

1 TABLE S1. Phenotypic and genotypic properties of challenge strains

	Challenge strains	Origin/ Year of isolation	Plasmids	Phenotypic resistance profile (by MIC) ^a	Genotypic resistance profile of pRH-1238	Genotypic resistance of others	Reference
Donor	NDM-1 producing <i>S. Corvallis</i> (12-SA01738)	Black kite (<i>Milvus migrans</i>) 2012	IncHI2 (~310 kb)	AMP, CHL, CIP, FFN, FOT, KAN SMX, STR, TAZ, TET, TMP	<i>bla</i> _{CMY-16} , <i>bla</i> _{NDM-1} , <i>floR</i> , <i>accA4</i> [<i>aac</i> (6')- <i>lb</i>], <i>tet</i> (A), <i>drfA1/7/17</i> , <i>strA/B</i> , <i>sul1</i> , <i>sul2</i> , <i>aadA5</i> , <i>fosA3</i> , <i>aphA6</i> , <i>mphA</i>	<i>qnrS</i>	(1, 2)
			ColRNAI (< 20 kb)				
Recipient	<i>S. Paratyphi B</i> (<i>dTa</i> +) (13-SA01617)	Chicken meat 2013	none	CIP, NAL, STR, TMP	-	<i>aadA1</i> , <i>dfrA1</i>	-

^a MIC carried out following CLSI guidelines, CLSI M07-A9 and using EUCAST epidemiological cut-off values (<http://www.eucast.org>)

Definition of abbreviations:

AMP (Ampicillin), CHL (Chloramphenicol), CIP (Ciprofloxacin), NAL (Nalidixic acid), FFN (Florfenicol), FOT (Cephotaxime),

KAN (Kanamycin), SMX (Sulphamethoxazole), STR (Streptomycin), TAZ (Cephtazidime), TET (Tetracycline), TMP (Trimethoprim)

3 TABLE S2. Average CTF rates based on filter mating conjugation experiments for donor and recipient strains

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Donor	Recipients	Strain no.	Conjugation transfer frequency (CTF) rate		
			RT	37°C	42°C
NDM-1 producing S. Corvallis (12-SA01738)	S. Enteritidis [with 60 kb <i>pSEV</i> virulence plasmid (3)]	07-SA03428	$5,08 \times 10^{-5}$	$8,71 \times 10^{-3}$	$1,88 \times 10^{-2}$
	S. Enteritidis (without 60 kb <i>pSEV</i> virulence plasmid)	04-SA02117	$8,56 \times 10^{-5}$	$1,50 \times 10^{-2}$	$1,57 \times 10^{-2}$
	S. Infantis	14-SA03263	$6,64 \times 10^{-5}$	$9,04 \times 10^{-3}$	$1,10 \times 10^{-2}$
	S. Paratyphi B (<i>dTa+</i>)	13-SA01617	$3,50 \times 10^{-4}$	$8,07 \times 10^{-3}$	$1,06 \times 10^{-2}$

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6 TABLE S3. Antibiotic supplementation of selective plates for target microorganisms

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Target microorganisms	Medium	Antibiotic supplementation		
		Cefotaxime (1 mg/l)	Meropenem (0.125 mg/l)	Nalidixic acid (50 mg/l)
S. Corvallis	XLD agar	+	+	-
S. Paratyphi B (dTa+)	XLD agar	-	-	+
NDM-1-producing S. Paratyphi B (dTa+)	XLD agar	+	+	+
Carbapenemase- producing Enterobacteriaceae (CPE)	chromID® CARBA agar	unknown	unknown	unknown

