

**Supplementary Table 1.** Primer sequences for PCR used in this study.

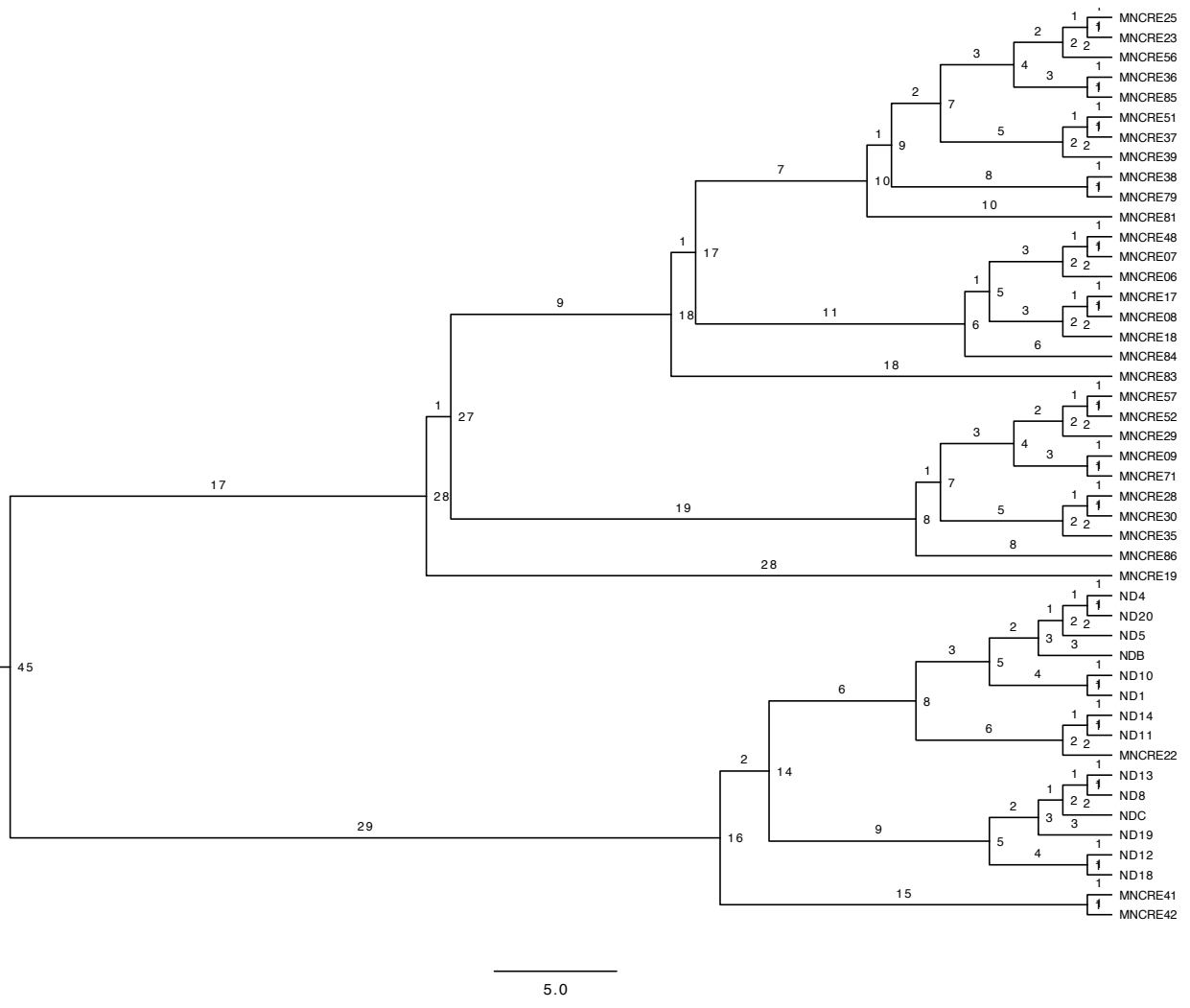
Locus	Forward/Reverse	Sequence (5'-3')
Junction 1	F	CAAACGCGCTGATTGCCATTC
Junction 1	R	CCCGCTTTGCCACGGACATA
Junction 2	F	CCCGCTTTGCCACGGACATA
Junction 2	R	CGGTGCGCGACAACCTACG
Junction 3	F	GTACGCCACCCGACCTGGAC
Junction 3	R	AAACGCGCTGATTGCCATTCT

