

Pietsch et al., Supplementary Files

Supplementary Table S1: Characteristics of clinical donor strains and the corresponding transconjugants (Kx) used for fitness experiments.

Isolate	Transconjugant ¹	Species	Year of isolation	MLST/ Phylogenetic group ²	Beta-lactamase gene	bla plasmid [kb] ³	Replicon type ⁴
102/04		<i>E. coli</i>	2004	D	<i>bla</i> _{CMY-16} , <i>bla</i> _{TEM-1}	160	
	102/04 K1	<i>E. coli</i>		A	<i>bla</i> _{CMY-16} , <i>bla</i> _{TEM-1}	160	IncA/C
	102/04 K2	<i>E. coli</i>		A	<i>bla</i> _{CMY-16} , <i>bla</i> _{TEM-1}	160	IncA/C
151/09		<i>E. cloacae</i>	2009		<i>bla</i> _{VIM-1}	100	
	151/09 K2	<i>E. coli</i>		A		100	IncN/IncR
17/11		<i>E. coli</i>	2011	B1	<i>bla</i> _{KPC-2}	210, 190, 85, 65	
	17/11 K1	<i>E. coli</i>		A	<i>bla</i> _{KPC-2}	190	IncA/C
252/09		<i>E. coli</i>	2009		<i>bla</i> _{CMY-2} , <i>bla</i> _{TEM-1}	85, 60, 30	IncI1, IncFII
	252/09 K3	<i>E. coli</i>		A	<i>bla</i> _{CMY-2}	85, 60	IncI1, IncFII
346/12		<i>K. pneumoniae</i>	2012		<i>bla</i> _{OXA-48} , <i>bla</i> _{OXA-1} , <i>bla</i> _{OXA-9}	105, 60, 35	IncL/M-1
	346/12 K2	<i>E. coli</i>		A	<i>bla</i> _{OXA-48}	60	IncL/M-1
370/12		<i>K. oxytoca</i>	2012		<i>bla</i> _{VIM-1} , <i>bla</i> _{OXA} ,	250, 150, 100	IncFIB, IncL/M-1
	370/12 K2	<i>E. coli</i>		A	<i>bla</i> _{VIM-1}	250	IncFIB
384/13		<i>K. pneumoniae</i>	2013		<i>bla</i> _{NDM-1} , <i>bla</i> _{SHV-like} , <i>bla</i> _{CTX-M-15} , <i>bla</i> _{OXA-232} ,	240, 110	IncFII, IncI1,
	384/13 K2	<i>E. coli</i>		A	<i>bla</i> _{OXA-1} , <i>bla</i> _{OXA-9} , <i>bla</i> _{TEM}		IncN?
467/13		<i>K. pneumoniae</i>			<i>bla</i> _{NDM} , <i>bla</i> _{CTX-M-15} , <i>bla</i> _{OXA-9} , <i>bla</i> _{TEM-1}	110	IncFII
	467/13 K2	<i>E. coli</i>		A	<i>bla</i> _{OXA-48}	60	IncL/M-1
531/12		<i>E. coli</i>			<i>bla</i> _{CMY-2}	190, 90, 55	IncI1
	531/12 K2	<i>E. coli</i>		A		90	IncI1
656/13		<i>E. coli</i>			<i>bla</i> _{SHV-12}	140, 105	
	656/13 K2	<i>E. coli</i>		A	<i>bla</i> _{SHV-12}	105	IncI1
RS014	negative	<i>E. coli</i>	2010	ST131	<i>bla</i> _{CTX-M-15}		
RS039		<i>E. coli</i>	2011	ST46	<i>bla</i> _{CTX-M-1} ,	80	IncI1
	RS039 K1	<i>E. coli</i>		A	<i>bla</i> _{TEM-1}		
RS060	negative	<i>E. coli</i>			<i>bla</i> _{CTX-M-1}		IncI1
RS135	negative	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-27}		
RS081	negative	<i>E. coli</i>	2011	ST410	<i>bla</i> _{CTX-M-15}		
RS165		<i>E. coli</i>	2011	D	<i>bla</i> _{CTX-M-1} , <i>bla</i> _{TEM-1}	90	IncI1
	RS165 K1	<i>E. coli</i>		ST73	<i>bla</i> _{CTX-M-14}		
RS292		<i>E. coli</i>	2012	D	<i>bla</i> _{CTX-M-14}	70	IncFII
	RS292 K1	<i>E. coli</i>		A	<i>bla</i> _{CTX-M-15} , <i>bla</i> _{TEM-1}		IncFII
104/15		<i>E. coli</i>	2015	B2, rfbO25 negative	<i>bla</i> _{CTX-M-15}	77	IncF

