

Supplementary material

Supplementary Table S1. NDM confirmed cases (N=122) from 2021-2022 by sample origin from the HSJD.

Sample origin	N	%
Sputum	60	49
Blood	23	19
Urine	17	14
Tissue	15	12
Peritoneal fluid	3	2
Abscess	1	1
Bone	1	1
Cerebrospinal fluid	1	1
Secretion	1	1

Supplementary Table S2. Chromosomal features of *bla*NDM-positive isolates.

TO_Code	Taxonomic identification	plasmidverify	Score	plasflow	Score	plasmidfinder	mob-suite	# scaffolds	# contigs	Topology	Genome size	GC	GC std	# ambiguous bases	Coding density	Translation table	# predicted genes	Completeness	Contamination
GN4720	<i>Acinetobacter baumannii</i>	Chromosome	-2345.95	chromosome	0.9825	Chromosome	chromosome	1	1	circular	4691780	0.553654263	0	0	0.891349125	11	4360	100	0
GN4722	<i>Acinetobacter baumannii</i>	Chromosome	-2345.95	chromosome	0.9826	Chromosome	chromosome	1	1	circular	5244654	0.574648394	0	0	0.879320352	11	4809	100	0
GN4725	<i>Acinetobacter baumannii</i>	Chromosome	-2345.95	chromosome	0.9821	Chromosome	chromosome	1	1	circular	5247538	0.574632713	0	0	0.879263571	11	4811	100	0
GN4736	<i>Acinetobacter baumannii</i>	Chromosome	-2345.95	chromosome	0.9837	Chromosome	chromosome	1	1	circular	5247706	0.574632611	0	0	0.879106413	11	4816	100	0
GN4742	<i>Acinetobacter baumannii</i>	Chromosome	-2345.95	chromosome	0.9877	Chromosome	chromosome	1	1	circular	5245204	0.574663445	0	0	0.87945159	11	4809	100	0
GN4753	<i>Acinetobacter baumannii</i>	Chromosome	-2315.49	chromosome	0.982	Chromosome	chromosome	1	1	circular	5240768	0.574701456	0	0	0.879472054	11	4831	100	0
GN4718	<i>Enterobacter xiangfangensis</i>	Chromosome	-3928.86	chromosome	0.8567	Chromosome	chromosome	1	1	circular	4099999	0.390056193	0	0	0.876248994	11	3859	99.77	0.43
GN4727	<i>Enterobacter xiangfangensis</i>	Chromosome	-3907.83	chromosome	0.8516	Chromosome	chromosome	1	1	circular	5247515	0.574625894	0	0	0.87931297	11	4812	99.77	0.45
GN4729	<i>Enterobacter xiangfangensis</i>	Chromosome	-3907.83	chromosome	0.8596	Chromosome	chromosome	1	1	circular	5247700	0.574632887	0	0	0.87908741	11	4815	99.77	0.43
GN4731	<i>Enterobacter xiangfangensis</i>	Chromosome	-3907.83	chromosome	0.8705	Chromosome	chromosome	1	1	circular	4691798	0.55365896	0	0	0.891477851	11	4353	99.77	0.43
GN4732	<i>Enterobacter xiangfangensis</i>	Chromosome	-3907.83	chromosome	0.8515	Chromosome	chromosome	1	1	circular	4691798	0.55365896	0	0	0.891477851	11	4353	99.77	0.43
GN4733	<i>Enterobacter xiangfangensis</i>	Chromosome	-3907.83	chromosome	0.8687	Chromosome	chromosome	1	1	circular	4691798	0.553657681	0	0	0.891491279	11	4353	99.77	0.43
GN4755	<i>Enterobacter xiangfangensis</i>	Chromosome	-3855.07	chromosome	0.8822	Chromosome	chromosome	1	1	circular	5344950	0.573802935	0	0	0.876600904	11	4919	99.47	0.55
GN4738	<i>Escherichia coli</i>	Chromosome	-4167.66	chromosome	0.9626	Chromosome	chromosome	1	1	circular	4099681	0.390048153	0	0	0.87598718	11	3860	99.97	0.39
GN4741	<i>Escherichia coli</i>	Chromosome	-4116.77	chromosome	0.9596	Chromosome	chromosome	1	1	circular	5204270	0.575759521	0	0	0.878295707	11	4829	99.93	0.26
GN4751	<i>Escherichia coli</i>	Chromosome	-4115.46	chromosome	0.9743	Chromosome	chromosome	1	1	circular	4831362	0.554350719	0	0	0.892742254	11	4500	99.93	0.1
GN4715	<i>Klebsiella pneumoniae</i>	Chromosome	-3900.35	chromosome	0.9226	Chromosome	chromosome	1	1	circular	4006508	0.387504031	0	0	0.847538056	11	3613	100	0.17
GN4717	<i>Klebsiella pneumoniae</i>	Chromosome	-3968.09	chromosome	0.9211	Chromosome	chromosome	1	1	circular	4100005	0.390056597	0	0	0.876181371	11	3858	99.99	0.17
GN4719	<i>Klebsiella pneumoniae</i>	Chromosome	-3968.09	chromosome	0.9212	Chromosome	chromosome	1	1	circular	4648246	0.55412192	0	0	0.891325459	11	4317	99.99	0.17
GN4721	<i>Klebsiella pneumoniae</i>	Chromosome	-3898.54	chromosome	0.9223	Chromosome	chromosome	1	1	circular	4691798	0.553658533	0	0	0.891491279	11	4353	100	0.17
GN4723	<i>Klebsiella pneumoniae</i>	Chromosome	-3898.6	chromosome	0.9222	Chromosome	chromosome	1	1	circular	5203921	0.575752207	0	0	0.878264101	11	4828	100	0.17
GN4724	<i>Klebsiella pneumoniae</i>	Chromosome	-3900.35	chromosome	0.9224	Chromosome	chromosome	1	1	circular	5204087	0.575758438	0	0	0.878464368	11	4831	100	0.17
GN4726	<i>Klebsiella pneumoniae</i>	Chromosome	-3896.79	chromosome	0.9222	Chromosome	chromosome	1	1	circular	5246448	0.574634877	0	0	0.879427948	11	4808	100	0.17
GN4728	<i>Klebsiella pneumoniae</i>	Chromosome	-3896.79	chromosome	0.9227	Chromosome	chromosome	1	1	circular	5246449	0.574634958	0	0	0.879428352	11	4811	100	0.17
GN4730	<i>Klebsiella pneumoniae</i>	Chromosome	-3898.6	chromosome	0.9248	Chromosome	chromosome	1	1	circular	5244601	0.574638566	0	0	0.879198055	11	4809	100	0.17
GN4734	<i>Klebsiella pneumoniae</i>	Chromosome	-3896.79	chromosome	0.9222	Chromosome	chromosome	1	1	circular	3909106	0.387794549	0	0	0.846109315	11	3520	100	0.17
GN4735	<i>Klebsiella pneumoniae</i>	Chromosome	-3898.6	chromosome	0.922	Chromosome	chromosome	1	1	circular	4099988	0.390055776	0	0	0.876227687	11	3857	100	0.17
GN4737	<i>Klebsiella pneumoniae</i>	Chromosome	-3968.09	chromosome	0.9212	Chromosome	chromosome	1	1	circular	5247710	0.574629124	0	0	0.87924428	11	4812	99.99	0.17
GN4739	<i>Klebsiella pneumoniae</i>	Chromosome	-3898.54	chromosome	0.9225	Chromosome	chromosome	1	1	circular	4720849	0.508764207	0	0	0.879628855	11	4338	100	0.17
GN4743	<i>Klebsiella pneumoniae</i>	Chromosome	-3897.36	chromosome	0.9248	Chromosome	chromosome	1	1	linear	5245181	0.574660245	0	0	0.879287292	11	4815	100	0.17
GN4744	<i>Klebsiella pneumoniae</i>	Chromosome	-3062.9	chromosome	0.9448	Chromosome	chromosome	1	1	circular	5240925	0.574573572	0	0	0.879097106	11	4806	99.97	0.17
GN4746	<i>Klebsiella pneumoniae</i>	Chromosome	-3870.6	chromosome	0.9313	Chromosome	chromosome	1	1	circular	5411392	0.580432909	0	0	0.876145177	11	5017	100	0.32
GN4747	<i>Klebsiella pneumoniae</i>	Chromosome	-3904.58	chromosome	0.9197	Chromosome	chromosome	1	1	linear	5341014	0.574042682	0	0	0.879213198	11	4930	100	0.56
GN4748	<i>Klebsiella pneumoniae</i>	Chromosome	-3976.18	chromosome	0.9087	Chromosome	chromosome	1	1	circular	3915690	0.389936384	0	0	0.877217042	11	3647		
GN4749	<i>Klebsiella pneumoniae</i>	Chromosome	-3991.26	chromosome	0.9208	Chromosome	chromosome	1	1	circular	4903224	0.50548537	0	0	0.873788552	11	4616	100	0.29
GN4750	<i>Klebsiella pneumoniae</i>	Chromosome	-3061.09	chromosome	0.9225	Chromosome	chromosome	1	1	circular	5350695	0.574294928	0	0	0.879582372	11	4969	100	0.17
GN4752	<i>Klebsiella pneumoniae</i>	Chromosome	-3888.25	chromosome	0.9618	Chromosome	chromosome	1	1	linear	5307156	0.574654109	0	0	0.877900518	11	4875	100	0.38
GN4745	<i>Klebsiella quasipneumoniae</i>	Chromosome	-3928.33	chromosome	0.9347	Chromosome	chromosome	1	1	circular	5435817	0.572349474	0	0	0.875315155	11	5038	99.99	0.43
GN4716	<i>Proteus mirabilis</i>	Chromosome	-3223.39	chromosome	0.9336	Chromosome	chromosome	1	1	circular	4100000	0.390056098	0	0	0.876201707	11	3857	100	0
GN4740	<i>Proteus mirabilis</i>	Chromosome	-3203.73	chromosome	0.9625	Chromosome	chromosome	1	1	circular	4947001	0.506287142	0	0	0.87810332	11	4604	100	0

*HCC: Healthcare center

Supplementary Table S3. Structural and in silico classification data for validated plasmid contigs from *bla*_{NDM}-positive isolates.