**Supplementary Table 2.** Genes under positive selection in the circulating CP-*E. cloacae* lineage.

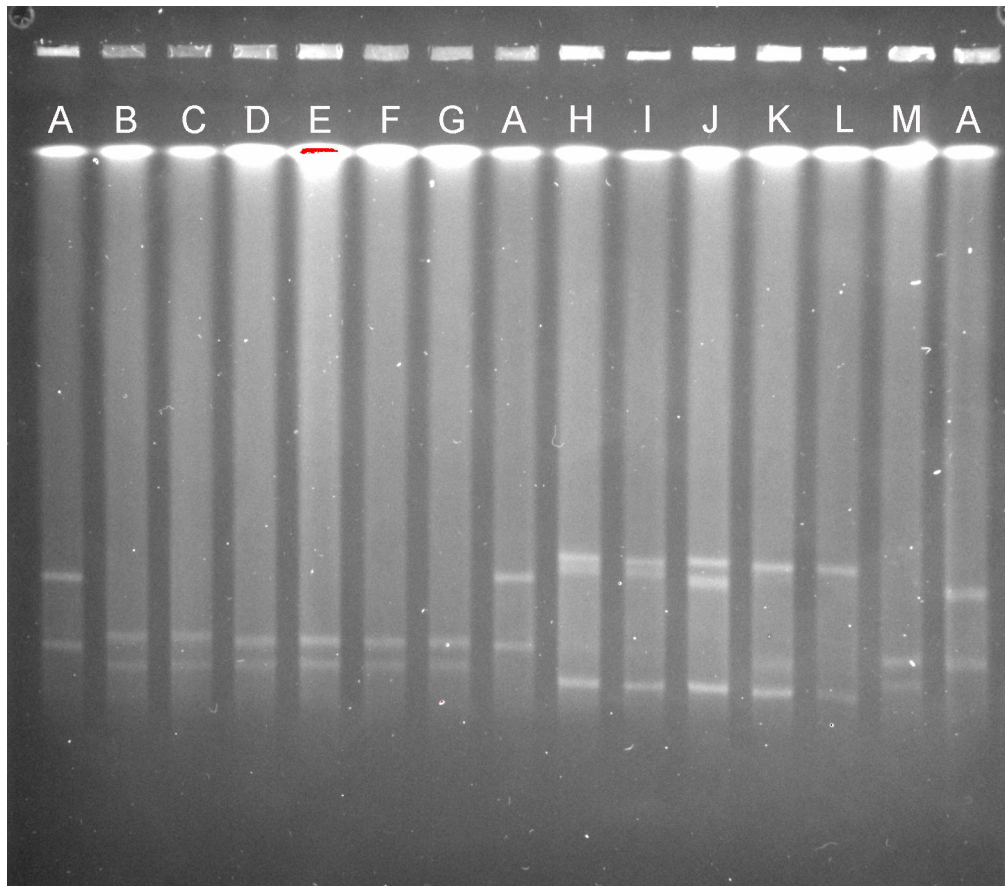
<b>groupid</b>	<b>dN/dS</b>	<b>dN</b>	<b>dS</b>	<b>Description</b>
group2056	306.9865	0.0359	0.0001	phospholipid:lipid A palmitoyltransferase
group5	188.0339	0.0101	0.0001	Hcp1 family type VI secretion system effector
group2142	8.0817	0.0301	0.0037	hypothetical protein
group640	4.5993	0.0102	0.0022	2'-5' RNA ligase
group1014	3.431	0.2088	0.0609	hypothetical protein
group1368	3.0634	0.0582	0.019	hypothetical protein
group2242	2.4204	0.0261	0.0108	polysaccharide export protein Wza
group168	2.1798	0.2044	0.0938	hypothetical protein
group3792	2.0738	0.0907	0.0437	antirepressor
group2648	2.0251	0.0128	0.0063	hydrogenase assembly chaperone
group2695	1.6815	0.0294	0.0175	hypothetical protein
group3671	1.6249	0.1056	0.065	hypothetical protein
group2417	1.5371	0.1378	0.0897	hypothetical protein
group3870	1.508	0.1786	0.1185	membrane protein
group527	1.2409	0.1138	0.0917	hypothetical protein
group785	1.1834	0.2276	0.1923	hypothetical protein
group730	1.1802	0.0208	0.0176	transcriptional regulator
group2241	1.127	0.0115	0.0102	phosphotyrosine-protein phosphatase
group2753	1.05	0.0132	0.0126	hypothetical protein
group3696	1.045	0.0138	0.0132	ATPase
group1709	1.014	0.0121	0.0119	hypothetical protein
group3668	1.0079	0.0313	0.031	transposase

**Supplementary Table 3.** Comparison of single nucleotide polymorphisms effects within the *E. cloacae* circulating lineage.

