

Table S1 (supplementary material): Probe sequences

probe name	probe sequence(5'-3') ^a	length w/o spacer ^b	T _m ^c
TEM-specific probes			
TEM 6	TTTTTTTTTTTTTATGAGTAT <u>TNA</u> ACATTTTCGTG	22	49.2
TEM 16	TTTTTTTTTTTTTATTCCTTT <u>NT</u> TGCGGCAT	20	53.1
TEM 21	TTTTTTTTTTTTTGCATTTTGC <u>NT</u> TCCTGTTTT	20	52.3
TEM 34	TTTTTTTTTTTTTGTGAAAGT <u>ANA</u> AGATGCTGAA	22	51.2
TEM 35 _{WT}	TTTTTTTTTTTTTGTGAAAGTAAAA <u>GAT</u> GCTGAAGAT	23	50.3
TEM 35 _{MUT}	TTTTTTTTTTTTTGTGAAAGTAAAA <u>CC</u> TGCTGAAGAT	23	52.5
TEM 39	TTTTTTTTTTTTTCTGAAGAT <u>NAG</u> TGGGTGC	19	53.4
TEM 42	TTTTTTTTTTTTTATCAGTTGGGT <u>GNA</u> CGAGTGGGTTA	25	62.2
TEM 51	TTTTTTTTTTTTTATCGAACTGGAT <u>CNCA</u> ACAGCGGTAAG	27	59.8
TEM 69.1	TTTTTTTTTTTTTTCGTTTCCAATG <u>NTG</u> AGCACTTTTAA	26	54.7
TEM 69.2	TTTTTTTTTTTTTTTTTCCAATGAT <u>NAG</u> CACTTTTAA	24	51.6
TEM 80	TTTTTTTTTTTTTATGTGGTGC <u>GNA</u> TTATCCC	20	54.7
TEM 84	TTTTTTTTTTTTTATCCCGT <u>NT</u> TGACGCCG	19	54.7
TEM 92	TTTTTTTTTTTTTGCAACTC <u>GN</u> TCGCCGA	17	62.0
TEM 104	TTTTTTTTTTTTTGACTTGGT <u>TNA</u> GACTCACC	20	52.6
TEM 114	TTTTTTTTTTTTTAAAAGCTTCTT <u>NC</u> GGATGGCA	21	50.4
TEM 115	TTTTTTTTTTTTTATCTTACG <u>NT</u> TGGCATGAC	19	52.1
TEM 124	TTTTTTTTTTTTTAGAATTATGCAN <u>TG</u> CTGCCATA	22	54.6
TEM 127	TTTTTTTTTTTTTGTGCTGCC <u>NTA</u> ACCATGA	18	52.7
TEM 130	TTTTTTTTTTTTTGCCATAACCATG <u>NGT</u> GATAAACACTG	26	57.0
TEM 145	TTTTTTTTTTTTTCGGAGGAN <u>C</u> GAAGGAGC	17	58.0
TEM 153	TTTTTTTTTTTTTCCGCTTTTTTGC <u>NC</u> AAATGGGGG	24	61.8
TEM 157	TTTTTTTTTTTTTGGGGG <u>AN</u> CATGTAACTC	18	50.9
TEM 158	TTTTTTTTTTTTTATGGGGGAT <u>NA</u> TGTAACTCG	20	54.1
TEM 163	TTTTTTTTTTTTTCTCGCCTT <u>GN</u> TCGTTGGGA	19	57.4
TEM 164.1	TTTTTTTTTTTTTGCCTTGAT <u>NGT</u> TGGGAA	17	52.4
TEM 164.2	TTTTTTTTTTTTTGCCTTGAT <u>CNT</u> TGGGAACC	19	56.4
TEM 165.1	TTTTTTTTTTTTTGTATCGT <u>NG</u> GGAACCG	17	52.4
TEM 165.2	TTTTTTTTTTTTTGTATCGT <u>TGN</u> GAACCGGAG	19	57.1
TEM 173	TTTTTTTTTTTTTGAATGAAGCC <u>NTA</u> CCAAAC	20	50.7
TEM 175	TTTTTTTTTTTTTCCATACCA <u>AN</u> CACGAGC	18	53.5
TEM 179	TTTTTTTTTTTTTACGAGCGT <u>GAN</u> ACCATGAT	19	54.5
TEM 182	TTTTTTTTTTTTTCACCAG <u>AN</u> GCCTGTAG	17	52.8
TEM 184	TTTTTTTTTTTTTCGATTCCT <u>GN</u> AGCAATGGCA	20	58.7
TEM 196.1	TTTTTTTTTTTTTAACTATTA <u>ACTNG</u> CGAACTACTT	23	51.8
TEM 196.2	TTTTTTTTTTTTTACTATTA <u>ACTGN</u> CGAACTACTT	22	51.3
TEM 204	TTTTTTTTTTTTTCTAGCTTCC <u>CNG</u> CAACAATTA	21	55.1
TEM 218	TTTTTTTTTTTTTAGTTGCAG <u>NA</u> CCACTTCT	18	53.6
TEM 221	TTTTTTTTTTTTTACCCTT <u>NT</u> TGCGCTCG	16	55.4
TEM 224	TTTTTTTTTTTTTGTTCGCTC <u>GGN</u> CCCTTC	17	53.5
TEM 237.1	TTTTTTTTTTTTTAAACTTGGA <u>AN</u> CCGGTGAGC	19	57.8
TEM 237.2	TTTTTTTTTTTTTATCTGGAG <u>ANC</u> CGTGAG	16	54.0
TEM 238.1	TTTTTTTTTTTTTCTGGAGCC <u>NGT</u> GAGCGT	17	60.7
TEM 238.2	TTTTTTTTTTTTTCTGGAGCC <u>GNT</u> GAGCGTG	18	61.5
TEM 240	TTTTTTTTTTTTTGTGAGCCGGT <u>NAG</u> CGTGGGT	18	63.3
TEM 244.1	TTTTTTTTTTTTTGTGGGTCT <u>NG</u> CGGTATC	17	55.3
TEM 244.2	TTTTTTTTTTTTTGTGGGTCT <u>CN</u> CGGTATCAT	19	56.9
TEM 262	TTTTTTTTTTTTTCCGTATCGT <u>ANT</u> TATCTACACG	22	52.0
TEM 265	TTTTTTTTTTTTTATCTAC <u>AN</u> GACGGGGA	18	52.1
TEM 268	TTTTTTTTTTTTTCGACGGGG <u>NGT</u> CAGGCA	17	60.1
TEM 275	TTTTTTTTTTTTTATGGATGAA <u>CN</u> AAATAGACAG	21	50.0