Genome_name	contig_name	organism	year	location	length	gc	depth	final prediction*	topology	blaNDM?	mobility class	CD-HIT-EST	inc_group(s)	relaxase_type(s)	orit_type(s)	AcinetobacterPlasmidTyping
GN4720	2_GN4720	<i>Acinetobacter baumannii</i>	2021	HSJD	29464	0.343198	5.31	plasmid	circular	No	conjugative	pCR-33		MOBQ	-	R3-T13, R3-T43
GN4722	2_GN4722	<i>Acinetobacter baumannii</i>	2021	HSJD	19569	0.33318	5.04	plasmid	circular	No	mobilizable	pCR-37		-	-	R3-T13, R3-T43
GN4725	2_GN4725	<i>Acinetobacter baumannii</i>	2021	HSJD	19569	0.333231	5.05	plasmid	circular	No	mobilizable	pCR-37		-	-	R3-T13, R3-T43
GN4736	2_GN4736	<i>Acinetobacter baumannii</i>	2021	HSJD	19569	0.333231	5.23	plasmid	circular	No	mobilizable	pCR-37		-	-	R3-T13, R3-T43
GN4742	2_GN4742	<i>Acinetobacter baumannii</i>	2021	HTFC	29464	0.343131	3.25	plasmid	circular	No	conjugative	pCR-34		MOBQ	-	R3-T13, R3-T43
GN4753	2_GN4753	<i>Acinetobacter baumannii</i>	2014	HCG	218111	0.398086	1.06	plasmid	circular	Yes	conjugative	pCR-8	Not determined	MOBP	-	No_result
GN4753	3_GN4753	<i>Acinetobacter baumannii</i>	2014	HCG	20970	0.360324	1.65	plasmid	circular	No	conjugative	pCR-35		MOBQ	-	R3-T50
GN4718	2_GN4718	<i>Enterobacter xiangfangensis</i>	2021	HSJD	340255	0.470162	1.99	plasmid	circular	No	conjugative	pCR-1	IncFIB(pQil),IncHI2,IncHI2A,IncN,IncR	MOBH	MOBF,MOBH	NA
GN4727	2_GN4727	<i>Enterobacter xiangfangensis</i>	2021	HSJD	297336	0.463718	1.6	plasmid	circular	No	conjugative	pCR-4	IncFIB(pQil),IncHI2,IncHI2A	MOBH	MOBH	NA
GN4729	2_GN4729	<i>Enterobacter xiangfangensis</i>	2021	HSJD	297610	0.464766	1	plasmid	circular	No	conjugative	pCR-4	IncFIB(pQil),IncHI2,IncHI2A	MOBH	MOBH	NA
GN4731	2_GN4731	<i>Enterobacter xiangfangensis</i>	2021	HSJD	263017	0.458294	1.09	plasmid	circular	No	conjugative	pCR-6	IncHI2,IncHI2A,	MOBH	MOBH	NA
GN4732	2_GN4732	<i>Enterobacter xiangfangensis</i>	2021	HSJD	298457	0.465002	1.08	plasmid	circular	No	conjugative	pCR-4	IncFIB(pQil),IncHI2,IncHI2A	MOBH	MOBH	NA
GN4733	2_GN4733	<i>Enterobacter xiangfangensis</i>	2021	HSJD	298457	0.464968	1.05	plasmid	circular	No	conjugative	pCR-4	IncFIB(pQil),IncHI2,IncHI2A	MOBH	MOBH	NA
GN4755	2_GN4755	<i>Enterobacter xiangfangensis</i>	2021	Hmex	172688	0.521907	1.52	plasmid	circular	No	conjugative	pCR-15	IncFIB(pECLA),IncFII(pECLA)	MOBF	-	NA
GN4718	3_GN4718	<i>Enterobacter xiangfangensis</i>	2021	HSJD	145152	0.526043	1.5	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4727	3_GN4727	<i>Enterobacter xiangfangensis</i>	2021	HSJD	140572	0.526708	1.39	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4729	3_GN4729	<i>Enterobacter xiangfangensis</i>	2021	HSJD	140672	0.526708	1.23	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4731	3_GN4731	<i>Enterobacter xiangfangensis</i>	2021	HSJD	140672	0.526708	1.3	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4732	3_GN4732	<i>Enterobacter xiangfangensis</i>	2021	HSJD	140672	0.526708	1.35	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4733	3_GN4733	<i>Enterobacter xiangfangensis</i>	2021	HSJD	140672	0.526708	1.32	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4755	3_GN4755	<i>Enterobacter xiangfangensis</i>	2021	Hmex	140672	0.526729	1.55	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4718	4_GN4718	<i>Enterobacter xiangfangensis</i>	2021	HSJD	52997	0.424262	1.46	plasmid	circular	No	mobilizable	pCR-28		MOBF	-	NA
GN4727	4_GN4727	<i>Enterobacter xiangfangensis</i>	2021	HSJD	52953	0.522936	1.65	plasmid	circular	No	mobilizable	pCR-29	IncN,IncR	-	MOBF	NA
GN4731	4_GN4731	<i>Enterobacter xiangfangensis</i>	2021	HSJD	53016	0.522918	1.42	plasmid	circular	No	mobilizable	pCR-29	IncN,IncR	-	MOBF	NA
GN4732	4_GN4732	<i>Enterobacter xiangfangensis</i>	2021	HSJD	53016	0.522918	1.59	plasmid	circular	No	mobilizable	pCR-29	IncN,IncR	-	MOBF	NA
GN4733	4_GN4733	<i>Enterobacter xiangfangensis</i>	2021	HSJD	53016	0.522918	1.53	plasmid	circular	No	mobilizable	pCR-29	IncN,IncR	-	MOBF	NA
GN4755	4_GN4755	<i>Enterobacter xiangfangensis</i>	2021	Hmex	36097	0.597889	3.83	plasmid	circular	No	mobilizable	pCR-32		MOBP	-	NA
GN4738	2_GN4738	<i>Escherichia coli</i>	2021	HTFC	186799	0.528541	0.87	plasmid	circular	Yes	conjugative	pCR-14	IncA/C2	MOBH,MOBH	MOBH	NA
GN4741	2_GN4741	<i>Escherichia coli</i>	2021	HCG	186799	0.528563	1.09	plasmid	circular	Yes	conjugative	pCR-14	IncA/C2	MOBH,MOBH	MOBH	NA
GN4751	2_GN4751	<i>Escherichia coli</i>	2014	HNN-2014	138998	0.518856	1.38	plasmid	circular	Yes	conjugative	pCR-21	IncA/C2	MOBH,MOBH	MOBH	NA
GN4738	3_GN4738	<i>Escherichia coli</i>	2021	HTFC	92193	0.492131	0.77	plasmid	circular	No	conjugative	pCR-25	IncFIA,IncI1	MOBP	MOBP	NA
GN4751	3_GN4751	<i>Escherichia coli</i>	2014	HNN-2014	117284	0.516567	1.23	plasmid	circular	No	mobilizable	pCR-22	IncFIA,IncFIB(AP001918),IncFII	-	-	NA
GN4738	4_GN4738	<i>Escherichia coli</i>	2021	HTFC	83671	0.517407	0.8	plasmid	circular	No	mobilizable	pCR-26	Col156,IncFIB(AP001918)	MOBP	-	NA
GN4715	2_GN4715	<i>Klebsiella pneumoniae</i>	2021	HSJD	162729	0.515704	1.05	plasmid	circular	No	conjugative	pCR-18	IncFIB(K)	MOBF,MOBF	-	NA
GN4717	2_GN4717	<i>Klebsiella pneumoniae</i>	2021	HSJD	241542	0.522919	1.13	plasmid	circular	No	conjugative	pCR-7	IncFIB(K),IncFII(K)	MOBF,MOBF	-	NA
GN4719	2_GN4719	<i>Klebsiella pneumoniae</i>	2021	HSJD	386821	0.52409	1.22	plasmid	circular	Yes	conjugative	pCR-0	IncA/C2,IncFIB(K),IncFII(K)	MOBF,MOBF,MOBH,MOBH	MOBH	NA
GN4721	2_GN4721	<i>Klebsiella pneumoniae</i>	2021	HSJD	286854	0.517071	1.39	plasmid	circular	Yes	conjugative	pCR-2	IncA/C2,IncFIB(K)	MOBF,MOBF,MOBH,MOBH	MOBH	NA
GN4723	2_GN4723	<i>Klebsiella pneumoniae</i>	2021	HSJD	159309	0.514572	1.05	plasmid	circular	No	conjugative	pCR-19	IncFIB(K)	MOBF,MOBF	-	NA
GN4724	2_GN4724	<i>Klebsiella pneumoniae</i>	2021	HSJD	286854	0.517071	1.31	plasmid	circular	Yes	conjugative	pCR-2	IncA/C2,IncFIB(K)	MOBF,MOBF,MOBH,MOBH	MOBH	NA
GN4726	2_GN4726	<i>Klebsiella pneumoniae</i>	2021	HSJD	299981	0.520263	1.38	plasmid	circular	Yes	conjugative	pCR-2	IncA/C2,IncFIB(K)	MOBF,MOBF,MOBH,MOBH	MOBH	NA
GN4728	2_GN4728	<i>Klebsiella pneumoniae</i>	2021	HSJD	159309	0.514572	1.1	plasmid	circular	No	conjugative	pCR-19	IncFIB(K)	MOBF,MOBF	-	NA
GN4730	2_GN4730	<i>Klebsiella pneumoniae</i>	2021	HSJD	299968	0.520255	1.65	plasmid	circular	Yes	conjugative	pCR-3	IncA/C2,IncFIB(K)	MOBF,MOBF,MOBH,MOBH	MOBH	NA
GN4734	2_GN4734	<i>Klebsiella pneumoniae</i>	2021	HSJD	159309	0.514572	1.11	plasmid	circular	No	conjugative	pCR-19	IncFIB(K)	MOBF,MOBF	-	NA
GN4735	2_GN4735	<i>Klebsiella pneumoniae</i>	2021	HSJD	159309	0.514572	1.06	plasmid	circular	No	conjugative	pCR-19	IncFIB(K)	MOBF,MOBF	-	NA
GN4737	2_GN4737	<i>Klebsiella pneumoniae</i>	2021	HSJD	241542	0.522915	1.21	plasmid	circular	No	conjugative	pCR-7	IncFIB(K),IncFII(K)	MOBF,MOBF	-	NA
GN4739	2_GN4739	<i>Klebsiella pneumoniae</i>	2021	HTFC	162729	0.515704	1.68	plasmid	circular	No	conjugative	pCR-18	IncFIB(K)	MOBF,MOBF	-	NA
GN4743	2_GN4743	<i>Klebsiella pneumoniae</i>	2021	HCG	167167	0.516801	1.35	plasmid	circular	No	conjugative	pCR-16	IncFIB(K)	MOBF,MOBF	-	NA
GN4744	2_GN4744	<i>Klebsiella pneumoniae</i>	2021	HTFC	280119	0.519497	1.8	plasmid	circular	Yes	conjugative	pCR-5	IncA/C2,IncFIB(K)	MOBF,MOBF,MOBH,MOBH	MOBH	NA
GN4746	2_GN4746	<i>Klebsiella pneumoniae</i>	2021	HMS	203108	0.517498	1.38	plasmid	circular	No	conjugative	pCR-10	IncFIB(K)	MOBF,MOBF	-	NA
GN4747	2_GN4747	<i>Klebsiella pneumoniae</i>	2021	Hmex	140672	0.526708	1.44	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4748	2_GN4748	<i>Klebsiella pneumoniae</i>	2021	HTFC	202186	0.520338	1.33	plasmid	circular	No	conjugative	pCR-11	IncFIB(K)	MOBF,MOBF	-	NA
GN4749	2_GN4749	<i>Klebsiella pneumoniae</i>	2021	CEACO	201798	0.50443	1.3	plasmid	circular	No	conjugative	pCR-12	IncFIB(K),IncHI1B	MOBH	-	NA
GN4750	2_GN4750	<i>Klebsiella pneumoniae</i>	2021	CEACO	202691	0.446488	1.15	plasmid	circular	No	conjugative	pCR-9	IncFIB(Mar),IncHI1B	MOBH	-	NA
GN4752	2_GN4752	<i>Klebsiella pneumoniae</i>	2014	Hmex-CIMA	138999	0.518853	0.78	plasmid	circular	Yes	conjugative	pCR-21	IncA/C2	MOBH,MOBH	MOBH	NA
GN4715	3_GN4715	<i>Klebsiella pneumoniae</i>	2021	HSJD	140672	0.526708	1.32	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4717	3_GN4717	<i>Klebsiella pneumoniae</i>	2021	HSJD	145279	0.526036	1.34	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4723	3_GN4723	<i>Klebsiella pneumoniae</i>	2021	HSJD	140672	0.526708	1.28	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4728	3_GN4728	<i>Klebsiella pneumoniae</i>	2021	HSJD	140672	0.526708	1.32	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4734	3_GN4734	<i>Klebsiella pneumoniae</i>	2021	HSJD	140672	0.526708	1.3	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4735	3_GN4735	<i>Klebsiella pneumoniae</i>	2021	HSJD	140672	0.526708	1.3	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4737	3_GN4737	<i>Klebsiella pneumoniae</i>	2021	HSJD	140672	0.526708	1.38	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4739	3_GN4739	<i>Klebsiella pneumoniae</i>	2021	HTFC	145279	0.526043	2.15	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4743	3_GN4743	<i>Klebsiella pneumoniae</i>	2021	HCG	140671	0.526704	1.61	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4746	3_GN4746	<i>Klebsiella pneumoniae</i>	2021	HMS	141616	0.524284	1.58	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA

GN4747	3_GN4747	<i>Klebsiella pneumoniae</i>	2021	Hmex	40587	0.497672	2.21	plasmid	circular	No	mobilizable	pCR-30	IncFII(pCTU2)	-	-	NA
GN4748	3_GN4748	<i>Klebsiella pneumoniae</i>	2021	HTFC	165190	0.524729	1.64	plasmid	circular	Yes	conjugative	pCR-17	IncA/C2	MOBH,MOBH	MOBH	NA
GN4749	3_GN4749	<i>Klebsiella pneumoniae</i>	2021	CEACO	144341	0.52757	1.52	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4750	3_GN4750	<i>Klebsiella pneumoniae</i>	2021	CEACO	160676	0.516717	1.38	plasmid	circular	No	conjugative	pCR-18	IncFIB(K)	MOBF,MOBF	-	NA
GN4752	3_GN4752	<i>Klebsiella pneumoniae</i>	2014	Hmex-CIMA	112300	0.489261	0.53	plasmid	circular	No	non-mobilizable	pCR-23	IncFIB(pKPHS1)	-	-	NA
GN4746	4_GN4746	<i>Klebsiella pneumoniae</i>	2021	HMS	116310	0.491342	1.25	plasmid	circular	No	non-mobilizable	pCR-23	IncFIB(pKPHS1)	-	-	NA
GN4748	4_GN4748	<i>Klebsiella pneumoniae</i>	2021	HTFC	39406	0.521139	2.03	plasmid	circular	No	conjugative	pCR-31	IncN,IncR	MOBF	MOBF	NA
GN4750	4_GN4750	<i>Klebsiella pneumoniae</i>	2021	CEACO	140672	0.526708	1.45	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4746	5_GN4746	<i>Klebsiella pneumoniae</i>	2021	HMS	20624	0.564343	6.98	plasmid	circular	No	mobilizable	pCR-36	ColRI	MOBC	-	NA
GN4745	2_GN4745	<i>Klebsiella quasipneumoniae</i>	2021	Hmex	193890	0.523168	1.67	plasmid	circular	No	conjugative	pCR-13	IncFIB(K),IncFII	MOBF,MOBF	-	NA
GN4745	3_GN4745	<i>Klebsiella quasipneumoniae</i>	2021	Hmex	138921	0.518806	1.65	plasmid	circular	Yes	conjugative	pCR-21	IncA/C2	MOBH,MOBH	MOBH	NA
GN4745	4_GN4745	<i>Klebsiella quasipneumoniae</i>	2021	Hmex	112126	0.520629	2.12	plasmid	circular	No	conjugative	pCR-24	IncFIB(pQil),IncFII(K)	MOBF,MOBF	-	NA
GN4745	5_GN4745	<i>Klebsiella quasipneumoniae</i>	2021	Hmex	73424	0.520565	1.94	plasmid	circular	No	conjugative	pCR-27	IncL/M,IncL/M(pMU407),IncL/M(pOXA-48)	MOBP	-	NA
GN4716	2_GN4716	<i>Proteus mirabilis</i>	2021	HSJD	145279	0.526043	2.05	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA
GN4740	2_GN4740	<i>Proteus mirabilis</i>	2021	HCG	145279	0.526043	1.67	plasmid	circular	Yes	conjugative	pCR-20	IncA/C2	MOBH,MOBH	MOBH	NA

* Contigs were classified/predicted as plasmids if at leaset two algorithms supported it, were circular, and were >10,000 bp.

