

Supplementary material 1: Isolated Enterobacteriaceae with resistance against 3rd generation methoxyimino cephalosporins or carbapenems, nonfermentative Gram-negative rod-shaped bacteria, and methicillin-resistant *Staphylococcus aureus* (MRSA) from Libyan and Syrian patients.

Isolates from Libyan patients								
Enterobacteriaceae with resistance against 3 rd generation methoxyimino cephalosporins or carbapenems								
Patient I.D.	Sample I.D.	Species	Isolation site	Day of isolation	Nosocomial	In rep-PCR 95% identical with	In NGS-based MLST ^a /ANI ^b identical with	Match NGS vs. rep-PCR
HBG-L1	2	<i>C. freundii</i>	Rectum	Day 2	No			
HBG-L1	3	<i>E. cloacae</i>	Rectum	Day 10	Yes	14 (WEST-L3), 48 (WEST-S6), 54 (WEST-S6)	14 (WEST-L3) ^{a,b}	14 (WEST-L3)
HBG-L1	4	<i>E. coli</i>	Rectum	Day 10	Yes			
HBG-L1	6	<i>E. coli</i>	Colostomy	Day 22	Yes		33 (WEST-S2) ^(b)	
HBG-L2	8	<i>K. pneumoniae</i>	Inguinal skin	Day 1	No		18 (HBG-L4) ^{a,b} , 20 (room 4 HBG-2) ^{a,b} , 26 (room 4 HBG- 2) ^{(a),(b)}	
HBG-L2	10	<i>E. cloacae</i>	Inguinal skin	Day 1	No	48 (WEST-S6), 54 (WEST-S6), 77 (HBG-S4)		

HBG-L2	12	<i>K. pneumoniae</i>	Inguinal skin	Day 10	Yes			
HBG-L3	16	<i>K. pneumoniae</i>	Inguinal skin	Day 1	No	27 (room 1 HBG-2), 28 (room 3 HBG-2)	27 (room 1 HBG-2) ^{a,b} , 28 (room 3 HBG-2) ^{a,b}	27 (room 1 HBG-2), 28 (room 3 HBG-2)
HBG-L3	17	<i>E. coli</i>	Perineal skin	Day 1	No		None	
HBG-L4	18	<i>K. pneumoniae</i>	Inguinal skin	Day 16	Yes	20 (room 4 HBG-2), 26 (room 4 HBG-2)	8 (HBG-L2) ^{a,b} , 20 (room 4 HBG-2) ^{a,b} , 26 (room 4 HBG-2) ^{(a),(b)}	20 (room 4 HBG-2), 26 (room 4 HBG-2)
WEST-L2	13	<i>K. pneumoniae</i>	Inguinal skin	Day 1	No		None	
West-L3	14	<i>E. cloacae</i>	External fixator of the left thigh	Day 1	No	3 (HBG-L1), 48 (WEST-S6), 54 (WEST-S6)	3 (HBG-L1) ^{a,b}	3 (HBG-L1)
West-L4	15	<i>K. pneumoniae</i>	Inguinal skin	Day 1	No			
Nonfermentative rod-shaped bacteria								
Patient I.D.	Sample I.D.	Species	Isolation site	Day of isolation	Nosocomial	In rep-PCR 95% identical with	In NGS-based MLST ^a /ANI ^b identical with	Match NGS vs. rep-PCR
HBG-L1	1	<i>A. baumannii</i> complex	Inguinal skin	2	no			

HBG-L1	5	<i>P. aeruginosa</i>	Perineal skin	16	yes			
HBG-L2	9	<i>A. baumannii</i> complex	Inguinal skin	1	no			
HBG-L2	11	<i>P. aeruginosa</i>	Orthopedic wound at the left hand	1	no		7 (WEST-L1) ^{a,(b)}	
WEST-L1	7	<i>P. aeruginosa</i>	Wound at the dorsal side of the left thigh	1	no		11 (HBG-L2) ^{a,(b)}	
Isolates from Syrian patients								
Enterobacteriaceae with resistance against 3 rd generation methoxyimino cephalosporins or carbapenems								
Patient I.D.	Sample I.D.	Species	Isolation site	Day of isolation	Nosocomial	In rep-PCR 95% identical with	In NGS-based MLST ^a /ANI ^b identical with	Match NGS vs. rep-PCR
HBG-S1	57	<i>E. cloacae</i>	Deep wound at the right heel	Day 2	No			
HBG-S1	75	<i>E. coli</i>	Perineal skin	Day 9	Yes			
HBG-S2	59	<i>K. pneumoniae</i>	Perineal skin	Day 2	No		78 (HBG-S4) ^{a,b}	
HBG-S2	60	<i>E. coli</i>	Perineal skin	Day 2	No	37 (WEST-S4), 61 (HBG-S3), 66 (HBG-S4),	37 (WEST-S4) ^{a,(b)} , 61 (HBG-S3) ^{a,(b)} , 72 (HBG-	37 (WEST-S4), 61 (HBG-S3), 72 (HBG-S6)

						72 (HBG-S6)	S6) ^{(a),(b)}	
HBG-S3	61	<i>E. coli</i>	Perineal skin	Day 2	No	37 (WEST-S4), 60 (HBG-S2), 66 (HBG-S4), 72 (HBG-S6)	37 (WEST-S4) ^{a,(b)} , 60 (HBG-S2) ^{a,(b)} , 72 (HBG-S6) ^{(a),(b)}	37 (WEST-S4), 60 (HBG-S2), 72 (HBG-S6)
HBG-S4	63	<i>E. coli</i>	Perineal skin	Day 2	No			
HBG-S4	65	<i>C. freundii</i>	Perineal skin	Day 2	No			
HBG-S4	66	<i>E. coli</i>	Deep wound at the right gluteal region	Day 2	No	37 (WEST-S4), 60 (HBG-S2), 61 (HBG-S3), 72 (HBG-S6)		
HBG-S4	76	<i>E. coli</i>	Catheter urine	Day 30	yes			
HBG-S4	77	<i>E. cloacae</i>	Perineal skin	Day 16	Yes	10 (HBG-L2), 54 (WEST-S6)	54 (WEST-S6) ^{a,(b)}	54 (WEST-S6)
HBG-S4	78	<i>K. pneumoniae</i>	Superficial wound at the groin	Day 32	Yes		59 (HBG-S2) ^{a,b}	
HBG-S5	68	<i>E. coli</i>	Perineal skin	Day 2	no		51 (WEST-S6) ^{a,(b)}	
HBG-S5	69	<i>Proteus mirabilis</i>	Perineal skin	Day 2	no			