probe name	probe sequence(5'-3') ^a	length w/o spacer ^b	T _M ^c
TEM 276	TTTTTTTTTTTTTTGGATGAACGANATAGACAGAT	21	49.8
TEM 280	TTTTTTTTTTTTTTAGACAGATCGNTGAGATAGGTG	23	55.3
SHV-specific probes			
SHV 7	TTTTTTTTTTTTTTATGCGTINATATTCGCCTGT	19	51.8
SHV 8	TTTTTTTTTTTTTTATGCGTTATNTTCGCCTGT	19	51.8
SHV 10	TTTTTTTTTTTTTTGTTATATTCGCCNNGTGTATATCT	24	50.4
SHV 18	TTTTTTTTTTTTTTCTGTAGCCNCCCTGCCG	18	58.8
SHV 19	TTTTTTTTTTTTTTAGCCACCNITGCCGC	15	58.6
SHV 25	TTTTTTTTTTTTTTTCGGTACACNCCAGCCC	16	59.5
SHV 35	TTTTTTTTTTTTTTAGCAAATTAACAAGCGAAAGCC	24	54.5
SHV 43 _{WT}	TTTTTTTTTTTTTTGTGCGGGCCGCGTAGG	16	61.1
SHV 43 _{MUT}	TTTTTTTTTTTTTTGTGCGGGCAGCGTAGG	16	57.8
SHV 48	TTTTTTTTTTTTTTGTAGGCATGATANAATGGATCTGG	25	55.1
SHV 61	TTTTTTTTTTTTTTGCCTGGNNGTGCCGAT	15	57.1
SHV 64	TTTTTTTTTTTTTTTCGCCGATGNACGCTTCC	18	57.2
SHV 69	TTTTTTTTTTTTTTTCCCATGATINAGCACCTTT	20	54.3
SHV 80	TTTTTTTTTTTTTTTCGGCGCANITGCTGGC	15	61.5
SHV 89	TTTTTTTTTTTTTTGCCGGTGACNAACAGCT	17	58.4
SHV 112	TTTTTTTTTTTTTTTCAGCGAAAAANACCTTGCC	19	55.2
SHV 112.SM	TTTTTTTTTTTTTTTCAGCGAAAAANATCTTGCC	20	54.0
SHV 113	TTTTTTTTTTTTTTTCGAAAAACACNITGCGGACG	20	57.3
SHV 114	TTTTTTTTTTTTTTTAAACACCTTNCCGACGG	17	56.0
SHV 114.SM	TTTTTTTTTTTTTTTGAAAAACATCTTNCCGACGG	20	54.7
SHV 119	TTTTTTTTTTTTTTTGCATGACGNITCGGCGAA	17	58.7
SHV 122	TTTTTTTTTTTTTTGTGCGCGAANTCTGCG	16	56.7
SHV 124	TTTTTTTTTTTTTTTAACTCTGCNCCGCCG	15	59.6
SHV 126	TTTTTTTTTTTTTTTCGCCGCCGNCAATTACC	16	60.6
SHV 129	TTTTTTTTTTTTTTTCGCCCATACCNTTAGCGATAACAG	25	55.0
SHV 130	TTTTTTTTTTTTTTTCCATTACCATGNCGATAACAGC	23	56.0
SHV 134	TTTTTTTTTTTTTTTAAACAGCGNCGCCAATC	17	56.1
SHV 140 _{WT}	TTTTTTTTTTTTTTTCTGCTACTGGCCACCGTCGG	20	62.9
SHV 140 _{MUT}	TTTTTTTTTTTTTTTCTGCTACTCCGGACCGTCGG	20	62.0
SHV 142	TTTTTTTTTTTTTTTGGCCACCNTCGGCGG	15	63.7
SHV 145	TTTTTTTTTTTTTTTGC GGCCNCGCAGGAT	15	62.7
SHV 146	TTTTTTTTTTTTTTTCGGCCCCGNAGGATTG	16	60.1
SHV 148	TTTTTTTTTTTTTTTCCCGCAGGANITGACTG	16	53.1
SHV 149	TTTTTTTTTTTTTTTAGGATTGNCTGCCTTT	16	47.4
SHV 156	TTTTTTTTTTTTTTTCCAGATCGNCGACAACG	17	56.4
SHV 158	TTTTTTTTTTTTTTTCGGCGACAANGTCAACC	17	59.6
SHV 167 _{WT}	TTTTTTTTTTTTTTTCTGGGAAACGGAACCTGAATG	20	53.7
SHV 167 _{MUT}	TTTTTTTTTTTTTTTCTGGGAAACTGACCGCTGGG	20	60.8
SHV 173	TTTTTTTTTTTTTTTATGAGCGGNTTCCCGG	16	58.3
SHV 175 _{WT}	TTTTTTTTTTTTTTTCTTCCCGGCGACGC	14	57.2
SHV 175 _{MUT}	TTTTTTTTTTTTTTTCTTCCCGCCGACGC	14	57.2
SHV 175 _{WT}	TTTTTTTTTTTTTTTGCTTCCCGGCGACTCC	16	54.0
SHV 175 _{MUT}	TTTTTTTTTTTTTTTGCTTCCCGCCGACTCC	16	54.0
SHV 179.1	TTTTTTTTTTTTTTTCGCCCGCNACACCAC	15	60.7
SHV 179.2	TTTTTTTTTTTTTTTGCCCGCGNACCACT	15	59.0
SHV 187	TTTTTTTTTTTTTTTCCAGCATGNCCGCGAC	16	60.6
SHV 192/3 _{WT}	TTTTTTTTTTTTTTTGCGCAAGCTGCTGACCA	17	59.4
SHV 192/3 _{MUT}	TTTTTTTTTTTTTTTGCGCAACGTGCTGACCA	17	59.5