Supplementary Table S4. Sequencing typing of Klebsiella spp. by Kleborate

Genome Name	species	Hospital	Isolation date	ST	YbST	Yersiniabactin	CbST	Colibactin	wzi	K locus	K type	K locus identity	K Missing expected genes	O locus	O type	O locus identity
GN4752	<i>Klebsiella pneumoniae</i>	Hmex-CIMA	July 16, 2014	ST147	177	ybt 9; ICEKp3	0	-	wzi64	KL64	K64	100.00%	-	O1/O2v1	O2a	99.03%
GN4715	<i>Klebsiella pneumoniae</i>	HSJD	January 15, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.40%	-	O1/O2v2	O1ab	99.22%
GN4717	<i>Klebsiella pneumoniae</i>	HSJD	February 2, 2021	ST37	0	-	0	-	wzi50	KL15	K15	99.84%	-	O4	O4	99.58%
GN4719	<i>Klebsiella pneumoniae</i>	HSJD	February 9, 2021	ST37	0	-	0	-	wzi50	KL15	K15	99.84%	-	O4	O4	99.58%
GN4739	<i>Klebsiella pneumoniae</i>	HTFC	April 16, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.40%	-	O1/O2v2	O1ab	99.22%
GN4744	<i>Klebsiella pneumoniae</i>	HTFC	May 23, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.40%	-	O1/O2v2	O1ab	99.22%
GN4743	<i>Klebsiella pneumoniae</i>	HCG	May 27, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.40%	-	O1/O2v2	O1ab	99.22%
GN4721	<i>Klebsiella pneumoniae</i>	HSJD	May 29, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.40%	-	O1/O2v2	O1ab	99.22%
GN4723	<i>Klebsiella pneumoniae</i>	HSJD	June 1, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.31%	-	O1/O2v2	O1ab	99.22%
GN4724	<i>Klebsiella pneumoniae</i>	HSJD	June 5, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.40%	-	O1/O2v2	O1ab	99.22%
GN4737	<i>Klebsiella pneumoniae</i>	HSJD	June 7, 2021	ST37	0	-	0	-	wzi50	KL15	K15	99.84%	-	O4	O4	99.58%
GN4726	<i>Klebsiella pneumoniae</i>	HSJD	June 29, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.31%	-	O1/O2v2	O1ab	99.22%
GN4734	<i>Klebsiella pneumoniae</i>	HSJD	June 30, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.31%	-	O1/O2v2	O1ab	99.22%
GN4735	<i>Klebsiella pneumoniae</i>	HSJD	June 30, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.31%	-	O1/O2v2	O1ab	99.22%
GN4728	<i>Klebsiella pneumoniae</i>	HSJD	July 2, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.31%	-	O1/O2v2	O1ab	99.22%
GN4730	<i>Klebsiella pneumoniae</i>	HSJD	July 5, 2021	ST342	0	-	0	-	wzi276	KL30	K30	97.31%	-	O1/O2v2	O1ab	99.22%
GN4746	<i>Klebsiella pneumoniae</i>	HMS	July 9, 2021	ST147	177	ybt 9; ICEKp3	0	-	wzi64	KL64	K64	100.00%	-	O1/O2v1	O2a	99.03%
GN4747	<i>Klebsiella pneumoniae</i>	Hmex	July 12, 2021	ST48	227	ybt 0; ICEKp10	17-2LV	clb 3	wzi167	KL124	unknown (KL124)	99.80%	-	O1/O2v1	O1ab	99.22%
GN4748	<i>Klebsiella pneumoniae</i>	HTFC	July 21, 2021	ST882	0	-	0	-	wzi248	KL16	K16	99.69%	-	O1/O2v1	O1ab	98.90%
GN4749	<i>Klebsiella pneumoniae</i>	CEACO	August 11, 2021	ST2098	65-1LV	ybt 4; plasmid	0	-	wzi23	KL31	K31	99.81%	-	O3b	O3b	99.73%
GN4750	<i>Klebsiella pneumoniae</i>	CEACO	August 23, 2021	ST342	0	-	0	-	-	KL30	K30	97.18%	KL30_01_galF;KL30_02_cpsACP	O1/O2v2	O1ab	99.22%
GN4745	<i>Klebsiella quasipneumoniae</i>	Hmex	July 1, 2021	ST696-3LV	0	-	0	-	-	KL64	K64	98.57%	-	O5	O5	98.31%

Supplementary Table S5. Prediction of virulence factors on the study CRE genomes by AMRfinderplus

genome	organism	tool	Contig id	Start	Stop	Strand	Element symbol	Element name	Scope	Type	Method	Target length	Reference sequence length	% Coverage of reference	% Identity to reference	Alignment length	Closest reference accession
GN4755	<i>Enterobacter xiangfangensis</i>	AMRfinderplus	1	1547935	1550106	+	iroN	siderophore salmochelin receptor IroN	plus	VIRULENCE	BLASTX	724	725	100	95.03	725	AAN76093.1
GN4755	<i>Enterobacter xiangfangensis</i>	AMRfinderplus	1	1552540	1556184	-	iroC	salmochelin/enterobactin export ABC transporter IroC	plus	VIRULENCE	BLASTX	1215	1219	99.75	90.79	1216	AUH19662.1
GN4755	<i>Enterobacter xiangfangensis</i>	AMRfinderplus	1	1556329	1557441	-	iroB	salmochelin biosynthesis C-glycosyltransferase IroB	plus	VIRULENCE	BLASTX	371	371	100	92.72	371	EOW04219.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	1015866	1018517	-	vactox	vacuolating autotransporter toxin Vat	plus	VIRULENCE	PARTIALX	884	1376	64.24	99.43	884	CAD66214.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	1039703	1043950	+	fdeC	inverse autotransporter adhesin FdeC	plus	VIRULENCE	BLASTX	1416	1416	100	99.58	1416	ABE05822.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	2760082	2761881	-	ybtQ	yersiniabactin ABC transporter ATP-binding/permease protein YbtQ	plus	VIRULENCE	BLASTX	600	600	100	99.67	600	AAC69584.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	2761871	2763670	-	ybtP	yersiniabactin ABC transporter ATP-binding/permease protein YbtP	plus	VIRULENCE	BLASTX	600	600	100	99.5	600	CAA21388.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3837156	3837440	-	papA	P fimbria major subunit PapA	plus	VIRULENCE	PARTIALX	95	185	51.89	87.5	96	CAA43562.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3847123	3848844	+	iucA	aerobactin synthase lucA	plus	VIRULENCE	BLASTX	574	576	100	98.61	576	EGI25746.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3848848	3849792	+	iucB	N(6)-hydroxylysine O-acetyltransferase lucB	plus	VIRULENCE	BLASTX	315	315	100	99.37	315	AAN82074.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3849795	3851534	+	iucC	NIS family aerobactin synthetase lucC	plus	VIRULENCE	BLASTX	580	580	100	99.14	580	AAN82073.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3851534	3852808	+	iucD	NADPH-dependent L-lysine N(6)-monooxygenase lucD	plus	VIRULENCE	BLASTX	425	445	95.51	97.65	425	AAD44749.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3852905	3855091	+	iutA	ferric aerobactin receptor iutA	plus	VIRULENCE	BLASTX	729	731	99.73	89.85	729	AAN45165.2
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3857047	3859926	+	sat	serine protease autotransporter toxin Sat	plus	VIRULENCE	PARTIALX	960	1295	74.13	99.58	960	CAE55775.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	1	3867667	3869754	-	iha	bifunctional siderophore receptor/adhesin Iha	plus	VIRULENCE	EXACTX	696	696	100	100	696	AEQ14190.1
GN4738	<i>Escherichia coli</i>	AMRfinderplus	4	25051	26223	+	senB	enterotoxin production-related protein TieB	plus	VIRULENCE	EXACTX	391	391	100	100	391	AAZ89288.1
GN4741	<i>Escherichia coli</i>	AMRfinderplus	1	2247357	2247647	-	iss	increased serum survival lipoprotein Iss	plus	VIRULENCE	EXACTX	97	97	100	100	97	CAR12622.1
GN4741	<i>Escherichia coli</i>	AMRfinderplus	1	3613531	3617772	-	fdeC	inverse autotransporter adhesin FdeC	plus	VIRULENCE	BLASTX	1414	1416	99.93	91.38	1415	ABE05822.1
GN4741	<i>Escherichia coli</i>	AMRfinderplus	1	3918036	3919451	+	espX1	type III secretion system effector EspX1	plus	VIRULENCE	BLASTX	472	473	99.79	91.53	472	ADD54679.1
GN4741	<i>Escherichia coli</i>	AMRfinderplus	1	4687907	4688476	+	lpfA-O113	long polar fimbria major subunit LpfA-O113	plus	VIRULENCE	EXACTX	190	190	100	100	190	AAT76975.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	1921564	1923363	+	ybtP	yersiniabactin ABC transporter ATP-binding/permease protein YbtP	plus	VIRULENCE	BLASTX	600	600	100	99.5	600	CAA21388.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	1923353	1925152	+	ybtQ	yersiniabactin ABC transporter ATP-binding/permease protein YbtQ	plus	VIRULENCE	BLASTX	600	600	100	99.5	600	AAC69584.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	3686941	3691188	-	fdeC	inverse autotransporter adhesin FdeC	plus	VIRULENCE	BLASTX	1416	1416	100	94.21	1416	ABE05822.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	3997425	3998498	+	espX1	type III secretion system effector EspX1	plus	VIRULENCE	PARTIALX	358	473	75.69	89.66	358	ADD54679.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	4342933	4343940	-	papG-II	P fimbria tip G-adhesin PapG-II	plus	VIRULENCE	BLASTX	336	337	100	98.52	337	AAA24293.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	4343987	4344484	-	papF	P fimbrial tip protein PapF	plus	VIRULENCE	BLASTX	166	167	100	91.62	167	CAA43569.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	4344562	4345080	-	papE	P fimbrial minor subunit PapE	plus	VIRULENCE	BLASTX	173	173	100	97.69	173	CAA43568.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	4347079	4349586	-	papC	P fimbrial usher protein PapC	plus	VIRULENCE	BLASTX	836	836	100	96.31	841	CAA43564.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	4349648	4350232	-	papH	P fimbrial minor subunit PapH	plus	VIRULENCE	BLASTX	195	195	100	98.97	195	CAA43563.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	4350299	4350850	-	papA	P fimbria major subunit PapA	plus	VIRULENCE	BLASTX	184	185	100	98.38	185	CAA43562.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	1	4870285	4870854	+	lpfA-O113	long polar fimbria major subunit LpfA-O113	plus	VIRULENCE	EXACTX	190	190	100	100	190	AAT76975.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	3	99554	101740	-	iutA	ferric aerobactin receptor iutA	plus	VIRULENCE	BLASTX	729	731	99.73	89.85	729	AAN45165.2
GN4751	<i>Escherichia coli</i>	AMRfinderplus	3	101837	103111	-	iucD	NADPH-dependent L-lysine N(6)-monooxygenase lucD	plus	VIRULENCE	BLASTX	425	445	95.51	97.65	425	AAD44749.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	3	103111	104850	-	iucC	NIS family aerobactin synthetase lucC	plus	VIRULENCE	BLASTX	580	580	100	97.59	580	AAN82073.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	3	104853	105797	-	iucB	N(6)-hydroxylysine O-acetyltransferase lucB	plus	VIRULENCE	BLASTX	315	315	100	96.19	315	AAN82074.1
GN4751	<i>Escherichia coli</i>	AMRfinderplus	3	105801	107522	-	iucA	aerobactin synthase lucA	plus	VIRULENCE	BLASTX	574	576	100	95.31	576	EGI25746.1
GN4746	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	1048068	1049867	+	ybtP	yersiniabactin ABC transporter ATP-binding/permease protein YbtP	plus	VIRULENCE	BLASTX	600	600	100	99.83	600	CAA21388.1
GN4746	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	1049857	1051656	+	ybtQ	yersiniabactin ABC transporter ATP-binding/permease protein YbtQ	plus	VIRULENCE	BLASTX	600	600	100	99.83	600	AAC69584.1
GN4747	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	998473	1008090	+	clbB	colibactin hybrid non-ribosomal peptide synthetase/type I polyketide synthase ClbB	plus	VIRULENCE	BLASTX	3206	3206	100	99.94	3206	AMQ58400.1
GN4747	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	1038189	1042553	+	clbN	colibactin non-ribosomal peptide synthetase ClbN	plus	VIRULENCE	EXACTX	1455	1455	100	100	1455	AMH08480.1
GN4747	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	1090697	1092496	+	ybtP	yersiniabactin ABC transporter ATP-binding/permease protein YbtP	plus	VIRULENCE	BLASTX	600	600	100	99.67	600	CAA21388.1
GN4747	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	1092486	1094285	+	ybtQ	yersiniabactin ABC transporter ATP-binding/permease protein YbtQ	plus	VIRULENCE	BLASTX	600	600	100	99.67	600	AAC69584.1
GN4748	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	4345205	4347298	-	mchF	microcin H47 export transporter peptidase/ATP-binding subunit MchF	plus	VIRULENCE	EXACTX	698	698	100	100	698	AAL08400.1
GN4749	<i>Klebsiella pneumoniae</i>	AMRfinderplus	2	124068	125867	+	ybtP	yersiniabactin ABC transporter ATP-binding/permease protein YbtP	plus	VIRULENCE	BLASTX	600	600	100	99.33	600	CAA21388.1
GN4749	<i>Klebsiella pneumoniae</i>	AMRfinderplus	2	125857	127656	+	ybtQ	yersiniabactin ABC transporter ATP-binding/permease protein YbtQ	plus	VIRULENCE	BLASTX	600	600	100	99.83	600	AAC69584.1
GN4752	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	18340	20139	-	ybtQ	yersiniabactin ABC transporter ATP-binding/permease protein YbtQ	plus	VIRULENCE	BLASTX	600	600	100	99.83	600	AAC69584.1
GN4752	<i>Klebsiella pneumoniae</i>	AMRfinderplus	1	20129	21928	-	ybtP	yersiniabactin ABC transporter ATP-binding/permease protein YbtP	plus	VIRULENCE	BLASTX	600	600	100	99.83	600	CAA21388.1

Supplementary Table S6. Metadata for reference blaNDM positive plasmids closely related to the studied plasmids.

