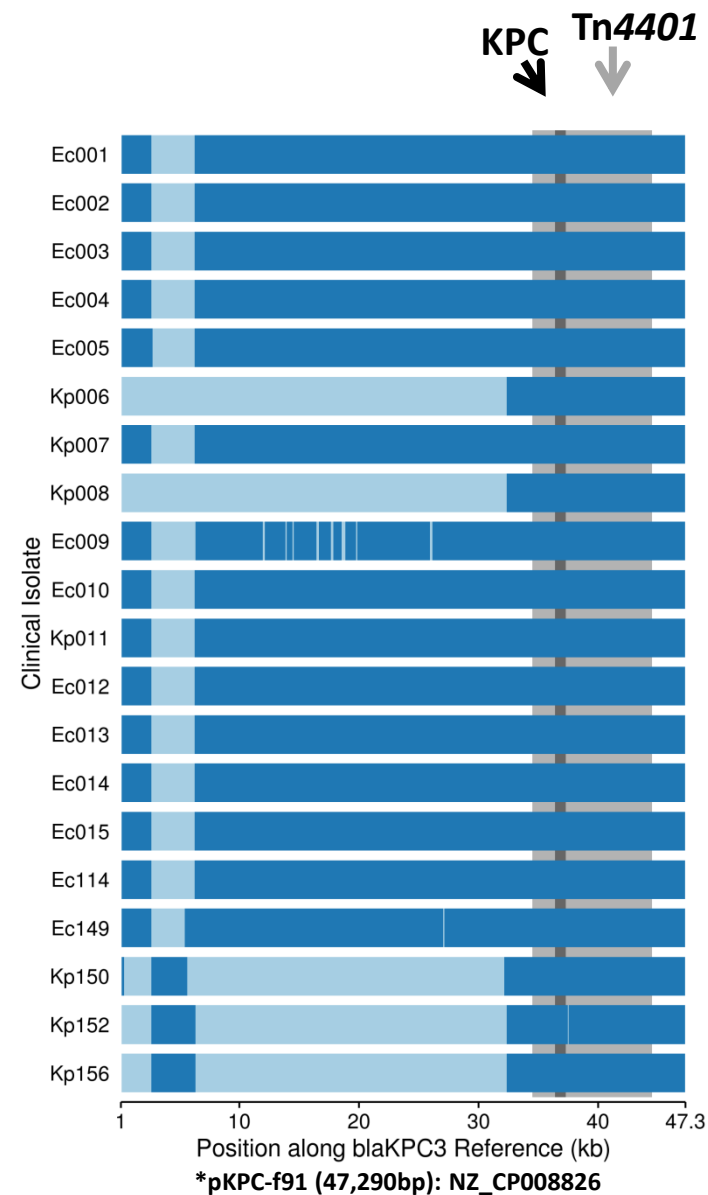
B

Figure S2. (A) Association of *bla*_{KPC}-containing contigs from *de novo* assemblies with publicly available plasmids on Blastn search. Presence (black) / absence (white) of plasmid references (RefSeq) for each isolate is shown. (B) The most common *bla*_{KPC-3}-containing *de novo* assembled contig/plasmid had high sequence homology with three previously described plasmids. For quality control purposes, short reads from all *bla*_{KPC}-containing isolates (n=20) were mapped against the longest of these (pKPC-f91, 47,290bp, NZ_CP008826), and the alignments were examined for evidence of plasmid closure (e.g. coverage breaks and terminal read splits). Dark blue is coverage > 25 and light blue is coverage < 25.

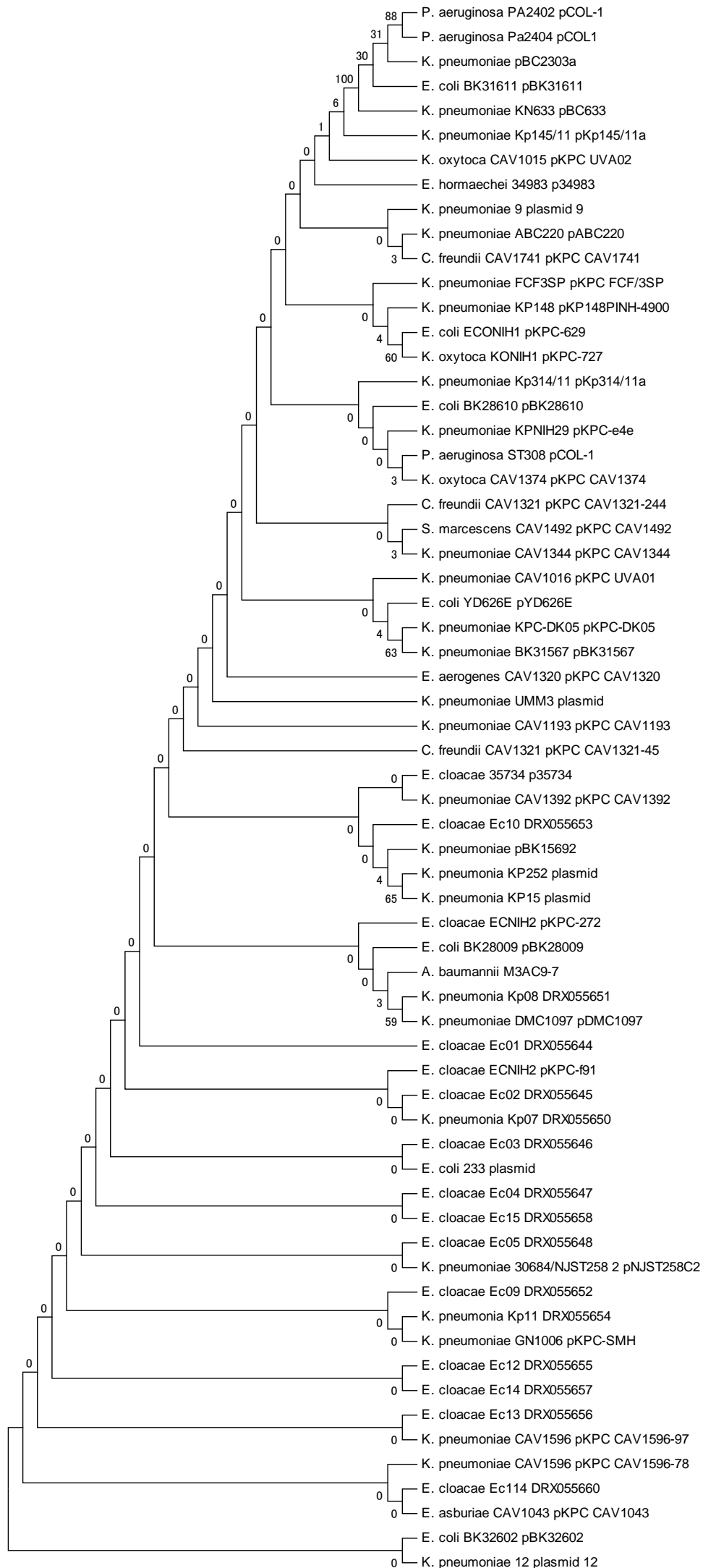


Figure S3. Tn4401b from the UNC outbreak cluster together when compared to Tn4401b elements from globally sourced samples. This phylogeny was inferred using the maximum-likelihood framework and the Tamura-Nei model. Maximum likelihood phylogeny of Tn4401b *de novo* assembled sequences from the UNC CRE outbreak were compared to all available Tn4401b sequences from GenBank. Branch confidence was confirmed using 500 bootstrap iterations. Evolutionary analyses were conducted in MEGA7 (<http://www.megasoftware.net/>).