probe name	probe sequence(5'-3') ^a	length w/o spacer ^b	T _m ^c
SHV 195	TTTTTTTTTTTTTGTCTGCTG <u>ANC</u> AGCCAGC	17	60.0
SHV 205	TTTTTTTTTTTTTGTTCGCA <u>ANC</u> NGCAGCTG	17	57.8
SHV 206	TTTTTTTTTTTTTGTGCAACGGC <u>AN</u> CTGCTG	16	58.2
SHV 226	TTTTTTTTTTTTTCCGTGCTG <u>CCG</u> TCG	14	50.6
SHV 238/240 _{GEg}	TTTTTTTTTTTTTGGAGCT <u>GCG</u> AGCG	14	57.0
SHV 238/240 _{SEg}	TTTTTTTTTTTTTCGGAGCT <u>AGC</u> AGCGG	16	58.8
SHV 238/240 _{SKg}	TTTTTTTTTTTTTCGGAGCT <u>AGCA</u> AGCGG	16	56.3
SHV 238/240 _{AEg}	TTTTTTTTTTTTTGGAGCT <u>GCG</u> AGCG	14	57.0
SHV 238/240 _{GEa}	TTTTTTTTTTTTTGGAGCT <u>GCG</u> AAACGG	15	56.7
SHV 238/240 _{SEa}	TTTTTTTTTTTTTCGGAGCT <u>AGCG</u> AAACGGG	17	58.6
SHV 238/240 _{SKa}	TTTTTTTTTTTTTGGAGCT <u>AGCA</u> AAACGGG	16	53.1
SHV 238/240 _{AEa}	TTTTTTTTTTTTTGGAGCT <u>GCG</u> AAACGG	15	56.7
SHV 238/240 _{AK}	TTTTTTTTTTTTTGGAGCT <u>GCA</u> AAACGG	15	54.0
SHV 243	TTTTTTTTTTTTTCCGGGGT <u>GNG</u> TGCG	14	54.1
SHV 268	TTTTTTTTTTTTTCTGCGT <u>GAT</u> NCCCGG	16	48.2
SHV 269	TTTTTTTTTTTTTGATA <u>CC</u> NGGCGAGCAT	17	57.6
SHV 278	TTTTTTTTTTTTTAAATCAGC <u>AN</u> ATCGCCGGG	19	56.4
CTX-M group discrimination			
CTX-M 73.M1/M2	TTTTTTTTTTTTTACCAGTA <u>ANG</u> TGATGGCCG	19	55.0
CTX-M 73.M9	TTTTTTTTTTTTTGTACCAGTA <u>ANG</u> TATGGCGG	21	53.2
CTX-M 132.M1	TTTTTTTTTTTTTGTGCATAACGT <u>NG</u> CAGTAA	19	55.7
CTX-M 267.M2	TTTTTTTTTTTTTT <u>TAC</u> CCA <u>ACC</u> GAGCAG	17	54.6
CTX-M 267.M1	TTTTTTTTTTTTTT <u>CAC</u> CCAG <u>CC</u> TCA <u>ACCT</u>	17	56.1
CTX-M 267.M8	TTTTTTTTTTTTTT <u>CAC</u> CCAG <u>CC</u> AGAGCAG	17	57.4
CTX-M 267.M9	TTTTTTTTTTTTTT <u>TAC</u> CCAG <u>CC</u> GCA <u>AC</u> CAG	17	55.5
probes specific for the CTX-M1 group			
CTX-M 12	TTTTTTTTTTTTTTCGACAGC <u>AN</u> CCGTACAG	17	50.4
CTX-M 23	TTTTTTTTTTTTT <u>AGT</u> GCC <u>ACT</u> G <u>NA</u> TGCACAAAC	21	-
CTX-M 27	TTTTTTTTTTTTTTCGCAAAAC <u>AGN</u> GGACGTACA	19	52.9
CTX-M 35	TTTTTTTTTTTTTTAAACT <u>TACC</u> GNATTAGAGCG	20	45.7
CTX-M 38	TTTTTTTTTTTTTGAATTAGAGC <u>NG</u> CAGTCGG	19	55.8
CTX-M 77	TTTTTTTTTTTTTGTATG <u>ACC</u> NGACCCACGGT	18	-
CTX-M 89	TTTTTTTTTTTTTGGCAACCA <u>ANT</u> CTGTAAA	19	42.0
CTX-M 106	TTTTTTTTTTTTTGTAACTAT <u>ANT</u> CCGATTGC	20	46.1
CTX-M 114	TTTTTTTTTTTTTAGCACGT <u>CNA</u> TGGAAACGA	18	49.7
CTX-M 119	TTTTTTTTTTTTTCGATGTC <u>CAN</u> GACTGAGC	18	47.3
CTX-M 140	TTTTTTTTTTTTTAAACTGAT <u>TNC</u> TACGTTGG	20	48.7
CTX-M 167.M1	TTTTTTTTTTTTTCCGTACCGAG <u>NC</u> AACGTTAA	20	52.9
CTX-M 239	TTTTTTTTTTTTTACCAGCAGC <u>NG</u> TGACTATG	19	51.5
CTX-M 240.M1	TTTTTTTTTTTTTGCAGCGGT <u>GNC</u> TATGG	16	53.1
CTX-M 278.M1	TTTTTTTTTTTTTAGCCATCGC <u>NA</u> TGTATTAG	19	47.6
CTX-M 288.M1	TTTTTTTTTTTTTAAATCGTCA <u>CCN</u> ACAGTTTGTA	22	47.2
probes specific for the CTX-M2 group			
CTX-M 48	TTTTTTTTTTTTTTCGCTGC <u>ACN</u> GATTAACACC	20	-
CTX-M 61.1	TTTTTTTTTTTTTAAATCTCTAC <u>NGT</u> ACCGATGA	21	-
CTX-M 61.2	TTTTTTTTTTTTTAAATCTCTAC <u>NTG</u> ACCGATGA	21	-
CTX-M 99	TTTTTTTTTTTTTGAATCAA <u>AA</u> ANGAGCGACCTG	22	49.8
CTX-M 121.M2	TTTTTTTTTTTTTACGCTGGCT <u>NA</u> GCTTGGC	18	61.6
CTX-M 159	TTTTTTTTTTTTTGGTGATGAG <u>NC</u> CTCCGTCT	20	56.3
CTX-M 230	TTTTTTTTTTTTTCATCATGG <u>GN</u> AGTGGACGAT	20	-
CTX-M 253	TTTTTTTTTTTTTATCTAGCC <u>AGN</u> AAACACGC	20	-
CTX-M 274.M2	TTTTTTTTTTTTTACGGAA <u>AGN</u> CGTCGAGAT	18	-