Contig	total_length	rep_types	Genus	species	strain	plasmid_name	source_category	year	country	NDM_variant	continent
NZ_KX636095.1	335317	IncA/C2, IncFIB,IncFII	<i>Klebsiella</i>	<i>pneumoniae</i>	RJ119	pRJ119-NDM1	feline	unknown	China	blaNDM	East Asia
OR041627.1	270446	IncA/C2I,IncFIA,IncFII,IncR,IncU	<i>Escherichia</i>	<i>coli</i>	J-JNKPN26-2	pJ-JNKPN26-2_HNK	unknown	unknown	unknown	blaNDM-1	unknown
OR041628.1	270443	IncA/C2,IncFIA,IncR,IncU	<i>Escherichia</i>	<i>coli</i>	J-JNKPN26-3	pJ-JNKPN26-3_HNK	unknown	unknown	unknown	blaNDM-1	unknown
OR041629.1	267313	IncA/C2,IncFIA,IncFII,IncR,IncU	<i>Escherichia</i>	<i>coli</i>	J-JNKPN26-4	pJ-JNKPN26-4_HNK	unknown	unknown	unknown	blaNDM-1	unknown
JF714412.2	165974	IncA/C2	<i>Escherichia</i>	<i>coli</i>	N10-2337	pNDM102337	human	2011	Canada	blaNDM-1	North America
JN157804.1	162746	IncA/C2	<i>Klebsiella</i>	<i>pneumoniae</i>	Kp7	pNDM-KN	unknown	unknown	Kenya	blaNDM-1	Africa
NZ_KX147633.1	154564	IncA/C2	<i>Citrobacter</i>	<i>freundii</i>	AMA332	pT1	unknown	unknown	Denmark	blaNDM-1	Europe
OR041626.1	144239	IncA/C2	<i>Escherichia</i>	<i>coli</i>	J-JNKPN26-1	pJ-JNKPN26-1_NDM	unknown	unknown	China	blaNDM-1	East Asia
CP006661.1	140825	IncA/C2	<i>Klebsiella</i>	<i>pneumoniae</i>	ATCC BAA-2146	pNDM-US	human	2010	United States	blaNDM-1	North America
NZ_MK041212.1	138998	IncA/C2	<i>Citrobacter</i>	<i>amalonaticus</i>	M21015	pNDM-M21015	human	unknown	Argentina	blaNDM-1	South America
NZ_MK123267.1	138998	IncA/C2	<i>Escherichia</i>	<i>coli</i>	M17386	pECO17386	human	2014	Argentina	blaNDM-1	South America
NZ_MK123268.1	138997	IncA/C2	<i>Serratia</i>	<i>marcescens</i>	M17468	pSMA17468	human	2014	Argentina	blaNDM-1	South America
KF992018.2	137552	IncA/C2	<i>Klebsiella</i>	<i>pneumoniae</i>	KP1	pKP1-NDM-1	unknown	unknown	Australia?	blaNDM-1	unknown
PV023092.1	137552	IncA/C2	<i>Klebsiella</i>	<i>pneumoniae</i>	11A19CPO062	p11A19062_A_NDM	human	2019	Canada	blaNDM-1	North America
NZ_MH263652.1	134802	IncA/C2	<i>Providencia</i>	<i>rettgeri</i>	QD51	pNDM-QD51	human	unknown	China	blaNDM-1	East Asia
MN310375.1	132407	IncA/C2	<i>Klebsiella</i>	<i>quasipneumoniae</i>	QD1501	pQD1501-Ct1	unknown	2015	China	blaNDM-1	East Asia
CP129246.1	166254		<i>Acinetobacter</i>	<i>baumannii</i>	13A297n	pNDM-9	Homo sapiens	2013	France	blaNDM-9	Europe

Supplementary Table S7. Metadata from the reference genomes used for genomic context analysis (figure 3) of the studied isolates.

Organism	ID	Status	Year	ST	Country	Database	accession_number
<i>A. baumannii</i>	GCA_001415835.1	Reference	2015	250	USA	GenBank	GCA_001415835.1
<i>A. baumannii</i>	GCA_001864575.1	Reference	2013	879	China	GenBank	GCA_001864575.1
<i>A. baumannii</i>	GCA_002014325.1	Reference	2009	250	USA	GenBank	GCA_002014325.1
<i>A. baumannii</i>	GCA_006494015.1	Reference	2013	250	Honduras	GenBank	GCA_006494015.1
<i>A. baumannii</i>	GCA_006494265.1	Reference	2010	108	USA	GenBank	GCA_006494265.1
<i>A. baumannii</i>	GCA_016473855.1	Reference	2019	250	USA	GenBank	GCA_016473855.1
<i>A. baumannii</i>	GCA_016515715.1	Reference	-	188	-	GenBank	GCA_016515715.1
<i>K.pneumoniae</i>	10625_MGH93.fasta	Reference	2014	147	USA	PasteurMLST	10625
<i>K.pneumoniae</i>	10633_CRK0306.fasta	Reference	2015	147	USA	PasteurMLST	10633
<i>K.pneumoniae</i>	25977_ERR4635721.fasta	Reference	2017	147	India	PasteurMLST	25977
<i>K.pneumoniae</i>	31041_SRR12509583.fasta	Reference	2017	147	USA	PasteurMLST	31041
<i>K.pneumoniae</i>	38061_SRR15695833	Reference	-	48	Singapore	PasteurMLST	38061
<i>K.pneumoniae</i>	38634_SRR16964816.fasta	Reference	2021	147	USA	PasteurMLST	38634
<i>K.pneumoniae</i>	41843_SRR18217218.fasta	Reference	2019	147	Turkey	PasteurMLST	41843
<i>K.pneumoniae</i>	44546_SRR9217825	Reference	2014	48	Singapore	PasteurMLST	44546
<i>K.pneumoniae</i>	46306_SRR5666405	Reference	2015	48	USA	PasteurMLST	46306
<i>K.pneumoniae</i>	48194_GCA_001902935.4	Reference	-	48	USA	PasteurMLST	48194
<i>K.pneumoniae</i>	54034_GCA_002936675_2.fasta	Reference	2015	147	USA	PasteurMLST	54034
<i>K.pneumoniae</i>	7106_NMI2273_16.fasta	Reference	2016	147	Poland	PasteurMLST	7106
<i>K.pneumoniae</i>	GCF_900501425.1	Reference	2013	882	Greece	EuSCAPE	GCF_900501425.1
<i>K.pneumoniae</i>	GCF_900501475.1	Reference	2013	37	Greece	EuSCAPE	GCF_900501475.1
<i>K.pneumoniae</i>	GCF_900503595.1	Reference	2014	37	Luxembourg	EuSCAPE	GCF_900503595.1
<i>K.pneumoniae</i>	GCF_900503655.1	Reference	2014	37	Luxembourg	EuSCAPE	GCF_900503655.1
<i>K.pneumoniae</i>	GCF_900503735.1	Reference	2014	37	Luxembourg	EuSCAPE	GCF_900503735.1
<i>K.pneumoniae</i>	GCF_900503805.1	Reference	2013	882	United Kingdom	EuSCAPE	GCF_900503805.1
<i>K.pneumoniae</i>	GCF_900504855.1	Reference	2014	147	Romania	EuSCAPE	GCF_900504855.1
<i>K.pneumoniae</i>	GCF_900505735.1	Reference	2014	48	Croatia	EuSCAPE	GCF_900505735.1
<i>K.pneumoniae</i>	GCF_900506475.1	Reference	2014	48	Ireland	EuSCAPE	GCF_900506475.1
<i>K.pneumoniae</i>	GCF_900507255.1	Reference	2013	37	Turkey	EuSCAPE	GCF_900507255.1
<i>K.pneumoniae</i>	GCF_900507265.1	Reference	2013	48	Turkey	EuSCAPE	GCF_900507265.1
<i>K.pneumoniae</i>	GCF_900507415.1	Reference	2014	882	Turkey	EuSCAPE	GCF_900507415.1
<i>K.pneumoniae</i>	GCF_900507565.1	Reference	2014	147	Belgium	EuSCAPE	GCF_900507565.1
<i>K.pneumoniae</i>	GCF_900508165.1	Reference	2014	48	Turkey	EuSCAPE	GCF_900508165.1
<i>K.pneumoniae</i>	GCF_900508285.1	Reference	2013	882	Turkey	EuSCAPE	GCF_900508285.1
<i>K.pneumoniae</i>	GCF_900509135.1	Reference	2013	882	Turkey	EuSCAPE	GCF_900509135.1
<i>K.pneumoniae</i>	GCF_900511365.1	Reference	2014	147	Poland	EuSCAPE	GCF_900511365.1
<i>K.pneumoniae</i>	GCF_900512345.1	Reference	2013	147	Germany	EuSCAPE	GCF_900512345.1
<i>K.pneumoniae</i>	GCF_900512745.1	Reference	2014	48	Germany	EuSCAPE	GCF_900512745.1
<i>K.pneumoniae</i>	GCF_900513215.1	Reference	2013	147	Italy	EuSCAPE	GCF_900513215.1
<i>K.pneumoniae</i>	GCF_900513505.1	Reference	2013	37	Israel	EuSCAPE	GCF_900513505.1
<i>K.pneumoniae</i>	GCF_900517145.1	Reference	2014	48	Spain	EuSCAPE	GCF_900517145.1
<i>K.pneumoniae</i>	GCF_900517655.1	Reference	2013	147	Spain	EuSCAPE	GCF_900517655.1
<i>K.pneumoniae</i>	GCF_900517665.1	Reference	2013	147	Spain	EuSCAPE	GCF_900517665.1
<i>K.pneumoniae</i>	ST147_10635_FDAARGOS_439	Reference	2014	147	Canada	PasteurMLST	10635
<i>K.pneumoniae</i>	ST147_10674_FDAARGOS_442	Reference	2010	147	Canada	PasteurMLST	10674
<i>K.pneumoniae</i>	ST147_22362_448_19	Reference	2019	147	Brazil	PasteurMLST	22362
<i>K.pneumoniae</i>	ST147_22364_466_21	Reference	2021	147	Brazil	PasteurMLST	22364
<i>K.pneumoniae</i>	ST147_34643_SRR11675972	Reference	2017	147	Canada	PasteurMLST	34643
<i>K.pneumoniae</i>	ST147_34743_SRR10490442	Reference	2012	147	Canada	PasteurMLST	34743
<i>K.pneumoniae</i>	ST147_36955_SRR15197816	Reference	2017	147	Canada	PasteurMLST	36955
<i>K.pneumoniae</i>	ST147_74202_144	Reference	2019	147	Brazil	PasteurMLST	74202
<i>K.pneumoniae</i>	ST2098_39052_SRR17302530	Reference	2015	2098	UK	PasteurMLST	39052
<i>K.pneumoniae</i>	ST342_25492_ERR4795599	Reference	2014	342	Colombia	PasteurMLST	25492