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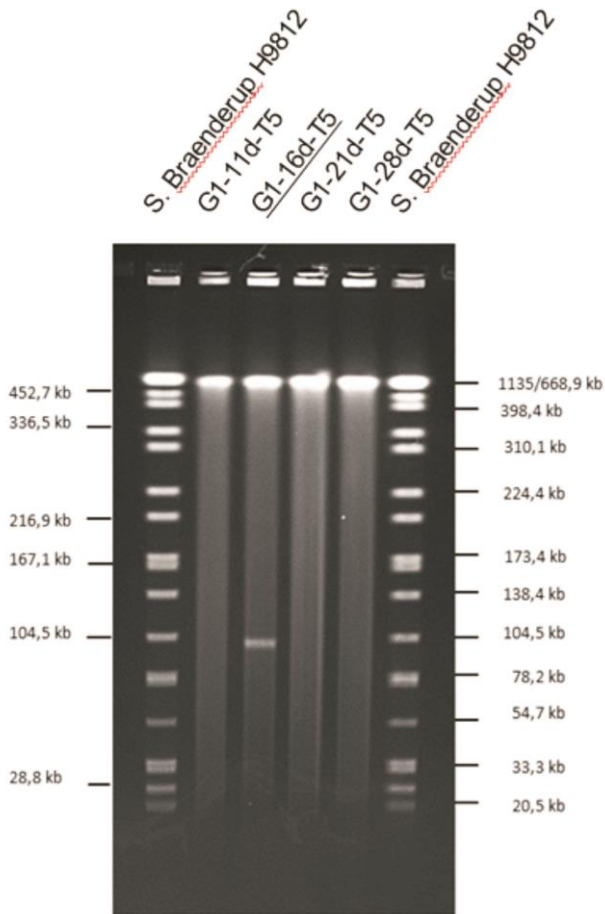
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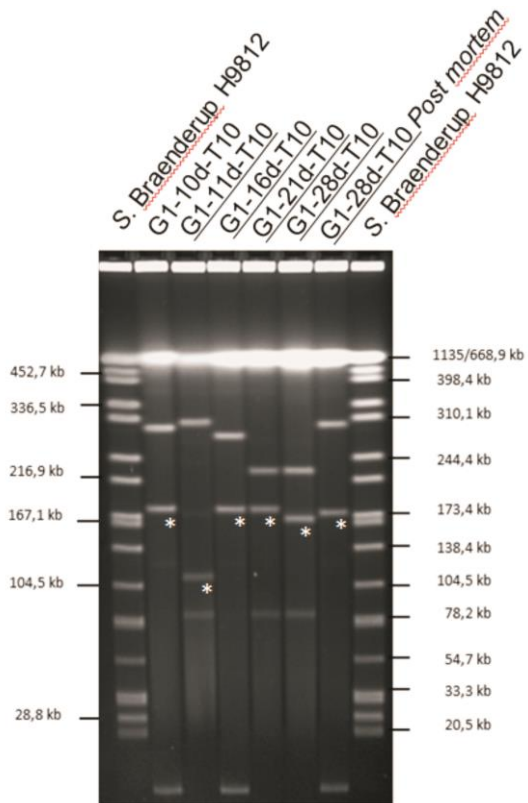
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FIGURE S1. S1-PFGE analysis of *S. Paratyphi B* (*dTa+*) reisolates from Group 1 in lanes 2-5 with molecular-sized standard, *Salmonella* Braenderup strain H9812 (restricted with XbaI) in lanes 1 and 6. Underlined strain selected for WGS.



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45 **FIGURE S2.** S1-PFGE analysis of *S. Corvallis* reisolates from Group 1 in lanes 2-7 with
 46 molecular-sized standard, *Salmonella* Braenderup strain H9812 (restricted with XbaI) in
 47 lanes 1 and 8. Asterix (*) marked *bla*_{NDM-1} hybridisation. Underlined strains selected for WGS.

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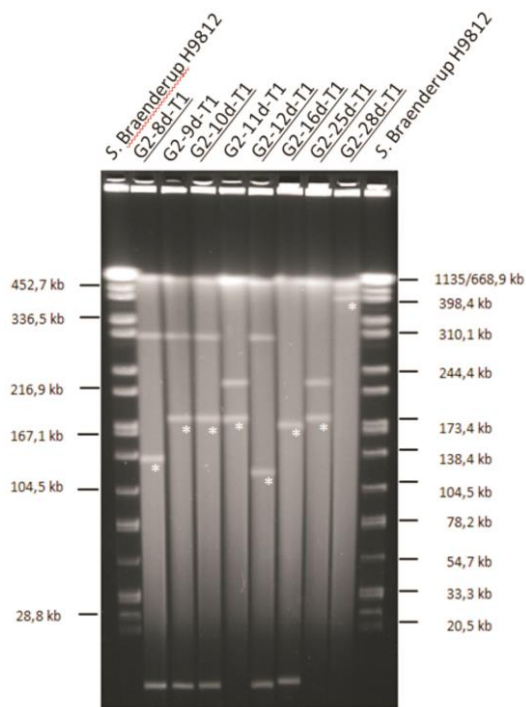
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62 **FIGURE S3.** S1-PFGE analysis of *S. Corvallis* reisolates from Group 2 in lanes 2-9 with
 63 molecular-sized standard, *Salmonella* Braenderup strain H9812 (restricted with XbaI) in
 64 lanes 1 and 10. Asterix (*) marked bla_{NDM-1} hybridisation. Underlined strains selected for
 65 WGS.