probe name	probe sequence(5'-3') ^a	length w/o spacer ^b	T _M ^c
CTX-M 278.M2	TTTTTTTTTTTTTCGTCG AGGAT <u>NTT</u> CTGGCTG	20	50.2
probes specific for the CTX-M8/25 group			
CTX-M 50	TTTTTTTTTTTTTGCTGATT NAC ACCTCC	16	43.2
CTX-M 55	TTTTTTTTTTTTTCTGATAAC NC ACAGACG	17	47.6
CTX-M 222	TTTTTTTTTTTTTCCAGCATT CN GGCT AGC	18	51.2
CTX-M 274.M8	TTTTTTTTTTTTTAGTCAG ANAG TTGTCTG	16	-
probes specific for the CTX-M9 group			
CTX-M 7	TTTTTTTTTTTTTCGGATGATG TNC AC AGC CGG	19	-
CTX-M 21	TTTTTTTTTTTTTTCGAGC ACGN CGCTTATG	18	52.1
CTX-M 29	TTTTTTTTTTTTTACGAGTGCC ANG CAGCAAAGC	22	59.6
CTX-M 52	TTTTTTTTTTTTTCATTGATAC NC AGATAATACG	22	48.4
CTX-M 121.M9	TTTTTTTTTTTTTGTGCTGGCAG AN CTGA ACGC	18	55.1
CTX-M 167.M9	TTTTTTTTTTTTTCA CACT GAA NCT ACGCTGA	19	48.5
CTX-M 183	TTTTTTTTTTTTTCCACCAC CGNCA CG AGC	19	-
CTX-M 220.1	TTTTTTTTTTTTTGC ACAGCC <u>NG</u> CATT CGG	17	51.2
CTX-M 220.2	TTTTTTTTTTTTTGCAGCC AGNA TT CGAGCC	18	55.3
CTX-M 231	TTTTTTTTTTTTTTCGTGGACT GN AGGTGATAAGA	22	57.8
CTX-M 240.M9	TTTTTTTTTTTTTTCAGC AGCGN CTACGGCAC	19	56.7
CTX-M 274.M9	TTTTTTTTTTTTTACGCAGAG NGCC ACCGC	17	55.4
CTX-M 288.M9	TTTTTTTTTTTTTAGAATCAT CAC NAAG AGCTGTAA	24	-

^a Sequence differences are highlighted bold. N assigns the position of the point mutation and is a substitution for A, G, C and T. The nucleotides, which encode the involved amino acid are displayed underlined.

^b The probe length refers to the specific sequence involved in hybridization and does not take into account the 13-thymidine spacer.