<i>K.pneumoniae</i>	ST342_25668_ERR4783372	Reference	2017	342	Nigeria	PasteurMLST	25668
<i>K.pneumoniae</i>	ST342_25723_ERR4783474	Reference	-	342	Nigeria	PasteurMLST	25723
<i>K.pneumoniae</i>	ST342_25862_ERR4795601	Reference	2014	342	Colombia	PasteurMLST	25862
<i>K.pneumoniae</i>	ST342_26047_ERR4795632	Reference	2017	342	Colombia	PasteurMLST	26047
<i>K.pneumoniae</i>	ST342_42468_SRR5387198	Reference	2015	342	USA	PasteurMLST	42468
<i>K.pneumoniae</i>	ST37_28014_ERR3712967	Reference	-	37	The Netherlands	PasteurMLST	28014
<i>K.pneumoniae</i>	ST37_32128_SRR13037727	Reference	2020	37	USA	PasteurMLST	32128
<i>K.pneumoniae</i>	ST37_34109_SRR10905988	Reference	2015	37	USA	PasteurMLST	34109
<i>K.pneumoniae</i>	ST37_38212_SRR16079151	Reference	-	37	Singapore	PasteurMLST	38212
<i>K.pneumoniae</i>	ST37_58186_MB8946	Reference	2019	37	USA	PasteurMLST	58186
<i>K.pneumoniae</i>	ST37_59698_ERR6057898	Reference	2018	37	Malawi	PasteurMLST	59698
<i>K.pneumoniae</i>	ST37_59719_ERR6057901	Reference	2017	37	Malawi	PasteurMLST	59719
<i>K.pneumoniae</i>	ST48_30449_SRR11819349	Reference	2017	48	USA	PasteurMLST	30449
<i>K.pneumoniae</i>	ST48_30925_SRR12509150	Reference	2017	48	USA	PasteurMLST	30925
<i>K.pneumoniae</i>	ST48_31166_SRR12509355	Reference	2017	48	USA	PasteurMLST	31166
<i>K.pneumoniae</i>	ST48_31625_SRR12902544	Reference	2013	48	USA	PasteurMLST	31625
<i>K.pneumoniae</i>	ST48_32507_SRR10376976	Reference	2016	48	USA	PasteurMLST	32507
<i>K.pneumoniae</i>	ST48_33946_SRR10376977	Reference	2016	48	USA	PasteurMLST	33946
<i>K.pneumoniae</i>	ST48_34307_SRR11193643	Reference	2013	48	USA	PasteurMLST	34307
<i>K.pneumoniae</i>	ST48_34422_SRR10376965	Reference	2016	48	USA	PasteurMLST	34422
<i>K.pneumoniae</i>	ST48_35206_SRR14402553	Reference	2017	48	USA	PasteurMLST	35206
<i>K.pneumoniae</i>	ST48_44681_SRR5973306	Reference	2017	48	USA	PasteurMLST	44681
<i>K.pneumoniae</i>	ST48_46109_SRR5386309	Reference	2012	48	USA	PasteurMLST	46109
<i>K.pneumoniae</i>	ST48_50040_GCA_000982085_1	Reference	2012	48	Honduras	PasteurMLST	50040
<i>K.pneumoniae</i>	ST882_12959_SPARK_1190_C1	Reference	2018	882	Italy	PasteurMLST	12959
<i>K.pneumoniae</i>	ST882_17376_KP_NORM_URN_57759	Reference	2009	882	Norway	PasteurMLST	17376
<i>K.pneumoniae</i>	ST882_17506_NK_H1_091	Reference	2018	882	Norway	PasteurMLST	17506
<i>K.pneumoniae</i>	ST882_17697_NK_H15_003	Reference	2018	882	Norway	PasteurMLST	17697
<i>K.pneumoniae</i>	ST882_17967_NK_H22_002	Reference	2016	882	Norway	PasteurMLST	17967
<i>K.pneumoniae</i>	ST882_18269_NK_H8_016	Reference	2018	882	Norway	PasteurMLST	18269
<i>K.pneumoniae</i>	ST882_18293_NK_H8_046	Reference	2018	882	Norway	PasteurMLST	18293
<i>K.pneumoniae</i>	ST882_18362_NK_H9_001	Reference	2018	882	Norway	PasteurMLST	18362
<i>K.pneumoniae</i>	ST882_22130_30862	Reference	2018	882	UK [Scotland]	PasteurMLST	22130
<i>K.pneumoniae</i>	ST882_36790_SRR15098077	Reference	2019	882	Australia	PasteurMLST	36790
<i>K.pneumoniae</i>	ST882_40606_SRR1610101	Reference	2010	882	USA	PasteurMLST	40606
<i>K.pneumoniae</i>	ST882_41174_SRR18175586	Reference	2019	882	USA	PasteurMLST	41174
<i>K.pneumoniae</i>	ST882_41453_SRR18208937	Reference	2020	882	Australia	PasteurMLST	41453
<i>K.pneumoniae</i>	ST882_41458_SRR18208943	Reference	2020	882	Australia	PasteurMLST	41458
<i>K.pneumoniae</i>	ST882_41472_SRR18208968	Reference	2020	882	Australia	PasteurMLST	41472
<i>K.pneumoniae</i>	ST882_52920_GCA_003346635_1	Reference	-	882	Algeria	PasteurMLST	52920
<i>K.pneumoniae</i>	ST882_56800_NK_H23_014	Reference	2017	882	Norway	PasteurMLST	56800
<i>K.pneumoniae</i>	ST882_59116_ERR1023784	Reference	2013	882	Australia	PasteurMLST	59116
<i>P. mirabilis</i>	1318_PR01166	Reference	2023	807	USA	PubMLST	1318
<i>P. mirabilis</i>	142_WGLW4	Reference	-	92	-	PubMLST	142
<i>P. mirabilis</i>	148_FDAARGOS_85	Reference	2013	92	USA	PubMLST	148
<i>P. mirabilis</i>	149_FDAARGOS_81	Reference	2013	99	USA	PubMLST	149
<i>P. mirabilis</i>	176_646_PMIR	Reference	-	92	USA	PubMLST	176
<i>P. mirabilis</i>	195_AR_0159	Reference	-	144	-	PubMLST	195
<i>P. mirabilis</i>	236_PMS_MEIH	Reference	2018	185	Lebanon	PubMLST	236
<i>P. mirabilis</i>	258_160A10	Reference	2018	185	France	PubMLST	258
<i>P. mirabilis</i>	260_4748	Reference	2017	92	Brazil	PubMLST	260
<i>P. mirabilis</i>	269_PmBR595	Reference	2015	99	Brazil	PubMLST	269
<i>P. mirabilis</i>	271_PmBR614	Reference	2015	92	Brazil	PubMLST	271
<i>P. mirabilis</i>	304_CC15031	Reference	2017	203	China	PubMLST	304
<i>P. mirabilis</i>	334_UMB0038	Reference	2020	92	USA	PubMLST	334

<i>P. mirabilis</i>	335_UMB1310	Reference	2020	92	USA	PubMLST	335
<i>P. mirabilis</i>	368_ChSC1905	Reference	2019	185	China	PubMLST	368
<i>P. mirabilis</i>	386_PM45467	Reference	2018	234	Czech Republic	PubMLST	386
<i>P. mirabilis</i>	460_HEDJ122	Reference	2019	185	China	PubMLST	460
<i>P. mirabilis</i>	466_SCRJC4FQ	Reference	2020	185	China	PubMLST	466
<i>P. mirabilis</i>	479_Survcare143	Reference	2019	234	Germany	PubMLST	479
<i>P. mirabilis</i>	480_2021EL_00141	Reference	2021	99	USA	PubMLST	480
<i>P. mirabilis</i>	517_L00022962	Reference	-	185	USA	PubMLST	517
<i>P. mirabilis</i>	529_L00022902	Reference	-	185	USA	PubMLST	529
<i>P. mirabilis</i>	557_PM3_9	Reference	2021	185	China	PubMLST	557
<i>P. mirabilis</i>	558_PM3_8	Reference	2021	185	China	PubMLST	558
<i>P. mirabilis</i>	559_PM3_10	Reference	2021	185	China	PubMLST	559
<i>P. mirabilis</i>	560_PM3_7	Reference	2021	185	China	PubMLST	560
<i>P. mirabilis</i>	569_PM3_6	Reference	2021	185	China	PubMLST	569
<i>P. mirabilis</i>	583_FZP2826	Reference	2021	185	China	PubMLST	583
<i>P. mirabilis</i>	616_FZP3803	Reference	2021	185	China	PubMLST	616
<i>P. mirabilis</i>	620_FZP2833	Reference	2021	185	China	PubMLST	620
<i>P. mirabilis</i>	643_63	Reference	2019	234	China	PubMLST	643
<i>P. mirabilis</i>	646_TUM5399	Reference	2009	234	Japan	PubMLST	646
<i>P. mirabilis</i>	647_TUM5408	Reference	2009	234	Japan	PubMLST	647
<i>P. mirabilis</i>	659_18111	Reference	-	185	Spain	PubMLST	659
<i>P. mirabilis</i>	766_WU_023_E1_U09	Reference	2018	99	USA	PubMLST	766
<i>P. mirabilis</i>	767_WU_023_E1_DxU	Reference	2018	99	USA	PubMLST	767
<i>P. mirabilis</i>	791_JZ76	Reference	2022	185	China	PubMLST	791
<i>P. mirabilis</i>	803_JZ64	Reference	2022	185	China	PubMLST	803
<i>P. mirabilis</i>	804_JZ57	Reference	2022	234	China	PubMLST	804
<i>P. mirabilis</i>	841_JZ18	Reference	2022	185	China	PubMLST	841
<i>P. mirabilis</i>	843_JZ17	Reference	2022	234	China	PubMLST	843
<i>P. mirabilis</i>	848_JZ121	Reference	2022	185	China	PubMLST	848
<i>P. mirabilis</i>	850_JZ119	Reference	2022	185	China	PubMLST	850
<i>P. mirabilis</i>	857_JZ111	Reference	2022	185	China	PubMLST	857
<i>P. mirabilis</i>	860_JZ109	Reference	2022	185	China	PubMLST	860
<i>P. mirabilis</i>	863_MAD23	Reference	2022	185	Iran	PubMLST	863
<i>P. mirabilis</i>	872_HJP16012	Reference	2022	234	China	PubMLST	872
<i>P. mirabilis</i>	905_NRZ_57448	Reference	-	92	Germany	PubMLST	905
<i>P. mirabilis</i>	919_Cont_28	Reference	-	92	Germany	PubMLST	919
<i>P. mirabilis</i>	922_Cont_24	Reference	-	185	Germany	PubMLST	922
<i>P. mirabilis</i>	928_Cont_20	Reference	-	185	Germany	PubMLST	928
<i>P. mirabilis</i>	933_Cont_12	Reference	-	99	Germany	PubMLST	933
<i>P. mirabilis</i>	941_Cont_07	Reference	-	185	Germany	PubMLST	941
<i>P. mirabilis</i>	955_Carb_34	Reference	-	479	Germany	PubMLST	955
<i>P. mirabilis</i>	964_NRZ_58292	Reference	-	234	Germany	PubMLST	964
<i>P. mirabilis</i>	977_NRZ_30483	Reference	-	479	Germany	PubMLST	977
<i>P. mirabilis</i>	996_NCTC12441	Reference	1990	144	United Kingdom	PubMLST	996
<i>Enterobacter sp.</i>	Eclo_117	Reference	2016	1583	Denmark	PubMLST	117
<i>Enterobacter sp.</i>	Eclo_121	Reference	2021	1583	Denmark	PubMLST	121
<i>Enterobacter sp.</i>	Eclo_123	Reference	2016	1583	Denmark	PubMLST	123
<i>Enterobacter sp.</i>	Eclo_127	Reference	2021	1583	Denmark	PubMLST	127
<i>Enterobacter sp.</i>	Eclo_328	Reference	2013	1722	USA	PubMLST	328
<i>Enterobacter sp.</i>	Eclo_358	Reference	2021	1833	Norway	PubMLST	358
<i>Enterobacter sp.</i>	Eclo_376	Reference	-	90	Spain	PubMLST	376
<i>Enterobacter sp.</i>	Eclo_420	Reference	2019	90	Spain	PubMLST	420
<i>Enterobacter sp.</i>	Eclo_520	Reference	-	1833	Norway	PubMLST	520
<i>Enterobacter sp.</i>	Eclo_529	Reference	2019	2195	India	PubMLST	529
<i>Enterobacter sp.</i>	Eclo_562	Reference	2016	544	Ethiopia	PubMLST	562

