

**Supplemental Table S3:** Primers used for the determination of genetic regions flanking the *bla*<sub>OXA-23</sub> and *bla*<sub>OXA-58</sub> genes in *Acinetobacter baumannii*

PCR	Target region	Primer name (Primer ID IHIT)	Primer sequence (5' - 3')	Amplicon size	Primer reference	OXA region with positive PCR reaction*
<b>OXA-23</b>						
1	ISAbal <i>ATPase</i>	ISAbal-A_RP ATPase-univ-R	CCACGATAAACGATTGCGAGCA GCAACCGTCGACATCTGTTA	1.703 bp	PS [1]	a, b, c, d, e
2	ISAbal <i>traL</i>	ISAbal-B_RP TraL_RP	CGGTGAGCAGTGGTTTACAT CTTCAAGACCGCATCCAACA	1.362 bp	PS PS	b, c, e
3	ISAbal <i>korB</i>	ISAbal_FWD KorB_RP	TTGGTTGGTCGGGTGAACT AAGAAGGCGTGGCAGAGAAT	3.660 bp	PS PS	e
4	<i>traD</i> <i>Hypothetical protein</i>	TraD_Fwd HP4_IHIT29996_REV	AGGCCGACTTACCCAATCAC TTGGCTGCATCATTTTCAGC	2.212 bp	PS PS	e
5	<i>Replication protein</i> <i>strB</i>	ReplP_FWD StrB_RP	TGGCACTATCATTGCCTGGAC CGATCAAGCAGGTGCGACA	3.023 bp	PS [3]	b
6	<i>strA</i> <i>topB</i>	StrA-RP TopB_RP	GCAACCAGTCAGAATGCGAT GGTCATGTTCTGCATATCCTA	1.856 bp	[3] PS	b
7	<i>ATPase</i> <i>parB</i>	ATPase-intern1 ParB-RP	TCAGGAAGATCGGACAGATC CATCTAGGAGAGCTTCGCAA	1.092 bp (b); 2.504 bp (c); 2.383 bp (d)	[1] PS	b, c, d
8	<i>Hypothetical protein</i> <i>higB2</i>	HP2_IHIT32289_REV HigB2_FWD	ATCCGGGTGCATGAGTGAC AACTGGGGCCAAATCTAGGC	2.192 bp	PS PS	e
9	<i>dnaJ</i> <i>Hypothetical protein</i>	DnaJ_FWD HP3_IHIT29996_REV	ATATCTTCAGTCGAGCCGCC AACGGTGGAGCAGAAGAAAGT	1.604 bp	PS PS	e
10	ISAbal <i>comM</i>	ISAbal_FWD ComM-REV	TTGGTTGGTCGGGTGAACT TTGCCTCTGGTCAACTTCCG	3.270 bp	PS PS	a
11	<i>bla</i> <sub>OXA-23</sub> <i>comM</i>	OXA-23_FWD ComM-REV	TGTCCTTGAACAATCTGACTC TTGCCTCTGGTCAACTTCCG	4.087 bp	[1] PS	a
12	<i>sulP</i> <i>ATPase</i>	SulP-FWD ATPase-intern1	TCAACGCCTGCAATAATGG TCAGGAAGATCGGACAGATC	2.258 bp	PS [1]	a

