

Supplementary Figures

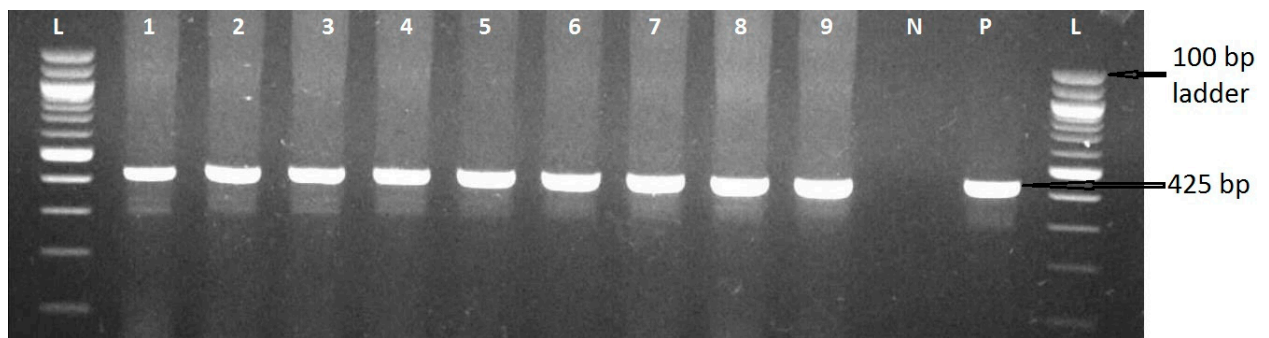


Figure S1: PCR analyses resolved by gel electrophoresis showing confirmed *Acinetobacter* spp. targeting the *recA* gene at 425 bp. L= DNA Ladder (100bp); Lane 1 to 9 = Selected *Acinetobacter* isolates; N= Negative control; P=Positive control (*A. baumannii*, DSM Number: 102929).

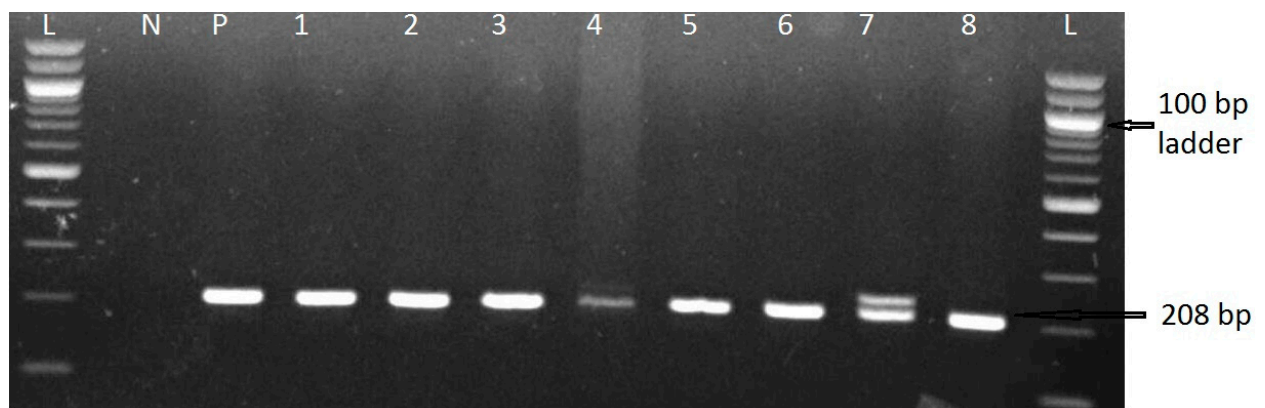


Figure S2: PCR analyses resolved by gel electrophoresis showing confirmed *A. baumannii* targeting the specific primer *Ab-ITS* gene at 208 bp. L= DNA Ladder (100bp); N= negative control, P= positive control (*A. baumannii*, DSM 102929); Lanes 1 to 8= selected *A. baumannii* samples.

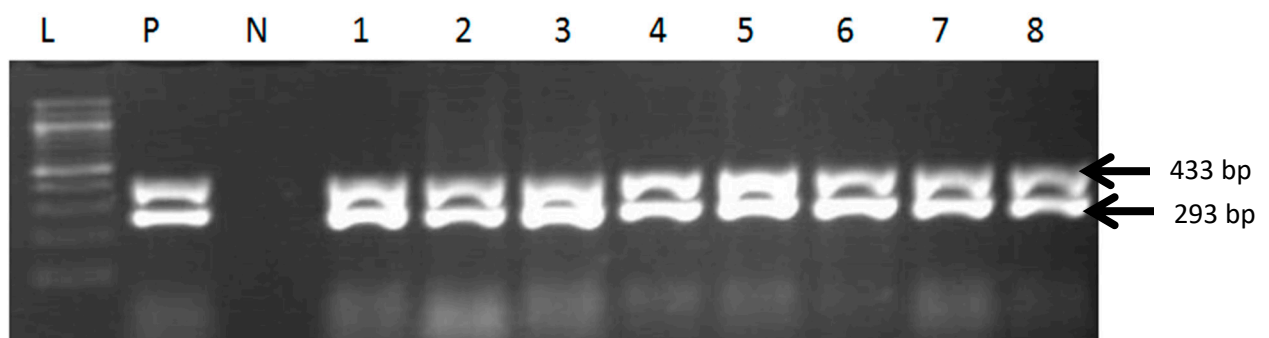


Figure S3: A gel electrophoresis showing sulfonamide resistance genes in *A. baumannii*. L= Ladder (100 bp); P= positive control, N= negative control, Lane 1 to 8 = Selected *A. baumannii* harbouring *sul1* (433 bp) and *sul2* (293 bp) genes.

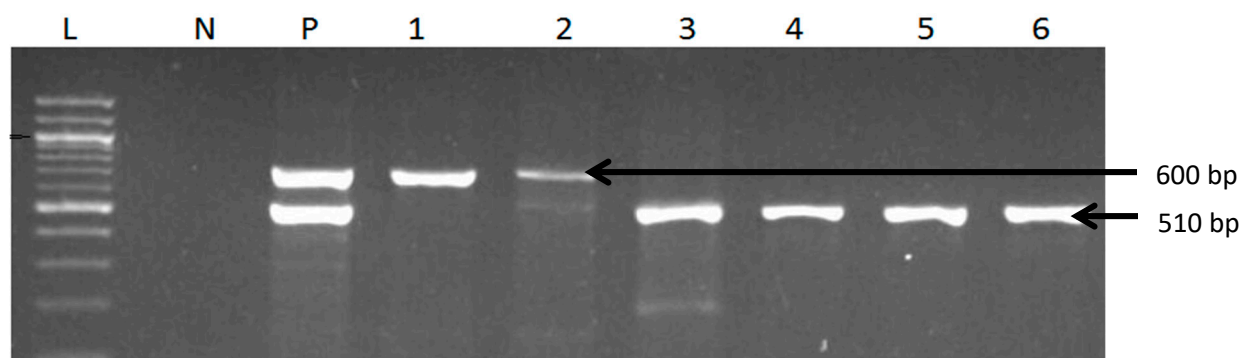


Figure S4: A gel electrophoresis showing aminoglycoside genes in *A. baumannii*. L= Ladder (100bp); P= positive control, N= negative control, Lane 1 and 2 = *apHA1* (600 bp) gene; lanes 3-6 = *apHA2* (510 bp) gene.