<i>Enterobacter sp.</i>	Eclo_575	Reference	2016	544	Ethiopia	PubMLST	575
<i>Enterobacter sp.</i>	Eclo_693	Reference	2018	2011	India	PubMLST	693
<i>Enterobacter sp.</i>	Eclo_739	Reference	2013	90	Australia	PubMLST	739
<i>Enterobacter sp.</i>	Eclo_760	Reference	2014	90	Australia	PubMLST	760
<i>Enterobacter sp.</i>	Eclo_765	Reference	2013	395	Brazil	PubMLST	765
<i>Enterobacter sp.</i>	Eclo_771	Reference	2015	90	Australia	PubMLST	771
<i>Enterobacter sp.</i>	Eclo_809	Reference	2015	459	Nigeria	PubMLST	809
<i>Enterobacter sp.</i>	Eclo_810	Reference	2015	459	Nigeria	PubMLST	810
<i>Enterobacter sp.</i>	Eclo_824	Reference	2015	90	France	PubMLST	824
<i>Enterobacter sp.</i>	Eclo_825	Reference	2015	90	France	PubMLST	825
<i>Enterobacter sp.</i>	Eclo_826	Reference	2016	90	France	PubMLST	826
<i>Enterobacter sp.</i>	Eclo_829	Reference	2017	90	France	PubMLST	829
<i>Enterobacter sp.</i>	Eclo_869	Reference	2014	66	Brazil	PubMLST	869
<i>Enterobacter sp.</i>	Eclo_870	Reference	2014	121	Nigeria	PubMLST	870
<i>Enterobacter sp.</i>	Eclo_883	Reference	2014	200	Brazil	PubMLST	883
<i>Enterobacter sp.</i>	Eclo_885	Reference	2016	90	France	PubMLST	885
<i>Enterobacter sp.</i>	Eclo_888	Reference	2015	544	France	PubMLST	888
<i>Enterobacter sp.</i>	Eclo_890	Reference	2015	90	France	PubMLST	890
<i>Enterobacter sp.</i>	Eclo_910	Reference	2007	90	Brazil	PubMLST	910
<i>Enterobacter sp.</i>	Eclo_924	Reference	2017	200	Myanmar	PubMLST	924
<i>Enterobacter sp.</i>	Eclo_925	Reference	2017	1053	Myanmar	PubMLST	925
<i>Enterobacter sp.</i>	Eclo_926	Reference	2017	90	Myanmar	PubMLST	926
<i>Enterobacter sp.</i>	Eclo_939	Reference	2016	544	Nigeria	PubMLST	939
<i>Enterobacter sp.</i>	Eclo_946	Reference	2020	121	Brazil	PubMLST	946
<i>Enterobacter sp.</i>	Eclo_947	Reference	2020	200	Brazil	PubMLST	947
<i>Enterobacter sp.</i>	Eclo_953	Reference	2020	303	Brazil	PubMLST	953
<i>Enterobacter sp.</i>	Eclo_965	Reference	2019	90	Australia	PubMLST	965
<i>Enterobacter sp.</i>	Eclo_970	Reference	2018	90	Australia	PubMLST	970
<i>Enterobacter sp.</i>	Eclo_977	Reference	2019	90	Australia	PubMLST	977
<i>Enterobacter sp.</i>	Eclo_985	Reference	2019	90	Australia	PubMLST	985
<i>Enterobacter sp.</i>	Eclo_1005	Reference	2015	90	Australia	PubMLST	1005
<i>Enterobacter sp.</i>	Eclo_1006	Reference	2020	66	Australia	PubMLST	1006
<i>Enterobacter sp.</i>	Eclo_1012	Reference	2018	90	Australia	PubMLST	1012
<i>Enterobacter sp.</i>	Eclo_1013	Reference	2018	90	Australia	PubMLST	1013
<i>Enterobacter sp.</i>	Eclo_1025	Reference	2020	90	Australia	PubMLST	1025
<i>Enterobacter sp.</i>	Eclo_1026	Reference	2019	90	Australia	PubMLST	1026
<i>Enterobacter sp.</i>	Eclo_1028	Reference	2017	1261	Brazil	PubMLST	1028
<i>Enterobacter sp.</i>	Eclo_1034	Reference	2021	121	Brazil	PubMLST	1034
<i>Enterobacter sp.</i>	Eclo_1035	Reference	2021	90	Brazil	PubMLST	1035
<i>Enterobacter sp.</i>	Eclo_1058	Reference	2016	171	France	PubMLST	1058
<i>Enterobacter sp.</i>	Eclo_1059	Reference	2016	136	France	PubMLST	1059
<i>Enterobacter sp.</i>	Eclo_1060	Reference	2014	171	France	PubMLST	1060
<i>Enterobacter sp.</i>	Eclo_1132	Reference	2018	90	Australia	PubMLST	1132
<i>Enterobacter sp.</i>	Eclo_1229	Reference	2006	90	France	PubMLST	1229
<i>Enterobacter sp.</i>	Eclo_1234	Reference	2022	2055	India	PubMLST	1234
<i>Enterobacter sp.</i>	Eclo_1236	Reference	2023		Switzerland	PubMLST	1236
<i>Enterobacter sp.</i>	Eclo_1269	Reference	2015	200	China	PubMLST	1269
<i>Enterobacter sp.</i>	Eclo_1301	Reference	2019	121	India	PubMLST	1301
<i>Enterobacter sp.</i>	Eclo_1302	Reference	2022	231	India	PubMLST	1302
<i>Enterobacter sp.</i>	Eclo_1354	Reference	2021	1518	India	PubMLST	1354
<i>Enterobacter sp.</i>	Eclo_1355	Reference	2021	231	India	PubMLST	1355
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<i>Enterobacter sp.</i>	Eclo_1399	Reference	2019	2256	China	PubMLST	1399
<i>Enterobacter sp.</i>	Eclo_1415	Reference	2019	2272	China	PubMLST	1415

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<i>Enterobacter sp.</i>	Eclo_1451	Reference	2015	2307	China	PubMLST	1451
<i>Enterobacter sp.</i>	Eclo_1631	Reference	2009	2401	Japan	PubMLST	1631
<i>Enterobacter sp.</i>	Eclo_1645	Reference	2015	2412	China	PubMLST	1645
<i>Enterobacter sp.</i>	Eclo_1819	Reference	2022	121	India	PubMLST	1819
<i>Enterobacter sp.</i>	Eclo_1940	Reference	2017	2592	China	PubMLST	1940
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<i>Enterobacter sp.</i>	Eclo_1942	Reference	2013	2594	China	PubMLST	1942
<i>Enterobacter sp.</i>	Eclo_1948	Reference	2019	2600	USA	PubMLST	1948
<i>Enterobacter sp.</i>	Eclo_1959	Reference	2003	2611	China	PubMLST	1959
<i>Enterobacter sp.</i>	Eclo_1960	Reference	2003	2611	China	PubMLST	1960
<i>Enterobacter sp.</i>	Eclo_2000	Reference	2010	2645	USA	PubMLST	2000
<i>Enterobacter sp.</i>	Eclo_2014	Reference	2015	2652	USA	PubMLST	2014
<i>Enterobacter sp.</i>	Eclo_2020	Reference	2013	2658	China	PubMLST	2020
<i>Enterobacter sp.</i>	Eclo_2021	Reference	2013	2658	China	PubMLST	2021
<i>Enterobacter sp.</i>	Eclo_2121	Reference	-	2735	Unknown	PubMLST	2121
<i>Enterobacter sp.</i>	Eclo_2137	Reference	2016	2685	Argentina	PubMLST	2137
<i>Enterobacter sp.</i>	Eclo_2195	Reference	2023	2836	France	PubMLST	2195
<i>Enterobacter sp.</i>	Eclo_2331	Reference	2024	2960	China	PubMLST	2331
<i>Enterobacter sp.</i>	Eclo_2344	Reference	2024	2969	China	PubMLST	2344
<i>Enterobacter sp.</i>	Eclo_2393	Reference	2023	3006	India	PubMLST	2393
<i>Enterobacter sp.</i>	Eclo_2739	Reference	2024	3234	France	PubMLST	2739
<i>Enterobacter sp.</i>	Eclo_2929	Reference	-	906	Belgium	PubMLST	2929
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<i>E. coli</i>	GCA_012663905.1	Reference	2011	88	USA	GenBank	GCA_012663905.1
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Supplementary figures

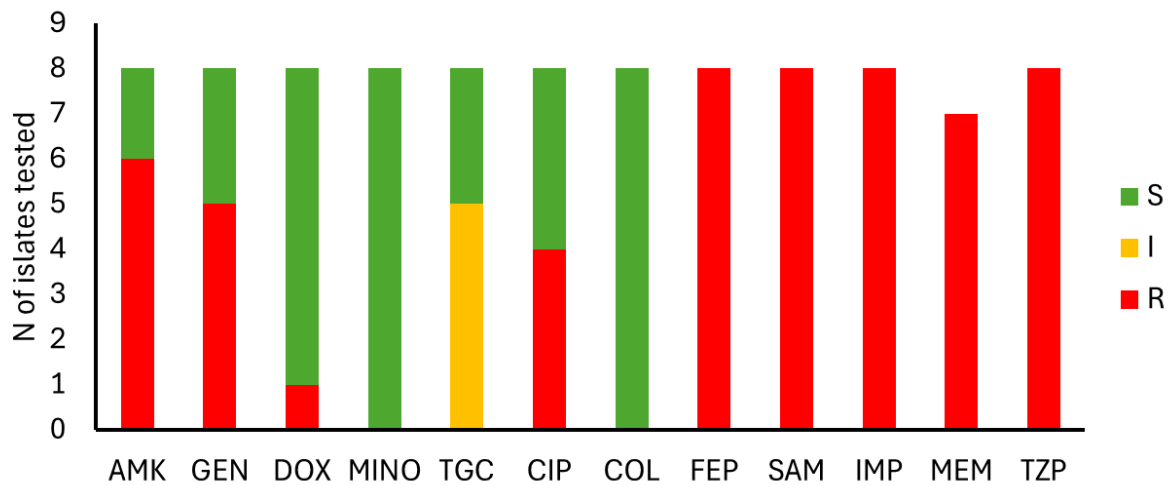


Fig. S1. Antimicrobial susceptibility profiles of *bl*_{NDM}-positive *Acinetobacter* isolates. Barplot showing the number of tested *Acinetobacter* isolates from HSJD (n = 8) and their susceptibility to selected antimicrobials. Bars are color-coded as susceptible (S, green), intermediate (I, yellow), or resistant (R, red). High resistance was observed to most β -lactams (FEP, SAM, IMP, MEM, TZP), while aminoglycosides (AMK, GEN), doxycycline (DOX), minocycline (MINO), tigecycline (TGC), and colistin (COL) retained variable activity. Susceptibility to ciprofloxacin (CIP) was reduced, with half of the isolates showing resistance or intermediate response. AST were interpreted according to CLSI M100, Ed. 23, 2023, expected for and TGC (tigecycline), colistin and fosfomycin for which EUCAST (https://www.eucast.org/clinical_breakpoints) and RELAVRA (<https://pmc.ncbi.nlm.nih.gov/articles/PMC6705331/>) breakpoints were employed.

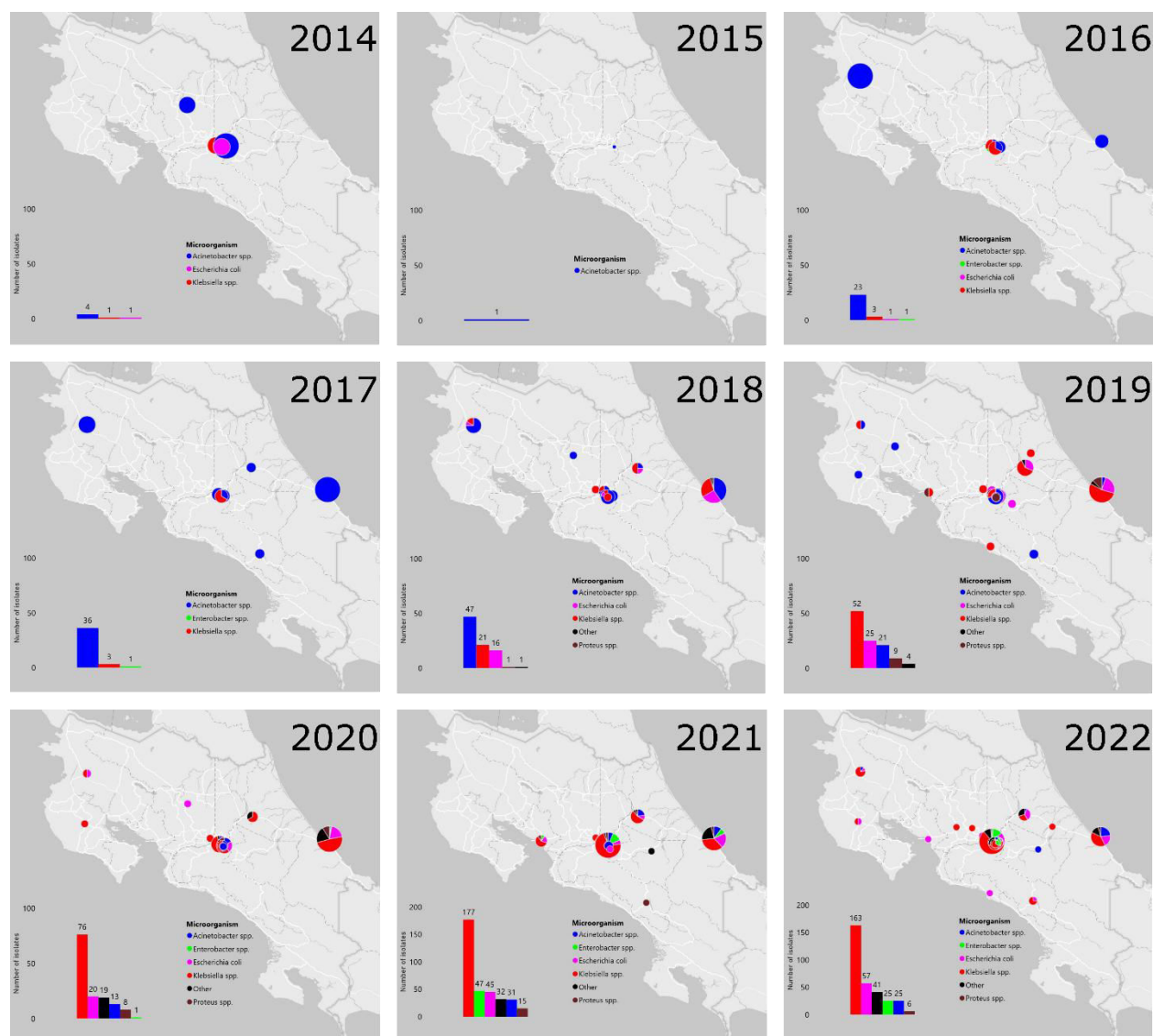


Fig. S2. Annual geographic distribution and species composition of *bla*_{NDM}-positive isolates in Costa Rica (2014–2022). Maps show the distribution of confirmed *bla*_{NDM}-producing isolates by year. Each circle corresponds to a healthcare facility, with circle size proportional to the number of isolates reported that year by the NRCB. Pie chart segments within circles indicate the proportion of bacterial species identified, including *Acinetobacter* spp., *E. coli*, *Enterobacter* spp., *Klebsiella* spp., *Proteus* spp., and others. Bar plots below each map summarize the total number of isolates per species for that year. The figure illustrates an epidemiological shift from sporadic *Acinetobacter* spp. detections in the early years (2014–2016) to a broader dissemination of *Klebsiella pneumoniae* and other Enterobacterales beginning in 2018, culminating in a nationwide outbreak during 2020–2022.