Isolate	Transconjugant ¹	Species	Year of isolation	MLST/ Phylogenetic group ²	Beta-lactamase gene	<i>bla</i> plasmid [kb] ³	Replicon type ⁴
	104/15 K3	<i>E. coli</i>		A	<i>bla</i> _{CTX-M-15}	77	IncFII
RS013	<i>negative</i>	<i>E. coli</i>	2010	ST131	<i>bla</i> _{CTX-M-15}		
RS014	<i>negative</i>	<i>E. coli</i>	2010	ST131	<i>bla</i> _{CTX-M-15}		
RS025	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS029	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS031	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS050	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS062	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS071	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS072	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS080	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS090	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS093	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS098	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS099	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS103	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS104	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS106	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS107	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS113	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS115	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS127	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS134	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS137	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		
RS143	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15} , <i>bla</i> _{TEM-1}		
RS184	<i>negative</i>	<i>E. coli</i>	2011	ST131	<i>bla</i> _{CTX-M-15}		

Legend: ¹ recipient *E. coli* K J53 Azi^r was used in mating experiments, ² PCR-based determination of *E. coli* phylogenetic group (Clermont O, Bonacorsi S, Bingen E. Rapid and simple determination of the *Escherichia coli* phylogenetic group. Appl Environ Microbiol. 2000;66(8):4555) and determination of sequence type (ST) by multilocus sequence typing (https://pubmlst.org/bigsubdb?db=pubmlst_ecoli_achtman_seqdef), ³ sizes of plasmids that contained the beta-lactamase (*bla*) gene of interest (printed in bold) were determined by S1 nuclease treatment and subsequent PFGE analyses, ⁴ PCR based replicon typing using the PRBT kit (Diatheva, Cartoceto, Italy).

Supplementary Table S2: Fitness values of the initial and evolved transconjugants from long-term growth experiments. Fitness values of the initial transconjugants relative to the fitness of the recipient *E. coli* J53 Azir⁽¹⁾ is given as generation G₀, values of the evolved transconjugants are presented for generations G₀, G₂₀₀, and G₅₀₀. The numbers of repeated experiments (*n* attempts) and the standard deviations (SD) are given.

Isolate	Generation G ₀ relative fitness [%] Average value (<i>n</i> attempts) SD		Generation G ₂₀₀ relative fitness [%] Average value (<i>n</i> attempts) SD		Generation G ₅₀₀ relative fitness [%] Average value (<i>n</i> attempts) SD	
	J53 ¹	100				
J53-1			102.03 (2)	0.36	96.87 (3)	1.86
J53-2			101.31 (2)	0.31	93.54 (3)	1.31
J53-3			bdl (2)		94.68 (3)	1.78
J53-4			102.81 (2)	2.77	97.41 (3)	2.20
RS165K1	98.47 (8)	1.76				
RS165 K1-1			113.19 (2)	2.85	99.08 (3)	1.12
RS165 K1-2			bdl (2)		99.95 (3)	0.55
RS165 K1-3			101.29 (2)	0.83	99.11 (3)	3.25
RS165 K1-4			112.63 (2)	3.18	97.66 (3)	2.18
102/04 K1	107.23 (4)	2.29				
102/04 K1-1			110.38 (2)	1.09	99.04 (3)	1.49
102/04 K1-2			96.16 (2)	0.65	102.68 (3)	3.63
102/04 K1-3			99.46 (1)		98.89 (3)	1.78
102/04 K1-4			100.49 (1)		102.10 (3)	2.33
102/04 K2	95.58 (3)	0.71				
102/04 K2-1			96.81 (2)	0.19	88.07 (3)	3.24
102/04 K2-2			97.99 (2)	0.64	104.53 (3)	0.57
102/04 K2-3			101.66 (1)		102.09 (3)	1.42
102/04 K2-4			99.89 (1)		94.75 (3)	0.60
252/09 K3	98.70 (3)	1.45				
252/09 K3-1			101.68 (1)		92.69 (3)	1.07
252/09 K3-2			101.39 (1)		95.65 (3)	2.12
252/09 K3-3			103.23 (1)		93.49 (3)	0.35
252/09 K3-4			93.57 (1)		97.86 (3)	2.02
151/09 K2	96.30 (3)	0.76				
151/09 K2-1			89.81 (1)		100.37 (3)	1.42
151/09 K2-2			93.74 (1)		97.60 (3)	0.58
151/09 K2-3			95.21 (1)		92.42 (3)	0.65
151/09 K2-4			90.82 (1)		95.59 (3)	1.36
104/15 K3	100.74 (3)	0.25				
104/15 K3-1			102.09 (2)	1.21	99.16 (3)	1.46
104/15 K3-2			101.26 (2)	1.51	97.99 (3)	1.40
104/15 K3-3			100.01 (2)	1.80	99.58 (3)	2.38
104/15 K3-4			100.70 (2)	1.81	95.20 (3)	1.93
346/12 K2	97.88 (3)	0.84				
346/12 K2-1			96.17 (1)		87.19 (3)	1.70
346/12 K2-2			97.60 (1)		83.70 (3)	0.60
346/12 K2-3			95.86 (1)		84.05 (2)	1.36
346/12 K2-4			95.50 (1)		88.07 (3)	1.40
RS039 K1*	99.02 (8)	2.15				
RS292K1*	100.02 (8)	1.93				
17/11K1*	99.76 (4)	1.52				
370/12K1*	100.82 (5)	1.46				
384/13K2*	100.01 (4)	2.33				
656/13 K2*	98.47 (3)	0.84				
531/12 K2*	98.34 (3)	0.16				