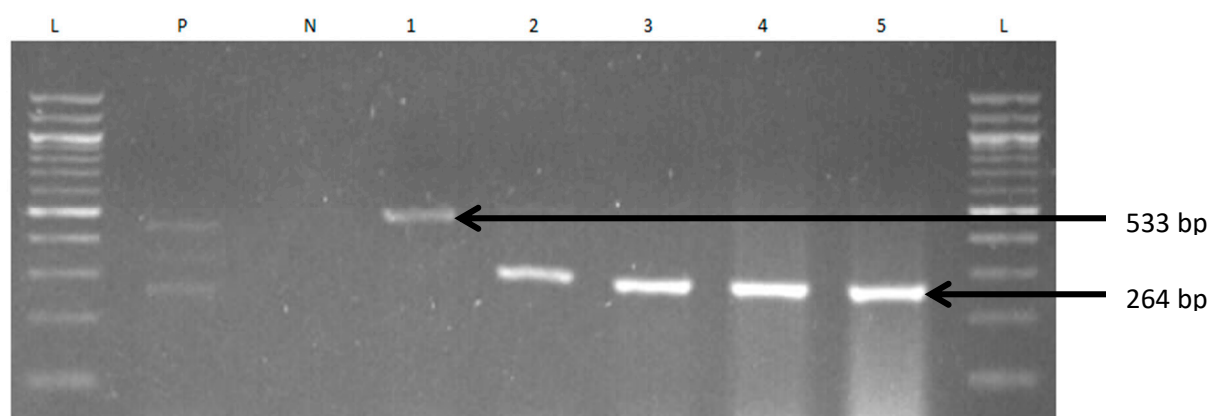


Figure S5: A gel electrophoresis showing Fluoroquinolones genes in *A. baumannii*. L= Ladder (100bp); P= positive control, N= negative control, Lane 1 = *qnrD* (533 bp) gene; lanes 2-5 = *qnrB* (264 bp) gene.

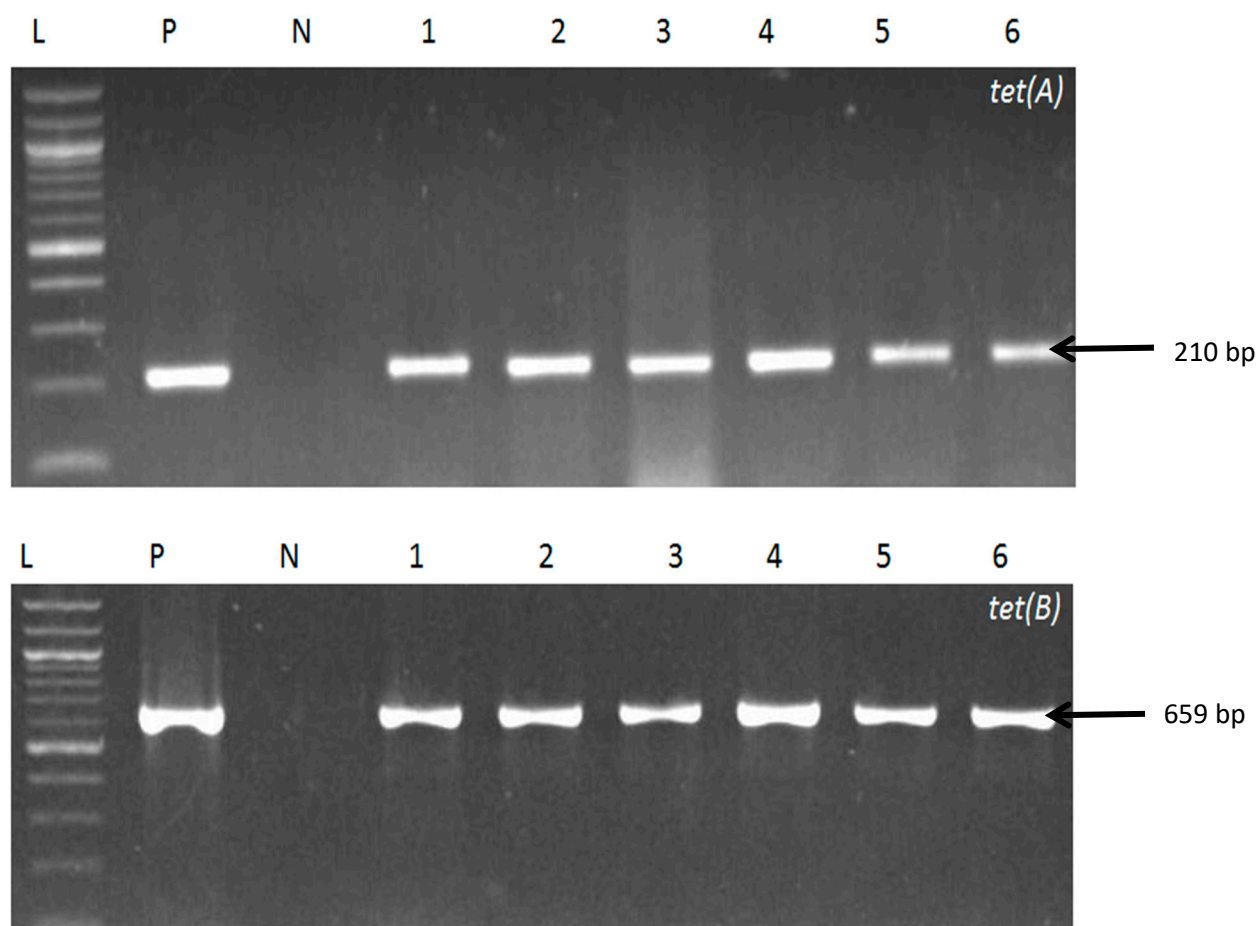


Figure S6: A gel electrophoresis showing Tetracycline genes *A. baumannii*. L= Ladder (100bp); P= positive control, N= negative control, Lane 1-6 = *tet(A)* (210 bp) and *tet(B)* (659 bp) genes respectively.

