

Table S2. Primers used in the study.

Oligonucleotide	Oligonucleotide sequence (5'→3')	Description
P-Ab-ITSF/ P-Ab-ITSB	CATTATCACGGTAATTAGTG/ AGAGCACTGTGCACTTAAG	<i>A. baumannii</i> specific identification primers [1]
sacB_F/ sacB_R	GTTGTCTAGAGATCCTTTTAAACCCATCAC/ GTTGGCATGCTGGGATTCACCTTTATGTTG	Amplification of <i>sacB</i> gene from <i>Bacillus subtilis</i> . <i>Xba</i> I and <i>Pae</i> I(<i>Sph</i> I) restriction sites are underlined
BfmR_Ptac_F/ BfmR_Ptac_R	CATGAGCCAAGAAGAAAAGTTACC/ TTACAATCCATTGGTTTCTTTAAC	Amplification of <i>bfmRS</i> operon, wild-type <i>bfmR</i> , and mutant <i>bfmR</i> (D58A). Cloning into inducible vector
BfmS_Ptac_R	GAACCTGATGCAACTCAG	Amplification of <i>bfmS</i> or <i>bfmRS</i> operon. Cloning into inducible vector
BfmS_Ptac_F	CGTGTTTAAACACAGTATATTCCTGC	Amplification of <i>bfmS</i> and cloning into inducible vector
hcp_compl_F/ hcp_compl_R	CATGAAAGATATATACGTTGAGTTTCGC/ CTTTATGTCAGCCTCCACCAA	Amplification of <i>hcp</i> . Cloning into inducible vector
BfmR_F	GTTGAAGCTTAAATGCAGCAACATCTCC	Verification for the $\Delta bfmRS$ deletion. Sequence obtained from [2]
ter_F/ ter_R	GGGCCATGGGCATGCGGTACCCTGTTTTG GCGGATGAGAG/ GTTGGAGCTCTTTGTAGAAACGCAAAAAG GC	Amplification of transcription termination site from pKK223-3 vector. <i>Kpn</i> I and <i>Sac</i> I restriction

		sites are underlined.
M13_rwd/ Aac3I_seqR	ACTGGCCGTCGTTTTAC/ CGAAGTCGAGGCATTTCTGT	Inverted amplification of pUC_gm_AcORI_Ptac_AcGFP_ter to remove Gm ^R
LacIq2_R/ LacIq2_F	CTCACTGCCCCGCTTTCCA/ ATCGAATGGTGCAAAAC	Amplification of <i>lacI^q</i> gene.
BfmR01F/ BfmRS01R	TCACGCATTGCACCATAA/ <u>GGAACCTGATGCAACTCAGTTATAAATCATT</u> GCCCTATAAATCTC	Amplification of <i>bfmRS</i> upstream region. Overlay with <i>bfmRS</i> downstream region is underlined
BfmS02F/ BfmS02Rgm	TTATAACTGAGTTGCATCAGG/ <u>CGTTCAAGCCGAGATGAATTCGATCGGCC</u> GAATTTGGTTATTG	Amplification of <i>bfmRS</i> downstream region. Overlay with <i>aac3I</i> downstream region is underlined
5_hcpFwd/ 5_hcpRev	TCAGGAAACGCCTTCAAATC/ <u>CTTTATGTCAGCCTCCACCAAGCTGACCTT</u> GATTAATTTGAGG	Amplification of <i>hcp</i> upstream region. Overlay with <i>hcp</i> downstream region is underlined
3_hcpFwd/ 3_hcpRev	TTGGTGGAGGCTGACATAAAG/ <u>CGTTCAAGCCGAGATGAATTCGATCGCTCA</u> AATTCGGATACATGCTG	Amplification of <i>hcp</i> downstream region. Overlay with <i>aac3I</i> downstream region is underlined
GentR_F/ GentR_R	GATC <u>GAGCTC</u> AGGACAGAAATGCCTCGAC T/ GATC <u>GAATTC</u> ATCTCGGCTTGAACGAATTG	Amplification of <i>aac3I</i> gene <i>SacI</i> and <i>EcoRI</i> restriction sites

CDI_3Fwd_final/ CDI_3Rev_final_gm	GGTCTATTACAGGTCGTTTACTTTAAATAG/ <u>CGTTCAAGCCGAGATGAATTCGATCACCCC</u> AAATCTTACTCCAATCG	Amplification of <i>cdiBAI</i> ^{V15} downstream region. Overlay with <i>aac3I</i> downstream region is underlined
Cdi_Imm_F/ Cdi_Imm_R	TTAAAGTAAACGACCTGTAATAGACC/ CATGATCGATTTTGTAAAGAATTATCTGC	Amplification of <i>cdiI</i> ^{V15} . Cloning into inducible vector.
CDI1F/ CDI1R	GGTAAATGGCCGCAATAGCATAC/ TGCTGTCAGGTGCAATCAGC	Detection of Type I CDI systems among <i>A. baumannii</i> ; and for the quantification of <i>cdiBAI</i> ^{V15} expression
CDI2F/ CDI2R	TTTATGCTTCGGGCAATCTGG/ GCACACCAAGTCGCAAAGAA	Detection of Type I CDI systems among <i>A. baumannii</i>
F_CDI_cluster3_4/ R_CDI_cluster3_4	CGGAGAGGTTGGTGGAAAACTGC/ CAAAGGCGCACCCACAAAAGC	Detection of Type II CDI system among <i>A. baumannii</i>

Gm^R, gentamicin resistance.

References

1. Chen T-L, Sin L-K, Wu RC-C, Shaio M-F, Huang L-Y, Fung C-P, et al. Comparison of one-tube multiplex PCR, automated ribotyping and intergenic spacer (ITS) sequencing for rapid identification of *Acinetobacter baumannii*. Clin Microbiol Infect. 2007;13(8):801-6.

2. Tomaras AP, Flagler MJ, Dorsey CW, Gaddy JA, Actis LA. Characterization of a two-component regulatory system from *Acinetobacter baumannii* that controls biofilm formation and cellular morphology. Microbiology. 2008;154(Pt 11):3398-409.