^c Melting temperatures (T_M) were calculated with OligoAnalyzer (<http://eu.idtdna.com/analyzer/Applications/OligoAnalyzer/>). For probes with artificial mismatches, the T_M-mismatch was calculated. For probes with more than one artificial mismatch the T_Ms could not be calculated and the probes were selected empirically.

Table S2 (supplementary material): Antibiotic susceptibility testing

a) MIC determination on a VITEK 2XL system using the Gram Negative Susceptibility Card AST-N062[#]. Numerical values are expressed in µg/ml. R, resistant; S, susceptible; I, intermediate; -, not tested. We did not consider the way the expert system of the VITEK interpreted or changed MICs.

No ^a	Isolate	ESBL ^b	PIP	AMX/MEZ	SAM/AMC	TZP	CFZ	CXM	CXM (axetil)	CPD	CTX/CRO	CAZ	IMP	MER	TET/DOX	GEN	TOB/AMK	SXT	CIP	LEV	NIT
24*	<i>E.sak.</i>	-	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	4 S	32 R	≤1 S	≤0.25 S	≤1 S	≥16 R	4 S	≥320 R	≤0.25 S	≤0.25 S	≤16 S
55*	<i>K.oxy.</i>	POS	≥128 R	≥32 R	≥32 R	≥128 R	≥64 R	≥64 R	≥64 R	≥8 R	4 S	8 S	≤1 S	≤0.25 S	≥16 S	≥16 R	≥16 R	≥320 R	≤0.25 S	≤0.25 S	32 S
25*	<i>K.spec.</i>	-	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	16 I	≥64 R	≤1 S	≤0.25 S	2 S	≤1 S	≥16 R	≤20 S	≤0.25 S	≤0.25 S	128 R
2 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	16 I	≤4 S	≥64 R	16 I	16 I	≥8 R	16 I	≥64 R	≤1 S	≤0.25 S	4 S	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	128 R
12 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	16 I	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≤1 S	≥16 R	≥16 R	≥320 R	0.5 S	1 S	32 S
36 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	4 S	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	64 I
1 ⁺	<i>K.ter.</i>	-	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	16 I	16 I	≥8 R	32 I	≥64 R	≤1 S	≤0.25 S	4 S	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	128 R
15 ⁺	<i>K.ter.</i>	-	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	16 I	16 I	≥8 R	32 I	≥64 R	≤1 S	≤0.25 S	≤1 S	≥16 R	≥16 R	≥320 R	≤0.25 S	0.5 S	128 R
17 ⁺	<i>K.ter.</i>	-	≥128 R	≥32 R	≥32 R	16 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≤1 S	≥16 R	8 I	≥320 I	1 S	1 S	64 I
52*	<i>K.oxy.</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	32 I	≥64 R	≤1 S	≤0.25 S	8 I	≥16 R	≥16 S	≥320 R	1 S	2 S	128 R
5 ⁺	<i>E.coli</i>	POS	16 S	≥32 R	4 S	≤4 S	≥64 R	8 S	8 I	≥8 R	≤1 S	≥64 R	≤1 S	≤0.25 S	≥16 R	≤1 S	≤1 S	≤20 S	≤0.25 S	≤0.25 S	≤16 S
19 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	16 I	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	2 S	≤1 S	≤1 S	≤20 S	≤0.25 S	≤0.25 S	128 R
49*	<i>K.spec.</i>	-	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
13 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	2 S	≥16 R	≤20 S	≥4 R	≥8 R	≤16 S
18 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≤1 S	≤1 S	≥320 S	≤0.25 S	≤0.25 S	≤16 S
20*	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	2 S	2 S	≤1 S	≤20 S	≥4 S	≥8 S	≤16 S
26 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	2 S	≥16 R	≥320 R	≥4 R	≥8 R	≤16 S
33*	<i>E.coli</i>	NEG	≥128 R	≥32 R	≥32 R	32 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	32 R	≤1 S	≤0.25 S	≥16 S	2 R	≥16 R	≤20 S	≥4 R	≥8 R	≤16 S
38 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≥128 R	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	≤16 S
40 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	64 I
48*	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	2 S	≥16 R	≤20 S	≥4 R	≥8 R	≤16 S
60 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	64 I
61 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≤1 S	≤1 S	≤1 S	≥320 R	≥4 R	≥8 R	≤16 S
6 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	64 I
9 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	≤16 S
30*	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≤20 S	≥4 R	≥8 R	≤16 S
32*	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	≤16 S
34 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≤1 S	≤1 S	≤1 S	≤20 S	≥4 R	≥8 R	≤16 S
57 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≤0.25 S	≤0.25 S	≤16 S