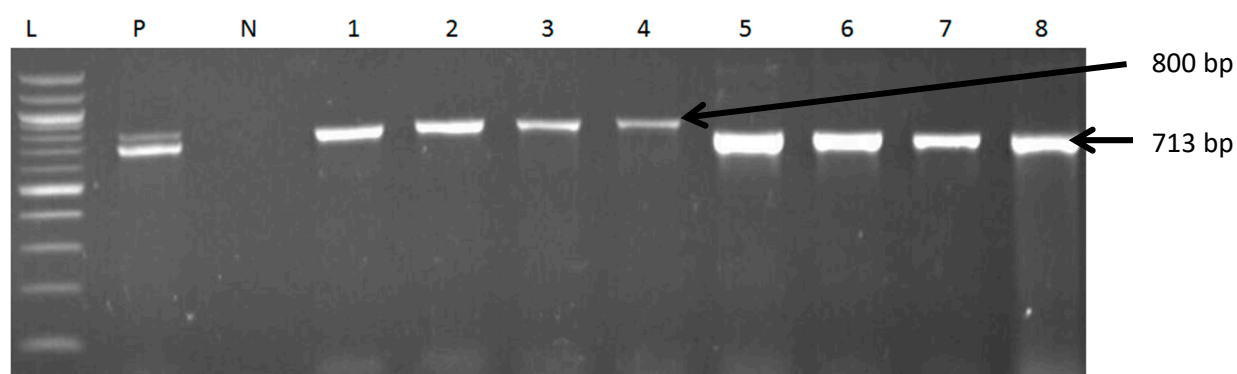


Figure S7A: A gel electrophoresis showing beta-lactamases genes in *A. baumannii*. L= Ladder (100bp); P= positive control, N= negative control, Lane 1-4 = *bla_{TEM}* (800 bp) and 5-8= *bla_{SHV}* (713 bp).

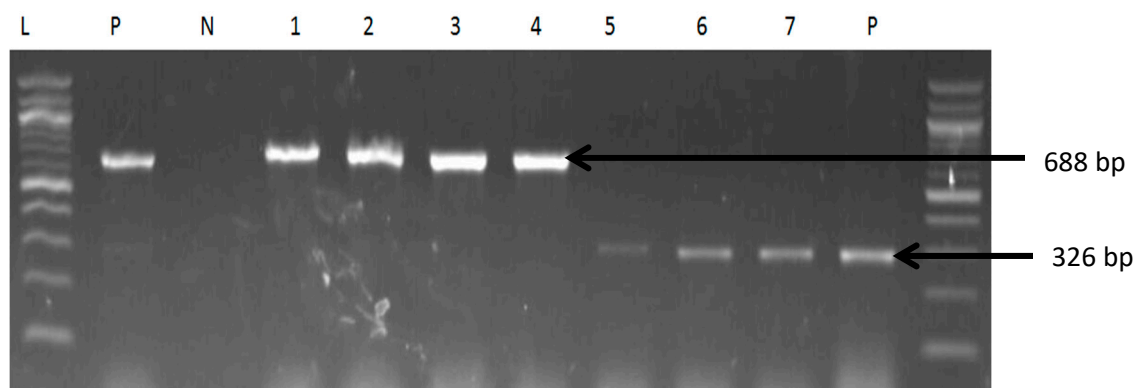


Figure S7B: A gel electrophoresis showing beta-lactamases genes in *A. baumannii*. L= Ladder (100bp), Lanes 1-4 = *bla_{CTX-M(1)}* (688 bp), Lanes 5-7 = *bla_{CTX-M-8/-25}* (326 bp).

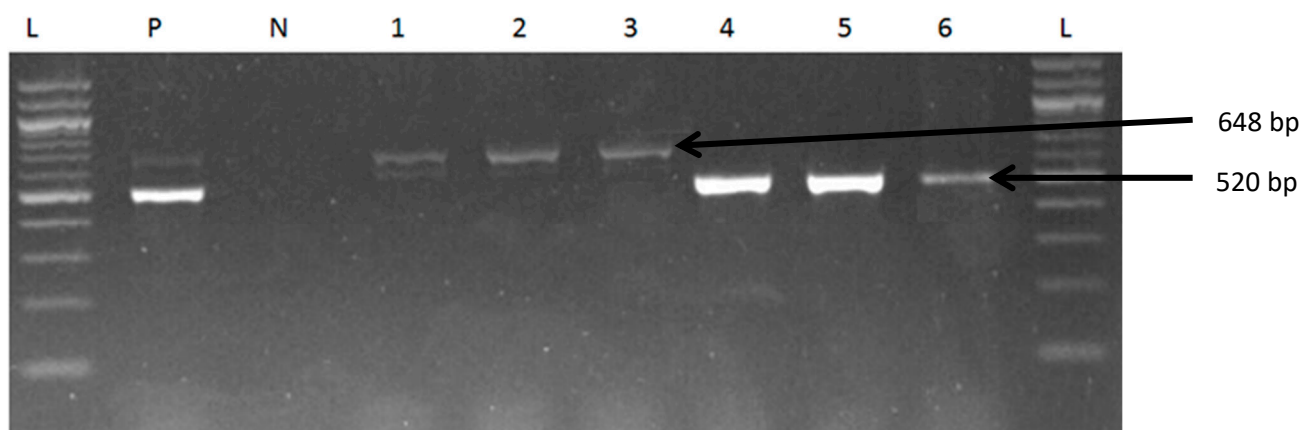


Figure S7C: A gel electrophoresis showing beta-lactamases genes in *A. baumannii*. Lane 1-3= *bla_{VEB}* (648 bp) and Lane 4-6 = *bla_{PER}* (520 bp) genes.

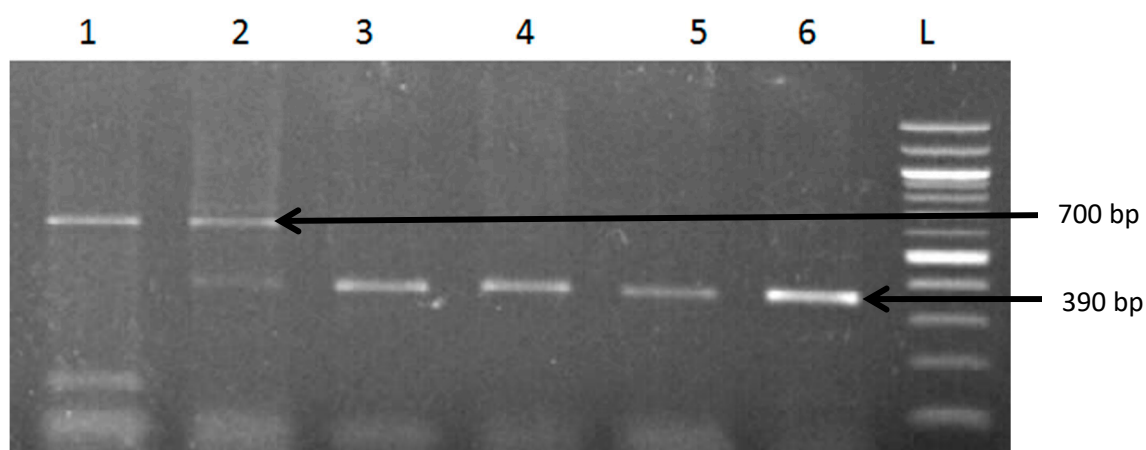


Figure S7D: A gel electrophoresis showing beta-lactamases genes in *A. baumannii*. L= Ladder (100bp), Lanes 1 and 2 = *bla_{KPC}* (700 bp) and Lanes 3-6= *bla_{VIM}* (390 bp). There were no positive and negative controls.