HBG-S5	70	<i>E. cloacae</i>	Deep wound at the upper side of a fixator	Day 2	no			
HBG-S5	71	<i>K. pneumoniae</i>	Perineal skin	Day 9	Yes			
HBG-S6	72	<i>E. coli</i>	Perineal skin	Day 2	No	37 (WEST-S4), 60 (HBG-S2), 61 (HBG-S3), 66 (HBG-S4)	37 (WEST-S4) ^{(a),b} , 60 (HBG-S2) ^{(a),b} , 61 (HBG-S3) ^{(a),b}	37 (WEST-S4), 60 (HBG-S2), 61 (HBG-S3)
HBG-S7	74	<i>E. coli</i>	Perineal skin	Day 9	Yes			
WEST-S1	32	<i>R. planticola</i>	Anus	Day 15	yes	52 (WEST-S6)	52 (West-S6) ^b	52 (WEST-S6)
WEST-S2	33	<i>E. coli</i>	Wound	Day 51	yes		6 (HBG-L1) ^(b)	
WEST-S2	38	<i>E. coli</i>	Anus	Day 1	no			
WEST-S2	39	<i>P. mirabilis</i>	Wound	Day 3	no			
WEST-S2	41	<i>M. morgani</i>	Wound	Day 69	yes			
WEST-S3	36	<i>M. morgani</i>	Wound	Day 1	no			
WEST-S4	37	<i>E. coli</i>	Wound	Day 1	No	60 (HBG-S2), 61 (HBG-S3), 66 (HBG-S4), 72 (HBG-S6)	60 (HBG-S2) ^{a,(b)} , 61 (HBG-S3) ^{a,(b)} , 72 (HBG-S6) ^{(a),(b)}	60 (HBG-S2), 61 (HBG-S3), 72 (HBG-S6)
WEST-S5	42	<i>K. pneumoniae</i>	Wound	Day 8	Yes			

WEST-S5	45	<i>C. freundii</i>	Wound	Day 1	no	55 (West-S7)	55 (West-S7) ^b	55 (West-S7)
WEST-S6	48	<i>E. cloacae</i>	Wound	Day 4	Yes	3 (HBG-L1), 10 (HBG-L2), 14 (WEST-L3), 54 (WEST-S6)		
WEST-S6	51	<i>E. coli</i>	Wound	Day 1	No		68 (HBG-S5) ^(b)	
WEST-S6	52	<i>R. planticola</i>	Wound	Day 1	No	32 (West-S1)	32 (West-S1) ^b	32 (West-S1)
WEST-S6	54	<i>E. cloacae</i>	Skin	Day 1	no	3 (HBG-L1), 10 (HBG-L2), 14 (WEST-L3), 48 (WEST-S6), 77 (HBG-S4)	77 (HBG-S4) ^{a,(b)}	77 (HBG-S4)
WEST-S7	55	<i>C. freundii</i>	Wound	Day 1	No	45 (WEST-S5)	45 (WEST-S5) ^b	45 (WEST-S5)
Nonfermentative rod-shaped bacteria								
Patient I.D.	Sample I.D.	Species	Isolation site	Day of isolation	Nosocomial	In rep-PCR 95% identical with	In NGS-based MLST ^a /ANI ^b identical with	Match NGS vs. rep-PCR
HBG-S1	56	<i>A. baumannii</i> complex	Deep wound at the right heel	Day 2	no		31 (WEST-S1) ^b , 50 (West-S6) ^b , 62 (HBG-S2) ^(b) , 64 (HBG-S4) ^b , 73 (HBG-S7) ^b	

HBG-S2	62	<i>A. baumannii</i> complex	Deep wound at the upper pin of the fixator at the thigh	Day 2	no	31 (WEST-S1), 50 (WEST-S6), 64 (HBG-S4), 73 (HBG-S7)	31 (WEST- S1) ^(b) , 50 (West-S6) ^(b) , 56 (HBG-S1) ^(b) , 64 (HBG-S4) ^(b) , 73 (HBG-S7) ^(b)	31 (WEST-S1), 50 (WEST-S6), 64 (HBG-S4), 73 (HBG-S7)
HBG-S4	64	<i>A. baumannii</i> complex	Perineal skin	Day 2	no	31 (WEST-S1), 50 (WEST-S6), 62 (HBG-S2), 73 (HBG-S7)	31 (WEST- S1) ^{a,b} , 50 (West-S6) ^{a,b} , 56 (HBG-S1) ^b , 62 (HBG-S2) ^(b) , 73 (HBG-S7) ^{a,b}	31 (WEST-S1), 50 (West-S6), 62 (HBG-S2), 73 (HBG-S7)
HBG-S7	73	<i>A. baumannii</i> complex	Pharynx	Day 9	yes	31 (WEST-S1), 50 (WEST-S6), 62 (HBG-S2), 64 (HBG-S4)	31 (WEST- S1) ^{a,b} , 50 (West-S6) ^{a,b} , 56 (HBG-S1) ^b , 62 (HBG-S2) ^(b) , 64 (HBG-S4) ^{a,b}	31 (WEST-S1), 50 (West-S6), 62 (HBG-S2), 64 (HBG-S4)
WEST-S1	31	<i>A. baumannii</i> complex	Anus	Day 21	yes	50 (WEST-S6), 62 (HBG-S2), 64 (HBG-S4), 73 (HBG-S7)	50 (West-S6) ^{a,b} , 56 (HBG-S1) ^b , 62 (HBG-S2) ^(b) , 64 (HBG-S4) ^{a,b} , 73 (HBG-S7) ^{a,b}	50 (West-S6), 62 (HBG-S2), 64 (HBG-S4), 73 (HBG-S7)
WEST-S2	40	<i>P. aeruginosa</i>	Wound	Day 3	no			
WEST-S5	44	<i>A.</i>	Wound	Day 2	no			

		<i>radioresistens</i>						
WEST-S5	46	<i>S. maltophilia</i>	Wound	Day 11	yes			
WEST-S6	47	<i>A. baumannii</i> complex	Wound	Day 4	yes			
WEST-S6	49	<i>A. baumannii</i> complex	Groin	Day 1	no			
WEST-S6	50	<i>A. baumannii</i> complex	Wound	Day 1	no	31 (WEST-S1), 62 (HBG-S2), 64 (HBG-S4), 73 (HBG-S7)	31 (WEST-S1) ^{a,b} , 56 (HBG-S1) ^b , 62 (HBG-S2) ^(b) , 64 (HBG-S4) ^{a,b} , 73 (HBG-S7) ^{a,b}	31 (WEST-S1), 62 (HBG-S2), 64 (HBG-S4), 73 (HBG-S7)
Methicillin-resistant <i>Staphylococcus aureus</i> (MRSA)								
Patient I.D.	Sample I.D.	Species	Isolation site	Day of isolation	Nosocomial	In spa-typing identical with	spa type	MLST type (according to BURP algorithm)
HBG-S1	58	<i>Staphylococcus aureus</i> (MRSA)	Deep wound at the left elbow	Day 2	no		t274	n.a.
HBG-S5	67	<i>Staphylococcus aureus</i> (MRSA)	Nasal vestibulum	Day 2	no	53 (WEST-S6)	t223	ST-22
WEST-S2	34	<i>Staphylococcus</i>	Groin	Day 23	yes		t026	ST-45, ST-47

		<i>aureus</i> (MRSA)						
WEST-S2	35	<i>Staphylococcus aureus</i> (MRSA)	Wound	Day 18	yes	43 (WEST-S5)	t376	n.a.
WEST-S5	43	<i>Staphylococcus aureus</i> (MRSA)	Groin	Day 64	yes	35 (WEST-S2)	t376	n.a.
WEST-S6	53	<i>Staphylococcus aureus</i> (MRSA)	Skin	Day 1	no	67 (HBG-S5)	t223	ST-22

^a Completely identical based on MLST, ^(a) identical based on MLST but not all markers complete due to lack of coverage.