Legend: bdl = below detection limit; *isolates not selected for further analyses

Supplementary Table S3: Antibiotic susceptibilities (MICs in mg/L) of transconjugants of the different generations, detected by broth microdilution (EUCAST v10.0; https://www.eu-cast.org/clinical_breakpoints/).

Isolate	AMP	CTA	CTZ	CXI ¹	GEN	KAN ¹	AMI	STR ¹	NAL ¹	CMP	CIP	MER	TRS
102/04 K1	>16	>16	>32	>32	1	>32	>32	>64	16	>32	≤0.063	≤0.063	>128
G200 -1	>16	16	32	>32	≤0.5	>32	16	64	8	>32	≤0.063	≤0.063	>128
G200 -2	>16	8	16	16	≤0.5	>32	8	16	16	>32	≤0.063	≤0.063	>128
G200 -5	>16	>16	>32	>32	4	>32	>32	>64	16	>32	≤0.063	≤0.063	>128
G200 -8	>16	>16	>32	>32	≤0.5	>32	32	64	16	>32	≤0.063	≤0.063	>128
G500 -1	>16	8	16	16	≤0.5	>32	4	16	16	>32	≤0.063	≤0.063	>128
G500 -2	>16	16	>32	>32	≤0.5	>32	8	16	8	>32	≤0.063	≤0.063	>128
G500 -3	>16	8	16	32	≤0.5	>32	8	16	16	>32	≤0.063	≤0.063	>128
G500 -4	>16	8	32	>32	≤0.5	>32	8	64	16	>32	≤0.063	≤0.063	>128
102/04 K2	>16	>16	>32	>32	≤0.5	>32	>32	>64	8	>32	≤0.063	≤0.063	>128
G200 -1	>16	>16	>32	>32	≤0.5	>32	>32	>64	<4	>32	≤0.063	≤0.063	>128
G200 -2	>16	>16	>32	>32	≤0.5	>32	>32	>64	<4	>32	≤0.063	≤0.063	>128
G200 -5	>16	>16	>32	>32	≤0.5	>32	>32	64	<4	>32	≤0.063	≤0.063	>128
G200 -8	>16	>16	>32	>32	≤0.5	>32	>32	>64	<4	>32	≤0.063	≤0.063	>128
G500 -1	>16	4	4	32	≤0.5	>32	4	8	<4	>32	≤0.063	≤0.063	>128
G500 -2	>16	>16	>32	>32	≤0.5	>32	>32	>64	<4	>32	≤0.063	≤0.063	>128
G500 -3	>16	>16	>32	>32	≤0.5	>32	>32	>64	<4	>32	≤0.063	≤0.063	>128
G500 -4	>16	16	32	>32	≤0.5	>32	16	32	<4	>32	≤0.063	≤0.063	>128
252/09 K3	>16	16	>32	>32	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G200 -1	>16	16	>32	>32	4	4	4	8	16	8	≤0.063	≤0.063	≤4
G200 -2	>16	16	>32	>32	1	4	4	8	16	8	≤0.063	≤0.063	≤4
G200 -3	>16	16	32	>32	1	4	4	≤4	8	8	≤0.063	≤0.063	≤4
G200 -4	>16	4	8	>32	2	≤2	4	8	16	8	≤0.063	≤0.063	≤4
G500 -1	>16	2	8	32	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G500 -2	>16	4	8	16	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G500 -3	>16	2	16	32	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G500 -4	>16	16	>32	>32	4	8	4	8	16	8	≤0.063	≤0.063	≤4
104/15 K3	>16	>16	32	16	8	8	4	8	8	>32	≤0.063	≤0.063	≤4
G200 -1	>16	>16	32	16	>8	16	<2	<4	16	>32	≤0.063	≤0.063	≤4
G200 -2	>16	>16	32	8	>8	8	8	8	16	>32	≤0.063	≤0.063	≤4
G200 -3	>16	>16	32	8	>8	8	4	<4	16	>32	≤0.063	≤0.063	≤4
G200 -4	>16	>16	>32	32	>8	8	<2	<4	16	>32	≤0.063	≤0.063	≤4
G500 -1	>16	>16	32	16	>8	4	≤2	≤4	8	>32	≤0.063	≤0.063	≤4
G500 -2	>16	>16	>32	8	>8	8	4	≤4	8	>32	≤0.063	≤0.063	≤4
G500 -3	>16	>16	32	8	>8	16	≤2	≤4	16	>32	≤0.063	≤0.063	≤4
G500 -4	>16	>16	32	8	>8	8	≤2	≤4	16	>32	≤0.063	≤0.063	≤4