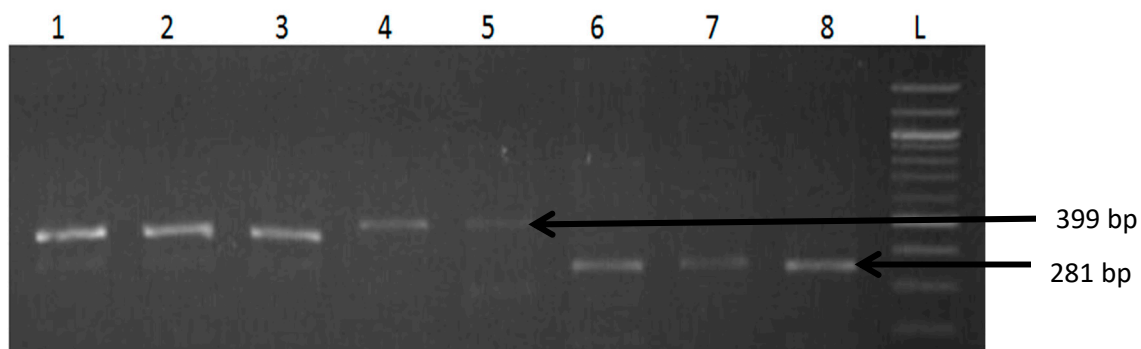


Figure S7E: A gel electrophoresis showing beta-lactamases genes in *A. baumannii*. L= Ladder (100bp); Lanes 1-5= *bla_{GES}* (399 bp) and Lanes 6-8= *bla_{OXA-48-like}* (281 bp). There were no positive and negative controls for both genes.

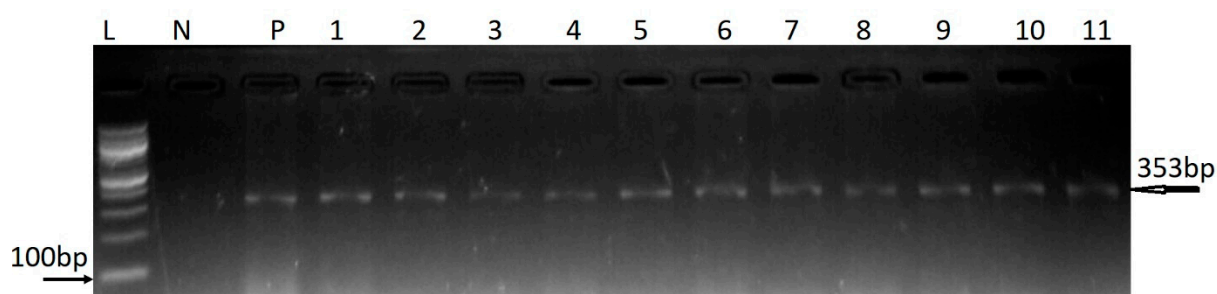


Figure S7F: A gel electrophoresis showing beta-lactamases genes in *A. baumannii*. L= Ladder (100bp); Lanes N = Negative control and Lanes P= Positive control. Lane 1-11= *bla_{OXA-51}* (353bp).

Supplementary Tables

Table S1: Phenotypic antibiotic resistance of *A. baumannii* recovered from each of the site where that water samples were collected along Great Fish, Kieskamma and Tyhume River. S, R and I stand for susceptible, resistance and intermediate resistance respectively.

Site	Isolates code	Resistance Phenotypes										
		AK	CPM	CTX	CAZ	CIP	GM	IMI	MEM	PTZ	TET	SXT
TY1	1	S	S	S	S	S	S	S	S	S	S	S
TY1	20	S	S	R	S	S	S	S	R	S	S	S
TY2	22	S	S	I	S	S	S	S	S	S	S	S
TY2	23	S	S	I	S	S	S	S	S	S	S	S
TY2	26	S	S	S	S	S	S	S	S	S	S	S
TY2	28	S	S	I	S	S	S	S	S	S	S	S
TY2	38	S	S	I	S	I	S	S	S	S	S	R
TY3	43	S	S	I	S	S	S	S	S	S	S	S
TY3	44	S	S	I	S	S	S	S	S	S	S	S
TY3	49	S	S	I	S	S	S	S	S	S	S	S
TY3	52	S	S	I	S	S	S	S	S	S	S	S
TY3	53	S	S	I	S	S	S	S	S	S	S	S
TY3	55	S	S	I	I	S	S	S	S	S	S	S
TY4	63	S	S	I	I	S	S	S	S	I	S	S
TY4	64	S	S	R	S	I	S	S	S	S	S	S
TY4	68	S	S	I	S	S	S	S	S	S	I	S
TY4	69	S	S	I	S	S	S	S	S	S	S	S
TY4	72	S	S	I	I	S	S	S	S	I	S	S
TY4	75	S	S	I	S	S	S	S	S	S	S	S
TY4	76	S	S	I	S	S	S	S	S	S	S	S
TY5	80	S	S	S	S	S	S	S	S	S	S	S
TY5	81	S	S	I	S	I	S	S	S	S	S	S
TY5	83	S	S	I	S	S	S	S	S	S	S	R
TY5	84	S	S	S	S	S	S	S	S	S	S	S
TY5	85	S	S	I	S	S	S	S	S	S	S	S
TY5	87	S	S	I	S	S	S	S	S	S	S	S
TY5	88	S	S	S	S	S	S	S	S	S	S	S
TY5	90	S	S	S	S	S	S	S	S	S	S	S
TY5	91	S	S	I	S	S	S	S	S	S	S	S
TY5	92	S	S	I	S	S	S	S	S	S	S	R
TY5	93	S	S	I	S	S	S	S	S	S	S	S
TY5	99	S	S	I	S	S	S	S	S	S	S	S
KE1	106	S	S	I	S	S	S	S	S	S	S	R
KE1	107	S	S	I	S	S	S	S	S	S	S	R
KE4	127	S	S	I	S	S	S	S	S	S	S	S
GF2	153	S	S	I	S	S	S	S	S	S	S	R