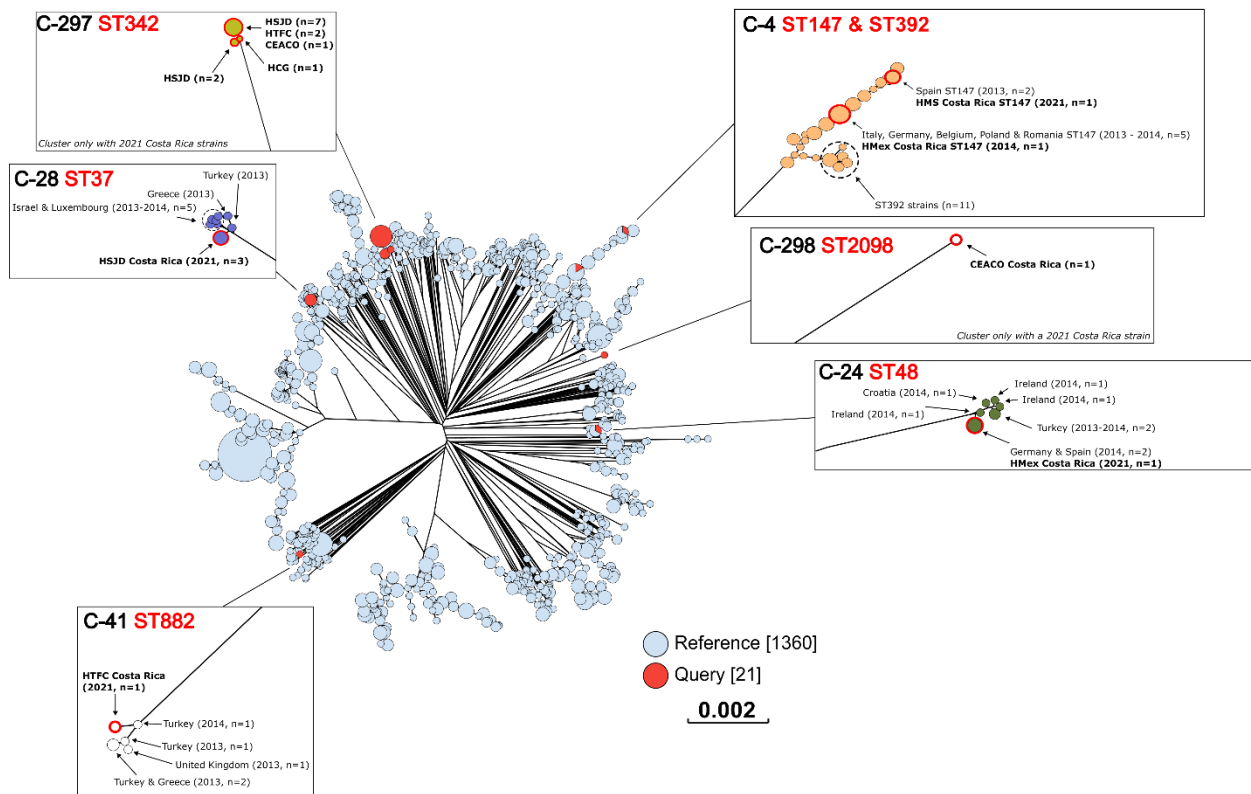


Fig. S3 Global population structure of *Klebsiella pneumoniae* based on core genome clustering. Core genome distances were calculated using popPUNK, and the resulting clusters were visualized with GrapeTree. Each node represents a group of closely related *K. pneumoniae* genomes, with publicly available reference genomes [1360 reference genomes from the European Survey of Carbapenemase-Producing Enterobacteriaceae (EuSCAPE)] shown in light blue and study isolates in red. Node size is proportional to the number of genomes within each cluster. Insets highlight zoomed regions containing closely related genomes, illustrating the phylogenetic placement of Costa Rican isolates (red stroke) within globally distributed *K. pneumoniae* lineages.

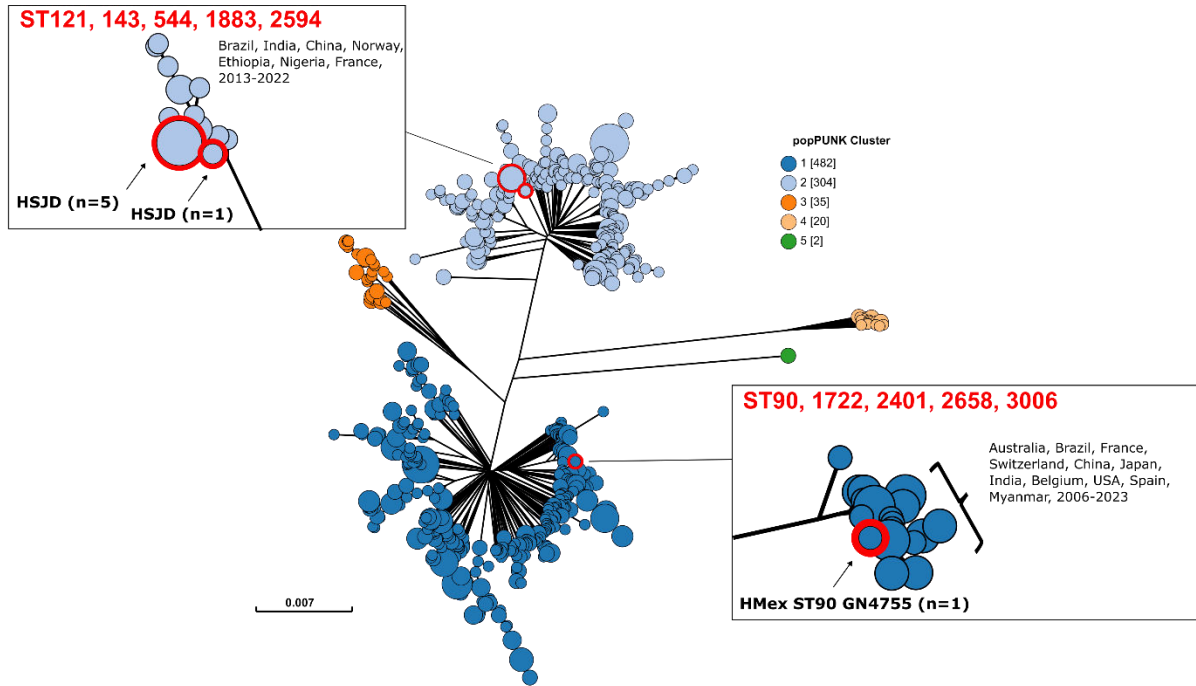


Fig. S4 Global population structure of *Enterobacter xiangfangensis* based on core genome clustering. Core genome distances were calculated using popPUNK, and the resulting clusters were visualized with GrapeTree. Each node represents a group of closely related *E. xiangfangensis* genomes, with publicly available reference genomes (836 genomes from PubMLST database) shown in light blue and study isolates in red. Node size is proportional to the number of genomes within each cluster. Insets highlight zoomed regions containing closely related genomes, illustrating the phylogenetic placement of Costa Rican isolates within globally distributed *E. xiangfangensis* lineages.

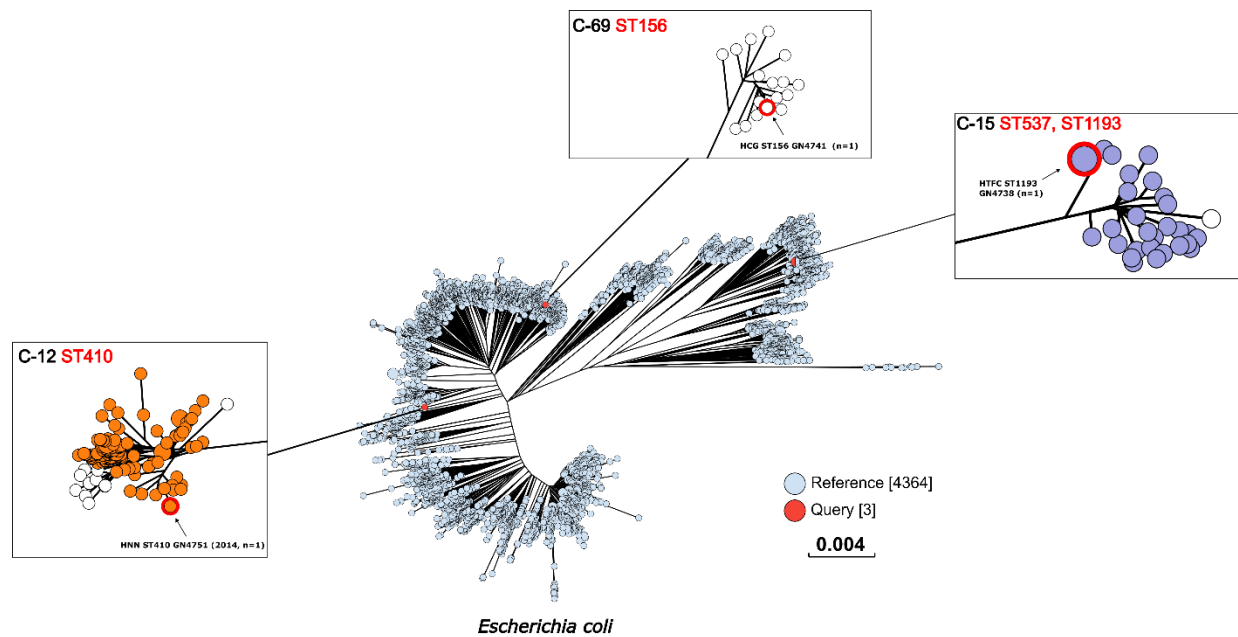


Fig. S5 Global population structure of *Escherichia coli* based on core genome clustering. Core genome distances were calculated using popPUNK, and the resulting clusters were visualized with GrapeTree. Each node represents a group of closely related *E. coli* genomes, with publicly available reference genomes (4,364 reference genomes from Horesh et al., 2021) shown in light blue and study isolates in red. Node size is proportional to the number of genomes within each cluster. Insets highlight zoomed regions containing closely related genomes, illustrating the phylogenetic placement of Costa Rican isolates within globally distributed *E. coli* lineages.

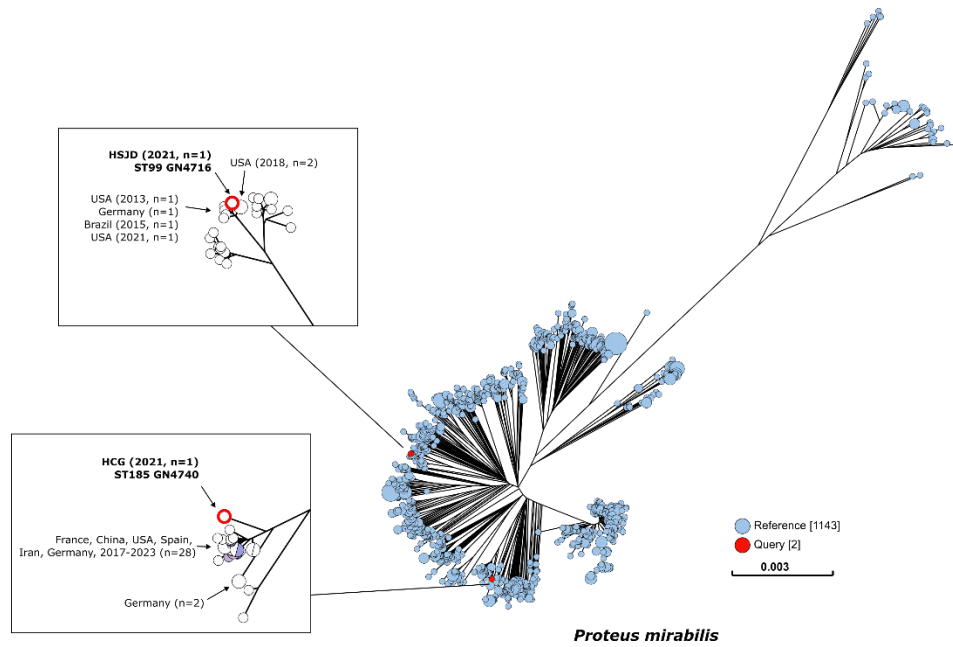


Fig. S6 Global population structure of *Proteus mirabilis* based on core genome clustering. Core genome distances were calculated using popPUNK, and the resulting clusters were visualized with GrapeTree. Each node represents a *P. mirabilis* genome, with publicly available reference genomes (PubMLST database, n=1,144 genomes) shown in light blue and study isolates in red. Node size is proportional to the number of genomes within each cluster. Insets highlight zoomed regions containing closely related genomes, illustrating the phylogenetic placement of Costa Rican isolates within globally distributed *P. mirabilis* lineages.