^b Identical based on ANI ($\geq 99.9\%$), ^(b) highly similar based on ANI ($\geq 99.5\%$, $< 99.9\%$).

Supplementary material 2: Isolated Enterobacteriaceae with resistance against 3rd generation methoxyimino cephalosporins or carbapenems, and nonfermentative Gram-negative rod-shaped bacteria, from the environment of Libyan patients at the Bundeswehr Hospital of Hamburg.

Isolates from the environment of Libyan patients at the Bundeswehr Hospital of Hamburg								
Enterobacteriaceae with resistance against 3 rd generation methoxyimino cephalosporins or carbapenems								
Ward	Room number	Sample I.D.	Species	Isolation site	Day of isolation	In rep-PCR 95% identical with	In NGS-based MLST ^a /ANI ^b identical with	NGS-based MLST type
HBG-2	Room 4	20	<i>K. pneumoniae</i>	hands	Day 11	18 (HBG-L4), 26 (room 4 HBG-2)	8 (HBG-L2) ^{a,b} , 18 (HBG-L4) ^{a,b} , 26 (room 4 HBG-2) ^{(a),(b)}	18 (HBG-L4), 26 (room 4 HBG-2) ^{(a),(b)}
HBG-2	Room 3	21	<i>K. pneumoniae</i>	hands	Day 11		None	
HBG-2	Room 4	26	<i>K. pneumoniae</i>	handle of a bag	Day 11	18 (HBG-L4), 20 (room 4 HBG-2)	8 (HBG-L2) ^{(a),b} , 18 (HBG-L4) ^{(a),b} , 20 (room 4 HBG-2) ^{(a),b}	18 (HBG-L4), 20 (room 4 HBG-2)
HBG-2	Room 1	27	<i>K. pneumoniae</i>	hands and beard	Day 11	16 (HBG-L3), 28 (room 3 HBG-2)	16 (HBG-L3) ^{a,b} , 28 (room 3 HBG-2) ^{a,b}	16 (HBG-L3), 28 (room 3 HBG-2)
HBG-2	Room 3	28	<i>K. pneumoniae</i>	walking frame	Day 11	16 (HBG-L3), 27 (room 1 HBG-2),	16 (HBG-L3) ^{a,b} , 27 (room 1 HBG-2) ^{a,b}	16 (HBG-L3), 27 (room 1 HBG-2),

Nonfermentative rod-shaped bacteria								
Ward	Room number	Sample I.D.	Species	Isolation site	Day of isolation	In rep-PCR 95% identical with	In NGS-based MLST ^a /ANI ^b identical with	NGS-based MLST type
HBG-2	Room 3	19	<i>P. aeruginosa</i>	walker	Day 11		29 (room 3 HBG-2) ^b	
HBG-2	Room 3	29	<i>P. aeruginosa</i>	hands	Day 11		19 (room 3 HBG-2) ^b	
HBG-1-ITS	Room 1	30	<i>P. putida</i>	sink (spout)	Day 11		None	

^a Completely identical based on MLST, ^(a) identical based on MLST but not all markers found/complete due to lack of coverage.

^b Identical based on ANI ($\geq 99.9\%$), ^(b) highly similar based ANI ($\geq 99.5\%$, $< 99.9\%$).

Supplementary material 3: Resistance of isolated Enterobacteriaceae with resistance against 3rd generation methoxyimino cephalosporins (n=49) and/or carbapenems (n=6/49) as identified by VITEK-II.

Enterobacteriaceae from Libyan patients at the Bundeswehr Hospitals of Hamburg and Westerstede (n=13)											
	Piperacillin / Tazobactam	Ceftazidime	Imipenem	Meropenem	Gentamicin	Ciprofloxacin	Levofloxacin	Tigecyclin	Fosfomycin	Nitrofurantoin	Cotrimoxazole
R	8	10		1	9	10	10	1		5	9
I	5	3	2	1		1		7		4	
S	0		11	11	4	2	3	5	13	4	4
Enterobacteriaceae from the environment of Libyan patients at the Bundeswehr Hospital of Hamburg (n=5)											
	Piperacillin / Tazobactam	Ceftazidime	Imipenem	Meropenem	Gentamicin	Ciprofloxacin	Levofloxacin	Tigecyclin	Fosfomycin	Nitrofurantoin	Cotrimoxazole
R	4	5	1		5	5	5	2	1	2	2
I	1		1	2				2		2	
S	0		3	3				1	4	1	3
Enterobacteriaceae from Syrian patients at the Bundeswehr Hospitals of Hamburg and Westerstede (n=31)											
	Piperacillin / Tazobactam	Ceftazidime	Imipenem	Meropenem	Gentamicin	Ciprofloxacin	Levofloxacin	Tigecyclin	Fosfomycin	Nitrofurantoin	Cotrimoxazole

R	9	25	2	2	16	18	17	4	7	7	18
I	21	6				6		5			
S	1		29	29	15	7	14	22	24	24	13

Supplementary material 4: Resistance of isolated *Acinetobacter baumannii* complex as identified by VITEK-II.

<i>Acinetobacter baumannii</i> complex from Libyan patients at the Bundeswehr Hospitals of Hamburg and Westerstede (n=2)											
	Piperacillin	Ceftazidime	Cefepime	Aztreonam	Imipenem	Meropenem	Gentamicin	Tobramycin	Ciprofloxacin	Colistin	Cotrimoxazole
R	2	2	2	2	1	1	2	2	2		2
I					1	1					
S										2	
<i>Acinetobacter baumannii</i> complex from Syrian patients at the Bundeswehr Hospitals of Hamburg and Westerstede (n=8)											
	Piperacillin	Ceftazidime	Cefepime	Aztreonam	Imipenem	Meropenem	Gentamicin	Tobramycin	Ciprofloxacin	Colistin	Cotrimoxazole
R	8	8	8	8	6	6	7	7	8	0	5
I					2	2					
S							1	1		8	3

S		1	1		1	1	1	1	1	1	1	1
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Supplementary material 6: Resistance of isolated MRSA as identified by VITEK-II.

MRSA isolates from Syria																	
	Levofloxacin	Moxifloxacin	Gentamicin	Clindamycin	Erythromycin	Cotrimoxazole	Tetracycline	Tigecycline	Teicoplanin	Vancomycin	Linezolid	Daptomycin	Fosfomycin	Fusidic acid	Rifampicin	Mupirocin	Nitrofurantoin
R				2	2	1								3			
I																	
S	6	6	6	4	4	5	6	6	6	6	6	6	6	3	6	6	6

Supplementary material 7: Detection of ESBL genes in Enterobacteriaceae that tested positive or not determined for ESBL by ABCD testing.

