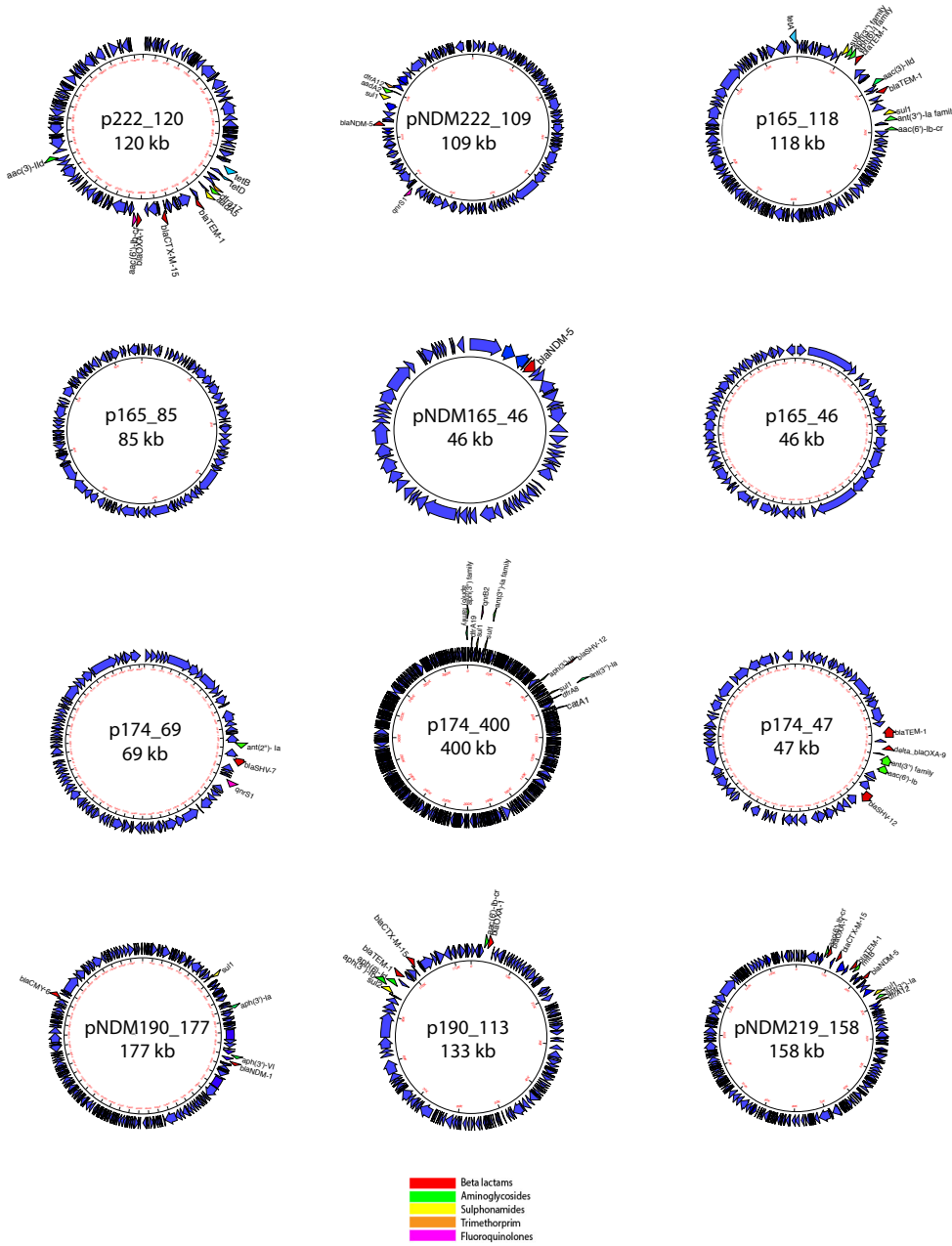


1 Supplementary Figure and Table Legends

S1



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3 **Figure S1) Plasmid Analyses:** Maps of all plasmids found in the *bla*<sub>NDM</sub>-carrying strains, with resistance genes

4 highlighted and color-coded according to drug class. Supplementary Table 3 indicates incompatibility (Inc) group

5 and the closest homologue of each plasmid found in Genbank, along with the corresponding %identity/% query  
 6 length, host bacterium species, and origin.