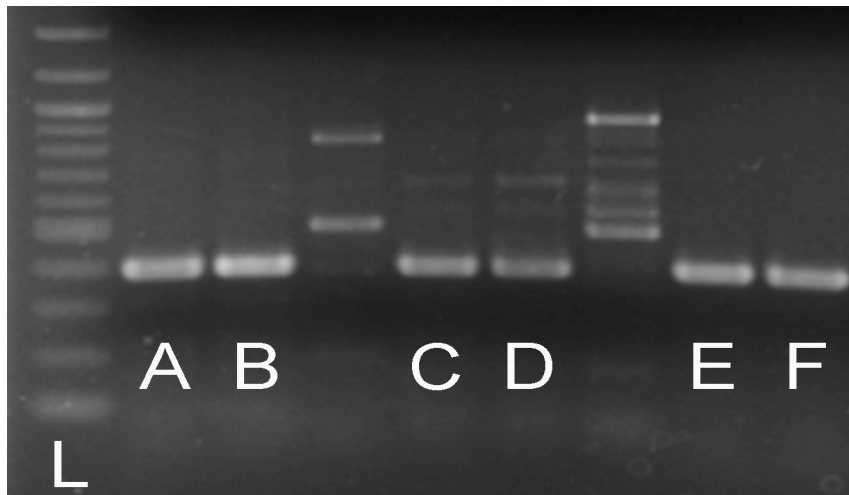
Strain	Synonymous	Non-synonymous	Total SNPs	Insertions	Deletions
MNCRE56	1	8	14	3	2
MNCRE79	1	10	17	3	3
MNCRE81	1	5	10	0	1
MNCRE28	1	7	13	3	1
MNCRE25	1	7	14	3	1
MNCRE23	1	7	13	2	1
MNCRE39	3	8	17	0	1
MNCRE51	3	6	14	3	1
MNCRE37	2	7	13	0	2
MNCRE41	5	7	27	4	1
MNCRE42	3	7	24	5	1
MNCRE36	1	7	13	3	1
MNCRE85	1	7	13	3	2
MNCRE83	2	9	16	0	1
MNCRE86	2	11	18	3	1
MNCRE84	2	7	13	0	2
MNCRE17	6	12	21	2	1
MNCRE08	3	6	12	1	1
MNCRE18	5	11	21	1	1
MNCRE06	3	9	16	1	3
MNCRE48	3	13	21	2	1
MNCRE07	2	8	13	1	1
MNCRE22	2	13	26	3	1
MNCRE35	2	14	20	1	3
MNCRE30	0	13	16	1	1
MNCRE28	0	16	19	1	1
MNCRE29	2	3	7	0	1
MNCRE52	3	7	12	0	1
MNCRE57	3	6	12	0	2
MNCRE71	3	16	27	0	1



**Supplementary Figure 1.** Reconstruction of the temporal history of the CP-*E. cloacae* circulating lineage using Bayesian coalescent molecular clock analyses.



**Supplementary Figure 2.** S1 nuclease pulsed-field gel electrophoresis of selected strains. Lane A = control *E. coli* strain JJ1886 with plasmids of sizes 110 kb and 56 kb; B = MNCRE22 (*E. cloacae*); C = MNCRE22 (*E. cloacae*); D and E = MNCRE41 (*E. cloacae*); F and G = MNCRE42 (*E. cloacae*); H and I = MNCRE44 (*E. coli*); J = MNCRE45 (*E. coli*); K = MNCRE46 (*E. coli*); L = MNCRE47 (*E. coli*); and M = MNCRE51 (*E. cloacae*).



**Supplementary Figure 3.** PCR for junctions spanning individual plasmids (junction 1) and co-integrate plasmid (junctions 2 and 3). Lane A = junction 1 with strain MNCRE41; B = junction 1 with MNCRE51; C = junction 2 with MNCRE44; D = junction 2 with MNCRE46; E = junction 3 with MNCRE44; and F = junction 3 with MNCRE46. L = 100 bp ladder.