	<i>bla</i> _{TEM}	<i>bla</i> _{SHV}	<i>bla</i> _{CTX-M} group I	<i>bla</i> _{CTX-M} group II	<i>bla</i> _{CTX-M} group III	<i>bla</i> _{CTX-M} group IV
Isolates from Libyan patients (n=13)	10 ^a (76.9%)	6 ^d (46.2%)	10 (76.9%)			1 (7.7%)
Isolates from the environment of Libyan patients at the Bundeswehr Hospital of Hamburg (n=5)	5 ^b (100%)	4 ^e (80%)	5 (100%)			
Isolates from Syrian patients (n=29)	15 ^c (51,7%)	5 ^f (17.2%)	26 (89.7%)			1 (3.4%)

^aDistribution of sequences: *bla*_{TEM-1} without exception. ^bDistribution of sequences: *bla*_{TEM-1} without exception. ^cDistribution of sequences: *bla*_{TEM-1} in 14 instances, not resolved due to different types with identical matching in 1 instance. ^dDistribution of sequences: *bla*_{SHV-12}, *bla*_{SHV-1}/*bla*_{SHV-28} (no further sequence discrimination possible), and *bla*_{SHV-33} in one instance each, insufficient discriminatory power in additional 3 instances. ^eDistribution of sequences: *bla*_{SHV-1}/*bla*_{SHV-1a} (no further sequence discrimination possible), *bla*_{SHV-11}, and *bla*_{SHV-33} in one instance each, insufficient discriminatory power in another instance; ^fDistribution of sequences: *bla*_{SHV-1} in two instances, *bla*_{SHV-12}/*bla*_{SHV-5} (no further sequence discrimination possible) and *bla*_{SHV-121}/*bla*_{SHV-136} (no further sequence discrimination possible) in one instance each, insufficient discriminatory power in another instance.

Supplementary material 8: Detection of carbapenemase genes in Enterobacteriaceae and nonfermentative, Gram-negative rod-shaped bacteria that did not test fully sensitive against carbapenems.

	<i>bla</i> _{NDM}	<i>bla</i> _{KPC}	<i>bla</i> _{BIC}	<i>bla</i> _{OXA48}	<i>bla</i> _{AIM}	<i>bla</i> _{GIM}	<i>bla</i> _{SIM}	<i>bla</i> _{DIM}	<i>bla</i> _{IMP}	<i>bla</i> _{VIM}	<i>bla</i> _{SPM}
Enterobacteriaceae from Libyan patients (n=2)				2x*							
<i>A. baumannii</i> complex from Libyan patients (n=2)											
Enterobacteriaceae from Syrian patients (n=2)			1°							1°	
<i>A. baumannii</i> complex from Syrian patients (n=8)											

*In 2 *K. pneumoniae* isolates. °In the same *E. cloacae* isolate.

Supplementary material 9: Resistance testing as determined by NGS with the ResFinder Software.

ID and species	Phenotypic resistance by Vitek II (acronyms of antibiotics that were not tested sensitive)	Genotypic detection of resistance genes by NGS with low coverage*	Phenotypic resistance without detected genotypic correlate	Genotypic resistance without detected phenotypic correlate
1 <i>Acinetobacter baumannii</i>	PRL, TZP, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP, COT	execution failed		
2 <i>Citrobacter freundii</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC	execution failed		
3 <i>Enterobacter cloacae</i> ssp. <i>cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC, NF, COT	<i>strA</i> , <i>aadB</i> , <i>aph(3')-Ic</i> , <i>bla_{OXA-23}</i> , <i>bla_{OXA-64}</i> , <i>bla_{ADC-25}</i> , <i>sul2</i>	fluoroquinolone, tetracycline, trimethoprim	none
4 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, COT	execution failed		
5 <i>Pseudomonas aeruginosa</i>	PRL, TZP, CAZ, ATM, CIP, COT	execution failed		
6. <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, COT	<i>aadA2</i> , <i>aadA1</i> , <i>bla_{SHV-12}</i> , <i>bla_{TEM-135}</i> , <i>sul3</i> , <i>sul2</i> , <i>dfrA12</i>	none	aminoglycoside
7 <i>Pseudomonas aeruginosa</i>	PRL, TZP, CAZ, FEP, ATM, AK, GC, NN, CIP, COT	<i>aph(3')-XV</i> , <i>strA</i> , <i>aph(3')-Ic</i> , <i>aacA4</i> , <i>strB</i> , <i>aadA6</i> , <i>aph(3')-IIb</i> , <i>bla_{PAO}</i> , <i>bla_{GES-1}</i> , <i>bla_{OXA-50}</i> , <i>aac(6')Ib-cr</i> , <i>fosA</i> , <i>catB7</i> , <i>sul1</i> , <i>tet(G)</i>	none	fosfomycin (not tested phenotypically)

8 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, NF	execution failed		
9 <i>Acinetobacter baumannii</i>	PRL, TZP, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP, COT	execution failed		
10 <i>Enterobacter cloacae</i> ssp. <i>cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC, NF, COT	execution failed		
11 <i>Pseudomonas</i> <i>aeruginosa</i>	PRL, TZP, CAZ, FEP, ATM, AK, GC, NN, CIP, COT	execution failed		
12 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, IPM, MEM, GC, CIP, LEV, NF, COT	execution failed		
13 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, IPM, MEM, GC, CIP, LEV, TGC, NF	execution failed		
14 <i>Enterobacter cloacae</i> ssp. <i>cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC, NF, COT	execution failed		
15 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, TGC, NF, COT	execution failed		
16 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ,	execution failed		

	GC, CIP, LEV, TGC, NF			
17 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, COT	execution failed		
18 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CN, CIP, LEV, TGC, NF, COT	execution failed		
19 <i>Pseudomonas aeruginosa</i>	ATM, COT	execution failed		
20 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, IMP, MEM, GC, CIP, LEV, TGC, NF, COT	execution failed		
21 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV	no sequence data		
26 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, IMP, MEM, GC, CIP, LEV, TGC, FOS, NF, COT	execution failed		
27 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC, NF	no sequence data		
28 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC, NF	execution failed		
29 <i>Pseudomonas aeruginosa</i>	ATM, COT	<i>aadB</i> , <i>aac(6')Ib-cr</i> , <i>aac(3)-IIa</i> , <i>strA</i> , <i>strB</i> , <i>aadA2</i> , <i>bla</i> _{TEM-1B} , <i>bla</i> _{CMY-4} , <i>bla</i> _{CTX-M}	trimethoprim	aminoglycoside, beta-lactam, fluoroquinolone, fosfomycin (not tested)