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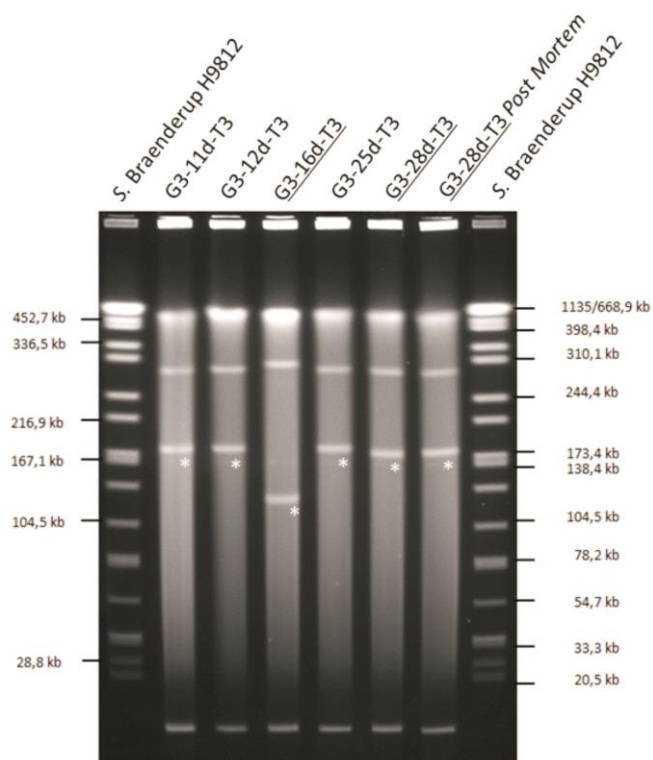
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79 **FIGURE S4.** S1-PFGE analysis of *S. Corvallis* reisolates from Group 3 in lanes 2-7 with
 80 molecular-sized standard, *Salmonella* Braenderup strain H9812 (restricted with XbaI) in
 81 lanes 1 and 8. Asterix (*) marked *bla*_{NDM-1} hybridisation. Underlined strains selected for WGS.

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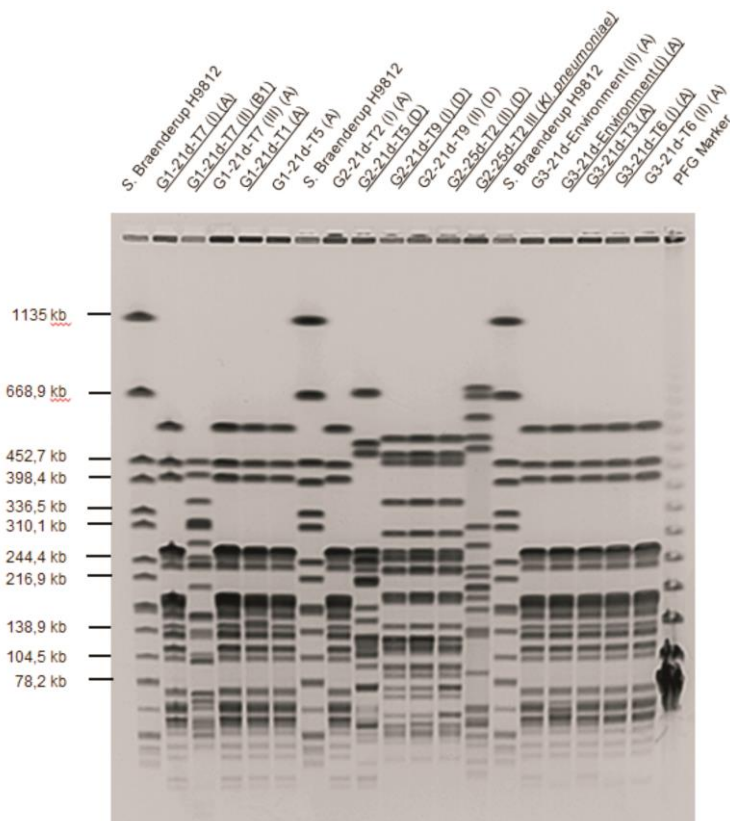
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97 **FIGURE S5.** XbaI-PFGE analysis of NDM-1 producing Enterobacteriaceae transconjugants
 98 from Group 1 (lanes 2-6), Group 2 (lanes 8-13), Group 3 (lanes 15-19) with *E. coli* phylogroups (A,
 99 B1 and D) designation in brackets and one *K. pneumoniae* strain. Molecular-sized standard
 100 *Salmonella* Braenderup strain H9812 (restricted with XbaI) in lanes 1, 7, 14 and MidRange
 101 PFG Marker in lane 20. Underlined strains selected for WGS.