No ^a	Isolate	ESBL ^b	PIP	AMX/MEZ	SAM/AMC	TZP	CFZ	CXM	CXM (axetil)	CPD	CTX/CRO	CAZ	IMP	MER	TET/DOX	GEN	TOB/AMK	SXT	CIP	LEV	NIT
3 ⁺	<i>E.int.</i>	-	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≤1 S	≥16 R	≤20 S	≥4 R	≥8 R	64 I
29 ⁺	<i>K.oxy.</i>	POS	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
7 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 S	16 I	≤1 S	≤0.25 S	8 I	≥16 R	8 R	≥320 R	≥4 R	≥8 R	64 I
16 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
37 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	32 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≤0.25 S	≤0.25 S	32 S
10 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	2 S	≥16 R	≥16 R	≤20 S	≤0.25 S	≤0.25 S	32 S
35 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	32 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
42 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
11 ⁺	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	2 I	1 S	64 I
22 [*]	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	40 S	≥4 R	≥8 R	512 R
50 [*]	<i>K.pneu.</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
14 ⁺	<i>K.ter.</i>	-	≥128 R	≥32 R	≥32 R	32 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≤20 S	≤0.25 S	0.5 S	32 S
28 ⁺	<i>K.ter.</i>	-	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
21 [*]	<i>K.ter.</i>	-	≥128 R	≥32 R	≥32 R	32 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
51 [*]	<i>K.spec.</i>	-	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	256 R
8 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	32 I	4 S	≤1 S	≤0.25 S	≤1 S	≤1 S	≤1 S	≥320 R	≤0.25 S	≤0.25 S	32 S
56 [*]	<i>E.coli</i>	POS	≥128 R	≥32 R	16 I	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	16 I	≤1 S	≤1 S	≤0.25 S	≥16 R	4 S	2 S	≤20 S	≤0.25 S	≤0.25 S	≤16 S
59 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	8 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	64 I
27 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	32 I	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	64 I
4 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≤1 S	≤1 S	≤0.25 S	≥16 R	≥16 R	8 I	≥320 R	≥4 R	≥8 R	≤16 S
39 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≤1 S	≤1 S	≤0.25 S	≥16 R	≥16 R	8 I	≤20 S	≥4 R	≥8 R	≤16 S
58 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	≤1 S	≤1 S	≤0.25 S	≥16 R	≤1 S	≤1 S	≤20 S	≤0.25 S	≤0.25 S	≤16 S
46 [*]	<i>E.coli</i>	POS	32 I	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	4 S	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	≤16 S
41 ⁺	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	4 S	≤1 S	≤0.25 S	2 S	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	32 S
47 ⁺	<i>P.vul.</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
44 [*]	<i>E.coli</i>	POS	64 I	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	32 I	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	≤16 S
53 [*]	<i>E.coli</i>	POS	≥128 R	≥32 R	≥32 R	16 S	≥64 R	≥64 R	≥64 R	≥8 R	≥64 R	16 I	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	64 I
31 [*]	<i>E.coli</i>	POS	64 I	≥32 R	≥32 R	≤4 S	≥64 R	≥64 R	≥64 R	≥8 R	32 I	≥64 R	≤1 S	≤0.25 S	≥16 R	≥16 R	≥16 R	≥320 R	≥4 R	≥8 R	≤16 S
54 [*]	<i>C.freu.</i>	-	≥128 R	≥32 R	≥32 R	64 I	≥64 R	≥64 R	≥64 R	≥8 R	32 I	≥64 R	≤1 S	≤0.25 S	≤1 S	≤1 S	≤1 S	≤20 S	≤0.25 S	≤0.25 S	32 S
62 [*]	<i>K.pneu.</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
23 [*]	<i>R.aqu.</i>	-	≤4 S	≥32 R	≤2 S	≤4 S	32 R	32 R	32 R	≥8 R	≤1 S	≤1 S	≤1 S	≤0.25 S	2 S	≤1 S	≤1 S	≤20 S	≤0.25 S	0.25 S	≤16 S

[#] MIC testing was performed at the Robert-Bosch-Hospital in Stuttgart, Germany

^a For better comparison the data was sorted as in Table 1. Samples originally collected in ⁺ Frankfurt and ^{*} Stuttgart.

^b The VITEK ESBL test is FDA approved only for *E. coli*, *K. pneumoniae* and *K. oxytoca*.

b) Susceptibility testing according to CLSI standards at the Institute of Medical Microbiology and Hygiene, J.W. Goethe-Universität, Frankfurt am Main, Germany. R, resistant; S, susceptible; I, intermediate; -, not tested.

No ^a	Isolate	AMX/MEZ	AMC	PIP	TZP	CEC/CFZ	CXM	FOX	CTX	CRO	CAZ	FEP	IMP	MER	GEN/TOB	AMK	DOX	SXT	FOF	LEV/CIP/MXF	Colistin
2	<i>K.pneu.</i>	R/R	S	R	I	R/R	R	R	R	R	R	R	S	S	R/R	S	S	R	S	R/I/R	S
12	<i>K.pneu.</i>	R/R	R	R	I	R/R	R	R	R	R	R	R	S	S	R/R	S	S	R	S	S/S/S	S
36	<i>K.pneu.</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	R	R/R/R	S-
1	<i>K.ter.</i>	R/R	I	R	I	R/R	R	S	R	R	R	R	S	S	R/R	S	I	R	R	I/I/R	S
15	<i>K.ter.</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	R	R	S	R	S/S/S	S
17	<i>K.ter.</i>	R/R	R	R	S	R/R	R	R	R	R	R	R	S	S	R/R	S	S	R	S	S/S/S	S
5	<i>E.coli</i>	R/R	R	R	S	R/R	R	R	R	R	R	R	S	S	S/S	S	R	R	S	S/S/S	S
19	<i>K.pneu.</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	S/S	S	S	S	S	S/S/S	S
13	<i>E.coli</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	S/S	S	R	R	S	S/S/S	S
18	<i>E.coli</i>	R/R	I	R	S	R/R	R	R	R	R	R	R	S	S	S/S	S	R	S	S	S/S/S	S
26	<i>E.coli</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	S/R	S	R	R	S	R/R/R	S
38	<i>E.coli</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	R	R	R	S	R/R/R	S
40	<i>E.coli</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	S/S	S	R	S	S	S/S/S	S
60	<i>E.coli</i>	R/R	R	R	I	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	R	R/R/R	S
61	<i>E.coli</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	S/S	S	S	S	R	R/R/R	S
6	<i>E.coli</i>	R/R	R	R	R	R/R	R	R	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
9	<i>E.coli</i>	R/R	R	R	S	R/R	R	R	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
34	<i>E.coli</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	S/S	S	R	R	S	R/R/R	S
57	<i>E.coli</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	S/S/S	S
3	<i>E.int.</i>	R/R	R	R	R	R/R	R	R	R	R	R	R	S	S	S/R	S	S	S	S	S/S/S	S
29	<i>K.oxy.</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	I	R/R/R	S
7	<i>K.pneu.</i>	R/R	R	R	R	R/R	R	R	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
16	<i>K.pneu.</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	R	R	R	R	R/R/R	S
37	<i>K.pneu.</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	R	S/S/S	S
10	<i>K.pneu.</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	R	R	R	R	S/S/S	-
35	<i>K.pneu.</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
42	<i>K.pneu.</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
11	<i>K.pneu.</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	I/I/I	S
14	<i>K.ter.</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	R	S	R	S	S/S/S	S
28	<i>K.ter.</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
8	<i>E.coli</i>	R/R	R	R	R	R/R	R	R	R	R	R	R	S	S	S/S	S	S	S	S	S/S/S	S
59	<i>E.coli</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
27	<i>E.coli</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	R	R/R/R	S
4	<i>E.coli</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
39	<i>E.coli</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	S	R	R	S	R/R/R	S
58	<i>E.coli</i>	R/R	R	R	R	R/R	R	S	R	R	R	R	S	S	S/S	S	R	S	S	S/S/S	S
41	<i>E.coli</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	-	I	R	R	R/R/R	S
47	<i>P.vul.</i>	R/R	R	R	S	R/R	R	S	R	R	R	R	S	S	R/R	S	R	S	R	S/S/S	R