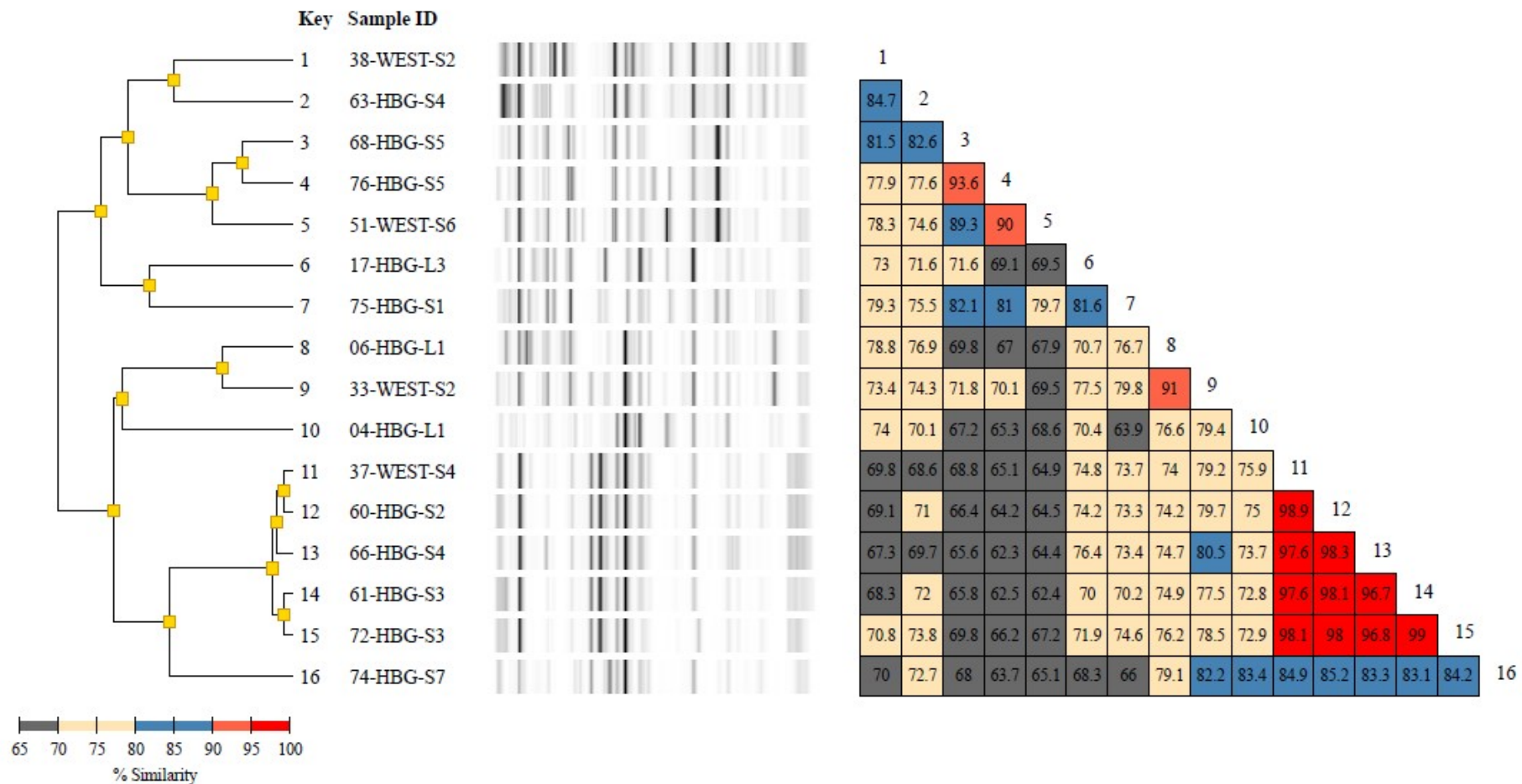
		<i>15, bla_{SHV-33}, bla_{OXA-1}, oqx_A, aac(6')_{lb-cr}, oqx_B, QnrA1, fosA, mph(E), msr(E), catB3, floR, sul1, sul2, tet(A)</i>		phenotypically)
30 <i>Pseudomonas putida</i>	PRL, MEM, CIP, LEV,	execution failed		
31 <i>Acinetobacter baumannii</i>	PRL, TZP, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP, COT	execution failed		
32 <i>Enterobacter cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, FOS, NF, COT	execution failed		
33 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ	execution failed		
36 <i>Morganella morganii</i> ssp. <i>morganii</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, TGC, FOS, NF, COT	<i>aac(3)-IId, aadA5, bla_{DHA-1}, mph(A), catA2, sul1, tet(B), dfrA17</i>	fosfomicin, fluoroquinolone, nitrofurantoin	none
37 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV	execution failed		
38 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, COT	execution failed		
39 <i>Proteus mirabilis</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, TGC, NF	execution failed		
40 <i>Pseudomonas</i>	PRL, PZP, ATM, COT	<i>aph(3')-IId, bla_{PAO}, bla_{OXA-50}, fosA, catB7</i>	sulfonamide, trimethoprim	aminoglycoside,

<i>aeruginosa</i>				fosfomycin
41 <i>Morganella morganii</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, TGC, FOS, NF, COT	<i>strA, aac(6')lb-cr, aph(3')-la, aadA5, strB, aadA1, bla_{TEM-1B}, bla_{DHA-1}, bla_{CTX-M-15}, bla_{OXA-1}, aac(6')lb-cr, catB3, catA2, catA1, sul1, sul2, tet(B), dfrA17, dfrA1</i>	fosfomycin	aminoglycoside
42 <i>Klebsiella pneumoniae</i> ssp. <i>pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, TGC, NF, COT	<i>aac(6')lb-cr, strB, strA, bla_{SHV-83}, bla_{CTX-M-15}, bla_{TEM-1B}, bla_{OXA-1}, aac(6')lb-cr, oqxB, oqxA, QnrB66, fosA, catB3, sul2, dfrA14</i>	tetracycline	aminoglycoside, fosfomycin
44 <i>Acinetobacter radioresistens</i>	no EUCAST breakpoints for VITEK available	<i>bla_{OXA-133}</i>		
45 <i>Citrobacter freundii</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, COT	execution failed		
46 <i>Stenotrophomonas maltophila</i>	no EUCAST breakpoints for VITEK available	<i>sph, blaL1</i>		
47 <i>Acinetobacter baumannii</i>	PRL, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP, COT	<i>aacA4, strB, strA, aadA2, aadB, aph(3')-VIa, bla_{ADC-25}, bla_{GES-11}, bla_{OXA-89}, aac(6')lb-cr, cmlA1, dfrA7</i>	sulphonamide	none
48 <i>Enterobacter cloacae</i> ssp. <i>cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, FOS, COT	<i>aac(6')lb-cr, strA, aadA1, strB, bla_{TEM-1B}, bla_{ACT-16}, bla_{CTX-M-15}, bla_{OXA-1}, aac(6')lb-cr, QnrB1, fosA, catB3, catA1, sul2, tet(A),</i>	none	tetracycline