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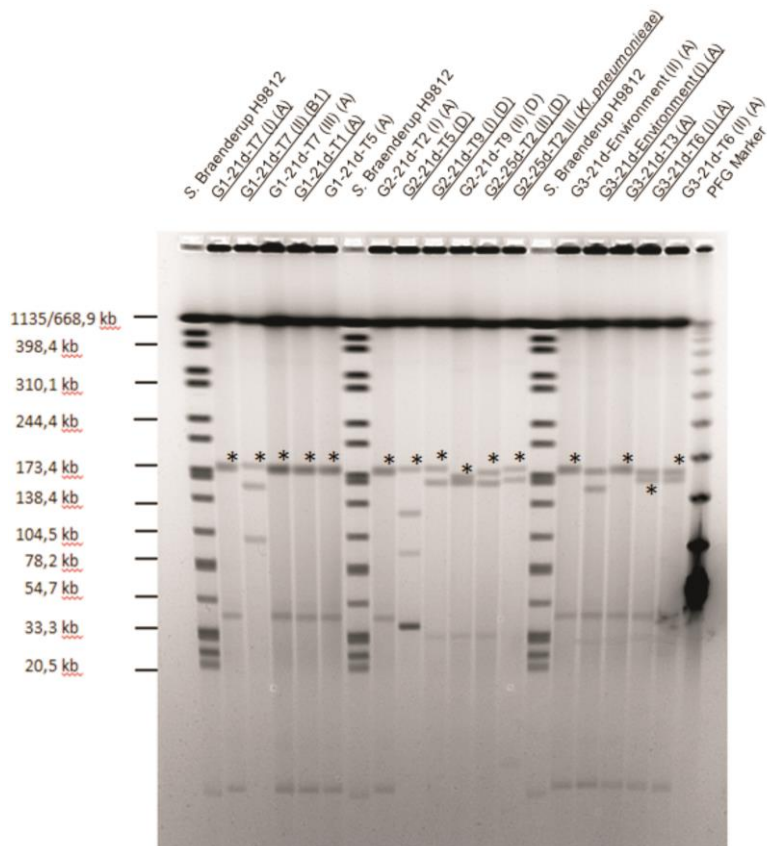
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111 **FIGURE S6.** S1-PFGE analysis analysis of NDM-1 producing Enterobacteriaceae
 112 transconjugants from Group 1 (lanes 2-6), Group 2 (lanes 8-13), Group 3 (15-19) with *E. coli*
 113 phylogroups (A, B1 and D) designation in brackets and one *K. pneumoniae* strain. Molecular-
 114 sized standard *Salmonella* Braenderup strain H9812 (restricted with XbaI) in lanes 1, 7, 14
 115 and MidRange PFG Marker in lane 20. Asterix (*) marked *bla*_{NDM-1} hybridisation. Underlined
 116 strains selected for WGS.

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125 **References**

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