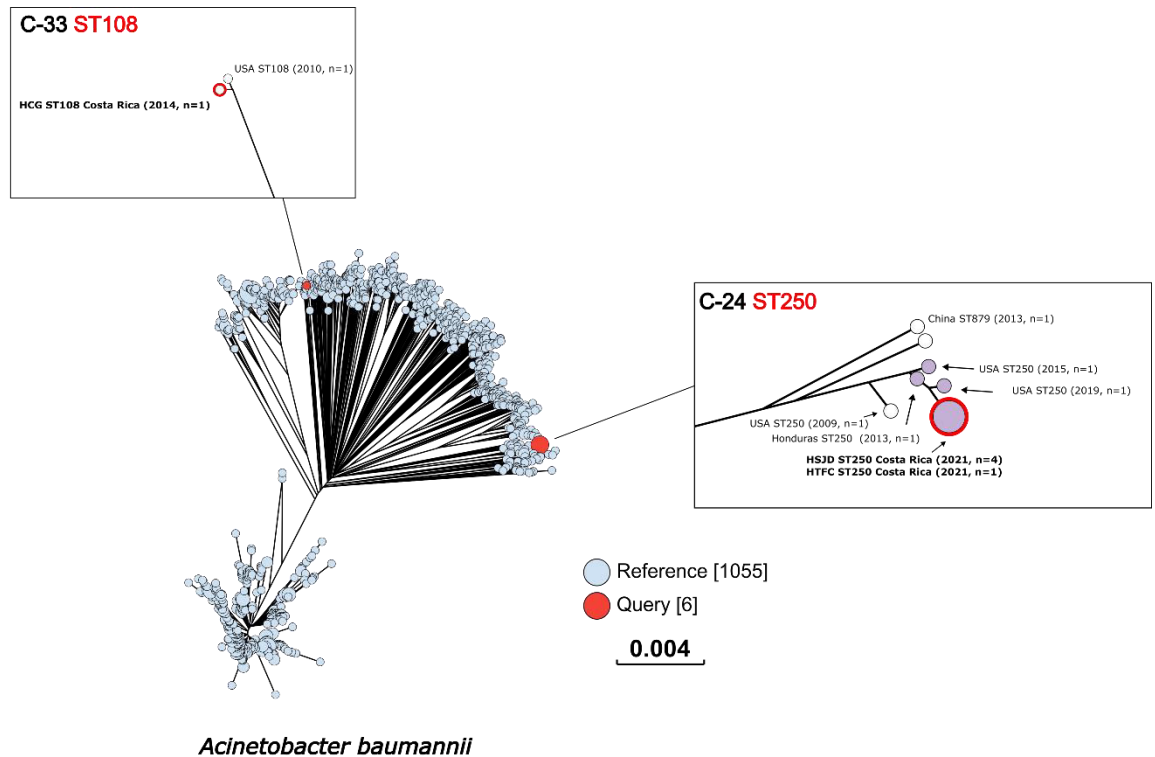


Fig. S7 Global population structure of *Acinetobacter baumannii* based on core genome clustering. Core genome distances were calculated using popPUNK, and the resulting clusters were visualized with GrapeTree. Each node represents an *A. baumannii* genome, with publicly available reference genomes (1,055 reference genomes from popPUNK database) shown in light blue and study isolates in red. Node size is proportional to the number of genomes within each cluster. Insets highlight zoomed regions containing closely related genomes, illustrating the phylogenetic placement of Costa Rican isolates within globally distributed *A. baumannii* lineages.

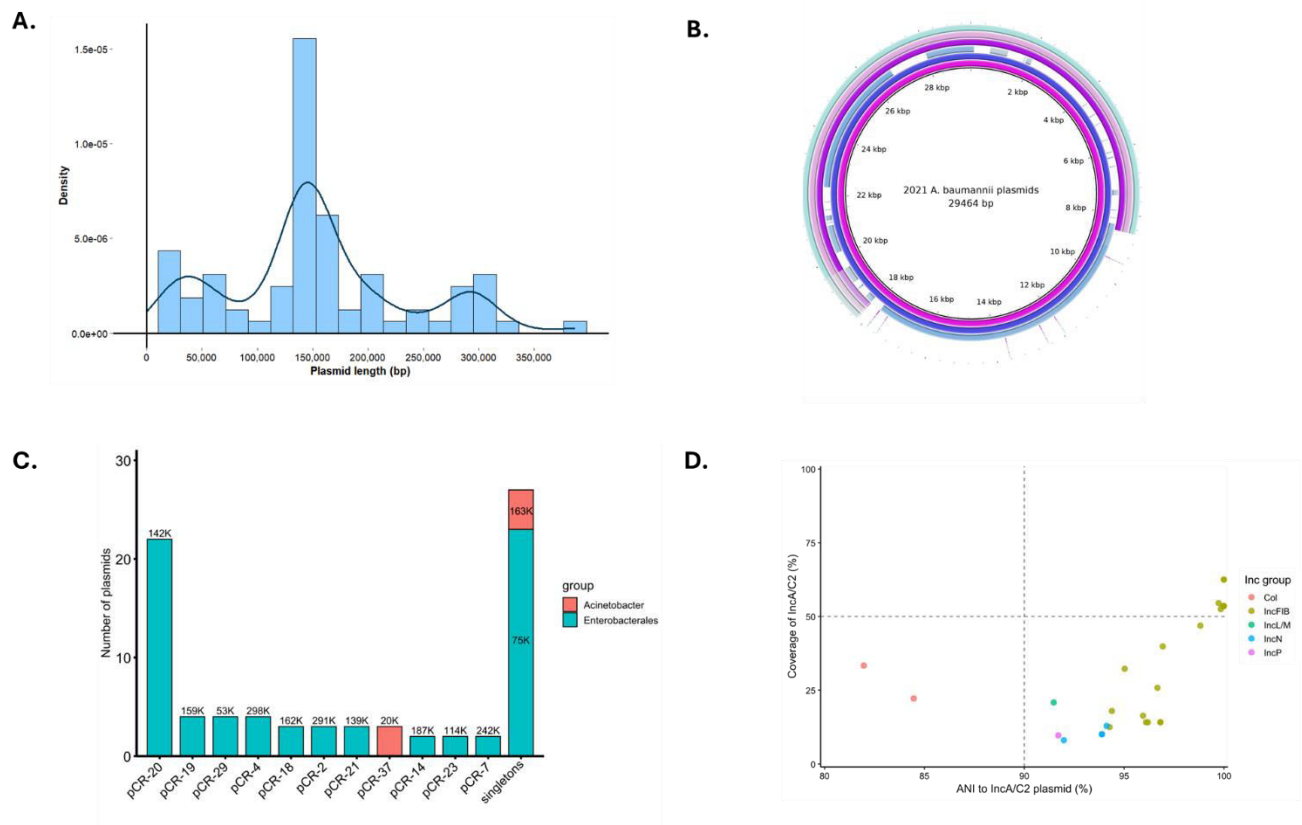


Fig. S8. Characterization of plasmid cargo. **A.**, Length distribution of plasmids. The plot displays the length distribution of all plasmid contigs in the dataset (bin=20), shown as a density-scaled histogram (blue bars) with an overlaid kernel density curve (dark blue). The distribution shows a prominent peak of mid-sized contigs (~130–150 kb) and additional modes corresponding to smaller and larger plasmids. **B.**, BRIG circular comparison of six *A. baumannii* plasmids recovered in 2021, using the 29,464-bp reference plasmid as the backbone. Colored rings represent individual plasmids, with shaded regions indicating sequence similarity across the plasmid backbone. **C.**, Distribution of plasmids across clusters generated using the CD-HIT-EST algorithm. Bars indicate the number of plasmids per cluster or singletons, color-coded by bacterial group. Numbers above bars denote the size (kb) of the representative plasmid in each cluster. **D.**, Scatter plot of average nucleotide identity (ANI) versus sequence coverage for non-*bla*_{NDM} plasmids relative to the *bla*_{NDM}(+) IncA/C2 plasmid set. Values were obtained from all-vs-all FastANI pairwise comparisons, and for each non-*bla*_{NDM} plasmid the highest ANI–coverage match is shown. Points represent individual non-*bla*_{NDM} plasmids, color-coded by incompatibility (Inc) group.

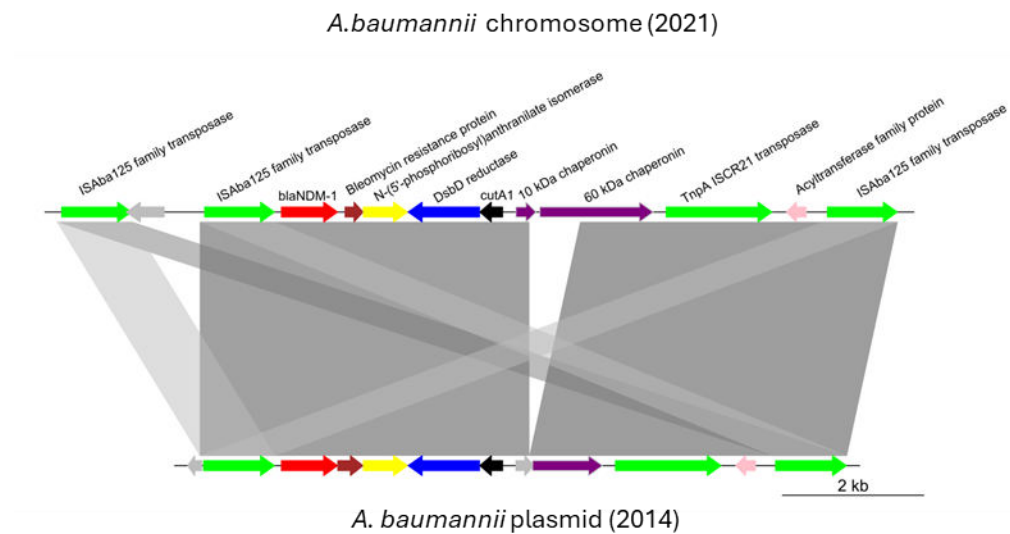


Fig. S9. Comparative genomic context of the *bla*NDM locus in *A. baumannii*. blastn alignment of the chromosomal *bla*NDM region from 2021 *A. baumannii* isolates against the plasmid-borne *bla*NDM genetic platform originally described in a 2014 *A. baumannii* isolate. Arrows denote predicted open reading frames and indicate direction of transcription. The *bla*NDM gene is highlighted in red, while insertion sequences and transposase-associated genes, including ISAbat125, are shown in green. Homologous regions are connected by shaded grey polygons, with grey-scale intensity proportional to nucleotide identity between aligned regions. The scale bar indicates 2 kb. The figure was generated in R using genoplotsR.

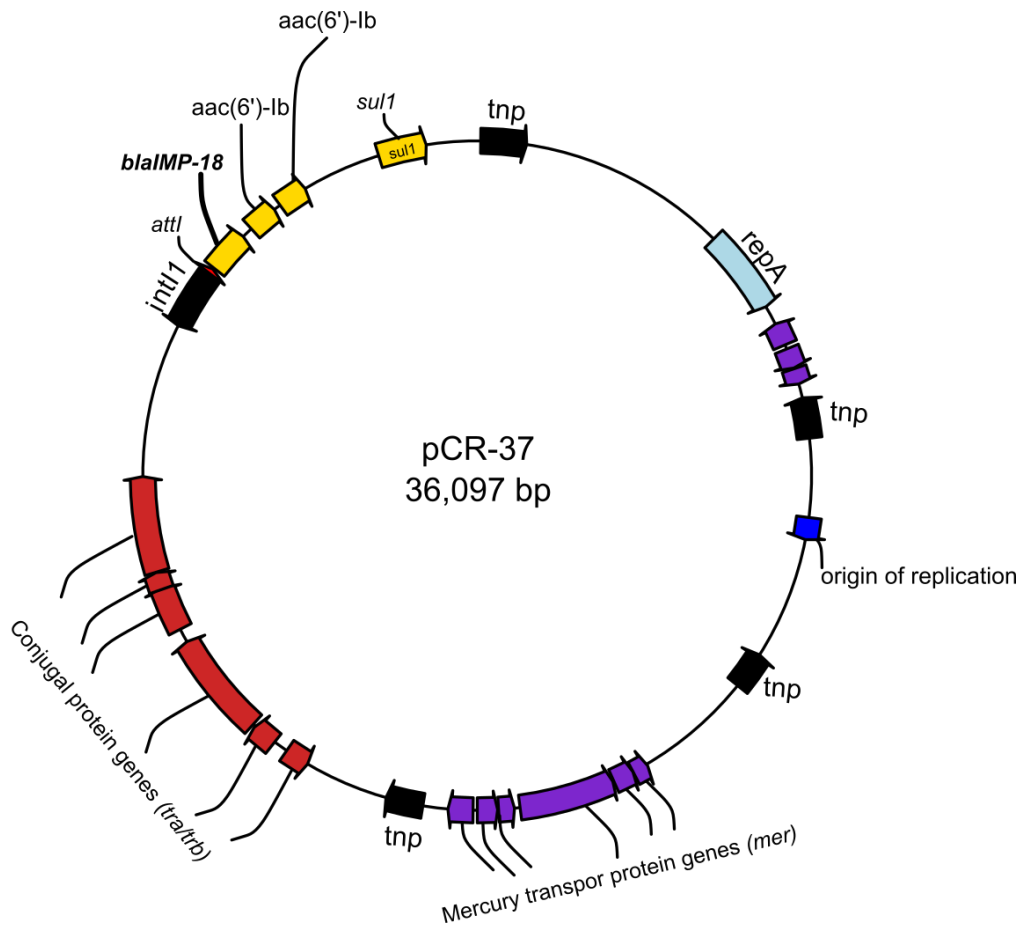


Fig. S10. Genetic architecture of the *bla*_{IMP-18}-carrying plasmid from *E. xiangfangensis*. Circular representation of the *bla*_{IMP-18}-harbouring plasmid identified in an *E. xiangfangensis* isolate recovered at HMex. Only selected, functionally relevant coding sequences (CDS) are depicted; all remaining plasmid CDS are omitted for clarity. Colored blocks represent predicted coding sequences grouped by functional categories, including antimicrobial resistance genes, integron-associated elements, mobile genetic elements, and plasmid maintenance functions. The class 1 integron region carrying *bla*_{IMP-18} and associated resistance genes, including *sul1*, is highlighted. Gene orientation is shown according to the direction of transcription. The figure was generated in R using plasmapR.