GF2	154	S	S	I	S	S	S	S	S	S	S	S
GF2	156	S	S	I	S	S	S	S	S	S	I	R
GF2	159	S	S	R	S	I	S	S	I	I	I	R
GF3	167	S	S	I	S	S	S	S	S	S	I	S
GF3	170	S	S	S	S	S	S	S	S	S	S	S
GF4	174	S	S	I	S	S	S	S	S	S	S	R
GF4	176	S	S	I	S	S	S	S	S	S	S	S
GF5	179	S	S	I	S	S	S	S	S	I	I	R
GF1	187	S	S	I	S	S	S	S	S	S	S	R
GF1	188	S	I	R	I	I	S	S	S	I	S	S
GF1	195	S	S	I	I	S	S	S	S	I	S	S
GF1	198	S	S	I	S	S	S	S	S	S	S	S
GF2	208	S	S	I	S	S	S	S	S	S	S	S
GF2	209	S	S	R	S	I	S	S	S	S	S	S
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GF2	214	S	S	I	S	S	S	S	S	S	S	S
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GF4	232	S	S	I	S	R	S	S	S	S	S	R
GF4	235	S	S	I	S	S	S	S	S	S	S	S
GF4	236	S	S	I	S	S	S	S	S	R	S	S
GF4	242	S	S	I	S	S	S	S	S	S	S	I
GF4	243	S	S	I	S	S	S	S	S	S	S	S
GF4	245	S	S	I	S	I	S	S	S	S	S	S
GF4	246	S	S	I	I	I	S	S	S	I	S	S
GF4	247	S	S	I	S	S	S	S	S	S	S	S
GF4	249	S	S	I	S	S	S	S	S	S	S	S
GF4	250	S	S	I	S	S	S	S	S	S	S	S
GF5	256	S	S	I	S	I	S	S	S	S	S	S
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TY3	273	S	S	I	S	I	S	S	S	S	S	S
TY3	274	S	S	I	S	I	S	S	S	I	S	S
TY3	278	S	S	I	S	I	S	S	S	S	S	S
TY3	279	S	S	I	S	S	S	S	S	S	S	S
TY3	282	S	S	I	S	S	S	S	S	S	S	S
TY3	283	S	S	I	S	I	S	S	S	S	S	S
TY3	286	S	S	I	S	S	S	S	S	S	S	S
TY3	289	S	S	I	S	S	S	S	S	S	S	S
TY3	290	S	S	I	S	I	S	S	S	I	S	S
TY3	294	S	S	I	S	I	S	S	S	S	S	S
TY5	303	S	S	I	S	I	S	S	S	S	S	S
KE1	306	S	S	I	I	S	S	S	S	S	S	S
KE1	308	S	S	I	S	S	S	S	S	I	S	S

KE1	309	S	S	S	S	S	S	S	S	S	S	S
KE1	315	S	S	I	S	S	S	S	S	S	S	S
KE1	316	S	S	I	I	I	S	S	S	S	S	S
KE2	319	S	S	I	S	S	S	S	S	I	S	S
KE4	333	S	S	I	S	S	S	S	S	S	S	S
TY2	346	S	S	I	S	S	S	S	S	S	S	S
TY2	348	S	S	S	S	S	S	S	S	S	I	S
TY2	353	S	S	I	I	S	S	S	S	I	S	S
TY2	356	S	R	I	S	S	S	S	S	S	S	S
TY2	358	S	S	I	S	S	S	S	S	S	S	S
TY3	361	S	S	I	I	I	S	S	S	S	S	S
TY3	364	S	S	I	S	I	S	S	S	S	S	S
TY3	367	S	S	I	I	I	S	S	S	I	S	S
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TY3	370	S	S	I	I	S	S	S	S	S	S	S
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TY3	385	R	R	R	R	R	R	S	S	S	S	S
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TY4	388	R	R	R	R	R	I	S	R	R	R	R
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TY4	397	S	S	R	I	S	S	S	S	I	S	I
TY4	398	S	R	R	I	R	S	S	S	R	R	S
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TY4	422	R	S	R	I	S	S	S	S	R	S	I
TY5	431	S	S	R	I	S	S	S	S	R	S	S
TY5	432	S	S	I	S	I	S	S	S	S	S	S
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TY5	434	S	S	R	R	S	S	S	S	I	S	S
TY5	436	S	S	I	I	S	S	S	S	S	I	S
GF1	441	S	S	I	S	S	S	S	S	S	S	S

GF2	444	S	S	I	S	S	S	S	S	S	S	S
GF2	449	S	S	I	S	S	S	S	S	R	S	S
GF2	450	S	S	I	I	R	S	S	S	S	S	S
GF3	454	S	S	I	S	S	S	S	S	R	S	S
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GF3	456	S	S	I	I	S	S	S	S	I	S	I
GF4	459	S	S	I	S	S	S	S	S	I	S	R
GF4	460	S	S	I	S	S	S	S	S	S	S	I
GF4	461	S	S	R	I	S	S	S	S	I	I	R
GF5	463	S	S	R	I	S	S	S	S	I	I	R
GF5	464	S	S	R	I	S	S	S	S	S	S	R
GF5	465	S	S	R	I	S	S	S	S	I	S	R
GF5	466	S	R	I	S	S	S	S	S	S	S	I
GF5	467	S	S	I	S	S	S	S	S	S	S	S
GF5	468	S	S	R	I	S	S	S	S	I	S	I
GF5	469	S	S	R	I	R	S	S	I	I	S	I
GF5	471	S	S	R	S	R	S	S	S	I	S	I
GF5	473	S	I	R	I	R	S	S	S	R	S	I
KE2	475	S	S	I	I	I	S	S	S	I	S	S
KE2	477	S	S	R	I	I	S	S	S	I	S	S
KE2	481	S	I	R	I	I	S	S	S	S	S	R
KE2	482	S	S	I	I	I	S	S	S	R	S	S
KE2	484	S	S	R	I	I	S	S	S	I	R	S
KE2	485	S	S	R	I	I	S	S	S	I	R	I
KE2	486	S	S	I	I	I	S	S	S	I	S	S
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KE3	499	S	I	I	I	S	S	S	R	S	S	S
KE4	501	S	S	I	S	S	S	S	S	S	S	S
KE5	504	S	S	I	S	S	S	S	S	S	S	S
TY2	505	S	S	I	S	S	S	S	S	S	S	S
TY2	509	S	S	I	S	I	S	S	S	S	S	S
TY2	510	S	S	I	S	I	S	S	S	S	S	S
TY2	511	S	S	S	S	I	S	S	S	S	S	S
TY3	513	S	S	I	I	S	S	S	S	R	R	R
TY3	514	S	S	I	I	S	S	S	S	S	S	S
TY3	515	S	S	I	I	S	S	S	S	S	S	I
TY3	516	R	S	I	I	S	S	S	S	S	S	S
TY4	519	S	S	I	S	S	S	S	S	S	S	S
TY4	520	R	S	I	I	R	S	S	S	I	S	I