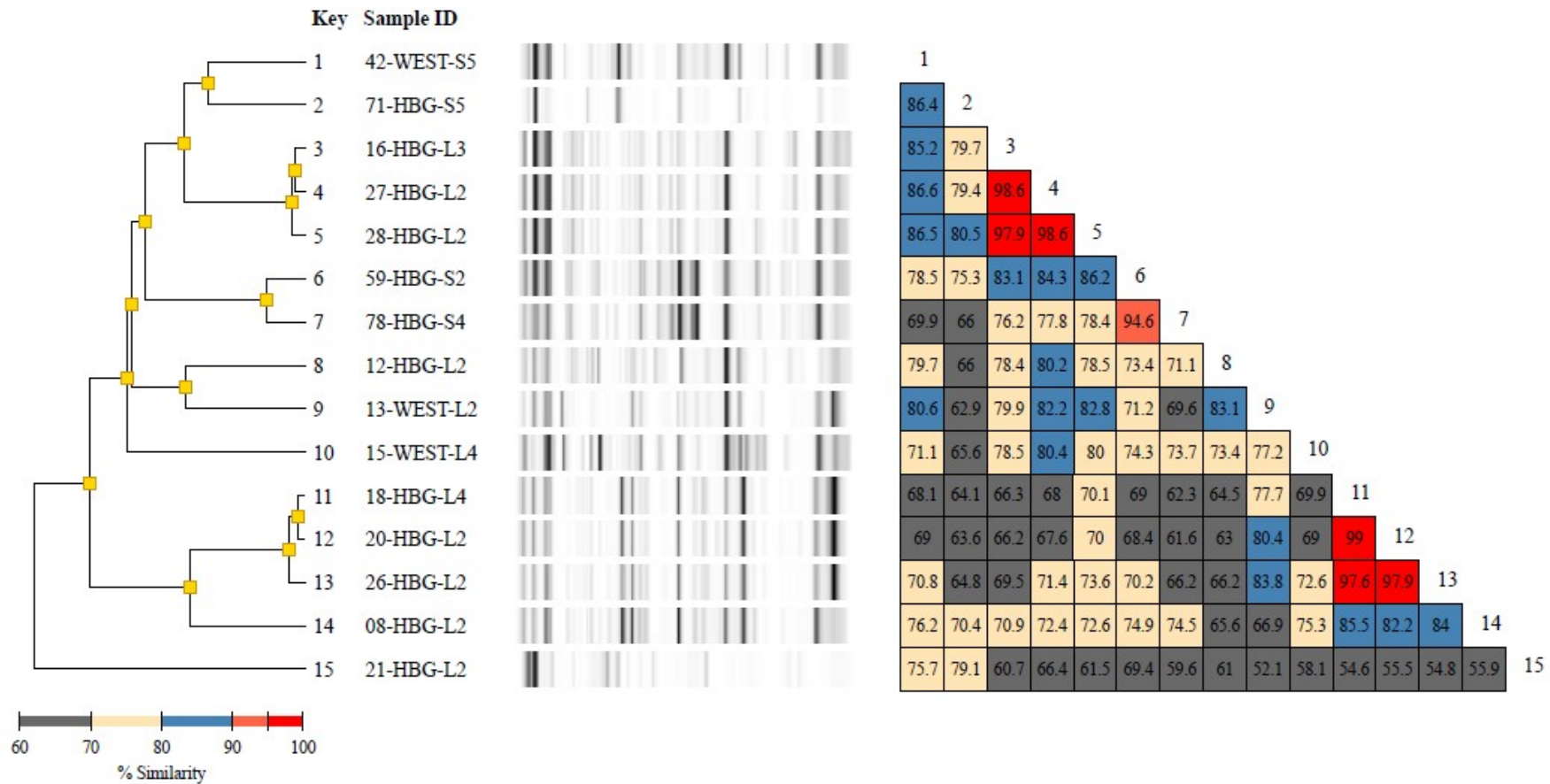
		<i>dfrA14</i>		
49 <i>Acinetobacter baumannii</i>	PRL, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP, COT	<i>aph(3')-VIa, aadB, bla_{ADC-25}, bla_{OXA-71}, tet(A)</i>	fluoroquinolone, sulphonamide, trimethoprim	tetracycline (not tested phenotypically)
50 <i>Acinetobacter baumannii</i>	PRL, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP, COT	<i>strB, aph(3')-Ic, strA, armA, bla_{ADC-25}, bla_{TEM-1D}, bla_{OXA-23}, bla_{OXA-66}, msr(E), mph(E), tet(B)</i>	sulphonamide, trimethoprim, fluoroquinolone	tetracycline (not tested phenotypically)
51 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, COT	<i>aac(3)-IId, strA, strB, bla_{TEM-1B}, bla_{CTX-M-15}, QnrS1, sul2, dfrA14</i>		
52 <i>Raoultella planticola</i>	AMP, SAM, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, FOS	<i>aac(3)-IIa, aac(6')Ib-cr, bla_{PLA1a}, bla_{CTX-M-15}, bla_{OXA-1}, fosA, catB3, tet(B)</i>	none	tetracycline
54 <i>Enterobacter cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, COT	execution failed		
55 <i>Citrobacter freundii</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, COT	<i>aac(6')-Ib-cr, aadA2, bla_{TEM}, bla_{CTX-M-15}, bla_{CMY-84}, bla_{OXA-1}, QnrS2, mph(A), catB3, ARR-3, sul1, dfrA12</i>		
56 <i>Acinetobacter baumannii</i>	PRL, CTX, CAZ, FEP, ATM, IPM, MEM, CIP	<i>aph(3')-Ic, strA, strB, bla_{OXA-23}, bla_{OXA-66}, bla_{ADC-25}, bla_{TEM-1D}, tet(B)</i>	fluoroquinolone	aminoglycoside, tetracycline (not tested phenotypically)
57 <i>Enterobacter cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, TGC, FOS, NF, COT	execution failed		

59 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC, NF	no resistance genes found		
60 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, COT	no resistance genes found		
61 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, COT	<i>aadA5, strB, strA, bla_{CTX-M-15}, bla_{TEM-1B}, mph(A), sul1, sul2, tet(A), dfrA17</i>	none	aminoglycoside, tetracycline
62 <i>Acinetobacter baumannii</i>	PRL, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP, COT	<i>aacA4, aadA2, aadB, strB, aph(3')-Ia, strA, bla_{OXA-23}, bla_{GES-11}, bla_{OXA-66}, bla_{OXA-117}, bla_{TEM-1D}, aac(6')Ib-cr, cmlA1, sul1, sul2, dfrA7</i>		
63 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP	no resistance genes found		
64 <i>Acinetobacter baumannii</i>	PRL, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP	execution failed		
65 <i>Citrobacter freundii</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ	<i>qnrS1</i>	beta-lactam	fluoroquinolone
66 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC	<i>aac(3')-IIa, aadA1, aadB, bla_{CTX-M-15}, mph(A), cmlA1, tet(B), dfrA17</i>	none	tetracycline
68 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV	<i>strA, strB, bla_{TEM-1B}</i>	fluoroquinolone	aminoglycoside
69 <i>Proteus mirabilis</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ,	execution failed		