^a For better comparison the data was also sorted for different genotypes detected and afterwards clustered for species.

c) Susceptibility testing according to CLSI standards at the Department of Laboratory Medicine, Robert-Bosch-Hospital, Stuttgart, Germany. R, resistant; S, susceptible; I, intermediate; -, not tested.

No ^a	Isolate	AMX/MEZ	AMC	PIP	TZP/PIP-SUL	CFZ	CXM	CPD	CTX	CRO	CAZ	FEP	IMP	FOX	Aztreonam	GEN/TOB	AMK	DOX	SXT	FOF	LEV/CIP
24	<i>E.sak.</i>	R/R	R	R	S	R	R	R	I	I	I	S	S	-	-	R/R	S	I	R	-	S/S
55	<i>K.oxy.</i>	R/R	R	R	R/-	R	R	R	R	R	R	S	S	-	-	R/R	S	R	R	-	S/S
25	<i>K.spec.</i>	-/-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-/-
52	<i>K.oxy.</i>	R/R	I	R	R	R	R	R	R	R	R	S	S	-	-	R/R	I	R	R	-	R/R
49	<i>K.spec.</i>	R/-	-	R	R	R	-	-	-	R	R	-	S	-	R	R/S	-	R	R	-	R/-
20	<i>E.coli</i>	R/R	I	R	S/-	R	R	R	R	R	R	R	S	-	-	S/S	S	S	S	-	R/R
33	<i>E.coli</i>	R/R	R	R	R/-	R	R	R	R	R	R	R	S	-	-	R/R	S	R	R	-	R/R
48	<i>E.coli</i>	R/R	R	R	R	R	R	R	R	R	R	R	S	-	-	R/R	S	R	S	-	R/R
30	<i>E.coli</i>	R/R	R	R	S/-	R	R	R	R	R	R	R	S	-	-	R/R	S	R	S	-	R/R
32	<i>E.coli</i>	R/R	R	R	R	R	R	R	R	R	R	R	S	-	-	R/R	R	R	R	-	R/R
22	<i>K.pneu.</i>	R/R	R	R	R	R	R	R	R	R	R	R	S	-	-	R/R	S	R	R	-	R/R
50	<i>K.pneu.</i>	R/R	R	R	R	R	R	R	R	R	R	R	S	S	-	R/R	I	R	R	-	R/R
21	<i>K.ter.</i>	R/R	R	R	R	R	R	R	R	R	R	R	S	-	-	R/R	S	R	R	-	R/R
51	<i>K.spec.</i>	R/-	R	R	R	R	-	-	-	R	R	-	S	-	-	R/R	-	R	R	-	R/-
56	<i>E.coli</i>	R/-	-	R	R/-	R	-	-	-	R	R	-	S	-	R	S/S	-	R	I	-	S/-
46	<i>E.coli</i>	R/R	R	R	-/R	R	R	R	R	R	R	R	S	S	R	R/R	S	R	R	-	R/R
44	<i>E.coli</i>	R/R	R	R	-/R	R	R	R	R	R	R	R	S	-	-	R/R	S	R	R	-	R/R
53	<i>E.coli</i>	R/R	R	R	R/R	R	R	R	R	R	R	R	S	-	-	R/R	S	R	R	S	R/R
31	<i>E.coli</i>	R/R	R	R	-/R	R	R	R	R	R	R	S	S	-	R	R/R	R	R	R	-	R/R
54	<i>C.freu.</i>	R/-	R	R	-	R	-	-	-	R	R	-	S	-	-	S/S	-	S	S	-	S/-
62	<i>K.pneu.</i>	R/-	R	R	-	R	-	-	-	S	I	-	S	-	-	S/S	-	R	R	-	S/-
23	<i>R.aqu.</i>	R/S	S-	R	S	R	R	R	S	S	S	S	S	-	-	S/S	S	S-	S	-	S/S

^a For better comparison the data was also sorted for different genotypes detected and afterwards clustered for species.