TY5	523	S	S	I	S	S	S	S	S	S	S	S
TY5	524	S	S	I	S	S	S	S	S	S	S	S
TY5	527	S	S	I	S	S	S	S	S	S	S	S
TY5	528	S	S	I	S	S	S	S	S	S	S	S
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TY5	531	S	R	R	R	S	S	S	S	I	R	S
KE2	536	S	R	R	R	I	R	S	I	R	S	R
KE2	537	S	R	I	R	S	R	S	S	S	R	R
KE2	538	S	S	I	R	R	R	I	I	R	R	R
KE2	539	S	R	R	R	S	R	S	S	I	I	R
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KE2	541	S	S	I	S	R	S	S	I	R	R	R
KE2	542	S	S	I	S	R	S	S	S	I	R	R
KE3	543	S	S	I	S	S	S	S	S	S	S	S
KE3	544	R	S	I	S	S	S	S	S	S	S	S
KE3	545	S	S	I	S	S	S	S	S	S	S	S
KE3	546	S	S	R	S	R	S	S	S	S	S	S
KE3	547	S	S	R	R	R	R	S	S	S	R	R
KE3	548	S	S	I	S	S	S	S	S	S	S	S
KE3	549	S	S	I	S	S	S	S	R	R	S	S
GF1	556	S	S	I	S	S	S	S	I	I	S	R
GF1	557	S	S	I	S	S	S	S	S	S	I	S
GF1	559	S	S	I	S	S	S	S	S	S	I	S
GF2	560	S	S	I	S	S	S	S	S	R	S	S
GF3	564	S	S	I	S	S	S	S	S	S	S	S
GF3	565	S	S	I	S	S	S	S	S	I	S	S
GF3	567	S	S	I	S	S	S	S	S	S	S	S
GF3	568	S	S	I	S	S	S	S	S	S	S	S
GF3	569	S	S	I	S	S	S	S	S	S	S	S
GF4	570	S	S	S	S	S	S	S	S	S	S	S
GF4	571	S	S	S	S	S	S	S	S	S	S	S
GF4	573	S	S	S	S	S	S	S	S	S	S	S
GF4	574	S	S	I	S	S	S	S	S	S	I	S
GF5	575	S	S	I	S	S	S	S	S	S	S	S
GF5	576	S	S	I	S	S	S	S	S	S	S	S
GF5	577	S	S	I	S	S	S	S	S	S	S	S
GF5	578	S	S	I	S	S	S	S	S	S	S	S
GF5	580	S	S	I	S	S	S	S	S	S	S	S
GF5	582	S	S	I	S	S	S	S	S	S	S	S
KE1	583	S	S	I	S	S	S	S	S	S	S	S
KE1	586	S	S	I	S	S	S	S	S	I	S	S
KE2	591	S	R	R	R	R	R	S	I	R	R	R
KE2	592	S	R	R	R	R	R	S	S	R	R	R

[illegible]

TY2	717	S	S	S	S	S	S	S	S	S	S	S
TY2	718	S	S	S	S	S	S	S	S	S	S	S
TY2	719	S	S	S	S	S	S	S	S	S	S	S
TY2	720	S	R	R	R	S	S	S	S	R	R	S
TY2	723	S	S	S	S	S	S	S	S	S	S	S
TY2	724	S	S	S	S	S	S	S	S	S	S	S
TY3	725	S	S	S	S	S	S	S	S	S	S	S
TY3	726	S	S	I	S	S	S	S	S	S	S	S
TY3	727	S	S	S	S	S	S	S	S	S	S	S
TY3	728	S	S	S	S	S	S	S	S	S	S	S
TY4	729	S	S	S	S	S	S	S	S	S	S	S
TY4	730	S	S	S	S	S	S	S	S	S	S	S
TY5	734	S	S	S	S	S	S	S	S	S	S	S
TY5	735	S	S	S	S	I	S	S	S	S	I	S
TY5	736	S	I	S	S	S	S	S	S	S	S	S
TY5	738	S	S	S	S	S	S	S	S	S	S	R
KE1	739	S	S	I	I	S	S	S	S	S	S	S
KE1	740	S	S	S	S	S	S	S	S	S	S	S
KE1	741	S	S	S	S	S	S	S	S	S	S	S
KE3	756	S	S	R	R	R	R	S	S	S	R	R
TY1	757	S	S	I	I	I	I	S	S	S	S	R
TY1	758	S	S	S	R	S	S	S	S	S	S	S
TY2	761	S	S	S	S	S	S	S	S	S	S	S
TY2	765	S	S	I	S	S	S	S	S	S	S	R
TY4	771	S	S	S	S	S	S	S	S	S	S	S
TY4	772	S	S	S	S	S	S	S	S	S	S	S
GF1	779	S	S	I	S	S	S	S	S	S	S	S
GF2	781	S	S	I	S	S	S	S	S	I	S	R
GF2	782	S	S	I	S	S	S	S	S	S	S	S
GF2	783	S	I	I	S	S	S	S	S	S	R	R
GF2	786	S	S	I	S	S	S	S	S	S	S	S
GF2	789	S	S	I	S	S	S	S	S	S	S	S
GF3	791	S	S	I	S	S	S	S	S	S	I	R
GF3	793	S	S	I	S	S	S	S	S	S	S	S
GF4	795	S	S	I	S	S	S	R	R	I	R	S
GF4	796	S	S	I	S	S	S	S	S	S	S	S
GF4	798	S	S	I	S	S	S	S	S	S	S	S
GF4	799	S	S	I	S	S	S	S	S	S	S	S
GF4	800	S	R	R	R	R	S	S	S	R	R	R
GF4	801	S	S	S	S	S	S	S	S	S	S	S
GF5	802	S	R	R	R	R	S	S	S	R	R	R
GF5	803	S	S	I	S	I	S	S	S	S	I	S
GF5	804	S	S	I	S	S	S	S	S	S	S	S

[illegible]