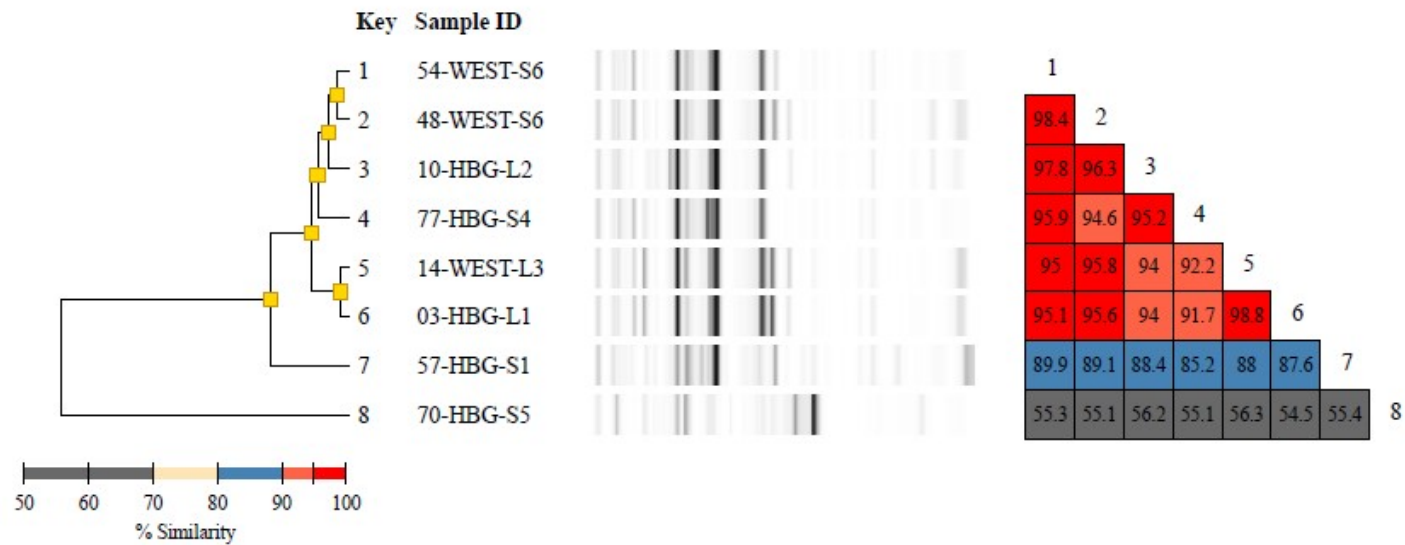
	GC, CIP, LEV, TGC, NF, COT			
70 <i>Enterobacter cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, IPM, MEM, CIP, LEV, TGC, FOS, COT	no resistance genes found		
71 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, CIP, LEV, NF	execution failed		
72 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, COT	execution failed		
73 <i>Acinetobacter baumannii</i>	PRL, CTX, CAZ, FEP, ATM, IPM, MEM, GC, NN, CIP	execution failed		
74 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ	execution failed		
75 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, COT	execution failed		
76 <i>Escherichia coli</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV	execution failed		
77 <i>Enterobacter cloacae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, NF, COT	execution failed		
78 <i>Klebsiella pneumoniae</i>	AMP, SAM, TZP, CXM, CXMAX, CPD, CTX, CAZ, GC, CIP, LEV, TGC, NF	execution failed		



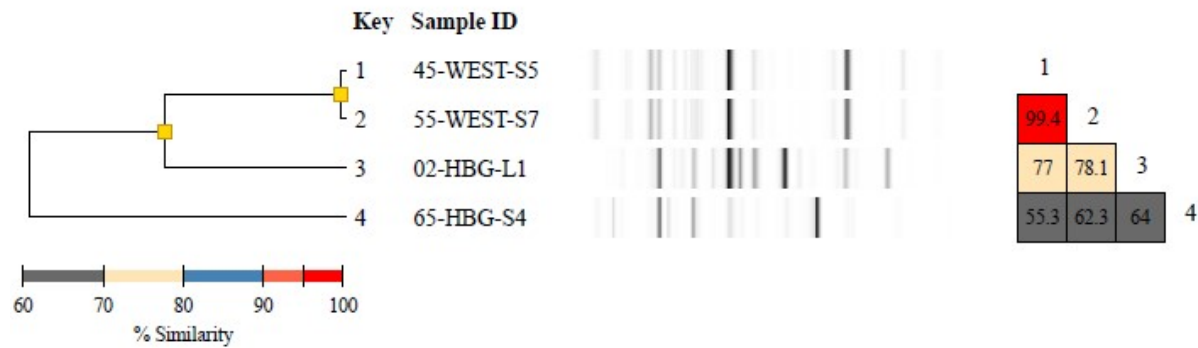
Supplementary material 10: Diversilab typing report of 16 *Escherichia coli* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. *Data interpretation criteria*—similarity matrix: lower than 95% means different, 95%–97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%.



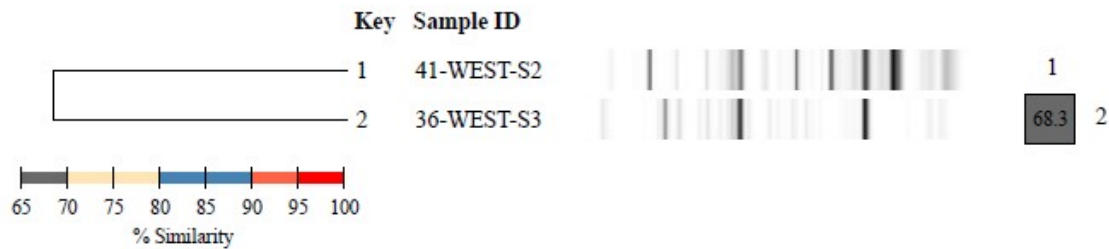
Supplementary material 11: Diversilab typing report of 15 *Klebsiella pneumoniae* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. **Data interpretation criteria**—similarity matrix: lower than 95% means different, 95%-97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%



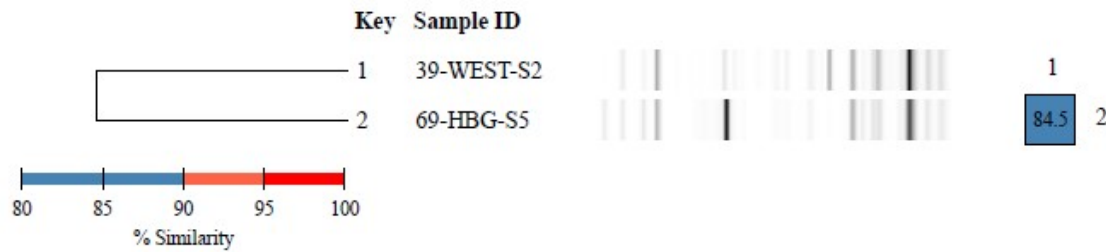
Supplementary material 12: Diversilab typing report of 8 *Enterobacter cloacae* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. *Data interpretation criteria*—similarity matrix: lower than 95% means different, 95%-97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%.