Abbreviations for antibacterial agents: AMC, amoxicillin-clavulanic acid; AMK, amikacin; AMX, ampicillin; CAZ, ceftazidime; CEC, cefaclor; CFZ, cefazolin; CIP, ciprofloxacin; CPD, cefpodoxime; CRO, ceftriaxone; CTX, cefotaxime; CXM, cefuroxime; DOX, doxycycline; FEP, cefepime; FOF, fosfomycin; FOX, ceftoxitin; GEN, gentamicin; IMP, imipenem; LEV, levofloxacin; MER, meropenem; MEZ, mezlocillin; MXF, moxifloxacin; NIT, nitrofurantoin; PIP, piperacillin; PIP-SUL, piperacillin-sulbactam; SAM, ampicillin-sulbactam; SXT, trimethoprim-sulfamethoxazole; TET, tetracycline; TOB, tobramycin; TZP, piperacillin-tazobactam.

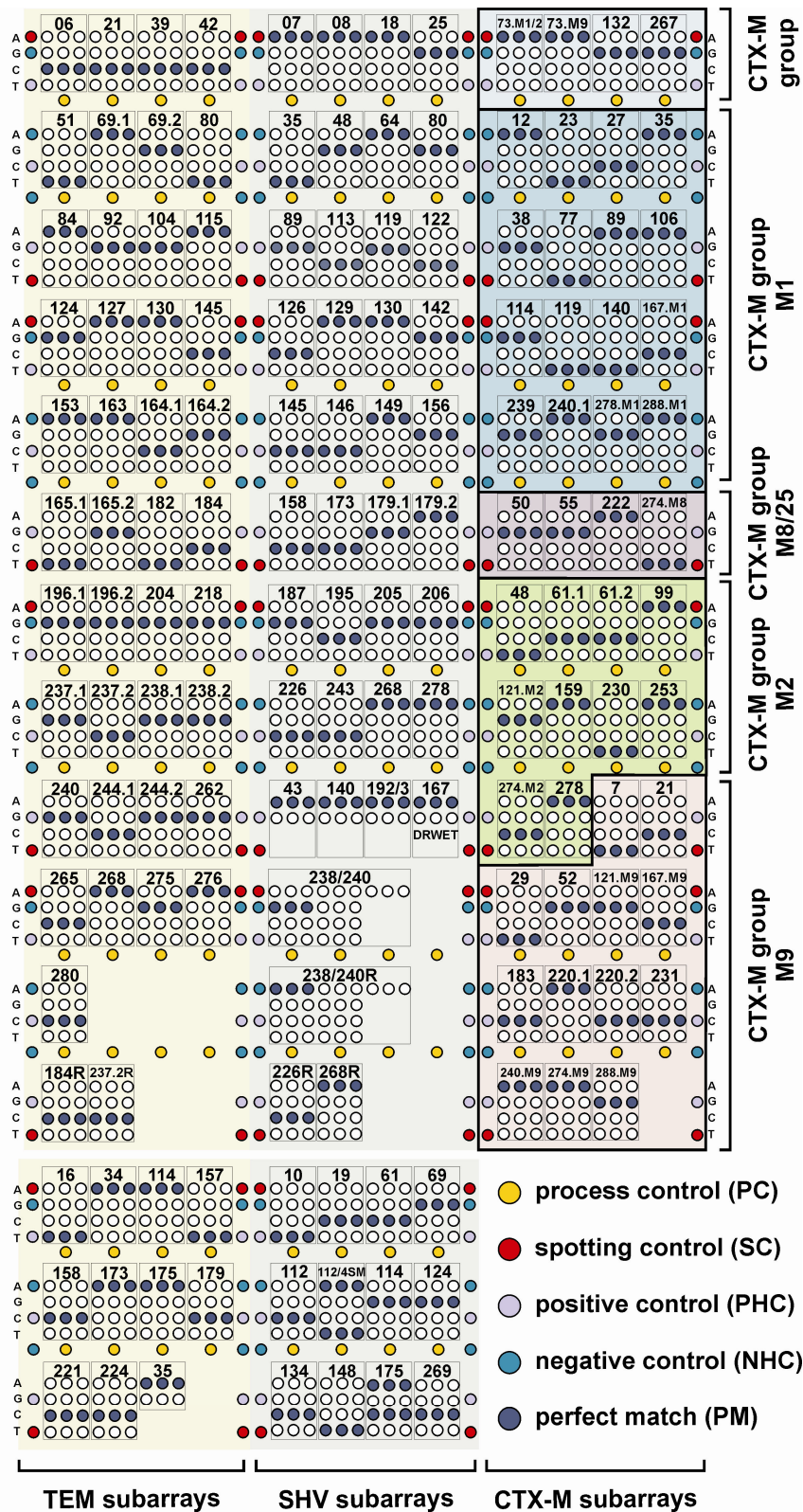


Figure S1 (supplementary material): Enlarged chip layout. Schematic representation of the modular layout of the oligonucleotide microarray. The areas specific for the different lactamase genes and the different subgroups of the CTX-M type genes are labeled. Theoretical perfect matches after hybridization with TEM-1, SHV-1, CTX M 1, CTX-M-2, CTX-M-8 and CTX-M-9 respectively are highlighted in dark blue.