PCR	Target region	Primer name (Primer ID IHIT)	Primer sequence (5` - 3`)	Amplicon size	Primer reference	OXA region with positive PCR reaction*
<b>OXA-58</b>						
<b>13</b>	<i>bla</i> <sub>OXA-58</sub> <i>araC</i>	OXA-58_FWD	AAGTATTGGGGCTTGTGCTG	2.110 bp (A-D); 3.395 bp (E)	[2]	A, B, C, D
		AraC_REV	CGTAGGGTTGATTTCGATAGCA		[3]	
<b>14</b>	<i>adh</i> <i>bla</i> <sub>OXA-58</sub>	Adh_FWD	ACCAAGATCCGTTCCACAAA	1.412 bp	PS	A, B
		OXA-58_REV	TCAACTTCCGTGCCTATTTG		[2]	
<b>15</b>	<i>repE</i> <i>adh</i>	RepE_FWD	ATGCTACAAGATCCCGCTCA	1.553 bp	PS	A
		Adh_REV	ACGTTGGTGTGCATGGTAAG		PS	
<b>16</b>	<i>adh</i> <i>tonB</i>	Adh_FWD	ACCAAGATCCGTTCCACAAA	1.536 bp	PS	A
		TonB_REV	ATTCCGTACCCAAGGCATCC		PS	
<b>17</b>	<i>araC</i> <i>vapC</i>	AraC_FP	ACAAACACTCTCAACATTGGTG	1.640 bp	[3]	A
		VapC_REV	CCATAAGCATGGGCACATTGT		PS	
<b>18</b>	<i>tonB</i> <i>spl</i>	TonB_FWD	TTACCTCCTGCTCGTTTGGG	958 bp	PS	C
		Spl_REV	ATGCCACTTTATTTCCCGCG		PS	
<b>19</b>	<i>Hypothetical protein</i> <i>bla</i> <sub>OXA-58</sub>	HP6_IHIT29997_FWD	ACAAGCCTGGAATTAGAGCCA	2.990 bp	PS	D
		OXA-58_REV	TCAACTTCCGTGCCTATTTG		[2]	
<b>20</b>	<i>repE</i> <i>bla</i> <sub>OXA-58</sub>	RepE_FWD	ATGCTACAAGATCCCGCTCA	2.730 bp	PS	C
		OXA-58_REV	TCAACTTCCGTGCCTATTTG		[2]	
<b>21</b>	<i>Hypothetical protein</i> <i>open reading frame</i>	HP3_IHIT29985_FWD	ACCTCATCTTTAGAAGCGCCA	699 bp	PS	C
		ORF_IHIT29985_REV	TTGTCACACACCACGCATCT		PS	

\* see Figures 2 and 3 of the main text for genetic structures of OXA regions; PS = present study

#### Primer references:

1. Klotz P, Goettig S, Leidner U, Semmler T, Scheufen S, Ewers C. 2017. Carbapenem-resistance and pathogenicity of bovine *Acinetobacter indicus*-like isolates. PLOS ONE 12(2):e0171986. doi: 10.1371/journal.pone.0171986
2. Groebner S, Linke D, Schutz W, Fladerer C, Madlung J, Autenrieth IB, Witte W, Pfeifer Y. 2009. Emergence of carbapenem-non-susceptible extended-spectrum  $\beta$ -lactamase-producing *Klebsiella pneumoniae* isolates at the university hospital of Tübingen, Germany. Journal of Medical Microbiology 58:912–922. doi: 10.1099/jmm.0.005850-0.
3. Klotz P, Jacobmeyer L, Leidner U, Stamm I, Semmler T, Ewers C. 2018. *Acinetobacter pittii* from Companion Animals Coharboring *bla*<sub>OXA-58</sub>, the *tet*(39) Region, and Other Resistance Genes on a Single Plasmid. Antimicrobial Agents and Chemotherapy 62(1):e01993-17. doi: 10.1128/AAC.01993-17.

## Supplemental Table S3 continued:

According to the different genetic environments of *bla*<sub>OXA-23</sub> and *bla*<sub>OXA-58</sub> genes (see Figure 2 and Figure 3 of the main text), *bla*<sub>OXA-23</sub> and *bla*<sub>OXA-58</sub>-positive *A. baumannii* strains revealed different PCR results:

		PCR numbers (positive PCR results are indicated by blue-filled boxes)																				
OXA gene flanking pattern	Location of <i>bla</i> <sub>OXA</sub> gene and/or plasmid size	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
		OXA-23																				
a	chromosome																					
b	48.4 kb																					
c	55.8 kb																					
d	unknown																					
e	71.3 kb																					
		OXA-58																				
A	21.1 kb																					
B	11.3 kb																					
C	12.6 kb																					
D	12.3 kb																					