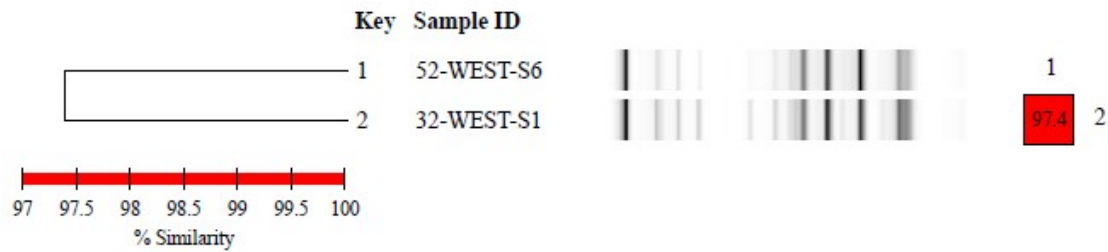
Supplementary material 13: Diversilab typing report of 4 *Citrobacter freundii* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. *Data interpretation criteria*—similarity matrix: lower than 95% means different, 95%–97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%.



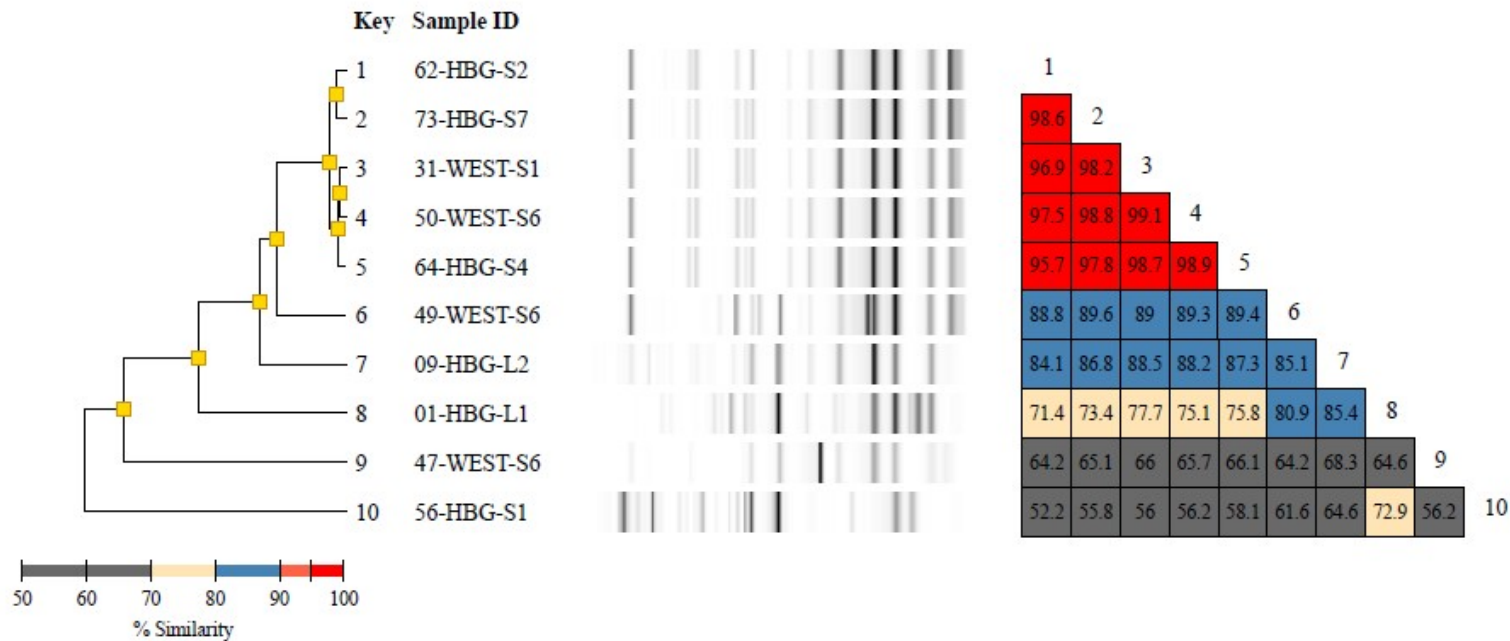
Supplementary material 14: Diversilab typing report of 2 *Morganella morganii* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. *Data interpretation criteria*—similarity matrix: lower than 95% means different, 95%–97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%



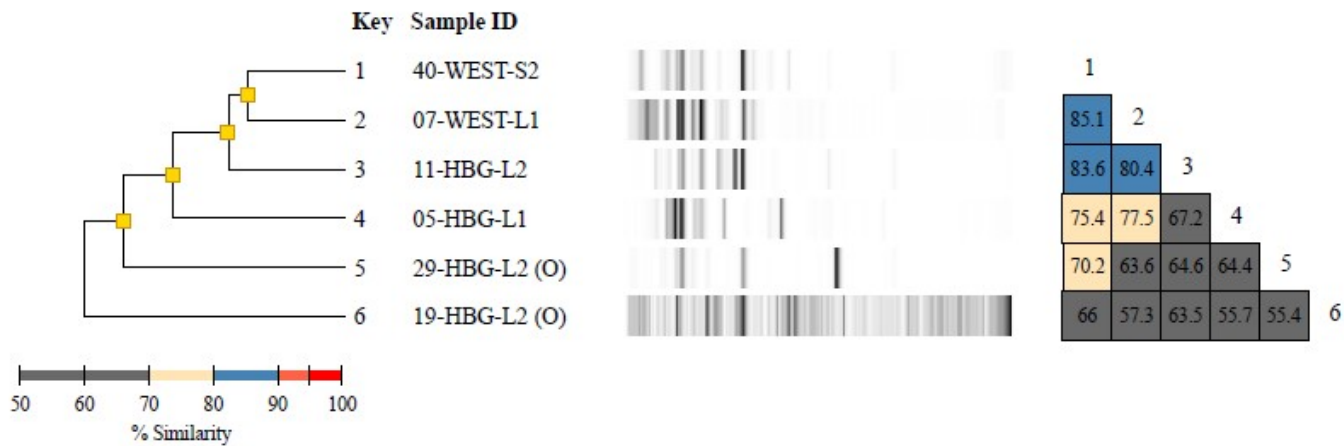
Supplementary material 15: Diversilab typing report of 2 *Proteus mirabilis* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. *Data interpretation criteria*—similarity matrix: lower than 95% means different, 95%–97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%



Supplementary material 16: Diversilab typing report of 2 *Raoultella planticola* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. *Data interpretation criteria*—similarity matrix: lower than 95% means different, 95%–97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%



Supplementary material 17: Diversilab typing report of 10 *Acinetobacter baumannii* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for easy data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. **Data interpretation criteria**—similarity matrix: lower than 95% means different, 95%–97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%



Supplementary material 18: Diversilab typing report of 6 *Pseudomonas aeruginosa* isolates including a dendrogram, band patterns of the virtual gels, and a similarity matrix for ease of data interpretation. The dendrogram shows fingerprint similarities as a treelike structure. The virtual band patterns give a short overview of the experimental data. The similarity matrix provides percentages of similarity between every pair of samples. **Data interpretation criteria**—similarity matrix: lower than 95% means different, 95%–97% means similar, above 97% means indistinguishable; color code of % similarity: bright red: 95% to 100%, dull red: 90% to 95%, blue: 80% to 90%, yellow: 70% to 80%, grey: less than 70%.