Isolate	AMP	CTA	CTZ	CXI ¹	GEN	KAN ¹	AMI	STR ¹	NAL ¹	CMP	CIP	MER	TRS
RS165 K1	>16	>16	≤2	2-16	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G200 -1	>16	16	≤2	4	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G200 -2	>16	8	≤2	8	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G200 -3	>16	16	≤2	4	≤0.5	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G200 -4	>16	16	≤2	4	≤0.5	≤2	≤2	≤4	16	8	≤0.063	≤0.063	≤4
G500 -1	>16	>16	<2	8	≤0.5	4	4	<4	8	8	≤0.063	≤0.063	≤4
G500 -2	>16	>16	4	4	≤0.5	<2	<2	<4	16	8	≤0.063	≤0.063	≤4
G500 -3	>16	>16	<2	8	2	4	<2	8	8	8	≤0.063	≤0.063	≤4
G500 -4	>16	>16	<2	8	2	4	4	<4	8	8	≤0.063	≤0.063	≤4
151/09 K2	>16	>16	>32	>32	4	>32	>32	>64	8	8	≤0.063	1	>128
G200 -1	>16	>16	>32	>32	1	32	32	>64	16	8	≤0.063	2	>128
G200 -2	>16	>16	>32	>32	4	32	16	>64	16	8	≤0.063	4	>128
G200 -3	>16	>16	>32	>32	8	32	>32	>64	16	8	≤0.063	4	>128
G200 -4	>16	>16	>32	>32	4	32	32	>64	16	8	≤0.063	4	>128
G500 -1	>16	>16	>32	>32	1	>32	4	>64	8	8	≤0.063	0.5	>128
G500 -2	>16	>16	>32	>32	<0.5	>32	4	4	8	8	≤0.063	0.25	>128
G500 -3	>16	>16	32	>32	<0.5	>32	<2	16	<4	<4	≤0.063	0.125	>128
G500 -4	>16	>16	32	>32	1	>32	16	>64	16	8	≤0.063	1	>128
346/12 K2	>16	≤1	≤2	2-16	≤0.5	4	≤2	8	8	8	≤0.063	0.25	≤4
G200 -1	>16	≤1	≤2	4	1	≤2	≤2	≤4	8	8	≤0.063	≤0.063	≤4
G200 -2	>16	<1	<2	8	≤0.5	<2	≤2	<4	8	8	≤0.063	0.125	≤4
G200 -3	>16	<1	<2	4	≤0.5	<2	≤2	<4	16	8	≤0.063	0.25	≤4
G200 -4	>16	<1	<2	4	≤0.5	2	≤2	<4	16	8	≤0.063	0.25	≤4
G500 -1	>16	<1	<2	4	≤0.5	<2	≤2	<4	8	8	≤0.063	0.25	≤4
G500 -2	>16	<1	<2	8	≤0.5	<2	≤2	<4	16	8	≤0.063	0.125	≤4
G500 -3	>16	<1	<2	4	≤0.5	<2	≤2	<4	8	8	≤0.063	0.125	<4
G500 -4	>16	<1	<2	8	<0.5	<2	<2	<4	8	8	≤0.063	≤0.063	<4