GF5	890	S	S	I	S	S	S	R	R	S	S	S
TY1	892	S	S	S	S	S	S	S	S	S	S	S
TY1	893	S	R	R	R	R	S	S	S	R	R	R
TY1	894	S	S	I	S	S	S	S	S	S	R	R
TY2	896	S	S	I	S	S	S	R	R	S	R	S
TY2	897	S	S	I	S	S	S	S	S	S	R	R
TY2	898	S	S	I	S	S	S	R	R	I	R	R
TY2	899	S	S	S	S	S	S	I	S	S	S	S
TY2	900	S	S	S	S	S	S	I	S	S	S	S
TY2	901	S	S	I	S	S	S	R	R	S	I	S
KE1	906	S	S	S	S	S	S	S	S	S	S	S
KE2	909	S	S	S	S	S	S	S	S	S	R	S
KE2	911	S	S	I	R	S	R	S	S	S	S	R
KE3	913	S	S	S	S	S	S	S	S	S	I	S
KE3	914	S	S	S	S	I	S	S	S	S	S	S
KE4	916	S	S	I	S	S	S	S	S	S	S	S
KE5	918	S	S	I	R	S	R	S	S	S	S	R
KE5	919	S	S	S	S	S	S	S	S	I	S	S
GF1	920	S	S	I	S	S	S	S	S	S	S	S
GF1	922	S	S	S	S	S	S	S	S	S	S	S
GF1	923	S	S	I	S	S	S	S	S	S	S	S
GF1	924	S	S	I	S	S	S	S	S	S	S	S
GF2	928	S	S	S	S	S	S	S	S	S	S	S
GF3	930	S	S	S	S	S	S	S	S	S	I	S
GF4	931	S	S	R	I	S	R	S	S	S	S	R
GF4	932	S	S	S	S	S	S	S	S	S	R	S
GF4	933	S	S	S	S	S	S	S	S	S	R	R
GF4	934	S	S	R	S	S	S	S	S	S	R	R
GF4	935	S	S	S	S	S	S	S	S	S	R	R
GF5	936	S	S	S	S	S	S	S	S	S	S	S
GF5	937	S	S	I	S	S	S	S	S	S	S	S
GF5	938	S	S	I	S	S	S	S	S	S	S	S
TY1	940	S	S	I	S	S	S	S	S	S	S	S
TY2	944	S	S	I	S	S	S	S	S	S	I	S
TY2	945	S	S	I	S	S	S	S	S	I	S	S
TY3	949	S	S	I	S	S	S	S	S	S	I	S
TY4	954	S	S	I	S	S	S	S	S	I	S	S
TY4	955	S	S	S	S	S	S	S	S	S	I	S
TY5	956	S	S	R	I	I	S	S	S	I	I	S
TY5	957	S	S	R	I	I	S	S	S	I	R	S
TY5	958	S	S	R	I	I	S	S	S	R	I	S
GF4	1019	S	R	R	R	I	S	R	R	R	R	R
GF4	1020	S	R	R	R	I	S	R	R	R	R	R

GF4	1022	S	I	I	R	I	S	S	S	S	S	S
GF5	1023	S	S	R	R	S	S	S	S	I	S	S
GF5	1024	S	R	R	R	S	R	S	S	I	S	R
GF5	1025	S	S	R	R	S	R	S	S	S	S	R
GF5	1026	S	I	R	R	R	R	S	S	R	R	R
TY1	1027	S	R	R	R	R	R	S	S	R	R	R
TY1	1028	S	R	R	R	R	R	S	S	R	R	R
TY2	1031	S	S	R	I	S	S	S	S	I	I	S
TY2	1032	S	S	R	I	I	S	S	S	R	R	R
TY3	1035	S	R	R	I	R	R	S	S	R	R	R
TY4	1041	S	S	R	I	I	S	S	S	I	I	S
TY4	1042	S	S	I	I	S	S	S	S	S	I	S
TY5	1045	S	S	I	I	S	S	S	S	S	S	S
TY5	1046	S	S	I	I	S	S	S	S	S	I	S
KE1	1047	S	S	I	S	S	S	S	S	S	I	S
KE1	1049	S	S	I	S	S	S	S	S	S	S	S
KE2	1053	S	S	I	S	S	S	S	S	S	S	S
KE2	1054	S	S	I	I	S	S	S	S	I	S	S
KE3	1055	S	S	I	I	S	S	S	S	I	S	S
KE3	1056	S	S	I	I	S	S	S	S	S	S	S
KE3	1057	S	S	I	I	S	S	S	S	I	S	S
KE3	1058	S	S	I	I	S	S	S	S	S	S	S
KE4	1059	S	S	R	I	I	S	S	S	I	S	S
KE4	1060	S	S	I	S	I	S	S	S	I	I	S
KE4	1061	S	S	I	S	S	S	S	S	S	S	S
KE4	1062	S	S	I	S	S	S	S	S	I	S	S
KE5	1063	S	S	I	S	S	S	S	S	S	S	S
KE5	1064	S	S	I	S	S	S	S	S	I	S	S
KE5	1065	S	S	I	I	S	S	S	S	S	S	S
KE5	1066	S	S	I	S	S	S	S	S	S	S	S

Table S2: Screening of *A. baumannii* that exhibited phenotypic resistance for antibiotics resistant genes

Antimicrobial Family	Primer Name	PCR primer sequence (5'-3')	Amplicon size (bp)	Gene name	PCR cycling condition	Reference
Aminoglycosides	aph(3)-Ia (<i>aphA1</i>)	F: ATGGGCTCGCGATAATGTC R: CTCACCGAGGCAGTTCCAT	600	<i>apHA1</i>	Initial denaturation step: 94°C for 5 min, followed by 30 cycles of 94°C for 30 s, annealing step: 50°C for 30 s and 72°C for 1.5 min and final elongation at 72°C for 5 min	[1]
	aph(3)-IIa (<i>aphA2</i>)	F: GAACAAGATGGATTGCACGC R: GCTCTTCAGCAATATCACGG	510	<i>apHA2</i>	Initial denaturation step: 94°C for 5 min, followed by 30 cycles of 94°C for 30 s, annealing step: 50°C for 30 s and 72°C for 1.5 min and final elongation at 72°C for 5 min	[1]
Beta-lactamases	MultiTSO-T	F: CATTTCGGTGTGCGCCCTTATTC R: CGTTCATCCATAGTTGCCTGAC	800	<i>bla_{TEM}</i>	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and a final elongation step at 72°C for 7 min	[2]
	MultiTSO-S	F: AGCCGCTTGAGCAAATTAAAC R: ATCCCGCAGATAAATCACCAC	713	<i>bla_{SHV}</i>	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	MultiCTXMGp 1	F: TTAGGAARTGTGCCGCTGYA R: CGATATCGTTGGTGGTRCCAT	688	<i>bla_{CTX-M(1)}</i>	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]