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 8 **Supplementary Table 1: Strain and Sequence Dataset Identifiers**

Strain ID	Crimson ID	BioProject ID	BioSample ID	Accession Number of Illumina DNA-seq reads	Location/Vector Name	Accession Number for PacBio Assembly
ECO-165	0055-8761	PRJNA278886	SAMN04393397	SRR3095381	chromosome	CP020509
					p165_118	CP020510
					p165_85	CP020511
					pNDM165_46	CP020512
ECC-174	0056-2175	PRJNA278886	SAMN04456586	SRR3168645	chromosome	CP020528
ECO-190	0057-1694	PRJNA278886	SAMN04622917	SRR3618626	p174_400	CP020529
					p174_69	CP020530
					p174_47	CP020531
					chromosome	CP020520
ECO-219	0058-7850	PRJNA278886	SAMN05194389	SRR3615372	pNDM190_177	CP020524
					p190_113	CP020523
					190_phage1_95kb	CP020522
					190_phage2_13kb	CP020521
ECO-222	0059-2033	PRJNA278886	SAMN05194390	SRR3615373	chromosome	CP020514
					pNDM219_158	CP020515
ECO-222	0059-2033	PRJNA278886	SAMN05194390	SRR3615373	chromosome	CP020516
					p222_120	CP020519
					222_phage_48kb	CP020518
					pNDM222_109	CP020517

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11 **Supplementary Table 2: PCR and Sequencing Primers used in Analyses**

Primer Target	Sequence	Target Size
NDM (NDM)	FW: CCAATATTATGCACCCGGTCGCGAAGCT RV: CCATGCGGGCCGTATGAGTGATTGC	798 bp
p222 (IncF conjugative transfer protein TraR)	FW: TTTCCATCTGGCCCCTAACC RV: ACCCTTTCCCGGCCATAAAG	458 bp
p165 (IncQ plasmid transfer nicking DNA)	FW: CCACACGTGCATGTCGTTTT RV: TGTTTTCTCCACGCCCTTGT	315 bp
p219 (IncF pilus TraC)	FW: GACGCAAAAATGGTGGTGCT RV: CTGCAGCAGGAAGGAACTGA	462 bp
p190 (Chromosome plasmid partitioning protein ParA)	FW: ATGCACTCTGGCCGATGAAA RV: CTGCGGTTTTGGTTCCAGTG	577 bp
J53 E. coli (CRISPR-associated protein Cse1/CasA)	FW: CATCGCGCCGTGGATAGATA RV: TGGGGCCATAGCCCATTAAC	588 bp
5' transposon boundary (Oxidoreductase-ISab125)	FW: ACATCAGCGCCTTCACGAGCAT RV: TCGCATGTGCCTTTTGCCAGG	9356 bp
5' transposon boundary sequencing	IS91: ACCGTTTGTGAGTGGGCG IS26: TATTGAGGTGATGCGTGC	N/A
3' transposon boundary (Integron-IS26)	FW: AACTGCGGGTCAAGGATCTG RV: ACTCCACGATTTACCGCTGG	1041 bp

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19 **Supplementary Table 3: Incompatibility (Inc) group typings and identification of homologues for all plasmids**  
 20 **identified in NDM-carrying strains.**

Carrying Strain	Plasmid	Inc Type	Genbank accession	Closest homologue (Accession #)	% Identity/ % Query Length	Host bacterium of homologous plasmid	Origin of homologous plasmid
ECO-222	P222_120	IncFIB/FIA	TBA	pM105_mF (AP018137)	99/63	<i>Escherichia coli</i>	Myanmar (Human)
ECO-222	pNDM222_109	IncFII	TBA	pCC1410-2 (KY288024)	99/76	<i>Klebsiella pneumoniae</i>	South Korea (Human)
ECO-165	p165_118	IncFII/IncF1B	TBA	pSCKLB138-1 (MH161192.1)	99/95	<i>Klebsiella pneumoniae</i>	China (unknown)
ECO-165	p165_85	IncL1	TBA	pEC014 (MG545910)	98/86	<i>Escherichia coli</i>	China (Chicken)
ECO-165	pNDM165_46	IncX	TBA	pSCM96-2 (CP028718.1)	99/100	<i>Klebsiella pneumoniae</i>	China (Human)
ECO-165	P165_46	IncC	TBA	p846 (CP029249.1)	99/99	<i>Salmonella enterica</i> subsp. enterica	Chine (Human)
ECC-174	P174_69	IncL/M	TBA	pKPN1705-3 (CP022826.1)	99/100	<i>Klebsiella quasivariicola</i>	USA (Human)
ECC-174	P174_400	IncH2/A	TBA	pKPC-272 (CP008825.1)	99/66	<i>Enterobacter sp.</i>	USA (Sink Drain)
ECC-174	P174_47	IncR	TBA	pKP-Goe-641-1 (CP018737.1)	100/89	<i>Klebsiella pneumoniae</i>	Germany (Human)
ECO-190	pNDM190_177	IncC1	TBA	unitig_2 (CP021536.1)	99/74	<i>Escherichia coli</i>	USA (Human)
ECO-190	P190_113	IncFII	TBA	pKDO1 (JX424423.1)	99/99	<i>Klebsiella pneumoniae</i>	Czech Republic (Human)
ECO-219	pNDM219_158	IncFII	TBA	P123 (CP023378.1)	99/68	<i>Escherichia coli</i>	Scotland (Canine)

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