Legend: All abbreviations according to EUCAST¹ for these substances only ECOFF values are available (https://www.eucast.org/mic_distributions_and_ecoffs/)-https://www.eucast.org/fileadmin/src/media/PDFs/EUCAST_files/Disk_test_documents/Disk_abbreviations/EUCAST_system_for_antimicrobial_abbreviations.pdf

Supplementary Table S4: Results of *de novo* Assembly of the reads of isolates 102/04 K1 G₀ und K2 G₀.

Heading	102/04K1 ¹	p102/04K1 ¹	102/04K2 ¹	p102/04K2 ¹	102/04K1 G ₅₀₀₋₁	p102/04K1 G ₅₀₀₋₁
Size	4,687,587	164,040	4,685,473	164,040	4,690,582	165,381
GC content	50.8 %	52.3 %	50.8 %	52.3 %	50.8 %	52.8 %
CDS	4,495	206	4,493	206	4,498	207
rRNA	22	-	22	-	22	-
tRNA	86	-	86	-	86	-

Legend: ¹ generation G₀.

Supplementary Table S5: Results of read mapping of illumina data for evolved transconjugants of RS165 K1 onto the reference sequence of 102/04 K1 G₀.

Heading	RS165K1 G ₀	pRS165K1 G ₀	RS165K1 G ₂₀₀₋₁	pRS165K1 G ₂₀₀₋₁	RS165K1 G ₂₀₀₋₃	pRS165K1 G ₂₀₀₋₃	RS165K1 G ₅₀₀₋₃	pRS165K1 G ₅₀₀₋₃
Size	4,682,662	70,269	4,686,841	70,269	4,687,417	70,269	4,688,104	70,269
GC content	50.8 %	52.3 %	50.8 %	52.3 %	50.8 %	52.3 %	50.8 %	52.3 %
CDS	4,508	96	4,511	96	4,512	96	4,512	96
rRNA	22	-	22	-	22	-	22	-
tRNA	86	-	86	-	86	-	86	-

Supplementary Table S6: Used PCR primer pairs in this study.

Primer	T _a [°C]	nM Multiplex	Product size [bp]	Sequence 5'-->3'	Reference
blaVIM fwd	55		216	AGTGGTGAGTATCCGACAG	1
blaVIM rev				ATGAAAGTGCCTGGAGAC	
ChuA fwd	55	200	279	GACGAACCAACGGTCAGGAT	2
ChuA rev				TGCCGCCAGTACCAAAGACA	
CITM fwd	60		462	TGGCCAGAAGTACAGGCAAAA	3
CITM rev				TTTCTCCTGAACGTGGCTGGC	
CTX-M universal fwd	55	267	551	CGCTTTGCGATGTGCAG	5
CTX-M universal rev				ACCGCGATATCGTTGGT	
CTX-M-9 MP fwd	55	200	356	GCAGTACAGCGACAATACCG	5
CTX-M-9 MP rev				TATCATTGGTGGTGCCGTAG	
gndbis fwd	59		300	ATACCGACGACGCCGATCTG	6
rfbO25b rev				TGCTATTCATTATGCGCAGC	
gndbis fwd	59		450	ATACCGACGACGCCGATCTG	6
rfbO16 rev				GGATCATTTATGCTGGTACG	
KPCu fwd	58		533	CAGTCATTCAAGGGCTTTC	5
KPCu rev				AGTCATTTGCCGTGCCATAC	
OXA-48 fwd	58		555	AAATCACAGGGCGTAGTTGTG	5
OXA-48 rev				GACCCACCAGCCAATCTTAG	
SHV MP1 fwd	55	267	750	TTCGCCTGTGTATTATCTCC	5
SHV MP1 rev				TCCGCTCTGCTTTGTTATTC	
TEM universal fwd	55	535	851	ATGAGTATTCAACATTTCGG	5
TEM universal rev				TTAATCAGTGAGGCACCTAT	
TspE4C fwd	55	267	152	GAGTAATGTCGGGGCATTCA	2
TspE4C rev				CGCGCCAACAAAGTATTACG	
Yja fwd	55	400	211	TGAAGTGTCAGGAGACGCTG	2
Yja rev				ATGGAGAATGCGTTTCCTCAAC	