	MultiCTXMGp 2	F: CGTTAACGGCACGATGAC R: CGATATCGTTGGTGGTRCCAT	404	<i>bla</i> _{CTX-M(2)}	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	MultiCTXMGp 9	F: TCAAGCCTGCCGATCTGGT R: TGATTCTCGCCGCTGAAG	561	<i>bla</i> _{CTX-M(9)}	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	CTX-Mg8/25	F: AACRCRCAGACGCTCTAC R: TCGAGCCGGAASGTGTAT	326	<i>bla</i> _{CTX-M-8/-25}	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	MultiGES	F: AGTCGGCTAGACCGGAAAG R: TTTGTCCGTGCTCAGGAT	399	<i>bla</i> _{GES}	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 57°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	MultiOXA-48	F: GCTTGATCGCCCTCGATT R: GATTTGCTCCGTGGCCGAAA	281	<i>bla</i> _{OXA-48-like}	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 57°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 mins	[2]
	OXA-51	F: TAATGCTTTGATCGGCCTTG R: TGGATTGCACTTCATCTTGG	353	<i>bla</i> _{OXA-51-like}	Initial denaturation step: 95°C for 1 min, followed by 30 cycles of 95°C for 15 s, annealing step: 52°C for 15 s and 72°C for 10 s; and final elongation step at 72°C for 10 mins	[3]
	OXA-23	F: GATCGGATTGGAGAACCAGA R: ATTCTTGACCGCATTTCCAT	501	<i>bla</i> _{OXA-23-like}		
	OXA-40	F: GGTTGTTGGCCCCCTTAAA R: AGTTGAGCGAAAAGGGGATT	246	<i>bla</i> _{OXA-40-like}		
	OXA-58	F: AAGTATTGGGGCTTGTGCTG R: CCCCTCTGCGCTCTACATAC	599	<i>bla</i> _{OXA-58-like}		

	MultiPER	F: GCTCCGATAATGAAAGCGT R: TTCGGCTTGACTCGGCTGA	520	<i>bla_{PER}</i>	Initial denaturation step: 94°C for 10 mins, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 mins	[2]
	MultiVEB	F: CATTTCCTCGATGCAAAGCGT R: CGAAGTTTCTTTGGACTCTG	648	<i>bla_{VEB}</i>	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 60°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	MultiIMP	F: TTGACACTCCATTTACDG R: GATYGAGAATTAAGCCACYCT	139	<i>bla_{IMP}</i>	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 55°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	MultiVIM	F: GATGGTGTTTGGTCGCATA R: CGAATGCGCAGCACCAG	390	<i>bla_{VIM}</i>	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 55°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
	MultiKPC	F: CATTCAAGGGCTTTCTTGCTGC R: ACGACGGCATAGTCATTTGC	700	<i>bla_{KPC}</i>	Initial denaturation step: 94°C for 10 min, followed by 30 cycles of 94°C for 40 s, annealing step: 55°C for 40 s and 72°C for 1 min; and final elongation step at 72°C for 7 min	[2]
Fluoroquinolones	QnrA	F: AGAGGATTTCTCACGCCAGG R: TGCCAGGCACAGATCTTGAC	580	<i>qnrA</i>	Initial denaturation step: 95°C for 15 min, followed by 32 cycles of 95°C for 1 min, annealing step: 55°C for 1 min, and 72°C for 5 min and final longation step at 72°C for 10 min	[4]

	QnrB	F: GGMATHGAAATTCGCCACTG R: TTTGCGYGYCGCCAGTCGAA	264	<i>qnrB</i>	Initial denaturation step: 95°C for 15 min, followed by 32 cycles of 95°C for 1 min, annealing step: 55°C for 1 min, and 72°C for 5 min and final elongation step at 72°C for 10 min	[4]
	QnrC	F: GGGTTGTACATTTATTGAATCG R: CACCTACCCATTTATTTTCA	307	<i>qnrC</i>	Initial denaturation step: 95°C for 15 min, followed by 32 cycles of 95°C for 1 min, annealing step: 55°C for 1 min, and 72°C for 5 min and final elongation step at 72°C for 10 min	[5]
	QnrD	F: CGAGATCAATTTACGGGGAATA R: AACAAAGCTGAAGCGCCTG	533	<i>qnrD</i>	Initial denaturation step: 95°C for 15 min, followed by 32 cycles of 95°C for 1 min, annealing step: 55°C for 1 min, and 72°C for 5 min and final elongation step at 72°C for 10 min	[4]
	QnrS	F: ACGACATTCGTCAACTGCAA R: TAAATTGGCACCCCTGTAGGC	417	<i>qnrS</i>	Initial denaturation step: 95°C for 15 min, followed by 32 cycles of 95°C for 1 min, annealing step: 55°C for 1 min, and 72°C for 5 min and final elongation step at 72°C for 10 min	[5]
Sulfonamides	sul1	F: CGGCGTGGGCTACCTGAACG R: GCCGATCGCGTGAAGTTCCG	433	<i>sul1</i>	Initial denaturation step: 94°C for 5 min, followed by 30 cycles of 94°C for 30 s, annealing step: 65°C for 30 s, 72°C for 2 min, and final extension step at 72°C for 10 min	[6]
	sul2	F: GCGCTCAAGGCAGATGGCATT R: GCGTTTGATACCGGCACCCGT	293	<i>sul2</i>	Initial denaturation step: 94°C for 5 min, followed by 30 cycles of 94°C for 30 s, annealing step: 65°C for 30 s, 72°C for 2 min, and final extension step at 72°C for 10 min	[6]

Tetracyclines	TetA	F: GCTACATCCTGCTTGCCTTC R: CATAGATCGCCGTGAAGAGG	210	<i>tet(A)</i>	Initial denaturation step: 94°C for 5 min, followed by 30 cycles of 94°C for 30 s, annealing step: 60°C for 30 s, 72°C for 2 min, and final extension step at 72°C for 10 min	[6]
	TetB	F: TTG GTT AGG GGC AAG TTT TG R: GTA ATG GGC CAA TAA CAC CG	659	<i>tet(B)</i>	Initial denaturation step: 94°C for 5 min, followed by 35 cycles of 94°C for 1 min, annealing step: 55°C for 1 min, 72°C for 2 min and final elongation step: 72°C for 1·5 min	[7]
	TetC	F: CTTGAGAGCCTTCAACCCAG R: ATGGTCGTCATCTACCTGCC	418	<i>tet(C)</i>	Initial denaturation step: 94°C for 5 min, followed by 30 cycles of 94°C for 30 s, annealing step: 60°C for 30 s, 72°C for 2 min, and final extension step at 72°C for 10 min	[6]
	TetL	F: TCG TTA GCG TGC TGT CAT TC R: GTA TCC CAC CAA TGT AGC CG	267	<i>tet(L)</i>	Initial denaturation step: 94°C for 5 min, followed by 35 cycles of 94°C for 1 min, annealing step: 55°C for 1 min and final elongation step: 72°C for 1·5 min	[7]
	TetM	F: GTG GAC AAA GGT ACA ACG AG R: CGG TAA AGT TCG TCA CAC AC	406	<i>tet(M)</i>	Initial denaturation step: 94°C for 5 min, followed by 35 cycles of 94°C for 1 min, annealing step: 55°C for 1 min and final elongation step: 72°C for 1·5 min	[7]
	TetO	F: ACGGARAGTTTATTGTATACC R: TGGCGTATCTATAATGTTGAC	171	<i>tet(O)</i>	Initial denaturation step: 94°C for 5 min, followed by 35 cycles of 94°C for 1 min, annealing step: 55°C for 1 min and final elongation step: 72°C for 1·5 min	[6]

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