References: (1) Miriagou V, Tzelepi E, Gianneli D, Tzouvelekis LS. *Escherichia coli* with a self-transferable, multiresistant plasmid coding for metallo-beta-lactamase VIM-1. *Antimicrob Agents Chemother.* 2003;47(1):395-7; (2) Clermont O, Bonacorsi S, Bingen E. Rapid and simple determination of the *Escherichia coli* phylogenetic group. *Appl Environ Microbiol.* 2000;66(8):4555; (3) Perez-Perez FJ, Hanson ND. Detection of plasmid-mediated AmpC beta-lactamase genes in clinical isolates by using multiplex PCR. *J Clin Microbiol.* 2002;40(6):2153-62; (5) Grobner S, Linke D, Schutz W, Fladerer C, Madlung J, Autenrieth IB, et al. Emergence of carbapenem-non-susceptible extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* isolates at the university hospital of Tübingen, Germany. *J Med Microbiol.* 2009;58(Pt 7):912-22; (6) Johnson JR, Clermont O, Johnston B, Clabots C, Tchesnokova V, Sokurenko E, et al. Rapid and specific detection, molecular epidemiology, and experimental virulence of the O16 subgroup within *Escherichia coli* sequence type 131. *J Clin Microbiol.* 2014;52(5):1358-65.

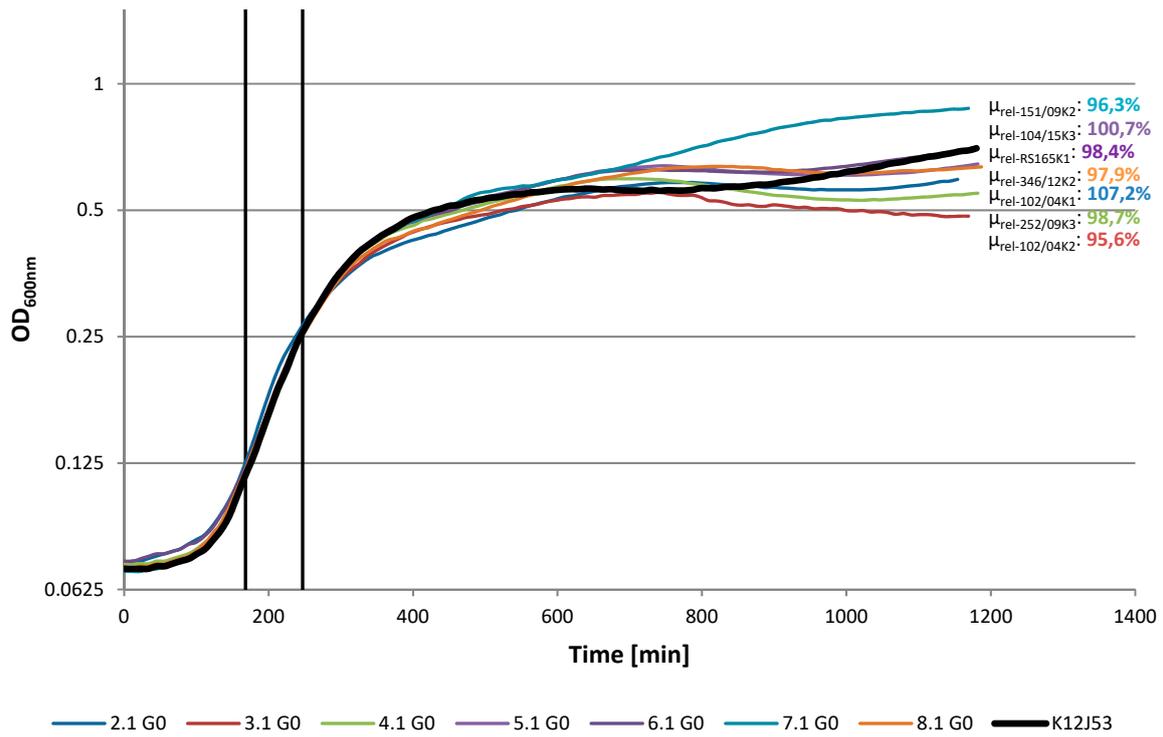


Figure S1. Growth curves of seven selected transconjugants with beta-lactamase gene carrying plasmids vs. the plasmid-free recipient *E. coli* J53 Azi^r. The black vertical lines frame the area of exponential growth used to determine the growth rates.